



The Complex Evolutionary Dynamics of Hsp70s: A Genomic and Functional Perspective

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Barry L. Williams

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Supplementary Fig. S1. Hsp70 orthologs identified in 57 fungal species with the 14 *S.c*
reciprocal best-blast hits against the *S. cerevisiae* proteins (rec-BLAST) are shown for each i

Group	Species / Strain	Data Source(s)
	<i>Ustilago maydis</i>	BROAD Institute
	<i>Cryptococcus neoformans grubii h99</i>	BROAD Institute
BASIDIOMYCOTA	<i>Phanerochaete chrysosporium</i>	JGI BROAD Institute
	<i>Coprinopsis cinerea okayama</i>	BROAD Institute
	<i>Schizosaccharomyces japonicus</i>	BROAD Institute
	<i>Schizosaccharomyces pombe 972h-</i>	BROAD Institute

SCHIZOSACCHAROMYCES

Fungi Hsp70

Schizosaccharomyces octosporus

BROAD Institute

Schizosaccharomyces cryophilus

BROAD Institute

Magnaporthe grisea 70-15 (MG6)

BROAD Institute

Neurospora crassa OR74A (NC10)

BROAD Institute

Podospora anserina

Podospora anserina Genome Project

Chaetomium globosum

BROAD Institute

Fungi Hsp70

PEZIZOMYCOTINA

Trichoderma reesei

JGI

Gibberella moniliformis
(*Fusarium verticillioides*)

BROAD Institute

Gibberella zeae
(*Fusarium graminearum*)

BROAD Institute

Botryotinia fuckeliana

BROAD Institute
Genoscope

Sclerotinia sclerotiorum

BROAD Institute

Phaeosphaeria nodorum

BROAD Institute

Fungi Hsp70

Ajellomyces capsulatus G186AR

BROAD Institute

Uncinocarpus reesii

BROAD Institute

Coccidioides immitis RS

BROAD Institute

Aspergillus nidulans FGSC A4

BROAD Institute

Aspergillus fumigatus

EBI Integr8

Aspergillus oryzae

BROAD Institute

Fungi Hsp70

Aspergillus terreus

BROAD Institute

Candida hispaniensis Y-5580

Cecile Neuveglise

Candida alimentaria

Cecile Neuveglise

Candida phangngensis CBS10407

Cecile Neuveglise

Candida yakushimensis CBS10253

Cecile Neuveglise

YARROWIA

Fungi Hsp70

Candida galli CBS9722

Cecile Neuveglise

Yarrowia lipolytica

Genolevures

Candida lusitanae

BROAD Institute

Meyerozyma guilliermondii
(*Pichia guilliermondii*)

BROAD Institute

CTG GROUP

<i>Debaryomyces hansenii</i>	Fungi Hsp70 BROAD Institute Genolevures
<i>Candida parapsilosis</i>	BROAD Institute
<i>Candida tropicalis</i>	BROAD Institute
<i>Candida dubliniensis</i>	Sanger Institute
<i>Candida albicans</i> WO-1	BROAD Institute
<i>Scheffersomyces stipitis</i>	NCBI

Fungi Hsp70

<i>Candida orthopsilosis</i> Co 90-125	NCBI
<i>Candida orthopsilosis</i> AY2	NCBI

<i>Candida tenuis</i>	NCBI
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<i>Lodderomyces elongisporus</i>	BROAD Institute
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<i>Spathaspora passalidarum</i>	NCBI
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<i>Lachancea kluyveri</i> (<i>Saccharomyces kluyveri</i>)	Genolevures
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Fungi Hsp70

Lachancea thermotolerans

Genolevures

Lachancea waltii

BROAD Institute
Kellis et al, 2004 (sup. materials)

Kluyveromyces lactis

Genolevures

Eremothecium gossypii

EBI Integr8

Zygosaccharomyces rouxii

Genolevures

<i>Vanderwaltozyma polyspora</i>	SGD
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<i>Naumovozyima castelli</i> (<i>Saccharomyces castelli</i>)	YGOB NCBI
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<i>Candida glabrata</i>	Genolevures
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<i>Saccharomyces uvarum</i> (<i>Saccharomyces bayanus</i> CBS 7001)	Saccharomyces Sensu Stricto Project SGD
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SACCHAROMYCETACEAE POST-WGD

Saccharomyces kudriavzevii IFO 1802 Saccharomyces Sensu Stricto Project

Saccharomyces mikatae IFO 1815 Saccharomyces Sensu Stricto Project

Saccharomyces paradoxus Saccharomyces Sensu Stricto Project

Fungi Hsp70

Saccharomyces cerevisiae

SGD



erevisiae Hsp70 proteins used as queries. Taxonom
identified Hsp70 ortholog. Specific issue encountered in

ORF ID(s) / Gene name

UM03791.1

UM04434+UM04435

UM05918.1

UM01209.1

UM05357.1

UM00904.1

CNAG_01750.2

CNAG_01727.2

CNAG_00334.2

CNAG_06208.2

CNAG_05199.2

CNAG_01404.2

CNAG_06443.2

CNAG_03899.2

e_gwh2.1.247.1

e_gwh2.1.301.1

fgenes1_pm.C_scaffold_6000005

fgenes1_pg.C_scaffold_12000350

Gww2.10.123.1

e_gww2.9.92.1

fgenes1_pg.C_scaffold_9000190

CC1G_13924.2

CC1G_13982.2

CC1G_09266.2

CC1G_06894.2

CC1G_05804.2

CC1G_12348.2

CC1G_09108.2

CC1G_14207.2

 SJAG_04055

SJAG_01186

SJAG_05779

SJAG_03237

SJAG_04511

SJAG_05709

SJAG_01510

SJAG_00790

SJAG_02875

SPAC13G7_02c / ssa1

SPCC1739_13 / ssa2

SPBC1709_05

Fungi Hsp70

SPAC110_04c
SPAC664_11
SPAC57A7_12
SPAC22A12_15c
SPAC1F5_06

SOCG_04298
SOCG_02770
SOCG_03479
SOCG_00373
SOCG_01535
SOCG_02356
SOCG_02212
SOCG_00522

SPOG_00242
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SPOG_04259
SPOG_02132
SPOG_05615
SPOG_05669
SPOG_00613
SPOG_01983

MGG_06958.6
MGG_11513.6
MGG_06065.6
MGG_04191.6
MGG_02842.6
MGG_02503.6
MGG_06648.6

NCU09602.4 / HSP70
NCU02075.4
NCU05269.4
NCU08693.4
NCU00692.4
NCU03982.4
NCU09485.4

Pa_6_4100
Pa_1_2670
Pa_3_4490
Pa_6_2570
Pa_1_18900
Pa_4_6420
Pa_3_10060

CHGG_08262.1
CHGG_01675.1
CHGG_04834.1

CHGG_04605.1
CHGG_06364.1
CHGG_09206.1
CHGG_01653.1
CHGG_10554.1

e_gw1.2.175.1
estExt_fgenesh5_pg.C_130159
estExt_GeneWisePlus.C_400011
estExt_fgenesh5_pg.C_20133
estExt_fgenesh1_pm.C_60103
estExt_fgenesh5_pg.C_160150
gw1.9.395.1

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FVEG_00688.2
FVEG_07295.2
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FVEG_02022.2
FVEG_04019.2
FVEG_11493.2

