

## SUPPLEMENT

### Additional genome analyses:

#### Genome expansion

Genome size varies greatly in fungi, even within the sub-phylum Saccharomycotina, from the 9 Mb *Ashbya gossypii* genome to the 20 Mb *Yarrowia lipolytica* genome [1]. Within *Metschnikowiaceae*, three species have been whole genome sequenced: *C. lusitaniae* [2], *M. bicuspisdata* [3], *M. fructicola* [4] and now *M. reukaufii*. Genome synteny mapping identified 4789 ortholog pairs between *M. reukaufii* and *M. bicuspisdata* and 4401 pairs against *C. lusitaniae*, suggesting high genomic collinearity (Fig. S5). *C. lusitaniae* has a smaller genome at 12 Mb, whereas both *Metschnikowia* species stand at approximately 15.5 Mb, indicating genome expansion prior to the *Metschnikowia* speciation. The relative sizes of syntenic blocks across the genomes of the three species followed closely the overall genome size difference (Fig. S5). In contrast, the number of coding sequences and average coding sequence length is similar, suggesting that the *Metschnikowia* genomes expanded either due to the abundance or size of introns or extension of the intergenic space. Comparison of highly syntenic blocks of *M. reukaufii* to *M. bicuspisdata* and *C. lusitaniae* revealed expansion of the intergenic space as the main contributor to the increased genome size in the *M. reukaufii* (Fig. S4).

#### Telomere identification

To detect chromosomal signatures within the 7 large scaffolds, we screened for telomeric motifs. Four of the 7 scaffolds (scaffold 2-4 & 7), harboured telomeric repeats at both ends, while scaffolds 1, 5, and 6 had telomeric

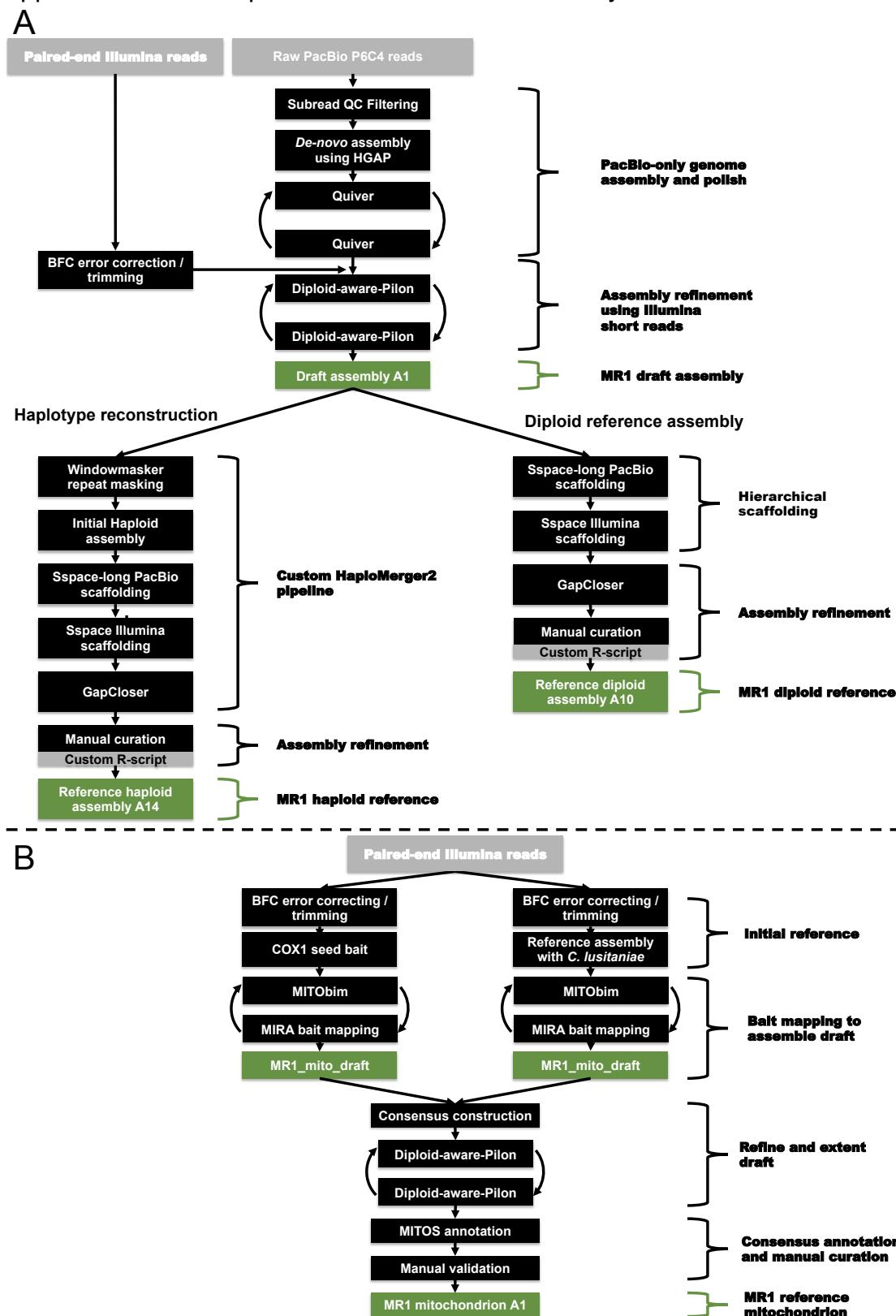
repeats at one end. The core motif was identified as 5' –

AAGATAAAATCAGTACATCCCT – 3', present as full- or partial sequence. This domain closely resembles the telomeric motif of 5' –

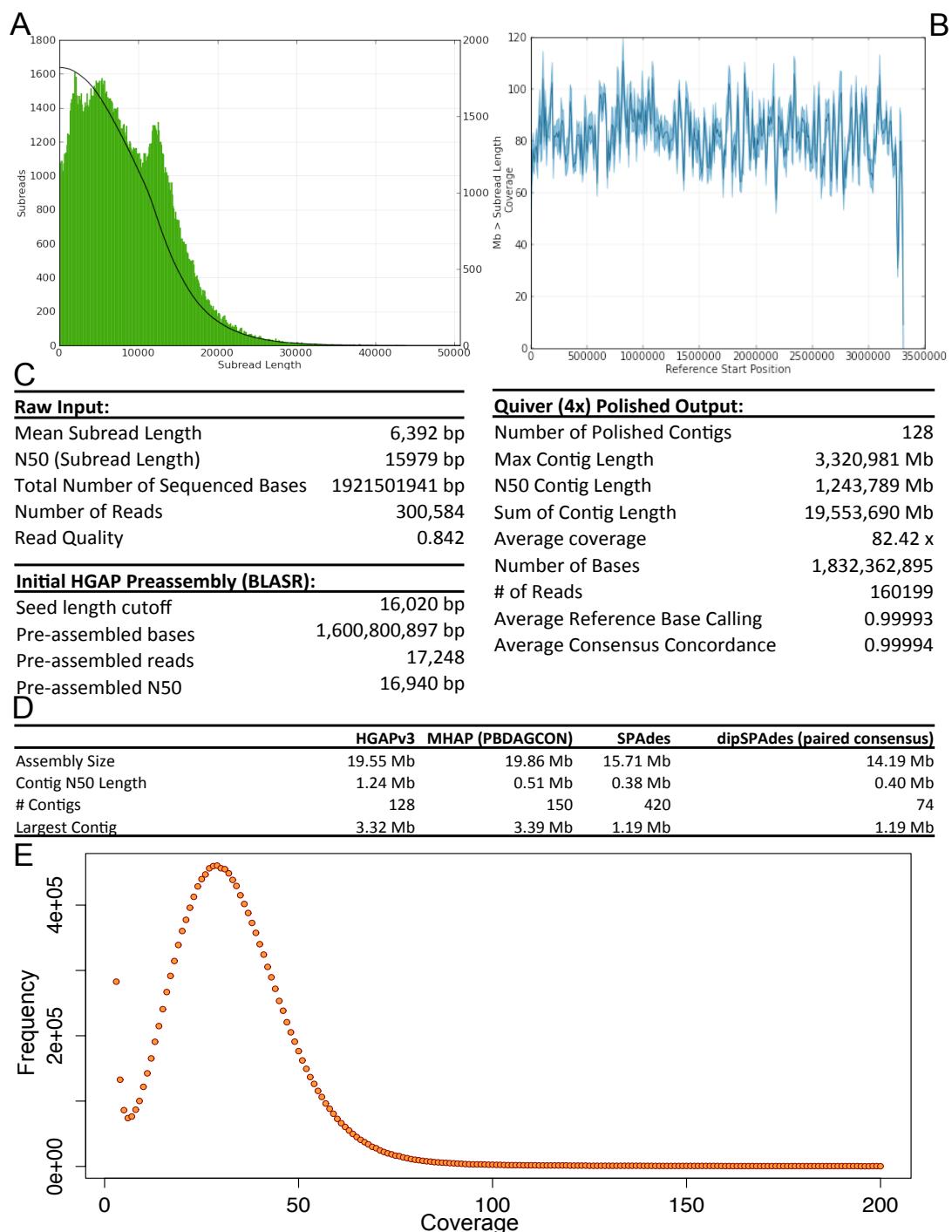
AAAGAACATCAGTACCTCCCT – 3' in *C. lusitaniae* [5]

