

Fig. S1. Non-metric multidimensional scaling plot based on Pearson coefficient similarities of genetic fingerprints obtained by M13 fingerprinting performed for all *Brettanomyces (Dekkera) bruxellensis* isolates investigated in this study and seven additional wine strains (ST05.12/63, MUCL 54014; ST05.12/64, MUCL 54015; ST05.12/65, CBS 1940; ST05.12/66, CBS 1941; ST05.12/67, CBS1942; ST05.12/68, CBS 1943 and ST05.12/69, CBS 2336). Open dark green squares, closed green squares, red circles and orange triangles represent *B. bruxellensis* isolates from the Cantillon brewery, beer, wine and soft drinks, respectively (stress of plot = 0.13).

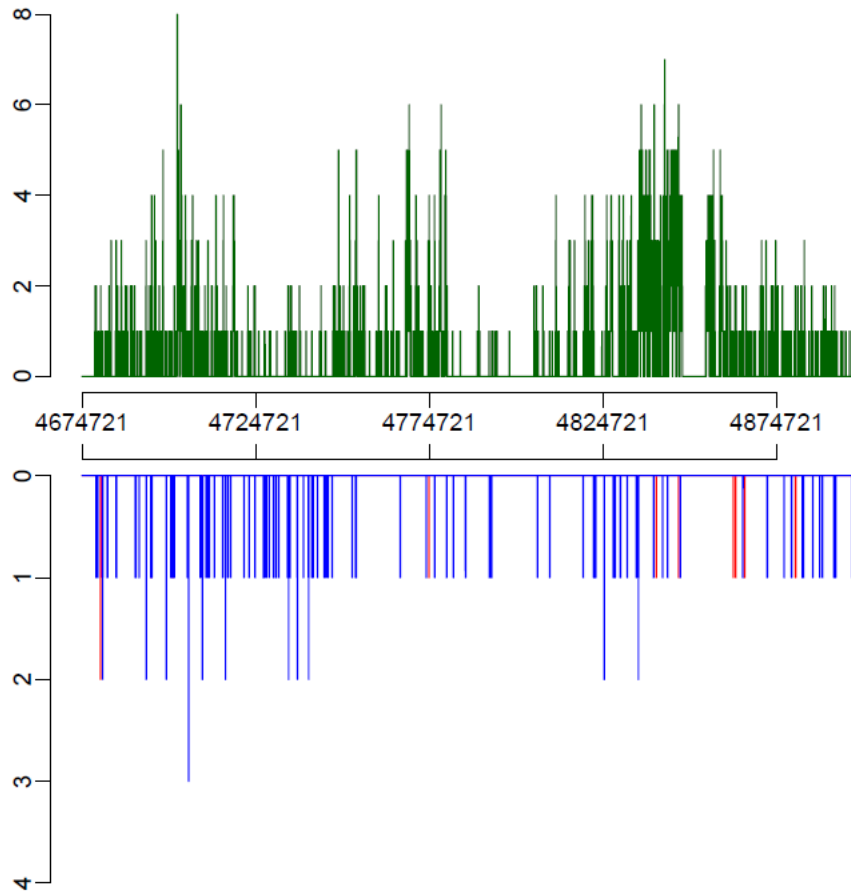


Fig. S2. Nucleotide variation in the genome of *Brettanomyces (Dekkera) bruxellensis* ST05.12/22 compared with AWRI 1499, showing single nucleotide polymorphisms (SNPs) (green bars), deletions (red bars) and insertions (blue bars), exemplified for scaffold 14. Variation is calculated as the number of variant bases in a 101 bp sliding window, centered at base 51 and with a 1 bp resolution.

AWRI 1499 contig AHIQ01000303

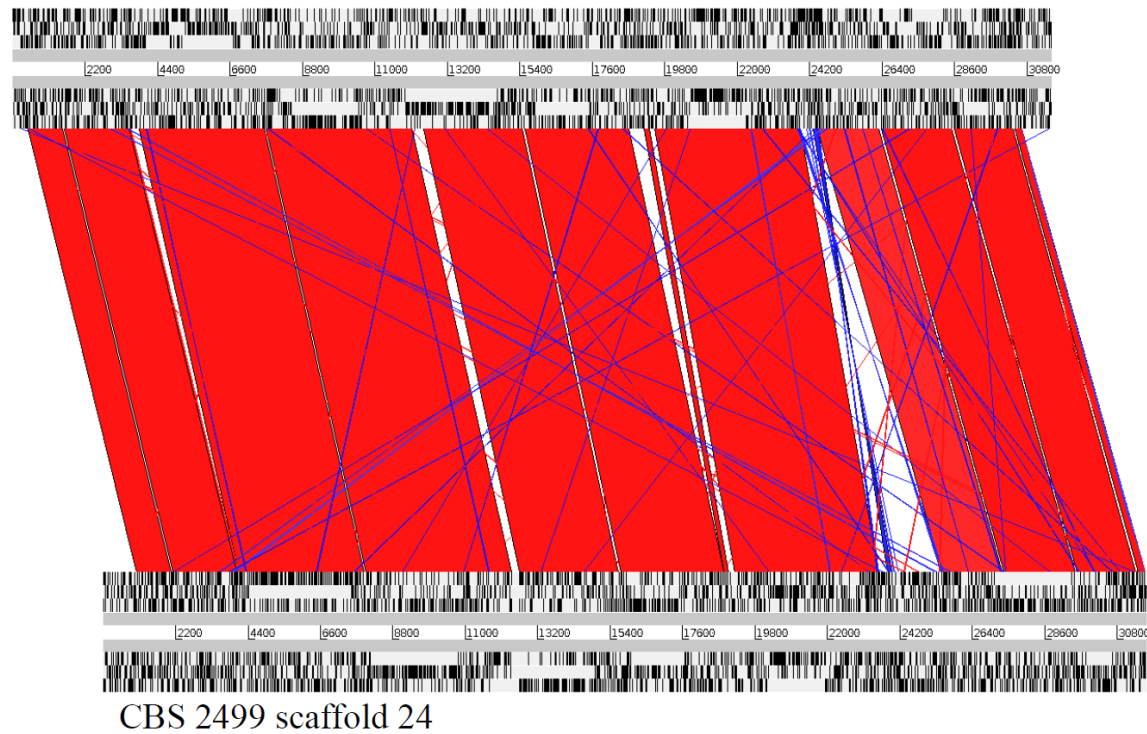


Fig. S3. Graphical representation (using ACT) of the presence of a β -galactosidase gene (1) together with the nitrate assimilation gene cluster (consisting of a nitrate reductase (2), nitrite reductase (3) and nitrate transporter gene (4)) in AWRI 1499 and CBS 2499. This gene cluster is absent in ST05.12/22.

