

protID	TmD	sorbitol	sorbitol + 1mM glucose	sorbitol + 60mM glucose	Description (conserved domains)
		rel. ab ± sd [%]	rel. ab ± sd [%]	rel. ab ± sd [%]	
Plasma membrane					
201546	4	0.984 ± 0.008	1.141 ± 0.039	0.353 ± 0.262	-
1145073;1115054;1186115	9;9;10	0.677 ± 0.152	0.908 ± 0.260	0.763 ± 0.063	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter ATPase, P-type cation-transporter, N-terminal Plasma-membrane proton-efflux P-type ATPase H+ transporting ATPase, proton pump E1-E2 ATPase-associated region
1180988	4	0.131 ± 0.011	0.151 ± 0.011	0.241 ± 0.008	Yip1 domain Bacterial surface antigen (D15)
1141113	1	0.116 ± 0.030	0.032 ± 0.001	0.089 ± 0.011	Glycoside hydrolase, catalytic core X8
1093022	11	0.116 ± 0.000	0.041 ± 0.001	0.080 ± 0.013	Amino acid transporter, transmembrane
1142721	3	0.103 ± 0.009	0.113 ± 0.013	0.060 ± 0.002	B-cell receptor-associated 31-like
1133629	6	0.098 ± 0.049	0.182 ± 0.008	0.238 ± 0.141	Formate/nitrite transporter Lipocalin
1084143	1	0.098 ± 0.013	0.043 ± 0.004	0.056 ± 0.001	Tricalbin C2 calcium/lipid-binding region, CaLB C2 calcium-dependent membrane targeting
1113589	11	0.097 ± 0.054	0.000 ± 0.000	0.061 ± 0.009	Rh-like protein/ammonium transporter Blood group Rhesus C/E and D polypeptide Ammonium transporter
1141872	12	0.096 ± 0.023	0.072 ± 0.008	0.099 ± 0.012	Amino acid/polyamine transporter I

1121621	12	0.091 ± 0.010	0.119 ± 0.048	0.095 ± 0.035	Major facilitator superfamily
1105147	14	0.089 ± 0.000	0.071 ± 0.020	0.117 ± 0.012	Major facilitator superfamily MFS-1 ATP-dependent DNA ligase, conserved site
1107420	4	0.087 ± 0.004	0.030 ± 0.001	0.073 ± 0.001	OST3/OST6 Thioredoxin-like fold Protein of unknown function DUF1774, fungi
1141471	6	0.085 ± 0.015	0.051 ± 0.002	0.108 ± 0.004	Major facilitator superfamily
1143598	10	0.064 ± 0.018	0.175 ± 0.024	0.000 ± 0.000	Major facilitator superfamily
1144791	12	0.062 ± 0.012	0.000 ± 0.000	0.000 ± 0.000	Major facilitator superfamily
1184281	1	0.061 ± 0.049	0.037 ± 0.003	0.110 ± 0.012	Alkaline-phosphatase-like, core domain Alkaline phosphatase
1101809	10	0.048 ± 0.005	0.020 ± 0.003	0.000 ± 0.000	Major facilitator superfamily General substrate transporter Sugar transporter, conserved site Sugar transporter MFS general substrate transporter
1026385	12	0.047 ± 0.004	0.027 ± 0.001	0.056 ± 0.003	Amino acid/polyamine transporter I Amino acid permease-associated region Amino acid permease subfamily
209668	2	0.046 ± 0.024	0.055 ± 0.022	0.082 ± 0.011	-
1177845	4	0.041 ± 0.032	0.098 ± 0.001	0.000 ± 0.000	Shr3 amino acid permease chaperone
1128338	9	0.037 ± 0.003	0.044 ± 0.000	0.065 ± 0.008	Major facilitator superfamily MFS-1
1141295	2	0.031 ± 0.014	0.033 ± 0.010	0.019 ± 0.002	GOLD emp24/gp25L/p24
1122987	1	0.030 ± 0.014	0.042 ± 0.012	0.071 ± 0.009	Ribophorin I
1148445	9	0.029 ± 0.003	0.000 ± 0.000	0.061 ± 0.014	Protein of unknown function DUF250
51992	15	0.028 ± 0.003	0.034 ± 0.004	0.022 ± 0.012	Na ⁺ /solute symporter
1186700	2	0.027 ± 0.003	0.016 ± 0.000	0.018 ± 0.005	VPS10 BNR repeat
1142882	11	0.022 ± 0.005	0.045 ± 0.002	0.000 ± 0.000	Major facilitator superfamily
1142864	1	0.022 ± 0.010	0.014 ± 0.001	0.019 ± 0.013	-