## Supplementary Figures and Tables

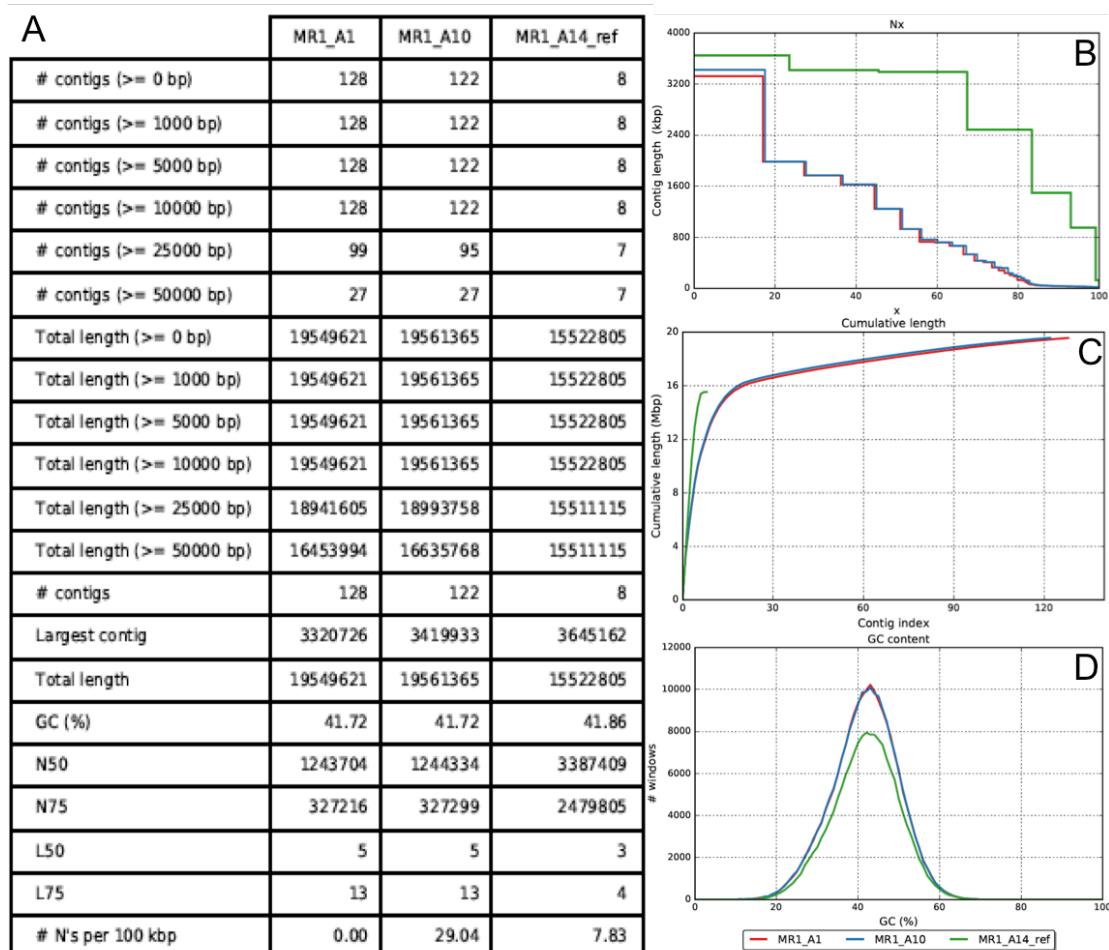
**Figure S1 Schematic of the *Metschnikowia reukaufii* genome assembly pipeline.** A, Genome assembly pipeline including diploid draft assembly, followed by reference haploid and diploid assemblies. B, Bait-mapping approach based independent mitochondrial assembly.



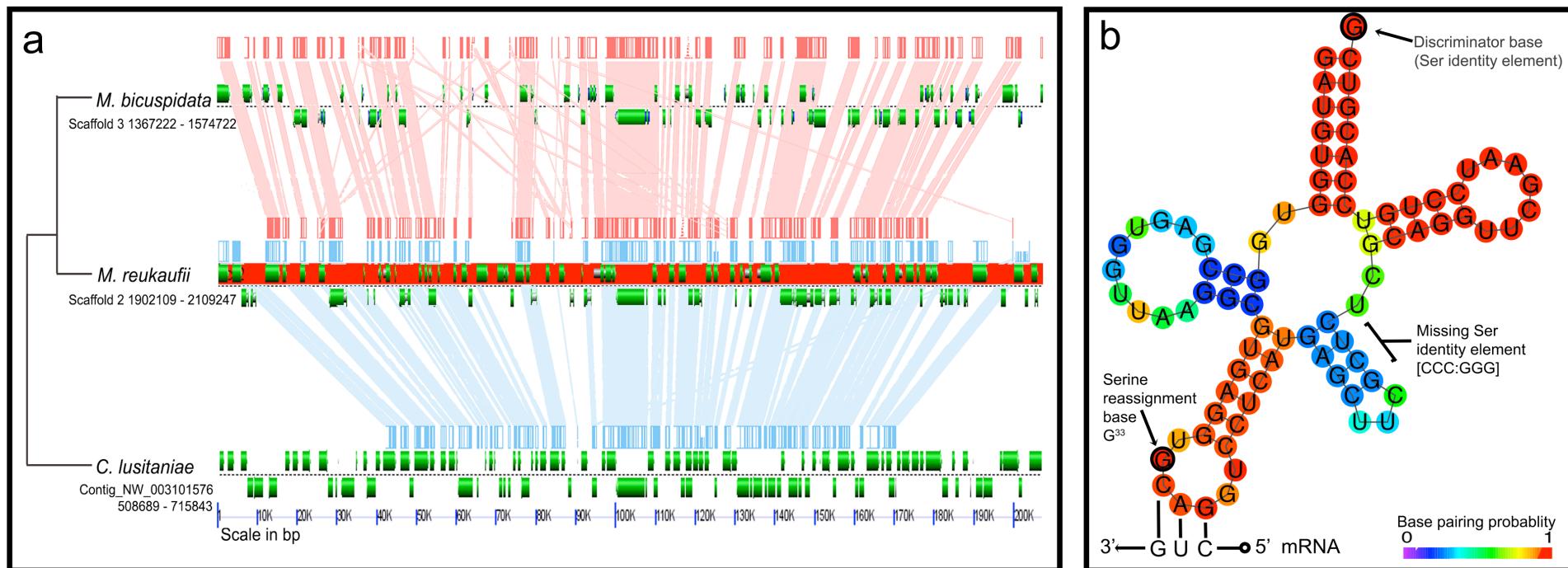
**Figure S2 Summary of *M. reukaufii* genome assembly statistics for the initial draft PacBio assembly MR1-A1.** A, Histogram of length distribution of raw P6C4 chemistry PacBio reads. The mean read length of the raw reads is 6,392 bp, and the N50 is 15,979 bp, B, Coverage across the length of the largest contig, final average coverage across the whole genome sequence was 82x, C, SMRT sequencing raw read, preassembly and assembly statistics, D, Comparison of HGAPv3, MHAP, SPAdes and dipSPAdes PacBio assemblers, and, E, Genome size estimation using *k*-mer distribution of unassembled *M. reukaufii* Illumina WGS reads. Frequency distribution suggests a genome size of ~18.4 Mb, also consistent with predictions from PacBio read data.



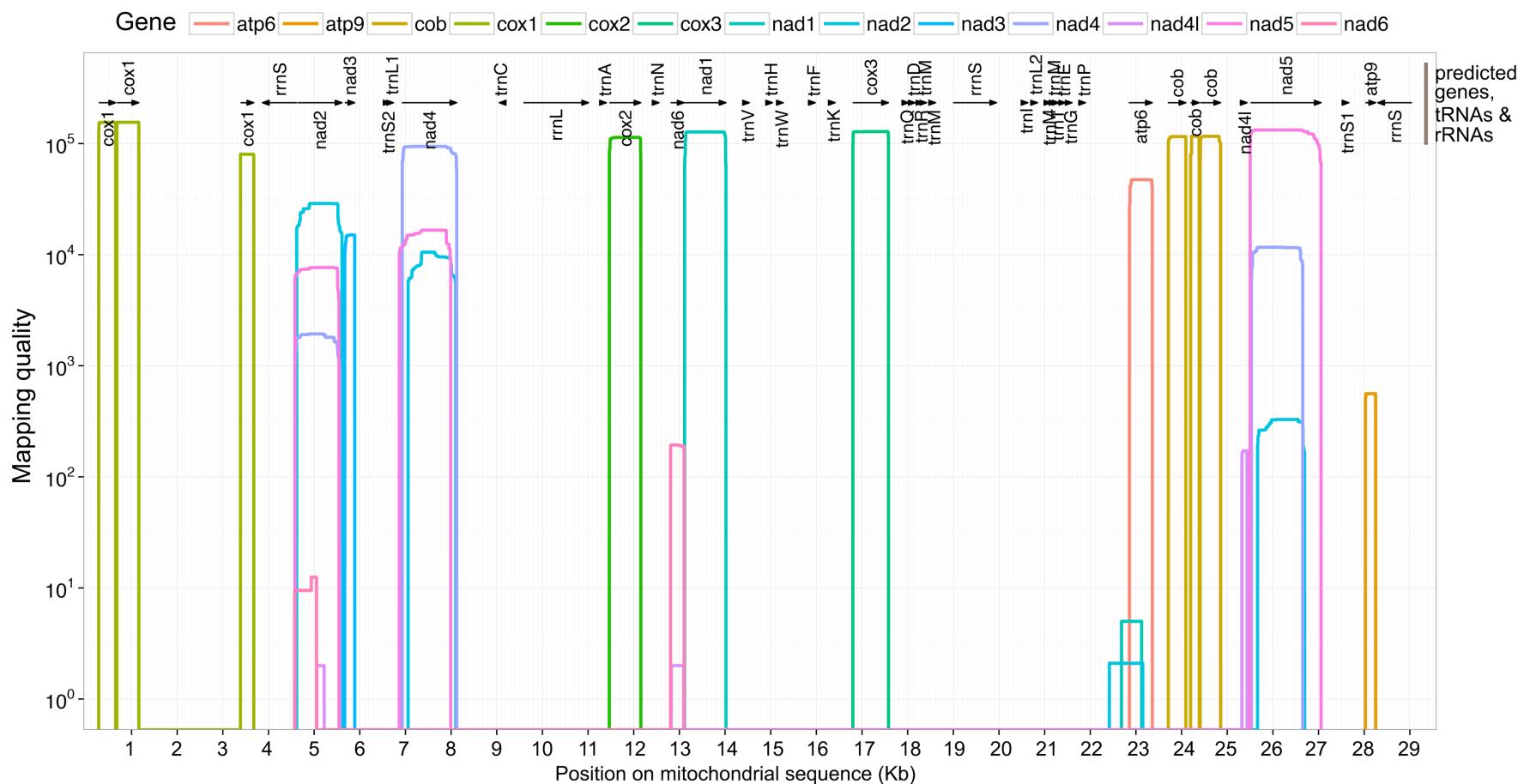
**Figure S3 Summary assembly statistics of initial draft MR1-A1, reference diploid (MR1-A10) and haploid (MR1-A14\_ref) *M. reukaufii* genome assemblies.** A, Summary table showing assembly parameters, B, Comparison of contig length *versus* number of contigs (x), C, Cumulative contig length *versus* contig index and D, GC content (%) across the three assemblies.