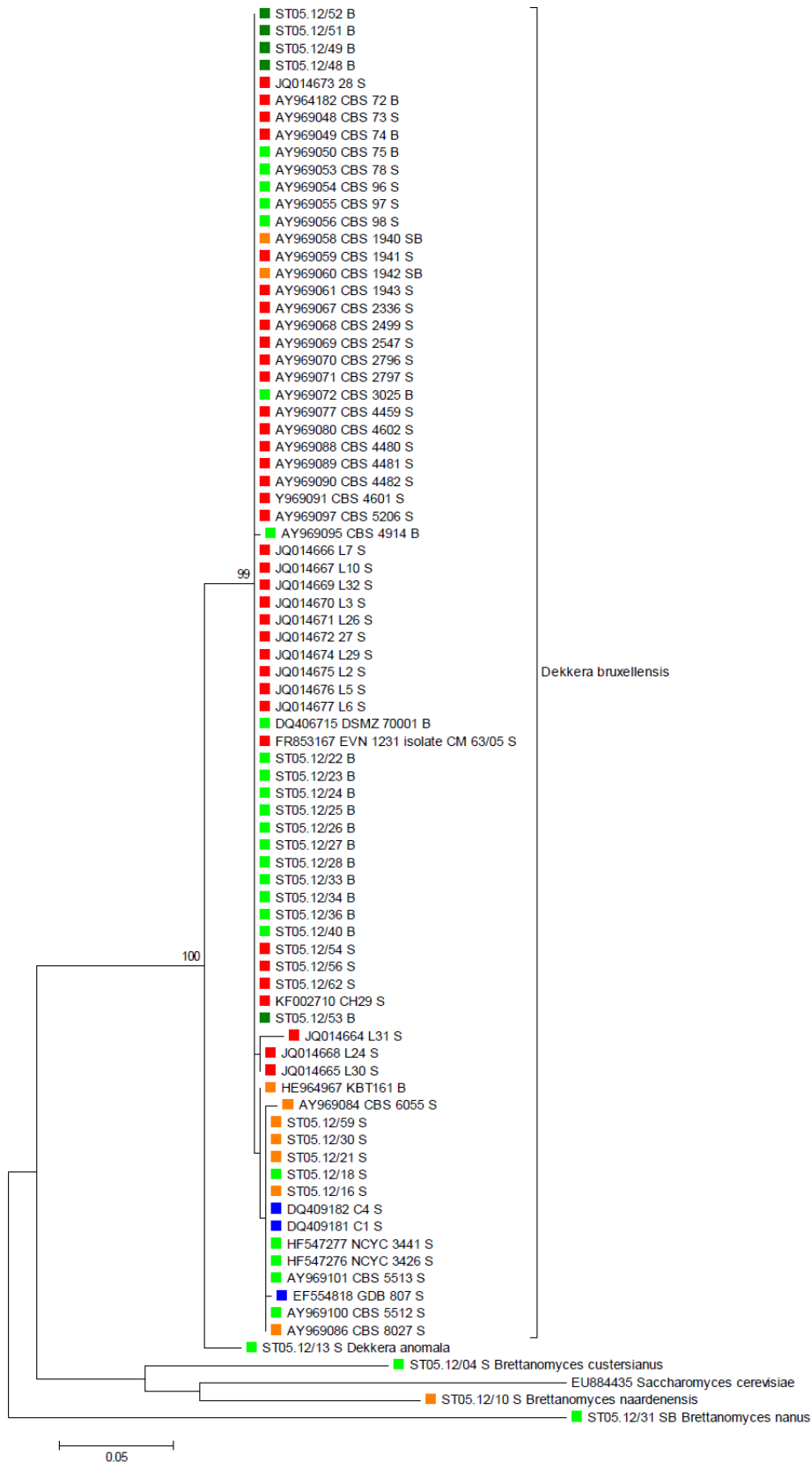


Fig. S4. Maximum likelihood tree (Tamura-Nei model) constructed with partial large subunit (LSU) ribosomal RNA (rRNA) gene sequences from all *Brettanomyces* strains investigated in this study and all *B. bruxellensis* LSU rRNA gene sequences available in GenBank (55 additional sequences; August 2013) (~400 bp). Bootstrap values >80% (based on 1,000 replicates) are given at the nodes of the tree. *Saccharomyces cerevisiae* was used as an outgroup. The origin of the different strains, i.e. beer, Cantillon brewery, soft drink, others and wine are highlighted in green, dark green, orange, blue and red, respectively.

Table S1. Primers used to complement/confirm bioinformatic analyses^a

Target (AWRI 1499 CDS Genbank Accession number, CBS 2499 JGI number or gene number in ST05.12/22)	Function target gene ^b	Primer Name	Direction	Sequence (5'-3')
EIF45194	fungal specific transcription factor domain protein	EIF45194_F	Forward	TACCAAACGAGCGAACCTT
EIF45194	fungal specific transcription factor domain protein	EIF45194_R	Reverse	GCAGGTTCTTTCGCATTCTC
EIF45195	hypothetical protein AWRI1499_4942	EIF45195_F	Forward	ATCCGTGTCTCCAAAAGGTG
EIF45195	hypothetical protein AWRI1499_4942	EIF45195_R	Reverse	CTCGGTAAATGCCGAAAGTC
EIF45196	lectin-like protein	AHIQ315_A1_F	Forward	TGCACCTTGCTTTTGAGGTTG
EIF45196	lectin-like protein	AHIQ315_A1_R	Reverse	AGCACGCTTTCACCTCGAAAT
EIF45229	putative trna pseudouridine synthase	EIF45229_F	Forward	GCCAATTTTGATAGGGCTCA
EIF45229	putative trna pseudouridine synthase	EIF45229_R	Reverse	GCCCATCTAAAGCCAGTTGA
EIF45248	beta-galactosidase	W54X_F	Forward	TTCCGTTGGAATTCGCTTTA
EIF45248	beta-galactosidase	W54X_R	Reverse	AGTGGTCCTACGCGAGAGTG
EIF45249	nitrate reductase	AHIQ303_A1_F	Forward	AAAATGGCGCTGTCTTCACT
EIF45249	nitrate reductase	AHIQ303_A1_R	Reverse	CATCTGTCCGATTGTGTTGG
EIF45250	nitrite reductase	W53X_F	Forward	GCCTCGTCTGGTAAAGCATC
EIF45250	nitrite reductase	W53X_R	Reverse	CCTAAAGCCGGGAATACCTC
EIF45251	nitrate transporter	AHIQ303_B1_R	Reverse	CTATTCGCATGGCTTGGATT
EIF45251	nitrate transporter	AHIQ303_B2_R	Reverse	GGCGGTGGTTAATCAGAGAA
EIF45252	maltase	AHIQ303_C1_F	Forward	GCTCCATGGTAATGGTGTCC
EIF45252	maltase	AHIQ303_C1_R	Reverse	GAGACAACCCAGAATGGTG
EIF45265	hypothetical protein AWRI1499_4878	W29_F	Forward	GCAACAGTTTCCTTTGCTGA
EIF45265	hypothetical protein AWRI1499_4878	W29_R	Reverse	TCTGAGAGTAGCAGCGAGGAG
EIF45400	carbohydrate esterase family 9 protein	AHIQ280_A1_F	Forward	GGGAGTTCACCTCTGAATGC
EIF45400	carbohydrate esterase family 9 protein	AHIQ280_A1_R	Reverse	CGGCAGGAACTGCTCTTACTA
EIF45401	carbohydrate esterase family 9 protein	AHIQ280_B1_F	Forward	CACCTTGACGACCATTTCT
EIF45401	carbohydrate esterase family 9 protein	AHIQ280_B1_R	Reverse	AAGGAAAATATGTACACCCAGGA
EIF45403	carbohydrate esterase family 9 protein	AHIQ280_C1_F	Forward	GACCTGTTGGGGAAGATTCA
EIF45403	carbohydrate esterase family 9 protein	AHIQ280_C1_R	Reverse	CGTTCGTCTATTGCATGAGC
EIF45404	mfs drug transporter	EIF45404_F	Forward	TCCCATCCTTATGGTGTGGT
EIF45404	mfs drug transporter	EIF45404_R	Reverse	ATGCTGCATCCAAAAGATCC
EIF45405	putative mfs-mdr transporter	EIF45405_F	Forward	CGGCCGAAACTAATGGATAA
EIF45405	putative mfs-mdr transporter	EIF45405_R	Reverse	AACGAAGCAAAGGGTAAAA
EIF45406	mfs multidrug	EIF4606_F	Forward	GACCTGTTGGGGAAGATTCA
EIF45406	mfs multidrug	EIF4606_R	Reverse	CTGCTGTCCAAGTGTGCAAT
EIF45407	high-affinity glucose transporter	EIF45407_F	Forward	TTTATCACCATGCGCCTGTA
EIF45407	high-affinity glucose transporter	EIF45407_R	Reverse	ACAGTTGCTCCCGTCTATGG
EIF45408	galactose-1-phosphate uridylyltransferase	EIF45408_F	Forward	AAAGGTGCTGCTATGGGTTG
EIF45408	galactose-1-phosphate uridylyltransferase	EIF45408_R	Reverse	AAAATGGAGCCTGATGGAGA

