



HAL
open science

Molecular Classification of Hepatocellular Adenoma Associates With Risk Factors, Bleeding, and Malignant Transformation

Jean-Charles Nault, Gabrielle Couchy, Charles Balabaud, Guillaume Morcrette, Stefano Caruso, Jean-Frederic Blanc, Yannick Bacq, Julien Calderaro, Valérie Paradis, Jeanne Ramos, et al.

► **To cite this version:**

Jean-Charles Nault, Gabrielle Couchy, Charles Balabaud, Guillaume Morcrette, Stefano Caruso, et al. Molecular Classification of Hepatocellular Adenoma Associates With Risk Factors, Bleeding, and Malignant Transformation. *Gastroenterology*, 2017, 152 (4), pp.880 - 894.e6. 10.1053/j.gastro.2016.11.042 . hal-01797602

HAL Id: hal-01797602

<https://hal.science/hal-01797602>

Submitted on 16 Jan 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Gastroenterology

Molecular Classification of Hepatocellular Adenoma: Interactions with Risk Factors and Clinical Outcomes

--Manuscript Draft--

Manuscript Number:	GASTRO-D-16-02075R1
Full Title:	Molecular Classification of Hepatocellular Adenoma: Interactions with Risk Factors and Clinical Outcomes
Article Type:	Basic - Liver
Section/Category:	Basic
Corresponding Author:	Jessica Zucman-Rossi, M.D., PhD INSERM Paris, P FRANCE
Corresponding Author Secondary Information:	
Corresponding Author's Institution:	INSERM
Corresponding Author's Secondary Institution:	
First Author:	Jean-Charles Nault
First Author Secondary Information:	
Order of Authors:	Jean-Charles Nault
	Gabrielle Couchy
	Charles Balabaud
	Guillaume Morcrette
	Stefano Caruso
	Jean Frederic Blanc
	Yannick Bacq
	Julien Calderaro
	Valérie Paradis
	Jeanne Ramos
	Jean-Yves Scoazec
	Viviane Gnemmi
	Nathalie Sturm
	Catherine Guettier
	Monique Fabre
	Eric Savier
	Laurence Chiche
	Philippe Labrune
	Janick Selves
	Dominique Wendum
	Camilla Pilati
	Alexis Laurent

	Anne De Muret
	Brigitte Lebail
	Sandra Rebouissou
	Sandrine Imbeaud
	Paulette Bioulac-Sage
	Eric Letouze
	Jessica Zucman-Rossi, M.D., PhD
Order of Authors Secondary Information:	
Abstract:	<p>Background and Aims Hepatocellular adenomas (HCA) are benign liver tumors divided in molecular subtypes characterized by mutations inactivating HNF1A, activating β-catenin or inflammatory pathway. We aimed to refine HCA natural history according to an updated molecular classification.</p> <p>Methods 607 samples of 533 HCA from 411 patients collected in 28 centers were systematically analyzed by expression profiling and sequencing 20 and 8 genes, respectively. Microarray analysis, RNA sequencing, whole-exome and genome sequencing were performed in selected cases. Clinical and pathological features were compared with molecular data.</p> <p>Results Symptomatic bleeding occurred in 14% of the patients (female 85%, median age 38 y), 7% of the nodules were borderline between adenoma and carcinoma (HCA/HCC) and in 3% HCC developed on HCA. We defined a new molecular classification of HCA in 8 molecular subgroups. Among them, we identified a new HCA subgroup (4%, previously unclassified) associated with obesity and bleeding. These tumors were characterized by a sonic Hedgehog pathway activation due to focal deletions creating INHBE promoter/GLI1 fusions. Analysis of inter-tumor genetic heterogeneity of multiple HCA in patients revealed a "molecular subtype field effect" with tumors harboring private mutations leading to similar pathway deregulation. Specific molecular HCA subtypes were associated with various risk factors and estrogen/androgen hormonal balances. Finally, the molecular classification enabled to stratify patients according to the risk of bleeding and malignant transformation.</p> <p>Conclusion INHBE-GLI1 fusion defined a new subgroup of HCA characterized by sonic hedgehog activation. Molecular classification identified subgroups of patients related to specific risk factors, clinical behavior and pathological features laying the foundations for personalized treatment.</p>

Molecular Classification of Hepatocellular Adenoma: Interactions with Risk Factors and Clinical Outcomes

Short title: molecular classification of liver adenomas

Jean Charles Nault^{1, 2, 3}, Gabrielle Couchy¹, Charles Balabaud⁴, Guillaume Morcrette¹, Stefano Caruso¹, Jean-Frederic Blanc^{4,5}, Yannick Bacq⁶, Julien Calderaro^{1,7}, Valérie Paradis⁸, Jeanne Ramos⁹, Jean-Yves Scoazec¹⁰, Viviane Gnemmi¹¹, Nathalie Sturm¹², Catherine Guettier¹³, Monique Fabre¹⁴, Eric Savier¹⁵, Laurence Chiche¹⁶, Philippe Labrune¹⁷, Janick Selves¹⁸, Dominique Wendum¹⁹, Camilla Pilati¹, Alexis Laurent²⁰, Anne De Muret²¹, Brigitte Le Bail^{4,22}, Sandra Rebouissou¹, Sandrine Imbeaud¹, GENTHEP investigators, Paulette Bioulac-Sage^{4,22}, Eric Letouzé¹, Jessica Zucman-Rossi¹

1. Unité Mixte de Recherche 1162, Génomique fonctionnelle des tumeurs solides, Institut National de la Santé et de la Recherche Médicale, Paris, France.
2. Liver unit, Hôpital Jean Verdier, Hôpitaux Universitaires Paris-Seine-Saint-Denis, Assistance-Publique Hôpitaux de Paris, Bondy, France
3. Unité de Formation et de Recherche Santé Médecine et Biologie Humaine, Université Paris 13, Communauté d'Universités et Etablissements Sorbonne Paris Cité, Paris, France
4. Univ. Bordeaux, UMR1053 Bordeaux Research In Translational Oncology, BaRITOn, F-33000 Bordeaux, France
5. Service Hépato-Gastroentérologie et oncologie digestive, Centre Medico-Chirurgical Magellan, Hôpital Haut-Lévêque, CHU de Bordeaux, F 33000 Bordeaux France
6. Service d'hépatogastroentérologie, CHRU de Tours, Tours
7. Service d'anatomopathologie, Hôpital Henri Mondor, Créteil ; Université Paris Est Créteil, Inserm U955, Team 18, Institut Mondor de Recherche Biomédicale
8. Service d'anatomopathologie, Hôpital Beaujon, Clichy
9. Service d'anatomopathologie, Gui de Chauliac, Montpellier
10. Service d'anatomopathologie, Institut Gustave Roussy, Villejuif
11. [Institut de Pathologie. CHRU de Lille](#).UMR-S 1172 - JPARC - Jean-Pierre Aubert Research Center, F-59000 Lille, France
12. Service d'anatomopathologie, CHU de Grenoble
13. Service d'anatomopathologie, Hôpitaux Paul Brousse et Bicêtre, Le Kremlin Bicêtre INSERM U 1193 Univ Paris Sud
14. Service d'anatomopathologie, Hôpital Necker-Enfants Malades, Paris
15. Service de chirurgie hépato-bilio-pancréatique, CHU Pitié Salpêtrière, Univ. Pierre et Marie Curie UPMC, Paris
16. Service de chirurgie digestive, Centre Medico-Chirurgical Magellan, Hôpital Haut-Lévêque, CHU Bordeaux

17. APHP, Hôpitaux Universitaires Paris Sud, Hôpital Antoine Bécclère, Centre de Référence des Maladies Héritaires du Métabolisme Hépatique, Clamart, and Univ- Paris Sud, and INSERM U 1169, France
18. Département d'anatomopathologie, Institut Universitaire du Cancer-Oncopole, Toulouse, France
19. Service d'Anatomie Pathologique, APHP Hôpital St Antoine, Sorbonne Universités, UPMC Univ Paris 06, Paris, France
20. Service de chirurgie digestive, Hôpital Henri Mondor, Créteil. Inserm U955 – Team 18 – Créteil France
21. Service d'anatomopathologie, CHRU de Tours
22. Service de Pathologie, Hôpital Pellegrin, CHU de Bordeaux, F 33000 Bordeaux France

Grants supports: ARC (2003), SNFGE (2005), Inca (2006), GENTHEP Inserm network (2003-2008), Equipe Labellisée Ligue contre le cancer, Labex OncoImmunology investissement d'avenir. the French Liver Biobanks network – INCa, BB-0033-00085, Hepatobio bank.

Abbreviations :

AP: alkaline phosphatase, b^{ex7,8}HCA: β -catenin mutated hepatocellular adenoma in exon 7 or 8, b^{ex7,8}IHCA : β -catenin mutated inflammatory hepatocellular adenoma in exon 7 or 8, b^{ex3}IHCA: β -catenin mutated inflammatory hepatocellular adenoma in exon 3, b^{ex3}HCA: β -catenin mutated hepatocellular adenoma in exon 3, BMI: body mass index, CTNFB1 : cadherin-associated protein beta 1, FRK : fyn related kinase, GLI1 : Glioma-Associated Oncogene 1, GNAS : Guanine Nucleotide Binding Protein Alpha Stimulating,, GGT: Gamma Glutamyl Transferase, HCA : hepatocellular adenoma, HCC : hepatocellular carcinoma, HHCA : HNF1A mutated hepatocellular adenoma, HNF1A : hepatocyte nuclear factor 1A, IL-6 : Interleukin 6, IHCA : inflammatory hepatocellular adenoma, INHBE : Inhibin Beta E, JAK : Janus Kinase, MRI: magnetic resonance imaging, OC: oral contraception, PTCH1: Patched Homolog 1, shHCA : sonic hedgehog hepatocellular adenoma, SMO: Smoothened, STAT : Signal transducer and activator of transcription , SUFU: Suppressor Of Fused Homolog, TERT : telomerase reverse transcriptase, UHCA : unclassified hepatocellular adenoma, WES: whole-exome sequencing, WGS: whole genome sequencing.

Correspondence:

Jessica Zucman-Rossi; MD, PhD
INSERM U 1162, Génomique fonctionnelle des tumeurs solides
27 Rue Juliette Dodu
75010 Paris, France
TEL: +33 1 53 72 51 66
FAX: +33 1 53 72 51 92
Email: jessica.zucman-rossi@inserm.fr

Conflict of interests for all authors: the authors have no conflicts of interests related to the manuscript, none to declare.

Transcripts profiling: accessions EGAS00001002091, GSE88839

Writing assistance: no writing assistance

List of investigators (GENTHEP network):

Christophe Laurent, service de chirurgie digestive, Centre Medico-Chirurgical Magellan, Hôpital Haut-Lévêque, CHU Bordeaux

Jean Saric, service de chirurgie digestive, Centre Medico-Chirurgical Magellan, Hôpital Haut-Lévêque, CHU Bordeaux

Nora Frulio, service de Pathologie, Hôpital Pellegrin, CHU-Bordeaux

Claire Castain , service de Pathologie, Hôpital Pellegrin, CHU-Bordeaux

Fanny Dujardin, service d'anatomopathologie, CHRU de Tours, Tours

Zin Benchellal, service de chirurgie digestive, CHRU de Tours, Tours

Pascal Bourlier, service de chirurgie digestive, CHRU de Tours, Tours

Daniel Azoulay, service de chirurgie digestive, hopital Henri Mondor, Créteil

Alain Luciani, service de radiologie, Hôpital Henri Mondor

Georges-Philippe Pageaux, service d'hépto-gastro-entérologie Hôpital St Eloi CHU Montpellier

Jean-Michel Fabre, service de chirurgie digestive Hôpital St Eloi CHU Montpellier

Valerie Vilgrain, service de radiologie, hopital Beaujon, Clichy sous bois

Jacques Belghiti, service de chirurgie hépatobiliaire, hopital Beaujon, Clichy sous bois

Brigitte Bancel, service d'Anatomie Pathologique, Hôpital de la Croix Rousse, Lyon

Emmanuel Boleslawski, service de chirurgie digestive et transplantation. Hôpital Huriez. Chru de lille. 59037 lille cedex.

Christophe letoublon, service de chirurgie digestive Chu Grenoble

Jean Christophe Vaillant, service de chirurgie hépto-bilio-pancréatique, CHU Pitié Salpetriere, Univ. Pierre et Marie Curie UPMC, Paris

Sophie Prévôt, APHP, HUPS, hôpital Antoine Béclère, Clamart, France.

Denis Castaing, Centre Hépatobiliaire Hôpital Paul Brousse 94804 Villejuif cedex France

Emmanuel Jacquemin, service d'Hépatologie et de Transplantation Hépatique Pédiatriques, Centre de référence de maladies rares du foie de l'enfant, CHU Bicêtre, AP-HP, Inserm U1174, DHU Hépatinov

Jean Marie Peron, service d'hépatogastroentérologie, CHU Toulouse

Sophie Michalak, département de Pathologie cellulaire et tissulaire, CHU ANGERS.

Alberto Quaglia, institute of Liver Studies, King's College Hospital, London, UK

François Paye, service de Chirurgie digestive, APHP Hôpital St Antoine, Paris

Luigi Terraciano, Basel University Hospital, Department of Pathology, Basel, Switzerland

Vincenzo Mazzaferro, university of Milan at the Istituto Nazionale Tumori IRCCS (National Cancer Institute)

Marie Christine Saint Paul, service d'Anatomie Pathologique, CHU de Nice, Nice

Benoit Terris, service d'Anatomie Pathologique, hôpital Cochin, Paris

Author contributions

Study design: JCN, JZR

Generation of experimental data: JCN, GC, SI, EL, SR, CP, GM, SC, JZR

Analysis and interpretation of data: JCN, GC, SI, EL, SR, CP, GM, SC, JZR

Collection of samples and related histological and clinical data: JCN, JZR, CB, GM, JFB, YB, JC, VP, JR, JYS, VG, NS, CG, MF, ES, LC, PL, JS, DW, AL, ADM, BL, PBS + investigators.

Drafting of the manuscript: JCN, JZR, SC, EL, SI

Revision of the manuscript and approval of the final version of the manuscript: JCN, JZR, GC, CB, GM, SC, JFB, YB, JC, VP, JR, JYS, VG, NS, CG, MF, ES, LC, PL, JS, DW, CP, AL, ADM, BL, SR, SI, PBS, EL+ investigators.

Abstract

Background and Aims

Hepatocellular adenomas (HCA) are benign liver tumors divided in molecular subtypes characterized by mutations inactivating *HNF1A*, activating β -catenin or inflammatory pathway. We aimed to refine HCA natural history according to an updated molecular classification.

Methods

607 samples of 533 HCA from 411 patients collected in 28 centers were systematically analyzed by expression profiling and sequencing 20 and 8 genes, respectively. Microarray analysis, RNA sequencing, whole-exome and genome sequencing were performed in selected cases. Clinical and pathological features were compared with molecular data.

Results

Symptomatic bleeding occurred in 14% of the patients (female 85%, median age 38 y), 7% of the nodules were borderline between adenoma and carcinoma (HCA/HCC) and in 3% HCC developed on HCA. We defined a new molecular classification of HCA in 8 molecular subgroups. Among them, we identified a new HCA subgroup (4%, previously unclassified) associated with obesity and bleeding. These tumors were characterized by a sonic Hedgehog pathway activation due to focal deletions creating *INHBE* promoter/*GLI1* fusions. Analysis of inter-tumor genetic heterogeneity of multiple HCA in patients revealed a “molecular subtype field effect” with tumors harboring private mutations leading to similar pathway deregulation. Specific molecular HCA subtypes were associated with various risk factors and estrogen/androgen hormonal balances. Finally, the molecular classification enabled to stratify patients according to the risk of bleeding and malignant transformation.

Conclusion

INHBE-GLI1 fusion defined a new subgroup of HCA characterized by sonic hedgehog activation. Molecular classification identified subgroups of patients related to specific risk factors, clinical behavior and pathological features laying the foundations for personalized treatment.

Keywords: sonic hedgehog, hepatocellular carcinoma, hepatocellular adenoma, benign liver tumor

Hepatocellular adenomas (HCA) are hormone-driven benign liver tumors mainly developed in young women with an incidence around 3/100,000^{1, 2}. Exposure to estrogens and androgens has been associated with HCA occurrence^{3, 4}. Complications such as hemorrhage (15-20%) or malignant transformation (5%)⁵⁻⁷ increase with tumor size leading to the recommendation to resect all HCA larger than 5 centimeters^{6, 8}.

We previously described a molecular classification of HCA dissecting the disease in 4 major subgroups strongly associated with risk factors, clinical features, and risk of complications as well as histological, immuno-histochemical and radiological features^{2, 9-11}. HHCA, are defined by inactivating mutations of *HNF1A* (Hepatocyte Nuclear Factor 1A)¹² with rare *HNF1A* germline mutations that predispose to liver adenomatosis with more than 10 adenomas in the liver¹²⁻¹⁵. Inflammatory HCA (IHCA) are defined by JAK/STAT pathway activation driven by somatic mutations activating different actors of this signaling pathway¹⁶ such as gp130 (encoded by *IL6ST*, 60% of mutations), *STAT3* (5%), *FRK* (10%), *JAK1* (3%) and *GNAS* (5%)¹⁶⁻²⁰. Mutations of *CTNNB1* exon 3, activating β -catenin, define the third group of tumors (b^{ex3}HCA)²¹. These tumors have an increased risk of malignant transformation in hepatocellular carcinoma (HCC) linked to *TERT* promoter mutations^{2, 20, 22, 23}. Interestingly, a subgroup of HCA shared both inflammatory phenotype and activating mutations of the exon 3 of *CTNNB1* (b^{ex3}IHCA). In contrast, mutations in *CTNNB1* exon 7 or 8 are associated with a mild activation of the Wnt/ β -catenin pathway in b^{ex7,8}HCA without an increased risk of malignant transformation^{20, 24}. Finally, around 10% of HCA are currently unclassified (UHCA) according to the molecular analysis. Our present study was constructed on a large series of 533 HCA collected to refine the HCA molecular classification and to precise its potential uses in clinical practice.

Material and Methods

Patients

Between 2000 and 2014, 777 frozen tumor samples of benign liver tumors were collected in 28 centers mainly in France and analyzed in the laboratory (Table 1 and Supplementary Table 1 and 2, Supplementary Fig. 1). All patients gave their informed consent according to French law and Paris Saint-Louis Institutional Review Board committee approved this study (Paris Saint-Louis, 2004; INSERM IRB 2010; the French Liver Biobanks network – AFAQ NF S96-900 and Hepatobio bank). All samples were frozen in nitrogen immediately after resection or biopsy and conserved at -80°C. After exclusion of focal nodular hyperplasia (FNH, n=71), tumors without diagnosis (n=19) or with poor RNA and DNA quality (n=80), 607 samples of HCA were finally included in the study. Among them, 6 malignant transformations (13 samples) and 46 HCA with multiple sampling (113 samples) were analyzed to assess intra-tumor heterogeneity. Finally, 533 different HCAs developed in 411 patients were analyzed in this study. Patients were treated by liver resection in 375 cases (92%), by liver transplantations in 10 cases (2%) or were only biopsied in 26 (6%). Multiple HCA analyzed in 73 patients (195 tumors) were used to study inter-tumor heterogeneity.

Gene sequencing and expression analysis

HNF1A (exon 1 to 10), *IL6ST* (exon 6 and 10), *CTNNB1* (exon 2,3,4, 7 and 8), *FRK* (exon 6), *STAT3* (exon 2, 5, 16 and 20), *GNAS* (exon 7, 8 and 9), *JAK1* (exon 15 and 16), *TERT* (promoter) were sequenced using Sanger sequencing (for detailed protocol see^{20, 24, 25}).

Somatic mutations were confirmed by sequencing a second amplification product of tumor and non-tumor samples. Microarray analysis was performed using Affymetrix U133.2 (accession number GSE88839). A RMA normalization was done and differential expression was investigated using a linear model followed by moderated *t*-test for the comparisons of interest, carried out with Limma package²⁶. Correction for multiple testing used Benjamini and Hochberg method²⁷. Unsupervised cluster analysis was done over the top 1000 most variable genes and spearman correlation with average linkage was measured using Gene Cluster 3.0 and Java TreeView²⁸.

Gene set enrichment analysis (GSEA) was applied as described by Subramanian et al²⁹. First, the genes were ranked according to their differential expression between the shHCA and normal liver classes. Then, hallmark gene sets were downloaded from the Molecular Signature Database (MSigDB) and were screened against the GSEA-ranked microarray data sets to determine concordant up- or downregulation of all genes in the signatures compared with the overall mean expression of genes. Statistical significances were set at a nominal $p < 0.001$. Gene expression was assessed by quantitative RT-PCR using Fluidigm technology and Taqman probes (Supplementary Table 3)^{24,30}. Data were normalized with the RNA ribosomal 18S as the calibrator and using the 2-delta delta CT method with the mean level of the corresponding gene expression in normal liver tissues, expressed as an n-fold ratio.

HHCA were defined by *HNF1A* bi-allelic mutations and/or silencing of *LFABP* and *UGT2B7* ($T/N < 0.2$), inflammatory HCA were defined by *IL-6/JAK/STAT3* activation (*SAA* and *CRP* overexpression $T/N > 5$) and/or activating mutations in *IL6ST*, *FRK*, *JAK1*, *STAT3*, *GNAS*. b^{ex3}HCA were defined by somatic mutations of *CTNNB1* exon 3 and/or strong over-expression of *GLUL* and *LGR5* ($T/N > 5$), two targets of the Wnt/catenin pathway. b^{ex7,8}HCA were defined by mutations of *CTNNB1* in exon 7 or 8. b^{ex3}IHCA were identified by the combination of b^{ex3}HCA and IHCA criteria, b^{ex7,8}IHCA by the combination of b^{ex7,8}HCA and IHCA criteria.

Immunohistochemistry

All stainings were performed on whole tumor sections. After dewaxing and rehydration, sections were placed into a boiling target retrieval solution (DiaPath Citrate Buffer pH 6) for 40 min, and left to cool down for 20 min. Slides were further processed on an automated immunostainer (Dako Autostainer). Endogenous peroxidase was blocked with H₂O₂ (Dako, 10 min) and nonspecific background staining with goat serum (20 min) and Avidin/Biotin blocking reagent (Vector Labs). Next, sections were incubated with a primary anti-PTGDS (HPA004938, Sigma-Aldrich, dilution 1/300) antibody for 1h at room temperature and washed with phosphate-buffered saline solution. After signal amplification with ABC Elite and staining with 3-diaminobenzidine (Dako) as chromogen, the slides were counterstained with Mayer's haematoxylin, dehydrated and mounting.

In each center, immunohistochemical analysis using glutamine synthase, β -catenin, *LFABP* and *SAA* was performed according to the method previously described¹⁰.

Whole exome sequencing

Whole exome sequencing was generated as described in Pilati et al. 2014. Briefly, sequence capture, enrichment and elution from 11 tumor genomic DNA and 11 corresponding non tumors genomic DNA were performed by IntegraGen (Evry, France)

using Agilent in-solution enrichment with their biotinylated oligonucleotides probes library (SureSelect Human All-Exon kit v4-70Mb (n=3 pairs); v5+UTRs-75Mb (n=8 pairs), Agilent technologies) according to manufacturer's instruction. Eluted-enriched DNA sample was sequenced on an Illumina HiSeq 2000 sequencer as paired-end 75b reads as previously described.

Image analysis and base-calling was performed using Illumina Real Time Analysis (RTA) Pipeline version 1.14 with default parameters. Whole-exome sequencing pre-analysis was based on the Illumina pipeline (CASAVA1.8.2) with the reference genome (hg19). The alignment algorithm used is ELANDv2. Only the positions included in the bait coordinates were conserved. The targeted regions in each sample were sequenced to an average depth of 76X, with ~98.3% of the targeted regions covered $\geq 1\times$, ~93.6% $\geq 10X$ and ~84.9% $\geq 25X$. Mapped reads were extracted from the original bam file and read counts for these were calculated using Bedtools Coverage (version 2.25) to find per-base fragment coverage across the targeted baits. A mean coverage was calculated relative to non-tumor tissues. The list of somatic variants in coding regions plus consensus splicing sites (± 2 bases) was generated according to Schulze et al. 2015 ³¹.

To detect focal deletions affecting *INHBE* gene in shHCA, we calculated the mean coverage log-ratio between tumor and normal samples across *INHBE* and *GLI1*. Ten samples with a log-ratio < -0.3 for *INHBE* and a log-ratio difference between *INHBE* and *GLI1* > 0.2 were considered to have a focal deletion within *INHBE*. In 6/10 samples, we identified chimeric reads that allowed us to map the deletions at single-base resolution using BLAST. Focal deletions were described in Supplementary Table 4.

All sequences has been deposited in the EGA (European genome-phenome archive - <http://www.ebi.ac.uk/ega/>) database (accessions EGAS00001000679 and EGAS00001002091).

RNA sequencing

Eight shHCA samples and 3 matched normal liver samples were analyzed by RNA-sequencing. Libraries were prepared by Integragen using Illumina TruSeq Stranded mRNA kit according to the manufacturer's instructions, and sequenced as paired-end 100bp reads on an Illumina HiSEQ 2000. Fastq files were aligned to the reference human genome hg19 with tophat2 (-p 10 -r 150 -g 2 --library-type fr-firststrand) ³². After removing reads mapping to multiple locations, we used HTSeq ³³ to obtain the number of reads associated to each gene in the Ensembl 65 database. To visualize fusion transcripts between *INHBE* and *GLI1* genes in shHCA, we loaded the bam files in Integrative Genomics Viewer (IGV) ³⁴ and we used the Sashimi plot function of IGV to identify and quantify fusion reads.

All sequences has been deposited in the EGA (European genome-phenome archive - <http://www.ebi.ac.uk/ega/>) database (accessions EGAS00001002091)

Whole genome sequencing

Three shHCA samples and matched normal liver samples were analyzed by whole genome sequencing. Genomic DNA libraries were prepared by Integragen using the Illumina Truseq DNA PCR-Free lib prep kit or the TruSeq DNA sample prep kit and sequenced on an Illumina HiSeq2500 as paired-end 125bp reads. The mean depth was 77X for tumor samples (range 54-93) and 55X for normal samples (range 50-60). Read alignment and variant calling were performed following GATK best practices. In short, we used BWA (version 0.7.15) ³⁵ to align sequences to the reference human genome hg19, Picard tools to remove PCR duplicates and GATK³⁶ for local indel realignment

and base quality recalibration. We used MuTect2³⁷ to identify somatic single nucleotide variants and indels, and Manta to detect somatic structural rearrangements³⁸. All sequences has been deposited in the EGA (European genome-phenome archive - <http://www.ebi.ac.uk/ega/>) database (accessions EGAS00001002091)

Statistical analysis

Statistical analysis was performed using the R software and the GraphPad Prism Software. Comparison between qualitative data was performed using Chi-square test and Fisher exact test. Monte-Carlo method was used to adjust the P value for multiple tests. Quantitative data were compared using Mann-Whitney U test and Kruskal-Wallis Test. All tests were two tailed and a P value < 0.05 was considered as significant. We scored estrogen exposure in women from 0 to 5: no oral contraception (OC, 0 point), number of years of OC < median (1 point), number of years of OC > median (2 points), BMI < 25 (0 point), BMI between 25-30 (1 point), BMI>30 (2 points), alcohol intake < 30 g/day (0 point), alcohol intake ≥ 30 g/day (1 point). We scored androgen exposure from 0 to 2 points: female (0 point), male (1 points), no androgen intake (0 points), androgen intake (1 points).

For statistical patient analysis, we assigned a molecular subgroup to each patient corresponding to that observed in the tumor. Only 21 patients harbored multiple HCA belonging to different molecular subgroups and one HCA harbored both *HNF1A* and *CTNNB1* mutations, consequently a molecular subgroup could not be assigned for these 22 patients and they were excluded of the correlation analysis performed with the clinical features.

Results

Patients and tumor features

A total of 533 HCA from 411 patients were analyzed (see flow chart, Supplementary Fig. 1). Among the 533 HCA, 36 were borderline tumors between HCA and HCC (HCA/HCC, 7%) and 15 demonstrated malignant transformation of HCA into HCC (HCC on HCA, 3%) (Supplementary Table 1). Clinical features were typical of a series of resected HCA (Supplementary Table 2). Briefly, HCA median size was 55 mm (Minimum-Maximum: 5-290), median age was 38 years (7-82), with a large predominance of female (85%) with oral contraception identified in 87% (median use 13 years (1-35)); 16% of the patients were obese, 6% had glycogen storage disease and 4% liver vascular diseases (other syndromic diseases were detailed in supplementary Table 5). HCA were discovered by chance (35%), pain (37%), symptomatic bleeding (14%), abnormal liver tests (14%) and/or inflammatory syndrome (5%) (Supplementary Table 2). Gamma Glutamyl Transferase (GGT) and alkaline phosphatase (AP) were increased in 55% and 35% of the patients, respectively. At histology, HCA were multiple in 45% of the cases and 47 patients (12%) had liver adenomatosis defined by more than 10 HCA at histology. The non-tumor liver parenchyma was steatotic in 42 patients (12%) and fibrotic (F2-F4) in 24 patients (7%) (Supplementary Table 2)³⁹. Six patients died, 3 due to a malignant transformation, 1 from HCA bleeding, 1 after liver resection for multiple HCA developed on cirrhosis and 1 after liver transplantation for HCA developed on glycogenosis.

Identification of a new subtype of HCA characterized by Sonic Hedgehog activation due to INBHE-GLI1 fusion.

To search for new molecular subtype of tumors, we performed an unsupervised hierarchical clustering of transcriptomic microarray in 36 HCA and 4 normal liver tissues that identified a homogeneous cluster of 4 previously unclassified HCA (Fig. 1a). Analysis of the genes differentially expressed in this subgroup of tumors revealed an activation of the sonic hedgehog pathway (Fig. 1b, Supplementary Table 6). We selected 6 genes (*PTGDS*, *HHIP*, *FRCLA*, *PTCH1*, *GPR97* and *TNNC1*) specifically over-expressed in this subgroup of HCA to analyze the whole series of 533 HCA by quantitative RT-PCR (Supplementary Fig. 2). One third of the unclassified HCA overexpressed these 6 genes and 22 tumors were re-classified as sonic hedgehog activated HCA (shHCA). Moreover, by immunohistochemistry, PTGDS protein over-expression was restricted to tumor hepatocytes (Fig. 1c). To unravel the molecular mechanism driving this tumor subgroup, we analyzed 11 cases by whole exome sequencing (WES), 9 of which were also analyzed by RNA-sequencing and 3 also by whole genome sequencing (WGS). shHCA displayed a median of 2,021 mutations (range 1952-2259) in the genome and 27 mutations (9-54) in coding regions, corresponding to a relatively low mutation rate of 0.7 mutations/Mb. We found no recurrent coding mutation in the series (Supplementary Table 7 and 8). In 9 cases, RNAseq analyses showed *GLI1* overexpression due its fusion with the 5' end of two different *INHBE* transcripts, a highly expressed gene located 2.1 kb upstream of *GLI1* (Fig. 1d and 1e). In all except one of the shHCA, the entire open reading frame of *GLI1*, the key transcription factor of sonic hedgehog pathway, was fused and over-expressed; the remaining one includes exons 6 to 12 coding for the DNA-binding and the transactivation domains (Fig. 1e and Supplementary Fig.3). All the 9 *INHBE-GLI1* fusions were validated as somatic by Sanger sequencing of the cDNA and specific *GLI1* overexpression in shHCA was validated by quantitative RT-PCR (Fig. 1d and Supplementary Fig. 4).

Whole genome and whole exome sequencing of the 9 shHCA harboring *INHBE-GLI1* fusion revealed a recurrent structural rearrangement within *INHBE* including 5 focal deletions and one inversion (Fig. 1e and Supplementary Table 9). We also observed another *INHBE* focal deletion in one shHCA not analyzed by RNAseq. Overall, *INHBE-GLI1* fusions were identified in 15 out 20 shHCA with a typical pattern of gene expression and investigated by sequencing. Thus, shHCA is a new molecular subgroup of HCA driven by structural rearrangements of *INHBE* producing a highly expressed *INHBE-GLI1* fusion leading to the constitutive activation of the sonic hedgehog pathway.

Mutations in 8 driver genes and expression analyses of 13 genes specifically over/underexpressed in each group allowed us to classify the 533 HCA into 8 different molecular subgroups (see method section, Supplementary Table 10): HHCA (n=179, 33.5%), IHCA (n=183, 34%), b^{ex3}HCA (n=37, 7%), b^{ex3}IHCA (n=34, 6%), b^{ex7,8}HCA (n=21, 4%), b^{ex7,8}IHCA (n=21, 4%), shHCA (n=22, 4%) and UHCA (n=40, 7.5%) (Table 1). In IHCA (n=183), we detected mutations of *IL6ST* (77%), *STAT3* (4%), *GNAS* (3%), *FRK* (9%) and *JAK1* (1%) whereas (6%) of the IHCA remained non-mutated (Supplementary Table 1 and 2). Interestingly, HNF1A mutations and shHCA were exclusive from all other subtypes. In contrast, whereas *CTNNB1* mutations in exon 3 were exclusive from the mutation in exons 7 or 8, half of the overall β -catenin HCA were associated with an IL-6/JAK/STAT activation and inflammation.

Intra-tumor and inter-tumor molecular subgroup homogeneity

To study intra-tumor heterogeneity in term of molecular subgroup, we analyzed multiple samples (2 to 4) in 52 tumors for mutations of 8 driver genes by Sanger sequencing and expression of 13 genes by quantitative RT-PCR including 46 HCA and 6 transformations in HCC. We identified molecular homogeneity, in 42/46 HCA (91%) with identical mutations and expression in the different parts of the tumors. A total of 4 HCA showed molecular heterogeneity. One multi-lobular HHCA (#462T/463T) harbored 3 different somatic HNF1A mutations in two different areas (Fig. 2A). Three additional cases showed different transcriptional (#2599T) or mutation (#1337 and #2768) profiles (Supplementary Fig. 5). Among the 6 HCA transformed in HCC, *TERT* promoter mutations were identified in the malignant part in two cases and not in the benign part whereas *TERT* promoter mutations was observed in both the HCA and HCC part in one case (Supplementary table 11).

Next, we focused on inter-tumor molecular subgroup heterogeneity and we analyzed 195 different tumors developed in 73 patients (from 2 to 8 analyzed tumors per patient) (Fig. 2B and 2C). In 52 patients (71%), all the analyzed tumors belonged to the same molecular subgroups (mainly HHCA and IHCA) (Fig. 2C) but with systematically private driver mutations, no common somatic mutations were identified showing the independent clonal origin of the multiple nodules (Fig. 2B). In contrast, in 21 patients (29%), the tumors from the same patient belonged to different molecular subgroups with *CTNNB1* exon3 mutation (b^{ex3}HCA or b^{ex3}IHCA) identified in the largest nodule in 8 out of 9 cases (Fig. 2C and supplementary Table 12).

Hormonal balance and other risk factors associated with molecular classes

A large predominance of female from 60% of b^{ex3}HCA to 100% of shHCA was observed in all subtypes (Fig. 3A, Table 1 and Supplementary Table 13). Several other features contribute to estrogen exposure: the cumulative intake of oral contraceptive (OC) but also obesity and alcohol intake. Interestingly, patients with IHCA and shHCA demonstrated higher BMI and/or cumulative consumption of OC in contrast to patients with b^{ex3}HCA and b^{ex7,8}HCA showing lower OC consumption (Fig. 3B, 3C and 3D, Table 1). *In fine*, a scoring of estrogen exposure revealed that patients with inflammatory HCA (with or without *CTNNB1* mutations) had a higher level of estrogen exposure compared to HHCA (Fig.3E). In the same line, women with multiple IHCA have also a higher level of estrogen exposure compared to women with multiple HHCA (P=0.0045, Supplementary Fig.6).

Androgen exposure also varied according to HCA molecular subtypes: androgen exposure due to gender or androgen intake was higher in b^{ex3}HCA with or without inflammation compared to other molecular subtypes (P<0.0001, Fig.3F).

Finally, other conditions modulate the occurrence of specific molecular subtypes: patients with b^{ex3}HCA and b^{ex7,8}HCA were 10 years younger compared to other patients (P<0.0001, Table 1, Fig. 3C). HCA arising on glycogenesis were never HHCA but enriched in inflammatory HCA as previously described⁴⁰. Interestingly, patients with liver vascular disease developed more frequently b^{ex3}HCA (P value=0.04)⁴¹ (Table 1).

Clinical presentation, risk factors of malignant transformation and hemorrhage

Clinical symptoms at presentation were less frequent in patients with IHCA (30%, P<0.0001,) in contrast they were more frequently diagnosed with abnormal biological tests showing inflammatory syndromes, raised GGT and AP (P <0.0001; Table 1). Liver adenomatosis was identified in 47 patients enriched in male (29.8% versus 13.2%

without adenomatosis, $P=0.008$), glycogenosis (16% versus 3% $P=0.005$) and microadenomas (41% versus 15% $P<0.0001$), *HNF1A* germline mutations (17% versus 1% $P<0.0001$) and HHCA molecular subtype (50% versus 32.4%, $P=0.038$) (Supplementary Table 14). In four patients (9%), liver adenomatosis was developed in a familial context; they were all related to *HNF1A* germline mutations. However, the rate of complications such as hemorrhage or malignant transformation was the same whatever the number of adenomas (Supplementary Table 14). Histological bleeding was observed in half of the tumors (52%) but only 14% of the patients presented with symptomatic HCA bleeding (Supplementary Table 1, 2 and 15). The classical cut off at 50mm was associated with more frequent histological hemorrhage (65%) in HCA >50mm versus 40% in HCA < 50mm ($P <0.0001$, Fig.4a, Supplementary Fig. 7) but not associated with symptomatic bleeding ($P=0.29$, Fig.4b). Interestingly, frequency of histological hemorrhages was closely related to the molecular subgroups; $b^{ex7,8}$ HCA and shHCA showed the highest rate of hemorrhages (92% and 81%) and HHCA the lowest (39%, $P<0.0001$, Fig.4a, Supplementary Fig. 7). Moreover, shHCA was the unique subgroup associated with symptomatic bleeding (71% of bleeding in shHCA versus 14% in other subgroups, $P<0.0001$, Fig.4b, Supplementary Fig. 7).

Patient features associated with malignant transformation in HCC on HCA or borderline HCA/HCC lesions were *TERT* promoter mutations (OR: 67.6 (CI95%: 8.3-3072), $P < 0.0001$), male (OR: 18.9 (CI95%: 8.5-44.2) $P<0.0001$), *CTNNB1* exon 3 mutations b^{ex3} HCA or b^{ex3} IHCA (OR: 9.3 (CI95%: 4.4-20.0) $P<0.0001$), unique nodule at imaging (OR: 4.1 (CI95%: 1.7-11.7) $P<0.0001$), high alcohol intake (OR: 4.85 (CI95%: 1.8-12.4) $P =0.001$), fibrosis in non-tumor liver (OR: 3.8 (1.1-11.4) $P = 0.02$) and diabetes type 2 (OR: 3.7 (CI95%: 1.3-9.9) $P=0.009$) (Fig. 4a and 4b). Several additional tumor features related to β -catenin activation (pseudoglandular formation, nuclear β -catenin, glutamine synthase expression and cholestasis) were also associated with malignant transformation (Fig.4a). Large tumor size at histology in the overall series tended to be associated with malignant transformation without reaching statistical significance (7.6% of borderline lesions or HCC on HCA in HCA < 50 mm versus 13.1% of borderline lesions or HCC on HCA in tumors > 50 mm, $P=0.053$).

Nosological definition of HCA classes and consequences for clinical care

Here we defined 8 different molecular subgroups that create a new nosology of HCA linked with risk factors, clinical presentation and risk of complications (Fig.5). HHCA, shHCA, bHCA and IHCA showed specific associations whereas mixed bIHCA shared features common to inflammatory and b-catenin activated subtypes (Fig.5). Finally, 7% of HCA remain unclassified and should be further analyzed. This molecular classification is currently translated in academic pathological laboratories using immunohistochemistry¹⁰. In the present series, we obtained the IHC data for 236 tumors from 17 hospitals (Supplementary Table 15). Interestingly, correlation of IHC results using a panel of 4 antibodies (SAA, LFABP, Glutamine Synthase and β -catenin) with major molecular subtypes (IHCA, HHCA, b^{ex3} HCA and b^{ex3} IHCA) were very good with sensitivity and specificity ranging from 0.85 to 0.93 (Supplementary Table 16). Next, we assessed whether if the molecular classification could help to identify more precisely patients at risk of major complications to refine therapeutic decision. Currently, in clinical practice, male gender and large tumor size (with a cut off of 5 cm) are used to identify patients that could benefit from tumor resection to prevent bleeding and malignant transformation^{6,8}. Here, we defined molecular subtypes of “at-risk-HCA”

including b^{ex3}HCA with or without inflammation associated to malignant transformation and shHCA with symptomatic bleeding. Overall, this classification identifies patients at risk of both complications in male and female (Table 2).

In male, the molecular classification is less useful due the global high risk of malignant transformation at baseline (41% versus 65%, see (Table 2). Of note, molecular classification is more contributive in small tumors developed in female and would help to guide treatment in this population. In women whatever the size of the tumor, the presence of at risk HCA was significantly associated with a higher rate of malignant transformation (17%) compared to other patients (1.5%, $P < 0.0001$). Women with at risk HCA still have a higher rate of malignant transformation after stratification by tumor size (14% in HCA < 5 cm and 18% in HCA > 5 cm) compared to women without at risk HCA (1% in HCA < 5 cm with $P < 0.038$ and 3% in HCA > 5 cm with $P=0.001$) (Table 2). Interestingly, no malignant transformation was observed in HHCA of less than 5 cm developed in women.

Discussion

In this study, we identified the role of sonic hedgehog activation in benign hepatocyte proliferation associated with a novel mechanism due to small somatic deletions of *INHBE* leading to *INHBE-GLI1* fusions. In the liver, sonic hedgehog pathway has been involved in regeneration and lipid metabolism in both humans and mice but its role in tumorigenesis is still unclear⁴². Interestingly, in other organs, sonic hedgehog pathway can be activated also mainly in benign (Pericytoma and Plexiform Fibromyxoma) or in non-metastatic (basal cell carcinoma) tumors and various genomic alterations were described including *MALAT1-GLI1* or *ACTB-GLI1* fusions, *PTCH1*, *SMO* and *SUFU* mutations⁴³⁻⁴⁵. Here, Sonic Hedgehog activation was identified in 4% of HCA previously unclassified and no similar alterations were found in our series of 120 HCC previously sequenced by whole exome sequencing³¹. Taking together, these findings reinforce the role of sonic Hedgehog activation in benign tumorigenesis.

Overall, our novel HCA molecular classification revealed an unexpected molecular diversity with alterations in four different pathways driving human benign clonal proliferation: activation of β -catenin, IL-6/JAK/STAT or Sonic Hedgehog and *HNF1A* inactivation. Interestingly, most of these alterations are exclusive each other except β -catenin and inflammatory pathways that can cooperate in mixed tumors. However, intra-tumor and inter-tumor genetic heterogeneity of the main driver genes was limited in our series and 71% of the patients with multiple HCA developed tumors belonging to the same molecular subtype. Moreover, in all the remaining heterogeneous cases, β -catenin exon 3 nodules associated with a highest risk of malignant transformation were the largest nodules. These results suggest that, in front of multiple HCA, biopsy of the largest nodule could be a valuable option in clinical practice to capture the prognostic information.

Analysis of inter-tumor genetic heterogeneity has also revealed a “molecular subtype field effect” in patients with multiple adenomas and private mutations were identified in each tumors leading to the same pathway de-regulation. It suggests that specific risk factors could predispose to the development of multiple independent HCA of the same molecular subgroup. In this line, we demonstrated the role of the hormonal balance between estrogen and androgen and of the magnitude of estrogen exposure in the

occurrence of the different molecular subgroups of HCA. Estrogen and androgen exposure is the conjunction of endogenous exposure due to gender and obesity and of exogenous exposure due to hormonal or alcohol intake. The occurrence of inflammatory and sonic hedgehog HCA could be fostered by high estrogen exposure (“estrogen intoxication”) during life. In contrast, the level of estrogen exposure is lower in patients with *HNF1A* mutated HCA suggesting that the genetic background such as *HNF1A* germline mutations or other unknown polymorphisms could sensitize the patient to lower doses of hormones (“estrogen sensitivity”) and estrogen metabolism alterations in HHCA could contribute to this mechanism⁴⁶. Finally, we also showed the role of androgen exposure due to male gender itself and/or androgen intake that promote HCA harboring *CTNNB1* exon 3 mutations and the malignant transformation of adenomas. This observation reinforced the association observed between androgen and the risk of HCC development described in mice and men⁴⁷.

The new HCA molecular classification enabled to stratify patients according to the risk of complication, malignant transformation and bleeding. Male and presence of *CTNNB1* mutations exon 3 were associated with a high risk of malignant transformation (10% of the tumors were borderline HCA/HCC or HCC on HCA in our series)^{21,22} together with new risk factors such as diabetes, alcohol intake, presence of a unique tumor and fibrosis on non-tumor liver. Only shHCA subtype was significantly associated with both histological hemorrhage (identified in 52% of the tumors) and symptomatic bleeding (identified in 14% of the patients) whereas large size of the HCA, that is currently used in clinical practice, was associated only with histological hemorrhage but not to symptomatic bleeding. Consequently, adding molecular subtyping with histology and imaging data could help to better assess the risk of bleeding in clinical practice. In male, classification of HCA in molecular subgroups of at-risk of complications (b^{ex3} HCA, b^{ex3} IHCA, shHCA) versus non-at-risk (HHCA, IHCA, $b^{x7,8}$ HCA, $b^{x7,8}$ IHCA) is not useful since gender *per se* is a strong risk factor of malignant transformation justifying systematic tumor destruction. In contrast, in women stratification according to molecular subgroups at-risk of complication could modify patient care. First, in small HCA, HHCA representing 41% of HCA < 5 cm can be efficiently identified at MRI in routine, as they were not associated with a risk of malignant transformation, patients could benefit of a non-aggressive treatment and surveillance¹¹. In contrast, in small non-HHCA at MRI, biopsy could be useful in order 1) to confirm the diagnosis of HCA and definitely exclude the diagnosis of FNH 2) identify molecular-at-risk HCA that could benefit from surgery. In women with large HCA (>5cm), molecular classification may be also helpful to identify patients the most at risk of complications particularly when surgery is difficult and discussed. However, several multidisciplinary teams also proposed to stop oral contraception and follow-up hepatocellular adenomas of more than 5 cm in women several months. Then, surgery is discussed only if the tumor increased in size despite stopping estrogens^{8,48}.

Candidate therapeutic targets can be defined according to the molecular classification taking into account the mechanism by which each pathway are dysregulated. We previously showed that ruxolutinib (a JAK1/JAK2 inhibitor) could be efficient to suppress the IL6/JAK/STAT pathway activation related to *IL6ST* or *JAK1* mutations whereas dasatinib (a src inhibitor) could be efficient against STAT3 and FRK mutations^{20,49}. Visdomegib (a SMO inhibitor) may not efficiently target sonic hedgehog activation in shHCA because of the downstream activation of GLI1, but GLI1 inhibitors

(such as GANT-61, under development) could be good candidates ^{50, 51}. Finally no efficient drugs are currently available for *HNF1A* inactivation and β -catenin activation.

In conclusion, the revisited molecular classification has redrawn the nosology of HCA according to risk factors, clinical presentation and histology. Personalized treatment based on genetic analysis could be proposed to stratify clinical care according to the risk of complications.

Table 1: genotype phenotype correlation according to molecular subgroups

	Available data ⁵	HHCA	b ^{ex} 7,8HCA	b ^{ex} 7,8IHCA	IHCA	b ^{ex} 3IHCA	b ^{ex} 3HCA	shHCA	UHCA	
	total n=389	n=133 (34%)	n=15 (4%)	n=21 (5%)	n=116 (30%)	n=30 (8%)	n=30 (8%)	n=16 (4%)	n=28 (7%)	
Gender (female)	381	118 (90%)	14 (100%)	16 (76%)	98 (85%)	19 (70%)*	18 (60%)**	16 (100%)	22 (81%)	
Age	381	37 (7-76)	27.5** (21-53)	41.0 (17-63)	40.0 (14-54)	39.0 (12-59)	28.5** (11-83)	43.0 (29-48)	38.0 (22-78)	
Transformed or borderline tumors	389	7 (5%)*	0 (0%)	1 (5%)	7 (6%)	8 (27%)**	14 (47%)**	1 (6%)	4 (14%)	
HCC on HCA	389	5 (4%)	0 (0%)	0 (0%)	1 (1%)	5 (17%)	4 (13%)	1 (6%)	3 (11%)*	
Borderline HCC/HCA	389	2 (1%)	0 (0%)	1 (5%)	6 (5%)	3 (10%)	10 (33%)**	0 (0%)	1 (3%)	
Children (yes) (women only)	204	54 (74%)	4 (40%)	7 (77%)	52 (79%)	6 (50%)	5 (38%)**	7 (88%)	10 (77%)	
Number of children (women only)	204	2 (0-4)	0** (0-2)	1 (0-3)	2 (0-5)	0 (0-3)	0** (0-9)	2 (0-3)	2 (0-2)	
Oral contraception (women only)	254	75 (85%)	11 (92%)	15 (100%)	65 (85%)	15 (100%)	13 (81%)	10 (77%)	17 (94%)	
Number of years of OC (women only)	170	12.0 (1-34)	9.5** (1-12)	22.0 (10-31)	20.0*** (3-35)	12.5 (4-28)	8.0** (1-13)	22.5 (10-30)	10.5 (5-23)	
BMI (kg/m ²)	290	21.0** (16-43)	20.0 (19-31)	27.0** (22-40)	25.0** (16-47)	22.0 (19-30)	22.5 (17-33)	32.0** (20-42)	25.0 (19-45)	
Diabetes	278	5 (5%)	1 (9%)	2 (13%)	13 (14%)	1 (7%)	4 (18%)	1 (10%)	2 (10%)	
Glycogenesis	263	0 (0%)**	2 (22%)	1 (7%)	10 (12%)**	1 (5%)	1 (5%)	0 (0%)	0 (0%)	
Hepatic vascular disease	262	4 (4%)	0 (0%)	0 (0%)	1 (1%)	1 (5%)	3 (14%)*	0 (0%)	0 (0%)	
High alcohol intake (yes)	250	3 (4%)**	1 (9%)	4 (31%)*	15 (19%)	4 (21%)	4 (17%)	0 (0%)	2 (12%)	
Symptomatic bleeding	332	20 (18%)	4 (33%)	1 (5%)	13 (13%)	1 (4%)	2 (7%)	10 (71%)**	3 (14%)	
Pain	332	47 (42%)	4 (33%)	10 (50%)	23 (23%)**	10 (44%)	11 (38%)	9 (64%)*	10 (45%)	
Discovery by chance	332	36 (32%)	3 (25%)	6 (30%)	42 (42%)	7 (30%)	13 (45%)	1 (7%)*	7 (32%)	
Abnormal liver function test	249	10 (12%)*	2 (22%)	3 (25%)	24 (31%)**	4 (24%)	3 (12%)	0 (0%)	2 (12%)	
Follow up of angioma/FNH	332	7 (8%)	1 (12%)	0 (0%)	1 (1%)	0 (0%)	1 (4%)	1 (14%)	2 (12%)	
Inflammatory syndrome	259	2 (2%)	1 (11%)	0 (0%)	11 (13%)**	2 (11%)	1 (4%)	0 (0%)	0 (0%)	
Symptomatic disease	332	51 (55%)	8 (67%)	12 (60%)	30 (30%)**	11 (48%)	13 (45%)	12 (86%)**	12 (55%)	
Raised GGT	273	21 (23%)**	7 (70%)	15 (88%)*	67 (79%)**	12 (71%)	10 (45%)	6 (50%)	9 (47%)	
Raised AP	181	13 (22%)*	1 (14%)	5 (50%)	31 (56%)**	5 (45%)	4 (27%)	1 (11%)	1 (7%)*	
Raised CRP	151	11 (25%)**	4 (67%)	9 (90%)*	45 (76%)**	5 (56%)	3 (27%)	5 (62%)	2 (40%)	
Germline HNF1A mutation	389	11 (8%)**	0 (0%)	0 (0%)	3 (3%)	1 (3%)	1 (3%)	0 (0%)	0 (0%)	
Number of adenomas	1	369	12 (92%)*	14 (67%)	57 (51%)	20 (77%)	65 (51%)	22 (76%)**	7 (44%)	17 (65%)
	2 to 5	369	1 (8%)*	4 (19%)	27 (24%)	5 (19%)	26 (20%)	2 (7%)**	5 (32%)	5 (19%)
	5 to 10	369	0 (0%)*	2 (9%)	14 (13%)	1 (4%)	15 (12%)	3 (10%)	2 (13%)	1 (4%)
	>=10	369	0 (0%)*	1 (5%)	13 (12%)	0 (0%)	21 (17%)	2 (7%)	2 (13%)	3 (10%)
Size of the largest nodule (mm)	358	60* (6-270)	93 (45-140)	70 (20-140)	68 (15-190)	70 (25-200)	80 (20-290)	70 (15-230)	47.5* (20-200)	
Steatosis on non tumor liver	356	13 (11%)**	4 (33%)	11 (52%)*	44 (40%)**	10 (38%)	9 (35%)*	10 (67%)**	10 (40%)	
Fibrosis non tumor liver (F2-F4)	353	5 (4%)	1 (8%)	1 (5%)	5 (7%)	2 (8%)	4 (16%)*	1 (7%)	0 (0%)	
Microadenoma at histology	345	43 (36%)**	1 (8%)	0 (0%)*	14 (13%)	1 (4%)	0 (0%)**	0 (0%)	2 (8%)	
Number of adenomas	1	316	10 (83%)*	13 (65%)	48 (49%)	15 (71%)	41 (39%)**	17 (63%)	3 (25%)	13 (59%)
	2 to 5	316	1 (8.5%)*	3 (15%)	15 (15%)	3 (14%)	26 (25%)**	5 (18%)	5 (42%)	2 (9%)
	5 to 10	316	0 (0%)*	2 (10%)	18 (19%)	1 (5%)	14 (13%)**	1 (4%)	1 (8%)	0 (0%)
	>=10	316	1 (8.5%)*	2 (10%)	16 (16%)	2 (10%)	24 (22%)**	4 (15%)	3 (25%)	7 (32%)
Size of adenomas > 5 cm	303	59 (57%)	10 (83%)	13 (68%)	64 (70%)	13 (65%)	17 (68%)	8 (73%)	10 (48%)	

Statistical test was Kruskal Wallis or Chi squared corrected using Monte Carlo resampling. * P < 0.05, ** P < 0.01, *** P < 0.001. *Patients with multiples tumors with discordant molecular features were excluded from the statistical analysis (n=22).

Table 2: risk of symptomatic bleeding and malignant transformation according to the molecular classification

	Molecular stratification	Symptomatic Bleeding	Malignant transformation	Both complications	P value
Male N=60	Non at-risk HCA N=40 (66%)	N= 2/33 (6%)	N= 14/40 (41%)	N= 14/33 (42%)	<i>P=0.047</i>
	At-risk HCA N=20 (34%)	N= 1/19 (5%)	N= 13/20 (65%)	N=14/19 (74%)	
Female All HCA N=319	Non at-risk HCA N=266 (83%)	N=38/230 (16%)	N=4/266 (1.5%)	N=40/230 (17%)	<i>P=0.0004</i>
	At-risk HCA N=53 (17%)	N=12/47 (26%)	N=9/53 (17%)	N=20/47 (42%)	
Female All HCA < 5 cm N=115	Non at-risk HCA N=101 (88%)	N= 13/90 (14%)	N= 1/101 (1%)	N= 14/90 (15%)	<i>P=0.007</i>
	At-risk HCA N=14 (12%)	N= 5/14 (36%)	N= 2/14 (14%)	N= 7/14 (50%)	
Female HCA < 5 cm excluding HHCA N=68	Non at-risk HCA N=54 (79%)	N= 7/49 (14%)	N= 1/54 (2%)	N= 8/49 (16%)	<i>P=0.015</i>
	At-risk HCA N=14 (21%)	N= 5/14 (36%)	N= 2/14 (14%)	N= 7/14 (50%)	
Female H-HCA < 5 cm N=47	Non at-risk HCA N=47 (100%)	N=6/41 (15%)	N=0/47 (0%)	N=6/41 (15%)	na
Female All HCA > 5 cm N=188	Non at-risk HCA N=150 (80%)	N= 26/136 (19%)	N= 4/150 (3%)	N= 28/136 (21%)	<i>P=0.087</i>
	At-risk HCA N=38 (20%)	N= 7/33 (21%)	N= 7/38 (18%)	N= 13/38 (34%)	

At risk HCA were b^{ex3}HCA, b^{ex3}IHCA and shHCA due to the high risk of malignant transformation and bleeding. Non at-risk HCA were HHCA, b^{ex7,8}HCA, b^{ex7,8}IHCA, IHCA and UHCA. Statistical analysis was performed using Fisher exact test.

Figure 1: a new subgroup of hepatocellular adenomas with sonic hedgehog pathway activation

(A) Unsupervised hierarchical clustering of 38 samples (normal liver n=3, HHCA n=4, b^{ex3}HCA n=7, b^{ex3}IHCA n=3, IHCA n=7, b^{ex7,8}HCA n=3, b^{ex7,8}IHCA n=3, shHCA n=4, UHCA n=4) analyzed in microarray.

(B) Differential expression analysis between shHCA and normal liver. The volcano plot (left) shows the expression fold-change (log₂ scale) between shHCA and normal liver on the x axis, and the p-value (-log₁₀ scale) on the y axis. Significantly down-regulated genes are indicated in green, and significantly up-regulated genes are indicated in red. Gene set enrichment analysis (GSEA) identified Hedgehog signaling as the most significant gene set associated with up-regulated genes (up right). Gene expression of the 6 Hedgehog signaling genes most significantly up-regulated in shHCA is represented as a heatmap (bottom right). Red: high expression; blue: low expression.

(C) Representative staining of PTGDS using immunohistochemistry in a sonic hedgehog HCA (shHCA).

(D) Expression of *GLI1* in the different molecular subtypes of HCA (HHCA n=123, IHCA n=151, b^{ex3}HCA n=30, b^{ex3}IHCA n=30, b^{ex7,8}HCA n=13, b^{ex7,8}IHCA n=19, shHCA n=7 and UHCA n=32) using quantitative RT-PCR (Kruskall Wallis Test).

(E) Representation of the *INHBE-GLI1* fusion in 8 HCA harboring sonic hedgehog pathway activation. The 2 transcripts of *INHBE* were represented in blue and the transcripts of *GLI1* in red. Deletion and inversion of *INHBE* were represented in gray; in 3 cases deletions of *INHBE* were unmapped.

Figure 2: Intertumor and intratumor heterogeneity

(A) *HNF1A* mutations of two samples from one multilobular HCA. (B) Multiples HCA all belonging of the same molecular subtype (IHCA) in one patient. All the tumors have somatic mutations in *IL6ST* but all these mutations were different. (C) Representation of intertumor heterogeneity with in each column one patient and in each line one tumor with the molecular subtype and borderline tumors between HCA/HCC or HCC on HCA represented using a panel of colors.

Figure 3: Correlation between molecular subgroups and clinical features

(A) Distribution of molecular subgroups according to the gender. (B) Mean value of years of uses of oral contraception (OC) in women, (C) of age, (D) of body mass index (BMI) of all the patients according to the molecular subgroups. (E) Distribution of the scoring of estrogen exposure according to the molecular subgroups. The scoring of exposition to estrogens in women from 0 to 5 was defined as follow: no OC (0 point), number of years of OC < median (1 point), number of years of OC > median (2 points), BMI < 25 (0 point), BMI between 25-30 (1 point), BMI>30 (2 points), alcohol intake < 30

g/day (0 point), alcohol intake \geq 30 g/day (1 point). (F) Distribution of the scoring of androgens exposure according to the molecular subgroups. The scoring of exposition to androgen from 0 to 2 points was defined as follow: female (0 point), male (1 points), no androgen intake (0 points), androgen intake (1 points)
Continuous data were represented using the mean with Confidence interval 95% (CI95) and compared using the Mann-Whitney test. Dichotomized variables were compared using Chi squared test with Monte carlo resampling.

Figure 4: risk of hemorrhage and malignant transformation

(A) Association between molecular, clinical and pathological features and the risk of haemorrhage and malignant transformation per tumors and (B) per patients. Odds ratio with the CI95% using a Chi squared with Monte carlo resampling.

Figure 5: a new nosology of hepatocellular adenomas

Supplementary Figure 1: flow chart of the study

Supplementary Figure 2: expression of genes upregulated in sonic hedgehog HCA

Expression of genes deregulated in sonic hedgehog HCA among the different molecular subtypes of HCA (HHCA n=92, IHCA n=113, b^{ex3}HCA n=24, b^{ex3}IHCA n=27, 6%, b^{ex7,8}HCA n=8, b^{ex7,8}IHCA n=17, shHCA n=22 and UHCA n=33) using quantitative RT-PCR (Kruskall Wallis Test).

Supplementary Figure 3: sashimi plot and *INHBE-GLI1* fusion

Sashimi plots exported from Integrative Genomics Viewer (IGV) showing RNA-seq alignments for 3 normal liver samples (top) and 9 cases of shHCA with *INHBE-GLI1* fusion (bottom). Alignments in exons are represented as read densities, and splice junction reads are drawn as arcs connecting a pair of exons, where arc width is proportional to the number of reads aligning to the junction. The canonical transcripts for the gene are shown above.

Supplementary Figure 4: validation of *INHBE-GLI1* fusion by Sanger sequencing

(A) Localization of primers used for Sanger validation of *INHBE-GLI1* fusion.
(B) Examples of *INHBE-GLI1* fusions identified by PCR. DNA amplifications were performed using different combinations of primers in *INHBE* and *GLI1* genes to amplify normal DNA (in green) and the corresponding tumors (in red)
(C) List of primers used for validation of *INHBE-GLI1* fusion by Sanger sequencing

Supplementary Figure 5: molecular intra-tumor heterogeneity

3 nodules with intratumor heterogeneity (2 samples per nodule) were represented.

Supplementary Figure 6: exposure to estrogens in multiples HCA

Distribution of the scoring of estrogen exposure in 23 patients with multiple HNF1A mutated HCA compared to 23 patients with multiple inflammatory HCA. The scoring of exposition to estrogens in women from 0 to 5 was defined as follow: no oral contraception (OC, 0 point), number of years of OC < median (1 point), number of years of OC > median (2 points), BMI < 25 (0 point), BMI between 25-30 (1 point), BMI>30 (2 points), alcohol intake < 30 g/day (0 point), alcohol intake \geq 30 g/day (1 point).

Supplementary Figure 7: risk of hemorrhage according to the size and the molecular classification

- A. Association between histological hemorrhage and tumor size as a continuous variable (Mann-Whitney Test)
- B. Association between histological hemorrhage and tumor size (Chi-squared test for trend)
- C. Association between histological hemorrhage and molecular subclasses (Chi-squared test). The size of the tumors of each molecular subclasses was represented in mean with standard deviation.
- D. Association between symptomatic bleeding and tumor size as a continuous variable (Mann-Whitney Test)
- E. Association between symptomatic bleeding and tumor size (Chi-squared test for trend)
- F. Association between symptomatic bleeding and molecular subclasses (Chi-squared test). The size of the tumors of each molecular subclasses was represented in mean with standard deviation.

1. Edmondson HA, Henderson B, Benton B. Liver-cell adenomas associated with use of oral contraceptives. *N Engl J Med* 1976;294:470-2.
2. Nault JC, Bioulac-Sage P, Zucman-Rossi J. Hepatocellular benign tumors-from molecular classification to personalized clinical care. *Gastroenterology* 2013;144:888-902.
3. Svrcek M, Jeannot E, Arrive L, et al. Regressive liver adenomatosis following androgenic progestin therapy withdrawal: a case report with a 10-year follow-up and a molecular analysis. *Eur J Endocrinol* 2007;156:617-21.
4. Buhler H, Pirovino M, Akobiantz A, et al. Regression of liver cell adenoma. A follow-up study of three consecutive patients after discontinuation of oral contraceptive use. *Gastroenterology* 1982;82:775-82.
5. Bioulac-Sage P, Laumonier H, Couchy G, et al. Hepatocellular adenoma management and phenotypic classification: the Bordeaux experience. *Hepatology* 2009;50:481-9.
6. Dokmak S, Paradis V, Vilgrain V, et al. A single-center surgical experience of 122 patients with single and multiple hepatocellular adenomas. *Gastroenterology* 2009;137:1698-705.
7. van Aalten SM, de Man RA, JN IJ, et al. Systematic review of haemorrhage and rupture of hepatocellular adenomas. *Br J Surg* 2012;99:911-6.
8. European Association for the Study of the Liver . Electronic address eee. EASL Clinical Practice Guidelines on the management of benign liver tumours. *J Hepatol* 2016;65:386-98.
9. Bioulac-Sage P, Rebouissou S, Sa Cunha A, et al. Clinical, morphologic, and molecular features defining so-called telangiectatic focal nodular hyperplasias of the liver. *Gastroenterology* 2005;128:1211-8.
10. **Bioulac-Sage P, Rebouissou S**, Thomas C, et al. Hepatocellular adenoma subtype classification using molecular markers and immunohistochemistry. *Hepatology* 2007;46:740-8.
11. Laumonier H, Bioulac-Sage P, Laurent C, et al. Hepatocellular adenomas: magnetic resonance imaging features as a function of molecular pathological classification. *Hepatology* 2008;48:808-18.
12. **Bluteau O, Jeannot E**, Bioulac-Sage P, et al. Bi-allelic inactivation of TCF1 in hepatic adenomas. *Nat Genet* 2002;32:312-5.
13. Flejou JF, Barge J, Menu Y, et al. Liver adenomatosis. An entity distinct from liver adenoma? *Gastroenterology* 1985;89:1132-8.
14. Bacq Y, Jacquemin E, Balabaud C, et al. Familial liver adenomatosis associated with hepatocyte nuclear factor 1alpha inactivation. *Gastroenterology* 2003;125:1470-5.
15. Reznik Y, Dao T, Coutant R, et al. Hepatocyte nuclear factor-1 alpha gene inactivation: cosegregation between liver adenomatosis and diabetes phenotypes in two maturity-onset diabetes of the young (MODY)3 families. *J Clin Endocrinol Metab* 2004;89:1476-80.
16. Pilati C, Zucman-Rossi J. Mutations leading to constitutive active gp130/JAK1/STAT3 pathway. *Cytokine Growth Factor Rev* 2015;26:499-506.
17. Rebouissou S, Amessou M, Couchy G, et al. Frequent in-frame somatic deletions activate gp130 in inflammatory hepatocellular tumours. *Nature* 2009;457:200-4.

18. Pilati C, Amessou M, Bihl MP, et al. Somatic mutations activating STAT3 in human inflammatory hepatocellular adenomas. *J Exp Med* 2011;208:1359-66.
19. Nault JC, Fabre M, Couchy G, et al. GNAS-activating mutations define a rare subgroup of inflammatory liver tumors characterized by STAT3 activation. *J Hepatol* 2012;56:184-91.
20. Pilati C, Letouze E, Nault JC, et al. Genomic Profiling of Hepatocellular Adenomas Reveals Recurrent FRK-Activating Mutations and the Mechanisms of Malignant Transformation. *Cancer Cell* 2014;25:428-41.
21. Zucman-Rossi J, Jeannot E, Nhieu JT, et al. Genotype-phenotype correlation in hepatocellular adenoma: new classification and relationship with HCC. *Hepatology* 2006;43:515-24.
22. Farges O, Ferreira N, Dokmak S, et al. Changing trends in malignant transformation of hepatocellular adenoma. *Gut* 2011;60:85-9.
23. van Aalten SM, Verheij J, Terkivatan T, et al. Validation of a liver adenoma classification system in a tertiary referral centre: implications for clinical practice. *J Hepatol* 2011;55:120-5.
24. **Rebouissou S, Franconi A**, Calderaro J, et al. Genotype-phenotype correlation of CTNNB1 mutations reveals different ss-catenin activity associated with liver tumor progression. *Hepatology* 2016.
25. Nault JC, Mallet M, Pilati C, et al. High frequency of telomerase reverse-transcriptase promoter somatic mutations in hepatocellular carcinoma and preneoplastic lesions. *Nat Commun* 2013;4:2218.
26. Smyth G. *Limma: Linear Models for Microarray Data*. Bioinformatics and Computational Biology Solutions Using R and Bioconductor 2005.
27. Benjamini Y, Y H. Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. *Journal of the Royal Statistical Society. Series B (Methodological)* 1995;Vol. 57, No. 1 (1995), pp. 289-300.
28. de Hoon MJ, Imoto S, Nolan J, et al. Open source clustering software. *Bioinformatics* 2004;20:1453-4.
29. Subramanian A, Tamayo P, Mootha VK, et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* 2005;102:15545-50.
30. **Boyault S, Rickman DS, de Reynies A**, et al. Transcriptome classification of HCC is related to gene alterations and to new therapeutic targets. *Hepatology* 2007;45:42-52.
31. **Schulze K, Imbeaud S, Letouze E**, et al. Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. *Nat Genet* 2015;47:505-11.
32. Kim D, Pertea G, Trapnell C, et al. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol* 2013;14:R36.
33. Anders S, Pyl PT, Huber W. HTSeq--a Python framework to work with high-throughput sequencing data. *Bioinformatics* 2015;31:166-9.
34. Robinson JT, Thorvaldsdottir H, Winckler W, et al. Integrative genomics viewer. *Nat Biotechnol* 2011;29:24-6.
35. Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 2009;25:1754-60.

36. DePristo MA, Banks E, Poplin R, et al. A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nat Genet* 2011;43:491-8.
37. Cibulskis K, Lawrence MS, Carter SL, et al. Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nat Biotechnol* 2013;31:213-9.
38. Chen X, Schulz-Trieglaff O, Shaw R, et al. Manta: rapid detection of structural variants and indels for germline and cancer sequencing applications. *Bioinformatics* 2016;32:1220-2.
39. Calderaro J, Nault JC, Balabaud C, et al. Inflammatory hepatocellular adenomas developed in the setting of chronic liver disease and cirrhosis. *Mod Pathol* 2016;29:43-50.
40. Calderaro J, Labrune P, Morcrette G, et al. Molecular characterization of hepatocellular adenomas developed in patients with glycogen storage disease type I. *J Hepatol* 2013;58:350-7.
41. Sempoux C, Paradis V, Komuta M, et al. Hepatocellular nodules expressing markers of hepatocellular adenomas in Budd-Chiari syndrome and other rare hepatic vascular disorders. *J Hepatol* 2015;63:1173-80.
42. Omenetti A, Choi S, Michelotti G, et al. Hedgehog signaling in the liver. *J Hepatol* 2011;54:366-73.
43. Amakye D, Jagani Z, Dorsch M. Unraveling the therapeutic potential of the Hedgehog pathway in cancer. *Nat Med* 2013;19:1410-22.
44. Spans L, Fletcher CD, Antonescu CR, et al. Recurrent MALAT1-GLI1 oncogenic fusion and GLI1 up-regulation define a subset of plexiform fibromyxoma. *J Pathol* 2016;239:335-43.
45. Dahlen A, Fletcher CD, Mertens F, et al. Activation of the GLI oncogene through fusion with the beta-actin gene (ACTB) in a group of distinctive pericytic neoplasms: pericytoma with t(7;12). *Am J Pathol* 2004;164:1645-53.
46. **Pelletier L, Rebouissou S**, Paris A, et al. Loss of hepatocyte nuclear factor 1alpha function in human hepatocellular adenomas leads to aberrant activation of signaling pathways involved in tumorigenesis. *Hepatology* 2010;51:557-66.
47. Li Z, Tuteja G, Schug J, et al. Foxa1 and Foxa2 are essential for sexual dimorphism in liver cancer. *Cell* 2012;148:72-83.
48. van Aalten SM, Witjes CD, de Man RA, et al. Can a decision-making model be justified in the management of hepatocellular adenoma? *Liver Int* 2012;32:28-37.
49. Poussin K, Pilati C, Couchy G, et al. Biochemical and functional analyses of gp130 mutants unveil JAK1 as a novel therapeutic target in human inflammatory hepatocellular adenoma. *Oncoimmunology* 2013;2:e27090.
50. Von Hoff DD, LoRusso PM, Rudin CM, et al. Inhibition of the hedgehog pathway in advanced basal-cell carcinoma. *N Engl J Med* 2009;361:1164-72.
51. Benvenuto M, Masuelli L, De Smaele E, et al. In vitro and in vivo inhibition of breast cancer cell growth by targeting the Hedgehog/GLI pathway with SMO (GDC-0449) or GLI (GANT-61) inhibitors. *Oncotarget* 2016;7:9250-70.

Shared authorship is indicated in bold

Figure 1

Figure 1

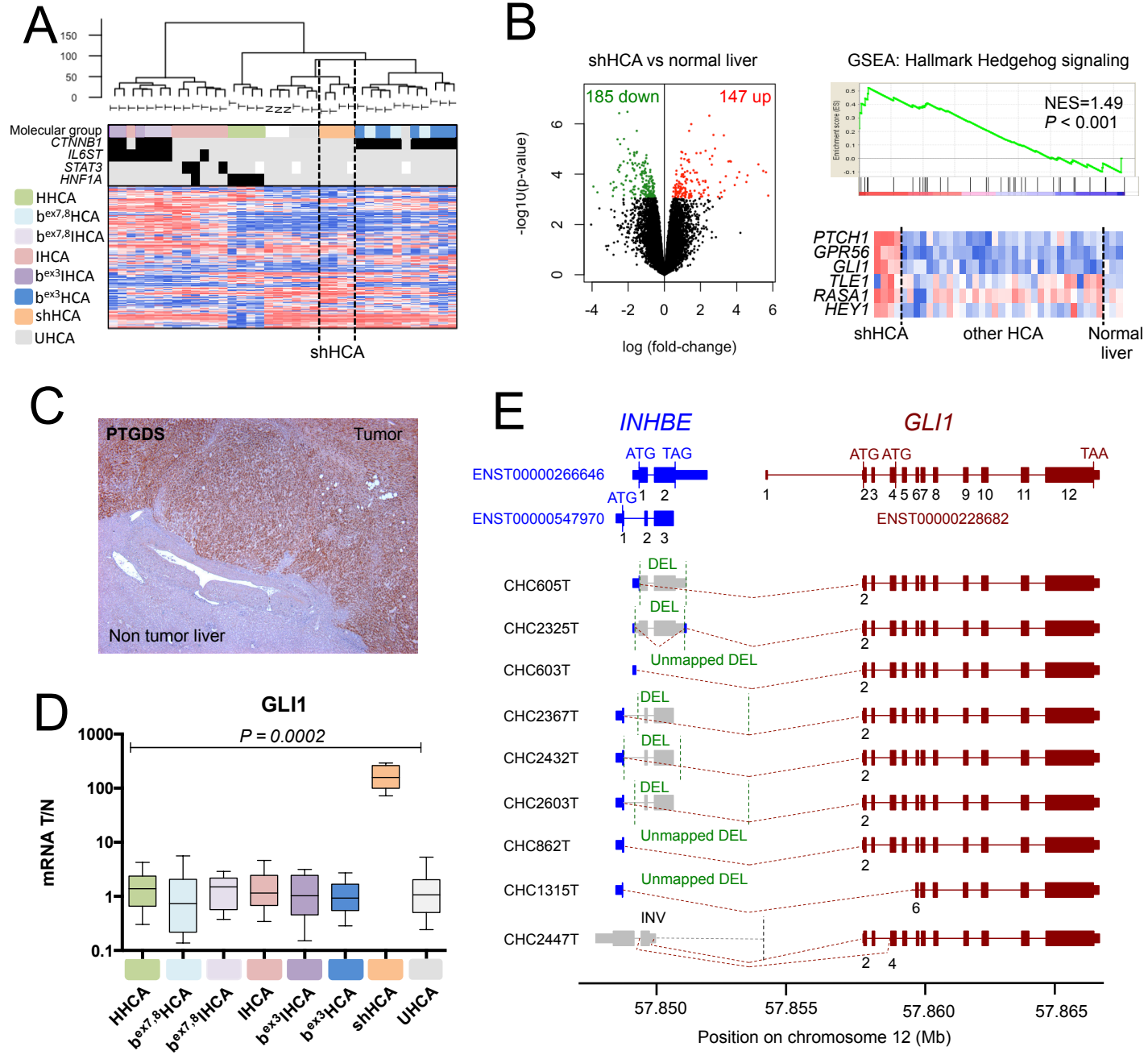
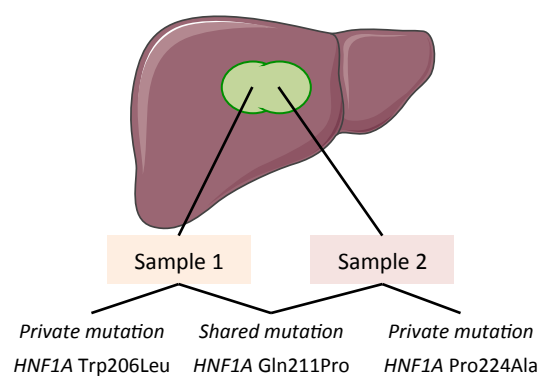
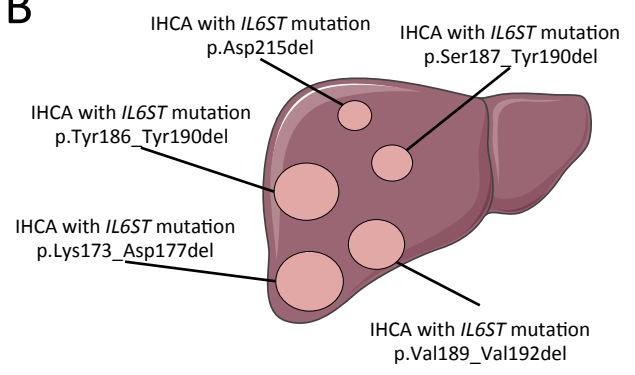


Figure 2

A



B



C

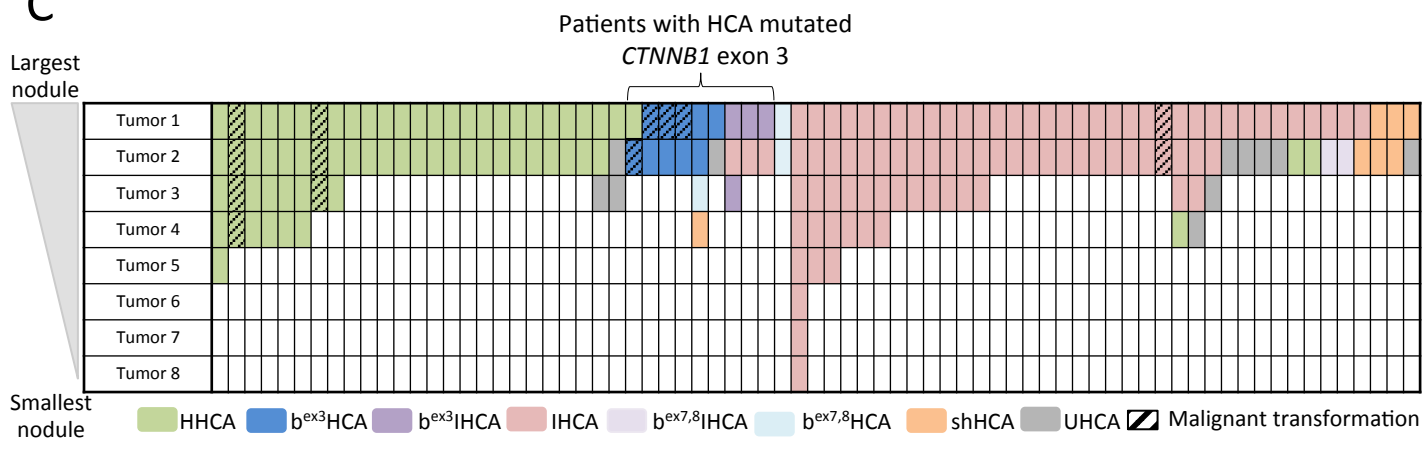


Figure 3

Figure 3

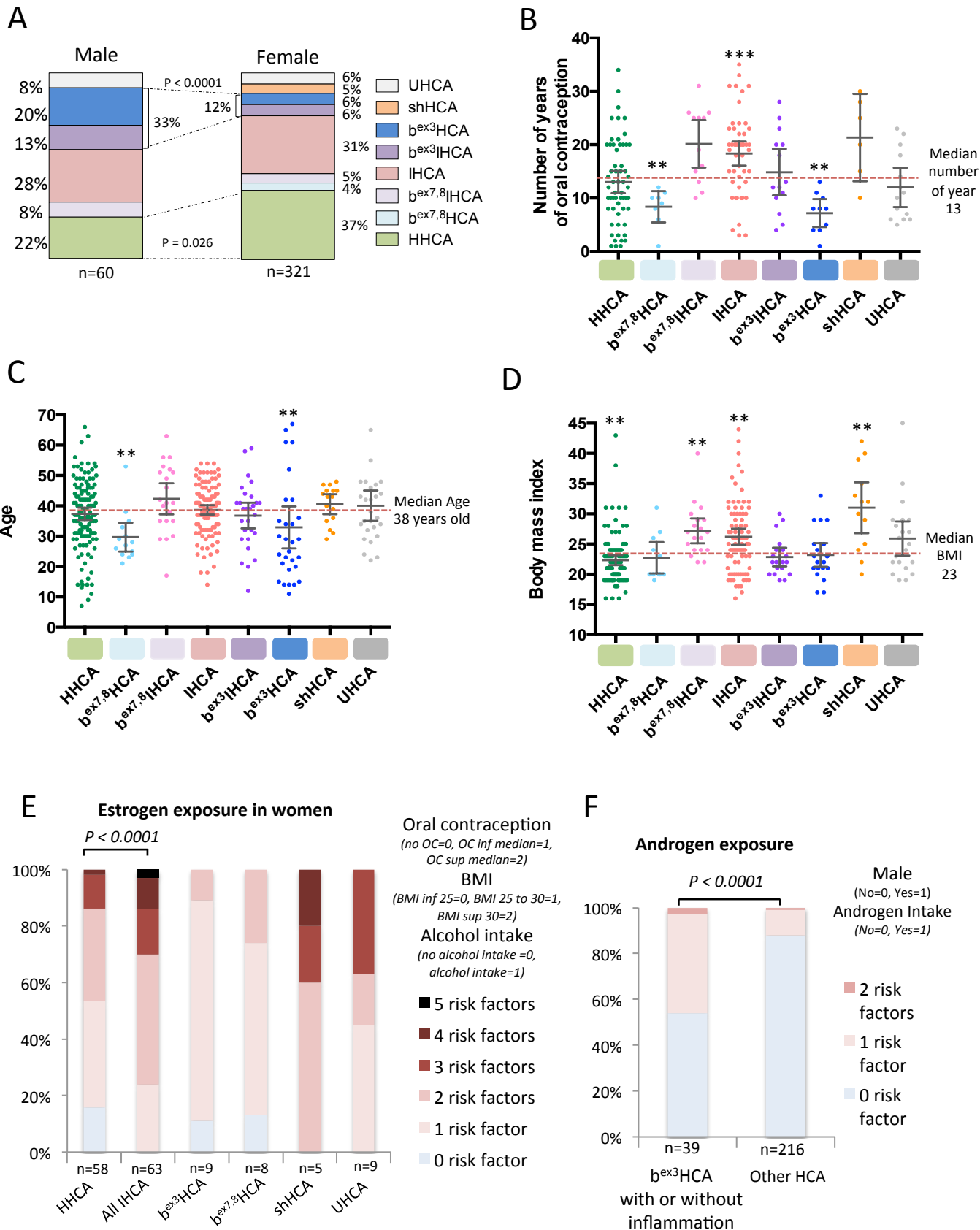


Figure 4

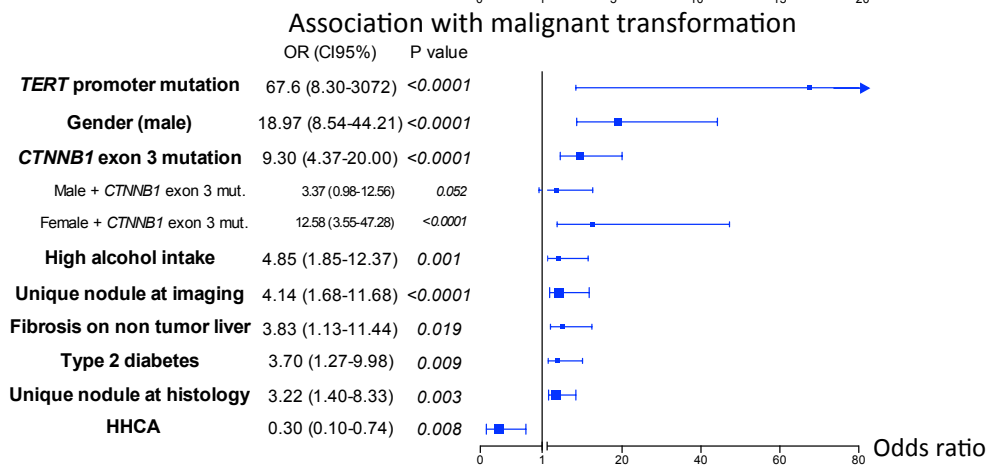
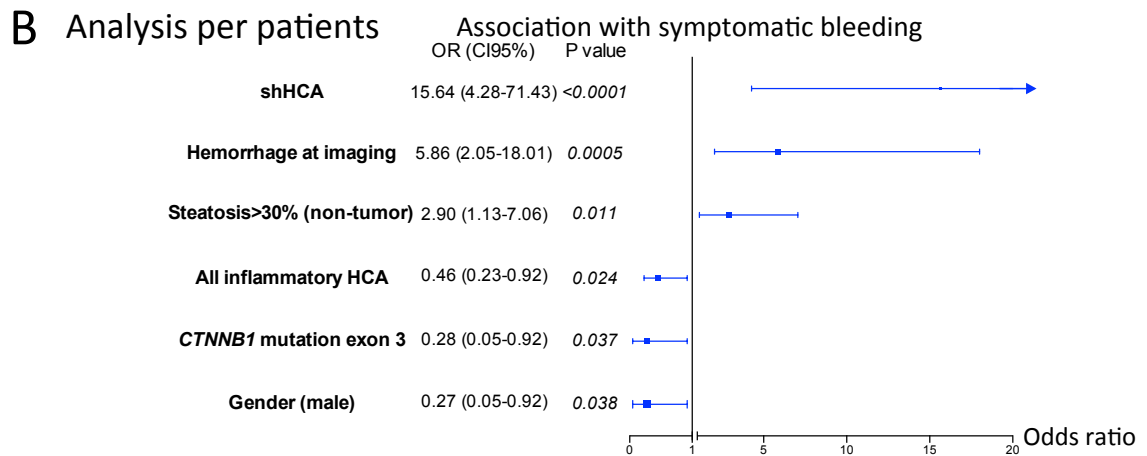
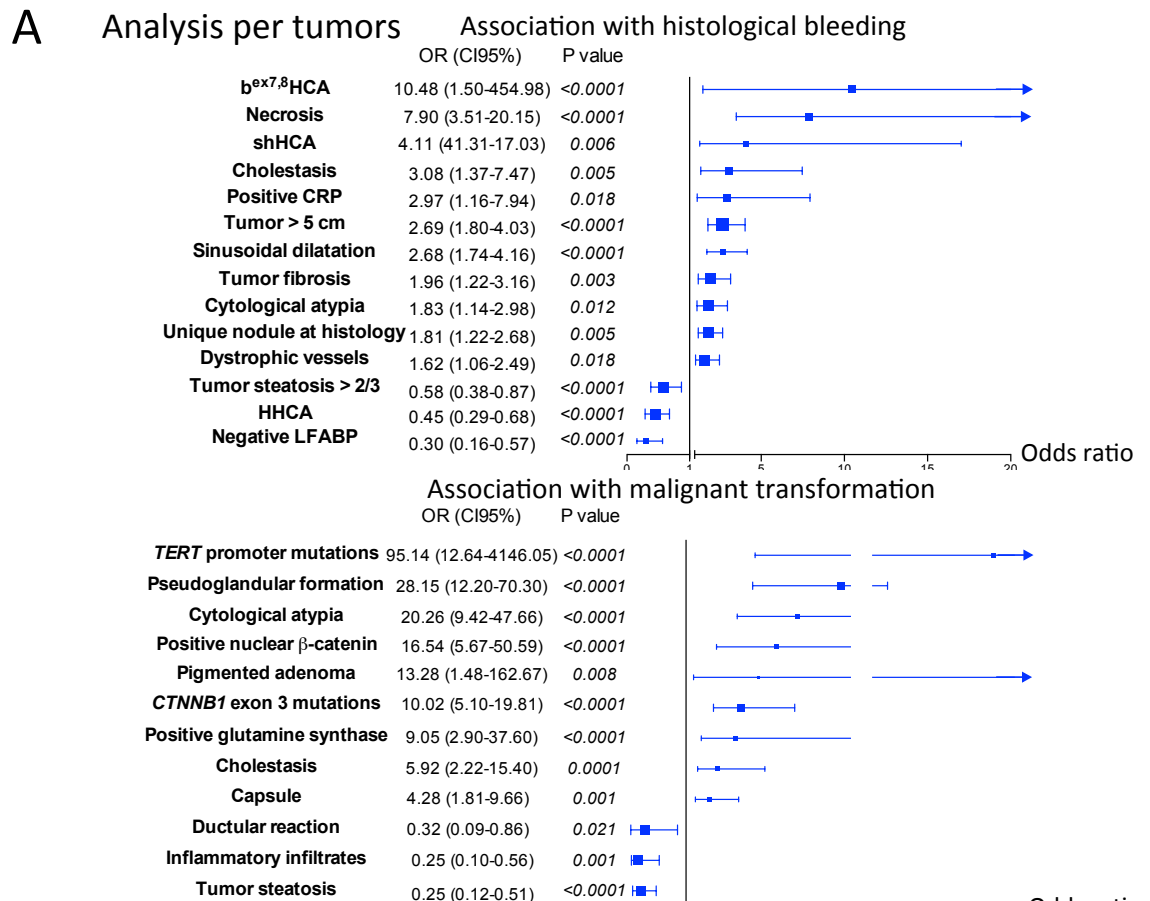
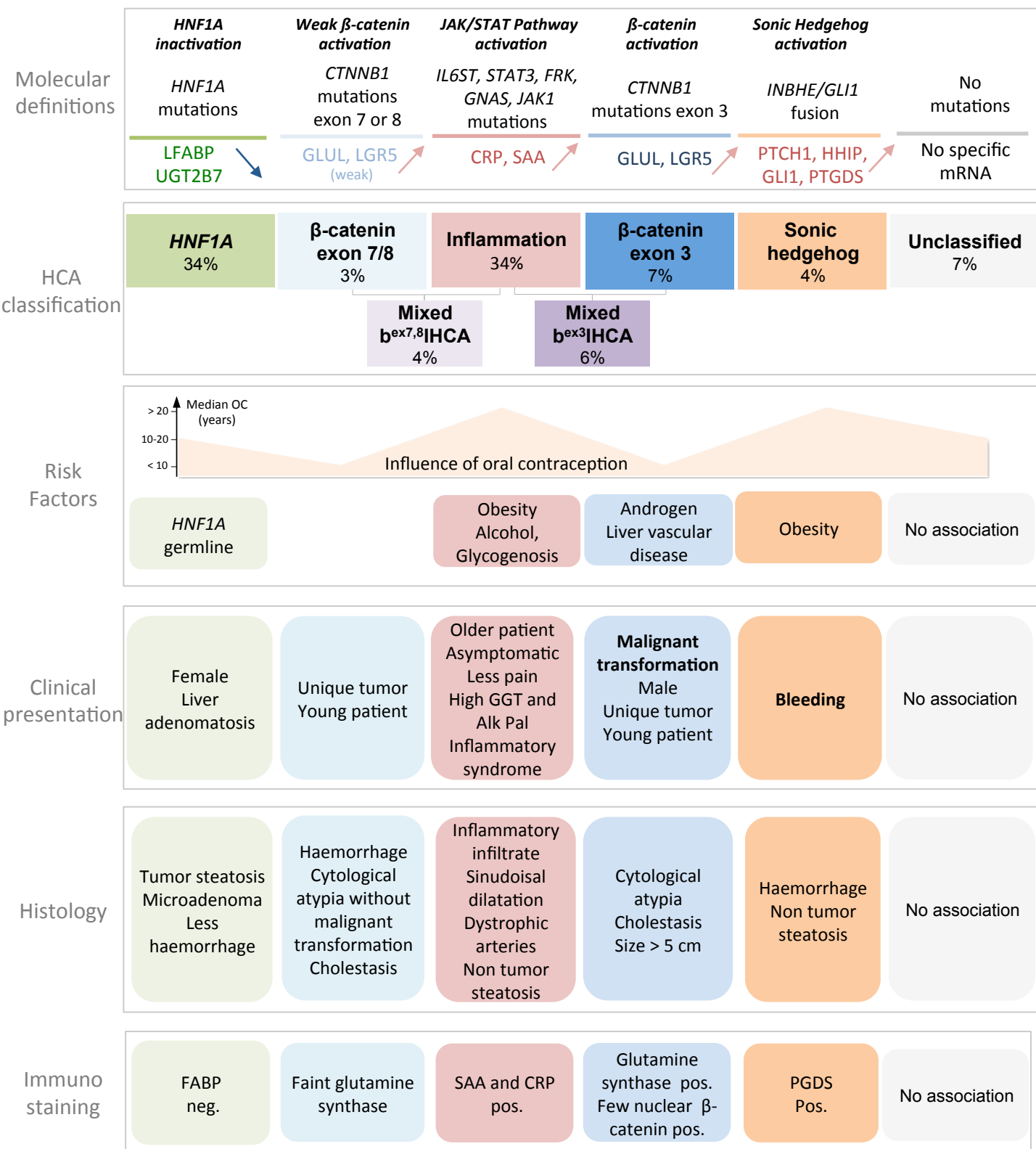
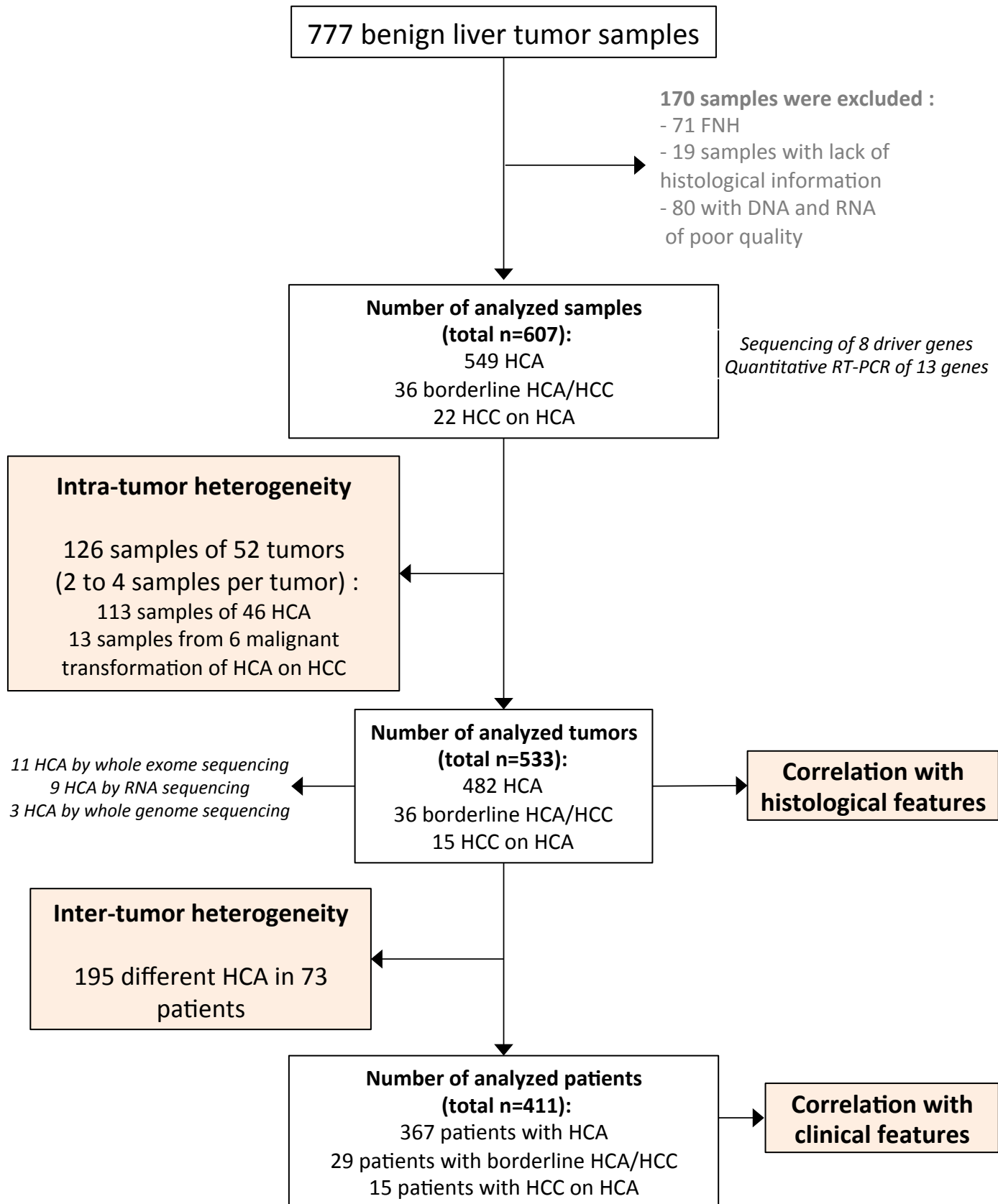