FGSG_00838.2
FGSG_00921.2
FGSG_01950.2
FGSG_06154.2
FGSG_08644.2
FGSG_09471.2
FGSG_10819.2

BC1G_06164.1 / BofuT4_P016860.1
BC1G_10845.1+BC1G_10846.1 / BofuT4_P147470.1
BC1G_09769.1
BC1G_11661.1
BC1G_00968.1
BC1G_04390.1
BC1G_12543.1

SS1G_00134.1
SS1G_05645.1
SS1G_01888.1
SS1G_09744.1
SS1G_09280.1
SS1G_02266.1
SS1G_10087.1

SNOG_14320.1+SNOG_14321.1+SNOG_14322.1
SNOG_04404.1
SNOG_06062.1
SNOG_13583.1

Fungi Hsp70

SNOG_00353.1
SNOG_12476.1
SNOG_02459.1

HCBG_07920.2
HCBG_04781.2
HCBG_04755.2
HCBG_08743.2
HCBG_02577.2
HCBG_05946.2
HCBG_03803.2

UREG_03219.1
UREG_01466.1
UREG_03621.1
UREG_01663.1
UREG_06810.1
UREG_01160.1
UREG_07090.1

CIMG_02494.3
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CIMG_01851.3
CIMG_01229.3
CIMG_03236.3

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Afu2g04620
Afu1g15050

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AO090003000257

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ATEG_10178.1
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ATEG_00453.1
ATEG_04432.1
ATEG_06952.1
ATEG_06040.1
ATEG_00843.1

YAHIOS3-06700g

YAHIOS6-03510g

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CLUG_05445.1
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PGUG_04519.1
PGUG_00144.1
PGUG_04934.1 (partial)
PGUG_02995.1

Fungi Hsp70

DEHA0D06116g
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DEHA0D17215g
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DEHA0A01749g
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DEHA2E03410g

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CPAG_04207.0
CPAG_00100.0
CPAG_03670.0
CPAG_04753.0
CPAG_01744.0
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CPAG_01321.0

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CTRG_03925.3
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CTRG_01349.3

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CD36_44350
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CAWG_04044.1

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CANTEDRAFT_128824

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SAKL0F12606g
SAKL0E13618g

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SAKL0D11638g
SAKL0H04004g
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SAKL0G11792g
SAKL0B11990g

KLTH0H08448g
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KLTH0B07744g
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KLTH0F07150g
KLTH0G07810g
KLTH0B04290g

Kwal_2130
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Kwal_4548
Kwal_12262
Kwal_14307 (partial)
Kwal_9278 (partial)
Kwal_14336
Kwal_2889
Kwal_14948

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KLLA0E20527g
KLLA0D19041g
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KLLA0C14652g
KLLA0D09559g
KLLA0F26455g

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EGOS_Q756R7 / AGOS_AER187W
EGOS_Q75E44 / AGOS_ABL174C
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EGOS_Q753R1 / AGOS_AFR352C
EGOS_Q752J2 / AGOS_AFR583W
EGOS_Q75EX1 / AGOS_AAL043C
EGOS_Q75C78 / AGOS_ACR038W
EGOS_Q759Z5 / AGOS_ADR128C

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ZYRO0B07524g
ZYRO0C14190g
ZYRO0A10846g
ZYRO0E01474g

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Kpol_1048.35
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Kpol_472.7
Kpol_1012.1
Kpol_1005.9
Kpol_339.4
Kpol_1004.11
Kpol_1019.2
Kpol_1073.18

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NCAS_0A14440
NCAS_0E02580
NCAS_0D00240
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NCAS_0C01870
NCAS_0B01860
NCAS_0A08260
NCAS_0J01260
NCAS_0H01530
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CAGL0G04917g
CAGL0I03322g
CAGL0I01496g
CAGL0L10560g
CAGL0D02948g
CAGL0F06369g

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Sbay_10.49 // Sbay_Contig566.14
Sbay_2.44 // Sbay_Contig616.26
Sbay_5.222 // Sbay_Contig677.58
Sbay_4.15 // Sbay_Contig538.4

Sbay_14.134 // Sbay_Contig667.61
Sbay_16.206
Sbay_4.422
Sbay_12.128
Sbay_10.485
Sbay_5.39
Sbay_15.253
Sbay_12.47
Sbay_11.150

Skud_1.58
Skud_12.44
Skud_2.32
Skud_5.228
Skud_4.25
Skud_14.127
Skud_16.177
Skud_2.297
Skud_10.263
Skud_5.61
Skud_12.454
Skud_8.121
Skud_10.188
Skud_11.153

Smik_1.63
Smik_12.40
Smik_2.43
Smik_5.249
Smik_1.64
Smik_4.12
Smik_14.123
Smik_16.131
Smik_2.310
Smik_10.320
Smik_5.73 / Smik_5.74
Smik_12.456
Smik_8.135
Smik_10.238
Smik_11.165

Spar_1.73
Spar_12.48
Spar_2.48
Spar_5.276
Spar_4.37
Spar_14.132
Spar_16.222
Spar_2.330
Spar_10.310
Spar_12.506
Spar_5.49

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Spar_8.141
Spar_10.229
Spar_11.184

YAL005C
YLL024C
YBL075C
YER103W
YDL229W
YNL209W
YPL106C
YBR169C
YJR045C
YLR369W
YEL030W
YHR064C
YJL034W
YKL073W

Fungi Hsp70

ic group, ORF/Gene names, their approximate genomic location, names given in this work (Given Name)
the identification process are explained in the Notes section.

Approximate genomic location of the ORF	Given Name
Contig 126: 117491-119428 +	UmaySSA
Contig 157: 150824 – 149484, 151718 – 151260, 152019 – 151956	UmaySSB1
Contig 216: 22904-25867 +	UmaySSE1
Contig 43: 12990-15309 -	UmaySSC1
Contig 192: 77460-79277 -	UmaySSZ1
Contig 32: 325 – 1 // Contig 31: 84996 – 83292	UmayKAR2
Contig 30: 62426-65185 -	UmayLHS1
Chromosome 11: 787758-790112 -	CneoSSA1
Chromosome 11: 729059-731645 +	CneoSSA2
Chromosome 1: 857472-859921 +	CneoSSB1
Chromosome 12: 630749-633499 +	CneoSSE1
Chromosome 4: 697170-699940 +	CneoSSC1
Chromosome 5: 394159-396194 +	CneoSSZ1
Chromosome 13: 499100-501759 -	CneoKAR2
Chromosome 2: 1130168-1133013 +	CneoLHS1
scaffold_1:1436212-1438391	PchrSSA
scaffold_1:1820168-1822284	PchrSSB1
scaffold_6:138921-141446	PchrSSE1
scaffold_12:1072737-1074905	PchrSSC1
scaffold_10:1261738-1263184	PchrSSZ1
scaffold_9:750951-753143	PchrKAR2
scaffold_9:620781-623737	PchrLHS1
Supercontig 2: 1783904-1786230 -	CcinSSA
Supercontig 2: 2701019-2703492 +	CcinSSB1
Supercontig 3: 3516070-3518798 +	CcinSSE1
Supercontig 3: 2451192-2453422 +	CcinSSC1
Supercontig 12: 216005-218031 +	CcinSSZ1
Supercontig 10: 1397150-1399622 -	CcinKAR2
Supercontig 10: 1064743-1067804 -	CcinLHS1
Supercontig 3: 1960479-1963567 +	CcinKAR2p
Chromosome 2: 3183743-3186117 +	SjapSSA-I
Chromosome 3: 1132068-1134327 -	SjapSSA-II
Chromosome 3: 2523408-2525449 +	SjapSSB1
Chromosome 2: 691851-693863 -	SjapSSB2
Chromosome 3: 714716-717686 +	SjapSSE1
Chromosome 3: 2001458-2003774 +	SjapSSC1
Chromosome 3: 1786066-1788033 +	SjapSSZ1
Chromosome 1: 2667113-2669515 -	SjapKAR2
Chromosome 1: 1651957-1654797 +	SjapLHS1
Supercontig 2: 2297753 – 2295819	SpomSSA-I
Supercontig 3: 2057243 – 2059186	SpomSSA-II
Supercontig 2: 1106456 – 1108297	SpomSSB1