1098273	16	0.022 ± 0.006	0.027 ± 0.001	0.031 ± 0.004	Glycosyl transferase, family 48
44753	1	0.020 ± 0.007	0.000 ± 0.000	0.000 ± 0.000	BAAT/Acyl-CoA thioester hydrolase C-terminal
1186946	5	0.019 ± 0.002	0.000 ± 0.000	0.026 ± 0.000	Cystinosin/ERS1p repeat Mannose-P-dolichol utilization defect 1 protein Protein of unknown function DUF284, transmembrane eukaryotic
1019516	2	0.018 ± 0.001	0.000 ± 0.000	0.007 ± 0.003	Cytochrome P450, E-class, group IV
1187492	2	0.018 ± 0.004	0.000 ± 0.000	0.011 ± 0.001	
1162850	1	0.016 ± 0.005	0.000 ± 0.000	0.000 ± 0.000	Mannose-6-phosphate receptor, binding
1038787	1	0.014 ± 0.008	0.017 ± 0.001	0.027 ± 0.015	Peptidase M28
1180715	13	0.013 ± 0.006	0.003 ± 0.000	0.019 ± 0.005	Transferrin receptor-like, dimerisation Protease-associated PA Glycoside hydrolase, catalytic core Glycosyl transferase, group 1 Starch synthase catalytic region Glycosyl hydrolase, family 13, catalytic region Glycosyl hydrolase, family 13, subfamily, catalytic region Cation-dependent mannose-6-phosphate receptor
202429	1	0.013 ± 0.001	0.000 0.000	0.011 ± 0.002	
1146541	3	0.012 ± 0.002	0.012 ± 0.002	0.011 ± 0.007	Mannose-6-phosphate receptor, binding Phosphatidic acid phosphatase type 2/haloperoxidase
1112865	1	0.012 ± 0.001	0.008 ± 0.001	0.003 ± 0.000	Cytochrome P450, E-class, group IV P-II protein uridylation site ERG4/ERG24 ergosterol biosynthesis protein
1101638	9	0.011 ± 0.004	0.000 ± 0.000	0.000 ± 0.000	
1188093	9	0.011 ± 0.004	0.008 ± 0.001	0.008 ± 0.003	Globin, subset Histone H4

					Oxidoreductase FAD-binding region Globin-like
1160579	9	0.011 ± 0.001	0.010 ± 0.003	0.008 ± 0.003	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter ATPase, P-type cation-transporter, C-terminal Calcium ATPase
1117429	1	0.010 ± 0.003	0.000 ± 0.000	0.005 ± 0.000	GOLD
1081653	2	0.010 ± 0.001	0.000 ± 0.000	0.016 ± 0.000	Cytochrome P450, E-class, group IV Cytochrome P450
1141222;1143346;1153587	7;8;6	0.026 ± 0.002	0.024 ± 0.006	0.029 ± 0.005	Legume lectin, beta domain Chitin synthase Chitin synthase N-terminal
1107559	1	0.008 ± 0.001	0.000 ± 0.000	0.022 ± 0.003	Glycoside hydrolase, catalytic core
1116513	12	0.008 ± 0.002	0.000 ± 0.000	0.005 ± 0.002	Glycolipid anchored surface protein GAS1 Amino acid/polyamine transporter I Amino acid permease, fungi Amino acid permease, conserved site ABC transporter, transmembrane region, type 1
1186153	14	0.007 ± 0.001	0.003 ± 0.001	0.012 ± 0.000	
41765	11	0.007 ± 0.000	0.007 ± 0.005	0.009 ± 0.001	Protein of unknown function DUF221 ERG4/ERG24 ergosterol biosynthesis
1087119	9	0.005 ± 0.003	0.005 ± 0.001	0.002 ± 0.000	protein Dienelactone hydrolase
1086577	5	0.004 ± 0.001	0.000 ± 0.000	0.013 ± 0.004	Cleft lip and palate transmembrane 1 TGF-beta receptor, type I/II extracellular region
1129336	9	0.003 ± 0.000	0.005 ± 0.001	0.011 ± 0.000	
1125334	5	0.003 ± 0.002	0.005 ± 0.001	0.000 ± 0.000	-
1160087	14	0.003 ± 0.001	0.013 ± 0.000	0.014 ± 0.002	Sterol-sensing 5TM box Patched