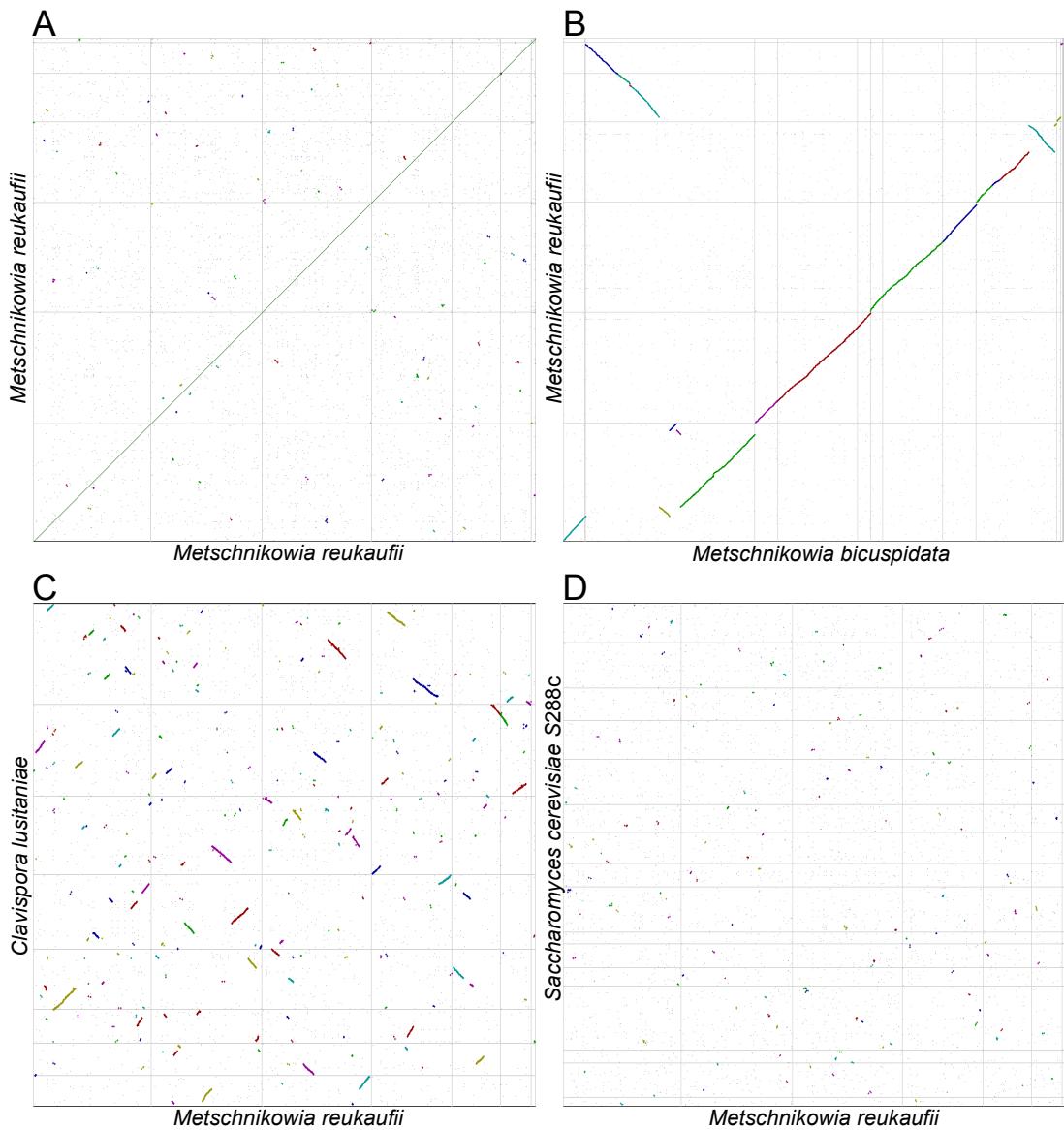
**Figure S4 Genomic features of *M. reukaufii* genome.** a, Intergenic expansion in the *Metschnikowia* genome. Comparison of a 200 Kb genomic region of *M. reukaufii* and *M. bicuspisdata* to closely related *Clavispora lusitaniae*. Green bars indicate predicted genes and red and blue tracks indicate genomic sequence conservation between *M. reukaufii* vs *M. bicuspisdata* and *M. reukaufii* vs *C. lusitaniae*, respectively. Conserved syntenic blocks are linked by shaded regions in their respective colours. b, The *M. reukaufii* tRNA<sub>CAG</sub><sup>Ser</sup> carries the CTG-clade characteristic purine G<sup>33</sup> instead of U<sup>33</sup>. In total, two of the three identity elements characteristic for Leu to Ser codon reassignment are present suggesting a hybrid tRNA<sub>CAG</sub><sup>Ser</sup>. The predicted anticodon CUG decoded by tRNA<sub>CAG</sub><sup>Ser</sup> is highlighted.



**Figure S5 Predicted genes, tRNAs and rRNAs along the length of the *M. reukaufii* mitochondrial sequence.** The mapping quality of mitochondrial genes compared to reference genes is indicated along the y-axis. Black arrows indicate the length and direction of the predicted genes and RNAs.



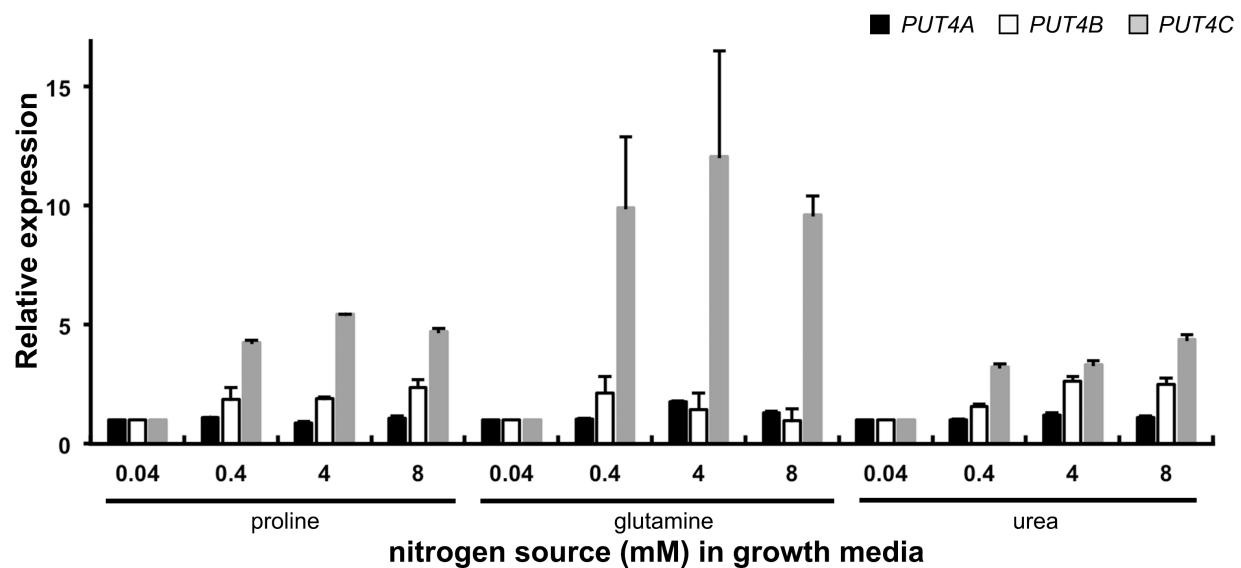
**Figure S6 Macrosynteny patterns between yeasts,** A, Macrosynteny of *M. reukaufii* versus *M. reukaufii*, B, *M. reukaufii* versus *M. bicuspidata*, C, *M. reukaufii* versus *C. lusitaniae*, and, D, *M. reukaufii* versus *S. cerevisiae* strain S288c.



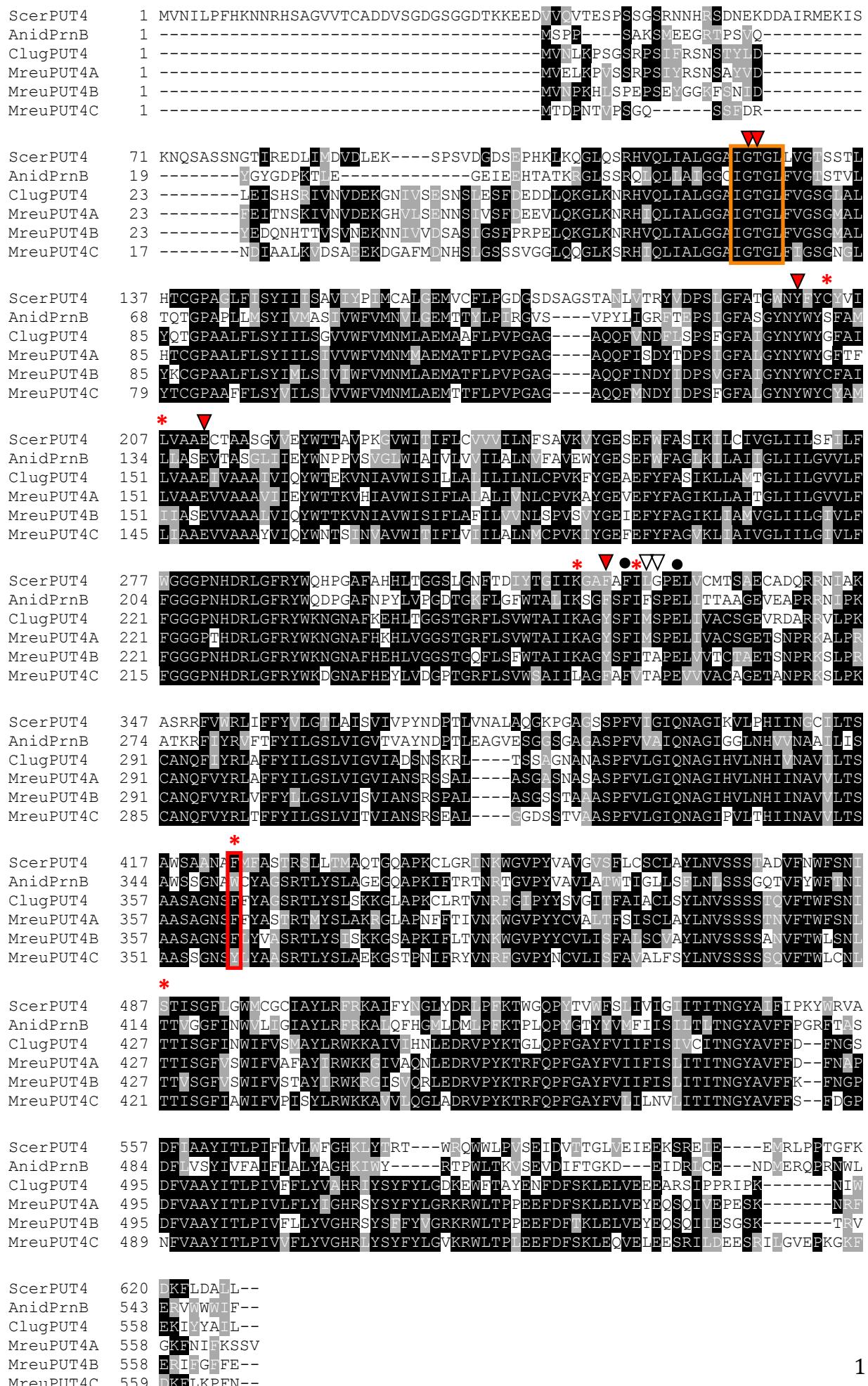
**Figure S7 Comparison of predicted conserved LysP domains (red \*) and AA permease domains (red rectangles) of GAP1 protein products from *M. reukaufii* GAP1 copies (MreuGAP1-1, MreuGAP1-2A to C) and *S. cerevisiae* (SceGAP1). These conserved regions are critical for transport function, which is predicted to be preserved across the *M reukaufii* copies. These domains are not conserved in closely-related YAT transporters found in the *M. reukaufii* genome (Mreu-scf3-4.234 and Mreu-scf5-0.170).**