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Supercontig 1: 1920160 – 1917998	SpomSSE1
Supercontig 1: 1726009 – 1728033	SpomSSC1
Supercontig 1: 1515089-1516914 -	SpomSSZ1
Supercontig 1: 1185303 – 1183312	SpomKAR2
Supercontig 1: 281367 – 278599	SpomLHS1
Chromosome 3: 576782-579147 -	SoctSSA-I
Chromosome 1: 320278-322202 -	SoctSSA-II
Chromosome 1: 2053617-2055908 -	SoctSSB1
Chromosome 2: 2092129-2094901 +	SoctSSE1
Chromosome 3: 2196974-2199415 -	SoctSSC1
Chromosome 1: 3427346-3429199 -	SoctSSZ1
Chromosome 1: 3105086-3107714 -	SoctKAR2
Chromosome 2: 2444159-2447187 -	SoctLHS1
Supercontig 3: 532003-534426 -	ScrySSA-I
Supercontig 4: 334784-337065 -	ScrySSA-II
Supercontig 9: 444495-446661 -	ScrySSB1
Supercontig 2: 1328159-1330917 -	ScrySSE1
Supercontig 1: 923558-926038 -	ScrySSC1
Supercontig 5: 927867-929974 -	ScrySSZ1
Supercontig 5: 614924-617571 -	ScryKAR2
Supercontig 2: 974957-977770 +	ScryLHS1
Supercontig 18: 935235-937726 -	MgriSSA
Supercontig 21: 1724419-1727245 +	MgriSSB1
Supercontig 24: 545033-548037 -	MgriSSE1
Supercontig 12: 486481-489423 +	MgriSSC1
Supercontig 23: 918967-920953 +	MgriSSZ1
Supercontig 18: 2064348-2066834 -	MgriKAR2
Supercontig 18: 2211652-2214877 -	MgriLHS1
Supercontig 2: 79807-82656 -	NcraSSA
Supercontig 1: 1450891-1453703 +	NcraSSB1
Supercontig 4: 5521208-5524832 -	NcraSSE1
Supercontig 4: 4072155-4075127 +	NcraSSC1
Supercontig 1: 7530307-7532510 +	NcraSSZ1
Supercontig 6: 2302462-2305332 -	NcraKAR2
Supercontig 2: 4430576-4433950 +	NcraLHS1
CHR 6: 160198 – 162442	PansSSA
CHR 1: 962007 – 964244	PansSSB1
CHR 3: 926456 – 929160	PansSSE1
CHR 6: 1429367 – 1431561	PansSSC1
CHR 1: 1696036 – 1697858	PansSSZ1
CHR 4: 1766710 – 1769004	PansKAR2
CHR 3: 2861974 – 2865069	PansLHS1
Supercontig 5: 4397131-4399392 +	CgloSSA
Supercontig 1: 5157151-5159397 -	CgloSSB1
Supercontig 4: 3438199-3440891 -	CgloSSE1

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Supercontig 4: 2692267-2694395 +	CgloSSC1
Supercontig 3: 3303639-3305447 +	CgloSSZ1
Supercontig 6: 2741846-2744216 -	CgloKAR2
Supercontig 1: 5081454-5083492 +	CgloKAR2p
Supercontig 7: 3076476-3079557 +	CgloLHS1
scaffold_2:1721232-1723250	TreeSSA
scaffold_13:501120-503692	TreeSSB1
scaffold_40:20191-23199	TreeSSE1
scaffold_2:459908-462223	TreeSSC1
scaffold_6:874716-876824	TreeSSZ1
scaffold_16:512482-515161	TreeKAR2
scaffold_9:508545-511499	TreeLHS1
Supercontig 1: 2118626-2121082 +	GmonSSA
Supercontig 1: 2008124-2011068 -	GmonSSB1
Supercontig 9: 379858-382935 -	GmonSSE1
Supercontig 7: 905127-908495 +	GmonSSC1
Supercontig 2: 1460770-1462601 +	GmonSSZ1
Supercontig 4: 1690107-1692628 +	GmonKAR2
Supercontig 17: 362696-366046 -	GmonLHS1
Supercontig 1: 2689098-2691457 -	GzeaSSA
Supercontig 1: 2987810-2990564 +	GzeaSSB1
Supercontig 1: 6393997-6397123 +	GzeaSSE1
Supercontig 3: 4480983-4483396 +	GzeaSSC1
Supercontig 5: 1135291-1137371 +	GzeaSSZ1
Supercontig 6: 1681356-1683917 +	GzeaKAR2
Supercontig 8: 1239854-1243148 +	GzeaLHS1
Supercontig 29: 217973-220426 -	BfucSSA
Supercontig 80: 115316-116955 - / Supercontig 80: 117318-119054 -	BfucSSB1
Supercontig 66: 142479-144980 +	BfucSSE1
Supercontig 91: 152354-154585 +	BfucSSC1
Supercontig 3: 72264-74141 -	BfucSSZ1
Supercontig 18: 306893-309142 -	BfucKAR2
Supercontig 103: 133202-136309 +	BfucLHS1
Supercontig 1: 360402-362841 +	SsclSSA
Supercontig 7: 85362-87846 +	SsclSSB1
Supercontig 2: 2131071-2133573 -	SsclSSE1
Supercontig 14: 356107-358330 +	SsclSSC1
Supercontig 13: 380553-382433 +	SsclSSZ1
Supercontig 3: 436178-438409 +	SsclKAR2
Supercontig 15: 78997-82107 +	SsclLHS1
Supercontig 31: 75420-79148 +	PnodSSA
Supercontig 6: 669855 - 672136	PnodSSB1
Supercontig 8: 1294925-1297418 -	PnodSSE1
Supercontig 27: 223556-225572 +	PnodSSC1

