Patient C	Cgl-C10	Cgl-D1	Cgl-D2	Cgl-D3	Cgl-D4	Cgl-D5	Cgl-D6	Cgl-D7	Cgl-D8	Cgl-D9	GENE	Gene-Name
ChrA_C_glabrata_CBS138	1	1	0	1	0	1	1	1	1	1	CAGL0A00105g	
ChrA_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0A00132g	
ChrA_C_glabrata_CBS138	0	0	1	0	1	1	0	1	1	0	CAGL0A00154g	
ChrA_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0A00385g	
ChrA_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0A00429g	ERG4
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	1	CAGL0A01221g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0A01243g	GIT1
ChrA_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0A01284g	EPA10
ChrA_C_glabrata_CBS138	1	0	0	1	1	1	1	0	1	1	CAGL0A01325g	PGD1
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	1	CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	0	1	0	1	1	0	0	0	1	0	CAGL0A01474g	
ChrA_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0A01738g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	1	CAGL0A02211g	HXT6/7
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0A02233g	HXT4/6/7
ChrA_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0A02299g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	0	1	1	1	0	CAGL0A02486g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	0	CAGL0A02552g	
ChrA_C_glabrata_CBS138	0	0	1	1	1	1	1	1	1	1	CAGL0A04587g	
ChrA_C_glabrata_CBS138	0	0	1	1	1	1	1	0	1	1	CAGL0A04873g	
ChrB_C_glabrata_CBS138	1	0	0	1	1	1	0	0	0	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	0	0	1	1	0	1	0	1	1	1	CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0B00264g	MTLalpha2
ChrB_C_glabrata_CBS138	1	2	1	1	1	1	1	1	1	1	CAGL0B02431g	
ChrB_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0B03608g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	0	1	0	1	1	1	0	1	1	0	CAGL0C00946g	
ChrC_C_glabrata_CBS138	0	0	1	1	0	1	0	1	0	1	CAGL0C00968g	
ChrC_C_glabrata_CBS138	1	2	2	1	2	2	2	1	2	2	CAGL0C01067g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	0	1	0	1	1	CAGL0C02343g	ARB1
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	1	1	0	0	CAGL0C03531g	
ChrC_C_glabrata_CBS138	0	1	0	1	1	0	1	0	1	1	CAGL0C05621g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0D03344g	
ChrD_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0D03872g	
ChrD_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0D04730g	
ChrD_C_glabrata_CBS138	0	0	1	0	1	0	0	1	0	0	CAGL0D05060g	
ChrD_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0D05082g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0D05192g	
ChrD_C_glabrata_CBS138	1	0	1	0	1	0	0	0	0	0	CAGL0D05478g	
ChrD_C_glabrata_CBS138	1	1	0	0	1	1	1	0	0	0	CAGL0D06512g	
ChrD_C_glabrata_CBS138	1	0	0	1	1	0	0	1	0	1	CAGL0D06556g	
ChrD_C_glabrata_CBS138	0	1	1	1	0	0	1	1	1	1	CAGL0D06600g	
ChrD_C_glabrata_CBS138	0	1	1	1	0	0	1	1	1	1	CAGL0D06622g	
ChrD_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1	0	CAGL0D06732g	EPA21

ChrE_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0E00105g	
ChrE_C_glabrata_CBS138	0	1	0	0	0	0	0	0	1	1	CAGL0E00110g	
ChrE_C_glabrata_CBS138	1	0	1	1	1	1	0	1	0	0	CAGL0E00187g	
ChrE_C_glabrata_CBS138	1	0	1	1	1	0	1	1	0	1	CAGL0E00231g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0E00627g	SRB8
ChrE_C_glabrata_CBS138	1	0	1	1	1	1	1	0	1	1	CAGL0E01287g	
ChrE_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	1	CAGL0E01661g	
ChrE_C_glabrata_CBS138	0	0	1	0	1	1	1	0	0	1	CAGL0E02783g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0E04092g	SIT1
ChrE_C_glabrata_CBS138	0	1	0	0	0	1	0	0	1	1	CAGL0E04114g	
ChrE_C_glabrata_CBS138	0	0	1	1	1	1	1	1	1	1	CAGL0E04774g	
ChrE_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0E05632g	
ChrE_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	0	CAGL0E06138g	
ChrE_C_glabrata_CBS138	1	1	0	1	1	1	1	0	0	1	CAGL0E06644g	EPA1
ChrE_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0E06688g	EPA3
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0F00105g	
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0F01089g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0F04191g	
ChrF_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0F04917g	
ChrF_C_glabrata_CBS138	1	1	0	1	0	0	1	0	1	0	CAGL0F07381g	
ChrF_C_glabrata_CBS138	1	1	1	0	0	1	0	1	1	1	CAGL0F07623g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0F07975g	
ChrG_C_glabrata_CBS138	1	1	1	0	1	1	0	0	1	1	CAGL0G00110g	
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	0	CAGL0G00814g	CHS5
ChrG_C_glabrata_CBS138	0	0	0	1	1	0	0	0	0	1	CAGL0G02695g	
ChrG_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0G02827g	
ChrG_C_glabrata_CBS138	1	1	1	0	1	1	1	1	2	1	CAGL0G03289g	SSA3
ChrG_C_glabrata_CBS138	0	1	0	0	1	0	0	0	0	0	CAGL0G05984g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0G06842g	
ChrG_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0G07293g	
ChrG_C_glabrata_CBS138	0	1	1	1	0	0	1	0	0	1	CAGL0G08151g	GRX4
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	1	0	CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	0	0	1	1	1	0	0	0	0	0	CAGL0H02189g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0H02959g	TOS8
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0H03465g	
ChrH_C_glabrata_CBS138	1	0	1	1	0	1	0	0	1	0	CAGL0H04895g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0H05511g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0H07007g	
ChrH_C_glabrata_CBS138	1	0	0	1	0	0	1	0	0	0	CAGL0H09592g	
ChrH_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0H10010g	
ChrH_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1	1	CAGL0H10032g	PST2
ChrH_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	0	CAGL0I00110g	
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	2	1	CAGL0I00726g	
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0I02156g	

ChrI_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0I05082g	
ChrI_C_glabrata_CBS138	1	0	0	0	1	0	0	0	1	0	CAGL0I05874g	
ChrI_C_glabrata_CBS138	0	1	0	0	1	0	1	0	0	1	CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	0	1	0	0	1	1	0	0	0	0	CAGL0I06204g	PIR1
ChrI_C_glabrata_CBS138	0	0	1	1	1	1	1	0	1	1	CAGL0I07139g	
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0I07821g	
ChrI_C_glabrata_CBS138	0	1	0	0	0	0	0	0	1	1	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	1	0	0	0	0	1	1	1	0	1	CAGL0I10147g	PWP1
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0I10200g	PWP3
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0I10246g	PWP2
ChrJ_C_glabrata_CBS138	0	0	1	0	0	0	1	0	1	1	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	1	1	1	0	0	0	1	0	0	0	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	0	CAGL0J02024g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	0	0	0	1	0	1	0	0	0	0	CAGL0J02530g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	0	0	1	1	0	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	0	0	1	1	1	0	1	1	0	0	CAGL0J05159g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0J07282g	
ChrJ_C_glabrata_CBS138	0	0	0	1	1	1	0	0	1	1	CAGL0J08316g	
ChrJ_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0J09548g	
ChrJ_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0J09702g	
ChrJ_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0J11462g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	0	1	1	0	1	0	1	1	0	1	CAGL0J11990g	AWP4
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0J12034g	
ChrK_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	0	0	1	0	0	1	0	1	1	0	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	0	0	1	0	1	1	0	1	1	1	CAGL0K01155g	
ChrK_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0K01177g	
ChrK_C_glabrata_CBS138	1	0	0	0	0	0	1	0	1	1	CAGL0K03443g	YKU80
ChrK_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0K03707g	
ChrK_C_glabrata_CBS138	0	1	1	1	1	1	1	0	1	1	CAGL0K04301g	
ChrK_C_glabrata_CBS138	0	1	0	0	0	1	0	0	1	1	CAGL0K04631g	
ChrK_C_glabrata_CBS138	0	1	0	0	1	1	1	1	1	1	CAGL0K05335g	
ChrK_C_glabrata_CBS138	0	1	1	1	1	1	1	0	1	1	CAGL0K07700g	
ChrK_C_glabrata_CBS138	0	0	1	0	1	0	1	0	1	0	CAGL0K11990g	
ChrK_C_glabrata_CBS138	0	1	0	1	1	1	1	1	1	1	CAGL0K12276g	PHO88
ChrK_C_glabrata_CBS138	0	0	1	0	0	1	0	0	1	0	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0L00157g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	1	0	1	0	CAGL0L00227g	
ChrL_C_glabrata_CBS138	0	0	0	1	0	0	1	0	0	1	CAGL0L00627g	
ChrL_C_glabrata_CBS138	1	1	0	0	0	1	0	0	0	0	CAGL0L00649g	
ChrL_C_glabrata_CBS138	0	0	1	2	2	2	0	0	0	2	CAGL0L02453g	
ChrL_C_glabrata_CBS138	1	1	0	1	1	1	0	1	1	1	CAGL0L06424g	
ChrL_C_glabrata_CBS138	1	1	1	1	0	0	0	0	0	1	CAGL0L08228g	
ChrL_C_glabrata_CBS138	1	1	1	1	0	1	1	1	0	1	CAGL0L08448g	
ChrL_C_glabrata_CBS138	0	0	0	0	1	0	0	1	0	0	CAGL0L09911g	

ChrL_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	0	CAGL0L10043g	
ChrL_C_glabrata_CBS138	0	0	1	1	0	0	0	0	0	1	CAGL0L10092g	
ChrL_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0L12254g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0L12320g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0L13299g	EPA11
ChrL_C_glabrata_CBS138	1	0	0	1	1	1	1	0	1	1	CAGL0L13332g	EPA13
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0L13354g	TNR1
ChrL_C_glabrata_CBS138	0	1	1	0	1	0	0	1	0	0	CAGL0L13431g	
ChrM_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	1	1	0	1	1	0	0	1	1	1	CAGL0M01320g	
ChrM_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0M03465g	
ChrM_C_glabrata_CBS138	1	1	1	0	0	1	1	1	0	1	CAGL0M07634g	
ChrM_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	1	CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0M09108g	
ChrM_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0M10395g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	0	1	1	0	1	CAGL0M10978g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0M13519g	
ChrM_C_glabrata_CBS138	0	1	0	1	0	0	0	0	0	0	CAGL0M13805g	MP65
ChrM_C_glabrata_CBS138	0	1	1	0	1	1	1	0	1	1	CAGL0M14069g	PWP6
ChrM_C_glabrata_CBS138	1	1	1	0	1	0	1	0	1	1	CAGL0M14091g	
ChrM_C_glabrata_CBS138	1	1	1	1	0	1	0	1	0	0	CAGL0M14113g	TNR2
mito_C_glabrata_CBS138	0	0	0	1	1	0	0	1	0	0	CaglfMp07	Cgai3
Patient D	**Cgl-D10**	**Cgl-D1**	**Cgl-D2**	**Cgl-D3**	**Cgl-D4**	**Cgl-D5**	**Cgl-D6**	**Cgl-D7**	**Cgl-D8**	**Cgl-D9**	**Tot**	**GENE**
ChrA_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0A00105g	
ChrA_C_glabrata_CBS138	0	0	0	1	1	0	0	0	0	0	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	0	1	0	1	0	0	0	0	CAGL0A00132g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	1	0	1	0	0	CAGL0A00154g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0A00385g	
ChrA_C_glabrata_CBS138	0	1	0	0	0	0	0	0	1	1	CAGL0A00429g	ERG4
ChrA_C_glabrata_CBS138	1	0	1	0	1	0	0	0	0	0	CAGL0A01221g	
ChrA_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0A01243g	GIT1
ChrA_C_glabrata_CBS138	1	1	1	0	0	1	1	1	1	1	CAGL0A01284g	EPA10
ChrA_C_glabrata_CBS138	1	0	1	0	1	0	0	1	0	0	CAGL0A01325g	PGD1
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0A01408g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0A01474g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0A02211g	HXT6/7
ChrA_C_glabrata_CBS138	1	0	0	1	1	0	1	1	1	0	CAGL0A02233g	HXT4/6/7
ChrA_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0A02299g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0A02321g	HXT3
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	1	CAGL0A02486g	
ChrA_C_glabrata_CBS138	1	0	1	0	0	1	1	1	0	1	CAGL0A02552g	
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0A04499g	
ChrA_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1	1	CAGL0A04587g	

ChrA_C_glabrata_CBS138	1	1	1	1	2	1	1	1	1	1	CAGL0A04785g	RTG2
ChrA_C_glabrata_CBS138	0	1	0	0	0	1	0	0	1	0	CAGL0A04873g	
ChrA_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0A04257g	
ChrB_C_glabrata_CBS138	0	0	1	1	0	0	1	0	0	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	1	0	1	1	0	1	0	0	1	0	CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	0	1	0	1	0	1	1	0	1	0	CAGL0B00264g	MTLalpha2
ChrB_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0B01243g	MATalpha1
ChrB_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0B03608g	
ChrB_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0B05093g	AWP9
ChrC_C_glabrata_CBS138	1	0	0	0	0	1	0	0	0	0	CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	0	0	1	0	0	1	0	1	0	0	CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0C00231g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	1	1	0	0	1	0	0	0	1	0	CAGL0C00946g	
ChrC_C_glabrata_CBS138	0	1	1	0	1	1	1	1	0	1	CAGL0C00968g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0C01056g	
ChrC_C_glabrata_CBS138	1	1	0	1	2	1	2	1	1	1	CAGL0C01067g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0C01133g	
ChrC_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1	1	CAGL0C01375g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0C01705g	GPX2
ChrC_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0C02343g	ARB1
ChrC_C_glabrata_CBS138	0	1	0	1	0	0	1	0	0	1	CAGL0C04763g	
ChrC_C_glabrata_CBS138	0	1	1	0	1	1	1	0	0	1	CAGL0C05643g	EPA7
ChrD_C_glabrata_CBS138	0	0	1	0	0	1	0	0	1	0	CAGL0D00105g&CAG	
ChrD_C_glabrata_CBS138	1	0	1	0	0	0	0	0	1	0	CAGL0D05478g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	1	1	1	0	0	CAGL0D06556g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	0	CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0E00105g	
ChrE_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0E00110g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0E00231g	
ChrE_C_glabrata_CBS138	1	0	1	0	1	1	0	0	1	0	CAGL0E00561g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0E04774g	
ChrE_C_glabrata_CBS138	1	1	0	0	0	0	0	0	1	0	CAGL0E05632g	
ChrE_C_glabrata_CBS138	1	1	0	0	1	1	0	1	0	0	CAGL0E06644g	EPA1
ChrF_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0F00105g	
ChrF_C_glabrata_CBS138	0	0	1	0	0	0	1	0	0	1	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	1	1	1	1	1	1	1	0	0	1	CAGL0F01089g	
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0F01463g	TIR1
ChrD_C_glabrata_CBS138	1	0	1	1	0	0	0	0	0	0	CAGL0D01188g	TEF1
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	0	CAGL0F02079g	
ChrF_C_glabrata_CBS138	0	0	1	0	0	0	0	0	1	0	CAGL0F03003g	
ChrF_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0F04015g	
ChrF_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0F04807g	
ChrF_C_glabrata_CBS138	0	1	0	0	1	0	0	1	1	1	CAGL0F04917g	
ChrF_C_glabrata_CBS138	0	0	0	0	0	1	0	0	1	0	CAGL0F06831g	
ChrF_C_glabrata_CBS138	0	0	0	1	0	0	1	0	0	0	CAGL0F07249g	
ChrF_C_glabrata_CBS138	0	1	0	1	0	1	1	0	1	0	CAGL0F07381g	

ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0F07623g	
ChrD_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0D05082g	
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0F07975g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0G00308g	SCW4
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0G00968g	
ChrD_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0D06622g	
ChrG_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0G02409g	SRP40
ChrG_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0G02695g	
ChrG_C_glabrata_CBS138	0	0	0	1	1	0	0	0	0	0	CAGL0G02827g	
ChrG_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0G03289g	SSA3
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0G07293g	
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	0	0	1	CAGL0G08151g	GRX4
ChrG_C_glabrata_CBS138	1	0	1	0	0	1	1	0	0	0	CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0H00110g	
ChrH_C_glabrata_CBS138	0	0	1	0	0	0	0	0	1	0	CAGL0H00737g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0H01309g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0H02057g	
ChrH_C_glabrata_CBS138	0	0	1	0	0	0	0	1	0	1	CAGL0H02189g	
ChrH_C_glabrata_CBS138	0	1	0	1	1	1	1	1	1	1	CAGL0H02343g	
ChrH_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	1	CAGL0H03465g	
ChrH_C_glabrata_CBS138	0	0	1	1	1	1	0	1	0	0	CAGL0H04059g	
ChrH_C_glabrata_CBS138	1	0	1	1	1	1	0	1	1	1	CAGL0H04235g	
ChrH_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0H04895g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0H04917g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0H05511g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0H06193g	
ChrH_C_glabrata_CBS138	0	0	0	0	1	0	1	1	0	0	CAGL0H09592g	
ChrH_C_glabrata_CBS138	0	1	0	0	0	1	1	0	0	0	CAGL0H09614g	
ChrI_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	1	CAGL0I00110g	
ChrI_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0I00572g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0I05060g	
ChrI_C_glabrata_CBS138	1	0	0	0	1	0	0	0	0	0	CAGL0I05082g	
ChrI_C_glabrata_CBS138	0	0	1	0	1	0	0	0	0	0	CAGL0I05874g	
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	2	0	0	CAGL0I07447g	
ChrI_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0I10200g	PWP3
ChrJ_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0J01529g	
ChrJ_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0J01595g	GLM6
ChrJ_C_glabrata_CBS138	1	1	0	0	0	1	1	0	1	1	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	1	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	0	0	0	1	1	1	1	1	0	CAGL0J02024g	
ChrJ_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	0	0	1	1	0	0	0	0	1	0	CAGL0J02530g	
ChrE_C_glabrata_CBS138	1	0	1	0	1	1	1	1	1	1	CAGL0E02783g	
ChrJ_C_glabrata_CBS138	0	1	0	0	1	1	0	0	0	0	CAGL0J06160g	
ChrE_C_glabrata_CBS138	0	0	0	0	1	0	0	1	0	0	CAGL0E06688g	EPA3

ChrJ_C_glabrata_CBS138	1	1	0	0	1	1	1	1	0	1	CAGL0J07568g	
ChrJ_C_glabrata_CBS138	0	1	1	0	1	0	0	0	1	0	CAGL0J08316g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	1	1	0	0	0	CAGL0J09064g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0J11352g	
ChrJ_C_glabrata_CBS138	0	0	1	1	1	1	1	1	0	0	CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0J11990g	AWP4
ChrK_C_glabrata_CBS138	0	0	0	0	0	1	1	1	0	0	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	0	1	1	1	1	1	1	0	1	1	CAGL0K01155g	
ChrK_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0K01177g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	1	CAGL0K03443g	YKU80
ChrK_C_glabrata_CBS138	1	0	0	1	0	1	1	1	0	0	CAGL0K05335g	
ChrK_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1	1	CAGL0K07502g	
ChrK_C_glabrata_CBS138	0	1	1	1	1	0	1	1	0	0	CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1	1	CAGL0K12276g	PHO88
ChrK_C_glabrata_CBS138	0	1	1	1	0	0	0	1	1	1	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0L00157g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0G05830g	
ChrL_C_glabrata_CBS138	0	0	1	1	1	1	0	1	0	0	CAGL0L00627g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	2	CAGL0L00649g	
ChrL_C_glabrata_CBS138	0	1	0	1	0	0	0	0	0	2	CAGL0L02453g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0L06424g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0L06776g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	0	1	1	1	CAGL0L10043g	
ChrL_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0L10582g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	1	CAGL0L13299g	EPA11
ChrL_C_glabrata_CBS138	1	0	1	0	1	0	1	0	0	0	CAGL0L13431g	
ChrM_C_glabrata_CBS138	0	0	1	0	0	0	1	0	0	1	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0M01320g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0M09108g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0M13519g	
ChrM_C_glabrata_CBS138	0	0	1	0	0	0	0	0	1	0	CAGL0M14069g	PWP6
ChrH_C_glabrata_CBS138	1	1	1	1	0	1	1	1	0	1	CAGL0H02783g	
ChrM_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0M14113g	TNR2
Patient EF	CgI-E1	CgI-E2	CgI-E3	CgI-E4	CgI-E5	CgI-F1	CgI-F2	CgI-F3	CgI-F4	CgI-F5	GENE	Gene-Name
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0A04873g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	1	1	0	0	1	CAGL0A00105g	
ChrA_C_glabrata_CBS138	1	0	1	0	1	0	0	0	0	1	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	0	1	0	0	0	0	1	0	CAGL0A00132g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0A00385g	
ChrA_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0A00429g	ERG4
ChrA_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0A00913g	
ChrA_C_glabrata_CBS138	1	0	0	1	0	0	0	1	0	0	CAGL0A01221g	
ChrA_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0A01243g	GIT1