SceGAP1	1 MSNTSSYEKNNPDNLKHNGITIDSEEL-IQEPITPSNGSA----VSIDETGSGSKWQDFKDSFKRVK-
MreuGAP1-1 (4.489)	1 -----MPEK-----ELNYVTSKGQASNEKDGGVYIDAFDAQAKAPMGWESEVDGFRREDE
MreuGAP1-2A (2.414)	1 -----MPEK-----ELNYVTSVEQASIEEKKGGV-TVQAFESPQSQKFSKRANEVDGFRRVDM
MreuGAP1-2B (2.519)	1 -----MPEK-----ELNYITSVEPVSLLEGKGGVVNVNDVFEEAKDNEKMSWESESFKDGFKRVEM
MreuGAP1-2C (2.599)	1 -----MPEK-----ELNYITSVEPVSLLEGKGGVVNVNDVFEEAKDNEKMSWESESFKDGFKRVEM
Mreu-scf3-4.234	1 -----MSSPTKSLETTNNSQEYASSLSLSDTHEQONGNWQNPFD <sup>*</sup> SFKPADO
Mreu-scf5-0.170	1 -----MSLSDKYGN-----IEEQYCRTESEFLWQNFFKDSFKRVNV
SceGAP1	64 -P-EVDPNLSEAEKVAILTAQTPLKHHHLKNRHLQMAIGGAIGTGLVGSGTALRTGGPASLILIGGST
MreuGAP1-1 (4.489)	53 AEGIJDPNLSEVEKAIAIVTANSPLSRLSLKGRHLQMAIGGSIGTGLFIGSCVLKNGGPASVLIAYLIG
MreuGAP1-2A (2.414)	52 DAMGIDPNLSEVEKAIAIVTANTPLSRLSLKGRHLQMAIGGSIGTGLFIGSCVLKNGGPASVLIAYLIG
MreuGAP1-2B (2.519)	53 DDLGIDPNLSEVEKAIAIVTANTPLSRLSLKGRHLQMAIGGSIGTGLFIGSCVLKNGGPASVLIAYLIG
MreuGAP1-2C (2.599)	53 DDLGIDPNLSEVEKAIAIVTANTPLSRLSLKGRHLQMAIGGSIGTGLFIGSCVLKNGGPASVLIAYLIG
Mreu-scf3-4.234	44 -VWLKLDLDAVEKANLRAANSOLAKKLKNRHLQMAIGGSIGTGLFGVGSCSALGTGGPCCVIAWLITA
Mreu-scf5-0.170	37 EQVEDMDDDNDEVERANLITAKSPDKRKLKSENISMIAIGGSIGSALSALFVGSCSALSTGGPACLLITWITG
SceGAP1	133 TMIVAMVVALGELAVIFPISCGETTYATRFIDESFGYANNENYMLQWLVLVPLEIVSASITVNFWGDPK
MreuGAP1-1 (4.489)	123 IMIVCTVHALGELAITFPVSGAEVTYNTNRFIDPSWGFMAMAWNYAMQWLVLVMELELVAAAITVRYWDTTTN
MreuGAP1-2A (2.414)	122 TMIVCTVHALGELAITFPVSGAEVTYNTNRFIDPSWGFMAMAWNYAMQWLVLVMELELVAAAITVRYWDTTTN
MreuGAP1-2B (2.519)	123 SMIVATVHALGELAITFPVSGAEFTYNTNRFIDPSWGFMAMAWNYAMQWLVLVMELELVAAAITVRYWDTTTN
MreuGAP1-2C (2.599)	123 SMIVATVHALGELAITFPVSGAEFTYNTNRFIDPSWGFMAMAWNYAMQWLVLVMELELVAAAITVRYWDTTTN
Mreu-scf3-4.234	113 TFEVTTMQLGELSTTFPISCGENIYATRFITEPAIGFAIGWNYELOEVILLELELVAAASISIQYWNKDN
Mreu-scf5-0.170	107 FAITTMQSLIGELSTFPVSGGENLYASRFIDPSVGFAVAUNYFIQFLVILPLELVSSSITMQFWNNNSIN
SceGAP1	203 YRDCEVALFWLAIVLINMFVGKVGYGEAEVFVFSFIKVITVVGFIILGIIINCGGGPIGGYIGCKYWHDPGA
MreuGAP1-1 (4.489)	193 -PAVVAIFYVVIINFFGVKGYGEAEVFVSTIKVIAVIGFIILGIVLVCGGPKGGYIGCKYWHNPGA
MreuGAP1-2A (2.414)	192 -IAAVALEFYVLIISINFFGVKGYGEAEVFVSAVKVLAVCGFIILGIVLVCGGPKGGYIGAKYWHNPGA
MreuGAP1-2B (2.519)	193 -PAVYVAVFYVLIINFFGVKGYGEAEFIFSAVKVLAVSGFIILGIVLVCGGPKGGYIGAKYWHDPGA
MreuGAP1-2C (2.599)	193 -PAVYVAVFYVLIINFFGVKGYGEAEFIFSAVKVLAVSGFIILGIVLVCGGPKGGYIGAKYWHDPGA
Mreu-scf3-4.234	183 -PDIFAVFVTFVFAITMMGVRYGEAEFVFCMIKVVIIGIFIILCVLICGGGPNHEFVCKYWHNPGA
Mreu-scf5-0.170	177 -ADIWVLFYVVCISINMFGRVARYCETEFVFSFIKVAVAFIIIVSIVLAAGGGPKGHSHGAEYWYNPG
SceGAP1	273 FAGDTPGAKFKGCVSVFTAASFAGSE-VGLAASESVEPRKSVPKAAKQVFWRITLFYIISLIMGILV
MreuGAP1-1 (4.489)	262 FNH-----GFKGLCSVFVTAAAFASCTELVGLAAAEVNPRKTMPPKAIKQVFWRITLFYIISLILVGCLV
MreuGAP1-2A (2.414)	261 FNH-----GFKGLCSVFVTAAAFAGCTELVGLAAAETVNPRKTMPPKAIKQVFWRITLFYIISLILVGMLV
MreuGAP1-2B (2.519)	262 FRN-----GFKGLCSVFVTAAAFAGCTELVGLAAAEMNPQCTMPKAIKQVFWRITLFYIISLILVGMLV
MreuGAP1-2C (2.599)	262 FRN-----GFKGLCSVFVTAAAFAGCTELVGLAAAEMNPQCTMPKAIKQVFWRITLFYIISLILVGMLV
Mreu-scf3-4.234	252 FAN-----GFKGVCSVFVTAASFAGCTEMISLGAAESENPAKALPKAIVQVLRITLFYIIVLTV
Mreu-scf5-0.170	246 FAN-----GFKGVSVFVTAAAFAGCTEMISLGAAESENPAKALPKAIVQVLRITLFYIIVLTV
SceGAP1	342 PYNDKSLI-CASSVDAAAASPFWIAIKTHG1KGLPSVNVVILIAVLSGVNSIYASRIMVALAEQRLIP *** **
MreuGAP1-1 (4.489)	327 PYNSEQLO-GS-DGSARYSPFWIAIRNAGISGLPSVMNVVILIAVLSGVNSVFGCSRITVALAAAGQAP
MreuGAP1-2A (2.414)	326 PYNSEELO-AS-DGIAARYSPFWIAIRNAGISGLPSVMNVVITISVLGVNSVFGCSRITVALAAAGQAP
MreuGAP1-2B (2.519)	327 PYNSEELO-AS-DGIAARYSPFWIAIRNAGISGLPSVMNVVIMISVLGVNSVFACSRITVALANAGQAP
MreuGAP1-2C (2.599)	327 PYNSEELO-AS-DGIAARYSPFWIAIRNAGISGLPSVMNVVIMISVLGVNSVFACSRITVALANAGQAP
Mreu-scf3-4.234	317 PYNDGRLLNCTSADAKITSPFWIAIVNSKGGLPSVINAIVLIAVLSGVNSVFACSRSLNSLAEGMAP
Mreu-scf5-0.170	311 PYNSPRLL-CASSVDTASPFWIAIEEGGIKGLPVMNAIVLVSIIISV-SIIVSYASRITLTLAEOQIAP
SceGAP1	411 EIFSYVDRKGRPLVGLIAVTSAGFLIAFVAASKKEGEVFNWLALSGLSSLFTWGGICICHIRFRKAIAAQ
MreuGAP1-1 (4.489)	395 KLFYIDKKGRPLGIILOSFLGLICFISASGKEGVFNWLALSGLSSLFTWGSICICHIRFRRALAVQ
MreuGAP1-2A (2.414)	394 KIGYIDKKGRPLVAILFOMVIAIMSFSASGKQCFMFNWLALSGLSSLFTWGSICICHIRFRRALAVQ
MreuGAP1-2B (2.519)	395 KIFGYIDKKGRPLGIILOSFLGLICFSSASGKQCFVNWLALSGLSSMFWSGSICMCHIRFRRALHVQ
MreuGAP1-2C (2.599)	395 KIFGYIDKKGRPLGIILOSFLGLICFSSASGKQCFVNWLALSGLSSMFWSGSICMCHIRFRRALHVQ
Mreu-scf3-4.234	387 KWTGYVDRKGRPLVAILVNMFGFLAFIAASDKOEVAFNWLALSGLSSLFTWMSINFSHIRFRRAAMKQ
Mreu-scf5-0.170	380 KICAYVDRKGRPLVAILCNLFLAASGKEEIFSWLISLSSIALSIALWISINWAHIRFRRALHVQ
SceGAP1	481 GRGLDELSFKSPTGWGSYWGLEYLIMFIAQFYAVFPGDPSAEGFFFYLSFFLVMVMMIGHKIKW
MreuGAP1-1 (4.489)	465 GRGKDEIAFTSQAGWIGSGWIGVILNLVLTIAQFWITALPIGGSPDASDFFQAYLSEFVILAFWIGHKIWK
MreuGAP1-2A (2.414)	464 KRDTSELAFKSOGLIGSWYGVILNLVLTIAQFWITALPIGGSPDASDFFQAYLSEFVILAFWIGHKIWK
MreuGAP1-2B (2.519)	465 KRDTSELAFKSOGLIGSWYGVILNLVLTIAQFWITALPIGGSPDASDFFQAYLSEFVILAFWIGHKIWK
MreuGAP1-2C (2.599)	465 GRDTSELAFKSOGLIGSWYGVILNLVLTIAQFWITALPIGGSPDASDFFQAYLSEFVILAFWIGHKIWK
Mreu-scf3-4.234	457 GRSLLDILVFRSATGVIGSWYGLVMNVLVIATFWSLFPGLICEAPNESSFFOCYIGLPTVIVSWMGKIKYS
Mreu-scf5-0.170	450 GRGVNEIPEVAQCTTGSTCGFISLVLVIAQFWIALFPGLCECPNAGFFFYLGCVILVIEVGHKIWK
SceGAP1	551 RNWKFLFIAEAKMDIDTGRREVLDLLKQEAEEKAIAIMATKPERWYRIWNFWC
MreuGAP1-1 (4.489)	535 RNWKFLFIRAKDIDIDTGRRELDLLKQEAEEKAIAEAKPYYIRYRFLC
MreuGAP1-2A (2.414)	534 RNWKFLFIRAKDIDIDTGRRELDLLKQEAEEKAIAEAKPYYIRYRFLC
MreuGAP1-2B (2.519)	535 CNWKEFIRAKDLDIDTGRRELDLLKQEAEEKAIAIMATKPFYYRMYRTVC
MreuGAP1-2C (2.599)	535 CNWKEFIRAKDLDIDTGRRELDLLKQEAEEKAIAEAKPYYRMYRTVC
Mreu-scf3-4.234	527 KSWRFLIKADIDIDTGRHVEFMDLIRQEAELASQSKKSWRRRLAYIF
Mreu-scf5-0.170	520 KNWLIQPAKDDIDTGRRETDLELLKEQIROEKLARPKWYFRLYHLWC