EIF45409	galactokinase	W52Y_F	Forward	TCAGTCGTGAAATGAACCAAA
EIF45409	galactokinase	W52Y_R	Reverse	TAAGCGCTTTACCCCTGAAA
EIF45410	gal10 bifunctional protein	EIF45410_F	Forward	ATGGAGAATCGCCTTGCTTA
EIF45410	gal10 bifunctional protein	EIF45410_R	Reverse	TTACCGGTACCCAAGTTCCA
EIF45411	dt dp-glucose -dehydratase	W28A	Forward	GGCGGACGCATTCTAATAAA
EIF45411	dt dp-glucose -dehydratase	W28A	Reverse	TTTGTCCGGTCTCCAGATTT
EIF45412	hexose transporter	EIF45412_F	Forward	CTTCCAGAAATACCCGCTTG
EIF45412	hexose transporter	EIF45412_R	Reverse	TTCCAGAATCTCCTCGTTGG
EIF45413	maltase	AHIQ280_D1_F	Forward	TCTGGAGACCTCCAAAAGGA
EIF45413	maltase	AHIQ280_D1_F	Reverse	TTTTCTCCCCCATCAGAGTG
EIF45414	multidrug resistance regulator 1	EIF45414_F	Forward	ACCACCTGATAGGCGAAATG
EIF45414	multidrug resistance regulator 1	EIF45414_R	Reverse	ACCGTAGCGATGTCGAGTCT
EIF45415	beta-glucosidase	AHIQ280_E1_F	Forward	GTGCCACTGCTGAAACAGAA
EIF45415	beta-glucosidase	AHIQ280_E1_F	Reverse	TGGCCCTAATGGAATCAGAG
EIF45416	hexose transporter	EIF45416_F	Forward	TCGTGGTACTTGGGAGCAAT
EIF45416	hexose transporter	EIF45416_R	Reverse	CTCGTGGCTTGTCTCTCTT
EIF45417	hypothetical protein AWRI1499_4714	W51_F	Forward	GAAGGAGGATGAGGGAGAGG
EIF45417	hypothetical protein AWRI1499_4714	W51_R	Reverse	TGCCTCTTAGAGAGTGAGAATCG
EIF45955	hypothetical protein AWRI1499_4159	W89_F	Forward	CGAGATCCTCGCTTAGCAGT
EIF45955	hypothetical protein AWRI1499_4159	W89_R	Reverse	GCGAGGATGTGATGCTGTTA
EIF45984	hypothetical protein AWRI1499_4155	W88_F	Forward	CTAAGAGAAAAGAAATGGCAAAGC
EIF45984	hypothetical protein AWRI1499_4155	W88_R	Reverse	CAGGAAGAGTGCTTGTCTCTTTT
EIF46173	hypothetical protein AWRI1499_3976	W49_F	Forward	GTGAGCAAGCGAAGGAAGTT
EIF46173	hypothetical protein AWRI1499_3976	W49_R	Reverse	TCTGCCTTTTCCCTTGCTTTT
EIF46260	hypothetical protein AWRI1499_3842	W87_F	Forward	CCAATATGGCCAGAACCAAT
EIF46260	hypothetical protein AWRI1499_3842	W87_R	Reverse	GGGACATCAGGTGAGATTGCG
EIF46377	hypothetical protein AWRI1499_3738	W23_F	Forward	TGAAGCAGGAGAATGAGGAGA
EIF46377	hypothetical protein AWRI1499_3738	W23_R	Reverse	GCCTCTGGAGCTGAGTTTTG
EIF46396	putative pyridoxine transport	EIF46396_F	Forward	TTCAACGGGAGGTATTCTCG
EIF46396	putative pyridoxine transport	EIF46396_R	Reverse	TGGTCCCAACAAAGATGTGA
EIF46397	hypothetical protein AWRI1499_3706	EIF46397_F	Forward	CTGTTAGCAGCGGTGGTATG
EIF46397	hypothetical protein AWRI1499_3706	EIF46397-R	Reverse	TATTGTTGCAGCGCTGATTT
EIF46398	hypothetical protein AWRI1499_3707	EIF46398_inclIntron	Forward	TTGCTGCTCTTCCGTTCTTT
EIF46398	hypothetical protein AWRI1499_3707	EIF46398_inclIntron	Reverse	AATGGCGATCCAAAGTCAAG
EIF46399	pantothenate transporter fen2	EIF46399_F	Forward	TGGGGACTTTTACTCTTGG
EIF46399	pantothenate transporter fen2	EIF46399_R	Reverse	CATGAACCCGGAAAAATATGG
EIF46400	upf0145 protein	EIF46400_F	Forward	TCCCTCACCAATTGATCCAC
EIF46400	upf0145 protein	EIF46400_R	Reverse	GCATTGGGAAAAATCGAGAAA
EIF46480	aspartate aminotransferase	AHIQ207_A1_F	Forward	CTGGGAAGGAGACAAAACAG
EIF46480	aspartate aminotransferase	AHIQ207_A1_R	Reverse	ATGTACGGCGAAAGAATTGG
EIF47162	hypothetical protein AWRI1499_2925	W44_F	Forward	CCAAGGAAGACCTCAGATGC
EIF47162	hypothetical protein AWRI1499_2925	W44_R	Reverse	TTAAAATCCTGGGCCACCT
EIF47495	hypothetical protein AWRI1499_2613	W67_F	Forward	AAATGGTGCCAGAAACATC
EIF47495	hypothetical protein AWRI1499_2613	W67_R	Reverse	AGACGAAGTCTTGACAGAAGTGG
EIF47553	hypothetical protein AWRI1499_2542	EIF47553_F	Forward	TTCAAGTTCGAATCAAAAATGG
EIF47553	hypothetical protein AWRI1499_2542	EIF47553_R	Reverse	TTTGAAGATAGACGCTTGATTTG
EIF47624	hypothetical protein AWRI1499_2416	W39_F	Forward	TCGTGGCATGCTGTTAGTA
EIF47624	hypothetical protein AWRI1499_2416	W39_R	Reverse	CGTATCCCAAGAATACGTCTGA
EIF47692	longevity-assurance protein 1	AHIQ132_A1_F	Forward	GCTGCTAACGCACACTACCA