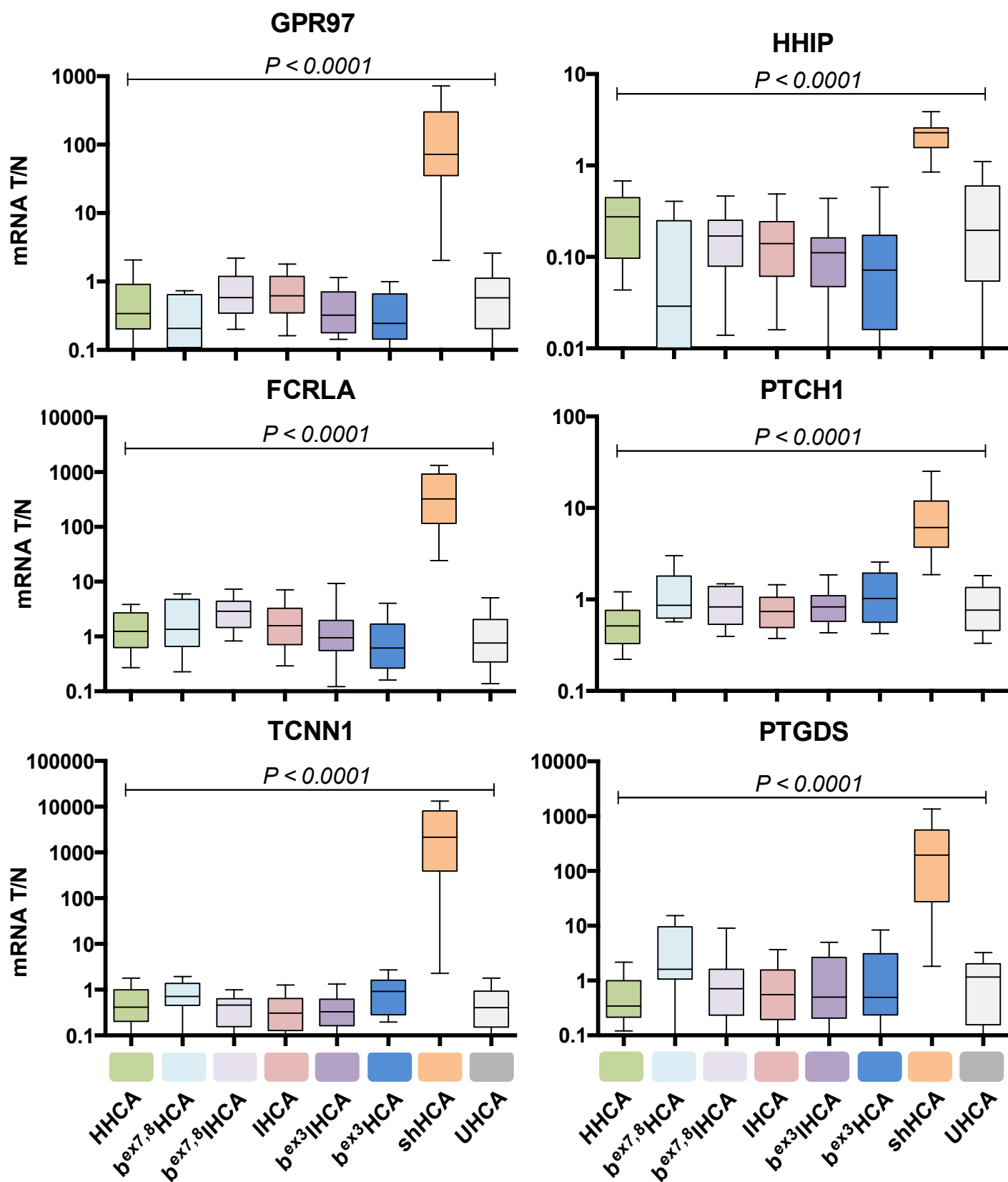
Figure 5



Supplementary Figure 1

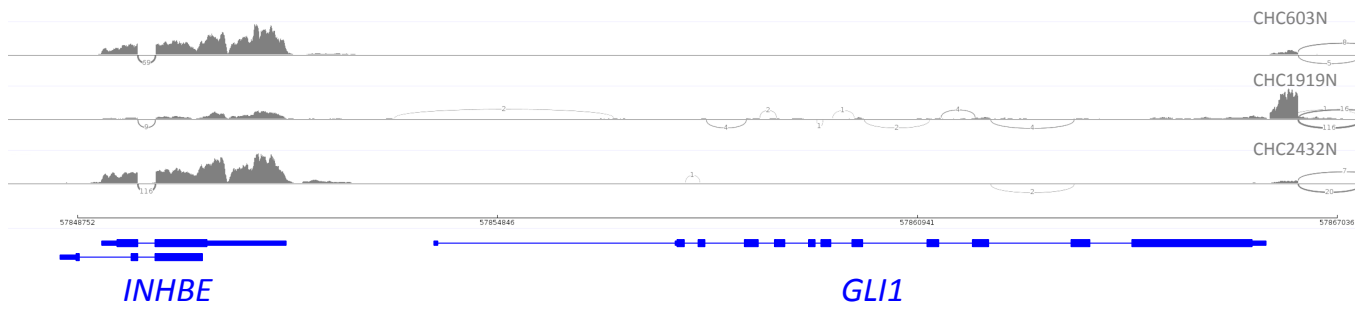


Supplementary figure 2

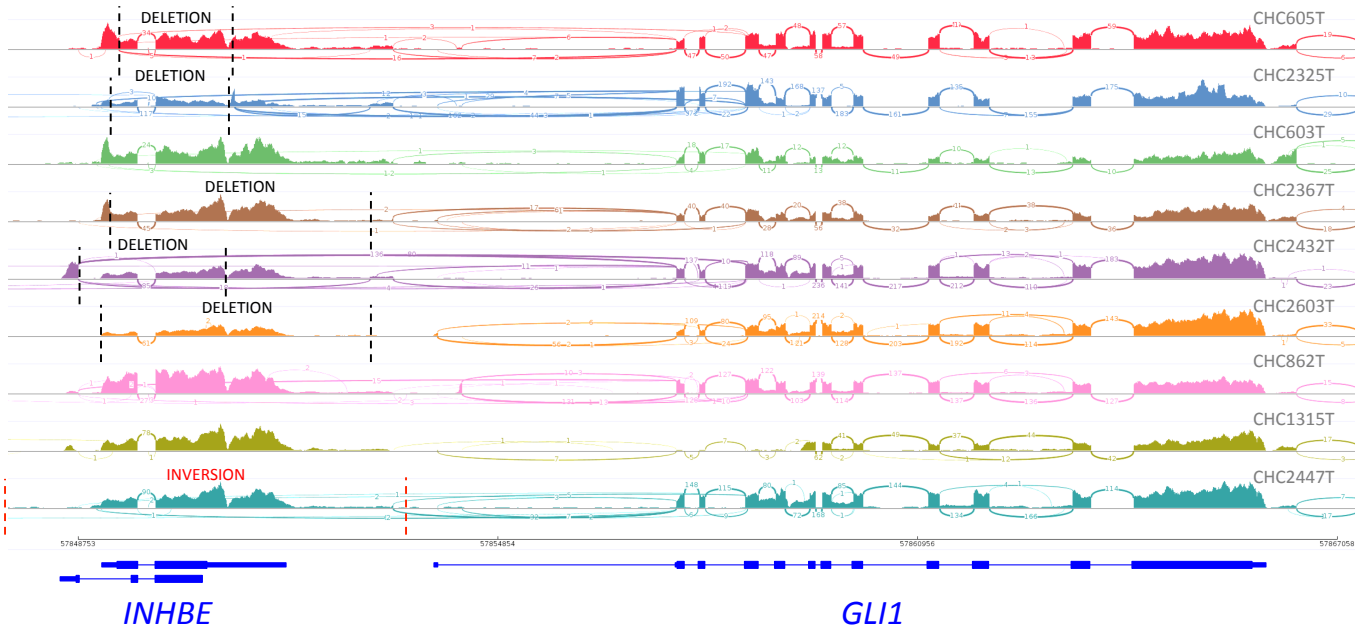




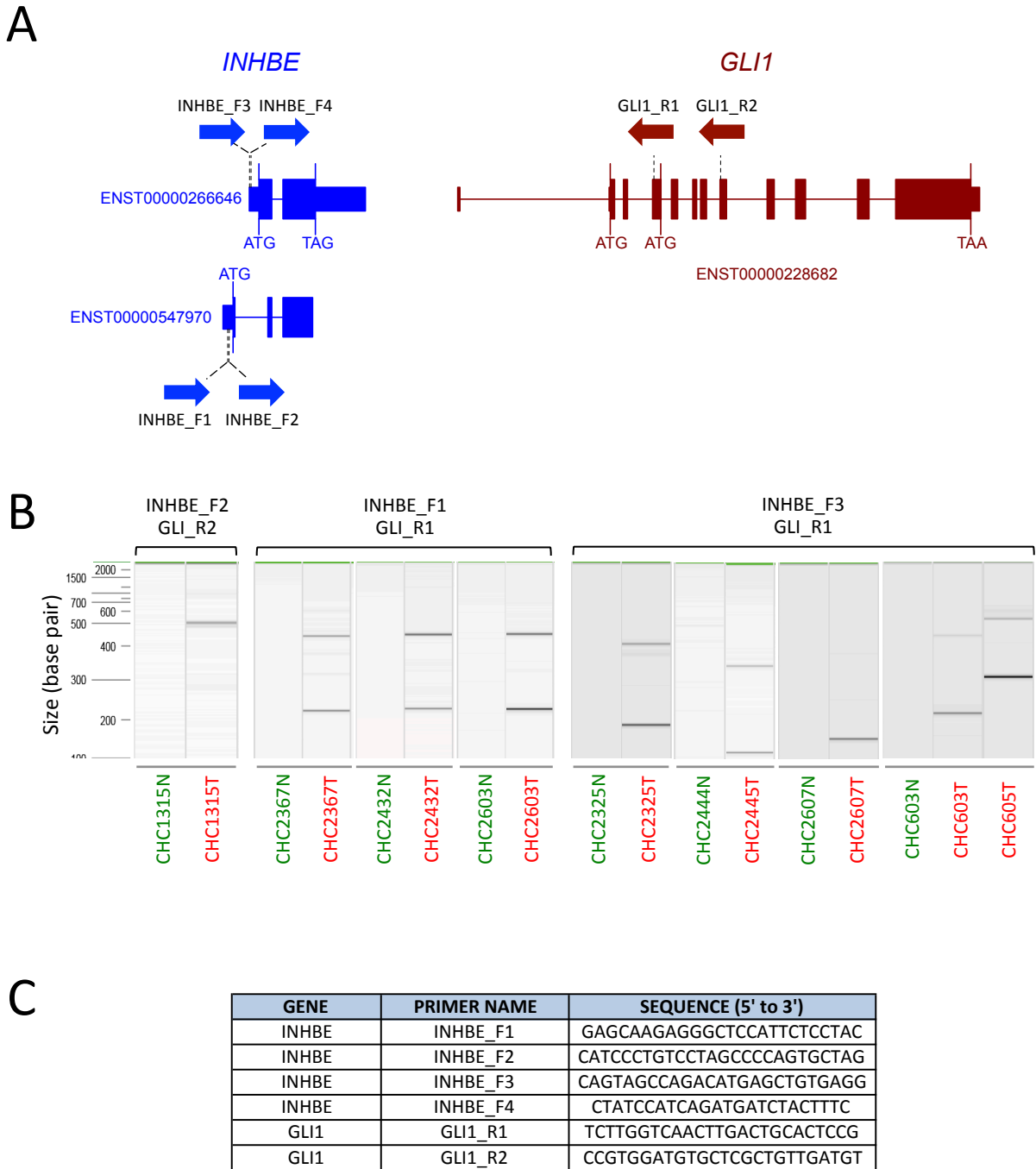
Non-Tumor shHCA



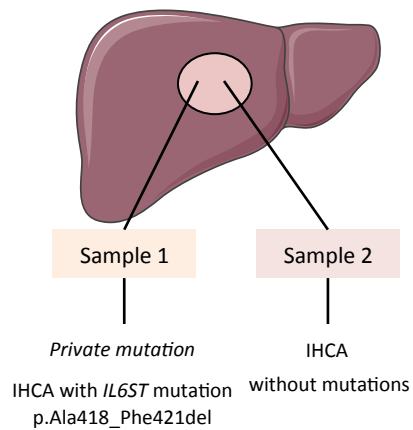
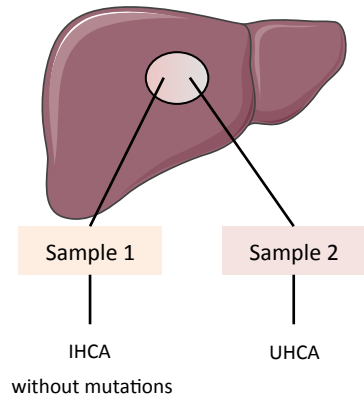
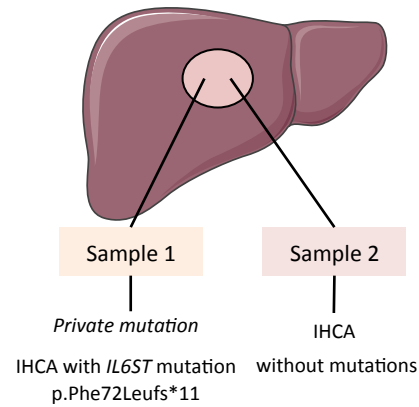
shHCA



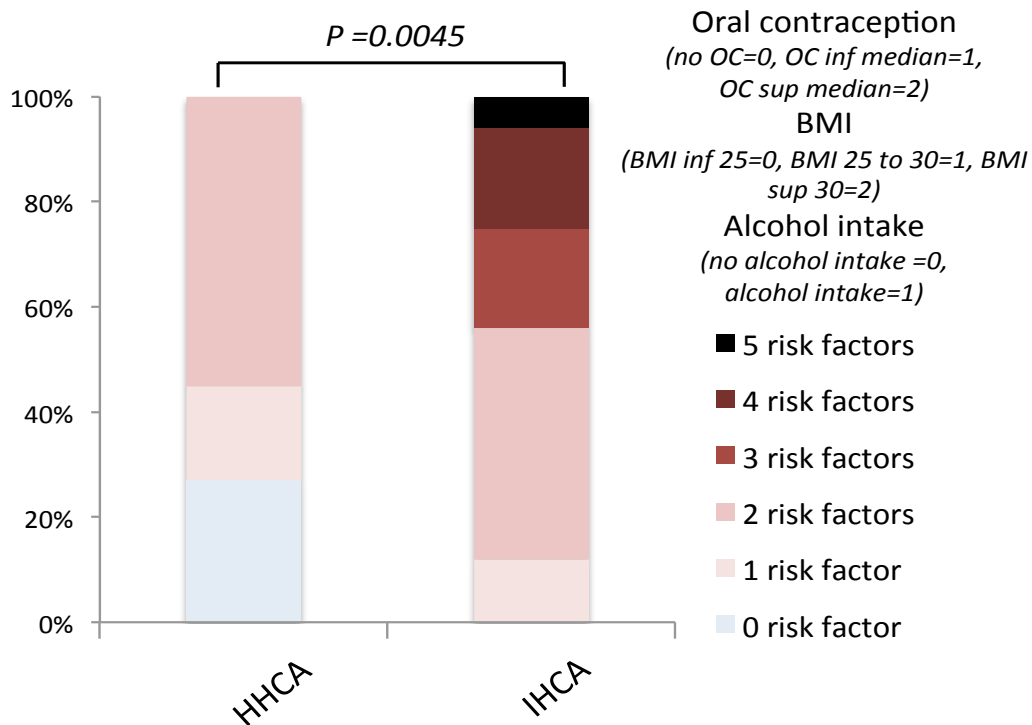
Supplementary Figure 4



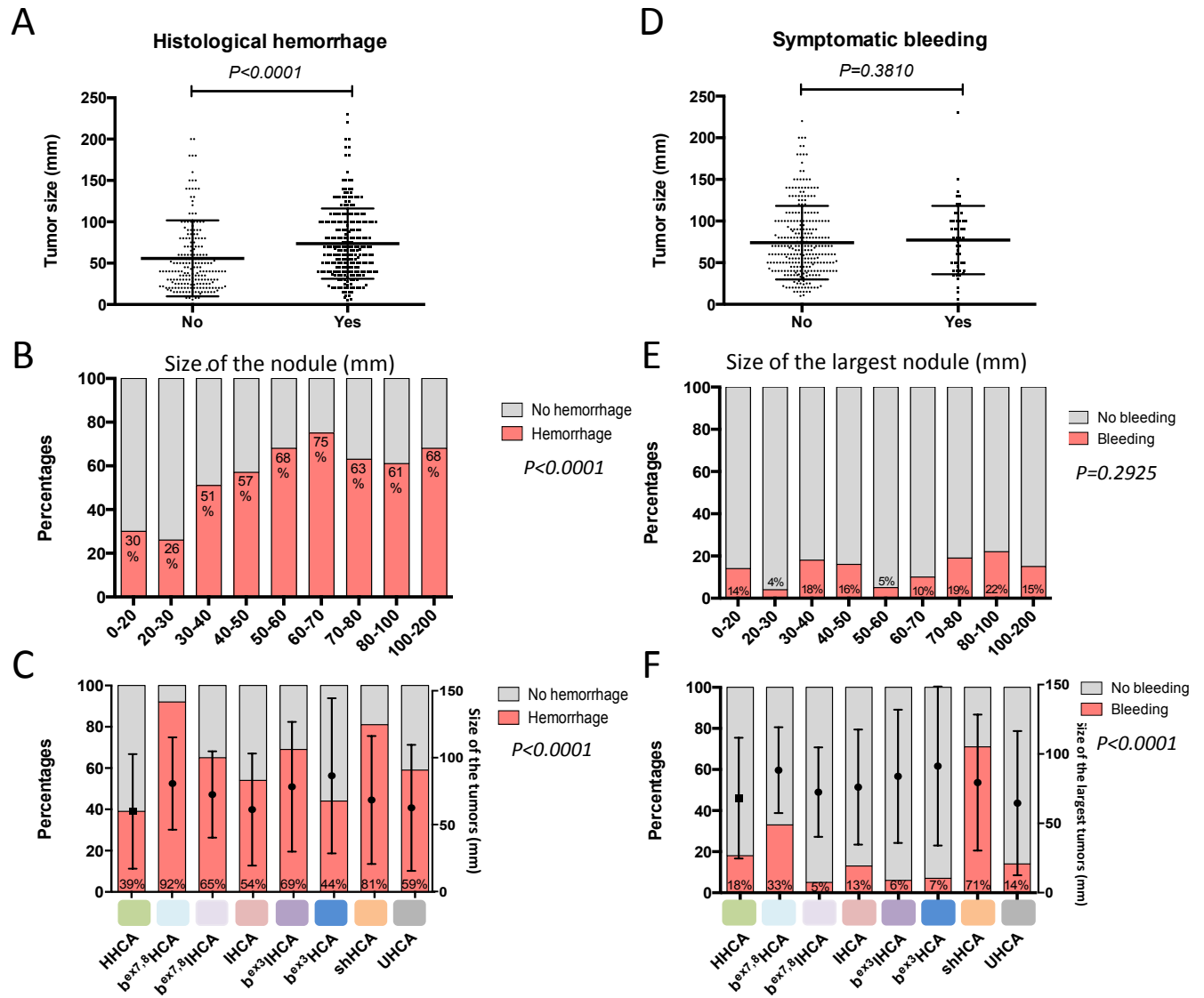
Supplementary Figure 5



Scoring of estrogen exposure in multiple HCA



Supplementary Figure 7



Supplementary Table 1: Description of the tumors

	Available data (n=533)	Number (%) Median (min-max)
PATHOLOGY		
HCA	533	482 (90%)
HCA/HCC	533	36 (7%)
HCC on HCA	533	15 (3%)
Size of the nodule	482	55 (5-290)
Size of the nodule≤5cm	482	237 (49%)
Size of the nodule>5cm	482	245 (51%)
Well limited nodule	433	311 (72%)
Encapsulated	419	43 (10%)
Hemorrhage	462	241 (52%)
Sinusoidal dilatation	455	292 (64%)
No tumor steatosis no	462	181 (39%)
Tumor steatosis < 1/3	462	100 (22%)
Tumor steatosis 1/3-2/3	462	81 (17%)
Tumor steatosis>2/3	462	100 (22%)
Dystrophic arteries	449	158 (35%)
Inflammatory infiltrate	438	227 (52%)
Ductular reaction	417	136 (32%)
Cytological atypia	478	110 (23%)
Pseudoglandular formation	389	65 (17%)
Cholestasis	282	39 (14%)
MOLECULAR CLASSIFICATION		
HHCA	533	179 (33.5%)
b ^{ex7,8} HCA	533	17 (3%)
b ^{ex7,8} IHCA	533	21 (4%)
IHCA	533	183 (34%)
b ^{ex3} IHCA	533	34 (6%)
b ^{ex3} HCA	533	37 (7%)
shHCA	533	22 (4%)
UHCA	533	40 (7.5%)
GENE MUTATIONS		
<i>HNF1A</i> mutations	509	178 (35%)
<i>CTNNB1</i> mutations exon 3	526	64 (12%)
<i>CTNNB1</i> mutations exon 7	521	27 (5%)
<i>CTNNB1</i> mutations exon 8	513	11 (2%)
<i>IL6ST</i> mutations	520	140 (27%)
<i>FRK</i> mutations	509	17 (3%)
<i>STAT3</i> mutations	502	8 (1.6%)
<i>JAK1</i> mutations	499	2 (0.4%)
<i>GNAS</i> mutations	510	6 (1%)
<i>TERT</i> promoter mutations	493	10 (2%)

Supplementary Table 2: Description of the patients

	Available Data n=411	Number (%) Median (min-max)	
RISK FACTORS			
Gender (female)	402	341 (85%)	
Age	402	38 (7-82)	
Children (yes) (female only)	215	152 (71%)	
Number of children (female only)	215	2 (0-9)	
Oral contraception (female only)	270	235 (87%)	
Age at first use of OC (female only)	141	18 (14-50)	
Number of years of OC (female only)	182	13 (1-35)	
Androgen	270	6 (2%)	
BMI (kg/m ²)	309	23 (14-47)	
Obesity (BMI≥30)	309	50 (16%)	
Diabetes	293	30 (10%)	
Glycogenesis	277	18 (6%)	
Liver vascular disease	276	10 (4%)	
Alcohol	264	34 (13%)	
CLINICAL PRESENTATION			
Presence of HCC on HCA	411	15 (4%)	
Presence of borderline HCC/HCA	411	29 (7%)	
Symptomatic bleeding	349	49 (14%)	
Pain	349	128 (37%)	
Discovery by chance	349	122 (35%)	
Abnormal liver function test	349	50 (14%)	
Discovery during follow up angioma/FNH	349	13 (4%)	
Inflammatory syndrome	349	18 (5%)	
Symptomatic disease	349	168 (48%)	
BIOLOGICAL DATA			
Raised Gammaglutamyl transferase	289	159 (55%)	
Raised Alkaline phosphatase	190	67 (35%)	
Raised C-reactive protein	163	92 (56%)	
HISTOLOGY			
Number of HCA	1	389	214 (55%)
	2 to 5	389	85 (22%)
	5 to 10	389	43 (11%)
	≥10	389	47 (12%)
Size of the largest HCA (mm)	379	65 (8-290)	
Size of the largest HCA >5cm	379	234 (62%)	
Steatosis on non tumor liver > 1/3	376	42 (11%)	
Fibrosis on non tumor liver (F2-F4)	373	24 (7%)	
Focal nodular hyperplasia	364	35 (10%)	
Angioma	359	10 (3%)	
Microadenoma	363	65 (18%)	
IMAGING DATA			
Number of HCA	1	334	163 (49%)
	2 to 5	334	67 (20%)
	5 to 10	334	39 (12%)
	≥10	334	65 (19%)
Size of the largest HCA > 5 cm	320	205 (64%)	
Focal nodular hyperplasia	193	34 (18%)	
Angioma	195	27 (14%)	
MOLECULAR CLASSIFICATION			
Germline <i>HNFI1A</i> mutation	375	11 (3%)	
HHCA	411	133 (32%)	
b ^{ex7,8} HCA	411	15 (4%)	
b ^{ex7,8} IHCA	411	21 (5%)	
IHCA	411	116 (28%)	
b ^{ex3} IHCA	411	30 (7%)	
b ^{ex3} HCA	411	30 (7%)	
shHCA	411	16 (4%)	
UHCA	411	28 (7%)	
Discordant molecular subgroups	411	22 (5%)	

Supplementary Table 3: Taqman probes used for quantitative RT-PCR

Gene	Taqman probe
<i>18S</i>	Hs03928990_g1
<i>FABP1</i>	Hs00155026_m1
<i>UGT2B7</i>	Hs00426592_m1
<i>CRP</i>	Hs04183452_g1
<i>SAA2</i>	Hs00754237_s1
<i>GLUL</i>	Hs00374213_m1
<i>LGR5</i>	Hs00173664_m1
<i>PTCH1</i>	Hs00181117_m1
<i>GLI1</i>	Hs00171790_m1
<i>HHIP</i>	Hs01011015_m1
<i>TNNC1</i>	Hs00896999_g1
<i>FCRLA</i>	Hs00262071_m1
<i>PTGDS</i>	Hs00168748_m1
<i>GPR97</i>	Hs00416887_m1

Supplementary Table 4: lists of samples analyzed by next generation sequencing and mapping of INHBE-GLI1 fusion

Sample	WES List	WGS List	RNAseq	Fusion_INHB E.RNA	Fusion_GLI1. RNA	SV_start. WES	SV_end. WES	SV_start. WGS	SV_end.WGS
CHC1315T	WXS.EGAS00 001000679	no WGS	PJ1306111	57848726	57859251				
CHC1854T	WXS.EGAS00 001000679	no WGS	no RNA seq	no RNA seq	no RNA seq				
CHC2325T	WXS.UNSUB MITTEDBAM	no WGS	PJ1212200	57851034	57857448	57849171	57850971		
CHC2367T	WXS.UNSUB MITTEDBAM	no WGS	PJ1312222	57848761	57857448	57849278	57853310		
CHC2432T	WXS.UNSUB MITTEDBAM	PJ1311194	PJ1312222	57848761	57857448	57848774	57850823	57848774	57850823
CHC2446T=C HC2247T	WXS.UNSUB MITTEDBAM	PJ1311194	PJ1312222	57849384	57858456			57845166	57853835
CHC2603T	WXS.UNSUB MITTEDBAM	no WGS	PJ1312222	57848761	57857448	57849163	57853308		
CHC603T	WXS.EGAS00 001000679	no WGS	PJ1306111	57849202	57857448				
CHC605T	WXS.EGAS00 001000679	PJ1311194	PJ1212200	57849348	57857448	57849348	57851031	57849348	57851031
CHC862T	WXS.UNSUB MITTEDBAM	no WGS	PJ1212200	57848761	57857448				
CHC949T	WXS.UNSUB MITTEDBAM	no WGS	no RNA seq	no RNA seq	no RNA seq	57849322	57853940		

Supplementary Table 5: Associated syndromic diseases

Associated Syndromic Diseases	CHC ID	Numbers of patients	Age	Gender	Molecular subtypes (number of nodules)
Rendu Osler disease	464T	1	53	F	HHCA (1)
Polycystic ovary syndrome	1246T	1	32	F	IHCA (1)
Trisomy 21	698T	1	31	F	IHCA (1)
Cavernoma due to neonatal portal thrombosis	1311T, 700T, 1876T, 1026T, 1117T	5	36, 30, 14, 15, 19	F, M, M, M, M	HHCA (4), b ^{ex3} HCA (4)
Fallot Tetratology	2774T	1	27	M	HHCA (4)
McCune Albright	1001T,1461T	2	31, 39	F, F	IHCA (2)
Congenital hepatic fibrosis	575T, 1256T	2	34, 54	F, F	HHCA (5)
Congenital portosystemic shunt	2219T, 2218T	2	14, 11	F, M	IHCA (1), b ^{ex3} HCA (1)
Familial adenomatous polyposis	591T	1	37	F	HHCA (1)
Alagille syndrome	1223T	1	11	F	HHCA (1)
Biliary atresia	1879T	1	7	F	HHCA (1)
Hepatorenal polycystic disease	358T	1	45	F	HHCA (1)
Turcot syndrome	2704T	1	37	M	HHCA (1)
Hereditary spastic paraplegia	2365T	1	26	F	shHCA (1)
Enchodromatosis	2436T	1	29	F	HHCA (1)
Primitive hyperoxaluria	540T	1	32	F	HHCA (1)

Supplementary Table 11: mutational analysis of multiples samples from HCC developed on HCA

	HCA sample	HCC sample #1	HCC sample #2
CHC361	<i>CTNNB1</i> exon 3 (p.Thr3_Ala126del)	<i>CTNNB1</i> exon 3 (p.Thr3_Ala126del) <i>TERT</i> prom (-124G>A)	<i>CTNNB1</i> exon 3 (p.Thr3_Ala126del) <i>TERT</i> prom (-124G>A)
CHC469	<i>CTNNB1</i> exon 3 (p.Gly34Arg) <i>IL6ST</i> (p.Tyr186_Tyr190del)	<i>CTNNB1</i> exon 3 (p.Gly34Arg) <i>IL6ST</i> (p.Tyr186_Tyr190del) <i>TERT</i> prom (-124G>A)	NA
CHC917	<i>CTNNB1</i> exon 3 (p.Ser33Tyr) <i>TERT</i> prom (-124G>A)	<i>CTNNB1</i> exon 3 (p.Ser45Phe) <i>TERT</i> prom (-124G>A)	NA
CHC464	<i>HNF1A</i> (p.Gln250_Gly255del; p.Ile27_Leu30del)	<i>HNF1A</i> (p.Gln250_Gly255del; p.Ile27_Leu30del)	NA
CHC1915	<i>CTNNB1</i> exon 3 (p.Leu31_Ile35del) <i>IL6ST</i> (p.Ser187_Tyr190del)	<i>CTNNB1</i> exon 3 (p.Leu31_Ile35del) <i>IL6ST</i> (p.Ser187_Tyr190del)	NA
CHC2581	Non mutated	<i>STAT3</i> (pTyr640Phe)	NA

Supplementary Table 12: CTNNB1 exon 3 mutations in multiple HCA

	Nodule 1 (molecular subgroup)	Nodule 1 (Size mm)	Nodule 2 (molecular subgroup)	Nodule 2 (Size mm)	Nodule 3 (molecular subgroup)	Nodule 3 (Size mm)	Nodule 4 (molecular subgroup)	Nodule 4 (Size mm)
Patient 1	HHCA	80	b ^{ex3} HCA	20				
Patient 2	b ^{ex3} HCA	180	b ^{ex3} HCA	140				
Patient 3	b ^{ex3} HCA	125	b ^{ex3} HCA	100				
Patient 4	b ^{ex3} HCA	60	b ^{ex3} HCA	35				
Patient 5	b ^{ex3} HCA	40	b ^{ex3} HCA	30	b ^{ex7,8} HCA	27	shHCA	25
Patient 6	b ^{ex3} HCA	40	UHCA	30				
Patient 7	b ^{ex3} IHCA	100	IHCA	30	b ^{ex3} IHCA	15		
Patient 8	b ^{ex3} IHCA	20	IHCA	15				
Patient 9	b ^{ex3} IHCA	37	IHCA	25				

Supplementary Table 13: HCA features according to gender

	Male (n=61)	Female (n=341)	P value corrigée
CLINICAL DATA			
Age	38 (9-82)	38 (7-76)	0.9
Androgen therapy	3 (7.3%)	3 (1.3%)	0.046
BMI (kg/m ²)	23.72 (13.72-40.40)	23.42 (15.54-46.88)	0.09
Obesity (BMI>=30)	10 (23.81%)	40 (15.09%)	0.049
Diabetes	11 (26%)	19 (7.63%)	<0.0001
Glycogenesis	8 (16%)	7 (3.15%)	0.002
Liver vascular disease	8 (16.33%)	2 (0.9%)	<0.0001
Alcohol (yes)	18 (41.86%)	16 (7.27%)	<0.0001
CLINICAL PRESENTATION			
Presence of HCC on HCA	8 (13.11%)	7 (2.05%)	<0.0001
Presence of borderline HCC/HCA	20 (32.79%)	8 (2.35%)	<0.0001
Symptomatic bleeding	2 (3.85%)	47 (15.93%)	0.034
Pain	14 (26.92%)	113 (38.31%)	0.121
Discovery by chance	26 (50%)	94 (31.86%)	0.01
Abnormal liver function test	8 (15.69%)	42 (14.24%)	0.825
Discovery during follow up angioma/FNH	2 (3.85%)	11 (3.73%)	1
Inflammatory syndrom	3 (6.67%)	15 (6.52%)	1
Symptomatic disease	17 (32.69%)	150 (50.85%)	0.025
BIOLOGICAL DATA			
Raised GGT	22 (52.38%)	136 (55.51%)	0.745
Raised AP	7 (25%)	59 (37.11%)	0.307
Raised CRP	11 (52.38%)	80 (57.14%)	0.812
HISTOLOGY			
Number of HCA	1	38 (64.41%)	0.002
	2 to 5	5 (8.47%)	
	5 to 10	2 (3.39%)	
	>=10	14 (23.73%)	
Size of the largest nodule(mm)	70 (15-200)	65 (6-290)	0.95
size of the largest nodule >5cm	33 (58.93%)	200 (62.11%)	
Steatosis on non tumor liver>1/3	8 (13.56%)	34 (10.76%)	0.641
Fibrosis on non-tumor liver	F0-F1	46 (79.31%)	<0.0001
	F2	9 (15.52%)	
	F3	2 (3.45%)	
	F4	1 (1.72%)	
FNH	3 (5.36%)	32 (10.42%)	0.33
Angioma	1 (1.79%)	9 (2.97%)	0.712
Microadenoma	8 (16.64%)	57 (18.69%)	0.457
IMAGING DATA			
Number of HCA	1	32 (67%)	0.028
	2 to 5	7 (15%)	
	5 to 10	1 (2%)	
	>=10	8 (17%)	
Size of HCA > 5 cm	24 (53.3%)	180 (65.93%)	
FNH	1 (4%)	33 (19.76%)	0.092
Angioma	1 (4%)	26 (15.38%)	0.206
MOLECULAR CLASSIFICATION			
Germline <i>HNF1A</i> mutation	3 (5%)	8 (3%)	0.217
HHCA	13 (21.7%)	119 (36.8%)	0.032
b ^{ex7,8} HCA	0 (0%)	14 (4.4%)	0.137
b ^{ex7,8} IHCA	5 (8.3%)	16 (5%)	0.344
IHCA	17 (28.3%)	98 (30.5%)	0.766
b ^{ex3} IHCA	8 (13.3%)	19 (5.9%)	0.052
b ^{ex3} HCA	12 (20%)	18 (5.6%)	0.003
shHCA	0 (0%)	16 (5%)	0.077
UHCA	5 (8.3%)	22 (6.9%)	0.785

Statistical tests were Mann Whitney Test or Chi squared test corrected using Monte Carlo resampling. *Patients with multiples tumors with discordant molecular features were excluded from the statistical analysis of molecular subgroups (n=22).

Supplementary Table 14: description of patients with liver adenomatosis

	Adenomatosis (n=47)	Others (n=342)	P value	
RISK FACTORS				
Gender (female)	33 (70,2%)	297 (86,8%)	0.008	
Age	35 (9-66)	38 (7-82)	0.12	
Children (yes) (female only)	14 (70%)	134 (70.5%)	1	
Number of children (female only)	1 (0-4)	2 (0-9)	0.6	
Oral contraception (female only)	18 (72%)	210 (88.2%)	0.029	
Number of years of OC (female only)	18 (1-31)	13 (1-35)	0.44	
Androgen therapy	2 (6.66%)	3 (0.01%)	0.0985	
BMI (kg/m2)	23.88 (14-38)	23.40 (16-47)	0.58	
Obesity (BMI>=30)	6 (16.2%)	43 (16.3%)	1	
Diabetes	4 (12.9%)	26 (10.2%)	0.757	
Glycogenesis	5 (16.1%)	8 (3.4%)	0.005	
Liver vascular disease	3 (9.7%)	7 (3%)	0.107	
Alcohol intake	2 (7.1%)	32 (13.7%)	0.405	
CLINICAL PRESENTATION				
Presence of HCC on HCA	2 (4.2%)	13 (3.8%)	1	
Presence of borderline HCC/HCA	3 (6.3%)	25 (7.3%)	1	
Symptomatic bleeding	5 (13.2%)	43 (14.1%)	1	
Pain	12 (31.6%)	114 (37.5%)	0.601	
Discovery by chance	15 (39.5%)	103 (33.9%)	0.571	
Abnormal liver function test	6 (15.8%)	43 (14.2%)	0.808	
Discovery during follow up angioma/FNH	1 (2.6%)	12 (3.9%)	1	
Inflammatory syndrome	1 (3%)	16 (6.8%)	0.504	
Symptomatic disease	16 (42.1%)	149 (49%)	0.495	
Liver resection	36 (76%)	324 (95%)	<0.0001	
Liver transplantation	8 (17%)	2 (0.05%)	<0.0001	
BIOLOGICAL DATA				
Raised GGT	17 (54.8%)	139 (55.2%)	1	
Raised AP	7 (33.3%)	58 (35.6%)	1	
Raised CRP	9 (52.9%)	80 (56.3%)	0.793	
HISTOLOGY				
Number of HCA	1	0 (0%)	214 (62.6%)	<0.0001
	2 to 5	0 (0%)	85 (24.9%)	
	5 to 10	0 (0%)	43 (12.6%)	
	>=10	47 (100%)	0 (0%)	
Size of the largest nodule (mm)	70 (20-220)	65 (6-290)	0.64	
Size of the largest nodule >5cm	27 (60%)	205 (62.1%)	1	
Steatosis on non tumor liver > 1/3	7 (15.2%)	35 (10.8%)	1	
Fibrosis of non tumor liver	F0-F1	40 (87%)	304 (94.1%)	0.002
	F2	2 (4.3%)	17 (5.3%)	
	F3	3 (6.5%)	1 (0.3%)	
	F4	1 (2.2%)	0 (0%)	
Microadenoma	18 (40.9%)	46 (14.6%)	<0.0001	
IMAGING DATA				
Number of HCA	1	4 (10.8%)	157 (54.1%)	<0.0001
	2 to 5	3 (8.1%)	64 (22.1%)	
	5 to 10	7 (18.9%)	31 (10.7%)	
	>=10	23 (62.2%)	38 (13.1%)	
Size of adenomas > 5 cm	24 (70.6%)	176 (63.3%)	0.454	
MOLECULAR CLASSIFICATION*				
Germline <i>HNF1A</i> mutation	7 (17%)	4 (1%)	<0.0001	
HHCA	21 (50%)	106 (32.4%)	0.032	
b ^{ex7,8} HCA	0 (0%)	13 (4%)	0.375	
b ^{ex7,8} IHCA	1 (2.4%)	20 (6.1%)	0.478	
IHCA	13 (31%)	98 (30%)	1	
b ^{ex3} IHCA	0 (0%)	26 (8%)	0.103	
b ^{ex3} HCA	2 (4.8%)	27 (8.3%)	0.546	
shHCA	2 (4.8%)	14 (4.3%)	1	
UHCA	3 (7.1%)	23 (7%)	1	

Liver adenomatosis was defined as ≥ 10 HCA at histology. Statistical tests were Mann Whitney Test or Chi squared test corrected using Monte Carlo resampling. *Patients with multiples tumors with discordant molecular features were excluded from the statistical analysis of molecular subgroups (n=22).

Supplementary Table 15: Description of the tumors according to the molecular classification

	Available data	All tumors n=533	H HCA n=179 (34%)	b ^{ex3} HCA n=37 (7%)	b ^{ex3} IHCA n=34 (6%)	b ^{ex7,8} HCA n=17 (3%)	b ^{ex7,8} IHCA n=21 (4%)	IHCA n=183 (34%)	shHCA n=22 (4%)	UHCA N=40 (7%)
PATHOLOGY										
HCA	533	482 (90%)	171 (95%)***	19 (51%)***	26 (76%)*	17 (100%)	20 (95%)	175 (96,5%)*	21 (95%)	36 (90%)
HCA/HCC	533	36 (7%)	10 (4,5%)***	12 (32%)***	5 (15%)*	0 (0%)	1 (5%)	7 (4%)*	0 (0%)	1 (3%)
HCC on HCA	533	15 (3%)	1 (0,5%)***	6 (16%)***	3 (9%)*	0 (0%)	0 (0%)	1 (0,5%)*	1 (5%)	3 (7%)
Size of the nodule	482	55 (5-290)	50 (5-270)	78 (20-290)*	70 (15-200)	83 (30-140)*	70 (20-140)	50 (6-190)	65 (15-230)	50 (20-200)
Size of the nodule>5cm	482	245 (51%)	78 (48%)	22 (61%)	20 (69%)	9 (64%)	14 (70%)	73 (45%)	13 (62%)	16 (47%)
Well limited nodule	433	311 (72%)	112 (75%)	27 (87%)	18 (67%)	13 (93%)	10 (56%)	95 (66%)	12 (71%)	25 (76%)
Encapsulated	419	43 (10%)	11 (7%)	8 (28%)**	5 (20%)	3 (23%)	2 (12%)	7 (5%)*	2 (11%)	5 (15%)
Hemorrhage	462	241 (52%)	59 (39%)**	15/34 (44%)	20 (69%)	11 (92%)**	13 (12%)	86 (54%)	17 (81%)*	20 (59%)
Sinusoidal dilatation	455	292 (64%)	63 (41%)***	13 (41%)**	25 (86%)*	6 (54%)	17 (89%)*	136 (83%)***	9 (56%)	23 (74%)
No tumor steatosis	462	181 (39%)	18 (11%)***	23 (74%)**	20 (74%)**	7 (70%)	7 (39%)	72 (45%)***	16 (84%)***	18 (60%)
Tumor steatosis < 1/3	462	100 (22%)	22 (13%)***	4 (13%)**	4 (15%)**	2 (20%)	6 (33%)	56 (35%)***	2 (11%)***	4 (13%)
Tumor steatosis 1/3-2/3	462	81 (17%)	47 (28%)***	1 (3%)**	2 (7%)**	1 (1%)	4 (22%)	20 (13%)***	1 (5%)***	5 (17%)
Tumor steatosis>2/3	462	100 (22%)	80 (48%)***	2 (6%)**	1 (4%)**	0 (0%)	1 (6%)	12 (7%)***	0 (0%)***	3 (10%)
Dystrophic arteries	449	158 (35%)	23 (15%)***	7 (21%)	17 (57%)*	3 (27%)	8 (42%)	84 (54%)***	4 (22%)	12 (44%)
Inflammatory infiltrate	438	227 (52%)	27 (18%)***	13 (43%)	20 (69%)	5 (50%)	19 (90%)***	131(83%)***	3 (19%)*	9 (36%)
Ductular reaction	417	136 (32%)	20 (14%)***	6 (25%)	13 (48%)	1 (8%)	7 (39%)	80 (53%)***	2 (12%)	7 (27%)
Cytological atypia	478	110 (23%)	13 (8%)***	20 (58%)***	23 (77%)***	7 (54%)*	9 (47%)*	31 (19%)	5 (24%)	2 (6%)*
Pseudoglandular formation	389	65 (17%)	25 (19%)	16 (62%)***	8 (35%)*	3 (30%)	2 (12%)	5 (4%)***	2 (11%)	4 (15%)
Cholestasis	282	39 (14%)	8 (9%)	8 (50%)**	9 (53%)***	3 (43%)	3 (38%)	5 (4%)**	1 (6%)	2 (13%)
IMMUNOHISTOCHEMISTRY										
LFABP negative	214	92 (43%)	79 (92%)***	0 (0%)**	0 (0%)**	2 (29%)	0 (0%)**	4 (6%)***	5 (50%)	2 (17%)
Glutamine synthase positive	236	46 (19%)	6 on 80 (7%)**	18 (90%)***	16 (94%)***	0 (0%)	0 (0%)	5 (6%)**	0 (0%)	1 (9%)
B-catenin nuclear positive	224	26 (12%)	2 on 71 (3%)**	15 (75%)***	7 (64%)**	1 (11%)	0 (0%)	1 (1%)***	0 (0%)	0 (0%)
SAA positive	214	111 (52%)	4 on 67 (6%)***	2 (20%)*	5 (71%)	1 (14%)	10 (100%)**	80 (90%)***	2 (18%)*	7 (54%)
GENE MUTATIONS										
Biallelic <i>HNF1A</i> mutations	509	178 (35%)	163 (94%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>CTNNB1</i> mutations exon 3	526	64 (12%)	1 (0,5%)	33 (89%)	30 (88%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>CTNNB1</i> mutations exon 7	521	27 (5%)	0 (0%)	0 (0%)	0 (0%)	12 (71%)	15 (71%)	0 (0%)	0 (0%)	0 (0%)
<i>CTNNB1</i> mutations exon 8	513	11 (2%)	0 (0%)	0 (0%)	0 (0%)	5 (29%)	6 (29%)	0 (0%)	0 (0%)	0 (0%)
<i>IL6ST</i> mutations	520	140 (27%)	0 (0%)	0 (0%)	22 (65%)	0 (0%)	15 (71%)	103 (58%)	0 (0%)	0 (0%)
<i>FRK</i> mutations	509	17 (3%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (5%)	16 (9%)	0 (0%)	0 (0%)
<i>STAT3</i> mutations	502	8 (1.6%)	0 (0%)	0 (0%)	1 (3%)	0 (0%)	1 (5%)	6 (3%)	0 (0%)	0 (0%)
<i>JAK1</i> mutations	499	2 (0.4%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	2 (1%)	0 (0%)	0 (0%)
<i>GNAS</i> mutations	510	6 (1%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	6 (3%)	0 (0%)	0 (0%)
<i>TERT</i> promoter mutations	493	10 (2%)	0 (0%)	8 (23%)	1 (3%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (3%)

β-catenin was considered as positive when nuclear translocation was observed and glutamine synthase when strong heterogeneous or strong homogeneous staining was observed. Statistical tests were Kruskal Wallis Test or Chi squared test corrected using Monte Carlo resampling. * P < 0.05, ** P < 0.01, *** P < 0.001

Supplementary Table 16: Accuracy of the immunohistochemical markers for the diagnosis of molecular subtypes

	Available data	Sensitivity	Specificity	Positive predictive value	Negative predictive value
LFABP for HHCA	214	0.92	0.90	0.86	0.94
SAA for all inflammatory HCA	214	0.90	0.85	0.86	0.89
Glutamine synthase for <i>CTNNB1</i> exon 3 mutations	236	0.92	0.94	0.74	0.98
β -catenin for <i>CTNNB1</i> exon 3 mutations	224	0.71	0.98	0.85	0.95
β -catenin and glutamine synthase for <i>CTNNB1</i> exon 3 mutations	198	0.90	0.93	0.70	0.98

Loss of LFABP and overexpression of SAA in the tumor were considered as positive. β -catenin was considered as positive when nuclear translocation was observed and glutamine synthase when strong heterogeneous or strong homogeneous staining was observed.

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
235638_at	RASSF6	0.231661856	16	5.13E-08
236307_at	BACH2	0.243006672	27	3.34E-07
218974_at	SOBP	5.603187406	161	4.77E-07
226931_at	TMTC1	2.803027149	95	1.03E-06
232472_at	FNDC3B	0.347524449	52	1.91E-06
236089_at	HECW2	2.585259103	28	1.91E-06
209815_at	PTCH1	6.562501277	186	2.77E-06
200696_s_at	GSN	9.780744755	691	2.88E-06
210511_s_at	INHBA	0.212842082	79	4.01E-06
213712_at	ELOVL2	0.16613848	365	4.15E-06
210587_at	INHBE	0.18384872	287	6.45E-06
235372_at	FCRLA	6.971390083	89	9.66E-06
209424_s_at	AMACR	0.250607978	325	1.01E-05
204159_at	CDKN2C	4.859922806	56	1.18E-05
202790_at	CLDN7	1.921262924	103	1.29E-05
241866_at	SLC16A7	0.349786904	12	1.30E-05
200973_s_at	TSPAN3	1.986375001	127	1.37E-05
210807_s_at	SLC16A7	0.314878745	53	1.38E-05
220404_at	GPR97	4.003595069	108	1.45E-05
227361_at	HS3ST3B1	0.3443369	923	1.45E-05
204856_at	B3GNT3	3.422340748	106	1.47E-05
209426_s_at	AMACR	0.266464012	432	1.52E-05
205613_at	SYT17	2.25863507	153	1.59E-05
221563_at	DUSP10	0.313519664	405	1.65E-05
243614_s_at	PRODH2	0.50277091	163	1.76E-05
230026_at	MRPL43	0.317123536	66	1.88E-05
226325_at	ADSSL1	6.272202747	217	1.90E-05
236365_at	AMACR	0.499322067	25	2.31E-05
1554821_a_at	ZBED1	1.910360671	53	2.38E-05
1553723_at	GPR97	5.717661721	25	2.49E-05
1553159_at	DNAH11	2.150606366	47	2.51E-05
219288_at	C3orf14	2.55061262	50	2.65E-05
230488_s_at	NCRNA00118	0.270549208	171	2.72E-05
208940_at	SEPHS1	2.426753337	146	2.86E-05
235401_s_at	FCRLA	12.38967191	21	3.05E-05
205139_s_at	UST	11.65725893	91	3.14E-05
239345_at	SLC19A3	0.209826569	76	3.14E-05
238029_s_at	SLC16A14	12.79915184	48	3.18E-05
217289_s_at	SLC37A4	2.578715794	602	3.32E-05
216381_x_at	AKR7A3	0.483041576	1749	3.38E-05
229526_at	AQP11	0.439290247	143	3.47E-05
209425_at	AMACR	0.291956578	548	3.60E-05
207584_at	LPA	0.243958886	408	3.64E-05
236236_at	WNK3	0.326869534	172	3.68E-05
230271_at	ONECUT2	0.467353066	201	3.69E-05
209614_at	ADH1B	0.37717982	1445	3.92E-05
211748_x_at	PTGDS	36.74454952	1705	4.10E-05
214329_x_at	TNFSF10	0.298670937	448	4.16E-05
235400_at	FCRLA	6.161031607	17	4.21E-05
225102_at	MGLL	0.423611483	516	4.37E-05
212695_at	CRY2	1.89587727	274	4.39E-05
206058_at	SLC6A12	0.181958855	339	4.45E-05
230003_at	SLC16A7	0.186380562	52	4.47E-05
236798_at	LINC00888	0.352476301	102	4.54E-05
227865_at	C9orf103	0.45274002	433	4.70E-05
203423_at	RBP1	0.175578151	496	5.44E-05
205498_at	GHR	0.392427119	2618	5.50E-05
215501_s_at	DUSP10	0.29675608	248	5.86E-05
229034_at	SOBP	1.985572543	26	5.99E-05
41660_at	CELSR1	0.481325089	49	6.11E-05
232098_at	DST	0.313923094	65	6.57E-05
52940_at	SIGIRR	0.583652727	507	6.78E-05
205862_at	GREB1	0.168830634	74	6.85E-05
236632_at	LOC646576	3.05412325	102	7.03E-05
220528_at	VNN3	0.31442564	116	7.22E-05
218024_at	BRP44L	0.469037964	2202	7.24E-05
211663_x_at	PTGDS	44.29186584	540	7.48E-05
206950_at	SCN9A	2.416094571	28	7.62E-05

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
234092_s_at	TM6SF2	0.436190897	185	7.87E-05
1558402_at	CTD-3080P12.3	0.423072768	18	7.94E-05
207057_at	SLC16A7	0.177589725	183	8.15E-05
225321_s_at	PILRB	0.580930761	310	8.26E-05
224959_at	SLC26A2	17.67437132	215	8.28E-05
206469_x_at	AKR7A3	0.481890785	1740	8.29E-05
217989_at	HSD17B11	2.196415111	1324	8.35E-05
212187_x_at	PTGDS	49.24062192	1701	8.46E-05
208763_s_at	TSC22D3	3.469639963	539	8.73E-05
229302_at	TMEM178	0.490313535	63	8.77E-05
212070_at	GPR56	3.235090408	137	8.80E-05
205954_at	RXRG	2.700906273	26	9.00E-05
239727_at	DIO3OS	0.486620035	68	9.04E-05
206894_at	APOA4	0.4235843	113	9.23E-05
221249_s_at	FAM117A	0.462610648	175	9.39E-05
1552727_s_at	ADAMTS17	0.42010459	100	9.57E-05
218579_s_at	DHX35	2.058972855	44	0.000100481
202688_at	TNFSF10	0.399848218	1393	0.000101975
202555_s_at	MYLK	1.575335017	953	0.000102413
204944_at	PTPRG	1.953791566	65	0.000103327
202830_s_at	SLC37A4	2.011475351	1180	0.000103535
219911_s_at	SLCO4A1	24.25775625	141	0.000111844
202820_at	AHR	0.418348437	400	0.000112276
221480_at	HNRNPD	2.011658455	53	0.000112762
214476_at	TFF2	0.341092384	26	0.000112973
218526_s_at	RANGRF	0.237707432	119	0.000113813
237460_x_at	C14orf182	0.5053048	27	0.000118726
202341_s_at	TRIM2	0.602388806	62	0.000120173
203919_at	TCEA2	10.55498703	927	0.000121614
218543_s_at	PARP12	0.555258968	155	0.000122759
205837_s_at	GYPA	1.918634219	8	0.000123406
208024_s_at	DGCR6 /// DGCR6l	2.162531839	680	0.000124411
236796_at	BACH2	0.230918866	34	0.000124673
229468_at	CDK3	0.619185799	171	0.000127083
208939_at	SEPHS1	2.079430968	216	0.000130579
229459_at	FAM19A5	16.2195346	50	0.000137983
242814_at	SERPINB9	0.42797402	65	0.000142082
215322_at	LONRF1	0.60434494	23	0.000143901
205244_s_at	SLC13A3	0.3279516	125	0.000147744
202687_s_at	TNFSF10	0.442556151	555	0.000153326
215146_s_at	TTC28	0.579290231	86	0.000156202
229053_at	SYT17	2.34680865	144	0.000159132
208158_s_at	OSBPL1A	2.351191702	214	0.000160195
227646_at	EBF1	3.52973736	37	0.000162627
215129_at	PIK3C2G	2.385384779	126	0.000166105
219316_s_at	FLVCR2	3.506167078	166	0.000169137
219462_at	TMEM53	0.641843422	169	0.000172743
229147_at	RASSF6	0.227373228	52	0.00017659
1552726_at	ADAMTS17	0.498657727	53	0.000178371
212820_at	DMXL2	2.782496958	136	0.00017885
229963_at	BEX5	1.619312903	39	0.000180617
206010_at	HABP2	0.618998592	2019	0.000184048
210404_x_at	CAMK2B	0.549948017	39	0.000185701
220736_at	SLC19A3	0.267623835	62	0.000186081
226096_at	FNDC5	4.390401076	305	0.000188872
241925_x_at	SLC16A7	0.280678193	20	0.000194629
214130_s_at	PDE4DIP	2.230971814	97	0.000194701
205355_at	ACADSB	0.613813459	1403	0.000195338
205221_at	HGD	2.886096427	3261	0.000196263
209581_at	PLA2G16	0.434731229	354	0.000202442
219221_at	ZBTB38	1.754370259	553	0.000203039
1556037_s_at	HHIP	4.8307447	29	0.000205155
205097_at	SLC26A2	23.17609998	161	0.000205603
213227_at	PGRMC2	0.549857773	287	0.000205693
217979_at	TSPAN13	0.142539161	613	0.000206929
202718_at	IGFBP2	8.499622299	1236	0.000210168
206008_at	TGM1	3.718062302	82	0.000213036
224706_at	KIAA2013	0.639074054	503	0.000226438

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
1554483_at	TMEM37	2.306144443	335	0.000227687
203726_s_at	LAMA3	0.555727859	48	0.000231118
202158_s_at	CELF2	1.767621106	28	0.000237442
220029_at	ELOVL2	0.193393601	91	0.000238694
217489_s_at	IL6R	1.862814185	42	0.000239751
227140_at	INHBA	0.127203995	167	0.000240336
215923_s_at	PSD4	1.605681959	73	0.000249451
228770_at	GPR146	0.510035577	93	0.000250494
208088_s_at	CFHR5	0.47592718	1383	0.000254451
229199_at	SCN9A	1.980329444	17	0.000256551
207251_at	MEP1B	3.852040401	33	0.000260016
223509_at	CLDN2	0.207131927	63	0.000268541
207308_at	SLCO1A2	14.85220199	48	0.000272086
211352_s_at	NCOA3	1.518525497	77	0.000277295
202834_at	AGT	0.641113121	9494	0.00028537
239911_at	ONECUT2	0.464055315	118	0.000286545
206262_at	ADH1C	0.639968771	4739	0.000296027
1563906_at	SOBP	1.71272599	21	0.000296783
1562921_at	EP300-AS1	0.49608752	101	0.000296998
1554077_a_at	TMEM53	0.629536193	246	0.000297118
226112_at	SGCB	0.503671966	179	0.000299069
206094_x_at	4 /// UGT1A5 ///	0.322666388	2523	0.000303537
203999_at	SYT1	0.540808533	32	0.000304085
218756_s_at	DHRS11	0.639281817	56	0.000305253
202156_s_at	CELF2	1.748241276	34	0.000308978
201599_at	OAT	0.472318562	3598	0.000311533
207330_at	PZP	0.065825686	721	0.000312839
223978_s_at	CRLS1	0.573376666	572	0.000314654
213872_at	C6orf62	1.863762057	274	0.00031507
207126_x_at	JGT1A4 /// UGT1,	0.311047258	2846	0.000321352
208788_at	ELOVL5	0.444272966	785	0.000322081
220581_at	C6orf97	0.490521318	29	0.000322915
205005_s_at	NMT2	0.557166205	106	0.000323987
230451_at	AS1 /// LOC1005	0.450031038	22	0.000324681
228653_at	SAMD5	0.454095017	113	0.000324729
218893_at	ISOC2	0.665033232	395	0.000326527
230645_at	FRMD3	1.529638305	21	0.000330406
211890_x_at	CAPN3	0.158637884	169	0.000333574
211480_s_at	SLCO1A2	5.311157467	53	0.000340233
220387_s_at	HHLA3	0.499883443	127	0.000340954
216696_s_at	PRODH2	0.47119246	996	0.000343043
207001_x_at	TSC22D3	2.075645522	102	0.000343706
219386_s_at	SLAMF8	1.902568359	24	0.000351158
214670_at	ZKSCAN1	1.684666443	415	0.000351234
215247_at	LOC100288570	1.533180187	44	0.000352985
205120_s_at	SGCB	0.489757051	133	0.000354745
205749_at	CYP1A1	0.146159395	161	0.000357344
218450_at	HEBP1	0.641152443	764	0.000357567
226322_at	TMT1C	2.2143466	105	0.000358673
225272_at	SAT2	0.499370853	1860	0.000373278
203972_s_at	PEX3	0.641386094	277	0.000381912
1557953_at	ZKSCAN1	1.835161163	217	0.000382066
204998_s_at	ATF5	0.370551815	1452	0.000382133
218921_at	SIGIRR	0.545518776	298	0.000385896
206068_s_at	ACADL	1.969356197	310	0.000392172
202157_s_at	CELF2	2.244526965	115	0.000396513
225099_at	FBXO45	1.538568363	78	0.000404815
204532_x_at	JGT1A4 /// UGT1,	0.302955382	2906	0.000405189
1556168_s_at	HEATR7B1	0.316321609	35	0.000411389
223103_at	STARD10	0.524775658	752	0.000415684
1554547_at	FAM13C	4.691823078	62	0.000424873
232095_at	/// SRGAP2C ///	1.852906706	54	0.000433542
214475_x_at	CAPN3	0.140826835	186	0.000440032
223020_at	CLPTM1L	10.02459227	2163	0.000454274
32837_at	AGPAT2	0.443955426	507	0.000455936
206756_at	CHST7	3.186001502	159	0.000457731
205006_s_at	NMT2	0.457805389	154	0.000459002
232180_at	UGP2	0.279626477	120	0.000461288

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
218477_at	TMEM14A	0.419333514	1618	0.000461537
202025_x_at	ACAA1	0.540882626	1192	0.000462265
233269_at	XXbac-B476C20.9	0.604243707	14	0.000464441
237262_at	GAREM	1.545120429	125	0.000471144
223080_at	GLS	0.567017816	26	0.000473495
217991_x_at	SSBP3	1.870951374	100	0.000477373
203760_s_at	SLA	2.243086806	107	0.000480832
209645_s_at	ALDH1B1	0.412908867	195	0.000481118
200972_at	TSPAN3	1.775352841	270	0.000483294
203339_at	SLC25A12	1.599389725	28	0.000485116
215125_s_at	4 /// UGT1A5 ///	0.271892648	2060	0.000486205
221523_s_at	RRAGD	1.776828519	44	0.000487354
204141_at	TUBB2A	0.48995017	906	0.000508024
205675_at	MTPP	0.574407832	1242	0.000513003
227585_at	ATAD1	1.648804892	47	0.000517727
214264_s_at	C14orf143	0.663124213	33	0.000517887
209288_s_at	CDC42EP3	2.363162784	61	0.000517993
238452_at	FCRLB	2.272414997	35	0.000519278
213349_at	TMCC1	0.41204291	144	0.000526653
209615_s_at	PAK1	1.807807512	11	0.000529397
235577_at	ZNF652	0.656457878	178	0.000529539
204623_at	TFF3	0.076859229	290	0.000530424
205511_at	FLJ10038	1.68929806	13	0.000530755
208596_s_at	4 /// UGT1A5 ///	0.293940988	2129	0.000540726
226935_s_at	CLPTM1L	8.728237965	1316	0.000541384
202800_at	SLC1A3	1.694251028	59	0.000546791
203865_s_at	ADARB1	2.117610015	90	0.000554168
203980_at	FABP4	3.784814187	107	0.000563108
226604_at	TMTC3	0.565942053	201	0.000566141
231918_s_at	GFM2	1.532001567	82	0.000569539
225747_at	COQ10A	0.57666422	233	0.000571232
203970_s_at	PEX3	0.602731003	180	0.00057246
228565_at	KIAA1804	0.434710283	56	0.000582577
228964_at	PRDM1	2.783304937	45	0.000589029
202754_at	R3HDM1	0.610015631	145	0.000589504
207097_s_at	SLC17A2	0.487128503	375	0.000594046
235099_at	CMTM8	0.639076069	345	0.00059686
204068_at	STK3	1.977476118	224	0.000600996
218383_at	HAUS4	2.017221538	239	0.00060257
226269_at	GDAP1	1.619673241	15	0.000608716
242370_at	MTHFD2L	2.241300645	35	0.000617927
203761_at	SLA	2.596980587	98	0.000623606
212297_at	ATP13A3	0.463413702	820	0.000624032
211682_x_at	UGT2B28	0.621774359	4077	0.000624443
210909_x_at	LPAL2	0.550402078	61	0.000627117
201185_at	HTRA1	0.550413959	431	0.000627557
226147_s_at	PIGR	0.329014275	309	0.000630435
229158_at	WNK4	4.07752343	48	0.000638865
221552_at	ABHD6	0.606622182	365	0.000639465
231693_at	FABP1	0.311221631	210	0.000641082
1553992_s_at	NBR2	0.56234762	82	0.000652344
212460_at	C14orf147	0.467170222	370	0.000654426
230907_at	GPRC5C	2.271263612	125	0.000655546
202179_at	BLMH	1.564270891	77	0.000656405
212606_at	WDFY3	1.536853523	90	0.000676264
202063_s_at	SEL1L	0.517113928	33	0.000680003
237365_at	ELOVL2-AS1	0.212882525	49	0.000683278
211026_s_at	MGLL	0.400790402	773	0.000684239
214308_s_at	HGD	2.764834608	1958	0.000689655
203304_at	BAMBI	5.428937206	307	0.000691565
232945_at	PUS10	0.511222009	20	0.000697223
209606_at	CYTIP	1.975481925	43	0.000707352
215171_s_at	TIMM17A	0.63728898	628	0.000709032
209904_at	TNNC1	53.57835683	106	0.000715675
225419_at	C7orf11	0.571814116	685	0.000716506
210678_s_at	AGPAT2	0.505711889	175	0.000716926
202177_at	GAS6	2.591890245	167	0.000727803
214307_at	HGD	2.150746133	1113	0.000728125

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
222592_s_at	ACSL5	0.516106553	757	0.000732287
209781_s_at	KHDRBS3	2.84122968	284	0.000734343
214129_at	PDE4DIP	1.700251809	334	0.000737252
230964_at	FREM2	0.138626998	18	0.000743753
210558_at	AKR1C4	0.575091608	2048	0.000749071
229655_at	FAM19A5	4.259557799	80	0.000771342
220626_at	SERPINA10	0.548798253	1606	0.000775232
231577_s_at	GBP1	0.493506905	1026	0.000778331
241114_s_at	ACAA2	0.547083859	291	0.000779682
233651_s_at	MPND	1.914726937	236	0.000787263
225816_at	PHF17	2.224356455	218	0.000789251
1559513_a_at	FANCC	4.033454141	31	0.000790728
209513_s_at	HSDL2	0.630677454	664	0.000794865
207378_at	TREH	7.825631536	120	0.000796406
212558_at	SPRY1	1.882265671	207	0.000797825
219948_x_at	UGT2A3	0.51390256	138	0.000799077
228027_at	GPRASP2	1.671116368	296	0.000807723
213479_at	NPTX2	9.028675442	43	0.000809449
212554_at	CAP2	2.797227903	55	0.000817184
203803_at	PCYOX1	0.604179799	580	0.00082059
222600_s_at	UBA6	0.65593758	121	0.000821609
218844_at	ACSF2	2.568811692	417	0.000843251
222482_at	SSBP3	2.230097154	224	0.00084431
209512_at	HSDL2	0.608970279	393	0.000846657
217734_s_at	WDR6	0.65721794	237	0.000857411
230647_at	TMEM53	0.627551392	41	0.000860436
204999_s_at	ATF5	0.322774344	509	0.00087138
221326_s_at	TUBD1	1.537610182	28	0.000877527
1555890_at	OR2A1-AS1 /// OI	1.665190115	11	0.000878707
206797_at	NAT2	0.403289885	734	0.000880799
232322_x_at	STARD10	0.527714746	1031	0.000892025
225204_at	PPTC7	1.567881152	599	0.000902376
232282_at	WNK3	0.285161266	228	0.000905002
225354_s_at	SH3BGR2	0.549891888	583	0.000909713
226278_at	SVIP	0.55616303	101	0.000921768
212800_at	STX6	1.53716964	14	0.000922897
224963_at	SLC26A2	8.321051709	159	0.000926959
1556606_at	NAV2	0.541204153	12	0.00093423
233403_x_at	TM6SF2	0.591312662	164	0.000940589
236064_at	SLC25A35	0.637828908	27	0.000947788
204544_at	HPS5	0.396102978	302	0.000949293
235349_at	FAM82A1	0.524646193	265	0.00095295
201761_at	MTHFD2	3.84924712	58	0.000954574
218147_s_at	GLT8D1	0.481010081	228	0.00095657
203725_at	GADD45A	0.56332326	958	0.000959178
1558733_at	ZBTB38	1.56025587	95	0.000961128
202375_at	SEC24D	0.457473377	153	0.000966968
230249_at	KHDRBS3	1.959968586	18	0.00097453
221782_at	DNAJC10	0.652520171	53	0.000974654
204067_at	SUOX	0.590831567	437	0.00097788
222870_s_at	B3GNT2	0.453129238	250	0.000980734
209566_at	INSIG2	0.326725561	346	0.00098241
1554863_s_at	DOK5	0.208088625	110	0.000983929
237466_s_at	HHIP	2.039144635	88	0.000989591
217963_s_at	NGFRAP1	1.77329581	1094	0.000991889
201859_at	SRGN	1.630603741	1506	0.001002302
205657_at	HAAO	1.504387216	682	0.001004155
207409_at	LECT2	1.605403107	4485	0.001008883
220663_at	IL1RAPL1	0.504057028	19	0.001011546
205542_at	STEAP1	0.482812775	86	0.001018064
232663_s_at	LOC390595	2.094316587	69	0.001018274
217857_s_at	RBM8A	1.639372414	65	0.001024231
213612_x_at	14 /// NBPF15 ///	1.669025504	1402	0.001029076
214681_at	GK	0.53178071	183	0.001031819
218412_s_at	GTF2IRD1	1.854226492	118	0.001036053
225612_s_at	B3GNT5	0.208524308	87	0.001039946
226193_x_at	/ CBWD5 /// CBW	0.644676382	571	0.001040185
48808_at	DHFR	0.597466341	190	0.001051483

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
230069_at	SFXN1	0.511119093	335	0.001053401
209956_s_at	CAMK2B	0.529069794	19	0.00105352
233463_at	RASSF6	0.443442502	12	0.001069563
238919_at	PCDH9	0.468797608	19	0.001074679
205883_at	ZBTB16	5.308021636	270	0.001078427
1554485_s_at	TMEM37	3.260201748	402	0.001090558
206784_at	AQP8	0.485509994	25	0.001091192
1554413_s_at	IX29P1 /// SNX29	1.556427295	13	0.001097663
210377_at	ACSM3	0.445022943	441	0.001097708
223630_at	C7orf13	1.58753925	75	0.001098194
207200_at	OTC	0.527764485	1010	0.001099771
202975_s_at	RHOBTB3	2.32115834	430	0.001103939
227812_at	TNFRSF19	0.358693496	12	0.001104872
205945_at	IL6R	1.951933063	506	0.001126746
209485_s_at	OSBPL1A	2.364002991	80	0.001133958
221864_at	ORAI3	0.656159175	390	0.00113478
204531_s_at	BRCA1	0.533717362	40	0.001135604
204672_s_at	ANKRD6	1.632737279	53	0.001143286
226287_at	CCDC34	1.626796093	33	0.00114677
1553976_a_at	DPCD	1.515565654	39	0.001153444
205429_s_at	MPP6	0.636907713	34	0.001156928
205942_s_at	ACSM3	0.479851163	301	0.001165798
204924_at	TLR2	2.100368528	123	0.001173219
202887_s_at	DDIT4	5.725962012	722	0.001178835
206753_at	RDH16	0.379481697	1576	0.001181367
237502_at	CRLS1	0.577538751	33	0.001183583
242055_at	PSMG4	0.346323947	38	0.001190075
219450_at	C4orf19	0.638780138	165	0.001204353
208606_s_at	WNT4	3.078182816	36	0.001207374
1554508_at	PIK3AP1	0.565403737	47	0.001207729
216048_s_at	RHOBTB3	2.337810863	77	0.001233596
231878_at	C16orf53	0.64462543	42	0.001254107
225150_s_at	RTKN	0.627713462	197	0.001267469
215712_s_at	IGFALS	0.461721261	330	0.001279422
200700_s_at	KDELRL2	0.662490458	712	0.001287882
212830_at	MEGF9	0.508038859	427	0.001288784
230265_at	SEL1L	0.591686451	147	0.001302639
224792_at	TNKS1BP1	0.530587654	80	0.001314176
212854_x_at	NBPF1	1.567173511	1159	0.001320026
232762_at	KIAA1217	0.648298862	42	0.001343059
221768_at	SFPQ	0.637269557	113	0.001346833
209917_s_at	TP53TG1	0.52256846	132	0.001349536
228275_at	LINC00888	0.447136388	130	0.001357115
49306_at	RASSF4	0.649996823	30	0.00136898
210944_s_at	CAPN3	0.209051454	375	0.001371498
236220_at	SLC16A10	0.351302511	73	0.00137688
226084_at	MAP1B	2.189609735	72	0.001379806
204713_s_at	F5	1.767236203	3801	0.001381189
242019_at	LASS6	1.633085813	12	0.001385515
230920_at	LOC284542	1.80042697	24	0.001386758
244804_at	SQSTM1	0.342687294	164	0.00138857
211360_s_at	ITPR2	0.630018544	68	0.001390201
205755_at	ITIH3	1.595022211	6464	0.001395805
224719_s_at	C12orf57	1.600245467	683	0.001402516
201104_x_at	NBPF19 /// NBPF2	1.825428825	620	0.001415155
202579_x_at	HMGN4	1.661638689	172	0.001416849
217744_s_at	PERP	0.519053913	503	0.001436205
1563792_at	AMN	1.588979488	52	0.00143834
214149_s_at	ATP6V0E1	0.65162545	131	0.001486064
212978_at	LRRRC8B	0.538355517	44	0.001487454
210278_s_at	AP4S1	1.542023287	19	0.001498126
217977_at	SEPX1	0.606475454	1085	0.00151446
218146_at	GLT8D1	0.562422639	820	0.001522876
203915_at	CXCL9	3.05633057	72	0.001523633
205303_at	KCNJ8	2.798301089	357	0.001529866
1552733_at	KLHDC1	1.554625233	85	0.001533773
226811_at	FAM46C	4.083894288	200	0.001534576
233446_at	ONECUT2	0.409803515	242	0.001537614

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
219464_at	CA14	1.732881978	82	0.001540015
211224_s_at	ABCB11	3.407284112	199	0.001543665
236205_at	ABCC6P1	0.648848294	192	0.001547411
224650_at	MAL2	0.455590684	162	0.001558259
209135_at	ASPH	0.569104241	342	0.001560241
232226_at	LRRC4C	0.640416678	22	0.001570456
228705_at	CAPN12	0.656397664	80	0.001590019
201689_s_at	TPD52	0.584881121	214	0.001600525
223594_at	TMEM117	0.484101819	59	0.001611751
202936_s_at	SOX9	0.478750185	45	0.001614133
204932_at	TNFRSF11B	0.211028758	24	0.001616097
212442_s_at	LASS6	2.128443509	324	0.001618338
204818_at	HSD17B2	0.313230586	1184	0.001621281
226517_at	BCAT1	2.433069593	24	0.001621818
204742_s_at	PDS5B	1.575618773	50	0.00162537
235019_at	CPM	1.730577608	337	0.001635187
215947_s_at	36A /// LOC10021	0.659254041	214	0.001637484
206340_at	NR1H4	0.527573016	615	0.001640343
219903_s_at	CYP2C8	0.503900174	40	0.001641509
209227_at	TUSC3	0.586400362	17	0.001647772
225426_at	PPP6C	1.563854338	91	0.001654161
228067_at	C2orf55	2.236667626	18	0.001667461
220305_at	MAVS	1.811078268	55	0.001678312
202269_x_at	GBP1	0.492349416	613	0.001690837
214461_at	LBP	0.490536497	1856	0.001696362
234728_s_at	DHX35	1.942658289	24	0.001699259
217649_at	ZFAND5	2.26120499	62	0.001709412
224884_at	AKAP13	2.02156395	153	0.001709937
234665_x_at	HHLA3	0.617899058	167	0.001712961
221911_at	ETV1	1.768676155	39	0.001744298
33494_at	ETFDH	0.571030317	727	0.001752368
209787_s_at	HMGN4	1.575240071	178	0.001756386
201690_s_at	TPD52	0.632815039	402	0.001768423
1557359_at	LOC285758	1.679382395	40	0.001777661
201853_s_at	CDC25B	0.538917553	194	0.001778564
231102_at	CROT	0.401164391	16	0.001781752
222939_s_at	SLC16A10	0.523683708	282	0.001789517
225202_at	RHOBTB3	2.459674407	577	0.001802349
207601_at	SULT1B1	0.501640141	67	0.001818436
214203_s_at	PRODH	4.52497993	202	0.001823068
203955_at	KIAA0649	1.514502318	98	0.001824309
223571_at	C1QTNF6	0.641590844	41	0.00184243
37201_at	ITIH4	0.548787735	621	0.0018453
212551_at	CAP2	2.866315266	84	0.001850998
227996_at	FARP1	1.511055497	53	0.001878492
214274_s_at	ACAA1	0.547020893	3560	0.001879413
228584_at	SGCB	0.425527528	70	0.001907722
209049_s_at	ZMYND8	1.681839169	148	0.001908426
215201_at	REPS1	2.03107983	38	0.001918619
233492_s_at	34P /// OR2A4 //	1.591547422	13	0.001923344
201200_at	REG1	0.663879256	3010	0.001927032
205530_at	ETFDH	0.572441556	474	0.001927914
230438_at	TBX15	0.32360559	41	0.001931736
230433_at	LOC729970	0.52246604	100	0.001934905
202284_s_at	CDKN1A	2.442695738	372	0.00194112
209786_at	HMGN4	1.774048611	94	0.001941203
244758_at	SCAND3	2.897946301	42	0.001942494
218544_s_at	RCL1	2.290126033	913	0.001959288
202976_s_at	RHOBTB3	2.597371121	342	0.001962265
204971_at	CSTA	3.504174513	388	0.001966437
209605_at	TST	0.627992682	3182	0.001969429
202792_s_at	PPP6R2	0.632960658	168	0.001972442
210553_x_at	PCSK6	0.580219409	78	0.001977505
222471_s_at	KCMF1	1.537949946	42	0.001982405
213455_at	FAM114A1	0.623306411	499	0.001984744
211048_s_at	PDI4A	0.606464127	680	0.001987979
224646_x_at	H19	6.373800752	1336	0.001997952
218299_at	C11orf24	0.601081992	140	0.002002086

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
210640_s_at	GPER	0.35327785	167	0.002011911
223194_s_at	SLC22A23	0.652381181	174	0.002040791
207635_s_at	KCNH1	1.846409193	16	0.002049882
206069_s_at	ACADL	2.241603262	146	0.002067553
226436_at	RASSF4	0.429608918	176	0.002069203
208325_s_at	AKAP13	1.955530712	87	0.002076431
221487_s_at	ENSA	1.633307068	54	0.00208594
214702_at	FN1	0.427170415	28	0.002088419
213820_s_at	STARD5	0.489552511	145	0.00209209
239562_at	MTHFD2L	2.969742361	116	0.002094541
225987_at	STEAP4	0.376321747	364	0.002096493
202270_at	GBP1	0.495392165	664	0.00210331
219753_at	STAG3	0.57500621	59	0.002106271
229736_at	TMEM86B	0.411556793	110	0.002135653
226844_at	MOBK12B	2.18626982	65	0.002143726
201506_at	TGFB1	1.712346681	1091	0.002153283
241234_at	LOC100506797	0.320456448	54	0.00217097
221847_at	LOC100129361	0.642267689	429	0.00217184
235898_at	LOC102723845	1.945981686	312	0.002176656
222866_s_at	FLVCR2	2.170927105	131	0.002178556
227173_s_at	BACH2	0.618059014	45	0.002203365
1555189_a_at	TAT	5.295205301	48	0.002218807
224690_at	C20orf108	0.591722045	1059	0.002231788
234098_at	SOBP	1.513856544	16	0.002237597
222083_at	GLYAT	0.621787701	2152	0.002239653
208147_s_at	CYP2C8	0.630103762	6524	0.002240755
233604_at	FLJ22763	0.398138031	72	0.002250744
204714_s_at	F5	1.667332798	2345	0.002270088
229331_at	SPATA18	0.335622588	106	0.002291959
229129_at	HNRNPD	1.706388482	27	0.002298512
226333_at	IL6R	1.785856234	912	0.002308493
206354_at	SLCO1B3	0.082758992	613	0.002308984
205478_at	PPP1R1A	1.873105738	778	0.002309603
217838_s_at	EVL	0.424102444	171	0.00231645
227900_at	CBLB	2.411542219	48	0.002319121
1555520_at	PTCH1	2.25093148	19	0.002320004
1552701_a_at	CARD16	2.324093266	93	0.002325977
231029_at	F5	2.478354089	770	0.002326884
218676_s_at	PCTP	1.801292975	828	0.002336042
228520_s_at	APLP2	0.6509165	205	0.002339518
201103_x_at	NBPF14 /// NBPF	1.643487299	1420	0.002349356
222392_x_at	PERP	0.595062501	1168	0.002364027
228785_at	ZNF281	1.890244663	580	0.002365609
1556185_a_at	CTB-167B5.2	0.376580697	38	0.002386918
215005_at	NECAB2	0.56186151	97	0.002386978
1554038_at	LARP1B	0.654149692	49	0.002393753
237421_at	RP11-76E1288 /// RP11-76E	0.626479971	40	0.002395304
228575_at	IL2ORB	0.51060371	18	0.002399249
226089_at	RABL3	1.858956319	49	0.00240065
209646_x_at	ALDH1B1	0.37466259	139	0.002404777
213970_at	RABL3	1.612674601	86	0.002427173
214073_at	CTTN	0.599117929	48	0.002431846
238365_s_at	C1orf228	0.630146324	16	0.002437099
222468_at	KIAA0319L	0.661948773	238	0.002455412
1555851_s_at	SEPW1	0.661340029	552	0.002459949
237094_at	FAM19A5	5.614562185	26	0.002460221
229374_at	EPHA4	2.703194845	26	0.002480856
232080_at	HECW2	1.694829829	121	0.002485243
213839_at	CLMN	2.203724029	128	0.002489891
208567_s_at	KCNJ18 /// LOC1	0.63911445	9	0.002529542
229666_s_at	CSTF3	0.463096631	61	0.002535882
213351_s_at	TMCC1	0.554247597	107	0.002545544
205892_s_at	FABP1	0.29817816	5269	0.002557018
45288_at	ABHD6	0.577066292	260	0.002566912
214844_s_at	DOK5	0.130043888	166	0.002572766
222100_at	CYP2E1	0.584139053	18	0.002581991
215977_x_at	GK	0.535662439	104	0.002596681
204056_s_at	MVK	0.610342469	114	0.002613478

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
223781_x_at	ADH4	0.615183263	2952	0.00264395
224397_s_at	TMT1C1	1.651161379	32	0.002651114
202319_at	SENP6	1.595824379	46	0.002670809
206249_at	MAP3K13	1.678880873	118	0.002676776
202743_at	PIK3R3	1.926376608	95	0.002688547
222243_s_at	TOB2	2.366668798	247	0.002713202
212392_s_at	PDE4DIP	1.702633765	21	0.002717167
209737_at	MAGI2	1.582062299	40	0.002720406
207387_s_at	GK	0.476705338	96	0.002724691
219167_at	RASL12	1.837456333	39	0.002726498
205888_s_at	JAKMIP2	0.49164704	86	0.002729568
1553995_a_at	NT5E	0.5545479	92	0.002731
226686_at	CISD2	0.626737857	144	0.002732173
1563160_at	F11	0.277591107	56	0.002735979
209286_at	CDC42EP3	1.876720099	45	0.002739349
226071_at	ADAMTSL4	1.639478191	90	0.002741143
203757_s_at	CEACAM6	0.607015797	15	0.002745311
1559026_at	PPP1R26-AS1	1.75916447	13	0.00277026
218653_at	SLC25A15	2.220766016	1414	0.002773151
221241_s_at	BCL2L14	4.988361098	62	0.002774634
230943_at	SOX17	1.601585598	16	0.002775309
222154_s_at	SPATS2L	0.60788467	1210	0.002793864
1553994_at	NT5E	0.565865348	126	0.002800606
204671_s_at	ANKRD6	1.993598322	52	0.002804962
214920_at	THSD7A	1.775037482	26	0.002805186
37512_at	HSD17B6	0.646783543	4420	0.002838046
202620_s_at	PLOD2	0.509995131	597	0.002842513
226210_s_at	MEG3	0.238316762	32	0.002848988
226863_at	FAM110C	0.325006126	332	0.002864243
206666_at	GZMK	1.685253349	59	0.002866587
208982_at	PECAM1	1.772210766	323	0.002868064
218658_s_at	ACTR8	1.594130957	25	0.002900115
203954_x_at	CLDN3	0.555598379	201	0.00292196
206118_at	STAT4	1.552410692	38	0.002925375
227190_at	TMEM37	2.581375355	276	0.002930346
209753_s_at	TMPO	1.759106294	36	0.002974027
218120_s_at	HMOX2	0.537353192	196	0.002977942
224657_at	ERRF1	1.70186227	4151	0.002979161
226459_at	PIK3AP1	0.51618217	641	0.002980418
225459_at	AMOTL1	1.920835456	50	0.00298475
213841_at	TNR	0.148197898	31	0.002992954
52255_s_at	COL5A3	0.438424259	76	0.003005621
233085_s_at	OBFC2A	1.966330888	35	0.00300835
235204_at	ENTPD7	0.532249235	76	0.003021029
227785_at	SDCCAG8	0.56290389	57	0.003029518
206100_at	CCPM	1.710180494	285	0.003035164
206197_at	NME5	1.782910676	16	0.003036069
202888_s_at	ANPEP	0.566660934	2052	0.003046567
205189_s_at	FANCC	3.278281782	289	0.003078671
226085_at	CBX5	1.725382409	170	0.003096481
1431_at	CYP2E1	0.402291681	6783	0.003130735
202746_at	ITM2A	1.996193541	44	0.003150968
213689_x_at	FAM69A	0.595438656	346	0.003161447
220954_s_at	PILRB	0.630653158	105	0.003161589
226634_at	METTL10	1.720876799	32	0.003166676
203354_s_at	PSD3	2.716168692	564	0.003177918
225030_at	BOD1	2.744683602	293	0.003178284
219915_s_at	SLC16A10	0.38360612	122	0.003184004
225785_at	REEP3	0.644516969	270	0.003190159
212594_at	PDCD4	0.602732808	87	0.003194813
211652_s_at	LBP	0.454298419	1150	0.003197415
227629_at	PRLR	0.531051851	121	0.003203762
213139_at	SNAI2	4.624708602	275	0.003226443
210199_at	CRYAA	0.577732816	82	0.003233333
1569020_at	NEDD9	1.906742424	42	0.003279448
226753_at	FAM76B	2.441137889	125	0.003296802
1570505_at	ABCB4	0.558895739	92	0.003300432
224348_s_at	HOTS	2.007071345	90	0.003311962