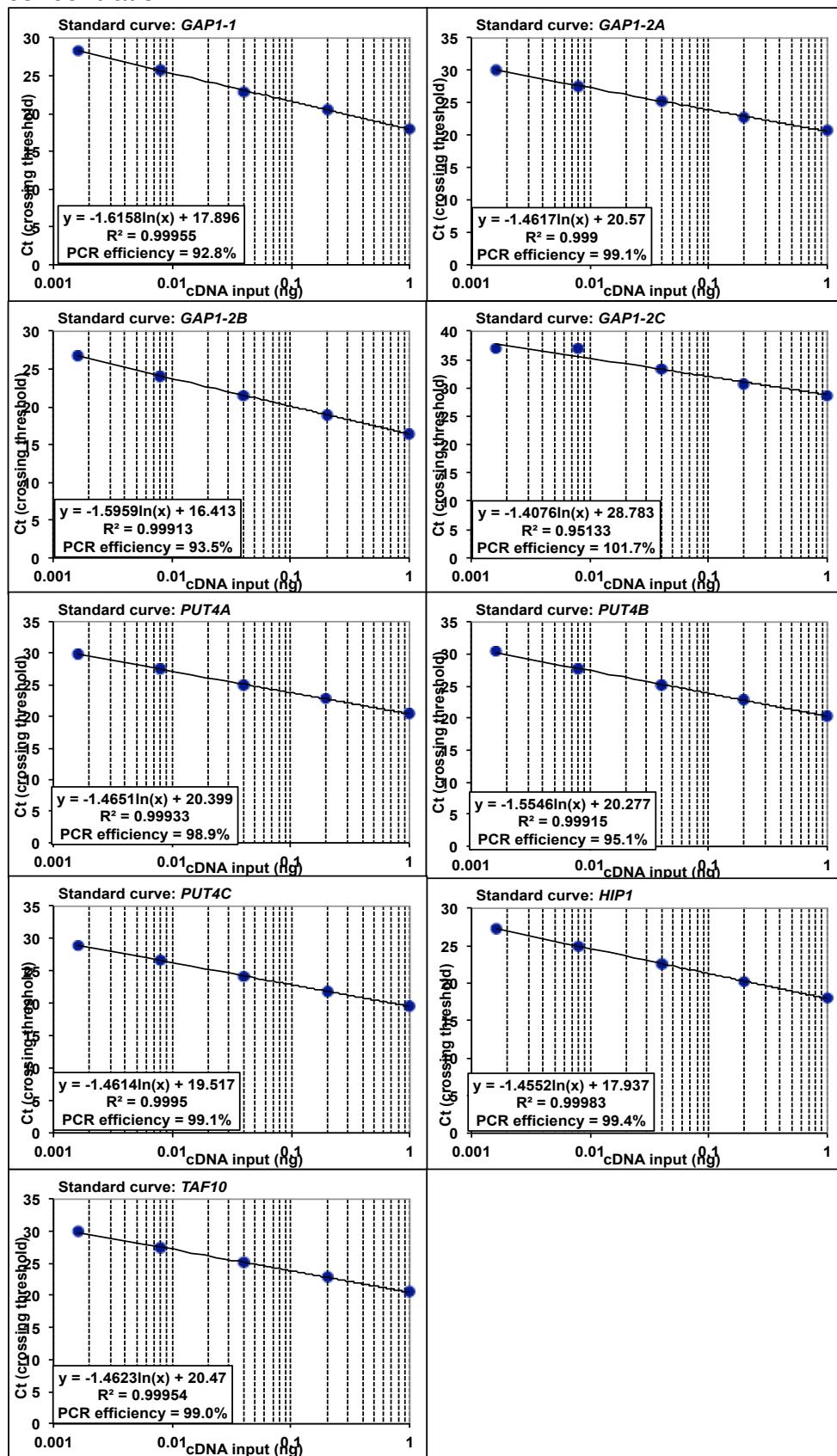
**Figure S8 Expression of *MreuPUT4* copies in nectar containing proline, glutamine or urea as nitrogen sources.** *M. reukaufii* cells were grown for 4 h in either synthetic nectar (20 % sucrose) with 0.04 mM, 0.4 mM, 4 mM, or 8 mM proline, glutamine or urea as nitrogen source. All data are normalized against the internal control gene *TAF10*. Data represent means  $\pm$  SD relative to 0.04 mM concentrations (set to 1); n = 2 to 3 biological replicates each with 2 technical replicates and at least 3 repetitions of the experiment.



**Figure S9 Sequence alignment of PUT4/PrnB proteins of known function from *S. cerevisiae* and *A. nidulans*, respectively, and their homologs in *C. lusitaniae* and *M. reukaufii*.** Red arrowheads indicate residues conserved in the YAT family, which are predicted to interact with the invariant part of amino acid substrates in PrnB (Gly<sup>56</sup>, Thr<sup>57</sup>, Glu<sup>138</sup>, and Phe<sup>248</sup>) and ScePUT4 (Gly<sup>125</sup>, Thr<sup>126</sup>, Glu<sup>211</sup> and Phe<sup>321</sup>). Tyr<sup>200</sup> of ScePUT4, necessary for transport activity in SceCAN1 is also highlighted. Red asterisks indicate residues non-conserved in the YAT family, which in PrnB (Trp<sup>351</sup> and Thr<sup>414</sup>) appear to participate in L-proline binding, as well as specificity determination residues of PrnB (Ser<sup>130</sup>, Lys<sup>245</sup>, Trp<sup>351</sup>, and Thr<sup>414</sup>). Residues Leu<sup>134</sup> and Ile<sup>251</sup> of PrnB shown to confer substrate specificity in SceCAN1 are also highlighted. Empty arrowheads indicate residues close to the substrate binding site which affect the specificity of PrnB (Phe<sup>252</sup> and Ser<sup>253</sup>), directly or indirectly. Black circles indicate residues conserved in the YAT family and important for PrnB function, that do not appear to directly participate in substrate binding (Phe<sup>250</sup> and Glu<sup>255</sup>). The orange frame indicates the YAT conserved G(T/S)G motif and the red frame highlights Phe<sup>424</sup> unique to PUT4 within the SceYAT family which facilitates L-alanine transport [6].



**Figure S10 Amplification efficiencies of developed qPCR primers range between 90-105%.** Amplification efficiencies were measured using a linear dilution series of cDNA and each reaction was run with 2 technical replicates at each cDNA concentration.