EIF47692	longevity-assurance protein 1	AHIQ132_A1_R	Reverse	GCATCCTCCTTGCTCATC
EIF47710	bleomycin resistance	AHIQ131_A1_F	Forward	CCAGGTGTCCTGTCTGGTTT
EIF47710	bleomycin resistance	AHIQ131_A1_R	Reverse	TTTTCGACATTCCTCGGCTCT
EIF47726	nadph-dependent 1-acyldihydroxyacetone phosphate reductase	AHIQ130_A1_F	Forward	TAGCGGAGGAACTTGCAAAAC
EIF47726	nadph-dependent 1-acyldihydroxyacetone phosphate reductase	AHIQ130_A1_R	Reverse	GGAAAGTAGGCAGCCACAAA
EIF47731	apoptosis-inducing taf9-like domain 1 family	AHIQ129_A1_F	Forward	TCAAGGGTCAGACAGTCCAA
EIF47731	apoptosis-inducing taf9-like domain 1 family	AHIQ129_A1_R	Reverse	TCCTCCTCCTCCTCCTCTTC
EIF47810	hypothetical protein AWRI1499_2284	EIF47810_F	Forward	TCTACCACACCCATCATCCA
EIF47810	hypothetical protein AWRI1499_2284	EIF47810_R	Reverse	CCGTCCGTTCCACTTAAACA
EIF47995	hypothetical protein AWRI1499_2081	W32A_F	Forward	CTTTATCCTTGGTCTCCTCAGC
EIF47995	hypothetical protein AWRI1499_2081	W32A_R	Reverse	ATGACCCAAAGTGAGGCAGT
EIF47999	serine threonine-protein kinase nrc-2	AHIQ112_A1_F	Forward	GATGTTGGCAAAGGTCTCGT
EIF47999	serine threonine-protein kinase nrc-2	AHIQ112_A1_R	Reverse	CTAGGCTCGTCGACCTCATC
EIF48066	cytochrome c	AHIQ107_A1_F	Forward	TGGCTGCTCCATACAAGAAA
EIF48066	cytochrome c	AHIQ107_A1_R	Reverse	CAGCCAAGTATGCAACAAGGT
EIF48111	hypothetical protein AWRI1499_1959	W63_F	Forward	TGGAGTTGAAGCAGTTGAGG
EIF48111	hypothetical protein AWRI1499_1959	W63_R	Reverse	CATTCTCTTCAACTTCCTCTTTG
EIF48158	hypothetical protein AWRI1499_1924	W31A_F	Forward	CATGGAATCGTTAGGGATGG
EIF48158	hypothetical protein AWRI1499_1924	W31A_R	Reverse	TTTTGCACCCCTCTTTCTTG
EIF48830	hypothetical protein AWRI1499_1218	EIF48830_InclIntron_F	Forward	GCCACGACAGAGGAAGAATG
EIF48830	hypothetical protein AWRI1499_1218	EIF48830_InclIntron_R	Reverse	TGCGTCCCAATGTTAGAGAA
EIF49042	glutamate synthase	AHIQ68_A1_F	Forward	TCGATGCCCGATAAGTTCAT
EIF49042	glutamate synthase	AHIQ68_A1_R	Reverse	ACAATCCGACCCTTCACAGT
EIF49054	thiamine biosynthesis	AHIQ66_A1_F	Forward	CGCAACTTTTCATTCTGTGC
EIF49054	thiamine biosynthesis	AHIQ66_A1_R	Reverse	TGCGAACAAGTTTTCTCTCT
EIF49314	peptide-n4-(n-acetyl-beta-d-glucosaminy) asparaginase amidase	AHIQ58_A1_F	Forward	TTCAACGTGTCGCTAGATGC
EIF49314	peptide-n4-(n-acetyl-beta-d-glucosaminy) asparaginase amidase	AHIQ58_A1_R	Reverse	GAGTCAGGCGGAAGAGATTG
EIF49824	nadph-dependent medium chain alcohol dehydrogenase with broad substrate specificity	AHIQ15_A1_F	Forward	GGCTTACCCAGACACTTTCCG
EIF49824	nadph-dependent medium chain alcohol dehydrogenase with broad substrate specificity	AHIQ15_A1_R	Reverse	CCTGGAAAGGCATCATCAAAA
X9085_gene1239	-	X9085_gene1239_F	Forward	ACATGGTGCAATCAATCCTG
X9085_gene1239	-	X9085_gene1239_R	Reverse	ATCATCAGCATGACCAACCA
X9085_gene1241	DEHA2G12782p	X9085_gene1241_F	Forward	GCGTTGATTTTTGAGAGCACA
X9085_gene1241	DEHA2G12782p	X9085_gene1241_R	Reverse	AGACCCTGTTACCTTGCAT
X9085_gene1242	protein BMH2	X9085_gene1242_F	Forward	TGAGCAAAGGAGGAGGCTA
X9085_gene1242	protein BMH2	X9085_gene1242_R	Reverse	CATGTCCGAAGTCCACAATG
X9085_gene1243	Shuttling pre-60S factor	X9085_gene1243_F	Forward	TGCAACCAACTGGACCATTA
X9085_gene1243	Shuttling pre-60S factor	X9085_gene1243_R	Reverse	GTAATGCCGAAATGCCAAGT

X9085_gene1637	-	X9085_gene1637_F	Forward	GCCATTGGTCATGGAAAAGTT
X9085_gene1637	-	X9085_gene1637_R	Reverse	CGTCAATGACCCGTTTGTTA
X9085_gene172	-	X9085_gene172_F	Forward	CCGATGTTTGCATTGTCAAG
X9085_gene172	-	X9085_gene172_R	Reverse	AGCACAGCTTCCTTCCAAAA
X9085_gene173	-	X9085_gene173_F	Forward	TGCTATCACGGGGATACAGAT
X9085_gene173	-	X9085_gene173_R	Reverse	CACGCTGCCTAGGACTTGTA
X9085_gene2	-	B1_F	Forward	GCAACCAAGAAAAAGACAAGG
X9085_gene2	-	B1_R	Reverse	AGTGCATGCAGTAAATGTTG
X9085_gene2206	hypothetical protein	X9085_gene2206_F	Forward	TGGGGAGGTTAAATTTGCTG
X9085_gene2206	hypothetical protein	X9085_gene2206_R	Reverse	TGGTCTGATTGGAAGCCATT
X9085_gene2208	N-acetyltransferase 9 isoform 2	X9085_gene2208_F	Forward	TTGAGAATATGCCAGCTTTGG
X9085_gene2208	N-acetyltransferase 9 isoform 2	X9085_gene2208_R	Reverse	TTTTTCCATGCGAATTATGG
X9085_gene2432	-	X9085_gene2432_F	Forward	CGAGAAAGATGGGGATACGA
X9085_gene2432	-	X9085_gene2432_R	Reverse	TCAAAGCCTCTGGAACGTCT
X9085_gene2697	-	X9085_gene2697_F	Forward	CTTCTGCTTTGGCTTCTGCT
X9085_gene2697	-	X9085_gene2697_R	Reverse	AAACCAGCACCGACGAAA
X9085_gene2883	-	X9085_gene2883_F	Forward	TGGCTGAAGAAACAAAAGCTG
X9085_gene2883	-	X9085_gene2883_R	Reverse	TACCCTCACCTTCTTCTCG
X9085_gene3	-	B1_F	Forward	GCAACCAAGAAAAAGACAAGG
X9085_gene3	-	B1_R	Reverse	AGTGCATGCAGTAAATGTTG
X9085_gene3090	DEHA2E17446p	X9085_gene3090_F	Forward	AGAGCCAAACGTGAGGAGAA
X9085_gene3090	DEHA2E17446p	X9085_gene3090_R	Reverse	CCCCTTGATCAGATGCACTT
X9085_gene3668	-	X9085_gene3668_F	Forward	AGGGACGTTTATGGCACAAG
X9085_gene3668	-	X9085_gene3668_R	Reverse	ACTTTGAGACCGCCCGTTAC
X9085_gene4	-	B1_F	Forward	GCAACCAAGAAAAAGACAAGG
X9085_gene4	-	B1_R	Reverse	AGTGCATGCAGTAAATGTTG
X9085_gene4202	hypothetical protein	X9085_gene4202_F	Forward	AAGTCAACGCAGGCTCTCAT
X9085_gene4202	hypothetical protein	X9085_gene4202_R	Reverse	CTTCTCGCTCTCCCTTTTT
X9085_gene4419	-	X9085_gene4419_F	Forward	ACCACAGCAGCAGTTGGAG
X9085_gene4419	-	X9085_gene4419_R	Reverse	AGCGTTTTTAGCCACAGGAG
X9085_gene4860	-	X9085_gene4860_F	Forward	ATATTCCGATTGGGGGAATC
X9085_gene4860	-	X9085_gene4860_R	Reverse	TCGAGCTGGTATCTTGCTGA
X9085_gene4861	-	X9085_gene4861_F	Forward	CATGCGAGAACGTTGAAAGA
X9085_gene4861	-	X9085_gene4861_R	Reverse	TCACCTTGTTTTCCAATTTGTT
X9085_gene4876	Nuclear SAM-dependent mono-and asymmetric arginine dimethylating methyltransferase	X9085_gene4876_F	Forward	TTACGAATCCATGCTGGACA
X9085_gene4876	Nuclear SAM-dependent mono-and asymmetric arginine dimethylating methyltransferase	X9085_gene4876_R	Reverse	CGTTCTTTGGGGAGTCAGAA
X9085_gene4877	GTPase	X9085_gene4877_F	Forward	TCATCGCAGCAACTTTTGAC
X9085_gene4877	GTPase	X9085_gene4877_R	Reverse	TATCTTCCCCACCACTTTGC
X9085_gene4952	TFIIH basal transcription factor complex subunit 2	X9085_gene4952_F	Forward	GGCTTCAGGCACTACACACA
X9085_gene4952	TFIIH basal transcription factor complex subunit 2	X9085_gene4952R	Reverse	CGACAAGCAGTACGAGTCCA
X9085_gene4987	mitochondrial ribosomal protein L11	X9085_gene4987_F	Forward	CACAGATGTGCCGATCAAGT
X9085_gene4987	mitochondrial ribosomal protein L11	X9085_gene4987R	Reverse	ACACCCTTGACACATCCTT
X9085_gene5044	-	X9085_gene5044_F	Forward	TGGAAAGGGGAGTACAGACCA