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
213467_at	RND2	0.612825071	23	0.00331677
207184_at	SLC6A13	0.477784787	119	0.0033277
225424_at	GPAM	0.559432557	1167	0.003334143
216687_x_at	UGT2B15	0.614913801	1436	0.003351993
228409_at	PLIN4	0.466284357	97	0.003361782
218517_at	PHF17	1.903024927	218	0.003371509
203706_s_at	FZD7	2.490212667	35	0.003390331
823_at	CX3CL1	0.642478704	69	0.003402199
225820_at	PHF17	2.213076274	54	0.003410737
225114_at	AGPS	0.575459138	85	0.00341259
244165_at	C10orf18	1.965196667	52	0.003441271
229362_at	PUS10	0.590867252	87	0.003448016
212956_at	TBC1D9	0.467430239	310	0.003451135
221575_at	SCLY	0.405164999	174	0.003458336
208983_s_at	PECAM1	2.11947932	83	0.003464928
219263_at	RNF128	0.64243534	2167	0.003468916
221433_at	FGF21	0.201272508	43	0.003478803
232231_at	RUNX2	1.818838986	19	0.003481773
236698_at	DYNC1I2	1.594126454	20	0.003493913
232654_s_at	UGT1A6	0.298420177	44	0.003501621
206636_at	RASA2	1.582540437	38	0.003504503
212057_at	KIAA0182	0.52228905	200	0.003507993
237031_at	RP11-21L23.2	0.20341519	99	0.003526502
208086_s_at	DMD	0.594530972	62	0.003528702
201015_s_at	JUP	1.669293619	364	0.003588558
200768_s_at	MAT2A	1.528786002	392	0.003621914
209976_s_at	CYP2E1	0.373271581	6754	0.003637151
1558199_at	FN1	0.535257442	17	0.003640136
227152_at	C12orf35	0.431171881	61	0.003641369
1553514_a_at	VNN3	0.566518468	22	0.003653268
214765_s_at	NAAA	0.650673858	221	0.003665551
201662_s_at	ACSL3	0.545027074	223	0.003667974
207262_at	APOF	0.624120325	1303	0.003680682
202323_s_at	ACBD3	0.443071769	93	0.003681848
224693_at	C20orf108	0.625383256	550	0.003687966
202304_at	FNDC3A	0.604710513	646	0.003689204
220070_at	JMJD5	0.365386584	134	0.003700569
204793_at	GPRASP1	2.312269548	43	0.003721168
209365_s_at	ECM1	0.382854077	300	0.00372417
228776_at	GJC1	2.394189561	22	0.003731614
207544_s_at	ADH6	0.596146899	653	0.003737271
242579_at	BMPR1B	0.66140574	16	0.003751559
206482_at	PTK6	0.621868788	17	0.003782101
209631_s_at	GPR37	0.527532328	181	0.003792202
1598_g_at	GAS6	1.942972878	422	0.003793507
243735_at	ELP2	1.886528041	30	0.003793956
203953_s_at	CLDN3	0.489546273	111	0.003801781
226846_at	PHYHD1	1.737511308	381	0.003808432
203638_s_at	FGFR2	0.635042206	303	0.003834959
226122_at	PLEKHG1	1.644206867	72	0.003836438
244111_at	KRT22	0.617724271	11	0.003855446
201858_s_at	SRGN	2.113265768	391	0.003855794
200795_at	SPARCL1	3.167935575	473	0.003858625
238723_at	ATXN3	1.945585261	29	0.003865895
225293_at	COL27A1	0.627609144	333	0.0038924
222908_at	FAM38B	1.698305261	35	0.003917652
205138_s_at	UST	3.512677354	31	0.003955673
208289_s_at	EI24	0.639130357	713	0.003962544
227150_at	MTF1	1.638806866	82	0.003979249
52164_at	C11orf24	0.484025245	319	0.004043427
227414_at	RHBDD1	0.524059336	57	0.004057402
221892_at	H6PD	1.974091154	213	0.004069747
212171_x_at	VEGFA	0.529452828	409	0.004071545
201508_at	IGFBP4	0.615404571	2210	0.004087245
208096_s_at	COL21A1	0.276450738	50	0.004091207
215689_s_at	SHBG	0.403807821	259	0.004110601
211996_s_at	3037 /// NPIPA5 /	0.618937698	178	0.004118761
222963_s_at	IL1RAPL1	0.548518116	15	0.004141022

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
209068_at	HNRPD1	1.767379544	187	0.004145102
235749_at	UGGT2	0.632691853	82	0.004147922
213566_at	RNASE6	2.533074847	60	0.004167727
223599_at	TRIM6	1.821325642	18	0.004172992
210788_s_at	DHRS7	0.516437154	516	0.004180905
208651_x_at	CD24	0.319740608	59	0.004233265
211596_s_at	LRIG1	0.607000913	147	0.004241672
207256_at	MBL2	0.222725929	898	0.004247573
202903_at	LSM5	1.807942918	37	0.004261509
231871_at	GPR180	0.406792626	50	0.004269953
212527_at	PPPDE2	0.641276816	246	0.00427568
221045_s_at	PER3	0.630980005	337	0.004288416
211821_x_at	GYPA	1.526920256	14	0.004302051
204693_at	CDC42EP1	0.604501285	98	0.004327864
200911_s_at	TACC1	1.893100059	561	0.00435132
228991_at	CDK13	0.568391704	123	0.004357953
222483_at	EFHD2	0.656475596	167	0.00438163
210971_s_at	ARNTL	1.705246162	29	0.004383939
204336_s_at	RG519	3.799325165	221	0.004392489
226218_at	IL7R	2.144109358	50	0.004402225
209919_x_at	GGT1	1.522993107	205	0.004403597
233059_at	KCNJ3	0.489132905	14	0.004408584
212183_at	NUDT4	2.91531138	240	0.004417122
225366_at	PGM2	0.377440495	99	0.004418114
222820_at	TNRC6C	2.060787623	89	0.004423222
64900_at	TMEM231	1.590502078	20	0.004436505
214142_at	ZG16	0.466094684	272	0.004437845
222525_s_at	CCDC25	0.628628125	378	0.004466094
201535_at	UBL3	1.724462535	488	0.004471277
209307_at	SWAP70	1.733749157	75	0.00447746
226909_at	ZNF518B	0.547697523	39	0.004481093
205328_at	CLDN10	0.428896432	18	0.004488565
212666_at	SMURF1	1.863958415	120	0.004509868
232380_at	FGGY	1.526376211	8	0.004522292
1552312_a_at	MFAP3	1.652604576	18	0.004524175
243221_at	FAM20A	1.580726744	84	0.004529576
1556387_at	LOC100507389	3.286736852	119	0.004542315
230179_at	LOC285812	1.988224918	102	0.004551352
219718_at	FGGY	2.60902542	549	0.00458727
212390_at	PDE4DIP	1.650138339	146	0.004629982
218208_at	PQLC1	1.640996951	512	0.004696154
218614_at	C12orf35	0.448927265	345	0.00470412
219562_at	RAB26	0.42849295	312	0.004712231
204933_s_at	TNFRSF11B	0.231766192	37	0.004748299
209306_s_at	SWAP70	1.594674261	48	0.00477364
234361_at	CREB3L3	0.569383579	93	0.004777009
216836_s_at	ERBB2	2.328589611	228	0.004784827
214455_at	HIST1H2BC	0.486982488	22	0.004786832
225029_at	LOC550643	1.62380253	141	0.004816268
219029_at	C5orf28	1.615613173	49	0.004841887
202534_x_at	DHFR	0.651045649	550	0.004865551
227600_at	MRPS30	1.502044976	53	0.004879497
201009_s_at	TXNIP	2.268644213	1591	0.004884001
231187_at	SLC28A1	0.548360923	75	0.004889958
215434_x_at	// NBP11 /// NBF	1.542929666	192	0.004894555
228235_at	MGC16121	0.649410387	43	0.004917089
228645_at	SNHG9	1.81430027	32	0.0049252
225282_at	SMAP2	1.630161388	299	0.004940267
50965_at	RAB26	0.448628737	228	0.004953192
223587_s_at	AMN	3.497552581	125	0.00496574
216950_s_at	^ /// FCGR1B /// F	1.60332517	46	0.004981662
236402_at	BRAF	1.543055529	21	0.00499303
219550_at	ROBO3	0.634040284	30	0.005024259
240681_at	EU250746	2.492087558	150	0.005043128
201008_s_at	TXNIP	2.667719025	865	0.005044245
204846_at	CP	0.609746824	4723	0.005049864
219913_s_at	CRNKL1	1.649822802	116	0.005052144
210241_s_at	TP53TG1	0.589096694	111	0.005054819

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
226403_at	TMC4	0.539324879	63	0.005056249
225160_x_at	MDM2	1.526417225	215	0.005067217
39549_at	NPAS2	0.592301846	15	0.005092334
209234_at	KIF1B	1.652040137	151	0.005094623
209228_x_at	TUSC3	0.449648183	57	0.005100352
228600_x_at	C7orf46	0.597140109	210	0.005119321
231698_at	FLJ36848	0.566942783	126	0.005119438
222675_s_at	BAIAP2L1	1.658056135	140	0.005127184
235221_at	CBLN3	0.147353759	82	0.005145493
211708_s_at	SCD	0.312172664	65	0.005145608
238805_at	C11orf52	0.608768896	94	0.005175367
201005_at	CD9	1.646683459	568	0.005177974
202039_at	VYO18A /// TIAF1	0.655736214	330	0.005191588
204608_at	ASL	2.048025811	2407	0.005198111
201785_at	RNASE1	2.00702895	150	0.005205907
220317_at	LRAT	0.460852166	15	0.005263721
218924_s_at	CTBS	0.564111887	307	0.005277392
241905_at	PIK3C2A	0.622935055	43	0.005306626
213982_s_at	RABGAP1L	1.868063558	86	0.005341033
201579_at	FAT1	3.674456321	334	0.005346628
210512_s_at	VEGFA	0.489921312	1261	0.005348423
209733_at	MID2	1.546581372	54	0.005383278
1569542_at	GPR125	2.619418477	69	0.00541859
218125_s_at	CCDC25	0.610955883	272	0.005420427
219629_at	FAM118A	2.216358133	29	0.005472308
219632_s_at	TRPV1	0.618972194	82	0.005494709
228752_at	EFCAB4B	1.501555882	28	0.005498872
229230_at	OSTalpha	2.427688443	656	0.005508924
213241_at	PLXNC1	1.932526316	36	0.005539983
218055_s_at	WDR41	1.585592844	75	0.005573075
241388_at	LOC101927451	1.626824929	33	0.005574079
222930_s_at	AGMAT	1.869114253	244	0.005588585
207317_s_at	CASQ2	1.808616395	39	0.005639348
206646_at	GLI1	1.619947193	32	0.00567517
224458_at	C9orf125	1.552041885	49	0.005696366
242149_at	C18orf19	1.640350751	32	0.005696538
202308_at	SREBF1	0.294102725	238	0.005701822
205513_at	TCN1	0.573862114	20	0.005715418
211481_at	SLCO1A2	1.57177631	17	0.005718248
209706_at	NKX3-1	0.470354636	61	0.00573171
208370_s_at	RCAN1	0.509171845	1634	0.005734418
225213_at	PPTC7	1.53880626	538	0.005771621
238752_at	GPLD1	0.562158611	500	0.005830174
204179_at	MB	2.59576513	54	0.005831879
206879_s_at	NRG2	1.585210818	30	0.005845672
201651_s_at	PACSIN2	0.479430768	718	0.005859836
228286_at	GEN1	0.514875433	56	0.005913384
237205_at	NCRNA00238	0.574827548	8	0.005922336
209782_s_at	DBP	0.388769318	84	0.00594066
207660_at	DMD	0.664380102	19	0.005941354
233493_at	OR2A4	1.506273482	16	0.005986324
229276_at	IGSF9	0.592147485	60	0.005987917
223911_at	LOC440330	1.648093859	159	0.006013784
1552880_at	SEC16B	1.555980393	62	0.006022511
222666_s_at	RCL1	1.900453817	727	0.006023338
219419_at	C18orf22	0.615629654	140	0.006044002
214771_x_at	MPRIIP	2.086749122	570	0.006062007
217167_x_at	GK	0.600165532	112	0.00606762
225420_at	GPAM	0.531646146	858	0.006068734
1556388_a_at	LOC100507389	3.43268798	271	0.006072066
205565_s_at	FXN	0.579141522	180	0.006073043
218136_s_at	SLC25A37	0.640072311	79	0.006081141
201146_at	NFE2L2	0.573378105	1219	0.006093863
206303_s_at	NUDT4	1.510786105	46	0.006099169
206386_at	SERPINA7	0.55781511	1369	0.006120057
217764_s_at	RAB31	1.611080229	129	0.006123827
226720_at	PWWP2A	0.636390696	57	0.006131495
209546_s_at	APOL1	0.63533653	346	0.006175339

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
203561_at	FCGR2A	1.881164754	38	0.006190111
228113_at	RAB37	1.574348057	107	0.006194898
215116_s_at	DNM1	0.373547001	35	0.006204025
229665_at	CSTF3	0.584239051	53	0.006252739
208288_at	ABCB11	3.681289811	109	0.006318037
222619_at	ZNF281	1.772568271	651	0.006406899
228463_at	FOXA3	0.441012066	372	0.006418097
226636_at	PLD1	0.560470234	192	0.006423862
232366_at	KIAA0232	1.728922436	48	0.006428942
236141_at	NBLA00301	0.6643388	12	0.006431768
220335_x_at	CES3	0.4464514	239	0.006468676
235024_at	PHF17	1.98589317	60	0.006514358
229127_at	JAM2	1.856533981	40	0.006551814
205831_at	CD2	1.755859318	39	0.00655362
202064_s_at	SEL1L	0.649213124	188	0.006586128
206862_at	ZNF254	0.554633814	18	0.006595626
211083_s_at	MAP3K13	1.511262127	11	0.006603319
222872_x_at	OBFC2A	1.80892607	83	0.006614494
228005_at	ZXDB	2.758909862	171	0.006642001
232158_x_at	NIPAL1	0.430195965	102	0.006659873
204215_at	C7orf23	1.650741972	72	0.006684058
226796_at	ABHD15	0.588600028	124	0.006697478
202457_s_at	PPP3CA	1.679945849	323	0.006753261
201751_at	JOSD1	1.506836681	239	0.006774102
212197_x_at	MPRIP	2.148837744	572	0.006832858
219250_s_at	FLRT3	0.513632635	50	0.006835928
206957_at	AGXT	0.569903678	430	0.006848648
206610_s_at	F11	0.650989262	845	0.006854226
222925_at	DCDC2	0.355319782	25	0.006864836
202619_s_at	PLOD2	0.564932737	337	0.006873267
226982_at	ELL2	1.729120358	568	0.00689718
224997_x_at	H19	1.736997834	922	0.006927881
242037_at	ASPH	0.628939599	19	0.006931568
204099_at	SMARCD3	5.052801321	110	0.006939801
218862_at	ASB13	2.079961966	557	0.006940943
202922_at	GCLC	0.569480749	686	0.006963904
1570523_s_at	ATG10	1.864330473	18	0.007003549
209243_s_at	PEG3	0.274119264	19	0.007039819
221794_at	DOCK6	0.636871291	90	0.007084726
204790_at	SMAD7	0.482154302	90	0.007100287
238160_at	ACOT12	0.282561578	554	0.00710577
204511_at	FARP2	0.556718443	77	0.007127516
237029_at	HGD	2.505378339	237	0.007189983
228726_at	SERPINB1	1.628203473	110	0.007192639
205610_at	MYOM1	1.741005122	157	0.007204173
203228_at	PAFAH1B3	1.55559511	81	0.007238368
203264_s_at	ARHGEF9	1.879098733	71	0.007247804
230352_at	PRPS2	1.534556973	87	0.007251677
223620_at	GPR34	2.785635917	40	0.007254123
219889_at	FRAT1	0.639324542	84	0.007279674
202069_s_at	IDH3A	1.535365849	84	0.007286117
225078_at	EMP2	1.684614237	249	0.007300016
235763_at	SLC44A5	0.607340933	8	0.007336633
221896_s_at	HIGD1A	0.644816206	1908	0.007337303
201688_s_at	TPD52	0.651271748	126	0.007340305
230238_at	ANKRD43	1.844913307	63	0.007341461
209187_at	DR1	1.533025853	121	0.007364431
235213_at	ITPKB	0.590301392	24	0.007371382
204304_s_at	PROM1	0.363351684	13	0.007382607
224224_s_at	PDE11A	0.472785376	12	0.007386168
212510_at	GPD1L	1.6614198	54	0.007405523
214319_at	FRY	0.409400785	59	0.007497113
227041_at	SESTD1	1.657531541	40	0.007527264
218501_at	ARHGEF3	1.704222587	58	0.00753308
210565_at	GCGR	1.640818589	235	0.007533477
1559266_s_at	C10orf140	0.514125153	28	0.007608547
209094_at	DDAH1	0.607062964	2010	0.007617677
208941_s_at	SEPHS1	1.50058129	228	0.007648971

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
218731_s_at	VWA1	0.608596392	116	0.00772709
204573_at	CROT	0.548204782	374	0.007733878
225450_at	AMOTL1	1.934068152	326	0.007734235
214446_at	ELL2	2.039218551	189	0.007738006
219113_x_at	HSD17B14	0.564408457	230	0.007747719
231015_at	KLF15	1.619469657	797	0.007784475
211715_s_at	BDH1	0.650137274	1140	0.007825393
215921_at	NPIP3 /// NPIP3	0.654358637	41	0.007935989
213587_s_at	ATP6V0E2	0.423063847	250	0.007939886
238197_at	GATA5	0.592646692	10	0.007943666
266_s_at	CD24	0.22509293	27	0.007954905
1558692_at	C1orf85	0.623689295	69	0.00796141
228922_at	SHF	0.648374322	77	0.007995579
212233_at	MAP1B	1.781714911	75	0.008000574
229096_at	00288570 /// LOC	1.94725914	63	0.008008162
216044_x_at	FAM69A	0.620708363	247	0.008066079
210327_s_at	AGXT	0.640062876	7712	0.008110398
203296_s_at	ATP1A2	1.854108524	13	0.008146483
228772_at	HNMT	1.589861576	522	0.008164804
1552703_s_at	CARD16 /// CASP1	1.816317107	81	0.008195423
228167_at	KLHL6	1.871380736	15	0.008219283
206979_at	C8B	1.554086157	3704	0.008219452
221868_at	PAIP2B	0.662147856	234	0.008228019
210170_at	PDLIM3	0.306031863	18	0.008249692
210305_at	PDE4DIP	3.66666484	46	0.00825837
222529_at	SLC25A37	0.619774265	184	0.008264216
1556148_s_at	LOC100287426	1.949194043	16	0.008278927
229441_at	PRSS23	1.609996814	18	0.008281566
225113_at	AGPS	0.557953439	114	0.008304603
215223_s_at	SOD2	1.784987158	417	0.008329611
221305_s_at	3 /// UGT1A5 /// U	0.398345248	166	0.008344797
227945_at	TBC1D1	1.560119301	113	0.008378576
229447_x_at	0 /// NBPF11 ///	1.524351285	1241	0.008390216
227605_at	AIMP1	1.798318811	69	0.008416653
225367_at	PGM2	0.514241601	241	0.008425844
1568620_at	CSAD	0.533038835	22	0.008445882
208782_at	FSTL1	2.352576025	632	0.008451771
202935_s_at	SOX9	0.38888197	33	0.008493125
214837_at	ALB	0.361497899	1074	0.008653251
223822_at	SUSD4	0.64437146	23	0.008665935
218613_at	PSD3	2.167292667	537	0.008679331
211071_s_at	MLLT11	2.385274862	83	0.008715688
209160_at	AKR1C3	0.58491345	1345	0.00871589
208996_s_at	POLR2C	1.638981767	390	0.008756375
203897_at	LYRM1	0.597726246	776	0.008789927
232633_at	XRCC5	1.779492547	13	0.008821423
209975_at	CYP2E1	0.611624343	11674	0.008834543
210326_at	AGXT	0.564617415	3438	0.008837143
209895_at	PTPN11	1.561957835	141	0.00885965
211577_s_at	IGF1	0.489871918	307	0.008879909
217763_s_at	RAB31	1.827551473	112	0.008894113
235706_at	CPM	1.515108624	232	0.008908778
235324_at	SRSF3	1.564409705	32	0.008911592
200708_at	GOT2	1.516536615	2197	0.008919751
217862_at	PIAS1	1.851861975	222	0.008936238
1556021_at	GPR180	0.576747452	14	0.00895434
242654_at	FANCC	1.80571431	12	0.008958711
243897_at	LOC101927287	1.797915322	66	0.009015878
231625_at	SLC22A9	1.71127343	145	0.009030307
225685_at	CDC42EP3	1.753154581	50	0.009038759
235144_at	RASEF	0.654967145	10	0.009063472
205502_at	CYP17A1	2.261676707	63	0.009094972
212151_at	PBX1	1.630833314	203	0.00911211
217542_at	MDM2	1.683851579	25	0.009191208
234850_at	MOGAT3	1.669609238	33	0.009248496
209906_at	C3AR1	1.941713891	192	0.00927803
242817_at	PGLYRP2	1.686756641	1106	0.009293445
217367_s_at	ZHX3	1.701422181	52	0.009296661

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
202017_at	EPHX1	0.525544754	3906	0.009297662
242979_at	IRS1	0.457331261	41	0.009316616
209682_at	CBLB	2.336760839	231	0.009319569
238880_at	GTF3A	0.620371105	97	0.009374877
205304_s_at	KCNJ8	1.972078768	421	0.009408772
205593_s_at	PDE9A	1.761386522	20	0.009410714
209242_at	PEG3	0.202146644	97	0.009415897
217521_at	HAL	2.829059449	637	0.009421754
222217_s_at	SLC27A3	1.631663391	261	0.009430555
201915_at	SEC63	1.520904658	139	0.009451579
204519_s_at	PLLP	0.658290563	108	0.009492664
207434_s_at	FXYD2	0.577466107	44	0.00949755
204111_at	HNMT	1.525166032	36	0.009509254
229337_at	USP2	0.56731329	83	0.009524208
210614_at	TTPA	0.566094478	187	0.009540849
225288_at	COL27A1	0.637439935	174	0.009544389
226855_at	PDP2	0.595191208	127	0.009550886
205517_at	GATA4	0.249727626	175	0.009566009
226237_at	COL8A1	1.95062452	18	0.009571757
219937_at	TRHDE	0.359846788	16	0.009573787
235142_at	ZBTB8A	1.896009622	89	0.00958423
226740_x_at	NUBP14	1.585160239	1366	0.009601594
210655_s_at	FOXO3	1.827951431	132	0.009609637
228713_s_at	HSD17B14	0.621651927	283	0.009637321
1558143_a_at	BCL2L11	1.790382916	120	0.009646221
217757_at	A2M	1.537027158	6735	0.009659978
1553962_s_at	RHOB	2.516049464	327	0.009660501
215966_x_at	GK3P	0.538769657	75	0.009684128
220390_at	AGBL2	0.664535481	33	0.009685519
209099_x_at	JAG1	1.555536313	373	0.00969267
220512_at	DLC1	0.399002085	23	0.009699996
203881_s_at	DMD	0.5472046	666	0.009723642
232912_at	GPR180	0.647989478	15	0.009753671
218251_at	MID1IP1	0.477894568	129	0.009763721
206011_at	CASP1	1.862011673	52	0.009778574
206302_s_at	NUDT4P1	1.971291603	188	0.009789252
229067_at	SRGAP2P1	1.531897664	120	0.009869418
204533_at	CXCL10	2.613104302	92	0.009903092
204706_at	INPP5E	2.063242921	177	0.009910479
210827_s_at	ELF3	0.490617949	83	0.009918611
38487_at	STAB1	0.498258662	286	0.009919973
225285_at	BCAT1	2.366385115	26	0.009956458
227443_at	C9orf150	3.393107742	431	0.009962959
242324_x_at	CCBE1	0.559915058	55	0.01002704
212923_s_at	C6orf145	0.578386517	697	0.010083524
219938_s_at	PSTPIP2	1.7513795	65	0.010089005
228023_x_at	AMY2B	1.667478619	109	0.010122218
203394_s_at	HES1	0.446391591	214	0.010127804
205807_s_at	TUFT1	0.424204558	47	0.010149371
206239_s_at	SPINK1	0.060384111	77	0.010172866
205697_at	SCGN	0.280348281	67	0.010196909
210390_s_at	CCL15-CCI	0.570777476	148	0.010204269
217961_at	SLC25A38	0.519049562	357	0.010219268
209542_x_at	IGF1	0.500355228	399	0.010235965
205668_at	LY75	1.864624411	23	0.010281907
233887_at	GPR126	1.959486985	71	0.010282135
213508_at	C14orf147	0.545326531	296	0.01030857
201701_s_at	PGRMC2	0.645545701	263	0.01033029
202345_s_at	FABP5	3.701223123	75	0.010333893
244352_at	CD84	1.520234204	33	0.010345721
212353_at	SULF1	3.025967781	38	0.010377098
221920_s_at	SLC25A37	0.617354076	42	0.010378697
205243_at	SLC13A3	0.642362103	83	0.010402023
235004_at	RBM24	2.378338382	27	0.010421782
231989_s_at	LOC641298	0.524916214	99	0.010474332
200769_s_at	MAT2A	1.876349668	77	0.010476307
228188_at	FOSL2	2.034485729	146	0.010513213
231675_s_at	ADH4	0.575948267	57	0.010528469

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
230178_s_at	ELP2	1.702615158	151	0.010555834
214279_s_at	NDRG2	1.655783264	417	0.010558746
203639_s_at	FGFR2	0.642802641	84	0.010599987
211162_x_at	SCD	0.372444751	63	0.010604451
220987_s_at	AKIP1 /// NUA2	0.516047101	63	0.010706094
203043_at	ZBED1	1.611410698	741	0.010714008
210461_s_at	ABLIM1	1.877670044	64	0.010738594
228732_at	GUCY1A2	0.53932903	21	0.010741294
229299_at	C5orf33	0.527117966	653	0.010783811
223839_s_at	SCD	0.16911432	143	0.010829584
200832_s_at	SCD	0.166443647	975	0.010831755
214420_s_at	CYP2C9	0.639897252	216	0.010851851
212148_at	PBX1	2.013552448	85	0.010888549
212912_at	RPS6KA2	1.816292949	112	0.010919496
225260_s_at	MRPL32	0.660092075	786	0.010926657
232530_at	PLD1	0.372530816	15	0.010928277
223278_at	GJB2	0.540500454	245	0.010955756
231726_at	PCDHB14	1.866162728	13	0.010970926
229144_at	KAZ	0.655993313	56	0.010984313
205372_at	PLAG1	0.608201933	13	0.010985138
212354_at	SULF1	2.372811652	77	0.010986182
205674_x_at	FXYD2	0.560314935	73	0.011031899
216316_x_at	RP11-548H18.2	0.651996416	76	0.011035302
209122_at	PLIN2	0.505554579	1356	0.011074963
204204_at	SLC31A2	1.673252353	190	0.011081377
221503_s_at	KPNA3	1.663416708	164	0.011157734
209771_x_at	CD24	0.186813942	90	0.011164834
205248_at	DOPEY2	0.332109205	40	0.011201918
211966_at	COL4A2	2.088070461	121	0.011217705
228696_at	SLC45A3	0.357316997	88	0.011218106
212579_at	SMCHD1	1.545471449	91	0.011329699
219594_at	NINJ2	0.347191665	77	0.011344688
223699_at	CNDP1	0.4555206	1076	0.011367899
213388_at	PDE4DIP	1.907367853	138	0.011393074
229659_s_at	PIGR	0.390480791	86	0.011402313
203344_s_at	RBBP8	2.466734292	150	0.011408243
1558034_s_at	CP	0.598814044	4205	0.011414368
223296_at	SLC25A33	1.556566821	275	0.011493142
1554079_at	GALNTL4	1.977422035	94	0.011498477
207609_s_at	CYP1A2	0.169406478	418	0.011502536
223089_at	VEZT	1.582921425	73	0.011560395
235199_at	RNF125	2.678875751	263	0.011592469
212796_s_at	TBC1D2B	1.570068578	296	0.01161994
212446_s_at	LASS6	1.936389732	155	0.011634204
223062_s_at	PSAT1	0.579458621	2097	0.0116449
219230_at	TMEM100	4.505459082	96	0.011727488
217762_s_at	RAB31	1.743786025	134	0.011727531
210275_s_at	ZFAND5	2.423810368	2467	0.011742873
242239_at	NSUN6	0.655512492	169	0.011754657
203961_at	NEBL	1.743881394	54	0.011770608
228049_x_at	SNHG19	2.239297171	325	0.011794636
201105_at	LGALS1	0.51173735	768	0.011807102
205194_at	PSPH	0.509861153	31	0.011830731
203434_s_at	MME	0.66432264	211	0.011913507
1554375_a_at	NR1H4	0.549268982	405	0.011919445
222484_s_at	CXCL14	0.190990679	160	0.011961675
204072_s_at	FRY	0.456326323	202	0.011996028
1555500_s_at	SLC2A4RG	0.643410018	114	0.01202331
202923_s_at	GCLC	0.582462903	1194	0.012026509
220643_s_at	FAIM	1.661906797	35	0.012031208
233123_at	SLC40A1	0.474449508	78	0.012050013
219155_at	PITPNC1	0.649775271	98	0.012068445
214064_at	TF	0.474942899	285	0.012135158
205253_at	PBX1	1.62346242	33	0.012144714
205844_at	VNN1	0.553381119	2044	0.012159757
225512_at	ZBTB38	1.769373414	464	0.012199956
226606_s_at	GTPBP5	0.48421234	99	0.012239251
229975_at	BMPR1B	0.588647202	11	0.012242158

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
208981_at	PECAM1	1.713238044	190	0.012243495
205380_at	PDZK1	0.61498591	315	0.012255614
222714_s_at	LACTB2	0.62550397	357	0.01227295
221718_s_at	AKAP13	1.883785079	408	0.012288733
242923_at	ZNF678	1.555205129	26	0.012309185
213352_at	TMCC1	0.58463639	46	0.012321749
215715_at	SLC6A2	0.500927776	47	0.012396351
226782_at	SLC25A30	2.623480368	515	0.012443647
212831_at	MEGF9	0.529485006	118	0.012458138
214099_s_at	PDE4DIP	1.520969671	56	0.012459541
230214_at	MRV11	1.891611986	44	0.012487795
200776_s_at	BZW1	1.911188967	680	0.01253252
211527_x_at	VEGFA	0.423995834	175	0.012558692
225721_at	SYNPO2	0.600286525	64	0.01256661
212056_at	KIAA0182	0.584576686	164	0.012576462
230741_at	P2RX7	0.448505525	45	0.012601834
213245_at	ADCY1	1.870610773	83	0.012604825
203828_s_at	IL32	3.102707477	465	0.012646401
1553105_s_at	DSG2	1.651841161	44	0.012652586
226425_at	CLIP4	2.252103315	42	0.012688247
222705_s_at	SLC25A15	2.305729016	373	0.012731061
219682_s_at	TBX3	0.418810878	124	0.012745863
216379_x_at	CD24	0.239661438	97	0.012753427
226090_x_at	RABL3	1.58568993	77	0.012762082
222317_at	PDE3B	2.40916907	165	0.012765433
201116_s_at	CPE	3.351234819	401	0.012784979
223605_at	SLC25A18	2.043847605	520	0.012857831
202286_s_at	TACSTD2	0.27983857	25	0.01288013
239394_at	SLC6A2	0.63935807	15	0.012897436
1554438_at	KIAA1217	0.579444541	18	0.012908382
217022_s_at	IGHA1 /// IGH	2.698209855	901	0.01291606
205141_at	ANG	0.621242397	4013	0.012973439
224480_s_at	AGPAT9	4.932196845	280	0.012975406
229476_s_at	THRSP	0.252523181	1015	0.012984348
1556178_x_at	TAF8	1.539416915	32	0.012988751
236335_at	GUCY1A2	0.375117433	42	0.013003579
214734_at	EXPH5	0.407363559	196	0.013027498
234331_s_at	FAM84A	0.564820982	13	0.013031569
200965_s_at	ABLIM1	2.722151369	429	0.0130628
226946_at	C5orf33	0.604108998	778	0.013065927
242957_at	VWCE	0.41344453	101	0.013069635
232422_at	A2LD1	0.43216951	86	0.013077871
230497_at	CELF5	2.499193205	14	0.013105614
1556049_at	RTN4	0.480238092	27	0.013136815
225079_at	EMP2	1.553457869	290	0.013183461
235362_at	LOC729970	0.560997609	38	0.013225959
223967_at	ANGPTL6	0.636969629	97	0.013301489
214417_s_at	FETUB	0.6335887	21	0.013347297
207608_x_at	CYP1A2	0.192730892	2366	0.013359649
204417_at	GALC	1.561832949	128	0.013376413
204678_s_at	KCNK1	0.652953273	49	0.013394509
210521_s_at	FETUB	0.424923735	617	0.013423381
228264_at	ACCS	0.548092546	77	0.013447638
230952_at	RP11-426C22.5	1.636898338	37	0.013456745
221933_at	NLGN4X	0.510821935	14	0.013518507
229389_at	ATG16L2	0.654761211	40	0.013543294
225100_at	FBXO45	1.674332737	52	0.013556173
221193_s_at	ZCCHC10	1.546493926	64	0.013566828
242363_at	DYNC1I2	1.709685113	110	0.01356689
202531_at	IRF1	0.506013171	151	0.013610641
242555_at	C16orf87	1.63312262	36	0.013634114
237765_at	SLC25A47	0.602386348	614	0.01368156
241741_at	CRLS1	0.61261396	153	0.01373779
217319_x_at	CYP4A22	0.584701496	1606	0.013823729
225720_at	SYNPO2	0.398955806	61	0.013829421
206143_at	SLC26A3	0.604359731	9	0.01387331
213524_s_at	GOS2	0.185176323	335	0.013882441
229546_at	LOC653602	0.542828506	7	0.013899663

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
244151_at	LOC285733	0.425940948	82	0.013948444
206271_at	TLR3	0.625594195	91	0.013982682
209255_at	KLHDC10	1.672784683	244	0.014021835
205815_at	REG3A	0.21215135	21	0.014066293
226211_at	MEG3	0.37287952	23	0.014177638
219588_s_at	NCAPG2	1.609212783	22	0.014228274
223240_at	FBXO8	0.599836916	253	0.014314481
204975_at	EMP2	1.791709168	424	0.01433137
213478_at	KAZ	0.343693682	129	0.014333942
228077_at	MRI1	0.588826462	269	0.0143755
205695_at	SDS	4.207198513	2593	0.014435661
203939_at	NT5E	0.526791619	168	0.014442859
203836_s_at	MAP3K5	2.977202668	207	0.014458449
241938_at	QKI	0.561316454	40	0.014556747
232683_s_at	PARP6	0.583564742	49	0.014588056
213929_at	EXPH5	0.345825215	80	0.014636089
221031_s_at	APOLD1	4.582790457	187	0.014641124
217741_s_at	ZFAND5	2.54349347	1416	0.014642314
221904_at	FAM131A	1.536507641	54	0.014727662
211964_at	COL4A2	2.277947784	546	0.014767739
244455_at	KCNT2	1.853562938	111	0.014768943
218322_s_at	ACSL5	0.647541308	820	0.014815589
215483_at	AKAP9	0.549993329	61	0.014882651
210289_at	NAT8	0.47508405	187	0.014894902
227475_at	FOXQ1	2.938123464	71	0.014914473
202295_s_at	CTSH	1.652571742	669	0.014928887
235616_at	TSHZ2	0.560233785	85	0.014999185
215253_s_at	RCAN1	0.661055302	241	0.01500396
224184_s_at	BOC	2.096246671	78	0.015053336
209780_at	PHTF2	1.534237039	101	0.01506329
224996_at	ASPH	0.593844695	321	0.015082094
207655_s_at	BLNK	0.579958837	414	0.015122766
227582_at	KLHDC9	1.509050806	150	0.015164502
239087_at	ANKS4B	0.555838814	51	0.015207609
219615_s_at	KCNK5	3.177081586	99	0.015236474
226490_at	NHSL1	0.558965736	333	0.015273729
229477_at	THRSP	0.266768011	561	0.015281083
201117_s_at	CPE	3.282543752	461	0.015303825
204310_s_at	NPR2	1.616247827	33	0.01531686
228948_at	EPHA4	3.58874537	27	0.01534281
240838_s_at	LOC145837	0.412344356	65	0.015457508
209816_at	PTCH1	1.537654849	12	0.015484031
223635_s_at	SSBP3	1.5328928	81	0.015498144
241765_at	CPM	1.508367559	22	0.01552072
209621_s_at	PDLIM3	0.49312824	134	0.015528138
218211_s_at	MLPH	0.539655411	360	0.015566464
240362_at	BRP44L	0.666608814	16	0.015571913
225236_at	RBM18	1.577462632	152	0.015580895
227471_at	HACE1	1.538770308	39	0.015609748
227449_at	EPHA4	5.117856973	22	0.015617345
231671_at	FGA	0.573262144	256	0.015630214
222846_at	RAB8B	1.731899991	47	0.015640243
229831_at	CNTN3	2.031854489	233	0.015641266
226622_at	MUC20	0.53742859	62	0.015647188
226651_at	HOMER1	0.579460338	27	0.015656417
206265_s_at	GPLD1	0.648450379	89	0.015697748
206963_s_at	NAT8 /// NAT8B	0.47585492	139	0.015790543
1553583_a_at	THRSP	0.352841405	158	0.015815445
208591_s_at	PDE3B	1.615935511	113	0.015819298
206002_at	GPR64	0.624010643	30	0.015886845
235048_at	FAM169A	2.663312595	104	0.015921431
239594_at	LOC145837	0.33923688	114	0.016073486
225895_at	SYNPO2	0.328655951	88	0.016087751
227295_at	IKBIP	1.639686055	22	0.016115631
206561_s_at	AKR1B10	0.465050909	37	0.016126403
220088_at	C5AR1	1.711393156	79	0.016175972
213880_at	LGR5	0.594012262	9	0.016214524
211980_at	COL4A1	2.06796686	498	0.016236206

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
221788_at	PGM3	0.531956282	117	0.016237052
209339_at	SIAH2	0.654860987	283	0.016237729
205669_at	NCAM2	1.629844986	10	0.016289373
210621_s_at	RASA1	1.520687588	131	0.016290605
244774_at	PHACTR2	0.178424987	28	0.016327703
205225_at	ESR1	0.540907963	352	0.01639939
225990_at	BOC	2.268663836	47	0.016526535
200777_s_at	BZW1	1.814611215	1270	0.016549694
227607_at	STAMBPL1	1.870776135	59	0.016612654
240951_at	RORA	2.934671615	20	0.016637663
216396_s_at	EI24	0.60322994	509	0.016683091
214295_at	KIAA0485	0.538228833	108	0.016703428
235420_at	HAPLN4	0.641279794	65	0.016803286
227526_at	CDON	0.661517431	19	0.016819948
1569701_at	PER3	0.361557285	19	0.016845308
204120_s_at	ADK	0.602158694	186	0.01688141
208228_s_at	FGFR2	0.65220957	129	0.016996369
236203_at	HLA-DQA1	0.533541841	10	0.017086004
1555095_at	C6orf123	1.610075426	84	0.017150889
226327_at	ZNF507	1.518372186	112	0.017181309
213682_at	NUP50	1.532795994	405	0.017193679
226875_at	DOCK11	1.990057268	52	0.017262047
213423_x_at	TUSC3	0.361895467	81	0.017333121
244359_s_at	CR936796	1.560136309	15	0.017337139
212088_at	PMPCA	1.594584573	577	0.017340269
235561_at	TXNL1	1.508225293	51	0.017350678
209403_at	LOC10272381	0.622039175	108	0.017394908
223125_s_at	C1orf21	0.659190193	259	0.017465475
226785_at	ATP11C	0.615835242	640	0.017496772
1556601_a_at	SPATA13	0.586476871	60	0.017522039
58916_at	KCTD14	0.60459311	49	0.01755114
214582_at	PDE3B	2.190419563	170	0.017560134
208308_s_at	GPI	1.579137117	609	0.017573682
233599_at	LOC728061	0.418012165	106	0.017675475
206155_at	ABCC2	0.657540941	325	0.017707512
207338_s_at	ZNF200	1.500486062	47	0.017844777
201010_s_at	TXNIP	2.344994912	1605	0.017849296
207735_at	RNF125	2.810419538	100	0.017888321
229903_x_at	RNPC3	1.750395445	65	0.017946955
219446_at	RIC8B	1.660263267	83	0.018014635
214282_at	CP	0.581158482	330	0.018058944
217889_s_at	CYBRD1	1.846469614	31	0.018078717
235395_at	SEC63	1.808781099	20	0.018115854
226701_at	GJA5	1.515488807	13	0.018124264
201695_s_at	PNP	0.644909851	321	0.018177687
229958_at	CLN8	0.645935535	62	0.018180626
221809_at	RANBP10	1.508339594	94	0.018187381
218401_s_at	ZNF281	1.790039945	181	0.018194451
218002_s_at	CXCL14	0.248653675	101	0.018212104
241459_at	LIMCH1	0.627113312	27	0.01823022
1556666_a_at	TTC6	0.637631581	9	0.01823681
227425_at	REPS2	1.602489706	96	0.018270595
203355_s_at	PSD3	2.382820104	524	0.018308592
211367_s_at	CASP1	1.677390657	41	0.018477152
207254_at	SLC15A1	1.942798175	69	0.018564561
216268_s_at	JAG1	1.509327537	262	0.018621786
200618_at	LASP1	0.58084724	564	0.018696312
220306_at	FAM46C	2.176917539	57	0.018699821
230085_at	PDK3	1.749001085	83	0.01871557
206114_at	EPHA4	2.625278333	77	0.01875469
221648_s_at	AGMAT	1.601458836	1719	0.018788373
1555539_at	SDS	2.903309976	55	0.018797728
229567_at	FITM1	0.255171448	117	0.018799499
222693_at	FNDC3B	0.530207574	69	0.018872834
1554691_a_at	PACIN2	0.541771798	145	0.018884801
207383_s_at	RHBDL1	3.536118923	29	0.018927945
227514_at	ITPRIPL2	1.570835691	59	0.018946461
213035_at	ANKRD28	1.764538652	215	0.01905483

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
214153_at	ELOVL5	0.66283943	36	0.019086218
228045_at	SUGT1	1.6053917	58	0.019146821
210041_s_at	PGM3	0.626033074	69	0.019196137
214318_s_at	FRY	0.531671519	33	0.019237043
205633_s_at	ALAS1	0.662139061	1990	0.019249258
232054_at	PCDH20	3.593430748	47	0.019250456
1562321_at	PDK4	2.137909497	17	0.019290878
209167_at	GPM6B	1.882031326	20	0.019320541
200783_s_at	STMN1	1.558868796	41	0.019338386
212184_s_at	TAB2	0.627672986	485	0.019473706
204547_at	RAB40B	0.637988782	191	0.019560242
226272_at	RCAN3	1.721085148	30	0.019606117
226292_at	CAPN5	0.588315118	207	0.019633897
213194_at	ROBO1	4.000863844	153	0.019659862
224497_x_at	HSD17B14	0.628264205	152	0.019733514
226697_at	FAM114A1	0.551621211	154	0.019774795
204150_at	STAB1	0.426541668	268	0.019779443
233540_s_at	CDK5RAP2	1.655487538	87	0.019781837
205858_at	NGFR	0.437021756	75	0.019828065
204057_at	IRF8	1.947645894	324	0.019838648
218923_at	CTBS	0.552942054	227	0.019858411
214204_at	PACRG	0.659604814	21	0.019881937
220346_at	MTHFD2L	1.781667721	47	0.01992397
210353_s_at	SLC6A2	0.651225595	22	0.019976222
207202_s_at	NR1I2	1.825337405	690	0.020017631
227448_at	ARGLU1	2.030392455	38	0.020037061
210643_at	TNFSF11	6.188254698	21	0.020046934
1554348_s_at	CDKN2AIPNL	0.630036859	24	0.020081425
227884_at	TAF15	0.657446238	48	0.020082616
229310_at	KLHL29	2.379016387	52	0.020343117
224494_x_at	HSD17B14	0.568894747	191	0.020349578
200831_s_at	SCD	0.438658381	414	0.020365999
211649_x_at	IGHG1	1.555006664	47	0.020367886
225510_at	OAF	0.599098581	778	0.0203841
207096_at	SAA4	0.627888129	2484	0.020392087
1555854_at	AKR1C2	0.473993622	188	0.020444093
218700_s_at	RAB7L1	0.660995744	91	0.020495645
226876_at	FAM101B	0.565406675	111	0.020559436
212192_at	KCTD12	1.649721558	305	0.020563402
1563298_at	LOC101927331	0.320379241	92	0.020563972
229865_at	FNDC3B	0.658867703	32	0.020613779
227961_at	CTSB	1.630876201	1531	0.020620517
228835_at	RP4-758J24.5	1.503262781	273	0.02065313
215458_s_at	SMURF1	1.566124072	48	0.020672596
217959_s_at	TRAPP4	1.500332701	159	0.02072169
231683_at	GLYAT	0.632713251	310	0.020731392
223361_at	C6orf115	2.425616168	297	0.020754025
204205_at	APOBEC3G	1.674645971	70	0.020754238
204040_at	RNF144A	2.894905809	51	0.020826841
204521_at	C12orf24	1.845988868	64	0.020884088
200790_at	ODC1	1.750591367	632	0.020938021
1560013_at	PDXDC1	0.643074878	32	0.020945135
226390_at	STARD4	0.573508923	168	0.020956826
223844_at	ADAMTS13	0.507329813	100	0.021006216
213293_s_at	TRIM22	1.710332177	404	0.021006719
232523_at	MEGF10	1.672627493	12	0.02101466
220106_at	NPC1L1	0.347634138	177	0.021032004
215126_at	LINC01314	0.539138508	61	0.02107888
235150_at	SESN3	1.647848283	15	0.021082941
242414_at	QPRT	0.65866151	653	0.021087411
53987_at	RANBP10	1.594644565	95	0.021162136
243623_at	SLC1A7	0.629235104	25	0.021241066
60474_at	FERMT1	1.720607175	19	0.021333881
238439_at	ANKRD22	0.242291292	52	0.02144578
219966_x_at	BANP	0.648497247	190	0.02155305
230360_at	GLDN	18.45471656	74	0.021617485
239196_at	ANKRD22	0.317805655	105	0.021655801
201123_s_at	EIF5A	0.353819827	248	0.021676024

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
236704_at	LOC101929787	1.997591365	52	0.021716436
227863_at	CTSD	0.557215617	28	0.021821471
218796_at	FERMT1	1.621743649	34	0.021834567
209185_s_at	IRS2	1.517973251	2061	0.021849467
1554696_s_at	TYMS	1.679962916	23	0.021874319
233375_at	EFCAB2	1.663647076	81	0.021877286
205363_at	BBOX1	1.698908375	691	0.021928583
202068_s_at	LDLR	0.490217451	1132	0.021940094
209098_s_at	JAG1	1.781369448	34	0.021999472
222528_s_at	SLC25A37	0.662728781	87	0.022100016
232000_at	TTC39B	2.293595364	74	0.022213934
219602_s_at	FAM38B	1.758902727	120	0.022411527
224856_at	FKBP5	3.929465289	892	0.022457114
239595_at	GPX2	0.661127088	16	0.022505526
231982_at	C19orf77	0.260919761	69	0.022516421
212960_at	TBC1D9	0.594083341	54	0.022532391
210408_s_at	CPNE6	0.4741172	87	0.022544082
221050_s_at	GTPBP2	1.593313547	53	0.022729743
219475_at	OSGIN1	0.626558165	148	0.022786168
204053_x_at	PTEN	0.642724861	440	0.022790706
201170_s_at	BHLHE40	0.454557429	1128	0.022838065
216834_at	RGS1	3.154344136	206	0.022882697
219575_s_at	COG8 /// PDF	0.653366062	152	0.022958865
231941_s_at	MUC20	0.468283976	24	0.023046113
210085_s_at	ANXA9	1.558374927	157	0.023148634
206840_at	AFM	0.640806597	2130	0.023455613
238762_at	MTHFD2L	1.880668284	169	0.023520417
221872_at	RARRES1	2.032355377	21	0.023569334
229487_at	EBF1	1.712541097	22	0.023570458
227994_x_at	PPDPF	0.41594975	234	0.0235916
203698_s_at	FRZB	1.7709537	45	0.023621335
230716_at	LOC285733	0.492446182	753	0.023778274
207996_s_at	C18orf1	1.743355959	165	0.023909021
221234_s_at	BACH2	0.44047299	19	0.024032312
238635_at	C5orf28	1.56990149	12	0.024058658
204836_at	GLDC	0.544187516	1259	0.024080027
215925_s_at	CD72	1.58644595	42	0.024101172
232055_at	SFXN1	0.5062761	24	0.024236995
206656_s_at	C20orf3	1.581514728	1435	0.02438769
229105_at	GPR39	0.639471622	43	0.024402425
206916_x_at	TAT	2.362008601	6178	0.024431738
226433_at	RNF157	1.761424313	19	0.024457415
227198_at	AFF3	0.484387831	41	0.024463535
209691_s_at	DOK4	1.517958732	162	0.024524767
212482_at	RMND5A	1.577835422	613	0.024543546
226609_at	DCBLD1	1.61561102	79	0.02455041
229429_x_at	LOC728855	1.842389811	714	0.024579501
237248_at	PDE11A	0.485835609	70	0.024644862
228740_at	RP11-999E24.3	0.664789409	13	0.024789924
222180_at	RP11-769O8.3	0.595133371	26	0.024871087
218330_s_at	NAV2	1.833601199	352	0.024970187
218852_at	PPP2R3C	1.521919186	115	0.025026105
234219_at	LOC101928820	0.197151198	54	0.025031605
1553322_s_at	TEAD1	1.747657985	14	0.025119529
235252_at	KSR1	2.022506712	67	0.02520273
207420_at	COLEC10	0.533495423	50	0.025205641
236513_at	PRELID2	3.73636795	20	0.025260028
202532_s_at	DHFR	0.641848058	174	0.02532622
202929_s_at	DDT	0.546599766	1416	0.025420377
205798_at	IL7R	1.613809872	80	0.025491798
231496_at	FCAMR	0.374871154	18	0.025554014
225207_at	PKM4	1.586098843	1897	0.025569541
213464_at	SHC2	0.609482358	242	0.025734797
1557724_a_at	LOC285847	2.157305043	16	0.025738667
1554668_a_at	FAM151A	0.540324632	93	0.025842755
227154_at	IGSF21	1.646568171	16	0.025871952
244840_x_at	DOCK4	0.636676633	19	0.025941063
244531_at	NNT	0.637304755	16	0.025951295

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
228456_s_at	LOC149832	1.526158732	110	0.025971868
1553204_at	C20orf200	2.393597561	44	0.025990823
203020_at	RABGAP1L	1.635463168	225	0.026011158
212944_at	SLC5A3	0.495813185	235	0.026012357
226228_at	AQP4	0.414036926	18	0.026065966
215543_s_at	LARGE	1.578882438	100	0.026140763
219087_at	ASPEN	0.393004249	361	0.026313338
226878_at	HLA-DOA	1.686423815	51	0.026528286
204073_s_at	C11orf9	0.614953994	79	0.026670649
223044_at	SLC40A1	0.589021831	2491	0.026723593
231821_x_at	'// LOC441124 ///	0.660589925	42	0.026795434
209825_s_at	UCK2	0.644171765	110	0.026919513
201294_s_at	WSB1	0.658098204	121	0.026937841
214511_x_at	FCGR1B	1.610890437	21	0.027053762
228101_at	APBA1	2.505967439	170	0.027189557
223075_s_at	AIF1L	1.815559285	53	0.02720382
231824_at	LARP1B	0.599627656	133	0.027218187
205418_at	FES	2.025712379	63	0.027248779
202589_at	TYMS	1.928419123	69	0.027299307
1556147_at	LOC100287426	2.162263244	8	0.027303559
211965_at	ZFP36L1	0.453134171	256	0.027338594
236302_at	PPM1E	1.951887215	65	0.027442923
224991_at	CMIP	1.605119814	111	0.027511648
229850_at	KDSR	0.593849519	265	0.027519874
209256_s_at	KLHDC10	1.676592859	301	0.027636806
232449_at	BCO2	0.628505362	357	0.027767079
202908_at	WFS1	0.656032291	106	0.027797232
219703_at	MNS1	3.155749142	56	0.027946634
220393_at	LGSN	1.81614553	105	0.027963676
238725_at	IRF1	0.494724198	116	0.028017644
205930_at	GTF2E1	1.853647702	82	0.028067618
229160_at	MUM1L1	3.029685133	58	0.028078558
218975_at	COL5A3	0.575317731	48	0.028141793
225805_at	HNRNPUL	1.556375537	52	0.028165459
212715_s_at	MICAL3	0.545534801	96	0.028181361
218036_x_at	NMD3	1.606423274	329	0.028268268
205890_s_at	GABBR1 /// UBD	2.406138884	123	0.028368057
232451_at	RP11-274H2.5	0.564448941	16	0.028379113
207203_s_at	NR112	1.567846422	182	0.02838917
214469_at	HIST1H2AE	0.620216343	18	0.028415267
1569484_s_at	MDN1	0.429796242	31	0.028422376
205968_at	KCNS3	2.918230496	47	0.028449278
224919_at	MRPS6	0.642102172	313	0.028489971
223843_at	SCARA3	0.581659678	19	0.028502449
218346_s_at	SESN1	3.050826124	368	0.028512479
222118_at	CENPN	1.523740914	16	0.028517515
216223_at	CPN2	0.655273594	707	0.02856065
228573_at	ANTXR2	0.620636813	95	0.02858416
219326_s_at	B3GNT2	0.556438421	88	0.028615361
203222_s_at	TLE1	1.655153876	92	0.028620291
203688_at	PKD2	0.652683335	174	0.028690785
1558549_s_at	VNN1	0.524145812	588	0.028945909
1554763_at	UBE2DNL	0.655240323	15	0.029038645
208691_at	TFRC	0.531331252	418	0.029186414
212181_s_at	'// NUDT4P1 /// N	1.600596826	548	0.029245863
238320_at	NEAT1	0.365681833	97	0.029446576
200947_s_at	GLUD1	0.648288898	2357	0.029455106
219300_s_at	CNTNAP2	0.519172096	14	0.02957844
228453_at	KIAA1632	1.507657505	45	0.029625176
204560_at	FKBP5	4.423746852	150	0.029714399
222602_at	UBA6	0.617609454	151	0.029720629
213817_at	IRAK3	1.843756694	14	0.029789925
224817_at	SH3PXD2A	1.612653251	251	0.029808551
219797_at	MGAT4A	0.601215802	47	0.02992389
227654_at	FAM65C	0.40830667	93	0.029962613
220139_at	DNMT3L	0.625772314	78	0.030310702
230481_at	ACY3	1.506547738	80	0.03031675
223382_s_at	ZNRF1	0.563996881	93	0.030398459

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
213649_at	SRSF7	0.647944221	357	0.030487023
233571_x_at	PPDPF	0.381640777	211	0.030518566
212651_at	RHOBTB1	0.430492279	45	0.030550196
228928_x_at	BANP	0.636241619	185	0.030650973
225896_at	MPRIP	1.921711883	102	0.030680121
232195_at	GPR158	0.643009438	11	0.030818778
1553722_s_at	RNF152	2.282568559	17	0.030952368
202145_at	LY6E	0.630101682	280	0.030980019
202067_s_at	LDLR	0.468340339	195	0.031015673
221027_s_at	PLA2G12A	0.641449852	173	0.031121019
204686_at	IRS1	0.552356945	371	0.031151933
204172_at	CPOX	0.640180942	316	0.031192607
226572_at	SOCS7	1.500070051	42	0.031229677
226756_at	CCDC71L	2.923355525	297	0.031251609
206643_at	HAL	2.395198713	1420	0.031280945
227753_at	TMEM139	0.612241263	57	0.031320367
211981_at	COL4A1	1.898747771	195	0.031322503
219157_at	KLHL2	1.559297985	560	0.03133319
238577_s_at	TSHZ2	0.500463227	53	0.031368607
215427_s_at	ZCCHC14	0.621801614	45	0.031379108
217437_s_at	TACC1	2.010584876	99	0.031481381
219065_s_at	JPY30 /// MEMO:	0.585876147	275	0.031565922
226525_at	STK17B	1.621775745	78	0.031595052
225912_at	TP53INP1	0.490478559	1129	0.031696279
206346_at	PRLR	0.652859384	13	0.03174516
1569566_at	TBC1D1	1.69311678	13	0.031771643
1557418_at	ACSL4	0.666217114	18	0.031835675
205203_at	PLD1	0.633712563	105	0.031856692
228202_at	PLN	2.688993255	10	0.032111657
212801_at	CIT	1.657523497	60	0.03216067
221577_x_at	GDF15	0.231141335	129	0.032162888
1554690_a_at	TACC1	1.864219305	76	0.032255113
206290_s_at	RGS7	7.220736756	23	0.032287371
228731_at	GUCY1A2	0.375108656	116	0.032346804
227787_s_at	MED30	1.557818049	88	0.032397812
203395_s_at	HES1	0.528079076	169	0.032404821
205373_at	CTNNA2	0.474090504	19	0.032524823
212736_at	C16orf45	1.664506317	188	0.03255195
1562102_at	AKR1C1	0.346980275	27	0.032560887
216233_at	CD163	1.909863044	14	0.03269116
201042_at	TGM2	0.580324733	261	0.032818876
224762_at	SERINC2	0.666344661	94	0.032839161
242488_at	CHRM3	0.575791805	25	0.032896836
225239_at	VIR612 /// NEAT1	0.252318407	777	0.032969258
204563_at	SELL	1.796062243	52	0.033043559
205666_at	FMO1	0.452812177	29	0.033103533
227918_s_at	ZYG11B	1.634696975	219	0.03313233
209531_at	GSTZ1	0.497352076	811	0.033134689
210534_s_at	B9D1	1.506492584	39	0.033146177
244472_at	LOC388630	1.916831661	36	0.033262588
1568609_s_at	0869 /// LINC011:	2.123530625	159	0.03327884
229318_at	LOC101060691	1.501679592	26	0.033369684
1558322_a_at	PAQR9	1.798677246	170	0.033443622
225752_at	NIPA1	0.622512474	64	0.03351994
227039_at	AKAP13	1.59331143	260	0.033642588
243874_at	LPP	0.588805505	27	0.033714929
234989_at	NEAT1	0.307473761	1269	0.033772712
202988_s_at	RGS1	2.842829621	40	0.03381424
235377_at	C6orf142	2.836863323	227	0.033839285
221024_s_at	SLC2A10	0.543612182	458	0.033898354
204939_s_at	PLN	3.363610605	43	0.033987252
242871_at	PAQR5	6.154534195	46	0.033991618
238008_at	PRR18	1.729210278	96	0.034074203
212480_at	CYTA	1.679202586	186	0.034083416
208650_s_at	CD24	0.358462414	19	0.034100461
211368_s_at	CASP1	1.591582355	113	0.034133312
208149_x_at	DDX11	0.662611967	109	0.034167808
210896_s_at	ASPH	0.596826851	166	0.03419317

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
205960_at	PDK4	2.132504764	201	0.034257564
225645_at	EHF	0.38657772	20	0.034267334
206396_at	SLC1A1	1.967926694	94	0.034338045
225390_s_at	KLF13	2.131451613	191	0.034417482
1553131_a_at	GATA4	0.350374062	78	0.034454481
218468_s_at	GREM1	2.094819451	11	0.034491939
225313_at	C20orf177	1.926817953	28	0.034592098
230577_at	LINC00844	0.520459073	1451	0.034622009
201502_s_at	NFKBIA	1.690634471	1825	0.034623511
212099_at	RHOB	1.660375281	5019	0.034696565
231562_at	APOC2	0.568118287	151	0.03486798
1563053_at	LOC729083	0.332259404	12	0.034907867
221529_s_at	PLVAP	1.622593849	83	0.035114967
217864_s_at	PIAS1	1.559444235	219	0.035129472
225008_at	ASPH	0.55679475	99	0.035177261
202561_at	TNKS	1.698101386	123	0.035226804
220276_at	REGL	2.155341724	20	0.035322992
1557126_a_at	PLD1	0.547773645	24	0.035323258
212928_at	TSPYL4	1.561986251	216	0.035360446
228925_at	AM1A /// ADAM	1.523471643	13	0.035384784
208978_at	CRIP2	1.700031224	116	0.035566668
201656_at	ITGA6	0.656793348	83	0.035566859
243609_at	CYP3A7-CYI	2.630291453	69	0.035603861
244043_at	TFDP2	1.89155309	45	0.035619229
210513_s_at	VEGFA	0.571228131	135	0.035648759
238900_at	HLA-DRB4 /// HLA	0.658338133	10	0.035677127
212670_at	ELN	0.665340837	102	0.035684888
227281_at	SLC29A4	1.573463215	51	0.035699811
233555_s_at	SULF2	1.572285142	29	0.035770139
230769_at	DENND2C	0.648883389	65	0.0357756
1552664_at	FLCN	1.704399615	106	0.035790078
227384_s_at	2725188 /// LOC7	1.585963394	165	0.035841585
218127_at	NFYB	1.575878822	155	0.035849937
225728_at	SORSB2	1.511090007	1397	0.035976843
225923_at	VAPB	1.877052475	103	0.036178435
204724_s_at	COL9A3	0.490054667	34	0.036178696
242691_at	CTC-444N24.11	1.527368704	43	0.036438465
224840_at	FKBP5	3.332233781	1641	0.036518266
230241_at	TOR1AIP2	2.028379262	80	0.036636028
209879_at	SELPLG	1.586920114	42	0.036664898
203987_at	FZD6	0.437269036	30	0.03669793
212256_at	GALNT10	1.555180451	24	0.036780822
223039_at	C22orf13	1.507947171	923	0.036854076
219499_at	SEC61A2	0.55064875	91	0.036869047
220187_at	STEAP4	0.609445863	9	0.03696488
230707_at	SORL1	0.342742289	208	0.03697436
223874_at	ACTR3C	0.621434305	102	0.037036399
241563_at	RP11-384L8.1	0.626478092	62	0.037062024
211657_at	CEACAM6	0.587876142	43	0.037159111
231358_at	MRO	0.511334753	77	0.037162628
1559110_x_at	LOC728613	0.605039995	261	0.037218783
1555122_at	GPR125	2.520011071	34	0.037318353
200600_at	MSN	1.633673454	556	0.037324994
210111_s_at	KLHDC10	1.685125855	849	0.037455438
239682_at	KANSL1L	1.683796761	70	0.037503214
1554806_a_at	FBXO8	0.619603072	219	0.037504257
203357_s_at	CAPN7	1.528688845	116	0.037580249
218469_at	GREM1	2.194359484	11	0.037598643
202436_s_at	CYP1B1	0.344116827	66	0.037611666
231969_at	STOX2	0.52241399	15	0.037623486
214315_x_at	CALR	0.658931003	460	0.03764292
217867_x_at	BACE2	2.098611866	49	0.037675721
217871_s_at	MIF	0.661456219	3101	0.03773101
243841_at	SYNE2	0.664498442	35	0.037785548
243940_at	TSHZ2	0.48429135	57	0.037920292
229088_at	ENPP1	0.616147344	134	0.038033016
229694_at	WDR11	0.654754545	106	0.038147434
222024_s_at	AKAP13	1.685546245	362	0.038170294

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
204361_s_at	SKAP2	1.64198908	25	0.038183794
227371_at	BAIAP2L1	1.558089601	69	0.038191618
201141_at	GNPMB	3.03141093	243	0.038294374
1555923_a_at	C10orf114	0.643392511	105	0.038576278
215498_s_at	MAP2K3	0.611985634	192	0.038588258
236826_at	TTC39B	1.562748649	50	0.038614118
212750_at	PPP1R16B	1.524906002	25	0.038729838
225544_at	TBX3	0.616046343	240	0.038747405
203221_at	TLE1	1.630605436	486	0.038828695
201363_s_at	IVNS1ABP	1.635908669	153	0.038862783
219892_at	TM6SF1	1.596048554	15	0.038926052
219195_at	PPARGC1A	1.942548707	402	0.038993056
227569_at	LNX2	1.69953944	200	0.038999896
222668_at	KCTD15	0.466885386	29	0.039026848
224968_at	CCDC104	1.594173727	51	0.03902983
225133_at	KLF3	0.563241661	371	0.039069092
229223_at	RP11-96D1.11	0.588289816	133	0.039270137
201829_at	NET1	1.669816889	406	0.039307775
213705_at	MAT2A	0.639189457	238	0.039399995
1568765_at	SERPINE1	0.392027566	53	0.039486534
235049_at	ADCY1	1.688304213	61	0.03955054
236273_at	NBPF1	1.677233716	20	0.03961707
201830_s_at	NET1	2.030514173	419	0.039622561
215649_s_at	MVK	0.650228223	44	0.039633539
217175_at	UGT2B15	0.597395048	19	0.039637983
211919_s_at	CXCR4	2.051905152	122	0.039646808
226939_at	CPEB2	0.643069024	440	0.039685752
221139_s_at	CSAD	0.612821093	288	0.039715
218039_at	NUSAP1	1.730128322	54	0.039734223
228821_at	ST6GAL2	0.482646876	20	0.039903256
205425_at	HIP1	1.535319271	50	0.039952871
226485_at	VSIG10	0.611864772	59	0.040011474
212964_at	HIC2	1.527286189	34	0.040179654
213594_x_at	SRSF10	1.540092224	119	0.04023547
217487_x_at	FOLH1	1.573423516	223	0.040246948
1556588_at	C15orf37	1.580550235	69	0.040665727
1569290_s_at	GRIA3	1.921797868	22	0.04084719
1566257_at	GPR180	0.521553512	24	0.040951363
206857_s_at	FKBP1B	0.553557369	20	0.040961467
205911_at	PTH1R	0.660617802	115	0.04101648
226905_at	FAM101B	0.529553203	149	0.04106697
213664_at	SLC1A1	2.322913131	922	0.041098412
36566_at	CTNS	0.660801484	61	0.041126181
213170_at	GPX7	1.629545993	41	0.04128284
209969_s_at	STAT1	0.598973973	156	0.041305991
1559321_at	LOC101928858	2.089975647	75	0.041372361
242947_at	RP4-680D5.8	1.542858619	154	0.041577868
228557_at	L3MBTL4	1.529281229	76	0.041848285
213920_at	CUX2	0.3899813	303	0.041906383
209474_s_at	ENTPD1	1.57129517	16	0.041962268
226264_at	SUSD1	1.540071628	34	0.042077251
239302_s_at	LOC100506922	0.61097907	39	0.042284898
1556314_a_at	RP11-389C8.2	1.88313787	31	0.042377843
238907_at	ZNF780A	1.562676222	14	0.042394122
206288_at	PGGT1B	1.563085436	34	0.042396922
217173_s_at	LDLR	0.555116369	117	0.04248942
204004_at	PAWR	1.68859935	255	0.042518227
210095_s_at	IGFBP3	0.431973291	2455	0.042531282
204039_at	CEBPA	0.292604108	569	0.042613112
202437_s_at	CYP1B1	0.292977847	43	0.042764005
1555728_a_at	MS4A4A	1.993680678	51	0.042796522
200859_x_at	FLNA	2.47443991	210	0.042995044
235745_at	ERN1	1.552704929	56	0.04302538
222717_at	SDPR	1.68700024	240	0.043049474
221215_s_at	RIPK4	0.524410836	360	0.043212279
238493_at	ZNF506	1.671007227	15	0.043272002
217992_s_at	EFHD2	0.622201916	182	0.043278329
209985_s_at	ASCL1	0.299273871	128	0.043365879

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
207571_x_at	C1orf38	1.618921081	74	0.043440314
208719_s_at	DDX17	0.500876521	80	0.043620375
225108_at	AGPS	0.650561956	103	0.043761764
227383_at	LOC727820	1.627599034	170	0.043773763
228004_at	NCRNA00261	0.623519256	1108	0.043990723
217373_x_at	MDM2	1.564337453	29	0.044008174
231996_at	N4BP2	0.655201334	114	0.044025584
205939_at	CYP3A7	3.660229338	1635	0.044061196
227894_at	WDR90	1.892772831	86	0.044103519
203576_at	BCAT2	0.546916147	99	0.044168886
214375_at	PPFIBP1	0.566867947	62	0.044170476
1557675_at	RAF1	0.652042763	82	0.044582737
231703_s_at	ADH4	0.609360621	68	0.044600991
203837_at	MAP3K5	2.867807039	363	0.044643989
214596_at	CHRM3	0.638698629	53	0.044784671
225278_at	PRKAB2	2.048214019	828	0.044790573
219873_at	COLEC11	0.396752661	622	0.045019568
223206_s_at	NMRAL1	0.651726488	204	0.045038241
203637_s_at	MID1	0.590874469	54	0.045078197
226621_at	FGG	1.686496471	95	0.045126491
242317_at	HIGD1A	0.652963617	180	0.045211071
230201_at	FXR1	1.518623105	51	0.045235108
227112_at	TMCC1	0.649658747	159	0.045253478
209475_at	USP15	1.878996285	181	0.045255756
230183_at	EXT1	1.839088254	110	0.045454501
226025_at	ANKRD28	1.782624231	397	0.04548325
221295_at	CIDEA	0.51958119	38	0.045551551
222315_at	LOC100996756	0.473621483	66	0.045692686
201169_s_at	BHLHE40	0.355518464	115	0.045816895
209343_at	EFHD1	2.36940293	449	0.045835723
230187_s_at	29855 /// LOC10	1.646894362	36	0.045990356
206363_at	MAF	0.638418745	178	0.046006219
228186_s_at	RSPO3	0.414921413	51	0.046156647
220437_at	LOC55908	0.333840661	191	0.046220258
203962_s_at	NEBL	1.652659789	53	0.046331828
209774_x_at	CXCL2	1.797349913	1915	0.046381972
224366_s_at	REPS1	1.932865179	464	0.046393352
218559_s_at	MAFB	1.601347748	827	0.046674724
235302_at	GPATCH2L	1.515195179	18	0.046678942
222692_s_at	FNDC3B	0.620894506	182	0.046815503
203697_at	FRZB	1.899568101	39	0.047080383
235740_at	MCTP1	1.52156026	9	0.04709347
229568_at	MOBK12B	2.228515514	34	0.047115777
209824_s_at	ARNTL	1.791509452	89	0.047343457
210397_at	DEFB1	0.16745668	322	0.047376427
202234_s_at	SLC16A1	0.562999718	136	0.047393054
221595_at	RBM48	1.594617405	18	0.047408799
214693_x_at	NBPF10	1.554118697	395	0.047475383
200946_x_at	GLUD1	0.66461286	1305	0.047496807
209304_x_at	GADD45B	1.560210954	1170	0.04777949
231283_at	MGAT4A	0.627416125	53	0.047796566
235945_at	SRD5A2	1.809268227	241	0.047874823
234835_at	LOC100506667	2.117374037	25	0.047891244
208151_x_at	DDX17	0.529895948	186	0.047909216
230407_at	SBNO1	1.606944184	84	0.047917299
229725_at	ACSL6	0.664517044	14	0.048174071
213746_s_at	FLNA	2.801889094	109	0.048287098
208623_s_at	EZR	0.560672337	347	0.048393183
224822_at	DLC1	0.468083696	261	0.048398761
238049_at	GRAMD3	0.509582221	38	0.048432253
209074_s_at	FAM107A	2.679527301	141	0.048558829
226152_at	TTC7B	0.444841999	51	0.048624509
208937_s_at	ID1	0.545852834	600	0.048641667
1569555_at	GDA	0.5645643	28	0.04869154
205935_at	FOXF1	0.440861617	50	0.04899906
217967_s_at	FAM129A	2.369776474	64	0.049051837
214752_x_at	FLNA	2.40944252	194	0.049054835
204938_s_at	PLN	1.795926157	10	0.049078831

Supplementary Table 6: genes significantly dysregulated in shHCA by microarray

Probe.set	Gene.symbol	Fold Change	AveExpr	P.Value
227062_at	NEAT1	0.236754951	622	0.049380265
240380_at	LOC728040	0.644360788	55	0.049649897

Supplementary Table 7: Somatic coding variants identified in shHCA by exome sequencing. Coordinates refers to hg19.

Sample ID	Ensembl Gene ID	Gene symbol	Chromosome	Mutation at	Mutations in Amino Acid
CHC1315T	ENSG00000155363	MOV10	1	g.113232679T>A	p.Pro265Pro
CHC1315T	ENSG00000204624	PTCHD2	1	g.11562096C>T	p.Gly349Gly
CHC1315T	ENSG00000059915	PSD	10	g.104173798C>T	p.Glu427Glu
CHC1315T	ENSG00000183389	OR56A4	11	g.6024362A>G	p.Leu6Ser
CHC1315T	ENSG00000151164	RAD9B	12	g.110956512T>C	p.Phe209Phe
CHC1315T	ENSG00000179912	R3HDM2	12	g.57662202C>T	p.Pro624Pro
CHC1315T	ENSG00000100644	HIF1A	14	g.62187110G>T	p.Glu16X
CHC1315T	ENSG00000140534	C15orf42	15	g.90119197G>A	p.Arg127Gln
CHC1315T	ENSG00000198650	TAT	16	g.71607507A>G	p.Phe115Leu
CHC1315T	ENSG00000121964	GTDC1	2	g.144764950T>C	p.His225Arg
CHC1315T	ENSG00000204335	SP5	2	g.171573406C>A	p.Ala230Asp
CHC1315T	ENSG00000185176	AQP12B	2	g.241622176C>A	p.Ala27Ser
CHC1315T	ENSG00000171055	FEZ2	2	g.36785587T>A	p.Thr352Ser
CHC1315T	ENSG00000142197	DOPEY2	21	g.37649375C>A	p.Gln1897Lys
CHC1315T	ENSG00000198836	OPA1	3	g.193360606G>T	p.Arg346Leu
CHC1315T	ENSG00000076242	MLH1	3	g.37090070G>A	p.Leu653Leu
CHC1315T	ENSG00000083896	YTHDC1	4	g.69203353T>G	p.Lys132Asn
CHC1315T	ENSG00000164403	SHROOM1	5	g.132161011T>C	p.Gly274Gly
CHC1315T	ENSG00000204970	PCDHA1	5	g.140166165A>G	p.Gln97Arg
CHC1315T	ENSG00000151914	DST	6	g.56391263G>C	p.Leu3386Val
CHC1854T	ENSG00000023902	PLEKHO1	1	g.150131291G>T	p.Arg268Leu
CHC1854T	ENSG00000163050	ADCK3	1	g.227153044C>T	p.Thr174Ile
CHC1854T	ENSG00000116544	DLGAP3	1	g.35365289C>T	p.Arg456His
CHC1854T	ENSG00000142892	PIGK	1	g.77627089T>C	p.His235Arg (Splice)
CHC1854T	ENSG00000170967	DDI1	11	g.103908255C>T	p.Pro235Pro
CHC1854T	ENSG00000187486	KCNJ11	11	g.17408832G>T	p.Asp269Glu
CHC1854T	ENSG00000110628	SLC22A18	11	g.2930839A>G	p.Ala145Ala
CHC1854T	ENSG00000161328	LRRC56	11	g.549945G>T	p.Ala124Ser
CHC1854T	ENSG00000134809	TIMM10	11	g.57296377C>T	p.Cys29Tyr
CHC1854T	ENSG00000110076	NRXN2	11	g.64402913A>G	p.Tyr1139His
CHC1854T	ENSG00000111700	SLCO1B3	12	g.21015782G>T	p.Asp241Tyr
CHC1854T	ENSG00000198353	HOXC4	12	g.54447926G>C	p.Gly74Arg
CHC1854T	ENSG00000083642	PDS5B	13	g.33349178G>A	p.Arg1444Arg
CHC1854T	ENSG00000166947	EPB42	15	g.43495325G>T	p.His619Gln
CHC1854T	ENSG00000170921	TANC2	17	g.61432654C>A	p.Arg755Ser
CHC1854T	ENSG00000064545	TMEM161A	19	g.19230883C>T	p.Ala432Ala
CHC1854T	ENSG00000104904	OAZ1	19	g.2271853C>G	p.Ala122Gly
CHC1854T	ENSG00000163286	ALPPL2	2	g.233274480C>G	p.Ala499Ala
CHC1854T	ENSG00000169564	PCBP1	2	g.70315833del	p.Glu320LysfsX23
CHC1854T	ENSG00000125846	ZNF133	20	g.18295898G>A	p.Glu134Lys
CHC1854T	ENSG00000100335	SMCR7L	22	g.39907934C>T	p.Asn75Asn
CHC1854T	ENSG00000100346	CACNA1I	22	g.40058881G>A	p.Arg1123Lys (Splice)
CHC1854T	ENSG00000113742	CPEB4	5	g.173316779G>T	p.Gly157Trp
CHC1854T	ENSG00000039123	SKIV2L2	5	g.54649023A>C	p.Met487Leu
CHC1854T	ENSG00000198339	HIST1H4I	6	g.27107338C>T	p.Ala84Val
CHC1854T	ENSG00000226807	FLJ43860	8	g.142484302G>T	p.Ala565Glu
CHC1854T	ENSG00000095397	DFNB31	9	g.117241018C>A	p.Val218Leu
CHC2325T	ENSG00000041515	MYO16	13	g.109459130A>T	p.His282Leu
CHC2325T	ENSG00000253309	SERPINE3	13	g.51921224A>G	p.Gln185Arg
CHC2325T	ENSG00000225190	PLEKHM1	17	g.43555393C>A	p.Val57Leu
CHC2325T	ENSG00000177511	ST8SIA3	18	g.55020091A>C	p.Lys5Thr
CHC2325T	ENSG00000197563	PIGN	18	g.59815561T>C	p.His187Arg
CHC2325T	ENSG00000129933	MAU2	19	g.19431701_19431715del	p.Ala13_Ala17del
CHC2325T	ENSG00000105063	PPP6R1	19	g.55748039C>A	p.Ala654Ser
CHC2325T	ENSG00000001617	SEMA3F	3	g.50211495C>A	p.Ala95Glu
CHC2325T	ENSG00000113312	TTC1	5	g.159492029C>G	p.Ser279Trp
CHC2325T	ENSG00000169067	ACTBL2	5	g.56778470A>G	p.Phe22Ser
CHC2325T	ENSG00000119326	CTNNA1	9	g.111754960C>G	p.Leu157Phe
CHC2367T	ENSG00000219073	CELA3B	1	g.22307385C>T	p.Asp66Asp
CHC2367T	ENSG00000054282	SDCCAG8	1	g.243652412G>T	p.Leu694Leu
CHC2367T	ENSG00000142765	SYTL1	1	g.27679790G>A	p.Asp442Asn
CHC2367T	ENSG00000173660	UQCRH	1	g.46774797G>C	p.Val27Leu
CHC2367T	ENSG00000188162	OTOG	11	g.17590832G>C	p.Asp531His
CHC2367T	ENSG00000182255	KCNA4	11	g.30034220C>T	p.Glu2Glu
CHC2367T	ENSG00000149091	DGKZ	11	g.46397162G>A	p.Ala819Thr
CHC2367T	ENSG00000174165	ZDHHC24	11	g.66307237A>C	p.Gly206Gly
CHC2367T	ENSG00000087470	DNM1L	12	g.32863902C>T	p.Pro137Ser
CHC2367T	ENSG00000119714	GPR68	14	g.91700722G>T	p.Gln225Lys

Supplementary Table 7: Somatic coding variants identified in shHCA by exome sequencing. Coordinates refers to hg19.

Sample ID	Ensembl Gene ID	Gene symbol	Chromosome	Mutation at	Mutations in Amino Acid
CHC2367T	ENSG00000137766	UNC13C	15	g.54630651C>A	p.Asp1559Glu
CHC2367T	ENSG00000197361	FBXL22	15	g.63889775_63889777del	p.Lys62del
CHC2367T	ENSG00000185924	RTN4RL1	17	g.1839874G>T	p.Ser414Arg
CHC2367T	ENSG00000101670	LIPG	18	g.47101745A>T	p.Asp193Val
CHC2367T	ENSG00000173572	NLRP13	19	g.56424117G>T	p.Leu356Met
CHC2367T	ENSG00000130508	PXDN	2	g.1677538C>T	p.Asp299Asn
CHC2367T	ENSG00000204217	BMPR2	2	g.203421124A>G	p.Glu912Glu
CHC2367T	ENSG00000163121	NEURL3	2	g.97166473A>C	p.Cys73Gly
CHC2367T	ENSG00000130702	LAMA5	20	g.60891827C>G	p.Thr2552Thr
CHC2367T	ENSG00000121211	MND1	4	g.154315486del	p.Thr117ArgfsX5
CHC2367T	ENSG00000222011	FAM185A	7	102392171_102392178c	p.Val162SerfsX4
CHC2367T	ENSG00000106628	POLD2	7	g.44161487T>G	p.Thr56Pro
CHC2367T	ENSG00000157927	RADIL	7	3214_4843215insCTGCC	p.Arg821delinsThrLeuAlaGly
CHC2367T	ENSG00000168300	PCMTD1	8	g.52733143A>G	p.Val281Ala
CHC2367T	ENSG00000171316	CHD7	8	g.61741297G>T	p.Glu1152X
CHC2367T	ENSG00000080503	SMARCA2	9	g.2039776A>G	p.Gln222Gln
CHC2367T	ENSG00000094631	HDAC6	X	g.48663862A>G	p.Glu110Gly
CHC2367T	ENSG00000102359	SRPX2	X	g.99917296G>A	p.Arg96Gln
CHC2432T	ENSG00000116701	NCF2	1	g.183529382G>T	p.Pro439Pro
CHC2432T	ENSG00000169598	DFFB	1	g.3789055G>T	p.Ser234Ile
CHC2432T	ENSG00000078618	NRD1	1	g.52306075T>C	p.Glu151Glu
CHC2432T	ENSG00000150867	PIP4K2A	10	g.22826180C>A	p.Glu391X
CHC2432T	ENSG00000133678	TMEM254	10	g.81841432G>A	p.Glu42Lys
CHC2432T	ENSG00000177103	DSCAML1	11	g.117376412C>T	p.Ala667Thr
CHC2432T	ENSG00000185670	ZBTB3	11	g.62520298G>A	p.Ser330Leu
CHC2432T	ENSG00000184014	DENND5A	11	g.9199780C>A	p.Arg602Leu
CHC2432T	ENSG00000172867	KRT2	12	g.53042806T>A	p.Lys314Asn
CHC2432T	ENSG00000183648	NDUFB1	14	g.92583963T>G	p.Ile54Leu
CHC2432T	ENSG00000140093	SERPINA10	14	g.94756406_94756407del	p.Lys175ArgfsX12
CHC2432T	ENSG00000138622	HCN4	15	g.73616592T>A	p.Ile661Phe
CHC2432T	ENSG00000103811	CTSH	15	g.79231512C>A	p.Glu31Asp (Splice)
CHC2432T	ENSG00000069188	SDK2	17	g.71434211T>C	p.Thr270Ala
CHC2432T	ENSG00000011485	PPP5C	19	g.46878881T>C	p.His128His
CHC2432T	ENSG00000105559	PLEKHA4	19	g.49362248G>A	p.Pro281Ser
CHC2432T	ENSG00000197951	ZNF71	19	g.57133813C>A	p.Ile386Ile
CHC2432T	ENSG00000144229	THSD7B	2	g.138425396C>A	p.Ile1539Ile
CHC2432T	ENSG00000101333	PLCB4	20	g.9404506A>G	p.Ile799Val
CHC2432T	ENSG00000163833	FBXO40	3	g.121340606C>T	p.Thr110Thr
CHC2432T	ENSG00000114204	SERPINI2	3	g.167183351C>T	p.Asp197Asn
CHC2432T	ENSG00000121879	PIK3CA	3	g.178936082G>A	p.Glu542Lys
CHC2432T	ENSG00000225697	SLC26A6	3	g.48669173_48669180del	p.Thr248CysfsX14
CHC2432T	ENSG00000168769	TET2	4	g.106155766G>T	p.Gly223Cys
CHC2432T	ENSG00000007062	PROM1	4	g.16026838T>G	p.Thr194Pro
CHC2432T	ENSG00000135083	CCNJL	5	g.159682561C>A	p.Leu294Leu
CHC2432T	ENSG00000168143	FAM83B	6	g.54805781C>A	p.Ser671X
CHC2432T	ENSG00000254184	TYW1B	7	g.72093938G>A	p.Asn517Asn
CHC2432T	ENSG00000178764	ZHX2	8	g.123964305del	p.Ile186SerfsX2
CHC2432T	ENSG00000178764	ZHX2	8	g.123964307T>A	p.Ile186Asn
CHC2432T	ENSG00000261150	EPPK1	8	g.144942212A>G	p.Leu1737Pro
CHC2432T	ENSG00000130224	LRCH2	X	g.114468600G>A	p.Ala2Val
CHC2432T	ENSG00000177485	ZBTB33	X	g.119389146C>A	p.Pro626Thr
CHC2432T	ENSG00000198889	DCAF12L1	X	g.125685608G>A	p.His328His
CHC2432T	ENSG00000147050	KDM6A	X	g.44870227C>T	p.Leu136Phe
CHC2432T	ENSG00000147050	KDM6A	X	g.44870231G>T	p.Gly137Val
CHC2432T	ENSG00000101945	SUV39H1	X	g.48557354G>A	p.Lys27Lys
CHC2446T	ENSG00000197323	TRIM33	1	g.115006106T>C	p.Thr240Ala
CHC2446T	ENSG00000143549	TPM3	1	g.154145571T>G	p.Lys125Gln
CHC2446T	ENSG00000198400	NTRK1	1	g.156845387C>A	p.Ser477Tyr
CHC2446T	ENSG00000162738	VANGL2	1	g.160390936G>C	p.Glu344Asp
CHC2446T	ENSG00000116809	ZBTB17	1	g.16271254G>T	p.Gln336X
CHC2446T	ENSG00000196482	ESRRG	1	g.216680437G>T	p.His384Gln
CHC2446T	ENSG00000107815	C10orf2	10	g.102750271G>A	p.Met521Ile
CHC2446T	ENSG00000023171	GRAMD1B	11	g.123484241C>G	p.Thr558Ser
CHC2446T	ENSG00000258588	TRIM34	11	g.5662434C>A	p.Ala263Asp
CHC2446T	ENSG00000149150	SLC43A1	11	g.57256774G>A	p.Leu429Leu
CHC2446T	ENSG00000205420	KRT6A	12	g.52882287C>A	p.Glu417X
CHC2446T	ENSG00000123384	LRP1	12	g.57552221G>T	p.Gly533Val
CHC2446T	ENSG00000151846	PABPC3	13	g.25671892G>T	p.Arg519Leu

Supplementary Table 7: Somatic coding variants identified in shHCA by exome sequencing. Coordinates refers to hg19.

Sample ID	Ensembl Gene ID	Gene symbol	Chromosome	Mutation at	Mutations in Amino Acid
CHC2446T	ENSG00000165572	KBTBD6	13	g.41705440G>T	p.Thr403Lys
CHC2446T	ENSG00000123200	ZC3H13	13	g.46538138A>T	p.Met1505Lys
CHC2446T	ENSG00000136155	SCEL	13	g.78138007G>T	p.Arg88Leu
CHC2446T	ENSG00000165300	SLITRK5	13	g.88330293C>T	p.Pro884Ser
CHC2446T	ENSG00000137802	MAPKBP1	15	g.42105273C>A	p.Leu265Ile
CHC2446T	ENSG00000171914	TLN2	15	g.63032892C>A	p.Leu1317Met
CHC2446T	ENSG00000166938	DIS3L	15	g.66624246C>A	p.Leu774Ile
CHC2446T	ENSG00000140853	NLRC5	16	g.57111266G>T	p.Gly1632Trp
CHC2446T	ENSG00000132142	ACACA	17	g.35548072C>A	p.Asp1484Tyr
CHC2446T	ENSG00000132142	ACACA	17	g.35548073C>A	p.Met1483Ile
CHC2446T	ENSG00000204347	BTBD17	17	g.72353504C>A	p.Pro243Pro
CHC2446T	ENSG00000065325	GLP2R	17	g.9763363G>T	p.Glu290Asp
CHC2446T	ENSG00000132199	ENOSF1	18	g.685922_685923del	p.Leu165AspfsX12
CHC2446T	ENSG00000127511	SIN3B	19	g.16989031C>A	p.Gln1030Lys
CHC2446T	ENSG00000105329	TGFB1	19	g.41858864C>T	p.Gly29Glu
CHC2446T	ENSG00000104888	SLC17A7	19	g.49934017C>A	p.Gly481Val
CHC2446T	ENSG00000125733	TRIP10	19	g.6743548C>A	p.Ala151Glu
CHC2446T	ENSG00000168702	LRP1B	2	g.141763012G>A	p.Arg799X
CHC2446T	ENSG00000168702	LRP1B	2	g.141771162T>G	p.Leu781Leu
CHC2446T	ENSG00000155657	TTN	2	g.179650750G>T	p.Thr732Asn
CHC2446T	ENSG00000099953	MMP11	22	g.24121490C>A	p.Leu75Leu
CHC2446T	ENSG00000163884	KLF15	3	g.126071130C>A	p.Thr212Thr
CHC2446T	ENSG00000127249	ATP13A4	3	g.193209127G>T	p.Leu198Leu
CHC2446T	ENSG00000196277	GRM7	3	g.7494454C>A	p.Gly445Gly
CHC2446T	ENSG00000227124	ZNF717	3	g.75786499C>T	p.Glu709Lys
CHC2446T	ENSG00000227124	ZNF717	3	g.75786506T>C	p.Lys06Lys
CHC2446T	ENSG00000156990	RPUSD3	3	g.9880818C>A	p.Gln254His
CHC2446T	ENSG00000064692	SNCAIP	5	g.121776375T>G	p.Leu450Val
CHC2446T	ENSG00000250120	PCDHA10	5	g.140237549C>A	p.Thr639Asn
CHC2446T	ENSG00000152818	UTRN	6	g.144765443A>T	p.Val513Val
CHC2446T	ENSG00000152818	UTRN	6	g.144765445G>T	p.Cys514Phe
CHC2446T	ENSG00000206503	HLA-A	6	g.29911317A>G	p.Thr206Ala
CHC2446T	ENSG00000137161	CNPY3	6	g.42906331C>A	p.Gly213Gly
CHC2446T	ENSG00000169876	MUC17	7	g.100683474T>G	p.Val2926Gly
CHC2446T	ENSG00000204983	PRSS1	7	g.142459626C>T	p.Arg68Cys (Splice)
CHC2446T	ENSG00000221836	OR2A5	7	g.143748345T>C	p.Met284Thr
CHC2446T	ENSG00000242802	AP5Z1	7	g.4820822G>T	p.Glu20X
CHC2446T	ENSG00000070501	POLB	8	g.42196143A>G	p.Met1?
CHC2446T	ENSG00000168300	PCMTD1	8	g.52733127G>A	p.Asn286Asn
CHC2446T	ENSG00000107186	MPDZ	9	g.13192152C>A	p.Cys649Phe
CHC2446T	ENSG00000198883	PNMA5	X	g.152159637C>A	p.Ser169Ile
CHC2603T	ENSG00000137992	DBT	1	g.100661841G>C	p.Asn473Lys
CHC2603T	ENSG00000054523	KIF1B	1	g.10331632T>C	p.Leu265Leu
CHC2603T	ENSG00000177272	KCNA3	1	g.111217256T>A	p.Asp59Val
CHC2603T	ENSG00000127481	UBR4	1	g.19455567G>A	p.Leu2970Leu (Splice)
CHC2603T	ENSG00000162585	C1orf86	1	g.2132527G>T	p.Ala4Glu
CHC2603T	ENSG00000120451	SNX19	11	g.130784716C>T	p.Leu373Leu
CHC2603T	ENSG00000175216	CKAP5	11	g.46783624G>A	p.Arg1383Cys
CHC2603T	ENSG00000133318	RTN3	11	g.63487784A>G	p.Ile585Val
CHC2603T	ENSG00000197891	SLC22A12	11	g.64367300C>T	p.Thr408Met
CHC2603T	ENSG00000256223	ZNF10	12	g.133732484A>G	p.Thr218Ala
CHC2603T	ENSG00000139496	NUPL1	13	g.25875951T>A	p.Ser14Thr
CHC2603T	ENSG00000151322	NPAS3	14	g.34269243C>A	p.Ser577Tyr
CHC2603T	ENSG00000205047		16	g.87735962T>G	p.Ala53Ala
CHC2603T	ENSG00000214860	EVPLL	17	g.18286677G>A	p.Ala255Ala
CHC2603T	ENSG00000121058	COIL	17	g.55023836G>T	p.Gln509Lys
CHC2603T	ENSG00000161270	NPHS1	19	g.36333318C>G	p.Ala823Ala
CHC2603T	ENSG00000105755	ETHE1	19	g.44011007C>A	p.Ala254Ser
CHC2603T	ENSG00000144406	UNC80	2	g.210783318A>C	p.Pro1692Pro
CHC2603T	ENSG00000021826	CPS1	2	g.211481202dup	p.Trp882ValfsX5
CHC2603T	ENSG00000185133	INPP5J	22	g.31521757A>C	p.Pro344Pro
CHC2603T	ENSG00000154174	TOMM70A	3	g.100096694T>C	p.Glu316Gly
CHC2603T	ENSG00000183960	KCNH8	3	g.19295334G>A	p.Glu89Lys
CHC2603T	ENSG00000138688	KIAA1109	4	g.123195523G>T	p.Glu2824Asp
CHC2603T	ENSG00000157796	WDR19	4	g.39233841C>T	p.Asn734Asn
CHC2603T	ENSG00000109265	KIAA1211	4	g.57180505G>A	p.Pro279Pro
CHC2603T	ENSG00000120318	ARAP3	5	141033715_141033726c	p.Gln1476_Gly1479del
CHC2603T	ENSG00000125354	06-sept	X	g.118763372T>C	p.Lys397Glu

Supplementary Table 7: Somatic coding variants identified in shHCA by exome sequencing. Coordinates refers to hg19.