ChrA_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0A01284g	EPA10
ChrA_C_glabrata_CBS138	0	1	1	0	1	1	0	0	0	0	CAGL0A01325g	PGD1
ChrA_C_glabrata_CBS138	1	0	0	0	1	0	0	0	0	0	CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	0	0	1	0	0	0	1	1	1	1	CAGL0A01408g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	1	0	1	1	1	CAGL0A01474g	
ChrA_C_glabrata_CBS138	0	0	1	1	0	1	1	0	1	1	CAGL0A02233g	HXT4/6/7
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0A02321g	HXT3
ChrA_C_glabrata_CBS138	0	1	0	1	1	1	1	1	0	1	CAGL0A02486g	
ChrA_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0A02552g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0A04257g	
ChrA_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0A04499g	
ChrA_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	0	CAGL0A04587g	
ChrB_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	0	1	1	0	1	0	0	0	0	0	CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0B02079g	
ChrB_C_glabrata_CBS138	0	0	1	1	1	1	1	0	1	1	CAGL0B02431g	
ChrB_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0B03817g	
ChrB_C_glabrata_CBS138	0	1	1	0	0	1	1	1	0	1		
ChrB_C_glabrata_CBS138	1	0	0	1	1	0	0	0	0	0	CAGL0B04103g	
ChrB_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0B05093g	AWP9
ChrC_C_glabrata_CBS138	1	1	0	0	1	1	1	1	0	1	CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	0	1	0	0	0	1	0	1	1	0	CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	0	0	0	0	0	1	1	1	0	0	CAGL0C00231g	
ChrC_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	0	1	0	0	1	1	0	0	0	1	CAGL0C00946g	
ChrC_C_glabrata_CBS138	0	0	1	0	1	1	0	1	1	1	CAGL0C00968g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0C01056g	
ChrC_C_glabrata_CBS138	1	2	1	2	1	2	1	1	2	2	CAGL0C01067g	
ChrC_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0C01133g	
ChrC_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0C01375g	
ChrC_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0C03399g	POP2
ChrC_C_glabrata_CBS138	1	1	0	0	1	1	0	0	0	1	CAGL0C03531g	
ChrC_C_glabrata_CBS138	1	1	0	0	0	1	0	1	0	0	CAGL0C03608g	TUP1
ChrC_C_glabrata_CBS138	0	0	0	0	1	1	0	0	0	1	CAGL0C03960g	
ChrC_C_glabrata_CBS138	0	1	0	0	0	0	1	0	0	0	CAGL0C04763g	
ChrC_C_glabrata_CBS138	1	0	0	1	0	0	0	0	0	0	CAGL0C05621g	
ChrC_C_glabrata_CBS138	0	1	0	0	1	0	1	1	0	1	CAGL0C05643g	EPA7
ChrD_C_glabrata_CBS138	0	1	0	0	0	0	0	1	0	0	CAGL0D00105g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0D00105g&CAGL0D00110g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	0	0	0	0	1	CAGL0D00110g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0D00264g	NUD1
ChrD_C_glabrata_CBS138	0	1	0	1	0	0	0	0	0	0	CAGL0D02266g	
ChrD_C_glabrata_CBS138	1	0	1	1	1	1	0	0	1	1	CAGL0D02618g	PEX11
ChrD_C_glabrata_CBS138	1	0	0	0	0	0	1	1	1	1	CAGL0D02640g	
ChrD_C_glabrata_CBS138	1	1	1	1	0	1	1	0	1	1	CAGL0D02662g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0D03344g	
ChrD_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0D03872g	

ChrD_C_glabrata_CBS138	0	0	1	1	0	0	0	0	1	1	CAGL0D04730g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0D05060g	
ChrD_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0D05082g	
ChrD_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0D05478g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0D05940g	ERG1
ChrD_C_glabrata_CBS138	1	1	2	1	1	1	1	1	1	1	CAGL0D06424g	ACO1
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	1	2	0	1	CAGL0D06512g	
ChrD_C_glabrata_CBS138	0	1	0	1	0	0	1	0	1	1	CAGL0D06556g	
ChrD_C_glabrata_CBS138	0	0	1	1	2	0	0	1	0	0	CAGL0D06600g	
ChrD_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0D06622g	
ChrD_C_glabrata_CBS138	0	1	1	1	1	1	1	0	1	1	CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	1	1	0	0	0	0	1	0	0	0	CAGL0E00110g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0E00187g	
ChrE_C_glabrata_CBS138	1	1	0	1	0	0	0	1	1	0	CAGL0E00231g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	0	0	1	1	CAGL0E00561g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	0	1	1	0	1	CAGL0E01661g	
ChrE_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0E01991g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	0	CAGL0E04774g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0E05632g	
ChrE_C_glabrata_CBS138	0	1	0	1	1	1	0	1	1	1	CAGL0E06644g	EPA1
ChrE_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0E06666g	EPA2
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	0	1	1	0	CAGL0F00105g	
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0F01089g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0F01463g	TIR1
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0F02079g	
ChrF_C_glabrata_CBS138	0	0	0	1	0	1	0	0	0	0	CAGL0F03003g	
ChrF_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0F04015g	
ChrF_C_glabrata_CBS138	1	1	0	1	1	1	0	1	1	1	CAGL0F04191g	
ChrF_C_glabrata_CBS138	1	0	0	1	0	0	0	0	0	1	CAGL0F04807g	
ChrF_C_glabrata_CBS138	1	1	1	0	0	1	0	1	1	1	CAGL0F04917g	
ChrF_C_glabrata_CBS138	0	0	0	0	1	0	0	1	1	0	CAGL0F06831g	
ChrF_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	1	CAGL0F07249g	
ChrF_C_glabrata_CBS138	1	1	0	0	0	0	1	1	0	1	CAGL0F07381g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0F07623g	
ChrF_C_glabrata_CBS138	0	0	1	1	1	0	0	0	0	0	CAGL0F07975g	
ChrG_C_glabrata_CBS138	0	0	0	0	1	0	0	1	1	1	CAGL0G00110g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0G00176g	ERV29
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0G00308g	SCW4
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0G00814g	CHS5
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G00968g	
ChrG_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0G02409g	SRP40
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G02695g	
ChrG_C_glabrata_CBS138	1	0	0	0	0	1	0	0	0	0	CAGL0G02827g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	1	CAGL0G05962g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G05984g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G07645g	

ChrG_C_glabrata_CBS138	0	0	1	1	1	1	1	0	0	0	CAGL0G08151g	GRX4
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G09537g	
ChrG_C_glabrata_CBS138	1	0	0	1	1	0	0	0	0	0	CAGL0G09999g	
ChrG_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	1	CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	0	0	1	0	0	0	0	1	0	1	CAGL0H00110g	
ChrH_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0H00121g	
ChrH_C_glabrata_CBS138	1	1	0	1	1	0	0	1	1	0	CAGL0H00737g	
ChrH_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0H01309g	
ChrH_C_glabrata_CBS138	0	1	0	1	0	0	0	1	0	0	CAGL0H02189g	
ChrH_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0H02299g	
ChrH_C_glabrata_CBS138	1	0	1	1	1	0	1	1	1	1	CAGL0H02343g	
ChrH_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0H02959g	TOS8
ChrH_C_glabrata_CBS138	1	0	0	0	1	0	0	0	0	0	CAGL0H03465g	
ChrH_C_glabrata_CBS138	1	0	0	1	0	0	1	1	0	0	CAGL0H04059g	
ChrH_C_glabrata_CBS138	1	1	0	0	1	0	1	1	1	1	CAGL0H04235g	
ChrH_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0H04895g	
ChrH_C_glabrata_CBS138	1	1	0	1	1	0	1	1	0	1	CAGL0H04917g	
ChrH_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0H04939g	
ChrH_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	0	CAGL0H05511g	
ChrH_C_glabrata_CBS138	1	0	1	0	0	0	0	0	1	0	CAGL0H06193g	
ChrH_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0H06237g	
ChrH_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0H07007g	
ChrH_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0H07997g	KNH1
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0H08129g	
ChrH_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0H08349g	
ChrH_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0H08844g	
ChrH_C_glabrata_CBS138	1	0	1	1	1	1	0	1	1	0	CAGL0H09592g	
ChrH_C_glabrata_CBS138	0	0	1	1	1	1	0	1	1	0	CAGL0H09614g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	0	0	0	1	1	0	0	1	1	0	CAGL0I00110g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	1	1	0	0	CAGL0I00105g	
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0I00572g	
ChrI_C_glabrata_CBS138	0	0	0	1	1	0	1	0	1	0	CAGL0I02134g	PEX21B
ChrI_C_glabrata_CBS138	1	1	0	1	2	1	1	1	1	1	CAGL0I03454g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0I03696g	LDB17
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0I03828g	RPB1
ChrI_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0I04994g	MET6
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0I05082g	
ChrI_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0I05170g	CST6
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0I05874g	
ChrI_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	1	CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	1	0	1	1	1	1	0	1	0	0	CAGL0I07139g	
ChrI_C_glabrata_CBS138	0	0	0	1	1	0	2	1	0	0	CAGL0I07447g	
ChrI_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	1	CAGL0I07821g	
ChrI_C_glabrata_CBS138	0	1	0	0	0	0	0	0	1	0	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	0	1	0	0	0	0	1	0	0	0	CAGL0I10147g	PWP1

ChrI_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0I10362g	PWP4
ChrJ_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0J00110g	
ChrJ_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0J00451g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0J01529g	
ChrJ_C_glabrata_CBS138	0	1	1	0	1	1	1	1	0	0	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	0	0	1	1	0	0	0	1	0	1	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0J01980g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0J02024g	
ChrJ_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0J02530g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	0	0	1	1	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1	0	CAGL0J05159g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	1	0	1	0	1	CAGL0J06160g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0J07282g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0J07568g	
ChrJ_C_glabrata_CBS138	0	0	1	1	0	1	0	0	0	1	CAGL0J08316g	
ChrJ_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0J09064g	
ChrJ_C_glabrata_CBS138	0	1	0	1	1	0	1	0	0	0	CAGL0J09548g	
ChrJ_C_glabrata_CBS138	1	0	0	1	1	1	0	1	1	1	CAGL0J09702g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0J09900g	
ChrJ_C_glabrata_CBS138	0	0	0	1	1	0	0	1	0	0	CAGL0J11352g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0J11462g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	0	1	0	0	1	CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0J11968g	EPA15
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J11990g	AWP4
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0J12034g	
ChrK_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1	1	CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	1	1	1	1	0	1	0	0	0	1	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	1	0	1	1	1	0	1	1	0	1	CAGL0K01155g	
ChrK_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0K01177g	
ChrK_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0K02079g	GLC7
ChrK_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0K02607r	tV(AAC)10
ChrK_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0K03399g	YPK2
ChrK_C_glabrata_CBS138	1	0	0	0	1	1	1	1	0	1	CAGL0K03443g	YKU80
ChrK_C_glabrata_CBS138	1	1	2	1	1	1	1	0	0	1	CAGL0K04257g	RME1
ChrK_C_glabrata_CBS138	1	1	1	1	2	1	1	1	1	1	CAGL0K04301g	
ChrK_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0K05115g	
ChrK_C_glabrata_CBS138	1	0	0	1	0	1	1	1	0	1	CAGL0K05335g	
ChrK_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0K07271g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	1	0	0	1	CAGL0K07502g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0K07700g	
ChrK_C_glabrata_CBS138	0	1	1	0	0	1	1	1	1	1	CAGL0K08096g	
ChrK_C_glabrata_CBS138	0	0	0	1	0	0	1	1	0	0	CAGL0K11990g	
ChrK_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	1	1	0	1	0	1	1	1	CAGL0K12078g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0K13024g	AED1

ChrL_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0L00157g	
ChrL_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0L00227g	
ChrL_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	0	CAGL0L00627g	
ChrL_C_glabrata_CBS138	0	0	0	1	0	0	0	2	0	1	CAGL0L00649g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	0	0	1	1	0	CAGL0L02453g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0L04598g	
ChrL_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0L06424g	
ChrL_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0L06776g	
ChrL_C_glabrata_CBS138	0	1	1	1	0	1	1	0	1	1	CAGL0L08228g	
ChrL_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	2	CAGL0L08448g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0L09372g	
ChrL_C_glabrata_CBS138	0	0	0	0	1	0	1	0	0	0	CAGL0L09911g	
ChrL_C_glabrata_CBS138	1	1	1	1	0	1	0	1	1	1	CAGL0L10043g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	1	0	0	0	CAGL0L10092g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	2	CAGL0L12320g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	1	1	0	0	0	CAGL0L13299g	EPA11
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0L13354g	TNR1
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0L13431g	
ChrM_C_glabrata_CBS138	1	1	0	1	0	0	0	1	1	0	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0M00330g	HOM6
ChrM_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0M00814g	
ChrM_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0M01320g	
ChrM_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0M01848g	
ChrM_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0M02035g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0M03465g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0M07920g	PDC
ChrM_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	0	CAGL0M09108g	
ChrM_C_glabrata_CBS138	0	0	0	0	1	0	0	1	0	1	CAGL0M10395g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	0	0	1	2	CAGL0M10978g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0M13519g	
ChrM_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0M13805g	MP65
ChrM_C_glabrata_CBS138	0	1	1	0	1	1	0	0	1	1	CAGL0M14069g	PWP6
ChrM_C_glabrata_CBS138	0	0	1	0	1	1	1	1	1	0	CAGL0M14091g	
ChrM_C_glabrata_CBS138	0	0	1	0	0	0	1	0	0	0	CAGL0M14113g	TNR2
Patient H	**Cgl-H10**	**Cgl-H1**	**Cgl-H2**	**Cgl-H3**	**Cgl-H4**	**Cgl-H5**	**Cgl-H6**	**Cgl-H7**	**Cgl-H8**	**Cgl-H9**	**GENE**	**Gene-Name**
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	0	CAGL0A00105g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0A00154g	
ChrA_C_glabrata_CBS138	0	1	1	0	2	0	1	1	1	1	CAGL0A00385g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0A01243g	GIT1
ChrA_C_glabrata_CBS138	0	1	1	1	1	0	1	1	1	1	CAGL0A01284g	EPA10
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	0	0	1	0	1	0	1	1	0	1	CAGL0A01474g	

ChrA_C_glabrata_CBS138	1	0	1	1	0	1	1	1	0	1	CAGL0A01738g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0A04873g	
ChrB_C_glabrata_CBS138	0	1	0	0	1	1	0	0	1	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0B00792g	
ChrB_C_glabrata_CBS138	1	0	2	1	0	1	2	1	0	0	CAGL0B00814g	
ChrB_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0B00990g	HBN1
ChrB_C_glabrata_CBS138	1	0	1	1	1	1	1	0	1	1	CAGL0B02431g	
ChrB_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0B03608g	
ChrB_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0B04103g	
ChrC_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0C00671g	
ChrC_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	0	CAGL0C00781g	
ChrC_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	0	1	1	0	1	0	1	0	1	1	CAGL0C00946g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0C00968g	
ChrC_C_glabrata_CBS138	1	0	0	1	0	0	0	0	0	0	CAGL0C01056g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	0	0	1	1	0	CAGL0C01067g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	0	0	1	1	0	CAGL0C01078g	
ChrC_C_glabrata_CBS138	1	0	0	0	0	1	0	0	0	0	CAGL0C01133g	
ChrC_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0C01375g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0C02343g	ARB1
ChrC_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0C03267g	FPS1
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0C03399g	POP2
ChrC_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0C03960g	
ChrC_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0C04543g	
ChrC_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0C05005g	
ChrC_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0C05137g	GPD2
ChrC_C_glabrata_CBS138	0	0	0	1	2	2	0	0	2	0	CAGL0C05379g	SSB1
ChrD_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0D00110g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0D00264g	NUD1
ChrD_C_glabrata_CBS138	1	1	1	0	1	0	1	1	1	1	CAGL0D02266g	
ChrD_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	0	CAGL0D02618g	PEX11
ChrD_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0D03344g	
ChrD_C_glabrata_CBS138	0	1	1	1	1	0	1	1	1	1	CAGL0D03872g	
ChrD_C_glabrata_CBS138	0	0	0	0	1	0	0	0	1	0	CAGL0D04730g	
ChrD_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0D05082g	
ChrD_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0D05544g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0D05940g	ERG1
ChrD_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0D06424g	ACO1
ChrD_C_glabrata_CBS138	1	0	0	0	1	0	1	0	0	0	CAGL0D06556g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0D06600g	
ChrD_C_glabrata_CBS138	1	1	1	0	0	1	1	1	1	1	CAGL0D06622g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0D06710g	
ChrD_C_glabrata_CBS138	1	0	0	1	0	1	0	0	0	1	CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0E00110g	
ChrE_C_glabrata_CBS138	0	1	0	1	1	1	1	1	1	0	CAGL0E00231g	

ChrE_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0E00561g	
ChrE_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0E00627g	SRB8
ChrE_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0E00847g	
ChrE_C_glabrata_CBS138	1	1	0	2	0	1	0	1	0	1	CAGL0E00891g	
ChrE_C_glabrata_CBS138	1	1	0	1	0	1	1	1	1	1	CAGL0E02189g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	2	1	1	1	1	CAGL0E02321g	
ChrE_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0E02783g	
ChrE_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0E03113g	
ChrE_C_glabrata_CBS138	1	1	1	0	1	1	1	0	1	0	CAGL0E03652g	ISA1
ChrE_C_glabrata_CBS138	0	1	0	0	1	1	1	0	0	0	CAGL0E03894g	FPS2
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0E04774g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0E04906g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0E05016g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	1	1	0	1	0	CAGL0E05830g	
ChrF_C_glabrata_CBS138	0	0	1	1	0	0	1	1	0	0	CAGL0F00105g	
ChrF_C_glabrata_CBS138	1	1	1	0	1	0	0	0	0	0	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0F00803g	GAL11B
ChrF_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0F01089g	
ChrF_C_glabrata_CBS138	0	1	1	0	0	1	1	0	0	0	CAGL0F01463g	TIR1
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	0	CAGL0F01837g	SPT8
ChrF_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0F02079g	
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	0	0	0	CAGL0F03003g	
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	0	1	1	1	CAGL0F04015g	
ChrF_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0F04917g	
ChrF_C_glabrata_CBS138	1	1	1	1	0	0	1	1	1	1	CAGL0F07623g	
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0F07975g	
ChrF_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0F08745g	
ChrG_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0G00264g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	1	0	0	0	CAGL0G00968g	
ChrG_C_glabrata_CBS138	0	0	0	0	1	1	0	0	0	1	CAGL0G02409g	SRP40
ChrG_C_glabrata_CBS138	1	1	1	1	0	0	1	0	1	1	CAGL0G02959g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0G03949g	
ChrG_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0G04125g	
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0G05830g	
ChrG_C_glabrata_CBS138	0	1	0	0	0	0	1	1	0	0	CAGL0G06446g	
ChrG_C_glabrata_CBS138	0	1	1	1	1	0	1	1	1	1	CAGL0G07315g	
ChrG_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0G07491g	MNN11
ChrG_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0G08173g	
ChrG_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0G09020g	
ChrG_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	0	0	0	0	0	1	0	0	1	0	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0H00110g	
ChrH_C_glabrata_CBS138	1	1	1	0	1	0	0	0	1	0	CAGL0H00121g	
ChrH_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0H00132g	
ChrH_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0H02123g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0H02959g	TOS8
ChrH_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0H03751g	

