Supplementary Information

Figure S1: Biofilm phenotypes of the 78-Strain panel.

Figure S2: A domain amino acid alignment.

Figure S3: C domain amino acid alignment.

Figure S4: Inferred breakpoints via GARD.

Figure S5: Genetic variation at *FLO11* compared to variation in genes that code for proteins with similar properties.

Figure S6: Upstream regulatory alignment.

Figure S7: Distribution of Tajima's D values.

Figure S8: Distribution of social scores among the regulatory clades

Figure S9: Functional assay of natural FLO11 alleles.

Table S1: Strain table and data summary

 Table S2: Genes for cell wall and GPI-anchored proteins

Table S3: Strains used in the cell wall and GPI-anchored genes analysis

Table S4: Strains for functional analysis

Table S5: Primers

Table S6: PAML model results for the full data set and various trees

Table S7: PAML significant sites associated with Table S2

 Table S8: PAML model results separating strains with and without the insert

Table S9: PAML significant sites associated with Table S4

Table S10: GARD results

 Table S11: PAML model results for recombination segments

Table S12: PAML significant sites associated with Table S6

 Table S13: ANOVA analysis of prFLO11-GFP expression

Data files: Fasta files and PAML files will be included.

Figure S1: Biofilm phenotypes of the 78-Strain panel. (A) Scale for scoring biofilm mats and colonies. (B) Distribution of average social scores. (C) Complex colony morphology on a low dextrose 2% agar plate. (D) Mat biofilms formed on low dextrose 0.3% agar plates. In both C and D, samples 1-78 (as described in Table S1) are arrayed in order from A1-A12, B1-B12, etc.







Figure S2: A domain amino acid alignment. Gray boxes are beta sheets; red, green and blue are apical regions, as in Figure 1. Black stars indicate aromatic band I in the apical region; gray stars indicate aromatic band II in the neck subdomain.

5288cRef_1/1=200	IMQRPFLLAYLVLSLL	NSALGFPIALVPRGSSEGISCNS	IVNGCPNLDFNWHMDQQNIMQ	YILDVISVSWVQDNIYQIIIHVKG	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENI 11/
YIM311 1/1-200	1 MORPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGC P N L D F NWHMDOO N I MO	YTLDVTSVSWVODNTYOITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V O L Y G Y	NENT 117
CBC2010 1/1 200	1 MOBBELLAVIVIELL	IN CALCEDTAL VDDCCCCCCCCCNC	VNCCRNLDENWHMNOOT I MO	VTI DVT SV SWVO DNTVO I TI HVVC	KENIDINVISSIVI	LOVICBEDIVOLVCC	NENT 117
CB32910_1/1=200	IMQKFFLLATLVLSLL	INSALUFFTALVFKUSSEUTSCNS	I VNGCPNEDPNWHMINQQI I MQ	TILDVISVSWVQDNITQIIIHVKG	KENIDENTESSERI	TUVIUP KDIVQLIGC	NENT 117
CBS1227_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	IVNGCPNLDFNWHMNQQTIMQ	Y T L D V T S V S W V Q D N T Y Q I T I H V K G	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
CBS7836 1/1-200	1 MORPELLAYIVISII	ENSALGEPTALVPRGSSEGTSCNS	LVNGCPNLDENWHMNOONIMO	YTI DVT SV SWVO DNTYO I TI HVKG	KENIDIKYIWSIKI	LGVTGPKGTVOLYGY	NENT 117
02 122 1/1 200	1 MODDELLAVIVIELL	INCALCED TALVED CEEEEEEE	UNICODAL DENMUMPOONLING	YT L DUT SU SWUO DNT YO LT LUVKC	KENLDLKYLWELKI	LOVICERCTVOLVCV	NENT 117
92-123_1/1-200	IMQKFFLLATLVLSLL	INSALUFFTALVFKUSSEUTSCNS	I VNGCPNEDPNWHMDQQNTMQ	TILDVISVSWVQDNITQIIIHVKG	KENIDEKTEWSEKI	TUVIUP KUTVQLTUT	NENT 117
YJM436_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	IVNGCPNLDFNWHMNQQTIMQ	Y T L D V T S V SWVQ D N T Y Q I T I H V K G	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
89-156 1/1-200	1 MORPELLAYIVISII	ENSALCEPTALVPROSSECTSONS	LVNGCPNLDENWHMNOON I MO	YTI DVTSVSWVO DNTYO I TI HVKG	KENIDIKYIWSIKI	LOVIGPKGTVOLYCY	NENT 117
VIII 455 1 (1 200	1 MORDELLAVIVIELL	IN SALCEDTAL VED CESECTECHE	UNCORNED ENWIRINGON INO	VTI DVT SV SWVO DNTVO I TI HVKC	KENIDLKYLWELKI	LOVICEKCTVOLVCV	NENT 117
TJM455_1/1=200	IMQKPFLLATLVLSLL	INSALUFPTALVPRUSSEUTSUNS	I VNGCPNEDPNWHMINQQN I MQ	TILDVISVSWVQDNITQIIIMVKG	KENIDEKTEWSERI	TUVIGPRGIVULTGT	NENT 11/
YJM523 1/1-200	1 MQRPFPFAYLVLSLL	F Y S A L G F P T A L V P R G S S E G T S C N S	I V NG C P N L D F NWHMNQQ N I MQ	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
R01_48 1/1_200	1 MORPELLAVIVISII	ENSALCEPTALVPRRSSECTSCNS	I V N C C P N L D E NWHM NOOT I MO	VTI DVTSVSWVO DNTVOITIHVKC	KENIDIKYISSIKI	LCLTCPEDTVOLVCW	NENT 117
00 00 1/1 200	1 MORDELLAVIVICILI		I VIICCONT DENVIRUNDO TINO	VTI DUT SV SWVQ DNTVQITI UVKC	KENIBLKYLWCLKI	LOVICERCIVOLNCE	NENT 117
96-98_1/1-200	IMQRPFLLAYLVLSLL	NSALGFPIALVPRGSSEGISCNS	IVNGCPNLDFNWHMNQQIIMQ	TILDVISVSWVQDNITQIIIHVKG	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENT 11/
NRRL YB-4348 1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NQ Q T I MQ	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
NCMH 125 1/1-200	1 MORPELLAVIVISII	ENSALCEPTALVPRCSSECTSCNS	I V N C C P N L D E NWHM NOOT I MO	VTI DVTSVSWVO DNTVOITIHVKC	KENIDIKYIWSIKI	LOVICPKCTVOLVCV	NENT 117
NCMN_125_1/1-200	INGREELEVESEE	NSALGEPTALWER COLORS		TTEDVTSV SWVQ DNTTQTTTNVKG	KENTDERTENSERT		
NRRL_Y-1546_1/1-199	IMQRPFLLAYLVLSLL	NSALGFPIALVPR-CSEGISCNS	IVNGCPNLDFNWHMDQQNIME	Y I L D V I S V SWVQ DN I YQ I I V H V K G	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENT 116
NRRL Y-6679 1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGC P N L D F NWHMNOO T I MO	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
NPPI V-062 1/1-200	1 MORRELLAVIVISII	ENSALCEPTALVPPCSSECTSCNS	I V N C C P N I D E NWHM NOOT I MO	VTI DVT SV SWVO DNTVOITIHVKC	KENIDINVISSIKI	LOVICEKDIVOLVCC	NENT 117
NRRL_1-303_1/1-200	IMORFFELATEVESEE	N SALUFFTAL VFRUSSLUTSCNS	I VINGER NEDENWINNINGQT I MQ	TTEDVISVSWVQDNTTQTTTHVKG	KENTDENTESSERT	TUVIUR KDIVQLIGC	NEWT 117
NRRL_Y-12638_1/1-200	IMQRPFLLAYLVLSLL	NSALGFPIALVPRGSSEGSSCNS	IVNGCPNLDFNWHMDQQNIME	Y I L DVI SV SWVQ DNI YQ I I I HVKG	KENIDLKYLWSLKV	IGVIGPKGIVQLYG <mark>Y</mark>	NENT 11/
NRRL YB-427 1/1-200	1 MORPFLLAYLVLSLL	FNSALGFPTALVPRGSSEGTSCNS	I V NGC P N L D F NWHMNOO N I MO	YTLDVTSVSWVODNTYOITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V O L Y G Y	NENT 117
NIDDI VP 000 1/1 200	1 MORDELLAVIVI SIL	ENGALCEDTALVDDCSSECTSCNS	I V N C C P N L D E NWHM NOON I MO	VTI DVT SV SWVO DNTVO I TI HVVC	KENTDIKATWELKT	ICVTCR/CTVOLVCT	NENT 117
NKKL_1B-308_1/1-200	IMORFFELATEVESEE	N SALUFFTAL VFRUSSLUTSCNS	I VINGER NEDENWITMINGQINTMQ	TTEDVISVSWVQDNITQTTINVKG	RENTDERTENSERT	TUVTUF KUTVQLTUT	NEWT III
NRRL_YB-4081_1/1-200	IMQRPFLLAYLVLSLL	NSALGFPIALVPRGSSEGISCNS	IVNGCPNLDFNWHMNQQNIMQ	Y I L DVI SV SWVQ DNI YQ I I I HVKG	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENT 11/
NRRL_Y-268_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NG C P N L D F NWHMNOO T I MO	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLNYLSSLKI	IGVTGPKDTVQLYGC	NENT 117
NRRI YR=2541 1/1-200	1 MORPELLAVIVISI	ENSALGEPTAL VPROSSECTSONS	I V NGCP NI DENWHMNOOT I MO	YTI DVT SV SWVO DNTYO I TI HVKC	KENIDINYISSIKI	LOVIGPKDTVOLVCC	NENT 117
NODI VD 4506 111 262	1 MODDELLAVIVICI			VTL DVT CV CWVO DNTVO LT LUVOC	KENIDLKVINCIKI	LOUTOBKOTVOLVOV	NEWT 117
NKKL_YB-4506_1/1-200	IMQRPFLLATLVLSLL	NSALUFPIALVPRUSSEUISUNS	I V NGCP NEDF NWHMINQQ NI MQ	TILDVISVSWVQDNITQIIIHVQG	KENIDEKTEWSEKI	IGVIGPKGIVQLTGT	NENT 11/
UWOPS83-787.3 1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NG C P N L D F NWHM DQ Q N I MQ	YTLDVTSVSWVQDNTYQVTIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
NRRI Y=6297 1/1-200	1 MORPELLAVIVISI	ENSALGEPTALVPROSSECTSONS	I V NGCP NI DENWHMNOON I MO	YTI DVT SV SWVO DNTYO I TI HVKC	KENIDIKYIWSIKI	LOVIGPKGTVOLVCY	NENT 117
01 212 1/1 200	1 MODDELLAVIVICI		LUNCCONT DE NUMBOOD	VTL DVT CVCWVQ DNTVQ LT LIVKG	KENIDLKYLWCLKI	LOUTOBKOTVOLVOV	NEWT 117
91-213_1/1-200	IMQKPFLLAYLVLSLL	-NSALGFPIALVPRGSSEGISCNS	I V NGCP NLDF NWHMDQQ NI MQ	TILDVISVSWVQDNIYQIIIHVKG	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENI 11/
NRRL Y-12603 1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NG C P N L D F NWHMDQQ N I MQ	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
\$288c 1/1=200	1 MORPELLAYLVISIL	ENSALGEPTALVPROSSECTSONS	LVNGCPNLDENWHMDOONLMO	YTI DVT SV SWVO DNTYO I TI HVKG	KENIDIKYIWSIKI	LOVTOPKOTVOLVOV	NENT 117
52000_1/1-200	1 MORD FLLAVEVESEE			TT DUT SU SWUQ DNT VQ I T HUVKG	KENIDERTERSERT	LOVI CDKDTVOLXCC	NENT 117
M22_1/1=200	IMQRPFLLATLVLSLL	NSALUFPTALVPRUSSEUTSUNS	IVNGCPNEDFNWHMNQQIIMQ	TILDVISVSWVQDNITQIIIHVKG	KENIDENTESSERI	TGVIGPKDIVQLTGC	NENT 11/
YPS128_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM D Q Q N I M Q	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
1-1528 1/1-200	1 MORPELLAYLVISIL	ENSALGEPTALVPROSSECTSONS	I V NGCPNI DENWHMNOONIMO	YTI DVT SV SWVO DNTYO I TI HVKG	KENIDIKYIWSIKI	LOVICPKCTVOLVCY	NENT 117
CK1 1/1 100	1 MORDELLAVIVICILI	NEALCEDTALVED CELETICNE	UNCONT DENVILLADOONTME	VTI DVT SV SWVQ DNTVQ I TVUVKC	KENIDLKYLWELKI	LOVICEKCTVOLVCV	NENT 110
SK1_1/1-199	IMQRPFLLATLVLSLL	FNSALGFPTALVPK-CSEGTSCNS	TVNGCPNLDFNWHMDQQNTME	TILDVISVSWVQDNITQIIVHVKG	KENIDEKTEWSERI	IGVIGPKGIVQLTGT	NENT 116
NCYC361_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	IVNGCPNLDFNWHMNQQTIMQ	Y T L D V T S V SWVQ D N T Y Q I T I H V K G	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
96-109 1/1-200	1 MORPELLAYIVISII	ENSALGEPTALVPRGSSEGTSCNS	I V NGCP N I D E NWHM NOOT I MO	YTI DVT SV SWVO DNTYO I TI HVKG	KENIDIKYIWSIKI	I GVT GPK GT VOL Y GY	NENT 117
VDCCOC 1/1 200	1 MORDELLAVIVICIL	ENCALCEDTALVDDCCCCCCCCNC	LVNCCRNLDENWHMDOONLMO	VTI DVT SV SWVO DNTVO I TI HVVC	KENIDIKVIWSIKI	LOVICERCTVOLVCY	NENT 117
TP3606_1/1=200	INQRFFLLATIVLSLL	INSALUFFTALVFRUSSEUTSCNS	TVNGCPNEDPNWHMDQQNTMQ	TILDVISVSWVQDNITQITIHVKG	KENIDEKTEVISEKI	I GVIGPKGIVQLIGI	NENT 117
NCYC110_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGC P N L D F NWHM NQQ T I MQ	Y T L D V T S V SWVQ DN T YQ I T I H V K G	KENIDLNYLSSLKI	IGVTGPKDTVQLYGC	NENT 117
378604X 1/1-200	1 MORP FLLAY LVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGCP N L D F NWHM NOOT I MO	YTLDVTSVSWVODNTYOITIHVKG	KENIDLKYLWSLKI	I GVT GPK GT VOLY GY	NENT 117
VDCC01 1/1 200	1 MORRELLAVIVICIL	ENCALCEDTALVDDCCCCCCCCNC	LVNCCRNLDENWHMDOONLMO	VTI DVT SV SWVO DNTVO I TI HVVC	VENIDIVVIWSIVI	LOVICBROTVOLVCV	NENT 117
175081_1/1-200	INQRFFLLATIVLSLL	FNSALGFFTALVFRUSSEGTSCNS	TVNGCFNEDFNWHMDQQNTMQ	TILDVISVSWVQDNITQTTIHVKG	KENTDERTEVISERT	I GVIGPKGIVQLIGI	NENT 117
YPS615_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGCP N L D F NWHM NQQ N I MQ	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	I GVTGPKGTVQLYGY	NENT 117
YPS617 1/1-200	1 MORPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NOO N I MO	YTLDVTSVSWVODNTYOITIHVKG	KENIDLKYLWSLKI	I GVT GPK GT VOLY GY	NENT 117
VDCCC1 1/1 200	1 MORDELLAVIVICIL	ENGALCEDTALVDDCCCCCCCCNC	LVNCCRNLDENWHMNOONLMO	VTI DVT SV SWVO DNTVO I TI HVVC	VENIDIVVIWSIVI	LOVICBROTVOLVCV	NENT 117
173001_1/1-200	IMQKFFLLATLVLJLL	INSALUFFTALVFRUSSEUTSCNS	I VINGER NEDENWINNING QINTING	TTEDVISVSWVQDNITQTTIHVKG	KENIDERI LWSERI	TUVTUFKUTVQLTUT	NEWT 117
YP5670_1/1-200	1 MQRPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGCP N L D F NWHMDQQ N I MQ	YTLDVTSVSWVQDNTYQITIHVKG	KENIDLKYLWSLKI	IGVIGPKGTVQLYGY	NENT 117
YPS630 1/1-200	1 MORPFLLAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V NGCP N L D F NWHM DOO N I MO	YTLDVTSVSWVODNTYOITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V O L Y G Y	NENT 117
11W/OPS2_461 4 1/1_200	1 MORPELLAVIVISI	ENSALCEPTALVPPCSSECTSCNS	I V N C C P N L D E NWHM NOON I MO	VTI DVT SV SWVO DNTVOITI HVKC	KENIDIKYIWSIKI	LOVICPKCTVOLVCV	NENT 117
000733-401.4_1/1-200	IMORFFELATEVESEE	N SALUFFTAL VFRUSSLUTSCNS	I VINGER NEDENWINNING ON I MO	TTEDVISVSWVQDNTIQTTINVKG	RENIDERIEWSERI	TUVTUFKUTVQLTUT	NEWT III
Y55_1/1-200	IMQRPFLLAYLVLSLL	NSALGFPIALVPRGSSEGISCNS	IVNGCPNLDFNWHMDQQNIMQ	Y I L DVI SV SWVQ DNI YQ I I I HVKG	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENT 11/
YS4 1/1-200	1 MQRPFPLAYLVLSLL	F Y S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NQ Q T I MQ	YTLDVTSVSWVQ DNTYQITIHVKG	KENIDLKYLWSLKI	I G V T G P K G T V Q L Y G Y	NENT 117
DRVPC1788 1/1-200	1 MORPELLAVIVISIL	ENSALGEPTALVPROSSECTSONS	I V N G C P N I D E NWHM NOOT I MO	VTI DVT SV SWVO DNT VOITIHVKG	KENIDIKYIWSIKI	LOVICPKCTVOLVCY	NENT 117
DDV/ 01/05_1/1-200	INORDELLAVIULEL		TVHOCT NEDT NUTHING OF TIME	TT DUT SU SWYQ DNT YQ I TYYYYG	KENTDERTENSERT	LOVI CD K CT VOL X CV	NEWT 117
DBVPG6044_1/1-199	IMQRPFLLAYLVLSLL	NSALGFPIALVPR-CSEGISCNS	I V NGCP NLDF NWHMDQQ NTME	Y I L DVI SV SWVQ DNI YQI I VHVKG	KENIDLKYLWSLKI	IGVIGPKGIVQLYGY	NENI 116
CBS7838 1/1-215	1 MQRPFPFAYLVLSLL	F Y S A L G F P T A L V P R G S S E G T S C N S	I V NG C P N L D F NWHM NQ Q N I MQ	YTLDVTSVSWVQDNTYQITIHVKG	EENIDLEYLSSLKI	IGVTGPKDTVQLYGYNEDT	YLIDNPL-VSRCDEYT 132
VIM522 1/1-215	1 MORREREAVIVISII	EVSALCEPTALVPPCSSECTSCNS	I V N C C P N L D E NWHM NOON I MO	VTI DVT SV SWVO DNTVOITIHVKC	FENIDLEVISSIKI	LOVIC PKDTVOLY CVNEDT	VIIDNRI-VSRCDEVT 132
1941522_1/1-215	INORDEREAVENESEE		TYNGCT NEDT NWTINNGQUITING	TT DUT SU SWUQ DNT VQ I T HUVKG	E ENI DI EVI COLKI	LOVI CDKDTVQLI CKNEDT	VILLENDL VCDCDEVT 132
TJM521_1/1-215	IMQKPFPFATLVLSLL	TSALGFPTALVPKGSSEGISCNS	I VNGCPNLDFNWHMNQQNTMQ	TILDVISVSWVQDNIYQIIIHVKG	LENIDLEYLSSLKI	GVIGPKDIVQLYGYNEDI	TETONPE-VSRCDETT 132
R93-1017_1/1-215	1 MQRLFPFAYLVLSLL	F N S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NQQ N I MQ	Y T L D V T S V S W V Q D N T Y Q I T I H V K G	EENIDLEYLSSLKI	IGVTGPKDTVQLYGYNEDT	YLIDNPL-VSRCDEYT 132
MMRL 125 1/1-215	1 MORLEPEAYLVLSII	ENSALGEPTALVPRGSSEGTSCNS	I V NGCP N L D F NWHM NOON I MO	YTLDVTSVSWV0DNTY0ITLHVKG	EENIDLEYLSSIKI	I G V T G P K D T V O L Y G Y N F D T	YLIDNPL-VSRCDEYT 132
VIM1115 1/1_315	1 MORIEREAVIVICI	ENSALCEDTALVADCSSECTSCH	IVNCCPNI DENWHMMOONING	VTI DVTSVSWVODNTVOIT LUVKC	FENIDIEVICELEI	LOVICER DIVOLVENDE	VIIDNEL-VERCDEVT 133
YJM1115_1/1-215	IMQKLFPFATLVLSLL	INSALGEPTALVPRUSSEGTSCNS	I VNGCPNED FNWHMNQQNIMQ	TILDVISVSWVQDNITQIIIHVKG	EENIDLETLSSLKI	IGVIGPKDIVQLTGTNEDI	TLIDNPL-VSKCDETI 132
NRRL_Y-961_1/1-215	1 MQRPFPFAYLVLSLL	Y SALGFP TALVP RGSSEGT SCNS	I V N G C P N L D F NWHM NQ Q N I MQ	Y I L D V T S V S W V Q D N T Y Q I T I H V K G	LENIDLEYLSSLKI	TGVTGPKDTVQLYG <mark>YNEDT</mark>	YLIDNPL-VSRCDEYT 132
NRRL YB-2625 1/1-214	1 MORP FP FAY LVLSLL	FY SALGEPTALVPRGSSEGTSCNS	I V NGC P N L D F NWHM NOO N I MO	YTLDVTSVSWV0DNTY0ITIHVKG	EENIDLKYLSSLKI	I G V T G P K D T V O L Y G Y H E N T	YLIDNPL-VSRCDENT 132
K11 1/1-216	1 MORREREAVIVISII	EVENICEDIALVEDCSSECTSCNS	LVNCCPNLDENWHMNOONLMO	VTI DVT SV SWVO DNTVOITI HVVC	FENIDIKVISSIKI	LOVICERDIVOLVERHENT	VIIDNPIDEVPCSENT 133
R11_1/1=210	INGREFFERIEVESEE	I JALOFFIALVERUJJEUTJUNJ	THE CENTER IN THE REPORT OF THE	TI DUT SU SWUQ DUT VOLTINIKU	E ENI DI EVI COLLA	LOUTONKDIVQLI UTHENI	VI IDNEL VCDCDENT 133
CBS7833_1/1-215	IMQRLFPFAYLVLSLL	N SALGEPTALVPRGSSEGTSCNS	I V NGCP N L D F NWHMNQQ N I MQ	TILDVISVSWVQDNTYQITIHVKG	LENIDLEYLSSLKI	I G V I G P K D I VQ L Y G Y N E D T	TLIDNPL-VSRCDEYT 132
Y12 1/1-215	1 MQRLFPFAYLVLSLL	FN SALGFP TALVP RGSSEGT SCNS	I V NGC P N L D F NWHM NOO N I MO	YTLDVTSVSWVQDNTYOITIHVKG	EENIDLKYLWSLKI	I G V T G P K D T V O L Y G Y D E D T	DWIDNPL-VSRCDENT 132
VS2 1/1-215	1 MORPEPEAVIVICI	EVSALGEPTALVPROSSECTSCNC	I V NGCPNI DENWHMNOON I MO	YTI DVT SV SWVO DNT YO I TI HVKC	FENIDIKVISSIVI	LOVICPKDIVOLVCVDENT	DWIDNPI-VSPCDENT 132
DDUDC110C 111 215	1 MODIEDEAVIVIET		LYNCCDNI DENWINNQQN IMQ	VTL DVT CV CW/VO DVTVO LT LIVY KG	EENI DI KYLWEI KI	LOUTONKDI VQLI GIDENI	DWI DNDI VCD CD CNT 132
DBVPG1106_1/1-215	IMQKLFPFAYLVLSLL	IN SALGEPTALVPRGSSEGTSCNS	I V NGC P N L D F NWHMNQQ N I MQ	TILDVISVSWVQDNIYQITIHVKG	LENIDLKYLWSLKI	TGVIGPKDIVQLYGYDEDT	DWIDNPL-VSRCDENT 132
Y9_1/1-215	1 MQRPFPFAYLVLSLL	F Y S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NQ Q N I MO	YT L D V T S V S W V Q D N T Y Q I T I H V K G	EENIDLKYLWSLKI	I G V T G P K D T V Q L Y G Y D E D T	DWIDNPL-VSRCDENT 132
YIM224 1/1-215	1 MORPEPEAVIVISI	EY SALGEPTAL VPROSSECTSONS	I V NGCP N I DE NWHMNOO N I MO	YTI DVT SV SWVO DNTYO I TI HVKC	FENIDIKYLSSIKI	LOVIGPKDIVOLYCYDENT	DWIDNPI-VSRCDENT 132
NDD/ V 10 000 1/1 315	1 MODDEDEAVING		LYNCCDNI DENWUMNOON MO	VTI DVT CVCWVO DNTVO I THIVKG	EENIDLKYLSSLKI	LOVICEKETVOLVCVEENT	DWIDNEL VERCOENT 132
NKKL_T-10_988_1/1-215	IMQKFFFFATLVLSLL	TJALUFFIALVPKUSSEUISCNS	I VINGEPINE DENWIMMINUQUN I MQ	TILDVISVSWVQDNIYQIIIHVKG	LENIDERTESSERI	TOVIGENDIVQLTGTDENI	DWIDNPL-VSKCDENT 132
YJM1119_1/1-215	1 MQRPFPFAYLVLSLL	F Y S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NQQ N I MQ	Y T L D V T S V S W V Q D N T Y Q I T I H V K G	EENIDLKYLWSLKI	I G V T G P K D T V Q L Y G Y D E D T	DWIDNPL-VSRCDENT 132
Sigma 1278b 1/1-215	1 MORPEPEAYLVISII	EY SALGEPTALVPRGSSEGTSCNS	I V NGCP N L D F NWHM NOO N I MO	YTLDVTSVSWV0DNTY0ITLHVKG	EENIDLKYLSSIKI	I GVT GPK DT VOL Y GY DENT	DWIDNPL-VSRCDENT 132
VIM1101 1/1-315	1 MORIEREAVIVIET	ENSALCEDTALVADCCCCCCCCC	IVNCCPNI DENWHMMOONING	VTI DVT SV SWVO DNT VO I T LUVKG	FENIDIKYLWSLOU	LOVICE KDTHOLYCYDEDT	DWIDNEL-VERCDENT 133
IJm1101_1/1-215	INGREFFFATEVESEE	N SALUFFIALVERUSSEUTSUNS	THE FREDERING WINNOUN INQUINING	TTEBVISVSWVQDNITQTTTHVKG	LENIDENTEWSLQI	LOVI OF KDIVQLIGIDEDI	DWIDNEL-VSKCDENT 132
NRRL_Y-17447_1/1-215	1 MQRPFPFAYLVLSLL	F Y S A L G F P T A L V P R G S S E G T S C N S	I V N G C P N L D F NWHM NQ Q N I MQ	Y I L D V T S V S W V Q D N T Y Q I T I H V K G	EENIDLKYLWSLKI	IGVTGPKDTVQLYGYDEDT	DWIDNPL-VSRCDENT 132
DBVPG6040 1/1-215	1 MORP FP FAY LVLSII	FY SALGFP TALVP RGS SEGT SCNS	I V NGCP N L D F NWHM NOO N I MO	YTLDVTSVSWVQDNTYOITLHVKG	EENIDLKYLWSIKI	I G V T G P K D T V O L Y G Y D F D T	DWIDNPL-VSRCDENT 132
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Consensus