					Aspartic acid and asparagine hydroxylation site
1189214	9	0.003 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	Major facilitator superfamily
1158555	1	0.002 ± 0.001	0.000 ± 0.000	0.000 ± 0.000	-
1214584	1	0.001 ± 0.000	0.002 ± 0.000	0.000 ± 0.000	Peptidase M28
1143191	12	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	Major facilitator superfamily
1089440	7	0.000 ± 0.000	0.012 ± 0.001	0.000 ± 0.000	Major facilitator superfamily MFS-1
1104422	14	0.000 ± 0.000	0.003 ± 0.001	0.000 ± 0.000	ABC transporter, transmembrane region, type 1
1113000	8	0.000 ± 0.000	0.001 ± 0.000	0.006 ± 0.000	Peptidase M28
					Leucine-rich repeat 2
					Leucine-rich repeat, cysteine-containing subtype
1127869	13	0.000 ± 0.000	0.006 ± 0.000	0.000 ± 0.000	Oligopeptide transporter OPT superfamily
1145364	3	0.000 ± 0.000	0.283 ± 0.064	0.000 ± 0.000	TB2/DP1 and HVA22 related protein
1185324	6	0.000 ± 0.000	0.045 ± 0.023	0.040 ± 0.012	Major intrinsic protein
1185987	11	0.000 ± 0.000	0.003 ± 0.001	0.002 ± 0.000	-
1188715	2	0.000 ± 0.000	0.003 ± 0.002	0.000 ± 0.000	ABC transporter, transmembrane region, type 1
1022562	11	0.000 ± 0.000	0.000 ± 0.000	0.029 ± 0.002	Protein of unknown function DUF250
1099906	5	0.000 ± 0.000	0.000 ± 0.000	0.002 ± 0.000	Protein of unknown function DUF590
1111630	10	0.000 ± 0.000	0.000 ± 0.000	0.011 ± 0.001	Major facilitator superfamily MFS-1
					TGF-beta receptor, type I/II extracellular region
1118545	11	0.000 ± 0.000	0.000 ± 0.000	0.039 ± 0.011	Major facilitator superfamily MFS-1
1124902	12	0.000 ± 0.000	0.000 ± 0.000	0.014 ± 0.004	Major facilitator superfamily MFS-1
1146101	14	0.000 ± 0.000	0.000 ± 0.000	0.012 ± 0.009	Major facilitator superfamily MFS-1
1156564	8	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	Glycoside hydrolase, catalytic core
					Amylo-alpha-1,6-glucosidase
					Glycogen debranching enzyme
					Six-hairpin glycosidase-like
					Protein of unknown function DUF221
1175877	9	0.000 ± 0.000	0.000 ± 0.000	0.008 ± 0.002	-
1180703	12	0.000 ± 0.000	0.000 ± 0.000	0.014 ± 0.001	Major facilitator superfamily