ChrH_C_glabrata_CBS138	1	1	1	0	0	1	1	1	1	0	CAGL0H04235g	
ChrH_C_glabrata_CBS138	1	0	1	1	0	1	1	1	1	0	CAGL0H04895g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0H05005g	
ChrH_C_glabrata_CBS138	0	1	1	1	1	1	1	0	1	1	CAGL0H05511g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	1	1	1	CAGL0H05577g	
ChrH_C_glabrata_CBS138	1	0	1	0	1	0	0	1	0	0	CAGL0H06193g	
ChrH_C_glabrata_CBS138	1	1	1	0	1	1	1	0	1	1	CAGL0H07469g	
ChrH_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0H08129g	
ChrH_C_glabrata_CBS138	0	0	1	1	0	1	0	0	1	1	CAGL0H08503g	
ChrH_C_glabrata_CBS138	1	1	1	2	1	1	1	1	1	1	CAGL0H08734g	
ChrH_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0H08844g	
ChrH_C_glabrata_CBS138	0	1	0	0	1	0	1	0	1	1	CAGL0H09614g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0I00105g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0I00110g	
ChrI_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0I03454g	
ChrI_C_glabrata_CBS138	1	1	1	0	0	0	1	1	1	1	CAGL0I04180g	AMT1
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0I04994g	MET6
ChrI_C_glabrata_CBS138	1	0	1	0	1	0	0	0	1	0	CAGL0I05082g	
ChrI_C_glabrata_CBS138	0	1	2	0	1	0	1	1	2	1	CAGL0I05500g	
ChrI_C_glabrata_CBS138	0	1	0	1	0	1	0	0	0	0	CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0I07821g	
ChrI_C_glabrata_CBS138	1	2	2	2	2	3	2	2	2	2	CAGL0I09878g	
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	0	0	1	1	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	1	1	1	0	1	1	0	0	0	1	CAGL0I10125g	
ChrI_C_glabrata_CBS138	1	2	0	2	2	2	2	2	2	2	CAGL0I10147g	PWP1
ChrI_C_glabrata_CBS138	0	0	0	1	0	1	0	0	0	0	CAGL0I10340g	PWP5
ChrI_C_glabrata_CBS138	1	1	1	1	1	0	0	1	1	1	CAGL0I10516g	
ChrJ_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0J00110g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	1	1	1	0	0	1	1	1	1	1	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0J01980g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	1	0	1	0	0	CAGL0J02024g	
ChrJ_C_glabrata_CBS138	1	0	0	1	1	1	0	1	0	1	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	1	1	1	0	1	0	0	1	0	1	CAGL0J04268g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0J05159g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0J06710g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0	1	0	0	1	1	CAGL0J07282g	
ChrJ_C_glabrata_CBS138	1	0	0	0	1	0	0	0	1	1	CAGL0J08613g	
ChrJ_C_glabrata_CBS138	0	0	0	1	1	1	0	0	1	1	CAGL0J09548g	
ChrJ_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0J09988g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0J10318g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0J11462g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0	1	CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	0	0	1	0	0	0	0	1	1	0	CAGL0J11990g	AWP4

ChrK_C_glabrata_CBS138	0	0	1	1	0	0	0	0	0	1	CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	1	1	0	1	1	1	0	1	1	1	CAGL0K00319g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0	0	CAGL0K01155g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	1	CAGL0K01177g	
ChrK_C_glabrata_CBS138	0	0	1	0	0	0	0	1	0	0	CAGL0K02079g	GLC7
ChrK_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0K03399g	YPK2
ChrK_C_glabrata_CBS138	1	0	0	0	0	0	0	1	2	0	CAGL0K03443g	YKU80
ChrK_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0K06105g	
ChrK_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1	0	CAGL0K07502g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0K10906g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	0	0	1	1	CAGL0K12034g	ENA1
ChrK_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0K12056g	
ChrK_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0K12276g	PHO88
ChrK_C_glabrata_CBS138	1	1	1	2	0	2	1	1	1	1	CAGL0K12342g	
ChrK_C_glabrata_CBS138	0	1	0	1	1	1	0	1	1	0	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	1	0	0	1	0	0	0	1	0	CAGL0L00157g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0	1	CAGL0L00627g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	0	0	0	0	CAGL0L00649g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0L01353g	
ChrL_C_glabrata_CBS138	1	1	0	1	1	0	1	0	1	1	CAGL0L02453g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0	1	CAGL0L03630g	GSH1
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0L05434g	SUN4
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0L05896g	
ChrL_C_glabrata_CBS138	0	1	0	1	1	1	0	1	0	0	CAGL0L06512g	
ChrL_C_glabrata_CBS138	0	1	1	1	0	1	0	0	1	1	CAGL0L08228g	
ChrL_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0L08448g	
ChrL_C_glabrata_CBS138	0	0	0	1	1	1	1	1	1	1	CAGL0L08932g	LSP1
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0L09251g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0L10043g	
ChrL_C_glabrata_CBS138	1	0	0	1	1	1	1	0	1	0	CAGL0L11770g	
ChrL_C_glabrata_CBS138	0	1	1	0	0	0	1	1	0	1	CAGL0L12936g	
ChrL_C_glabrata_CBS138	1	0	0	1	0	0	0	1	0	0	CAGL0L13431g	
ChrM_C_glabrata_CBS138	1	0	1	1	0	1	1	0	0	0	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0M01826g	ECM33
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0M01914g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0M03465g	
ChrM_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0M07315g	
ChrM_C_glabrata_CBS138	0	0	0	1	1	1	1	1	1	1	CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	0	1	0	0	0	0	1	0	0	0	CAGL0M08624g	
ChrM_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0M09020g	
ChrM_C_glabrata_CBS138	0	0	0	0	1	0	1	0	0	0	CAGL0M10395g	
ChrM_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0M12056g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0M13519g	
ChrM_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0M13805g	MP65
ChrM_C_glabrata_CBS138	0	1	0	1	1	1	0	1	1	1	CAGL0M14069g	PWP6
ChrM_C_glabrata_CBS138	1	0	0	0	1	1	0	0	0	1	CAGL0M14091g	

ChrM_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0M14113g	TNR2
Patient I	**Cgl-I1**	**Cgl-I2**	**Cgl-I3**	**Cgl-I4**	**Cgl-I5**						**GENE**	**Gene-Name**
ChrA_C_glabrata_CBS138	1	0	1	0	1						CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	1	1	0	0	1						CAGL0A00105g	
ChrA_C_glabrata_CBS138	1	0	0	0	0						CAGL0A00429g	ERG4
ChrA_C_glabrata_CBS138	1	1	0	1	1						CAGL0A01243g	GIT1
ChrA_C_glabrata_CBS138	1	1	0	0	1						CAGL0A01325g	PGD1
ChrA_C_glabrata_CBS138	1	0	0	0	0						CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	1	1	0	1	1						CAGL0A01474g	
ChrA_C_glabrata_CBS138	0	0	1	0	0						CAGL0A02321g	HXT3
ChrA_C_glabrata_CBS138	0	0	0	1	1						CAGL0A02486g	
ChrA_C_glabrata_CBS138	0	0	1	0	0						CAGL0A02552g	
ChrB_C_glabrata_CBS138	0	0	0	0	1						CAGL0B00105g	
ChrB_C_glabrata_CBS138	0	1	0	0	1						CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	1	0	0	0	0						CAGL0B03817g	
ChrB_C_glabrata_CBS138	1	0	0	0	0						CAGL0B05093g	AWP9
ChrC_C_glabrata_CBS138	1	0	0	0	0						CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	0	1	0	0	2						CAGL0C00231g	
ChrC_C_glabrata_CBS138	1	0	0	0	1						CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	1	0	0	0	0						CAGL0C00946g	
ChrC_C_glabrata_CBS138	0	0	1	1	1						CAGL0C00968g	
ChrC_C_glabrata_CBS138	1	1	1	0	1						CAGL0C01056g	
ChrC_C_glabrata_CBS138	1	1	1	2	0						CAGL0C01067g	
ChrD_C_glabrata_CBS138	1	1	1	1	0						CAGL0D02662g	
ChrD_C_glabrata_CBS138	1	1	0	1	0						CAGL0D05478g	
ChrD_C_glabrata_CBS138	1	0	1	0	0						CAGL0D06556g	
ChrD_C_glabrata_CBS138	1	0	1	1	0						CAGL0D06622g	
ChrD_C_glabrata_CBS138	1	1	1	1	0						CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	0	0	0	0	1						CAGL0E00187g	
ChrE_C_glabrata_CBS138	1	1	1	1	0						CAGL0E00231g	
ChrE_C_glabrata_CBS138	0	0	0	1	1						CAGL0E00561g	
ChrE_C_glabrata_CBS138	1	1	1	1	0						CAGL0E00627g	SRB8
ChrE_C_glabrata_CBS138	1	1	1	1	0						CAGL0E00671g	
ChrE_C_glabrata_CBS138	1	1	0	1	0						CAGL0E01661g	
ChrE_C_glabrata_CBS138	1	1	1	1	0						CAGL0E02321g	
ChrE_C_glabrata_CBS138	0	1	1	1	1						CAGL0E04092g	SIT1
ChrE_C_glabrata_CBS138	1	1	0	1	0						CAGL0E04906g	
ChrE_C_glabrata_CBS138	0	1	2	0	0						CAGL0E05632g	
ChrE_C_glabrata_CBS138	0	1	0	0	1						CAGL0E06644g	EPA1
ChrE_C_glabrata_CBS138	0	1	0	1	0						CAGL0E06688g	EPA3
ChrF_C_glabrata_CBS138	0	0	0	1	0						CAGL0F00105g	
ChrF_C_glabrata_CBS138	0	0	0	0	1						CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	1	0	0	1	0						CAGL0F06831g	
ChrF_C_glabrata_CBS138	1	0	0	0	1						CAGL0F07381g	

ChrG_C_glabrata_CBS138	1	1	1	0	1						CAGL0G00110g	
ChrG_C_glabrata_CBS138	1	0	1	0	0						CAGL0G00968g	
ChrG_C_glabrata_CBS138	1	0	0	0	1						CAGL0G02827g	
ChrG_C_glabrata_CBS138	0	1	0	0	0						CAGL0G07645g	
ChrG_C_glabrata_CBS138	1	0	1	1	1						CAGL0G09020g	
ChrG_C_glabrata_CBS138	1	1	1	1	0						CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	0	0	0	1	0						CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	1	0	0	0	0						CAGL0H00121g	
ChrH_C_glabrata_CBS138	0	1	0	0	0						CAGL0H00737g	
ChrH_C_glabrata_CBS138	1	0	0	1	1						CAGL0H01309g	
ChrH_C_glabrata_CBS138	1	0	0	0	0						CAGL0H02189g	
ChrH_C_glabrata_CBS138	0	0	0	1	1						CAGL0H03465g	
ChrH_C_glabrata_CBS138	0	0	1	1	1						CAGL0H05511g	
ChrH_C_glabrata_CBS138	1	0	0	0	1						CAGL0H06193g	
ChrH_C_glabrata_CBS138	1	0	1	0	0						CAGL0H06237g	
ChrH_C_glabrata_CBS138	1	1	1	0	0						CAGL0H07007g	
ChrH_C_glabrata_CBS138	1	1	1	1	0						CAGL0H07997g	KNH1
ChrH_C_glabrata_CBS138	1	1	1	1	0						CAGL0H08844g	
ChrH_C_glabrata_CBS138	1	1	1	2	1						CAGL0H10010g	
ChrH_C_glabrata_CBS138	1	1	1	0	1						CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	0	0	1	0	1						CAGL0I00105g	
ChrI_C_glabrata_CBS138	0	0	0	0	1						CAGL0I00110g	
ChrI_C_glabrata_CBS138	1	1	1	1	0						CAGL0I00572g	
ChrI_C_glabrata_CBS138	1	1	0	1	1						CAGL0I00726g	
ChrI_C_glabrata_CBS138	1	0	0	0	0						CAGL0I02134g	PEX21B
ChrI_C_glabrata_CBS138	1	1	0	1	1						CAGL0I02156g	
ChrI_C_glabrata_CBS138	1	1	0	0	1						CAGL0I03454g	
ChrI_C_glabrata_CBS138	1	1	0	1	0						CAGL0I05082g	
ChrI_C_glabrata_CBS138	1	0	0	0	1						CAGL0I05874g	
ChrI_C_glabrata_CBS138	1	1	1	0	0						CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	0	0	1	0	0						CAGL0I07139g	
ChrI_C_glabrata_CBS138	0	1	0	1	0						CAGL0I07249g	
ChrI_C_glabrata_CBS138	0	1	0	0	0						CAGL0I07293g	
ChrI_C_glabrata_CBS138	0	0	0	1	0						CAGL0I07447g	
ChrI_C_glabrata_CBS138	1	0	0	0	1						CAGL0I07821g	
ChrI_C_glabrata_CBS138	0	1	0	0	0						CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	1	0	1	1	1						CAGL0I10362g	PWP4
ChrI_C_glabrata_CBS138	1	0	0	0	0						CAGL0I11011g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0						CAGL0J00869g	
ChrJ_C_glabrata_CBS138	0	0	0	0	1						CAGL0J01800g	
ChrJ_C_glabrata_CBS138	0	1	1	1	1						CAGL0J02024g	
ChrJ_C_glabrata_CBS138	0	0	1	1	1						CAGL0J02530g	
ChrJ_C_glabrata_CBS138	1	2	1	1	1						CAGL0J02552g	
ChrJ_C_glabrata_CBS138	0	1	1	1	1						CAGL0J03454g	HDA1
ChrJ_C_glabrata_CBS138	0	0	1	0	1						CAGL0J05159g	
ChrJ_C_glabrata_CBS138	1	0	0	0	0						CAGL0J06160g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0						CAGL0J06710g	

ChrJ_C_glabrata_CBS138	1	1	0	0	0						CAGL0J08316g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0						CAGL0J09064g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1						CAGL0J09548g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0						CAGL0J09702g	
ChrJ_C_glabrata_CBS138	1	1	1	1	2						CAGL0J09988g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1						CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	0	0	0	1	0						CAGL0J11990g	AWP4
ChrK_C_glabrata_CBS138	1	1	0	0	1						CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	0	1	1	1	1						CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	0	0	1	0	0						CAGL0K03443g	YKU80
ChrK_C_glabrata_CBS138	1	1	1	1	0						CAGL0K07271g	
ChrK_C_glabrata_CBS138	0	0	0	0	1						CAGL0K11990g	
ChrK_C_glabrata_CBS138	0	1	0	1	1						CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	0	1	0						CAGL0K12078g	
ChrK_C_glabrata_CBS138	1	0	1	1	1						CAGL0K12276g	PHO88
ChrK_C_glabrata_CBS138	1	1	1	1	0						CAGL0K12672g	
ChrK_C_glabrata_CBS138	0	0	1	0	0						CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	1	0	1	0						CAGL0L00627g	
ChrL_C_glabrata_CBS138	1	0	1	1	1						CAGL0L02453g	
ChrL_C_glabrata_CBS138	0	0	1	1	1						CAGL0L06424g	
ChrL_C_glabrata_CBS138	1	0	0	1	0						CAGL0L08228g	
ChrL_C_glabrata_CBS138	0	1	1	1	0						CAGL0L12254g	
ChrM_C_glabrata_CBS138	0	0	0	0	1						CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	0	0	0	1	0						CAGL0M10395g	
ChrM_C_glabrata_CBS138	0	0	1	1	0						CAGL0M14069g	PWP6
ChrM_C_glabrata_CBS138	1	1	0	0	1						CAGL0M14091g	
ChrM_C_glabrata_CBS138	1	0	0	0	0						CAGL0M14113g	TNR2

Patient J	**Cgl-J10**	**Cgl-J1**	**Cgl-J2**	**Cgl-J3**	**Cgl-J4**	**Cgl-J5**	**Cgl-J6**	**Cgl-J7**	**Cgl-J8**	**Cgl-J9**	**GENE**	**Gene-Name**
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	0	CAGL0A04873g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0A00105g	
ChrA_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0A00132g	
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0A02299g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	0	1	0	0	0	CAGL0A02552g	
ChrA_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0A04367g	
ChrA_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0A04587g	
ChrB_C_glabrata_CBS138	0	1	0	0	0	0	0	1	0	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	0	0	1	0	1	0	2	0	0	0	CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0B00286g	
ChrB_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0B01243g	MATalpha1
ChrB_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0B02904g	BMT6
ChrC_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0C00209g&CAG	
ChrC_C_glabrata_CBS138	0	1	1	0	0	1	0	0	0	0	CAGL0C00231g	

ChrC_C_glabrata_CBS138	0	1	1	1	0	0	1	0	1	0	CAGL0C00253g	
ChrC_C_glabrata_CBS138	1	0	0	0	0	1	0	0	1	1	CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0C00968g	
ChrC_C_glabrata_CBS138	0	1	0	0	0	0	1	0	0	0	CAGL0C01056g	
ChrC_C_glabrata_CBS138	0	0	0	0	1	0	1	1	1	1	CAGL0C01133g	
ChrC_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0C01881g	
ChrC_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0C03267g	FPS1
ChrC_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0C04807g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0C05379g	SSB1
ChrD_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0D02266g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0D03344g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0D03872g	
ChrD_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	1	CAGL0D05082g	
ChrD_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0D06226g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0D06600g	
ChrD_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0D06710g	
ChrE_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0E00231g	
ChrE_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0E00561g	
ChrE_C_glabrata_CBS138	0	0	1	0	0	0	1	0	0	0	CAGL0E01155g	
ChrE_C_glabrata_CBS138	0	0	1	0	1	0	0	0	0	0	CAGL0E01661g	
ChrE_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0E04136g	
ChrE_C_glabrata_CBS138	0	0	1	1	1	1	1	1	1	1	CAGL0E05214g	
ChrE_C_glabrata_CBS138	0	1	1	0	0	1	1	0	0	1	CAGL0E06644g	EPA1
ChrE_C_glabrata_CBS138	1	0	1	1	1	0	1	1	1	1	CAGL0E06666g	EPA2
ChrE_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0E06688g	EPA3
ChrF_C_glabrata_CBS138	1	1	1	0	1	0	1	0	0	1	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	1	1	1	0	0	1	1	1	0	0	CAGL0F00105g	
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0F00803g	GAL11B
ChrF_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0F01463g	TIR1
ChrF_C_glabrata_CBS138	0	1	0	0	0	1	1	1	1	0	CAGL0F03003g	
ChrF_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0F04345g	
ChrF_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0F04807g	
ChrF_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0F04917g	
ChrF_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0F06831g	
ChrF_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0F07007g	
ChrF_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0F07315g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G00110g	
ChrG_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0G00814g	CHS5
ChrG_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0G00924g	GLM5
ChrG_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0G00968g	
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0G02409g	SRP40
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0G02695g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G03267g	
ChrG_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0G03289g	SSA3
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0G04125g	
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0G05522g	
ChrG_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0G05830g	

ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0G05984g	
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0G06842g	
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0G10109g	
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0G10175g	AWP6
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0H00110g	
ChrH_C_glabrata_CBS138	1	1	0	0	1	1	0	1	1	0	CAGL0H00132g	
ChrH_C_glabrata_CBS138	1	1	0	0	1	1	0	1	1	0	CAGL0H00121g	
ChrH_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0H02123g	
ChrH_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0H02189g	
ChrH_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0H02959g	TOS8
ChrH_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0H06215g	GAL11A
ChrI_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0I02134g	PEX21B
ChrI_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0I03454g	
ChrI_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0I04378g	
ChrI_C_glabrata_CBS138	1	0	0	1	0	2	0	1	0	1	CAGL0I05082g	
ChrI_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0I05610g	
ChrI_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0I06028g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0I07183g	
ChrI_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0I07447g	
ChrI_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0I09108g	
ChrI_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0I10147g	PWP1
ChrI_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0I10125g	
ChrI_C_glabrata_CBS138	1	1	1	1	1	0	0	0	1	1	CAGL0I10362g	PWP4
ChrJ_C_glabrata_CBS138	1	0	0	1	0	0	0	0	1	0	CAGL0J00105g	
ChrJ_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0J00110g	
ChrJ_C_glabrata_CBS138	0	0	0	1	1	1	0	0	0	1	CAGL0J00110g&CAG	
ChrJ_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0J01529g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	1	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J02024g	
ChrJ_C_glabrata_CBS138	1	0	0	1	0	1	1	1	1	0	CAGL0J02530g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	1	0	0	0	0	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	0	1	1	0	0	0	1	1	1	0	CAGL0J05159g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J06072g	CBK1
ChrJ_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0J07018g	
ChrJ_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0J09548g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J09592g	
ChrJ_C_glabrata_CBS138	1	0	1	1	1	1	0	1	0	1	CAGL0J09988g	
ChrJ_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0J10494g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J11352g	
ChrK_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0K05115g	
ChrK_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0K10164g	
ChrK_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0K11990g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0K12078g	