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Supercontig 1: 825701-827510 -	PnodSSZ1
Supercontig 22: 436572 – 432968 -	PnodKAR2
Supercontig 3: 1389497-1392654 +	PnodLHS1
Supercontig 14: 787633-790545 -	AcapSSA
Supercontig 6: 246375-249081 +	AcapSSB1
Supercontig 6: 175186-178648 -	AcapSSE1
Supercontig 17: 332729-336038 -	AcapSSC1
Supercontig 3: 1241446-1243861 +	AcapSSZ1
Supercontig 8: 462625-465850 +	AcapKAR2
Supercontig 4: 2258060-2261385 -	AcapLHS1
Supercontig 2: 732847-734942 -	UreeSSA
Supercontig 1: 3706657-3708820 +	UreeSSB1
Supercontig 2: 1898773-1901396 +	UreeSSE1
Supercontig 1: 4304912-4307119 +	UreeSSC1
Supercontig 4: 2000023-2001905 +	UreeSSZ1
Supercontig 1: 2836596-2838920 -	UreeKAR2
Supercontig 5: 207815-210859 +	UreeLHS1
Supercontig 1: 1675495-1678079 -	CimmSSA
Supercontig 1: 2256912-2259616 +	CimmSSB1
Supercontig 2: 3686703-3689818 -	CimmSSE1
Supercontig 4: 521504-524476 +	CimmSSC1
Supercontig 1: 3583856-3586135 -	CimmSSZ1
Supercontig 1: 5252843-5255630 +	CimmKAR2
Supercontig 6: 809068-812503 +	CimmLHS1
Contig 88: 88007-90384 +	AnidSSA
Contig 175: 18168-19865 + / Contig 22: 134-1579 +	AnidSSB1
Contig 16: 8192-11153 +	AnidSSE1
Contig 103: 5334-7986 +	AnidSSC1
Contig 79: 68926-71101 -	AnidSSZ1
Contig 32: 187084-189402 -	AnidKAR2
Contig 13: 191288-194278 -	AnidLHS1
Chromosome 1: 2102587-2104621 +	AfumSSA
Chromosome 8: 839316-841607 +	AfumSSB1
Chromosome 1: 3331407-3333764 +	AfumSSE1
Chromosome 2: 2551872-2554095 -	AfumSSC1
Chromosome 2: 584085-586013 -	AfumSSZ1
Chromosome 2: 1258486-1260682 -	AfumKAR2
Chromosome 1: 4045354-4048347 -	AfumLHS1
Supercontig 12: 2578981-2581024 +	AorySSA
Supercontig 25: 21617-23874 +	AorySSB1
Supercontig 17: 1656464-1658958 +	AorySSE1
Supercontig 22: 1645256-1647468 +	AorySSC1
Supercontig 22: 1284917-1286908 -	AorySSZ1
Supercontig 6: 682684-684869 +	AoryKAR2

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Supercontig 2: 3237941-3240898 +	AoryLHS1
Supercontig 16: 632123-634104 +	AterSSA
Supercontig 1: 13213-15416 -	AterSSB1
Supercontig 1: 1283326-1285800 +	AterSSE1
Supercontig 6: 524851-527117 -	AterSSC1
Supercontig 10: 305711-307663 +	AterSSZ1
Supercontig 8: 1156564-1158740 +	AterKAR2
Supercontig 1: 2352335-2361162 +	AterLHS1
YAHIOS3_545647..547605	ChisSSA-X1
YAHIOS6_270881..272824	ChisSSA-A
YAHI_scf4343_434777..436777	ChisKAR2
YAHI_scf4344_84637..86862	ChisSSC1
YAHI_scf4340_426683..428518	ChisSSB1
YAHI_scf4343_680889..682967	ChisSSE1
YAHI_scf4345_178227..179846	ChisSSZ1
YAHI_scf4341_168515..171424	ChisLHS1
YAAL_scf8585_2882264..2884198	CaliSSA-E
YAAL_scf8609_2533460..2535394	CaliSSA-X2
YAAL_scf8610_806196..808157	CaliSSA-G
YAAL_scf8611_3130179..3132134	CaliSSA-A
YAAL_scf8613_411018..412976	CaliSSA-C
YAAL_scf8613_155349..155953[pseudo]	CaliSSA-X3p
YAAL_scf8611_2204030..2206042	CaliKAR2
YAAL_scf8585_1668335..1670537	CaliSSC1
YAAL_scf8605_54251..56086	CaliSSB1
YAAL_scf8611_1242441..1244495	CaliSSE1
YAAL_scf8609_1004967..1006577	CaliSSZ1
YAAL_scf8609_1683712-1686792.	CaliLHS1
YAPH233-YALIOD08184g complement(1614545..1616491)	CphaSSA-C
YAPH233-YALIOD22352g complement(3197089..3199029)	CphaSSA-G
YAPH240-YALIOD08184g complement(1417672..1419603)	CphaSSA-X4
YAPH240-YALIOD08184g complement(444452..446380)	CphaSSA-X5
YAPH242-YALIOD08184g complement(1854555..1856501)	CphaSSA-A
YAPH239-YALIOE13706g 1641771..1643789	CphaKAR2
YAPH233-YALIOC17347g join(618522..618560,618773..620680)	CphaSSC1
YAPH242-YALIOA00132g complement(168836..170671)	CphaSSB1
YAPH239-YALIOE13255g complement(1675854..1677911)	CphaSSE1
YAPH241-YALIOB12474g 199154..200764	CphaSSZ1
YAPH241-YALIOB08778g complement(1092513..1095374)	CphaLHS1
YAYA_scf25028_28151..30081	YyakSSA-Fp
YAYA_scf25030_10981..12897	YyakSSA-D
YAYA_scf25030_622567..624501	YyakSSA-E
YAYA_scf25031_2026191..2028137	YyakSSA-A
YAYA_scf25031_2677312..2679276	YyakSSA-B
YAYA_scf25032_1078054..1080003	YyakSSA-C
YAYA_scf25030_2324415..2326427	YyakKAR2
YAYA_scf25033_736061..738306	YyakSSC1

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YAYA_scf25032_13901..15736	YyakSSB1
YAYA_scf25030_1569979..1572036	YyakSSE1
YAYA_scf25034_2297654..2299264	YyakSSZ1
YAYA_scf25034_3835205..3838159	YyakLHS1
Yaga0C-YALIO0D08184g complement(join(1301102..1302967,1302967..1303059))	CgalSSA-A
Yaga0D-YALIO0D22352g 1595424..1597382	CgalSSA-B
Yaga0D-YALIOE35046g complement(3125512..3127443)	CgalSSA-X6
Yaga0E-YALIOE35046g 718090..720036	CgalSSA-E
Yaga0E-YALIOE35046g complement(4952556..4954487)	CgalSSA-F
Yaga0E-YALIOE35046g3 19404..21335	CgalSSA-D
Yaga0F-YALIOF25289g 5231772..5233733	CgalSSA-C
Yaga0E-YALIOE13706g complement(4384451..4386463)	CgalKAR2
Yaga0B-YALIO0C17347g 2599322..2601641	CgalSSC1
Yaga0D-YALIOA00132g 39754..41589	CgalSSB1
Yaga0E-YALIOE13255g 2867376.. 2869433	CgalSSE1
Yaga0F-YALIOB12474g complement(2631902..2633512)	CgalSSZ1
Yaga0E-YALIOB08778g 3129789.. 3132875	CgalLHS1
CHR D: 1045550 – 1043604	YlipSSA-A
CHR D: 2843487 – 2845436	YlipSSA-B
CHR F: 3260540 – 3258579	YlipSSA-C
CHR E: 4190297 – 4188366	YlipSSA-D
CHR E: 3493589 – 3493885	YlipSSA-Ep
CHR A: 7045 – 8880	YlipSSB1
CHR E: 1595877 – 1597934	YlipSSE1
CHR C: 2440654 – 2440692, 2438437 – 2440341	YlipSSC1
CHR B: 1664503 – 1666113	YlipSSZ1
CHR E: 1658116 – 1656104	YlipKAR2
CHR B: 1207977 – 1204954	YlipLHS1
Supercontig 4: 77068-79032 -	ClusSSA-a
Supercontig 2: 390531-392468 +	ClusSSA-b
Supercontig 3: 1072350-1074239 -	ClusSSB1
Supercontig 2: 1623249-1625318 +	ClusSSE1
Supercontig 5: 42250-44184 +	ClusSSC1
Supercontig 4: 1315749-1317701 -	ClusSSQ1
Supercontig 8: 549826-551862 +	ClusKAR2
Supercontig 7: 427265-428886 +	ClusSSZ1
Supercontig 5: 879033-882343 +	ClusLHS1
Supercontig 7: 760966-762921 +	MguiSSA-ap
Supercontig 6: 360136 – 358199	MguiSSA-b
Supercontig 2: 1331754 – 1329913	MguiSSB1
Supercontig 1:1030838 – 1032948	MguiSSE1
Supercontig 5: 350855 – 352801	MguiSSC1
Supercontig 5: 1055829 – 1057802	MguiSSQ1
Supercontig 1: 244452-242821	MguiSSZ1
Supercontig 6: 596018 – 593982	MguiKAR2
Supercontig 3: 1231598 – 1228821	MguiLHS1