**Table S1 Functional annotation of the 227 tandem duplicated genes unique to *M. reukaufii*.**

<b>MarkerID of TGA anchor gene</b>	<b>Manuscript ID</b>	<b>Protein annotation (Blast2GO)</b>	<b>Seq. Length</b>	<b>Min. eValue</b>	<b>Mean Similarity</b>
maker-scf2-snap-gene-0.85-mRNA-1		wd40 repeat-like protein	2539	0	61.40%
snap_masked-scf2-processed-gene-0.71-mRNA-1		general amino acid permease	635	0	78.00%
snap_masked-scf2-processed-gene-0.42-mRNA-1		DEHA2G00946p	516	0	78.90%
maker-scf2-snap-gene-0.402-mRNA-1		multidrug resistance protein 2	1081	0	74.00%
augustus_masked-scf2-processed-gene-0.549-mRNA-1		hypothetical protein CLUG_01432	1059	0	49.80%
genemark-scf2-processed-gene-0.632-mRNA-1		copper resistance protein	594	2.17E-87	49.40%
genemark-scf2-processed-gene-0.574-mRNA-1		hypothetical protein CLUG_01452	2790	0	73.50%
snap_masked-scf2-processed-gene-0.80-mRNA-1		pmc1 vacuolar calcium p-type atpase	102	8.28E-11	80.25%
snap_masked-scf2-processed-gene-0.583-mRNA-1		---NA---	74		
maker-scf2-snap-gene-1.581-mRNA-1		hypothetical protein CLUG_01538	609	6.30E-91	78.40%
genemark-scf2-processed-gene-1.134-mRNA-1		transcriptional repressor	325	2.61E-67	64.80%
snap_masked-scf2-processed-gene-1.358-mRNA-1		hypothetical protein QG37_03270	142	1.42E-46	82.00%
snap_masked-scf2-processed-gene-1.414-mRNA-1		---NA---	87		
snap_masked-scf2-processed-gene-1.95-mRNA-1		---NA---	71		
maker-scf2-snap-gene-1.612-mRNA-1	<i>MreuOPT2A, -B, -C, -D, -E</i>	opt family small oligopeptide transporter	904	0	83.10%
snap_masked-scf2-processed-gene-1.546-mRNA-1		histone-fold-containing protein	347	3.61E-81	80.20%
genemark-scf2-processed-gene-1.199-mRNA-1		spf3 protein	323	0	89.10%
augustus_masked-scf2-processed-gene-1.335-mRNA-1		ion transporter	340	1.02E-153	66.00%
maker-scf2-snap-gene-1.603-mRNA-1		v-type proton atpase proteolipid subunit	158	1.51E-94	95.10%
snap_masked-scf2-processed-gene-1.388-mRNA-1		nadp-dependent alcohol dehydrogenase 7	405	0	72.60%
snap_masked-scf2-processed-gene-1.371-mRNA-1		hypothetical protein V494_05488	132	1.34E-21	64.00%
snap_masked-scf2-processed-gene-1.541-mRNA-1		---NA---	81		
maker-scf2-snap-gene-2.591-mRNA-1		mmd1 mitochondrial protein	114	7.17E-50	71.00%
maker-scf2-snap-gene-2.587-mRNA-1		cu zn superoxide dismutase	919	1.74E-41	68.30%
maker-scf2-snap-gene-2.579-mRNA-1		gaba-specific high-affinity permease	733	0	80.60%
snap_masked-scf2-processed-gene-2.445-mRNA-1		---NA---	306		
snap_masked-scf2-processed-gene-2.555-mRNA-1		---NA---	81		
snap_masked-scf2-processed-gene-2.578-mRNA-1		60s ribosomal protein l5	320	0	92.70%
snap_masked-scf2-processed-gene-2.595-mRNA-1		sporulation-specific protein 73	145	2.21E-35	63.50%
genemark-scf2-processed-gene-2.408-mRNA-1		histidine acid inositol hexakisphosphate and inositol heptakisphosphate inositol pyrophosphate	651	0	81.20%
snap_masked-scf2-processed-gene-2.559-mRNA-1		translation elongation factor 1- partial	307	8.17E-119	73.40%
augustus_masked-scf2-processed-gene-2.184-mRNA-1		lysine-specific permease	482	1.35E-177	60.30%
genemark-scf2-processed-gene-3.527-mRNA-1		hypothetical protein QG37_07532	656	7.25E-64	49.80%
maker-scf2-snap-gene-3.8-mRNA-1		folylpolyglutamate synthase	1225	1.44E-155	63.20%
augustus_masked-scf2-processed-gene-3.322-mRNA-1		aspartic proteinase 3	944	5.21E-128	56.60%
maker-scf2-snap-gene-3.640-mRNA-1		aspartic protease	725	5.11E-114	60.30%
maker-scf2-snap-gene-3.178-mRNA-1		hypothetical protein AC631_00105	3269	0	62.30%
snap_masked-scf2-processed-gene-3.549-mRNA-1		hypothetical protein QG37_06724	471	1.20E-178	64.80%
maker-scf2-snap-gene-3.691-mRNA-1		a-chain sccts1_apo crystal structure	363	4.62E-125	67.10%
maker-scf2-snap-gene-3.38-mRNA-1		histone acetyltransferase subunit	766	2.06E-178	76.80%
genemark-scf2-processed-gene-4.347-mRNA-1		hypothetical protein QG37_01280	566	3.85E-101	59.20%
genemark-scf2-processed-gene-4.263-mRNA-1		hypothetical protein CLUG_02597	245	2.07E-113	75.00%
snap_masked-scf2-processed-gene-4.473-mRNA-1		gpi inositol-deacylase	1025	0	61.50%
maker-scf2-snap-gene-4.623-mRNA-1		dna-directed rna polymerase iii 130 kda polypeptide	1206	0	93.70%
snap_masked-scf2-processed-gene-4.478-mRNA-1		hypothetical protein QG37_01345	332	6.75E-60	51.83%
snap_masked-scf2-processed-gene-4.495-mRNA-1		autophagy-related protein 7 (autophagy-related e1-like activating enzyme atg7)	228	4.77E-66	62.30%
snap_masked-scf2-processed-gene-4.498-mRNA-1		conserved hypothetical protein	340	1.61E-27	82.00%
snap_masked-scf2-processed-gene-4.8-mRNA-1		---NA---	204		
genemark-scf2-processed-gene-4.426-mRNA-1		histone acetyltransferase gon5	516	0	90.40%
snap_masked-scf2-processed-gene-4.551-mRNA-1		---NA---	59		
snap_masked-scf2-processed-gene-5.43-mRNA-1		rna polymerase ii mediator complex	457	9.49E-102	70.90%
genemark-scf2-processed-gene-5.459-mRNA-1		mitochondrial chaperone bcs1	445	0	88.00%
maker-scf2-exonerase_protein2genome-gene-5.173-mRNA-1		hypothetical protein CLUG_04708	97	1.25E-42	79.70%
snap_masked-scf2-processed-gene-5.382-mRNA-1		hypothetical protein CLUG_03518	641	0	55.40%
snap_masked-scf2-processed-gene-5.441-mRNA-1		translation initiation factor 3 subunit h	373	0	81.60%

*Continued overleaf...*

snap_masked-scf2-processed-gene-5.526-mRNA-1	solute carrier family 24 (sodium potassium calcium exchanger) member 6	666	1.99E-172	56.20%
augustus_masked-scf2-processed-gene-5.595-mRNA-1	hypothetical wd-40 repeat protein	1040	0	63.30%
snap_masked-scf2-processed-gene-5.661-mRNA-1	pff1_cla4 ame: full=vacuolar membrane protease ame: full=fxna-related family	1325	0	69.00%
protease 1				
maker-scf2-snap-gene-5.423-mRNA-1	translation initiation factor subunit a (eif-3a)	1282	0	80.70%
genemark-scf2-processed-gene-5.615-mRNA-1	snare-like likely involved in golgi	209	5.73E-94	75.30%
snap_masked-scf2-processed-gene-5.1130-mRNA-1	hypothetical protein VP1G_11002	227	1.61E-23	63.50%
genemark-scf2-processed-gene-5.696-mRNA-1	acetyl- carboxylase biotin carboxylase	2565	0	87.80%
genemark-scf2-processed-gene-5.695-mRNA-1	beta-glucan synthase	1715	0	69.30%
snap_masked-scf2-processed-gene-5.388-mRNA-1	---NA---	345		
maker-scf3-snap-gene-0.152-mRNA-1	aspartic proteinase 3	1599	0	54.10%
snap_masked-scf3-processed-gene-0.445-mRNA-1	utp-glucose-1-phosphate uridylyltransferase	82	3.08E-31	87.30%
snap_masked-scf3-processed-gene-0.424-mRNA-1	5'-phosphoribosylformyl glycaminidine synthetase	1366	0	86.30%
maker-scf3-snap-gene-0.39-mRNA-1	hypothetical protein G7K_2802-t1	129	2.74E-17	68.00%
snap_masked-scf3-processed-gene-0.436-mRNA-1	---NA---	81		
maker-scf3-snap-gene-1.194-mRNA-1	kynureninase	1029	0	79.70%
genemark-scf3-processed-gene-1.26-mRNA-1	srp9 protein	1776	0	54.90%
genemark-scf3-processed-gene-1.89-mRNA-1	phosphopantethenoylcysteine decarboxylase	701	3.04E-144	68.50%
snap_masked-scf3-processed-gene-1.319-mRNA-1	---NA---	59		
snap_masked-scf3-processed-gene-1.539-mRNA-1	set2_debha ame: full=histone-lysine n- h3 lysine-36 specific ame: full=set	2283	0	75.90%
genemark-scf3-processed-gene-1.103-mRNA-1	domain-containing protein 2			
protein phosphatase methylesterase 1	385	3.15E-114	61.40%	
40S ribosomal protein s18	145	2.94E-99	97.50%	
snap_masked-scf3-processed-gene-2.413-mRNA-1	hypothetical protein SPAPADRAFT_52739	556	0	65.30%
maker-scf3-exonerate_protein2genome-gene-2.58-mRNA-1	batten s disease protein cln3	410	6.62E-169	74.20%
genemark-scf3-processed-gene-2.45-mRNA-1	fungal zinc cluster transcription	651	1.06E-61	46.50%
snap_masked-scf3-processed-gene-2.451-mRNA-1	60S ribosomal subunit assembly export protein loc1	270	1.09E-79	85.70%
maker-scf3-exonerate_protein2genome-gene-2.141-mRNA-1	hypothetical protein CLUG_00537	617	0	71.20%
genemark-scf3-processed-gene-2.177-mRNA-1	paxneb-domain-containing protein	422	3.69E-169	68.30%
genemark-scf3-processed-gene-2.196-mRNA-1	cation diffusion facilitator family transporter	713	0	61.30%
maker-scf3-snap-gene-2.28-mRNA-1	cell division control protein 48	273	1.05E-34	69.10%
snap_masked-scf3-processed-gene-2.592-mRNA-1	---NA---	491		
snap_masked-scf3-processed-gene-2.521-mRNA-1	---NA---	96		
maker-scf3-snap-gene-3.10-mRNA-1	hypothetical protein CLUG_01671	933	0	73.20%
snap_masked-scf3-processed-gene-3.270-mRNA-1	hypothetical protein CLUG_03063	1118	0	67.70%
snap_masked-scf3-processed-gene-3.51-mRNA-1	---NA---	83		
augustus_masked-scf3-processed-gene-3.355-mRNA-1	alkyl hydroperoxide reductase 1	190	7.97E-96	69.00%
genemark-scf3-processed-gene-3.458-mRNA-1	bifunctional 6-phosphofructo-2-kinase fructose- -bisphosphate 2-phosphatase	566	0	75.00%
snap_masked-scf3-processed-gene-3.139-mRNA-1	hypothetical protein CLUG_01744	459	3.86E-33	58.00%
snap_masked-scf3-processed-gene-4.391-mRNA-1	mcp-domain signal transduction protein	553	3.67E-86	54.40%
maker-scf3-exonerate_protein2genome-gene-4.611-mRNA-1	plasma membrane proteolipid 3	55	2.33E-24	85.60%
maker-scf3-snap-gene-4.453-mRNA-1	serine threonine-protein phosphatase pp1-gamma catalytic subunit	783	0	76.10%
genemark-scf3-processed-gene-4.286-mRNA-1	cerevisin	471	0	68.40%
genemark-scf3-processed-gene-4.268-mRNA-1	hypothetical protein CLUG_00700	732	0	58.10%
snap_masked-scf3-processed-gene-4.445-mRNA-1	---NA---	735		
snap_masked-scf3-processed-gene-4.396-mRNA-1	hypothetical protein BN1708_003876	355	4.24E-49	60.00%
snap_masked-scf3-processed-gene-4.489-mRNA-1	general amino acid permease	589	0	85.80%
genemark-scf3-processed-gene-4.339-mRNA-1	hypothetical protein CLUG_00742	350	4.35E-150	70.60%
genemark-scf3-processed-gene-5.570-mRNA-1	dnak hsp70 family atpase and chaperone	1336	0	85.90%
snap_masked-scf3-processed-gene-5.740-mRNA-1	fch-domain-containing protein	821	0	75.90%
snap_masked-scf3-processed-gene-5.81-mRNA-1	hypothetical protein BN1723_005673	317	2.53E-11	60.00%
snap_masked-scf3-processed-gene-5.113-mRNA-1	---NA---	240		
genemark-scf3-processed-gene-5.637-mRNA-1	pre-mrna-splicing factor clf1	710	0	63.80%
snap_masked-scf3-processed-gene-5.238-mRNA-1	trs120 targeting complex component involved in er to golgi membrane traffic	1447	0	56.30%
maker-scf3-snap-gene-5.619-mRNA-1	phosphoribosylglycinamide formyltransferase	600	1.95E-122	91.40%
maker-scf3-snap-gene-5.386-mRNA-1	gtp-binding protein	510	0	92.40%
snap_masked-scf3-processed-gene-5.285-mRNA-1	heat shock protein ssb1	527	0	69.40%
snap_masked-scf3-processed-gene-5.251-mRNA-1	---NA---	221		
snap_masked-scf3-processed-gene-5.932-mRNA-1	---NA---	68		
augustus_masked-scf3-processed-gene-5.850-mRNA-1	hypothetical protein CLUG_02757	296	3.13E-131	80.60%
genemark-scf1-processed-gene-0.15-mRNA-1	hypothetical protein CLUG_05245	764	0	56.90%
snap_masked-scf1-processed-gene-0.61-mRNA-1	hypothetical protein VP1G_11265	311	2.26E-67	72.00%