ChrK_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	0	CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0K12276g	PHO88
ChrK_C_glabrata_CBS138	1	1	0	0	0	0	1	1	1	1	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0L00157g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0L00227g	
ChrL_C_glabrata_CBS138	0	1	0	0	0	0	0	0	1	1	CAGL0L00627g	
ChrL_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0L00649g	
ChrL_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0L01067g	
ChrL_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0L04598g	
ChrL_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0L06424g	
ChrL_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0L06512g	
ChrL_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0L08580g	RPN10
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0L08602g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0L09911g	
ChrL_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0L10043g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0	1	CAGL0L10092g	
ChrL_C_glabrata_CBS138	0	1	0	1	0	1	1	0	0	0	CAGL0L11660g	
ChrL_C_glabrata_CBS138	1	1	0	0	1	1	0	1	1	1	CAGL0L13354g	TNR1
ChrM_C_glabrata_CBS138	0	0	1	1	0	0	1	0	0	1	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0M00374g	
ChrM_C_glabrata_CBS138	1	0	0	1	1	0	1	0	1	1	CAGL0M01276g	
ChrM_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0M03773g	
ChrM_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0M05115g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0M07315g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0M07898g	
ChrM_C_glabrata_CBS138	1	1	2	1	1	1	1	1	1	1	CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0M09020g	
ChrM_C_glabrata_CBS138	1	0	0	0	0	1	1	0	1	1	CAGL0M10395g	
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CaglfMt15	tM(CAU)8mt
mito_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	1	CaglfMp02	VAR1
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CaglfMt20	tW(UCA)1mt
mito_C_glabrata_CBS138	0	1	1	1	1	1	0	1	0	0	CaglfMr13	LSU
mito_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	0	CaglfMt21	tT(UGU)4mt
mito_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CaglfMt22	tH(GUG)7mt
mito_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	0	CaglfMt23	tE(UUC)10mt
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CaglfMp03	cytB
mito_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	1	CaglfMt24	tM(CAU)9mt
mito_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	1	CaglfM01	RPR1
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CaglfMt25	tP(UGG)8mt
mito_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CaglfMp05	Cgai1
mito_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CaglfMp06	Cgai2
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CaglfMp07	Cgai3
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CaglfMp09	ATP6
mito_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	1	CaglfMp11	COX2
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CaglfMt28	tC(GCA)4mt
mito_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	1	CaglfMp12	COX3
mito_C_glabrata_CBS138	1	0	0	0	0	0	1	0	0	1	CaglfMt30	tL(UAA)4mt

mito_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CaglfMt33	tR(UCU)10mt
Patient K	**Cgl-K10**	**Cgl-K1**	**Cgl-K2**	**Cgl-K3**	**Cgl-K4**	**Cgl-K5**	**Cgl-K6**	**Cgl-K7**	**Cgl-K8**	**Cgl-K9**	**GENE**	**Gene-Name**
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0A04873g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0	1	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	1	0	1	0	0	0	0	0	CAGL0A00154g	
ChrA_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	0	CAGL0A01325g	PGD1
ChrA_C_glabrata_CBS138	0	0	0	0	1	0	1	0	0	1	CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0A01408g	
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0A02552g	
ChrB_C_glabrata_CBS138	0	0	0	0	0	0	0	1	1	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	1	0	1	0	0	0	0	0	1	0	CAGL0B00110g	AWP8
ChrC_C_glabrata_CBS138	0	1	1	1	0	0	1	1	0	0	CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	0	0	1	0	0	0	1	0	1	0	CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	1	0	1	0	CAGL0C00231g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0C00253g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	0	0	0	1	0	0	1	1	0	0	CAGL0C00968g	
ChrC_C_glabrata_CBS138	0	1	1	0	0	0	0	0	1	0	CAGL0C01056g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0C01067g	
ChrC_C_glabrata_CBS138	0	0	1	0	1	0	0	1	0	0	CAGL0C01133g	
ChrC_C_glabrata_CBS138	0	1	0	0	1	0	1	0	0	0	CAGL0C04807g	
ChrD_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0D00264g	NUD1
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	0	0	0	0	CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	0	0	1	0	0	1	1	0	0	1	CAGL0E00231g	
ChrE_C_glabrata_CBS138	0	0	0	1	1	1	1	1	1	1	CAGL0E05214g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	0	0	1	1	1	1	1	1	0	1	CAGL0F07007g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	0	1	1	0	1	CAGL0G00814g	CHS5
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0G02695g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	0	CAGL0H00121g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0H08844g	
ChrI_C_glabrata_CBS138	1	1	1	1	0	1	1	0	1	1	CAGL0I05016g	TRP2
ChrI_C_glabrata_CBS138	0	1	0	0	1	0	1	0	2	1	CAGL0I05082g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	1	1	1	1	0	0	1	1	1	1	CAGL0I10362g	PWP4
ChrJ_C_glabrata_CBS138	0	1	0	1	1	1	0	1	0	1	CAGL0J00110g	
ChrJ_C_glabrata_CBS138	0	1	0	0	0	0	0	1	0	0	CAGL0J00110g&CAG	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0J02530g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	1	1	0	0	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	1	1	1	0	1	1	0	1	1	1	CAGL0J09988g	

ChrK_C_glabrata_CBS138	0	1	0	0	1	0	0	0	0	0	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	0	0	1	1	CAGL0K01177g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0K07700g	
ChrK_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	1	CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0K12078g	
ChrK_C_glabrata_CBS138	1	0	1	0	1	0	1	1	1	1	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0L00157g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0L00227g	
ChrL_C_glabrata_CBS138	0	1	0	1	0	0	1	1	1	0	CAGL0L00627g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0L08602g	
ChrL_C_glabrata_CBS138	1	0	0	0	1	0	1	0	0	0	CAGL0L09911g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0L10043g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0L10092g	
ChrL_C_glabrata_CBS138	1	0	0	0	1	0	1	0	0	0	CAGL0L11660g	
ChrL_C_glabrata_CBS138	0	0	1	1	0	1	0	0	1	0	CAGL0L13299g	EPA11
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	1	CAGL0L13354g	TNR1
ChrL_C_glabrata_CBS138	1	0	1	0	1	0	1	1	1	1	CAGL0L13431g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0M05115g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0M05181g	

Patient L	Cgl-L10	Cgl-L1	Cgl-L2	Cgl-L3	Cgl-L4	Cgl-L5	Cgl-L6	Cgl-L7	Cgl-L8	Cgl-L9	**Gene**	**Gene-Name**
ChrA_C_glabrata_CBS138	0	1	1	1	1	1	0	1	0	1	CAGL0A00105g	
ChrA_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0A00132g	
ChrA_C_glabrata_CBS138	1	0	1	1	1	0	1	0	0	1	CAGL0A00154g	
ChrA_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0A00451g	PDR1
ChrA_C_glabrata_CBS138	0	1	0	1	1	1	0	0	0	1	CAGL0A01325g	PGD1
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0A01408g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0A02211g	HXT6/7
ChrA_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0A02233g	HXT4/6/7
ChrA_C_glabrata_CBS138	0	1	2	3	3	0	3	3	0	4	CAGL0A02321g	HXT3
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0A02552g	
ChrA_C_glabrata_CBS138	1	1	0	0	1	0	1	1	1	1	CAGL0A04257g	
ChrA_C_glabrata_CBS138	1	0	0	0	1	0	1	0	1	1	CAGL0A04499g	
ChrB_C_glabrata_CBS138	0	0	0	0	1	0	1	0	0	0	CAGL0B00105g	
ChrB_C_glabrata_CBS138	1	0	1	1	0	1	1	0	1	1	CAGL0B00264g	MTLalpha2
ChrB_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0B00792g	
ChrB_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0B01265g	MATalpha2
ChrB_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0		
ChrC_C_glabrata_CBS138	0	1	1	0	0	1	1	2	1	1	CAGL0C00231g	
ChrC_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0C01056g	
ChrC_C_glabrata_CBS138	0	0	1	1	0	1	0	1	1	1	CAGL0C03267g	FPS1
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0C03960g	
ChrC_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0C04763g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0D00105g&CAG	

ChrD_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0D00264g	NUD1
ChrD_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0D02486g	
ChrD_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0D02618g	PEX11
ChrD_C_glabrata_CBS138	1	1	0	1	0	1	1	1	1	0	CAGL0D02640g	
ChrD_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	0	CAGL0D03872g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	1	0	1	1	1	CAGL0D05082g	
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0D05478g	
ChrD_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0D06710g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0E00627g	SRB8
ChrE_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0E05632g	
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	0	1	0	1	CAGL0F00105g	
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	0	CAGL0F04015g	
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0F06831g	
ChrF_C_glabrata_CBS138	0	1	1	1	0	0	1	1	0	1	CAGL0F07249g	
ChrF_C_glabrata_CBS138	0	0	1	1	1	1	0	0	1	1	CAGL0F07381g	
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0F08745g	
ChrG_C_glabrata_CBS138	0	0	1	1	0	0	1	1	1	0	CAGL0G02409g	SRP40
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0G05830g	
ChrG_C_glabrata_CBS138	0	1	0	1	0	0	0	0	1	0	CAGL0G07645g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0H00121g	
ChrH_C_glabrata_CBS138	1	1	1	1	2	1	1	1	1	1	CAGL0H02343g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0H03465g	
ChrH_C_glabrata_CBS138	1	1	0	1	0	0	1	0	1	1	CAGL0H04235g	
ChrH_C_glabrata_CBS138	0	0	1	1	0	1	0	0	1	1	CAGL0H06193g	
ChrH_C_glabrata_CBS138	1	1	1	1	0	1	0	1	1	1	CAGL0H07997g	KNH1
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0H09592g	
ChrH_C_glabrata_CBS138	0	1	1	0	0	0	1	0	0	0	CAGL0H09614g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0I00105g	
ChrI_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0I03828g	RPB1
ChrI_C_glabrata_CBS138	0	1	0	0	1	0	1	1	0	1	CAGL0I05082g	
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	1	CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0I06204g	PIR1
ChrJ_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0J09702g	
ChrJ_C_glabrata_CBS138	0	0	1	0	0	0	1	0	0	0	CAGL0J11462g	
ChrJ_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0J12034g	
ChrK_C_glabrata_CBS138	1	1	0	1	1	0	1	1	1	1	CAGL0K07502g	
ChrK_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0K07700g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0K12078g	
ChrL_C_glabrata_CBS138	0	1	1	1	1	0	1	1	0	0	CAGL0L00627g	
ChrL_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0L06776g	
ChrL_C_glabrata_CBS138	0	0	0	1	0	0	1	0	0	1	CAGL0L10043g	
ChrL_C_glabrata_CBS138	1	2	1	1	1	1	1	1	1	1	CAGL0L12320g	
ChrL_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0L13354g	TNR1
ChrL_C_glabrata_CBS138	0	0	1	0	1	0	1	1	1	0	CAGL0L13431g	
ChrM_C_glabrata_CBS138	0	0	1	0	1	1	1	1	0	1	CAGL0M07634g	
ChrM_C_glabrata_CBS138	0	0	1	0	0	0	0	0	1	0	CAGL0M08492g	PIR3

ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	0	0	1	CAGL0M10395g	
ChrM_C_glabrata_CBS138	1	0	1	1	1	1	1	0	1	1	CAGL0M14091g	
ChrM_C_glabrata_CBS138	1	1	1	0	1	1	1	1	0	1	CAGL0M14113g	TNR2
mito_C_glabrata_CBS138	1	1	0	0	1	0	0	1	0	0	CaglfMp07	Cgai3
ChrA_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0A04873g	
ChrA_C_glabrata_CBS138	0	1	1	1	1	1	0	1	1	1	CAGL0A00110g	EPA19
ChrA_C_glabrata_CBS138	0	0	0	0	1	1	0	0	0	0	CAGL0A01284g	EPA10
ChrA_C_glabrata_CBS138	0	1	1	0	0	1	1	1	1	1	CAGL0A01366g	EPA9
ChrB_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0B05093g	AWP9
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0C00968g	
ChrC_C_glabrata_CBS138	1	0	1	0	0	0	1	1	1	1	CAGL0C01067g	
ChrC_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	1	CAGL0C01133g	
ChrC_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1	1	CAGL0C05643g	EPA7
ChrD_C_glabrata_CBS138	0	0	0	0	0	0	1	0	1	1	CAGL0D00110g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	1	CAGL0E00110g	
ChrE_C_glabrata_CBS138	0	0	0	0	1	1	1	1	1	1	CAGL0E00187g	
ChrE_C_glabrata_CBS138	1	1	0	1	1	1	1	1	0	1	CAGL0E00231g	
ChrE_C_glabrata_CBS138	0	1	1	0	0	1	0	0	1	0	CAGL0E01661g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0E06666g	EPA2
ChrE_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0E06688g	EPA3
ChrF_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0F00110g	AWP10
ChrG_C_glabrata_CBS138	1	0	0	1	1	1	1	0	0	1	CAGL0G00110g	
ChrG_C_glabrata_CBS138	1	1	0	0	1	1	1	0	0	0	CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	0	0	1	1	0	0	1	1	1	1	CAGL0H00110g	
ChrH_C_glabrata_CBS138	0	0	0	0	1	0	1	0	1	0	CAGL0H08844g	
ChrH_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	0	0	1	0	0	1	1	0	0	0	CAGL0I00110g	
ChrI_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0I07293g	
ChrI_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	0	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	0	0	1	1	1	0	0	0	0	0	CAGL0I10147g	PWP1
ChrI_C_glabrata_CBS138	1	1	1	0	0	0	1	1	1	0	CAGL0I10200g	PWP3
ChrI_C_glabrata_CBS138	0	0	0	0	1	1	0	0	0	0	CAGL0I10362g	PWP4
ChrJ_C_glabrata_CBS138	0	1	1	0	0	0	0	1	0	1	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	0	1	0	1	1	1	1	1	1	1	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	0	0	1	0	2	2	2	2	2	2	CAGL0J02530g	
ChrJ_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	1	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0J05159g	
ChrJ_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0J11968g	EPA15

ChrJ_C_glabrata_CBS138	1	0	1	1	1	0	1	1	1	0	CAGL0J11990g	AWP4
ChrK_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	1	CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	1	1	0	1	1	0	0	1	1	1	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	1	1	1	1	1	0	0	0	0	0	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	0	0	0	1	0	0	0	1	1	CAGL0L00157g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	1	0	0	1	0	CAGL0L00227g	
ChrL_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0L09911g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	1	1	0	0	1	CAGL0L10092g	
ChrL_C_glabrata_CBS138	0	1	1	0	1	1	1	0	0	1	CAGL0L13299g	EPA11
ChrM_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0M00132g	EPA12

Patient P	**CgI-P10**	**CgI-P1**	**CgI-P2**	**CgI-P3**	**CgI-P4**	**CgI-P5**	**CgI-P6**	**CgI-P7**	**CgI-P9**		**GENE**	**Gene-Name**
ChrA_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1		CAGL0A04873g	
ChrA_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0		CAGL0A00105g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0		CAGL0A00154g	
ChrA_C_glabrata_CBS138	0	1	1	0	1	0	0	1	1		CAGL0A01284g	EPA10
ChrA_C_glabrata_CBS138	1	1	1	1	1	1	1	0	0		CAGL0A01366g	EPA9
ChrA_C_glabrata_CBS138	1	0	0	0	0	0	1	1	1		CAGL0A02211g	HXT6/7
ChrA_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0A02233g	HXT4/6/7
ChrB_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0		CAGL0B00105g	
ChrB_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0B01243g	MATalpha1
ChrB_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1		CAGL0B02882g	BMT2
ChrC_C_glabrata_CBS138	1	1	1	0	0	0	0	0	1		CAGL0C00110g	EPA6
ChrC_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1		CAGL0C00209g&CAG	
ChrC_C_glabrata_CBS138	0	0	0	1	1	0	0	1	0		CAGL0C00209g	AWP7
ChrC_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0		CAGL0C00847g	EPA8
ChrC_C_glabrata_CBS138	1	0	1	1	1	1	1	0	0		CAGL0C00968g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0		CAGL0C01056g	
ChrC_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0		CAGL0C01067g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0		CAGL0C01133g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0C04807g	
ChrC_C_glabrata_CBS138	1	1	0	1	0	1	1	1	1		CAGL0C05379g	SSB1
ChrD_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0		CAGL0D00105g	
ChrD_C_glabrata_CBS138	0	0	1	0	0	1	0	0	0		CAGL0D00264g	NUD1
ChrD_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1		CAGL0D05082g	
ChrD_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0		CAGL0D06226g	
ChrD_C_glabrata_CBS138	1	1	0	1	1	0	1	1	1		CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0		CAGL0E00231g	
ChrE_C_glabrata_CBS138	1	0	0	0	1	0	0	0	0		CAGL0E01155g	
ChrE_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1		CAGL0E01661g	
ChrE_C_glabrata_CBS138	1	1	1	0	1	1	1	0	0		CAGL0E05214g	
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0		CAGL0E06644g	EPA1
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	1	0	0		CAGL0E06666g	EPA2
ChrE_C_glabrata_CBS138	0	1	1	0	1	1	1	1	1		CAGL0E06688g	EPA3
ChrF_C_glabrata_CBS138	0	0	0	0	1	0	0	1	0		CAGL0F00110g	AWP10

ChrF_C_glabrata_CBS138	0	0	0	0	1	1	0	1	0		CAGL0F00105g	
ChrF_C_glabrata_CBS138	0	1	1	1	1	1	1	1	2		CAGL0F00605g	GLK1
ChrF_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1		CAGL0F03003g	
ChrF_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1		CAGL0F04763g	
ChrF_C_glabrata_CBS138	0	0	0	1	1	0	0	1	0		CAGL0F04917g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1		CAGL0F06831g	
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0F07007g	
ChrG_C_glabrata_CBS138	0	1	1	1	0	0	0	0	0		CAGL0G00105g	
ChrG_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0		CAGL0G00110g	
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1		CAGL0G00814g	CHS5
ChrG_C_glabrata_CBS138	0	1	0	0	0	1	0	0	1		CAGL0G05830g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	0	1	0	1		CAGL0G06842g	
ChrG_C_glabrata_CBS138	0	0	0	1	1	0	0	0	0		CAGL0G07293g	
ChrG_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1		CAGL0G07491g	MNN11
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1		CAGL0G10109g	
ChrG_C_glabrata_CBS138	1	0	0	0	0	0	0	0	1		CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0		CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0		CAGL0H00110g	
ChrH_C_glabrata_CBS138	0	1	0	1	1	1	1	1	1		CAGL0H00132g	
ChrH_C_glabrata_CBS138	0	1	0	1	1	1	1	1	1		CAGL0H00121g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0		CAGL0H04235g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0		CAGL0H08844g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0		CAGL0H09592g	
ChrH_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0		CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0		CAGL0I00110g	
ChrI_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0		CAGL0I00105g	
ChrI_C_glabrata_CBS138	1	2	2	2	0	1	2	2	2		CAGL0I04180g	AMT1
ChrI_C_glabrata_CBS138	0	1	1	0	0	1	0	0	1		CAGL0I04378g	
ChrI_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1		CAGL0I05016g	TRP2
ChrI_C_glabrata_CBS138	0	1	0	0	0	2	0	1	0		CAGL0I05082g	
ChrI_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0		CAGL0I05170g	CST6
ChrI_C_glabrata_CBS138	0	0	1	1	0	0	1	1	1		CAGL0I05874g	
ChrI_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1		CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1		CAGL0I06204g	PIR1
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	1	1	1	1	0	0	1	1	1		CAGL0I10362g	PWP4
ChrJ_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0		CAGL0J00110g	
ChrJ_C_glabrata_CBS138	0	0	1	0	1	0	0	0	0		CAGL0J00105g	
ChrJ_C_glabrata_CBS138	1	1	0	1	0	0	0	0	0		CAGL0J01727g	
ChrJ_C_glabrata_CBS138	0	0	0	1	1	0	1	0	0		CAGL0J01774g	
ChrJ_C_glabrata_CBS138	0	1	1	1	1	0	1	1	1		CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1		CAGL0J02530g	
ChrJ_C_glabrata_CBS138	1	0	0	1	0	0	0	1	1		CAGL0J02552g	
ChrJ_C_glabrata_CBS138	1	0	1	0	1	0	0	1	0		CAGL0J05159g	
ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0		CAGL0J07018g	
ChrJ_C_glabrata_CBS138	1	0	0	0	0	1	0	0	0		CAGL0J09988g	
ChrJ_C_glabrata_CBS138	1	0	0	0	0	1	0	0	0		CAGL0J10010g	