1187342	13	0.000 ± 0.000	0.000 ± 0.000	0.003 ± 0.001	Glycoside hydrolase, catalytic core
1188840	12	0.000 ± 0.000	0.000 ± 0.000	0.030 ± 0.013	Major facilitator superfamily MFS-1 Nitrate transporter
1168100	1	0.000 ± 0.000	0.000 ± 0.000	0.013 ± 0.003	-
1039419	1	0.000 ± 0.000	0.000 ± 0.000	0.003 ± 0.000	Octicosapeptide/Phox/Bem1p Cystathionine beta-synthase, core ABC transporter, transmembrane region, type 1
1227231	12	0.000 ± 0.000	0.000 ± 0.000	0.001 ± 0.000	Calcium-binding EF-hand
1166284	5	0.000 ± 0.000	0.000 ± 0.000	0.001 ± 0.000	
Membrane bound mitochondrial					
1147568	4	1.360 ± 0.317	1.372 ± 0.292	1.563 ± 0.244	Mitochondrial carrier protein
1103448	1	0.455 ± 0.120	0.321 ± 0.099	0.381 ± 0.041	Prohibitin Band 7 protein
1142070	3	0.362 ± 0.047	0.633 ± 0.150	0.445 ± 0.072	- Ubiquinol-cytochrome C reductase, UQCRX/QCR9-like
1146906	1	0.347 ± 0.016	0.495 ± 0.029	0.247 ± 0.007	-
1141403	2	0.294 ± 0.102	0.564 ± 0.078	0.344 ± 0.102	GRIM-19
1145529	1	0.217 ± 0.060	0.144 ± 0.078	0.093 ± 0.013	-
1164228	3	0.167 ± 0.119	0.167 ± 0.036	0.106 ± 0.016	Protein of unknown function DUF543
1179969	1	0.166 ± 0.081	0.363 ± 0.003	0.192 ± 0.070	Concanavalin A-like lectin/glucanase Hypoxia induced protein conserved region
1167367	1	0.126 ± 0.005	0.050 ± 0.011	0.052 ± 0.005	Mitochondrial carrier protein Mitochondrial substrate carrier Adenine nucleotide translocator 1
1148052	3	0.123 ± 0.021	0.083 ± 0.025	0.096 ± 0.013	
1113466	2	0.108 ± 0.021	0.082 ± 0.010	0.034 ± 0.003	Mitochondrial import inner membrane translocase, subunit Tim17/22
1148385	3	0.073 ± 0.011	0.322 ± 0.007	0.144 ± 0.058	Cytochrome P450, E-class, group I Protein of unknown function UPF0136, Transmembrane
1112854	2	0.066 ± 0.017	0.053 ± 0.014	0.053 ± 0.002	Mpv17/PMP22
1104685	3	0.059 ± 0.024	0.038 ± 0.010	0.054 ± 0.009	
1146802	3	0.058 ± 0.019	0.000 ± 0.000	0.008 ± 0.004	

1211786	2	0.031 ± 0.017	0.005 ± 0.001	0.019 ± 0.000	AMP-dependent synthetase and ligase
1143042	1	0.026 ± 0.001	0.006 ± 0.001	0.021 ± 0.004	Ras GTPase
1129330	2	0.021 ± 0.000	0.008 ± 0.000	0.010 ± 0.001	Root hair defective 3 GTP-binding Protein of unknown function DUF1772, fungi
1187028	4	0.014 ± 0.003	0.236 ± 0.053	0.158 ± 0.003	AAA ATPase, conserved site
1126414	1	0.011 ± 0.001	0.000 ± 0.000	0.013 ± 0.002	AAA ATPase, core Peptidase M41, FtsH Peptidase M41
1145516	1	0.010 ± 0.001	0.000 ± 0.000	0.005 ± 0.003	Inorganic phosphate transport PHO88
1141800	1	0.051 ± 0.003	0.084 ± 0.006	0.059 ± 0.003	Mitochondrial substrate carrier
213531	1	0.023 ± 0.003	0.021 ± 0.004	0.034 ± 0.010	Protease inhibitor I4, serpin Tetratricopeptide TPR2 Tetratricopeptide TPR-1 Tetratricopeptide region Mitochondrial import translocase, subunit Tom70
1186873	5	0.008 ± 0.003	0.012 ± 0.005	0.000 ± 0.000	Insulin-induced
1188148	1	0.005 ± 0.002	0.007 ± 0.000	0.009 ± 0.003	Cytochrome P450, E-class, group IV
213721	3	0.005 ± 0.003	0.007 ± 0.001	0.005 ± 0.003	EXS, C-terminal
1139856	1	0.005 ± 0.002	0.000 ± 0.000	0.000 ± 0.000	Alpha/beta hydrolase fold-1
1182144	1	0.003 ± 0.001	0.000 ± 0.000	0.000 ± 0.000	-
1161772	1	0.003 ± 0.001	0.000 ± 0.000	0.000 ± 0.000	Apc13p Initiation factor 2B related
1102272	1	0.001 ± 0.001	0.000 ± 0.000	0.001 ± 0.000	Sel1-like
1142582	1	0.000 ± 0.000	0.202 ± 0.040	0.197 ± 0.020	- Fungal transcriptional regulatory protein, N-terminal
1183694	3	0.000 ± 0.000	0.003 ± 0.000	0.000 ± 0.000	NAD(P)-binding
1122081	1	0.000 ± 0.000	0.000 ± 0.000	0.005 ± 0.001	Aspartate/homoserine dehydrogenase, NAD-binding Homoserine dehydrogenase, catalytic