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snap_masked-scf1-processed-gene-0.194-mRNA-1		98		
genemark-scf1-processed-gene-0.121-mRNA-1		410	0	83.80%
snap_masked-scf1-processed-gene-0.279-mRNA-1		164	4.69E-70	75.00%
snap_masked-scf1-abinit-gene-1.198-mRNA-1		307	1.79E-21	47.78%
genemark-scf1-processed-gene-1.241-mRNA-1		419	0	77.30%
genemark-scf1-processed-gene-1.267-mRNA-1		198	9.97E-42	48.80%
genemark-scf1-processed-gene-1.447-mRNA-1		390	0	70.10%
snap_masked-scf1-processed-gene-1.180-mRNA-1		1231	2.49E-136	54.20%
snap_masked-scf1-processed-gene-1.142-mRNA-1		110		
snap_masked-scf1-processed-gene-2.143-mRNA-1		987	2.46E-63	82.40%
genemark-scf1-processed-gene-2.403-mRNA-1		380	0	86.80%
maker-scf1-snap-gene-2.342-mRNA-1		1246	0	62.60%
maker-scf1-snap-gene-2.10-mRNA-1		696	0	62.70%
genemark-scf1-processed-gene-2.529-mRNA-1		476	0	63.80%
maker-scf1-snap-gene-2.414-mRNA-1		1692	0	88.50%
maker-scf1-snap-gene-3.386-mRNA-1		358	4.03E-100	87.10%
snap_masked-scf1-processed-gene-3.460-mRNA-1		321	0	95.40%
snap_masked-scf1-processed-gene-3.491-mRNA-1		145	4.82E-56	76.20%
snap_masked-scf1-processed-gene-3.109-mRNA-1		541	2.25E-35	65.50%
maker-scf1-snap-gene-3.392-mRNA-1		700	3.93E-98	72.50%
maker-scf1-snap-gene-3.619-mRNA-1		1789	0	64.80%
genemark-scf1-processed-gene-3.450-mRNA-1		462	0	85.20%
snap_masked-scf1-processed-gene-3.599-mRNA-1		539	1.50E-178	64.50%
snap_masked-scf1-processed-gene-3.537-mRNA-1		70	4.14E-11	72.00%
snap_masked-scf1-processed-gene-4.516-mRNA-1		991	0	70.00%
genemark-scf1-processed-gene-4.295-mRNA-1		410	0	84.90%
genemark-scf1-processed-gene-4.277-mRNA-1		381	5.07E-162	63.30%
maker-scf1-snap-gene-4.12-mRNA-1		713	0	83.80%
snap_masked-scf1-processed-gene-4.152-mRNA-1		551	0	92.10%
maker-scf1-snap-gene-4.661-mRNA-1		1275	0	84.90%
snap_masked-scf1-processed-gene-4.555-mRNA-1		395	6.82E-42	61.50%
snap_masked-scf1-processed-gene-5.48-mRNA-1		110	9.51E-34	79.40%
snap_masked-scf1-processed-gene-5.12-mRNA-1		313	3.14E-29	65.67%
snap_masked-scf1-processed-gene-5.45-mRNA-1		159		
maker-scf1-snap-gene-5.613-mRNA-1		379	0	87.90%
snap_masked-scf1-processed-gene-5.565-mRNA-1		576	0	59.80%
genemark-scf1-processed-gene-6.422-mRNA-1		472	0	72.00%
genemark-scf1-processed-gene-6.443-mRNA-1		324	4.58E-171	97.30%
maker-scf1-snap-gene-6.571-mRNA-1		172	6.78E-77	92.70%
snap_masked-scf1-processed-gene-6.748-mRNA-1		580	4.58E-152	57.70%
snap_masked-scf1-processed-gene-6.706-mRNA-1		556	0	71.20%
maker-scf1-snap-gene-6.848-mRNA-1		1040	0	84.60%
genemark-scf1-processed-gene-6.562-mRNA-1		759	0	73.80%
maker-scf1-snap-gene-6.890-mRNA-1		358	5.69E-74	61.10%
maker-scf1-augustus-gene-6.15-mRNA-1		1158	0	85.50%
snap_masked-scf1-processed-gene-6.851-mRNA-1		241	6.12E-29	59.80%
augustus_masked-scf1-processed-gene-6.246-mRNA-1		1128	0	56.40%
snap_masked-scf1-processed-gene-6.209-mRNA-1		86	8.58E-08	78.00%
maker-scf6-snap-gene-0.746-mRNA-1		2263	4.54E-131	64.20%
maker-scf6-snap-gene-0.730-mRNA-1		622	0	77.70%
genemark-scf6-processed-gene-0.670-mRNA-1		1118	0	66.80%
maker-scf6-snap-gene-0.1105-mRNA-1		1105	0	77.90%
genemark-scf5-processed-gene-0.323-mRNA-1		1085	0	74.10%
maker-scf5-snap-gene-0.351-mRNA-1		1101	0	67.70%
snap_masked-scf5-processed-gene-0.134-mRNA-1		879	4.46E-174	54.50%
snap_masked-scf5-processed-gene-0.30-mRNA-1		779	0	58.00%
augustus_masked-scf5-processed-gene-0.282-mRNA-1		122	1.02E-66	92.60%
genemark-scf5-processed-gene-0.316-mRNA-1		807	0	63.00%
snap_masked-scf5-processed-gene-0.576-mRNA-1		766	2.18E-109	61.80%
genemark-scf5-processed-gene-0.362-mRNA-1		1369	0	75.40%
genemark-scf5-processed-gene-0.343-mRNA-1		720	0	82.50%
maker-scf5-snap-gene-1.1120-mRNA-1		2758	1.10E-116	53.00%