ChrJ_C_glabrata_CBS138	0	0	0	1	0	0	1	0	0		CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	1	1	0	0	0	0	1	0	0		CAGL0J11968g	EPA15
ChrJ_C_glabrata_CBS138	1	1	0	0	0	1	1	1	1		CAGL0J11990g	AWP4
ChrJ_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1		CAGL0J12034g	
ChrK_C_glabrata_CBS138	0	1	0	0	0	0	0	1	1		CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0		CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1		CAGL0K01177g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0		CAGL0K07700g	
ChrK_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0		CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	0	1	0		CAGL0K12078g	
ChrK_C_glabrata_CBS138	1	0	1	1	1	0	1	1	1		CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0L00157g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1		CAGL0L00227g	
ChrL_C_glabrata_CBS138	0	1	0	1	0	1	0	1	0		CAGL0L00627g	
ChrL_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0		CAGL0L01067g	
ChrL_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0		CAGL0L01331g	ANP1
ChrL_C_glabrata_CBS138	0	1	1	0	0	0	0	0	1		CAGL0L09911g	
ChrL_C_glabrata_CBS138	1	1	0	0	0	0	0	0	0		CAGL0L10043g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0		CAGL0L10092g	
ChrL_C_glabrata_CBS138	0	1	2	2	0	0	0	0	1		CAGL0L11660g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0		CAGL0L13431g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	0	1	1	1		CAGL0M01276g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1		CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	1	1	0	1	1	0	1	1	1		CAGL0M10395g	
ChrM_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1		CAGL0M12430g	RHR2

Patient ST	**Cgl-S1**	**Cgl-S2**	**Cgl-S3**	**Cgl-S4**	**Cgl-S5**	**Cgl-T1**	**Cgl-T2**	**Cgl-T3**	**Cgl-T4**	**Cgl-T5**	**GENE**	**Gene-Name**
ChrA_C_glabrata_CBS138	1	0	1	0	1	0	1	1	1	0	CAGL0A00105g	
ChrA_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	1	CAGL0A00132g	
ChrA_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0A00154g	
ChrA_C_glabrata_CBS138	0	1	1	1	0	0	0	1	0	0	CAGL0A01408g	
ChrA_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	0	CAGL0A03872g	
ChrB_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0B00110g	AWP8
ChrB_C_glabrata_CBS138	1	0	1	0	0	1	1	1	1	0	CAGL0B00242g	
ChrB_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0B01243g	MATalpha1
ChrB_C_glabrata_CBS138	1	1	1	0	1	1	1	1	1	1	CAGL0B03608g	
ChrB_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	AWP9&CAGL0B0514	
ChrB_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1		
ChrC_C_glabrata_CBS138	1	0	1	0	0	0	0	0	1	0	CAGL0C00231g	
ChrC_C_glabrata_CBS138	0	0	0	1	0	0	0	1	1	1	CAGL0C00781g	
ChrC_C_glabrata_CBS138	0	0	0	0	0	1	0	0	0	0	CAGL0C00968g	
ChrC_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0C01056g	
ChrC_C_glabrata_CBS138	0	0	1	1	0	0	0	0	0	1	CAGL0C01133g	
ChrC_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	0	CAGL0C05379g	SSB1
ChrC_C_glabrata_CBS138	0	0	0	1	1	1	1	1	1	0	CAGL0C05643g	EPA7

ChrD_C_glabrata_CBS138	0	1	0	0	0	1	0	0	0	1	CAGL0D00105g	
ChrD_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0D00110g	
ChrD_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0D02618g	PEX11
ChrD_C_glabrata_CBS138	1	1	1	1	1	0	0	1	0	1	CAGL0D05082g	
ChrD_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0D06226g	
ChrD_C_glabrata_CBS138	1	0	0	1	1	1	1	1	1	1	CAGL0D06732g	EPA21
ChrE_C_glabrata_CBS138	1	1	1	1	0	0	1	1	1	1	CAGL0E00105g	
ChrE_C_glabrata_CBS138	0	0	0	1	1	1	0	0	0	1	CAGL0E00110g	
ChrE_C_glabrata_CBS138	1	0	1	1	0	1	1	0	0	1	CAGL0E00116g	
ChrE_C_glabrata_CBS138	0	0	0	1	1	1	1	0	0	0	CAGL0E00187g	
ChrE_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0E00231g	
ChrE_C_glabrata_CBS138	1	2	2	0	0	0	2	2	2	2	CAGL0E00715g	
ChrE_C_glabrata_CBS138	0	0	1	0	0	1	0	0	0	0	CAGL0E01155g	
ChrE_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0E01661g	
ChrE_C_glabrata_CBS138	0	1	1	1	0	1	1	1	1	1	CAGL0E05192g	
ChrE_C_glabrata_CBS138	0	1	1	1	1	1	1	1	1	0	CAGL0E05214g	
ChrE_C_glabrata_CBS138	1	0	2	2	2	2	2	2	2	2	CAGL0E05940g	
ChrE_C_glabrata_CBS138	0	1	0	0	0	1	1	1	0	0	CAGL0E06644g	EPA1
ChrE_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0E06666g	EPA2
ChrE_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0E06688g	EPA3
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0F00105g	
ChrF_C_glabrata_CBS138	1	0	0	0	0	0	0	1	0	0	CAGL0F00110g	AWP10
ChrF_C_glabrata_CBS138	0	1	1	1	0	1	1	0	0	1	CAGL0F00605g	GLK1
ChrF_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	1	CAGL0F00803g	GAL11B
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0F03003g	
ChrF_C_glabrata_CBS138	0	0	1	1	0	0	1	0	1	1	CAGL0F03861g	
ChrF_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0F04807g	
ChrF_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0F06831g	
ChrF_C_glabrata_CBS138	0	0	0	0	0	0	0	1	1	0	CAGL0F07007g	
ChrF_C_glabrata_CBS138	1	1	1	1	0	0	1	1	1	1	CAGL0F07249g	
ChrF_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0F07381g	
ChrF_C_glabrata_CBS138	0	1	0	1	1	1	0	1	1	1	CAGL0F08745g	
ChrG_C_glabrata_CBS138	1	1	0	0	1	0	0	0	1	1	CAGL0G00105g	
ChrG_C_glabrata_CBS138	0	0	0	1	0	0	0	0	0	0	CAGL0G00110g	
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0G00814g	CHS5
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0G04125g	
ChrG_C_glabrata_CBS138	0	0	1	0	0	0	1	0	1	1	CAGL0G05830g	
ChrG_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0G06842g	
ChrG_C_glabrata_CBS138	0	0	0	0	0	1	0	0	1	0	CAGL0G07293g	
ChrG_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0G07491g	MNN11
ChrG_C_glabrata_CBS138	1	0	2	0	0	1	1	0	0	0	CAGL0G09064g	
ChrG_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0G10175g	AWP6
ChrG_C_glabrata_CBS138	1	0	1	0	0	1	1	1	1	1	CAGL0G10219g	AWP12
ChrH_C_glabrata_CBS138	0	1	0	0	1	1	0	0	0	0	CAGL0H00110g	
ChrH_C_glabrata_CBS138	1	1	1	0	1	1	0	0	1	0	CAGL0H00132g	
ChrH_C_glabrata_CBS138	1	1	1	0	1	1	0	0	1	0	CAGL0H00121g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0H02959g	TOS8

ChrH_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0H04235g	
ChrH_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0H04257g	MT-II
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0H07469g	
ChrH_C_glabrata_CBS138	1	0	1	1	1	1	1	1	0	1	CAGL0H08844g	
ChrH_C_glabrata_CBS138	1	1	1	1	1	1	1	0	1	1	CAGL0H09592g	
ChrH_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	0	CAGL0H09614g	
ChrH_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0H10626g	AWP13
ChrI_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0I00110g	
ChrI_C_glabrata_CBS138	0	0	0	0	0	1	1	1	0	0	CAGL0I00105g	
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0I00220g	EPA23
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0I00726g	
ChrI_C_glabrata_CBS138	1	2	2	2	2	2	2	2	3	2	CAGL0I04180g	AMT1
ChrI_C_glabrata_CBS138	1	0	0	0	1	1	0	1	0	1	CAGL0I04378g	
ChrI_C_glabrata_CBS138	1	1	1	1	0	1	1	1	2	1	CAGL0I05016g	TRP2
ChrI_C_glabrata_CBS138	0	0	0	0	0	0	0	1	0	0	CAGL0I05082g	
ChrI_C_glabrata_CBS138	0	1	1	0	0	0	0	0	0	0	CAGL0I05170g	CST6
ChrI_C_glabrata_CBS138	1	1	0	0	1	1	1	1	1	1	CAGL0I06182g	PIR2
ChrI_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0I06204g	PIR1
ChrI_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0I07447g	
ChrI_C_glabrata_CBS138	1	1	1	0	0	0	0	0	1	0	CAGL0I10098g	PWP7
ChrI_C_glabrata_CBS138	0	0	1	1	0	0	0	1	0	0	CAGL0I10147g	PWP1
ChrI_C_glabrata_CBS138	0	1	1	1	0	0	0	1	1	0	CAGL0I10200g	PWP3
ChrI_C_glabrata_CBS138	1	1	0	1	0	0	1	1	0	0	CAGL0I10362g	PWP4
ChrJ_C_glabrata_CBS138	1	0	0	1	0	1	1	0	1	1	CAGL0J00105g	
ChrJ_C_glabrata_CBS138	1	0	0	1	0	1	1	0	1	1	CAGL0J00110g	
ChrJ_C_glabrata_CBS138	0	0	1	1	0	0	0	1	1	0	CAGL0J00110g&CAG	
ChrJ_C_glabrata_CBS138	1	1	0	0	1	0	0	0	0	0	CAGL0J01727g	
ChrJ_C_glabrata_CBS138	0	1	0	0	0	1	0	0	0	0	CAGL0J01774g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0J01800g	
ChrJ_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0J02024g	
ChrJ_C_glabrata_CBS138	1	1	1	1	0	1	1	1	1	1	CAGL0J02508g	AWP1
ChrJ_C_glabrata_CBS138	1	0	1	0	0	1	0	0	0	1	CAGL0J02552g	
ChrJ_C_glabrata_CBS138	1	0	0	0	1	0	0	0	1	1	CAGL0J05159g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	1	1	0	0	0	CAGL0J09988g	
ChrJ_C_glabrata_CBS138	0	0	0	0	0	1	1	0	0	0	CAGL0J10010g	
ChrJ_C_glabrata_CBS138	1	1	0	0	1	0	0	0	0	0	CAGL0J11462g	
ChrJ_C_glabrata_CBS138	0	1	0	0	0	0	0	0	0	0	CAGL0J11891g	AWP3
ChrJ_C_glabrata_CBS138	0	1	0	0	1	0	1	1	1	1	CAGL0J11968g	EPA15
ChrJ_C_glabrata_CBS138	0	0	1	1	1	1	0	0	0	0	CAGL0J11990g	AWP4
ChrK_C_glabrata_CBS138	1	1	0	1	0	0	1	0	0	0	CAGL0K00110g	AWP2
ChrK_C_glabrata_CBS138	1	0	0	0	0	0	0	0	0	0	CAGL0K00170g	EPA22
ChrK_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0K01177g	
ChrK_C_glabrata_CBS138	0	1	1	1	1	1	1	1	0	1	CAGL0K02079g	GLC7
ChrK_C_glabrata_CBS138	1	2	1	1	1	1	1	1	1	1	CAGL0K05335g	
ChrK_C_glabrata_CBS138	0	0	0	0	1	0	0	0	0	0	CAGL0K07700g	
ChrK_C_glabrata_CBS138	0	0	0	0	0	0	1	0	0	0	CAGL0K12056g	
ChrK_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0K12078g	

ChrK_C_glabrata_CBS138	1	1	0	1	0	1	1	0	0	1	CAGL0K13024g	AED1
ChrL_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	0	CAGL0L00157g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0L00227g	
ChrL_C_glabrata_CBS138	0	0	1	0	1	0	1	0	1	1	CAGL0L00627g	
ChrL_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	2	CAGL0L01067g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0L01837g	VPS24
ChrL_C_glabrata_CBS138	1	1	1	1	1	0	0	0	0	0	CAGL0L01903g	RGT1
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0L08580g	RPN10
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0L09911g	
ChrL_C_glabrata_CBS138	0	0	0	0	0	0	0	0	0	1	CAGL0L10043g	
ChrL_C_glabrata_CBS138	0	1	0	1	0	1	0	0	0	0	CAGL0L10092g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	1	0	1	1	1	CAGL0L10208g	
ChrL_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0L10406g	CYT1
ChrL_C_glabrata_CBS138	1	0	0	0	1	2	0	2	1	0	CAGL0L11660g	
ChrL_C_glabrata_CBS138	1	1	1	1	2	1	1	1	1	1	CAGL0L12254g	
ChrL_C_glabrata_CBS138	0	1	1	1	0	0	0	1	0	0	CAGL0L13299g	EPA11
ChrL_C_glabrata_CBS138	1	1	1	1	1	0	1	1	1	1	CAGL0L13332g	EPA13
ChrL_C_glabrata_CBS138	0	1	0	0	1	0	1	0	0	0	CAGL0L13354g	TNR1
ChrL_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	0	CAGL0L13431g	
ChrM_C_glabrata_CBS138	1	1	0	1	0	0	1	1	0	1	CAGL0M00132g	EPA12
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	0	1	CAGL0M01276g	
ChrM_C_glabrata_CBS138	0	0	1	0	0	0	0	0	0	0	CAGL0M05115g	
ChrM_C_glabrata_CBS138	1	1	0	1	1	1	1	1	1	1	CAGL0M05181g	
ChrM_C_glabrata_CBS138	1	0	1	1	1	1	1	1	1	1	CAGL0M08492g	PIR3
ChrM_C_glabrata_CBS138	0	0	0	0	0	0	0	0	1	0	CAGL0M10395g	
ChrM_C_glabrata_CBS138	0	0	1	1	1	1	1	1	1	1	CAGL0M12320g	
ChrM_C_glabrata_CBS138	1	1	1	1	1	1	1	1	1	0	CAGL0M14113g	TNR2
mito_C_glabrata_CBS138	1	1	0	1	0	0	0	0	0	0	CaglfMp07	Cgai3

Description
Protein of unknown function
Putative adhesin-like protein; belongs to adhesin cluster I; appears artificially broken into fragments due to seque
Protein of unknown function
Protein of unknown function
Ortholog(s) have nuclear import signal receptor activity, role in protein import into nucleus and cytoplasm, nucleu
Putative C24 sterol reductase
Has domain(s) with predicted channel activity, role in transmembrane transport and membrane localization
Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral c
Putative adhesin-like protein; belongs to adhesin cluster I
Has domain(s) with predicted transcription coregulator activity, role in regulation of transcription by RNA polymer
Putative adhesin; belongs to adhesin cluster I
Ortholog(s) have fungal-type cell wall localization
Putative mannosyltransferase of cis-Golgi apparatus; gene is upregulated in azole-resistant strain
Ortholog(s) have glucose transmembrane transporter activity, pentose transmembrane transporter activity, role i
Ortholog(s) have glucose transmembrane transporter activity and mitochondrial membrane localization
Protein of unknown function
Ortholog(s) have role in fungal-type cell wall organization and Golgi apparatus localization
Has domain(s) with predicted GTP binding activity and role in cell cycle
Ortholog(s) have dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase activity
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Homeobox-domain protein alpha2
Ortholog(s) have NADH dehydrogenase (ubiquinone) activity, role in NADH oxidation, mitochondrial electron trans
Has domain(s) with predicted mitochondrial inner membrane peptidase complex localization
Sub-telomerically encoded adhesin with a role in cell adhesion; binds to ligands containing a terminal galactose re
Protein of unknown function
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have ATPase activity, role in ribosomal small subunit export from nucleus, ribosome biogenesis and nu
Ortholog(s) have protein methyltransferase activity, rRNA (guanine) methyltransferase activity, tRNA (guanine-N2
Protein of unknown function
Ortholog(s) have ubiquitin-protein transferase activity and role in cytoplasm protein quality control by the ubiquit
Protein of unknown function
Ortholog(s) have role in potassium ion transport, protein insertion into mitochondrial inner membrane from matri
Has domain(s) with predicted hydrolase activity
Protein of unknown function
Ortholog(s) have ubiquinol-cytochrome-c reductase activity and role in aerobic respiration, mitochondrial electror
Ortholog(s) have protein phosphatase activator activity
Putative membrane bound guanine nucleotide exchange factor; gene is upregulated in azole-resistant strain
Ortholog(s) have RNA binding, aspartate-tRNA ligase activity, role in aspartyl-tRNA aminoacylation and cytoplasm,
Ortholog(s) have protein serine/threonine kinase activity, protein tyrosine kinase activity
Ortholog(s) have MAP-kinase scaffold activity
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I

Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative adhesin-like protein; belongs to adhesin cluster IV
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
DNA-directed RNA polymerase II
Ortholog(s) have role in 2-oxoglutarate metabolic process and mitochondrial nucleoid, mitochondrial oxoglutarate
Adhesin-like protein with tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have cargo adaptor activity, ubiquitin binding activity and role in actin cortical patch assembly, endocy
Putative siderophore-iron transporter with 14 transmembrane domains; required for iron-dependent survival in m
Ortholog(s) have role in cellular response to oxidative stress, protein quality control for misfolded or incompletely
Has domain(s) with predicted role in response to oxidative stress
Ortholog(s) have L-proline transmembrane transporter activity, neutral amino acid transmembrane transporter ac
Ortholog(s) have fatty acid synthase activity, role in fatty acid biosynthetic process, long-chain fatty acid biosynthe
Sub-telomerically encoded adhesin with a role in cell adhesion; GPI-anchored cell wall protein; N-terminal ligand b
Epithelial adhesion protein, involved in biofilm formation and azole drug resistance; belongs to adhesin cluster I; G
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Ortholog(s) have adenyl-nucleotide exchange factor activity and role in SRP-dependent cotranslational protein tar
Ortholog of S. cerevisiae : YBL029C-A, C. albicans SC5314 : C1_02060W_A, C. dubliniensis CD36 : Cd36_01920, C. p
Putative regulatory subunit for protein phosphatase; gene is upregulated in azole-resistant strain
Has domain(s) with predicted protein heterodimerization activity and role in DNA-templated transcription, initiati
Ortholog of S. cerevisiae : MTC2 and Saccharomyces cerevisiae S288C : YKL098W
Ortholog of S. cerevisiae : YGR237C, C. albicans SC5314 : C5_04960W_A, C. dubliniensis CD36 : Cd36_54560, C. pa
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have small GTPase binding activity
Ortholog(s) have role in macroautophagy, mitochondrial proton-transporting ATP synthase complex assembly and
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate binding, sphingolipid binding activity
Heat shock protein of the HSP70 family
Ortholog(s) have role in ascospore wall assembly
Ortholog(s) have role in actin cytoskeleton organization, negative regulation of Arp2/3 complex-mediated actin nu
Ortholog(s) have molecular adaptor activity and role in mRNA splicing, via spliceosome, positive regulation of prot
Putative glutathione-dependent oxidoreductase; induced by excess iron; likely functional homolog of S. cerevisiae
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Ortholog(s) have role in ribosomal small subunit biogenesis and nucleolus localization
Ortholog(s) have chromatin binding activity and nuclear chromatin localization
Protein of unknown function
Ortholog(s) have role in DNA recombinase assembly, error-free translesion synthesis, recombinational repair and S
Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA fro
Ortholog(s) have role in proteasomal ubiquitin-independent protein catabolic process, proteasome-mediated ubic
Putative GPI-linked cell wall protein
Protein of unknown function
Ortholog(s) have cytoplasm, membrane raft localization
Predicted cell wall adhesin with a role in adhesion; belongs to adhesin cluster III; predicted GPI anchor; contains ta
Putative adhesin-like with multiple tandem repeats; ORF appears artificially broken into fragments due to sequenc
Ortholog(s) have role in ascospore wall assembly
Ortholog(s) have clathrin binding activity and role in endocytosis

Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Haloacid dehalogenase-like hydrolase
Pir protein family member, putative cell wall component
Pir protein family member, putative cell wall component
Ortholog(s) have succinate-CoA ligase (ADP-forming) activity, role in succinyl-CoA metabolic process and mitochor
Ortholog(s) have ubiquitin binding activity
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Protein with 32 tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Adhesin-like protein with tandem repeats; contains a PA14 domain; belongs to adhesin cluster II
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Protein of unknown function
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI; predicted
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Putative adhesin-like protein
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Ortholog(s) have homoserine O-acetyltransferase activity and role in 'de novo' L-methionine biosynthetic process,
Ortholog(s) have DNA translocase activity, RNA polymerase II activating transcription factor binding activity
Ortholog(s) have role in fungal-type cell wall organization, positive regulation of signal transduction
Predicted GPI-linked cell wall protein
Putative adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI
Putative adhesin-like protein with internal repeats; identified in cell wall extracts by mass spectrometry; ORF appe
Protein of unknown function
Putative adhesin; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster V; predicted GPI
Putative adhesin-like protein; belongs to adhesin cluster I
Ortholog of S. cerevisiae : YGR079W and Saccharomyces cerevisiae S288C : YGR079W
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefoldin co
Putative component of the telomeric Ku complex, involved in maintenance of telomere length and nonhomologou
Ortholog(s) have role in endoplasmic reticulum polarization and cellular bud neck localization
Putative mitochondrial Ser/Thr protein kinase; gene is upregulated in azole-resistant strain
Has domain(s) with predicted nucleic acid binding, zinc ion binding activity
Ortholog(s) have DNA translocase activity
Ortholog(s) have role in RNA polymerase I assembly, RNA polymerase II core complex assembly, RNA polymerase
Has domain(s) with predicted ATP binding, protein kinase activity, protein tyrosine kinase activity and role in prote
Ortholog(s) have role in protein maturation, protein targeting to ER and endoplasmic reticulum, membrane localiz
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Putative adhesin with glycine and serine rich repeats; belongs to adhesin cluster V
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Acetyl-coenzyme A synthetase
Ortholog of S. cerevisiae : MIT1, C. albicans SC5314 : C1_10150W_A/WOR1, C. dubliniensis CD36 : Cd36_09540, C.
Predicted GPI-linked adhesin-like protein
Has domain(s) with predicted ribokinase activity and role in D-ribose metabolic process
Ortholog(s) have role in eisosome assembly, negative regulation of protein phosphorylation, negative regulation o
Putative adhesin-like cell wall protein; 5 tandem repeats; predicted GPI-anchor

Ortholog(s) have protein kinase activator activity
Putative adhesin-like cell wall protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster
Ortholog(s) have L-alanine:2-oxoglutarate aminotransferase activity, role in alanine biosynthetic process, alanine c
Ortholog(s) have role in mitochondrial genome maintenance, mitochondrial tRNA 5'-end processing and matrix sic
Putative adhesin; belongs to adhesin cluster I
Sub-telomerically encoded lectin-like adhesin with a role in cell adhesion; contains multiple tandem repeats; predi
Putative nicotinamide transporter; strongly induced under niacin-limiting conditions
Protein of unknown function
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Ortholog(s) have ubiquitin binding activity and role in proteasome-mediated ubiquitin-dependent protein catabolı
Ortholog(s) have acetate transmembrane transporter activity, ammonium transmembrane transporter activity, ro
Ortholog(s) have role in pseudohyphal growth and cytosol, nucleus localization
Pir protein family member, putative cell wall component
Ortholog(s) have mRNA binding activity and role in cellular protein-containing complex localization, establishment
Protein of unknown function
Protein of unknown function
Ortholog(s) have RNA binding, RNA helicase activity, RNA-dependent ATPase activity
65 kDa mannoprotein
Adhesin-like protein with similarity to S. cerevisiae flocculins, cell wall proteins that mediate adhesion; predicted C
Putative quinone reductase/NADPH dehydrogenase; gene is upregulated in azole-resistant strain
High-affinity transporter of NAD+ precursors; strongly induced under niacin-limiting conditions
Putative endonuclease with similarity to S. cerevisiae AI5_alpha (I-SceIV) endonuclease; encoded by the first three

Gene-Name
Protein of unknown function
Putative adhesin-like protein; belongs to adhesin cluster I; appears artificially broken into fragments due to sequer
Protein of unknown function
Protein of unknown function
Ortholog(s) have nuclear import signal receptor activity, role in protein import into nucleus and cytoplasm, nucleu
Putative C24 sterol reductase
Has domain(s) with predicted channel activity, role in transmembrane transport and membrane localization
Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral c
Putative adhesin-like protein; belongs to adhesin cluster I
Has domain(s) with predicted transcription coregulator activity, role in regulation of transcription by RNA polymer
Putative adhesin; belongs to adhesin cluster I
Ortholog(s) have RNA polymerase II activating transcription factor binding, RNA polymerase II core promoter sequ
Ortholog(s) have fungal-type cell wall localization
Ortholog(s) have glucose transmembrane transporter activity, pentose transmembrane transporter activity, role in
Ortholog(s) have glucose transmembrane transporter activity and mitochondrial membrane localization
Protein of unknown function
Ortholog(s) have fructose transmembrane transporter activity, glucose transmembrane transporter activity, mann
Ortholog(s) have role in fungal-type cell wall organization and Golgi apparatus localization
Has domain(s) with predicted GTP binding activity and role in cell cycle
Ortholog(s) have iron ion binding, oxidoreductase activity, acting on iron-sulfur proteins as donors, zinc ion bindin
Ortholog(s) have dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase activity

Protein of unknown function
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Ortholog(s) have sequence-specific DNA binding activity and role in regulation of transcription by RNA polymerase
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Homeobox-domain protein alpha2
Alpha-domain mating-type protein alpha1p; expressed in all MTLalpha strains and not in MTLa strains
Has domain(s) with predicted mitochondrial inner membrane peptidase complex localization
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Sub-telomerically encoded adhesin with a role in cell adhesion; binds to ligands containing a terminal galactose re
Putative adhesin-like cell wall protein; belongs to adhesin cluster IV; predicted GPI-anchor
Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport, trans
Putative adhesin-like protein; belongs to adhesin cluster I
Protein of unknown function
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Ortholog of S. cerevisiae : YIL108W, C. albicans SC5314 : C3_02570W_A, C. dubliniensis CD36 : Cd36_82530, C. par
Putative glutathione peroxidase
Ortholog(s) have ATPase activity, role in ribosomal small subunit export from nucleus, ribosome biogenesis and nu
Has domain(s) with predicted integral component of membrane localization
Adhesin-like protein with a predicted GPI-anchor; belongs to adhesin cluster I; strain BG14 encodes the full-length
Ortholog(s) have protein phosphatase activator activity
Ortholog(s) have RNA binding, aspartate-tRNA ligase activity, role in aspartyl-tRNA aminoacylation and cytoplasm,
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have histone binding, histone deacetylase binding, mediator complex binding, phosphatidylinositol-3,5
Has domain(s) with predicted role in response to oxidative stress
Ortholog(s) have L-proline transmembrane transporter activity, neutral amino acid transmembrane transporter ac
Sub-telomerically encoded adhesin with a role in cell adhesion; GPI-anchored cell wall protein; N-terminal ligand b
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Ortholog(s) have adenyl-nucleotide exchange factor activity and role in SRP-dependent cotranslational protein tar
Putative GPI-linked cell wall mannoprotein of the Srp1p/Tip1p family
Translation elongation factor eEF1 alpha-A chain
Ortholog(s) have DNA secondary structure binding, cohesin ATPase activity, double-stranded DNA binding, minor g
Ortholog(s) have osmosensor activity and role in (1->3)-beta-D-glucan biosynthetic process, cellular bud site selec
Ortholog of S. cerevisiae : FMP42, C. albicans SC5314 : CR_04760C_A, C. dubliniensis CD36 : Cd36_30130, C. parap
Ortholog(s) have integral component of mitochondrial outer membrane, mitochondrial outer membrane, mitocho
Putative regulatory subunit for protein phosphatase; gene is upregulated in azole-resistant strain
Ortholog(s) have role in cellular response to cold, mRNA stabilization and positive regulation of transcription by RN
Ortholog(s) have RNA polymerase II activating transcription factor binding, chromatin binding, molecular adaptor
Has domain(s) with predicted protein heterodimerization activity and role in DNA-templated transcription, initiati

Ortholog of S. cerevisiae : MTC2 and Saccharomyces cerevisiae S288C : YKL098W
Protein of unknown function
Ortholog of S. cerevisiae : YGR237C, C. albicans SC5314 : C5_04960W_A, C. dubliniensis CD36 : Cd36_54560, C. pa
Putative transglycosidase with a predicted role in the modification of 1,3-beta-glucan
Ortholog(s) have actin binding activity and role in actin cortical patch localization, bipolar cellular bud site selectio
Ortholog(s) have MAP-kinase scaffold activity
Ortholog(s) have nucleolus localization
Ortholog(s) have role in macroautophagy, mitochondrial proton-transporting ATP synthase complex assembly and
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate binding, sphingolipid binding activity
Heat shock protein of the HSP70 family
Ortholog(s) have molecular adaptor activity and role in mRNA splicing, via spliceosome, positive regulation of prot
Putative glutathione-dependent oxidoreductase; induced by excess iron; likely functional homolog of S. cerevisiae
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Adhesin-like protein with internal repeats; predicted GPI-anchor; likely a C-terminal fragment of a single ORF with
Ortholog(s) have GTPase activator activity and role in endoplasmic reticulum to Golgi vesicle-mediated transport,
Ortholog(s) have sphinganine-1-phosphate aldolase activity and role in calcium-mediated signaling, cellular respor
Ortholog(s) have box H/ACA snoRNA binding activity, role in snRNA pseudouridine synthesis and box H/ACA snoRN
Ortholog(s) have role in ribosomal small subunit biogenesis and nucleolus localization
Ortholog(s) have transcription corepressor activity
Protein of unknown function
Protein of unknown function
Ortholog(s) have tRNA dihydrouridine synthase activity and role in tRNA modification
Ortholog(s) have role in DNA recombinase assembly, error-free translesion synthesis, recombinational repair and S
Protein of unknown function
Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA fro
Ortholog(s) have DNA binding, DNA-dependent ATPase activity, chromatin binding activity
Putative GPI-linked cell wall protein
Putative GPI-linked cell wall protein
Putative adhesin-like with multiple tandem repeats; ORF appears artificially broken into fragments due to sequenc
Ortholog(s) have ATPase activity, proton-transporting ATP synthase activity, rotational mechanism activity
Ortholog(s) have sequence-specific DNA binding activity and role in chromatin silencing at telomere, rDNA heteroc
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Haloacid dehalogenase-like hydrolase
Ortholog(s) have myo-inositol transmembrane transporter activity, role in myo-inositol import across plasma mem
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Ortholog(s) have role in histone deacetylation, negative regulation of antisense RNA transcription and positive reg
Gene used for molecular typing of C. glabrata strain isolates
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Protein of unknown function
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI; predicted
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Ortholog(s) have cargo adaptor activity, ubiquitin binding activity and role in actin cortical patch assembly, endocy
Ortholog(s) have myosin II tail binding, protein-macromolecule adaptor activity, role in protein localization to cell
Epithelial adhesion protein, involved in biofilm formation and azole drug resistance; belongs to adhesin cluster I; G

Ortholog(s) have RNA polymerase II cis-regulatory region sequence-specific DNA binding, cysteine-type peptidase
Ortholog(s) have homoserine O-acetyltransferase activity and role in 'de novo' L-methionine biosynthetic process,
Ortholog(s) have GTPase activity, role in Golgi to plasma membrane transport, endoplasmic reticulum to Golgi ves
Ortholog(s) have thiol-dependent ubiquitin-specific protease activity, role in chromatin silencing at telomere, histo
Putative adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI
Putative adhesin-like protein with internal repeats; identified in cell wall extracts by mass spectrometry; ORF appe
Putative adhesin-like protein; belongs to adhesin cluster I
Ortholog of S. cerevisiae : YGR079W and Saccharomyces cerevisiae S288C : YGR079W
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefoldin co
Putative component of the telomeric Ku complex, involved in maintenance of telomere length and nonhomologou
Ortholog(s) have DNA translocase activity
Protein of unknown function
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have role in protein maturation, protein targeting to ER and endoplasmic reticulum, membrane localiz
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have DNA binding activity
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Acetyl-coenzyme A synthetase
Ortholog of S. cerevisiae : MIT1, C. albicans SC5314 : C1_10150W_A/WOR1, C. dubliniensis CD36 : Cd36_09540, C.
Predicted GPI-linked adhesin-like protein
Has domain(s) with predicted DNA-binding transcription factor activity, sequence-specific DNA binding, zinc ion bi
Ortholog(s) have protein kinase activator activity
Has domain(s) with predicted mannosyl-oligosaccharide glucosidase activity and role in oligosaccharide metabolic
Putative adhesin; belongs to adhesin cluster I
Protein of unknown function
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Ortholog(s) have ubiquitin binding activity and role in proteasome-mediated ubiquitin-dependent protein catabol
Pir protein family member, putative cell wall component
Ortholog(s) have mRNA binding activity and role in cellular protein-containing complex localization, establishment
Ortholog(s) have RNA binding, RNA helicase activity, RNA-dependent ATPase activity
Adhesin-like protein with similarity to S. cerevisiae flocculins, cell wall proteins that mediate adhesion; predicted G
Ortholog(s) have protein phosphatase inhibitor activity, rDNA binding activity
High-affinity transporter of NAD+ precursors; strongly induced under niacin-limiting conditions
[redacted]

Feature-type
pseudogene
ORF|Uncharacterized
pseudogene
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pseudogene
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ORF|Verified
ORF|Uncharacterized
ORF|Uncharacterized
ORF|Uncharacterized
tRNA|Uncharacterized
ORF|Uncharacterized
ORF|Verified
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ORF|Uncharacterized
ORF|Uncharacterized
ORF|Verified

Description
Protein of unknown function
Putative adhesin-like protein; belongs to adhesin cluster I; appears artificially broken into fragments due to seque
Protein of unknown function
Ortholog(s) have nuclear import signal receptor activity, role in protein import into nucleus and cytoplasm, nucleu
Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral c
Putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin; belongs to adhesin cluster I
Ortholog(s) have fungal-type cell wall localization

Putative mannosyltransferase of cis-Golgi apparatus; gene is upregulated in azole-resistant strain
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Protein of unknown function
Ortholog(s) have RNA binding activity, role in regulation of translation and cytoplasmic stress granule, polysome lo
Ortholog(s) have role in actin cortical patch localization, actin cytoskeleton organization, actin filament organizatio
Ortholog(s) have oxidoreductase activity, acting on NAD(P)H, nitrogenous group as acceptor activity and role in ce
Ortholog(s) have NADH dehydrogenase (ubiquinone) activity, role in NADH oxidation, mitochondrial electron trans
Has domain(s) with predicted mitochondrial inner membrane peptidase complex localization
Ortholog(s) have role in cellular protein-containing complex localization and Dsc E3 ubiquitin ligase complex localiz
Sub-telomerically encoded adhesin with a role in cell adhesion; binds to ligands containing a terminal galactose re
Putative adhesin-like cell wall protein; belongs to adhesin cluster IV; predicted GPI-anchor
Ortholog(s) have role in reciprocal meiotic recombination
Protein of unknown function
Putative adhesin-like protein; belongs to adhesin cluster I
Protein of unknown function
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Protein of unknown function
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Ortholog of S. cerevisiae : YIL108W, C. albicans SC5314 : C3_02570W_A, C. dubliniensis CD36 : Cd36_82530, C. par
Ortholog(s) have ATPase activity, role in ribosomal small subunit export from nucleus, ribosome biogenesis and nu
Glycerol transporter; involved in flucytosine resistance; double fps1/fps2 mutant accumulates glycerol, has constit
Ortholog(s) have 3'-5'-exoribonuclease activity
Has domain(s) with predicted transferase activity, transferring glycosyl groups activity and role in protein glycosyla
Ortholog(s) have alditol:NADP+ 1-oxidoreductase activity, aldo-keto reductase (NADP) activity and role in D-xylose
Ortholog(s) have protein serine/threonine kinase activity and role in meiotic spindle disassembly, mitotic cytokine
Putative glycerol 3-phosphate dehydrogenase; protein differentially expressed in azole resistant strain
Heat shock protein
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative nuclear phosphatase regulatory subunit; gene is downregulated in azole-resistant strain
Ortholog(s) have transcription factor TFIIH holo complex localization
Ortholog(s) have role in fatty acid metabolic process, fatty acid oxidation, peroxisome fission and endoplasmic ret
Ortholog(s) have ubiquitin-protein transferase activity and role in cytoplasm protein quality control by the ubiquit
Protein of unknown function
Ortholog(s) have role in potassium ion transport, protein insertion into mitochondrial inner membrane from matri
Protein of unknown function
Ortholog(s) have mRNA binding activity
Squalene epoxidase with a role in ergosterol synthesis; involved in growth under conditions of low oxygen tension
Putative aconitate hydratase
Ortholog(s) have RNA binding, aspartate-tRNA ligase activity, role in aspartyl-tRNA aminoacylation and cytoplasm,
Ortholog(s) have protein serine/threonine kinase activity, protein tyrosine kinase activity
Ortholog(s) have MAP-kinase scaffold activity
Protein of unknown function
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III

Ortholog(s) have histone binding, histone deacetylase binding, mediator complex binding, phosphatidylinositol-3,5
DNA-directed RNA polymerase II
Ortholog(s) have ARF guanyl-nucleotide exchange factor activity and role in autophagosome assembly, endoplasm
Ortholog(s) have DNA-binding transcription activator activity, RNA polymerase II-specific, sequence-specific DNA b
Ortholog(s) have palmitoyltransferase activity, role in protein palmitoylation, protein targeting to membrane and
Putative phospholipase B; predicted GPI-anchor
Ortholog(s) have cargo adaptor activity, ubiquitin binding activity and role in actin cortical patch assembly, endocy
Ortholog(s) have GTPase activity
Has domain(s) with predicted iron-sulfur cluster binding, structural molecule activity and role in iron-sulfur cluster
Glycerol transporter; involved in flucytosine resistance; double fps1/fps2 mutant accumulates glycerol, has constit
Has domain(s) with predicted role in response to oxidative stress
Ortholog(s) have ATPase activator activity, chaperone binding activity, role in cellular response to heat, protein fol
Ortholog(s) have chorismate synthase activity, riboflavin reductase (NADPH) activity, role in aromatic amino acid f
Ortholog(s) have mRNA binding, ribosome binding activity and role in mitochondrial respiratory chain complex III a
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Component of the transcriptional Mediator complex that provides interfaces between RNA polymerase II and upst
Ortholog(s) have adenyl-nucleotide exchange factor activity and role in SRP-dependent cotranslational protein tar
Putative GPI-linked cell wall mannoprotein of the Srp1p/Tip1p family
Ortholog(s) have TBP-class protein binding, transcription coregulator activity
Ortholog(s) have DNA secondary structure binding, cohesin ATPase activity, double-stranded DNA binding, minor g
Ortholog(s) have osmosensor activity and role in (1->3)-beta-D-glucan biosynthetic process, cellular bud site select
Ortholog of S. cerevisiae : FMP42, C. albicans SC5314 : CR_04760C_A, C. dubliniensis CD36 : Cd36_30130, C. parap
Putative regulatory subunit for protein phosphatase; gene is upregulated in azole-resistant strain
Ortholog of S. cerevisiae : MTC2 and Saccharomyces cerevisiae S288C : YKL098W
Ortholog of S. cerevisiae : YGR237C, C. albicans SC5314 : C5_04960W_A, C. dubliniensis CD36 : Cd36_54560, C. pa
Ortholog(s) have role in cellular response to desiccation and cytoplasm localization
Ortholog(s) have enzyme activator activity, telomerase inhibitor activity, role in box C/D snoRNA 3'-end processing
Ortholog(s) have actin binding activity and role in actin cortical patch localization, bipolar cellular bud site selectio
Ortholog(s) have nucleolus localization
Ortholog of S. cerevisiae : NNF2, C. albicans SC5314 : C2_00120C_A/EMC9, C. dubliniensis CD36 : Cd36_15110, C. p
Protein of unknown function
Protein with similarity to S. cerevisiae Sag1 agglutinin, involved in cell adhesion; predicted GPI-anchor
Ortholog(s) have DNA binding activity
Protein of unknown function
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly, mitochondrial respirasome assembly, regu
Alpha-1,6-mannosyltransferase with a role in protein glycosylation
Ortholog(s) have protein tag activity, role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,
Ortholog(s) have cAMP-dependent protein kinase activity, protein serine/threonine kinase activity, translation init
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Adhesin-like protein with internal repeats; predicted GPI-anchor; likely a C-terminal fragment of a single ORF with
Protein of unknown function
Putative adhesin-like protein with 4 tandem repeats; appears artificially broken into fragments due to sequencing
Ortholog(s) have mRNA binding activity and role in mRNA splice site selection, mRNA splicing, via spliceosome, po
Ortholog(s) have chromatin binding activity and nuclear chromatin localization
Ortholog(s) have DNA-binding transcription activator activity, RNA polymerase II-specific activity, role in positive r