MQ R P F L L A Y L V L S L L F N S A L G F P T A L V P R G S S E G T S C N S I V NG C P N L D F NWHMNQQ N I MQYT L D V T S V SWVQ D N T YQ I T I H V K G K E N I D L K Y L W S L K I I G V T G P K G T VQ L Y G Y D E D T D W I D N P L D V S R C N E N I

S288cRef_1/1-200	118 Y L I DNP TD FT AT FEVY AT QDVNS CQVWMPNFQ I QFEY LQ <mark>G SAAQYA SSWQWGTT</mark> SFDL ST GCNNY DNQGH SQT DFPG FYWN I D
YJM311_1/1-200	118 Y L I DNPTDFTATFEVY ATQDVN SCOVWMPNFQI QFEYLQGSAAEYACSW EWGTTSFDLSTGCNNYDNQGHSQTDFPGFYWN I D
CBS1227 1/1-200	118 Y L DNY TDEFTAT FEV ATODVS COVMPNENCIOFFY LOGSAAOYAS SWKWGTTS FDLSTGCNNTDNQGHSQTDFPGFYWDKD
CBS7836 1/1-200	118 Y L I DNP TDFTATFEVY ATQDVNSCQVWMP NFQ I Q FEY LQGSAAQYACSWEWGTTSFDLSTGCNNYDNQGHSQTDFP GFYWN I D
92-123_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q G S A A Q Y A S SW K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
YJM436_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q G S A A Q Y A S SW K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
89-156_1/1-200	118 Y L I DNP TD FT AT FEV Y AT Q DANS COVWMPN FQ I Q FEY LQ C SAAQY AS TW TWG TT S FD L ST CCNNY DNQ CH SQ TD FP C FYWN I D
YJM455_1/1=200 VIM522_1/1=200	118 Y LI DNP T DFI A I FEVTA I QUVNSCOVMPNIQ I QFET LOG SA AQYAS SWKWGTI SFDLSI GCNNT DNQCHSQI DFPG FI WI I D
R91-48 1/1-200	118 Y L DNP TDFTATFEV ATODVS COVMP DE OLOFFY L HGEP ARYKR SWKWGTTS FULSTGCNNTDRUGGS OT DEP GETWIND
96-98_1/1-200	118 Y L I DNP TDFTATFEVY ATQUVNS CQVWMP NFQ I Q FEY LQ G SAAQYAS SWKWGTTS FDL STGCNNY DNQ GH SQT DFP GFYWN I D
NRRL_YB-4348_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q <mark>G S A A Q Y A S SW</mark> K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W D K D
NCMH_125_1/1-200	118 Y L I DNP TD FTAT FEVY ATQ DVN S CQ VWMP N FQ I Q FEY LQ G SAAQYAS SWKWGTT S FD L STGCNNY DNQ GH SQ TD FP G FYWN I D
NRRL_Y-1546_1/1-199	11/ Y LI DNP I DFIAI FEVYA I QDV NSCQVWMP NFQ I QFEY LQCSAAQYASSWKWGTI SFDLSI CCNNY DNQCHSQI DFP GFYWN I D
NRRL_1-6679_1/1-200	118 Y LI DNP T DETATEVYATODVNSCOVWPN POTOFEV OG FAQYAS SWKWGTTSEN I STOCNNY DNOCH SOTOFPGFTWID
NRRL Y-12638 1/1-200	118 Y L I DNP TDFTAT FEVYATODVNSCOVWMPNFO I OFEY LOGSAAOYAS SWKWGTTS FDL STGCNNY DNOGHSOTDFPGFYWN I D
NRRL_YB-427_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q G S A A Q Y A S SW K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
NRRL_YB-908_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q <mark>G S A A Q Y A S SW</mark> K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
NRRL_YB-4081_1/1-200	118 Y L I DNPTDFTATFEVYATQDVNSCQVWMPNFQIQFEYLQGSAAQYASSWKWGTTSFDLSTGCNNYDNQGHSQTDFPGFYWNID
NRRL_Y-268_1/1-200	118 Y L I DNP TDFTATFEVY AT ODVINS COVIMP NEO 10 FEY LOG SAAQYAS SWKWGTTS FNLSTGCNNY DNQGHSQTDFPGFYWN I D
NRRL_TB=2541_1/1=200 NRRL_YR=4506_1/1=200	118 Y LI DNY TDETATFEVIALQUVINS QUVINPNE QIQFET LOGSAAQYASSWKWGTISENUS IGCNNT DNQGISQI DEPGETIMI D
UWOP583-787.3 1/1-200	118 Y L I DNP TDFTAT FEVYATODVNSCOVWMPNFO I OFEY LOGSAAOYASTWTWGTTS FDL STGCNNY DNOGHSOTDFPGFYWN I D
NRRL_Y-6297_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q G S A A Q Y A S SW K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
91-213_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q <mark>G S A A Q Y A S SW</mark> QWGT T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
NRRL_Y-12603_1/1-200	118 Y L I DNPTDFTATFEVYATODVNSCOVWMPNFQIQFEYLQGSAAQYASSWKWGTTSFDLSTGCNNYDNQGHSQTDFPGFYWNID
S288c_1/1-200	118 Y LI DNPT DFI A I FEVY A TODVINSCOVIMPNED TO FEV LOGSA A QYAS SWOWGTI SFDLST GCNNY DNOCHSQI DFPG FYWN I D
W22_1/1=200 VP\$128_1/1=200	118 Y LI DNP TDETA TEVYA TODVNSCOVWMPNEQ TOFEVLOG SA ADYA S SWEWGTTSEDISTCENNY DNOCH SCOVWPNEQ FUNID
L-1528 1/1-200	118 Y L I DNP TDFTAT FEVY ATODVN SCOVWMP NFO I OF EY LOGCAAQYA STWTWGTTS FDL STGCNNY DNOGH SQT DFP GFYWN I D
SK1_1/1-199	117 Y L I DNP TD FTAT F E VY ATQ DV N S CQ VWMP N FQ I Q F E Y L Q G S A A Q Y A S SW KWGTT S FD L ST R C N NY D NQ G H SQ T D F P G F Y W N I D
NCYC361_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V WMP N F Q I Q F E Y L Q <mark>G S A A Q Y A S SW</mark> K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
96-109_1/1-200	118 Y L I DNP TD FTAT FEVY ATODVNS COVWMPNFO I OFEY LOGSAAQYAS SWRWGTTS FDL ST GCNNY DNOGHSOTDFPG FYWN I D
YPS606_1/1-200	118 Y LI DNP T DFI A I FEVY A TODVINS COVIMP NED TO FEV LOGS A A QY AS SWKWGTT SENI ST CONNY DNOCHSQI DFP G FYWN I D
378604X 1/1-200	118 Y L I DNP TD FT AT FEVY ATO DVN S COVWMP NEO I O FEY LOG SAAO YAS SWKWGTT SEDL ST GCNNY DNOGHSOT DEP G FYWN I D
YPS681_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V WMP N F Q I Q F E Y L Q G S A A Q Y A S SWKWGT T S F D L S T G C NNY D N Q G H S Q T D F P G F Y W N I D
YPS615_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D A N S C Q V W M P N F Q I Q F E Y L Q <mark>G S A A Q Y A S T W</mark> T W G T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
YPS617_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D A N S C Q V W M P N F Q I Q F E Y L Q G S A A Q Y A S T W T W G T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
YPS661_1/1-200	118 Y L I DNP TDFTATFEVY AT ODVINS COVIMP NEO 10 FEY LOG SAAQYASTWTWGTTS FDLSTGCNNY DNQGHSQTDFPGFYWN ID
VPS620 1/1-200	118 Y LI DNP TDETA TEVYA TODVNSCOVWMPNEQTOFEVLOG SA A OYAS SWEWGTTSEDESTOCNNY DNOCH SO TOFF GETWID
UWOP53-461.4 1/1-200	118 Y L I DNP TDFTAT FEVY ATODVN SCOVWP NFD I O FEY LOGCAAOYA STWTWGTTS FDL STGCNNY DNO GH SOT DFP GFYWN I D
Y55_1/1-200	118 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q G S A A Q Y A S SW K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
YS4_1/1-200	118 Y L I DNPTDFTATFEVYATQDVNSCQVWMPDFQIQFEYLQDSAAQYASSWKWGTTSFALSTGCNNYDNQGHSQTDFPGFYWNID
DBVPG1788_1/1-200	118 Y L I DNP TD FTAT FEVYATODVNS COVWMPNFQ I Q FEY LOC SAAQYAS SWRWCTTS FDL ST CONNY DNGCHSQTDFP C FYWN I D
DBVPG6044_1/1-199 CPS7828_1/1_215	117 Y LI DNP T DFI A I FEVTA I QUVNSCOVMPNE U QEFELOG SA QTASSWKWGTI SFIDESI GCNNT DNQCHSQI DFP G FIWNI D
YIM522 1/1-215	133 Y L DNP TD FT AT FFVY ATO DVN S COVWMP NEOLOFFYLOD LAPEDEC SWEWGTTS FTLSTGCDNY DNOGY SOTDFPG FFWN I D
YJM521_1/1-215	133 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V WMP N F Q I Q F E Y L Q D I A P E D E C SW EWGT T S F T L S T G C D N Y D N Q G Y S Q T D F P G F Y W N I D
R93-1017_1/1-215	133 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q D I A P E D E C S W E W G T T S F T L S T G C D N Y D N Q G Y S Q T D F P G F Y W N I D
MMRL_125_1/1-215	133 Y L I DNP TD FTAT FEVY ATQ DVN S CQ VWMP N FQ I Q FEY LQ DI APEDEC SW EWGTTS FTL STGCDNY DNQ GY SQ TD FP G FYWN I D
YJM1115_1/1-215	133 Y LI DNP TDFTA TFEVYA TODVNSCOVWPNFQ TOFEYLODIAPEDEC SWEWGTTSFTLSTCCDNYDNOCYSQTDFPG FYWN ID
NRRL_T-901_1/1-215 NRRL_VR_2625_1/1_214	133 TELEDRY TO FTAT FEV VATODVINS COVIMPNED LOFEVLOGES 4 A EVECES WEWGTTS FYLSTCC-NY DDOCHSOTDEFC FYWID
K11 1/1-216	134 H L I DNP TDFTATFEVY ATODVNSCOVWPNFO I OFEY LOGSAAQYAC SWEWGTTS FY LSTGCNNY DHOGH SQTDFPGFYWN I D
CBS7833_1/1-215	133 Y L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q D I A P E D E C S W E W G T T S F T L S T G C D N Y D N Q G Y S Q T D F P G F Y W N I D
Y12_1/1-215	133 H L I DNP T D F T A T F E V Y A T Q D V N S C Q V WMP N F Q I Q F E Y L Q <mark>G S A A Q Y A C SW</mark> EWGT T S F Y L S T G C N N Y D H Q G H S Q T D F P G F Y W N I D
YS2_1/1-215	133 Y L I DNP TD FTAT FEVY ATODVNS COVWMPNFO I OFEY LOGSAAEYACSWEWGTTS FY L ST GCDNY DNGGY SOTDFPG FYWN I D
DBVPG1106_1/1-215	133 H LIDNPTDFTATFEVTATQDVNSQQVMPNFQTQFETQGSAAQYACSWEWGTTSFYLSTGCNNYDHQHSQTDFPGFTWNTD 133 H LIDNPTDFTATFEVYATQDVNSQQVMPNFQTQFEYLQGSAAQYACSWEWGTTSFYLSTGCNNYDHQGHSQTDFPGFYWNTD
YIM224 1/1-215	133 Y L I DNP T D F T A T F E VY A T O D V N S C O VWMP N F O I O F E Y L O G S A A E Y A C SW EWGT T S F Y L S T G C D N Y D N G Y S O T D F P G F Y W I D
NRRL_Y-10_988_1/1-215	133 Y L I DNPT DFTAT F EVY ATQ DVNS CQVWMPN FQ I Q F EY LQ G SAA EY AC SW EWGTT S FY L ST GCDNY DNQ GY SQT D FP G F YWN I D
YJM1119_1/1-215	133 H L I DNP T D F T A T F E V Y A T Q D V N S C Q V W M P N F Q I Q F E Y L Q <mark>G S A A Q Y A S SW</mark> K W G T T S F D L S T G C N N Y D N Q G H S Q T D F P G F Y W N I D
Sigma1278b_1/1-215	133 Y L I DNPTDFTATFEVYATQDVNSCQVWMPNFQIQFEYLQGSAAEYACSWEWGTTSFYLSTGCDNYDNQGYSQTDFPGFYWNID
YJM1101_1/1-215	133 H LI DNP T DF LA T FEVY A TODVINS COVIMP NFO TO FEV LOG SAAEHAC SWEWGTT SFYLST GCDNY DNOCY SQI DFP G FYWN LD
DRVPC6040 1/1=215	133 H L DNP TDETAT FEVY A TODVNSCOVWMPNED OF EYLOG SA A OYA S SWKWGTTSEDISTGCNNY DNOCH SCOVMPNED
221. 30010_1/1-213	* * * *
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	Y L I DNP T D F T A T F E V Y A T O D V N S C O VWMP N F O I O F E Y L O G S A A O Y A S SWKWGT T S F D L S T G C NNY D N O G H S O T D F P G F Y W N I D

Figure S3: C domain amino acid alignment. Black line indicates location that defined C-domain in our analysis. Gray domain indicates GPI-anchored area.