X9085_gene5044	-	X9085_gene5044_R	Reverse	CATCATCACCGTCATCATCA
X9085_gene5174	-	X9085_gene5174_F	Forward	CAAATGCAGCAACAACAACC
X9085_gene5174	-	X9085_gene5174_R	Reverse	TTAAAATCCTGGGCCACCT
X9085_gene5208	Cox2p	X9085_gene5208_F	Forward	GATGCAGTTCAGGTCGTTT
X9085_gene5208	Cox2p	X9085_gene5208_R	Reverse	GGCATAGATGAATGCATAACAC
X9085_gene5217	-	X9085_gene5217_F	Forward	GATCAAGATGCCTCGGTTTC
X9085_gene5217	-	X9085_gene5217_R	Reverse	GCAATTTGCGGTGCTTCTAT
X9085_gene5218	-	X9085_gene5218_F	Forward	CAGTTCCAGATGGGTCACATT
X9085_gene5218	-	X9085_gene5218_R	Reverse	GCATAGCCCTGTTGATTCTGT
X9085_gene5231	copia protein-like	X9085_gene5231_F	Forward	TAAAGCTGCGAGTTGTCTGT
X9085_gene5231	copia protein-like	X9085_gene5231_R	Reverse	TCGCTGGAATGTAAGCAGTG
X9085_gene1048	Autophagy-related protein 12	X9085_gene1048_F	Forward	GCGATGAGGATGAGGATGAT
X9085_gene1048	Autophagy-related protein 12	X9085_gene1048_R	Reverse	CAACTCGCTATCTCCCGATT
X9085_gene1561	-	X9085_gene1561_F	Forward	CGTGCGAAGAACGTTTATGA
X9085_gene1561	-	X9085_gene1561_R	Reverse	TCTTCTCCAACCCCATCTTG
X9085_gene2040	-	X9085_gene2040_F	Forward	GGATTGCCAGAAAACCTGGAC
X9085_gene2040	-	X9085_gene20402_R	Reverse	AAACTTGGCTGCATTTCTCC
X9085_gene2356	Conserved hypothetical protein	X9085_gene2356_F	Forward	TGAGCGCAGTGATAGCAAAC
X9085_gene2356	Conserved hypothetical protein	X9085_gene2356_R	Reverse	ATGATATCCGGTTGGCATGT
X9085_gene2436	SPAPADRAFT_58771 hypothetical protein	X9085_gene2436_F	Forward	CAGCATCGAAAGTGGCAGT
X9085_gene2436	SPAPADRAFT_58771	X9085_gene2436_R	Reverse	CACCTGCACCTCTAAACACG
X9085_gene2697	-	X9085_gene2697_F	Forward	CTTCTGCTTTGGCTTCTGCT
X9085_gene2697	-	X9085_gene2697_R	Reverse	AAACCAGCACCGACGAAA
X9085_gene2842	-	X9085_gene2842_F	Forward	TTGCCTTGGAGGAAGAACTG
X9085_gene2842	-	X9085_gene2842_R	Reverse	CCACCGAATTATCAAAGTCCA
X9085_gene2883	-	X9085_gene2883_F	Forward	TGGCTGAAGAAACAAAAGCTG
X9085_gene2883	-	X9085_gene2883_R	Reverse	TACCCTCACCTTCCTTCTCG
X9085_gene3697	-	X9085_gene3697_F	Forward	AGCGACCCGTCAGAATACAC
X9085_gene3697	-	X9085_gene3697_R	Reverse	AGAGCCAACAGCAGCAGAAAT
X9085_gene4359	-	X9085_gene4359_F	Forward	GGCACTGATATCGGCAAAAA
X9085_gene4359	-	X9085_gene4359_R	Reverse	AAAACGAGTTCTGGCTGCTT
X9085_gene4419	-	X9085_gene4419_F	Forward	ACCACAGCAGCAGTTGGAG
X9085_gene4419	-	X9085_gene4419_R	Reverse	AGCGTTTTTAGCCACAGGAG
X9085_gene4593	Mitochondrial ribosomal protein of the large subunit	X9085_gene4593_F	Forward	CGATCCTTTTGGATCAGAGG
X9085_gene4593	Mitochondrial ribosomal protein of the large subunit	X9085_gene4593_R	Reverse	TGCCCTGGAATGTCTATCAA
X9085_gene4903	-	X9085_gene4903_F	Forward	GATGGGATTACGCTGGAAGA
X9085_gene4903	-	X9085_gene4903_R	Reverse	GCGGAAGCTTCTGTGTTTCT
X9085_gene5174	-	X9085_gene5174_F	Forward	CAAATGCAGCAACAACAACC
X9085_gene5174	-	X9085_gene5174_R	Reverse	TTAAAATCCTGGGCCACCT
CE57870_27783	Nitrate transporter	CE57870_27783_F	Forward	GGCGGTGGTTAATCAGAGAA
CE57870_27783	Nitrate transporter	CE57870_27783_R	Reverse	AGCGCAACAACAATGATG
gm1.2653_g	-	gm1.2653_g_F	Forward	AAACTTGCAGCTGCTGATGA
gm1.2653_g	-	gm1.2653_g_R	Reverse	GCTCGAGTTAGTCGAAGCGTA
gm1.2653_g	Nitrite reductase [NAD(P)H] large subunit, NirD	fgenesh1_kg.24_#_3_#_Locus2869v1rpkm42.70_F	Forward	GGTGCCCGTGCTCTATTTA