Sample ID	Ensembl Gene ID	Gene symbol	Chromosome	Mutation at	Mutations in Amino Acid
CHC603T	ENSG00000160753	RUSC1-AS1	1	g.155291166A>G	p.Ser38Ser
CHC603T	ENSG00000117501	C1orf129	1	g.170955824G>A	p.Leu284Leu
CHC603T		CCDC147	10	g.106118337A>G	p.Lys83Arg
CHC603T	ENSG00000188906	LRRK2	12	g.40716288G>T	p.Asp1829Tyr
CHC603T	ENSG00000198033	TUBA3C	13	g.19751340C>T	p.Pro261Pro
CHC603T	ENSG00000158270	COLEC12	18	g.321726C>T	p.Gly715Gly
CHC603T	ENSG00000131864	USP29	19	g.57641414C>T	p.Asn457Asn
CHC603T	ENSG00000123636	BAZ2B	2	g.160239244C>A	p.Glu1277Asp
CHC603T	ENSG00000168397	ATG4B	2	g.242593011G>A	p.Arg90Gln
CHC603T	ENSG00000099960	SLC7A4	22	g.21385289del	p.Ile272SerfsX19
CHC603T	ENSG00000181789	COPG1	3	g.128984459G>T	p.Ser431Ile
CHC603T	ENSG00000215375	MYL5	4	g.675718G>T	p.Ala153Ser
CHC603T	ENSG00000132405	TBC1D14	4	g.6925651G>A	p.Asp179Asn
CHC603T	ENSG00000153404	PLEKHG4B	5	g.143575G>T	p.Ala234Ser
CHC603T	ENSG00000038382	TRIO	5	g.14488125G>T	p.Ser2463Ile
CHC603T	ENSG00000164418	GRIK2	6	g.102513730C>T	p.Ser874Phe
CHC603T	ENSG00000170915	PAQR8	6	g.52268471T>A	p.Tyr154Asn
CHC603T	ENSG00000160948	VPS28	8	g.145649377G>A	p.Leu199Phe
CHC605T	ENSG00000131591	C1orf159	1	g.1026913C>T	p.Arg4Gln
CHC605T	ENSG00000160753	RUSC1-AS1	1	g.155291166A>G	p.Ser38Ser
CHC605T		KIAA0754	1	g.39877706C>G	p.Ala590Gly
CHC605T	ENSG00000171502	COL24A1	1	g.86307795C>T	p.Gly1176Ser
CHC605T	ENSG00000048740	CELF2	10	g.11308625G>T	p.Gln170His
CHC605T	ENSG00000179817	MRGPRX4	11	g.18195553T>C	p.Tyr250Tyr
CHC605T	ENSG00000181761	OR8H3	11	g.55889957C>A	p.Leu37Ile
CHC605T	ENSG00000175536	LIPT2	11	g.74204650C>T	p.Glu33Glu
CHC605T	ENSG00000013573	DDX11	12	g.31256569T>C	p.Cys864Arg
CHC605T	ENSG00000165805	C12orf50	12	g.88376933C>T	p.Arg389Gln
CHC605T	ENSG00000100583	SAMD15	14	g.77845223_77845224del	p.Val488GlnfsX2
CHC605T	ENSG00000254585	MAGEL2	15	g.23890891G>C	p.Gln667Glu
CHC605T	ENSG00000254585	MAGEL2	15	g.23890895_23890927del	p.Ser655_Pro665del
CHC605T	ENSG00000183655	KLHL25	15	g.86312352G>A	p.Pro230Pro
CHC605T	ENSG00000007545	CRAMP1L	16	g.1675986G>T	p.Gly120Val
CHC605T		LOC81691	16	g.20826371G>A	p.Arg125Ser
CHC605T	ENSG00000172716	SLFN11	17	g.33690405C>A	p.Arg141Leu
CHC605T	ENSG00000166398	KIAA0355	19	g.34821229_34821243del	p.Leu414_Gln418del
CHC605T	ENSG00000118997	DNAH7	2	g.196822084A>G	p.Ile993Ile
CHC605T	ENSG00000123485	HJURP	2	g.234758503G>A	p.Asp81Asp
CHC605T	ENSG00000168397	ATG4B	2	g.242593011G>A	p.Arg90Gln
CHC605T	ENSG00000115760	BIRC6	2	g.32724727A>G	p.Glu2861Gly
CHC605T	ENSG00000155066	PROM2	2	g.95954724G>C	p.Val829Leu
CHC605T	ENSG00000250588	SCHIP1	3	g.159604077G>T	p.Lys320Asn
CHC605T	ENSG00000145113	MUC4	3	g.195487872A>G	p.Ser675Pro
CHC605T	ENSG00000131711	MAP1B	5	g.71489906C>A	p.Pro242Thr
CHC605T	ENSG00000137166	FOXP4	6	g.41565582G>A	p.Ala597Thr
CHC605T	ENSG00000170950	PGK2	6	g.49753880C>T	p.Gly341Arg
CHC605T	ENSG00000197157	SND1	7	g.127729599G>T	p.Cys826Phe
CHC605T	ENSG00000178209	PLEC	8	g.145006815G>A	p.Tyr738Tyr
CHC605T	ENSG00000036448	MYOM2	8	g.2007298C>T	p.Cys195Cys
CHC605T	ENSG00000184661	CDCA2	8	g.25360917G>A	p.Gly567Glu
CHC605T		TMEM66	8	g.29924341G>A	p.Thr265Ile
CHC605T	ENSG00000165078	CPA6	8	g.68658266A>G	p.Tyr33Tyr
CHC605T	ENSG00000160339	FCN2	9	g.137777113C>T	p.Asp110Asp
CHC605T	ENSG00000107281	NPDC1	9	g.139934875C>T	p.Arg241Gln
CHC605T	ENSG00000169895	SYAP1	X	g.16759892C>A	p.Gln139Lys
CHC862T	ENSG00000178104	PDE4DIP	1	g.144994681_144994683del	p.Lys154del
CHC862T	ENSG00000067704	IARS2	1	g.220316359T>G	p.Ala878Ala
CHC862T	ENSG00000203697	CAPN8	1	g.22749_223722755delAA	p.?
CHC862T	ENSG00000126107	HECTD3	1	g.45469202C>A	p.Val850Leu
CHC862T	ENSG00000091262	ABCC6	16	g.16248528C>A	p.Gly1389Cys
CHC862T	ENSG00000171487	NLRP5	19	g.56539519C>T	p.Leu640Leu
CHC862T	ENSG00000159399	HK2	2	g.75116514G>A	p.Ala840Thr
CHC862T	ENSG00000134313	KIDINS220	2	g.8940534C>A	p.Gly299Val
CHC862T	ENSG00000136939	OR1L4	9	g.125487125T>A	p.Leu286Gln
CHC949T	ENSG00000196177	ACADSB	10	g.124810597C>A	p.Thr341Thr
CHC949T	ENSG00000198250	ANTXRL	10	g.47669146C>A	p.Ala245Asp (Splice)
CHC949T	ENSG00000138316	ADAMTS14	10	g.72520142G>A	p.Val1072Ile
CHC949T	ENSG00000149294	NCAM1	11	g.113075154G>A	p.Gly92Ser

Supplementary Table 7: Somatic coding variants identified in shHCA by exome sequencing. Coordinates refers to hg19.

Sample ID	Ensembl Gene ID	Gene symbol	Chromosome	Mutation at	Mutations in Amino Acid
CHC949T	ENSG00000180785	OR51E1	11	g.4674374C>G	p.Ile206Met
CHC949T	ENSG00000168959	GRM5	11	g.88300296G>A	p.Ser852Leu
CHC949T	ENSG00000168959	GRM5	11	g.88300298C>A	p.Lys851Asn
CHC949T	ENSG00000230657	PRB4	12	g.11461633T>C	p.His95Arg
CHC949T	ENSG00000073614	KDM5A	12	g.430193G>T	p.Pro837Thr
CHC949T	ENSG00000261308	FIGNL2	12	g.52214698C>G	p.Arg500Arg
CHC949T	ENSG00000110955	ATP5B	12	g.57038956C>T	p.Leu103Leu (Splice)
CHC949T	ENSG00000165480	SKA3	13	21746645_21746646ins	p.D56_splice
CHC949T	ENSG00000151835	SACS	13	g.23912436T>G	p.Lys1860Thr
CHC949T	ENSG00000102786	INTS6	13	g.51952480T>C	p.Lys499Lys
CHC949T	ENSG00000102786	INTS6	13	g.51952573A>C	p.Asp468Glu
CHC949T	ENSG00000151320	AKAP6	14	g.33291246A>C	p.Leu1409Phe
CHC949T	ENSG00000187535	IFT140	16	g.1637944C>A	p.Ala298Ser
CHC949T	ENSG00000069345	DNAJA2	16	g.47001529del	p.Lys158SerfsX13
CHC949T	ENSG00000132475	H3F3B	17	g.73774772G>A	p.Phe105Phe
CHC949T	ENSG00000205209	SCGB2B2	19	g.35085242A>G	p.Asp28Asp
CHC949T	ENSG00000167676	PLIN4	19	g.4511504_4511602del	p.Ala784_Asp816del
CHC949T	ENSG00000167676	PLIN4	19	g.4512848_4512946del	p.Met331_Ala363del
CHC949T	ENSG00000181781	ODF3L2	19	g.464293G>T	p.Pro141Thr
CHC949T	ENSG00000259009	TPRX2P	19	g.48364219G>T	p.Arg144Met
CHC949T	ENSG00000170909	OSCAR	19	g.54599356C>G	p.Val150Leu
CHC949T	ENSG00000175497	DPP10	2	g.116485400T>A	p.Ile195Ile
CHC949T		LOC100652824	2	g.203019531del	p.Lys682ArgfsX32
CHC949T	ENSG00000152154	TMEM178A	2	g.39893305A>C	p.His64Pro
CHC949T	ENSG00000183773	AIFM3	22	g.21331338G>T	p.Leu412Leu
CHC949T	ENSG00000128203	ASPHD2	22	g.26839121C>A	p.Val353Val
CHC949T	ENSG00000138650	PCDH10	4	g.134073692G>T	p.Pro799Pro
CHC949T	ENSG00000183090	FREM3	4	g.144619987C>T	p.Leu614Leu
CHC949T	ENSG00000109654	TRIM2	4	g.154216813G>T	p.Asp352Tyr
CHC949T	ENSG00000205678	TECRL	4	g.65188509G>A	p.Gly111Gly (Splice)
CHC949T	ENSG00000112146	FBXO9	6	g.52958305C>T	p.Thr312Ile
CHC949T	ENSG00000146147	MLIP	6	g.53976348C>A	p.Ser24X
CHC949T	ENSG00000091138	SLC26A3	7	g.107418685T>C	p.Gly483Gly
CHC949T	ENSG00000133612	AGAP3	7	g.150831568G>T	p.Ala470Ser
CHC949T	ENSG00000170852	KBTBD2	7	g.32910283A>G	p.Ser182Ser
CHC949T	ENSG00000164916	FOXK1	7	g.4801940A>C	p.Thr683Pro
CHC949T	ENSG00000255394	C8orf49	8	g.11619105_11619110del	p.Thr162del
CHC949T	ENSG00000255394	C8orf49	8	g.11619112A>T	p.Ile64Leu
CHC949T	ENSG00000171428	NAT1	8	g.18079724T>G	p.Phe56Leu
CHC949T	ENSG00000180828	BHLHE22	8	g.65494020G>A	p.Gly225Ser
CHC949T	ENSG00000182752	PAPPA	9	g.119124880A>T	p.Ser1453Cys
CHC949T	ENSG00000126767	ELK1	X	g.47497205C>A	p.Gly344Val
CHC949T	ENSG00000130385	BMP15	X	g.50653924G>A	p.Glu47Glu

Supplementary Table 8: somatic structural variation of whole genome sequencing of 3 shHCA (hg19)

Sample	CHROM	Start	End	Type	Affected genes
CHC605T	chr1	106563124	106651394	Deletion	
CHC605T	chr4	136754079	136754079	Insertion	
CHC605T	chr6	75010330	75010395	Deletion	
CHC605T	chr7	6489307	6490046	Tandem duplication	
CHC605T	chr7	158882944	158883213	Deletion	VIPR2
CHC605T	chr9	135938360	135958876	Deletion	CEL,CELP
CHC605T	chr10	134637770	134638616	Tandem duplication	
CHC605T	chr11	50277770	50278724	Deletion	
CHC605T	chr12	57849348	57851031	Deletion	INHBE
CHC605T	chr14	21538480	21538540	Deletion	FLJ10357
CHC605T	chr16	22019828	22092003	Deletion	C16orf52
CHC605T	chr18	50827381	50827442	Deletion	DCC
CHC605T	chr19	49539572	49551507	Deletion	CGB1,CGB8,CGB5,SNAR-G1
CHC605T	chr20	50484700	50484982	Deletion	
CHC605T	chrX	1756734	1761268	Deletion	ASMT
CHC605T	chrX	1760194	1761268	Deletion	ASMT
CHC605T	chrX	153430952	153431368	Deletion	
CHC2432T	chr4	154405748	154406122	Deletion	KIAA0922
CHC2432T	chr9	131472056	131472332	Deletion	PKN3
CHC2432T	chr12	57848774	57850823	Deletion	INHBE
CHC2432T	chr12	97323366	97323989	Deletion	NEDD1
CHC2432T	chr12	105693905	105707968	Deletion	
CHC2432T	chr19	43382572	43420764	Deletion	PSG6,PSG1
CHC2432T	chr19	49439834	49440198	Deletion	DHDH
CHC2432T	chr21	15232004	15251319	Tandem duplication	
CHC2446T	chr1	51255587	51449320	Deletion	CDKN2C,FAF1
CHC2446T	chr3	125443141	125465796	Deletion	
CHC2446T	chr4	164014407	164018700	Deletion	
CHC2446T	chr6	21146116	24665276	Deletion	KIAA0319,CDKAL1,DCDC2,GPLD1,SOX
CHC2446T	chr6	32516663	32541489	Deletion	HLA-DRB6
CHC2446T	chr7	38392991	38401885	Deletion	
CHC2446T	chr7	88091180	88091890	Deletion	
CHC2446T	chr8	59322909	59323104	Deletion	
CHC2446T	chr9	68160916	68161012	Deletion	
CHC2446T	chr9	117090025	117096975	Deletion	ORM2,AKNA
CHC2446T	chr10	35597002	35597244	Deletion	CCNY
CHC2446T	chr11	15285461	15286038	Tandem duplication	
CHC2446T	chr11	18963943	18986218	Deletion	
CHC2446T	chr11	60998172	61017889	Deletion	PGA4,PGA5
CHC2446T	chr12	11428201	11473727	Deletion	PRB4
CHC2446T	chr12	57845166	57853835	Inversion	INHBE
CHC2446T	chr14	24428122	24463091	Deletion	DHRS4L2,DHRS4
CHC2446T	chr16	29717022	29717335	Deletion	
CHC2446T	chr17	63496272	63496368	Deletion	
CHC2446T	chr18	14269347	14288962	Deletion	
CHC2446T	chr19	43694129	43713139	Deletion	PSG4
CHC2446T	chr19	45835675	45904288	Tandem duplication	PPP1R13L,KLC3,ERCC2
CHC2446T	chr19	54754860	54778696	Deletion	LILRB2,LILRB5
CHC2446T	chr19	55250841	55267353	Deletion	KIR3DP1,KIR2DL3
CHC2446T	chr20	42762824	42763258	Deletion	JPH2
CHC2446T	chr20	42762845	42763258	Deletion	JPH2
CHC2446T	chr22	20710992	20712319	Tandem duplication	



Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr10:9657442T>C	Unknown		
CHC2432T	g.chr12:77538599C>A	Unknown		
CHC2432T	g.chr14:88671874T>A	KCNK10		
CHC2432T	g.chr15:49297789T>G	SECISBP2L		
CHC2432T	g.chr16:49956171A>G	RP11-305A4.3		
CHC2432T	g.chr19:32339187G>T	Unknown		
CHC2432T	g.chr19:419655G>A	SHC2		
CHC2432T	g.chr19:49670838C>T	TRPM4		
CHC2432T	g.chr21:46127331T>A	TSPEAR		
CHC2432T	g.chr3:44419885C>T	TCAIM		
CHC2432T	g.chr5:110450512A>C	WDR36		
CHC2432T	g.chr6:83008698A>G	Unknown		
CHC2432T	g.chr7:83692042G>T	SEMA3A		
CHC2432T	g.chr8:106889522A>T	RP11-152P17.2		
CHC2432T	g.chr8:122291025C>T	Unknown		
CHC2432T	g.chr8:66404453A>G	Unknown		
CHC2432T	g.chr8:84607800T>C	Unknown		
CHC2432T	g.chr9:70976112T>C	PGM5		
CHC2432T	g.chr1:100188428G>A	FRRS1		
CHC2432T	g.chr1:101845142A>G	RP11-157N3.1		
CHC2432T	g.chr1:102926989C>T	Unknown		
CHC2432T	g.chr1:103019957T>A	Unknown		
CHC2432T	g.chr1:103259720A>G	RP5-936J12.1		
CHC2432T	g.chr1:104624411G>C	Unknown		
CHC2432T	g.chr1:105067128A>T	Unknown		
CHC2432T	g.chr1:105349642C>A	Unknown		
CHC2432T	g.chr1:105608293G>C	Unknown		
CHC2432T	g.chr1:106494698G>A	RP11-24P14.1		
CHC2432T	g.chr1:107214489A>T	Unknown		
CHC2432T	g.chr1:107442150T>G	Unknown		
CHC2432T	g.chr1:107709783T>C	NTNG1		
CHC2432T	g.chr1:109108098T>G	FAM102B		
CHC2432T	g.chr1:111083842G>T	Unknown		
CHC2432T	g.chr1:111095687T>G	Unknown		
CHC2432T	g.chr1:111479186C>T	RP11-96K19.4		
CHC2432T	g.chr1:115182626A>G	DENND2C		
CHC2432T	g.chr1:115330662T>G	Unknown		
CHC2432T	g.chr1:115598024C>T	TSPAN2		
CHC2432T	g.chr1:115768683C>A	Unknown		
CHC2432T	g.chr1:115928104G>T	Unknown		
CHC2432T	g.chr1:117198048C>A	IGSF3		
CHC2432T	g.chr1:120854780A>G	FAM72B		
CHC2432T	g.chr1:120884992G>A	RP11-439A17.4		
CHC2432T	g.chr1:14033506A>G	PRDM2		
CHC2432T	g.chr1:143129315G>T	RP11-782C8.2		
CHC2432T	g.chr1:146859170A>G	Unknown		
CHC2432T	g.chr1:147239752C>T	GJA5		
CHC2432T	g.chr1:14765669T>G	Unknown		
CHC2432T	g.chr1:1484471T>A	SSU72		
CHC2432T	g.chr1:14972852G>C	KAZN		
CHC2432T	g.chr1:149938189T>C	OTUD7B		
CHC2432T	g.chr1:151756053C>T	TDRKH		
CHC2432T	g.chr1:153270232C>A	Unknown		
CHC2432T	g.chr1:154935137C>G	SHC1		
CHC2432T	g.chr1:156346811A>C	RHBG		
CHC2432T	g.chr1:158851397C>A	Unknown		
CHC2432T	g.chr1:160878780C>T	Unknown		
CHC2432T	g.chr1:162894381C>A	Unknown		
CHC2432T	g.chr1:165302228T>A	LMX1A		
CHC2432T	g.chr1:165521156A>C	LRRC52		
CHC2432T	g.chr1:168225288A>G	Unknown		
CHC2432T	g.chr1:171456506A>G	PRRC2C		
CHC2432T	g.chr1:175013004G>A	Unknown		
CHC2432T	g.chr1:175449378C>A	TNR		
CHC2432T	g.chr1:175694553T>C	TNR		
CHC2432T	g.chr1:176734640T>C	PAPPA2		
CHC2432T	g.chr1:177810006T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr1:179852367C>T	TOR1AIP1		
CHC2432T	g.chr1:180232512C>T	LHX4		
CHC2432T	g.chr1:181991250T>C	Unknown		
CHC2432T	g.chr1:182627616G>A	RGS8		
CHC2432T	g.chr1:183529382G>T	NCF2	c.1317C>A	p.P439P
CHC2432T	g.chr1:187463340A>G	Unknown		
CHC2432T	g.chr1:187824420T>C	Unknown		
CHC2432T	g.chr1:188621511T>A	Unknown		
CHC2432T	g.chr1:189457974A>G	Unknown		
CHC2432T	g.chr1:190990307G>T	Unknown		
CHC2432T	g.chr1:191074286A>G	Unknown		
CHC2432T	g.chr1:191607735T>A	Unknown		
CHC2432T	g.chr1:192047692C>G	Unknown		
CHC2432T	g.chr1:192064705G>T	Unknown		
CHC2432T	g.chr1:192261910C>T	Unknown		
CHC2432T	g.chr1:192271124C>A	Unknown		
CHC2432T	g.chr1:192528095C>A	RP5-1011O1.2		
CHC2432T	g.chr1:192569925A>G	Unknown		
CHC2432T	g.chr1:192754478C>A	Unknown		
CHC2432T	g.chr1:194474222G>A	Unknown		
CHC2432T	g.chr1:194862550A>T	Unknown		
CHC2432T	g.chr1:195103012T>C	Unknown		
CHC2432T	g.chr1:198653822A>G	PTPRC		
CHC2432T	g.chr1:201705148A>G	NAV1		
CHC2432T	g.chr1:203360636G>T	Unknown		
CHC2432T	g.chr1:20356595A>C	PLA2G5		
CHC2432T	g.chr1:203896566A>G	Unknown		
CHC2432T	g.chr1:206602484A>C	SRGAP2		
CHC2432T	g.chr1:207263103T>C	C4BPB		
CHC2432T	g.chr1:208857020A>G	Unknown		
CHC2432T	g.chr1:211246039G>C	KCNH1		
CHC2432T	g.chr1:211736801G>T	Unknown		
CHC2432T	g.chr1:212609843G>A	NENF		
CHC2432T	g.chr1:215067717T>C	Unknown		
CHC2432T	g.chr1:21525172C>G	Unknown		
CHC2432T	g.chr1:216701827C>T	ESRRG		
CHC2432T	g.chr1:229799461A>C	Unknown		
CHC2432T	g.chr1:232908596C>G	Unknown		
CHC2432T	g.chr1:233166182T>C	PCNXL2		
CHC2432T	g.chr1:237582158A>T	RYR2		
CHC2432T	g.chr1:237731905T>C	RYR2		
CHC2432T	g.chr1:237889963G>T	RYR2		
CHC2432T	g.chr1:238054393T>C	RP11-193H5.1		
CHC2432T	g.chr1:238429737C>T	Unknown		
CHC2432T	g.chr1:239095571C>A	Unknown		
CHC2432T	g.chr1:239961695T>C	CHRM3		
CHC2432T	g.chr1:243839093C>A	AKT3		
CHC2432T	g.chr1:24537521C>T	RP11-10N16.2		
CHC2432T	g.chr1:246407225A>G	SMYD3		
CHC2432T	g.chr1:247647088C>T	Unknown		
CHC2432T	g.chr1:248329662C>A	Unknown		
CHC2432T	g.chr1:26910093G>T	Unknown		
CHC2432T	g.chr1:27213168G>T	GPN2		
CHC2432T	g.chr1:27615712C>G	WDTC1		
CHC2432T	g.chr1:30159854G>A	Unknown		
CHC2432T	g.chr1:30722012A>G	Unknown		
CHC2432T	g.chr1:32540781T>G	TMEM39B		
CHC2432T	g.chr1:34400446A>C	CSMD2		
CHC2432T	g.chr1:34599292C>G	CSMD2		
CHC2432T	g.chr1:3474457G>A	MEGF6		
CHC2432T	g.chr1:34976063G>T	Unknown		
CHC2432T	g.chr1:35407883T>A	Unknown		
CHC2432T	g.chr1:3789055G>T	DFFB	c.701G>T	p.S234I
CHC2432T	g.chr1:41160133A>G	NFYC		
CHC2432T	g.chr1:43290410G>A	ERMAP		
CHC2432T	g.chr1:44050296T>C	PTPRF		
CHC2432T	g.chr1:46358966G>A	MAST2		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr1:49243280G>A	AGBL4		
CHC2432T	g.chr1:50312863A>G	AGBL4		
CHC2432T	g.chr1:54122260C>T	GLIS1		
CHC2432T	g.chr1:56193961A>G	RP11-466L17.1		
CHC2432T	g.chr1:61645620A>G	NFIA		
CHC2432T	g.chr1:64499088G>A	ROR1		
CHC2432T	g.chr1:70435829G>T	LRRC7		
CHC2432T	g.chr1:70682177A>G	SRSF11		
CHC2432T	g.chr1:74808945C>T	FPGT-TNNI3K		
CHC2432T	g.chr1:74998817A>T	TNNI3K		
CHC2432T	g.chr1:75075740T>A	C1orf173		
CHC2432T	g.chr1:75425943C>A	Unknown		
CHC2432T	g.chr1:76344880G>C	MSH4		
CHC2432T	g.chr1:77823780T>C	AK5		
CHC2432T	g.chr1:7844388G>T	PER3		
CHC2432T	g.chr1:81820014C>A	LPHN2		
CHC2432T	g.chr1:8455367C>A	RERE		
CHC2432T	g.chr1:84641713A>G	PRKACB		
CHC2432T	g.chr1:86362444G>T	COL24A1		
CHC2432T	g.chr1:86716498A>G	Unknown		
CHC2432T	g.chr1:89986456A>G	Unknown		
CHC2432T	g.chr1:90603412A>G	Unknown		
CHC2432T	g.chr1:91101938C>T	Unknown		
CHC2432T	g.chr1:91606033T>C	Unknown		
CHC2432T	g.chr1:93070229A>G	EVI5		
CHC2432T	g.chr1:94327821C>A	Unknown		
CHC2432T	g.chr1:95176033G>A	LINC01057		
CHC2432T	g.chr1:95905523A>G	Unknown		
CHC2432T	g.chr1:96563347A>G	Unknown		
CHC2432T	g.chr1:97463757C>G	Unknown		
CHC2432T	g.chr1:98710765T>C	RP5-1070A16.1		
CHC2432T	g.chr1:99032160T>C	Unknown		
CHC2432T	g.chr10:100586164T>C	HPSE2		
CHC2432T	g.chr10:101111803A>G	CNNM1		
CHC2432T	g.chr10:102296676C>T	HIF1AN		
CHC2432T	g.chr10:105440925G>C	SH3PXD2A		
CHC2432T	g.chr10:106196558G>C	CCDC147		
CHC2432T	g.chr10:106642337G>A	SORCS3		
CHC2432T	g.chr10:109020985G>A	Unknown		
CHC2432T	g.chr10:110339124G>A	Unknown		
CHC2432T	g.chr10:111415419A>T	Unknown		
CHC2432T	g.chr10:115769800C>A	Unknown		
CHC2432T	g.chr10:116385412A>T	ABLIM1		
CHC2432T	g.chr10:118753096T>C	KIAA1598		
CHC2432T	g.chr10:119572006T>C	Unknown		
CHC2432T	g.chr10:120308930G>A	Unknown		
CHC2432T	g.chr10:120616957G>T	Unknown		
CHC2432T	g.chr10:124123982A>G	Unknown		
CHC2432T	g.chr10:126843454G>A	CTBP2		
CHC2432T	g.chr10:130120862C>A	Unknown		
CHC2432T	g.chr10:130150762C>T	Unknown		
CHC2432T	g.chr10:132878747C>T	Unknown		
CHC2432T	g.chr10:132914231G>T	TCERG1L		
CHC2432T	g.chr10:132914255A>T	TCERG1L		
CHC2432T	g.chr10:133181512G>A	Unknown		
CHC2432T	g.chr10:133207146G>T	Unknown		
CHC2432T	g.chr10:133324851A>G	Unknown		
CHC2432T	g.chr10:133962521C>A	JAKMIP3		
CHC2432T	g.chr10:14242150C>T	FRMD4A		
CHC2432T	g.chr10:1510636C>T	ADARB2		
CHC2432T	g.chr10:15560066A>G	ITGA8		
CHC2432T	g.chr10:20112336G>A	PLXDC2		
CHC2432T	g.chr10:22826180C>A	PIP4K2A	c.1171G>T	p.E391*
CHC2432T	g.chr10:2577563A>T	RP11-526P5.2		
CHC2432T	g.chr10:28182898G>A	ARMC4		
CHC2432T	g.chr10:2957004T>C	Unknown		
CHC2432T	g.chr10:32800781C>G	CCDC7		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr10:32936728T>G	C10orf68		
CHC2432T	g.chr10:33369756T>C	RP11-462L8.1		
CHC2432T	g.chr10:34987983T>C	PARD3		
CHC2432T	g.chr10:35879526C>A	Unknown		
CHC2432T	g.chr10:37124116G>A	Unknown		
CHC2432T	g.chr10:4228819C>A	Unknown		
CHC2432T	g.chr10:42829768G>T	RP11-313J2.1		
CHC2432T	g.chr10:42921539A>T	CCNYL2		
CHC2432T	g.chr10:4509128T>A	Unknown		
CHC2432T	g.chr10:45932569G>A	ALOX5		
CHC2432T	g.chr10:51557656T>C	MSMB		
CHC2432T	g.chr10:52341877T>C	SGMS1		
CHC2432T	g.chr10:52437409C>T	Unknown		
CHC2432T	g.chr10:52775054C>T	PRKG1		
CHC2432T	g.chr10:54306609T>C	Unknown		
CHC2432T	g.chr10:56119431C>T	PCDH15		
CHC2432T	g.chr10:56295376A>G	PCDH15		
CHC2432T	g.chr10:56936265C>T	PCDH15		
CHC2432T	g.chr10:56979388C>A	PCDH15		
CHC2432T	g.chr10:57023247G>A	PCDH15		
CHC2432T	g.chr10:57652139C>A	Unknown		
CHC2432T	g.chr10:57821759T>G	Unknown		
CHC2432T	g.chr10:58099833A>T	Unknown		
CHC2432T	g.chr10:58257868G>T	Unknown		
CHC2432T	g.chr10:63150109C>T	Unknown		
CHC2432T	g.chr10:64078907C>T	Unknown		
CHC2432T	g.chr10:6472598C>A	PRKCQ		
CHC2432T	g.chr10:65414565A>T	Unknown		
CHC2432T	g.chr10:66478413T>G	Unknown		
CHC2432T	g.chr10:66827286T>C	Unknown		
CHC2432T	g.chr10:67172507G>T	Unknown		
CHC2432T	g.chr10:68350381T>C	CTNNA3		
CHC2432T	g.chr10:69152737C>T	CTNNA3		
CHC2432T	g.chr10:70103983C>A	RUFY2		
CHC2432T	g.chr10:70809002A>G	Unknown		
CHC2432T	g.chr10:77315846G>T	Unknown		
CHC2432T	g.chr10:7962381C>G	TAF3		
CHC2432T	g.chr10:80931745C>G	ZMIZ1		
CHC2432T	g.chr10:80947392G>T	ZMIZ1		
CHC2432T	g.chr10:82686340C>T	Unknown		
CHC2432T	g.chr10:82777341A>G	Unknown		
CHC2432T	g.chr10:83478634T>C	Unknown		
CHC2432T	g.chr10:85289239A>T	Unknown		
CHC2432T	g.chr10:86295107G>T	Unknown		
CHC2432T	g.chr10:86933537A>T	Unknown		
CHC2432T	g.chr10:87016178G>T	Unknown		
CHC2432T	g.chr10:87660303A>G	GRID1		
CHC2432T	g.chr10:8806802C>G	Unknown		
CHC2432T	g.chr10:8813862A>G	Unknown		
CHC2432T	g.chr10:89936184G>C	Unknown		
CHC2432T	g.chr10:90060979A>C	RNLS		
CHC2432T	g.chr10:91033260C>A	LIPA		
CHC2432T	g.chr10:91529395A>G	KIF20B		
CHC2432T	g.chr10:93949810C>T	CPEB3		
CHC2432T	g.chr10:94440948C>T	Unknown		
CHC2432T	g.chr10:94537063G>A	Unknown		
CHC2432T	g.chr10:9461263T>A	Unknown		
CHC2432T	g.chr10:94793980C>G	EXOC6		
CHC2432T	g.chr10:97587368G>T	ENTPD1		
CHC2432T	g.chr10:98843205G>T	SLIT1		
CHC2432T	g.chr11:103269622A>G	DYNC2H1		
CHC2432T	g.chr11:104399174C>T	RP11-886D15.1		
CHC2432T	g.chr11:104912497T>C	CARD16		
CHC2432T	g.chr11:105144901A>G	RP11-94P11.4		
CHC2432T	g.chr11:105847096C>A	GRIA4		
CHC2432T	g.chr11:108011543A>G	ACAT1		
CHC2432T	g.chr11:110155975T>C	RDX		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr11:111622698T>C	PPP2R1B		
CHC2432T	g.chr11:111622709A>C	PPP2R1B		
CHC2432T	g.chr11:111833610C>T	DIXDC1		
CHC2432T	g.chr11:112491810C>A	Unknown		
CHC2432T	g.chr11:114354482G>T	Unknown		
CHC2432T	g.chr11:116043317G>A	Unknown		
CHC2432T	g.chr11:116318018C>A	Unknown		
CHC2432T	g.chr11:117228551G>A	CEP164		
CHC2432T	g.chr11:118837086A>T	Unknown		
CHC2432T	g.chr11:120298344G>C	ARHGEF12		
CHC2432T	g.chr11:122020511T>C	Unknown		
CHC2432T	g.chr11:123482575C>A	GRAMD1B		
CHC2432T	g.chr11:124708783G>A	Unknown		
CHC2432T	g.chr11:126021256G>A	Unknown		
CHC2432T	g.chr11:127541120C>A	Unknown		
CHC2432T	g.chr11:127582395C>A	Unknown		
CHC2432T	g.chr11:129744531A>C	NFRKB		
CHC2432T	g.chr11:130101933A>C	ZBTB44		
CHC2432T	g.chr11:130597837G>A	Unknown		
CHC2432T	g.chr11:131036817T>A	Unknown		
CHC2432T	g.chr11:131275828C>A	NTM		
CHC2432T	g.chr11:131711792A>C	NTM		
CHC2432T	g.chr11:14729880C>T	PDE3B		
CHC2432T	g.chr11:16272574A>G	SOX6		
CHC2432T	g.chr11:18820928T>A	Unknown		
CHC2432T	g.chr11:21046659G>T	NELL1		
CHC2432T	g.chr11:21644096A>C	Unknown		
CHC2432T	g.chr11:22331290T>G	CTD-2140G10.2		
CHC2432T	g.chr11:23559169G>T	Unknown		
CHC2432T	g.chr11:24126152A>T	Unknown		
CHC2432T	g.chr11:24886728T>C	LUZP2		
CHC2432T	g.chr11:25551340C>A	Unknown		
CHC2432T	g.chr11:25918319A>G	Unknown		
CHC2432T	g.chr11:26018549G>A	Unknown		
CHC2432T	g.chr11:26819560T>C	Unknown		
CHC2432T	g.chr11:26865679G>T	Unknown		
CHC2432T	g.chr11:28992100G>T	RP11-115J23.1		
CHC2432T	g.chr11:30077490T>C	RP11-624D11.2		
CHC2432T	g.chr11:30553714T>A	MPPED2		
CHC2432T	g.chr11:30662078G>A	Unknown		
CHC2432T	g.chr11:31815786G>A	PAX6		
CHC2432T	g.chr11:32322477C>T	RP1-65P5.1		
CHC2432T	g.chr11:36345369G>T	PRR5L		
CHC2432T	g.chr11:36725545T>C	Unknown		
CHC2432T	g.chr11:38521942A>G	Unknown		
CHC2432T	g.chr11:38662897C>G	RP11-277K23.1		
CHC2432T	g.chr11:38792172G>A	Unknown		
CHC2432T	g.chr11:40506472A>G	LRR4C		
CHC2432T	g.chr11:410311C>T	SIGIRR		
CHC2432T	g.chr11:42021976G>A	Unknown		
CHC2432T	g.chr11:42299761C>A	Unknown		
CHC2432T	g.chr11:42362201T>G	Unknown		
CHC2432T	g.chr11:42468509C>A	Unknown		
CHC2432T	g.chr11:42846623A>C	Unknown		
CHC2432T	g.chr11:45985214C>G	PHF21A		
CHC2432T	g.chr11:46671327A>G	ATG13		
CHC2432T	g.chr11:47636462G>A	Y_RNA		
CHC2432T	g.chr11:49082100C>G	Unknown		
CHC2432T	g.chr11:5202127C>A	OR52A1		
CHC2432T	g.chr11:5351187T>A	HBG2		
CHC2432T	g.chr11:56395615T>A	Unknown		
CHC2432T	g.chr11:58011082T>C	Unknown		
CHC2432T	g.chr11:60314021T>G	Unknown		
CHC2432T	g.chr11:62520298G>A	ZBTB3	c.989C>T	p.S330L
CHC2432T	g.chr11:64690914A>G	PPP2R5B		
CHC2432T	g.chr11:65490253A>G	Unknown		
CHC2432T	g.chr11:67148123C>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr11:6718629G>A	Unknown		
CHC2432T	g.chr11:6878874C>A	Unknown		
CHC2432T	g.chr11:7254238T>A	Unknown		
CHC2432T	g.chr11:78130834C>T	RP11-452H21.1		
CHC2432T	g.chr11:79975536T>G	Unknown		
CHC2432T	g.chr11:80025736G>T	Unknown		
CHC2432T	g.chr11:80619618G>A	Unknown		
CHC2432T	g.chr11:80932438G>A	Unknown		
CHC2432T	g.chr11:81388081G>C	Unknown		
CHC2432T	g.chr11:82492618C>A	Unknown		
CHC2432T	g.chr11:86050878G>T	C11orf73		
CHC2432T	g.chr11:90629702T>A	Unknown		
CHC2432T	g.chr11:9199780C>A	DENND5A	c.1805G>T	p.R602L
CHC2432T	g.chr11:92587324C>A	FAT3		
CHC2432T	g.chr11:9517638A>G	ZNF143		
CHC2432T	g.chr11:95451891A>G	Unknown		
CHC2432T	g.chr11:9578349G>C	Unknown		
CHC2432T	g.chr11:96617870C>A	Unknown		
CHC2432T	g.chr11:96656870C>T	Unknown		
CHC2432T	g.chr11:98122927G>T	Unknown		
CHC2432T	g.chr11:98463403T>C	Unknown		
CHC2432T	g.chr11:99751747A>T	CNTN5		
CHC2432T	g.chr12:103266923T>C	PAH		
CHC2432T	g.chr12:103717175A>C	C12orf42		
CHC2432T	g.chr12:106295110A>T	Unknown		
CHC2432T	g.chr12:107034984G>A	RP11-144F15.1		
CHC2432T	g.chr12:120644061T>C	PXN-AS1		
CHC2432T	g.chr12:121163577C>G	ACADS		
CHC2432T	g.chr12:121567052C>T	Unknown		
CHC2432T	g.chr12:122412813G>T	WDR66		
CHC2432T	g.chr12:122469728G>T	BCL7A		
CHC2432T	g.chr12:122929864T>A	Unknown		
CHC2432T	g.chr12:128005583G>A	Unknown		
CHC2432T	g.chr12:129771410T>A	TMEM132D		
CHC2432T	g.chr12:129771411G>T	TMEM132D		
CHC2432T	g.chr12:130063059C>A	TMEM132D		
CHC2432T	g.chr12:130745954C>A	RP11-143E21.6		
CHC2432T	g.chr12:130784300C>T	Unknown		
CHC2432T	g.chr12:133043353C>G	Unknown		
CHC2432T	g.chr12:133321966C>T	ANKLE2		
CHC2432T	g.chr12:15611743C>T	PTPRO		
CHC2432T	g.chr12:15821692T>C	EPS8		
CHC2432T	g.chr12:1952756T>C	CACNA2D4		
CHC2432T	g.chr12:24325493A>C	Unknown		
CHC2432T	g.chr12:24506572T>C	Unknown		
CHC2432T	g.chr12:2454025G>T	CACNA1C		
CHC2432T	g.chr12:24580455C>T	RP11-444D3.1		
CHC2432T	g.chr12:2758913C>T	CACNA1C		
CHC2432T	g.chr12:30701091A>C	Unknown		
CHC2432T	g.chr12:32213376G>A	Unknown		
CHC2432T	g.chr12:34039720A>G	Unknown		
CHC2432T	g.chr12:34060604A>G	Unknown		
CHC2432T	g.chr12:39970213G>A	ABCD2		
CHC2432T	g.chr12:40531830C>A	Unknown		
CHC2432T	g.chr12:41872161G>A	PDZRN4		
CHC2432T	g.chr12:42709648T>C	ZCRB1		
CHC2432T	g.chr12:43773751C>T	ADAMTS20		
CHC2432T	g.chr12:45303151C>A	NELL2		
CHC2432T	g.chr12:45648481A>G	ANO6		
CHC2432T	g.chr12:45854023G>T	Unknown		
CHC2432T	g.chr12:52479583G>A	RP1-288H2.4		
CHC2432T	g.chr12:54770249A>G	ZNF385A		
CHC2432T	g.chr12:55118437A>G	Unknown		
CHC2432T	g.chr12:55696659G>A	Unknown		
CHC2432T	g.chr12:57261325T>C	RP11-74M13.4		
CHC2432T	g.chr12:57850896A>C	INHBE		
CHC2432T	g.chr12:59077263G>A	RP11-362K2.2		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr12:59433914G>T	RP11-150C16.1		
CHC2432T	g.chr12:61628521C>T	Unknown		
CHC2432T	g.chr12:61967054G>T	Unknown		
CHC2432T	g.chr12:61967055C>T	Unknown		
CHC2432T	g.chr12:62573115T>C	FAM19A2		
CHC2432T	g.chr12:63802613C>A	Unknown		
CHC2432T	g.chr12:64254924T>A	SRGAP1		
CHC2432T	g.chr12:65299942T>C	RP11-766N7.3		
CHC2432T	g.chr12:66490032A>C	Unknown		
CHC2432T	g.chr12:70261423T>G	MYRFL		
CHC2432T	g.chr12:71042367C>T	PTPRR		
CHC2432T	g.chr12:71242880G>A	PTPRR		
CHC2432T	g.chr12:71524932A>G	TSPAN8		
CHC2432T	g.chr12:71531122T>C	TSPAN8		
CHC2432T	g.chr12:71566536T>A	TSPAN8		
CHC2432T	g.chr12:72886965G>T	TRHDE		
CHC2432T	g.chr12:7316357T>C	Unknown		
CHC2432T	g.chr12:74367451T>C	Unknown		
CHC2432T	g.chr12:75281992C>T	Unknown		
CHC2432T	g.chr12:76034033C>T	RP11-114H23.1		
CHC2432T	g.chr12:76634059G>T	Unknown		
CHC2432T	g.chr12:78017952T>C	Unknown		
CHC2432T	g.chr12:78103319C>A	Unknown		
CHC2432T	g.chr12:79642599A>C	SYT1		
CHC2432T	g.chr12:80072858T>C	PAWR		
CHC2432T	g.chr12:82448545C>A	Unknown		
CHC2432T	g.chr12:84125673T>C	Unknown		
CHC2432T	g.chr12:85324929A>G	Unknown		
CHC2432T	g.chr12:85324935C>G	Unknown		
CHC2432T	g.chr12:85771967A>G	Unknown		
CHC2432T	g.chr12:86611217G>A	MGAT4C		
CHC2432T	g.chr12:87091510A>T	MGAT4C		
CHC2432T	g.chr12:87250950A>G	Unknown		
CHC2432T	g.chr12:88577469G>T	TMTC3		
CHC2432T	g.chr12:89821784G>C	POC1B		
CHC2432T	g.chr12:90988536G>A	Unknown		
CHC2432T	g.chr12:91509171G>T	Unknown		
CHC2432T	g.chr12:94037428C>T	Unknown		
CHC2432T	g.chr12:94501818G>A	Unknown		
CHC2432T	g.chr12:95095563A>G	Unknown		
CHC2432T	g.chr12:97077065T>A	C12orf55		
CHC2432T	g.chr12:98791903G>A	Unknown		
CHC2432T	g.chr12:99360766T>C	ANKS1B		
CHC2432T	g.chr13:105340223G>T	Unknown		
CHC2432T	g.chr13:105452910G>A	Unknown		
CHC2432T	g.chr13:105869970G>C	Unknown		
CHC2432T	g.chr13:110170270T>C	Unknown		
CHC2432T	g.chr13:111212286C>T	RAB20		
CHC2432T	g.chr13:20807694G>A	Unknown		
CHC2432T	g.chr13:22065376G>A	Unknown		
CHC2432T	g.chr13:23485818C>A	LINC00621		
CHC2432T	g.chr13:25757484G>A	LINC01053		
CHC2432T	g.chr13:26034115G>A	ATP8A2		
CHC2432T	g.chr13:26214349A>G	ATP8A2		
CHC2432T	g.chr13:26725946T>C	RNF6		
CHC2432T	g.chr13:27245106G>A	WASF3		
CHC2432T	g.chr13:32094032C>G	Unknown		
CHC2432T	g.chr13:35465541G>A	Unknown		
CHC2432T	g.chr13:36172675C>T	NBEA		
CHC2432T	g.chr13:36269782G>A	Unknown		
CHC2432T	g.chr13:36488285G>A	DCLK1		
CHC2432T	g.chr13:40005744A>G	LHFP		
CHC2432T	g.chr13:40390201A>G	Unknown		
CHC2432T	g.chr13:40974354C>T	Unknown		
CHC2432T	g.chr13:44002184T>C	ENOX1		
CHC2432T	g.chr13:46124530A>T	FAM194B		
CHC2432T	g.chr13:48197160G>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr13:53483702G>A	Unknown		
CHC2432T	g.chr13:54375857C>A	Unknown		
CHC2432T	g.chr13:54507088G>T	Unknown		
CHC2432T	g.chr13:57969728T>C	Unknown		
CHC2432T	g.chr13:58056504G>A	Unknown		
CHC2432T	g.chr13:58086113T>C	Unknown		
CHC2432T	g.chr13:61939862T>C	Unknown		
CHC2432T	g.chr13:63555910C>A	Unknown		
CHC2432T	g.chr13:64040408C>A	Unknown		
CHC2432T	g.chr13:64810233C>G	Unknown		
CHC2432T	g.chr13:66271032G>T	Unknown		
CHC2432T	g.chr13:66301051A>T	Unknown		
CHC2432T	g.chr13:67064694G>A	PCDH9		
CHC2432T	g.chr13:67089075C>G	PCDH9		
CHC2432T	g.chr13:69632615G>C	Unknown		
CHC2432T	g.chr13:70658747C>T	KLHL1		
CHC2432T	g.chr13:71719642A>C	LINC00348		
CHC2432T	g.chr13:71921349G>T	Unknown		
CHC2432T	g.chr13:72122855C>A	DACH1		
CHC2432T	g.chr13:72313332C>T	DACH1		
CHC2432T	g.chr13:77222845C>A	Unknown		
CHC2432T	g.chr13:78239554C>A	Unknown		
CHC2432T	g.chr13:78591062G>C	RNF219-AS1		
CHC2432T	g.chr13:78726369C>T	RNF219-AS1		
CHC2432T	g.chr13:79331187A>G	Unknown		
CHC2432T	g.chr13:79703709G>T	Unknown		
CHC2432T	g.chr13:82518310T>C	Unknown		
CHC2432T	g.chr13:82723814C>A	Unknown		
CHC2432T	g.chr13:83043923A>T	Unknown		
CHC2432T	g.chr13:84266435C>A	Unknown		
CHC2432T	g.chr13:84760959G>A	Unknown		
CHC2432T	g.chr13:85581282T>C	Unknown		
CHC2432T	g.chr13:85701085A>G	Unknown		
CHC2432T	g.chr13:85932800T>C	Unknown		
CHC2432T	g.chr13:86705599G>T	RP11-30L8.1		
CHC2432T	g.chr13:87252781C>T	Unknown		
CHC2432T	g.chr13:88761758T>A	Unknown		
CHC2432T	g.chr13:89252460A>C	Unknown		
CHC2432T	g.chr13:90124398A>G	Unknown		
CHC2432T	g.chr13:91614647G>C	Unknown		
CHC2432T	g.chr13:91743656G>T	Unknown		
CHC2432T	g.chr13:92515698T>C	GPC5		
CHC2432T	g.chr13:93843952T>C	Unknown		
CHC2432T	g.chr13:94573488C>T	GPC6		
CHC2432T	g.chr13:98826790A>G	FARP1		
CHC2432T	g.chr14:100430633C>T	Unknown		
CHC2432T	g.chr14:101066587A>T	Unknown		
CHC2432T	g.chr14:102715165C>A	MOK		
CHC2432T	g.chr14:104394644G>C	Unknown		
CHC2432T	g.chr14:21063286G>A	RNASE11		
CHC2432T	g.chr14:22129055T>C	Unknown		
CHC2432T	g.chr14:22863058T>A	AE000661.37		
CHC2432T	g.chr14:25981672G>A	Unknown		
CHC2432T	g.chr14:26715267A>G	Unknown		
CHC2432T	g.chr14:26877826G>A	Unknown		
CHC2432T	g.chr14:27015280G>T	NOVA1		
CHC2432T	g.chr14:27225641G>A	NOVA1-AS1		
CHC2432T	g.chr14:28279680G>T	Unknown		
CHC2432T	g.chr14:28475278C>T	Unknown		
CHC2432T	g.chr14:29097963T>A	Unknown		
CHC2432T	g.chr14:31623642G>A	HECTD1		
CHC2432T	g.chr14:34777403T>A	Unknown		
CHC2432T	g.chr14:35911079T>C	Unknown		
CHC2432T	g.chr14:36597758G>A	LINC00609		
CHC2432T	g.chr14:41008578A>T	Unknown		
CHC2432T	g.chr14:42402220A>C	Unknown		
CHC2432T	g.chr14:43127139G>A	CTD-2307P3.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr14:46447856A>G	Unknown		
CHC2432T	g.chr14:46559063C>T	LINC00871		
CHC2432T	g.chr14:47033779A>G	Unknown		
CHC2432T	g.chr14:47187006C>T	Unknown		
CHC2432T	g.chr14:47707512A>C	MDGA2		
CHC2432T	g.chr14:47871775C>T	MDGA2		
CHC2432T	g.chr14:48087562A>G	MDGA2		
CHC2432T	g.chr14:48675743A>G	Unknown		
CHC2432T	g.chr14:48764251C>A	Unknown		
CHC2432T	g.chr14:48884285A>T	RP11-2G1.1		
CHC2432T	g.chr14:49334226G>T	Unknown		
CHC2432T	g.chr14:49711278A>G	Unknown		
CHC2432T	g.chr14:51551378A>T	TRIM9		
CHC2432T	g.chr14:52694370T>C	Unknown		
CHC2432T	g.chr14:57033964G>C	Unknown		
CHC2432T	g.chr14:59501264C>T	Unknown		
CHC2432T	g.chr14:60060773A>G	Unknown		
CHC2432T	g.chr14:61009419T>C	RP11-1042B17.3		
CHC2432T	g.chr14:61385339A>G	MNAT1		
CHC2432T	g.chr14:61758117G>A	Unknown		
CHC2432T	g.chr14:65549733C>T	MAX		
CHC2432T	g.chr14:66554985T>A	Unknown		
CHC2432T	g.chr14:70245254G>T	SLC10A1		
CHC2432T	g.chr14:72496132G>T	RGS6		
CHC2432T	g.chr14:73856422T>C	NUMB		
CHC2432T	g.chr14:75639253C>A	TMED10		
CHC2432T	g.chr14:75837503G>C	Unknown		
CHC2432T	g.chr14:78482914C>T	Unknown		
CHC2432T	g.chr14:78796981C>T	Unknown		
CHC2432T	g.chr14:78808273A>G	Unknown		
CHC2432T	g.chr14:78956392G>A	NRXN3		
CHC2432T	g.chr14:79062633T>C	NRXN3		
CHC2432T	g.chr14:81007066T>C	CEP128		
CHC2432T	g.chr14:84226640C>T	Unknown		
CHC2432T	g.chr14:84455997T>A	Unknown		
CHC2432T	g.chr14:84556593A>T	Unknown		
CHC2432T	g.chr14:84813206A>G	Unknown		
CHC2432T	g.chr14:86964672A>G	Unknown		
CHC2432T	g.chr14:87155688C>T	Unknown		
CHC2432T	g.chr14:87403422G>T	RP11-736P16.1		
CHC2432T	g.chr14:87921300T>C	RP11-594C13.1		
CHC2432T	g.chr14:88381293C>T	Unknown		
CHC2432T	g.chr14:89711271G>A	FOXP3		
CHC2432T	g.chr14:92583963T>G	NDUFB1	c.19A>C	p.I7L
CHC2432T	g.chr14:94310550T>C	Unknown		
CHC2432T	g.chr14:94315292T>A	Unknown		
CHC2432T	g.chr14:96797041C>A	ATG2B		
CHC2432T	g.chr14:97171783T>C	Unknown		
CHC2432T	g.chr15:100026126A>T	MEF2A		
CHC2432T	g.chr15:22516247C>T	Unknown		
CHC2432T	g.chr15:24122118G>A	Unknown		
CHC2432T	g.chr15:24254606T>C	Unknown		
CHC2432T	g.chr15:27451206C>T	GABRG3		
CHC2432T	g.chr15:28075371C>G	OCA2		
CHC2432T	g.chr15:28500625A>G	HERC2		
CHC2432T	g.chr15:28528371A>C	HERC2		
CHC2432T	g.chr15:33380676A>T	FMN1		
CHC2432T	g.chr15:33879800T>C	RYR3		
CHC2432T	g.chr15:34241743T>C	AVEN		
CHC2432T	g.chr15:35445366T>C	RP11-323I15.5		
CHC2432T	g.chr15:35542386C>A	DPH6		
CHC2432T	g.chr15:37064526A>G	C15orf41		
CHC2432T	g.chr15:37500206C>G	Unknown		
CHC2432T	g.chr15:41217806C>T	Unknown		
CHC2432T	g.chr15:41844552G>A	Unknown		
CHC2432T	g.chr15:41927909T>C	MGA		
CHC2432T	g.chr15:43212876G>C	TTBK2		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr15:43787488G>C	TP53BP1		
CHC2432T	g.chr15:44316575C>T	FRMD5		
CHC2432T	g.chr15:47025438G>A	RP11-627D16.1		
CHC2432T	g.chr15:47703751A>C	SEMA6D		
CHC2432T	g.chr15:52493178T>C	MYO5C		
CHC2432T	g.chr15:54819184T>A	UNC13C		
CHC2432T	g.chr15:55200199A>G	Unknown		
CHC2432T	g.chr15:55944670G>C	PRTG		
CHC2432T	g.chr15:60497779T>C	Unknown		
CHC2432T	g.chr15:60669308C>A	ANXA2		
CHC2432T	g.chr15:61049443T>C	RORA		
CHC2432T	g.chr15:62493707T>A	RP11-299H22.1		
CHC2432T	g.chr15:63325759A>G	Unknown		
CHC2432T	g.chr15:65320525A>G	MTFMT		
CHC2432T	g.chr15:66452055G>C	MEGF11		
CHC2432T	g.chr15:71689375G>C	THSD4		
CHC2432T	g.chr15:73616592T>A	HCN4	c.1981A>T	p.I661F
CHC2432T	g.chr15:76716288T>A	SCAPER		
CHC2432T	g.chr15:79231512C>A	CTSH	c.93G>T	p.E31D
CHC2432T	g.chr15:80764444C>T	ARNT2		
CHC2432T	g.chr15:80840944C>T	ARNT2		
CHC2432T	g.chr15:82080461T>C	RP11-499F3.2		
CHC2432T	g.chr15:83741519G>T	RP11-382A20.5		
CHC2432T	g.chr15:85609877A>G	PDE8A		
CHC2432T	g.chr15:87406526C>A	AGBL1		
CHC2432T	g.chr15:88411844T>A	Unknown		
CHC2432T	g.chr15:89081064T>C	DET1		
CHC2432T	g.chr15:89267059T>C	Unknown		
CHC2432T	g.chr15:90126316C>T	TICRR		
CHC2432T	g.chr15:93879267A>T	RP11-266O8.1		
CHC2432T	g.chr15:94363439T>C	CTD-3049M7.1		
CHC2432T	g.chr15:97898542G>C	CTD-2147F2.1		
CHC2432T	g.chr15:97944591A>T	CTD-2147F2.2		
CHC2432T	g.chr15:98761974C>A	CTD-2544M6.1		
CHC2432T	g.chr15:99216640A>G	IGF1R		
CHC2432T	g.chr15:99235282G>T	IGF1R		
CHC2432T	g.chr15:99630636A>T	RP11-654A16.3		
CHC2432T	g.chr16:10837495G>A	Unknown		
CHC2432T	g.chr16:11565740C>T	CTD-3088G3.8		
CHC2432T	g.chr16:12959447A>C	Unknown		
CHC2432T	g.chr16:13268927A>C	SHISA9		
CHC2432T	g.chr16:13307533G>A	SHISA9		
CHC2432T	g.chr16:1582084C>G	IFT140		
CHC2432T	g.chr16:16356750C>T	NOMO3		
CHC2432T	g.chr16:18140817T>C	CTA-481E9.3		
CHC2432T	g.chr16:18968214A>T	Unknown		
CHC2432T	g.chr16:19828577T>G	IQCK		
CHC2432T	g.chr16:20159651A>T	Unknown		
CHC2432T	g.chr16:20428861G>A	ACSM5		
CHC2432T	g.chr16:22852898A>G	HS3ST2		
CHC2432T	g.chr16:24967717G>C	ARHGAP17		
CHC2432T	g.chr16:25921157A>T	HS3ST4		
CHC2432T	g.chr16:26065982T>G	HS3ST4		
CHC2432T	g.chr16:27952723G>T	GSG1L		
CHC2432T	g.chr16:2947218G>A	FLYWCH2		
CHC2432T	g.chr16:29857617G>A	MVP		
CHC2432T	g.chr16:30933472G>C	FBXL19-AS1		
CHC2432T	g.chr16:31480793C>T	Unknown		
CHC2432T	g.chr16:47156117G>A	NETO2		
CHC2432T	g.chr16:49268980T>A	Unknown		
CHC2432T	g.chr16:51810157T>C	Unknown		
CHC2432T	g.chr16:53463041A>G	Unknown		
CHC2432T	g.chr16:55448168T>C	MMP2		
CHC2432T	g.chr16:57176739G>T	CPNE2		
CHC2432T	g.chr16:61440883T>C	Unknown		
CHC2432T	g.chr16:62095485T>A	Unknown		
CHC2432T	g.chr16:62394017G>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr16:62440791G>A	Unknown		
CHC2432T	g.chr16:62620439T>C	Unknown		
CHC2432T	g.chr16:64658440T>A	Unknown		
CHC2432T	g.chr16:65532033A>G	LINC00922		
CHC2432T	g.chr16:66097254G>A	Unknown		
CHC2432T	g.chr16:71291289C>G	Unknown		
CHC2432T	g.chr16:7244790G>A	RBFOX1		
CHC2432T	g.chr16:73186617T>C	Unknown		
CHC2432T	g.chr16:76009623G>C	Unknown		
CHC2432T	g.chr16:7706192C>T	RBFOX1		
CHC2432T	g.chr16:79318289C>A	Unknown		
CHC2432T	g.chr16:8042117T>A	Unknown		
CHC2432T	g.chr16:84328094C>T	Unknown		
CHC2432T	g.chr16:85124768G>T	KIAA0513		
CHC2432T	g.chr16:85655915G>C	GSE1		
CHC2432T	g.chr16:85863538C>T	Unknown		
CHC2432T	g.chr16:86218829C>T	Unknown		
CHC2432T	g.chr16:86397193T>A	Unknown		
CHC2432T	g.chr16:86659422G>A	Unknown		
CHC2432T	g.chr16:9252538C>T	Unknown		
CHC2432T	g.chr17:10034086A>G	GAS7		
CHC2432T	g.chr17:1018515C>T	ABR		
CHC2432T	g.chr17:12307852C>G	Unknown		
CHC2432T	g.chr17:12310787G>T	Unknown		
CHC2432T	g.chr17:14614630T>A	Unknown		
CHC2432T	g.chr17:15723828C>A	Unknown		
CHC2432T	g.chr17:22054965C>T	Unknown		
CHC2432T	g.chr17:25442485A>G	Unknown		
CHC2432T	g.chr17:26969591C>A	KIAA0100		
CHC2432T	g.chr17:27166023C>T	FAM222B		
CHC2432T	g.chr17:29887748C>T	Unknown		
CHC2432T	g.chr17:32228257C>G	ASIC2		
CHC2432T	g.chr17:35238745C>T	RP11-445F12.1		
CHC2432T	g.chr17:3676463C>A	ITGAE		
CHC2432T	g.chr17:38307597T>A	CASC3		
CHC2432T	g.chr17:39609951C>T	Unknown		
CHC2432T	g.chr17:39845792C>A	EIF1		
CHC2432T	g.chr17:40311678T>G	KCNH4		
CHC2432T	g.chr17:40669212C>T	ATP6V0A1		
CHC2432T	g.chr17:43832107G>T	CRHR1		
CHC2432T	g.chr17:46004516G>A	SP2		
CHC2432T	g.chr17:50368288A>G	Unknown		
CHC2432T	g.chr17:51761505T>C	Unknown		
CHC2432T	g.chr17:54101777C>T	Unknown		
CHC2432T	g.chr17:5474269G>T	NLRP1		
CHC2432T	g.chr17:56836177A>T	PPM1E		
CHC2432T	g.chr17:60129081A>C	MED13		
CHC2432T	g.chr17:6314926C>A	Unknown		
CHC2432T	g.chr17:64991589T>C	CACNG4		
CHC2432T	g.chr17:662204G>C	GLOD4		
CHC2432T	g.chr17:68961021A>G	Unknown		
CHC2432T	g.chr17:69438232T>C	Unknown		
CHC2432T	g.chr17:70091870G>T	AC005152.2		
CHC2432T	g.chr17:70659375G>A	SLC39A11		
CHC2432T	g.chr17:71434211T>C	SDK2	c.808A>G	p.T270A
CHC2432T	g.chr17:73175267A>C	SUMO2		
CHC2432T	g.chr17:74559115C>A	Unknown		
CHC2432T	g.chr17:76920715G>T	TIMP2		
CHC2432T	g.chr17:7736610A>C	DNAH2		
CHC2432T	g.chr17:78171053G>T	CARD14		
CHC2432T	g.chr17:79248288G>A	SLC38A10		
CHC2432T	g.chr18:10228980G>T	Unknown		
CHC2432T	g.chr18:13813983A>G	Unknown		
CHC2432T	g.chr18:1939199T>G	Unknown		
CHC2432T	g.chr18:22154888G>C	Unknown		
CHC2432T	g.chr18:25829125A>G	Unknown		
CHC2432T	g.chr18:26794559A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr18:26893192C>A	CTD-2515C13.2		
CHC2432T	g.chr18:27597949A>G	Unknown		
CHC2432T	g.chr18:2814090C>T	RP11-703M24.5		
CHC2432T	g.chr18:30533576T>C	CCDC178		
CHC2432T	g.chr18:30661331T>C	CCDC178		
CHC2432T	g.chr18:34912909G>A	CELF4		
CHC2432T	g.chr18:35361417C>T	Unknown		
CHC2432T	g.chr18:35491673A>G	Unknown		
CHC2432T	g.chr18:3611386A>T	DLGAP1		
CHC2432T	g.chr18:38501664A>C	Unknown		
CHC2432T	g.chr18:42607723A>G	SETBP1		
CHC2432T	g.chr18:43076143T>G	SLC14A2		
CHC2432T	g.chr18:43092806G>T	SLC14A2		
CHC2432T	g.chr18:43457353C>A	EPG5		
CHC2432T	g.chr18:4347746C>A	DLGAP1		
CHC2432T	g.chr18:43545891T>C	EPG5		
CHC2432T	g.chr18:4356950G>C	DLGAP1		
CHC2432T	g.chr18:43594981G>C	PSTPIP2		
CHC2432T	g.chr18:44066747T>A	LOXHD1		
CHC2432T	g.chr18:4583142A>G	Unknown		
CHC2432T	g.chr18:47620773G>A	MYO5B		
CHC2432T	g.chr18:51078722G>T	RP11-671P2.1		
CHC2432T	g.chr18:52570169A>G	CCDC68		
CHC2432T	g.chr18:58190900G>A	Unknown		
CHC2432T	g.chr18:5869973G>T	Unknown		
CHC2432T	g.chr18:6056264C>A	L3MBTL4		
CHC2432T	g.chr18:6177148A>C	L3MBTL4		
CHC2432T	g.chr18:63500039T>C	CDH7		
CHC2432T	g.chr18:63767637T>C	Unknown		
CHC2432T	g.chr18:64066717A>T	Unknown		
CHC2432T	g.chr18:64148100A>G	Unknown		
CHC2432T	g.chr18:66154682G>A	Unknown		
CHC2432T	g.chr18:66412939A>G	CCDC102B		
CHC2432T	g.chr18:70586128C>T	Unknown		
CHC2432T	g.chr18:7304956C>T	Unknown		
CHC2432T	g.chr18:73499360G>A	Unknown		
CHC2432T	g.chr18:73621872T>C	Unknown		
CHC2432T	g.chr18:75430585C>T	Unknown		
CHC2432T	g.chr18:75806355C>A	Unknown		
CHC2432T	g.chr18:7812268T>G	PTPRM		
CHC2432T	g.chr18:9319959G>A	RP11-888D10.3		
CHC2432T	g.chr19:11180853T>A	Unknown		
CHC2432T	g.chr19:13348128T>A	CACNA1A		
CHC2432T	g.chr19:14178451A>T	Unknown		
CHC2432T	g.chr19:15825627T>C	Unknown		
CHC2432T	g.chr19:18148312G>A	Unknown		
CHC2432T	g.chr19:18865886C>T	CRTC1		
CHC2432T	g.chr19:1909001G>T	SCAMP4		
CHC2432T	g.chr19:19575669A>G	GATAD2A		
CHC2432T	g.chr19:21827122T>C	Unknown		
CHC2432T	g.chr19:22291142G>T	Unknown		
CHC2432T	g.chr19:22489726G>A	ZNF729		
CHC2432T	g.chr19:22489919A>G	ZNF729		
CHC2432T	g.chr19:22719952C>A	Unknown		
CHC2432T	g.chr19:22786104G>T	CTC-457E21.6		
CHC2432T	g.chr19:29438116G>A	AC011524.1		
CHC2432T	g.chr19:29806033A>T	CTC-525D6.1		
CHC2432T	g.chr19:30866041C>A	ZNF536		
CHC2432T	g.chr19:30912789A>G	ZNF536		
CHC2432T	g.chr19:30914770G>T	ZNF536		
CHC2432T	g.chr19:34436416C>A	Unknown		
CHC2432T	g.chr19:34557612G>T	Unknown		
CHC2432T	g.chr19:37665805C>T	CTC-454I21.3		
CHC2432T	g.chr19:40358045A>G	FCGBP		
CHC2432T	g.chr19:42015128G>A	Unknown		
CHC2432T	g.chr19:44553471C>T	ZNF223		
CHC2432T	g.chr19:46166107C>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr19:47545411A>G	NPAS1		
CHC2432T	g.chr19:49285346T>G	Unknown		
CHC2432T	g.chr19:49362248G>A	PLEKHA4	c.841C>T	p.P281S
CHC2432T	g.chr19:5092916C>A	KDM4B		
CHC2432T	g.chr19:51024172G>T	LRR4B		
CHC2432T	g.chr19:51752726A>C	Unknown		
CHC2432T	g.chr19:52174916C>A	Unknown		
CHC2432T	g.chr19:52361327C>A	ZNF577		
CHC2432T	g.chr19:52668798A>G	ZNF836		
CHC2432T	g.chr19:54280814T>C	Unknown		
CHC2432T	g.chr19:5551699C>A	Unknown		
CHC2432T	g.chr19:57133813C>A	ZNF71	c.1158C>A	p.I386I
CHC2432T	g.chr19:7237097T>C	INSR		
CHC2432T	g.chr19:804946G>T	PTBP1		
CHC2432T	g.chr19:8082200A>G	Unknown		
CHC2432T	g.chr2:100662616A>T	AFF3		
CHC2432T	g.chr2:101234220C>G	Unknown		
CHC2432T	g.chr2:101376582T>C	Unknown		
CHC2432T	g.chr2:10994181T>G	AC092687.4		
CHC2432T	g.chr2:115255317G>T	DPP10		
CHC2432T	g.chr2:116759807G>T	Unknown		
CHC2432T	g.chr2:118029913A>G	Unknown		
CHC2432T	g.chr2:118194113A>T	Unknown		
CHC2432T	g.chr2:118522880G>T	AC009312.1		
CHC2432T	g.chr2:121161043G>A	Unknown		
CHC2432T	g.chr2:122393748A>C	CLASP1		
CHC2432T	g.chr2:124038335G>T	Unknown		
CHC2432T	g.chr2:124914398T>A	CNTNAP5		
CHC2432T	g.chr2:125057046A>G	CNTNAP5		
CHC2432T	g.chr2:126034359T>A	Unknown		
CHC2432T	g.chr2:126085326T>G	Unknown		
CHC2432T	g.chr2:126124820T>C	Unknown		
CHC2432T	g.chr2:127306910A>C	Unknown		
CHC2432T	g.chr2:127772774T>C	Unknown		
CHC2432T	g.chr2:130496192A>T	Unknown		
CHC2432T	g.chr2:133361466A>G	GPR39		
CHC2432T	g.chr2:135574629G>A	AC016725.4		
CHC2432T	g.chr2:1368888G>A	SNTG2		
CHC2432T	g.chr2:13709098C>T	AC092635.1		
CHC2432T	g.chr2:138425396C>A	THSD7B	c.4704C>A	p.I1568I
CHC2432T	g.chr2:139854391A>C	Unknown		
CHC2432T	g.chr2:142175019A>T	LRP1B		
CHC2432T	g.chr2:145347663C>A	Unknown		
CHC2432T	g.chr2:146896392T>C	Unknown		
CHC2432T	g.chr2:149222561A>G	MBD5		
CHC2432T	g.chr2:153826920C>T	Unknown		
CHC2432T	g.chr2:154030677C>T	AC011901.2		
CHC2432T	g.chr2:157395474T>C	GPD2		
CHC2432T	g.chr2:157591975G>A	Unknown		
CHC2432T	g.chr2:158018953T>C	Unknown		
CHC2432T	g.chr2:158067134T>A	Unknown		
CHC2432T	g.chr2:158715948T>C	ACVR1		
CHC2432T	g.chr2:160029811G>A	TANC1		
CHC2432T	g.chr2:160712565C>G	LY75-CD302		
CHC2432T	g.chr2:160717627A>G	LY75-CD302		
CHC2432T	g.chr2:160918868G>T	PLA2R1	c.47C>A	p.P16Q
CHC2432T	g.chr2:163977966A>G	Unknown		
CHC2432T	g.chr2:167814375T>G	XIRP2		
CHC2432T	g.chr2:170534668T>C	CCDC173		
CHC2432T	g.chr2:174814983T>C	SP3		
CHC2432T	g.chr2:176878307A>C	Unknown		
CHC2432T	g.chr2:177294492G>T	Unknown		
CHC2432T	g.chr2:17769088T>A	VSNL1		
CHC2432T	g.chr2:181600658C>T	Unknown		
CHC2432T	g.chr2:181738121C>A	Unknown		
CHC2432T	g.chr2:181958862T>C	AC068196.1		
CHC2432T	g.chr2:182731565A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr2:184082183C>G	Unknown		
CHC2432T	g.chr2:184271360A>G	Unknown		
CHC2432T	g.chr2:185867761G>A	Unknown		
CHC2432T	g.chr2:18660059G>A	Unknown		
CHC2432T	g.chr2:188029718G>A	AC007319.1		
CHC2432T	g.chr2:188243418T>G	CALCRL		
CHC2432T	g.chr2:190433263A>T	SLC40A1		
CHC2432T	g.chr2:192452042A>T	Unknown		
CHC2432T	g.chr2:193793700G>A	Unknown		
CHC2432T	g.chr2:194872178C>A	Unknown		
CHC2432T	g.chr2:197897198C>T	ANKRD44		
CHC2432T	g.chr2:19831212C>T	Unknown		
CHC2432T	g.chr2:198437183T>C	RFTN2		
CHC2432T	g.chr2:198470171C>A	RFTN2		
CHC2432T	g.chr2:200213151T>C	SATB2		
CHC2432T	g.chr2:202609971G>A	ALS2		
CHC2432T	g.chr2:202745871A>T	CDK15		
CHC2432T	g.chr2:203548914C>T	FAM117B		
CHC2432T	g.chr2:207020488G>C	NDUFS1		
CHC2432T	g.chr2:207401884C>G	ADAM23		
CHC2432T	g.chr2:208630936A>G	FZD5		
CHC2432T	g.chr2:209548035G>T	Unknown		
CHC2432T	g.chr2:210365117T>A	MAP2		
CHC2432T	g.chr2:211757426A>G	Unknown		
CHC2432T	g.chr2:213064271C>T	ERBB4		
CHC2432T	g.chr2:21322702A>G	Unknown		
CHC2432T	g.chr2:213229756G>A	ERBB4		
CHC2432T	g.chr2:214593551A>T	SPAG16		
CHC2432T	g.chr2:214626343T>C	SPAG16		
CHC2432T	g.chr2:215938368G>A	ABCA12		
CHC2432T	g.chr2:217065881C>T	XRCC5		
CHC2432T	g.chr2:218199021A>C	DIRC3		
CHC2432T	g.chr2:21821318T>C	Unknown		
CHC2432T	g.chr2:218949204C>A	RUFY4		
CHC2432T	g.chr2:219387785G>C	USP37		
CHC2432T	g.chr2:221134359C>A	AC114765.1		
CHC2432T	g.chr2:22116366C>G	Unknown		
CHC2432T	g.chr2:222194313C>A	Unknown		
CHC2432T	g.chr2:222485277T>A	Unknown		
CHC2432T	g.chr2:222635849G>A	Unknown		
CHC2432T	g.chr2:222680374C>A	Unknown		
CHC2432T	g.chr2:226418877A>T	NYAP2		
CHC2432T	g.chr2:227160135T>C	Unknown		
CHC2432T	g.chr2:227203654C>G	Unknown		
CHC2432T	g.chr2:228747363C>A	DAW1		
CHC2432T	g.chr2:229790746G>T	PID1		
CHC2432T	g.chr2:23253599C>A	AC016768.1		
CHC2432T	g.chr2:23253600A>T	AC016768.1		
CHC2432T	g.chr2:237110662G>T	ASB18		
CHC2432T	g.chr2:237335503T>C	IQCA1		
CHC2432T	g.chr2:239506962A>G	Unknown		
CHC2432T	g.chr2:239795410T>C	TWIST2		
CHC2432T	g.chr2:25879260T>A	DTNB		
CHC2432T	g.chr2:26140259C>A	Unknown		
CHC2432T	g.chr2:26473134A>C	HADHB		
CHC2432T	g.chr2:27554114C>A	GTF3C2		
CHC2432T	g.chr2:27933715C>A	AC074091.13		
CHC2432T	g.chr2:28588073A>C	Unknown		
CHC2432T	g.chr2:31079253A>T	Unknown		
CHC2432T	g.chr2:32445088A>G	SLC30A6		
CHC2432T	g.chr2:36499237G>T	Unknown		
CHC2432T	g.chr2:36613572A>G	CRIM1		
CHC2432T	g.chr2:38803623T>C	HNRNPLL		
CHC2432T	g.chr2:40524451A>G	SLC8A1		
CHC2432T	g.chr2:40537149C>T	SLC8A1		
CHC2432T	g.chr2:40747945C>A	SLC8A1		
CHC2432T	g.chr2:40860657T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr2:42446923G>T	EML4		
CHC2432T	g.chr2:42631963G>A	Unknown		
CHC2432T	g.chr2:42765188C>G	MTA3		
CHC2432T	g.chr2:43188852G>C	Unknown		
CHC2432T	g.chr2:43380360C>T	Unknown		
CHC2432T	g.chr2:43837713T>C	Unknown		
CHC2432T	g.chr2:45276289C>G	Unknown		
CHC2432T	g.chr2:48844222A>C	STON1-GTF2A1L		
CHC2432T	g.chr2:49276145G>A	FSHR		
CHC2432T	g.chr2:49562025G>A	Unknown		
CHC2432T	g.chr2:52657853T>C	Unknown		
CHC2432T	g.chr2:53950420T>A	GPR75-ASB3		
CHC2432T	g.chr2:54981432G>T	EML6		
CHC2432T	g.chr2:5680726C>T	Unknown		
CHC2432T	g.chr2:57550394C>T	Unknown		
CHC2432T	g.chr2:58232888G>T	VRK2		
CHC2432T	g.chr2:59658698T>C	RP11-444A22.1		
CHC2432T	g.chr2:59687507G>A	RP11-444A22.1		
CHC2432T	g.chr2:59836809A>G	RP11-444A22.1		
CHC2432T	g.chr2:62274292T>G	COMMD1		
CHC2432T	g.chr2:6526273T>A	Unknown		
CHC2432T	g.chr2:66122301A>C	Unknown		
CHC2432T	g.chr2:6653943T>C	Unknown		
CHC2432T	g.chr2:6835913G>A	Unknown		
CHC2432T	g.chr2:70566317G>T	Unknown		
CHC2432T	g.chr2:71786384C>G	DYSF		
CHC2432T	g.chr2:72296302A>G	Unknown		
CHC2432T	g.chr2:72710223A>C	EXOC6B		
CHC2432T	g.chr2:73536838A>G	Unknown		
CHC2432T	g.chr2:75421300G>T	TACR1		
CHC2432T	g.chr2:76464014C>T	Unknown		
CHC2432T	g.chr2:76835693A>G	Unknown		
CHC2432T	g.chr2:78670233T>A	Unknown		
CHC2432T	g.chr2:80127827T>C	CTNNA2		
CHC2432T	g.chr2:81026915C>T	AC084193.1		
CHC2432T	g.chr2:82158350C>T	Unknown		
CHC2432T	g.chr2:82343814G>A	Unknown		
CHC2432T	g.chr2:83245640A>G	Unknown		
CHC2432T	g.chr2:83788511G>C	Unknown		
CHC2432T	g.chr2:86903778A>G	RNF103-CHMP3		
CHC2432T	g.chr2:87248045C>G	PLGLB1		
CHC2432T	g.chr2:95666976A>T	Unknown		
CHC2432T	g.chr2:98580959G>A	TMEM131		
CHC2432T	g.chr2:98580960G>A	TMEM131		
CHC2432T	g.chr20:21020720G>T	Unknown		
CHC2432T	g.chr20:21310053T>C	XRN2		
CHC2432T	g.chr20:22119173C>T	Unknown		
CHC2432T	g.chr20:23452553C>G	Unknown		
CHC2432T	g.chr20:24963322G>A	APMAP		
CHC2432T	g.chr20:30461345C>T	TTL9		
CHC2432T	g.chr20:31583715T>C	SUN5		
CHC2432T	g.chr20:31811107G>T	BPIFA3		
CHC2432T	g.chr20:34743905G>T	EPB41L1		
CHC2432T	g.chr20:40490605A>G	Unknown		
CHC2432T	g.chr20:42726682C>A	Unknown		
CHC2432T	g.chr20:44271681G>A	Unknown		
CHC2432T	g.chr20:44611144C>A	Unknown		
CHC2432T	g.chr20:49394062T>A	Unknown		
CHC2432T	g.chr20:49461288C>T	BCAS4		
CHC2432T	g.chr20:51023640T>A	Unknown		
CHC2432T	g.chr20:53716884A>G	Unknown		
CHC2432T	g.chr20:57833015C>A	ZNF831		
CHC2432T	g.chr20:57933823C>A	Unknown		
CHC2432T	g.chr20:57943051G>A	Unknown		
CHC2432T	g.chr20:58283134G>T	PHACTR3		
CHC2432T	g.chr20:58726011C>A	RP5-1043L13.1		
CHC2432T	g.chr20:58759595T>C	RP5-1043L13.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr20:59884279C>A	CDH4		
CHC2432T	g.chr20:60473553C>A	CDH4		
CHC2432T	g.chr20:61031550G>A	Unknown		
CHC2432T	g.chr20:61795357G>T	Unknown		
CHC2432T	g.chr21:15558584T>C	LIPI		
CHC2432T	g.chr21:15739153T>C	Unknown		
CHC2432T	g.chr21:16051425T>C	Unknown		
CHC2432T	g.chr21:18206411C>T	Unknown		
CHC2432T	g.chr21:18281668C>T	Unknown		
CHC2432T	g.chr21:19429430G>T	CHODL		
CHC2432T	g.chr21:21505317A>G	Unknown		
CHC2432T	g.chr21:21514879T>C	Unknown		
CHC2432T	g.chr21:22056683A>C	Unknown		
CHC2432T	g.chr21:23332648C>A	AP000472.3		
CHC2432T	g.chr21:23554762C>G	Unknown		
CHC2432T	g.chr21:24377936G>A	Unknown		
CHC2432T	g.chr21:24615211T>A	Unknown		
CHC2432T	g.chr21:25997145G>A	Unknown		
CHC2432T	g.chr21:27913311C>T	CYR1		
CHC2432T	g.chr21:28330219G>A	ADAMT5		
CHC2432T	g.chr21:28421900G>A	Unknown		
CHC2432T	g.chr21:28670429C>A	Unknown		
CHC2432T	g.chr21:31502345C>A	Unknown		
CHC2432T	g.chr21:32092424T>G	Unknown		
CHC2432T	g.chr21:33685823A>T	URB1		
CHC2432T	g.chr21:37141542A>G	Unknown		
CHC2432T	g.chr21:40199205C>T	Unknown		
CHC2432T	g.chr21:40436776C>A	Unknown		
CHC2432T	g.chr21:41237508T>G	Unknown		
CHC2432T	g.chr21:42459122C>A	Unknown		
CHC2432T	g.chr21:42751061C>G	MX2		
CHC2432T	g.chr21:43346491A>G	C2CD2		
CHC2432T	g.chr21:44795733G>A	Unknown		
CHC2432T	g.chr21:45446338A>G	TRAPPC10		
CHC2432T	g.chr22:22716703C>A	Unknown		
CHC2432T	g.chr22:23935623G>A	Unknown		
CHC2432T	g.chr22:24044427T>G	KB-1572G7.2		
CHC2432T	g.chr22:24164582T>A	SMARCB1		
CHC2432T	g.chr22:25668741C>A	Unknown		
CHC2432T	g.chr22:27539042G>T	Unknown		
CHC2432T	g.chr22:34118638T>C	LARGE		
CHC2432T	g.chr22:34713180A>G	Unknown		
CHC2432T	g.chr22:34954720A>C	Unknown		
CHC2432T	g.chr22:34994510C>T	Unknown		
CHC2432T	g.chr22:35272663G>T	Unknown		
CHC2432T	g.chr22:37005349C>G	CACNG2		
CHC2432T	g.chr22:45474247C>T	Unknown		
CHC2432T	g.chr22:47067510G>T	GRAMD4		
CHC2432T	g.chr22:47135816C>T	Unknown		
CHC2432T	g.chr22:47739286C>T	Unknown		
CHC2432T	g.chr22:47798026G>A	Unknown		
CHC2432T	g.chr22:49749177G>T	Unknown		
CHC2432T	g.chr3:100321252G>C	Unknown		
CHC2432T	g.chr3:100757342T>C	Unknown		
CHC2432T	g.chr3:1015544T>G	Unknown		
CHC2432T	g.chr3:102999843C>A	Unknown		
CHC2432T	g.chr3:103121950T>C	Unknown		
CHC2432T	g.chr3:10329849C>A	GHRL		
CHC2432T	g.chr3:103764340G>A	Unknown		
CHC2432T	g.chr3:104227550T>C	Unknown		
CHC2432T	g.chr3:104263504G>A	Unknown		
CHC2432T	g.chr3:104897371C>T	Unknown		
CHC2432T	g.chr3:106148896T>C	Unknown		
CHC2432T	g.chr3:106208800C>A	Unknown		
CHC2432T	g.chr3:109096761G>C	Unknown		
CHC2432T	g.chr3:109740589T>C	Unknown		
CHC2432T	g.chr3:112073079C>T	CD200		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr3:112509031C>T	Unknown		
CHC2432T	g.chr3:114393485A>C	ZBTB20		
CHC2432T	g.chr3:115401824A>C	GAP43		
CHC2432T	g.chr3:115782702C>A	LSAMP		
CHC2432T	g.chr3:118139439T>A	RP11-384F7.1		
CHC2432T	g.chr3:118675497G>A	IGSF11		
CHC2432T	g.chr3:119834496A>G	Unknown		
CHC2432T	g.chr3:121340606C>T	FBXO40	c.330C>T	p.T110T
CHC2432T	g.chr3:123507369T>C	MYLK		
CHC2432T	g.chr3:123659746A>C	CCDC14		
CHC2432T	g.chr3:126653838A>G	CHCHD6		
CHC2432T	g.chr3:130881089C>G	NEK11		
CHC2432T	g.chr3:131113296C>A	Unknown		
CHC2432T	g.chr3:131431580G>T	CPNE4		
CHC2432T	g.chr3:131872761T>C	CPNE4		
CHC2432T	g.chr3:132049909G>T	ACPP		
CHC2432T	g.chr3:134177421G>T	Unknown		
CHC2432T	g.chr3:137045055G>C	Unknown		
CHC2432T	g.chr3:143665684A>G	Unknown		
CHC2432T	g.chr3:145496384G>T	Unknown		
CHC2432T	g.chr3:145709672T>C	Unknown		
CHC2432T	g.chr3:147211236G>A	ZIC1		
CHC2432T	g.chr3:151660923T>C	Unknown		
CHC2432T	g.chr3:152431970C>T	Unknown		
CHC2432T	g.chr3:153073339G>T	Unknown		
CHC2432T	g.chr3:153073340A>T	Unknown		
CHC2432T	g.chr3:153392839T>C	RP11-23D24.2		
CHC2432T	g.chr3:154139513T>C	GPR149		
CHC2432T	g.chr3:1542204A>T	Unknown		
CHC2432T	g.chr3:157454095T>A	Unknown		
CHC2432T	g.chr3:162052671G>T	Unknown		
CHC2432T	g.chr3:162980181G>A	CT64		
CHC2432T	g.chr3:163802434A>G	Unknown		
CHC2432T	g.chr3:163870585C>A	Unknown		
CHC2432T	g.chr3:164186550C>T	Unknown		
CHC2432T	g.chr3:165696676A>T	Unknown		
CHC2432T	g.chr3:166294235C>A	Unknown		
CHC2432T	g.chr3:166625194C>T	Unknown		
CHC2432T	g.chr3:166920706C>A	Unknown		
CHC2432T	g.chr3:167183351C>T	SERPINI2	c.589G>A	p.D197N
CHC2432T	g.chr3:167294492G>T	WDR49		
CHC2432T	g.chr3:167358277A>C	WDR49		
CHC2432T	g.chr3:168982458C>T	MECOM		
CHC2432T	g.chr3:171989607C>T	FNDC3B		
CHC2432T	g.chr3:175685911A>G	Unknown		
CHC2432T	g.chr3:176983026G>A	Unknown		
CHC2432T	g.chr3:178556075T>C	KCNMB2		
CHC2432T	g.chr3:178861272G>T	RP11-360P21.2		
CHC2432T	g.chr3:178936082G>A	PIK3CA	c.1624G>A	p.E542K
CHC2432T	g.chr3:179668384G>T	PEX5L		
CHC2432T	g.chr3:182683176C>T	DCUN1D1		
CHC2432T	g.chr3:189712740C>A	LEPREL1		
CHC2432T	g.chr3:18977470G>T	Unknown		
CHC2432T	g.chr3:19105616C>A	Unknown		
CHC2432T	g.chr3:191886996G>T	FGF12		
CHC2432T	g.chr3:192536748C>A	MB21D2		
CHC2432T	g.chr3:197196101G>C	Unknown		
CHC2432T	g.chr3:19730776G>A	Unknown		
CHC2432T	g.chr3:197759738G>T	LMLN		
CHC2432T	g.chr3:19887289C>A	Unknown		
CHC2432T	g.chr3:21275046A>T	Unknown		
CHC2432T	g.chr3:28677746G>T	LINC00693		
CHC2432T	g.chr3:30044241C>T	RBMS3		
CHC2432T	g.chr3:3035950C>T	CNTN4		
CHC2432T	g.chr3:30884519C>A	GADL1		
CHC2432T	g.chr3:32785430G>T	CNOT10		
CHC2432T	g.chr3:33067082T>A	GLB1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr3:33440275A>T	UBP1		
CHC2432T	g.chr3:34090115T>A	Unknown		
CHC2432T	g.chr3:36656761G>T	Unknown		
CHC2432T	g.chr3:38244521G>A	OXSR1		
CHC2432T	g.chr3:4115285C>A	SUMF1		
CHC2432T	g.chr3:41374186T>A	ULK4		
CHC2432T	g.chr3:4388224G>A	SUMF1		
CHC2432T	g.chr3:43991362G>A	Unknown		
CHC2432T	g.chr3:47414183T>C	Unknown		
CHC2432T	g.chr3:49006487T>A	ARIH2		
CHC2432T	g.chr3:52673290C>T	PBRM1		
CHC2432T	g.chr3:53492149T>G	Unknown		
CHC2432T	g.chr3:53826453A>G	CACNA1D		
CHC2432T	g.chr3:54133994T>C	Unknown		
CHC2432T	g.chr3:54313064A>T	CACNA2D3		
CHC2432T	g.chr3:55974527T>C	ERC2		
CHC2432T	g.chr3:57379996A>G	DNAH12		
CHC2432T	g.chr3:60797480T>C	FHIT		
CHC2432T	g.chr3:62394912G>T	CADPS		
CHC2432T	g.chr3:6351063A>G	AC026167.1		
CHC2432T	g.chr3:64946200C>T	ADAMTS9-AS2		
CHC2432T	g.chr3:65422559G>A	MAGI1		
CHC2432T	g.chr3:66649004C>A	Unknown		
CHC2432T	g.chr3:6691125G>T	AC069277.2		
CHC2432T	g.chr3:684937T>C	AC090044.1		
CHC2432T	g.chr3:68738798C>T	Unknown		
CHC2432T	g.chr3:69001150A>T	Unknown		
CHC2432T	g.chr3:70998697C>T	Unknown		
CHC2432T	g.chr3:72153342C>T	Unknown		
CHC2432T	g.chr3:73333793A>C	Unknown		
CHC2432T	g.chr3:75078495C>A	Unknown		
CHC2432T	g.chr3:75658398T>G	Unknown		
CHC2432T	g.chr3:75976756T>C	ROBO2		
CHC2432T	g.chr3:76348168C>G	ROBO2		
CHC2432T	g.chr3:76850181A>G	ROBO2		
CHC2432T	g.chr3:76911678G>A	ROBO2		
CHC2432T	g.chr3:77197872C>A	ROBO2		
CHC2432T	g.chr3:7731331G>A	GRM7		
CHC2432T	g.chr3:81543124A>G	GBE1		
CHC2432T	g.chr3:82673289A>T	Unknown		
CHC2432T	g.chr3:83530257G>T	Unknown		
CHC2432T	g.chr3:83766408T>A	Unknown		
CHC2432T	g.chr3:85252392C>T	CADM2		
CHC2432T	g.chr3:85270416G>C	CADM2		
CHC2432T	g.chr3:86129311A>G	Unknown		
CHC2432T	g.chr3:86317787G>T	Unknown		
CHC2432T	g.chr3:87433769C>T	Unknown		
CHC2432T	g.chr3:87793254A>C	RP11-451B8.1		
CHC2432T	g.chr3:88498288T>G	Unknown		
CHC2432T	g.chr3:88740621A>G	Unknown		
CHC2432T	g.chr3:89356285T>A	EPHA3		
CHC2432T	g.chr3:89951885G>A	Unknown		
CHC2432T	g.chr3:94782278G>T	Unknown		
CHC2432T	g.chr3:94796785T>C	Unknown		
CHC2432T	g.chr3:95215386T>C	Unknown		
CHC2432T	g.chr3:95614375C>A	Unknown		
CHC2432T	g.chr3:95835477C>G	Unknown		
CHC2432T	g.chr3:97171022G>T	EPHA6		
CHC2432T	g.chr3:97818431G>T	Unknown		
CHC2432T	g.chr3:99750674T>C	FILIP1L		
CHC2432T	g.chr4:100104096T>C	RP11-696N14.1		
CHC2432T	g.chr4:100268528A>C	ADH1C		
CHC2432T	g.chr4:101505203A>T	Unknown		
CHC2432T	g.chr4:101678007G>A	Unknown		
CHC2432T	g.chr4:103800224A>G	CISD2		
CHC2432T	g.chr4:104979631T>C	Unknown		
CHC2432T	g.chr4:105344058A>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr4:105791610A>G	RP11-556114.2		
CHC2432T	g.chr4:105848565C>T	RP11-556114.2		
CHC2432T	g.chr4:105970555T>C	RP11-556114.1		
CHC2432T	g.chr4:106155766G>T	TET2	c.667G>T	p.G223C
CHC2432T	g.chr4:106369762T>C	PPA2		
CHC2432T	g.chr4:106673436T>A	GSTCD		
CHC2432T	g.chr4:107340715G>A	Unknown		
CHC2432T	g.chr4:108204441T>C	DKK2		
CHC2432T	g.chr4:111244985T>C	Unknown		
CHC2432T	g.chr4:112314995G>C	Unknown		
CHC2432T	g.chr4:112437784C>T	Unknown		
CHC2432T	g.chr4:113082029T>G	C4orf32		
CHC2432T	g.chr4:114685545T>C	Unknown		
CHC2432T	g.chr4:116266378C>A	Unknown		
CHC2432T	g.chr4:117015228A>G	Unknown		
CHC2432T	g.chr4:117081152A>G	RP11-65903.1		
CHC2432T	g.chr4:11743992A>C	RP11-281P23.2		
CHC2432T	g.chr4:11941394A>G	Unknown		
CHC2432T	g.chr4:120429273A>G	PDE5A		
CHC2432T	g.chr4:120891640T>C	Unknown		
CHC2432T	g.chr4:121483372C>T	Unknown		
CHC2432T	g.chr4:121537499C>A	Unknown		
CHC2432T	g.chr4:125966349A>G	Unknown		
CHC2432T	g.chr4:128728455T>G	HSPA4L		
CHC2432T	g.chr4:133006773T>C	RP11-789C2.1		
CHC2432T	g.chr4:134456018T>A	Unknown		
CHC2432T	g.chr4:136107000C>T	Unknown		
CHC2432T	g.chr4:136959240T>A	Unknown		
CHC2432T	g.chr4:136991794A>G	Unknown		
CHC2432T	g.chr4:137196632C>A	RP11-775H9.2		
CHC2432T	g.chr4:137351796C>G	Unknown		
CHC2432T	g.chr4:138656332A>G	Unknown		
CHC2432T	g.chr4:143574128A>G	INPP4B		
CHC2432T	g.chr4:143646989T>G	INPP4B		
CHC2432T	g.chr4:144592871A>G	FREM3		
CHC2432T	g.chr4:144936023G>T	GYPB		
CHC2432T	g.chr4:145296776G>T	Unknown		
CHC2432T	g.chr4:146694787T>C	ZNF827		
CHC2432T	g.chr4:147425224C>A	SLC10A7		
CHC2432T	g.chr4:147523091C>A	Unknown		
CHC2432T	g.chr4:147755523G>A	TTC29		
CHC2432T	g.chr4:151991130T>C	Unknown		
CHC2432T	g.chr4:153280593T>C	FBXW7		
CHC2432T	g.chr4:154156823T>C	TRIM2		
CHC2432T	g.chr4:155231256G>T	DCHS2		
CHC2432T	g.chr4:156244390C>T	AC097467.2		
CHC2432T	g.chr4:156492302T>C	Unknown		
CHC2432T	g.chr4:157896318G>T	Unknown		
CHC2432T	g.chr4:158448258C>G	Unknown		
CHC2432T	g.chr4:159461242C>A	RXFP1		
CHC2432T	g.chr4:159529971C>A	RXFP1		
CHC2432T	g.chr4:16026838T>G	PROM1	c.580A>C	p.T194P
CHC2432T	g.chr4:161139234G>T	Unknown		
CHC2432T	g.chr4:165398633G>T	Unknown		
CHC2432T	g.chr4:165928557C>A	RP11-366M4.13		
CHC2432T	g.chr4:167316155C>T	RP11-217C7.1		
CHC2432T	g.chr4:168692809A>G	Unknown		
CHC2432T	g.chr4:171116884A>G	Unknown		
CHC2432T	g.chr4:171891729T>A	Unknown		
CHC2432T	g.chr4:173074348G>A	GALNTL6		
CHC2432T	g.chr4:173564495C>T	GALNTL6		
CHC2432T	g.chr4:175044561C>T	RP11-148L24.1		
CHC2432T	g.chr4:176574847G>A	GPM6A		
CHC2432T	g.chr4:177460145G>T	Unknown		
CHC2432T	g.chr4:178203293A>G	Unknown		
CHC2432T	g.chr4:178286671C>A	Unknown		
CHC2432T	g.chr4:178691010G>T	RP11-389E17.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr4:178954522G>T	Unknown		
CHC2432T	g.chr4:178976366A>G	Unknown		
CHC2432T	g.chr4:179372697C>T	Unknown		
CHC2432T	g.chr4:179658204C>A	Unknown		
CHC2432T	g.chr4:180205864A>G	Unknown		
CHC2432T	g.chr4:181513979T>G	Unknown		
CHC2432T	g.chr4:182086323G>T	Unknown		
CHC2432T	g.chr4:183830187T>G	DCTD		
CHC2432T	g.chr4:188591872G>A	Unknown		
CHC2432T	g.chr4:189122083C>T	Unknown		
CHC2432T	g.chr4:19004321A>C	Unknown		
CHC2432T	g.chr4:19799323A>G	RP11-608O21.1		
CHC2432T	g.chr4:22371901C>A	Unknown		
CHC2432T	g.chr4:25467414G>T	Unknown		
CHC2432T	g.chr4:25512492T>C	Unknown		
CHC2432T	g.chr4:277813C>A	ZNF732		
CHC2432T	g.chr4:27790592G>T	Unknown		
CHC2432T	g.chr4:29373049G>T	Unknown		
CHC2432T	g.chr4:29581854G>T	Unknown		
CHC2432T	g.chr4:31231916C>T	Unknown		
CHC2432T	g.chr4:34375674A>G	Unknown		
CHC2432T	g.chr4:36062347G>C	Unknown		
CHC2432T	g.chr4:41075230T>A	APBB2		
CHC2432T	g.chr4:42623549A>G	ATP8A1		
CHC2432T	g.chr4:43882356A>G	Unknown		
CHC2432T	g.chr4:44532606G>A	Unknown		
CHC2432T	g.chr4:44552501T>C	Unknown		
CHC2432T	g.chr4:45385871C>T	Unknown		
CHC2432T	g.chr4:48555753G>T	FRYL		
CHC2432T	g.chr4:4929544A>T	Unknown		
CHC2432T	g.chr4:53305868A>T	Unknown		
CHC2432T	g.chr4:5379767G>C	STK32B		
CHC2432T	g.chr4:54777990A>T	FIP1L1		
CHC2432T	g.chr4:55049707T>C	FIP1L1		
CHC2432T	g.chr4:55745881G>T	Unknown		
CHC2432T	g.chr4:57090624C>G	KIAA1211		
CHC2432T	g.chr4:58478820T>G	RP11-4O3.1		
CHC2432T	g.chr4:58737759C>G	Unknown		
CHC2432T	g.chr4:58943187A>G	Unknown		
CHC2432T	g.chr4:60260968A>G	Unknown		
CHC2432T	g.chr4:60405072T>A	Unknown		
CHC2432T	g.chr4:60417216G>A	RP11-725D20.1		
CHC2432T	g.chr4:61672555C>G	Unknown		
CHC2432T	g.chr4:62948905A>G	RP11-84A1.3		
CHC2432T	g.chr4:63122540A>T	Unknown		
CHC2432T	g.chr4:63336401G>A	Unknown		
CHC2432T	g.chr4:65002962T>C	Unknown		
CHC2432T	g.chr4:65905919A>G	Unknown		
CHC2432T	g.chr4:66564304C>T	Unknown		
CHC2432T	g.chr4:66652864C>T	Unknown		
CHC2432T	g.chr4:67220245G>T	Unknown		
CHC2432T	g.chr4:67375149C>G	Unknown		
CHC2432T	g.chr4:67375150C>A	Unknown		
CHC2432T	g.chr4:67856218A>T	Unknown		
CHC2432T	g.chr4:68022770A>G	Unknown		
CHC2432T	g.chr4:68030355C>A	Unknown		
CHC2432T	g.chr4:6854634T>G	KIAA0232		
CHC2432T	g.chr4:68927123C>A	TMPRSS11F		
CHC2432T	g.chr4:69815245T>A	UGT2A3		
CHC2432T	g.chr4:70383936C>A	UGT2B4		
CHC2432T	g.chr4:72099715A>G	SLC4A4		
CHC2432T	g.chr4:73771069A>G	Unknown		
CHC2432T	g.chr4:73771073T>A	Unknown		
CHC2432T	g.chr4:75221064C>T	Unknown		
CHC2432T	g.chr4:76294835A>T	RP11-567N4.2		
CHC2432T	g.chr4:77298797G>C	CCDC158		
CHC2432T	g.chr4:81640413C>A	C4orf22		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr4:82321982G>T	Unknown		
CHC2432T	g.chr4:83105360G>C	Unknown		
CHC2432T	g.chr4:87073690A>G	MAPK10		
CHC2432T	g.chr4:87187082C>T	MAPK10		
CHC2432T	g.chr4:87378040A>G	MAPK10		
CHC2432T	g.chr4:88390413A>G	Unknown		
CHC2432T	g.chr4:9070601C>A	Unknown		
CHC2432T	g.chr4:92039568G>T	CCSER1		
CHC2432T	g.chr4:93851884T>C	GRID2		
CHC2432T	g.chr4:94843909C>T	Unknown		
CHC2432T	g.chr4:95733968C>A	BMPR1B		
CHC2432T	g.chr4:96543568G>T	Unknown		
CHC2432T	g.chr4:96556620C>T	Unknown		
CHC2432T	g.chr4:97246872T>A	RP11-145G20.1		
CHC2432T	g.chr4:97516637A>G	Unknown		
CHC2432T	g.chr4:97776942A>G	Unknown		
CHC2432T	g.chr5:10202813C>A	Unknown		
CHC2432T	g.chr5:103072959C>A	Unknown		
CHC2432T	g.chr5:103787952G>A	Unknown		
CHC2432T	g.chr5:103842576G>A	RP11-6N13.1		
CHC2432T	g.chr5:104206374G>T	RP11-6N13.1		
CHC2432T	g.chr5:104230857C>A	RP11-6N13.1		
CHC2432T	g.chr5:104714918T>A	RP11-6N13.1		
CHC2432T	g.chr5:10497713T>C	RP11-1C1.4		
CHC2432T	g.chr5:105088729G>T	Unknown		
CHC2432T	g.chr5:105573047C>A	Unknown		
CHC2432T	g.chr5:107249524C>A	FBXL17		
CHC2432T	g.chr5:107443631C>A	FBXL17		
CHC2432T	g.chr5:112122163T>G	APC		
CHC2432T	g.chr5:112143652G>T	APC		
CHC2432T	g.chr5:113909914A>C	RP11-492A10.1		
CHC2432T	g.chr5:114956723C>T	TMED7		
CHC2432T	g.chr5:116642129C>T	Unknown		
CHC2432T	g.chr5:117843459T>G	CTD-2281M20.1		
CHC2432T	g.chr5:118404403T>A	CTB-161M19.4		
CHC2432T	g.chr5:118404404G>A	CTB-161M19.4		
CHC2432T	g.chr5:119423803C>T	Unknown		
CHC2432T	g.chr5:119599885T>C	CTC-552D5.1		
CHC2432T	g.chr5:121276238C>A	Unknown		
CHC2432T	g.chr5:121426060A>T	Unknown		
CHC2432T	g.chr5:122644615G>C	Unknown		
CHC2432T	g.chr5:122987617T>C	Unknown		
CHC2432T	g.chr5:123583226G>T	Unknown		
CHC2432T	g.chr5:124074228C>A	ZNF608		
CHC2432T	g.chr5:12636744T>A	CT49		
CHC2432T	g.chr5:129102334A>C	KIAA1024L		
CHC2432T	g.chr5:130763019C>A	RAPGEF6		
CHC2432T	g.chr5:130813613C>A	RAPGEF6		
CHC2432T	g.chr5:132918993T>C	FSTL4		
CHC2432T	g.chr5:135362250T>C	Unknown		
CHC2432T	g.chr5:13754669T>C	DNAH5		
CHC2432T	g.chr5:138013507T>A	Unknown		
CHC2432T	g.chr5:138903475G>A	Unknown		
CHC2432T	g.chr5:148779015C>T	IL17B		
CHC2432T	g.chr5:149747537G>A	TCOF1		
CHC2432T	g.chr5:149973249T>A	Unknown		
CHC2432T	g.chr5:150324727T>C	Unknown		
CHC2432T	g.chr5:150991914A>G	Unknown		
CHC2432T	g.chr5:151049506C>A	SPARC		
CHC2432T	g.chr5:151469064T>C	CTB-1202.1		
CHC2432T	g.chr5:153538896T>A	MFAP3		
CHC2432T	g.chr5:155202614T>A	Unknown		
CHC2432T	g.chr5:156946684G>T	ADAM19		
CHC2432T	g.chr5:157883291C>T	Unknown		
CHC2432T	g.chr5:157914259C>A	RP11-32D16.1		
CHC2432T	g.chr5:159101437C>A	Unknown		
CHC2432T	g.chr5:159102441T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr5:159682561C>A	CCNJL	c.738G>T	p.L246L
CHC2432T	g.chr5:160438503G>A	Unknown		
CHC2432T	g.chr5:161435571T>G	Unknown		
CHC2432T	g.chr5:161843933C>A	Unknown		
CHC2432T	g.chr5:162358751T>A	Unknown		
CHC2432T	g.chr5:162539329C>T	RP11-541P9.3		
CHC2432T	g.chr5:163334661C>T	Unknown		
CHC2432T	g.chr5:163852609G>A	CTC-340A15.2		
CHC2432T	g.chr5:16795336G>T	MYO10		
CHC2432T	g.chr5:1695599T>A	Unknown		
CHC2432T	g.chr5:172223149A>G	Unknown		
CHC2432T	g.chr5:1724019A>T	Unknown		
CHC2432T	g.chr5:173350832T>G	CPEB4		
CHC2432T	g.chr5:17343440A>G	Unknown		
CHC2432T	g.chr5:173733515T>C	Unknown		
CHC2432T	g.chr5:174105004G>T	Unknown		
CHC2432T	g.chr5:178922531A>T	Unknown		
CHC2432T	g.chr5:19720920T>C	CDH18		
CHC2432T	g.chr5:21455558C>G	Unknown		
CHC2432T	g.chr5:21703928C>A	RP11-804N13.1		
CHC2432T	g.chr5:22179112G>A	CDH12		
CHC2432T	g.chr5:22217034A>C	CDH12		
CHC2432T	g.chr5:22536126T>C	CDH12		
CHC2432T	g.chr5:22585842G>A	CDH12		
CHC2432T	g.chr5:2336045C>T	Unknown		
CHC2432T	g.chr5:23850140T>C	Unknown		
CHC2432T	g.chr5:25476459T>G	Unknown		
CHC2432T	g.chr5:25476467C>T	Unknown		
CHC2432T	g.chr5:25722026G>A	Unknown		
CHC2432T	g.chr5:26753508G>A	Unknown		
CHC2432T	g.chr5:27061915G>A	Unknown		
CHC2432T	g.chr5:28366667G>A	Unknown		
CHC2432T	g.chr5:28882172C>A	Unknown		
CHC2432T	g.chr5:30031314G>A	Unknown		
CHC2432T	g.chr5:31207375T>A	CDH6		
CHC2432T	g.chr5:32991295G>A	Unknown		
CHC2432T	g.chr5:3423739G>T	LINC01019		
CHC2432T	g.chr5:3521885C>T	LINC01019		
CHC2432T	g.chr5:37257183C>T	Unknown		
CHC2432T	g.chr5:38459950A>G	EGFLAM		
CHC2432T	g.chr5:40015904C>A	Unknown		
CHC2432T	g.chr5:44787051G>A	RP11-53019.1		
CHC2432T	g.chr5:45613721T>C	HCN1		
CHC2432T	g.chr5:49816321T>C	Unknown		
CHC2432T	g.chr5:50197146T>C	Unknown		
CHC2432T	g.chr5:50637415G>A	Unknown		
CHC2432T	g.chr5:51249785C>A	Unknown		
CHC2432T	g.chr5:52667676G>C	Unknown		
CHC2432T	g.chr5:5459539G>T	KIAA0947		
CHC2432T	g.chr5:55514645A>T	ANKRD55		
CHC2432T	g.chr5:55779860G>A	Unknown		
CHC2432T	g.chr5:56449871T>C	Unknown		
CHC2432T	g.chr5:57369399A>C	Unknown		
CHC2432T	g.chr5:57644679T>C	Unknown		
CHC2432T	g.chr5:5788148C>T	Unknown		
CHC2432T	g.chr5:58727895A>G	PDE4D		
CHC2432T	g.chr5:59217286G>A	PDE4D		
CHC2432T	g.chr5:6001761C>T	Unknown		
CHC2432T	g.chr5:61945227G>C	Unknown		
CHC2432T	g.chr5:62316196G>A	Unknown		
CHC2432T	g.chr5:63248922A>G	Unknown		
CHC2432T	g.chr5:70993936C>T	Unknown		
CHC2432T	g.chr5:71637658A>G	PTCD2		
CHC2432T	g.chr5:71884674C>T	CTC-347C20.2		
CHC2432T	g.chr5:7326806G>A	Unknown		
CHC2432T	g.chr5:73456311G>A	Unknown		
CHC2432T	g.chr5:75367291T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr5:78831555T>C	Unknown		
CHC2432T	g.chr5:7973095G>T	Unknown		
CHC2432T	g.chr5:8039959C>G	Unknown		
CHC2432T	g.chr5:81413279A>G	ATG10		
CHC2432T	g.chr5:82556947A>G	XRCC4		
CHC2432T	g.chr5:82881887A>C	Unknown		
CHC2432T	g.chr5:84091491G>A	Unknown		
CHC2432T	g.chr5:84402299C>A	Unknown		
CHC2432T	g.chr5:84508606A>G	Unknown		
CHC2432T	g.chr5:84743691T>C	Unknown		
CHC2432T	g.chr5:84991423T>C	Unknown		
CHC2432T	g.chr5:85852495A>C	Unknown		
CHC2432T	g.chr5:86035402A>G	Unknown		
CHC2432T	g.chr5:8664841T>C	Unknown		
CHC2432T	g.chr5:89399897T>G	Unknown		
CHC2432T	g.chr5:89676269C>G	Unknown		
CHC2432T	g.chr5:9161621C>A	SEMA5A		
CHC2432T	g.chr5:92457808A>T	Unknown		
CHC2432T	g.chr5:97729781G>T	Unknown		
CHC2432T	g.chr5:99540022A>G	Unknown		
CHC2432T	g.chr5:99951253C>T	Unknown		
CHC2432T	g.chr6:103771936G>T	Unknown		
CHC2432T	g.chr6:104169521C>T	Unknown		
CHC2432T	g.chr6:113149075C>T	Unknown		
CHC2432T	g.chr6:113523213T>A	Unknown		
CHC2432T	g.chr6:116728893T>A	DSE		
CHC2432T	g.chr6:117118266A>G	GPRC6A		
CHC2432T	g.chr6:118157287A>G	Unknown		
CHC2432T	g.chr6:118313896T>C	SLC35F1		
CHC2432T	g.chr6:119715068G>T	Unknown		
CHC2432T	g.chr6:120291369A>T	Unknown		
CHC2432T	g.chr6:125704671T>C	Unknown		
CHC2432T	g.chr6:12613324T>A	Unknown		
CHC2432T	g.chr6:127714533A>G	Unknown		
CHC2432T	g.chr6:127714544A>G	Unknown		
CHC2432T	g.chr6:128070365T>C	THEMIS		
CHC2432T	g.chr6:129359912C>A	LAMA2		
CHC2432T	g.chr6:129882654G>C	Unknown		
CHC2432T	g.chr6:130025832C>A	ARHGAP18		
CHC2432T	g.chr6:132718209G>A	MOXD1		
CHC2432T	g.chr6:132935187G>C	Unknown		
CHC2432T	g.chr6:13472679C>T	GFOD1		
CHC2432T	g.chr6:134886036T>C	Unknown		
CHC2432T	g.chr6:135455001A>T	Unknown		
CHC2432T	g.chr6:135636813T>G	AHI1		
CHC2432T	g.chr6:136143822T>C	Unknown		
CHC2432T	g.chr6:136852571T>A	MAP7		
CHC2432T	g.chr6:137954534G>A	Unknown		
CHC2432T	g.chr6:142613844C>T	Unknown		
CHC2432T	g.chr6:147210687T>C	STXBP5-AS1		
CHC2432T	g.chr6:147633935G>A	STXBP5		
CHC2432T	g.chr6:148438516C>A	Unknown		
CHC2432T	g.chr6:149512932T>A	Unknown		
CHC2432T	g.chr6:149513170C>A	Unknown		
CHC2432T	g.chr6:150006597C>A	LATS1		
CHC2432T	g.chr6:150126773T>A	PCMT1		
CHC2432T	g.chr6:150716901C>A	IYD		
CHC2432T	g.chr6:150751023T>C	Unknown		
CHC2432T	g.chr6:15097438G>A	Unknown		
CHC2432T	g.chr6:151754637G>T	RMND1		
CHC2432T	g.chr6:152860213T>A	SYNE1		
CHC2432T	g.chr6:153674535G>T	Unknown		
CHC2432T	g.chr6:153680559G>A	Unknown		
CHC2432T	g.chr6:154065841C>A	Unknown		
CHC2432T	g.chr6:154084818G>C	Unknown		
CHC2432T	g.chr6:154422170C>T	OPRM1		
CHC2432T	g.chr6:159983834C>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr6:161495558A>G	MAP3K4		
CHC2432T	g.chr6:162070888G>T	PARK2		
CHC2432T	g.chr6:162952362C>T	PARK2		
CHC2432T	g.chr6:163009606C>A	PARK2		
CHC2432T	g.chr6:163929745G>A	QKI		
CHC2432T	g.chr6:170781273C>A	Unknown		
CHC2432T	g.chr6:17395325A>G	CAP2		
CHC2432T	g.chr6:18150921A>G	TPMT		
CHC2432T	g.chr6:19192420C>A	Unknown		
CHC2432T	g.chr6:19215856C>T	Unknown		
CHC2432T	g.chr6:19254616A>G	Unknown		
CHC2432T	g.chr6:20520805G>A	Unknown		
CHC2432T	g.chr6:22191021A>C	Unknown		
CHC2432T	g.chr6:22196171T>C	Unknown		
CHC2432T	g.chr6:22257554T>C	Unknown		
CHC2432T	g.chr6:22860084T>C	RP1-209A6.1		
CHC2432T	g.chr6:24351128A>G	DCDC2		
CHC2432T	g.chr6:29784891A>T	Unknown		
CHC2432T	g.chr6:3022101C>T	RP1-90J20.12		
CHC2432T	g.chr6:34026914A>G	GRM4		
CHC2432T	g.chr6:37640613T>C	MDGA1		
CHC2432T	g.chr6:42866376G>C	Unknown		
CHC2432T	g.chr6:44214362T>A	Unknown		
CHC2432T	g.chr6:44388630C>T	CDC5L		
CHC2432T	g.chr6:44533953A>G	Unknown		
CHC2432T	g.chr6:45956995C>T	CLIC5		
CHC2432T	g.chr6:47972958G>T	PTCHD4		
CHC2432T	g.chr6:53804318A>G	RP11-411K7.1		
CHC2432T	g.chr6:54411675G>A	Unknown		
CHC2432T	g.chr6:54805781C>A	FAM83B	c.2012C>A	p.S671*
CHC2432T	g.chr6:55222741A>G	GFRAL		
CHC2432T	g.chr6:55445417G>A	Unknown		
CHC2432T	g.chr6:55582368A>G	Unknown		
CHC2432T	g.chr6:55805614T>A	Unknown		
CHC2432T	g.chr6:56065036G>C	COL21A1		
CHC2432T	g.chr6:57176440G>T	Unknown		
CHC2432T	g.chr6:5923782C>T	Unknown		
CHC2432T	g.chr6:62387729C>T	RP1-240B8.3		
CHC2432T	g.chr6:6461788C>T	LY86-AS1		
CHC2432T	g.chr6:65037514T>C	EYS		
CHC2432T	g.chr6:66286645A>T	EYS		
CHC2432T	g.chr6:66482123C>T	Unknown		
CHC2432T	g.chr6:66681517T>A	Unknown		
CHC2432T	g.chr6:66914533A>C	Unknown		
CHC2432T	g.chr6:68511385G>A	Unknown		
CHC2432T	g.chr6:71702550T>A	Unknown		
CHC2432T	g.chr6:72164503C>A	RP1-288M22.2		
CHC2432T	g.chr6:73111894G>T	RIMS1		
CHC2432T	g.chr6:73940079C>A	RP11-257K9.8		
CHC2432T	g.chr6:74337091C>T	SLC17A5		
CHC2432T	g.chr6:74737912C>G	Unknown		
CHC2432T	g.chr6:74889460A>T	RP11-554D15.1		
CHC2432T	g.chr6:74963661T>A	RP11-554D15.1		
CHC2432T	g.chr6:75052855C>T	RP11-554D15.1		
CHC2432T	g.chr6:76254680C>T	Unknown		
CHC2432T	g.chr6:77502258C>G	Unknown		
CHC2432T	g.chr6:78114986A>C	Unknown		
CHC2432T	g.chr6:78824911C>A	Unknown		
CHC2432T	g.chr6:8036605T>C	BLOC1S5-TXNDC5		
CHC2432T	g.chr6:81815914C>T	Unknown		
CHC2432T	g.chr6:83524209C>T	Unknown		
CHC2432T	g.chr6:8390635C>T	Unknown		
CHC2432T	g.chr6:89268480T>C	Unknown		
CHC2432T	g.chr6:91864528C>T	Unknown		
CHC2432T	g.chr6:92538685A>G	Unknown		
CHC2432T	g.chr6:93070399T>A	Unknown		
CHC2432T	g.chr6:93383880A>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr6:93598439T>C	Unknown		
CHC2432T	g.chr6:93921264C>T	Unknown		
CHC2432T	g.chr6:94131887A>T	Unknown		
CHC2432T	g.chr6:95128343C>A	Unknown		
CHC2432T	g.chr6:983066G>A	Unknown		
CHC2432T	g.chr6:98505361C>A	RP11-436D23.1		
CHC2432T	g.chr6:98505364T>G	RP11-436D23.1		
CHC2432T	g.chr6:98690214G>T	RP11-436D23.1		
CHC2432T	g.chr6:98690215G>T	RP11-436D23.1		
CHC2432T	g.chr6:99005779G>A	Unknown		
CHC2432T	g.chr6:99475792C>A	Unknown		
CHC2432T	g.chr7:100406287A>C	EPHB4		
CHC2432T	g.chr7:102463763A>G	FBXL13		
CHC2432T	g.chr7:10368854G>C	Unknown		
CHC2432T	g.chr7:104778347T>C	SRPK2		
CHC2432T	g.chr7:106376265A>C	Unknown		
CHC2432T	g.chr7:106393175A>G	Unknown		
CHC2432T	g.chr7:107885956T>C	NRCAM		
CHC2432T	g.chr7:107885980A>C	NRCAM		
CHC2432T	g.chr7:108699197G>C	Unknown		
CHC2432T	g.chr7:109599125C>T	Unknown		
CHC2432T	g.chr7:110524846A>G	IMMP2L		
CHC2432T	g.chr7:111771105G>C	DOCK4		
CHC2432T	g.chr7:115422118G>T	Unknown		
CHC2432T	g.chr7:116005193C>A	CAV2		
CHC2432T	g.chr7:116408082A>G	MET		
CHC2432T	g.chr7:116650650G>T	ST7		
CHC2432T	g.chr7:117624044A>C	Unknown		
CHC2432T	g.chr7:11838982T>C	THSD7A		
CHC2432T	g.chr7:119224975C>A	Unknown		
CHC2432T	g.chr7:120396714T>C	Unknown		
CHC2432T	g.chr7:120997297C>A	FAM3C		
CHC2432T	g.chr7:122939552A>C	Unknown		
CHC2432T	g.chr7:123066103T>A	Unknown		
CHC2432T	g.chr7:124917433C>A	RP11-3B12.2		
CHC2432T	g.chr7:125446033A>C	Unknown		
CHC2432T	g.chr7:125459108C>A	Unknown		
CHC2432T	g.chr7:125900075T>G	Unknown		
CHC2432T	g.chr7:126672671T>A	GRM8		
CHC2432T	g.chr7:12682582C>T	SCIN		
CHC2432T	g.chr7:127059244T>C	Unknown		
CHC2432T	g.chr7:130402789T>C	Unknown		
CHC2432T	g.chr7:130497086C>T	Unknown		
CHC2432T	g.chr7:131419617G>T	Unknown		
CHC2432T	g.chr7:132446512A>G	Unknown		
CHC2432T	g.chr7:13434107C>T	Unknown		
CHC2432T	g.chr7:135924580A>C	AC009784.3		
CHC2432T	g.chr7:137487378T>G	DGKI		
CHC2432T	g.chr7:138062425C>A	Unknown		
CHC2432T	g.chr7:13866380G>T	Unknown		
CHC2432T	g.chr7:139294485C>A	HIPK2		
CHC2432T	g.chr7:140331283C>G	DENND2A		
CHC2432T	g.chr7:140873017G>T	TMEM178B		
CHC2432T	g.chr7:142616247A>G	TRPV5		
CHC2432T	g.chr7:142616256G>T	TRPV5		
CHC2432T	g.chr7:144975052T>C	Unknown		
CHC2432T	g.chr7:145345244A>C	Unknown		
CHC2432T	g.chr7:146591174G>T	CNTNAP2		
CHC2432T	g.chr7:147230040C>A	CNTNAP2		
CHC2432T	g.chr7:147836838G>T	CNTNAP2		
CHC2432T	g.chr7:147836839G>T	CNTNAP2		
CHC2432T	g.chr7:149289838G>A	ZNF767		
CHC2432T	g.chr7:149798458A>G	Unknown		
CHC2432T	g.chr7:15153610T>A	Unknown		
CHC2432T	g.chr7:152165990A>T	Unknown		
CHC2432T	g.chr7:152281612T>G	Unknown		
CHC2432T	g.chr7:152389008T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr7:153760113C>T	DPP6		
CHC2432T	g.chr7:155230833G>A	AC008060.8		
CHC2432T	g.chr7:155779265C>T	Unknown		
CHC2432T	g.chr7:157807692C>A	PTPRN2		
CHC2432T	g.chr7:157933083T>C	PTPRN2		
CHC2432T	g.chr7:158002928C>A	PTPRN2		
CHC2432T	g.chr7:158919780T>A	VIPR2		
CHC2432T	g.chr7:16970077A>C	Unknown		
CHC2432T	g.chr7:18280173C>T	HDAC9		
CHC2432T	g.chr7:18433571T>C	HDAC9		
CHC2432T	g.chr7:18650011C>A	HDAC9		
CHC2432T	g.chr7:19064493A>T	Unknown		
CHC2432T	g.chr7:19078534C>A	Unknown		
CHC2432T	g.chr7:20302528A>T	Unknown		
CHC2432T	g.chr7:21704974G>A	DNAH11		
CHC2432T	g.chr7:23142990A>G	KLHL7-AS1		
CHC2432T	g.chr7:26267501C>T	Unknown		
CHC2432T	g.chr7:26949000G>A	Unknown		
CHC2432T	g.chr7:29241055C>T	CHN2		
CHC2432T	g.chr7:29380705C>T	CHN2		
CHC2432T	g.chr7:29841735C>A	Unknown		
CHC2432T	g.chr7:30036315A>G	AC007285.6		
CHC2432T	g.chr7:31128191A>G	ADCYAP1R1		
CHC2432T	g.chr7:31727411C>A	PPP1R17		
CHC2432T	g.chr7:33095463C>A	NT5C3A		
CHC2432T	g.chr7:34143810G>A	BMPER		
CHC2432T	g.chr7:39283459C>G	POU6F2		
CHC2432T	g.chr7:39485434G>T	POU6F2		
CHC2432T	g.chr7:42327696G>A	Unknown		
CHC2432T	g.chr7:46516779T>C	AC004869.3		
CHC2432T	g.chr7:47028735T>C	AC004901.1		
CHC2432T	g.chr7:47196508T>C	Unknown		
CHC2432T	g.chr7:47299877A>C	Unknown		
CHC2432T	g.chr7:48419841A>T	ABCA13		
CHC2432T	g.chr7:48712023C>A	Unknown		
CHC2432T	g.chr7:48981158C>A	Unknown		
CHC2432T	g.chr7:49099313G>T	Unknown		
CHC2432T	g.chr7:49545708T>C	Unknown		
CHC2432T	g.chr7:51061173A>T	RP4-724E13.2		
CHC2432T	g.chr7:52107596T>C	Unknown		
CHC2432T	g.chr7:52181376A>G	Unknown		
CHC2432T	g.chr7:53025790T>A	Unknown		
CHC2432T	g.chr7:57329179G>A	Unknown		
CHC2432T	g.chr7:5868999G>A	ZNF815P		
CHC2432T	g.chr7:63720919A>G	ZNF679		
CHC2432T	g.chr7:66074181A>T	Unknown		
CHC2432T	g.chr7:69273615G>T	AUTS2		
CHC2432T	g.chr7:69273616C>G	AUTS2		
CHC2432T	g.chr7:70967810A>C	WBSCR17		
CHC2432T	g.chr7:77833668A>G	MAGI2		
CHC2432T	g.chr7:79153265C>G	Unknown		
CHC2432T	g.chr7:80039436C>A	CD36		
CHC2432T	g.chr7:82192987C>A	Unknown		
CHC2432T	g.chr7:84795219G>T	SEMA3D		
CHC2432T	g.chr7:85000815T>C	Unknown		
CHC2432T	g.chr7:86149473T>C	Unknown		
CHC2432T	g.chr7:87111548A>G	Unknown		
CHC2432T	g.chr7:88004171G>A	Unknown		
CHC2432T	g.chr7:92671180G>A	Unknown		
CHC2432T	g.chr7:94836099A>G	PPP1R9A		
CHC2432T	g.chr7:95491129T>C	DYNC111		
CHC2432T	g.chr7:96370868C>A	Unknown		
CHC2432T	g.chr7:96680618G>T	Unknown		
CHC2432T	g.chr8:102329590T>C	Unknown		
CHC2432T	g.chr8:102997272C>G	NCALD		
CHC2432T	g.chr8:103108193C>T	NCALD		
CHC2432T	g.chr8:104041550G>A	ATP6V1C1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr8:104433142A>C	DCAF13		
CHC2432T	g.chr8:105296959G>T	Unknown		
CHC2432T	g.chr8:105501518T>G	LRP12		
CHC2432T	g.chr8:105819050C>T	RP11-127H5.1		
CHC2432T	g.chr8:105969913A>T	Unknown		
CHC2432T	g.chr8:107209649A>C	Unknown		
CHC2432T	g.chr8:111378693A>T	Unknown		
CHC2432T	g.chr8:111472379A>T	Unknown		
CHC2432T	g.chr8:112564404G>A	Unknown		
CHC2432T	g.chr8:112567896G>T	Unknown		
CHC2432T	g.chr8:113024474C>A	Unknown		
CHC2432T	g.chr8:113105118C>T	Unknown		
CHC2432T	g.chr8:114602327T>C	Unknown		
CHC2432T	g.chr8:114766843A>T	Unknown		
CHC2432T	g.chr8:115230533G>T	Unknown		
CHC2432T	g.chr8:115424814C>A	Unknown		
CHC2432T	g.chr8:115715435C>T	Unknown		
CHC2432T	g.chr8:116279437T>C	Unknown		
CHC2432T	g.chr8:117854017G>T	UTP23		
CHC2432T	g.chr8:120254784T>A	MAL2		
CHC2432T	g.chr8:121715011T>C	SNTB1		
CHC2432T	g.chr8:121796573T>C	SNTB1		
CHC2432T	g.chr8:122942452A>G	Unknown		
CHC2432T	g.chr8:123643949T>C	Unknown		
CHC2432T	g.chr8:123964307T>A	ZHX2	c.557T>A	p.I186N
CHC2432T	g.chr8:126934802A>G	Unknown		
CHC2432T	g.chr8:128413297G>A	CASC8		
CHC2432T	g.chr8:128495458C>A	Unknown		
CHC2432T	g.chr8:132605123A>G	Unknown		
CHC2432T	g.chr8:132733489A>T	Unknown		
CHC2432T	g.chr8:134209120G>T	WISP1		
CHC2432T	g.chr8:13620396G>A	Unknown		
CHC2432T	g.chr8:13663352T>A	Unknown		
CHC2432T	g.chr8:138308824G>A	Unknown		
CHC2432T	g.chr8:138596273C>A	Unknown		
CHC2432T	g.chr8:139007504T>G	RP11-238K6.1		
CHC2432T	g.chr8:143594269A>C	BAI1		
CHC2432T	g.chr8:144942212A>G	EPPK1	c.5210T>C	p.L1737P
CHC2432T	g.chr8:145911710A>G	Unknown		
CHC2432T	g.chr8:15005689A>G	SGCZ		
CHC2432T	g.chr8:1762760C>G	Unknown		
CHC2432T	g.chr8:18346903T>C	Unknown		
CHC2432T	g.chr8:19798529G>A	LPL		
CHC2432T	g.chr8:20547309G>A	RP11-108E14.1		
CHC2432T	g.chr8:21004742T>A	Unknown		
CHC2432T	g.chr8:21004743C>T	Unknown		
CHC2432T	g.chr8:22796411C>T	PEBP4		
CHC2432T	g.chr8:23654809C>A	Unknown		
CHC2432T	g.chr8:24119059C>A	Unknown		
CHC2432T	g.chr8:24269785G>T	RP11-624C23.1		
CHC2432T	g.chr8:26435458T>G	DPYSL2		
CHC2432T	g.chr8:26557293C>A	Unknown		
CHC2432T	g.chr8:26703597T>C	ADRA1A		
CHC2432T	g.chr8:2760866A>T	Unknown		
CHC2432T	g.chr8:27619842C>T	CCDC25		
CHC2432T	g.chr8:27624336C>A	CCDC25		
CHC2432T	g.chr8:27963701G>A	ELP3		
CHC2432T	g.chr8:28443762A>G	Unknown		
CHC2432T	g.chr8:28998867A>C	KIF13B		
CHC2432T	g.chr8:29254929C>T	Unknown		
CHC2432T	g.chr8:3291988C>A	CSMD1		
CHC2432T	g.chr8:34396641A>G	Unknown		
CHC2432T	g.chr8:35591778A>G	UNC5D		
CHC2432T	g.chr8:36393795G>T	Unknown		
CHC2432T	g.chr8:36393796G>T	Unknown		
CHC2432T	g.chr8:37555101C>G	ZNF703	c.682C>G	p.H228D
CHC2432T	g.chr8:38785321G>T	PLEKHA2		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr8:38935719A>G	ADAM9		
CHC2432T	g.chr8:40182544T>G	Unknown		
CHC2432T	g.chr8:40751873C>T	ZMAT4		
CHC2432T	g.chr8:40943793T>C	Unknown		
CHC2432T	g.chr8:4638320G>A	CSMD1		
CHC2432T	g.chr8:47899644G>A	Unknown		
CHC2432T	g.chr8:49074222A>G	Unknown		
CHC2432T	g.chr8:50327738C>A	Unknown		
CHC2432T	g.chr8:5444544T>C	Unknown		
CHC2432T	g.chr8:57968104T>A	Unknown		
CHC2432T	g.chr8:60809861C>T	Unknown		
CHC2432T	g.chr8:60952958C>A	Unknown		
CHC2432T	g.chr8:61179031T>C	CA8		
CHC2432T	g.chr8:6134372C>A	Unknown		
CHC2432T	g.chr8:6181021C>A	Unknown		
CHC2432T	g.chr8:63308165T>C	NKAIN3		
CHC2432T	g.chr8:64058949A>G	Unknown		
CHC2432T	g.chr8:69016852A>G	PREX2		
CHC2432T	g.chr8:69772419A>G	Unknown		
CHC2432T	g.chr8:70005382A>G	RP11-600K15.1		
CHC2432T	g.chr8:71386067C>T	RP11-333A23.4		
CHC2432T	g.chr8:71488938T>C	TRAM1		
CHC2432T	g.chr8:72677008T>C	Unknown		
CHC2432T	g.chr8:73113463C>T	RP11-142A23.1		
CHC2432T	g.chr8:75593151A>G	RP11-758M4.1		
CHC2432T	g.chr8:75663158A>C	RP11-758M4.1		
CHC2432T	g.chr8:76021288C>A	Unknown		
CHC2432T	g.chr8:80176011C>T	Unknown		
CHC2432T	g.chr8:81273794C>T	Unknown		
CHC2432T	g.chr8:82287410C>A	Unknown		
CHC2432T	g.chr8:84121768C>G	Unknown		
CHC2432T	g.chr8:85834324T>A	Unknown		
CHC2432T	g.chr8:8627198C>G	RP11-211C9.1		
CHC2432T	g.chr8:87232440C>G	SLC7A13		
CHC2432T	g.chr8:88104246T>A	CNBD1		
CHC2432T	g.chr8:89745547C>G	RP11-586K2.1		
CHC2432T	g.chr8:89935492T>A	Unknown		
CHC2432T	g.chr8:89963699C>T	Unknown		
CHC2432T	g.chr8:93682693T>C	RP11-100L22.1		
CHC2432T	g.chr8:95526448T>C	KIAA1429		
CHC2432T	g.chr8:97867797C>T	CPQ		
CHC2432T	g.chr8:98797203T>C	LAPTM4B		
CHC2432T	g.chr9:101332545G>A	GABBR2		
CHC2432T	g.chr9:102312783C>T	Unknown		
CHC2432T	g.chr9:103459930T>A	Unknown		
CHC2432T	g.chr9:104555818G>A	Unknown		
CHC2432T	g.chr9:105015087A>G	Unknown		
CHC2432T	g.chr9:105279639A>G	Unknown		
CHC2432T	g.chr9:105649839G>A	Unknown		
CHC2432T	g.chr9:10578288G>T	PTPRD		
CHC2432T	g.chr9:10640076G>A	Unknown		
CHC2432T	g.chr9:108294431C>T	FSD1L		
CHC2432T	g.chr9:108505271A>G	TMEM38B		
CHC2432T	g.chr9:109674085G>A	ZNF462		
CHC2432T	g.chr9:109899717C>A	Unknown		
CHC2432T	g.chr9:11064704A>T	Unknown		
CHC2432T	g.chr9:110672379T>C	Unknown		
CHC2432T	g.chr9:112684042T>G	PALM2-AKAP2		
CHC2432T	g.chr9:11331446A>G	Unknown		
CHC2432T	g.chr9:114363147G>A	Unknown		
CHC2432T	g.chr9:114363148G>T	Unknown		
CHC2432T	g.chr9:115674319G>A	Unknown		
CHC2432T	g.chr9:11738906C>A	Unknown		
CHC2432T	g.chr9:118219135G>A	Unknown		
CHC2432T	g.chr9:118273345C>A	Unknown		
CHC2432T	g.chr9:118320826A>G	Unknown		
CHC2432T	g.chr9:120897561A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr9:126987064G>C	Unknown		
CHC2432T	g.chr9:127029504G>A	NEK6		
CHC2432T	g.chr9:127194375C>T	Unknown		
CHC2432T	g.chr9:127356070A>C	NR6A1		
CHC2432T	g.chr9:128724711G>A	PBX3		
CHC2432T	g.chr9:128788525A>G	Unknown		
CHC2432T	g.chr9:130457846A>G	Unknown		
CHC2432T	g.chr9:131161514T>C	Unknown		
CHC2432T	g.chr9:134341905C>T	PRRC2B		
CHC2432T	g.chr9:134914276C>T	MED27		
CHC2432T	g.chr9:136439541G>A	ADAMTSL2		
CHC2432T	g.chr9:13681881G>T	Unknown		
CHC2432T	g.chr9:136919892G>A	BRD3		
CHC2432T	g.chr9:137429796G>T	RP11-473E2.4		
CHC2432T	g.chr9:139472475G>T	Unknown		
CHC2432T	g.chr9:139862153A>G	Unknown		
CHC2432T	g.chr9:140393649C>A	PNPLA7		
CHC2432T	g.chr9:15336704A>G	Unknown		
CHC2432T	g.chr9:15894393A>C	CCDC171		
CHC2432T	g.chr9:1792635A>G	Unknown		
CHC2432T	g.chr9:18144034G>T	Unknown		
CHC2432T	g.chr9:19704311A>T	SLC24A2		
CHC2432T	g.chr9:19966362C>T	Unknown		
CHC2432T	g.chr9:21210063G>C	Unknown		
CHC2432T	g.chr9:21312374C>G	Unknown		
CHC2432T	g.chr9:2184051T>A	SMARCA2		
CHC2432T	g.chr9:25211569T>C	Unknown		
CHC2432T	g.chr9:26288282C>T	Unknown		
CHC2432T	g.chr9:27132682T>G	TEK		
CHC2432T	g.chr9:27150779T>C	TEK		
CHC2432T	g.chr9:27924016A>T	Unknown		
CHC2432T	g.chr9:2869259A>G	Unknown		
CHC2432T	g.chr9:29575486C>A	Unknown		
CHC2432T	g.chr9:30442618T>C	Unknown		
CHC2432T	g.chr9:30573141T>C	Unknown		
CHC2432T	g.chr9:30806403A>T	Unknown		
CHC2432T	g.chr9:31391123G>T	Unknown		
CHC2432T	g.chr9:35470246C>A	Unknown		
CHC2432T	g.chr9:37323574A>G	ZCCHC7		
CHC2432T	g.chr9:40312221G>A	Unknown		
CHC2432T	g.chr9:43436537A>G	Unknown		
CHC2432T	g.chr9:69914857C>T	Unknown		
CHC2432T	g.chr9:71181844T>C	RP11-274B18.4		
CHC2432T	g.chr9:72884703A>G	SMC5		
CHC2432T	g.chr9:74006554T>C	TRPM3		
CHC2432T	g.chr9:76235192G>A	Unknown		
CHC2432T	g.chr9:77410295A>G	TRPM6		
CHC2432T	g.chr9:77455637G>T	TRPM6		
CHC2432T	g.chr9:79713850T>C	Unknown		
CHC2432T	g.chr9:79821456A>G	VPS13A		
CHC2432T	g.chr9:81698647A>T	Unknown		
CHC2432T	g.chr9:82995549C>T	Unknown		
CHC2432T	g.chr9:83408120C>T	Unknown		
CHC2432T	g.chr9:89266125G>A	RP11-395D3.1		
CHC2432T	g.chr9:89668903G>A	Unknown		
CHC2432T	g.chr9:93151218T>C	RP11-389K14.3		
CHC2432T	g.chr9:93175280C>T	RP11-389K14.3		
CHC2432T	g.chr9:97288546C>T	Unknown		
CHC2432T	g.chrX:102784492T>C	Unknown		
CHC2432T	g.chrX:103134590G>T	Unknown		
CHC2432T	g.chrX:10427267T>A	MID1		
CHC2432T	g.chrX:104423114C>T	IL1RAPL2		
CHC2432T	g.chrX:105055783C>A	Unknown		
CHC2432T	g.chrX:105287717T>C	Unknown		
CHC2432T	g.chrX:105822721T>G	Unknown		
CHC2432T	g.chrX:107776742T>C	COL4A5		
CHC2432T	g.chrX:109017186C>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chrX:109274597G>A	TMEM164		
CHC2432T	g.chrX:110976193C>G	ALG13		
CHC2432T	g.chrX:111203095A>C	TRPC5		
CHC2432T	g.chrX:112565272G>A	Unknown		
CHC2432T	g.chrX:113841138C>G	HTR2C		
CHC2432T	g.chrX:114116978T>A	HTR2C		
CHC2432T	g.chrX:115735267T>C	Unknown		
CHC2432T	g.chrX:115809440C>A	Unknown		
CHC2432T	g.chrX:118839022T>C	Unknown		
CHC2432T	g.chrX:119389146C>A	ZBTB33	c.1876C>A	p.P626T
CHC2432T	g.chrX:121111311C>A	Unknown		
CHC2432T	g.chrX:123160695T>A	STAG2		
CHC2432T	g.chrX:123840366A>G	TENM1		
CHC2432T	g.chrX:124807005A>G	Unknown		
CHC2432T	g.chrX:125685608G>A	DCAF12L1	c.984C>T	p.H328H
CHC2432T	g.chrX:126262886T>A	Unknown		
CHC2432T	g.chrX:126342454T>C	Unknown		
CHC2432T	g.chrX:126947919A>G	Unknown		
CHC2432T	g.chrX:126968602C>T	Unknown		
CHC2432T	g.chrX:127346113A>G	Unknown		
CHC2432T	g.chrX:12866629C>G	Unknown		
CHC2432T	g.chrX:128839456C>A	Unknown		
CHC2432T	g.chrX:128903662G>C	Unknown		
CHC2432T	g.chrX:130299370G>C	Unknown		
CHC2432T	g.chrX:130838402A>T	RP11-453F18__B.1		
CHC2432T	g.chrX:131594886C>A	MBNL3		
CHC2432T	g.chrX:132619656C>A	Unknown		
CHC2432T	g.chrX:133378773T>A	CCDC160		
CHC2432T	g.chrX:133776259T>C	PLAC1		
CHC2432T	g.chrX:13575554T>C	Unknown		
CHC2432T	g.chrX:138086203G>C	FGF13		
CHC2432T	g.chrX:138410934T>C	Unknown		
CHC2432T	g.chrX:138776152G>A	MCF2		
CHC2432T	g.chrX:139273238C>A	Unknown		
CHC2432T	g.chrX:140521463T>G	Unknown		
CHC2432T	g.chrX:142001436A>G	Unknown		
CHC2432T	g.chrX:142091970T>C	Unknown		
CHC2432T	g.chrX:14233331T>C	Unknown		
CHC2432T	g.chrX:142924777C>T	Unknown		
CHC2432T	g.chrX:142961719C>T	Unknown		
CHC2432T	g.chrX:145431426G>A	Unknown		
CHC2432T	g.chrX:146343735C>T	Unknown		
CHC2432T	g.chrX:146476271C>T	Unknown		
CHC2432T	g.chrX:147157120G>T	Unknown		
CHC2432T	g.chrX:147426484A>G	Unknown		
CHC2432T	g.chrX:147874896T>G	AFF2		
CHC2432T	g.chrX:148044734C>T	AFF2		
CHC2432T	g.chrX:148091896C>A	Unknown		
CHC2432T	g.chrX:149611333G>A	MAMLD1		
CHC2432T	g.chrX:150016203C>T	CD99L2		
CHC2432T	g.chrX:152746016C>G	HAUS7		
CHC2432T	g.chrX:153934410G>A	GAB3		
CHC2432T	g.chrX:17244032G>A	Unknown		
CHC2432T	g.chrX:18182331G>A	BEND2		
CHC2432T	g.chrX:18211733C>A	BEND2		
CHC2432T	g.chrX:19437597G>C	MAP3K15		
CHC2432T	g.chrX:20706719T>C	Unknown		
CHC2432T	g.chrX:21688464A>G	Unknown		
CHC2432T	g.chrX:21785078G>T	Unknown		
CHC2432T	g.chrX:22221708T>G	PHEX		
CHC2432T	g.chrX:23846865C>A	Unknown		
CHC2432T	g.chrX:25810244G>T	Unknown		
CHC2432T	g.chrX:30315212C>T	Unknown		
CHC2432T	g.chrX:31463677T>C	DMD		
CHC2432T	g.chrX:31686932T>G	DMD		
CHC2432T	g.chrX:32978464C>T	DMD		
CHC2432T	g.chrX:33115244G>T	DMD		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chrX:34335049C>T	RP11-545D19.1		
CHC2432T	g.chrX:35156060A>G	Unknown		
CHC2432T	g.chrX:39264715G>A	RP11-157D23.2		
CHC2432T	g.chrX:40694367G>T	Unknown		
CHC2432T	g.chrX:41396697A>G	CASK		
CHC2432T	g.chrX:42527429A>C	RP1-154K9.2		
CHC2432T	g.chrX:42554109C>G	RP1-154K9.2		
CHC2432T	g.chrX:43658196C>T	MAOB		
CHC2432T	g.chrX:43845566T>C	Unknown		
CHC2432T	g.chrX:44870227C>T	KDM6A	c.406C>T	p.L136F
CHC2432T	g.chrX:44870231G>T	KDM6A	c.410G>T	p.G137V
CHC2432T	g.chrX:4532480C>A	Unknown		
CHC2432T	g.chrX:45400023G>A	Unknown		
CHC2432T	g.chrX:45507993T>C	Unknown		
CHC2432T	g.chrX:47776290T>C	ZNF81		
CHC2432T	g.chrX:48557354G>A	SUV39H1	c.81G>A	p.K27K
CHC2432T	g.chrX:4870169A>G	Unknown		
CHC2432T	g.chrX:5010680A>T	Unknown		
CHC2432T	g.chrX:50498875A>T	SHROOM4		
CHC2432T	g.chrX:50958767C>A	Unknown		
CHC2432T	g.chrX:51345283C>A	Unknown		
CHC2432T	g.chrX:51718001A>G	Unknown		
CHC2432T	g.chrX:55086692T>C	Unknown		
CHC2432T	g.chrX:55969582G>T	RP13-188A5.1		
CHC2432T	g.chrX:56943039G>A	Unknown		
CHC2432T	g.chrX:58497345T>A	Unknown		
CHC2432T	g.chrX:6183887C>T	Unknown		
CHC2432T	g.chrX:6240409C>A	Unknown		
CHC2432T	g.chrX:62668044C>A	RP11-357C3.3		
CHC2432T	g.chrX:63263795C>A	Unknown		
CHC2432T	g.chrX:65736819T>C	Unknown		
CHC2432T	g.chrX:65756473T>A	Unknown		
CHC2432T	g.chrX:66054334G>T	Unknown		
CHC2432T	g.chrX:66791344A>G	AR		
CHC2432T	g.chrX:67395616G>T	OPHN1		
CHC2432T	g.chrX:68220756A>C	Unknown		
CHC2432T	g.chrX:68598604C>A	Unknown		
CHC2432T	g.chrX:70406209G>A	RP5-1091N2.9		
CHC2432T	g.chrX:71240035G>T	NHSL2		
CHC2432T	g.chrX:7399895A>G	Unknown		
CHC2432T	g.chrX:74484390T>G	Unknown		
CHC2432T	g.chrX:74894210T>C	Unknown		
CHC2432T	g.chrX:75194543T>A	Unknown		
CHC2432T	g.chrX:77646457T>C	Unknown		
CHC2432T	g.chrX:78447840A>G	Unknown		
CHC2432T	g.chrX:78520347G>A	Unknown		
CHC2432T	g.chrX:80032414T>C	BRWD3		
CHC2432T	g.chrX:81587786G>A	Unknown		
CHC2432T	g.chrX:82382504G>A	Unknown		
CHC2432T	g.chrX:8248101C>G	Unknown		
CHC2432T	g.chrX:83253059G>T	Unknown		
CHC2432T	g.chrX:86048477A>G	DACH2		
CHC2432T	g.chrX:86152827G>T	Unknown		
CHC2432T	g.chrX:86162071C>A	Unknown		
CHC2432T	g.chrX:86363144T>C	Unknown		
CHC2432T	g.chrX:87133132C>T	Unknown		
CHC2432T	g.chrX:89548967A>G	Unknown		
CHC2432T	g.chrX:91716436G>A	PCDH11X		
CHC2432T	g.chrX:93174690T>G	Unknown		
CHC2432T	g.chrX:95139600C>G	Unknown		
CHC2432T	g.chrX:9568188T>C	TBL1X		
CHC2432T	g.chrX:96714356G>T	DIAPH2		
CHC2432T	g.chrX:98255375G>C	Unknown		
CHC2432T	g.chrX:98872610C>T	Unknown		
CHC2432T	chr1:111168956_111168956ins	KCNA2		
CHC2432T	g.chr1:160365675delGA	Unknown		
CHC2432T	g.chr1:161191110delAAAT	AL590714.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	hr1:188541782_188541782ins	Unknown		
CHC2432T	g.chr1:190082610delAT	BRINP3		
CHC2432T	rr1:190082612delAATCCAAT	BRINP3		
CHC2432T	g.chr1:210533017delCATGGG	HHAT		
CHC2432T	g.chr1:220517597delGT	Unknown		
CHC2432T	g.chr1:226774051delCT	C1orf95		
CHC2432T	hr1:247559707_247559707ins	Unknown		
CHC2432T	1:43471051delTCAAGTGGA/	Unknown		
CHC2432T	g.chr1:5228389delAG	Unknown		
CHC2432T	792_58101792insCTGGGGCC/	DAB1		
CHC2432T	g.chr1:72239618delCA	NEGR1		
CHC2432T	g.chr1:8875088delTC	RERE		
CHC2432T	g.chr1:96700954delAAG	Unknown		
CHC2432T	g.chr10:101034388delTAAAA	Unknown		
CHC2432T	:hr10:10949721_10949721ins	Unknown		
CHC2432T	g.chr10:132247736delGT	RP11-540N6.1		
CHC2432T	gGGGCTTTTGATACATTGACAA/	KIAA1217		
CHC2432T	.chr10:2543369_2543369insC	Unknown		
CHC2432T	g.chr10:25964692delGA	Unknown		
CHC2432T	:hr10:37566427_37566427ins	ANKRD30A		
CHC2432T	10:58169631delGAAAATGCCA	Unknown		
CHC2432T	g.chr10:61278178delCA	Unknown		
CHC2432T	g.chr10:80282699delCT	Unknown		
CHC2432T	g.chr10:84648473delGA	NRG3		
CHC2432T	g.chr10:90191998delTA	RNLS		
CHC2432T	g.chr10:90687304delGT	STAMBPL1		
CHC2432T	g.chr11:101058091delGC	RP11-788M5.3		
CHC2432T	.chr11:1070525_1070525insA	Unknown		
CHC2432T	g.chr11:118751945delCACT	Unknown		
CHC2432T	8751949delGTGGAAGTGTGT	Unknown		
CHC2432T	g.chr11:120298342delCG	ARHGEF12		
CHC2432T	:hr11:14729876_14729876ins	PDE3B		
CHC2432T	g.chr11:18941284delCAA	Unknown		
CHC2432T	rr11:21250240delCTCTCCTTC/	NELL1		
CHC2432T	g.chr11:45898214delCCCCT	CRY2		
CHC2432T	g.chr11:46801406delAG	CKAP5		
CHC2432T	g.chr11:60089265delATT	Unknown		
CHC2432T	g.chr11:65959101delAC	PACS1		
CHC2432T	:hr11:69144470_69144470ins	Unknown		
CHC2432T	g.chr11:79580386delGA	Unknown		
CHC2432T	(TCAGGAAGTCATAATCTTTGG/	TMEM135		
CHC2432T	:hr11:93102933_93102933ins	CCDC67		
CHC2432T	rr12:118658922_118658922in	TAOK3		
CHC2432T	g6544delTGGGAGGGGAGTGT	IQSEC3		
CHC2432T	g.chr12:820586delGT	Unknown		
CHC2432T	g.chr13:105452907delCT	Unknown		
CHC2432T	g.chr13:110912881delAC	COL4A1		
CHC2432T	g.chr13:44658119delTATTA	Unknown		
CHC2432T	g.chr13:59854375delCA	Unknown		
CHC2432T	g.chr13:63047736delAG	Unknown		
CHC2432T	g.chr13:98072560delGA	Unknown		
CHC2432T	g.chr14:104579449delAC	Unknown		
CHC2432T	g.chr14:62606580delGA	LINC00644		
CHC2432T	g.chr14:94756405delCTT	SERPINA10	c.526delAAG	p.K176fs
CHC2432T	g.chr15:26898046delTTCC	GABRB3		
CHC2432T	15:57965432delTTAGGCCCCC	MYZAP		
CHC2432T	g:60909281delTTTCTGTCCTAG	RORA		
CHC2432T	:hr16:18960114_18960114ins	Unknown		
CHC2432T	g.chr16:24584828delTA	Unknown		
CHC2432T	g.chr16:25505985delCT	Unknown		
CHC2432T	7insTTAGGGCAGAAAGCCGCA/	RP11-67H24.2		
CHC2432T	g.chr16:5967421delAT	RP11-420N3.2		
CHC2432T	gAGTGTGATTTTTCTTAGGAC	Unknown		
CHC2432T	g.chr16:65613299delAT	Unknown		
CHC2432T	.chr16:7909151_7909151insT	Unknown		
CHC2432T	:hr16:79736255_79736255ins	Unknown		
CHC2432T	g.chr17:2315737delCA	AC006435.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr17:595289delGA	VPS53		
CHC2432T	g.chr18:3611384delGC	DLGAP1		
CHC2432T	g.chr18:48814933delAC	Unknown		
CHC2432T	g.chr18:48814935delACACAC	Unknown		
CHC2432T	g.chr18:57908356delCATGT	Unknown		
CHC2432T	g.chr18:65749448delTG	Unknown		
CHC2432T	CTTTTGTCTGATTCAACTTTCA	Unknown		
CHC2432T	chr19:12789582delCAAAAAA/	DHPS		
CHC2432T	19:14796584_14796584insAT	EMR3		
CHC2432T	6016insTATATATATAAATATAT	AC005307.3		
CHC2432T	g.chr19:41261189delCA	SNRPA		
CHC2432T	hr2:102441549_102441549in:	MAP4K4		
CHC2432T	g.chr2:106368493delAT	NCK2		
CHC2432T	5_120463566insATATATATAT	Unknown		
CHC2432T	g.chr2:126522002delTA	AC097499.1		
CHC2432T	hr2:130313589delTGTCAAAA/	Unknown		
CHC2432T	hr2:132364374_132364374in:	Unknown		
CHC2432T	g.chr2:14324297delCAGAT	Unknown		
CHC2432T	g.chr2:149340695delCT	Unknown		
CHC2432T	2:162610388_162610388insA	SLC4A10		
CHC2432T	g.chr2:171663946delTG	Unknown		
CHC2432T	g.chr2:188674297delAAGT	Unknown		
CHC2432T	g.chr2:216274157delGTT	FN1		
CHC2432T	g.chr2:222751764delCT	Unknown		
CHC2432T	g.chr2:228653813delCT	Unknown		
CHC2432T	g.chr2:240434020delAT	Unknown		
CHC2432T	g.chr2:29124370delCT	WDR43		
CHC2432T	g.chr2:49593266delAT	Unknown		
CHC2432T	g.chr2:73776021delGAA	ALMS1		
CHC2432T	g.chr2:81849627delCA	Unknown		
CHC2432T	chr2:84663693_84663693ins1	SUCLG1		
CHC2432T	g.chr20:46239749delCT	NCOA3		
CHC2432T	21:38945961_38945961insAT	Unknown		
CHC2432T	g.chr22:32908845delAGTG	SYN3		
CHC2432T	g.chr22:33283305delCTGCA	SYN3		
CHC2432T	g.chr22:47539254delGA	TBC1D22A		
CHC2432T	103664186_103664186insAT	Unknown		
CHC2432T	g.chr3:104318379delAC	Unknown		
CHC2432T	hr3:114360585_114360585in:	ZBTB20		
CHC2432T	g.chr3:161673462delTA	Unknown		
CHC2432T	g.chr3:172668748delCG	SPATA16		
CHC2432T	g.chr3:178838496delCTCTG	RP11-360P21.2		
CHC2432T	g.chr3:20955067delTC	Unknown		
CHC2432T	g.chr3:22197355delATTT	ZNF385D		
CHC2432T	chr3:48669172delAGCTGCAG	SLC26A6	.705delACTGCAGC	p.A235fs
CHC2432T	g.chr4:100076382delATC	ADH4		
CHC2432T	hr4:115324244_115324244ins:	Unknown		
CHC2432T	hr4:132224872_132224872in:	Unknown		
CHC2432T	g.chr4:137260050delAGGT	Unknown		
CHC2432T	g.chr4:145123786delAT	Unknown		
CHC2432T	g.chr4:152552426delTA	FAM160A1		
CHC2432T	g.chr4:155504319delAAT	FGA		
CHC2432T	hr4:185606003_185606003in:	PRIMPOL		
CHC2432T	g.chr4:65660183delTC	Unknown		
CHC2432T	g.chr4:67197700delTA	Unknown		
CHC2432T	g.chr4:7974839delTAG	ABLIM2		
CHC2432T	_7974842insGTGTGTGTGTGTG	ABLIM2		
CHC2432T	hr4:903825delCAGCTGCCAGG	GAK		
CHC2432T	hr5:119604743_119604743ins:	CTC-552D5.1		
CHC2432T	ACGTATATACGTATATACATGTA	Unknown		
CHC2432T	g.chr5:163462279delCT	Unknown		
CHC2432T	g.chr5:164396489delGT	CTC-340A15.2		
CHC2432T	g.chr5:2287374delCT	Unknown		
CHC2432T	g.chr5:23169733delCA	Unknown		
CHC2432T	43512885delTTTTTTTTTTTTTT	C5orf34		
CHC2432T	g.chr5:44544796delTAA	Unknown		
CHC2432T	chr5:54517111_54517111ins1	MCIDAS		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2432T	g.chr5:84294535delCT	Unknown		
CHC2432T	g.chr5:97729779delITG	Unknown		
CHC2432T	chr5:99517433_99517433insA	Unknown		
CHC2432T	hr6:161005768delCCTTTAGTG	LPA		
CHC2432T	g.chr6:30256607delAG	HCG17		
CHC2432T	r6:36589257_36589257insCT.	Unknown		
CHC2432T	g.chr6:40783012delCAA	Unknown		
CHC2432T	g.chr6:40783015delICT	Unknown		
CHC2432T	g.chr6:47816610delAAAAT	Unknown		
CHC2432T	hr6:57902955_57902955insT	Unknown		
CHC2432T	g.chr6:84248155delTAGGCTAC	Unknown		
CHC2432T	7:101040694delCTTCTTTCTTT	COL26A1		
CHC2432T	g.chr7:141227274delTC	Unknown		
CHC2432T	g.chr7:157864106delCCTG	PTPRN2		
CHC2432T	g.chr7:1816646delIGC	Unknown		
CHC2432T	g.chr7:21068669delICT	Unknown		
CHC2432T	hr7:33223279delAACTGCTTG.	BBS9		
CHC2432T	g.chr7:51061167delITAGAGC	RP4-724E13.2		
CHC2432T	g.chr7:56752108delICA	Unknown		
CHC2432T	g.chr7:67494197delITC	RP11-358M3.1		
CHC2432T	r7:73099278delAAAAAAAAAAA	WBSCR22		
CHC2432T	g.chr7:84069513delITG	Unknown		
CHC2432T	hr7:93936776_93936776insA	Unknown		
CHC2432T	l05472649delACCTTCTAACAT	DPYS		
CHC2432T	g.chr8:123964300delIAC	ZHX2	c.550delAC	p.T184fs
CHC2432T	g.chr8:16234534delITAG	MSR1		
CHC2432T	g.chr8:18664557delATGG	PSD3		
CHC2432T	chr8:63267839_63267839insC	NKAIN3		
CHC2432T	g.chr8:75126176delITA	Unknown		
CHC2432T	g.chr8:77046283delIGC	Unknown		
CHC2432T	g.chr8:88663121delIAC	AF121898.3		
CHC2432T	g.chr9:1065664delIAC	Unknown		
CHC2432T	g.chr9:122672228delICT	Unknown		
CHC2432T	g.chr9:140318571delCCCTG	NOXA1		
CHC2432T	.chr9:140318577delACGGAGC	NOXA1		
CHC2432T	g.chr9:14158592delITA	NFIB		
CHC2432T	g.chr9:19966357delITA	Unknown		
CHC2432T	g.chr9:73003847delGGAGTT	KLF9		
CHC2432T	g.chr9:93852635delIAT	Unknown		
CHC2432T	g.chrX:101031536delICA	Unknown		
CHC2432T	g.chrX:139273235delIAG	Unknown		
CHC2432T	g.chrX:15988400delIGT	Unknown		
CHC2432T	g.chrX:31686928delITCAA	DMD		
CHC2432T	chrX:42093140_42093140insA	Unknown		
CHC2432T	800004delTATATATATATATAT	Unknown		
CHC2432T	chrX:58034701_58034701insC	Unknown		
CHC2432T	chrX:63212245_63212245insC	Unknown		
CHC2432T	g.chrX:76545627delITA	Unknown		
CHC2446T	g.chr1:114173033G>A	MAGI3		
CHC2446T	g.chr1:87145183G>C	RP4-651E10.4		
CHC2446T	g.chr10:130435954A>T	Unknown		
CHC2446T	g.chr10:78828541A>G	KCNMA1		
CHC2446T	g.chr10:98245770G>A	TLL2		
CHC2446T	g.chr11:114404606G>A	NXPE1		
CHC2446T	g.chr11:7836305T>C	RP11-35J10.5		
CHC2446T	g.chr12:121962185G>A	KDM2B		
CHC2446T	g.chr12:12329812G>T	LRP6		
CHC2446T	g.chr12:131514754C>T	GPR133		
CHC2446T	g.chr13:77407061G>T	Unknown		
CHC2446T	g.chr14:64402963G>A	SYNE2		
CHC2446T	g.chr15:88298297G>A	Unknown		
CHC2446T	g.chr16:75377764G>A	CFDP1		
CHC2446T	g.chr17:28437109A>G	RP11-1148O4.2		
CHC2446T	g.chr19:18491104C>A	GDF15		
CHC2446T	g.chr19:31841349C>T	AC007796.1		
CHC2446T	g.chr2:107948620C>A	AC006227.1		
CHC2446T	g.chr2:113179630A>C	RGPD8	c.234T>G	p.L78L

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr2:240215245G>C	HDAC4		
CHC2446T	g.chr2:4195680G>T	Unknown		
CHC2446T	g.chr2:87356694A>G	Unknown		
CHC2446T	g.chr21:44019511C>T	AP001626.1		
CHC2446T	g.chr3:176724567T>G	Unknown		
CHC2446T	g.chr3:186084905G>T	Unknown		
CHC2446T	g.chr4:73464399C>G	Unknown		
CHC2446T	g.chr5:112986139A>C	Unknown		
CHC2446T	g.chr5:135718834C>T	TRPC7		
CHC2446T	g.chr5:24554607G>A	CDH10		
CHC2446T	g.chr5:97407640A>T	Unknown		
CHC2446T	g.chr6:109068643C>T	Unknown		
CHC2446T	g.chr6:66373790A>G	EYS		
CHC2446T	g.chr7:17606585T>C	Unknown		
CHC2446T	g.chr7:88143647G>A	Unknown		
CHC2446T	g.chrX:30134823T>A	Unknown		
CHC2446T	g.chr1:102753795A>G	RP11-202K23.1		
CHC2446T	g.chr1:103727829G>T	Unknown		
CHC2446T	g.chr1:104522802G>C	Unknown		
CHC2446T	g.chr1:104877669G>T	Unknown		
CHC2446T	g.chr1:105364362C>T	Unknown		
CHC2446T	g.chr1:106861211G>A	Unknown		
CHC2446T	g.chr1:106904433G>T	Unknown		
CHC2446T	g.chr1:107778680A>G	NTNG1		
CHC2446T	g.chr1:108169104A>G	VAV3		
CHC2446T	g.chr1:112256172A>C	RAP1A		
CHC2446T	g.chr1:113021593A>G	WNT2B		
CHC2446T	g.chr1:115006106T>C	TRIM33	c.718A>G	p.T240A
CHC2446T	g.chr1:115614250G>C	TSPAN2		
CHC2446T	g.chr1:116777880A>C	Unknown		
CHC2446T	g.chr1:1181600G>A	FAM132A		
CHC2446T	g.chr1:120347742A>G	REG4		
CHC2446T	g.chr1:120912308C>T	RP11-439A17.10		
CHC2446T	g.chr1:14229373C>T	Unknown		
CHC2446T	g.chr1:151317132G>C	RFX5		
CHC2446T	g.chr1:152710453C>A	Unknown		
CHC2446T	g.chr1:153095528A>T	SPRR2B		
CHC2446T	g.chr1:153117472C>A	Unknown		
CHC2446T	g.chr1:153146750C>T	Unknown		
CHC2446T	g.chr1:154145571T>G	TPM3	c.484A>C	p.K162Q
CHC2446T	g.chr1:15423593G>A	KAZN		
CHC2446T	g.chr1:155275651G>T	Unknown		
CHC2446T	g.chr1:157066296C>T	ETV3L		
CHC2446T	g.chr1:157729548A>C	FCRL2		
CHC2446T	g.chr1:158145556T>C	Unknown		
CHC2446T	g.chr1:158169108G>T	RP11-404O13.5		
CHC2446T	g.chr1:158730558T>A	Unknown		
CHC2446T	g.chr1:160390936G>C	VANGL2	c.1032G>C	p.E344D
CHC2446T	g.chr1:160420262A>T	Unknown		
CHC2446T	g.chr1:166492263C>A	Unknown		
CHC2446T	g.chr1:168604249T>C	Unknown		
CHC2446T	g.chr1:170906077C>T	MROH9		
CHC2446T	g.chr1:172620213G>C	Unknown		
CHC2446T	g.chr1:174682580A>G	RABGAP1L		
CHC2446T	g.chr1:174752154T>G	RABGAP1L		
CHC2446T	g.chr1:180569924G>C	Unknown		
CHC2446T	g.chr1:181911927T>C	Unknown		
CHC2446T	g.chr1:183583195C>T	Unknown		
CHC2446T	g.chr1:183800312T>C	RGL1		
CHC2446T	g.chr1:187347023A>G	Unknown		
CHC2446T	g.chr1:188057550C>A	Unknown		
CHC2446T	g.chr1:188822295T>G	Unknown		
CHC2446T	g.chr1:188849457G>A	RP11-316I3.2		
CHC2446T	g.chr1:189828688C>G	Unknown		
CHC2446T	g.chr1:189889778A>G	Unknown		
CHC2446T	g.chr1:195255342C>T	Unknown		
CHC2446T	g.chr1:195428887T>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr1:19968474T>C	MINOS1-NBL1		
CHC2446T	g.chr1:20459471A>G	Unknown		
CHC2446T	g.chr1:205028177C>T	CNTN2		
CHC2446T	g.chr1:20662268A>T	VWA5B1		
CHC2446T	g.chr1:208140433G>T	Unknown		
CHC2446T	g.chr1:208142395A>G	Unknown		
CHC2446T	g.chr1:209481380C>A	Unknown		
CHC2446T	g.chr1:213219829G>A	Unknown		
CHC2446T	g.chr1:215177960G>T	Unknown		
CHC2446T	g.chr1:216132965C>A	USH2A		
CHC2446T	g.chr1:218602278A>G	TGFB2		
CHC2446T	g.chr1:222037215C>T	Unknown		
CHC2446T	g.chr1:222435275T>A	RP11-400N13.1		
CHC2446T	g.chr1:223585934A>G	Unknown		
CHC2446T	g.chr1:228248658C>T	WNT3A		
CHC2446T	g.chr1:229622398C>T	NUP133		
CHC2446T	g.chr1:229622399A>C	NUP133		
CHC2446T	g.chr1:236158989C>A	NID1		
CHC2446T	g.chr1:237774057G>A	RYR2		
CHC2446T	g.chr1:238267852G>A	Unknown		
CHC2446T	g.chr1:239308397T>C	Unknown		
CHC2446T	g.chr1:239938895T>C	CHRM3		
CHC2446T	g.chr1:242331872T>C	PLD5		
CHC2446T	g.chr1:243026558T>A	Unknown		
CHC2446T	g.chr1:245003833A>G	COX20		
CHC2446T	g.chr1:246942788G>C	RP11-439E19.8		
CHC2446T	g.chr1:247424991T>A	Unknown		
CHC2446T	g.chr1:247762523T>C	RP11-978I15.10		
CHC2446T	g.chr1:26206704G>T	Unknown		
CHC2446T	g.chr1:26907544C>T	Unknown		
CHC2446T	g.chr1:27472348G>C	SLC9A1		
CHC2446T	g.chr1:30366935C>T	Unknown		
CHC2446T	g.chr1:31317990C>T	Unknown		
CHC2446T	g.chr1:32968688T>A	RP1-27O5.3		
CHC2446T	g.chr1:35119207G>A	Unknown		
CHC2446T	g.chr1:40587764A>G	Unknown		
CHC2446T	g.chr1:43590302G>A	Unknown		
CHC2446T	g.chr1:4857469A>G	Unknown		
CHC2446T	g.chr1:48871333G>C	SPATA6		
CHC2446T	g.chr1:50886305A>T	DMRTA2		
CHC2446T	g.chr1:51846116A>T	EPS15		
CHC2446T	g.chr1:56040812G>T	Unknown		
CHC2446T	g.chr1:56230397G>A	Unknown		
CHC2446T	g.chr1:61471271G>T	NFIA		
CHC2446T	g.chr1:61592015A>G	NFIA		
CHC2446T	g.chr1:62711652G>T	KANK4		
CHC2446T	g.chr1:6730760G>C	DNAJC11		
CHC2446T	g.chr1:69557189C>T	RP11-424D14.1		
CHC2446T	g.chr1:71113595G>T	Unknown		
CHC2446T	g.chr1:7313634A>G	CAMTA1		
CHC2446T	g.chr1:73190629G>A	Unknown		
CHC2446T	g.chr1:77324340G>T	Unknown		
CHC2446T	g.chr1:77397319T>A	ST6GALNAC5		
CHC2446T	g.chr1:78780585A>T	PTGFR		
CHC2446T	g.chr1:79374678G>T	ELTD1		
CHC2446T	g.chr1:79707460T>C	Unknown		
CHC2446T	g.chr1:82361688G>A	LPHN2		
CHC2446T	g.chr1:84532434C>T	Unknown		
CHC2446T	g.chr1:85161984C>T	Unknown		
CHC2446T	g.chr1:90465483T>A	ZNF326		
CHC2446T	g.chr1:94456111T>C	Unknown		
CHC2446T	g.chr1:945484G>T	Unknown		
CHC2446T	g.chr1:98070576C>A	DPYD		
CHC2446T	g.chr10:100482273G>T	HPSE2		
CHC2446T	g.chr10:10062658G>T	Unknown		
CHC2446T	g.chr10:100927968A>G	HPSE2		
CHC2446T	g.chr10:102750271G>A	C10orf2	c.1563G>A	p.M521I