S288c 1/1-516	1 APVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T T I V T K T T T S V T T P S T T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T T I T T 134
YJM224/1-491	1 A P V S S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 114
YJM311/1-486	1 AP VT S STT E S S S AP V P T P C T T V AP S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T A V T T S S T T I T T T V C S T G T N S A G E T T S E C S P K T V T T T V P T S P T T P V T T S P T T T I T 109
CB52910/1-511	1 APVTSSTTESSSAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S KY P G SQT ET S V S S T T ET T I V P T T T T S V T T S S T T I T T T V C S T G T N S A G E T S G C S P K T I T T V P T S P T T P V T S P T T I T T 134
CBS1227/1=511	1 APVSSSIIESSVAPVPIPSSSSNIISSAPSSIPFSSSIESFSIGIIVIPS	SSKYPGSQ1E1SVSSITETTIVPIIIISVIISSIIIIIVCSIGINSAGEIISGCSPKIIIIVPISPIIPVIISPIIIII154
CB57836/1-447	1 APVT S STT F S S V AP V P T P S S S S N T S S A P S	SKYPGSOTETSVSSTETTIVPTTTTSVTTPSTT
92-123/1-491	1 AP V S S S T T E S S V AP V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T T I T 1 1 4
YJM436/1-511	1 APVSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T T S S T T I T T T V C S T G T N S A G E T T S G C S P K T I T T T V P T S P T T P V T T S P T T T I T 134
89-156/1-472	1 APVTSSTTESSSAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T I V P T T T T T S V T P S T T I T T T V C S T G T N
YJM455/1-467	1 APVTSSTTESSVAPVPTPCSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	\$ \$ \$ K Y P G \$ Q T E T \$ V \$ \$ T T E T I V P T T T T \$ V T \$ \$
YJM522/1-447 VIME21/1-447	1 APVSSSIIESSVAPVPIPSSSSNIISSAPS	S SKYPG SQTET SV SSTTETT IVPTTTTSVTTP STT
YIM523/1-491	1 AP VT S STT E S S V AP V P T P S S S S N T S S A P S	S K Y P G S OT ET S V S S T ET T I V P T T T T S V T P S T T I T T T V C S T G T N S A G E T S G C S P K T V T T V P T T T T S V T P S T T I T T 14
R91-48/1-512	1 S S T T E S S V A P V P T P S S S S N I T S S A P S S T P F S S T T E S F S T G T T V T P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 130
96-98/1-511	1 AP V S S S T T E S S V AP V P T P S S S S N I T S S AP S S T P F S S S T E S F S T G T T V T P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T T S S T T I T T T V C S T G T N S A G E T T S G C S P K T I T T T V P T S P T T P V T T S P T T T I T 134
R93-1017/1-491	1 AP V S S S T T E S S S AP V P T P S S S S N I T S S A P S	S S K Y P G S T T E T T I V P T A T T S V T P S T T I T T T V C S T G T N S A G E T T S G S P K T V T T V P T T T T S V T T S V T T S T T I T T T V P T A T T S V T P S T T T I T T V C S T G T N S A G E T T S G C S P K T V T T V P T T T T S V T T S S T T I T T I 14
96-100/1-511 NPDI VP 4348/1 511	1 APV15511E55VAPVP1P5555N1155AP551PF5511E5F51G11V1P5	S SK YP G SQT ET SV S ST TET T VP T T TT SV T S ST T T T T VC ST G I N SA GET I SGC SP K T T T VP T SP T T P V T S P T T T T V ST ST T T T VC ST G T N SA GET SGC SP K T T T VP T SP T T T V ST ST T T T T VC ST G T T N SA GET SGC SP K T T T VP T SP T T T T T T T T T T T T T T T T T
NRRL_1D=4348/1=311 NRRL_Y=10_988/1=491	1 APVSSSTTESSVAPVPTPSSSSNTTSSAFSSTFFSSSTESFSTGTTVTFS	S S KY P G S O T E T S V S S T E T T I V P T T T T S V T S S T T I T T V C S T G N S A G E T S G C F P K T V T T V P T T T S V T S S T T I T T I I A
NCMH_125/1-511	1 APVSSSTTESSVAPVPTPSSSSNITSSAPSSTPSSSTTESSSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T T S S T T I T T T V C S T G T N S A G E T T S G C S P K T I T T T V P T S P T T T T T T T T 134
MMRL_125/1-479	1 A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T A T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 102
YJM1115/1-491	1 A P V S S S T T E S S S A P V P T P S S S S N I T S S A P S	S SKYP G SQTET SV S STT ETT I VPTATTT SVTTP STTT I TTTVC STGTN SAGETT SGC SPKTVTTTVPTTTTTS VTTS STTT I TT 114
YJM1119/1-491		SSKYPGSQTETSVSSTELTIVPTTTTSVTPSTTTTTVCSTGTNSAGETSGCSPKIVTTVPTTTTSVTSSTTTTTT
NRRL_1-1540/1-491 NRRL_Y=6679/1-467	1 APVSSSTTESSVAPVPTPSSSSNTTSSA	SKYPGSQTETSVSSTTETTIVPTTTTTSVTTSS
Sigma 1278b/1-447	1 APVS SSTTESSVAPVPTPSSSSNITSSAPS	S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T
NRRL_Y-961/1-447	1 A P V S S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T
YJM1101/1-491	1 AP V S S S T T E S S V AP V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 114
NRRL_Y-963/1-511		SSKYPGSQTETSVSSTELTTVPTTTTSVTTSS
NRRL_1-12038/1-404 NRRI_VR_427/1_491	1 AP XT S S T T E S S S AP V P T P S S S S N T S S AP S S T F S S S T E S S S I U T V T P - 1 AP V T S S T T E S S S AP V P T P S S S S N T S S AP S S T P S S S T E S S S I U T V T P - 2 P S	3 SKTP U SUTET ST ST TETTT I V F TT TT SV T 5 ST TT TT TV C ST CT NS & C FT SC C SP KT V TT TV P TT TT SV T F ST TT T T
NRRL_Y-17447/1-491	1 APVSSSTTESSVAPVPTPSSSSNITSSAPS	S SKYP G SQ T ET SV S STT ETT I VP TTTTTAVTTP STTT I TTTVC ST GT NS AGETT S G C SP K TVTT VP TTTT SV TT S STTT I TT 114
NRRL_YB-908/1-472	1 APVTSSTTESSSSPVPTPSCSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S K T E T S V S S T T E T T I V P T T T T T S V I T P S T T T I T T 90
NRRL_YB-4081/1-491	1 APVTSSTTESSVAPVPTPSSSSNITSSAPS	\$ \$ \$ KYP G SQT ET \$ V \$ \$ TT ETT I V P TTTTT \$ V TT P \$ TTT I TTTV C \$ TG TN \$ A G ETT \$ G C \$ P K TV TT V P TTTT \$ V TT \$ \$ TTT I TT1 4
NRRL_1-208/1-511 NRRI_VR_2541/1_511	1 APVSSSTTESSVAPVPTPSSSSNTTSSAPSSTPFSSTTESFSTUTIVTPS	3 SKTP USQLET SVS STTETT I VPTTTTT SVTTS STTTTT I VCS I GINSA GETT SGC SPKTTTT VPT SPTTP VTT SPTTTTT I TT I A
NRRL YB-4506/1-491	1 S S N I T S S A P S S T P S S T T E S F S T G T T V T P S	S K Y P G S K T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T V P T T T T S V T S S T T I T T 114
NRRL_YB-2625/1-491	1 A P V S S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T A V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 114
Yllc17_E5/1-511	1 APVTSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T I V P T T T T T S V T T S S T T I T T T V C S T G T N S A G E T S G C S P K T I T T T V P T S P T T P V T S P T T I T T 1 3 A
UWOP583-787.3/1-516	1 APVSSSTTESSSAPVPTPSSSSNTTSSAPSSTPFSSTESFSTGTTVTPS	\$ \$ K Y P G \$ Q E \$ V \$ \$ 1 E V P \$ V P \$ V \$ G G N \$ A G E \$ G \$ S P K V V P \$ V \$ S 14
91-213/1-516	1 APVSSSTTESSVAPVPTPSSSSNTSSAPSSIPFSSTESFSTGTTVTPS	S KY P G S OT ET S V S S T ET T I V P T K T T S V T P S T T I T T T V C S T G T N S A G ET S G C S P K T V T T V P T T T T S V T S S T T I T T 134
NRRL_Y-12603/1-491	1 A P V S S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T V P T T T T S V T S S T T I T T 114
S288c/1-516	1 APVSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S SKYP G SQTET SV S STTETT I VPTKTTT SVTTP STTT I TTTVC STGTN SAGETT SGC SPKTVTTTVPTTTTTSVTTS STTT I TT 134
M22/1-511 VPS128/1-480	1 APVSSSIIESSSAPVPIPSSSSNIISSAPSSIPFSSIIESFSIGIIVIPS	\$ \$ K Y P G \$ Q E \$ V \$ S E V P \$ V \$ S V \$ G G N \$ A G E \$ G \$ S P K V P \$ P P V \$ P 134 \$ \$ K Y P G \$ O T E T \$ V \$ S T T E T V P T T T \$ V T T S T T T T V \$ S T T C \$ S T T C \$ S T T T T \$ V T S \$ T T T T \$ V \$ S T T 144
96-101/1-511	1 PPVSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S K Y P G S O T E T S V S S T T E T I V P T T T T T S V T S S T T I T T T V C S T G T N S A G E T S G C S P K T I T T V P T S P T T P V T S P T T T T T 134
L-1528/1-472	1 PPVTSSTTESSSTPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C F T G T N
SK1/1-491	1 A P V T S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T I I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T S G C S P K T V T T V P T T T T S V T S S T T I T T 114
K11/1-491	1 APVSSSTTESSVAPVPTPSSSSNITSSAPS	SSKYPGSQTETSVSSTTETTIVPTTTTSVTTPSTTTITTTVCSTGTNSAGETTSGCSPKTVTTTVPTTTTTSVTTSSTTTITT1
NCYC361/1-425	1TGTTVTPS	5 SKYPG SQT FT SV S STT FT I VPT I TT SVT F ST I TT I VC F G IN
DBVPG6765/1-467	1 PPVSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S 5 K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T T S S
DBVPG6040/1-467	1 APVTSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T T S S
DBVPG1853/1-511	1 APVSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S T T E T T I V P T T T T T S V T T S T T T I T T T V C S T G T N S A G E T T S G C S P K T I T T V P T S P T T P V T S P T T I T T 134
CB5_7833/1-491 06_100/1_511	1 APVSSSIIESSSAPVPIPSSSSNIISSAPS	3 S K Y U S Q I E I S Y S S I E I I I Y Y I A I I S Y I Y S I I I I I I V S I G I N SA GE I I S G S Y K I Y I I Y Y I I I S Y I S S I I I I I I
YPS606/1-480	1 VAPVPTPSSSSNITSSA	S S K Y P G S O T E T S V S S T T E T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T S G C S P K T V T T V P T T T T S V T T S S T T I T T 103
L-1374/1-467	1 APVSSSTTESSVAPVPTPSSSSNITSSAPSSTPSSSTTESSSTGTTVTPS	S 5 K Y P G 5 Q T E T S V S S T T E T T I V P T T T T T S V T T S S
Y12/1-491	1 AP V S S S T T E S S V AP V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 114
Y52/1-491		SSRYPGSQTETSVSSTELTTVPTTTTSVTPSTTTTVCSTGTNSAGETSGCSPRTVTTVPTTTSVTSSTTTTT
DRVPC110/1-511	1 APVSSSTTFSSVAPVPTPSSSSNTTSSAPSSTPFSSTTESPSTUTIVTPS	S S KY P G S Q T E T S V S S T F T T I V P T T T T S V T S S T T T T T V S T G T N S G C F T S G C S P K T T T V P T T T T S V T S T T T T I I I I I I I I I I I I I I
378604X/1-425	1 TGTTVTP S	S 5 K Y P G SQ T E T S V S S T T E T I V P T T T T T S V T T S S T T I T T 48
YPS681/1-480	1 V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T V P T T T T S V T S S T T I T T 103
YPS615/1-472	1 APVTSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	S S K Y P G S Q T E T S V S S T E E T I V P T T T T S V T P S T T I T T T V C S T G T N
YP5617/1=472 VP5661/1=472	1 APVISSIIESSSAPVPIPSSSSNIISSAPSSIPFSSIIESFSIGIIVIPS	S \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
YPS670/1-491	1 AP V S S S T T E S S V AP V P T P S S S S N T S S A P S	S S K Y P G S OT ET S V S S T T ET T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T S G C S P K T V T T V P T T T T S V T S S T T I T T 1 1 4
YPS630/1-491	1 A P V S S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G SQ T E T S V S S T T E T T I V P T T T T T S V T P S T T I T T T V C S T G T N S A G E T T S G C S P K T V T T T V P T T T T T S V T T S S T T I T T 114
UWOP53-461.4/1-388	1	14
Y55/1-491 VS4/1-426	1 AF V 5 5 5 1 1 E 5 5 V AF V F I F 5 5 5 5 N I T 5 5 A	SSKYPGSQIELSVSSILEIIIVPIIIISVIIPSIIIIIIVVCSGINSAGETTSGCSPKIVTTVPTTTTSVTTSSTTTIT114
DBVPG1788/1-511	1 PPVTSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSTTESFSTGTTVTPS	SKYPGSQTETSVSSTETIVPTTTTSVTTSSTTTITTVCSTGTNSAGETTSGCSPKTITTVPTSPTTPVTTSPTTIT1134
DBVPG6044/1-491	1 A P V T S S T T E S S V A P V P T P S S S S N I T S S A P S	S S K Y P G S Q T E T S V S S T E T T I V P T T T T T S V T P S T T T I T T V C S T G T N S A G E T S G C S P K T V T T V P T T T T S V T S S T T I T T 114
Y9/1-486	1 E S T T T S P T T P V T T V V S T T V V T T E Y	TSTKPGGEITTTFVTKNITTIASTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTITTTVPTTTTSVTTSSTTTITT109
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Conservation		
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5288c_1/1-516	135 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T T I A P T P S V T T V T N F T P T T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 268
VIM224/1-491	115 TVCSTCTN	δα C FTT SCC SP KT I TTTVP C ST SP S FTA S F STTT SP TTP VTTVV STTVVTT FY ST STKP C C F I TTT FVTK N I PTTY I TT I Δ PTP S VTTVT N FTP TT I TTTVC ST CT N S Δ C FTT SCC SP KTVTTVP 248
19822471-451	110 TVCSTCT	
TJM311/1-480	110 1 V C S I G I K	SAGETTSGCSPRTTTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTETSTSTRPGGETTTTPVTRNTPTTTTTTASTPSVTTVTNPTPTTTTTVCSTGTNSAGETTSGCSPRTVTTTVP245
CBS2910/1-511	135 T V C S T G T N	NS A G ETTS G C S P KT I TTTV P C ST S P S ETA S E S TTT S P TTP V TTV V S TTV V TT EY S T S TK P G G E I TTT F V TK N I P TTY L TT I A P TP S V TTV TN FTP TT I TTTV C S T G TN S A G E TT S G C S P K TV TTTV P 268
CBS1227/1-511	135 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 268
CR57838/1-447	71 TVCSTCTN	SACETTSCCSPKT Ι ΤΤΤΥΡCSTSPSETASESTTTSPTTPVTTVVSTTVVTEPSSTSTKPCCE Ι ΤΤΓΕVΤΚΝΙΡΤΥΙ ΤΤΙ ΔΡΤΡSVTTVTNETPTT Ι ΤΤΤVCSTCTNSACETTSCCSPKTVTTVP204
CDC703C/1 447	71 TVCSTCT	
CB5/836/1-44/	71 1 V C S I G I N	AGETTSGCSPRTTTTTVPCSTSPSETASESTTSPTPVTVVSTTVVTTETSTSTRPGGETTTFVTRNIPTTTLTTAPTPSVTVTNFTPTTTTTVCSTGINSAGETTSGCSPRTVTTVP204