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snap_masked-scf5-processed-gene-1.863-mRNA-1	membrane signaling protein	1096	0	65.30%
maker-scf5-exonrate_protein2genome-gene-1.834-mRNA-1	hypothetical protein QG37_04139	108	2.85E-44	71.30%
genemark-scf5-processed-gene-1.855-mRNA-1	hypothetical protein QG37_05716	634	0	70.90%
augustus_masked-scf5-processed-gene-1.463-mRNA-1	wd repeat	1542	0	59.00%
snap_masked-scf5-processed-gene-1.827-mRNA-1	isocitrate dehydrogenase subunit mitochondrial precursor	322	6.65E-130	69.00%
genemark-scf5-processed-gene-1.543-mRNA-1	hypothetical protein CLUG_02685	365	3.96E-115	60.80%
snap_masked-scf5-processed-gene-1.372-mRNA-1	---NA---	108		
snap_masked-scf5-processed-gene-1.804-mRNA-1	---NA---	82		
snap_masked-scf5-processed-gene-1.955-mRNA-1	glycerol kinase	812	0	89.30%
genemark-scf5-processed-gene-1.1001-mRNA-1	amino acid transporter	519	0	78.60%
genemark-scf5-processed-gene-1.994-mRNA-1	p-loop containing nucleoside triphosphate hydrolase protein	367	0	95.80%
snap_masked-scf5-processed-gene-1.225-mRNA-1	conserved nucleotide binding protein	293	1.36E-156	83.50%
maker-scf5-snap-gene-1.749-mRNA-1	elongation factor mitochondrial	901	0	86.90%
genemark-scf5-processed-gene-1.1072-mRNA-1	atp-dependent rna helicase dbp2	540	0	88.90%
snap_masked-scf5-processed-gene-1.318-mRNA-1	---NA---	199		
snap_masked-scf5-abinit-gene-1.124-mRNA-1	cytochrome c oxidase subunit vb	139	1.87E-27	89.00%
snap_masked-scf4-processed-gene-0.306-mRNA-1	rna pol ii transcription cofactor	338	8.16E-180	79.20%
snap_masked-scf4-processed-gene-0.115-mRNA-1	pyridoxamine 5'-phosphate oxidase	700	9.84E-120	80.70%
genemark-scf4-processed-gene-0.411-mRNA-1	potential transmembrane protein	476	1.57E-172	67.80%
genemark-scf4-processed-gene-0.350-mRNA-1	lysophospholipase-like protein	767	0	74.40%
snap_masked-scf4-processed-gene-0.167-mRNA-1	heat shock protein ssb1	572	9.26E-132	71.10%
snap_masked-scf4-processed-gene-0.567-mRNA-1	hypothetical protein G7K_2802-t1	217	1.92E-17	73.00%
genemark-scf4-processed-gene-1.226-mRNA-1	molecular chaperone	701	0	92.70%
genemark-scf4-processed-gene-1.237-mRNA-1	transcriptional regulator	424	0	92.30%
snap_masked-scf4-processed-gene-1.375-mRNA-1	hypothetical protein CLUG_01071	580	1.71E-66	52.50%
snap_masked-scf4-processed-gene-1.325-mRNA-1	40S ribosomal protein s3ae	260	5.17E-114	82.00%
genemark-scf4-processed-gene-1.269-mRNA-1	regulator of phospholipid metabolism	582	9.58E-117	61.50%
snap_masked-scf4-processed-gene-0.178-mRNA-1	---NA---	195		
snap_masked-scf4-processed-gene-1.490-mRNA-1	aconitate mitochondrial precursor	755	0	69.80%
snap_masked-scf4-processed-gene-1.489-mRNA-1	60S ribosomal protein I33-a	114	1.42E-50	73.60%
snap_masked-scf4-processed-gene-2.511-mRNA-1	prolyl-tRNA cytoplasmic	634	0	74.20%
genemark-scf4-processed-gene-2.186-mRNA-1	hypothetical protein CLUG_00949	736	0	58.10%
snap_masked-scf4-processed-gene-2.281-mRNA-1	ribonucleoside-diphosphate reductase small chain	434	0	87.10%
augustus_masked-scf4-processed-gene-2.26-mRNA-1	tbc domain protein	484	7.30E-171	64.60%
genemark-scf4-processed-gene-2.575-mRNA-1	DEHA2F05654p	428	3.13E-140	68.10%
augustus_masked-scf4-processed-gene-3.116-mRNA-1	cell surface glycoprotein	4183	1.38E-16	59.50%
snap_masked-scf4-processed-gene-3.49-mRNA-1	alcohol dehydrogenase 2	358	0	87.70%
maker-scf4-snap-gene-3.320-mRNA-1	zrt2 zinc transporter	733	2.61E-176	77.70%
genemark-scf4-processed-gene-3.697-mRNA-1	peroxisomal catalase	488	0	86.70%
snap_masked-scf4-processed-gene-3.138-mRNA-1	hexose transporter 2	679	0	78.90%
snap_masked-scf4-processed-gene-3.33-mRNA-1	translation elongation factor 1- partial	306	2.37E-97	75.40%
snap_masked-scf4-processed-gene-3.127-mRNA-1	---NA---	109		
snap_masked-scf4-processed-gene-3.316-mRNA-1	u3 small nucleolar rna-associated protein 12	997	0	79.90%
genemark-scf4-processed-gene-3.881-mRNA-1	mannan endo- -alpha-mannosidase	451	0	70.80%
genemark-scf4-processed-gene-3.975-mRNA-1	cap-associated protein cat20	165	1.95E-83	77.10%
maker-scf4-snap-gene-3.720-mRNA-1	aroB0 protein	771	0	62.60%
snap_masked-scf4-processed-gene-3.427-mRNA-1	hypothetical protein CLUG_04053	296	9.54E-103	69.30%
maker-scf4-snap-gene-3.349-mRNA-1	cip1 protein	319	4.57E-102	64.80%
snap_masked-scf4-processed-gene-3.347-mRNA-1	hypothetical protein CaO19.1558	273	4.81E-49	74.00%
snap_masked-scf4-processed-gene-3.302-mRNA-1	hypothetical protein CTRG_03479	100	7.77E-19	66.00%

**Table S2 Primer pairs developed and/or used in this study.** Primer sequences, amplicon melting temperature and cycling conditions. PCR efficiency for the developed qPCR primers are given in Figure S10.

Target gene	Name	Sequence	Source	Amplicon melting temperature °C
16SrDNA-bacterial	27F	AGAGTTGATCMTGGCTCAG	Lane et al 1991	NA
16SrDNA-bacterial	1492R	TACCTTGTACGACTT	Lane et al 1991	
<i>MreuTAF10</i>	TAF10_F	GACGCTGAGTTGATGACGA	this study	84.09
<i>MreuTAF10</i>	TAF10_R	TCGAGCGTCTTGTCCCTTTT	this study	
<i>MreuHIP</i>	HIP1F	ACGGCCACGTTGTCTTTAC	this study	81.44
<i>MreuHIP</i>	HIP1R	ACCGCAACAAAAATGTCAGG	this study	
<i>MreuGAP1_1</i>	GAP1_1F	TGGAGGCGTCTACATTGAC	this study	81.98
<i>MreuGAP1_1</i>	GAP1_1R	AGCAGCCTTTCGACTTCA	this study	
<i>MreuGAP1_2A</i>	GAP1_2AF	AAAGGAGGAGTTACTGTCCAA	this study	79.45
<i>MreuGAP1_2A</i>	GAP1_2AR	ATTAGGGTCAATTCCCATTG	this study	
<i>MreuGAP1_2B</i>	GAP1_2BF	CTGTATGTGTCACATCCGTTTC	this study	81.71
<i>MreuGAP1_2B</i>	GAP1_2BR	AGAATGGCTTGGTTGCCATA	this study	
<i>MreuGAP1_2C</i>	GAP1_2CF	TTTAGACGGCGCTTCATA	this study	79.89
<i>MreuGAP1_2C</i>	GAP1_2CR	TTTTATGACCAAGCCAAAATG	this study	
<i>MreuPUT4_A</i>	PUT4_AF	GACGCTGAGTTGATGACGA	this study	83.92
<i>MreuPUT4_A</i>	PUT4_AR	TCGAGCGTCTTGTCCCTTTT	this study	
<i>MreuPUT4_B</i>	PUT4_BF	ACGGCCACGTTGTCTTTAC	this study	81.54
<i>MreuPUT4_B</i>	PUT4_BR	ACCGCAACAAAAATGTCAGG	this study	
<i>MreuPUT4_C</i>	PUT4_C5F	AAGATGGCGCATTTATGGAC	this study	84.15
<i>MreuPUT4_C</i>	PUT4_C5R	GACGACCAAAGATAAAATCACATAC	this study	

**Cycling conditions for qPCR primers developed in this study:**

Step	Time (HH/MM/SS)	Temp (°C)	Cycles
Initial Denat.	0:12:00	95	1
Denaturing	0:00:10	95	45

<b>Annealing</b>	0:00:15	62	45
<b>Elongation</b>	0:00:15	72	45
<b>Melting Curve</b>	0:01:00	65-97	1
<b>Cooling</b>	0:00:30	40	-

**Table S3 Bagheera CUG-codon usage prediction for *M. reukaufii* conserved proteins.** A total of 30 *M. reukaufii* proteins containing 196 CUG-sites were analysed of which 81 showed alternative codon usage and 32 showed standard codon usage and 57 sites had no CTG-site matches in the reference collection. Table shows a selection of proteins.

Gene	Sequences in alignment	CTG Position	CTG usage in reference data	Number of CTG codons
Myosin heavy chain Class	80	29	S: 100%, L: 0%	2
		48	S: 100%, L: 0%	1
Mhc		56	S: 100%, L: 0%	1
		111	S: 100%, L: 0%	2
		119	S: 100%, L: 0%	1
		190	S: 100%, L: 0%	3
		218	S: 100%, L: 0%	1
		327	S: 100%, L: 0%	5
		678	S: 100%, L: 0%	1
		879	S: 67%, L: 33%	3
Kinesin Class	80	48	S: 25%, L: 75%	4
8		164	S: 100%, L: 0%	17
		186	S: 100%, L: 0%	2
		226	S: 100%, L: 0%	1
		236	S: 100%, L: 0%	8
		259	S: 100%, L: 0%	2
		281	S: 100%, L: 0%	3
		298	S: 100%, L: 0%	1
		353	S: 100%, L: 0%	3
		378	S: 100%, L: 0%	10

	415	S: 100%, L: 0%	1
	454	S: 0%, L: 100%	5
	480	S: 100%, L: 0%	2
<b>Actin related protein Class 6</b>	83	S: 100%, L: 0%	1
	14	S: 100%, L: 0%	1
	24	S: 100%, L: 0%	1
	85	S: 100%, L: 0%	3
	132	S: 100%, L: 0%	1
	133	S: 100%, L: 0%	1
<b>Kinesin Class 15</b>	318	S: 100%, L: 0%	20
	77	S: 100%, L: 0%	1
	13	S: 100%, L: 0%	1
	341	S: 100%, L: 0%	22
	353	S: 100%, L: 0%	1
	435	S: 50%, L: 50%	2
<b>Kinesin Class 3</b>	553	S: 100%, L: 0%	1
	51	S: 100%, L: 0%	2
	14	S: 100%, L: 0%	2
<b>Kinesin Class 1</b>	285	S: 100%, L: 0%	2
	43	S: 100%, L: 0%	2
	20	S: 100%, L: 0%	5
	466	S: 100%, L: 0%	
	25	S: 100%, L: 0%	1

## REFERENCES TO THE SUPPLEMENT

- [1] Grigoriev, I.V., Nikitin, R., Haridas, S., Kuo, A., Ohm, R., Otiilar, R., Riley, R., Salamov, A., Zhao, X., Korzeniewski, F., et al. 2014 MycoCosm portal: gearing up for 1000 fungal genomes. *Nucleic Acids Res* **42**, D699-704. (doi:10.1093/nar/gkt1183).
- [2] Fitzpatrick, D.A., Logue, M.E., Stajich, J.E. & Butler, G. 2006 A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. *BMC Evol. Biol.* **6**, 1-15. (doi:10.1186/1471-2148-6-99).
- [3] Riley, R., Haridas, S., Wolfe, K.H., Lopes, M.R., Hittinger, C.T., Göker, M., Salamov, A., Wisecaver, J., Long, T.M., Aerts, A.L., et al. 2016 Comparative genomics of biotechnologically important yeasts. *Proc Natl Acad Sci USA In Press*. (doi:10.1073/pnas.1603941113).
- [4] Hershkovitz, V., Sela, N., Taha-Salaime, L., Liu, J., Rafael, G., Kessler, C., Aly, R., Levy, M., Wisniewski, M. & Droby, S. 2013 De-novo assembly and characterization of the transcriptome of *Metschnikowia fructicola* reveals differences in gene expression following interaction with *Penicillium digitatum* and grapefruit peel. *BMC Genomics* **14**, 1-13. (doi:10.1186/1471-2164-14-168).
- [5] McEachern, M.J. & Blackburn, E.H. 1994 A conserved sequence motif within the exceptionally diverse telomeric sequences of budding yeasts. *Proc Natl Acad Sci USA* **91**, 3453-3457.
- [6] Gournas, C., Evangelidis, T., Athanasopoulos, A., Mikros, E. & Sophianopoulou, V. 2015 The *Aspergillus nidulans* Proline Permease as a model for understanding the factors determining substrate binding and specificity of fungal amino acid transporters. *J Biol Chem* **290**, 6141-6155. (doi:10.1074/jbc.M114.612069).