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Supercontig 4: 436738-438699 -	DhanSSA-a
Supercontig 4: 1059116-1061062 +	DhanSSA-b
Supercontig 1: 937961-939802 +	DhanSSB1
Supercontig 4: 1324520-1326607 +	DhanSSE1
Supercontig 3: 727170-729113 +	DhanSSC1
Supercontig 7: 1354668-1356635 +	DhanSSQ1
Supercontig 1: 108699-110750 -	DhanKAR2
Supercontig 7: 349980-352748 +	DhanLHS1
Supercontig 5/E: 291711 - 293339	DhanSSZ1
Contig 136: 73482-75437 -	CparSSA-a
Contig 140: 211688-213628 +	CparSSA-b
Contig 135: 255883-257724 -	CparSSB1
Contig 35: 3304-5424 +	CparSSE1
Contig 130: 154581-156536 -	CparSSC1
Contig 139: 220038-221975 -	CparSSQ1
Contig 102: 106644-108257 -	CparSSZ1
Contig 138: 269187-271241 +	CparKAR2
Contig 93: 11466-14276 -	CparLHS1
Supercontig 4: 1466594-1468540 -	CtroSSA-a
Supercontig 6: 1007504-1009438 +	CtroSSA-b
Supercontig 4: 164218-166059 -	CtroSSB1
Supercontig 5: 1351392-1353467 -	CtroSSE1
Supercontig 2: 1395100-1397040 +	CtroSSC1
Supercontig 7: 759503-761413 -	CtroSSQ1
Supercontig 5: 470629-472251 +	CtroSSZ1
Supercontig 2: 483729-485789 -	CtroKAR2
Supercontig 2: 594327-597200 +	CtroLHS1
CHR 1: 2990554 – 2992533 +	CdubSSA-a
CHR 1: 919866 – 921809 -	CdubSSA-b
CHR R: 1735413 – 1737254 +	CdubSSB1
CHR 1: 1317430 – 1319556 -	CdubSSE1
CHR 2: 1509835 – 1511781 +	CdubSSC1
CHR 7: 922410 – 924329 +	CdubSSQ1
CHR 4: 1045493 – 1047115 +	CdubSSZ1
CHR 2: 188912 – 190969 +	CdubKAR1
CHR 2: 579192 - 576394 -	CdubLHS1
Supercontig 1: 238582-240513 -	CalbSSA-a
Supercontig 1: 2302015-2303952 +	CalbSSA-b
Supercontig 2: 1758887-1760728 +	CalbSSB1
Supercontig 1: 1913171-1915279 +	CalbSSE1
Supercontig 9: 139233-141179 +	CalbSSC1
Supercontig 8: 876839-878755 +	CalbSSQ1
Supercontig 4: 601054-602676 -	CalbSSZ1
Supercontig 5: 180920-182983 +	CalbKAR2
Supercontig 5: 549902-552700 +	CalbLHS1
Chr1 (2017568..2019526)	SstiSSA-a

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Chr6 complement(630721..632652)	SstiSSA-b
Chr7 (460467..462308)	SstiSSB1
Chr6 complement(1635139..1637082)	SstiSSC1
Chr2 complement(1594863..1596815)	SstiSSQ1
Chr2 complement(255860..257905)	SstiKAR2
Chr1 complement(975511..977601)	SstiSSE1
Chr7 (119178..120815)	SstiSSZ1
Chr2 complement(543302..546091)	SstiLHS1
c7 complement(79787..80419) // contig64 (7490-12309)	CortSSA-a
c2 (1696261..1696893) // contig718 (5506-10334)	CortSSA-b
c4 complement(1161719..1163560)	CortSSB1
c2 (1324900..1326855)	CortSSC1
c7 (512271..514211)	CortSSQ1
c1 complement(2866861..2868912)	CortKAR2
c2 (1077703..1079796)	CortSSE1
c5 complement(1009642..1011255)	CortSSZ1
c1 complement(2559395..2562205)	CortLHS1
c21 (2016600..2018534)	CtenSSA-a
c15 complement(524416..526344)	CtenSSA-b
c4 (8246..10087)	CtenSSB1
c4 complement(664208..666142)	CtenSSC1
c8 complement(14877..16799)	CtenSSQ1
c6 complement(590787..592832)	CtenKAR2
c6 complement(790531..792627)	CtenSSE1
c15 complement(211510..213153)	CtenSSZ1
c4 complement(148956..151730)	CtenLHS1
Supercontig 4: 1593130-1595073	LeloSSA-a
Supercontig 2: 873906-875840	LeloSSA-b
Supercontig 4: 106976-108817 +	LeloSSB1
Supercontig 2: 1348570-1350534 -	LeloSSC1
Supercontig 8: 92736-94691 -	LeloSSQ1
Supercontig 1: 3106363-3108426 -	LeloKAR2
Supercontig 2: 1666184-1668286 -	LeloSSE1
Supercontig 11: 22203-23828 -	LeloSSZ1
Supercontig 1: 2866724-2869447 -	LeloLHS1
c4 complement(1647522..1649483)	SpasSSA-a
c1 (809852..811786)	SpasSSA-b
c2 (523624..525465)	SpasSSB1
c3 complement(677675..679606)	SpasSSC1
c8 complement(367554..369449)	SpasSSQ1
c3 complement(1879782..1881326)	SpasKAR2
c1 complement(1429380..1431207)	SpasSSE1
c1 complement(2173195..2174832)	SpasSSZ1
c3 (1602011..1604749)	SpasLHS1
CHR H: 1754166 – 1752241	LkluSSA2
CHR F: 981486 – 983453	LkluSSA3
CHR E: 1124772 – 1122931	LkluSSB1