Ortholog(s) have tRNA dihydrouridine synthase activity and role in tRNA modification
Ortholog(s) have role in DNA recombinase assembly, error-free translesion synthesis, recombinational repair and
Ortholog(s) have phosphatidylinositol transfer activity
Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA fro
Ortholog(s) have protein-membrane adaptor activity and role in COPII vesicle coating, macroautophagy, protein lo
Ortholog(s) have DNA binding, DNA-dependent ATPase activity, chromatin binding activity
Putative adhesin-like protein
Ortholog(s) have role in protein processing, pseudohyphal growth and plasma membrane localization
Has domain(s) with predicted hydrolase activity, tubulin-tyrosine ligase activity and role in cellular protein modific
Ortholog(s) have cytosolic large ribosomal subunit localization
Putative adhesin-like protein
Putative GPI-linked cell wall protein
Predicted cell wall adhesin with a role in adhesion; belongs to adhesin cluster III; predicted GPI anchor; contains ta
Protein of unknown function
Putative adhesin-like with multiple tandem repeats; ORF appears artificially broken into fragments due to sequenc
Protein of unknown function
Metal-activated transcription factor; binds promoters of metallothionein genes; autoregulates its own expression;
5-methyltetrahydropteroyltriglutamate homocysteine methyltransferase; protein abundance increased in ace2 m
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Ortholog(s) have ribose phosphate diphosphokinase activity, role in 5-phosphoribose 1-diphosphate biosynthetic
Pir protein family member, putative cell wall component
Ortholog(s) have ubiquitin binding activity
Ortholog(s) have long-chain fatty acid-CoA ligase activity, medium-chain fatty acid-CoA ligase activity, myristoyl-Co
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Protein of unknown function
Protein with 32 tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Cell wall adhesin; predicted GPI anchor; contains tandem repeats; belongs to adhesin cluster II
Ortholog(s) have eisosome, membrane raft localization
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Ortholog(s) have 3'-5' DNA helicase activity, DNA/RNA helicase activity, flap-structured DNA binding, four-way jun
Protein of unknown function
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI; predicted
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Ortholog(s) have CoA-transferase activity, acetate CoA-transferase activity, hydrolase activity, acting on ester bon
Putative adhesin-like protein
Ortholog(s) have 2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity, role in aerobic respiratio
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Ortholog(s) have calcium activated cation channel activity, calcium channel activity, potassium channel activity, so
Ortholog(s) have DNA translocase activity, RNA polymerase II activating transcription factor binding activity
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in translational readthroug
Ortholog(s) have role in axial cellular bud site selection, establishment of protein localization, mitotic nuclear divis
Predicted GPI-linked cell wall protein
Putative adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI
Putative adhesin-like protein with internal repeats; identified in cell wall extracts by mass spectrometry; ORF appe

Putative adhesin; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster V; predicted GPI
Putative adhesin-like protein; belongs to adhesin cluster I
Ortholog(s) have ATP binding, magnesium ion binding, ubiquitin activating enzyme activity, role in protein ubiquiti
Ortholog of S. cerevisiae : YGR079W and Saccharomyces cerevisiae S288C : YGR079W
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefoldin co
Putative serine-threonine phosphoprotein phosphatase 1, catalytic chain
Ortholog(s) have kinase activity, protein kinase activity, protein serine/threonine kinase activity, protein serine/th
Putative component of the telomeric Ku complex, involved in maintenance of telomere length and nonhomologou
Ortholog of S. cerevisiae : BOP2 and Saccharomyces cerevisiae S288C : YLR267W
Protein of unknown function
Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytos
Na(+)-ATPase with broad substrate specificity; plays a role in sodium detoxification; highly upregulated by increase
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have role in protein maturation, protein targeting to ER and endoplasmic reticulum, membrane localiz
Ortholog(s) have beta-1,4-mannosyltransferase activity, role in oligosaccharide-lipid intermediate biosynthetic pro
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Acetyl-coenzyme A synthetase
Ortholog(s) have RNA binding, ribosome binding, translation elongation factor activity, translation initiation factor
Ortholog of S. cerevisiae : MIT1, C. albicans SC5314 : C1_10150W_A/WOR1, C. dubliniensis CD36 : Cd36_09540, C.
Putative gamma glutamylcysteine synthetase, essential for viability; role in glutathione biosynthesis; required to k
Ortholog(s) have role in fungal-type cell wall organization or biogenesis, mitochondrial ATP synthesis coupled prot
Ortholog(s) have role in mRNA splicing, via spliceosome and RES complex, U2-type spliceosomal complex, nucleus
Ortholog(s) have role in meiotic cell cycle, negative regulation of protein localization to nucleolus
Has domain(s) with predicted ribokinase activity and role in D-ribose metabolic process
Ortholog(s) have role in eisosome assembly, negative regulation of protein phosphorylation, negative regulation o
Long chain base-responsive inhibitor of protein kinases; protein abundance decreased in ace2 mutant cells
Ortholog(s) have role in positive regulation of transcription by RNA polymerase II, response to salt stress and cyto
Ortholog(s) have protein kinase activator activity
Ortholog(s) have DNA binding, DNA-dependent ATPase activity, chromatin DNA binding, methylated histone bindi
Ortholog(s) have role in protein targeting to mitochondrion and integral component of mitochondrial outer memb
Protein of unknown function
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Ecm33-family protein with a predicted role in cell wall biogenesis and organization; predicted GPI-anchor
Protein of unknown function
Ortholog(s) have acetate transmembrane transporter activity, ammonium transmembrane transporter activity, ro
Ortholog(s) have mannosyltransferase activity and role in glycosphingolipid biosynthetic process, mannosyl-inosito
Pir protein family member, putative cell wall component
Ortholog(s) have tryptophan-tRNA ligase activity, role in mitochondrial tryptophanyl-tRNA aminoacylation and mit
Ortholog(s) have succinate:fumarate antiporter activity, role in acetate catabolic process, carbon utilization, fatty
Protein of unknown function
Protein of unknown function
Ortholog(s) have RNA binding, RNA helicase activity, RNA-dependent ATPase activity
65 kDa mannoprotein
Adhesin-like protein with similarity to S. cerevisiae flocculins, cell wall proteins that mediate adhesion; predicted G
Putative quinone reductase/NADPH dehydrogenase; gene is upregulated in azole-resistant strain

High-affinity transporter of NAD+ precursors; strongly induced under niacin-limiting conditions
Feature-type
pseudogene
ORF|Uncharacterized
ORF|Uncharacterized
ORF|Uncharacterized
ORF|Uncharacterized
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ORF|Verified
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ORF|Verified

Description
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Putative adhesin-like protein; belongs to adhesin cluster I; appears artificially broken into fragments due to seque
Protein of unknown function
Protein of unknown function
Protein of unknown function
Has domain(s) with predicted GTP binding activity and role in cell cycle
Ortholog of S. cerevisiae : YBL059W and Saccharomyces cerevisiae S288C : YBL059W
Ortholog(s) have dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase activity
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Ortholog(s) have L-serine ammonia-lyase activity, L-threonine ammonia-lyase activity, role in L-serine catabolic pr
Alpha-domain mating-type protein alpha1p; expressed in all MTLalpha strains and not in MTLa strains
Beta mannosyltransferase
Putative adhesin-like cell wall protein; belongs to adhesin cluster IV; predicted GPI-anchor
Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport, trans

Putative cell wall adhesin; belongs to adhesin cluster III; predicted GPI anchor; contains 6 tandem repeats
Putative adhesin-like protein; belongs to adhesin cluster I
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Protein of unknown function
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Ortholog(s) have phospholipid binding activity, role in actin filament organization, budding cell apical bud growth,
Glycerol transporter; involved in flucytosine resistance; double fps1/fps2 mutant accumulates glycerol, has constit
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Heat shock protein
Ortholog(s) have transcription factor TFIIH holo complex localization
Ortholog(s) have ubiquitin-protein transferase activity and role in cytoplasm protein quality control by the ubiquit
Protein of unknown function
Protein of unknown function
Putative adhesin-like protein
Ortholog(s) have protein serine/threonine kinase activity, protein tyrosine kinase activity
Protein of unknown function
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have histone binding, histone deacetylase binding, mediator complex binding, phosphatidylinositol-3,5
Ortholog(s) have RNA polymerase I activity, role in nucleolar large rRNA transcription by RNA polymerase I, transc
Adhesin-like protein with tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have peptide alpha-N-acetyltransferase activity, role in N-terminal protein amino acid acetylation, ma
Protein of unknown function
Sub-telomerically encoded adhesin with a role in cell adhesion; GPI-anchored cell wall protein; N-terminal ligand b
Epithelial adhesion protein; predicted GPI-anchor; belongs to adhesin cluster I
Epithelial adhesion protein, involved in biofilm formation and azole drug resistance; belongs to adhesin cluster I; G
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Protein of unknown function
Component of the transcriptional Mediator complex that provides interfaces between RNA polymerase II and upst
Putative GPI-linked cell wall mannoprotein of the Srp1p/Tip1p family
Ortholog(s) have osmosensor activity and role in (1->3)-beta-D-glucan biosynthetic process, cellular bud site selec
Protein of unknown function
Ortholog(s) have integral component of mitochondrial outer membrane, mitochondrial outer membrane, mitocho
Putative regulatory subunit for protein phosphatase; gene is upregulated in azole-resistant strain
Ortholog(s) have role in cellular response to cold, mRNA stabilization and positive regulation of transcription by RN
Ortholog(s) have protein kinase activity, pyruvate dehydrogenase (acetyl-transferring) kinase activity
Ortholog(s) have AMP binding, AMP-activated protein kinase activity, ATP binding, protein serine/threonine kinas
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have small GTPase binding activity
Gene used for molecular typing of C. glabrata strain isolates
Ortholog(s) have actin binding activity and role in actin cortical patch localization, bipolar cellular bud site selectio
Ortholog(s) have nucleolus localization
Ortholog(s) have role in macroautophagy, mitochondrial proton-transporting ATP synthase complex assembly and
Ortholog(s) have role in protein targeting to membrane
Heat shock protein of the HSP70 family
Protein with similarity to S. cerevisiae Sag1 agglutinin, involved in cell adhesion; predicted GPI-anchor
Protein of unknown function
Ortholog(s) have DNA binding activity

Ortholog(s) have role in ascospore wall assembly
Ortholog(s) have role in actin cytoskeleton organization, negative regulation of Arp2/3 complex-mediated actin nu
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA polymeras
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with internal repeats; predicted GPI-anchor; likely a C-terminal fragment of a single ORF with
Putative adhesin-like protein with 4 tandem repeats; appears artificially broken into fragments due to sequencing
Protein of unknown function
Ortholog(s) have mRNA binding activity and role in mRNA splice site selection, mRNA splicing, via spliceosome, po
Ortholog(s) have role in ribosomal small subunit biogenesis and nucleolus localization
Ortholog(s) have chromatin binding activity and nuclear chromatin localization
Component of the transcriptional Mediator complex that provides interfaces between RNA polymerase II and upst
Ortholog(s) have role in protein import into peroxisome matrix and cytosol, peroxisome localization
Protein of unknown function
Ortholog(s) have mannosyltransferase activity, role in cell wall mannoprotein biosynthetic process, protein N-linke
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Ortholog of S. cerevisiae : YNR014W and Saccharomyces cerevisiae S288C : YNR014W
Ortholog(s) have SCF ubiquitin ligase complex localization
Pir protein family member, putative cell wall component
Ortholog(s) have DNA-binding transcription factor activity, RNA polymerase II-specific and RNA polymerase II cis-r
Ortholog(s) have myo-inositol transmembrane transporter activity, role in myo-inositol import across plasma mem
Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral c
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Protein with 32 tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Protein of unknown function
Cell wall adhesin; predicted GPI anchor; contains tandem repeats; belongs to adhesin cluster II
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have role in histone deacetylation, negative regulation of antisense RNA transcription and positive reg
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Protein of unknown function
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Putative adhesin-like protein
Ortholog(s) have protein serine/threonine kinase activity
Ortholog of S. cerevisiae : YPL109C, C. albicans SC5314 : C4_02160C_A, C. dubliniensis CD36 : Cd36_42050, C. para
Ortholog(s) have DNA translocase activity, RNA polymerase II activating transcription factor binding activity
Ortholog(s) have U6 snRNA binding activity and role in mRNA cis splicing, via spliceosome, mRNA splicing, via splic
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in translational readthroug
Has domain(s) with predicted adenine phosphoribosyltransferase activity, role in adenine salvage, nucleoside met
Ortholog(s) have thiol-dependent ubiquitin-specific protease activity, role in chromatin silencing at telomere, histo
Ortholog(s) have cyclin-dependent protein kinase activating kinase regulator activity, cyclin-dependent protein ser
Predicted GPI-linked protein; putative adhesin-like protein
Has domain(s) with predicted ATP binding, protein kinase activity, protein tyrosine kinase activity and role in prote
Ortholog(s) have DNA-binding transcription repressor activity, RNA polymerase II-specific, RNA polymerase II cis-r

Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have role in protein maturation, protein targeting to ER and endoplasmic reticulum, membrane localiz
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Putative adhesin with glycine and serine rich repeats; belongs to adhesin cluster V
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Acetyl-coenzyme A synthetase
Ortholog(s) have cytoplasm localization
Ortholog(s) have RNA 7-methylguanosine cap binding, m7G(5')pppN diphosphatase activity, role in cellular respon
Predicted GPI-linked adhesin-like protein
Ortholog(s) have role in meiotic cell cycle, negative regulation of protein localization to nucleolus
Putative 26S proteasome regulatory subunit; protein abundance decreased in ace2 mutant cells
Ortholog(s) have exopolyphosphatase activity, role in polyphosphate catabolic process and cytoplasm localization
Putative adhesin-like cell wall protein; 5 tandem repeats; predicted GPI-anchor
Ortholog(s) have protein kinase activator activity
Putative adhesin-like cell wall protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA polymeras
Putative nicotinamide transporter; strongly induced under niacin-limiting conditions
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Ortholog(s) have sulfite reductase (NADPH) activity, role in hydrogen sulfide biosynthetic process, sulfate assimila
Ortholog(s) have double-stranded DNA helicase activity, role in mitochondrial DNA metabolic process and mitoch
Predicted GPI-linked adhesin-like protein
Protein of unknown function
Ortholog(s) have mannosyltransferase activity and role in glycosphingolipid biosynthetic process, mannosyl-inosit
Ortholog(s) have microtubule binding, microtubule plus end polymerase activity
Pir protein family member, putative cell wall component
Ortholog(s) have succinate:fumarate antiporter activity, role in acetate catabolic process, carbon utilization, fatty
Protein of unknown function
Mitochondrial methionine tRNA, one of two tRNA-Met encoded on the mitochondrial genome; has CAU anticodon
Probable mitochondrial ribosomal protein of the small subunit, orthologous to S. cerevisiae VAR1
Mitochondrial tryptophan tRNA, has UCA anticodon
Mitochondrial 21S rRNA of the large ribosomal subunit
Mitochondrial threonine tRNA, one of two tRNA-Thr encoded on the mitochondrial genome; has UGU anticodon
Mitochondrial histidine tRNA, has GUG anticodon
Mitochondrial glutamate tRNA, has UUC anticodon
Cytochrome b, mitochondrially encoded subunit of the ubiquinol-cytochrome c reductase complex
Mitochondrial methionine tRNA, one of two tRNA-Met encoded on the mitochondrial genome; has CAU anticodon
RNA component of mitochondrial RNAse P; initially synthesized as a polycistronic precursor RNA
Mitochondrial proline tRNA, has UGG anticodon
Putative endonuclease with similarity to S. cerevisiae AI3 (I-SceIII), encoded by the first exon and part of the first i
Putative endonuclease containing motifs common to fungal intron-encoded endonucleases; encoded by the first t
Putative endonuclease with similarity to S. cerevisiae AI5_alpha (I-SceIV) endonuclease; encoded by the first three
Mitochondrially encoded subunit a of the F0 sector of mitochondrial F1F0 ATP synthase
Subunit II of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron
Mitochondrial cysteine tRNA, has GCA anticodon
Subunit III of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron
Mitochondrial leucine tRNA, has UAA anticodon

Mitochondrial arginine tRNA, has UCU anticodon

Description

Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Putative adhesin-like protein; belongs to adhesin cluster I; appears artificially broken into fragments due to seque
Protein of unknown function
Has domain(s) with predicted transcription coregulator activity, role in regulation of transcription by RNA polymer
Putative adhesin; belongs to adhesin cluster I
Ortholog(s) have RNA polymerase II activating transcription factor binding, RNA polymerase II core promoter sequ
Has domain(s) with predicted GTP binding activity and role in cell cycle
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Sub-telomerically encoded adhesin with a role in cell adhesion; binds to ligands containing a terminal galactose re
Putative adhesin-like cell wall protein; belongs to adhesin cluster IV; predicted GPI-anchor
Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport, trans
Putative cell wall adhesin; belongs to adhesin cluster III; predicted GPI anchor; contains 6 tandem repeats
Putative adhesin-like protein; belongs to adhesin cluster I
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Putative nuclear phosphatase regulatory subunit; gene is downregulated in azole-resistant strain
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Ortholog(s) have protein kinase activity, pyruvate dehydrogenase (acetyl-transferring) kinase activity
Ortholog(s) have small GTPase binding activity
Ortholog(s) have role in macroautophagy, mitochondrial proton-transporting ATP synthase complex assembly and
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Protein of unknown function
Putative adhesin-like protein
Putative anthranilate synthase component I; protein abundance increased in ace2 mutant cells
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Cell wall adhesin; predicted GPI anchor; contains tandem repeats; belongs to adhesin cluster II
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to

Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI; predicted
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in translational readthroug

Putative adhesin-like protein; belongs to adhesin cluster I
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefoldin co
Ortholog(s) have role in RNA polymerase I assembly, RNA polymerase II core complex assembly, RNA polymerase
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have DNA-binding transcription repressor activity, RNA polymerase II-specific, RNA polymerase II cis-r
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Putative adhesin with glycine and serine rich repeats; belongs to adhesin cluster V
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Ortholog(s) have exopolyphosphatase activity, role in polyphosphate catabolic process and cytoplasm localization
Putative adhesin-like cell wall protein; 5 tandem repeats; predicted GPI-anchor
Ortholog(s) have protein kinase activator activity
Putative adhesin-like cell wall protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA polymeras
Putative adhesin; belongs to adhesin cluster I
Putative nicotinamide transporter; strongly induced under niacin-limiting conditions
Protein of unknown function
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Protein of unknown function
Ortholog(s) have role in mRNA splicing, via spliceosome, spliceosomal complex assembly and U2 snRNP, U2-type p