92-123/1-491	115 TVCSTGTN	NSAGETTSGCSPKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVP248
YJM436/1-511	135 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 268
89-156/1-472	99	SACETTS CCSPKT I TTTVPCSTSPSETASESTTTS PTTPVTTVVSTTVVTTEVSTSTKPCCE I TTTEVTKNI PTTY I TTI APTPSVTTVTNETPTT I TTVCSTCTNSACETTS CCSPKTVTTVP224
05-150/1-4/2	01 TYCSTCT	
TJM455/1-407	91 1 4 C 5 1 G 1 4	SAGETT SUCSPRITTER VPCSTSPSETASESTT SPTPVTVVSTTVVTTETSTSTRPGGETTT PVTRNIPTTELTTAPTPSVTVTNFTPTTTTTVCSTGINSAGETT SUCSPRIVTTVP224
YJM522/1-447	71 TVCSTGTN	NSAGETTSGCSPKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVP204
YJM521/1-447	71 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 204
VIM523/1-491	115 TVCSTCTN	δα C FTT SCC SP KT I TTTVP C ST SP S FTA S F STTT SP TTP VTTVV STTVVTT FY ST STKP C C F I TTT FVTK N I P TTY I TT I Δ P TP S VTTVT N FTP TT I TTTVC ST CT N S AC FTT SCC SP KTVTTVP 248
DO1 48/1 512	121 TVCSTCT	CACETY CCCENT I TTYD CST S CETA CST TTO TTY TY TTY TTY TTY CST C C C C C C C C C C C C C C C C C C
K91-48/1-512	151 1 V C 5 1 G I N	SAGETTSGCSPRTTTTVPCSTSPSETASESTTSPTPVTVVSTTVVTTETSTSTRPGGETTTPVTRNIPTTTLTTAPTPSVTVTNFTPTTTTTVCSTGINSAGETTSGCSPRTVTTVP204
96-98/1-511	135 T V C S T G T N	NS A G ETTS G C S P KT I TTTV P C ST S P S ETA S E S TTT S P TTP V TTV V S TTV V TT EY S T S TK P G G E I TTT F V TK N I P TTY L TT I A P TP S V TTV TN FTP TT I TTTV C S T G TN S A G E TT S G C S P K TV TTTV P 268
R93-1017/1-491	115 TVCSTGTN	VISAGETT S G C S P KT I TTT V P C S T S P S ETA S E S TTT S P TT P V TT V V S TT V V TT E Y S T S T K P G G E I TTT F V TK N I P TTY L T I A P T P S V TT V TN F T P TT I TT V C S T G T N S A G E TT S G C S P K T V TT V P 248
96-100/1-511	135 TVCSTCTN	SACETTSCCSPKT Ι ΤΤΤΥΡCSTSPSETASESTTTSPTTPVTTVVSTTVVTEPSSTSTKPCCE Ι ΤΤΓΕVΤΚΝΙΡΤΥΙ ΤΙ ΔΡΤΡSVTTVTNETPTT Ι ΤΤΤVCSTCTNSACETTSCCSPKTVTTVP268
NDDI VD 4340/1 511	125 TVCSTCT	CALETY COLORY I TTY DOCTO SETASES TTY ONTO WITH WITH STATE OF THE VIEW OF THE STATE
NKKL_TB-4348/1-311	155 TVC 5TGTF	SAGETT SUCSPRITTER VESTSP SETASESTT SPTEPVTVVSTEVVTTETSTSTRPGGETTTEPVTRNIPTTELTTAPTPSVTVTNPTPTTTTTVCSTGINSAGETT SUCSPRIVTTVP200
NRRL_Y-10_988/1-491	115 TVCSTGTN	NSAGETTSGCSPKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVP248
NCMH 125/1-511	135 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 268
MMRI 125/1-479	103 TVCSTCTN	SACETTSCCSPKT TTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTFYSTSTKPCCE TTTEVTKN PTTY TT APTPSVTTVTNETPTT TTTVCSTCTNSACETTSCCSPKTVTTVP236
VM111E/1 401	115 TVCSTCTA	
IJM1113/1-491	115 TVC STGT	SAGET SUCSEKTTTEVECSTSE SETASESTTTSFTEVETVVSTEVVTEETSTSTKEGGETTTEVEKKIPTETETTAFTE SVTEVEKEFFTTTTEVESTGENSAGETTSGCSEKTVTTEVE 240
YJM1119/1-491	115 I V C S I G I N	NSAGETTSGCSPKTTTTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTGTKPGGETTTTFVTKNTPTTYLTTAPTPSVTTVTNFTPTTTTTVCSTGTNSAGETTSGCSPKTVTTTVP248
NRRL_Y-1546/1-491	115 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T T V C S T G T N S A G E T T S G C S P K T V T T V P 248
NRRL Y-6679/1-467	91 TVCSTGTN	NS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 224
Sigma 1278h / 1-447	71 TVCSTCTN	SACETTS CCSPKT I TTTVPCSTSPSETASESTTTS PTTPVTTVVSTTVVTTEYSTSTKPCCE I TTTEVTKN I PTTY I TT I APTPSVTTVTNETPTT I TTTVCSTCTNSACETTS CCSPKTVTTVP204
Signa12760/1-447	71 TVCSTGT	
NRRL_Y-961/1-447	71 1 1 0 C S 1 G 1 N	BAGETTSGCSPRTTTTTVPCSTSPSETASESTTSPTPVTVVSTTVVTTEPSTSTRPGGETTTFVTRNIPTTPTTTTTTVCSTGTNSAGETTSGCSPRTVTTVP204
YJM1101/1-491	115 TVCSTGTN	NS A G ETT S G C S P KT I TTT V P C ST S P S ET A S E S TTT S P TTP V TT V V S TT V V TT EY S T S T K P G G E I TTT F V T K N I P TTY L TT I A P T P S V TT V T N F T P TT I TTT V C S T G T N S A G E TT S G C S P K T V TT V P 248
NRRL Y-963/1-511	135 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 268
NRRI V=12638/1-464	89 TVCSTCTN	SACETTSCCSPKT Ι ΤΤΤΥΡCSTSPSETASESTTTSPTTPVTTVVSTTVVTEYSTSTKPCCE I ΤΤΓΕVΤΚΝΙΡΤΥΙ ΤΙ ΔΡΤΡSVTTVTNETPTT I ΤΤΤVCSTCTNSACETTSCCSPKTVTTVP222
NPPI VP_427/1_401	115 TVCSTCTA	
NKKL_1B-427/1-491	115 1 VC 5 1 G 1 K	SAGETT SUCSPRITTER VESTSP SETASESTT SPTTPVTVVSTTVVTTETSTUTKPGGETTT FVTRNIPTT LITTAPTPSVTVTNFTPTTTTTVCSTGINSAGETT SUCSPRIVTTVP240
NRRL_Y-17447/1-491	115 TVCSTGTN	NSAGETTSGCSPKTTTTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGETTTTFVTKNTPTTYLTTTAPTPSVTTVTNFTPTTTTTTVCSTGTNSAGETTSGCSPKTVTTTVP248
NRRL_YB-908/1-472	91 TVCSTGTN	\ S A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T KQ G G E I T T T F V T K N I P T T Y L T I A P T S S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T I T T T V P 2 4
NRRL YB-4081/1-491	115 TVCSTGTN	NS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 248
NPRI V-268/1-511	135 TVCSTCTN	SACETTS CCSPKT I TTY PCSTSPSETASESTTS PTTPVTTVVSTTVVTEYSTSTKPCCE I TTEVTKN I PTTY I TTI APTPSVTTVTNETPTT I TTY CSTCTNSACETTS CCSPKTVTTVP 268
NDD/ VD 2541/1 511	125 TVCSTCT	CALETY COLORYTITY DOCTOR CETAL CETTLE OTTOWN TO WITH THE STATE OF THE
NKKL_TB=2541/1=511	155 TVC 5TGTF	SAGETT SUCSPRITTER VESTSP SETASESTT SPTEPVTVVSTEVVTTETSTSTRPGGETTTEPVTRNIPTTELTTAPTPSVTVTNPTPTTTTTVCSTGINSAGETT SUCSPRIVTTVP200
NRRL_YB-4506/1-491	115 TVCSTGTN	VSAGETTSGCSPKTITTTVPCSTSPSETASESTTTSPTTPVTTVISTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVP248
NRRL_YB-2625/1-491	115 TVCSTGTN	\ S A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 248
YIIc17 E5/1-511	135 TVCSTGTN	SAGETT S G C S P KT I TT T V P C S T S P S F T A S F S T T T S P T T P V T T V V S T T V V T T F Y S T S T K P G G E I T T F V T K N I P T T Y I T T I A P T P S V T V T N F T P T I T T V C S T G T N S A G F T T S G C S P K T V T T V P 268
11W/0P583_7873/1_516	135 TVCSTCTN	A GETT S G S P KT I TT V P C ST S P S ET A S E S T T S P TT P V T V V S T V V T E Y S T S T K P G G E I T T F V T K N I P T Y I T I A P T P S V T V V N E T P T I T T V C S T C T N S A G E T S G C S P KT V T T V P 268
0007383-787.371-310	135 TVC5TGT	
NKKL_1-6297/1-491	115 1 V C S I G I N	SAGETTSGCSPRTTTTVPCSTSPSETASESTTSPTPVTVVSTTVVTTETSTSTRPGGETTTFVTRNIPTTTLTTAPTPSVTVTNFTPTTTTTVCSTGINSAGETTSGCSPRTVTTVP246
91-213/1-516	135 T V C S T G T N	NS A G ETT S G C S P KT I TTT V P C ST S P S ETA S E S TTT S P TT P V TT V V S TT V V TT E Y S T S T K P G G E I TTT F V TK N I P TTY L TT I A P T P S V TT V TN F T P TT I TT V C S T G T N S A G E TT S G C S P K T V TT T V P 268
NRRL Y-12603/1-491	115 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 248
\$288c/1=516	135 TVCSTCTN	SAGETTS CCSPKT TTTVPCSTSPSFTASFSTTTSPTTPVTTVVSTTVVTFYSTSTKPCCF TTTFVTKN PTTY TT APTPSVTTVTNFTPTT TTTVCSTCTNSACETTS CCSPKTVTTVP268
M22/1_F11	125 TVCSTCTA	
M22/1-311	133 TVC 3TGTF	a den sucsex intervent verses en second verses and the second verse and the second verse intervent verses and the second verses and
YPS128/1-480	104 IVCSIGIN	NSAGETTSGCSPKTTTTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGETTTTFVTKNTPTTYLTTTAPTPSVTTVTNFTPTTTTTTVCSTGTNSAGETTSGCSPKTVTTTVP237
96-101/1-511	135 T V C S T G T N	NS A G ETT S G C S P KT I TTT V P C ST S P S ET A S E S TTT S P TTP V TT V V S TT V V TT EY S T S T K P G G E I TTT F V T K N I P TT Y L TT I A P T P S V TT V T N F T P TT I TT T V C S T G T N S A G E TT S G C S P K T V TT V P 268
L-1528/1-472	99	IS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 224
SK1/1_401	115 TVCSTCTN	A CETTS CCSPKT I TTY PCSTSPSETASESTTS PTTPVTTVVSTVVTEVSTSKPCCE I TTEVTKN I PTTV I TT I APTPSVTVV NETPTT I TTVCSTCTNSACETTS CCSPKTVTTVP 248
K11/1 401	115 TVCSTCT	CACETY CCCENT ITTUD CTC SECTATES TTTO TTUTT VITE STATES CCCENT TO TTUTT AND SUTTUTNETS TO TTUT CCCENT TO TTUTT AND SUTTUTNETS TO TTUTT CCCENT TTUTT AND SUTTUTNETS TO TTUTNETS TO TTUTNETS ACCENT SUTTUTNETS ACCEN
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UWOP505-217.3/1-472	99	-SAGETTSGCSPKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVP224
NCYC361/1-425	49 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 182
DBVPC6765/1-467	91 TVCSTGTN	SAGETTS GC SP KT I TTTVPC ST SP S FTA S F STTT SP TTP V TTVV STTVV TFY ST STKP GG F I TTT F V TK N I P TTY I TA I AP TP S V TTV TN FTP TT I TTTVC ST GT N S AG F TT S GC S P KTV TT V P 224
DRVPC6040/1_467	91 TVCSTCTN	A CETTS CCSPKT I TTY PCSTSPSETASESTTS PTTPVTTVVSTTVVTEVSTCKPCCE I TTEVTKN I PTTV I TT I APTPSVTVV NETPTT I TTVCSTCTNSACETTS CCSPKTVTTVP 24
00040/1-407	31 1 1 2 3 1 6 1 6	
DBVPG1853/1-511	135 1 V C S I G I N	BAGETTSGCSPRTTTTTVPCSTSPSETASESTTSPTPVTVVSTTVVTTEFSTSTRPGGETTTFVTRNIPTTFLTTAPTPSVTVTNFTPTTTTTVCSTGINSAGETTSGCSPRTVTTTVP28
CBS_7833/1-491	115 TVCSTGTN	NSAGE115GC5PK11111VPC515P5ETASE51115P11PV11VV511VV11EY5151KPGGE1111FV1KN1P11YL111AP1P5V11V1NF1P111111VC51G1N5AGE115GC5PK1V111VP248
96-109/1-511	135 TVCSTGTN	VS A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T S P T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 268
YPS606/1-480	104 TVCSTGTN	SAGETTSGCSPKTITTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTFYSTSTKPGGEITTTEVTKNIPTTYITTIAPTPSVTTVTNFTPTTITTVCSTGTNSAGETTSGCSPKTVTTVP237
1-1274/1-467	01 TVCSTCTA	A CETTS CCS PKT I TTY PCSTS PSETASESTTTS PTTPVTTVVSTTVVTEVSTS KPCCE I TTEVTVNI PTTVI TTI A PTP SVTVTNETPTT I TTVCSTCTNSACETTS CCS PKTVTTVP 2/4
L-1374/1-407	31 1 V C S T G T A	
Y12/1-491	115 1 V C S I G I N	SAGETTSGCSPRTTTTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTRPGGETTTTPVTRNIPTTYLTTAPTPSVTTVTNFTPTTTTTTVCSTGTNSAGETTSGCSPRTVTTTVP248
YS2/1-491	115 TVCSTGTN	NSAGETTSGCSPKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVP248
NCYC110/1-511	135 TVCSTGTN	NS A G ETT S G C S P KT I TTT V P C S T S P S ETA S E S TTT S P TT P V TT V V S TT V V TT EY S T S T K P G G E I TTT F V TK N I P TTY L TT I A P T P S V TT V TN F T P TT I TT V C S T G T N S A G ETT S G C S P K T V TT V P 268
DRVPC1106/1-491	115 TVCSTCTN	SACETTS CCSPKT I TTTVPCSTSPSETASESTTTS PTTPVTTVVSTTVVTTEYSTSTKPCCE I TTTEVTKN I PTTY I TT I APTPSVTTVTNETPTT I TTTVCSTCTNSACETTS CCSPKTVTTVP 248
378604V/1 435	40 TVCSTCT	
3780044/1-423	49 1 0 C 3 1 G 1 6	a de la sucse ki i la vecto de la sesta sesta se si la se
YP5681/1-480	104 IVCSIGTN	NDAGETTSUCSPRTTTTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTRPGGETTTFVTKNTPTTYLTTTAPTPSVTTVTNFTPTTTTTVCSTGTNSAGETTSGCSPKTVTTTVP237
YPS615/1-472	99	-ISAGETT SGC SP KT I TTTVP C ST SP S ETA S E STTT SP TTP V TTV V STTVV TT EY ST ST KP GG E I TTT FV TKN I P TTY L TT I AP TP S V TTV TN FT P TT I TTT V C ST G TN SAG E TT SGC SP KT V TTT V P 224
YPS617/1-472	99	IS A GETT S G C S P KT I TTT V P C S T S P S E TA S E S T TT S P T P V T T V V S T T V V T T E Y S T S T K P G G E I T T F V T K N I P T T Y L T T I A P T P S V T V T N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T T V P 224
YPS661/1-472	99	SAGETTSGCSPKTITTVPCSTSPSETASESTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTFVTKNIPTTYITTIAPTPSVTTVNFTPTTITTVCSTGTNSAGETTSGCSPKTVTTVP224
VPS670/1_401	115 TVCSTCT	A A CETTS C S D V T I TT V D C S T S D C ETA S E S TT V V T T V V S T V V T E V S T S T V D C S T T V V T T V D S T S D C E TA S C S D V T V V V T S V S T V V S T V S T V S
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UWOPS3-461.4/1-388	15	- ISAGETT SGCSPKT I TTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGE I TTTFVTKN I PTTYLTTI APTPSVTTVTNFTPTT I TTTVCSTGTNSAGETTSGCSPKTVTTTVP140
Y55/1-491	115 TVCSTGTN	\ S A G E T T S G C S P K T I T T T V P C S T S P S E T A S E S T T T P V T T V V S T T V V T T E Y S T S T K P G G E I T T T F V T K N I P T T Y L T T I A P T P S V T T V N F T P T I T T V C S T G T N S A G E T T S G C S P K T V T T V P 248
YS4/1-426	50 TVCSTGTN	A SAGETT SGC SP KT I TTTVP CST SP SETA SE STTT SP TTP VTTVV STTVVTTEY ST ST KP GGE I TTT FVTK N I P TTY L TT I AP TP SVTTV N FTP TT I TTTVC STGTN SAG FTT SGC SP KTVTTTVP 183
DBVPC1788/1_511	135 TVCSTCTN	A A G F T S G C S P K T I T T V P C S T S P S F T A S F S T T S P T T P V T T V V S T C V V T T F Y S T S T K P G G F I T T F V T K N I P T V I T T I A P T P S V T V T V P S T S C S C V T V T T V P S S S S S S S S S S S S S S S S S S
DRVDC6044/1_401	115 TVCSTCT	$u_{a} = v_{a} = v_{a$
DBVPGB044/1-491	110 TVCSTGIN	NDAUET 13 U.S.R.T.T.T.T.V.R.S.S.F.T.S.F.T.T.V.T.V.S.T.V.T.T.V.S.T.V.T.T.T.T.T.T
Y9/1-486	110 IVCSTGTN	NDAGETTSGCSPKTTTTVPCSTSPSETASESTTTSPTPVTTVVSTTVVTTEYSTSTKPGGETTTFVTKNIPTTYLTTTAPTPSVTTVTNFTPTTTTTVCSTGTNSAGETTSGCSPKTVTTTVP243
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	23232322	δ-++++++++++++++++++++++++++++++++