1145832	2	0.000 ± 0.000	0.000 ± 0.000	0.037 ± 0.000	Microsomal signal peptidase 25 kDa subunit
1148034	2	0.000 ± 0.000	0.000 ± 0.000	0.036 ± 0.016	-
Membrane bound ER					
1147042	1	0.587 ± 0.047	0.833 ± 0.081	0.381 ± 0.064	Cytochrome b5
1030262	10	0.334 ± 0.157	0.381 ± 0.002	0.121 ± 0.014	SecY protein
1148233	1	0.183 ± 0.051	0.149 ± 0.007	0.219 ± 0.010	FAD-binding, type 1 Flavodoxin-like Oxidoreductase FAD/NAD(P)-binding Flavoprotein pyridine nucleotide cytochrome reductase Flavodoxin/nitric oxide synthase Cyclopropane-fatty-acyl-phospholipid synthase
1141865	2	0.144 ± 0.047	0.057 ± 0.006	0.041 ± 0.006	Cyclophilin-like
1126047	2	0.134 ± 0.047	0.018 ± 0.000	0.046 ± 0.004	Surface protein from Gram-positive cocci, anchor region Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
1111800	1	0.133 ± 0.011	0.067 ± 0.015	0.059 ± 0.026	Heat shock protein 70 Heat shock protein Hsp70
1161167	15	0.116 ± 0.038	0.016 ± 0.011	0.113 ± 0.009	Tetrapeptide transporter, OPT1/isp4
1142917	1	0.099 ± 0.030	0.085 ± 0.026	0.085 ± 0.004	Oligopeptide transporter OPT superfamily Terpenoid synthase
187424	3	0.085 ± 0.023	0.035 ± 0.007	0.048 ± 0.003	Farnesyl-diphosphate farnesyltransferase Squalene/phytoene synthase
1156469	1	0.064 ± 0.002	0.228 ± 0.052	0.142 ± 0.014	Defender against death DAD protein
1022934	7	0.052 ± 0.011	0.040 ± 0.011	0.038 ± 0.003	ERG2 and sigma1 receptor-like
1126035	5	0.041 ± 0.010	0.038 ± 0.016	0.045 ± 0.025	GNS1/SUR4 membrane protein Peptidase M48, Ste24p

1129295	7	0.038 ± 0.014	0.051 ± 0.004	0.080 ± 0.001	Peptidase M, neutral zinc metallopeptidases, zinc-binding site Cytochrome c oxidase, subunit VIa Surfeit locus 4-related Surfeit locus 4
1141391	5	0.035 ± 0.012	0.034 ± 0.010	0.028 ± 0.001	ER lumen protein retaining receptor
1176663	13	0.032 ± 0.002	0.037 ± 0.000	0.035 ± 0.003	Oligosaccharyl transferase, STT3 subunit
1150065	1	0.030 ± 0.004	0.004 ± 0.001	0.024 ± 0.004	Heat shock protein 70
1122380	10	0.022 ± 0.000	0.015 ± 0.005	0.019 ± 0.004	E1-E2 ATPase-associated region ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter P-type ATPase of unknown pump specificity (type V)
1126550	6	0.020 ± 0.006	0.021 ± 0.007	0.032 ± 0.004	Haloacid dehalogenase-like hydrolase Cof protein 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal Phosphotransferase system, HPr serine phosphorylation site
1112450	10	0.018 ± 0.001	0.014 ± 0.002	0.009 ± 0.006	Glycosyl transferase, family 39 MIR motif MIR
1185951	17	0.016 ± 0.006	0.019 ± 0.006	0.052 ± 0.006	Endonuclease/exonuclease/phosphatase Inositolphosphorylceramide-B
1142806	3	0.016 ± 0.000	0.012 ± 0.008	0.037 ± 0.004	hydroxylase Cytochrome b5 Fatty acid hydroxylase
1184388	7	0.015 ± 0.003	0.006 ± 0.000	0.009 ± 0.002	ABC-2 type transporter EGF-like, type 3 EGF, extracellular