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr10:105969860A>C	WDR96		
CHC2446T	g.chr10:106925637G>A	SORCS3		
CHC2446T	g.chr10:107483634C>A	Unknown		
CHC2446T	g.chr10:108221016C>T	Unknown		
CHC2446T	g.chr10:108309323G>T	Unknown		
CHC2446T	g.chr10:10894540T>C	Unknown		
CHC2446T	g.chr10:109310247A>G	Unknown		
CHC2446T	g.chr10:110827947G>T	Unknown		
CHC2446T	g.chr10:111410473C>A	Unknown		
CHC2446T	g.chr10:113607205G>A	Unknown		
CHC2446T	g.chr10:127357529A>G	TEX36		
CHC2446T	g.chr10:128054982C>T	ADAM12		
CHC2446T	g.chr10:129255962A>C	Unknown		
CHC2446T	g.chr10:129295237C>T	Unknown		
CHC2446T	g.chr10:130333989G>A	Unknown		
CHC2446T	g.chr10:13327459T>C	PHYH		
CHC2446T	g.chr10:15613553T>C	ITGA8		
CHC2446T	g.chr10:15871475A>C	FAM188A		
CHC2446T	g.chr10:22563848T>A	Unknown		
CHC2446T	g.chr10:24548699G>T	KIAA1217		
CHC2446T	g.chr10:25593630C>A	GPR158		
CHC2446T	g.chr10:25908548C>T	Unknown		
CHC2446T	g.chr10:26570057C>T	GAD2		
CHC2446T	g.chr10:27345847G>T	ANKRD26		
CHC2446T	g.chr10:30222186A>T	Unknown		
CHC2446T	g.chr10:30663033G>A	MTPAP		
CHC2446T	g.chr10:33389580G>A	RP11-342D11.3		
CHC2446T	g.chr10:34401550C>A	PARD3		
CHC2446T	g.chr10:35976588T>C	Unknown		
CHC2446T	g.chr10:37112815C>A	Unknown		
CHC2446T	g.chr10:38515370C>A	Unknown		
CHC2446T	g.chr10:39014908G>T	Unknown		
CHC2446T	g.chr10:44262438A>G	Unknown		
CHC2446T	g.chr10:49703669C>A	ARHGAP22		
CHC2446T	g.chr10:54285886G>A	Unknown		
CHC2446T	g.chr10:54697176C>G	Unknown		
CHC2446T	g.chr10:55102791A>C	Unknown		
CHC2446T	g.chr10:57753646G>A	Unknown		
CHC2446T	g.chr10:57826817G>A	Unknown		
CHC2446T	g.chr10:59048420G>A	Unknown		
CHC2446T	g.chr10:66955347G>A	Unknown		
CHC2446T	g.chr10:70850598T>C	SRGN		
CHC2446T	g.chr10:72299531C>A	PALD1		
CHC2446T	g.chr10:7236133C>A	SFMBT2		
CHC2446T	g.chr10:77190360C>T	RP11-399K21.10		
CHC2446T	g.chr10:77791833T>A	C10orf11		
CHC2446T	g.chr10:80204163C>T	Unknown		
CHC2446T	g.chr10:80722664A>G	ZMIZ1-AS1		
CHC2446T	g.chr10:82613008T>G	Unknown		
CHC2446T	g.chr10:82981956A>G	Unknown		
CHC2446T	g.chr10:83770676C>T	NRG3		
CHC2446T	g.chr10:85558122T>A	Unknown		
CHC2446T	g.chr10:86680547G>A	Unknown		
CHC2446T	g.chr10:90833433A>C	Unknown		
CHC2446T	g.chr10:92157121T>G	Unknown		
CHC2446T	g.chr10:93859065T>A	CPEB3		
CHC2446T	g.chr10:93859067C>A	CPEB3		
CHC2446T	g.chr10:96281433A>G	TBC1D12		
CHC2446T	g.chr10:96794995A>G	Unknown		
CHC2446T	g.chr10:97302318T>C	SORBS1		
CHC2446T	g.chr10:97631854C>G	RP11-248J23.7		
CHC2446T	g.chr10:97985776G>A	BLNK		
CHC2446T	g.chr10:99966030T>C	R3HCC1L		
CHC2446T	g.chr11:101152607A>C	Unknown		
CHC2446T	g.chr11:101190254C>G	Unknown		
CHC2446T	g.chr11:103937724G>A	PDGFD		
CHC2446T	g.chr11:103955948T>C	PDGFD		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr11:104975269C>A	Unknown		
CHC2446T	g.chr11:105176724G>T	RP11-94P11.4		
CHC2446T	g.chr11:105444074C>T	Unknown		
CHC2446T	g.chr11:106912555A>G	Unknown		
CHC2446T	g.chr11:107674579T>C	SLC35F2		
CHC2446T	g.chr11:110564587T>A	ARHGAP20		
CHC2446T	g.chr11:110953317A>T	Unknown		
CHC2446T	g.chr11:112142455T>A	RP11-356J5.12		
CHC2446T	g.chr11:115235454C>A	CADM1		
CHC2446T	g.chr11:116558743G>A	Unknown		
CHC2446T	g.chr11:117661022G>A	DSCAML1		
CHC2446T	g.chr11:123484241C>G	GRAMD1B	c.1673C>G	p.T558S
CHC2446T	g.chr11:130327663A>T	ADAMTS15		
CHC2446T	g.chr11:130975126G>T	Unknown		
CHC2446T	g.chr11:131350176C>A	NTM		
CHC2446T	g.chr11:133674245T>C	RP11-448P19.1		
CHC2446T	g.chr11:13768936T>C	Unknown		
CHC2446T	g.chr11:17622357G>T	OTOG		
CHC2446T	g.chr11:21163496G>T	NELL1		
CHC2446T	g.chr11:21379084G>A	NELL1		
CHC2446T	g.chr11:2187034C>T	TH		
CHC2446T	g.chr11:23248916T>C	Unknown		
CHC2446T	g.chr11:23552452C>A	Unknown		
CHC2446T	g.chr11:25263176C>A	Unknown		
CHC2446T	g.chr11:26021218T>C	Unknown		
CHC2446T	g.chr11:26349974C>T	ANO3		
CHC2446T	g.chr11:26646080G>C	ANO3		
CHC2446T	g.chr11:2685175G>A	KCNQ1		
CHC2446T	g.chr11:27773031A>T	RP11-587D21.4		
CHC2446T	g.chr11:27773032G>T	RP11-587D21.4		
CHC2446T	g.chr11:28958642T>A	RP11-115J23.1		
CHC2446T	g.chr11:35434336C>T	SLC1A2		
CHC2446T	g.chr11:39340560A>G	Unknown		
CHC2446T	g.chr11:39487542T>A	Unknown		
CHC2446T	g.chr11:39751273T>C	Unknown		
CHC2446T	g.chr11:42436054T>C	Unknown		
CHC2446T	g.chr11:42480289C>A	Unknown		
CHC2446T	g.chr11:44824735T>G	TSPAN18		
CHC2446T	g.chr11:45757647C>G	CTD-2210P24.1		
CHC2446T	g.chr11:49269384A>G	Unknown		
CHC2446T	g.chr11:49781499C>A	RP11-707M1.1		
CHC2446T	g.chr11:5213240A>T	Unknown		
CHC2446T	g.chr11:55276835G>A	Unknown		
CHC2446T	g.chr11:55968020C>A	Unknown		
CHC2446T	g.chr11:55991837T>C	Unknown		
CHC2446T	g.chr11:56809766G>A	Unknown		
CHC2446T	g.chr11:57256774G>A	SLC43A1	c.1285C>T	p.L429L
CHC2446T	g.chr11:57297673C>A	TIMM10		
CHC2446T	g.chr11:57458231A>G	ZDHHC5		
CHC2446T	g.chr11:59442676C>G	AP000640.2		
CHC2446T	g.chr11:62854969T>G	SLC22A24		
CHC2446T	g.chr11:67271234C>T	PITPNM1		
CHC2446T	g.chr11:69032475C>T	Unknown		
CHC2446T	g.chr11:719436C>T	EPS8L2		
CHC2446T	g.chr11:73098906C>G	RELT		
CHC2446T	g.chr11:73852838G>C	C2CD3		
CHC2446T	g.chr11:74992822C>T	ARRB1		
CHC2446T	g.chr11:75743368T>A	UVRAG		
CHC2446T	g.chr11:76529831A>C	Unknown		
CHC2446T	g.chr11:7740474T>A	RP11-35J10.5		
CHC2446T	g.chr11:81714169C>A	RP11-179A16.1		
CHC2446T	g.chr11:9520210G>T	ZNF143		
CHC2446T	g.chr11:96445209T>C	Unknown		
CHC2446T	g.chr11:96765386T>A	Unknown		
CHC2446T	g.chr11:96792310T>A	Unknown		
CHC2446T	g.chr11:99358166T>C	CNTN5		
CHC2446T	g.chr11:99358766T>C	CNTN5		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr12:102638860G>C	Unknown		
CHC2446T	g.chr12:103785555T>C	C12orf42		
CHC2446T	g.chr12:104067004T>A	STAB2		
CHC2446T	g.chr12:105011385C>A	CHST11		
CHC2446T	g.chr12:108262922C>G	Unknown		
CHC2446T	g.chr12:109599573A>G	ACACB		
CHC2446T	g.chr12:111728268G>T	CUX2		
CHC2446T	g.chr12:113580073A>C	Unknown		
CHC2446T	g.chr12:114386587C>A	RBM19		
CHC2446T	g.chr12:114860923T>C	Unknown		
CHC2446T	g.chr12:115423538G>T	Unknown		
CHC2446T	g.chr12:117365668G>T	FBXW8		
CHC2446T	g.chr12:118462597G>A	RFC5		
CHC2446T	g.chr12:119553041G>T	SRRM4		
CHC2446T	g.chr12:119907630A>G	CCDC60		
CHC2446T	g.chr12:120399951G>A	Unknown		
CHC2446T	g.chr12:12058810T>C	Unknown		
CHC2446T	g.chr12:124481290G>T	ZNF664		
CHC2446T	g.chr12:124481291G>T	ZNF664		
CHC2446T	g.chr12:126994568C>A	Unknown		
CHC2446T	g.chr12:127903841C>T	Unknown		
CHC2446T	g.chr12:13035429C>T	Unknown		
CHC2446T	g.chr12:17709074A>G	RP11-871F6.3		
CHC2446T	g.chr12:19434295G>C	PLEKHA5		
CHC2446T	g.chr12:23937632T>A	SOX5		
CHC2446T	g.chr12:24172146G>C	Unknown		
CHC2446T	g.chr12:25620808C>T	Unknown		
CHC2446T	g.chr12:27458031A>G	STK38L		
CHC2446T	g.chr12:30187973G>T	Unknown		
CHC2446T	g.chr12:33875102C>T	Unknown		
CHC2446T	g.chr12:3466074G>A	Unknown		
CHC2446T	g.chr12:37988508C>G	Unknown		
CHC2446T	g.chr12:38828903C>T	Unknown		
CHC2446T	g.chr12:41977613T>C	Unknown		
CHC2446T	g.chr12:42768033C>A	PPHLN1		
CHC2446T	g.chr12:43206140T>C	Unknown		
CHC2446T	g.chr12:44561964G>A	TMEM117		
CHC2446T	g.chr12:44719586A>T	TMEM117		
CHC2446T	g.chr12:44804601C>G	Unknown		
CHC2446T	g.chr12:44858802A>G	Unknown		
CHC2446T	g.chr12:45272358A>T	NELL2		
CHC2446T	g.chr12:4633595C>T	C12orf4		
CHC2446T	g.chr12:47843665A>G	Unknown		
CHC2446T	g.chr12:4811092G>C	RP11-234B24.6		
CHC2446T	g.chr12:48705360C>A	Unknown		
CHC2446T	g.chr12:48926368T>C	Unknown		
CHC2446T	g.chr12:51386709C>A	SLC11A2	c.1168G>T	p.V390F
CHC2446T	g.chr12:5189802A>T	Unknown		
CHC2446T	g.chr12:52409539G>A	GRASP		
CHC2446T	g.chr12:54668013G>C	CBX5		
CHC2446T	g.chr12:55933043C>A	RP11-110A12.2		
CHC2446T	g.chr12:57259694T>C	RP11-74M13.4		
CHC2446T	g.chr12:57868033G>A	ARHGAP9		
CHC2446T	g.chr12:59103987A>G	RP11-362K2.2		
CHC2446T	g.chr12:59213313G>A	Unknown		
CHC2446T	g.chr12:60529565T>A	Unknown		
CHC2446T	g.chr12:66597234G>T	IRAK3		
CHC2446T	g.chr12:66967141G>T	GRIP1		
CHC2446T	g.chr12:70743726T>A	CNOT2		
CHC2446T	g.chr12:70816535C>T	KCNMB4		
CHC2446T	g.chr12:71003501A>T	PTPRB		
CHC2446T	g.chr12:73905415T>A	Unknown		
CHC2446T	g.chr12:77542582G>T	Unknown		
CHC2446T	g.chr12:79337406C>A	SYT1		
CHC2446T	g.chr12:81114057C>T	Unknown		
CHC2446T	g.chr12:83187699C>T	TMTC2		
CHC2446T	g.chr12:83754335G>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr12:84054279A>G	Unknown		
CHC2446T	g.chr12:86187246G>A	Unknown		
CHC2446T	g.chr12:86837349A>G	MGAT4C		
CHC2446T	g.chr12:86917128A>G	MGAT4C		
CHC2446T	g.chr12:88372789T>C	Unknown		
CHC2446T	g.chr12:9131479T>A	KLRG1		
CHC2446T	g.chr12:91618169T>C	Unknown		
CHC2446T	g.chr12:91989504A>G	Unknown		
CHC2446T	g.chr12:92536612T>C	BTG1		
CHC2446T	g.chr12:92635014C>G	Unknown		
CHC2446T	g.chr12:94356929G>C	Unknown		
CHC2446T	g.chr12:98422380G>A	Unknown		
CHC2446T	g.chr12:99750488G>C	ANKS1B		
CHC2446T	g.chr13:104967709C>A	Unknown		
CHC2446T	g.chr13:106765984G>T	Unknown		
CHC2446T	g.chr13:107204359C>A	ARGLU1		
CHC2446T	g.chr13:107204360T>G	ARGLU1		
CHC2446T	g.chr13:107626742T>G	Unknown		
CHC2446T	g.chr13:109069779A>T	Unknown		
CHC2446T	g.chr13:109454973A>G	MYO16		
CHC2446T	g.chr13:110227489A>C	Unknown		
CHC2446T	g.chr13:111219497C>A	Unknown		
CHC2446T	g.chr13:112338561T>A	Unknown		
CHC2446T	g.chr13:112630498A>C	Unknown		
CHC2446T	g.chr13:113540444C>A	ATP11A		
CHC2446T	g.chr13:28473930T>C	PDX1-AS1		
CHC2446T	g.chr13:32382722T>G	Unknown		
CHC2446T	g.chr13:33451197C>A	Unknown		
CHC2446T	g.chr13:34554251A>G	Unknown		
CHC2446T	g.chr13:35893861C>T	NBEA		
CHC2446T	g.chr13:35897515G>A	NBEA		
CHC2446T	g.chr13:36326339C>A	Unknown		
CHC2446T	g.chr13:38006154T>A	Unknown		
CHC2446T	g.chr13:38317741G>T	TRPC4		
CHC2446T	g.chr13:38620123T>C	Unknown		
CHC2446T	g.chr13:38757809G>T	Unknown		
CHC2446T	g.chr13:39918199C>T	LHFP		
CHC2446T	g.chr13:41634961T>C	Unknown		
CHC2446T	g.chr13:42294682C>A	VWA8		
CHC2446T	g.chr13:43401116C>A	Unknown		
CHC2446T	g.chr13:45130847C>A	TSC22D1		
CHC2446T	g.chr13:46538138A>T	ZC3H13	c.4514T>A	p.M1505K
CHC2446T	g.chr13:47657021A>G	Unknown		
CHC2446T	g.chr13:48424374C>T	Unknown		
CHC2446T	g.chr13:49039523G>T	RB1		
CHC2446T	g.chr13:52721755G>A	NEK3		
CHC2446T	g.chr13:53036494A>G	CKAP2		
CHC2446T	g.chr13:53277117G>T	Unknown		
CHC2446T	g.chr13:53799589G>T	Unknown		
CHC2446T	g.chr13:54455202G>A	Unknown		
CHC2446T	g.chr13:55880081T>C	Unknown		
CHC2446T	g.chr13:56526021G>T	Unknown		
CHC2446T	g.chr13:57682759T>C	Unknown		
CHC2446T	g.chr13:57841342G>C	Unknown		
CHC2446T	g.chr13:59785274G>A	Unknown		
CHC2446T	g.chr13:60205575C>A	Unknown		
CHC2446T	g.chr13:61409491A>T	Unknown		
CHC2446T	g.chr13:62351746G>A	Unknown		
CHC2446T	g.chr13:63083328A>G	Unknown		
CHC2446T	g.chr13:63216668C>G	Unknown		
CHC2446T	g.chr13:63573030T>A	Unknown		
CHC2446T	g.chr13:63774348C>G	LINC00376		
CHC2446T	g.chr13:63788195A>G	LINC00376		
CHC2446T	g.chr13:64457725T>G	Unknown		
CHC2446T	g.chr13:65192781A>T	Unknown		
CHC2446T	g.chr13:67725318C>A	PCDH9		
CHC2446T	g.chr13:70099514T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr13:70868143C>T	Unknown		
CHC2446T	g.chr13:71048135T>C	Unknown		
CHC2446T	g.chr13:72920469G>A	Unknown		
CHC2446T	g.chr13:76675843C>A	Unknown		
CHC2446T	g.chr13:77366620A>G	Unknown		
CHC2446T	g.chr13:79872597A>C	Unknown		
CHC2446T	g.chr13:80161751G>C	Unknown		
CHC2446T	g.chr13:81644026G>A	Unknown		
CHC2446T	g.chr13:82003604A>T	Unknown		
CHC2446T	g.chr13:82048293T>A	Unknown		
CHC2446T	g.chr13:82207144C>A	Unknown		
CHC2446T	g.chr13:82562667C>G	Unknown		
CHC2446T	g.chr13:82682065C>A	Unknown		
CHC2446T	g.chr13:82702314G>T	Unknown		
CHC2446T	g.chr13:83043478T>C	Unknown		
CHC2446T	g.chr13:84095706A>G	Unknown		
CHC2446T	g.chr13:84105632A>T	Unknown		
CHC2446T	g.chr13:87784716C>T	Unknown		
CHC2446T	g.chr13:88330293C>T	SLITRK5	c.2650C>T	p.P884S
CHC2446T	g.chr13:88626456T>G	Unknown		
CHC2446T	g.chr13:89862956T>C	Unknown		
CHC2446T	g.chr13:90517741T>A	Unknown		
CHC2446T	g.chr13:90583114C>T	Unknown		
CHC2446T	g.chr13:90726646G>T	LINC00559		
CHC2446T	g.chr13:91948432G>A	Unknown		
CHC2446T	g.chr13:93863520C>A	Unknown		
CHC2446T	g.chr13:97022674G>A	HS6ST3		
CHC2446T	g.chr13:97462308G>T	HS6ST3		
CHC2446T	g.chr13:97694844G>T	Unknown		
CHC2446T	g.chr14:100208014G>A	Unknown		
CHC2446T	g.chr14:101905877C>G	Unknown		
CHC2446T	g.chr14:102078310C>T	Unknown		
CHC2446T	g.chr14:106179553G>A	Unknown		
CHC2446T	g.chr14:24778267G>A	LTB4R2		
CHC2446T	g.chr14:26747357C>T	Unknown		
CHC2446T	g.chr14:28061640G>A	CTD-3006G17.2		
CHC2446T	g.chr14:33059491G>C	AKAP6		
CHC2446T	g.chr14:33871515C>A	NPAS3		
CHC2446T	g.chr14:34009723C>A	NPAS3		
CHC2446T	g.chr14:34042448C>A	NPAS3		
CHC2446T	g.chr14:34201933C>A	NPAS3		
CHC2446T	g.chr14:34772766C>T	Unknown		
CHC2446T	g.chr14:35479738C>T	SRP54		
CHC2446T	g.chr14:36282685C>T	Unknown		
CHC2446T	g.chr14:39114513G>A	Unknown		
CHC2446T	g.chr14:40180304C>T	Unknown		
CHC2446T	g.chr14:42173533T>A	LRFN5		
CHC2446T	g.chr14:42855219C>A	CTD-2307P3.1		
CHC2446T	g.chr14:48333106C>A	Unknown		
CHC2446T	g.chr14:48758180G>A	Unknown		
CHC2446T	g.chr14:51806236C>A	LINC00640		
CHC2446T	g.chr14:53128905T>A	ERO1L		
CHC2446T	g.chr14:54787026G>A	Unknown		
CHC2446T	g.chr14:55167015G>A	SAMD4A		
CHC2446T	g.chr14:57473398T>A	OTX2-AS1		
CHC2446T	g.chr14:59207995A>G	Unknown		
CHC2446T	g.chr14:60733212A>G	PPM1A		
CHC2446T	g.chr14:62219520A>G	RP11-618G20.1		
CHC2446T	g.chr14:63300401A>G	KCNH5		
CHC2446T	g.chr14:67742827T>C	MPP5		
CHC2446T	g.chr14:70125299A>G	KIAA0247		
CHC2446T	g.chr14:70960219G>A	RP11-486O13.4		
CHC2446T	g.chr14:71001202C>T	ADAM20		
CHC2446T	g.chr14:71144843G>A	Unknown		
CHC2446T	g.chr14:71768908T>C	RP1-261D10.2		
CHC2446T	g.chr14:72269940C>T	Unknown		
CHC2446T	g.chr14:72307703C>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr14:72356775T>C	RP6-114E22.1		
CHC2446T	g.chr14:73500837G>A	Unknown		
CHC2446T	g.chr14:77572768T>G	KIAA1737		
CHC2446T	g.chr14:78698477C>T	Unknown		
CHC2446T	g.chr14:80033425T>C	NRXN3		
CHC2446T	g.chr14:80091594T>C	NRXN3		
CHC2446T	g.chr14:80346444T>A	Unknown		
CHC2446T	g.chr14:80634360A>T	Unknown		
CHC2446T	g.chr14:83117827C>T	RP11-406A9.2		
CHC2446T	g.chr14:84092065C>A	Unknown		
CHC2446T	g.chr14:84538065T>A	Unknown		
CHC2446T	g.chr14:86219364G>A	Unknown		
CHC2446T	g.chr14:87875955T>C	RP11-594C13.1		
CHC2446T	g.chr14:88286727G>T	RP11-1152H15.1		
CHC2446T	g.chr14:91048280C>A	TTC7B		
CHC2446T	g.chr14:91669930A>G	C14orf159		
CHC2446T	g.chr14:91676107T>C	C14orf159		
CHC2446T	g.chr14:93875819T>C	UNC79		
CHC2446T	g.chr14:95307759G>T	Unknown		
CHC2446T	g.chr14:95540228C>A	Unknown		
CHC2446T	g.chr14:95586441A>C	DICER1		
CHC2446T	g.chr14:96686960A>C	BDKRB2		
CHC2446T	g.chr14:97839357C>T	Unknown		
CHC2446T	g.chr14:98153750G>A	Unknown		
CHC2446T	g.chr14:99201790C>T	Unknown		
CHC2446T	g.chr14:99853253T>A	Unknown		
CHC2446T	g.chr14:99997688G>A	CCDC85C		
CHC2446T	g.chr15:102268024C>A	Unknown		
CHC2446T	g.chr15:20653630T>A	HERC2P3		
CHC2446T	g.chr15:24740222C>T	Unknown		
CHC2446T	g.chr15:25320313T>C	SNHG14		
CHC2446T	g.chr15:26092183C>T	ATP10A		
CHC2446T	g.chr15:26384708A>G	Unknown		
CHC2446T	g.chr15:27975294C>A	Unknown		
CHC2446T	g.chr15:35499044A>G	ANP32AP1		
CHC2446T	g.chr15:36606721T>A	Unknown		
CHC2446T	g.chr15:40421208G>T	Unknown		
CHC2446T	g.chr15:41694686T>C	Unknown		
CHC2446T	g.chr15:43259058A>G	UBR1		
CHC2446T	g.chr15:44253110A>G	FRMD5		
CHC2446T	g.chr15:45689988G>C	GATM		
CHC2446T	g.chr15:46592282A>T	Unknown		
CHC2446T	g.chr15:46776036C>A	Unknown		
CHC2446T	g.chr15:50822988A>G	USP50		
CHC2446T	g.chr15:53185010T>C	Unknown		
CHC2446T	g.chr15:54091380C>A	Unknown		
CHC2446T	g.chr15:54201989C>T	Unknown		
CHC2446T	g.chr15:55891304C>G	Unknown		
CHC2446T	g.chr15:55891305C>A	Unknown		
CHC2446T	g.chr15:56832627C>T	Unknown		
CHC2446T	g.chr15:58226647A>G	Unknown		
CHC2446T	g.chr15:60474544A>G	Unknown		
CHC2446T	g.chr15:60512879G>A	Unknown		
CHC2446T	g.chr15:61049143T>G	RORA		
CHC2446T	g.chr15:67578424T>A	IQCH		
CHC2446T	g.chr15:69512814A>G	GLCE		
CHC2446T	g.chr15:72462581C>A	GRAMD2		
CHC2446T	g.chr15:72762805A>C	Unknown		
CHC2446T	g.chr15:74168985A>G	TBC1D21		
CHC2446T	g.chr15:76069878G>T	RP11-24M17.5		
CHC2446T	g.chr15:77218637A>G	Unknown		
CHC2446T	g.chr15:80027233T>A	Unknown		
CHC2446T	g.chr15:80300848A>G	Unknown		
CHC2446T	g.chr15:80357254A>G	ZFAND6		
CHC2446T	g.chr15:81624117T>C	TMC3		
CHC2446T	g.chr15:83523522C>T	HOMER2	c.558G>A	p.E186E
CHC2446T	g.chr15:87033490A>T	AGBL1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr15:92035271T>C	RP11-661P17.1		
CHC2446T	g.chr15:93299133T>C	Unknown		
CHC2446T	g.chr15:93396429C>A	Unknown		
CHC2446T	g.chr15:93458257A>G	CHD2		
CHC2446T	g.chr15:94330516C>T	CTD-3049M7.1		
CHC2446T	g.chr15:94413071T>C	CTD-3049M7.1		
CHC2446T	g.chr15:95246689C>A	Unknown		
CHC2446T	g.chr15:97993464T>C	Unknown		
CHC2446T	g.chr16:10375598C>A	Unknown		
CHC2446T	g.chr16:13043700A>T	SHISA9		
CHC2446T	g.chr16:1687786G>T	CRAMP1L		
CHC2446T	g.chr16:22902810T>C	HS3ST2		
CHC2446T	g.chr16:2379950G>T	ABCA3		
CHC2446T	g.chr16:24373529A>T	CACNG3		
CHC2446T	g.chr16:26172827G>C	Unknown		
CHC2446T	g.chr16:32200312G>T	RP11-17M15.1		
CHC2446T	g.chr16:34899289T>C	Unknown		
CHC2446T	g.chr16:3799977C>A	CREBBP		
CHC2446T	g.chr16:4481798C>A	DNAJA3		
CHC2446T	g.chr16:4481799G>A	DNAJA3		
CHC2446T	g.chr16:49141969A>G	Unknown		
CHC2446T	g.chr16:50747419T>C	NOD2		
CHC2446T	g.chr16:53889327T>G	FTO		
CHC2446T	g.chr16:5721845T>C	RP11-420N3.2		
CHC2446T	g.chr16:57349165A>T	Unknown		
CHC2446T	g.chr16:59599388G>A	Unknown		
CHC2446T	g.chr16:59821097C>T	Unknown		
CHC2446T	g.chr16:59845763A>T	Unknown		
CHC2446T	g.chr16:6057393G>A	RP11-420N3.2		
CHC2446T	g.chr16:60583478G>A	Unknown		
CHC2446T	g.chr16:61139357T>C	Unknown		
CHC2446T	g.chr16:61613688C>T	Unknown		
CHC2446T	g.chr16:62424056T>G	Unknown		
CHC2446T	g.chr16:62947636G>T	Unknown		
CHC2446T	g.chr16:64122550G>T	Unknown		
CHC2446T	g.chr16:6433634T>C	RBFOX1		
CHC2446T	g.chr16:65415052A>C	LINC00922		
CHC2446T	g.chr16:68703969T>C	CDH3		
CHC2446T	g.chr16:7404747A>G	RBFOX1		
CHC2446T	g.chr16:7588319C>G	RBFOX1		
CHC2446T	g.chr16:76685027G>A	RP11-96P7.1		
CHC2446T	g.chr16:77422799G>T	ADAMTS18		
CHC2446T	g.chr16:78024492A>G	Unknown		
CHC2446T	g.chr16:7985330T>A	Unknown		
CHC2446T	g.chr16:8084281C>T	Unknown		
CHC2446T	g.chr16:81399629G>A	GAN		
CHC2446T	g.chr16:83370693G>A	CDH13		
CHC2446T	g.chr16:86170134G>C	Unknown		
CHC2446T	g.chr16:86398278C>T	Unknown		
CHC2446T	g.chr16:87346535C>T	RP11-178L8.4		
CHC2446T	g.chr16:88516595A>G	Unknown		
CHC2446T	g.chr17:11284665A>C	SHISA6		
CHC2446T	g.chr17:12668448A>G	MYOCD		
CHC2446T	g.chr17:16990171G>A	MPRIP		
CHC2446T	g.chr17:1884996T>G	RTN4RL1		
CHC2446T	g.chr17:21395645A>G	Unknown		
CHC2446T	g.chr17:25340821G>T	Unknown		
CHC2446T	g.chr17:26009248G>T	Unknown		
CHC2446T	g.chr17:26246921C>T	Unknown		
CHC2446T	g.chr17:28662450C>T	Unknown		
CHC2446T	g.chr17:35548072C>A	ACACA	c.4450G>T	p.D1484Y
CHC2446T	g.chr17:35548073C>A	ACACA	c.4449G>T	p.M1483I
CHC2446T	g.chr17:35564364A>C	ACACA		
CHC2446T	g.chr17:35669316T>C	ACACA		
CHC2446T	g.chr17:40461464T>C	STAT5A	c.2091T>C	p.A697A
CHC2446T	g.chr17:41207673C>T	BRCA1		
CHC2446T	g.chr17:4125411G>A	ANKFY1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr17:4392638C>T	Unknown		
CHC2446T	g.chr17:47028000C>T	Unknown		
CHC2446T	g.chr17:48344516A>G	Unknown		
CHC2446T	g.chr17:49428572C>T	Unknown		
CHC2446T	g.chr17:49876424A>G	CA10		
CHC2446T	g.chr17:51632679C>T	Unknown		
CHC2446T	g.chr17:51877850T>A	Unknown		
CHC2446T	g.chr17:52495772A>G	Unknown		
CHC2446T	g.chr17:56078899T>C	RP11-159D12.5		
CHC2446T	g.chr17:58182050C>T	Unknown		
CHC2446T	g.chr17:61465324C>G	TANC2		
CHC2446T	g.chr17:6329807C>T	AIP1		
CHC2446T	g.chr17:64381483G>T	PRKCA		
CHC2446T	g.chr17:66016305G>T	Unknown		
CHC2446T	g.chr17:66887189T>A	ABCA8		
CHC2446T	g.chr17:67274543C>T	ABCA5		
CHC2446T	g.chr17:675805T>C	GLOD4		
CHC2446T	g.chr17:68446053C>A	Unknown		
CHC2446T	g.chr17:70030993G>A	RP11-84E24.3		
CHC2446T	g.chr17:70315328T>A	Unknown		
CHC2446T	g.chr17:71157767C>A	Unknown		
CHC2446T	g.chr17:71632797G>T	SDK2		
CHC2446T	g.chr17:71959703C>A	Unknown		
CHC2446T	g.chr17:72581195T>C	C17orf77		
CHC2446T	g.chr17:75006814A>C	Unknown		
CHC2446T	g.chr17:76317187T>G	AC061992.2		
CHC2446T	g.chr17:79230214C>A	SLC38A10		
CHC2446T	g.chr17:79875089C>A	SIRT7		
CHC2446T	g.chr17:79875090C>T	SIRT7		
CHC2446T	g.chr17:8712710G>A	PIK3R6		
CHC2446T	g.chr17:9726541T>C	GLP2R		
CHC2446T	g.chr17:9763363G>T	GLP2R	c.870G>T	p.E290D
CHC2446T	g.chr18:10459735C>T	APCDD1		
CHC2446T	g.chr18:11063870T>C	PIEZO2		
CHC2446T	g.chr18:1304608G>C	LINC00470		
CHC2446T	g.chr18:1356827G>A	LINC00470		
CHC2446T	g.chr18:14453860G>T	Unknown		
CHC2446T	g.chr18:14563299T>C	Unknown		
CHC2446T	g.chr18:14708391T>C	Unknown		
CHC2446T	g.chr18:1771560C>G	CTD-2015H3.2		
CHC2446T	g.chr18:18633101C>T	ROCK1		
CHC2446T	g.chr18:23297956T>C	Unknown		
CHC2446T	g.chr18:25006290C>A	RP11-739N10.1		
CHC2446T	g.chr18:26919471A>G	CTD-2515C13.2		
CHC2446T	g.chr18:27370997A>G	Unknown		
CHC2446T	g.chr18:28023720T>G	Unknown		
CHC2446T	g.chr18:28073329A>C	Unknown		
CHC2446T	g.chr18:32183180G>T	DTNA		
CHC2446T	g.chr18:36570625G>T	Unknown		
CHC2446T	g.chr18:37650685A>G	RP11-653G8.2		
CHC2446T	g.chr18:38844388A>G	Unknown		
CHC2446T	g.chr18:3902256C>T	DLGAP1		
CHC2446T	g.chr18:39581024A>G	PIK3C3		
CHC2446T	g.chr18:39939050G>T	LINC00907		
CHC2446T	g.chr18:42999073T>C	SLC14A2		
CHC2446T	g.chr18:48853880T>G	Unknown		
CHC2446T	g.chr18:50220480G>T	DCC		
CHC2446T	g.chr18:51966880A>C	Unknown		
CHC2446T	g.chr18:57286532T>C	CCBE1		
CHC2446T	g.chr18:57542999C>T	Unknown		
CHC2446T	g.chr18:59195065C>T	CDH20		
CHC2446T	g.chr18:63079045T>G	Unknown		
CHC2446T	g.chr18:6413796C>G	L3MBTL4		
CHC2446T	g.chr18:65152315A>G	Unknown		
CHC2446T	g.chr18:68290588G>A	Unknown		
CHC2446T	g.chr18:68561539C>A	Unknown		
CHC2446T	g.chr18:68837629T>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr18:69340896A>G	Unknown		
CHC2446T	g.chr18:69673787G>C	Unknown		
CHC2446T	g.chr18:70193722G>A	Unknown		
CHC2446T	g.chr18:8684189G>A	Unknown		
CHC2446T	g.chr18:8931723A>T	Unknown		
CHC2446T	g.chr18:8931728T>G	Unknown		
CHC2446T	g.chr19:13729660G>T	Unknown		
CHC2446T	g.chr19:14604147A>G	GIPC1		
CHC2446T	g.chr19:14640688A>T	TECR		
CHC2446T	g.chr19:14950784A>G	Unknown		
CHC2446T	g.chr19:19257734T>C	MEF2B		
CHC2446T	g.chr19:20416276A>G	CTC-260E6.6		
CHC2446T	g.chr19:20476174A>G	Unknown		
CHC2446T	g.chr19:21091403A>G	Unknown		
CHC2446T	g.chr19:22662953A>G	ZNF98		
CHC2446T	g.chr19:22697761G>T	ZNF98		
CHC2446T	g.chr19:22837594G>A	ZNF492		
CHC2446T	g.chr19:23160343T>C	ZNF728		
CHC2446T	g.chr19:24130867G>A	CTB-92J24.3		
CHC2446T	g.chr19:28905772T>G	Unknown		
CHC2446T	g.chr19:29887386G>T	CTC-525D6.1		
CHC2446T	g.chr19:30955546T>C	ZNF536		
CHC2446T	g.chr19:31790143C>A	TSHZ3		
CHC2446T	g.chr19:32226355G>T	Unknown		
CHC2446T	g.chr19:33104760G>A	ANKRD27		
CHC2446T	g.chr19:42167510G>T	Unknown		
CHC2446T	g.chr19:48874089G>T	SYNGR4		
CHC2446T	g.chr19:49322537T>C	HSD17B14		
CHC2446T	g.chr19:49574101G>A	KCNA7	c.590C>T	p.P197L
CHC2446T	g.chr19:51139794C>T	SYT3		
CHC2446T	g.chr19:51238438T>C	Unknown		
CHC2446T	g.chr19:52325058A>G	FPR3		
CHC2446T	g.chr19:53769958A>G	VN1R4		
CHC2446T	g.chr2:102685756G>T	Unknown		
CHC2446T	g.chr2:104661566A>G	Unknown		
CHC2446T	g.chr2:106100940G>A	Unknown		
CHC2446T	g.chr2:109320883C>A	Unknown		
CHC2446T	g.chr2:11126068A>C	Unknown		
CHC2446T	g.chr2:115112483G>A	Unknown		
CHC2446T	g.chr2:115885026C>A	DPP10		
CHC2446T	g.chr2:11656309A>G	Unknown		
CHC2446T	g.chr2:116815581T>C	Unknown		
CHC2446T	g.chr2:116844650G>C	Unknown		
CHC2446T	g.chr2:117066017T>C	Unknown		
CHC2446T	g.chr2:117543325T>C	Unknown		
CHC2446T	g.chr2:118978307A>T	Unknown		
CHC2446T	g.chr2:1258928C>T	SNTG2		
CHC2446T	g.chr2:129897686T>C	Unknown		
CHC2446T	g.chr2:130685333C>T	AC079776.3		
CHC2446T	g.chr2:131565080T>A	Unknown		
CHC2446T	g.chr2:133384639G>A	GPR39		
CHC2446T	g.chr2:140028519G>A	Unknown		
CHC2446T	g.chr2:1409868A>G	TPO		
CHC2446T	g.chr2:141171223A>G	LRP1B		
CHC2446T	g.chr2:141763012G>A	LRP1B	c.2395C>T	p.R799*
CHC2446T	g.chr2:142152404A>T	LRP1B		
CHC2446T	g.chr2:142841645T>A	LRP1B		
CHC2446T	g.chr2:143321619A>G	Unknown		
CHC2446T	g.chr2:143988768G>A	ARHGAP15		
CHC2446T	g.chr2:144653951A>G	Unknown		
CHC2446T	g.chr2:146253474A>T	Unknown		
CHC2446T	g.chr2:147278335G>A	Unknown		
CHC2446T	g.chr2:152631313T>C	Unknown		
CHC2446T	g.chr2:15377670A>G	NBAS		
CHC2446T	g.chr2:157546937T>A	Unknown		
CHC2446T	g.chr2:159785523C>T	Unknown		
CHC2446T	g.chr2:160264741T>C	BAZ2B		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr2:160737007T>A	LY75-CD302		
CHC2446T	g.chr2:163054239G>T	FAP		
CHC2446T	g.chr2:164474462C>T	FIGN		
CHC2446T	g.chr2:165524449C>T	Unknown		
CHC2446T	g.chr2:16733153T>G	FAM49A		
CHC2446T	g.chr2:170745295C>G	UBR3		
CHC2446T	g.chr2:170982621C>T	Unknown		
CHC2446T	g.chr2:170992558G>A	Unknown		
CHC2446T	g.chr2:172545768G>T	DYNC112		
CHC2446T	g.chr2:172911208A>G	METAP1D		
CHC2446T	g.chr2:174573679G>A	Unknown		
CHC2446T	g.chr2:174967217T>C	OLA1		
CHC2446T	g.chr2:178794825T>C	PDE11A		
CHC2446T	g.chr2:179650750G>T	TTN	c.2195C>A	p.T732N
CHC2446T	g.chr2:180550181T>C	ZNF385B		
CHC2446T	g.chr2:182036456A>T	AC104820.2		
CHC2446T	g.chr2:184442924A>G	Unknown		
CHC2446T	g.chr2:186625742G>A	FSIP2	c.1106G>A	p.R369H
CHC2446T	g.chr2:187952348G>T	AC007319.1		
CHC2446T	g.chr2:190997364A>T	Unknown		
CHC2446T	g.chr2:19341402G>A	Unknown		
CHC2446T	g.chr2:193523484A>G	Unknown		
CHC2446T	g.chr2:194658791T>C	Unknown		
CHC2446T	g.chr2:194799874T>C	Unknown		
CHC2446T	g.chr2:195143783G>A	Unknown		
CHC2446T	g.chr2:196207119T>C	Unknown		
CHC2446T	g.chr2:199059877C>G	Unknown		
CHC2446T	g.chr2:203085302T>C	SUMO1		
CHC2446T	g.chr2:203596682T>G	FAM117B		
CHC2446T	g.chr2:205199544T>C	Unknown		
CHC2446T	g.chr2:20520846G>C	PUM2		
CHC2446T	g.chr2:209722830C>A	Unknown		
CHC2446T	g.chr2:210279895T>C	Unknown		
CHC2446T	g.chr2:210556727G>T	MAP2		
CHC2446T	g.chr2:212480076A>T	ERBB4		
CHC2446T	g.chr2:212811854C>T	ERBB4		
CHC2446T	g.chr2:214049220A>G	Unknown		
CHC2446T	g.chr2:215198886T>G	SPAG16		
CHC2446T	g.chr2:215767338G>A	AC072062.1		
CHC2446T	g.chr2:217375245A>G	RPL37A		
CHC2446T	g.chr2:217943256T>G	Unknown		
CHC2446T	g.chr2:221241228G>T	AC114765.1		
CHC2446T	g.chr2:221928807C>T	Unknown		
CHC2446T	g.chr2:221956061G>A	Unknown		
CHC2446T	g.chr2:222561290C>T	Unknown		
CHC2446T	g.chr2:222937709C>A	Unknown		
CHC2446T	g.chr2:224756801C>A	WDFY1		
CHC2446T	g.chr2:225967747A>G	Unknown		
CHC2446T	g.chr2:229316548C>T	Unknown		
CHC2446T	g.chr2:237429520A>T	Unknown		
CHC2446T	g.chr2:238009479A>T	Unknown		
CHC2446T	g.chr2:238376105G>A	Unknown		
CHC2446T	g.chr2:241145033C>A	Unknown		
CHC2446T	g.chr2:241811220C>G	AGXT		
CHC2446T	g.chr2:29579350A>G	ALK		
CHC2446T	g.chr2:30066959C>T	ALK		
CHC2446T	g.chr2:3052011G>T	AC019118.2		
CHC2446T	g.chr2:31734702A>G	Unknown		
CHC2446T	g.chr2:32732090A>G	BIRC6		
CHC2446T	g.chr2:33644633G>C	Unknown		
CHC2446T	g.chr2:34830881C>A	AC073218.1		
CHC2446T	g.chr2:36642871T>A	CRIM1		
CHC2446T	g.chr2:38554367A>C	ATL2		
CHC2446T	g.chr2:39363726C>T	Unknown		
CHC2446T	g.chr2:39904868T>G	TMEM178A		
CHC2446T	g.chr2:40640695A>T	SLC8A1		
CHC2446T	g.chr2:43135252T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr2:45113964A>G	Unknown		
CHC2446T	g.chr2:47015474C>T	Unknown		
CHC2446T	g.chr2:4772834C>A	Unknown		
CHC2446T	g.chr2:5132169G>A	Unknown		
CHC2446T	g.chr2:52415751A>G	AC007682.1		
CHC2446T	g.chr2:5663795C>T	Unknown		
CHC2446T	g.chr2:57194123C>G	Unknown		
CHC2446T	g.chr2:57311578A>G	Unknown		
CHC2446T	g.chr2:57922239T>C	Unknown		
CHC2446T	g.chr2:59406000G>C	Unknown		
CHC2446T	g.chr2:61970386G>A	Unknown		
CHC2446T	g.chr2:64057724C>T	Unknown		
CHC2446T	g.chr2:64067574G>A	Unknown		
CHC2446T	g.chr2:64451200A>G	AC074289.1		
CHC2446T	g.chr2:66121226G>A	Unknown		
CHC2446T	g.chr2:67127779A>T	Unknown		
CHC2446T	g.chr2:68057993A>G	Unknown		
CHC2446T	g.chr2:73267958A>G	SFXN5		
CHC2446T	g.chr2:75313226A>G	TACR1		
CHC2446T	g.chr2:76489822G>T	Unknown		
CHC2446T	g.chr2:76839550C>T	Unknown		
CHC2446T	g.chr2:77355408T>C	LRRTM4		
CHC2446T	g.chr2:78049399C>T	Unknown		
CHC2446T	g.chr2:7872272A>G	Unknown		
CHC2446T	g.chr2:79431080C>A	CTNNA2		
CHC2446T	g.chr2:79549323T>A	CTNNA2		
CHC2446T	g.chr2:7960427T>C	Unknown		
CHC2446T	g.chr2:7993983C>A	Unknown		
CHC2446T	g.chr2:81216510A>C	Unknown		
CHC2446T	g.chr2:8220424A>G	Unknown		
CHC2446T	g.chr2:8649885C>T	Unknown		
CHC2446T	g.chr2:89110123G>A	AC096579.13		
CHC2446T	g.chr2:96227936T>A	Unknown		
CHC2446T	g.chr20:22284113G>A	Unknown		
CHC2446T	g.chr20:24521982T>G	SYNDIG1		
CHC2446T	g.chr20:29567458A>T	RP4-610C12.1		
CHC2446T	g.chr20:32967019A>G	ITCH		
CHC2446T	g.chr20:33357238C>T	NCOA6		
CHC2446T	g.chr20:38197012A>G	Unknown		
CHC2446T	g.chr20:38273636C>A	Unknown		
CHC2446T	g.chr20:39951349C>G	Unknown		
CHC2446T	g.chr20:46506860T>C	Unknown		
CHC2446T	g.chr20:46686154C>T	Unknown		
CHC2446T	g.chr20:50167518T>A	NFATC2		
CHC2446T	g.chr20:52217704C>G	ZNF217		
CHC2446T	g.chr20:52736681C>G	Unknown		
CHC2446T	g.chr20:53066575C>T	Unknown		
CHC2446T	g.chr20:54374105G>A	Unknown		
CHC2446T	g.chr20:54886273A>G	Unknown		
CHC2446T	g.chr20:55322610G>A	Unknown		
CHC2446T	g.chr20:55486155T>C	Unknown		
CHC2446T	g.chr20:56543579C>T	Unknown		
CHC2446T	g.chr20:56919731G>C	RAB22A		
CHC2446T	g.chr20:58898169T>A	Unknown		
CHC2446T	g.chr20:59198374G>A	Unknown		
CHC2446T	g.chr20:61455721C>T	COL9A3		
CHC2446T	g.chr21:15874062C>T	SAMSN1		
CHC2446T	g.chr21:15893527C>A	SAMSN1	c.73G>T	p.G25W
CHC2446T	g.chr21:20018232T>A	AF240627.2		
CHC2446T	g.chr21:22006384G>A	Unknown		
CHC2446T	g.chr21:22059092T>C	Unknown		
CHC2446T	g.chr21:24191478C>A	Unknown		
CHC2446T	g.chr21:27929749A>C	CYYR1		
CHC2446T	g.chr21:28427016T>C	Unknown		
CHC2446T	g.chr21:29684980G>C	Unknown		
CHC2446T	g.chr21:30696751G>T	BACH1		
CHC2446T	g.chr21:34718892T>G	IFNAR1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr21:36334944G>A	RUNX1		
CHC2446T	g.chr21:36997111C>A	Unknown		
CHC2446T	g.chr21:38663590G>A	Unknown		
CHC2446T	g.chr21:38987867T>G	KCNJ6		
CHC2446T	g.chr21:39631340A>G	KCNJ15		
CHC2446T	g.chr21:40508276G>A	Unknown		
CHC2446T	g.chr21:46295479T>C	Unknown		
CHC2446T	g.chr21:47002612G>A	Unknown		
CHC2446T	g.chr22:17411120C>T	Unknown		
CHC2446T	g.chr22:20842746G>C	KLHL22		
CHC2446T	g.chr22:21266255G>A	Unknown		
CHC2446T	g.chr22:21296996T>C	CRKL		
CHC2446T	g.chr22:24707301A>G	SPECC1L		
CHC2446T	g.chr22:27442190A>C	Unknown		
CHC2446T	g.chr22:27667137G>A	Unknown		
CHC2446T	g.chr22:29114942T>A	CHEK2		
CHC2446T	g.chr22:31420806T>C	Unknown		
CHC2446T	g.chr22:35004324G>C	Unknown		
CHC2446T	g.chr22:35697641C>G	TOM1		
CHC2446T	g.chr22:37816034C>T	ELFN2		
CHC2446T	g.chr22:42344574C>A	Unknown		
CHC2446T	g.chr22:43030420T>C	CYB5R3		
CHC2446T	g.chr22:45894020C>T	Unknown		
CHC2446T	g.chr22:47491173A>T	TBC1D22A		
CHC2446T	g.chr22:48286793C>A	Unknown		
CHC2446T	g.chr22:48888322T>G	FAM19A5		
CHC2446T	g.chr22:48888323T>C	FAM19A5		
CHC2446T	g.chr3:103320010G>A	Unknown		
CHC2446T	g.chr3:105251968A>G	ALCAM		
CHC2446T	g.chr3:106820087C>A	LINC00882		
CHC2446T	g.chr3:106930760T>C	LINC00882		
CHC2446T	g.chr3:108229726A>C	MYH15		
CHC2446T	g.chr3:109204894A>C	RP11-702L6.4		
CHC2446T	g.chr3:1106893A>G	Unknown		
CHC2446T	g.chr3:112380860A>T	Unknown		
CHC2446T	g.chr3:112449181C>A	Unknown		
CHC2446T	g.chr3:112717652G>C	GTPBP8		
CHC2446T	g.chr3:115095164T>G	Unknown		
CHC2446T	g.chr3:11734918C>A	VGLL4		
CHC2446T	g.chr3:12017793C>T	Unknown		
CHC2446T	g.chr3:120940998T>G	STXBPL5		
CHC2446T	g.chr3:121491725T>C	IQCB1		
CHC2446T	g.chr3:12154322A>G	SYN2		
CHC2446T	g.chr3:124209615C>T	KALRN	c.4465C>T	p.L1489L
CHC2446T	g.chr3:125118729A>G	Unknown		
CHC2446T	g.chr3:126071130C>A	KLF15	c.636G>T	p.T212T
CHC2446T	g.chr3:128053596C>T	EEFSEC		
CHC2446T	g.chr3:131934091T>A	CPNE4		
CHC2446T	g.chr3:132364890G>T	ACAD11		
CHC2446T	g.chr3:133083316T>C	TMEM108		
CHC2446T	g.chr3:133281466A>C	Unknown		
CHC2446T	g.chr3:134576063C>T	EPHB1		
CHC2446T	g.chr3:138777805C>G	MRPS22		
CHC2446T	g.chr3:138777949A>C	MRPS22		
CHC2446T	g.chr3:139594612A>G	Unknown		
CHC2446T	g.chr3:142821291T>C	Unknown		
CHC2446T	g.chr3:145097206T>C	Unknown		
CHC2446T	g.chr3:145833432C>T	PLOD2		
CHC2446T	g.chr3:148258088T>A	Unknown		
CHC2446T	g.chr3:148904713A>C	CP		
CHC2446T	g.chr3:148973867A>C	Unknown		
CHC2446T	g.chr3:149018562T>C	RP11-206M11.7		
CHC2446T	g.chr3:149957270T>C	RP11-167H9.6		
CHC2446T	g.chr3:15250595G>T	CAPN7		
CHC2446T	g.chr3:153034567T>C	Unknown		
CHC2446T	g.chr3:153681469T>A	RP11-23D24.2		
CHC2446T	g.chr3:154552284A>G	RP11-439C8.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr3:155890246T>G	KCNAB1		
CHC2446T	g.chr3:155911737A>G	KCNAB1		
CHC2446T	g.chr3:158254524A>T	RSRC1		
CHC2446T	g.chr3:158776139C>T	IQCI-SCHIP1		
CHC2446T	g.chr3:159966974T>C	RP11-432B6.3		
CHC2446T	g.chr3:161255169A>G	Unknown		
CHC2446T	g.chr3:161793703T>A	Unknown		
CHC2446T	g.chr3:16246460G>T	GALNT15		
CHC2446T	g.chr3:162599309G>T	Unknown		
CHC2446T	g.chr3:164221997A>G	Unknown		
CHC2446T	g.chr3:166678901C>A	Unknown		
CHC2446T	g.chr3:166748017G>A	Unknown		
CHC2446T	g.chr3:167870402A>C	Unknown		
CHC2446T	g.chr3:168741387G>A	Unknown		
CHC2446T	g.chr3:169791459A>C	GPR160		
CHC2446T	g.chr3:171855658A>G	FNDC3B		
CHC2446T	g.chr3:173308197C>T	NLGN1		
CHC2446T	g.chr3:173553401T>A	NLGN1		
CHC2446T	g.chr3:175871492T>G	Unknown		
CHC2446T	g.chr3:17605531C>T	TBC1D5		
CHC2446T	g.chr3:176313895T>C	Unknown		
CHC2446T	g.chr3:177966130T>A	Unknown		
CHC2446T	g.chr3:178301420G>A	KCNMB2		
CHC2446T	g.chr3:179338606G>T	NDUFB5		
CHC2446T	g.chr3:180979572G>T	Unknown		
CHC2446T	g.chr3:182330637G>T	Unknown		
CHC2446T	g.chr3:187764330T>C	Unknown		
CHC2446T	g.chr3:187984449A>G	LPP		
CHC2446T	g.chr3:18806236G>T	AC144521.1		
CHC2446T	g.chr3:188707581C>T	TPRG1		
CHC2446T	g.chr3:195480475G>T	MUC4		
CHC2446T	g.chr3:19627688A>T	Unknown		
CHC2446T	g.chr3:20007373C>A	RAB5A		
CHC2446T	g.chr3:2032477G>T	Unknown		
CHC2446T	g.chr3:20887724A>G	Unknown		
CHC2446T	g.chr3:2101839T>A	Unknown		
CHC2446T	g.chr3:21490764T>C	ZNF385D		
CHC2446T	g.chr3:25408861A>G	RARB		
CHC2446T	g.chr3:2553908C>A	CNTN4		
CHC2446T	g.chr3:26071229C>A	Unknown		
CHC2446T	g.chr3:26247498A>T	Unknown		
CHC2446T	g.chr3:26669003G>T	LRR3B		
CHC2446T	g.chr3:26916094G>A	Unknown		
CHC2446T	g.chr3:27916368G>A	AC098973.2		
CHC2446T	g.chr3:27980753T>C	Unknown		
CHC2446T	g.chr3:28862730C>A	Unknown		
CHC2446T	g.chr3:29435174C>A	RBMS3		
CHC2446T	g.chr3:29435175C>G	RBMS3		
CHC2446T	g.chr3:29447000G>T	RBMS3		
CHC2446T	g.chr3:30510379A>G	Unknown		
CHC2446T	g.chr3:32140740C>A	Unknown		
CHC2446T	g.chr3:3313912C>T	Unknown		
CHC2446T	g.chr3:34867909G>A	Unknown		
CHC2446T	g.chr3:3601143C>T	Unknown		
CHC2446T	g.chr3:41828980C>T	ULK4		
CHC2446T	g.chr3:44565215A>G	Unknown		
CHC2446T	g.chr3:46887314G>C	Unknown		
CHC2446T	g.chr3:58625238C>T	FAM3D		
CHC2446T	g.chr3:59362997T>C	Unknown		
CHC2446T	g.chr3:61441942G>T	Unknown		
CHC2446T	g.chr3:64016445T>C	Unknown		
CHC2446T	g.chr3:64234136A>T	PRICKLE2		
CHC2446T	g.chr3:64456313T>C	Unknown		
CHC2446T	g.chr3:67566975A>G	SUCLG2		
CHC2446T	g.chr3:69197364T>G	Unknown		
CHC2446T	g.chr3:72346306T>A	Unknown		
CHC2446T	g.chr3:7494454C>A	GRM7	c.1335C>A	p.G445G

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr3:75869506G>T	Unknown		
CHC2446T	g.chr3:75959366C>T	ROBO2		
CHC2446T	g.chr3:793754T>C	AC090044.1		
CHC2446T	g.chr3:81439429T>G	Unknown		
CHC2446T	g.chr3:82637431A>G	Unknown		
CHC2446T	g.chr3:84395426C>T	Unknown		
CHC2446T	g.chr3:84799247A>G	LINC00971		
CHC2446T	g.chr3:85425574T>C	CADM2		
CHC2446T	g.chr3:86053127G>T	CADM2		
CHC2446T	g.chr3:86336765G>A	Unknown		
CHC2446T	g.chr3:87964475C>A	Unknown		
CHC2446T	g.chr3:88662724G>A	Unknown		
CHC2446T	g.chr3:90224832C>T	Unknown		
CHC2446T	g.chr3:9214352A>C	SRGAP3		
CHC2446T	g.chr3:95063179C>T	Unknown		
CHC2446T	g.chr3:96092686T>A	Unknown		
CHC2446T	g.chr3:96172419G>A	Unknown		
CHC2446T	g.chr3:97560122A>G	CRYBG3		
CHC2446T	g.chr4:102426663A>C	BANK1		
CHC2446T	g.chr4:102481848T>C	BANK1		
CHC2446T	g.chr4:104778365A>G	Unknown		
CHC2446T	g.chr4:105415953G>C	CXXC4		
CHC2446T	g.chr4:10691418T>C	RP11-61G19.1		
CHC2446T	g.chr4:108067043A>G	DKK2		
CHC2446T	g.chr4:110185429C>T	COL25A1		
CHC2446T	g.chr4:111046334C>A	ELOVL6		
CHC2446T	g.chr4:11152990G>T	Unknown		
CHC2446T	g.chr4:111635941G>A	Unknown		
CHC2446T	g.chr4:11198499A>C	Unknown		
CHC2446T	g.chr4:11225610C>T	Unknown		
CHC2446T	g.chr4:114832623C>A	AR SJ		
CHC2446T	g.chr4:11657597G>C	Unknown		
CHC2446T	g.chr4:117003596G>A	Unknown		
CHC2446T	g.chr4:117824194T>C	Unknown		
CHC2446T	g.chr4:117857115A>C	Unknown		
CHC2446T	g.chr4:118859798A>C	Unknown		
CHC2446T	g.chr4:119009442T>C	NDST3		
CHC2446T	g.chr4:119862426G>A	SYNPO2		
CHC2446T	g.chr4:121247278C>T	RP11-679C8.2		
CHC2446T	g.chr4:125995502A>G	Unknown		
CHC2446T	g.chr4:127105400G>A	Unknown		
CHC2446T	g.chr4:127788988A>G	Unknown		
CHC2446T	g.chr4:129090868T>A	LARP1B		
CHC2446T	g.chr4:130150950C>A	Unknown		
CHC2446T	g.chr4:130491247C>T	Unknown		
CHC2446T	g.chr4:133176858T>C	Unknown		
CHC2446T	g.chr4:134617304C>T	Unknown		
CHC2446T	g.chr4:136128636T>C	Unknown		
CHC2446T	g.chr4:136601768A>T	Unknown		
CHC2446T	g.chr4:137735165G>C	RP11-138I17.1		
CHC2446T	g.chr4:140768059G>A	MAML3		
CHC2446T	g.chr4:141682864A>G	Unknown		
CHC2446T	g.chr4:144237003T>G	RP11-364L4.3		
CHC2446T	g.chr4:145211729C>T	Unknown		
CHC2446T	g.chr4:145474692G>C	Unknown		
CHC2446T	g.chr4:14616675T>C	LINC00504		
CHC2446T	g.chr4:148361164G>C	Unknown		
CHC2446T	g.chr4:149812395T>A	Unknown		
CHC2446T	g.chr4:151470556T>C	LRBA		
CHC2446T	g.chr4:151470557C>A	LRBA		
CHC2446T	g.chr4:154734148C>T	Unknown		
CHC2446T	g.chr4:156087031C>T	Unknown		
CHC2446T	g.chr4:157800626A>C	PDGFC		
CHC2446T	g.chr4:158077259T>A	GLRB		
CHC2446T	g.chr4:158563393G>T	RP11-364P22.2		
CHC2446T	g.chr4:158751553A>T	Unknown		
CHC2446T	g.chr4:158913031T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr4:162740282A>G	FSTL5		
CHC2446T	g.chr4:163324639T>A	Unknown		
CHC2446T	g.chr4:164441058T>C	TMA16		
CHC2446T	g.chr4:165240769C>A	01-mars		
CHC2446T	g.chr4:166655892C>A	RP11-340B18.1		
CHC2446T	g.chr4:167152827C>G	Unknown		
CHC2446T	g.chr4:167938706C>T	SPOCK3		
CHC2446T	g.chr4:172158409C>G	Unknown		
CHC2446T	g.chr4:172475781T>C	RP11-97E7.1		
CHC2446T	g.chr4:173005880G>T	GALNTL6		
CHC2446T	g.chr4:173508009G>T	GALNTL6		
CHC2446T	g.chr4:173527245A>G	GALNTL6		
CHC2446T	g.chr4:174790878A>G	Unknown		
CHC2446T	g.chr4:174814629T>C	Unknown		
CHC2446T	g.chr4:176351081C>A	Unknown		
CHC2446T	g.chr4:176993034C>A	WDR17		
CHC2446T	g.chr4:177724579C>A	Unknown		
CHC2446T	g.chr4:178421116A>G	RP11-130F10.1		
CHC2446T	g.chr4:181871993G>T	Unknown		
CHC2446T	g.chr4:183036767A>G	AC108142.1		
CHC2446T	g.chr4:183369051A>T	TENM3		
CHC2446T	g.chr4:18506657T>A	Unknown		
CHC2446T	g.chr4:186005604A>T	RP11-386B13.3		
CHC2446T	g.chr4:186530214T>C	SORBS2		
CHC2446T	g.chr4:186599090T>C	SORBS2		
CHC2446T	g.chr4:186989204A>G	Unknown		
CHC2446T	g.chr4:18745758C>T	Unknown		
CHC2446T	g.chr4:19096009A>G	Unknown		
CHC2446T	g.chr4:19153567T>A	Unknown		
CHC2446T	g.chr4:19265778T>C	RP11-3J1.1		
CHC2446T	g.chr4:19868377A>T	RP11-608O21.1		
CHC2446T	g.chr4:22091538T>C	RP11-17E2.2		
CHC2446T	g.chr4:29179679C>A	RP11-472K22.1		
CHC2446T	g.chr4:30307741G>A	Unknown		
CHC2446T	g.chr4:31231231G>T	Unknown		
CHC2446T	g.chr4:31295516T>C	Unknown		
CHC2446T	g.chr4:32518796T>A	Unknown		
CHC2446T	g.chr4:33300555C>T	Unknown		
CHC2446T	g.chr4:34855760C>T	Unknown		
CHC2446T	g.chr4:34891306T>G	Unknown		
CHC2446T	g.chr4:35021237A>G	Unknown		
CHC2446T	g.chr4:35454752G>T	Unknown		
CHC2446T	g.chr4:39530527A>G	UGDH-AS1		
CHC2446T	g.chr4:40549788T>C	RBM47		
CHC2446T	g.chr4:43199635C>A	RP11-395F4.1		
CHC2446T	g.chr4:44020878G>T	RP11-328N19.1		
CHC2446T	g.chr4:44403835T>G	KCTD8		
CHC2446T	g.chr4:46717876C>A	Unknown		
CHC2446T	g.chr4:47816380G>C	CORIN		
CHC2446T	g.chr4:493065G>T	PIGG		
CHC2446T	g.chr4:5459155G>T	STK32B		
CHC2446T	g.chr4:55186404T>A	Unknown		
CHC2446T	g.chr4:55405262T>C	Unknown		
CHC2446T	g.chr4:55532178T>A	KIT		
CHC2446T	g.chr4:57387255T>C	ARL9		
CHC2446T	g.chr4:57896670A>C	POLR2B		
CHC2446T	g.chr4:5798998C>T	EVC		
CHC2446T	g.chr4:58688801A>G	Unknown		
CHC2446T	g.chr4:59651863G>T	RP11-506N2.1		
CHC2446T	g.chr4:59802855A>G	RP11-506N2.1		
CHC2446T	g.chr4:60826777C>A	Unknown		
CHC2446T	g.chr4:62430863T>G	LPHN3		
CHC2446T	g.chr4:6504703C>T	PPP2R2C		
CHC2446T	g.chr4:65580368G>C	Unknown		
CHC2446T	g.chr4:6731884C>A	Unknown		
CHC2446T	g.chr4:67436715T>C	Unknown		
CHC2446T	g.chr4:67647440G>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr4:67870960T>C	Unknown		
CHC2446T	g.chr4:69300574C>A	Unknown		
CHC2446T	g.chr4:69563728C>T	Unknown		
CHC2446T	g.chr4:71121540T>C	Unknown		
CHC2446T	g.chr4:71230548T>C	SMR3A		
CHC2446T	g.chr4:7189789G>A	Unknown		
CHC2446T	g.chr4:72338703T>A	SLC4A4		
CHC2446T	g.chr4:73488974A>T	Unknown		
CHC2446T	g.chr4:75890651G>C	PARM1		
CHC2446T	g.chr4:75936807C>T	PARM1		
CHC2446T	g.chr4:76226985T>A	RP11-542G1.1		
CHC2446T	g.chr4:76979468T>A	ART3		
CHC2446T	g.chr4:77245422C>A	CCDC158		
CHC2446T	g.chr4:78332626C>A	CCNG2		
CHC2446T	g.chr4:78373833G>T	RP11-625I7.1		
CHC2446T	g.chr4:79297834C>A	FRAS1		
CHC2446T	g.chr4:79417136G>C	FRAS1		
CHC2446T	g.chr4:8203644T>A	SH3TC1		
CHC2446T	g.chr4:84962676T>G	Unknown		
CHC2446T	g.chr4:86260534C>T	Unknown		
CHC2446T	g.chr4:8774676C>T	Unknown		
CHC2446T	g.chr4:87766745C>T	SLC10A6		
CHC2446T	g.chr4:89152386G>C	ABCG2		
CHC2446T	g.chr4:89327794T>C	HERC6		
CHC2446T	g.chr4:89900356C>A	FAM13A		
CHC2446T	g.chr4:90337563T>G	Unknown		
CHC2446T	g.chr4:90386679C>A	Unknown		
CHC2446T	g.chr4:91705966T>C	CCSER1		
CHC2446T	g.chr4:91795748A>T	CCSER1		
CHC2446T	g.chr4:91810832A>T	CCSER1		
CHC2446T	g.chr4:91829374A>G	CCSER1		
CHC2446T	g.chr4:91931002T>C	CCSER1		
CHC2446T	g.chr4:92038190T>C	CCSER1		
CHC2446T	g.chr4:92406907A>G	CCSER1		
CHC2446T	g.chr4:92830034G>A	Unknown		
CHC2446T	g.chr4:93615547C>A	GRID2		
CHC2446T	g.chr4:93705973G>A	GRID2		
CHC2446T	g.chr4:94801003T>G	Unknown		
CHC2446T	g.chr4:96054525C>T	BMPR1B		
CHC2446T	g.chr4:96719672T>C	Unknown		
CHC2446T	g.chr4:97086895G>A	Unknown		
CHC2446T	g.chr4:97610506A>T	Unknown		
CHC2446T	g.chr5:100328158G>C	Unknown		
CHC2446T	g.chr5:103565517T>A	Unknown		
CHC2446T	g.chr5:103672411T>C	Unknown		
CHC2446T	g.chr5:104462394A>G	CTD-2374C24.1		
CHC2446T	g.chr5:104958852G>T	Unknown		
CHC2446T	g.chr5:104992942G>T	Unknown		
CHC2446T	g.chr5:105578823C>A	Unknown		
CHC2446T	g.chr5:105605500C>T	Unknown		
CHC2446T	g.chr5:109839677C>G	TMEM232		
CHC2446T	g.chr5:1099818T>A	SLC12A7		
CHC2446T	g.chr5:113387217A>G	Unknown		
CHC2446T	g.chr5:116155053T>C	Unknown		
CHC2446T	g.chr5:117117416T>C	Unknown		
CHC2446T	g.chr5:120254717T>A	Unknown		
CHC2446T	g.chr5:120800442A>T	Unknown		
CHC2446T	g.chr5:120953373A>C	Unknown		
CHC2446T	g.chr5:122689997T>C	CEP120		
CHC2446T	g.chr5:122997855T>C	Unknown		
CHC2446T	g.chr5:124516379T>G	Unknown		
CHC2446T	g.chr5:124566947C>A	Unknown		
CHC2446T	g.chr5:125323064G>C	Unknown		
CHC2446T	g.chr5:128340843T>G	SLC27A6		
CHC2446T	g.chr5:128605545C>A	Unknown		
CHC2446T	g.chr5:129770610T>A	Unknown		
CHC2446T	g.chr5:130436271T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr5:133246074G>A	Unknown		
CHC2446T	g.chr5:136210442C>A	Unknown		
CHC2446T	g.chr5:1413847C>T	SLC6A3		
CHC2446T	g.chr5:144529870C>A	Unknown		
CHC2446T	g.chr5:145575262T>C	Unknown		
CHC2446T	g.chr5:146073764G>A	PPP2R2B		
CHC2446T	g.chr5:146210369T>C	PPP2R2B		
CHC2446T	g.chr5:147700175C>T	AC091948.1		
CHC2446T	g.chr5:148364661T>C	Unknown		
CHC2446T	g.chr5:149081717T>C	Unknown		
CHC2446T	g.chr5:1493630C>G	LPCAT1		
CHC2446T	g.chr5:150155736G>A	Unknown		
CHC2446T	g.chr5:151742990G>A	Unknown		
CHC2446T	g.chr5:152981134G>A	GRIA1		
CHC2446T	g.chr5:153251985G>A	Unknown		
CHC2446T	g.chr5:156461591C>A	HAVCR1		
CHC2446T	g.chr5:156753441T>C	CYFIP2		
CHC2446T	g.chr5:159378619C>G	ADRA1B		
CHC2446T	g.chr5:161380592C>A	Unknown		
CHC2446T	g.chr5:161539876C>T	GABRG2		
CHC2446T	g.chr5:161797749C>A	Unknown		
CHC2446T	g.chr5:164152785T>G	CTC-340A15.2		
CHC2446T	g.chr5:164175689T>C	CTC-340A15.2		
CHC2446T	g.chr5:167553739A>G	TENM2		
CHC2446T	g.chr5:169737202T>C	CTB-114C7.4		
CHC2446T	g.chr5:177747332C>T	COL23A1		
CHC2446T	g.chr5:178832548A>G	Unknown		
CHC2446T	g.chr5:179916889C>T	Unknown		
CHC2446T	g.chr5:180032732A>T	FLT4		
CHC2446T	g.chr5:18343173C>G	Unknown		
CHC2446T	g.chr5:19188194G>T	Unknown		
CHC2446T	g.chr5:2000048G>T	Unknown		
CHC2446T	g.chr5:21814318A>C	CDH12		
CHC2446T	g.chr5:24787294A>G	Unknown		
CHC2446T	g.chr5:26517196C>T	Unknown		
CHC2446T	g.chr5:2661764T>A	Unknown		
CHC2446T	g.chr5:26689642T>C	Unknown		
CHC2446T	g.chr5:26872260A>G	Unknown		
CHC2446T	g.chr5:27144234T>A	Unknown		
CHC2446T	g.chr5:27751326A>T	Unknown		
CHC2446T	g.chr5:29203405A>C	Unknown		
CHC2446T	g.chr5:29337822A>G	Unknown		
CHC2446T	g.chr5:30154643C>T	Unknown		
CHC2446T	g.chr5:32320759C>T	Unknown		
CHC2446T	g.chr5:35912948C>G	CAPSL		
CHC2446T	g.chr5:38374913G>A	EGFLAM		
CHC2446T	g.chr5:38629215G>T	LIFR-AS1		
CHC2446T	g.chr5:38749786C>A	Unknown		
CHC2446T	g.chr5:3875764T>A	Unknown		
CHC2446T	g.chr5:39168875T>C	FYB		
CHC2446T	g.chr5:39808856A>G	Unknown		
CHC2446T	g.chr5:41026653G>A	MROH2B		
CHC2446T	g.chr5:4152637T>C	Unknown		
CHC2446T	g.chr5:41561397A>G	Unknown		
CHC2446T	g.chr5:4253378C>A	Unknown		
CHC2446T	g.chr5:42781932C>T	CCDC152		
CHC2446T	g.chr5:44917177G>A	Unknown		
CHC2446T	g.chr5:49787104T>C	Unknown		
CHC2446T	g.chr5:51430055T>A	Unknown		
CHC2446T	g.chr5:5191312T>C	ADAMTS16		
CHC2446T	g.chr5:5221348C>T	ADAMTS16		
CHC2446T	g.chr5:53802189T>C	Unknown		
CHC2446T	g.chr5:54503749C>A	Unknown		
CHC2446T	g.chr5:54539886A>C	RP11-506H20.1		
CHC2446T	g.chr5:55039316G>T	DDX4		
CHC2446T	g.chr5:56760304C>T	CTD-2023N9.1		
CHC2446T	g.chr5:5705497A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr5:5870789G>A	Unknown		
CHC2446T	g.chr5:67430802T>C	Unknown		
CHC2446T	g.chr5:67803646G>C	Unknown		
CHC2446T	g.chr5:67812415C>G	Unknown		
CHC2446T	g.chr5:71391780T>C	Unknown		
CHC2446T	g.chr5:73222558C>G	ARHGEF28		
CHC2446T	g.chr5:74606985G>C	Unknown		
CHC2446T	g.chr5:76662681C>G	PDE8B		
CHC2446T	g.chr5:7806776C>A	ADCY2		
CHC2446T	g.chr5:79161024T>C	Unknown		
CHC2446T	g.chr5:80145623T>A	MSH3		
CHC2446T	g.chr5:82120178C>A	Unknown		
CHC2446T	g.chr5:82730416T>C	Unknown		
CHC2446T	g.chr5:85723468T>A	Unknown		
CHC2446T	g.chr5:88798308G>T	Unknown		
CHC2446T	g.chr5:89825309G>A	LYSMD3		
CHC2446T	g.chr5:90519180A>G	Unknown		
CHC2446T	g.chr5:91978774T>C	Unknown		
CHC2446T	g.chr5:92709959A>G	Unknown		
CHC2446T	g.chr5:93051697T>C	FAM172A		
CHC2446T	g.chr5:93884284G>T	KIAA0825		
CHC2446T	g.chr5:93886568A>C	KIAA0825		
CHC2446T	g.chr5:94746113A>G	FAM81B		
CHC2446T	g.chr5:97427735C>A	AC008834.1		
CHC2446T	g.chr5:97493282T>A	AC008834.1		
CHC2446T	g.chr5:98408972T>C	Unknown		
CHC2446T	g.chr6:101066586T>A	ASCC3		
CHC2446T	g.chr6:101859030A>G	GRIK2		
CHC2446T	g.chr6:102747867A>G	Unknown		
CHC2446T	g.chr6:103260680C>A	Unknown		
CHC2446T	g.chr6:103853470C>T	Unknown		
CHC2446T	g.chr6:104331931G>C	Unknown		
CHC2446T	g.chr6:109079687A>G	LINC00222		
CHC2446T	g.chr6:110892964G>A	Unknown		
CHC2446T	g.chr6:114703144C>A	RP3-399L15.3		
CHC2446T	g.chr6:114955170C>A	Unknown		
CHC2446T	g.chr6:115316241G>T	Unknown		
CHC2446T	g.chr6:116501456A>G	NT5DC1		
CHC2446T	g.chr6:117813719T>C	DCBLD1		
CHC2446T	g.chr6:12087848T>C	HIVEP1		
CHC2446T	g.chr6:121607224C>A	TBC1D32		
CHC2446T	g.chr6:123173223A>G	Unknown		
CHC2446T	g.chr6:123465688A>G	Unknown		
CHC2446T	g.chr6:126742242A>G	Unknown		
CHC2446T	g.chr6:129417747G>A	LAMA2		
CHC2446T	g.chr6:129481738C>T	LAMA2		
CHC2446T	g.chr6:1353135T>A	Unknown		
CHC2446T	g.chr6:1449406G>A	Unknown		
CHC2446T	g.chr6:145821219C>A	Unknown		
CHC2446T	g.chr6:14599243T>A	RP11-330A16.1		
CHC2446T	g.chr6:147577967G>A	STXBP5		
CHC2446T	g.chr6:147739405C>A	Unknown		
CHC2446T	g.chr6:150347320G>T	Unknown		
CHC2446T	g.chr6:151329937A>C	MTHFD1L		
CHC2446T	g.chr6:152054521T>G	ESR1		
CHC2446T	g.chr6:152210214T>A	ESR1		
CHC2446T	g.chr6:153027886A>T	MYCT1		
CHC2446T	g.chr6:153278356A>G	Unknown		
CHC2446T	g.chr6:153674859G>C	Unknown		
CHC2446T	g.chr6:154631054C>T	IPCEF1		
CHC2446T	g.chr6:156890917A>G	Unknown		
CHC2446T	g.chr6:161158785T>G	PLG		
CHC2446T	g.chr6:162404451T>G	PARK2		
CHC2446T	g.chr6:162404454G>C	PARK2		
CHC2446T	g.chr6:18795495C>T	Unknown		
CHC2446T	g.chr6:21713168T>C	Unknown		
CHC2446T	g.chr6:28595309C>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr6:31104778A>G	PSORS1C1		
CHC2446T	g.chr6:32525862G>T	HLA-DRB6		
CHC2446T	g.chr6:33810841G>A	Unknown		
CHC2446T	g.chr6:34222382G>A	Unknown		
CHC2446T	g.chr6:34288148C>T	NUDT3		
CHC2446T	g.chr6:43606257G>C	MAD2L1BP		
CHC2446T	g.chr6:44087335C>T	MRPL14		
CHC2446T	g.chr6:45328815G>T	SUPT3H		
CHC2446T	g.chr6:46072747T>C	RP1-8B1.4		
CHC2446T	g.chr6:46886324G>A	GPR116		
CHC2446T	g.chr6:47785898C>G	OPN5		
CHC2446T	g.chr6:49744613A>G	Unknown		
CHC2446T	g.chr6:50357499A>T	Unknown		
CHC2446T	g.chr6:50399798G>T	Unknown		
CHC2446T	g.chr6:50843554T>C	Unknown		
CHC2446T	g.chr6:52111755C>A	Unknown		
CHC2446T	g.chr6:54951074C>A	Unknown		
CHC2446T	g.chr6:54976147A>G	Unknown		
CHC2446T	g.chr6:55089411A>T	HCRT2		
CHC2446T	g.chr6:56111098T>C	COL21A1		
CHC2446T	g.chr6:56608915C>A	DST		
CHC2446T	g.chr6:57880846G>C	Unknown		
CHC2446T	g.chr6:5985058G>A	Unknown		
CHC2446T	g.chr6:6066304T>C	Unknown		
CHC2446T	g.chr6:62017088A>G	Unknown		
CHC2446T	g.chr6:62751418C>A	KHDRBS2		
CHC2446T	g.chr6:65869032T>C	EYS		
CHC2446T	g.chr6:66097741A>T	EYS		
CHC2446T	g.chr6:66467117T>C	Unknown		
CHC2446T	g.chr6:66580221C>T	Unknown		
CHC2446T	g.chr6:66779530C>T	Unknown		
CHC2446T	g.chr6:67495605C>G	Unknown		
CHC2446T	g.chr6:67744367T>A	Unknown		
CHC2446T	g.chr6:68034464G>T	Unknown		
CHC2446T	g.chr6:68066478A>G	Unknown		
CHC2446T	g.chr6:69139736T>A	Unknown		
CHC2446T	g.chr6:69650739G>A	BAI3		
CHC2446T	g.chr6:69764306G>T	BAI3		
CHC2446T	g.chr6:70122933T>C	Unknown		
CHC2446T	g.chr6:74540177C>G	Unknown		
CHC2446T	g.chr6:74941039T>C	RP11-554D15.1		
CHC2446T	g.chr6:75676738T>C	Unknown		
CHC2446T	g.chr6:75863820A>T	COL12A1		
CHC2446T	g.chr6:78780537A>G	Unknown		
CHC2446T	g.chr6:79570053A>C	Unknown		
CHC2446T	g.chr6:82294632T>A	Unknown		
CHC2446T	g.chr6:8582076C>T	Unknown		
CHC2446T	g.chr6:87459931G>T	Unknown		
CHC2446T	g.chr6:89093139C>A	RP11-459O1.2		
CHC2446T	g.chr6:93584700G>T	Unknown		
CHC2446T	g.chr6:93898124T>A	Unknown		
CHC2446T	g.chr6:95519151A>T	Unknown		
CHC2446T	g.chr6:95970066T>C	Unknown		
CHC2446T	g.chr6:95981608A>C	Unknown		
CHC2446T	g.chr7:100184642A>G	FBXO24		
CHC2446T	g.chr7:103801399C>T	ORC5		
CHC2446T	g.chr7:104432324A>C	LHFPL3		
CHC2446T	g.chr7:105791229A>G	Unknown		
CHC2446T	g.chr7:108750648A>G	Unknown		
CHC2446T	g.chr7:109814710A>C	Unknown		
CHC2446T	g.chr7:110450200C>T	IMMP2L		
CHC2446T	g.chr7:111137624C>T	IMMP2L		
CHC2446T	g.chr7:113143599G>A	Unknown		
CHC2446T	g.chr7:118336917T>C	Unknown		
CHC2446T	g.chr7:118347695T>C	Unknown		
CHC2446T	g.chr7:118934941C>A	Unknown		
CHC2446T	g.chr7:118951443A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr7:119256916T>C	Unknown		
CHC2446T	g.chr7:121220939T>G	Unknown		
CHC2446T	g.chr7:121273570A>G	Unknown		
CHC2446T	g.chr7:122937252G>A	Unknown		
CHC2446T	g.chr7:125062959C>G	Unknown		
CHC2446T	g.chr7:125765396T>G	Unknown		
CHC2446T	g.chr7:125981380A>G	Unknown		
CHC2446T	g.chr7:133914864G>T	LRGUK		
CHC2446T	g.chr7:135127128T>C	CNOT4		
CHC2446T	g.chr7:137609151A>C	CREB3L2		
CHC2446T	g.chr7:138396587G>A	ATP6V0A4		
CHC2446T	g.chr7:14092977C>T	Unknown		
CHC2446T	g.chr7:143055797T>G	FAM131B		
CHC2446T	g.chr7:143748345T>C	OR2A5	c.851T>C	p.M284T
CHC2446T	g.chr7:144684000G>T	Unknown		
CHC2446T	g.chr7:147920308T>G	CNTNAP2		
CHC2446T	g.chr7:153121264C>G	Unknown		
CHC2446T	g.chr7:156023935T>C	Unknown		
CHC2446T	g.chr7:157484181C>A	PTPRN2		
CHC2446T	g.chr7:158004387T>C	PTPRN2		
CHC2446T	g.chr7:17856468G>A	SNX13		
CHC2446T	g.chr7:19548564C>T	AC007091.1		
CHC2446T	g.chr7:19572541A>G	AC007091.1		
CHC2446T	g.chr7:2209838C>A	MAD1L1		
CHC2446T	g.chr7:22115826G>A	Unknown		
CHC2446T	g.chr7:23982638C>T	Unknown		
CHC2446T	g.chr7:24519403A>G	Unknown		
CHC2446T	g.chr7:24963815T>C	OSBPL3		
CHC2446T	g.chr7:25031247A>G	Unknown		
CHC2446T	g.chr7:26958463T>G	Unknown		
CHC2446T	g.chr7:27848515G>A	TAX1BP1		
CHC2446T	g.chr7:34501824A>C	NPSR1-AS1		
CHC2446T	g.chr7:34501827A>G	NPSR1-AS1		
CHC2446T	g.chr7:37012589T>G	ELMO1		
CHC2446T	g.chr7:39132894G>T	POU6F2		
CHC2446T	g.chr7:42282893A>G	Unknown		
CHC2446T	g.chr7:42443236T>C	Unknown		
CHC2446T	g.chr7:43590619C>T	HECW1		
CHC2446T	g.chr7:44644592T>C	Unknown		
CHC2446T	g.chr7:46559780G>T	Unknown		
CHC2446T	g.chr7:49350492A>T	Unknown		
CHC2446T	g.chr7:50341626A>C	Unknown		
CHC2446T	g.chr7:51785189C>T	Unknown		
CHC2446T	g.chr7:53122511A>G	Unknown		
CHC2446T	g.chr7:54096315C>A	Unknown		
CHC2446T	g.chr7:57462145T>A	Unknown		
CHC2446T	g.chr7:66305908C>A	GTF2IRD1P1		
CHC2446T	g.chr7:67645573C>T	RP5-945F2.3		
CHC2446T	g.chr7:68238711G>A	Unknown		
CHC2446T	g.chr7:6872726T>C	Unknown		
CHC2446T	g.chr7:68831985T>C	RP11-3P22.2		
CHC2446T	g.chr7:70564000G>T	Unknown		
CHC2446T	g.chr7:71601004G>T	CALN1		
CHC2446T	g.chr7:72019503G>A	Unknown		
CHC2446T	g.chr7:74641241A>T	Unknown		
CHC2446T	g.chr7:78001941T>G	MAGI2		
CHC2446T	g.chr7:78964117T>C	MAGI2		
CHC2446T	g.chr7:7985477C>T	RPA3-AS1		
CHC2446T	g.chr7:82143719C>A	Unknown		
CHC2446T	g.chr7:83109374C>A	SEMA3E		
CHC2446T	g.chr7:83692567C>A	SEMA3A		
CHC2446T	g.chr7:84173533C>G	AC003984.1		
CHC2446T	g.chr7:84434296A>G	Unknown		
CHC2446T	g.chr7:85538458C>A	Unknown		
CHC2446T	g.chr7:86189867A>T	Unknown		
CHC2446T	g.chr7:86283422T>C	GRM3		
CHC2446T	g.chr7:86808105A>T	DMTF1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr7:87244958C>T	ABCB1		
CHC2446T	g.chr7:88148556A>G	Unknown		
CHC2446T	g.chr7:8822314T>G	Unknown		
CHC2446T	g.chr7:91139782T>A	RP11-142A5.1		
CHC2446T	g.chr7:96798761A>G	ACN9		
CHC2446T	g.chr7:97252751G>T	Unknown		
CHC2446T	g.chr8:102394221A>C	Unknown		
CHC2446T	g.chr8:104853376T>C	RIMS2		
CHC2446T	g.chr8:106159731A>G	RP11-57407.1		
CHC2446T	g.chr8:106987233C>A	RP11-152P17.2		
CHC2446T	g.chr8:108967667C>T	RSPO2		
CHC2446T	g.chr8:109370123T>C	Unknown		
CHC2446T	g.chr8:110672924A>G	SYBU		
CHC2446T	g.chr8:111268312A>T	Unknown		
CHC2446T	g.chr8:112507295T>C	RP11-1101K5.1		
CHC2446T	g.chr8:113073069C>A	Unknown		
CHC2446T	g.chr8:113263342C>G	CSMD3		
CHC2446T	g.chr8:113463012G>T	CSMD3		
CHC2446T	g.chr8:113835914A>G	CSMD3		
CHC2446T	g.chr8:114079351G>T	CSMD3		
CHC2446T	g.chr8:114601116C>A	Unknown		
CHC2446T	g.chr8:115122635C>A	Unknown		
CHC2446T	g.chr8:115344186G>C	Unknown		
CHC2446T	g.chr8:115648166A>C	Unknown		
CHC2446T	g.chr8:116707285C>A	Unknown		
CHC2446T	g.chr8:117082463A>G	LINC00536		
CHC2446T	g.chr8:117543485G>A	Unknown		
CHC2446T	g.chr8:118585124C>A	Unknown		
CHC2446T	g.chr8:120602928T>C	ENPP2		
CHC2446T	g.chr8:12523674A>T	Unknown		
CHC2446T	g.chr8:126102223T>C	KIAA0196		
CHC2446T	g.chr8:129943273T>C	Unknown		
CHC2446T	g.chr8:130997103C>T	FAM49B		
CHC2446T	g.chr8:132992873A>G	EFR3A		
CHC2446T	g.chr8:133353046A>G	KCNQ3		
CHC2446T	g.chr8:133370489A>G	KCNQ3		
CHC2446T	g.chr8:134204959A>G	WISP1		
CHC2446T	g.chr8:134285781G>A	NDRG1		
CHC2446T	g.chr8:134656748T>G	Unknown		
CHC2446T	g.chr8:135630152G>C	ZFAT		
CHC2446T	g.chr8:137330844G>A	Unknown		
CHC2446T	g.chr8:137643079G>A	Unknown		
CHC2446T	g.chr8:137866959T>C	Unknown		
CHC2446T	g.chr8:13817654A>G	Unknown		
CHC2446T	g.chr8:138590800G>A	Unknown		
CHC2446T	g.chr8:139240322T>C	FAM135B		
CHC2446T	g.chr8:14015911C>A	SGCZ		
CHC2446T	g.chr8:142537893T>C	Unknown		
CHC2446T	g.chr8:15469752G>T	TUSC3		
CHC2446T	g.chr8:17658173G>A	MTUS1		
CHC2446T	g.chr8:19812570G>A	LPL		
CHC2446T	g.chr8:21400143C>A	Unknown		
CHC2446T	g.chr8:22807597C>T	Unknown		
CHC2446T	g.chr8:25518581G>A	Unknown		
CHC2446T	g.chr8:25768890C>T	EBF2		
CHC2446T	g.chr8:25907481A>C	Unknown		
CHC2446T	g.chr8:27764952C>A	SCARA5		
CHC2446T	g.chr8:29114141C>T	KIF13B		
CHC2446T	g.chr8:29435656G>T	Unknown		
CHC2446T	g.chr8:29981951A>G	LEPROTL1		
CHC2446T	g.chr8:30792608G>A	Unknown		
CHC2446T	g.chr8:31034704G>A	Unknown		
CHC2446T	g.chr8:31547423C>A	NRG1		
CHC2446T	g.chr8:35901140G>T	RP11-89M20.2		
CHC2446T	g.chr8:3683525C>A	Unknown		
CHC2446T	g.chr8:42196143A>G	POLB	c.1A>G	p.M1V
CHC2446T	g.chr8:4221428G>T	CSMD1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr8:43140838C>A	Unknown		
CHC2446T	g.chr8:43342878A>C	Unknown		
CHC2446T	g.chr8:47570217A>T	Unknown		
CHC2446T	g.chr8:48002888C>T	Unknown		
CHC2446T	g.chr8:48074059A>G	Unknown		
CHC2446T	g.chr8:5117088T>A	Unknown		
CHC2446T	g.chr8:54104282G>A	RP11-162D9.3		
CHC2446T	g.chr8:54371821C>A	Unknown		
CHC2446T	g.chr8:54493195C>A	Unknown		
CHC2446T	g.chr8:54615118G>A	Unknown		
CHC2446T	g.chr8:54755340T>G	ATP6V1H		
CHC2446T	g.chr8:55750603C>T	Unknown		
CHC2446T	g.chr8:62671568A>G	Unknown		
CHC2446T	g.chr8:64677448T>C	RP11-32K4.1		
CHC2446T	g.chr8:65287030C>T	LINC00966		
CHC2446T	g.chr8:66466350A>T	CTD-3025N20.2		
CHC2446T	g.chr8:67889274T>G	PPP1R42		
CHC2446T	g.chr8:69106166T>A	PREX2		
CHC2446T	g.chr8:69734597C>A	Unknown		
CHC2446T	g.chr8:71148605C>T	NCOA2		
CHC2446T	g.chr8:74165540A>C	Unknown		
CHC2446T	g.chr8:75257479C>T	GDAP1		
CHC2446T	g.chr8:76141570G>A	CASC9		
CHC2446T	g.chr8:76650003T>A	Unknown		
CHC2446T	g.chr8:78527282C>G	Unknown		
CHC2446T	g.chr8:78914586A>G	Unknown		
CHC2446T	g.chr8:80059276A>G	Unknown		
CHC2446T	g.chr8:80681451G>A	RP11-27N21.3		
CHC2446T	g.chr8:82926680T>C	Unknown		
CHC2446T	g.chr8:83034610C>A	RP11-99H20.1		
CHC2446T	g.chr8:84042865T>C	Unknown		
CHC2446T	g.chr8:84636835A>G	Unknown		
CHC2446T	g.chr8:86429725G>T	Unknown		
CHC2446T	g.chr8:87005441T>C	Unknown		
CHC2446T	g.chr8:87807898G>A	RP11-386D6.2		
CHC2446T	g.chr8:88785738T>C	Unknown		
CHC2446T	g.chr8:89678898C>T	RP11-586K2.1		
CHC2446T	g.chr8:90277703A>G	Unknown		
CHC2446T	g.chr8:90376335T>C	Unknown		
CHC2446T	g.chr8:92500552T>C	Unknown		
CHC2446T	g.chr8:94045964A>G	Unknown		
CHC2446T	g.chr8:97016644G>A	Unknown		
CHC2446T	g.chr8:99349301G>T	Unknown		
CHC2446T	g.chr9:100091836A>G	CCDC180		
CHC2446T	g.chr9:10366770C>G	PTPRD		
CHC2446T	g.chr9:105859183T>A	Unknown		
CHC2446T	g.chr9:105976821C>G	RP11-341A22.2		
CHC2446T	g.chr9:106590745C>A	Unknown		
CHC2446T	g.chr9:111555041C>A	Unknown		
CHC2446T	g.chr9:11321263C>A	Unknown		
CHC2446T	g.chr9:113565163A>G	Unknown		
CHC2446T	g.chr9:11419878C>G	Unknown		
CHC2446T	g.chr9:115796883A>T	Unknown		
CHC2446T	g.chr9:116089646C>A	WDR31		
CHC2446T	g.chr9:116620184A>T	Unknown		
CHC2446T	g.chr9:118108622C>A	1-Dec		
CHC2446T	g.chr9:118241456T>C	Unknown		
CHC2446T	g.chr9:122135905C>A	Unknown		
CHC2446T	g.chr9:122489864C>A	Unknown		
CHC2446T	g.chr9:125308024T>G	Unknown		
CHC2446T	g.chr9:125742441G>T	RABGAP1		
CHC2446T	g.chr9:125928824G>A	STRBP		
CHC2446T	g.chr9:126933677T>C	Unknown		
CHC2446T	g.chr9:128703665G>A	PBX3		
CHC2446T	g.chr9:12992766T>A	Unknown		
CHC2446T	g.chr9:130558863G>A	Unknown		
CHC2446T	g.chr9:13192152C>A	MPDZ	c.1946G>T	p.C649F