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S288c_1/1-516 YJM224/1-491 YIM211/1-486	269 C ST G T G E Y T E A T T L V T T A V T T V V T T E S ST G T N S A G K T T G Y T K S V P T T Y V T T L AP S AP V T P A T NA V P T T I T T T E C S AA T NA AG E T T S V C S AKT I V S S A S AG E NT AP V T T A I P T T V I T E S S V G T N S A' S A O Y T P A T S AV P T T I T T T E C S AA T NA AG E T T S V C S AKT I V S S A S AG E N T AP V T T A I P T T V I T E S S V G T N S A' S A O Y T P A T S AV P T T I T T T E C S AA T NA AG E T T S V C S AKT I V S S A S AG E N T AP V T T A I P T T V T T E S S V G T N S A' S A O Y T P A T S AV P T T I T T T E C S AA T NA AG E T T S V C S AKT I V S S A S AG E N T T P V T T A I P T T V T T E S S V G T N S A' S A O Y T P A T S AV P T T I T T E C S AA T NA AG E T T S V C S AKT I V S S AS AG E N T T P V T T A I P T T V T T E S S V G T N S A' S AO Y T P A T S AV P T T T T T E C S AA T NA AG E T T S V C S AKT I V S S AS AG E N T T P V T T A I P T T V T T E S S V G T N S A' S AO Y T P A T S AV P T T T T T E C S AA T NA AG E T T S V C S AKT I V S S AS AG E N T T P V T T A I P T T V T T E S S V G T N S A' S AO Y T P A T S AV P T T T T T T T T C S AA T NA AG E T T S V C S AKT I V S S AS AG E N T T P V T T A I P T T V T T E S V C T N S A' T D V T T E S S V G T N S A' T D V T T A I P T T V T T E S V G T N S A' S AO Y T A I P T T V T T E S Y G T N S A' T D V T T E S S V G T N S A' S AO Y T A I P T T V T T E S Y G T N S A' S AO Y T A I P T T V T T I D S AO Y T D Y T A I P T T V T T I D S AO Y T D Y T A I P T T V T T I D S AO Y T A I P T T V T T I D S AO Y T A I P T T V T T I D S AO Y T A' I P T T V T T I D S AO Y T A' I P T T A I P T T V T T I D S AO Y T A I P T T Y T A I P T T V T T I D S AO Y T A' I P T T A I P T T V T T I D S AO Y T A' I P T T Y T A I P T T A I P T T V T T I D S AO Y T A' I P T T A' I P T T Y T A' I P T T Y T A I P T T Y T A I P T T Y T A I P T T Y T A I P T T Y T A I P T T Y T A I P T T Y T A I P T T Y T A' I P T T Y T A' I P T T A I P T T Y T A I P T T Y T A I P T T Y T A I P T T Y T A' I P T T A' I P T T Y T A I P T T A I P T
CBS2910/1-511	249 CSTGTGEVTT EATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTVVTLAPSAPVTPATNAIPTTITTECSAATMAAGETTSVCSAKTIVSSASAGENTPVTTAIPTTVVTTESSVGTNS397
CBS1227/1-511 CBS7838/1-447	269 C ST G G E V T E A T P V T A V T T V V T E S ST G T N S A C KT T G V T T K S V P T Y V T T L A P S A P V T P A T NA I P T T I T T T E C S A A T NA A G E T T S V C S A KT I V S S A S G E N T T P V T A I P T T V V T T E S S V G T N S 30 ? 205 C ST G G E V T F A T P V T A V T T V V T F S S T G T N S A C F T T S V T T A Y T D Y T A V T T V V T F S S T C T N S A C F T S V C S A KT I V S S A S G E N T T P V T A I P T T V V T T E S S V G T N S 33 ?
CB57836/1-447	205 C 5 T G T G E Y T E A T P V T A V T T V V T T E S S T G T N S A G E T T G Y T K S V P T T Y V T L A P S A P V T P A T N A V P T T I T T T E C S A A T N A A G E T T S V C S A K T I V S S A S A G E N T T P V T T A I P T T V V T E S S V G T N S 333
92-123/1-491 YIM436/1-511	249 C ST GT GE VTT E ATT P V TT A V TT T V V TT E S ST GT N S A GET T T G V TT K S V P TT V V T T L AP SA P V T P A T NA V P T T I T T T E C SA A T NA A G E T T S V C SA K T I V S SA SA GEN T T P V T T A I P T T V V T T E S S V G T N S 37 269 C ST GT GE V T T A T T T V V T T T S ST GT N S A GET T G V T T K S V P T T V V T T I AP SA P V T P A T NA I P T I T T T F C SA A T NA A G E T T S V C SA K T I V S SA SA GEN T T P V T T A I P T T V V T T E S S V G T N S 37
89-156/1-472	225 CSTGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSAGKTTTGYTTKSVPTTYVTTLAP SAP VTPATNAVPTTITTTECSAATNAAGETTSVCSAKTIVSSASAGENTAP SATTPVTTAIPTTVVTTESSVGTNS358
YJM455/1-467 YIM522/1-447	225 C STGTGEYTTEATTP VTTAVTTTVVTTESSTGTNSAGETTTGVTTK SVP TTVVTTLAP SAP VTP AT NA IP TTI TTTECSAATNAAGETTSVCSAKTI VS SASAGENTTP VTTA IP TTVVTTESSVGTNS 333 205 C STGTGEYTTEATTP VTTAVTTTVVTTESSTGTNSAGETTTGVTTK SVP TTVVTTI AP SAP VTP AT SAVP TT ITTTECSAATNAAGETTSVCSAKTI VS SASAGENTTP VTTA IP TTVVTTESSTGTS33
YJM521/1-447	205 C 5 T G T G E Y T E A T P V T A V T T V V T T E S S T G T N S A G E T T G Y T K S V P T T Y V T T L A P S A P V T P A T S A V P T T I T T T E C S A A T N A A G E T T S V C S A K T I V S S A S A G E N T T P V T T A I P T T V V T E S S V G T N S 333
YJM523/1-491 R91-48/1-512	249 C ST GT GEVTT E ATT P V T A V T T T V V T E S ST GT N SA GETT T G V T T K S V P T T V V T L AP SA P V T P AT SA V P T T T T T E C SA A T MA A G ETT S V C SA KT I V S SA SA GE C T P V T T A I P T T V V T T E S ST G T N SA GETT S V C SA KT I V S SA SA SA C M SA ST T V T T N V T T E S T G T N SA GETT S V C T N SA V P T T V T T E S T G T N SA GETT S V C SA KT I V S SA SA SA SA SA ST T S V C SA KT I V S SA SA SA SA ST T S V C SA KT I V S SA S
96-98/1-511	269 C S T G T G T D V T A V T T V V T T S S T G T N S A G K T T G V T K S V P T T V T T L A P S A P V T P A T NA I P T T I T T T C S A A T N A A G E T S V C S A K T I V S S A S A G E N T P V T A I P T T V V T E S S V G T N S 397
R93-1017/1-491 96-100/1-511	249 CSIGIGEYTIEATIPVITAVITIVVITESSIGINSAGETIGYTIKSVPITYVITLAPSAPVIPATSVPITTITTECSAATMAAGETISVCSAKTIVSSASAGENTIPVITAIPTIVVITESSVGINS3/7 269 CSIGGEYTIEATIPVITAVITTVVITESSIGINSAGETIGYTIKSVPITYVITLAPSAPVIPATNAIPTITTITTECSAATMAAGETISVCSAKTIVSSASAGENTIPVITAIPTIVVITESSVGINS3/7
NRRL_YB-4348/1-511	269 C ST GT GEVIT EATTP VTT AVTTT VVTT ESST GT NS AGKTTT GYTT KSVPTT VVTT LAP SAP VTP AT NA I PTT I TTT ECSAAT NA AG ETT SVC SAKT I VS SASAGEN TTP VTT A I PTT VVTT ESS VGT NS 397
NRRL_Y-10_988/1-491 NCMH_125/1-511	249 CSIGIGEVITEATIPVITAVITIVVITESSIGINSAGETIGTIKSVPITYVILLAPSAPVIPATSAVPITTIECSAATMAAGETISVCSAKTIVSSASAGENTIPVITAIPTIVVITESSVGINS3/7
MMRL_125/1-479	237 C ST G T G E V T E A T T P V T A V T T V V T E S S T G T N S A G E T T G V T T K S V P T T V T T L A P S A P V T P A T S V V P T T I T T E C S A A T N A A G E T S V C S A K T I V S S A S A G E N T P V T A I P T T V V T E S S V G T N S 365
YJM1115/1-491 YJM1119/1-491	249 CSTGTGEYTTEATTPVTTAVTTVVTTESSTGTNSAGETTGYTTKSVPTTVVTLAPSAPVTPATSVPTTTTTTECSAATMAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS377
NRRL_Y-1546/1-491	249 CST GT GEVTT EATTP VTT AVTT VVTT ESST GT NSAGETT TG VTT KSVP TT VVTT LAP SAP VTP AT NA VP TT I TT TE CSAAT NA AGETT SV CSAKT I VS SASAGEN TTP VTT A I PTT VVTT ESS VGT NS 377
Sigma1278b/1-447	225 CSTGTGEVTTEATTPVTTAVTTVVTTESSTGTNSAGETTTGVTTKSVPTTVVTLAPSAPVTPATSAVPTTTTTECSAATMAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS333
NRRL_Y-961/1-447	205 C ST G T G E Y T E A T T P V T A V T T V V T E S ST G T N SA G E T T G V T T K SV P T T V V T L A P SA P V T P A T SA V P T I T T T E C SA A T NA A G E T T S V C SA K T I V S SA SA G E N T T P V T A I P T T V V T E S S V G T N S 33 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5
NRRL_Y-963/1-511	249 CSTGTGEVTTEATTPVTTAVTTTVVTTESSTGTNSAGETTGYTTKSVPTTVVTLAPSAPVTPATNAIPTTITTECSAATMAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS397
NRRL_Y-12638/1-464	223 C ST G T G E YT E G T F P VT A V T T V V T E S ST G T N SA G K T T G V T T K S V P T I V YT T L AP SA P A T P A T NA V P T I I T T E C SA A T NA A G E T T S V C SA K T I V S SA SA G E N T T P I T T A I P T T V YT T E S S V C T N S 35 37 30 37 37 37 37 37 37 37 37 37 37 37 37 37
NRRL_Y=17447/1=491	249 CSTGTGEVTT EATTP VTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTYVTLAP SAPVTP AT SAVPTTITTECSAATMAAGETTSVCSAKTIVSSASAGENTTP VTTAIPTTVVTTESSVGTNS377
NRRL_YB-908/1-472	225 C ST G T G E YT T E A T A P V T A V T T V V T E S ST G T N S A G K T T G V T K S V P T Y V T T L A P S A P V T P A T NA V P T T I T I T E C S A A T N A G E T T S V C S A K T I V S G S S G E NT A P S A T T P V T A I P T T V V T E S S V C N S 375 240 C ST C E V T E A T D V T T A V T T V V T E S ST C T N S A C E T T C V T K S V P T Y V T I L A P S A V Y P A T NA V D T I T T I C S C A A T NA G E T T S V C S A K T I V S S S S A C E N
NRRL_Y-268/1-511	269 CSTGTGEVTTEATTPVTTAVTTTVVTTESSTGTNSAGKTTTGYTTKSVPTTYVTTLAPSAPVTPATNAIPTTITTECSAATNAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS397
NRRL_YB-2541/1-511 NRRL_YB-4506/1-491	269 C ST G T G F YT T E AT T P V T A V T T V V T E S ST G T N S A C KT T G YT T K S V P T T V V T T L A P S A P V T P A T NA I P T T I T T T E C S A A T NA A G E T T S V C S A KT I V S S A S G E N T T P V T T A I P T T V V T T E S S V G T N S 37 249 C ST G G F YT T F A T P V T T A V T T V V T T F S T G T N S A C KT T G V T K S V P T T V V T T F S T G T N S A C F T S V C S A KT I V S S A S G E N T T P V T T A I P T T V T T E S V G T N S 37
NRRL_YB-2625/1-491	249 CSTGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTYVTTLAP SAP VTPATSAVPTTITTTECSAATNAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS377
Yllc17_E5/1-511 UWOP\$83-787.3/1-516	269 C ST GT GE VTT E ATT P V TT A V TT T V V T E S ST GT N SA GKT T C Y T TK S V P T T V V T L AP SA P V T P A T NA I P T T I T T T E C SA A T NA A G E T T S V C SA KT I V S SA SA GE N T P V T T A I P T T V V T T E S V GT N S 397 269 C ST GT GE V T T A T T P V T T A V T T V V T T F S T G T N A GKT T G V T K S V P T T V V T T I P ST P V T T A I P T T V V T F S ST G T N SA GKT T G V T K S V P T Y V T I AP SA P V P A T NA V P T T V T T F S SA T NA A G E T T S V C SA KT I V S SA SA GE N T A ST T V V T T F S ST G T N A GKT T G V T K S V P T Y V T I AP SA P V P A T NA V P T M T T F C SA A T NA A G E T T S V C SA KT I N S SA SA GE N T A ST T V V T T I S SA V S SA SA GE N T A ST T V V T T I S SA V S SA S
NRRL_Y-6297/1-491	249 CSTGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTYVTTLAPSAPVTPATNAVPTTITTTECSAATNAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS377
91–213/1–516 NRRL Y–12603/1–491	269 C ST GT GE YT T E ATT L V T T A V T T T V V T T E S ST GT N S AG KT T C YT T K S V P T T V T T L AP SA P V T P A T NA V P T T I T T T C S AA T NA AG E T T S V C S AKT I V S S AS AG E NT AP SAT T P V T T A I P T T V I T T E S S V G T N S 402 249 C ST G C E YT T E ATT P V T T A V T T T V V T T E S ST G T N S AG E T T T G V T T K S V P T T V T T I AP SA P V T P A T NA V P T I T T T E C S AA T NA AG E T T S V C S AKT I V S S AS AG E N T T P V T T A I P T T V T T E S T G T N S AG E T T S V C S AKT I N S S AS AG E N T T T V T T I S T T V T T E S T G T N S AG E T T S V C S AKT I N S S AS AG E N T AP S T T V T T E S T G T N S AG E N T S O T N S AG E N T S O T N S AG E N T S O T N S AG E N T S O T N S AG E N T S O T N S O
S288c/1-516	269 C ST G T G T T L VT T A VT T V VT T E ST G T N S A G K T T G VT K S V P T T V VT L AP S A P VT P A T NA VP T T I T T T C S A A T NA A G E T S V C S A K T I V S S A S A G E N T A P VT A I P T V I T E S S V G T N S 402
M22/1-511 YPS128/1-480	269 CSIGIGEYTIEATIPVITAVITIVVITESSIGINSAGKTIGYTIKSVPITYVILAPSAPVIPATNAIPTITITIECSAATNAAGETISVCSAKTIVSSASAGENTTPVITAIPTIVVITESSVGINS399 238 CSIGGEYTIEATTPVITAVITTVVITESSIGINSAGETIGVITKSVPITYVTILAPSAPVIPATNAVPTITITIECSAATNAAGETISVCSAKTIVSSASAGEN
96-101/1-511	269 C 5 T G T G E V T F A T T P V T A V T T V V T E S S T G T N S A G K T T G V T K S V P T T V V T L A P S A P V T P A T NA I P T T I T T E C S A A T N A A G E T S V C S A K T I V S S A S A G E N T P V T A I P T T V V T E S S V G T N S 397
L=1528/1=472 SK1/1=491	229 CSTGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTVVTLAPSAPVTPATNAVPTTTTTECSAATMAAGETTSVCSAKTIVSSASAGENTVTTAIPTTVVTTESSVGTNS377
K11/1-491	249 C ST G T G E V T E A T T P V T T A V T T V V T E S S T G T N S A C E T T G V T T K S V P T T V V T L A P S A P V T P A T S A V P T T I T T E C S A A T N A A G E T T S V C S A K T I V S S A S A G E N T T P V T A I P T T V V T E S S V G T N S 37 246 C C T C E V T E A T N V T T V V T E S T C T N S A V T T C V T T N S A P V T P A T N A V D T V T A T N A V T N S A S A C E N T S A V T N S A S A C E N T S A V T N S A S A S A T N A G E T T S V C S A K T I V S S A S A C E N T A V T T V T T E S V G T N S 37 256 C C T C E V T E A T N V T T V V T E S T C T N S A V T T C V T T N S A V T N T N A T N A V T N V T S S A C E N T S A V T N S A S A S A T N A G E T T S V C S A K T I V S S A S A C E N T S A V T N S A S A S A T N A S A V T N S A S A S A T N A S A V T N S A S A S A T N A S A V T N A T N A V T N Y T N S A S A S A C E N T S A V T N S A S A S A C E N T S A S A S A S A S A S A S A S A S A S
NCYC361/1-425	223 CSTGTGEVTTEATTPVTTAVTTTVVTTESSTGTNSAGKTTGYTTKSVPTTVVTLAPSAPVTPATNAIPTTITTECSAATMAAGETTSVCSAKTIVSSASAGENTPVTTAIPTTVVTTESSVGTNS311
DBVPG6765/1-467	225 C STGTGEYTTEATTPYTTAVTTTVVTTESSTGTNSACKTTGHTTKSVPTTYVTTLAPSAPVTPATNAIPTTITTTECSAATNAAGETTSVCSAKTIVSSASACENTTPVTIAIPTTVVTTESSVCTNS353 235 C STGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSACETTTCVTTESSVCTNS353
DBVPG1853/1-511	269 CSTGTGEVTT EATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTYVTTLAPSAPVTPATNAIPTTITTECSAATMAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS397
CBS_7833/1-491	249 C STGTGEYTTEATTP VTTAVTTTVVTTESSTGTNSACETTTGVTK SVP TTYVTTLAP SAP VTP AT SAVP TT I TTTECSAATNAAGETTSVCSAKTI VSSASAGENTTP VTTAI P TTVVTTESSVGTNS 37 DGG C STGTGEYTTEATTP VTTAVTTTVVTTESSTGTNSACETTTGVTK SVP TTVVTTI AP SAP VTP ATNAI D TTI VTTESSACANAGETTSVCSAKTI VSSASAGENTTP VTTAI P TTVVTTESSVGTNS 307
YPS606/1-480	238 CSTGTGEVTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTYVTTLAPSAPVTPATNAVPTTITTTECSAATNAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS366
L-1374/1-467 ¥12/1-491	225 C 5 T G T G E V T E A T I V V T T V V T E S 5 T G T N S A G KT T G V T T K S V P T T V V T L A P S A P V T P A T NA I P T I T T T E C S A A T NA A G E T T S V C S A K I I V S S A S G E N T T P V T A I P T T V V T T E S S V G T N S 37 24 G C 5 T G E V T F A T P V T T A V T T V V T F S 5 T G T N S A G F T T G V T T K S V P T T V V T T E S S V G N S 37
Y52/1-491	249 CSTGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTYVTTLAPSAPVTPATSAVPTTITTTECSAATNAAGETTSVCSAKTIVSSASAGENTTPVTTAIPTTVVTTESSVGTNS377
NCYC110/1-511 DBVPG1106/1-491	269 C ST G T G E Y T E A T I P V T A V T T V V T E S ST G T N S A G K T T C Y T T K S V P T T V V T L A P S A P V T P A T NA I P T T I T T T E C S A A T NA A G E T T S V C S A K T I V S S A S A G E N T T P V T T A I P T T V V T T E S S V G T N S 37 249 C ST G C E Y T E A T P V T T A V T T V V T E S ST G T N S A G E T T G V T T K S V P T T Y V T I L A P S A P V T P A T S A V P T T I T T T E C S A A T NA A G E T T S V C S A K T I V S S A S A G E N T T P V T T A I P T T V V T T E S S T G T N S A G E T T G V T T K S V P T T Y T T L A P S A P V T P A T S A V P T T T T T E C S A A T NA A G E T T S V C S A K T I V S S A S A G E N T T P V T T A I P T T V T T E S T G T N S A G E N T T P V T T A I P T T V T T E S T G T N S A G E N T T P V T A I P T T V T T E S T G T N S A G E N T T P V T T A I P T T V T T E S T G T N S A G E N T T P V T A I P T I V T T E S T G T N S A G E N T T P V T A I P T I V T T E S T G T N S A G E N T T P V T A I P T I V T T E S T G T N S A G E N T T P V T A I P T I V T T E S T G T N S A G E N T T P V T A I P T I V T T E S T G N S A G E N T T P V T A I P T I V T T E S T G N S A G E N T T P V T A I P T I V T T E S T G N S A G E N T T P V T A I P T I V T T E S T G N S A G E N T T P V T A I P T I V T T E S T G N S A G E N
378604X/1-425	183 C S T G T G E Y T F A T T P V T A V T T V V T E S S T G T N S A G K T T G Y T K S V P T T Y V T L A P S A P V T P A T NA I P T T I T T T E C S A A T NA A G E T S V C S A K I V S S A S G E N T P V T A I P T T V V T E S S V G T N S 31 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
YPS681/1-480 YPS615/1-472	238 CSIGIGEYTIEATIPVITAVITIVVITESSIGINSAGETIGYTIKSVPITYVILAPSAPVIPATNAVPITITIECSAATNAAGETISVCSAKTIVSSASAGENTIPVITAIPTIVVITESSUGNS366 225 CSIGGEYTIEATIPVITAVITIVVITESSIGINSAGETIGYTIKSVPITYVTILAPSAPVIPATNAVPITITITECSAATNAAGETISVCSAKTIVSSASAGENTAPSATIPVITAIPTIVVITESSUGNS358
YPS617/1-472	225 CSTGTGEVITEATTPVTTAVTTVVTTESSTGTNSAGKTTTGVTTKSVPTTVVTTLAPSAPVTPATNAVPTTITTECSAATNAAGETTSVCSAKTIVSSASAGENTAPSATTPVTTAIPTTVVTTESSVGTNS358
YPS661/1-472 YPS670/1-491	229 CSTGTGEYTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTVVTLAPSAPVTPATNAVPTTTTTTECSAATMAAGETTSVCSAKTIVSSASAGENTVTTAIPTTVVTTESSVGTNS377
YPS630/1-491	249 CSTGTGEYTTEATTPYTTAVTTTVVTTESSTGTNSACETTTGYTTKSVPTTYVTTLAPSAPVTPATNAVPTTITTTECSAATNAAGETTSVCSAKTIVSSASSACENTTPVTTAIPTTVVTTESSVGTNS377
Y55/1-491	249 CSTGTGEVTTEATTPVTTAVTTTVVTTESSTGTNSAGETTTGYTTKSVPTTTVTTLAPSAPVTPATNAVPTTTTTECSAATMAAGETTSVCSAKTIVSSASAGENTPVTTAIPTTVVTTESSVGTNS377
YS4/1-426	184 C ST G T G E Y T F A T T P V T T A V T T V V T T E S ST G T N S A G E T T G Y T T K S V P T T Y V T T L A P S A P V T P A T S A V P T T I T T T E C S A A T N A A G E T S V C S A K T I V S S A S A G E N T T P V T T A I P T T V V T E S S V G T N S 3 12 269 C S T G T G E Y T F A T T P V T T A V T T V V T E S S T G T N S A G E T T G Y T A V T T A V T T Y V T T E S S V G T N S 3 12
DBVPG6044/1-491	249 C S T G T G T T A V T A V T T V T T E S S T G T N S A G E T T G Y T N S V T T Y T T L A F S A F V T A T NA T T T T T T E C S A A T NA A G E T S Y C S A KT I Y S A S A G E N T T P Y T A I P T T Y Y T E S S Y G T N S 39 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
Y9/1-486	244 C STGTGEYTTEATTP VTTAVTTTVVTTE S STGTN SAGETTTGYTTK SVP TTYVTT LAP SAP VTP AT SAVP TT I TTTEC SAAT NAAGETT SVC SAKT I V S SA SAGEN TTP VTTA I P TTVVTTE S SVGTN S 372
Conservation	