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CHR H: 757260 – 755179	LkluSSE1
CHR D: 966535 – 964598	LkluSSC1
CHR H: 373807 – 371864	LkluSSQ1
CHR G: 804704 – 806323	LkluSSZ1
CHR G: 1003865 – 1001826	LkluKAR2
CHR B: 1034223 – 1031509	LkluLHS1
Klth0H: 736897 - 738819	LtheSSA2
Klth0C: 573991 - 575820	LtheSSA3
Klth0B: 628227 - 630065	LtheSSB1
Klth0E: 1209958 – 1212039	LtheSSE1
Klth0F: 612749 – 614689	LtheSSC1
Klth0D: 1102731 – 1104581	LtheSSQ1
Klth0F: 624087 – 625703	LtheSSZ1
Klth0G: 629654 – 631633	LtheKAR2
Klth0B: 346782 – 349325	LtheLHS1
Contig 228: 2784 – 862	LwalSSA2
Contig 33: 80028 – 78076	LwalSSA3
Contig 4: 15848 – 17689	LwalSSB1
Contig 22: 32828 – 34909	LwalSSE1
Contig 104: 28507 – 30452	LwalSSC1
Contig 70: 67493 – 68860 // contig 71: 5 – 589	LwalSSQ1
Contig 104: 39418 – 41034	LwalSSZ1
Contig 246: 63588 – 61549	LwalKAR2
Contig 396: 13355 – 16012	LwalLHS1
CHR D: 363732 – 365654	KlacSSA2
CHR E: 1822412 – 1824364	KlacSSA3
CHR D: 1602756 – 1600915	KlacSSB1
CHR E: 2183993 – 2186077	KlacSSE1
CHR E: 1990670 – 1992595	KlacSSC1
CHR B: 690308 – 688371	KlacSSQ1
CHR C: 1280333 – 1281970	KlacSSZ1
CHR D: 807614 – 805574	KlacKAR2
CHR F: 2450871 – 2453462	KlacLHS1
CHR 6: 641037 – 642962	EgosSSA2
CHR 5: 983874 – 985823	EgosSSA-X1
CHR 2: 78053 – 76212	EgosSSB1
CHR 7: 1153862 – 1155955	EgosSSE1
CHR 6: 1075912 – 1073984	EgosSSC1
CHR 6: 1485413 – 1487323	EgosSSQ1
CHR 1: 266861 – 268474	EgosSSZ1
CHR 3: 428006 – 430030	EgosKAR2
CHR 4: 937048 – 934445	EgosLHS1
Zyro0B: 65436 – 67271	ZrouSSA2
Zyro0B: 284311 – 286137	ZrouSSA3
Zyro0C: 800876 – 802714	ZrouSSB1
Zyro0A: 849544 – 851625	ZrouSSE1
Zyro0F: 420062 – 421960	ZrouSSC1

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Zyro0B: 589928 – 591784	ZrouSSQ1
Zyro0C: 1111922 – 1113544	ZrouSSZ1
Zyro0A: 872493 – 874520	ZrouKAR2
Zyro0E: 105281 – 107740	ZrouLHS1
KpolContig1054a: 45398 – 47320	VpolSSA2
KpolContig1041a: 5803 – 7725	VpolSSA-X2
KpolContig1018c: 256463 – 258388	VpolSSA3
KpolContig1045c: 85701..87641	VpolSSA4
KpolContig1054a: 83386 – 85227	VpolSSB2
KpolContig1014d: 65303 – 67144	VpolSSB1
KpolContig1048b: 7671 – 9689	VpolSSE1
KpolContig242: 2796 – 4775	VpolSSE2
KpolContig1061c: 6149 – 8089	VpolSSC1
KpolContig472: 17347 – 19218	VpolSSQ1
KpolContig1012a: 631 – 2532	VpolSSC3
KpolContig1005: 13821..15440	VpolSSZ1
KpolContig339: 6900 – 8510	VpolSSZ2
KpolContig1004a: 21700 – 23670	VpolKAR2
KpolContig1019a: 4142 – 6757	VpolLHS1
KpolContig1073b: 26498 – 29009	VpolLHS2
Chr3 (1183153..1185075)	NcasSSA2
Chr1 (2840790..2842730)	NcasSSA4
Chr5 complement(515573..517513)	NcasSSA3
Chr4 (27261..29102)	NcasSSB1
Chr7 (278345..280186)	NcasSSB2
Chr3 complement(344877..346679)	NcasSSE1
Chr2 complement(304736..306832)	NcasSSE2
Chr1 complement(1631053..1633017)	NcasSSC1
Chr10 (217723..219678)	NcasSSQ1
Chr8 (295003..296628)	NcasSSZ1
Chr1 (238768..240819)	NcasKAR2
Chr8 (621613..624528)	NcasLHS1
CHR G: 363008 – 364930	CglaSSA2
CHR G: 312871 – 314814	CglaSSA4
CHR K: 465701 – 463860	CglaSSB2
CHR C: 514118 – 512277	CglaSSB1
CHR M: 637047 – 634963	CglaSSE2
CHR G: 472650 – 470710	CglaSSQ1
CHR I: 285239 – 283299	CglaSSC1
CHR I: 120258 – 122201	CglaSSC3
CHR L: 1129742 – 1128132	CglaSSZ1
CHR D: 308191 – 310194	CglaKAR2
CHR F: 630723 – 628054	CglaLHS1
Contig 669: 32964 – 34901	SuvaSSA1
Sbay_10 (100174-101864) // Contig 566: 31167 – 33086	SuvaSSA2
Sbay_2 (81093-83647) // Contig c616 48192-50150	SuvaSSA3
Sbay_5 (338527-340952) // Contig c677 127431-129359	SuvaSSA4
Sbay_4 (31421-33858) // Contig c538 6878-8719	SuvaSSB1

Fungi Hsp70

Sbay_14 (246668-248568) // Contig c667 103948-105789	SuvaSSB2
Sbay_16 (359654-362331)	SuvaSSE1
Sbay_4 (743056-745733)	SuvaSSE2
Sbay_12 (193086-195649)	SuvaSSC1
Sbay_10 (824352-826918)	SuvaSSQ1
Sbay_5 (69830-72354)	SuvaSSC3
Sbay_15 (426849-429061)	SuvaSSZ1
Sbay_12 (63913-66470)	SuvaKAR2
Sbay_11 (282486-285727)	SuvaLHS1
Skud_1 (114404-116823)	SkudSSA1
Skud_12 (86537-88956)	SkudSSA2
Skud_2 (67960-70385)	SkudSSA3
Skud_5 (360315-362740)	SkudSSA4
Skud_4 (40909-43346)	SkudSSB1
Skud_14 (240586-243023)	SkudSSB2
Skud_16 (321332-324009)	SkudSSE1
Skud_2 (541084-543698)	SkudSSE2
Skud_10 (475604-478185)	SkudSSC1
Skud_5 (92310-94819)	SkudSSC3
Skud_12 (798802-801371)	SkudSSQ1
Skud_8 (198489-200701)	SkudSSZ1
Skud_10 (348964-351521)	SkudKAR2
Skud_11 (281438-284679)	SkudLHS1
Smik_1 (123006-124621)	SmikSSA1
Smik_12 (81603-83479)	SmikSSA2
Smik_2 (78473-80412)	SmikSSA3
Smik_5 (373523-375348)	SmikSSA4
Smik_1 (123006-124621)	SmikSSA1p
Smik_4 (22025-23862)	SmikSSB1
Smik_14 (231362-233199)	SmikSSB2
Smik_16 (233516-235593)	SmikSSE1
Smik_2 (560159-562173)	SmikSSE2
Smik_10 (505806-507703)	SmikSSC1
Smik_5 (103210-104729)	SmikSSC3p
Smik_12 (798229-800180)	SmikSSQ1
Smik_8 (200825-202437)	SmikSSZ1
Smik_10 (377587-379544)	SmikKAR2
Smik_11 (282629-285270)	SmikLHS1
Spar_1 (114869-116688)	SparSSA1
Spar_12 (82826-84645)	SparSSA2
Spar_2 (79731-81676)	SparSSA3
Spar_5 (375605-377430)	SparSSA4
Spar_4 (49681-51518)	SparSSB1
Spar_14 (236135-237972)	SparSSB2
Spar_16 (375298-377375)	SparSSE1
Spar_2 (546730-548744)	SparSSE2
Spar_10 (495494-497445)	SparSSC1
Spar_12 (814208-816177)	SparSSQ1
Spar_5 (72542-74469)	SparSSC3