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr9:13300100G>A	Unknown		
CHC2446T	g.chr9:134675703C>T	Unknown		
CHC2446T	g.chr9:134827011A>G	MED27		
CHC2446T	g.chr9:13582372G>A	Unknown		
CHC2446T	g.chr9:136370277G>T	Unknown		
CHC2446T	g.chr9:137925249G>A	Unknown		
CHC2446T	g.chr9:138125055G>A	RP11-399H11.3		
CHC2446T	g.chr9:138164018C>T	Unknown		
CHC2446T	g.chr9:139555523A>G	EGFL7		
CHC2446T	g.chr9:16006871A>G	CCDC171		
CHC2446T	g.chr9:21403832A>G	Unknown		
CHC2446T	g.chr9:21622066G>A	Unknown		
CHC2446T	g.chr9:21708833C>A	Unknown		
CHC2446T	g.chr9:2302767T>A	Unknown		
CHC2446T	g.chr9:24001279T>A	Unknown		
CHC2446T	g.chr9:24276951G>A	Unknown		
CHC2446T	g.chr9:24276952C>A	Unknown		
CHC2446T	g.chr9:24792934G>T	Unknown		
CHC2446T	g.chr9:24825121T>A	Unknown		
CHC2446T	g.chr9:24972640G>A	Unknown		
CHC2446T	g.chr9:25250586G>T	Unknown		
CHC2446T	g.chr9:25849594A>G	Unknown		
CHC2446T	g.chr9:26561734A>C	Unknown		
CHC2446T	g.chr9:30011857T>C	Unknown		
CHC2446T	g.chr9:30344972A>G	Unknown		
CHC2446T	g.chr9:30353618T>C	Unknown		
CHC2446T	g.chr9:31049988G>T	Unknown		
CHC2446T	g.chr9:3122139G>A	Unknown		
CHC2446T	g.chr9:32789998G>T	Unknown		
CHC2446T	g.chr9:33371417C>T	Unknown		
CHC2446T	g.chr9:34528791T>C	Unknown		
CHC2446T	g.chr9:3527128G>A	RP11-509J21.1		
CHC2446T	g.chr9:36271465G>T	GENE		
CHC2446T	g.chr9:3938846T>G	GLIS3		
CHC2446T	g.chr9:41236318T>C	Unknown		
CHC2446T	g.chr9:43402867G>T	Unknown		
CHC2446T	g.chr9:4488145T>C	Unknown		
CHC2446T	g.chr9:45992780A>T	Unknown		
CHC2446T	g.chr9:68172072G>C	Unknown		
CHC2446T	g.chr9:68348694G>C	Unknown		
CHC2446T	g.chr9:69352463T>G	Unknown		
CHC2446T	g.chr9:71783259A>T	TJP2		
CHC2446T	g.chr9:72196441A>G	APBA1		
CHC2446T	g.chr9:76020940A>T	Unknown		
CHC2446T	g.chr9:79698526T>C	Unknown		
CHC2446T	g.chr9:809793G>T	Unknown		
CHC2446T	g.chr9:83096403G>A	Unknown		
CHC2446T	g.chr9:83427672A>G	Unknown		
CHC2446T	g.chr9:85353095G>C	Unknown		
CHC2446T	g.chr9:85387926T>G	Unknown		
CHC2446T	g.chr9:90069561C>G	Unknown		
CHC2446T	g.chr9:90256566C>T	DAPK1		
CHC2446T	g.chr9:93080035G>A	RP11-389K14.3		
CHC2446T	g.chr9:96213958G>C	FAM120AOS		
CHC2446T	g.chr9:96767907C>T	Unknown		
CHC2446T	g.chr9:97061927G>T	ZNF169		
CHC2446T	g.chrX:101945181T>A	Unknown		
CHC2446T	g.chrX:105036665G>T	Unknown		
CHC2446T	g.chrX:10615266G>T	MID1		
CHC2446T	g.chrX:108601800C>G	Unknown		
CHC2446T	g.chrX:108677458A>T	GUCY2F		
CHC2446T	g.chrX:108848017A>G	Unknown		
CHC2446T	g.chrX:10987252A>C	RP11-120D5.1		
CHC2446T	g.chrX:110345109G>T	PAK3		
CHC2446T	g.chrX:114045185C>T	HTR2C		
CHC2446T	g.chrX:115034639T>G	RP11-761E20.1		
CHC2446T	g.chrX:115825577T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chrX:11632576C>A	ARHGAP6		
CHC2446T	g.chrX:117258035A>T	Unknown		
CHC2446T	g.chrX:117974437G>A	RP4-562J12.2		
CHC2446T	g.chrX:118348447A>T	Unknown		
CHC2446T	g.chrX:119081973A>T	Unknown		
CHC2446T	g.chrX:119221373C>A	RP4-755D9.1		
CHC2446T	g.chrX:11937856C>A	Unknown		
CHC2446T	g.chrX:11983832C>T	Unknown		
CHC2446T	g.chrX:12064640G>C	Unknown		
CHC2446T	g.chrX:121865067G>A	Unknown		
CHC2446T	g.chrX:122859824C>A	THOC2		
CHC2446T	g.chrX:123493615A>G	SH2D1A		
CHC2446T	g.chrX:124356432C>A	Unknown		
CHC2446T	g.chrX:124666233C>A	Unknown		
CHC2446T	g.chrX:125650693T>C	Unknown		
CHC2446T	g.chrX:125854298G>A	Unknown		
CHC2446T	g.chrX:126921814A>G	Unknown		
CHC2446T	g.chrX:127232358A>T	Unknown		
CHC2446T	g.chrX:128815238A>C	Unknown		
CHC2446T	g.chrX:133001994C>G	GPC3		
CHC2446T	g.chrX:134144737T>A	Unknown		
CHC2446T	g.chrX:137177724G>T	Unknown		
CHC2446T	g.chrX:138641536A>G	F9		
CHC2446T	g.chrX:140440433T>C	Unknown		
CHC2446T	g.chrX:140764422C>T	Unknown		
CHC2446T	g.chrX:142115859A>T	SPANXN4		
CHC2446T	g.chrX:144181570C>T	Unknown		
CHC2446T	g.chrX:144498872C>T	Unknown		
CHC2446T	g.chrX:14463369C>T	Unknown		
CHC2446T	g.chrX:145614471A>G	Unknown		
CHC2446T	g.chrX:146339206A>T	Unknown		
CHC2446T	g.chrX:146919651C>A	Unknown		
CHC2446T	g.chrX:148772958T>A	MAGEA11		
CHC2446T	g.chrX:149014761G>T	Unknown		
CHC2446T	g.chrX:151617296G>A	GABRA3		
CHC2446T	g.chrX:152188621A>G	Unknown		
CHC2446T	g.chrX:15537277C>A	BMX		
CHC2446T	g.chrX:17735829G>T	NHS		
CHC2446T	g.chrX:20043504C>A	MAP7D2		
CHC2446T	g.chrX:20740774A>G	Unknown		
CHC2446T	g.chrX:24966567G>A	POLA1		
CHC2446T	g.chrX:28232647C>A	Unknown		
CHC2446T	g.chrX:28588572C>T	Unknown		
CHC2446T	g.chrX:2863194G>A	ARSE		
CHC2446T	g.chrX:30083506G>C	Unknown		
CHC2446T	g.chrX:30083507G>A	Unknown		
CHC2446T	g.chrX:30888950C>T	TAB3		
CHC2446T	g.chrX:30990667G>A	TAB3		
CHC2446T	g.chrX:32109129G>T	DMD		
CHC2446T	g.chrX:3357356C>G	Unknown		
CHC2446T	g.chrX:34193244C>A	Unknown		
CHC2446T	g.chrX:35100652A>G	Unknown		
CHC2446T	g.chrX:35281836G>T	Unknown		
CHC2446T	g.chrX:36251372T>A	Unknown		
CHC2446T	g.chrX:40699527C>T	Unknown		
CHC2446T	g.chrX:42021944C>T	Unknown		
CHC2446T	g.chrX:42428855C>T	RP1-154K9.2		
CHC2446T	g.chrX:44380967T>C	Unknown		
CHC2446T	g.chrX:46753460A>G	CXorf31		
CHC2446T	g.chrX:47489502T>A	CFP		
CHC2446T	g.chrX:47846047T>A	ZNF182		
CHC2446T	g.chrX:48226191G>C	Unknown		
CHC2446T	g.chrX:49516184C>G	Unknown		
CHC2446T	g.chrX:50181833G>T	DGKK		
CHC2446T	g.chrX:50830805G>T	Unknown		
CHC2446T	g.chrX:54197912G>A	FAM120C		
CHC2446T	g.chrX:55639710A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chrX:55762884A>G	RRAGB		
CHC2446T	g.chrX:56075999C>T	Unknown		
CHC2446T	g.chrX:56326479T>C	Unknown		
CHC2446T	g.chrX:57055718A>G	Unknown		
CHC2446T	g.chrX:6247096A>G	Unknown		
CHC2446T	g.chrX:62868716G>A	ARHGEF9		
CHC2446T	g.chrX:63738333T>A	Unknown		
CHC2446T	g.chrX:65313813A>G	Unknown		
CHC2446T	g.chrX:67508336G>A	OPHN1		
CHC2446T	g.chrX:71594314G>T	HDAC8		
CHC2446T	g.chrX:72442987G>A	Unknown		
CHC2446T	g.chrX:72511906A>C	Unknown		
CHC2446T	g.chrX:74332177A>G	ABCB7		
CHC2446T	g.chrX:75726481G>A	Unknown		
CHC2446T	g.chrX:78132797G>A	Unknown		
CHC2446T	g.chrX:79862442T>C	Unknown		
CHC2446T	g.chrX:81720367G>T	Unknown		
CHC2446T	g.chrX:82583531C>T	Unknown		
CHC2446T	g.chrX:83069128G>C	Unknown		
CHC2446T	g.chrX:83850608G>T	Unknown		
CHC2446T	g.chrX:84779663C>T	Unknown		
CHC2446T	g.chrX:86602527A>T	Unknown		
CHC2446T	g.chrX:87434058C>T	Unknown		
CHC2446T	g.chrX:87459261G>A	Unknown		
CHC2446T	g.chrX:88389216T>A	Unknown		
CHC2446T	g.chrX:8892469G>A	Unknown		
CHC2446T	g.chrX:89646322T>G	Unknown		
CHC2446T	g.chrX:89711627A>T	Unknown		
CHC2446T	g.chrX:90604147T>G	Unknown		
CHC2446T	g.chrX:94771339G>A	Unknown		
CHC2446T	g.chrX:96171280C>A	DIAPH2		
CHC2446T	g.chrX:96896281C>G	DIAPH2-AS1		
CHC2446T	g.chrX:97262492G>A	Unknown		
CHC2446T	g.chrX:97640623T>G	Unknown		
CHC2446T	g.chrX:97640627G>T	Unknown		
CHC2446T	g.chrX:98137984C>T	Unknown		
CHC2446T	g.chrX:98753402C>A	Unknown		
CHC2446T	g.chrX:99232522G>T	Unknown		
CHC2446T	102300669delTAGTTTATATAG	OLFM3		
CHC2446T	g.chr1:106625014delGA	RP5-947P14.1		
CHC2446T	:12286495delCCAGCACTTTGG	Unknown		
CHC2446T	g.chr1:21613511delTA	ECE1		
CHC2446T	:24489192delTTTTCTTTCTTT	IFNLR1		
CHC2446T	:71113579_71113579insTATA	Unknown		
CHC2446T	:75597delCCAATTCATGTGGT	RERE		
CHC2446T	g.chr1:9447975delTA	Unknown		
CHC2446T	r10:341529_341529insAGGCT	DIP2C		
CHC2446T	rr10:70592432_70592432insA	STOX1		
CHC2446T	rr11:105020786_105020786in	Unknown		
CHC2446T	g.chr11:11277975delGTGTA	Unknown		
CHC2446T	1:117162604delCTGGGGCCCC	BACE1		
CHC2446T	g.chr11:43440123delGTAA	TTC17		
CHC2446T	g.chr11:56915389delTA	Unknown		
CHC2446T	g.chr12:104631788delCA	TXNRD1		
CHC2446T	g.chr12:112941846delAT	PTPN11		
CHC2446T	l3282_28803282insTATTATAT.	Unknown		
CHC2446T	g.chr12:41304181delAT	CNTN1		
CHC2446T	g.chr12:57343680delGTTTGT	Unknown		
CHC2446T	3GAATGGGCAAGGGCGGGAGC	R3HDM2		
CHC2446T	g.chr12:72107540delCA	Unknown		
CHC2446T	:hr12:80576902_80576902ins.	Unknown		
CHC2446T	rr13:100444022_100444022in	CLYBL		
CHC2446T	g.chr13:105326023delGC	Unknown		
CHC2446T	g.chr13:107818883delATT	Unknown		
CHC2446T	:hr13:20208212_20208212ins	MPHOSPH8		
CHC2446T	g.chr13:72488852delAG	Unknown		
CHC2446T	g.chr13:73653782delCT	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	g.chr14:47700968delAG	MDGA2		
CHC2446T	g.chr14:85497722delGC	Unknown		
CHC2446T	4224delCCATCCCCATCTCACCT	ZC3H14		
CHC2446T	g.chr15:20178104delGT	Unknown		
CHC2446T	g.chr15:59202990delCTGGAG	SLTM		
CHC2446T	:hr15:63370083_63370083ins	Unknown		
CHC2446T	rr15:63370084_63370084insT	Unknown		
CHC2446T	g.chr16:28100738delCACACA	Unknown		
CHC2446T	:hr16:48239494_48239494ins	ABCC11		
CHC2446T	:hr16:51726792_51726792ins	Unknown		
CHC2446T	g.chr16:63661389delCA	Unknown		
CHC2446T	rr17:37420597_37420597insT	FBXL20	.1034_1034insGTC	p.-344fs
CHC2446T	g.chr17:42379019delAG	AC003102.3		
CHC2446T	g.chr17:50535715delAT	RP11-429O1.1		
CHC2446T	:hr17:63236804_63236804ins	Unknown		
CHC2446T	:hr18:38182920_38182920ins	Unknown		
CHC2446T	g.chr18:64111109delGTTGA	Unknown		
CHC2446T	g.chr18:66041738delTTG	Unknown		
CHC2446T	g.chr18:685921delCAA	ENOSF1	c.741delTTG	p.F247fs
CHC2446T	g.chr18:70898517delGATAAT	RP11-169F17.1		
CHC2446T	:hr19:14121233delTAAAATAC	Unknown		
CHC2446T	:hr19:22314848_22314848ins	Unknown		
CHC2446T	r19:42355824delATATTTAGTC	DMRTC2		
CHC2446T	rr19:56048836_56048836insG	Unknown		
CHC2446T	g.chr19:5820747delAAG	Unknown		
CHC2446T	g.chr2:115052857delTC	Unknown		
CHC2446T	g.chr2:115251323delTC	DPP10		
CHC2446T	l7231916delGGTCCCGAAAAA	Unknown		
CHC2446T	.8035953_118035953insTATA	Unknown		
CHC2446T	g.chr2:169591228delTAAAAG	CERS6		
CHC2446T	g.chr2:170890084delCACAA	UBR3		
CHC2446T	g.chr2:195837838delCT	Unknown		
CHC2446T	g.chr2:211468545delTC	CPS1		
CHC2446T	hr2:237139383_237139383ins	ASB18		
CHC2446T	g.chr2:25241442delCACACA	DNAJC27-AS1		
CHC2446T	g.chr2:37322335delCA	GPATCH11		
CHC2446T	chr2:41184113_41184113insC	Unknown		
CHC2446T	g.chr2:42748734delAG	MTA3		
CHC2446T	g.chr2:44176020delGT	LRPPRC		
CHC2446T	g.chr2:50023240delAC	Unknown		
CHC2446T	chr2:71117100_71117100insA	Unknown		
CHC2446T	g.chr2:9445657_9445657insG	ASAP2		
CHC2446T	r20:61399646_61399646insCC	Unknown		
CHC2446T	26_62408426insCCACTGGGAA	ZBTB46		
CHC2446T	:hr21:30204053_30204053ins	Unknown		
CHC2446T	37420354_37420354insAGAC	SETD4		
CHC2446T	g.chr21:42260907delCT	Unknown		
CHC2446T	24763948delTTCTGTCCACTT	SPECC1L		
CHC2446T	g.chr22:37454458delAG	KCTD17		
CHC2446T	g.chr22:47035099delCTG	GRAMD4		
CHC2446T	g.chr22:49726484delGA	Unknown		
CHC2446T	g.chr3:107140396delAT	Unknown		
CHC2446T	3:119381052delGGAAGGAAA	POPDC2		
CHC2446T	g.chr3:186447190delTAGCC	KNG1		
CHC2446T	delCTTTTTTCCACCTATATCTGA	PAK2		
CHC2446T	g.chr3:3375087_3375087insCA	AC026188.1		
CHC2446T	GGGCGGGGGCTGACCCCCC	HYAL1		
CHC2446T	chr3:50496739_50496739insC	CACNA2D2		
CHC2446T	chr3:76666525_76666525insT	ROBO2		
CHC2446T	g.chr4:115479816delTA	Unknown		
CHC2446T	hr4:124648689_124648689ins	Unknown		
CHC2446T	g.chr4:138318842delTG	Unknown		
CHC2446T	g.chr4:14435628delAT	Unknown		
CHC2446T	g.chr4:170902195delCT	Unknown		
CHC2446T	l170_177099170insAAAAAAA	WDR17		
CHC2446T	g.chr4:27313726delAG	Unknown		
CHC2446T	g.chr4:3058952_3058952insG	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC2446T	5056600_46056600insCATGA/	GABRG1		
CHC2446T	g.chr4:56513139delGGC	Unknown		
CHC2446T	g.chr4:74274642delTATG	ALB		
CHC2446T	g.chr4:74285187delTTC	ALB		
CHC2446T	g.chr4:8920536delTTTTTC	Unknown		
CHC2446T	g.chr4:98881952delTC	STPG2		
CHC2446T	hr5:103619664_103619664ins	Unknown		
CHC2446T	288insGTTTAGGGTGTCTGAAA	PCBD2		
CHC2446T	g.chr5:14519169delAG	Unknown		
CHC2446T	g.chr5:19116424delAT	RP11-124N3.3		
CHC2446T	g.chr5:2037132delAT	Unknown		
CHC2446T	TATTTTTTTTTTTTTGTATTTTT	HCN1		
CHC2446T	:hr5:5493120_5493120insAGC	Unknown		
CHC2446T	chr5:64769371_64769371ins/	ADAMTS6		
CHC2446T	g.chr5:66665086delTCAAA	Unknown		
CHC2446T	g.chr5:77574758delAC	AP3B1		
CHC2446T	:101275755_101275755insGG	ASCC3		
CHC2446T	g.chr6:108682058delCA	LACE1		
CHC2446T	g.chr6:120433093delAC	Unknown		
CHC2446T	g.chr6:130629109delGA	SAMD3		
CHC2446T	hr6:155195658_155195658ins	TIAM2		
CHC2446T	g.chr6:166016477delTC	PDE10A		
CHC2446T	chr6:20757084_20757084insC	CDKAL1		
CHC2446T	rr6:20757093_20757093insTC	CDKAL1		
CHC2446T	g.chr6:31149090delITG	Unknown		
CHC2446T	g.chr7:126899676delACCT	Unknown		
CHC2446T	:hr7:17352048_17352048insC	AHR		
CHC2446T	g.chr7:21090363delCAGGCTT	Unknown		
CHC2446T	g.chr7:50798239delTCAAA	GRB10		
CHC2446T	:hr7:50798244delTTTTTTAAA	GRB10		
CHC2446T	g.chr7:56687584delICT	Unknown		
CHC2446T	chr7:57249222_57249222insC	Unknown		
CHC2446T	rr7:64709392_64709392insCC	Unknown		
CHC2446T	rr7:64709393_64709393insTA	Unknown		
CHC2446T	CCCCCACCCTGCGGTGTGGAT	Unknown		
CHC2446T	g.chr8:122236181delTA	Unknown		
CHC2446T	chr8:20256794_20256794insC	Unknown		
CHC2446T	g.chr8:49105356delAGAG	Unknown		
CHC2446T	chr8:77925885_77925885insC	Unknown		
CHC2446T	g.chr8:92335987delTAAA	SLC26A7		
CHC2446T	g.chr9:13582369delAG	Unknown		
CHC2446T	chr9:19563824_19563824insC	SLC24A2		
CHC2446T	g.chr9:21102952delTC	Unknown		
CHC2446T	chr9:74039261_74039261ins/	TRPM3		
CHC2446T	g.chr9:79643934delICT	Unknown		
CHC2446T	g.chr9:87933091delGA	Unknown		
CHC2446T	9:94477817_94477817insGTT	ROR2		
CHC2446T	g.chr9:95781604delIGT	FGD3		
CHC2446T	chr9:98782445_98782445insC	LINC00092		
CHC2446T	541_122788641insAAAAAAA	THOC2		
CHC2446T	g.chrX:15105544delITG	Unknown		
CHC2446T	g.chrX:24686543delIGA	PCYT1B		
CHC2446T	2794093insTTTTTTTTTTTTTG	GYG2		
CHC2446T	g.chrX:54780345delITG	ITIH6		
CHC2446T	g.chrX:56778173delCTTTA	RP11-622K12.1		
CHC2446T	3:chrX:70847534delGACACCA/	Unknown		
CHC2446T	3:chrX:77041292delCGTCGGAC	ATRX		
CHC605T	g.chr1:11483107G>A	Unknown		
CHC605T	g.chr1:234935032A>G	Unknown		
CHC605T	g.chr1:237311876A>T	RYR2		
CHC605T	g.chr10:1307686T>C	ADARB2		
CHC605T	g.chr11:32629084A>C	CCDC73		
CHC605T	g.chr11:5284451C>T	HBG2		
CHC605T	g.chr11:85606566A>G	CCDC83		
CHC605T	g.chr12:123065759T>G	KNTC1		
CHC605T	g.chr12:133115933G>C	FBRSL1		
CHC605T	g.chr12:74365786G>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr15:56803956G>A	Unknown		
CHC605T	g.chr16:1152779C>G	Unknown		
CHC605T	g.chr16:3257170G>A	AJ003147.9		
CHC605T	g.chr17:65821566C>A	Unknown		
CHC605T	g.chr18:32136296A>T	DTNA		
CHC605T	g.chr2:105830734C>T	Unknown		
CHC605T	g.chr2:226236756C>T	Unknown		
CHC605T	g.chr20:26191611G>T	Unknown		
CHC605T	g.chr3:100725617G>A	Unknown		
CHC605T	g.chr3:165011576A>C	Unknown		
CHC605T	g.chr4:116897314T>C	Unknown		
CHC605T	g.chr4:28218786A>G	Unknown		
CHC605T	g.chr4:91704177C>A	CCSER1		
CHC605T	g.chr5:170125632C>A	KCNIP1		
CHC605T	g.chr5:57266568C>T	Unknown		
CHC605T	g.chr6:54637970C>A	Unknown		
CHC605T	g.chr6:82349266C>G	Unknown		
CHC605T	g.chr8:127035167C>T	Unknown		
CHC605T	g.chr8:142458675T>A	MROH5		
CHC605T	g.chr9:100559138C>T	Unknown		
CHC605T	g.chr9:38743831A>T	Unknown		
CHC605T	g.chr9:83345948A>T	Unknown		
CHC605T	g.chr9:8334671G>T	PTPRD		
CHC605T	g.chrX:28634714C>G	IL1RAPL1		
CHC605T	g.chr1:103554714C>A	COL11A1		
CHC605T	g.chr1:104490437A>G	Unknown		
CHC605T	g.chr1:104849745C>T	Unknown		
CHC605T	g.chr1:105161540G>T	Unknown		
CHC605T	g.chr1:106245540T>C	Unknown		
CHC605T	g.chr1:106951256T>C	Unknown		
CHC605T	g.chr1:109248224T>G	Unknown		
CHC605T	g.chr1:112934916G>T	Unknown		
CHC605T	g.chr1:115613895G>A	TSPAN2		
CHC605T	g.chr1:115651340T>C	Unknown		
CHC605T	g.chr1:117827125G>T	Unknown		
CHC605T	g.chr1:118756560C>G	Unknown		
CHC605T	g.chr1:14954242A>T	KAZN		
CHC605T	g.chr1:150266551T>G	MRPS21		
CHC605T	g.chr1:154034939A>G	NUP210L		
CHC605T	g.chr1:155765355C>A	GON4L		
CHC605T	g.chr1:157725115G>A	FCRL2		
CHC605T	g.chr1:161068218G>C	KLHDC9		
CHC605T	g.chr1:162615256G>A	DDR2		
CHC605T	g.chr1:165694411T>C	Unknown		
CHC605T	g.chr1:166305348T>C	Unknown		
CHC605T	g.chr1:166350882T>C	Unknown		
CHC605T	g.chr1:167532157G>T	Unknown		
CHC605T	g.chr1:172657699T>G	Unknown		
CHC605T	g.chr1:17446329T>A	Unknown		
CHC605T	g.chr1:179424103C>A	AXDND1		
CHC605T	g.chr1:184249524C>A	Unknown		
CHC605T	g.chr1:185392004C>T	Unknown		
CHC605T	g.chr1:186773420A>G	Unknown		
CHC605T	g.chr1:187080415C>A	LINC01036		
CHC605T	g.chr1:187289114A>G	LINC01036		
CHC605T	g.chr1:187411955G>C	Unknown		
CHC605T	g.chr1:188149804G>T	Unknown		
CHC605T	g.chr1:189725435G>T	Unknown		
CHC605T	g.chr1:190161506G>A	BRINP3		
CHC605T	g.chr1:190839994C>G	Unknown		
CHC605T	g.chr1:191329680C>A	Unknown		
CHC605T	g.chr1:191804398C>A	Unknown		
CHC605T	g.chr1:191870455T>C	RP11-541F9.2		
CHC605T	g.chr1:192150785A>G	RGS18		
CHC605T	g.chr1:192205894C>A	Unknown		
CHC605T	g.chr1:195276253T>G	Unknown		
CHC605T	g.chr1:195460500A>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr1:195823623T>C	Unknown		
CHC605T	g.chr1:196003083A>T	Unknown		
CHC605T	g.chr1:196138672T>A	Unknown		
CHC605T	g.chr1:19814370G>A	Unknown		
CHC605T	g.chr1:200564080T>C	KIF14		
CHC605T	g.chr1:201361794G>C	LAD1		
CHC605T	g.chr1:201513085A>G	Unknown		
CHC605T	g.chr1:201533606G>T	Unknown		
CHC605T	g.chr1:201826350A>G	IPO9		
CHC605T	g.chr1:204095804T>G	SOX13		
CHC605T	g.chr1:208103677C>T	Unknown		
CHC605T	g.chr1:208271134C>T	PLXNA2		
CHC605T	g.chr1:209183971A>T	Unknown		
CHC605T	g.chr1:209224963T>A	Unknown		
CHC605T	g.chr1:213244183A>G	RPS6KC1		
CHC605T	g.chr1:215058264G>C	Unknown		
CHC605T	g.chr1:215168230T>C	Unknown		
CHC605T	g.chr1:215583596T>C	Unknown		
CHC605T	g.chr1:215598063A>T	Unknown		
CHC605T	g.chr1:216945192T>A	ESRRG		
CHC605T	g.chr1:217174470G>T	ESRRG		
CHC605T	g.chr1:218668724G>T	Unknown		
CHC605T	g.chr1:218714500G>A	Unknown		
CHC605T	g.chr1:220648015C>T	Unknown		
CHC605T	g.chr1:220905599A>G	Unknown		
CHC605T	g.chr1:222355436A>T	RP11-400N13.1		
CHC605T	g.chr1:222363666C>T	RP11-400N13.1		
CHC605T	g.chr1:222471875A>G	RP11-400N13.1		
CHC605T	g.chr1:227723604T>C	Unknown		
CHC605T	g.chr1:227747404C>T	Unknown		
CHC605T	g.chr1:228990801C>A	Unknown		
CHC605T	g.chr1:229632498G>C	NUP133		
CHC605T	g.chr1:23308137G>T	Unknown		
CHC605T	g.chr1:23494303G>C	LUZP1		
CHC605T	g.chr1:235461011C>A	ARID4B		
CHC605T	g.chr1:237112897C>T	Unknown		
CHC605T	g.chr1:238786813T>C	Unknown		
CHC605T	g.chr1:239150974T>A	Unknown		
CHC605T	g.chr1:239847144C>A	CHRM3		
CHC605T	g.chr1:242857686A>G	Unknown		
CHC605T	g.chr1:247926739T>A	Unknown		
CHC605T	g.chr1:26739637A>T	LIN28A		
CHC605T	g.chr1:2707732G>A	TTC34		
CHC605T	g.chr1:30115119G>A	Unknown		
CHC605T	g.chr1:30670714A>G	Unknown		
CHC605T	g.chr1:31710132C>A	NKAIN1		
CHC605T	g.chr1:31737736C>T	SNRNP40		
CHC605T	g.chr1:34354748T>A	CSMD2		
CHC605T	g.chr1:35308342T>C	Unknown		
CHC605T	g.chr1:3533019C>T	Unknown		
CHC605T	g.chr1:36092724C>A	PSMB2		
CHC605T	g.chr1:3758295C>A	CEP104		
CHC605T	g.chr1:39064328A>C	Unknown		
CHC605T	g.chr1:39877706C>G	MACF1		
CHC605T	g.chr1:39932352G>A	MACF1		
CHC605T	g.chr1:42402405A>C	Unknown		
CHC605T	g.chr1:4697946C>G	Unknown		
CHC605T	g.chr1:47193593T>C	Unknown		
CHC605T	g.chr1:47353225T>A	CYP4Z2P		
CHC605T	g.chr1:47509444T>C	CYP4X1		
CHC605T	g.chr1:4778910G>T	AJAP1		
CHC605T	g.chr1:48476815T>C	Unknown		
CHC605T	g.chr1:49749721C>T	AGBL4		
CHC605T	g.chr1:50690622G>A	Unknown		
CHC605T	g.chr1:53303178G>A	Unknown		
CHC605T	g.chr1:55294874G>A	C1orf177		
CHC605T	g.chr1:5640543C>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr1:57049079C>T	Unknown		
CHC605T	g.chr1:60963697A>T	Unknown		
CHC605T	g.chr1:60967641G>A	Unknown		
CHC605T	g.chr1:6330524G>T	ACOT7		
CHC605T	g.chr1:67532503C>T	Unknown		
CHC605T	g.chr1:6811881T>G	Unknown		
CHC605T	g.chr1:68364832A>G	GNG12-AS1		
CHC605T	g.chr1:68633796G>T	WLS		
CHC605T	g.chr1:71897176G>A	NEGR1		
CHC605T	g.chr1:71990841A>G	NEGR1		
CHC605T	g.chr1:72140467C>T	NEGR1		
CHC605T	g.chr1:73068011T>C	Unknown		
CHC605T	g.chr1:74423719T>A	Unknown		
CHC605T	g.chr1:75381219G>A	Unknown		
CHC605T	g.chr1:75473691G>T	Unknown		
CHC605T	g.chr1:75480307C>G	Unknown		
CHC605T	g.chr1:77175620G>C	Unknown		
CHC605T	g.chr1:79363452C>G	ELTD1		
CHC605T	g.chr1:79435738A>T	ELTD1		
CHC605T	g.chr1:79858325T>C	Unknown		
CHC605T	g.chr1:81366421G>A	Unknown		
CHC605T	g.chr1:81669123G>T	Unknown		
CHC605T	g.chr1:83525488G>A	RP4-601K24.1		
CHC605T	g.chr1:86307795C>T	COL24A1	c.3526G>A	p.G1176S
CHC605T	g.chr1:86604123A>G	COL24A1		
CHC605T	g.chr1:88478795A>G	Unknown		
CHC605T	g.chr1:93851404T>C	Unknown		
CHC605T	g.chr1:96072962G>A	Unknown		
CHC605T	g.chr1:99180428G>A	SNX7		
CHC605T	g.chr10:100083042G>T	Unknown		
CHC605T	g.chr10:101436486C>T	ENTPD7		
CHC605T	g.chr10:105894131G>A	WDR96		
CHC605T	g.chr10:106653336C>G	SORCS3		
CHC605T	g.chr10:106695054T>C	SORCS3		
CHC605T	g.chr10:107010086G>A	SORCS3		
CHC605T	g.chr10:107302179A>T	Unknown		
CHC605T	g.chr10:109365453T>C	Unknown		
CHC605T	g.chr10:109484173C>A	Unknown		
CHC605T	g.chr10:109803361C>A	RP11-215N21.1		
CHC605T	g.chr10:110117063T>C	Unknown		
CHC605T	g.chr10:112005603T>C	MX11		
CHC605T	g.chr10:113033923A>G	Unknown		
CHC605T	g.chr10:11308625G>T	CELF2	c.510G>T	p.Q170H
CHC605T	g.chr10:115561043G>A	Unknown		
CHC605T	g.chr10:116815412T>C	Unknown		
CHC605T	g.chr10:119478737G>A	Unknown		
CHC605T	g.chr10:120267969A>G	Unknown		
CHC605T	g.chr10:120537472C>A	Unknown		
CHC605T	g.chr10:120773472C>A	Unknown		
CHC605T	g.chr10:121806044G>T	Unknown		
CHC605T	g.chr10:122048073T>G	Unknown		
CHC605T	g.chr10:122195114C>A	Unknown		
CHC605T	g.chr10:122425070C>T	Unknown		
CHC605T	g.chr10:122527477C>T	WDR11-AS1		
CHC605T	g.chr10:124256033T>C	HTRA1		
CHC605T	g.chr10:1244540G>A	ADARB2		
CHC605T	g.chr10:125047525A>G	Unknown		
CHC605T	g.chr10:125189130C>A	RP11-2821.1		
CHC605T	g.chr10:126317776G>A	FAM53B		
CHC605T	g.chr10:12650547G>A	CAMK1D		
CHC605T	g.chr10:127681744A>G	FANK1		
CHC605T	g.chr10:128008535C>T	ADAM12		
CHC605T	g.chr10:128410796T>C	Unknown		
CHC605T	g.chr10:130542187T>A	Unknown		
CHC605T	g.chr10:133002202G>T	TCERG1L		
CHC605T	g.chr10:134955098G>A	Unknown		
CHC605T	g.chr10:14976166A>T	DCLRE1C		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr10:20311194G>A	PLXDC2		
CHC605T	g.chr10:2235295C>T	Unknown		
CHC605T	g.chr10:22774203C>A	Unknown		
CHC605T	g.chr10:2366544G>C	Unknown		
CHC605T	g.chr10:24241219G>T	KIAA1217		
CHC605T	g.chr10:2486479A>G	Unknown		
CHC605T	g.chr10:26419825T>A	MYO3A		
CHC605T	g.chr10:26986293T>C	Unknown		
CHC605T	g.chr10:2983941G>A	Unknown		
CHC605T	g.chr10:32228345A>G	Unknown		
CHC605T	g.chr10:37925109C>A	Unknown		
CHC605T	g.chr10:38627126C>T	Unknown		
CHC605T	g.chr10:42621054G>A	Unknown		
CHC605T	g.chr10:43305005G>A	BMS1		
CHC605T	g.chr10:43497131C>T	Unknown		
CHC605T	g.chr10:46038085G>C	08-mars		
CHC605T	g.chr10:54430719A>G	RP11-556E13.1		
CHC605T	g.chr10:55100141G>A	Unknown		
CHC605T	g.chr10:57698814C>A	Unknown		
CHC605T	g.chr10:5879923T>C	Unknown		
CHC605T	g.chr10:62091012T>G	ANK3		
CHC605T	g.chr10:62134415C>A	ANK3		
CHC605T	g.chr10:63465839C>A	C10orf107		
CHC605T	g.chr10:65811470T>G	Unknown		
CHC605T	g.chr10:65838693T>C	Unknown		
CHC605T	g.chr10:66332242T>C	Unknown		
CHC605T	g.chr10:68792100A>C	CTNNA3		
CHC605T	g.chr10:72687067A>T	Unknown		
CHC605T	g.chr10:72816099G>C	Unknown		
CHC605T	g.chr10:73007347C>T	UNC5B		
CHC605T	g.chr10:7374763G>A	SFMBT2		
CHC605T	g.chr10:77418802C>T	C10orf11		
CHC605T	g.chr10:79494144T>C	Unknown		
CHC605T	g.chr10:8044914A>T	TAF3		
CHC605T	g.chr10:84507366T>G	NRG3		
CHC605T	g.chr10:85294232C>A	Unknown		
CHC605T	g.chr10:88251263C>A	WAPAL		
CHC605T	g.chr10:91913793C>A	Unknown		
CHC605T	g.chr10:92490365C>T	Unknown		
CHC605T	g.chr10:98463567A>C	PIK3AP1		
CHC605T	g.chr11:100319419G>A	Unknown		
CHC605T	g.chr11:10067077T>G	SBF2		
CHC605T	g.chr11:103660610C>T	RP11-563P16.1		
CHC605T	g.chr11:104544281T>C	Unknown		
CHC605T	g.chr11:105174304T>A	RP11-94P11.4		
CHC605T	g.chr11:105629067C>A	GRIA4		
CHC605T	g.chr11:107796709A>C	SLC35F2		
CHC605T	g.chr11:109326921A>G	RP11-708B6.2		
CHC605T	g.chr11:110925036C>T	Unknown		
CHC605T	g.chr11:113391718G>A	Unknown		
CHC605T	g.chr11:115038910C>A	Unknown		
CHC605T	g.chr11:117345240G>T	DSCAML1		
CHC605T	g.chr11:118493473G>T	PHLDB1		
CHC605T	g.chr11:119574493T>G	PVRL1		
CHC605T	g.chr11:12053392G>A	RP13-631K18.2		
CHC605T	g.chr11:126699800C>T	KIRREL3		
CHC605T	g.chr11:129467064T>C	Unknown		
CHC605T	g.chr11:130286356G>A	ADAMTS8		
CHC605T	g.chr11:131322129C>T	NTM		
CHC605T	g.chr11:131449806A>G	NTM		
CHC605T	g.chr11:132068932G>A	NTM		
CHC605T	g.chr11:132119583A>T	NTM		
CHC605T	g.chr11:133022927G>T	OPCML		
CHC605T	g.chr11:133291961C>T	OPCML		
CHC605T	g.chr11:13921969G>A	Unknown		
CHC605T	g.chr11:14971740G>T	CALCB		
CHC605T	g.chr11:15021718T>A	CALCB		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr11:17070160T>C	OR7E14P		
CHC605T	g.chr11:17620153G>A	OTOG		
CHC605T	g.chr11:17670062C>T	Unknown		
CHC605T	g.chr11:18195553T>C	MRGPRX4	c.750T>C	p.Y250Y
CHC605T	g.chr11:18332908C>A	HPS5		
CHC605T	g.chr11:20322109G>T	Unknown		
CHC605T	g.chr11:21503777C>G	NELL1		
CHC605T	g.chr11:23693731G>T	Unknown		
CHC605T	g.chr11:23747210A>G	Unknown		
CHC605T	g.chr11:26304791C>T	ANO3		
CHC605T	g.chr11:32206342G>T	Unknown		
CHC605T	g.chr11:34376131G>T	ABTB2		
CHC605T	g.chr11:36363450G>C	PRR5L		
CHC605T	g.chr11:37296812G>A	Unknown		
CHC605T	g.chr11:39170215C>A	Unknown		
CHC605T	g.chr11:39608926T>C	Unknown		
CHC605T	g.chr11:39866507G>A	Unknown		
CHC605T	g.chr11:42382952G>A	Unknown		
CHC605T	g.chr11:48558356T>A	Unknown		
CHC605T	g.chr11:50240170G>A	Unknown		
CHC605T	g.chr11:51464199G>T	Unknown		
CHC605T	g.chr11:5185221T>C	OR52A1		
CHC605T	g.chr11:5251884G>A	Unknown		
CHC605T	g.chr11:55100212C>A	Unknown		
CHC605T	g.chr11:55889957C>A	OR8H3	c.109C>A	p.L37I
CHC605T	g.chr11:55970415A>G	Unknown		
CHC605T	g.chr11:56738807C>A	Unknown		
CHC605T	g.chr11:5846655C>A	TRIM5		
CHC605T	g.chr11:58556634A>G	Unknown		
CHC605T	g.chr11:60697847T>C	TMEM132A		
CHC605T	g.chr11:60998388C>T	PGA4		
CHC605T	g.chr11:64247473C>A	Unknown		
CHC605T	g.chr11:66639651C>T	PC		
CHC605T	g.chr11:69013037G>A	Unknown		
CHC605T	g.chr11:71367684T>C	Unknown		
CHC605T	g.chr11:73251130T>C	FAM168A		
CHC605T	g.chr11:7776144G>A	RP11-35J10.5		
CHC605T	g.chr11:81182626A>T	Unknown		
CHC605T	g.chr11:82208320A>G	Unknown		
CHC605T	g.chr11:82395332A>T	Unknown		
CHC605T	g.chr11:8746638T>C	ST5		
CHC605T	g.chr11:9004024G>A	NRIP3		
CHC605T	g.chr11:90469014G>T	DISC1FP1		
CHC605T	g.chr11:92610079G>A	FAT3		
CHC605T	g.chr11:93625453G>A	Unknown		
CHC605T	g.chr11:96177255T>A	JRKL		
CHC605T	g.chr11:96212739C>T	JRKL		
CHC605T	g.chr11:96499416G>A	RP11-360K13.1		
CHC605T	g.chr11:96919525T>A	Unknown		
CHC605T	g.chr11:99734991T>A	CNTN5		
CHC605T	g.chr12:100289974A>C	ANKS1B		
CHC605T	g.chr12:108096594T>C	PWP1		
CHC605T	g.chr12:108832777G>T	RP11-13G14.4		
CHC605T	g.chr12:110115957A>G	Unknown		
CHC605T	g.chr12:113050562A>G	RPH3A		
CHC605T	g.chr12:113809573G>A	PLBD2		
CHC605T	g.chr12:115808206G>T	Unknown		
CHC605T	g.chr12:117880333T>C	NOS1		
CHC605T	g.chr12:11926611A>G	ETV6		
CHC605T	g.chr12:123476487C>G	PITPNM2		
CHC605T	g.chr12:125058185T>C	Unknown		
CHC605T	g.chr12:12833393A>T	GPR19		
CHC605T	g.chr12:12885733A>C	APOLD1		
CHC605T	g.chr12:130110233T>A	TMEM132D		
CHC605T	g.chr12:130355972G>T	TMEM132D		
CHC605T	g.chr12:130419026G>T	Unknown		
CHC605T	g.chr12:131058357G>A	RIMBP2		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr12:13162546A>G	RP11-377D9.3		
CHC605T	g.chr12:133183595C>T	Unknown		
CHC605T	g.chr12:15449034T>C	Unknown		
CHC605T	g.chr12:17464532A>T	Unknown		
CHC605T	g.chr12:18159871T>C	Unknown		
CHC605T	g.chr12:18978335G>A	Unknown		
CHC605T	g.chr12:19500288G>T	PLEKHA5		
CHC605T	g.chr12:25460248C>A	Unknown		
CHC605T	g.chr12:25630739A>G	IFLTD1		
CHC605T	g.chr12:26315489T>C	SSPN		
CHC605T	g.chr12:2710304G>T	CACNA1C		
CHC605T	g.chr12:29414920G>A	FAR2		
CHC605T	g.chr12:30075517C>A	Unknown		
CHC605T	g.chr12:31545689T>C	DENND5B		
CHC605T	g.chr12:32694766G>A	FGD4		
CHC605T	g.chr12:33172832C>A	Unknown		
CHC605T	g.chr12:38482929C>T	Unknown		
CHC605T	g.chr12:43281113C>A	Unknown		
CHC605T	g.chr12:43782975A>G	ADAMTS20		
CHC605T	g.chr12:44484680G>T	TMEM117		
CHC605T	g.chr12:47255846C>T	Unknown		
CHC605T	g.chr12:48015171C>T	Unknown		
CHC605T	g.chr12:48525733G>A	PFKM		
CHC605T	g.chr12:52427526G>A	NR4A1		
CHC605T	g.chr12:52589932C>T	Unknown		
CHC605T	g.chr12:53664979A>G	ESPL1		
CHC605T	g.chr12:55299834T>C	Unknown		
CHC605T	g.chr12:55319392T>C	Unknown		
CHC605T	g.chr12:55432463G>A	Unknown		
CHC605T	g.chr12:56162491C>T	RP11-762I7.5		
CHC605T	g.chr12:5917604C>T	ANO2		
CHC605T	g.chr12:60658663T>A	Unknown		
CHC605T	g.chr12:60971452G>A	Unknown		
CHC605T	g.chr12:61519388T>C	Unknown		
CHC605T	g.chr12:62183904C>A	FAM19A2		
CHC605T	g.chr12:62245668G>A	FAM19A2		
CHC605T	g.chr12:64335837C>T	SRGAP1		
CHC605T	g.chr12:66428283C>A	Unknown		
CHC605T	g.chr12:66781415A>G	GRIP1		
CHC605T	g.chr12:66952361A>G	GRIP1		
CHC605T	g.chr12:67447881C>T	RP11-123O10.3		
CHC605T	g.chr12:71374288G>T	Unknown		
CHC605T	g.chr12:71374289A>T	Unknown		
CHC605T	g.chr12:72924624G>A	TRHDE		
CHC605T	g.chr12:74145210G>A	Unknown		
CHC605T	g.chr12:74304416T>C	RP11-711C17.1		
CHC605T	g.chr12:74435005A>C	RP11-711C17.2		
CHC605T	g.chr12:7462109G>A	ACSM4		
CHC605T	g.chr12:75014561A>T	Unknown		
CHC605T	g.chr12:78854764G>A	RP11-754N21.1		
CHC605T	g.chr12:79310870C>T	SYT1		
CHC605T	g.chr12:82218298G>A	Unknown		
CHC605T	g.chr12:84142026C>T	Unknown		
CHC605T	g.chr12:85720662C>A	RP11-408B11.2		
CHC605T	g.chr12:86710622C>T	MGAT4C		
CHC605T	g.chr12:87840126T>A	Unknown		
CHC605T	g.chr12:88376933C>T	C12orf50	c.1166G>A	p.R389Q
CHC605T	g.chr12:89116426T>A	Unknown		
CHC605T	g.chr12:89360559G>A	Unknown		
CHC605T	g.chr12:89749655G>T	Unknown		
CHC605T	g.chr12:89749656T>G	Unknown		
CHC605T	g.chr12:9002037C>A	A2ML1		
CHC605T	g.chr12:91346286G>A	CCER1		
CHC605T	g.chr12:91626615T>C	Unknown		
CHC605T	g.chr12:9623436A>T	Unknown		
CHC605T	g.chr12:99697427A>G	ANKS1B		
CHC605T	g.chr13:104377815A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr13:105061354A>G	Unknown		
CHC605T	g.chr13:105173217G>A	Unknown		
CHC605T	g.chr13:105500360C>T	Unknown		
CHC605T	g.chr13:106336438C>T	Unknown		
CHC605T	g.chr13:111977576G>A	TEX29		
CHC605T	g.chr13:112988758T>A	Unknown		
CHC605T	g.chr13:113492682G>A	ATP11A		
CHC605T	g.chr13:24788258C>G	RP11-307N16.6		
CHC605T	g.chr13:25246000C>A	Unknown		
CHC605T	g.chr13:26180000T>C	ATP8A2		
CHC605T	g.chr13:34421211G>A	RFC3		
CHC605T	g.chr13:38340422C>T	TRPC4		
CHC605T	g.chr13:46808781A>T	LRR63		
CHC605T	g.chr13:52454924C>A	Unknown		
CHC605T	g.chr13:52693715A>G	NEK5		
CHC605T	g.chr13:52800905A>T	RP11-248G5.8		
CHC605T	g.chr13:53762613A>T	Unknown		
CHC605T	g.chr13:54589263T>A	Unknown		
CHC605T	g.chr13:54589270G>T	Unknown		
CHC605T	g.chr13:55466347G>T	Unknown		
CHC605T	g.chr13:55531572G>A	Unknown		
CHC605T	g.chr13:56012259T>C	Unknown		
CHC605T	g.chr13:58616204T>C	Unknown		
CHC605T	g.chr13:58744346G>T	Unknown		
CHC605T	g.chr13:58755850C>A	Unknown		
CHC605T	g.chr13:61583741G>A	Unknown		
CHC605T	g.chr13:62279777T>A	Unknown		
CHC605T	g.chr13:62579992C>A	LINC00358		
CHC605T	g.chr13:62604797T>C	Unknown		
CHC605T	g.chr13:63518902C>T	Unknown		
CHC605T	g.chr13:63518903C>A	Unknown		
CHC605T	g.chr13:64763950T>C	Unknown		
CHC605T	g.chr13:66108567T>C	Unknown		
CHC605T	g.chr13:66980801C>T	PCDH9		
CHC605T	g.chr13:68731683T>C	Unknown		
CHC605T	g.chr13:71002719G>C	Unknown		
CHC605T	g.chr13:71076593C>A	Unknown		
CHC605T	g.chr13:71211069G>A	Unknown		
CHC605T	g.chr13:71422924A>G	Unknown		
CHC605T	g.chr13:72147374T>C	DACH1		
CHC605T	g.chr13:72231856C>A	DACH1		
CHC605T	g.chr13:72537574T>C	Unknown		
CHC605T	g.chr13:72638415T>C	Unknown		
CHC605T	g.chr13:73204862G>A	Unknown		
CHC605T	g.chr13:77004965C>A	Unknown		
CHC605T	g.chr13:77276338G>A	Unknown		
CHC605T	g.chr13:77959093C>T	Unknown		
CHC605T	g.chr13:78356987A>G	Unknown		
CHC605T	g.chr13:82715576T>C	Unknown		
CHC605T	g.chr13:83358692C>A	Unknown		
CHC605T	g.chr13:87154500G>T	Unknown		
CHC605T	g.chr13:87852951A>G	Unknown		
CHC605T	g.chr13:88315123C>T	MIR4500HG		
CHC605T	g.chr13:88386777T>C	Unknown		
CHC605T	g.chr13:90868307C>T	Unknown		
CHC605T	g.chr13:91113078C>T	Unknown		
CHC605T	g.chr13:92669442C>T	GPC5		
CHC605T	g.chr13:93616670C>A	Unknown		
CHC605T	g.chr13:97447796A>G	HS6ST3		
CHC605T	g.chr13:97508164C>T	Unknown		
CHC605T	g.chr14:100325622G>A	EML1		
CHC605T	g.chr14:100470476G>A	EVL		
CHC605T	g.chr14:102964283C>T	TECPR2		
CHC605T	g.chr14:106431227G>T	Unknown		
CHC605T	g.chr14:106431228G>T	Unknown		
CHC605T	g.chr14:107002829T>C	Unknown		
CHC605T	g.chr14:21419701G>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr14:22501386C>T	Unknown		
CHC605T	g.chr14:25766131C>T	Unknown		
CHC605T	g.chr14:27425867A>T	RP11-384J4.2		
CHC605T	g.chr14:27627997C>T	RP11-384J4.2		
CHC605T	g.chr14:27636437C>A	Unknown		
CHC605T	g.chr14:29937820T>C	Unknown		
CHC605T	g.chr14:33877064C>T	NPAS3		
CHC605T	g.chr14:33936455T>C	NPAS3		
CHC605T	g.chr14:34182674G>T	NPAS3		
CHC605T	g.chr14:35866800T>C	Unknown		
CHC605T	g.chr14:35945853G>A	Unknown		
CHC605T	g.chr14:38063216C>T	FOXA1		
CHC605T	g.chr14:38848187G>A	Unknown		
CHC605T	g.chr14:38848188C>A	Unknown		
CHC605T	g.chr14:38972382A>T	Unknown		
CHC605T	g.chr14:39130696T>A	Unknown		
CHC605T	g.chr14:41227716A>T	Unknown		
CHC605T	g.chr14:41669929G>A	Unknown		
CHC605T	g.chr14:42000844A>G	Unknown		
CHC605T	g.chr14:42689728C>T	Unknown		
CHC605T	g.chr14:43084388T>A	CTD-2307P3.1		
CHC605T	g.chr14:43168177G>A	CTD-2307P3.1		
CHC605T	g.chr14:47408776T>A	MDGA2		
CHC605T	g.chr14:47760640C>A	MDGA2		
CHC605T	g.chr14:48124104G>T	MDGA2		
CHC605T	g.chr14:48165531T>C	Unknown		
CHC605T	g.chr14:49923683A>C	Unknown		
CHC605T	g.chr14:50454045A>T	C14orf182		
CHC605T	g.chr14:52343032T>G	GNG2		
CHC605T	g.chr14:53503627T>C	RP11-368P15.3		
CHC605T	g.chr14:54583820T>G	Unknown		
CHC605T	g.chr14:59765890T>G	DAAM1		
CHC605T	g.chr14:59837956A>C	DAAM1		
CHC605T	g.chr14:60049299G>A	Unknown		
CHC605T	g.chr14:60277455A>G	RTN1		
CHC605T	g.chr14:60964445T>A	Unknown		
CHC605T	g.chr14:61225036A>C	MNAT1		
CHC605T	g.chr14:62482315A>G	SYT16		
CHC605T	g.chr14:62764115G>A	Unknown		
CHC605T	g.chr14:62856791G>A	Unknown		
CHC605T	g.chr14:64415724G>C	SYNE2		
CHC605T	g.chr14:64480446A>T	SYNE2		
CHC605T	g.chr14:65482320T>G	FNTB		
CHC605T	g.chr14:65757198T>A	CTD-2509G16.5		
CHC605T	g.chr14:67137170C>G	GPHN		
CHC605T	g.chr14:67777748G>T	MPP5		
CHC605T	g.chr14:68198248A>G	RDH12		
CHC605T	g.chr14:70587369C>G	SLC8A3		
CHC605T	g.chr14:71940145A>G	Unknown		
CHC605T	g.chr14:72673339T>C	RGS6		
CHC605T	g.chr14:74284910C>G	Unknown		
CHC605T	g.chr14:79209455A>T	NRXN3		
CHC605T	g.chr14:79794409T>A	NRXN3		
CHC605T	g.chr14:79794410G>T	NRXN3		
CHC605T	g.chr14:80542820T>C	Unknown		
CHC605T	g.chr14:81963069C>T	SEL1L		
CHC605T	g.chr14:82388179C>A	RP11-666E17.1		
CHC605T	g.chr14:83460694T>A	Unknown		
CHC605T	g.chr14:83779693C>T	Unknown		
CHC605T	g.chr14:84232746G>T	Unknown		
CHC605T	g.chr14:85035335A>G	Unknown		
CHC605T	g.chr14:85922141A>G	CTD-2128A3.2		
CHC605T	g.chr14:86046253T>C	FLRT2		
CHC605T	g.chr14:86229174T>C	Unknown		
CHC605T	g.chr14:90646399G>A	KCNK13		
CHC605T	g.chr14:91017464C>A	TTC7B		
CHC605T	g.chr14:91972841C>T	SMEK1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr14:92573214G>A	Unknown		
CHC605T	g.chr14:94259371G>C	Unknown		
CHC605T	g.chr14:98044324T>C	Unknown		
CHC605T	g.chr14:98164038C>T	Unknown		
CHC605T	g.chr14:98445541A>G	Unknown		
CHC605T	g.chr15:100019655G>C	MEF2A		
CHC605T	g.chr15:101969223G>C	PCSK6		
CHC605T	g.chr15:20226397G>A	Unknown		
CHC605T	g.chr15:23176092T>A	Unknown		
CHC605T	g.chr15:23855299G>A	MKRN3		
CHC605T	g.chr15:23890891G>C	MAGEL2	c.190C>G	p.Q64E
CHC605T	g.chr15:24167592A>G	RP11-484P15.1		
CHC605T	g.chr15:24332825A>T	Unknown		
CHC605T	g.chr15:24343823A>G	Unknown		
CHC605T	g.chr15:24473954G>T	Unknown		
CHC605T	g.chr15:25358540A>T	SNHG14		
CHC605T	g.chr15:27812567A>G	Unknown		
CHC605T	g.chr15:28098376A>G	OCA2		
CHC605T	g.chr15:28886335G>T	Unknown		
CHC605T	g.chr15:29235951G>A	APBA2		
CHC605T	g.chr15:29453287G>A	FAM189A1		
CHC605T	g.chr15:29558319C>T	FAM189A1		
CHC605T	g.chr15:32403975T>G	CHRNA7		
CHC605T	g.chr15:33847722G>A	RYR3		
CHC605T	g.chr15:40763216C>G	CHST14		
CHC605T	g.chr15:41371368G>A	INO80		
CHC605T	g.chr15:45186356C>A	Unknown		
CHC605T	g.chr15:45400755C>T	DUOX2		
CHC605T	g.chr15:46072349A>G	RP11-718O11.1		
CHC605T	g.chr15:51084741T>A	Unknown		
CHC605T	g.chr15:51730841T>A	RP11-707P17.1		
CHC605T	g.chr15:53664405G>T	Unknown		
CHC605T	g.chr15:53664406C>T	Unknown		
CHC605T	g.chr15:53822537C>T	WDR72		
CHC605T	g.chr15:56720439G>A	TEX9		
CHC605T	g.chr15:58628312G>T	Unknown		
CHC605T	g.chr15:61095989T>C	RORA		
CHC605T	g.chr15:65781925T>C	DPP8		
CHC605T	g.chr15:65986925A>G	DENND4A		
CHC605T	g.chr15:66444741A>T	MEGF11		
CHC605T	g.chr15:70325532G>A	Unknown		
CHC605T	g.chr15:71728544G>A	THSD4		
CHC605T	g.chr15:73768444A>G	C15orf60		
CHC605T	g.chr15:76610332G>A	Unknown		
CHC605T	g.chr15:77182191C>A	SCAPER		
CHC605T	g.chr15:77666126A>T	PEAK1		
CHC605T	g.chr15:80957348G>T	Unknown		
CHC605T	g.chr15:86312352G>A	KLHL25	c.690C>T	p.P230P
CHC605T	g.chr15:88180135G>T	RP11-648K4.2		
CHC605T	g.chr15:88560007G>A	NTRK3		
CHC605T	g.chr15:90645329G>C	IDH2		
CHC605T	g.chr15:91184306C>T	CRTC3		
CHC605T	g.chr15:91283730G>A	BLM		
CHC605T	g.chr15:93517981T>G	CHD2		
CHC605T	g.chr15:94621924G>C	CTD-2643K12.3		
CHC605T	g.chr15:95243346T>C	Unknown		
CHC605T	g.chr15:99955489C>T	Unknown		
CHC605T	g.chr16:11599188T>C	Unknown		
CHC605T	g.chr16:13139806G>T	SHISA9		
CHC605T	g.chr16:16343998C>A	NOMO3		
CHC605T	g.chr16:18666977A>T	Unknown		
CHC605T	g.chr16:19131685C>T	ITPR1PL2		
CHC605T	g.chr16:19322202G>T	CLEC19A		
CHC605T	g.chr16:21646219A>G	METTL9		
CHC605T	g.chr16:23692768A>C	PLK1		
CHC605T	g.chr16:25408553A>G	Unknown		
CHC605T	g.chr16:26306611G>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr16:26440543T>C	Unknown		
CHC605T	g.chr16:2645617G>T	PDPK1		
CHC605T	g.chr16:29275520C>A	RP11-426C22.6		
CHC605T	g.chr16:31309721C>T	ITGAM		
CHC605T	g.chr16:32915578G>C	Unknown		
CHC605T	g.chr16:34649510C>A	Unknown		
CHC605T	g.chr16:35019088C>T	Unknown		
CHC605T	g.chr16:47829060T>C	Unknown		
CHC605T	g.chr16:50056922C>A	Unknown		
CHC605T	g.chr16:58720807G>A	Unknown		
CHC605T	g.chr16:61074279G>A	Unknown		
CHC605T	g.chr16:61223543C>T	Unknown		
CHC605T	g.chr16:61264797C>A	Unknown		
CHC605T	g.chr16:6165395T>C	RBFOX1		
CHC605T	g.chr16:62653146G>A	Unknown		
CHC605T	g.chr16:6337766C>T	RBFOX1		
CHC605T	g.chr16:63519333C>A	Unknown		
CHC605T	g.chr16:64552565C>A	RP11-467L24.1		
CHC605T	g.chr16:65051681G>A	CDH11		
CHC605T	g.chr16:65705351G>A	Unknown		
CHC605T	g.chr16:6852147G>A	RBFOX1		
CHC605T	g.chr16:69804639G>T	WWP2		
CHC605T	g.chr16:7017306A>T	RBFOX1		
CHC605T	g.chr16:7017308G>T	RBFOX1		
CHC605T	g.chr16:73505787G>A	Unknown		
CHC605T	g.chr16:79474963T>C	Unknown		
CHC605T	g.chr16:80879305T>C	RP11-314O13.1		
CHC605T	g.chr16:84188187G>C	DNAAF1	c.358G>C	p.D120H
CHC605T	g.chr16:891711G>A	Unknown		
CHC605T	g.chr16:9561554A>G	RP11-418I22.2		
CHC605T	g.chr17:10205972C>G	MYH13		
CHC605T	g.chr17:11559528T>C	DNAH9		
CHC605T	g.chr17:11559530C>A	DNAH9		
CHC605T	g.chr17:12752385G>C	ARHGAP44		
CHC605T	g.chr17:17666714C>G	RAI1		
CHC605T	g.chr17:1770916G>C	RPA1		
CHC605T	g.chr17:19015884C>T	SNORD3D		
CHC605T	g.chr17:22107500C>A	Unknown		
CHC605T	g.chr17:29769514C>G	RAB11FIP4		
CHC605T	g.chr17:31563901G>A	ASIC2		
CHC605T	g.chr17:33690405C>A	SLFN11	c.422G>T	p.R141L
CHC605T	g.chr17:35483603T>C	ACACA		
CHC605T	g.chr17:36846731G>C	Unknown		
CHC605T	g.chr17:37515630C>A	FBXL20		
CHC605T	g.chr17:38416227A>G	WIPF2		
CHC605T	g.chr17:39901079G>A	JUP		
CHC605T	g.chr17:4040292G>C	ZZEF1		
CHC605T	g.chr17:41335283G>T	NBR1		
CHC605T	g.chr17:43462678C>T	Unknown		
CHC605T	g.chr17:44880288A>T	WNT3		
CHC605T	g.chr17:44941601C>G	WNT9B		
CHC605T	g.chr17:46385349T>A	SKAP1		
CHC605T	g.chr17:48365958A>T	Unknown		
CHC605T	g.chr17:48692243C>T	CACNA1G		
CHC605T	g.chr17:48830711A>G	LUC7L3		
CHC605T	g.chr17:51191578A>T	Unknown		
CHC605T	g.chr17:51193378C>T	Unknown		
CHC605T	g.chr17:51943421A>G	Unknown		
CHC605T	g.chr17:52431645C>T	Unknown		
CHC605T	g.chr17:53863057T>G	PCTP		
CHC605T	g.chr17:54823995G>C	Unknown		
CHC605T	g.chr17:55305151A>G	Unknown		
CHC605T	g.chr17:5699278G>T	WSCD1		
CHC605T	g.chr17:58682578C>T	PPM1D		
CHC605T	g.chr17:62771638C>T	hsa-mir-6080		
CHC605T	g.chr17:62771640C>G	hsa-mir-6080		
CHC605T	g.chr17:64666798G>A	PRKCA		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr17:68144016C>T	Unknown		
CHC605T	g.chr17:68629593A>C	Unknown		
CHC605T	g.chr17:68745154C>T	Unknown		
CHC605T	g.chr17:69488847T>A	Unknown		
CHC605T	g.chr17:70903937A>C	SLC39A11		
CHC605T	g.chr17:70909734T>C	SLC39A11		
CHC605T	g.chr17:75041042T>A	Unknown		
CHC605T	g.chr17:76416885G>T	PGS1		
CHC605T	g.chr17:77050075A>G	Unknown		
CHC605T	g.chr18:10140488A>T	RP11-419J16.1		
CHC605T	g.chr18:12229358G>A	Unknown		
CHC605T	g.chr18:13322554C>A	LDLRAD4		
CHC605T	g.chr18:13695326C>T	FAM210A		
CHC605T	g.chr18:19729190C>G	Unknown		
CHC605T	g.chr18:20955045C>A	TMEM241		
CHC605T	g.chr18:24007215G>T	Unknown		
CHC605T	g.chr18:25789964G>T	Unknown		
CHC605T	g.chr18:2912069T>C	EMILIN2		
CHC605T	g.chr18:2944600G>A	LPIN2		
CHC605T	g.chr18:31557494G>C	NOL4		
CHC605T	g.chr18:31817922T>C	Unknown		
CHC605T	g.chr18:32331620G>A	DTNA		
CHC605T	g.chr18:33687225C>T	Unknown		
CHC605T	g.chr18:34895708G>C	CELF4		
CHC605T	g.chr18:36539467G>A	Unknown		
CHC605T	g.chr18:37743020C>T	Unknown		
CHC605T	g.chr18:37774934G>A	Unknown		
CHC605T	g.chr18:39537286T>C	PIK3C3		
CHC605T	g.chr18:3980180A>G	DLGAP1		
CHC605T	g.chr18:40662703A>G	RIT2		
CHC605T	g.chr18:40967680G>A	Unknown		
CHC605T	g.chr18:43589834T>A	PSTPIP2		
CHC605T	g.chr18:44190168A>G	LOXHD1		
CHC605T	g.chr18:45033509G>C	RP11-157P23.2		
CHC605T	g.chr18:45879110G>A	ZBTB7C		
CHC605T	g.chr18:46653431T>C	DYM		
CHC605T	g.chr18:4757537G>A	Unknown		
CHC605T	g.chr18:4802966C>G	Unknown		
CHC605T	g.chr18:49450117G>A	Unknown		
CHC605T	g.chr18:49511118G>A	Unknown		
CHC605T	g.chr18:49604572C>T	Unknown		
CHC605T	g.chr18:49655306C>G	Unknown		
CHC605T	g.chr18:5086040G>C	Unknown		
CHC605T	g.chr18:5337530A>C	Unknown		
CHC605T	g.chr18:57400598C>T	Unknown		
CHC605T	g.chr18:58312100G>T	RP11-325K19.1		
CHC605T	g.chr18:58334797C>A	RP11-325K19.1		
CHC605T	g.chr18:58903239C>T	Unknown		
CHC605T	g.chr18:59358204A>G	RP11-879F14.1		
CHC605T	g.chr18:59726214A>C	PIGN		
CHC605T	g.chr18:61229010A>T	SERPINB12		
CHC605T	g.chr18:61738266A>G	Unknown		
CHC605T	g.chr18:62063576T>A	RP11-146N18.1		
CHC605T	g.chr18:62411931A>G	Unknown		
CHC605T	g.chr18:63205772G>A	Unknown		
CHC605T	g.chr18:66364234A>C	TMX3		
CHC605T	g.chr18:66974440A>G	Unknown		
CHC605T	g.chr18:70510047A>G	NETO1		
CHC605T	g.chr18:70572304A>G	Unknown		
CHC605T	g.chr18:73336042A>T	Unknown		
CHC605T	g.chr18:73825346T>C	Unknown		
CHC605T	g.chr18:73965654T>G	Unknown		
CHC605T	g.chr18:7410413G>A	Unknown		
CHC605T	g.chr18:75188487G>T	RP11-176N18.2		
CHC605T	g.chr18:75570048G>T	Unknown		
CHC605T	g.chr18:75699054G>T	Unknown		
CHC605T	g.chr18:76249564C>T	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr18:77555993C>T	RP11-154H12.3		
CHC605T	g.chr19:10061377G>A	Unknown		
CHC605T	g.chr19:11921376C>G	Unknown		
CHC605T	g.chr19:18040189G>A	Unknown		
CHC605T	g.chr19:19180925C>T	SLC25A42		
CHC605T	g.chr19:19451318G>T	MAU2		
CHC605T	g.chr19:20346659G>A	CTC-260E6.6		
CHC605T	g.chr19:22432538T>G	Unknown		
CHC605T	g.chr19:22969256G>T	Unknown		
CHC605T	g.chr19:23960383G>A	RPSAP58		
CHC605T	g.chr19:2703886C>G	Unknown		
CHC605T	g.chr19:28623092C>T	Unknown		
CHC605T	g.chr19:40538245T>C	ZNF780B		
CHC605T	g.chr19:40868317G>T	PLD3		
CHC605T	g.chr19:43242562T>C	PSG3		
CHC605T	g.chr19:43242563G>T	PSG3		
CHC605T	g.chr19:44169268G>A	PLAUR		
CHC605T	g.chr19:45417762G>A	APOC1		
CHC605T	g.chr19:46542344A>G	Unknown		
CHC605T	g.chr19:52944626G>T	ZNF534		
CHC605T	g.chr19:56489776A>G	NLRP8		
CHC605T	g.chr19:56725495C>T	Unknown		
CHC605T	g.chr19:627390G>A	POLRMT		
CHC605T	g.chr19:9336124G>T	Unknown		
CHC605T	g.chr2:101148175T>A	Unknown		
CHC605T	g.chr2:102456850A>G	MAP4K4		
CHC605T	g.chr2:106312358C>T	Unknown		
CHC605T	g.chr2:106747868A>G	UXS1		
CHC605T	g.chr2:107978496G>A	AC006227.1		
CHC605T	g.chr2:108793843T>C	AC019100.3		
CHC605T	g.chr2:111531197T>C	ACOXL		
CHC605T	g.chr2:112861725G>T	TMEM87B		
CHC605T	g.chr2:115162700G>T	Unknown		
CHC605T	g.chr2:118678313G>A	CCDC93		
CHC605T	g.chr2:122830112C>A	Unknown		
CHC605T	g.chr2:124028286T>A	Unknown		
CHC605T	g.chr2:124045849C>A	Unknown		
CHC605T	g.chr2:124045850C>G	Unknown		
CHC605T	g.chr2:124114993C>A	Unknown		
CHC605T	g.chr2:124202803A>G	Unknown		
CHC605T	g.chr2:124531887T>C	Unknown		
CHC605T	g.chr2:124947502C>T	CNTNAP5		
CHC605T	g.chr2:129391590A>T	Unknown		
CHC605T	g.chr2:129995500C>A	Unknown		
CHC605T	g.chr2:130230903A>C	Unknown		
CHC605T	g.chr2:132692978A>G	Unknown		
CHC605T	g.chr2:133187598T>C	GPR39		
CHC605T	g.chr2:133779008T>C	NCKAP5		
CHC605T	g.chr2:13441815T>C	Unknown		
CHC605T	g.chr2:136067386A>C	ZRANB3		
CHC605T	g.chr2:139296138A>G	SPOPL		
CHC605T	g.chr2:139768646A>G	Unknown		
CHC605T	g.chr2:140422037C>T	Unknown		
CHC605T	g.chr2:140526996G>A	Unknown		
CHC605T	g.chr2:141541265A>T	LRP1B		
CHC605T	g.chr2:142194450C>A	LRP1B		
CHC605T	g.chr2:142343920A>G	LRP1B		
CHC605T	g.chr2:14267760C>T	Unknown		
CHC605T	g.chr2:145417311T>G	Unknown		
CHC605T	g.chr2:145828701G>A	TEX41		
CHC605T	g.chr2:1459334G>A	TPO		
CHC605T	g.chr2:14935687A>T	Unknown		
CHC605T	g.chr2:15113513C>G	Unknown		
CHC605T	g.chr2:15317956C>A	NBAS		
CHC605T	g.chr2:15319026G>A	NBAS		
CHC605T	g.chr2:153620580A>G	Unknown		
CHC605T	g.chr2:153688646A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr2:154312690T>A	AC012501.2		
CHC605T	g.chr2:154722758G>T	Unknown		
CHC605T	g.chr2:155659618C>A	KCNJ3		
CHC605T	g.chr2:156433599T>A	Unknown		
CHC605T	g.chr2:157006037G>C	Unknown		
CHC605T	g.chr2:160013238T>C	TANC1		
CHC605T	g.chr2:16220580G>T	AC130710.1		
CHC605T	g.chr2:164604854C>T	Unknown		
CHC605T	g.chr2:165177879C>T	AC092684.1		
CHC605T	g.chr2:1665822G>T	PXDN		
CHC605T	g.chr2:171436499T>G	MYO3B		
CHC605T	g.chr2:17199285G>C	Unknown		
CHC605T	g.chr2:173472395C>G	PDK1		
CHC605T	g.chr2:17391129G>A	Unknown		
CHC605T	g.chr2:174873154T>C	Unknown		
CHC605T	g.chr2:175929165G>T	Unknown		
CHC605T	g.chr2:176986678G>A	HOXD-AS2		
CHC605T	g.chr2:178043775C>G	AC079305.8		
CHC605T	g.chr2:181220872T>G	Unknown		
CHC605T	g.chr2:182005379G>T	AC104820.2		
CHC605T	g.chr2:184219212A>T	Unknown		
CHC605T	g.chr2:184925465C>A	Unknown		
CHC605T	g.chr2:185523892C>T	ZNF804A		
CHC605T	g.chr2:185524264T>C	ZNF804A		
CHC605T	g.chr2:185898844G>T	Unknown		
CHC605T	g.chr2:186489600C>T	Unknown		
CHC605T	g.chr2:187976116G>A	AC007319.1		
CHC605T	g.chr2:188903731C>T	Unknown		
CHC605T	g.chr2:190614254C>T	OSGEPL1		
CHC605T	g.chr2:192693926G>T	Unknown		
CHC605T	g.chr2:193368894T>C	Unknown		
CHC605T	g.chr2:194129736G>A	Unknown		
CHC605T	g.chr2:195064186G>T	Unknown		
CHC605T	g.chr2:195848635C>T	Unknown		
CHC605T	g.chr2:196404727A>G	Unknown		
CHC605T	g.chr2:196698561C>A	DNAH7		
CHC605T	g.chr2:196822084A>G	DNAH7	c.2979T>C	p.I993I
CHC605T	g.chr2:200262968A>G	SATB2		
CHC605T	g.chr2:200411004C>A	Unknown		
CHC605T	g.chr2:201705452C>A	Unknown		
CHC605T	g.chr2:201960390C>A	Unknown		
CHC605T	g.chr2:203505997G>A	FAM117B		
CHC605T	g.chr2:205935121G>T	PARD3B		
CHC605T	g.chr2:209477295C>T	Unknown		
CHC605T	g.chr2:210548442G>A	MAP2		
CHC605T	g.chr2:211207681C>A	AC007970.1		
CHC605T	g.chr2:212773920C>T	ERBB4		
CHC605T	g.chr2:214067379G>T	Unknown		
CHC605T	g.chr2:218413767C>A	DIRC3		
CHC605T	g.chr2:219414775A>G	USP37		
CHC605T	g.chr2:220494992C>A	SLC4A3	c.729C>A	p.N243K
CHC605T	g.chr2:221290711A>G	AC114765.1		
CHC605T	g.chr2:222131534C>A	Unknown		
CHC605T	g.chr2:226305073T>G	NYAP2		
CHC605T	g.chr2:228863386T>C	SPHKAP		
CHC605T	g.chr2:230078731G>A	PID1		
CHC605T	g.chr2:231196225A>G	SP140L		
CHC605T	g.chr2:23865892G>A	KLHL29		
CHC605T	g.chr2:241721364C>T	KIF1A		
CHC605T	g.chr2:26793869G>T	C2orf70		
CHC605T	g.chr2:29161277T>A	WDR43		
CHC605T	g.chr2:29313184C>A	Unknown		
CHC605T	g.chr2:31419626A>G	CAPN14		
CHC605T	g.chr2:32724727A>G	BIRC6	c.8582A>G	p.E2861G
CHC605T	g.chr2:33055801G>A	LINC00486		
CHC605T	g.chr2:33128993G>T	LINC00486		
CHC605T	g.chr2:33753114C>T	RASGRP3		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr2:35510345A>G	Unknown		
CHC605T	g.chr2:35708689C>T	Unknown		
CHC605T	g.chr2:37385292A>G	Unknown		
CHC605T	g.chr2:38261872A>T	RMDN2		
CHC605T	g.chr2:41134470C>A	Unknown		
CHC605T	g.chr2:41762181C>A	Unknown		
CHC605T	g.chr2:48404834G>A	AC079807.4		
CHC605T	g.chr2:49685901G>T	Unknown		
CHC605T	g.chr2:51493854C>T	AC007682.1		
CHC605T	g.chr2:51554739T>C	AC007682.1		
CHC605T	g.chr2:56013056C>A	Unknown		
CHC605T	g.chr2:56081108G>A	Unknown		
CHC605T	g.chr2:56126670A>G	EFEMP1		
CHC605T	g.chr2:5761751C>A	AC108025.2		
CHC605T	g.chr2:59762277A>G	RP11-444A22.1		
CHC605T	g.chr2:59811815G>A	RP11-444A22.1		
CHC605T	g.chr2:63510542T>C	WDPCP		
CHC605T	g.chr2:64607231T>C	Unknown		
CHC605T	g.chr2:64788384C>G	AFTPH		
CHC605T	g.chr2:65340882G>T	RAB1A		
CHC605T	g.chr2:65933647A>C	Unknown		
CHC605T	g.chr2:66258063C>T	Unknown		
CHC605T	g.chr2:66577728G>T	Unknown		
CHC605T	g.chr2:67280448A>G	Unknown		
CHC605T	g.chr2:70575198G>A	Unknown		
CHC605T	g.chr2:71001381T>C	Unknown		
CHC605T	g.chr2:75933387T>C	GFCF2		
CHC605T	g.chr2:77928240G>T	Unknown		
CHC605T	g.chr2:78159331T>C	Unknown		
CHC605T	g.chr2:82926198A>G	Unknown		
CHC605T	g.chr2:84129707C>A	Unknown		
CHC605T	g.chr2:88733668G>T	Unknown		
CHC605T	g.chr2:95954724G>C	PROM2	c.2485G>C	p.V829L
CHC605T	g.chr2:966852G>T	SNTG2		
CHC605T	g.chr2:9834895G>A	RP11-521D12.2		
CHC605T	g.chr2:9834896G>C	RP11-521D12.2		
CHC605T	g.chr2:99812236A>G	MRPL30		
CHC605T	g.chr20:20919477G>T	Unknown		
CHC605T	g.chr20:23427886G>A	Unknown		
CHC605T	g.chr20:23675652G>A	Unknown		
CHC605T	g.chr20:23872480T>A	Unknown		
CHC605T	g.chr20:24122600T>C	Unknown		
CHC605T	g.chr20:29510637G>A	Unknown		
CHC605T	g.chr20:31784213C>T	BPIFA4P		
CHC605T	g.chr20:34719676G>T	EPB41L1		
CHC605T	g.chr20:34797975C>A	EPB41L1		
CHC605T	g.chr20:37453714G>T	PPP1R16B		
CHC605T	g.chr20:40359284C>G	Unknown		
CHC605T	g.chr20:41116839T>C	PTPRT		
CHC605T	g.chr20:41325072A>T	PTPRT		
CHC605T	g.chr20:41709972T>C	PTPRT		
CHC605T	g.chr20:42402696G>T	Unknown		
CHC605T	g.chr20:47712880T>A	CSE1L		
CHC605T	g.chr20:48001845C>A	KCNB1		
CHC605T	g.chr20:49417956C>G	BCAS4		
CHC605T	g.chr20:49668513G>C	Unknown		
CHC605T	g.chr20:50301764C>A	ATP9A		
CHC605T	g.chr20:53147063C>A	DOK5		
CHC605T	g.chr20:53441837C>T	Unknown		
CHC605T	g.chr20:53517736C>A	Unknown		
CHC605T	g.chr20:53995026G>T	Unknown		
CHC605T	g.chr20:54208113G>A	Unknown		
CHC605T	g.chr20:54303932A>G	Unknown		
CHC605T	g.chr20:58329454T>A	PHACTR3		
CHC605T	g.chr20:58391669G>T	PHACTR3		
CHC605T	g.chr20:58742713A>G	RP5-1043L13.1		
CHC605T	g.chr20:59141815T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr20:59707984C>T	Unknown		
CHC605T	g.chr20:60208307A>G	CDH4		
CHC605T	g.chr20:60239119G>A	CDH4		
CHC605T	g.chr20:60689907G>A	Unknown		
CHC605T	g.chr20:60863691G>T	OSBPL2		
CHC605T	g.chr20:62759366C>T	Unknown		
CHC605T	g.chr21:23220089C>A	Unknown		
CHC605T	g.chr21:23654152T>C	AP000705.7		
CHC605T	g.chr21:24717642T>A	Unknown		
CHC605T	g.chr21:25135765G>C	Unknown		
CHC605T	g.chr21:25508801C>T	Unknown		
CHC605T	g.chr21:28094062C>T	Unknown		
CHC605T	g.chr21:29072226C>A	Unknown		
CHC605T	g.chr21:33696724T>C	URB1		
CHC605T	g.chr21:36707295C>A	Unknown		
CHC605T	g.chr21:38497513G>A	TTC3		
CHC605T	g.chr21:39914821T>A	ERG		
CHC605T	g.chr21:40558725T>A	BRWD1		
CHC605T	g.chr21:42848000C>G	TMPRSS2		
CHC605T	g.chr21:44603137G>T	Unknown		
CHC605T	g.chr21:47567670G>T	FTCD		
CHC605T	g.chr22:18525678A>G	Unknown		
CHC605T	g.chr22:20990830G>A	SMPD4P1		
CHC605T	g.chr22:21247089G>T	Unknown		
CHC605T	g.chr22:22930774C>G	IGLV2-33		
CHC605T	g.chr22:23105711C>T	Unknown		
CHC605T	g.chr22:29776113T>C	AP1B1		
CHC605T	g.chr22:30794107G>T	SEC14L2		
CHC605T	g.chr22:31024730A>T	Unknown		
CHC605T	g.chr22:31406539A>C	Unknown		
CHC605T	g.chr22:32144765C>A	PRR14L		
CHC605T	g.chr22:32347438G>T	YWHAH		
CHC605T	g.chr22:34811292A>T	Unknown		
CHC605T	g.chr22:34999752C>T	Unknown		
CHC605T	g.chr22:35535206A>G	CTA-714B7.5		
CHC605T	g.chr22:36488515T>C	Unknown		
CHC605T	g.chr22:38277325T>G	EIF3L		
CHC605T	g.chr22:38556325T>C	PLA2G6		
CHC605T	g.chr22:49600988A>G	Unknown		
CHC605T	g.chr3:100734556A>C	Unknown		
CHC605T	g.chr3:102017814G>C	ZPLD1		
CHC605T	g.chr3:103177866C>G	Unknown		
CHC605T	g.chr3:103419360C>A	Unknown		
CHC605T	g.chr3:103419376A>T	Unknown		
CHC605T	g.chr3:103953465T>C	Unknown		
CHC605T	g.chr3:104031087G>A	Unknown		
CHC605T	g.chr3:10819740G>T	Unknown		
CHC605T	g.chr3:10819741T>A	Unknown		
CHC605T	g.chr3:11079492G>T	SLC6A1		
CHC605T	g.chr3:112156220T>C	Unknown		
CHC605T	g.chr3:113959645G>A	Unknown		
CHC605T	g.chr3:11518587G>T	ATG7		
CHC605T	g.chr3:115721625A>G	LSAMP		
CHC605T	g.chr3:116368083T>A	LSAMP		
CHC605T	g.chr3:117593872C>G	LSAMP		
CHC605T	g.chr3:118548159C>T	Unknown		
CHC605T	g.chr3:118701313C>A	IGSF11		
CHC605T	g.chr3:119055751G>T	ARHGAP31		
CHC605T	g.chr3:121943517C>T	CASR		
CHC605T	g.chr3:127758892G>A	Unknown		
CHC605T	g.chr3:130265191G>A	Unknown		
CHC605T	g.chr3:135206239G>T	Unknown		
CHC605T	g.chr3:137681702A>G	Unknown		
CHC605T	g.chr3:140069301G>T	CLSTN2		
CHC605T	g.chr3:141152794T>C	ZBTB38		
CHC605T	g.chr3:144181621C>A	Unknown		
CHC605T	g.chr3:145352850A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr3:146791901C>A	RP11-649A16.1		
CHC605T	g.chr3:148611505T>A	CPA3		
CHC605T	g.chr3:150599947G>C	FAM188B2		
CHC605T	g.chr3:1506045G>A	Unknown		
CHC605T	g.chr3:153021808A>G	Unknown		
CHC605T	g.chr3:154025210A>G	DHX36		
CHC605T	g.chr3:157781099C>T	RP11-290K4.2		
CHC605T	g.chr3:159751523C>G	IL12A-AS1		
CHC605T	g.chr3:160884574A>G	Unknown		
CHC605T	g.chr3:161763837T>A	Unknown		
CHC605T	g.chr3:161861050T>C	Unknown		
CHC605T	g.chr3:161908356G>A	Unknown		
CHC605T	g.chr3:162411879G>A	Unknown		
CHC605T	g.chr3:162899098C>A	RP11-10022.1		
CHC605T	g.chr3:163386999T>A	Unknown		
CHC605T	g.chr3:163690438A>T	Unknown		
CHC605T	g.chr3:165816155G>A	Unknown		
CHC605T	g.chr3:166278402C>A	Unknown		
CHC605T	g.chr3:168505622A>G	Unknown		
CHC605T	g.chr3:168516973T>A	Unknown		
CHC605T	g.chr3:168548582T>A	Unknown		
CHC605T	g.chr3:168927522G>A	MECOM		
CHC605T	g.chr3:172153351G>C	Unknown		
CHC605T	g.chr3:173723620G>A	NLGN1		
CHC605T	g.chr3:17555071C>A	TBC1D5		
CHC605T	g.chr3:175939407A>G	Unknown		
CHC605T	g.chr3:176631015T>A	Unknown		
CHC605T	g.chr3:177949548G>T	Unknown		
CHC605T	g.chr3:179482371C>A	USP13		
CHC605T	g.chr3:18093391A>G	TBC1D5		
CHC605T	g.chr3:181750743T>A	Unknown		
CHC605T	g.chr3:187307333A>G	Unknown		
CHC605T	g.chr3:187449962G>C	RP11-211G3.3		
CHC605T	g.chr3:189433713G>A	TP63		
CHC605T	g.chr3:190384206C>G	Unknown		
CHC605T	g.chr3:190858747A>G	Unknown		
CHC605T	g.chr3:192096254C>T	FGF12		
CHC605T	g.chr3:193015907A>G	ATP13A5		
CHC605T	g.chr3:193482372T>C	Unknown		
CHC605T	g.chr3:195487872A>G	MUC4	c.2023T>C	p.S675P
CHC605T	g.chr3:196960592T>C	DLG1		
CHC605T	g.chr3:21389924G>A	Unknown		
CHC605T	g.chr3:21568168C>T	ZNF385D		
CHC605T	g.chr3:2418008C>T	CNTN4		
CHC605T	g.chr3:25901280T>C	LINC00692		
CHC605T	g.chr3:2679882G>T	CNTN4		
CHC605T	g.chr3:27985955T>G	Unknown		
CHC605T	g.chr3:29155641G>A	Unknown		
CHC605T	g.chr3:29547679T>A	RBMS3		
CHC605T	g.chr3:349390T>A	CHL1		
CHC605T	g.chr3:349447G>A	CHL1		
CHC605T	g.chr3:37915442T>A	CTDSPL		
CHC605T	g.chr3:39907505T>C	MYRIP		
CHC605T	g.chr3:4365948C>A	SUMF1		
CHC605T	g.chr3:4470704C>G	SUMF1		
CHC605T	g.chr3:46499301G>A	LTF		
CHC605T	g.chr3:48447949C>T	PLXNB1		
CHC605T	g.chr3:50770803T>A	DOCK3		
CHC605T	g.chr3:54767066G>T	CACNA2D3		
CHC605T	g.chr3:55212781A>G	RP11-889D3.2		
CHC605T	g.chr3:57900923C>G	SLMAP		
CHC605T	g.chr3:6135235T>A	AC027119.1		
CHC605T	g.chr3:62941064G>A	LINC00698		
CHC605T	g.chr3:63144754A>G	Unknown		
CHC605T	g.chr3:63818947T>C	C3orf49		
CHC605T	g.chr3:64129337C>G	PRICKLE2		
CHC605T	g.chr3:64428096G>A	PRICKLE2		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr3:65187395G>A	Unknown		
CHC605T	g.chr3:6535939G>T	AC069277.2		
CHC605T	g.chr3:66718368G>A	Unknown		
CHC605T	g.chr3:68262715G>T	FAM19A1		
CHC605T	g.chr3:6849156T>C	Unknown		
CHC605T	g.chr3:68589880G>C	FAM19A1		
CHC605T	g.chr3:69229111G>T	FRMD4B		
CHC605T	g.chr3:70214626C>T	Unknown		
CHC605T	g.chr3:70228513G>A	Unknown		
CHC605T	g.chr3:7076230A>G	GRM7		
CHC605T	g.chr3:71379157T>G	FOXP1		
CHC605T	g.chr3:73930477T>A	RP11-20B7.1		
CHC605T	g.chr3:74972303C>A	Unknown		
CHC605T	g.chr3:76322660G>A	ROBO2		
CHC605T	g.chr3:79165856C>T	ROBO1		
CHC605T	g.chr3:79421178G>C	ROBO1		
CHC605T	g.chr3:80327808G>T	Unknown		
CHC605T	g.chr3:80647751A>G	Unknown		
CHC605T	g.chr3:8082341G>T	LMCD1-AS1		
CHC605T	g.chr3:81122983A>G	RP11-6B4.1		
CHC605T	g.chr3:81819024C>T	Unknown		
CHC605T	g.chr3:84041743G>T	Unknown		
CHC605T	g.chr3:84136110G>A	Unknown		
CHC605T	g.chr3:85738703T>G	CADM2		
CHC605T	g.chr3:85764687G>T	CADM2		
CHC605T	g.chr3:8584063C>T	LMCD1		
CHC605T	g.chr3:87827988A>G	RP11-451B8.1		
CHC605T	g.chr3:88387993A>C	Unknown		
CHC605T	g.chr3:88549477C>A	Unknown		
CHC605T	g.chr3:88618495A>T	Unknown		
CHC605T	g.chr3:89059186T>C	Unknown		
CHC605T	g.chr3:90229373G>T	Unknown		
CHC605T	g.chr3:94030841G>A	Unknown		
CHC605T	g.chr3:94139262A>T	Unknown		
CHC605T	g.chr3:95873611C>A	Unknown		
CHC605T	g.chr3:96819485C>G	EPHA6		
CHC605T	g.chr3:97710750A>G	GABRR3		
CHC605T	g.chr4:102705415G>A	BANK1		
CHC605T	g.chr4:107434182G>A	Unknown		
CHC605T	g.chr4:10992011C>T	Unknown		
CHC605T	g.chr4:113024751C>A	Unknown		
CHC605T	g.chr4:113375687G>A	Unknown		
CHC605T	g.chr4:114012744G>A	ANK2		
CHC605T	g.chr4:114837820T>C	ARSJ		
CHC605T	g.chr4:11539058T>C	Unknown		
CHC605T	g.chr4:118077308A>T	Unknown		
CHC605T	g.chr4:118294306C>G	Unknown		
CHC605T	g.chr4:118538149A>C	AC092661.1		
CHC605T	g.chr4:119144463T>C	NDST3		
CHC605T	g.chr4:12070502C>T	Unknown		
CHC605T	g.chr4:121088141A>G	RP11-679C8.2		
CHC605T	g.chr4:121889670T>C	Unknown		
CHC605T	g.chr4:121896331T>A	Unknown		
CHC605T	g.chr4:123781597G>A	FGF2		
CHC605T	g.chr4:126175049G>A	Unknown		
CHC605T	g.chr4:126933064G>A	Unknown		
CHC605T	g.chr4:126966762T>C	Unknown		
CHC605T	g.chr4:127263545G>T	Unknown		
CHC605T	g.chr4:127314781G>T	Unknown		
CHC605T	g.chr4:131252982A>G	Unknown		
CHC605T	g.chr4:133465357A>G	Unknown		
CHC605T	g.chr4:134283818A>T	Unknown		
CHC605T	g.chr4:134293354A>G	Unknown		
CHC605T	g.chr4:134734353C>A	Unknown		
CHC605T	g.chr4:135149081A>T	Unknown		
CHC605T	g.chr4:135281336G>C	Unknown		
CHC605T	g.chr4:135361385G>T	RP11-400D2.3		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr4:135597945C>T	Unknown		
CHC605T	g.chr4:136129421G>T	Unknown		
CHC605T	g.chr4:136274073C>A	Unknown		
CHC605T	g.chr4:136853561C>T	Unknown		
CHC605T	g.chr4:137288857C>A	Unknown		
CHC605T	g.chr4:137352918T>C	Unknown		
CHC605T	g.chr4:137352965G>C	Unknown		
CHC605T	g.chr4:137699759T>A	Unknown		
CHC605T	g.chr4:137725727G>C	RP11-138117.1		
CHC605T	g.chr4:138700232C>T	Unknown		
CHC605T	g.chr4:14078078T>A	Unknown		
CHC605T	g.chr4:142503189A>T	Unknown		
CHC605T	g.chr4:143779423C>A	Unknown		
CHC605T	g.chr4:144446310A>T	SMARCA5		
CHC605T	g.chr4:147794362C>T	TTC29		
CHC605T	g.chr4:147970419C>A	Unknown		
CHC605T	g.chr4:149639430T>C	Unknown		
CHC605T	g.chr4:149817468C>G	Unknown		
CHC605T	g.chr4:150365906A>G	RP11-526A4.1		
CHC605T	g.chr4:150471566G>A	RP11-526A4.1		
CHC605T	g.chr4:151542188C>T	LRBA		
CHC605T	g.chr4:152879489C>A	RP11-73G16.1		
CHC605T	g.chr4:154907358G>A	Unknown		
CHC605T	g.chr4:157737974C>A	PDGFC		
CHC605T	g.chr4:15904176T>A	Unknown		
CHC605T	g.chr4:160789327G>A	Unknown		
CHC605T	g.chr4:16124025A>G	Unknown		
CHC605T	g.chr4:163591892C>T	Unknown		
CHC605T	g.chr4:164861539C>T	01-mars		
CHC605T	g.chr4:164967397T>A	01-mars		
CHC605T	g.chr4:165913373C>T	Unknown		
CHC605T	g.chr4:166862791C>T	TLL1		
CHC605T	g.chr4:168611443G>T	Unknown		
CHC605T	g.chr4:172419656C>G	Unknown		
CHC605T	g.chr4:173476394A>G	GALNTL6		
CHC605T	g.chr4:175917351A>G	Unknown		
CHC605T	g.chr4:180996882G>T	Unknown		
CHC605T	g.chr4:18102098T>C	Unknown		
CHC605T	g.chr4:181836084A>G	Unknown		
CHC605T	g.chr4:182450330T>A	Unknown		
CHC605T	g.chr4:182535875C>A	Unknown		
CHC605T	g.chr4:184175407T>C	WWC2		
CHC605T	g.chr4:184670088A>T	Unknown		
CHC605T	g.chr4:186939273C>T	Unknown		
CHC605T	g.chr4:187114581A>G	CYP4V2		
CHC605T	g.chr4:188510180A>G	Unknown		
CHC605T	g.chr4:189400938G>T	LINC01060		
CHC605T	g.chr4:189400939A>T	LINC01060		
CHC605T	g.chr4:189507180C>T	Unknown		
CHC605T	g.chr4:190157870A>G	Unknown		
CHC605T	g.chr4:190725441C>G	Unknown		
CHC605T	g.chr4:19648151T>C	RP11-608O21.1		
CHC605T	g.chr4:20133125G>A	Unknown		
CHC605T	g.chr4:21325057G>T	KCNIP4		
CHC605T	g.chr4:21620479A>G	KCNIP4		
CHC605T	g.chr4:23246975G>T	RP11-453O5.1		
CHC605T	g.chr4:26476761T>A	Unknown		
CHC605T	g.chr4:2765087C>T	Unknown		
CHC605T	g.chr4:27822830A>G	Unknown		
CHC605T	g.chr4:28538542T>C	RP11-123O22.1		
CHC605T	g.chr4:29356742C>A	Unknown		
CHC605T	g.chr4:29435204C>A	Unknown		
CHC605T	g.chr4:30200558G>T	Unknown		
CHC605T	g.chr4:31302929G>A	Unknown		
CHC605T	g.chr4:31306768T>A	Unknown		
CHC605T	g.chr4:32020806T>C	RP11-734I18.1		
CHC605T	g.chr4:35099823T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr4:35760482G>T	Unknown		
CHC605T	g.chr4:38404723A>G	Unknown		
CHC605T	g.chr4:41788090C>T	RP11-227F19.1		
CHC605T	g.chr4:42733717C>G	Unknown		
CHC605T	g.chr4:43564795A>G	Unknown		
CHC605T	g.chr4:44192233A>G	KCTD8		
CHC605T	g.chr4:45765238T>A	Unknown		
CHC605T	g.chr4:48165684G>T	TEC		
CHC605T	g.chr4:55258333T>C	Unknown		
CHC605T	g.chr4:5682721G>A	EVC2		
CHC605T	g.chr4:5789529C>T	EVC		
CHC605T	g.chr4:58400709G>T	Unknown		
CHC605T	g.chr4:59085581C>T	Unknown		
CHC605T	g.chr4:6099062T>A	JAKMIP1		
CHC605T	g.chr4:6104717C>A	JAKMIP1		
CHC605T	g.chr4:63468708C>T	Unknown		
CHC605T	g.chr4:64219673G>T	Unknown		
CHC605T	g.chr4:64826584G>T	Unknown		
CHC605T	g.chr4:64860638C>G	Unknown		
CHC605T	g.chr4:64861935T>A	Unknown		
CHC605T	g.chr4:6540133T>C	PPP2R2C		
CHC605T	g.chr4:65634675C>A	Unknown		
CHC605T	g.chr4:66389353C>T	EPHA5		
CHC605T	g.chr4:66573661G>T	Unknown		
CHC605T	g.chr4:67042565G>T	Unknown		
CHC605T	g.chr4:68776140G>T	TMPRSS11A		
CHC605T	g.chr4:71506398G>A	ENAM		
CHC605T	g.chr4:72310130T>A	SLC4A4		
CHC605T	g.chr4:72379800A>G	SLC4A4		
CHC605T	g.chr4:76547739C>A	CDKL2		
CHC605T	g.chr4:78338260C>A	CCNG2		
CHC605T	g.chr4:78750628G>A	Unknown		
CHC605T	g.chr4:80167351C>G	NAA11		
CHC605T	g.chr4:80794778T>C	Unknown		
CHC605T	g.chr4:81750244A>G	C4orf22		
CHC605T	g.chr4:8214985T>A	SH3TC1		
CHC605T	g.chr4:83191287T>C	Unknown		
CHC605T	g.chr4:83697247C>T	SCD5		
CHC605T	g.chr4:86257833G>T	Unknown		
CHC605T	g.chr4:89951334A>G	FAM13A		
CHC605T	g.chr4:91009331T>A	Unknown		
CHC605T	g.chr4:91783148G>A	CCSER1		
CHC605T	g.chr4:92227898G>T	CCSER1		
CHC605T	g.chr4:92397506T>C	CCSER1		
CHC605T	g.chr4:92685667A>G	Unknown		
CHC605T	g.chr4:94426267C>A	GRID2		
CHC605T	g.chr4:94858661A>T	Unknown		
CHC605T	g.chr4:94996180A>G	Unknown		
CHC605T	g.chr4:96031115A>C	BMPR1B		
CHC605T	g.chr4:96441955A>G	UNC5C		
CHC605T	g.chr4:96836431G>T	Unknown		
CHC605T	g.chr4:98727997C>G	STPG2		
CHC605T	g.chr5:102986886A>T	Unknown		
CHC605T	g.chr5:103532986G>A	Unknown		
CHC605T	g.chr5:104565060T>C	CTD-2374C24.1		
CHC605T	g.chr5:104768658T>G	Unknown		
CHC605T	g.chr5:105070337C>A	Unknown		
CHC605T	g.chr5:105116996A>G	Unknown		
CHC605T	g.chr5:105379225A>G	Unknown		
CHC605T	g.chr5:107997081T>C	Unknown		
CHC605T	g.chr5:112320891G>A	DCP2		
CHC605T	g.chr5:114252984A>G	Unknown		
CHC605T	g.chr5:115987223T>A	Unknown		
CHC605T	g.chr5:117147142A>C	Unknown		
CHC605T	g.chr5:117147143C>A	Unknown		
CHC605T	g.chr5:117293238T>C	Unknown		
CHC605T	g.chr5:119430483T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr5:119838781G>A	PRR16		
CHC605T	g.chr5:120509749G>A	Unknown		
CHC605T	g.chr5:120518870C>A	Unknown		
CHC605T	g.chr5:121039744G>A	Unknown		
CHC605T	g.chr5:122936060C>T	CSNK1G3		
CHC605T	g.chr5:123039334C>T	Unknown		
CHC605T	g.chr5:128006343C>T	CTC-573M9.1		
CHC605T	g.chr5:128838758A>G	ADAMTS19		
CHC605T	g.chr5:13294181C>T	Unknown		
CHC605T	g.chr5:134744965G>T	Unknown		
CHC605T	g.chr5:135061821G>A	Unknown		
CHC605T	g.chr5:135514004A>G	SMAD5		
CHC605T	g.chr5:137456104T>G	NME5		
CHC605T	g.chr5:1376622C>G	RP11-325I22.2		
CHC605T	g.chr5:140617122T>C	Unknown		
CHC605T	g.chr5:141648226C>A	Unknown		
CHC605T	g.chr5:14394013A>G	TRIO		
CHC605T	g.chr5:151628373G>T	CTB-1202.1		
CHC605T	g.chr5:153120829C>T	GRIA1		
CHC605T	g.chr5:154690741T>G	Unknown		
CHC605T	g.chr5:154729549G>A	Unknown		
CHC605T	g.chr5:154731947C>A	Unknown		
CHC605T	g.chr5:154860228A>G	Unknown		
CHC605T	g.chr5:156940426A>G	ADAM19		
CHC605T	g.chr5:157542889C>T	Unknown		
CHC605T	g.chr5:160990725G>T	GABRA6		
CHC605T	g.chr5:16152960G>A	11-mars		
CHC605T	g.chr5:165773354G>C	Unknown		
CHC605T	g.chr5:166903455C>A	TENM2		
CHC605T	g.chr5:168164675G>A	SLIT3		
CHC605T	g.chr5:168731380C>A	Unknown		
CHC605T	g.chr5:171805000C>T	SH3PXD2B		
CHC605T	g.chr5:173270768C>A	Unknown		
CHC605T	g.chr5:177906911G>T	COL23A1		
CHC605T	g.chr5:179661665G>T	MAPK9		
CHC605T	g.chr5:20991098G>T	Unknown		
CHC605T	g.chr5:21499206G>T	GUSBP1		
CHC605T	g.chr5:22116475C>A	CDH12		
CHC605T	g.chr5:2248770A>G	Unknown		
CHC605T	g.chr5:24452157G>T	Unknown		
CHC605T	g.chr5:27741962G>T	Unknown		
CHC605T	g.chr5:29558871G>C	Unknown		
CHC605T	g.chr5:29666461C>T	Unknown		
CHC605T	g.chr5:30004770G>A	Unknown		
CHC605T	g.chr5:30812207C>T	Unknown		
CHC605T	g.chr5:36899729T>C	NIPBL		
CHC605T	g.chr5:37650319G>A	WDR70		
CHC605T	g.chr5:3790864G>T	Unknown		
CHC605T	g.chr5:38913919G>A	OSMR		
CHC605T	g.chr5:39567619A>G	Unknown		
CHC605T	g.chr5:40762279C>A	PRKAA1		
CHC605T	g.chr5:4336071A>T	Unknown		
CHC605T	g.chr5:44979125G>C	Unknown		
CHC605T	g.chr5:50265171C>G	CTD-2089N3.2		
CHC605T	g.chr5:5099362T>G	Unknown		
CHC605T	g.chr5:51664629C>T	Unknown		
CHC605T	g.chr5:52431617G>T	Unknown		
CHC605T	g.chr5:55131095C>T	Unknown		
CHC605T	g.chr5:55597648A>T	Unknown		
CHC605T	g.chr5:5711343C>T	Unknown		
CHC605T	g.chr5:57839901C>T	CTD-2117L12.1		
CHC605T	g.chr5:59946760T>C	DEPDC1B		
CHC605T	g.chr5:60750374G>A	ZSWIM6		
CHC605T	g.chr5:6083961C>A	Unknown		
CHC605T	g.chr5:62034118T>C	Unknown		
CHC605T	g.chr5:62522802C>T	Unknown		
CHC605T	g.chr5:63047729C>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr5:64331382T>A	Unknown		
CHC605T	g.chr5:71489906C>A	MAP1B	c.724C>A	p.P242T
CHC605T	g.chr5:72314158C>T	FCHO2		
CHC605T	g.chr5:7264664G>A	Unknown		
CHC605T	g.chr5:76788693A>G	Unknown		
CHC605T	g.chr5:78924636T>A	PAPD4		
CHC605T	g.chr5:80126681A>C	MSH3		
CHC605T	g.chr5:82984339A>G	HAPLN1		
CHC605T	g.chr5:83562215T>A	EDIL3		
CHC605T	g.chr5:83669809T>C	EDIL3		
CHC605T	g.chr5:83753933T>C	CTD-2269F5.1		
CHC605T	g.chr5:84189488C>A	Unknown		
CHC605T	g.chr5:84189489C>A	Unknown		
CHC605T	g.chr5:87042397A>G	Unknown		
CHC605T	g.chr5:87150759C>T	Unknown		
CHC605T	g.chr5:89271404C>T	Unknown		
CHC605T	g.chr5:89443308C>A	Unknown		
CHC605T	g.chr5:89886130C>T	GPR98		
CHC605T	g.chr5:9154684T>C	SEMA5A	c.1397A>G	p.H466R
CHC605T	g.chr5:95321664T>C	CTD-2337A12.1		
CHC605T	g.chr5:95811947A>G	CTD-2337A12.1		
CHC605T	g.chr5:98055690G>T	Unknown		
CHC605T	g.chr6:100158545C>T	Unknown		
CHC605T	g.chr6:100388354A>T	MCHR2		
CHC605T	g.chr6:103144045G>C	Unknown		
CHC605T	g.chr6:104522509A>G	Unknown		
CHC605T	g.chr6:104656884G>T	Unknown		
CHC605T	g.chr6:105346613G>T	Unknown		
CHC605T	g.chr6:106121143T>C	Unknown		
CHC605T	g.chr6:106619717T>C	Unknown		
CHC605T	g.chr6:108519671A>G	Unknown		
CHC605T	g.chr6:109199329A>G	ARMC2		
CHC605T	g.chr6:110881303G>T	Unknown		
CHC605T	g.chr6:11176355A>G	RP3-510L9.1		
CHC605T	g.chr6:120567789T>C	Unknown		
CHC605T	g.chr6:121443973A>G	TBC1D32		
CHC605T	g.chr6:123489407C>T	Unknown		
CHC605T	g.chr6:125505661T>C	TPD52L1		
CHC605T	g.chr6:127502196C>A	RSPO3		
CHC605T	g.chr6:127883064C>A	C6orf58		
CHC605T	g.chr6:128984878C>T	Unknown		
CHC605T	g.chr6:13199731G>A	PHACTR1		
CHC605T	g.chr6:135937664C>A	LINC00271		
CHC605T	g.chr6:135959579G>A	LINC00271		
CHC605T	g.chr6:138473758T>C	Unknown		
CHC605T	g.chr6:141528643G>A	Unknown		
CHC605T	g.chr6:145619802C>T	Unknown		
CHC605T	g.chr6:149501963A>T	Unknown		
CHC605T	g.chr6:153520867G>T	Unknown		
CHC605T	g.chr6:153925205A>G	Unknown		
CHC605T	g.chr6:154178289C>T	Unknown		
CHC605T	g.chr6:156178220T>A	Unknown		
CHC605T	g.chr6:156672632G>C	Unknown		
CHC605T	g.chr6:156727776T>C	Unknown		
CHC605T	g.chr6:157445140C>T	ARID1B		
CHC605T	g.chr6:158058196A>G	ZDHHC14		
CHC605T	g.chr6:16452354A>C	ATXN1		
CHC605T	g.chr6:16511791G>A	ATXN1		
CHC605T	g.chr6:165250392T>A	Unknown		
CHC605T	g.chr6:165450664G>C	Unknown		
CHC605T	g.chr6:167567354C>T	Unknown		
CHC605T	g.chr6:168048559T>C	Unknown		
CHC605T	g.chr6:169517647C>T	Unknown		
CHC605T	g.chr6:170577868G>A	RP5-894D12.5		
CHC605T	g.chr6:18726846A>G	Unknown		
CHC605T	g.chr6:19216530G>C	Unknown		
CHC605T	g.chr6:19398052T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr6:19697126G>T	RP1-167F1.2		
CHC605T	g.chr6:19778151A>G	RP1-167F1.2		
CHC605T	g.chr6:26470707A>G	BTN2A1		
CHC605T	g.chr6:27913787A>G	Unknown		
CHC605T	g.chr6:33904212A>G	Unknown		
CHC605T	g.chr6:34560824C>T	C6orf106		
CHC605T	g.chr6:35491738C>G	Unknown		
CHC605T	g.chr6:37469652C>G	Unknown		
CHC605T	g.chr6:40228892A>G	Unknown		
CHC605T	g.chr6:44190829G>T	SLC29A1		
CHC605T	g.chr6:45094878C>T	SUPT3H		
CHC605T	g.chr6:47811942C>T	Unknown		
CHC605T	g.chr6:48776400T>C	Unknown		
CHC605T	g.chr6:48827873A>G	Unknown		
CHC605T	g.chr6:48841725G>A	Unknown		
CHC605T	g.chr6:49058251A>C	Unknown		
CHC605T	g.chr6:49143133T>C	Unknown		
CHC605T	g.chr6:49158431G>C	Unknown		
CHC605T	g.chr6:49753880C>T	PGK2	c.1021G>A	p.G341R
CHC605T	g.chr6:49866368A>G	Unknown		
CHC605T	g.chr6:50364841A>T	Unknown		
CHC605T	g.chr6:55073133A>T	HCRTR2		
CHC605T	g.chr6:56234953C>T	COL21A1		
CHC605T	g.chr6:57684660G>A	Unknown		
CHC605T	g.chr6:64908456G>A	EYS		
CHC605T	g.chr6:66821365C>A	Unknown		
CHC605T	g.chr6:6921282G>T	Unknown		
CHC605T	g.chr6:72317102T>A	Unknown		
CHC605T	g.chr6:72567708T>C	Unknown		
CHC605T	g.chr6:75484244A>T	Unknown		
CHC605T	g.chr6:76665382C>G	IMPG1		
CHC605T	g.chr6:76799417C>A	Unknown		
CHC605T	g.chr6:76842250G>T	Unknown		
CHC605T	g.chr6:77145257C>A	Unknown		
CHC605T	g.chr6:78720726C>A	Unknown		
CHC605T	g.chr6:79979337A>G	Unknown		
CHC605T	g.chr6:80226474C>A	LCA5		
CHC605T	g.chr6:80241977A>T	LCA5		
CHC605T	g.chr6:85950468G>T	Unknown		
CHC605T	g.chr6:91273230A>G	MAP3K7		
CHC605T	g.chr6:92494625C>G	Unknown		
CHC605T	g.chr6:94274963C>G	Unknown		
CHC605T	g.chr6:94830651T>C	Unknown		
CHC605T	g.chr6:94930399C>T	Unknown		
CHC605T	g.chr6:94969409T>A	Unknown		
CHC605T	g.chr6:95094522G>T	Unknown		
CHC605T	g.chr6:96680909A>G	Unknown		
CHC605T	g.chr6:97225657A>T	Unknown		
CHC605T	g.chr6:9840804C>A	Unknown		
CHC605T	g.chr6:99297870C>T	Unknown		
CHC605T	g.chr7:101878254C>A	CUX1		
CHC605T	g.chr7:106162853C>A	Unknown		
CHC605T	g.chr7:106991803G>A	COG5		
CHC605T	g.chr7:107246186G>T	BCAP29		
CHC605T	g.chr7:107911651C>T	NRCAM		
CHC605T	g.chr7:108391472C>T	Unknown		
CHC605T	g.chr7:108610172G>A	Unknown		
CHC605T	g.chr7:109311001A>T	Unknown		
CHC605T	g.chr7:111228156C>A	Unknown		
CHC605T	g.chr7:111476324A>G	DOCK4		
CHC605T	g.chr7:113247484G>A	Unknown		
CHC605T	g.chr7:114177499T>C	FOXP2		
CHC605T	g.chr7:115411167A>G	Unknown		
CHC605T	g.chr7:120004879C>T	KCND2		
CHC605T	g.chr7:120163937A>G	KCND2		
CHC605T	g.chr7:122928441A>G	Unknown		
CHC605T	g.chr7:125082545C>A	RP11-807H17.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr7:125445295T>C	Unknown		
CHC605T	g.chr7:12560713A>C	AC005281.1		
CHC605T	g.chr7:127729599G>T	SND1	c.2477G>T	p.C826F
CHC605T	g.chr7:130147674A>G	RP11-2E11.9		
CHC605T	g.chr7:131461867C>A	Unknown		
CHC605T	g.chr7:133981985A>C	SLC35B4		
CHC605T	g.chr7:134471942T>C	CALD1		
CHC605T	g.chr7:136208717C>G	Unknown		
CHC605T	g.chr7:137493636C>T	DGKI		
CHC605T	g.chr7:139873549T>G	JHDM1D		
CHC605T	g.chr7:142727900G>T	Unknown		
CHC605T	g.chr7:143786422T>C	Unknown		
CHC605T	g.chr7:144815122A>T	Unknown		
CHC605T	g.chr7:146284345A>G	CNTNAP2		
CHC605T	g.chr7:146389076C>T	CNTNAP2		
CHC605T	g.chr7:149821686T>C	Unknown		
CHC605T	g.chr7:151200747A>C	RHEB		
CHC605T	g.chr7:152412192A>G	Unknown		
CHC605T	g.chr7:153293068C>A	Unknown		
CHC605T	g.chr7:153374093T>C	Unknown		
CHC605T	g.chr7:153801967A>G	DPP6		
CHC605T	g.chr7:155805135A>G	Unknown		
CHC605T	g.chr7:156583847A>C	LMBR1		
CHC605T	g.chr7:159113445G>T	Unknown		
CHC605T	g.chr7:16320070T>A	ISPD		
CHC605T	g.chr7:18717176C>A	HDAC9		
CHC605T	g.chr7:19498016C>G	AC007091.1		
CHC605T	g.chr7:20329472A>G	Unknown		
CHC605T	g.chr7:23297661T>C	GPNMB		
CHC605T	g.chr7:23554788C>A	TRA2A		
CHC605T	g.chr7:25321364T>A	Unknown		
CHC605T	g.chr7:27620921G>C	HIBADH		
CHC605T	g.chr7:30155681C>T	PLEKHA8		
CHC605T	g.chr7:30917174C>G	FAM188B		
CHC605T	g.chr7:31023397A>C	GHRHR		
CHC605T	g.chr7:32107781T>A	PDE1C		
CHC605T	g.chr7:34447795C>A	NPSR1-AS1		
CHC605T	g.chr7:34756588G>C	NPSR1		
CHC605T	g.chr7:34957530G>A	Unknown		
CHC605T	g.chr7:34978474T>G	DPY19L1		
CHC605T	g.chr7:35521325C>T	Unknown		
CHC605T	g.chr7:35610588T>C	Unknown		
CHC605T	g.chr7:38604892G>A	AMPH		
CHC605T	g.chr7:4355611G>A	Unknown		
CHC605T	g.chr7:4508722G>T	Unknown		
CHC605T	g.chr7:47705605G>A	Unknown		
CHC605T	g.chr7:49458859C>T	Unknown		
CHC605T	g.chr7:50613416C>T	DDC		
CHC605T	g.chr7:51445484G>T	Unknown		
CHC605T	g.chr7:51445485C>T	Unknown		
CHC605T	g.chr7:51845480G>T	Unknown		
CHC605T	g.chr7:51932259C>T	Unknown		
CHC605T	g.chr7:52847657A>C	Unknown		
CHC605T	g.chr7:52860554G>T	Unknown		
CHC605T	g.chr7:53075833C>A	Unknown		
CHC605T	g.chr7:53410020A>G	Unknown		
CHC605T	g.chr7:56088515C>T	PSPH		
CHC605T	g.chr7:57042274A>G	Unknown		
CHC605T	g.chr7:6114248A>G	Unknown		
CHC605T	g.chr7:63088582G>T	Unknown		
CHC605T	g.chr7:67270225G>A	Unknown		
CHC605T	g.chr7:67283379G>A	Unknown		
CHC605T	g.chr7:69003834G>C	Unknown		
CHC605T	g.chr7:73403371G>A	Unknown		
CHC605T	g.chr7:73888324C>T	GTF2IRD1		
CHC605T	g.chr7:78735356G>C	MAGI2		
CHC605T	g.chr7:79733289A>G	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr7:82092775A>G	Unknown		
CHC605T	g.chr7:82352350C>A	Unknown		
CHC605T	g.chr7:82896449T>C	Unknown		
CHC605T	g.chr7:84080052C>G	Unknown		
CHC605T	g.chr7:84335114C>A	Unknown		
CHC605T	g.chr7:84409116G>A	Unknown		
CHC605T	g.chr7:85306375T>C	Unknown		
CHC605T	g.chr7:85537022G>T	Unknown		
CHC605T	g.chr7:85541192A>G	Unknown		
CHC605T	g.chr7:88330436C>A	Unknown		
CHC605T	g.chr7:88382027G>T	AC002127.4		
CHC605T	g.chr7:9005034G>A	Unknown		
CHC605T	g.chr7:9005035G>T	Unknown		
CHC605T	g.chr7:91559339A>T	Unknown		
CHC605T	g.chr7:93322150A>G	NGT1		
CHC605T	g.chr7:93837639G>C	Unknown		
CHC605T	g.chr7:96133088C>G	Unknown		
CHC605T	g.chr7:99249810A>T	CYP3A5		
CHC605T	g.chr8:102905039G>A	NCALD		
CHC605T	g.chr8:103526665G>T	Unknown		
CHC605T	g.chr8:105889241A>C	RP11-127H5.1		
CHC605T	g.chr8:106067798C>G	Unknown		
CHC605T	g.chr8:106406085A>G	ZFPM2		
CHC605T	g.chr8:106496205G>A	ZFPM2		
CHC605T	g.chr8:107223424A>G	Unknown		
CHC605T	g.chr8:107539005T>A	OXR1		
CHC605T	g.chr8:109584808C>T	Unknown		
CHC605T	g.chr8:110010828A>C	RP11-1084E5.1		
CHC605T	g.chr8:110991287A>T	Unknown		
CHC605T	g.chr8:111525717T>G	Unknown		
CHC605T	g.chr8:112088672T>A	Unknown		
CHC605T	g.chr8:113401928T>G	CSMD3		
CHC605T	g.chr8:114406203T>C	CSMD3		
CHC605T	g.chr8:115283922G>T	Unknown		
CHC605T	g.chr8:116413393T>C	Unknown		
CHC605T	g.chr8:116511253G>A	TRPS1		
CHC605T	g.chr8:118262002C>A	Unknown		
CHC605T	g.chr8:122752245C>A	Unknown		
CHC605T	g.chr8:124369353T>A	ATAD2		
CHC605T	g.chr8:1249336C>T	CTD-2281E23.1		
CHC605T	g.chr8:125673646G>A	MTSS1		
CHC605T	g.chr8:127650464T>A	RP11-89K10.1		
CHC605T	g.chr8:128338922G>T	CASC8		
CHC605T	g.chr8:130244868T>G	LINC00977		
CHC605T	g.chr8:131435421C>A	ASAP1		
CHC605T	g.chr8:131516847A>C	Unknown		
CHC605T	g.chr8:13457018T>C	RP11-145O15.3		
CHC605T	g.chr8:134965338T>C	Unknown		
CHC605T	g.chr8:136022317A>G	Unknown		
CHC605T	g.chr8:136602467G>A	KHDRBS3		
CHC605T	g.chr8:137134978C>T	RP11-149P24.1		
CHC605T	g.chr8:137273304C>T	Unknown		
CHC605T	g.chr8:137695850A>G	Unknown		
CHC605T	g.chr8:137898442G>A	Unknown		
CHC605T	g.chr8:13995108T>C	SGCZ		
CHC605T	g.chr8:142113462G>A	Unknown		
CHC605T	g.chr8:142578204G>C	Unknown		
CHC605T	g.chr8:142578205A>T	Unknown		
CHC605T	g.chr8:14595935G>T	SGCZ		
CHC605T	g.chr8:1462058C>T	DLGAP2		
CHC605T	g.chr8:16336035T>C	MSR1		
CHC605T	g.chr8:19885254G>C	Unknown		
CHC605T	g.chr8:19905318C>G	Unknown		
CHC605T	g.chr8:2007298C>T	MYOM2	c.585C>T	p.C195C
CHC605T	g.chr8:21176008C>T	Unknown		
CHC605T	g.chr8:23223249C>A	LOXL2		
CHC605T	g.chr8:24629634C>T	RP11-624C23.1		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr8:25360917G>A	CDCA2	c.1700G>A	p.G567E
CHC605T	g.chr8:2689457C>A	Unknown		
CHC605T	g.chr8:27386168C>T	EPHX2		
CHC605T	g.chr8:29649958G>A	Unknown		
CHC605T	g.chr8:29924341G>A	TMEM66	c.794C>T	p.T265I
CHC605T	g.chr8:32875894G>T	RP11-11N9.4		
CHC605T	g.chr8:33516342G>A	Unknown		
CHC605T	g.chr8:3450624G>T	CSMD1		
CHC605T	g.chr8:35179212A>G	UNC5D		
CHC605T	g.chr8:35981115C>A	Unknown		
CHC605T	g.chr8:36165878T>G	Unknown		
CHC605T	g.chr8:37102748G>A	Unknown		
CHC605T	g.chr8:38321040C>T	FGFR1		
CHC605T	g.chr8:41275538A>G	Unknown		
CHC605T	g.chr8:4318669C>A	CSMD1		
CHC605T	g.chr8:4753896T>G	CSMD1		
CHC605T	g.chr8:51051441A>T	SNTG1		
CHC605T	g.chr8:5172180G>T	Unknown		
CHC605T	g.chr8:52654171A>C	PXDNL		
CHC605T	g.chr8:54299224T>C	Unknown		
CHC605T	g.chr8:54455977T>C	Unknown		
CHC605T	g.chr8:54579052C>A	Unknown		
CHC605T	g.chr8:55737140C>A	Unknown		
CHC605T	g.chr8:60215368A>T	Unknown		
CHC605T	g.chr8:60654602C>T	Unknown		
CHC605T	g.chr8:61139071T>C	CA8		
CHC605T	g.chr8:6278779G>T	MCPH1		
CHC605T	g.chr8:63055122T>C	Unknown		
CHC605T	g.chr8:64803355T>C	RP11-32K4.1		
CHC605T	g.chr8:65387365C>G	Unknown		
CHC605T	g.chr8:68622246G>A	CPA6		
CHC605T	g.chr8:68658266A>G	CPA6	c.99T>C	p.Y33Y
CHC605T	g.chr8:68729290C>G	Unknown		
CHC605T	g.chr8:69119410A>G	PREX2		
CHC605T	g.chr8:71888084C>T	Unknown		
CHC605T	g.chr8:72402360G>T	RP11-1102P16.1		
CHC605T	g.chr8:74483612C>T	STAU2		
CHC605T	g.chr8:74676241A>T	RP11-463D19.2		
CHC605T	g.chr8:76550223T>C	Unknown		
CHC605T	g.chr8:76554578C>A	Unknown		
CHC605T	g.chr8:76919463A>G	Unknown		
CHC605T	g.chr8:81822809A>C	Unknown		
CHC605T	g.chr8:83404692T>C	Unknown		
CHC605T	g.chr8:85125660A>G	RALYL		
CHC605T	g.chr8:87824075G>T	RP11-386D6.2		
CHC605T	g.chr8:92658516T>A	RP11-122C21.1		
CHC605T	g.chr8:92836508C>T	RP11-122C21.1		
CHC605T	g.chr8:92954396A>G	Unknown		
CHC605T	g.chr8:963595C>T	ERICH1-AS1		
CHC605T	g.chr8:96392710A>C	KB-1047C11.2		
CHC605T	g.chr8:97274713C>T	PTDSS1		
CHC605T	g.chr8:97472674A>G	Unknown		
CHC605T	g.chr8:97599218T>A	SDC2		
CHC605T	g.chr9:10136263T>C	PTPRD		
CHC605T	g.chr9:105427818T>C	Unknown		
CHC605T	g.chr9:105919877G>A	RP11-341A22.2		
CHC605T	g.chr9:106123228C>G	Unknown		
CHC605T	g.chr9:109278264A>G	RP11-308N19.1		
CHC605T	g.chr9:111590282C>T	Unknown		
CHC605T	g.chr9:11214419G>A	Unknown		
CHC605T	g.chr9:11337170C>A	Unknown		
CHC605T	g.chr9:113522163A>G	MUSK		
CHC605T	g.chr9:114018889T>G	RP11-202G18.1		
CHC605T	g.chr9:115451665G>C	INIP		
CHC605T	g.chr9:11590603A>G	Unknown		
CHC605T	g.chr9:116714815T>A	ZNF618		
CHC605T	g.chr9:117996700A>G	1-Dec		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chr9:11855817G>C	Unknown		
CHC605T	g.chr9:118912188T>A	Unknown		
CHC605T	g.chr9:121119773A>C	Unknown		
CHC605T	g.chr9:121289989T>C	Unknown		
CHC605T	g.chr9:121535935C>T	Unknown		
CHC605T	g.chr9:122157661A>G	Unknown		
CHC605T	g.chr9:122324500T>G	Unknown		
CHC605T	g.chr9:122661082G>A	Unknown		
CHC605T	g.chr9:124250936A>C	GGTA1P		
CHC605T	g.chr9:12508529A>G	Unknown		
CHC605T	g.chr9:127568222G>A	OLFML2A		
CHC605T	g.chr9:130019846G>T	Unknown		
CHC605T	g.chr9:131904046G>A	PPP2R4		
CHC605T	g.chr9:133268490G>A	HMCN2		
CHC605T	g.chr9:133422308G>A	Unknown		
CHC605T	g.chr9:136435969G>A	ADAMTSL2		
CHC605T	g.chr9:137410555C>T	RP11-473E2.2		
CHC605T	g.chr9:137777113C>T	FCN2	c.330C>T	p.D110D
CHC605T	g.chr9:13839658A>C	Unknown		
CHC605T	g.chr9:16526560T>A	BNC2		
CHC605T	g.chr9:17146696A>G	CNTLN		
CHC605T	g.chr9:19004737G>A	FAM154A		
CHC605T	g.chr9:20022747C>T	Unknown		
CHC605T	g.chr9:21424998G>C	Unknown		
CHC605T	g.chr9:2749987T>C	Unknown		
CHC605T	g.chr9:28157954A>G	LINGO2		
CHC605T	g.chr9:28480820T>A	LINGO2		
CHC605T	g.chr9:28665180A>G	LINGO2		
CHC605T	g.chr9:30318220T>C	Unknown		
CHC605T	g.chr9:3056245C>A	Unknown		
CHC605T	g.chr9:31092895A>G	Unknown		
CHC605T	g.chr9:31245860G>T	Unknown		
CHC605T	g.chr9:32079781G>T	Unknown		
CHC605T	g.chr9:3388882C>A	RFX3		
CHC605T	g.chr9:36711223A>G	Unknown		
CHC605T	g.chr9:37565192T>C	FBXO10		
CHC605T	g.chr9:37842076G>T	DCAF10		
CHC605T	g.chr9:4401835T>C	Unknown		
CHC605T	g.chr9:45110938G>A	RP11-374M1.2		
CHC605T	g.chr9:45742552G>T	Unknown		
CHC605T	g.chr9:5273391C>T	Unknown		
CHC605T	g.chr9:5739325G>A	KIAA1432		
CHC605T	g.chr9:66274871C>G	Unknown		
CHC605T	g.chr9:66682144G>T	Unknown		
CHC605T	g.chr9:68328877A>T	RP11-149F8.5		
CHC605T	g.chr9:7115723C>A	KDM4C		
CHC605T	g.chr9:74605337T>A	Unknown		
CHC605T	g.chr9:76472010T>G	Unknown		
CHC605T	g.chr9:77364668C>A	TRPM6		
CHC605T	g.chr9:7847667G>A	Unknown		
CHC605T	g.chr9:80036298T>G	VPS13A		
CHC605T	g.chr9:83311052T>G	Unknown		
CHC605T	g.chr9:86836314C>T	Unknown		
CHC605T	g.chr9:87192360T>C	Unknown		
CHC605T	g.chr9:88570493T>C	NAA35		
CHC605T	g.chr9:9613783A>T	PTPRD		
CHC605T	g.chr9:9673520G>A	PTPRD		
CHC605T	g.chr9:9733004A>G	PTPRD		
CHC605T	g.chr9:99300121C>A	CDC14B		
CHC605T	g.chrX:100920384G>T	Unknown		
CHC605T	g.chrX:102560853T>C	Unknown		
CHC605T	g.chrX:103136380G>A	Unknown		
CHC605T	g.chrX:10510681C>T	MID1		
CHC605T	g.chrX:105459295G>T	Unknown		
CHC605T	g.chrX:105802210C>T	Unknown		
CHC605T	g.chrX:106760926G>A	FRMPD3-AS1		
CHC605T	g.chrX:108135591C>A	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chrX:110476519C>A	Unknown		
CHC605T	g.chrX:112811471C>T	Unknown		
CHC605T	g.chrX:114025276T>C	HTR2C		
CHC605T	g.chrX:117082906T>C	KLHL13		
CHC605T	g.chrX:117382890C>G	Unknown		
CHC605T	g.chrX:117922523T>C	IL13RA1		
CHC605T	g.chrX:118089528T>C	Unknown		
CHC605T	g.chrX:118767626C>T	06-sept		
CHC605T	g.chrX:11918317T>C	Unknown		
CHC605T	g.chrX:121424675G>A	Unknown		
CHC605T	g.chrX:12186187C>T	FRMPD4		
CHC605T	g.chrX:12512075A>T	FRMPD4		
CHC605T	g.chrX:127099003T>C	Unknown		
CHC605T	g.chrX:127553685T>C	RP1-30E17.2		
CHC605T	g.chrX:128134841T>A	Unknown		
CHC605T	g.chrX:128169088C>A	Unknown		
CHC605T	g.chrX:128619572G>T	SMARCA1		
CHC605T	g.chrX:129952043T>A	ENOX2		
CHC605T	g.chrX:130047493T>C	Unknown		
CHC605T	g.chrX:132227528C>T	USP26		
CHC605T	g.chrX:132290353T>A	Unknown		
CHC605T	g.chrX:133438107A>G	Unknown		
CHC605T	g.chrX:136197087G>T	Unknown		
CHC605T	g.chrX:138439580T>G	Unknown		
CHC605T	g.chrX:138933346A>T	ATP11C		
CHC605T	g.chrX:14071597A>C	Unknown		
CHC605T	g.chrX:141420482G>T	Unknown		
CHC605T	g.chrX:14200405T>G	Unknown		
CHC605T	g.chrX:143736281G>C	Unknown		
CHC605T	g.chrX:144276342C>T	Unknown		
CHC605T	g.chrX:144319413C>T	Unknown		
CHC605T	g.chrX:144687644T>C	Unknown		
CHC605T	g.chrX:14527134A>G	Unknown		
CHC605T	g.chrX:146417786G>T	Unknown		
CHC605T	g.chrX:146856019C>T	Unknown		
CHC605T	g.chrX:147301744T>C	Unknown		
CHC605T	g.chrX:147857481C>T	AFF2		
CHC605T	g.chrX:149886409A>T	MTMR1		
CHC605T	g.chrX:150702569G>T	Unknown		
CHC605T	g.chrX:151268446A>G	Unknown		
CHC605T	g.chrX:151713195G>A	Unknown		
CHC605T	g.chrX:153272964G>T	Unknown		
CHC605T	g.chrX:153540650A>C	TKTL1		
CHC605T	g.chrX:154492169C>T	RAB39B		
CHC605T	g.chrX:15853123T>G	AP1S2		
CHC605T	g.chrX:16759892C>A	SYAP1	c.415C>A	p.Q139K
CHC605T	g.chrX:17549558C>A	NHS		
CHC605T	g.chrX:19281185C>A	Unknown		
CHC605T	g.chrX:21880935C>A	MBTPS2		
CHC605T	g.chrX:21880949A>T	MBTPS2		
CHC605T	g.chrX:24019008G>A	KLHL15		
CHC605T	g.chrX:27196816A>C	RP11-268G12.1		
CHC605T	g.chrX:27446048C>T	Unknown		
CHC605T	g.chrX:30544175C>A	Unknown		
CHC605T	g.chrX:31032140A>T	Unknown		
CHC605T	g.chrX:31059707A>T	Unknown		
CHC605T	g.chrX:32701004C>T	DMD		
CHC605T	g.chrX:33106252C>T	DMD		
CHC605T	g.chrX:34988674G>A	Unknown		
CHC605T	g.chrX:34991095T>C	Unknown		
CHC605T	g.chrX:36750686A>C	Unknown		
CHC605T	g.chrX:39654785G>T	Unknown		
CHC605T	g.chrX:41061308C>G	USP9X		
CHC605T	g.chrX:41066985G>A	USP9X		
CHC605T	g.chrX:42766796T>G	Unknown		
CHC605T	g.chrX:46063975T>C	Unknown		
CHC605T	g.chrX:46204649T>C	Unknown		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	g.chrX:48017100C>A	Unknown		
CHC605T	g.chrX:4943833T>A	Unknown		
CHC605T	g.chrX:5050613T>A	Unknown		
CHC605T	g.chrX:51317690G>T	Unknown		
CHC605T	g.chrX:51510475G>T	Unknown		
CHC605T	g.chrX:5435392T>A	Unknown		
CHC605T	g.chrX:55044322C>A	ALAS2		
CHC605T	g.chrX:55992994T>C	RP13-188A5.1		
CHC605T	g.chrX:56491862T>G	Unknown		
CHC605T	g.chrX:56491905G>A	Unknown		
CHC605T	g.chrX:58185661G>A	Unknown		
CHC605T	g.chrX:63899840T>C	Unknown		
CHC605T	g.chrX:64547555G>C	Unknown		
CHC605T	g.chrX:65750097G>T	Unknown		
CHC605T	g.chrX:67061260G>C	Unknown		
CHC605T	g.chrX:67658963T>G	Unknown		
CHC605T	g.chrX:69125813G>T	EDA		
CHC605T	g.chrX:73044027C>A	TSIX		
CHC605T	g.chrX:73707057A>G	SLC16A2		
CHC605T	g.chrX:74603881A>G	ZDHHC15		
CHC605T	g.chrX:77010403G>A	ATRX		
CHC605T	g.chrX:80092862G>C	Unknown		
CHC605T	g.chrX:80653137T>C	Unknown		
CHC605T	g.chrX:80863135A>G	Unknown		
CHC605T	g.chrX:80987062G>T	Unknown		
CHC605T	g.chrX:82299204T>C	Unknown		
CHC605T	g.chrX:82581028G>A	Unknown		
CHC605T	g.chrX:85416453C>A	DACH2		
CHC605T	g.chrX:87122420A>T	Unknown		
CHC605T	g.chrX:88067261T>C	Unknown		
CHC605T	g.chrX:89647412C>A	Unknown		
CHC605T	g.chrX:92002443T>A	Unknown		
CHC605T	g.chrX:92209272G>A	Unknown		
CHC605T	g.chrX:92612459C>T	Unknown		
CHC605T	g.chrX:93573943C>T	Unknown		
CHC605T	g.chrX:94415565C>A	Unknown		
CHC605T	g.chrX:97364587C>T	Unknown		
CHC605T	g.chrX:97756161T>C	Unknown		
CHC605T	g.chrX:99676090T>G	Unknown		
CHC605T	g.chr1:10876700delAC	Unknown		
CHC605T	848522_116848522insTATAT	Unknown		
CHC605T	hr1:117972970delGCGGAGAC	MAN1A2		
CHC605T	delTCCTCACTCCAGATGGG	MAN1A2		
CHC605T	g.chr1:179016470delCTTA	FAM20B		
CHC605T	1:181595460_181595460insG	CACNA1E		
CHC605T	g.chr1:181883180delAC	Unknown		
CHC605T	hr1:197880615delCGGGTCCC	Unknown		
CHC605T	g.chr1:202014443delAAAAG	Unknown		
CHC605T	g.chr1:215430580delTA	Unknown		
CHC605T	5_3393885insACCCCATCACC	ARHGEF16		
CHC605T	g.chr1:57275728delAAG	C1orf168		
CHC605T	g.chr1:98061146delTA	DPYD		
CHC605T	g.chr10:114612085delAT	Unknown		
CHC605T	g.chr10:13836693delTC	FRMD4A		
CHC605T	g.chr10:2366548delTA	Unknown		
CHC605T	g.chr10:25633096delGA	GPR158		
CHC605T	g.chr10:58350673delGA	Unknown		
CHC605T	g.chr10:61454451delTG	SLC16A9		
CHC605T	g.chr10:73575117delCG	CDH23		
CHC605T	g.chr10:84507361delGT	NRG3		
CHC605T	.chr10:9609240_9609240insA	Unknown		
CHC605T	ir11:116699020_116699020in	Unknown		
CHC605T	g.chr11:13731754delAT	FAR1		
CHC605T	7209211delAAATCCAGGAGGA	Unknown		
CHC605T	00289978delCTGAAATTTATA	ANKS1B		
CHC605T	g.chr12:127041407delTC	Unknown		
CHC605T	12:51892621_51892621insAT	SLC4A8		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	:hr12:59505438_59505438ins	Unknown		
CHC605T	g.chr12:65151854delTG	GNS		
CHC605T	93insTTTATATATAATGGATT	Unknown		
CHC605T	g.chr12:86897214delAT	MGAT4C		
CHC605T	.chr12:9591342_9591342insT	Unknown		
CHC605T	g.chr13:96669929delGT	UGGT2		
CHC605T	g.chr14:77845221delATG	SAMD15	c.1460delATG	p.N487fs
CHC605T	g.chr14:79209449delCA	NRXN3		
CHC605T	g.chr14:83828903delGA	Unknown		
CHC605T	g.chr14:93788516delTG	BTBD7		
CHC605T	g.chr15:20364382delTGGGG	Unknown		
CHC605T	r15:20364386_20364386insG	Unknown		
CHC605T	elGGGGGGGTAGCTGGATTTGC	MAGEL2	AAGCCGTGCAAATC	p.S63fs
CHC605T	g.chr15:29354738delCT	APBA2		
CHC605T	g.chr15:34092010delGTAGT	RXR3		
CHC605T	g.chr15:40242810delAAAG	EIF2AK4		
CHC605T	g.chr15:44043829delGA	PDIA3		
CHC605T	g.chr16:10191814delTA	GRIN2A		
CHC605T	g.chr16:17286026delGCT	XYLT1		
CHC605T	delCTTGAGCCGCGCTGCTGGC	PGP		
CHC605T	g.chr16:61026866delCT	Unknown		
CHC605T	:hr16:63235317_63235317ins	Unknown		
CHC605T	g.chr16:79829881delGGCCT	RP11-345M22.1		
CHC605T	:hr16:84207141_84207141ins	DNAAF1		
CHC605T	;chr17:48978303delCAAGTGC	TOB1-AS1		
CHC605T	g.chr18:23364168delTG	Unknown		
CHC605T	g.chr18:36083825delCAGA	Unknown		
CHC605T	g.chr18:55413398delGT	ATP8B1		
CHC605T	:75344600delGTGGGTCCCAA	Unknown		
CHC605T	g.chr19:1164908delGCAC	SBNO2		
CHC605T	8457156delTGCAGGCAACTGT	PGPEP1		
CHC605T	.9:34821227delAGCTGCTGTTT	KIAA0355	8delAGCTGCTGTTT	p.Q413fs
CHC605T	g.chr19:34821242delAG	KIAA0355	c.1253delAG	p.Q418fs
CHC605T	9:45060883_45060883insCAA	Unknown		
CHC605T	rr19:51397405_51397405insA	Unknown		
CHC605T	2:114139015delTTTTTTTTTTT	Unknown		
CHC605T	g.chr2:115699965delTATAC	DPP10		
CHC605T	hr2:124792592_124792592in:	CNTNAP5		
CHC605T	hr2:144077979_144077979ins:	ARHGAP15		
CHC605T	g.chr2:161322328delCT	RBMS1		
CHC605T	hr2:180248815_180248815ins:	Unknown		
CHC605T	g.chr2:187889431delCA	AC007319.1		
CHC605T	g.chr2:204963722delCA	AC009965.2		
CHC605T	g.chr2:40646903delAT	SLC8A1		
CHC605T	g.chr2:6057634delTC	Unknown		
CHC605T	GACTCAGTTTCCTTATAGGTAA	Unknown		
CHC605T	g.chr2:87226775delGA	RGPD1		
CHC605T	g.chr20:38087755delCT	Unknown		
CHC605T	l2378486delCGGGACACCACA	Unknown		
CHC605T	g.chr20:48042187delAAT	KCNB1		
CHC605T	g.chr20:53517731delAC	Unknown		
CHC605T):56335980delCTAACATCAAA	Unknown		
CHC605T	g.chr21:36221778delTTA	RUNX1		
CHC605T	:hr22:21520812_21520812ins	Unknown		
CHC605T	g.chr22:44254387delGA	SULT4A1		
CHC605T	g.chr3:118540523delTA	Unknown		
CHC605T	g.chr3:119055749delAC	ARHGAP31		
CHC605T	hr3:123107159_123107159ins:	ADCY5		
CHC605T	g.chr3:142501735delCT	TRPC1		
CHC605T	g.chr3:145230612delTCAGGA	Unknown		
CHC605T	g.chr3:153346757delGA	RP11-23D24.2		
CHC605T	g.chr3:165694436delTG	Unknown		
CHC605T	g.chr3:17372462delCT	TBC1D5		
CHC605T	g.chr3:179481978delTG	USP13		
CHC605T	g.chr3:179481980delTG	USP13		
CHC605T	g.chr3:180710027delTAG	Unknown		
CHC605T	g.chr3:19525208delAC	KCNH8		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	chr3:43293633_43293633insA	Unknown		
CHC605T	g.chr3:59146126delTA	Unknown		
CHC605T	g.chr3:82791301delAT	Unknown		
CHC605T	g.chr3:95365270delAG	Unknown		
CHC605T	.04870663_104870663insTAA	Unknown		
CHC605T	hr4:115843109_115843109in:	NDST4		
CHC605T	g.chr4:127103739delCT	Unknown		
CHC605T	g.chr4:142918424delCT	Unknown		
CHC605T	g.chr4:145633808delGATA	HHIP		
CHC605T	g.chr4:149739904delAT	Unknown		
CHC605T	chr4:149739906delGAAGCTAC	Unknown		
CHC605T	g.chr4:31326540delGT	Unknown		
CHC605T	g.chr4:69860017delTC	Unknown		
CHC605T	g.chr4:7876287delTTTTTAG	AFAP1		
CHC605T	chr4:92766376_92766376insA	Unknown		
CHC605T	g.chr5:101048999delAT	Unknown		
CHC605T	g.chr5:10250222delAG	CCT5		
CHC605T	g.chr5:123108809delTG	Unknown		
CHC605T	hr5:156993506_156993506ins:	ADAM19		
CHC605T	g.chr5:176107110delTG	Unknown		
CHC605T	g.chr5:53381742delCAT	ARL15		
CHC605T	g.chr5:59556811delACTGT	PDE4D		
CHC605T	g.chr5:7467828delCTG	ADCY2		
CHC605T	39789520_89789520insTAAA	POLR3G		
CHC605T	g.chr5:9525530delCCAGA	SEMA5A		
CHC605T	g.chr6:135339019delCA	HBS1L		
CHC605T	g.chr6:135339023delTTC	HBS1L		
CHC605T	g.chr6:156178217delGC	Unknown		
CHC605T	g.chr6:19693990delGAT	RP1-167F1.2		
CHC605T	6:25658274_25658274insTGC	SCGN		
CHC605T	g.chr6:34588791delCATCAAG	C6orf106		
CHC605T	g.chr6:43838540delCT	Unknown		
CHC605T	g.chr6:50364844delGA	Unknown		
CHC605T	g.chr6:70141682delTA	Unknown		
CHC605T	:71160445delTTTTTTTTTTTTT	FAM135A		
CHC605T	elATATATATTATATATATAA	SSR1		
CHC605T	chr6:94236210_94236210insC	Unknown		
CHC605T	g.chr7:101696089delTATC	CUX1		
CHC605T	g.chr7:10218766delAT	Unknown		
CHC605T	g.chr7:121346612delTC	Unknown		
CHC605T	g.chr7:124850772delTG	RP11-3B12.2		
CHC605T	r7:1320490delGGAGGAAGGA	Unknown		
CHC605T	g.chr7:33175373delGATT	BBS9		
CHC605T	g.chr7:38628791delTA	AMPH		
CHC605T	g.chr8:127098151delTC	Unknown		
CHC605T	g.chr8:54145551delGC	OPRK1		
CHC605T	g.chr8:67415431delGGC	C8orf46		
CHC605T	g.chr8:7339517delTG	Unknown		
CHC605T	:8:76378867delCCTTCTCCCTT	HNF4G		
CHC605T	r8:89608833delTGCATATACTA	RP11-586K2.1		
CHC605T	g.chr8:93339522delCT	Unknown		
CHC605T	g.chr8:96239612delGT	Unknown		
CHC605T	chr9:12541891_12541891insC	Unknown		
CHC605T	g.chr9:25573050delTCAAA	Unknown		
CHC605T	g.chr9:29865015delAT	Unknown		
CHC605T	g.chr9:35001699delAT	Unknown		
CHC605T	chrX:112512384_112512384ins:	Unknown		
CHC605T	g.chrX:119743361delGA	MCTS1		
CHC605T	:hrX:144999942delCCAAAATT	Unknown		
CHC605T	hrX:152999874_152999874ins:	ABCD1		
CHC605T	g.chrX:20636893delTA	Unknown		
CHC605T	g.chrX:22502436delAT	RP11-40F8.2		
CHC605T	g.chrX:4458573delGT	Unknown		
CHC605T	g.chrX:4684334delGC	Unknown		
CHC605T	g.chrX:49931900delTC	Unknown		
CHC605T	g.chrX:68107158delGT	Unknown		
CHC605T	chrX:84633791_84633791insC	POF1B		