Description
Protein of unknown function
Protein of unknown function
Protein of unknown function
Zinc finger transcription factor, activator of drug resistance genes via pleiotropic drug response elements (PDRE); r
Has domain(s) with predicted transcription coregulator activity, role in regulation of transcription by RNA polymer
Ortholog(s) have RNA polymerase II activating transcription factor binding, RNA polymerase II core promoter sequ
Ortholog(s) have glucose transmembrane transporter activity, pentose transmembrane transporter activity, role i
Ortholog(s) have glucose transmembrane transporter activity and mitochondrial membrane localization
Ortholog(s) have fructose transmembrane transporter activity, glucose transmembrane transporter activity, mann
Has domain(s) with predicted GTP binding activity and role in cell cycle
Ortholog(s) have sequence-specific DNA binding activity and role in regulation of transcription by RNA polymerase
Ortholog(s) have iron ion binding, oxidoreductase activity, acting on iron-sulfur proteins as donors, zinc ion bindin
Protein of unknown function
Homeobox-domain protein alpha2
Ortholog(s) have RNA binding activity, role in regulation of translation and cytoplasmic stress granule, polysome lo
Mating-type regulatory protein alpha2; expressed in all MTLalpha strains and not in MTLa strains
Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport, trans
Protein of unknown function
Glycerol transporter; involved in flucytosine resistance; double fps1/fps2 mutant accumulates glycerol, has constit
Has domain(s) with predicted transferase activity, transferring glycosyl groups activity and role in protein glycosyla
Has domain(s) with predicted integral component of membrane localization

Putative nuclear phosphatase regulatory subunit; gene is downregulated in azole-resistant strain
Has domain(s) with predicted DNA-binding transcription factor activity, RNA polymerase II-specific, zinc ion bindin
Ortholog(s) have role in fatty acid metabolic process, fatty acid oxidation, peroxisome fission and endoplasmic ret
Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral c
Protein of unknown function
Protein of unknown function
Ortholog(s) have protein phosphatase activator activity
Protein of unknown function
DNA-directed RNA polymerase II
Ortholog(s) have L-proline transmembrane transporter activity, neutral amino acid transmembrane transporter ac
Protein of unknown function
Ortholog of S. cerevisiae : FMP42, C. albicans SC5314 : CR_04760C_A, C. dubliniensis CD36 : Cd36_30130, C. parap
Ortholog(s) have role in cellular response to cold, mRNA stabilization and positive regulation of transcription by RN
Ortholog(s) have RNA polymerase II activating transcription factor binding, chromatin binding, molecular adaptor
Has domain(s) with predicted protein heterodimerization activity and role in DNA-templated transcription, initiati
Ortholog(s) have role in cellular response to desiccation and cytoplasm localization
Ortholog(s) have nucleolus localization
Ortholog(s) have DNA binding activity
Protein of unknown function
Protein of unknown function
Ortholog(s) have transcription corepressor activity
Protein of unknown function
Ortholog(s) have tRNA dihydrouridine synthase activity and role in tRNA modification
Ortholog(s) have DNA binding, DNA-dependent ATPase activity, chromatin binding activity
Protein involved in cell wall beta 1,6-glucan synthesis, similar to Kre9p,
Putative GPI-linked cell wall protein
Putative GPI-linked cell wall protein
Protein of unknown function
RNA polymerase II largest subunit
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Pir protein family member, putative cell wall component
Pir protein family member, putative cell wall component
Ortholog(s) have role in fungal-type cell wall organization, positive regulation of signal transduction
Predicted GPI-linked cell wall protein
Protein of unknown function
Protein of unknown function
Ortholog(s) have role in RNA polymerase I assembly, RNA polymerase II core complex assembly, RNA polymerase
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have DNA-binding transcription repressor activity, RNA polymerase II-specific, RNA polymerase II cis-r
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Has domain(s) with predicted DNA-binding transcription factor activity, sequence-specific DNA binding, zinc ion bi
Ortholog(s) have protein kinase activator activity
Ortholog(s) have role in mitochondrial genome maintenance, mitochondrial tRNA 5'-end processing and matrix sic
Putative nicotinamide transporter; strongly induced under niacin-limiting conditions
Protein of unknown function
Ortholog(s) have role in pseudohyphal growth and cytosol, nucleus localization
Pir protein family member, putative cell wall component

Protein of unknown function
Putative quinone reductase/NADPH dehydrogenase; gene is upregulated in azole-resistant strain
High-affinity transporter of NAD+ precursors; strongly induced under niacin-limiting conditions
Putative endonuclease with similarity to S. cerevisiae AI5_alpha (I-SceIV) endonuclease; encoded by the first three
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Putative adhesin-like protein; belongs to adhesin cluster I; appears artificially broken into fragments due to seque
Putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin; belongs to adhesin cluster I
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Sub-telomerically encoded adhesin with a role in cell adhesion; binds to ligands containing a terminal galactose re
Putative adhesin-like cell wall protein; belongs to adhesin cluster IV; predicted GPI-anchor
Putative adhesin-like protein; belongs to adhesin cluster I
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Adhesin-like protein with a predicted GPI-anchor; belongs to adhesin cluster I; strain BG14 encodes the full-length
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative adhesin-like protein; belongs to adhesin cluster IV
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
Adhesin-like protein with tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Epithelial adhesion protein; predicted GPI-anchor; belongs to adhesin cluster I
Epithelial adhesion protein, involved in biofilm formation and azole drug resistance; belongs to adhesin cluster I; G
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Adhesin-like protein with internal repeats; predicted GPI-anchor; likely a C-terminal fragment of a single ORF with
Putative adhesin-like protein
Predicted cell wall adhesin with a role in adhesion; belongs to adhesin cluster III; predicted GPI anchor; contains ta
Putative adhesin-like with multiple tandem repeats; ORF appears artificially broken into fragments due to sequenc
Adhesin-like cell wall protein; predicted GPI-anchor; belongs to adhesin cluster V
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Protein with 32 tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Cell wall adhesin; predicted GPI anchor; contains tandem repeats; belongs to adhesin cluster II
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI; predicted
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Putative adhesin-like protein
Putative adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI
Putative adhesin-like cell wall protein; belongs to adhesin cluster I

Putative adhesin-like protein with internal repeats; identified in cell wall extracts by mass spectrometry; ORF appe
Putative adhesin; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster V; predicted GPI
Putative adhesin-like protein; belongs to adhesin cluster I
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Putative adhesin with glycine and serine rich repeats; belongs to adhesin cluster V
Putative adhesin-like cell wall protein; 5 tandem repeats; predicted GPI-anchor
Putative adhesin-like cell wall protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster
Putative adhesin; belongs to adhesin cluster I
Putative adhesin-like cell wall protein; belongs to adhesin cluster I

Description
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster III
Protein of unknown function
Protein of unknown function
Putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin; belongs to adhesin cluster I
Ortholog(s) have glucose transmembrane transporter activity, pentose transmembrane transporter activity, role i
Ortholog(s) have glucose transmembrane transporter activity and mitochondrial membrane localization
Protein of unknown function
Alpha-domain mating-type protein alpha1p; expressed in all MTLalpha strains and not in MTLa strains
Beta mannosyltransferase; transmembrane domain protein similar to C. albicans WRY family; gene is downregulat
Sub-telomerically encoded adhesin with a role in cell adhesion; binds to ligands containing a terminal galactose re
Putative adhesin-like cell wall protein; belongs to adhesin cluster IV; predicted GPI-anchor
Putative adhesin-like protein; belongs to adhesin cluster I
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Heat shock protein
Protein of unknown function
Putative nuclear phosphatase regulatory subunit; gene is downregulated in azole-resistant strain
Protein of unknown function
Putative adhesin-like protein
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have RNA polymerase I activity, role in nucleolar large rRNA transcription by RNA polymerase I, transc
Adhesin-like protein with tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Protein of unknown function
Sub-telomerically encoded adhesin with a role in cell adhesion; GPI-anchored cell wall protein; N-terminal ligand b
Epithelial adhesion protein; predicted GPI-anchor; belongs to adhesin cluster I
Epithelial adhesion protein, involved in biofilm formation and azole drug resistance; belongs to adhesin cluster I; G
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag

Protein of unknown function
Aldohexose specific glucokinase
Ortholog(s) have osmosensor activity and role in (1->3)-beta-D-glucan biosynthetic process, cellular bud site selec
Ortholog(s) have role in chromatin silencing, sister chromatid cohesion and nucleus localization
Putative regulatory subunit for protein phosphatase; gene is upregulated in azole-resistant strain
Ortholog(s) have role in cellular response to cold, mRNA stabilization and positive regulation of transcription by R
Ortholog(s) have protein kinase activity, pyruvate dehydrogenase (acetyl-transferring) kinase activity
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have small GTPase binding activity
Ortholog(s) have DNA binding activity
Ortholog(s) have role in actin cytoskeleton organization, negative regulation of Arp2/3 complex-mediated actin nu
Ortholog(s) have molecular adaptor activity and role in mRNA splicing, via spliceosome, positive regulation of prot
Alpha-1,6-mannosyltransferase with a role in protein glycosylation
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA polymeras
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Adhesin-like protein with internal repeats; predicted GPI-anchor; likely a C-terminal fragment of a single ORF with
Putative adhesin-like protein with 4 tandem repeats; appears artificially broken into fragments due to sequencing
Protein of unknown function
Ortholog(s) have tRNA dihydrouridine synthase activity and role in tRNA modification
Putative adhesin-like protein
Putative GPI-linked cell wall protein
Predicted cell wall adhesin with a role in adhesion; belongs to adhesin cluster III; predicted GPI anchor; contains ta
Putative adhesin-like with multiple tandem repeats; ORF appears artificially broken into fragments due to sequenc
Protein of unknown function
Metal-activated transcription factor; binds promoters of metallothionein genes; autoregulates its own expression;
Ortholog(s) have mannosyltransferase activity, role in cell wall mannoprotein biosynthetic process, protein N-linke
Putative anthranilate synthase component I; protein abundance increased in ace2 mutant cells
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
bZIP domain-containing protein involved in regulation of biofilm formation; negatively regulates expression of the
Haloacid dehalogenase-like hydrolase
Pir protein family member, putative cell wall component
Pir protein family member, putative cell wall component
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Cell wall adhesin; predicted GPI anchor; contains tandem repeats; belongs to adhesin cluster II
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Protein of unknown function
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Putative adhesin-like protein
Ortholog of S. cerevisiae : YPL109C, C. albicans SC5314 : C4_02160C_A, C. dubliniensis CD36 : Cd36_42050, C. para
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in translational readthroug
Ortholog(s) have tRNA (adenine-N1-)-methyltransferase activity, role in tRNA methylation and nucleus, tRNA (m1A

Putative adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Putative adhesin-like protein with internal repeats; identified in cell wall extracts by mass spectrometry; ORF appe
Protein of unknown function
Putative adhesin; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster V; predicted GPI
Putative adhesin-like protein; belongs to adhesin cluster I
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefoldin co
Ortholog(s) have role in RNA polymerase I assembly, RNA polymerase II core complex assembly, RNA polymerase
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have DNA-binding transcription repressor activity, RNA polymerase II-specific, RNA polymerase II cis-r
Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Putative adhesin with glycine and serine rich repeats; belongs to adhesin cluster V
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Ortholog(s) have cytoplasm localization
Alpha-1,6-mannosyltransferase with a role in protein N-linked glycosylation in Golgi
Putative adhesin-like cell wall protein; 5 tandem repeats; predicted GPI-anchor
Ortholog(s) have protein kinase activator activity
Putative adhesin-like cell wall protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA polymeras
Protein of unknown function
Ortholog(s) have double-stranded DNA helicase activity, role in mitochondrial DNA metabolic process and mitoch
Pir protein family member, putative cell wall component
Protein of unknown function
Putative DL-glycerol phosphatase

Description
Protein of unknown function
Protein of unknown function
Protein of unknown function
Ortholog(s) have RNA polymerase II activating transcription factor binding, RNA polymerase II core promoter sequ
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate binding activity, role in actin cortical patch assembly, acti
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Alpha-domain mating-type protein alpha1p
Alpha-domain mating-type protein alpha1p; expressed in all MTLalpha strains and not in MTLa strains
Has domain(s) with predicted mitochondrial inner membrane peptidase complex localization
Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport, trans
Protein of unknown function
Adhesin-like protein with a predicted role in cell adhesion; belongs to adhesin cluster VII; predicted GPI-anchor
Protein of unknown function
Adhesin-like protein; belongs to adhesin cluster VII; predicted GPI anchor
Heat shock protein
Adhesin-like protein with a predicted GPI-anchor; belongs to adhesin cluster I; strain BG14 encodes the full-length

Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have role in fatty acid metabolic process, fatty acid oxidation, peroxisome fission and endoplasmic ret
Protein of unknown function
Putative adhesin-like protein
Pseudogene with a predicted GPI-anchor sequence; putative adhesin-like protein; belongs to adhesin cluster I
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Protein of unknown function
Putative adhesin-like protein; belongs to adhesin cluster IV
Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor; belongs to adhesin cluster III
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have RNA polymerase I activity, role in nucleolar large rRNA transcription by RNA polymerase I, transc
Adhesin-like protein with tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Protein of unknown function
Protein of unknown function
Ortholog(s) have FAD transmembrane transporter activity, calcium channel activity
Sub-telomerically encoded adhesin with a role in cell adhesion; GPI-anchored cell wall protein; N-terminal ligand b
Epithelial adhesion protein; predicted GPI-anchor; belongs to adhesin cluster I
Epithelial adhesion protein, involved in biofilm formation and azole drug resistance; belongs to adhesin cluster I; G
Protein of unknown function
Putative adhesin-like protein; GPI-anchored; belongs to adhesin cluster V; ORF appears artificially broken into frag
Aldohexose specific glucokinase
Component of the transcriptional Mediator complex that provides interfaces between RNA polymerase II and upst
Ortholog(s) have osmosensor activity and role in (1->3)-beta-D-glucan biosynthetic process, cellular bud site select
Ortholog(s) have mevalonate kinase activity and role in ergosterol biosynthetic process, farnesyl diphosphate bios
Ortholog(s) have integral component of mitochondrial outer membrane, mitochondrial outer membrane, mitocho
Ortholog(s) have role in cellular response to cold, mRNA stabilization and positive regulation of transcription by RN
Ortholog(s) have protein kinase activity, pyruvate dehydrogenase (acetyl-transferring) kinase activity
Ortholog(s) have RNA polymerase II activating transcription factor binding, chromatin binding, molecular adaptor
Has domain(s) with predicted protein heterodimerization activity and role in DNA-templated transcription, initiati
Ortholog(s) have role in cellular response to desiccation and cytoplasm localization
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Ortholog(s) have small GTPase binding activity
Protein with similarity to S. cerevisiae Sag1 agglutinin, involved in cell adhesion; predicted GPI-anchor
Ortholog(s) have DNA binding activity
Ortholog(s) have role in actin cytoskeleton organization, negative regulation of Arp2/3 complex-mediated actin nu
Ortholog(s) have molecular adaptor activity and role in mRNA splicing, via spliceosome, positive regulation of prot
Alpha-1,6-mannosyltransferase with a role in protein glycosylation
Ortholog(s) have role in glycerol biosynthetic process and cytosol, nucleus localization
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster IV; predicted
Adhesin-like protein with 5 tandem repeats; belongs to adhesin cluster VII; predicted GPI-anchor; similarity to S. c
Adhesin-like protein with internal repeats; predicted GPI-anchor; likely a C-terminal fragment of a single ORF with
Putative adhesin-like protein with 4 tandem repeats; appears artificially broken into fragments due to sequencing
Protein of unknown function
Ortholog(s) have chromatin binding activity and nuclear chromatin localization

Ortholog(s) have tRNA dihydrouridine synthase activity and role in tRNA modification
Copper-binding metallothionein, involved in sequestration of metal ions; inducible by copper and silver; present ir
Putative adhesin-like protein
Putative adhesin-like protein
Putative GPI-linked cell wall protein
Putative GPI-linked cell wall protein
Predicted cell wall adhesin with a role in adhesion; belongs to adhesin cluster III; predicted GPI anchor; contains ta
Putative adhesin-like with multiple tandem repeats; ORF appears artificially broken into fragments due to sequenc
Protein of unknown function
Predicted GPI-linked adhesin-like protein; belongs to adhesin cluster I
Ortholog(s) have role in ascospore wall assembly
Metal-activated transcription factor; binds promoters of metallothionein genes; autoregulates its own expression;
Ortholog(s) have mannosyltransferase activity, role in cell wall mannoprotein biosynthetic process, protein N-linke
Putative anthranilate synthase component I; protein abundance increased in ace2 mutant cells
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
bZIP domain-containing protein involved in regulation of biofilm formation; negatively regulates expression of the
Pir protein family member, putative cell wall component
Pir protein family member, putative cell wall component
Ortholog(s) have myo-inositol transmembrane transporter activity, role in myo-inositol import across plasma mem
Cell wall protein that mediates adhesion to endothelial cells; predicted GPI anchor and signal peptide; contains mu
Protein with 32 tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Protein with tandem repeats; putative adhesin-like protein; belongs to adhesin cluster II
Cell wall adhesin; predicted GPI anchor; contains tandem repeats; belongs to adhesin cluster II
Protein of unknown function
Putative adhesin-like protein; ORF appears artificially broken into fragments due to sequencing errors; belongs to
Putative adhesion protein; predicted GPI-anchor; belongs to adhesin cluster VI
Putative adhesin-like protein; has glycine and serine rich repeats; belongs to adhesin cluster VI
Putative adhesin-like protein; belongs to adhesin cluster VI
Protein of unknown function
Adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI; predicted
Adhesin-like protein; predicted GPI anchor; belongs to adhesin cluster VI
Putative adhesin-like protein
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in translational readthroug
Ortholog(s) have tRNA (adenine-N1-)-methyltransferase activity, role in tRNA methylation and nucleus, tRNA (m1A
Predicted GPI-linked cell wall protein
Putative adhesin-like protein; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster VI
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Putative adhesin-like protein with internal repeats; identified in cell wall extracts by mass spectrometry; ORF appe
Putative adhesin; identified in cell wall extracts by mass spectrometry; belongs to adhesin cluster V; predicted GPI
Putative adhesin-like protein; belongs to adhesin cluster I
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefoldin co
Putative serine-threonine phosphoprotein phosphatase 1, catalytic chain
Ortholog(s) have DNA translocase activity
Ortholog(s) have role in RNA polymerase I assembly, RNA polymerase II core complex assembly, RNA polymerase
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localizatio
Ortholog(s) have DNA-binding transcription repressor activity, RNA polymerase II-specific, RNA polymerase II cis-r

Adhesin-like protein required for adherence to endothelial cells; identified in cell wall extracts by mass spectrome
Putative adhesin-like protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster III
Putative adhesin with glycine and serine rich repeats; belongs to adhesin cluster V
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Ortholog(s) have cytoplasm localization
Ortholog(s) have role in ATP export, cellular response to pH, intralumenal vesicle formation and late endosome to
Ortholog(s) have DNA binding, DNA-binding transcription activator activity, RNA polymerase II-specific, RNA polym
Putative 26S proteasome regulatory subunit; protein abundance decreased in ace2 mutant cells
Putative adhesin-like cell wall protein; 5 tandem repeats; predicted GPI-anchor
Ortholog(s) have protein kinase activator activity
Putative adhesin-like cell wall protein; multiple tandem repeats; predicted GPI-anchor; belongs to adhesin cluster
Ortholog(s) have phosphopantothenoylcysteine decarboxylase activity, protein phosphatase inhibitor activity and
Ortholog(s) have electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activ
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA polymeras
Ortholog(s) have L-alanine:2-oxoglutarate aminotransferase activity, role in alanine biosynthetic process, alanine c
Putative adhesin; belongs to adhesin cluster I
Sub-telomerically encoded lectin-like adhesin with a role in cell adhesion; contains multiple tandem repeats; predi
Putative nicotinamide transporter; strongly induced under niacin-limiting conditions
Protein of unknown function
Putative adhesin-like cell wall protein; belongs to adhesin cluster I
Ortholog(s) have double-stranded DNA helicase activity, role in mitochondrial DNA metabolic process and mitocho
Protein of unknown function
Ortholog(s) have role in mRNA splicing, via spliceosome, spliceosomal complex assembly and U2 snRNP, U2-type p
Pir protein family member, putative cell wall component
Protein of unknown function
Ortholog(s) have FAD transmembrane transporter activity
High-affinity transporter of NAD+ precursors; strongly induced under niacin-limiting conditions
Putative endonuclease with similarity to S. cerevisiae AI5_alpha (I-SceIV) endonuclease; encoded by the first three
[redacted]