fgenes1_kg.24_#_3_#_Locus2869v1rpkm42.70	Nitrite reductase [NAD(P)H] large subunit, NirD	fgenes1_kg.24_#_3_#_Locus2869v1rpkm42.70_R	Reverse	TTCAGCTCGCTTTCCAAAAT
fgenes1_kg.17_#_19_#_Locus4180v1rpkm7.35	NAD-dependent epimerase/dehydratase	fgenes1_kg.17_#_19_#_Locus4180v1rpkm7.35_F	Forward	ATGTTTGTCCGGTCTCCAGA
fgenes1_kg.17_#_19_#_Locus4180v1rpkm7.35	NAD-dependent epimerase/dehydratase	fgenes1_kg.17_#_19_#_Locus4180v1rpkm7.35_R	Reverse	TCTACTGCCTCCCCAGATTG
fgenes1_kg.19_#_13_#_Locus985v1rpkm163.02	-	fgenes1_kg.19_#_13_#_Locus985v1rpkm163.02_F	Forward	TCGTTTCGCCTGTATTCTCT
fgenes1_kg.19_#_13_#_Locus985v1rpkm163.02	-	fgenes1_kg.19_#_13_#_Locus985v1rpkm163.02_R	Reverse	CGCTTGACTGTTTTGCACAT
fgenes1_kg.17_#_17_#_Locus4025v1rpkm10.11	Galactose-1-phosphate uridyl transferase, class I	fgenes1_kg.17_#_17_#_Locus4025v1rpkm10.11_F	Forward	TCTCCATCAGGCTCCATTTT
fgenes1_kg.17_#_17_#_Locus4025v1rpkm10.11	Galactose-1-phosphate uridyl transferase, class I	fgenes1_kg.17_#_17_#_Locus4025v1rpkm10.11_R	Reverse	CCCGCAGTTGGAAGTTGTAT
CE13834_2308	Retrotransposon gag protein	CE13834_2308_F	Forward	AGTTTGCCTTAGCCGACAAC
CE13834_2308	Retrotransposon gag protein	CE13834_2308_R	Reverse	AGAAGACGGAAGCGGAAGTT
fgenes1_pg.18_#_5	Protein of unknown function DUF74	fgenes1_pg.18_#_5_F	Forward	GCATTGGGAAAATCGAGAAA
fgenes1_pg.18_#_5	Protein of unknown function DUF74	fgenes1_pg.18_#_5_R	Reverse	CACACCGTTCCGCAATAAC
e_gw1.1.1978.1	Ribosomal protein L2	e_gw1.1.1978.1_F	Forward	GCCACAACCCAGATGAGAAC
e_gw1.1.1978.1	Ribosomal protein L2	e_gw1.1.1978.1_R	Reverse	CTCCTCAAGAGCCTTCTCCTT
gm1.1418_g	SMP-30/Gluconolactonase/LRE-like region	gm1.1418_g_F	Forward	GCGGATAGTTCAGTGGGTGT
gm1.1418_g	SMP-30/Gluconolactonase/LRE-like region	gm1.1418_g_R	Reverse	GATCTGCATCTGGCTCATCA
e_gw1.4.652.1	Alcohol dehydrogenase, zinc-binding	e_gw1.4.652.1_F	Forward	CGATGGGACTCTTTGTCTGTT
e_gw1.4.652.1	Alcohol dehydrogenase, zinc-binding	e_gw1.4.652.1_R	Reverse	CAAGCTAGAAGGACCCGGA
fgenes1_pg.5_#_301	Shr3 amino acid permease chaperone	fgenes1_pg.5_#_301_F	Forward	GATCGCATCATGTTCCGTAAT
fgenes1_pg.5_#_301	Shr3 amino acid permease chaperone	fgenes1_pg.5_#_301_R	Reverse	CCCCTTTGTCTTTCTGGA
gm1.3526_g	6-phosphogluconate dehydrogenase, C-terminal-like	gm1.3526_g_F	Forward	ATTGTGGCGAAGAACAGCTT
gm1.3526_g	6-phosphogluconate dehydrogenase, C-terminal-like	gm1.3526_g_R	Reverse	GTCCGTTTTCTGCCTCATGT
fgenes1_kg.7_#_28_#_Locus3256v1rpkm30.45	Inner centromere protein, ARK binding region	fgenes1_kg.7_#_28_#_Locus3256v1rpkm30.45_F	Forward	CGATTGGCAGAGAGGAAAAG
fgenes1_kg.7_#_28_#_Locus3256v1rpkm30.45	Inner centromere protein, ARK binding region	fgenes1_kg.7_#_28_#_Locus3256v1rpkm30.45_R	Reverse	TTGGATCTTCAATCGTTCC
fgenes1_pg.8_#_19	Peptidase aspartic, catalytic	fgenes1_pg.8_#_19_F	Forward	GGGACCCCTTATCTCACAT
fgenes1_pg.8_#_19	Peptidase aspartic, catalytic	fgenes1_pg.8_#_19_R	Reverse	GTGGCTTGTCGTGTAAGT
estExt_Genewise1Plus.C_90065	Cyclin, N-terminal	estExt_Genewise1Plus.C_90065_F	Forward	GCCGATCTTCGTGTTCTAGC
estExt_Genewise1Plus.C_90065	Cyclin, N-terminal	estExt_Genewise1Plus.C_90065_R	Reverse	CCTTAATCTGGCGCTTCTTG
fgenes1_pg.10_#_55	Arginase	fgenes1_pg.10_#_55_F	Forward	TGGAGTTGAACAAGCACCAG
fgenes1_pg.10_#_55	Arginase	fgenes1_pg.10_#_55_R	Reverse	GAGTACCAGTTGCAGCGACA
fgenes1_kg.11_#_4_#_Locus4839v2rpkm0.09_PRE	Biotin synthase	fgenes1_kg.11_#_4_#_Locus4839v2rpkm0.09_PRE_F	Forward	AAAGGTGCAACCAGTTTTTG
fgenes1_kg.11_#_4_#_Locus4839v2rpkm0.09_PRE	Biotin synthase	fgenes1_kg.11_#_4_#_Locus4839v2rpkm0.09_PRE_R	Reverse	GAAGGATTTTCATCGGAACGA
estExt_Genewise1Plus.C_120009	Imidazole glycerol-phosphate dehydratase	estExt_Genewise1Plus.C_120009_F	Forward	CGGTCATCGATATCGGTCTT
estExt_Genewise1Plus.C_120009	Imidazole glycerol-phosphate dehydratase	estExt_Genewise1Plus.C_120009_R	Reverse	AGAATGGCCTGAACAAGGTG
estExt_Genemark1.C_130002	mRNA splicing factor, Cwf21	estExt_Genemark1.C_130002_F	Forward	TCATACAACGGGATCGGATT
estExt_Genemark1.C_130002	mRNA splicing factor, Cwf21	estExt_Genemark1.C_130002_r	Reverse	CTCTTCGGGCTTCCCTTACT
fgenes1_kg.14_#_20_#_Locus994v1rpkm161.74	Glutathione reductase, animal and	fgenes1_kg.14_#_20_#_Locus994v1rpkm161.74_F	Forward	TTGTTGACGCTTTGTTCTGG