Consensus	

C S T G T G E Y T T E A T T P V T T A V T T V V T T E S S T G T T T G Y T T K S V P T T Y V T T L A P S A P V T P A T N A V P T T I T T T E C S A A T N A A G E T T S V C S A K T I V S S A S A G E N T A P S A T T P V T T A I P T T V V T E S S V G T N S

S288c_1/1-516	403 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSVAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVF
YJM224/1-491	378 A G ETTT GYTTK SI PTTY I TTL I P G S NGAK NY ETVATATNP I SI KTT SQLATTA SA SSMAP VVT SP SLTGP LQSA SG SAVATY SVP SI SSTYQGAAN I KVLGN FMVL	LLALPVVF
YJM311/1-486	3/3 A G E T T GY T K S I P T T Y I T T L I P G S NGAK NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MAP V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S I Y Q G A A N K V L G N F MWL	LLALPVVF
CBS2910/1-511	398 A GETTTGYTTKSIPTTYTTLTPGSNGAKNYETVATATNPISTKITSGLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSTSSTYQGAANKVLGNFMUL	LLALPVVF
CBS1227/1-511	396 AGETTTGVTTKSIDTTVTTLLIPGSNGAKNTEIVATATNDISIKITSQLATTASASSMAPVVTSPSLIGPLQSASGSAVATTSVPSTSSTTQGAANIKVLGNEMMU	
CB57838/1-447	334 AUGT TIKSTETTTVTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
CB3/830/1-44/	334 AGETTTEVTTEVITETTETTETTETTETTETTETTETTETTETTETTETSULATTASASSMAR VVISYSQLGEVQASQLGAVATTSVYSISSITQGAAN IN VLONEMMU 278 AGETTEVTTEVITETTETTEVITETTETCSULATVASTASTADISING SCANADVVIS SQLGEVASASULGAVATTSVSISSITQGAAN IN VLONEMMU	
92-125/1-491 VIM426/1-511	3/0 A GETTT CYTT K SI PTT VITTI I DE SNEAK NV ETVATATND I SI KIT SOLATTASA SIMAF VVI 3E SLIGE LOSAS GAVATI SVEJISTI SU ANANI KVI CNEMNI 302 A GETTT CYTT K SI PTT VITTI I DE SNEAK NV ETVATATND I SI KIT SOLATTASA SEMA DVI SE SLIGE LOSAS GAVATI SVEJISTI SU ANANI KVI CNEMNI	
1JM450/1-311 80-156/1-472	300 A GETTT CYTT KILDT VITTI I LLFGSNUARN Y ETVATATND I SI KITSOLATTASAS 3MAF VYTSFSLIGE LQSASU SAVATTSYFSI SI TQAAN I KVL CMFMWL 300 A GETTT CYTT KILD TVITTI LD CSNCARN V ETVATATND I SI KITSOLATTASAS 3MAF VYTSFSLIGE LQSASU SAVATTSYFSI SI TQ	
VIM455/1-467	354 AGETTTGYTTK SI PTTYITTI I FG SNGAK NY ETVATATNO I SI KITSOLATTASA SIMAD VY 57 SI GELOSA GSAVATY SV DSI STYOGAAN I KVI GNEMVI	
VIM522/1=447	344 GETTTGYTTK SI PTTY I TT I PG SNG & NY FTVATATNP I SI KTT SOLATTA SA SSMAP VVT SP SI TG PLO SA SG SAVATY SVP SI SSTYOGAAN I KVI GERWU	LLALPVVF
VIM521/1-447	344 GETTTGYTTK SI PTTY I TT I PG SNG & NY FTVATATNP I SI KTT SOLATTA SA SSMAP VVT SP SI TG PLO SA SG SAVATY SVP SI SSTYOGAAN I KVI GERWU	
YIM523/1-491	378 A GETTT GYTTK SIPTTY ITTI IPG SNGAKNYETVATATNPI SIKTTSOLATTA SA SSMAP VYTSP SI TGPI O SA SG SA VATY SVP SI SSTYOGAAN I KVI GNEMVI	LIALPVVF
R91-48/1-512	399 A G E T T G Y T K S I P T T Y I T T L I P G SNGAK NY ET VATAT NP I S I K T T SO LATTA SA SSVAP V V T SP S L T G P LO SA SG SA VAT Y SV P S I S ST Y O GAAN I K V L G N F MVL	LLALPVVF
96-98/1-511	398 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSOLATTASASSMAPVVTSPSLTGPLOSASGSAVATYSVPSISSTYOGAAN KVLGNFMWL	LLALPVVF
R93-1017/1-491	378 A G E T T G Y T T K S I P T T Y I T T L I P G S NG A K NY E T V A T A T N P I S I K T T S Q LA T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MWL	LLALPVVF
96-100/1-511	398 A G E T T G Y T T K S I P T T Y I T L I P G S N G A K NY E T V A T A T NP I S I K T T S Q L A T T A S A S S MAP V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MWL	LLALPVVF
NRRL_YB-4348/1-511	398 A G E T T G Y T T K S I P T T Y I T T L I P G S NGAK NY E T V A T A T NP I S I K T T SQ L A T T A S A S S MAP V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MW L	LLALPVVF
NRRL_Y-10_988/1-491	378 A G E T T G Y T T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVF
NCMH_125/1-511	398 A G E T T G Y T T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVF
MMRL_125/1-479	366 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVF
YJM1115/1-491	378 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVF
YJM1119/1-491	378 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MW L	LLALPVVF
NRRL_Y-1546/1-491	378 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T VA T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MW L	LLALPVVF
NRRL_Y-6679/1-467	354 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T VA T A T NP I S I K T T S Q L A T T A S G S S MAP V V T S P S L T G P V Q S A S G P A V A T Y S A P A I S S T Y Q G A A I K V L G N F MWL	LVALPIVI
Sigma1278b/1-447	334 AGETTTGYTTKSIPTTYITTLIPGSNCAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMUL	LLALPVVF
NKRL_Y-961/1-447	334 AGETTTUTTUSTTUSTTUSTUSTUSTUSTUSTUSTUSTUSTUS	LLALPVVF
YJM1101/1-491	3/8 AUEITI GYTIKSIPITYITTI POSNGAKNY ETVATATNPISIKITSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSI SSTYQGAANI KVLGN FMVL	LLALPVVF
NRRL_Y-963/1-511	398 AGETTTGYTTKSTPTTYTTTTTPGSNGAKNYETVATATNPTSTKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSTSSTYQGAANTKVLGNFMWL	LLALPVVF
NRRL_Y-12638/1-464	352 A GETTTGYTTKS I PTTYTTL I PGSNGAKNYETVATATNPI STKITSQL I TA SA SSMAP VVTSP SL GPLQS - SG SAVATY SVPST SS TYQGAAN KVLGNEMU	LLALPVVF
NRRL_YB-42//1-491	3/8 AGETTTGVTTKSIDTTVTTTLLFYGSNGAKNTETVATATNDISIKTSGLATTASASSMAP VVTSYSLIGFLGSASGSAVATTSYFSTSSTTGGAAN KVLGNFMUL 278 AGETTGVTTKSIDTVTTLLFGSNGAVVETVATATNDISIKTSGLATTASASSMAP VVTSYSLIGFLGSASGSAVATTSYFSTSSTTGGAAN KVLGNFMUL	
NRRL_Y-1/44//1-491	3/8 AGETTIGYTIKSIPTIYTTILIPGSNGAKNTEIVATATNDISIKITSQLATTASASSMAPVVISPSLIGPLQSASGSAVATTSYPSISSITQGAANIKVLGNEMUU 200 AGETTGYTTGVITTILIPGSNGAVVETVATATNDISIKITSQLATTASASSMAPVVISPSLIGPLQSASGSAVATTSYPSISSITQGAANIKVLGNEMUU	
NPPI VP_4081/1_401	337 A GETTT GYTT KSI PTTY I TTI I DE SNEAKNY ETVATATNO I SI KITSOLATTASAS SVAP VYTSESLI GELQSAS GSAVATI SVESTS STOGAAN I KVI CNEMMI 278 A GETTT GYTT KSI PTTY I TTI I DE SNEAKNY ETVATATNO I SI KITSOLATTASAS SVAP VYTSESLI GELQSAS GSAVATI SVESTS	
NRRI V-268/1-511		LLALPVVF
NRRI YR-2541/1-511	308 AGETTTGYTTK SI PTTY ITTI I PG SNGAK NY FTVATATNP I SI KTT SOLATTA SA SSMAP VVT SP SI TGP I O SA SG SA VATY SVP SI S STYOGAAN I KVI GYEMWI	LLALPVVF
NRRI YB-4506/1-491	378 A G F T T G Y T K S I P T Y I T T I I P G SNG AK NY F T V AT AT NP I S I K T T SO I AT T A SA SSMAP V V T SP S I T G P I O SA SG SA VAT Y SV P S I S ST Y O G A A I K V I G Y F WI	LIALPVVF
NRRL YB-2625/1-491	378 A G ETTT GYTTK SI PTTY I TT LI P G SNG AK NY ETVATATNPI SI KTTSOLATTA SA SSMAP VVT SP SLTGPLOSA SG SA VATY SVP SI SSTYOGAAN I KVLGN FMVL	LLALPVVF
YIIc17 E5/1-511	398 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAAN KVLGNFMWL	LLALPVVF
UWOPS83-787.3/1-516	403 A G E T T G Y T K S I P T T Y V T T L I P G S N G A K NY E T V A T A T NP I S I K T T S Q L A T T A S A S S MAP V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVV
NRRL_Y-6297/1-491	378 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T VA T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MW L	LLALPVVF
91-213/1-516	403 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSVAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVF
NRRL_Y-12603/1-491	378 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMVL	LLALPVVF
52886/1-516	403 A GETTTGYTTKS I PTTYTTL I PGSNGAKNYETVATATNPI STKITSQLATTASASSVAPVI SPSLIGPLQSASGSAVATYSVPSTSSTYQGAANKV LGNFMU	LLALPVVF
M22/1-511 VDS138/1_480	390 AGETTTEVTTEVITETTETTETTETTETTETTETTETTETTETTETSTETTSGLATTASASSMAR VVISYSLIGELQSASGSAVATTSVYSTSSTIGGAVALVULAUMMU 267 AGETTEVTTEVITETTETTEVITETTEGSAAVVEEVATATADELSIVETSGLATTASASSMAR VVISYSLIGELGSASGSAVATTSVYSTSSTIGGAVALVULAUMMU	
96-101/1-511	307 A GETTTGYTTK SI PTTY I TTI I PG SNGAKNI EI VATATNPI SI KTI SGI ATTA SA SGMAP VY SP SI GTGI GSA SGAVATY SV SI SI TGGANATY V GY SI TGGANATY V GY SI SI SI TGGANATY V GY SI SI SI TGGANATY V GY SI SI SI SI SI TGGANATY V GY SI S	
L = 1528/1 = 472	359 A G ETTTGYTTK SI PTTY I TT LIP G SNGAK NY ETVATATNPI SI KTT SOLATTA SA SSMAP VVT SP SI TGPI O SA SG SA VATY SVP SI S STYOGAAN I KVI GNEMVI	LLALPVVV
SK1/1-491	378 A G E T T G Y T T K S I P T T Y I T T L I P G S NG A K NY E T V A T A T N P I S I K T T S Q LAT T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MWL	LLALPVVF
K11/1-491	378 A G E T T G Y T T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVF
UWOPS05-217.3/1-472	359 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T NP I S I K T T S Q L A T T A S A S S MAP V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVV
NCYC361/1-425	312 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVF
DBVPG6765/1-467	354 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T VA T A T N P I S I K T T S Q L A T T A S A S SMAP V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MWL	LLALPVVF
DBVPG6040/1-467	354 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T VA T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MWL	LLALPVVF
DBVPG1853/1-511	398 AGETTTGYTTK SIPTTY ITTLIPG SNGAKNY ETVATATNP I SIKTT SQLATTA SA S SMAP VVT SP SLTGP LQ SA SG SAVATY SVP SI S STYQGAAN I KVLGN FMWL	LLALPVVF
CBS_7833/1-491	378 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVF
96-109/1-511	398 AGETTTGYTTKSIPTTYITTLIPGSNCAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMUL	LLALPVVF
YPS606/1-480	367 A GETTT GYTT KSTPTTYTT LTP GSNCAKNYET VATA TNP IST KTT SQLATTA SA SSMAP VVT SP SETGPLQSA SG SA VATY SVP ST SSTYQGAAN I KVL CNFMWL	LLALPVVF
L=13/4/1-46/	334 AGETTTGGTTKS IPTTYTTTLIPGSNGARNTETVATATNPTSKTTSQLATASAS MAPYVTSPSLTGPLQSASGSAVATTSVPSTSGTTQGAANIKVLGNPMVL	LLALPVVF
Y12/1-491 Y52/1-401	J/0 AGETTTEVTTEVITETTETTETTETTETTETVATANNETVATANNETSINITSQLATTASASSMAP VVISYSLIGELQSASGSAVATTSVYSISSITQGAANINVLONEMUL 270 AGETTEVTTEVITETTETTEVITETTEDESNAAVVEEVATANNETSINITSQLATTASASSMAP VVISYSLIGELQSASGSAVATTSVYSISSITQGAANINVLONEMUL	
NCVC110/1_511	3/0 A GETTT CYTT SI DT TY ITT I LEF GSNUARN TE EVALATIN DISINT SOLATIASA SIMAF VYTSF SELGE LQSAS GSAVATT SYTST ST TQAAN I KVE GUNFMWE 308 A GETTT CYTT SI DT TY ITT I LE CSNCAR VY ETVATATND I SI KTT SOLATTASAS SIMAF VYTSF SELGE LQSAS GSAVATT SYTST	
DRVPC1106/1-491	378 AGETTTGYTTK SI PTTYITTI I FG SNGAK NY ETVATATNO I SI KITSOLATTASA SIMAD VY SP SI TGP I O SA SGAVATY SV PSI STYOGAAN I KVI GHEMWI	
378604X/1=425	312 AGETTTGYTTK SI PTTY I TT I PG SNGAK NY FTVATATNP I SI KTT SOLATTA SA SSMAP VVT SP SI TGP I O SA SG SAVATY SVP SI SSTYOGAAN I KVI GPENWI	LLALPVVF
YPS681/1-480	367 A G F T T G Y T K S I P T Y I T T I I P G SNG AK NY F T V AT AT NP I S I K T T SO I AT T A SA SSMAP V V T SP S I T G P I O SA SG SA VAT Y SV P S I S ST Y O G A A I K V I G Y F WI	LIALPVVF
YPS615/1-472	359 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K N Y E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MWL	LLALPVVV
YPS617/1-472	359 A G E T T G Y T T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A N I K V L G N F MW L	LLALPVVV
YPS661/1-472	359 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T VA T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MW L	LLALPVVV
YPS670/1-491	378 A G E T T G Y T K S I P T T Y I T T L I P G S N G A K NY E T V A T A T N P I S I K T T S Q L A T T A S A S S MA P V V T S P S L T G P L Q S A S G S A V A T Y S V P S I S S T Y Q G A A I K V L G N F MW L	LLALPVVF
YPS630/1-491	378 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVF
UWOPS3-461.4/1-388	275 AGETTTGYTTKSIPTTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNFMWL	LLALPVVV
Y55/1-491	3/8 AGEIIIIGYIIKSIPIIYIIIIPGSNGAKNYETVATATNPISIKTTSQLATTASASSMAPVVTSPSLTGPLQSASGSAVATYSVPSISSTYQGAANIKVLGNEMUL	LLALPVVF
Y54/1-426	513 AUETTT GVTT KSTPTT VTT LIP GSNGAKNY ETVATATNETSTKTT SQLATTASASSMAP VVT SPSLTGPLQSASGSAVATY SVPSTSSTYQGAANTKVLGN FMVL	LLALPVVF
DBVPG1788/1-511	398 AUETTTGVTTKSTPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	LLALPVVF
VPG0044/1-491	3/0 AUGLITUTTIN STETTTITTITLE VOJNUARNI E I VATATINETS INTI SULATIASAS SMAP VVI SPISLI UPLUSASUSAVATTS VESTISSI TVUGAN IN VULGEN IMVL 373 AUGLITUTTI VTI TI I DE OKCAKNY E TVATATINE I SI KETKOLI ATTAKAK SMAP VVI SPISLI OPLO CAACAAVITVU SU SI VUGA	
13/1-400	A SAGE TECHTER TETTETETE SIGARATE ET ATALIKE ESTATATIVE STATE SOUTH AS AS SMART VETSES ET OF EQSAS GAAVATES VETSES STUDIAN I KVEGAVIK	LLALFVVF
Conservation	*	
conservation		
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Consensus

A GETTT GYTTK SIPTTY ITT LIP G SNGAKNY ETVATATNP I SIKTT SO LATTA SA SSMAP VVT SP SLTGP LO SA SG SAVATY SVP SIS STYOGAAN I KVLGNFMWLL LA LP VVF

Figure S4: Detection of recombination breakpoints within the FLO11 coding region. The data were analyzed with the A domain alone, the A-C domains concatenated, and data that included a part of the B domain that could be resolved and aligned. x-axis is the nucleotide position in the gene and the y-axis is support for a breakpoint, as determined via GARD (note the different scales).



Figure S5: Genetic variation at *FLO11* **compared to variation in genes that code for proteins with similar properties.** Each data point represents a pairwise comparison between strains, for a given gene, as estimated in PAML using the yn00 function (N=54 strains and 43 genes for a total of ~65,000 data points). Red points represent *FLO11* comparisons.



Figure S6: Upstream regulatory alignment. Position 1 is -3544; positions 3545-6 are the start codon.

		10	20	30	40	50	60	70	80	90		100	110	120	130	140	150	160	170	180	190	200
S288cRef/1-3541														g			a	.t				
YJM224/1-3537				t								. t		g			a .	.t				
YJM311_Allele1/1-3541 VIM211_Allele2/1_2541				t								. t	• • • • • • • • • • •	g			a .	. t				
CBS2910/1-3539												. t		a				. t				
CBS1227/1-3540																						
CBS7838/1-3538																						
CBS7836/1-3541 02_122/1_2541													• • • • • • • • • • •					*			.a	
YIM436/1-3539																						
89-156/1-3506															.g							
YJM455/1-3540																						
TJM522/1=3538 YIM521/1=3538																						
YJM523/1-3541														g			a	. t				
R91-48/1-3540																					. a	
96-98/1-3539												•	• • • • • • • • • • •					•				
96-100/1-3540														y								
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NRRL_Y-10_988/1-3537				t								. t	• • • • • • • • • • •	g			a .	. t		c		
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YJM1119/1-3541												. t		g			a .	.t		c		
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NRRL_Y-961/1-3538																						
YJM1101/1-3540																						
NRRL_Y-963/1-3539																						
NRRL_1=12038/1=3329 NRRL_YB=427/1=3539														g			a					
NRRL_Y-11878/1-3541				t.								.t		g			a.	.t		c		
NRRL_Y-17447/1-3538				t							t.			g			a .	. t				
NRRL_YB-908/1-3537														g	g			.t				
NRRL Y-268/1-3540																						
NRRL_YB-2541/1-3539																					. a	
NRRL_YB-4506/1-3538														g			c	. <u>t</u>				
NKKL_TB-2625/1-3541 YIIc17 F5/1-3540														g			a .					
UWOPS83-787.3/1-3540															.g							
NRRL_Y-6297/1-3539														g				. t				
91-213/1-3541													• • • • • • • • • • •	g			a	. t				
S288c/1-3541														g								
M22/1-3539																					.a	
YPS128/1-3541														g				. t				
96-101/1-3539 1-1528/1-3505																						
K11/1-3538												. t		q				. t				
UWOPS05-217.3/1-3505															.g							
NCYC361/1-3540																					.a	
DBVPG6040/1-3541																						
DBVPG6040-2/1-3541				t.								.t		g			a.	.t		c		
DBVPG1853/1-3540																						
CBS_7833-1/1-3536 CBS_7833-2/1-3536				t									• • • • • • • • • • •	9			· · · · · · · · · · · · · · · · · · ·	. t				
96-109/1-3539																						
YPS606/1-3541														g				. t				
L-1374/1-3540																						
YS2/1-3537				· · · · · · · · · · · · · · · · · · ·										g								
NCYC110/1-3539																					.a	
DBVPG1106/1-3538				t							t.			g			a .	.t				
378604X/1-3540													• • • • • • • • • • •					• • • • • • • • • • •			.a	
YPS615/1-3506															. a							
YPS617/1-3506															.g							
YPS661/1-3506															.g							
YPS670/1-3541 YPS630/1-3541														g				.t				
UWOPS3-461.4/1-3505														g	. q							
YS4/1-3538				t.								.t		g			a.	.t				
DBVPG1788/1-3539																						
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Occupancy

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COOUNAAACU	UNCCUINACA	COARTUTUAA	ICCUCIMATE		CCACATUAAA	CETUCIACII	TTERUTCET	CITCUINIUC	ATTICCCAAP	ALICALICUI	AUCCITUICA	ACTIAGACIC	AGLICCACO	GCOTOCAGUA	COOUCHAITAI	GAALAAAA	GOALCEACUU	GIGAGATITUT	COMPOSITION OF A DECEMPOSITION OF A DECEMPOSITICA A DECEMPOSIC	AGGIATUGAUTT

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ACT	ACCACTAC	ACTICIT		CANTECAT	AAAGGATGT	TICCITCCI			CTATICATC	CTTATACTC	CCTCATCAT	CIICLCCT	CT	ATATACTTE	TACCCCTCA	ATCOATATION	ACACTATC
ACTI	ACCAGIACA	AUTTUIT		CAATIGATAA	AAAGGATCTT	TIGCITCCI/	AAAATAAACGTA	AAAAAGCACC	CIAIICAICA	GITATACIC	CUTCATCAT	GITGIGGIT	CIAATIAAA	ATATACITI	JIAGGEETEAAAA	AICCATATACG	ACACIAIG

Figure S7: Distribution of Tajima's D values in the upstream and downstream regions. Red points represent the region implicated in binding to the histone deacetylase RpdL3.