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Spar_8 (201371-202983)
Spar_10 (371921-373878)
Spar_11 (306855-309496)

SparSSZ1
SparKAR2
SparLHS1

Chr I 141433-139505
Chr XII 97484-95565
Chr II 86446-84497
Chr V 364585-366513
CHR IV 44066-45907
CHR XIV 252060-253901
CHR XVI 352272-350191
CHR II: 575991-573910
CHR X 521594-519630
CHR XII: 859551-861524
Chr V 94644-96578
CHR 8: 227143-225527
Chr X 381321-383369
Chr XI 296074-298719

ScerSSA1
ScerSSA2
ScerSSA3
ScerSSA4
ScerSSB1
ScerSSB2
ScerSSE1
ScerSSE2
ScerSSC1
ScerSSQ1
ScerSSC3
ScerSSZ1
ScerKAR2
ScerLHS1

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rec-BLAST

SSA1
SSB2
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SSC1
SSZ1
KAR2
LHS1

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SSA1
SSB2
SSE1
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LHS1

SSA4
SSB2
SSE1
SSC1
SSZ1
KAR2
LHS1

SSA3
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SSE1
SSC1
SSZ1
KAR2
LHS1
KAR2

SSA4
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SSB2
SSB2
SSE1
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SSZ1
KAR2
LHS1

SSA1
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SSE1
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SSZ1
KAR2
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SSA4
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SSC1
SSZ1
KAR2
LHS1

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Fungi Hsp70

SSC1
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KAR2
LHS1

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Fungi Hsp70

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KAR2
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SSZ1
KAR2
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KAR2

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KAR2
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KAR2
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KAR2
SSE1
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KAR2
LHS1
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SSQ1
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KAR2
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KAR2
LHS1

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SSB2
SSE1
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SSZ1
KAR2
LHS1

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SSZ1
KAR2
LHS1

SSA1
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SSB1
SSB2
SSE1
SSE2
SSC1
SSQ1
SSC3

Fungi Hsp70

SSZ1
KAR2
LHS1

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SSA3
SSA4
SSB1
SSB2
SSE1
SSE2
SSC1
SSQ1
SSC3
SSZ1
KAR2
LHS1

Notes

ORFs contains partial sequences, full sequence reconstructed using genomic data and homology with Ccinerea

contigs contain partial sequences, because the gene is located at a contig break

ORF contains partial sequence, full sequence reconstructed using PCHR_78864, genomic data and homology v

ORF contains partial sequence, full sequence reconstructed from genomic data and homology with Pchrysospo

ORF contains partial sequence, full sequence reconstructed from genomic data and homology with Cneoformar

putative pseudogene, not used

Fungi Hsp70

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with Scryophilus

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with Mgrisea, Pi

Fungi Hsp70

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with *Panseria*

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with *Panseria*,
ORF contains partial sequence, full sequence reconstructed using genomic data, trace archive and homology w

ORF contains a unique insertion/intron, full sequence reconstructed using using homology with *G.zeae* and *G. r*

ORF contains partial sequence, nearly full sequence reconstructed using genomic data and homology with *Gmc*

ORF contains partial sequence, full sequence reconstructed using *BofuT4_P016860.1*

ORFs contains partial sequences, full sequence reconstructed using *BofuT4_P147470.1*, genomic data and hor

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with *Ssclerotioru*

ORFs contained partial sequence, full sequence reconstructed using genomic data, trace archive and homology
ORFs contained partial sequence, full sequence reconstructed using genomic data

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with *Ssclerotioru*

Fungi Hsp70

ORFs contained partial sequence, full sequence reconstructed using genomic data

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with Cimmitis

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with Cimmitis

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with Cimmitis

ORF contains partial sequence, full sequence reconstructed using genomic data, trace archive and homology w

contigs contain partial sequences, full sequence reconstructed using combined data from both contigs

ORF contains partial sequence, full sequence reconstructed using genomic data and homology with Aterreus, Ai

ORF contains a very long protein, the LHS1 homolog forms the 2nd exon

ORF contains a frameshifted sequence, full sequence reconstructed using genomic data and trace archive
ORF contains partial sequence, nearly full sequence reconstructed using genomic data, trace archive and using

ORFs contains partial sequences, full sequence reconstructed using genomic data and trace archive

ORFs contains partial sequences, full sequence reconstructed using genomic data and trace archive

Fungi Hsp70

Co 90-125 ORF contains a partial sequence, full sequence reconstructed using data from the AY2 strain, paralogs
Co 90-125 ORF contains a partial sequence, full sequence reconstructed using data from the AY2 strain, paralogs

ORF contains partial sequence, full sequence reconstructed using genomic data and similarity with other CTG genes
ORF contains partial sequence, full sequence reconstructed using genomic data and similarity with other CTG genes

Fungi Hsp70

ORF contains a frameshifted sequence, full sequence reconstructed using genomic data and trace archive
contigs contain partial sequences, full sequence reconstructed using combined data from both contigs

ORF contains a frameshifted sequence, full sequence reconstructed using genomic data and trace archive

ORF has CTG as the starting codon, instead of ATG

SSS assembly contained only SSA3 and SSA4, extracted all four SSAs from SGD data
SSS assembly contained only SSA3 and SSA4, extracted all four SSAs from SGD data
SSS assembly contained only SSA3 and SSA4, extracted all four SSAs from SGD data
SSS assembly contained only SSA3 and SSA4, extracted all four SSAs from SGD data
SSS assembly contained partial SSB2, extracted both SSBs from SGD data

Fungi Hsp70

SSS assembly contained partial SSB2, extracted both SSBs from SGD data

Alternative transcript to Smik_1.63



l and Cneoformans

with Ccinerea

rium
is, Pchrysosporium and Umaydis

5

anserina and Cglobosum

Ncrassa and Mgrisea
with Panzerina, Ncrassa and Mgrisea
noniliformis

noniliformis, but a missing fragment is absent even from trace data, so probably wasn't sequenced at a

nology with Sscleoriorum

im

/ with Ssclerotiorum and Ureesii

um and Ureesii

with Cimmitis and Acapsulatus

nidulans and Afumigatus

| homology with Dhansenii

ig synteny determined based on sequence similarity
ig synteny determined based on sequence similarity