fgenes1_kg.14_#_20_#_Locus994v1rpkm161.74	bacterial Glutathione reductase, animal and bacterial	fgenes1_kg.14_#_20_#_Locus994v1rpkm161.74_R	Reverse	TGATGTTTCGTGTTGGCAAAT
gm1.5011_g	Fungal transcriptional regulatory protein, N-terminal	gm1.5011_g_F	Forward	GCATGCCGTGAGAAGAAAAAT
gm1.5011_g	Fungal transcriptional regulatory protein, N-terminal	gm1.5011_g_R	Reverse	CAGCTCCGTGTCCGTATTCT
fgenes1_kg.16_#_33_#_Locus2982v1rpkm39.26	Sulphate transporter	fgenes1_kg.16_#_33_#_Locus2982v1rpkm39.26_F	Forward	TAGTGACGCTGGCCTTTTCT
fgenes1_kg.16_#_33_#_Locus2982v1rpkm39.26	Sulphate transporter	fgenes1_kg.16_#_33_#_Locus2982v1rpkm39.26_R	Reverse	TGAAGAGCACCGAGTTTGTG
fgenes1_pm.21_#_6	Homeobox	fgenes1_pm.21_#_6_F	Forward	CCATCCATGTGGATTGAGAA
fgenes1_pm.21_#_6	Homeobox	fgenes1_pm.21_#_6_R	Reverse	CCTCATCTGAGATAGCGGAAC
gm1.5241_g	FAD dependent oxidoreductase	gm1.5241_g_F	Forward	GTTGTTGGTGCCGGAATATC
gm1.5241_g	FAD dependent oxidoreductase	gm1.5241_g_R	Reverse	CCAGCTGTAGCTTCGACCTT
e_gw1.23.26.1	-	e_gw1.23.26.1_F	Forward	TGGATGTTCCCAAAGCAGAT
e_gw1.23.26.1	-	e_gw1.23.26.1_R	Reverse	TGGCACTAATCTCCCAAACC
gm1.5276_g	Inositol polyphosphate related phosphatase	gm1.5276_g_F	Forward	GGAGGGAAAGGTTGAGAAGG
gm1.5276_g	Inositol polyphosphate related phosphatase	gm1.5276_g_R	Reverse	ATTGCCTTGAAATCCTGGTG
gw1.27.10.1	Molybdopterin dehydrogenase, FAD-binding	gw1.27.10.1_F	Forward	AATCGGGATGTAATGCTTGC
gw1.27.10.1	Molybdopterin dehydrogenase, FAD-binding	gw1.27.10.1_R	Reverse	TTTCGCATCCGGATAGATTC
estExt_Genewise1Plus.C_300001	6-phosphogluconate dehydrogenase, C-terminal-like	estExt_Genewise1Plus.C_300001_F	Forward	ATTGTGGCGAAGAACAGCTT
estExt_Genewise1Plus.C_300001	6-phosphogluconate dehydrogenase, C-terminal-like	estExt_Genewise1Plus.C_300001_R	Reverse	GTCCGTTTTCTGCCTCATGT
e_gw1.31.2.1	WD40 repeat	e_gw1.31.2.1_F	Forward	GCATCAGGTGAAAAACACGA
e_gw1.31.2.1	WD40 repeat	e_gw1.31.2.1_R	Reverse	GGCGATCTTAGTGTCTTTCG
estExtgenes1_pm.C_320002	Zinc finger, N-recognin	estExt_fgenes1_pm.C_320002_F	Forward	CAGCTGCAAAAAGCCATACA
estExtgenes1_pm.C_320002	Zinc finger, N-recognin	estExt_fgenes1_pm.C_320002_R	Reverse	CCGGTTATTGCCTGCTCTAC
gw1.35.3.1	Lysophospholipase, catalytic region	gw1.35.3.1_F	Forward	CAGCGATAACCCAATCAACA
gw1.35.3.1	Lysophospholipase, catalytic region	gw1.35.3.1_R	Reverse	AGAAATCGGAAGAGCAAGCA
gm1.5307_g	-	gm1.5307_g_F	Forward	GAGGCTGTTTTCTGCTTGC
gm1.5307_g	-	gm1.5307_g_R	Reverse	GATGCTAGGCCATTCTGCTC
gm1.5309_g	-	gm1.5309_g_F	Forward	CTGCTGTGCCCGTAGTAAG
gm1.5309_g	-	gm1.5309_g_R	Reverse	CCTACCAGGCGTATCCAAAC
gm1.5316_g	-	gm1.5316_g_F	Forward	AAAATTGTCAAGGCCCAAT
gm1.5316_g	-	gm1.5316_g_R	Reverse	TGTCCAAGCCCGTCTTTATC
MIX1345_2881_99	-	MIX1345_2881_99_F	Forward	CACAAGGAAAAGGCTGGTTT
MIX1345_2881_99	-	MIX1345_2881_99_R	Reverse	CAAAAATGGTTCCGGATTCC
fgenes1_kg.56_#_1_#_Locus2611v1rpkm50.81	Sodium/hydrogen exchanger	fgenes1_kg.56_#_1_#_Locus2611v1rpkm50.81_F	Forward	ACGCTCAGAACCCCATACAG
fgenes1_kg.56_#_1_#_Locus2611v1rpkm50.81	Sodium/hydrogen exchanger	fgenes1_kg.56_#_1_#_Locus2611v1rpkm50.81_R	Reverse	CTGGAAAATGCCGAGAGAAC
gm1.5337_g	Armadillo-type fold	gm1.5337_g_F	Forward	GCAGTGAAGTACCACGGACA
gm1.5337_g	Armadillo-type fold	gm1.5337_g_R	Reverse	CTGCAGCTCCTTCAACTTCC
e_gw1.20.48.1	Zinc/iron permease	e_gw1.20.48.1_F	Forward	GCGTTTTTCCCCTTTTGTG
e_gw1.20.48.1	Zinc/iron permease	e_gw1.20.48.1_R	Reverse	AGCCTGGAGTCGTAAGACCA
e_gw1.20.53.1	-	e_gw1.20.53.1_F	Forward	CAACTGGCGTTCTAAATCCAA
e_gw1.20.53.1	-	e_gw1.20.53.1_R	Reverse	CGGAAGGATCAACAACCTCA