Supplementary Table 9: somatic single nucleotide variation and small indels (WGS) of 3 shHCA

Sample	Genome_Change	Hugo_Symbol	cDNA_Change	Protein_Change
CHC605T	chrX:95122451_95122451insC	Unknown		

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC1018T	ENST00000257555	<i>HNF1A</i>	LOH	NM
CHC1026T ²	ENST00000257555	<i>HNF1A</i>	c.99_105del; p.Gly34ThrfsX119	c.872dup; p.Gly292ArgfsX25
CHC1117T ²	ENST00000257555	<i>HNF1A</i>	c.646del; p.Gln216ArgfsX17	c.872del; p.Pro291GlnfsX51
CHC1120T	ENST00000257555	<i>HNF1A</i>	c.815G>A; p.Arg272His	c.592_605del; p.Lys198ProfsX17
CHC1132T ²	ENST00000257555	<i>HNF1A</i>	c.34_35insAG; p.Leu12GlnfsX11	LOH
CHC1214T	ENST00000257555	<i>HNF1A</i>	c.714-45_753del:p.?	del13bases+dup11basesCCTCTCCTCC
CHC1223T ²	ENST00000257555	<i>HNF1A</i>	c.476G>C; p.Arg159Pro	c.872dup; p.Gly292ArgfsX25
CHC1259T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	LOH
CHC1311T	ENST00000257555	<i>HNF1A</i>	c.1004C>G; p.Ser335X	LOH
CHC1312T	ENST00000257555	<i>HNF1A</i>	c.2T>C; p.Met1?	Splice
CHC1318T	ENST00000257555	<i>HNF1A</i>	c.68_69insCTGATCCA; p.Lys23Asnfs	c.665_666dup; p.Asn223ArgfsX11
CHC1320T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.802T>C; p.Phe268Leu
CHC1322T	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	c.872dup; p.Gly292ArgfsX25
CHC1323T	ENST00000257555	<i>HNF1A</i>	c.671C>G; p.Pro224Arg	c.710A>G; p.Asn237Ser
CHC1324T	ENST00000257555	<i>HNF1A</i>	c.527-29_529del;	c.618G>T; p.Trp206Cys
CHC1326T	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	c.710A>G; p.Asn237Ser
CHC1327T	ENST00000257555	<i>HNF1A</i>	c.870_878del; p.Pro291_Pro293del	c.869_879delinsT; p.Pro290LeufsX49
CHC1333T	ENST00000257555	<i>HNF1A</i>	c.56C>T; p.Ser19Leu	c.640C>G; p.Leu214Val
CHC1334T	ENST00000257555	<i>HNF1A</i>	c.1483C>T; p.Gln495X	LOH
CHC1340T ²	ENST00000257555	<i>HNF1A</i>	c.370C>T; p.Gln124X	c.618G>T; p.Trp206Cys
CHC1341T	ENST00000257555	<i>HNF1A</i>	c.209_231del; p.Ser70TrpfsX18	c.815G>A; p.Arg272His
CHC1348T ²	ENST00000257555	<i>HNF1A</i>	LOH	c.618G>T; p.Trp206Cys
CHC1355T	ENST00000257555	<i>HNF1A</i>	c.379A>T; p.Asn127Tyr	c.688G>A; p.Glu230Lys
CHC1364T	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.872_873del; p.Pro291ArgfsX25
CHC1378T ²	ENST00000257555	<i>HNF1A</i>	LOH	c.787C>T; p.Arg263Cys
CHC1379T ²	ENST00000257555	<i>HNF1A</i>	c.1232_1233insGG; p.Met412AlafsX	LOH
CHC1390T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.800_835dup; p.Arg278_His279ins12
CHC1406T	ENST00000257555	<i>HNF1A</i>	LOH	c.618G>T; p.Trp206Cys
CHC1414T	ENST00000257555	<i>HNF1A</i>	c.795_817del; p.Tyr265X	c.829_830del; p.Phe277ProfsX39
CHC1415T	ENST00000257555	<i>HNF1A</i>	c.1113_1117del; p.Ala372TrpfsX45	c.1441C>T; p.Gln481X
CHC1416T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	NM
CHC1417T	ENST00000257555	<i>HNF1A</i>	c.614A>T; p.Lys205Met	c.189_198dup; p.Thr67AlafsX32
CHC1420T	ENST00000257555	<i>HNF1A</i>	c.814C>T; p.Arg272Cys	c.1043_1044dup; p.His349SerfsX16
CHC1425T ²	ENST00000257555	<i>HNF1A</i>	c.816delinsGCGC; p.Arg272dup	c.1340C>T; p.Pro447Leu
CHC1426T ²	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	NM
CHC1427T ²	ENST00000257555	<i>HNF1A</i>	c.614A>T; p.Lys205Met	c.326+6del; p.?
CHC1428T ²	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.1378C>T; p.Gln460X
CHC1429T ²	ENST00000257555	<i>HNF1A</i>	c.731G>T; p.Arg244Ile	c.1441C>T; p.Gln481X
CHC1431T ²	ENST00000257555	<i>HNF1A</i>	c.202_234del; p.Arg68_Gly78del	NM
CHC1436T	ENST00000257555	<i>HNF1A</i>	c.620G>A; p.Gly207Asp	c.641T>C; p.Leu214Pro
CHC1437T ²	ENST00000257555	<i>HNF1A</i>	c.692C>T; p.Thr231Met	c.732A>T; p.Arg244Ser
CHC1438T ²	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	NM
CHC1510T	ENST00000257555	<i>HNF1A</i>	c.607C>T; p.Arg203Cys	c.617G>T; p.Trp206Leu
CHC1515T ²	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	NA
CHC1517T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.872_873del; p.Pro291ArgfsX25
CHC1525T	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	nd
CHC1526T	ENST00000257555	<i>HNF1A</i>	c.392_393delins; p.Arg131LeufsX24	NM
CHC1669T	ENST00000257555	<i>HNF1A</i>	LOH	c.872dup; p.Gly292ArgfsX25
CHC1679T	ENST00000257555	<i>HNF1A</i>	c.815G>A; p.Arg272His	c.872dup; p.Gly292ArgfsX25
CHC1680T	ENST00000257555	<i>HNF1A</i>	c.815G>A; p.Arg272His	c.378dup; p.Asn127GlnfsX61
CHC1681T	ENST00000257555	<i>HNF1A</i>	c.815G>A; p.Arg272His	c.103_106del; p.Pro35ThrfsX119
CHC1853T	ENST00000257555	<i>HNF1A</i>	c.731G>C; p.Arg244Thr	LOH
CHC1856T	ENST00000257555	<i>HNF1A</i>	c.788G>A; p.Arg263His	c.829_831del; p.Phe277del
CHC1877T	ENST00000257555	<i>HNF1A</i>	LOH	c.731G>T; p.Arg244Ile
CHC1878T	ENST00000257555	<i>HNF1A</i>	c.685C>T; p.Arg229X	
CHC1882T	ENST00000257555	<i>HNF1A</i>	c.709A>T; p.Asn237Tyr	c.98_99insT; p.Pro35AlafsX25
CHC1926T	ENST00000257555	<i>HNF1A</i>	LOH	c.1120delinsCT; p.Gly374LeufsX45
CHC1928T	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	c.130_131del; p.Leu44GlyfsX15
CHC1933T	ENST00000257555	<i>HNF1A</i>	c.589A>T; p.Lys197X	c.710A>G; p.Asn237Ser
CHC1934T	ENST00000257555	<i>HNF1A</i>	LOH	c.235dup; p.Glu79GlyfsX17

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC1941T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	LOH
CHC1942T	ENST00000257555	<i>HNF1A</i>	c.709A>T; p.Asn237Tyr	c.*5G>A; p.?
CHC2198T	ENST00000257555	<i>HNF1A</i>	c.36_39del; p.Leu13ArgfsX8	c.815G>A; p.Arg272His
CHC2326T	ENST00000257555	<i>HNF1A</i>	c.872_873del; p.Pro291ArgfsX25	LOH
CHC2366T	ENST00000257555	<i>HNF1A</i>	c.646C>T; p.Gln216X	
CHC2368T	ENST00000257555	<i>HNF1A</i>	c.251_258dup; p.Lys87ProfsX71	
CHC2436T	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	c.715_784del; p.Ala239CysfsX80
CHC2570T	ENST00000257555	<i>HNF1A</i>	c.618G>T; p.Trp206Cys	c.872_873del; p.Pro291ArgfsX25
CHC2583T	ENST00000257555	<i>HNF1A</i>	c.495_526del; p.Trp165X	NM
CHC2594T	ENST00000257555	<i>HNF1A</i>	c.452G>A; p.Gly151Asp	NM
CHC2601T	ENST00000257555	<i>HNF1A</i>	c.56C>T; p.Ser19Leu	c.638T>G; p.Ile213Ser
CHC2606T	ENST00000257555	<i>HNF1A</i>	c.686G>T; p.Arg229Leu	c.1107+1G>A; p.?
CHC2617T	ENST00000257555	<i>HNF1A</i>	c.198_199del; p.Glu66AspfsX29	c.711T>A; p.Asn237Lys
CHC2619T	ENST00000257555	<i>HNF1A</i>	c.685_705del; p.Arg229_Glu235del	LOH
CHC2704T	ENST00000257555	<i>HNF1A</i>	c.364T>C; p.Tyr122His	c.800G>A; p.Trp267X
CHC2774T	ENST00000257555	<i>HNF1A</i>	c.2T>A; p.Met1?	
CHC2776T	ENST00000257555	<i>HNF1A</i>	c.218_219insT; p.Glu73AspfsX23	c.799T>C; p.Trp267Arg
CHC2779T	ENST00000257555	<i>HNF1A</i>	c.653A>G; p.Tyr218Cys	
CHC2782T	ENST00000257555	<i>HNF1A</i>	c.82del; p.Gln28ArgfsX127	
CHC2784T	ENST00000257555	<i>HNF1A</i>	c.620del; p.Gly207AlafsX26	c.713+1G>T; p.?
CHC340T ²	ENST00000257555	<i>HNF1A</i>	c.685C>T; p.Arg229X	LOH
CHC357T ²	ENST00000257555	<i>HNF1A</i>	c.526+1G>A; p.?	c.618G>T; p.Trp206Cys
CHC358T ²	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.872_884del; p.Pro291ArgfsX47
CHC368T ²	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	LOH
CHC369T ²	ENST00000257555	<i>HNF1A</i>	c.436_437del; p.Gln146ThrfsX41	LOH
CHC370T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.803T>G; p.Phe268Cys
CHC371T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.730A>G; p.Arg244Gly
CHC373T ²	ENST00000257555	<i>HNF1A</i>	c.82C>T; p.Gln28X	LOH
CHC380T	ENST00000257555	<i>HNF1A</i>	c.196G>T; p.Glu66X	c.779C>T; p.Thr260Met
CHC383T ²	ENST00000257555	<i>HNF1A</i>	c.493T>A; p.Trp165Arg	c.1340C>T; p.Pro447Leu
CHC384T ²	ENST00000257555	<i>HNF1A</i>	c.17_35delinsT; p.Ser6_Leu12delins	c.26_32del; p.Gln9ArgfsX11
CHC385T ²	ENST00000257555	<i>HNF1A</i>	c.817A>G; p.Lys273Glu	LOH
CHC461T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.872del; p.Pro291GlnfsX51
CHC462T ²	ENST00000257555	<i>HNF1A</i>	c.632A>C; p.Gln211Pro	c.670C>G; p.Pro224Ala
CHC463T ²	ENST00000257555	<i>HNF1A</i>	c.632A>C; p.Gln211Pro	c.617G>T; p.Trp206Leu
CHC464T ²	ENST00000257555	<i>HNF1A</i>	c.747_764del; p.Gln250_Gly255del	c.79_90del; p.Ile27_Leu30del
CHC474T	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	LOH
CHC476T	ENST00000257555	<i>HNF1A</i>	c.233_246dup; p.Pro83GlyfsX77	c.1288_1289del; p.Gly430CysfsX118
CHC479T	ENST00000257555	<i>HNF1A</i>	c.476_479del; p.Arg159ProfsX26	c.811C>T; p.Arg271Trp
CHC482T	ENST00000257555	<i>HNF1A</i>	c.653A>G; p.Tyr218Cys	LOH
CHC487T	ENST00000257555	<i>HNF1A</i>	c.814C>A; p.Arg272Ser	LOH
CHC489T	ENST00000257555	<i>HNF1A</i>	c.327-2A>T; p.?	c.1072_1073delinsTACAGGCTCA; p.Pro358TyrfsX9
CHC508T ²	ENST00000257555	<i>HNF1A</i>	c.77T>A; p.Leu26Gln	c.872del; p.Pro291GlnfsX51
CHC509T ²	ENST00000257555	<i>HNF1A</i>	c.391C>T; p.Arg131Trp	c.872del; p.Pro291GlnfsX51
CHC514T	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.829_837del; p.Phe277_His279del
CHC516T	ENST00000257555	<i>HNF1A</i>	c.185_194del; p.Asn62ArgfsX90	c.788G>A; p.Arg263His
CHC518T ²	ENST00000257555	<i>HNF1A</i>	c.164_168del; p.Gly55AlafsX3	LOH
CHC523T	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	LOH
CHC532T ²	ENST00000257555	<i>HNF1A</i>	c.199_203del; p.Thr67GlyfsX27	c.618G>T; p.Trp206Cys
CHC535T ²	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.872dup; p.Gly292ArgfsX25
CHC539T ²	ENST00000257555	<i>HNF1A</i>	c.686G>T; p.Arg229Leu	c.775G>C; p.Val259Leu
CHC540T ²	ENST00000257555	<i>HNF1A</i>	c.618G>T; p.Trp206Cys	LOH
CHC546T	ENST00000257555	<i>HNF1A</i>	c.1A>G; p.Met1?	c.620G>A; p.Gly207Asp
CHC548T	ENST00000257555	<i>HNF1A</i>	c.327-1G>T; p.?	nd
CHC549T	ENST00000257555	<i>HNF1A</i>	c.327-1G>T; p.?	c.1072_1073delinsTACAGGCTCA; p.Pro358TyrfsX9
CHC575T ²	ENST00000257555	<i>HNF1A</i>	c.526+1_526+13del; p.?	c.956del; p.Gly319ValfsX23
CHC578T ²	ENST00000257555	<i>HNF1A</i>	c.788G>T; p.Arg263Leu	c.1107+1G>T; p.?
CHC579T ²	ENST00000257555	<i>HNF1A</i>	c.134_158del; p.Asp45ValfsX102	c.872dup; p.Gly292ArgfsX25
CHC580T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	nd
CHC583T	ENST00000257555	<i>HNF1A</i>	c.811_818del; p.Lys273SerfsX41	c.815G>A; p.Arg272His

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC584T	ENST00000257555	<i>HNF1A</i>	c.607C>T; p.Arg203Cys	c.710A>G; p.Asn237Ser
CHC590T ²	ENST00000257555	<i>HNF1A</i>	c.526+1G>A; p.?	c.257_258del; p.Leu86GlnfsX9
CHC591T ²	ENST00000257555	<i>HNF1A</i>	c.787C>T; p.Arg263Cys	LOH
CHC592T ²	ENST00000257555	<i>HNF1A</i>	c.526C>T; p.Gln176X	c.956-2A>G; p.?
CHC621T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.19C>T; p.Gln7X
CHC633T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.650_654del; p.Ala217GlyfsX7
CHC634T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.650_654del; p.Ala217GlyfsX7
CHC635T ²	ENST00000257555	<i>HNF1A</i>	c.618G>T; p.Trp206Cys	c.872dup; p.Gly292ArgfsX25
CHC682T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.197dup; p.Thr67AspfsX29
CHC683T ²	ENST00000257555	<i>HNF1A</i>	c.696_698del; p.Val233del	c.613A>C; p.Lys205Gln
CHC687T ²	ENST00000257555	<i>HNF1A</i>	c.814C>A; p.Arg272Ser	LOH
CHC688T ²	ENST00000257555	<i>HNF1A</i>	c.710A>G; p.Asn237Ser	LOH
CHC689T ²	ENST00000257555	<i>HNF1A</i>	c.326+2_326+3del; p.?	c.56C>A; p.Ser19X
CHC690T ²	ENST00000257555	<i>HNF1A</i>	c.327-2A>T; p.?	c.872dup; p.Gly292ArgfsX25
CHC694T	ENST00000257555	<i>HNF1A</i>	c.527-2A>G; p.?	c.682G>T; p.Glu228X
CHC695T	ENST00000257555	<i>HNF1A</i>	c.527-2A>G; p.?	c.105_144delinsTTC; p.Tyr36SerfsX107
CHC696T	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.1168G>T; p.Glu390X
CHC699T	ENST00000257555	<i>HNF1A</i>	c.685C>G; p.Arg229Gly	c.710dup; p.Asn237LysfsX2
CHC705T ²	ENST00000257555	<i>HNF1A</i>	c.618G>T; p.Trp206Cys	c.631C>T; p.Gln211X
CHC749T	ENST00000257555	<i>HNF1A</i>	c.618G>T; p.Trp206Cys	LOH
CHC759T	ENST00000257555	<i>HNF1A</i>	c.526+1G>A; p.?	c.608G>T; p.Arg203Leu
CHC761T ²	ENST00000257555	<i>HNF1A</i>	c.617G>T; p.Trp206Leu	c.618_628del; p.Trp206CysfsX10
CHC763T ²	ENST00000257555	<i>HNF1A</i>	c.526+1G>A; p.?	c.872dup; p.Gly292ArgfsX25
CHC764T ²	ENST00000257555	<i>HNF1A</i>	c.526+1G>A; p.?	LOH
CHC778T	ENST00000257555	<i>HNF1A</i>	c.1441C>T; p.Gln481X	c.1067_1073del; p.Leu356ProfsX6
CHC814T ²	ENST00000257555	<i>HNF1A</i>	c.476G>A; p.Arg159Gln	c.872dup; p.Gly292ArgfsX25
CHC815T ²	ENST00000257555	<i>HNF1A</i>	c.779C>T; p.Thr260Met	c.872dup; p.Gly292ArgfsX25
CHC816T ²	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.713+8_713+9ins87; p.?
CHC817T	ENST00000257555	<i>HNF1A</i>	c.196G>T; p.Glu66X	c.711T>A; p.Asn237Lys
CHC818T	ENST00000257555	<i>HNF1A</i>	c.872_873del; p.Pro291ArgfsX25	c.710A>G; p.Asn237Ser
CHC829T	ENST00000257555	<i>HNF1A</i>	c.695T>A; p.Leu232Gln	c.931_932delinsACCTA; p.Ala311delinsThrTyr
CHC831T	ENST00000257555	<i>HNF1A</i>	c.815G>A; p.Arg272His	c.872dup; p.Gly292ArgfsX25
CHC833T	ENST00000257555	<i>HNF1A</i>	c.607C>T; p.Arg203Cys	LOH
CHC834T	ENST00000257555	<i>HNF1A</i>	c.607C>T; p.Arg203Cys	LOH
CHC850T	ENST00000257555	<i>HNF1A</i>	c.872dup; p.Gly292ArgfsX25	c.133_149del; p.Asp45ArgfsX9
CHC851T	ENST00000257555	<i>HNF1A</i>	c.872_873del; p.Pro291ArgfsX25	LOH
CHC856T	ENST00000257555	<i>HNF1A</i>	c.872_873del; p.Pro291ArgfsX25	c.770A>C; p.Asn257Thr
CHC951T ²	ENST00000257555	<i>HNF1A</i>	c.534_535insA; p.His179ThrfsX9	c.779C>T; p.Thr260Met
CHC957T	ENST00000257555	<i>HNF1A</i>	c.730A>G; p.Arg244Gly	c.1274_1275del; p.Thr425IlefsX123
CHC964T	ENST00000257555	<i>HNF1A</i>	c.629C>T; p.Ser210Phe	LOH exon1
CHC965T	ENST00000257555	<i>HNF1A</i>	c.815G>A; p.Arg272His	c.252_258del; p.Ile85LysfsX68
CHC971T	ENST00000257555	<i>HNF1A</i>	c.620G>A; p.Gly207Asp	c.872del; p.Pro291GlnfsX51
CHC972T	ENST00000257555	<i>HNF1A</i>	c.618G>T; p.Trp206Cys	c.1249_1250insT; p.Gly417ValfsX2
CHC1023T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC1118T ²	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1123T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC1124T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC1129T	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC1131T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC1217T ²	ENST00000396185	<i>CTNNB1</i>	c.102_104del; p.Ile35del	
CHC1234T ²	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1250T	ENST00000396185	<i>CTNNB1</i>	c.65_379del; p.Val22_Ala126del	
CHC1264T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1275T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC1279T	ENST00000396185	<i>CTNNB1</i>	c.134C>A; p.Ser45Tyr	
CHC1281T	ENST00000396185	<i>CTNNB1</i>	c.58_426del; p.Ala20_Tyr142del	

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC1287T	ENST00000396185	<i>CTNNB1</i>	c.121_153del; p.Thr41_Asn51del	
CHC1298T	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC1334T	ENST00000396185	<i>CTNNB1</i>	c.134C>G; p.Ser45Cys	
CHC1342T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1346T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC1347T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>A; p.Asn387Lys	
CHC1350T ²	ENST00000396185	<i>CTNNB1</i>	c.860A>G; p.Asn287Ser	
CHC1351T ²	ENST00000396185	<i>CTNNB1</i>	c.860A>G; p.Asn287Ser	
CHC1352T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1354T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1358T ²	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1365T ²	ENST00000396185	<i>CTNNB1</i>	c.30_428del; p.Met12_Asp144del	
CHC1382T	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1383T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1385T	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1387T	ENST00000396185	<i>CTNNB1</i>	c.1161T>A; p.Asn387Lys	
CHC1391T	ENST00000396185	<i>CTNNB1</i>	c.23_397del; p.Met8_Leu132del	
CHC1396T	ENST00000396185	<i>CTNNB1</i>	c.64_291del; p.Val22_Ala97del	
CHC1424T ²	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1441T	ENST00000396185	<i>CTNNB1</i>	c.1161T>A; p.Asn387Lys	
CHC1496T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1509T ²	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1516T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1662T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1663T	ENST00000396185	<i>CTNNB1</i>	c.45_429delinsT; p.Glu15_Gln143delinsAsp	
CHC1665T ²	ENST00000396185	<i>CTNNB1</i>	c.134C>T; p.Ser45Phe	
CHC1666T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC1667T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1851T	ENST00000396185	<i>CTNNB1</i>	c.128C>G; p.Ala43Gly	c.130_150del; p.Pro44_Gly50del
CHC1876T	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC1891T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC1897T	ENST00000396185	<i>CTNNB1</i>	c.65_424del; p.Val22_Tyr142delinsAsp	
CHC1915T	ENST00000396185	<i>CTNNB1</i>	c.92_106del; p.Leu31_Ile35del	
CHC2188T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC2192T	ENST00000396185	<i>CTNNB1</i>	c.486C>T; p.Asp162Asp	
CHC2196T	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC2217T	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC2218T	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC222T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>C; p.Lys335Thr	
CHC2321T ²	ENST00000396185	<i>CTNNB1</i>	c.7_378del; p.Thr3_Ala126del	
CHC2328T	ENST00000396185	<i>CTNNB1</i>	c.128_146delinsGTAC; p.Ala43_Lys49delinsGlyThr	
CHC2363T	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC2366T	ENST00000396185	<i>CTNNB1</i>	c.670C>T; p.His224Tyr	
CHC2562T	ENST00000396185	<i>CTNNB1</i>	c.18_380del; p.Asp6_Ala126del	
CHC343T ²	ENST00000396185	<i>CTNNB1</i>	c.134C>A; p.Ser45Tyr	
CHC361TA ²	ENST00000396185	<i>CTNNB1</i>	c.7_378del; p.Thr3_Ala126del	
CHC364T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>C; p.Lys335Thr	

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC372T ²	ENST00000396185	<i>CTNNB1</i>	c.101G>A; p.Gly34Glu	
CHC376T ²	ENST00000396185	<i>CTNNB1</i>	c.98C>G; p.Ser33Cys	
CHC377T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC378T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>C; p.Lys335Thr	
CHC390T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC454T ²	ENST00000396185	<i>CTNNB1</i>	c.13+147_241+62del; p.?	
CHC458T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC469T ²	ENST00000396185	<i>CTNNB1</i>	c.100G>A; p.Gly34Arg	
CHC477T	ENST00000396185	<i>CTNNB1</i>	c.13+3_241+2del; p.Ala5_Ala80del	
CHC505T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC506T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC517T ²	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC534T	ENST00000396185	<i>CTNNB1</i>	c.55_423del; p.Lys19_Asn141del	
CHC536T ²	ENST00000396185	<i>CTNNB1</i>	c.94G>A; p.Asp32Asn	
CHC543T ²	ENST00000396185	<i>CTNNB1</i>	c.60_446del; p.Ala21_Ala149del	
CHC554T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC573T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC574T ²	ENST00000396185	<i>CTNNB1</i>	c.1004A>C; p.Lys335Thr	
CHC582T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC663T	ENST00000396185	<i>CTNNB1</i>	c.133T>G; p.Ser45Ala	
CHC678T ²	ENST00000396185	<i>CTNNB1</i>	c.13+49_426del; p.?	
CHC680T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC684T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC691T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC700T ²	ENST00000396185	<i>CTNNB1</i>	c.134C>T; p.Ser45Phe	
CHC701T ²	ENST00000396185	<i>CTNNB1</i>	c.134C>T; p.Ser45Phe	
CHC711T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC742T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC747T	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC754T	ENST00000396185	<i>CTNNB1</i>	c.72_428del; p.His24_Tyr142del	
CHC755T	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC756T	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC786T ²	ENST00000396185	<i>CTNNB1</i>	c.13+12_402del; p.?	
CHC820T ²	ENST00000396185	<i>CTNNB1</i>	c.116C>G; p.Ala39Gly	
CHC823T ²	ENST00000396185	<i>CTNNB1</i>	c.116C>G; p.Ala39Gly	
CHC846T ²	ENST00000396185	<i>CTNNB1</i>	c.121A>G; p.Thr41Ala	
CHC870T ²	ENST00000396185	<i>CTNNB1</i>	c.134C>T; p.Ser45Phe	
CHC917T	ENST00000396185	<i>CTNNB1</i>	c.98C>A; p.Ser33Tyr	
CHC955T ²	ENST00000396185	<i>CTNNB1</i>	c.1161T>G; p.Asn387Lys	
CHC967T	ENST00000396185	<i>CTNNB1</i>	c.133T>C; p.Ser45Pro	
CHC974T	ENST00000396185	<i>CTNNB1</i>	c.134C>T; p.Ser45Phe	
CHC976T	ENST00000396185	<i>CTNNB1</i>	c.1004A>T; p.Lys335Ile	
CHC979T	ENST00000396185	<i>CTNNB1</i>	c.97T>C; p.Ser33Pro	
CHC1002T	ENST00000381298	<i>IL6ST</i>	c.594_620del; p.Glu199_Val207del	
CHC1004T	ENST00000381298	<i>IL6ST</i>	c.594_620del; p.Glu199_Val207del	
CHC1020T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1023T ²	ENST00000381298	<i>IL6ST</i>	c.646_647ins33; p.Asp215_Pro216ins11	
CHC1121T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC1123T ²	ENST00000381298	<i>IL6ST</i>	c.647C>A; p.Pro216His	
CHC1124T ²	ENST00000381298	<i>IL6ST</i>	c.571_579del; p.Phe191_Asn193del	
CHC1129T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1131T ²	ENST00000381298	<i>IL6ST</i>	c.564_576delinsA; p.Val189_Val192del	
CHC1216T	ENST00000381298	<i>IL6ST</i>	c.1252_1263del; p.Ala418_Phe421del	
CHC1232T ²	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	
CHC1237T ²	ENST00000381298	<i>IL6ST</i>	c.565_574delinsT; p.Val189_Val192delinsPhe	
CHC1238T ²	ENST00000381298	<i>IL6ST</i>	c.573_582delinsG; p.Phe191_Ile194delinsLeu	
CHC1243T	ENST00000381298	<i>IL6ST</i>	c.557_574del; p.Tyr186_Val192delinsPhe	
CHC1251T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1252T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1275T ²	ENST00000381298	<i>IL6ST</i>	c.643_645del; p.Asp215del	
CHC1285T	ENST00000381298	<i>IL6ST</i>	c.568_579del; p.Tyr190_Asn193del	
CHC1287T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1289T	ENST00000381298	<i>IL6ST</i>	c.518_535delinsCCG; p.Lys173_Pro179delinsThrAla	
CHC1290T	ENST00000381298	<i>IL6ST</i>	c.577_580delinsT; p.Asn193_Ile194delinsPhe	
CHC1291T	ENST00000381298	<i>IL6ST</i>	c.564_575del; p.Val189_Val192del	
CHC1296T	ENST00000381298	<i>IL6ST</i>	c.567_578del; p.Tyr190_Asn193del	
CHC1297T	ENST00000381298	<i>IL6ST</i>	c.562_573del; p.Thr188_Phe191del	
CHC1301T ²	ENST00000381298	<i>IL6ST</i>	c.643_645del; p.Asp215del	
CHC1302T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1304T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC1305T ²	ENST00000381298	<i>IL6ST</i>	c.518_532del; p.Lys173_Asp177del	
CHC1306T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1313T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1319T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1321T	ENST00000381298	<i>IL6ST</i>	c.573_582delinsG; p.Phe191_Ile194delinsLeu	
CHC1328T ²	ENST00000381298	<i>IL6ST</i>	c.567_578del; p.Tyr190_Asn193del	
CHC1329T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1330T ²	ENST00000381298	<i>IL6ST</i>	c.518_532del; p.Lys173_Asp177del	
CHC1331T ²	ENST00000381298	<i>IL6ST</i>	c.567_578del; p.Tyr190_Asn193del	
CHC1335T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1336T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1337T ²	ENST00000381298	<i>IL6ST</i>	c.1252_1263del; p.Ala418_Phe421del	
CHC1339T ²	ENST00000381298	<i>IL6ST</i>	c.564_576delinsA; p.Val189_Val192del	
CHC1342T ²	ENST00000381298	<i>IL6ST</i>	c.518_532del; p.Lys173_Asp177del	
CHC1350T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1354T	ENST00000381298	<i>IL6ST</i>	c.556_573del; p.Tyr186_Phe191del	
CHC1356T	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	
CHC1386T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1388T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1399T	ENST00000381298	<i>IL6ST</i>	c.575_577del; p.Val192_Asn193delinsAsp	
CHC1407T	ENST00000381298	<i>IL6ST</i>	c.567_579delinsT; p.Tyr190_Asn193del	
CHC1410T	ENST00000381298	<i>IL6ST</i>	c.640_642del; p.Phe214del	
CHC1412T	ENST00000381298	<i>IL6ST</i>	c.556_573del; p.Tyr186_Phe191del	
CHC1413T	ENST00000381298	<i>IL6ST</i>	c.564_575del; p.Val189_Val192del	
CHC1421T	ENST00000381298	<i>IL6ST</i>	c.565_577delinsT; p.Val189_Asn193delinsTyr	
CHC1432T ²	ENST00000381298	<i>IL6ST</i>	c.1841-2A>T; p.?	
CHC1433T ²	ENST00000381298	<i>IL6ST</i>	c.618_641dup; p.Asn213_Phe214ins8	
CHC1434T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1435T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1440T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1518T	ENST00000381298	<i>IL6ST</i>	c.556_571delinsA; p.Tyr186_Phe191delinsIle	
CHC1521T	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	
CHC1664T	ENST00000381298	<i>IL6ST</i>	c.643_645del; p.Asp215del	
CHC1666T ²	ENST00000381298	<i>IL6ST</i>	c.564_576delinsA; p.Val189_Val192del	
CHC1676T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC1677T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1768T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1851T	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC1880T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC1915T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC2191T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC2196T	ENST00000381298	<i>IL6ST</i>	c.522_536del; p.Lys175_Pro179del	
CHC2329T	ENST00000381298	<i>IL6ST</i>	c.580_585del; p.Ile194_Glu195del	
CHC2370T	ENST00000381298	<i>IL6ST</i>	c.565_579del; p.Val189_Asn193del	
CHC2371T	ENST00000381298	<i>IL6ST</i>	c.556_573del; p.Tyr186_Phe191del	
CHC2372T	ENST00000381298	<i>IL6ST</i>	c.565_579del; p.Val189_Asn193del	
CHC2373T	ENST00000381298	<i>IL6ST</i>	c.570_578del; p.Phe191_Asn193del	
CHC2374T	ENST00000381298	<i>IL6ST</i>	c.557_572del; p.Tyr186LeufsX8	
CHC2375T	ENST00000381298	<i>IL6ST</i>	c.575_583del; p.Val192_Ile194del	
CHC2377T	ENST00000381298	<i>IL6ST</i>	c.565_579del; p.Val189_Asn193del	
CHC2561T	ENST00000381298	<i>IL6ST</i>	c.647C>A; p.Pro216His	
CHC2568T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC2571T	ENST00000381298	<i>IL6ST</i>	c.570_578del; p.Phe191_Asn193del	
CHC2574T	ENST00000381298	<i>IL6ST</i>	c.564_575del; p.Val189_Val192del	
CHC2575T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC2576T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC2585T	ENST00000381298	<i>IL6ST</i>	c.579_584del; p.Asn193_Glu195delinsLys	
CHC2620T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC2769T	ENST00000381298	<i>IL6ST</i>	c.216del; p.Phe72LeufsX11	
CHC344T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC362T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC364T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC377T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC382T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC390T ²	ENST00000381298	<i>IL6ST</i>	c.557_574del; p.Tyr186_Val192delinsPhe	
CHC455T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC456T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC457T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC466T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC468T ²	ENST00000381298	<i>IL6ST</i>	c.647C>A; p.Pro216His	
CHC469T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC473T	ENST00000381298	<i>IL6ST</i>	c.564_575del; p.Val189_Val192del	
CHC481T	ENST00000381298	<i>IL6ST</i>	c.615_644dup; p.Phe214_Asp215ins10	
CHC490T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC503T ²	ENST00000381298	<i>IL6ST</i>	c.566_580delinsATG; p.Val189_Ile194delinsAspVal	
CHC528T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC536T ²	ENST00000381298	<i>IL6ST</i>	c.566_577del; p.Val189_Asn193delinsAsp	
CHC552T ²	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	
CHC555T ²	ENST00000381298	<i>IL6ST</i>	c.503_580del; p.Lys168_Asn193del	
CHC560T	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC581T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC594T	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	
CHC631T	ENST00000381298	<i>IL6ST</i>	c.636_644del; p.Asn213_Asp215del	
CHC670T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC680T ²	ENST00000381298	<i>IL6ST</i>	c.563_577del; p.Thr188_Val192del	
CHC684T ²	ENST00000381298	<i>IL6ST</i>	c.565_576del; p.Val189_Val192del	
CHC691T ²	ENST00000381298	<i>IL6ST</i>	c.518_532del; p.Lys173_Asp177del	
CHC698T	ENST00000381298	<i>IL6ST</i>	c.568_579del; p.Tyr190_Asn193del	
CHC711T ²	ENST00000381298	<i>IL6ST</i>	c.643_645del; p.Asp215del	
CHC742T	ENST00000381298	<i>IL6ST</i>	c.518_532del; p.Lys173_Asp177del	
CHC745T	ENST00000381298	<i>IL6ST</i>	c.562_573del; p.Thr188_Phe191del	
CHC751T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC754T	ENST00000381298	<i>IL6ST</i>	c.647C>A; p.Pro216His	
CHC756T	ENST00000381298	<i>IL6ST</i>	c.552_566del; p.Asp185_Val189del	
CHC770T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC771T ²	ENST00000381298	<i>IL6ST</i>	c.564_575del; p.Val189_Val192del	
CHC772T ²	ENST00000381298	<i>IL6ST</i>	c.562_573del; p.Thr188_Phe191del	
CHC786T ²	ENST00000381298	<i>IL6ST</i>	c.551_559del; p.Val184_Ser187delinsAla	

Supplementary Table 10, Catalog of somatic mutations in 8 driver genes.

Sample ID	Ensembl Transcript	Gene symbol	Allele 1 Mutation	Allele 2 Mutation
CHC820T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC821T ²	ENST00000381298	<i>IL6ST</i>	c.557_571del; p.Tyr186_Tyr190del	
CHC823T ²	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC839T ²	ENST00000381298	<i>IL6ST</i>	c.647C>A; p.Pro216His	
CHC844T	ENST00000381298	<i>IL6ST</i>	c.562_573del; p.Thr188_Phe191del	
CHC857T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC858T	ENST00000381298	<i>IL6ST</i>	c.563_574del; p.Thr188_Val192delinsIle	
CHC861T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC864T	ENST00000381298	<i>IL6ST</i>	c.1252_1263del; p.Ala418_Phe421del	
CHC867T ²	ENST00000381298	<i>IL6ST</i>	c.583_588del; p.Glu195_Val196del	
CHC955T ²	ENST00000381298	<i>IL6ST</i>	c.556_571delinsA; p.Tyr186_Phe191delinsIle	
CHC973T	ENST00000381298	<i>IL6ST</i>	c.569_578delinsC; p.Tyr190_Asn193delinsSer	
CHC974T	ENST00000381298	<i>IL6ST</i>	c.647C>A; p.Pro216His	
CHC975T	ENST00000381298	<i>IL6ST</i>	c.560_571del; p.Ser187_Tyr190del	
CHC976T	ENST00000381298	<i>IL6ST</i>	c.570_578del; p.Phe191_Asn193del	
CHC979T	ENST00000381298	<i>IL6ST</i>	c.646_648del; p.Pro216del	
CHC1001T ²	ENST00000371085	<i>GNAS</i>	c.601C>T; p.Arg201Cys	
CHC1286T	ENST00000371085	<i>GNAS</i>	c.602G>A; p.Arg201His	
CHC1461T	ENST00000371085	<i>GNAS</i>	c.601C>T; p.Arg201Cys	
CHC1519T	ENST00000371085	<i>GNAS</i>	c.602G>A; p.Arg201His	
CHC478T	ENST00000371085	<i>GNAS</i>	c.602G>A; p.Arg201His	
CHC854T	ENST00000371085	<i>GNAS</i>	c.602G>A; p.Arg201His	
CHC1021T ²	ENST00000264657	<i>STAT3</i>	c.1969_1980dup; p.Tyr657_Met660dup	
CHC1351T ²	ENST00000264657	<i>STAT3</i>	c.1969_1970insTTT; p.Gly656_Tyr657insPhe	
CHC2363T	ENST00000264657	<i>STAT3</i>	c.1972A>T; p.Lys658*	
CHC2773T	ENST00000264657	<i>STAT3</i>	c.1969_1970insCATGATCTTATA; p.Tyr657_Met769delinsSerX	
CHC341T ²	ENST00000264657	<i>STAT3</i>	c.233T>G; p.Leu78Arg	
CHC379T ²	ENST00000264657	<i>STAT3</i>	c.1972_1974delinsTAT; p.Lys658Tyr	
CHC574T ²	ENST00000264657	<i>STAT3</i>	c.496G>C; p.Glu166Gln	
CHC966T	ENST00000264657	<i>STAT3</i>	c.1919A>T; p.Tyr640Phe	
CHC1432T ²	ENST00000342505	<i>JAK1</i>	c.2108G>T; p.Ser703Ile	
CHC1490T ²	ENST00000342505	<i>JAK1</i>	c.2168C>A; p.Ala723Asp	
CHC1130T ²	ENST00000368626	<i>FRK</i>	c.1037A>G; p.Glu346Gly	c.1049A>G; p.Tyr350Cys
CHC1239T ²	ENST00000368626	<i>FRK</i>	c.1037A>G; p.Glu346Gly	
CHC1240T ²	ENST00000368626	<i>FRK</i>	c.1132_1137del; p.Val378_Phe379del	
CHC1263T ²	ENST00000368626	<i>FRK</i>	c.1132_1133delinsAAACTAAA; p.Val378delinsLysLeuAsn	
CHC1325T	ENST00000368626	<i>FRK</i>	c.1037A>G; p.Glu346Gly	c.1049A>G; p.Tyr350Cys
CHC1488T ²	ENST00000368626	<i>FRK</i>	c.1132_1137del; p.Val378_Phe379del	
CHC1489T ²	ENST00000368626	<i>FRK</i>	c.1133_1138del; p.Val378_Lys380delinsGlu	
CHC1496T ²	ENST00000368626	<i>FRK</i>	c.1037A>G; p.Glu346Gly	
CHC2193T	ENST00000368626	<i>FRK</i>	c.1133_1138del; p.Val378_Lys380delinsGlu	
CHC2197T	ENST00000368626	<i>FRK</i>	c.1131_1137delinsG; p.Val378_Phe379del	
CHC2331T	ENST00000368626	<i>FRK</i>	c.1132_1133insAAA; p.Val378delinsGluIle	
CHC341T ²	ENST00000368626	<i>FRK</i>	c.1037A>G; p.Glu346Gly	
CHC544T ²	ENST00000368626	<i>FRK</i>	c.1132_1137del; p.Val378_Phe379del	
CHC624T ²	ENST00000368626	<i>FRK</i>	c.1133_1138del; p.Val378_Lys380delinsGlu	
CHC627T ²	ENST00000368626	<i>FRK</i>	c.1137_1140delinsA; p.Phe379_Lys380delinsLeu	
CHC782T ²	ENST00000368626	<i>FRK</i>	c.1132_1137del; p.Val378_Phe379del	
CHC970T	ENST00000368626	<i>FRK</i>	c.1132_1137del; p.Val378_Phe379del	
CHC1279T	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC1349T	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC1391T	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC2321T ²	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC361TA ²	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC469T ²	ENST00000310581	<i>TERT</i> prom	c.-146G>A	
CHC663T	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC700T ²	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC701T ²	ENST00000310581	<i>TERT</i> prom	c.-124G>A	
CHC917T	ENST00000310581	<i>TERT</i> prom	c.-124G>A	

² Previously described in Pilati C *et al* (Cancer cell 2014)



Click here to access/download

**Revised Manuscript in Word or RTF (no changes
marked)**

NaultetalGastroenterologyWITHOUTCHANGES.docx

