

Heading	
HG19_End	Mutation start coordinates using HG19 as reference
HG19_Start	Mutation end coordinates using HG19 as reference
NG_017013.2_Variant	Mutation nomenclature according to HGVS standards using the RefSeq Gene NG_017013. sequence as reference <a href="http://www.ncbi.nlm.nih.gov/nuccore/NG_017013.2">http://www.ncbi.nlm.nih.gov/nuccore/NG_017013.2</a> This sequence is also the reference used by the Locus Reference Genomic ( <a href="http://ftp.ebi.ac.uk/pub/databases/LRG/LRG_321.xml">http://ftp.ebi.ac.uk/pub/databases/LRG_321.xml</a> )
HGVS_Genomic_GRCh37	Mutation nomenclature according to HGVS standards using the genomic sequence as reference Reference sequence: NC_000017.10 for genome build NCBI37/hg19
HGVS_Genomic_GRCh38	Mutation nomenclature according to HGVS standards using the genomic sequence as reference Reference sequence: NC_000017.11 for genome build GRCh38.p2
Variant_Type	Variant type as defined in MAF file : SNP: Single Nucleotide Variant DNP: Change in two consecutive bases (dinucleotide polymorphism) TNP: Change in three consecutive bases (trinucleotide polymorphism) ONP: Change in four or more consecutive bases (oligo-nucleotide polymorphism) INS: Insertion DEL: Deletion
Event_type_db	Mutational event: NR: not relevant
Consequence_protein	Indicates whether or not the TP53 variant is expressed
Mutation_effect	Translational effect of the mutation (Missense, Nonsense, Synonymous, Nonstop, In_frame_Del, Inframe_Ins, Frameshift_Del or Frameshift_Ins).
Gene_effect	Location of the mutation in the TP53 gene
Protein P1 TP53_alpha NP_000537.3	Protein variant description; reference sequence NP_000537.3
Protein P3 TP53_beta NP_001119586.1	Protein variant description; reference sequence NP_001119586.1
Protein P4 TP53_gamma NP_001119585.1	Protein variant description; reference sequence NP_001119585.1
Genome_Base_Non_Coding	Nucleotide at the start position of the mutation
Mutant_Allele	Mutant nucleotide
Base_Change_Size	Size of the substitution
Del_Size	Size of the deletion
Ins_Size	Size of the insertion; the sequence of the insertion is available for a few cases
Exon_start	<p>Location of the mutation start in the introns or exons of the TP53 gene. In most cases, Exon:intron_Start and Exon:intron_stop are similar.</p> <p>A few large deletions encompass several exons and introns.</p> <p>Although all intronic variations described in the literature have been included in the database, only mutations that target the canonical AG spliceacceptor site or GT splice-donor site (-1,-2, +1, +2) are considered to be pathogenic (see splice comment for more information).</p>
Exon_End	<p>Location of the mutation end in the introns or exons of the TP53 gene. In most cases, Exon:intron_Start and Exon:intron_stop are similar.</p> <p>A few large deletions encompass several exons and introns.</p> <p>Although all intronic variations described in the literature have been included in the database, only mutations that target the canonical AG spliceacceptor site or GT splice-donor site (-1,-2, +1, +2) are considered to be pathogenic (see splice comment for more information).</p>
Codon_start	Codon position using TP53 alpha (p1) as reference (NP_000537.2)
Codon_end	Codon position using TP53 alpha (p1) as reference (NP_000537.2)
LRG_321t1	Mutation nomenclature according to HGVS standards using the coding sequence as reference (position 1 refers to the A of the start ATG); reference sequence NM_000546.5
Disease_Name	Cancer type
Oncotree	Cancer classification according to oncotree: <a href="http://oncotree.mskcc.org">http://oncotree.mskcc.org</a>
Sample_ID	Patient ID
Complexity	<b>SM</b> : Single mutational event in the tumour; ; <b>DMU</b> (Double Mutation Unknown): Two p53 mutations in the same tumour, but their allelic distribution is unknown.; <b>DMD</b> (Double Mutation Different allele): Two p53 mutations in the same tumour on two different p53 alleles.; <b>DMS</b> ; (Double Mutation Same allele): Two p53 mutations in the same tumour on the same p53 allele. ; <b>MM</b> (Multiple Mutation): More than two p53 mutations in the same tumour.
Project_ID	Method used for the analysis, NGS or Sanger
True_complexity	Total number of variants in the sample
SNP_Tag	SNP status
tag_Splice	Potential defect in splicing
VAF	Variant allele frequency when available