gm1.5197_g	Cytochrome b5	gm1.5197_g_F	Forward	ATTGCAATCGACGGAGAAGT
gm1.5197_g	Cytochrome b5	gm1.5197_g_R	Reverse	GATCCTCGGCTTCCCTAATC
gm1.5120_g	Protein of unknown function DUF74	gm1.5120_g_F	Forward	GGCCCTATTTCGAATCATCAA
gm1.5120_g	Protein of unknown function DUF74	gm1.5120_g_R	Reverse	AAAAGCAGACACCGGAAAGA
gm1.5119_g	Amidase signature enzyme	gm1.5119_g_F	Forward	CCGTCTTTTGAGTCTGGAG
gm1.5119_g	Amidase signature enzyme	gm1.5119_g_R	Reverse	TCCAGTCCCCGTTGTTTTAG
gm1.5118_g	-	gm1.5118_g_F	Forward	TGTGCTTGTGGAAGAACCAA
gm1.5118_g	-	gm1.5118_g_R	Reverse	CATATTC AAGCTTGCACCA
gw1.18.30.1	-	gw1.18.30.1_F	Forward	GGTATTGTTAGCCCAACACTTAG
gw1.18.30.1	-	gw1.18.30.1-R	Reverse	TCCGTCAATGTTAACGAAGCTG
gw1.17.85.1	-	gw1.17.85.1_F	Forward	GGATTCTTTTCGGTGACGGTA
gw1.17.85.1	-	gw1.17.85.1_R	Reverse	AAGTCGAATCCACGACCAAC
gm1.5099_g	Glycosyl hydrolase, family 13, catalytic region	gm1.5099_g_F	Forward	ATTCCAAGCTCCCTGGTCTT
gm1.5099_g	Glycosyl hydrolase, family 13, catalytic region	gm1.5099_g_R	Reverse	GATGACCATGGGAAAGGTGT
estExt_Genewise1.C_170061	Sugar transporter	estExt_Genewise1.C_170061_F	Forward	TTCCAGAATCTCCTCGTTGG
estExt_Genewise1.C_170061	Sugar transporter	estExt_Genewise1.C_170061_R	Reverse	AACTTCCAGCCAACAGCATC
fgenesh1_kg.17_#_18_#_Locus3414v1rpkm26.35	Glycoside hydrolase-type carbohydrate-binding	fgenesh1_kg.17_#_18_#_Locus3414v1rpkm26.35_F	Forward	ATCCGGGGTAATGCATACAA
fgenesh1_kg.17_#_18_#_Locus3414v1rpkm26.35	Glycoside hydrolase-type carbohydrate-binding	fgenesh1_kg.17_#_18_#_Locus3414v1rpkm26.35_R	Reverse	AGACCGGCAAAATGAATCAC
gm1.5092_g	Major facilitator superfamily MFS-1	gm1.5092_g_F	Forward	TCCACAGTGGTTGTGTGGAC
gm1.5092_g	Major facilitator superfamily MFS-1	gm1.5092_g_R	Reverse	AGTTGCGGGCAAAAATTGAAC
e_gw1.17.116.1	Major facilitator superfamily MFS-1	e_gw1.17.116.1_F	Forward	CTTTGTTTTGGAGCCGTGAT
e_gw1.17.116.1	Major facilitator superfamily MFS-1	e_gw1.17.116.1_R	Reverse	TCAA AATTGTGCAACCAGCA
CE38200_26352	Fungal transcriptional regulatory protein, N-terminal	CE38200_26352_F	Forward	CGTGTGAAGAGGGACAGGTT
CE38200_26352	Fungal transcriptional regulatory protein, N-terminal	CE38200_26352_R	Reverse	TCCTTGCTTCGATTTCCCTA
fgenesh1_kg.17_#_14_#_Locus4237v1rpkm6.64	Major facilitator superfamily MFS-1	fgenesh1_kg.17_#_14_#_Locus4237v1rpkm6.64_F	Forward	TTTGATTGCCGCTGTTACAA
fgenesh1_kg.17_#_14_#_Locus4237v1rpkm6.64	Major facilitator superfamily MFS-1	fgenesh1_kg.17_#_14_#_Locus4237v1rpkm6.64_R	Reverse	CTGCGTTCCATCAGGAAAAT
gw1.17.11.1	Amidohydrolase 1	gw1.17.11.1_F	Forward	TTTGAACAGACCTCAACC
gw1.17.11.1	Amidohydrolase 1	gw1.17.11.1_R	Reverse	TTTCTCGCCCCAACTATCTG
e_gw1.17.17.1	Sugar transporter	e_gw1.17.17.1_F	Forward	ATTAGGACAGCAGCCAATCG
e_gw1.17.17.1	Sugar transporter	e_gw1.17.17.1_R	Reverse	TTAAGCTTGCCCTCTTCCAA
e_gw1.17.69.1	Major facilitator superfamily MFS-1	e_gw1.17.69.1_F	Forward	TTTTGCCTGGGGTATAGTGG
e_gw1.17.69.1	Major facilitator superfamily MFS-1	e_gw1.17.69.1_R	Reverse	AATCATCGGAGCGACAAAAA
e_gw1.17.12.1	Major facilitator superfamily MFS-1	e_gw1.17.12.1_F	Forward	GCACATATGGCGTGGTAGAT
e_gw1.17.12.1	Major facilitator superfamily MFS-1	e_gw1.17.12.1_R	Reverse	TCAATGCCTCAATGACCTGA
fgenesh1_pg.17_#_34	FAD dependent oxidoreductase	fgenesh1_pg.17_#_34_F	Forward	CGGGATATGTCAGGTTTCGAT
fgenesh1_pg.17_#_34	FAD dependent oxidoreductase	fgenesh1_pg.17_#_34_R	Reverse	TGGCGTGCTAACATTTTTTCA
e_gw1.17.59.1	FAD dependent oxidoreductase	e_gw1.17.59.1_F	Forward	TGGAAGACCACATCCAGTGA
e_gw1.17.59.1	FAD dependent oxidoreductase	e_gw1.17.59.1_R	Reverse	GGGCAGTTGATCCATTCTGT
fgenesh1_kg.17_#_29_#_Locus4199v1rpkm7.15	Major facilitator superfamily MFS-1	fgenesh1_kg.17_#_29_#_Locus4199v1rpkm7.15_F	Forward	GGCAGATTCCATCGCATTAT
fgenesh1_kg.17_#_29_#_Locus4199v1rpkm7.15	Major facilitator superfamily MFS-1	fgenesh1_kg.17_#_29_#_Locus4199v1rpkm7.15_R	Reverse	CATAAGAAGAGCCCCACAA
gm1.5110_g	-	gm1.5110_g_F	Forward	GAAGCAAGCTTGCCATTC
gm1.5110_g	-	gm1.5110_g_R	Reverse	AATTGCCAAGTCTCCTGGAA
gw1.17.105.1	-	gw1.17.105.1_F	Forward	CTGAGTCAGGTTTCGTCAGTTG

gw1.17.105.1	-	gw1.17.105.1_R	Reverse	GGTTTCGATGGAAGAAGTGG
gm1.5112_g	Major facilitator superfamily MFS-1	gm1.5112_g_F	Forward	GCACCAATGCTTTCTGGATT
gm1.5112_g	Major facilitator superfamily MFS-1	gm1.5112_g_R	Reverse	GCAGCGCCTACACCATAAAT
gm1.5113_g	Amidase signature enzyme	gm1.5113_g_F	Forward	TGAAGGTGCTTTAGCAGCAA
gm1.5113_g	Amidase signature enzyme	gm1.5113_g_R	Reverse	TGAAACATATGCCGGTGCTA
gm1.5095_g	Galactokinase	gm1.5095_g_F	Forward	GCTAGAGCCCCAGGAAGAGT
gm1.5095_g	Galactokinase	gm1.5095_g_R	Reverse	CCTAACGTTGAAGCCACACA
fgenes1_kg.24_#_1_#_Locus2959v1rpkm39.78	Glycoside hydrolase, family 2	fgenes1_kg.24_#_1_#_Locus2959v1rpkm39.78_F	Forward	GGGAAAGTATGACGCGGTTA
fgenes1_kg.24_#_1_#_Locus2959v1rpkm39.78	Glycoside hydrolase, family 2	fgenes1_kg.24_#_1_#_Locus2959v1rpkm39.78_R	Reverse	CCTTAAAGCGAATTCCAACG
CE38776_32	-	CE38776_32_F	Forward	CCATCGGTAAGGTCACAAAA
CE38776_32	-	CE38776_32_R	Reverse	GGTCTCCTTAATCGATGCTTTG

^a All amplifications were performed using a Bio-Rad T100 thermal cycler in a total volume of 20 µl containing 0.5 µM of each primer, 0.15 mM of each dNTP, 1.0 unit Titanium Taq DNA polymerase, 1× Titanium Taq. Before amplification, DNA samples were denatured at 94°C for 2 min. Subsequently, 30 cycles were run of 1 min at 94°C, 45 s at 60°C, and 1 min at 72°C, with a final extension step for 10 min at 72°C;

^b -, Function not known.