group homologs
group homologs

Fungi Hsp70

Fungi Hsp70

archive

51	<i>Saccharomyces castelli</i>	SGD	SCAS_604.10 / NCAS_0C05760 SCAS_609.2 / NCAS_0A14440 SCAS_599.14 / NCAS_0E02580 SCAS_677.4 / NCAS_0D00240 SCAS_606.17 / NCAS_0G01560 SCAS_700.8 / NCAS_0C01870 SCAS_721.2 / NCAS_0B01860 SCAS_560.8 / NCAS_0A08260 SCAS_670.6 / NCAS_0J01260 SCAS_686.12 / NCAS_0H01530 SCAS_690.24 / NCAS_0A01220 SCAS_649.13 / NCAS_0H03240
53	<i>Saccharomyces bayanus</i> MCYC 623	BROAD Institute data	SBAY_566.14 SBAY_669.15 SBAY_677.58 SBAY_616.26 SBAY_538.4 SBAY_667.61 SBAY_632.46 SBAY_678.54 SBAY_670.9 SBAY_545.8 SBAY_676.18 SBAY_572.7 Sbay_12.47 SBAY_652.55
54	<i>Saccharomyces kudriavzevii</i> IFO 1802	SGD GenBank Saccharomyces Sensu	Skud_1.58 Skud_12.44 Skud_2.32 Skud_5.228 Skud_4.25 Skud_14.127 Skud_16.177 Skud_2.297 Skud_10.263 Skud_5.61 Skud_12.454 Skud_8.121 Skud_10.188 Skud_11.153
55	<i>Saccharomyces mikatae</i>	SGD Saccharomyces Sensu	SM291 / Smik_1.63 SM14300 / Smik_12.40 SM1586 / Smik_2.43 SM6476 / Smik_5.249 Smik_1.64 SM2387 / Smik_4.12 SM18133 / Smik_14.123 SM21895 / Smik_16.131 SM606 / Smik_2.310

archive

SM12335 / Smik_10.320
SM15845 / Smik_12.456
SM9845 / Smik_8.135
SM12089+SM12090 (partials) / Sn
SM13389 / Smik_11.165

56 *Saccharomyces paradoxus*

SGD
BROAD Institute Yeast

SPAR_198
SPAR_14937
SPAR_622
SPAR_6601
SPAR_2913
SPAR_18569
SPAR_22509
SPAR_1684
SPAR_12469
SPAR_15481
SPAR_5843
SPAR_10162
SPAR_12205 (partial)
SPAR_13762+SPAR_13760

archive

Contig 604: 20560 – 18638	ScasSSA2	SSA2
Contig 609: 5097 – 3157	ScasSSA4	SSA3
Contig 599: 31680 – 29740	ScasSSA3	SSA3
Contig 677: 6276 – 8117	ScasSSB1	SSB2
Contig 606: 31979 – 33820	ScasSSB2	SSB2
Contig 700: 10577 – 12634	ScasSSE1	SSE1
Contig 721: 2855 – 759	ScasSSE2	SSE1
Contig 560: 12871 – 14835	ScasSSC1	SSC1
Contig 670: 10634 – 8679	ScasSSQ1	SSQ1
Contig 686: 23678 – 22053	ScasSSZ1	SSZ1
Contig 690: 44044 – 46092	ScasKAR2	KAR2
Contig 649: 22106 – 19191	ScasLHS1	LHS1
Contig 566: 31167 – 33086	SbaySSA2	SSA2
Contig 669: 32964 – 34901	SbaySSA1	SSA1
Contig 677: 129359 – 127431	SbaySSA4	SSA4
Contig 616: 48192 – 50150	SbaySSA3	SSA3
Contig 538: 6878 – 8719	SbaySSB1	SSB1
Contig 667: 105789 – 103948	SbaySSB2	SSB2
Contig 632: 88503 – 90584	SbaySSE1	SSE1
Contig 678: 104314 – 106395	SbaySSE2	SSE2
Contig 670: 21960 – 19993	SbaySSC1	SSC1
Contig 545: 14061 – 12085	SbaySSQ1	SSQ1
Contig 676: 52934 – 50994	SbayECM10	ECM10
Contig 572: 9920 – 11536	SbaySSZ1	SSZ1
Contig 646: 1 – 1506 // Contig 628: 62914 – 63438	SbayKAR2	KAR2
Contig 652: 114002 – 111357	SbayLHS1	LHS1
Contig 889: 2102-2371 +contig 239: 2-610 +contig 1561: 6659 – 7513	SkudSSA1	SSA1
Contig 1030: 1-387 + contig 761: 10-861 +contig 1993: 17168-17551	SkudSSA2	SSA2
Contig 1957: 4484 – 2535	SkudSSA3	SSA3
Contig 2041: 3737 – 1809	SkudSSA4	SSA4
Contig 1659: 4792 – 2951	SkudSSB1	SSB1
Contig 2014: 4170 – 6011	SkudSSB2	SSB1
Contig 1742: 8645 – 6564	SkudSSE1	SSE1
Contig 2007: 11553 – 13634	SkudSSE2	SSE2
Contig 303: 34 – 711, contig 281: 444-896	SkudSSC1	SSC1
Contig 1575: 1711 – 3651	SkudECM10	ECM10
Contig 2058: 17319 – 15346	SkudSSQ1	SSQ1
Contig 1838: 1117 – 2733	SkudSSZ1	SSZ1
Contig 1462: 1 – 1380 // contig 1953: 570 – 1	SkudKAR2	KAR2
Contig 1372: 3424 – 779	SkudLHS1	LHS1
Contig 1032: 44755 – 42815	SmikSSA1	SSA1
Contig 1119: 4865 – 2946	SmikSSA2	SSA2
Contig 132: 43949 – 45892	SmikSSA3	SSA3
Contig 620: 69841 – 67913	SmikSSA4	SSA4
Contig 1163: 1-669	SmikSSA1p	SSA1
Contig 196: 7736 – 9577	SmikSSB1	SSB1
Contig 428: 6289 – 8130	SmikSSB2	SSB2
Contig 32: 14854 – 12773	SmikSSE1	SSE1
Contig 99: 7345 – 9426	SmikSSE2	SSE2

archive

Contig 326: 6089 – 4110	SmikSSC1	SSC1
Contig 1173: 23494 – 21530	SmikSSQ1	SSQ1
Contig 315: 20754 – 19138	SmikSSZ1	SSZ1
Contig 336: 7975 – 8396 // contig 335: 3 – 1505	SmikKAR2	KAR2
Contig 702: 134244 – 134346 // contig 703: 1-2576	SmikLHS1	LHS1
Contig 218: 34679 – 36607	SparSSA1	SSA1
Contig 53: 19353 - 21272	SparSSA2	SSA2
Contig 449: 46719 – 48668	SparSSA3	SSA3
Contig 333: 73988 – 72060	SparSSA4	SSA4
Contig 429: 27707 – 29548	SparSSB1	SSB1
Contig 238: 51353 - 53194	SparSSB2	SSB2
Contig 387: 12334 – ¹⁰²⁵³	SparSSE1	SSE1
Contig 210: 13973 – 11892	SparSSE2	SSE2
Contig 301: 71152 – 69197	SparSSC1	SSC1
Contig 152: 54225 – 52252	SparSSQ1	SSQ1
Contig 354: 45341 – 43410	SparECM10	ECM10
Contig 37: 10943 – 12559	SparSSZ1	SSZ1
Contig 298: 3159 – 3194 // contig 299: 1-1979	SparKAR2	KAR2
Contig 322: 1548 – 1 // contig 323: 34600 – 33493	SparLHS1	LHS1

archive

c628(1-175aa)+c646(183-684aa), contig breaks, filled with Ns

c889 (1-90), c239 (91-293), c1561 (323-x)
c1030 (1-129), c761 (206-489), c1993 (489-x)

pseudogene (found in SkudJSSS)
c303 (132-359), c281(511-x)

c1953(1-190aa)+c1462(224-682aa), contig breaks

Alternative transcript to Smik_1.63, not used

archive

c336(1-141aa)+c335(184-683aa), contig breaks, filled with Ns
c702(1-29aa)+c703(29-881aa), contig breaks, filled with Ns

c298(1-12aa)+c299(25-683aa), contig breaks, filled with Ns
c322(1-516aa)+c323(514-881aa), contig breaks, filled with Ns