1142025	1	0.015 ± 0.005	0.013 ± 0.001	0.000 ± 0.000	Peptidase S26A, signal peptidase I Peptidase S24, S26A, S26B and S26C Peptidase S26B, eukaryotic signal peptidase
1167021	2	0.013 ± 0.000	0.000 ± 0.000	0.015 ± 0.008	Peptidase S24, S26A and S26B, C-terminal Synaptojanin, N-terminal
1128516	2	0.013 ± 0.002	0.017 ± 0.003	0.009 ± 0.000	Cytochrome P450, E-class, group I UDP-glucuronosyl/UDP-
1159100	1	0.013 ± 0.006	0.012 ± 0.003	0.018 ± 0.004	glucosyltransferase Short-chain dehydrogenase/reductase
1151842	3	0.012 ± 0.005	0.032 ± 0.004	0.023 ± 0.010	SDR Glucose/ribitol dehydrogenase NAD(P)-binding
1087806	1	0.012 ± 0.001	0.004 ± 0.001	0.021 ± 0.002	Glycosyl transferase, family 15
1164538;1188786	10;11	0.021 ± 0.001	0.000 ± 0.000	0.026 ± 0.002	Major facilitator superfamily MFS-1
1165478	9	0.006 ± 0.001	0.002 ± 0.000	0.008 ± 0.001	ALG6, ALG8 glycosyltransferase
1180885	1	0.006 ± 0.002	0.004 ± 0.001	0.009 ± 0.002	Glycoside hydrolase, catalytic core Glycoside hydrolase, family 31
1119913	4	0.006 ± 0.003	0.000 ± 0.000	0.008 ± 0.001	Calcium-binding EF-hand Like-Sm ribonucleoprotein-related, core Membrane protein, At2g17000, predicted Mechanosensitive ion channel MscS
1212687	6	0.005 ± 0.001	0.000 ± 0.000	0.002 ± 0.001	Hydroxymethylglutaryl-CoA reductase, class I/II, substrate-binding Hydroxymethylglutaryl-CoA reductase, class I, catalytic Ribosomal protein S2 Hydroxymethylglutaryl-CoA reductase, class I/II, NAD/NADP-binding

						Sterol-sensing 5TM box
						Hydroxymethylglutaryl-CoA reductase, class I/II, catalytic
1105077	5	0.004 ± 0.003	0.011 ± 0.001	0.005 ± 0.001		Spermine synthase
1184634	9	0.003 ± 0.000	0.000 ± 0.000	0.000 ± 0.000		Major facilitator superfamily
1102309	3	0.002 ± 0.001	0.005 ± 0.001	0.000 ± 0.000		Sec63
						Heat shock protein DnaJ, N-terminal
1126795	11	0.000 ± 0.000	0.007 ± 0.001	0.006 ± 0.001		ALG6, ALG8 glycosyltransferase
1141396	2	0.000 ± 0.000	0.001 ± 0.000	0.016 ± 0.007		Sterol desaturase
1141926	12	0.000 ± 0.000	0.007 ± 0.000	0.000 ± 0.000		Tetrapeptide transporter, OPT1/isp4
						Translocation protein Sec62, ascomycota
1164790	2	0.000 ± 0.000	0.010 ± 0.001	0.000 ± 0.000		Translocation protein Sec62
						Protein of unknown function UPF0136, Transmembrane
1038793	4	0.000 ± 0.000	0.000 ± 0.000	0.014 ± 0.004		Cytochrome b5
1145703	1	0.000 ± 0.000	0.000 ± 0.000	0.032 ± 0.011		Major facilitator superfamily MFS-1
1165706	11	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000		Flagellar basal body rod protein
						Fatty acid desaturase, type 1, core
1173782	3	0.000 ± 0.000	0.000 ± 0.000	0.022 ± 0.002		Delta-9 acyl-CoA desaturase with haem/steroid binding region
						Fatty acid desaturase, type 1, C-terminal
						Fatty acid desaturase, type 1, N-terminal
1178623	11	0.000 ± 0.000	0.000 ± 0.000	0.047 ± 0.011		Major facilitator superfamily MFS-1
1180615	12	0.000 ± 0.000	0.000 ± 0.000	0.015 ± 0.005		Oligopeptide transporter OPT superfamily
129462	9	0.000 ± 0.000	0.000 ± 0.000	0.003 ± 0.000		Alg9-like mannosyltransferase
Membrane bound golgi						
1121885	1	0.095 ± 0.005	0.054 ± 0.009	0.053 ± 0.012		Thioredoxin domain
						Thioredoxin-related
1145709	4	0.035 ± 0.016	0.000 ± 0.000	0.000 ± 0.000		-