Pure Backgrounds



HMY433xHMY434

HMY439xHMY436 HMY432x

HMY432xHMY435 HM

HMY465xHMY463

HMY446xHMY444

HMY467xHMY464



Figure S9: Functional assay of natural FLO11 alleles. Ratios indicate the volume of each strain used to create a mixed inoculum.

- (A) Three genetic backgrounds with varying levels of social phenotypes. (B) Hybrids of the three strains, hemizygous for the FLO11 locus. Different alleles generate different mat architectures. Mixed colonies of GFP and mCherry versions of the same strain demonstrate no fitness cost to the
- fluorescence; numerically disadvantaged strains remain rare in the final mat. (C) Mixed colonies of hybrids with different FLO11 alleles. The FLO11 allele from NRRL Y-10988 appears to dominate the edge of the biofilm in mixed communities with other alleles, even when it is numerically
- disadvantaged. In contrast, in mixed communities with YJM311 and YPS681 FLO11 alleles, neither appears to have a fitness advantage.

Hemizygous Hybrid Backgrounds: Different FLO11 Alleles

YJM311 x YPS681 NRRL Y-10988 x YPS681 NRRL Y-10988 x YJM311 FLO11₁₀₉₈₈ + FLO11₃₁₁ FLO11₃₁₁ + FLO11₁₀₉₈₈ FLO11₃₁₁ + FLO11₆₈₁ FLO11₆₈₁ + FLO11₃₁₁ FLO11₁₀₉₈₈ + FLO11₆₈₁ FLO11₆₈₁ + FLO11₁₀₉₈₈ 1:1 10:**1** 1:10 HMY439xHMY435 HMY432xHMY436 HMY446xHMY464 HMY467xHMY444 HMY442xHMY468 HMY462xHMY441

Sample	НМҮ	Strain	Parental isolate/ isogenic with	Isolate source or other name	Geographic origin	Origin	Population	Upstream	Domain A	Domain C	Downstream	B Length	Reference
1	2		YJM224		Unknown	Distillery		✓	~	~	~	✓	
2	3		YJM311	91-212	CA, USA	Clinical	Mosaic	~	~	~	~	✓	
4	25	YJM244	YJM210	CBS 1227	Romania	Clinical	Wine/Eur	~	~	✓	~	•	1
3	26	YJM248	YJM218	CBS 2910	Unknown	Clinical (feces)	Wine/Eur	~	•	•	•	~	1
5	27	YJM270	YJM215	CBS 2807	Slovenia	Wine	Wine/Eur	Х	х	Х	х	х	1
6	30	YJM326	YJM310	CBS 7838	CA, USA	Clinical	Mosaic	✓	•	•	~	Х	1
7	31	YJM428	YJM308	CBS 7836	CA, USA	Clinical	Mosaic	✓	•	•	~	✓	1
8	32	YJM450	YJM440	92-123	CA, USA	Clinical	Mosaic	~	~	~	~	✓	1
9	33	YJM451	YJM436	B70302(b)	Unknown	Clinical	Mosaic	✓	~	~	~	✓	1
10	35	YJM456	YJM454	89-156	CA, USA	Clinical	Mosaic	~	~	~	~	Х	1
11	36	YJM470	YJM455	SUH	CA, USA	Clinical	Mosaic	✓	~	✓	~	✓	1
12	37	YJM541	YJM522	SUH	CA, USA	Clinical	Mosaic	✓	~	•	~	✓	1
13	38	YJM554	YJM521	SUH	CA, USA	Clinical	Mosaic	~	•	•	~	Х	1
14	39	YJM555	YJM523	SUH	CA, USA	Clinical	Mosaic	✓	•	•	~	Х	1
15	43	YJM693	YJM669	R91-48	TX, USA	Clinical	Mosaic	✓	•	•	~	✓	1
16	45	YJM969	YJM967	96-98	Italy	Clinical	Wine/Eur	✓	•	•	~	✓	1
17	46	YJM689	YJM675	R93-1017	TX, USA	Clinical	Mosaic	~	~	~	~	•	1
18	47	YJM972	YJM947	96-100	Italy	Clinical	Wine/Eur	~	Х	Х	~	Х	1
19	57	YJM1078	YJM1075	NRRL YB-4348	Portugal	Clinical	Wine/Eur	~	~	~	~	•	1
20	58	YJM1083	YJM1073	NRRL Y-10,988	NC, USA	Clinical	Mosaic	~	~	~	~	~	1
21	59	YJM1129	YJM1123	NCMH 125	OH, USA	Distillery	Wine/Eur	~	~	•	~	~	1
22	60	YJM1133	YJM1125	MMRL 125	NC, USA	Clinical	Mosaic	~	~	~	~	•	1
23	62	YJM1199	YJM1115		MI, USA	Clinical	Mosaic	~	~	~	~	Х	1
24	64	YJM1208	YJM1119	1882	MI, USA	Clinical	Mosaic	~	~	~	~	•	1

25	67	YJM1248	YJM1219	NRRL Y-1546	West Africa	Wine	West African	~	✓	✓	✓	•	1
26	69	YJM1252	YJM1224	NRRL Y-6679	Spain	Alpechin	Wine/Eur	~	~	✓	~	~	1
27	72	YJM1290		Sigma1278b	Unknown	Laboratory	Mosaic	•	~	✓	~	Х	1
28	75	YJM1307	YJM1071	NRRL Y-961	DC, USA	Clinical	Mosaic	•	~	✓	~	~	1
29	76	YJM1311	YJM1101	C. Kaufman	MI, USA	Clinical	Mosaic	•	~	~	~	~	1
30	80	YJM1338	YJM1315	NRRL Y-963	MD, USA	Sour fig	Mosaic	•	~	~	~	•	1
31	82	YJM1342	YJM1324	NRRL Y-12638	South Africa	Soil	Mosaic	~	~	~	~	~	1
32	85	YJM1381	YJM1357	NRRL YB-427	Trinidad	Rum fermentation	Mosaic	~	•	~	•	•	1
33	88	YJM1386	YJM1365	NRRL Y-11878	Jamaica	Sugar cane	Mosaic	•	~	Х	~	•	1
34	91	YJM1389	YJM1368	NRRL Y-17447	Thailand	Sewage	Sake	~	~	~	~	~	1
35	92	YJM1399	YJM1393	NRRL YB-908	Unknown	Wild cherry tree gum	Mosaic	•	~	~	~	~	1
36	93	YJM1400	YJM1394	NRRL YB-4081	Philippines	Guava	Mosaic	•	~	~	~	~	1
37	96	YJM1415	YJM1407	NRRL Y-268	France	Wine	Wine/Eur	•	~	•	~	~	1
38	97	YJM1417	YJM1411	NRRL YB-2541	HI, USA	ND	Wine/Eur	•	~	~	~	•	1
39	98	YJM1418	YJM1413	NRRL YB-4506	Japan	Oak tree	Mosaic	•	~	~	~	~	1
40	99	YJM1419	YJM1412	NRRL YB-2625	Unknown	Bagasse	Mosaic	•	~	~	~	~	1
41	100	YJM1433		YIIc17_E5	France	Wine	Wine/Eur	•	Х	Х	~	Х	1,2
42	103	YJM1443		UWOPS83-787.3	Bahamas	Fruit	Mosaic	•	~	~	~	~	1,2
43	111	YJM1479	YJM1474	NRRL Y-6297	Phillipines	Coconut tuba	Mosaic	~	~	•	~	~	1
44	117	YJM1615	YJM312	91-213	CA, USA	Clinical	Mosaic	•	~	✓	~	~	1
45	121	YJM1573	YJM1566	NRRL Y-12603	India	Fermented food	Mosaic	~	•	~	•	~	1
46	122	YJM1552	S1	S288c	CA, USA	Rotten fig	Mosaic	•	~	~	~	✓	1
47	124	YJM1529		M22	Unknown	Wine	Wine/Eur	•	~	~	~	~	1
48	158			YPS128	PA, USA	Oak	North American	•	~	•	~	~	3
50	160			L-1528	Chile	Wine	Wine/Eur	•	~	•	~	Х	2
49	161	YJM975	YJM948	96-101	Italy	Clinical	Wine/Eur	~	Х	Х	~	~	1
51	169			SK1	USA	Soil, lab strain	West African	Х	~	•	~	~	2
52	170			K11	Japan	Sake strain	Sake	~	~	~	~	~	2
53	171			UWOPS05-217.3	Malaysia	Bertam Palm	Malaysian	~	Х	Х	~	~	2
54	172			NCYC361	Ireland- S.	Beer spoilage	Mosaic	~	•	•	~	•	2

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55	173			DBVPG6765	unknown- S. boulardi	Unknown	Wine/Eur	•	х	х	~	х	2
56	174	YJM1549		DBVPG6040	Netherlands- S. fructum	Fermenting fruit juice	Mosaic	~	•	•	•	~	1,2
57	175	YJM1463		DBVPG1853	Ethiopia	White tecc	Wine/Eur	•	Х	Х	•	•	1,2
58	217	YJM145	YJM128	CBS 7833	MO, USA	Clinical		•	~	•	•	Х	1
59	261	YJM978	YJM954	96-109	Italy	Clinical	Wine/Eur	•	~	✓	•	•	1
60	262	YJM1434		YPS606	PA, USA	Oak	North American	•	~	•	•	•	3
61	263			L-1374	Chile	Wine	Wine/Eur	~	Х	Х	~	•	2
62	264	YJM1460		Y12	Africa	Palm Wine	Sake	•	~	✓	•	•	1,2
63	265			YS2	Australia	Baker strain	Mosaic	•	~	~	•	•	2
64	266	YJM1439		NCYC110	West Africa	Ginger beer	West African	•	~	~	•	Х	1,2
65	267			DBVPG1106	Australia	Grape	Wine/Eur	•	~	~	•	•	2
66	268			378604X	Newcastle, UK	Clinical	Mosaic	•	~	~	•	•	2
67	270			YPS681	PA, USA	Oak	North American	•	~	~	•	•	4
68	271			YPS615	PA, USA	Oak	North American	•	~	~	•	•	4
69	272			YPS617	PA, USA	Oak	North American	•	~	~	•	•	4
70	273			YPS661	PA, USA	Oak	North American	•	~	~	•	•	4
71	274			YPS670	PA, USA	Oak	North American	•	~	✓	~	~	4
72	275			YPS630	PA, USA	Oak	North American	~	~	~	~	~	4
73	276			UWOPS3-461.4	Malaysia	Bertam Palm, nectar	Malaysian	•	•	•	Х	•	2
74	277			Y55	France	Wine, lab strain		х	•	•	•	•	2
75	278			YS4	Netherlands	Baker strain	Mosaic	•	~	~	•	•	2
76	279			DBVPG1788	Finland	Soil	Wine/Eur	•	~	~	•	•	2
77	280			DBVPG6044	West Africa	Bili wine	West African	•	~	~	•	•	2
78	281			Y9; NRRL-Y5997	Japan	Ragi wine	Sake	•	~	~	•	Х	2

Table S1. List of the 78 strains, along with their parental isolate name, geographic and environmental origin, as well as population membership (according to ref 1.). The data obtained for each strain is indicated with a check. (1) Strope, P.K., et al. (2015), *Genome Research*, 25(5):762-774. (2) Liti, G., et al. (2009), *Nature*, 458: 337-341. (3) Sniegowski, P.D., et al. (2002), *FEMS Yeast Research*, 1: 299-306. (4) Murphy, H.A. and C.W. Zeyl (2012), *Evolution*, 66(4): 1196-1209.

Systematic Name	Standard Name	cont'd	cont'd	cont'd	cont'd
YBR067C	TIP1	YIL011W	TIR3	YLR390W-A	CCW14
YBR162C	TOS1	YJL158C	CIS3	YMR238W	DFG5
YDR055W	PST1	YJL159W	HSP150	YMR305C	SCW10
YDR077W	SED1	YJL171C	TOH1	YMR307W	GAS1
YDR261C	EXG1	YJR004C	SAG1	YNL190W	n/a
YDR349C	YPS7	YKL046C	DCW1	YNL300W	TOS6
YEL040W	UTR2	YKL096W	CWP1	YNL322C	KRE1
YER150W	SPI1	YKL096W-A	CWP2	YNL327W	EGT2
YGL028C	SCW11	YLR040C	AFB1	YNR044W	AGA1
YGL228W	SHE10	YLR042C	n/a	YOL132W	GAS4
YGR279C	SCW4	YLR110C	CCW12	YOR009W	TIR4
YHL009C	YAP3	YLR194C	NCW2	YOR010C	TIR2
YHR126C	ANS1	YLR342W	FKS1	YOR214C	SPR2
YHR143W	DSE2	YLR343W	GAS2	YPR159W	KRE6

Table S2: Genes recovered from literature search for GPI-anchored and cell wall associated proteins.

Sample	HMY	Strain	cont'd	cont'd	cont'd	cont'd	cont'd	cont'd
3	HMY26	CBS29101	22	HMY60	MMRL 125 ¹	44	HMY117	91-213 ¹
4	HMY25	CBS1227 ¹	23	HMY62	YJM1115 ¹	45	HMY121	NRRL Y-12603 ¹
5	HMY27	CBS28071	24	HMY64	YJM1119 ¹	46	HMY122	S288c ²
6	HMY30	CBS78381	25	HMY67	NRRL Y-1546 ¹	48	HMY158	YPS128 ²
7	HMY31	CBS7836 ¹	26	HMY69	NRRL Y-6679 ¹	49	HMY161	96-101 ¹
8	HMY32	92-123 ¹	28	HMY75	NRRL Y-961 ¹	51	HMY169	SK1 ²
9	HMY33	YJM436 ¹	29	HMY76	YJM1101 ¹	55	HMY173	DBVPG6765 ²
10	HMY35	89-156 ¹	30	HMY80	NRRL Y-963 ¹	56	HMY174	DBVPG6040 ¹
11	HMY36	YJM455 ¹	32	HMY85	NRRL YB-427 ¹	57	HMY175	DBVPG1853 ¹
12	HMY37	YJM522 ¹	34	HMY91	NRRL Y-17447 ¹	57	HMY175	DBVPG1853
13	HMY38	YJM521 ¹	35	HMY92	NRRL YB-908 ¹	59	HMY261	96-109 ¹
14	HMY39	YJM523 ¹	36	HMY93	NRRL YB-4081 ¹	60	HMY262	YPS606
15	HMY43	R91-48 ¹	37	HMY96	NRRL Y-268 ¹	62	HMY264	Y12 ¹
16	HMY45	96-98 ¹	38	HMY97	NRRL YB-2541 ¹	62	HMY264	Y12 ²
17	HMY46	R93-1017 ¹	39	HMY98	NRRL YB-4506 ¹	64	HMY266	NCYC110 ¹
18	HMY47	96-100 ¹	40	HMY99	NRRL YB-2625 ¹	73	HMY276	UWOPS3-461.4 ²
20	HMY58	NRRL Y-10988 ¹	41	HMY100	YJM1433 ¹	77	HMY280	DBVPG6044 ²
21	HMY59	NCMH 125 ¹	43	HMY111	NRRL Y-6297 ¹	-	HMY269	UWOPS83-787.3 ¹

Table S3: Strains with available genomes used for gene comparison to *FLO11*. ¹ Strope, P.K., et al. (2015), *Genome Research*, 25(5):762-774; ² Yue, J.-X., et al. (2017), *Nature Genetics*, 49(6):913-924.

	HMY	Genetic Background	PGK1-Fluorescence	FLO11
	390	YPS681	GFP-KanMX	FLO11/FLO11
	388	YPS681	GFP-KanMX	FLO11/Δflo11
7	391	YPS681	GFP-KanMX	$\Delta flo11/\Delta flo11$
ŭ	414	YPS681	mCherry-KanMX	FLO11/FLO11
<u>o</u>	402	YPS681	mCherry-KanMX	FLO11/Δflo11
Ś	403	YPS681	mCherry-KanMX	$\Delta flo11/\Delta flo11$
3ac	411	YJM311	mCherry-HphMX	FLO11/FLO11
е	409	YJM311	mCherry-HphMX	FLO11/Δflo11
'n	412	YJM311	mCherry-HphMX	$\Delta flo11/\Delta flo11$
ш	401	NRRL Y-10988	GFP-KanMX	FLO11/FLO11
	450	NRRL Y-10988	GFP-KanMX	FLO11/Δflo11
	458	NRRL Y-10988	GFP-KanMX	$\Delta flo11/\Delta flo11$
	435	YPS681 x YJM311	mCherry-HphMX	FLO11 ₆₈₁ /∆flo11
	436	YPS681 x YJM311	mCherry-HphMX	FLO11 ₃₁₁ /Δflo11
	434	YPS681 x YJM311	mCherry-HphMX	$\Delta flo11/\Delta flo11$
	432	YPS681 x YJM311	GFP-KanMX	FLO11 ₆₈₁ /Δflo11
	439	YPS681 x YJM311	GFP-KanMX	FLO11 ₃₁₁ /Δflo11
p	433	YPS681 x YJM311	GFP-KanMX	$\Delta flo11/\Delta flo11$
JUL	464	YPS681 x NRRL Y-10988	mCherry-KanMX	FLO11 ₆₈₁ /Δflo11
grc	444	YPS681 x NRRL Y-10988	mCherry-KanMX	FLO11 ₁₀₉₈₈ /Δflo11
Š	463	YPS681 x NRRL Y-10988	mCherry-KanMX	$\Delta flo11/\Delta flo11$
B	467	YPS681 x NRRL Y-10988	GFP-KanMX	FLO11 ₆₈₁ /Δflo11
ĿĽ	446	YPS681 x NRRL Y-10988	GFP-KanMX	FLO11 ₁₀₉₈₈ /Δflo11
ybi	465	YPS681 x NRRL Y-10988	GFP-KanMX	$\Delta flo11/\Delta flo11$
I	468	YJM311 x NRRL Y-10988	mCherry-HphMX	FLO11 ₃₁₁ /Δflo11
	441	YJM311 x NRRL Y-10988	mCherry-HphMX	FLO11 ₁₀₉₈₈ /Δflo11
	475	YJM311 x NRRL Y-10988	mCherry-HphMX	$\Delta flo11/\Delta flo11$
	462	YJM311 x NRRL Y-10988	GFP-KanMX	FLO11 ₃₁₁ /Δflo11
	442	YJM311 x NRRL Y-10988	GFP-KanMX	FLO11₁0988/∆flo11
	466	YJM311 x NRRL Y-10988	GFP-KanMX	Δflo11/Δflo11
	нмү	Genetic Background	Fluorescence	FLO11
	483	NRRI Y-10988	prEL 011-GEP	FL 01110000/ Aflo11"GEP-KanMX
	484	Y.IM311 x NRRI Y-10988	prFI 011311-GEP	FL O1110088/ Aflo11"GEP-KanMX
	485	Y.IM311	prELO11-GEP	FL O11211/ Aflo11:GEP-KanMX
	486	Y.IM311 x NRRI Y-10988	prELO111000-GEP	FL O11211/ Aflo11::GFP-KanMX
	400			

Table S4: Strains engineered for functional analysis of *FLO11*.

Primer	Sequence	Design/Purpose
FLO11A-for	TTGGTCAATCAGAACAGGCAAC	To amplify FLO11 and its associated regulatory
FLO11A-rev	GAGACATCTTTAGAGTAACCACAGATATTC	regions
PCK1-VPC-for	GGTAAGGAATTGCCAGGTGTTGCTTTCTTATCCGAAAAGA	To generate a cassette to produce fluorescence.
FGRI-TRC-IOI	AA GGTCGACGGATCCCCGGG	40 bp upstream and downstream of the PGK1 stop
PCK1 VPC rov	GAAAAGAAAAAATTGATCTATCGATTTCAATTCAATTCA	codon plus homology to the pFA6a plasmid (GFP-
FGRI-TRC-Iev	ATCGATGAATTCGAGCTCG	KanMX cassette) and pBS34 (mCherry-KanMX)
ELO11 MX for	GACCCCTTTTCGTACAGAAGCCTTGGTCAATCAGAACAGG	To generate a cassette to delete FLO11 and replace
FLOTI-IMA-IOI	CAACG CGTACGCTGCAGGTC	with antibiotic resistance gene. 45 bp homology to
FLO11-MX-rev	ACAGT GGCTTCAAAG AACTGCTGATTGCTCAAGGC	upstream and downstream of FLO11 plus homology
	AATCAGTCCG ATCGATGAATTCGAG	to antibiotic MX cassettes.
FL O11-end-Kan-for	AACATCGTAATGAAGAAACGAACATGTTGGAATTGTATCA	To generate a cassette to replace FLO11 with GFP.
1 LOTT-end-Ran-tor	ATCGATGAATTCGAGCTCG	Homology to promoter of FLO11, ATG, and the 2nd
ELO11_pr_CEP_rov	TACTTTTGTAGGCCTCAAAAATCCATATACGCACACT ATG	codon on in GFP; homology to downstream of
ΤΕΘΤΙ-βΙ-ΘΙ Ε-Ιέν	AGTAAAGGAGAAGAACTTTT	FLO11 and the end of the KanMX cassette.
FLO11-Repeat-for	GGTTTCGCTTGGACTGGTTGAACATGGAAC	To even life the D demain for low oth events
FLO11-Repeat-rev	GATTTCCCAGGCTTCTATTGGAACATAGAT	I o amplity the B-domain for length analysis.

Table S5. Primers used in this study

Tree	Model	Parameter estimates	Log Likelihood	No. Param.	AIC	Comparison	Chi- squared	P-value
	Model1	p ₀ =0.70, p ₁ = 0.30, ω ₀ =0.016, κ=2.23	-2059.398	103	4324.8	2 vs. 1	49.106	<0.0001
-	Model2	$p_0=0.70, p_1=0.21, p_2=0.09, \omega_0=0.045, \omega_1=1, \omega_2=5.24, \kappa=3.04$	-2034.845	105	4279.7			
Jair	Model7	p=0.008, q= 0.016, к=2.24	-2059.504	104	4327.0	8 vs. 7	48.966	<0.0001
A-dom	Model8	p=0.06, q= 0.18, p₀=0.91, p₁= 0.09 ω=5.25, κ=3.05	-2035.021	106	4282.0			
4	ModelC	ω=0.60,π=3.32, κ=2.79	-2100.346	113	4426.7	E vs. C	39.858	<0.0001
	ModelE	ω ₁ =0.43, ω ₂ =4.51, π=3.09, κ ₁ =3.71, κ ₂ =1.30	-2080.417	115	4390.8			
	Model1	p₀=0.71, p₁=0.29 , ω₀=0, κ=3.82	-4485.937	111	9193.9	2 vs. 1	222.014	<0.0001
enate	Model2	p₀=0.69, p₁=0.27, p₂=0.04, ω₀=0.02, ω₁=1, ω₂=15.98, κ=5.04	-4374.93	113	8975.9			
ate	Model7	p=0.005, q=.012 , к=3.76	-4484.238	112	9192.5	8 vs. 7	218.568	<0.0001
Conc	Model8	p=0.005, q=0.01, p₀=0.96, p₁= 0.04, ω=16.25, κ=5.05	-4374.954	114	8977.9			
Ģ	ModelC	ω=0.62,π=5.69, κ=3.83	-4506.825	121	9255.7	E vs. C	47.642	<0.0001
-A	ModelE	ω ₁ =0.50, ω ₂ =4.60, π=5.24, κ ₁ =5.08, κ ₂ =1.30	-4483.004	123	9212.0			
4	Model1	p ₀ =0.70, p ₁ = 0.30, ω ₀ =0.007, κ=2.69	-6626.686	111	13475.4	2 vs. 1	250.794	<0.0001
enate	Model2	p ₀ =0.67, p ₁ = 0.31, p ₂ =0.02, ω ₀ =0, ω ₁ =1, ω ₂ =15.63, κ=3.18	-6501.289	113	13228.6			
cat	Model7	p=0.01, q= 0.02, к=2.70	-6626.727	112	13477.5	8 vs. 7	284.204	<0.0001
Con	Model8	p=0.007, q= 0.01, p₀=0.97, p₁= 0.03, ω=13.7, κ=3.25	-6484.625	114	13197.3			
U m	ModelC	ω=0.53, π=3.46, κ=2.63	-6724.781	121	13691.6	E vs. C	41.526	<0.0001
A-F	ModelE	ω ₁ =0.46, ω ₂ =5.32, π=3.22, κ ₁ =2.69, κ ₂ =1.45	-6704.018	123	13654.0			
	Model1	p ₀ =0.83, p ₁ = 0.17, ω ₀ =0.003, κ=3.05	-7310.787	77	14775.6	2 vs. 1	888.794	<0.0001
red	Model2	p ₀ =0.81, p ₁ = 0.13, p ₂ =0.06, ω ₀ =0.009, ω ₁ =1, ω ₂ =16.2, κ=4.28	-6866.390	79	13890.8			
sho ins	Model7	p=0.009, q= 0.055, к=3.03	-7320.583	78	14797.2	8 vs. 7	906.836	<0.0001
I-Ancl Proteii	Model8	p=0.009, q= 0.051, p ₀ =0.94, p ₁ = 0.06, ω=15.9, κ=4.27	-6867.165	80	13894.3			
ц Ц	ModelC	ω=0.72,π=6.16, κ=3.15	-7527.352	87	15228.7	E vs. C	103.500	<0.0001
	ModelE	ω ₁ =0.57, ω ₂ =7.82, π=5.81, κ ₁ =4.02, κ ₂ =1.35	-7475.602	89	15129.2			

Table S6: Results of the evolutionary analysis conducted in PAML using three different phylogenetic trees with their associated alignment, as well as a "strain" tree with an alignment of the fullest data set (i.e., including the part of the B domain that could be resolved and aligned). Parameter estimates associated with each model are listed: $\omega = dN/dS$ rate; $\pi =$ synonymous transversion rate; $\kappa =$ transition/transversion rate; parameters with subscripts refer to estimates for a given site class; $p_i =$ proportion of codons in a given site class; p and q are parameters describing a β distribution. For each data set, the random sites models that allow for the possibility of positive selection (2 and 8) were significantly better fits than those that did not (1 and 7), as determined by a likelihood ratio test. Likewise, the fixed sites model that allowed the dN/dS value to differ between the site partitions (E) was a significantly better model of the data than the model that held dN/dS constant between the partitions (C).

	A-Domain Tree								
Model 2	54D, 57N, 94W, 177Q, 183Q, 190D								
Model 8	17N, 54D, 57N, 94W, <mark>113Y</mark> , <mark>119-</mark> , 177Q, 179A, 180S, 183Q, 190D								
	Concatenated A- and C-Domains Tree								
Model 2	17N, 54D, 57N, 94W, <mark>113Y, 114-, 118-, 119-, 177Q, 179A, 180S,</mark> 183Q, 190D, 200N, 203H, 406V(1188)								
Model 8	17N, 54D, 57N, 94W, <mark>113Y</mark> , <mark>114-</mark> , <mark>118-</mark> , <mark>119-</mark> , 134Y, 177Q, 179A, 180S, 183Q, 190D, 203H, 375K(1157), 406V(1188)								
	Concatenated A-, minor B- and C- Domains Tree								
Model 2	54D, 94W, 113Y, 114-, 116-, 119-, 177Q, 190D, 203H, [220S(855), 228V(863), 299P(934)] 522K(1157)								
Model 8	54D, 94W, 113Y, 114-, 116-, 118-, 119-, 177Q, 183Q, 190D, 203H, [220S(855), 228V(863), 299P(934)] 522K(1157)								
	Genes of GPI-Anchored and Cell Wall Proteins Tree								
Model 2	4P, 6L, 7L, 17N, 54D, 57N, 60Q, 85K, 91K, 94W, 106G, 113Y, 114-, 118-, 119-, 129-, 131E, 133T, 172Q, 173G, 176A, 177Q, 178Y, 179A, 182W, 189F, 195C, 202G, [219V(854), 227S(862), 290T(925), 298T(933), 327T(962), 334T(969), 335T(970), 338T(973), 343S(978),] 521G(1156), 550T(1185), 552A(1187), 675S(1310), 731V(1366)								
Model 8	4P, 6L, 7L, 17N, 54D, 57N, 60Q, 85K, 91K, 94W, 106G, 113Y, 114-, 118-, 119-, 129-, 131E, 133T, 172Q, 173G, 175A, 176A, 177Q, 178Y, 179A, 182W, 189F, 195C, 202G, [219V(854), 227S(862), 290T(925), 298T(933), 327T(962), 334T(969), 335T(970), 338T(973), 343S(978),] 521G(1156), 550T(1185), 552A(1187), 675S(1310), 731V(1366)								

Table S7: Under random sites models that allowed for positive selection (M2 and M8), individual codons were identified as being under significant positive selection. Red and blue codons are associated with the apical regions of the A-domain and grey codons fall within the part of the B-domain that was included in the analysis (see Figure S4). Numbers refer to the amino acid within the concatenated A and C-domain alignment and numbers in parentheses refer to the amino acid within the reference strain, S288c, *FLO11* sequence (P>0.95).

Tree	Model	Parameter estimates	Log Likelihood	No. Param.	AIC	Comparison	Chi- squared	P-value
	Model1	p₀=0.58, p₁= 0.42, ω₀=0.00, κ=1.83	-2741.054	43		2 vs. 1	105.82	<0.0001
with	Model2	p ₀ =0.96, p ₁ = 0.0003, p ₂ =0.04, ω ₀ =0.439, ω ₁ =1, ω ₂ =63.9, κ=2.97	-2688.146	45				
us T	Model7	p=2.28, q= 0.005, к=1.93	-2747.600	44		8 vs. 7	118.91	<0.0001
straii inse	Model8	p=65.4, q= 83.7, p₀=0.96, p₁= 0.04 ω=63.9, κ=2.97	-2688.146	46				
U V	ModelC	ω=11.90,π=2.14, κ=2.14	-2691.529	53		E vs. C	11.52	0.00069
4	ModelE	ω ₁ =1.30, ω ₂ =999, π=11.59, κ ₁ =3.16, κ ₂ =1.42	-2685.768	55				
	Model1	p₀=0.72, p₁=0.28 , ω₀=0, κ=4.61	-3774.625	76		2 vs. 1	91.292	<0.0001
ithout	Model2	p ₀ =0.75, p ₁ =0.23, p ₂ =0.02, ω ₀ =0.058, ω ₁ =1, ω ₂ =17.29, κ=5.46	-3728.979	78				
≥ t	Model7	р=0.005, q=.012 , к=4.63	-3774.725	77		8 vs. 7	92.664	<0.0001
trains inse	Model8	p=0.006, q=0.01, p₀=0.99, p₁= 0.01, ω=36.66, κ=5.52	-3728.393	79				
S C	ModelC	ω=0.42,π=3.95, κ=4.61	-3787.932	86		E vs. C	23.772	<0.0001
A-(ModelE	ω ₁ =0.37, ω ₂ =1.9, π=3.52, κ ₁ =5.62, κ ₂ =1.19	-3776.046	88				

Table S8: The sequence data that included the A- and C- domains concatenated was used to investigate whether separating the strains into groups with and without the insert (in the first interacting region of the protein) would affect the results. Models and parameters are as in Table S2. For both data sets, the random sites models that allow for the possibility of positive selection (2 and 8) were significantly better fits than those that did not (1 and 7), as determined by a likelihood ratio test. Likewise, the fixed sites model that allowed the dN/dS value to differ between the site partitions (E) was a significantly better model of the data than the model that held dN/dS constant between the partitions (C).

Model 2	4P, 17Y, 94S, 114D, 116N, 118D, 119W, 130D, 134Y, 177E, 178Y, 179A, 190Y, 196D, 200N, 203Y						
Model 8	4P, 17Y, 94S, <mark>114D, 116N, 118D, 119W, 130D</mark> , 134Y, <mark>177E</mark> , 178Y, 179A, 190D, 196D, 200N, 203Y						
Concatenated A- and C- Domains: Strains without Insert							
Model 2	54D, 57N, 113Y, 164S(180)*, 167Q(183), 359K(375,1010), 390V(406,1188), 569F(585,1204)*						
Model 8	54D, 57N, 113Y, 161Q (177)*, 164S(180), 167Q(183), 359K(375,1010), 390V(406,1188), 513V(529,1164)*, 569F(585,1204)						

Concatenated A- and C- Domains: Strains with Insert

Table S9: Under random sites models that allowed for positive selection (M2 and M8), individual codons were identified as being under significant positive selection. Red and blue codons are associated with the apical regions of the A-domain (see Figure S4). Numbers refer to the amino acid within the concatenated A and C-domain alignment and numbers in parentheses refer to the amino acid when the insert is included in the sequence followed by the location in the reference sequence of S288C (P>0.95). * P>0.92

	Break Points	AICc	Δ AICc	Segment	p-value
A Domain	0	4025.05		1-648	
A Domain	1	3935.37	89.68	1-399, 400-648	0.0002
	0	8739.24		1-1755	
A-C Concatenated	1	8538.30	200.94	1-617, 618-1755	0.0004
	2	8471.75	66.55	1-440, 441-890, 891-1755	0.0004
	0	13263.88		1-2199	
A-B-C Concatenated	1	12728.38	535.50	1-698, 699-2199	0.0004
	2	12700.43	27.96	1-461, 462-727, 728-2199	0.0004

Table S10: Results from the GARD analysis for each data set. In the concatenated data sets, the locations refer to the location of the input sequence and not the reference genome sequence (i.e., the majority of the B-domain is missing). The A-domain is the first 648 nucleotides; the interacting domains are 336-393 and 513-546.

Tree	Model	Parameter estimates	Log Likelihood	No. Param.	AIC	Comparison	Chi- squared	P-value
	Model1	p ₀ =0.74, p ₁ = 0.26, ω ₀ =0.025, κ=2.71	-1364.213	100	2928.4	2 vs. 1	49.778	<0.0001
	Model2	p ₀ =0.74, p ₁ = 0.19, p ₂ =0.07, ω ₀ =0.055, ω ₁ =1, ω ₂ =9.63, κ=4.00	-1339.324	102	2882.6			
n 1 32	Model7	р=0.008, q=0.016, к=2.79	-1364.425	101	2934.9	8 vs. 7	49.978	<0.0001
sectic 1-46	Model8	p=0.089, q= 0.276, p₀=0.93, p₁= 0.07, ω=9.54, κ=4.02	-1339.436	103	2886.9			
0)	ModelC	ω=0.48,π=4.34, κ=3.10	-1392.434	110	3004.9	E vs. C	17.42	<0.0001
	ModelE	ω ₁ =0.379, ω ₂ =3.53, π=4.28, κ ₁ =3.72, κ ₂ =1.92	-1383.724	112	2991.5			
	Model1	p₀=0.77, p₁=0.23 , ω₀=0.077, κ=1.49	-1617.268	97	3428.5	2 vs. 1	126.38	<0.0001
	Model2	p ₀ =0.63, p ₁ =0.30, p ₂ =0.07, ω ₀ =0.059, ω ₁ =1, ω ₂ =8.55, κ=2.23	-1554.078	99	3306.2			
n 2 30	Model7	р=0.146, q= 0.35, к=1.49	-1618.957	98	3433.9	8 vs. 7	130.89	<0.0001
sectio 463-7	Model8	p=0.157, q= 0.316, p₀=0.93, p₁= 0.07, ω=8.06, κ=2.19	1553.513	100	3307.1			
0)	ModelC	ω=0.72,π=1.64, κ=2.09	-1703.781	107	3621.6	E vs. C	48.11	<0.0001
	ModelE	ω ₁ =0.49, ω ₂ =21.59, π=1.49, κ ₁ =2.16, κ ₂ =1.48	-1679.725	109	3577.5			
	Model1	p ₀ =0.66, p ₁ = 0.34, ω ₀ =0, κ=3.6	-3445.500	97	7085	2 vs. 1	68.266	<0.0001
on 3: 2199	Model2	p ₀ =0.8, p ₁ = 0.16, p ₂ =0.04, ω ₀ =0.125, ω ₁ =1, ω ₂ =9.835, κ=3.99	-3411.367	99	7020.7			
ecti 31-:	Model7	р=0.005, q=0.0096, к=3.61	-3446.033	98	7088.1	8 vs. 7	61.236	<0.0001
Se 73	Model8	p=0.331, q=0.923, p₀=0.96, p₁= 0.04, ω=9.588, κ=4.01	-3415.415	100	7030.83			

Table S11: The sequence data that included the A-, minor B-, and C- domains concatenated was divided into three recombination blocks by the program GARD (nucleotides 1-462, 463-730, 731-2199); this division separated the two cell-cell interacting regions of the protein. Each block was separately analyzed by the program PAML; models and parameters as in Table S2. For all individual recombination blocks, the random sites models that allow for the possibility of positive selection (2 and 8) were significantly better fits than those that did not (1 and 7), as determined by a likelihood ratio test. Likewise, the fixed sites model that allowed the dN/dS value to differ between the site partitions (E) was a significantly better model of the data than the model that held dN/dS constant between the partitions (C).

Each Recombination Block Analyzed Separately

Model	54D, 57N, 94W, 113Y*, 114-**, 116-*, 118-**, 119-**, 177Q, 180S, 183Q, 190D, [220S(855), 228V(863), 256S(891), 274Q(909),			
2	295S(930), 299P(934)], 551N(1186)			
Model	54D, 57N, 94W, 113Y**, 114-**, 116-**, 118-**, 119-, 177Q, 180S, 183Q, 190D, [220S(855), 228V(863), 256S(891), 257F(892),			
8	274Q(909), 295S(930), 299P(934)], 551N(1186), 732F(1367)			

Table S12: Under random sites models that allowed for positive selection (M2 and M8), individual codons were identified as being under significant positive selection. Red and blue codons are associated with the apical regions of the A-domain and grey codons fall within the part of the B-domain that was included in the analysis (see Figure S4). Numbers refer to the amino acid within the concatenated A, B, and C-domain alignment and numbers in parentheses refer to the amino acid within the reference strain, S288c, *FLO11* sequence (P>0.95). **P>0.9, * P>0.86;

Source	Sum of Squares	F-ratio	p-value
Allele	0.1819	26.47 (1,82)	<0.0001
Medium	3.2845	478.09 (1,82)	<0.0001
Genetic Background	1.5437	224.70 (1,82)	<0.0001
Allele*Medium	0.0306	4.45 (1,82)	0.038
Allele*Background	0.0653	9.51(1,82)	0.0028
Medium*Background	1.1716	170.54 (1,82)	<0.0001
Allele*Medium*Background	0.0057	0.83 (1,82)	0.3657
Genetic Background Contrast: Hy	brid <i>pFLO11</i> ₁₀₉₈₈ vs. Hybrid <i>pFLO11</i> ₃₁₁	2.18 (1,82)	0.1439

 Table S13. ANOVA results for *prFLO11-GFP* expression.