1189177	9	0.025 ± 0.005	0.023 ± 0.000	0.021 ± 0.001	Nonaspanin (TM9SF)
1025773	9	0.022 ± 0.004	0.011 ± 0.000	0.035 ± 0.001	Protein of unknown function DUF250 UDP-galactose transporter
1134649	1	0.022 ± 0.013	0.000 ± 0.000	0.008 ± 0.005	Dolichyl-diphosphooligosaccharide- protein glycosyltransferase 48kDa subunit
1182240	5	0.012 ± 0.009	0.014 ± 0.001	0.000 ± 0.000	SNARE associated Golgi protein
1150734	1	0.009 ± 0.005	0.034 ± 0.000	0.007 ± 0.001	-
1169091	7	0.006 ± 0.001	0.000 ± 0.000	0.000 ± 0.000	Nucleotide-sugar transporter
1163105	2	0.000 ± 0.000	0.004 ± 0.000	0.000 ± 0.000	Cytochrome P450, E-class, group I
1157289	1	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	Cytochrome P450, E-class, group I
Membrane bound vacuolar					
1104971	1	0.041 ± 0.005	0.040 ± 0.003	0.032 ± 0.005	Protein of unknown function DUF1620 Pyrrolo-quinoline quinone WD40 repeat-like Quinonprotein alcohol dehydrogenase- like
1142522	7	0.039 ± 0.037	0.000 ± 0.000	0.000 ± 0.000	Iron permease FTR1
1167192	6	0.035 ± 0.003	0.131 ± 0.009	0.130 ± 0.013	ATPase, V0/A0 complex, 116-kDa subunit
1122202	13	0.009 ± 0.001	0.000 ± 0.000	0.005 ± 0.003	Major facilitator superfamily MFS-1 Major facilitator superfamily Tetracycline resistance protein, TetB ABC transporter, transmembrane region, type 1
1093419	12	0.004 ± 0.002	0.001 ± 0.000	0.001 ± 0.001	AAA+ ATPase, core ABC transporter-like
1080879	12	0.000 ± 0.000	0.000 ± 0.000	0.020 ± 0.001	ABC transporter, transmembrane region Citrate synthase-like, core Amino acid/polyamine transporter I
1208596	3	0.000 ± 0.000	0.000 ± 0.000	0.002 ± 0.000	SPX, N-terminal

Membrane bound lysosomal					
1100508	7	0.027 ± 0.003	0.011 ± 0.001	0.010 ± 0.007	Transmembrane receptor, eukaryota
Membrane bound extracellular (secreted)					
1034818	1	0.009 ± 0.002	0.007 ± 0.001	0.000 ± 0.000	-
1139200	1	0.000 ± 0.000	0.031 ± 0.009	0.000 ± 0.000	-
1145281	1	0.000 ± 0.000	0.000 ± 0.000	0.145 ± 0.084	NADH-ubiquinone oxidoreductase B12 subunit
Mitochondrial - with targeting sequence					
1141664	1	0.856 ± 0.081	1.836 ± 0.108	1.898 ± 0.373	Cytochrome c oxidase subunit IV
1101772	1	0.597 ± 0.104	0.258 ± 0.049	0.356 ± 0.056	Concanavalin A-like lectin/glucanase Calreticulin/calnexin Calreticulin/calnexin, P
1098376	1	0.316 ± 0.019	0.134 ± 0.031	0.195 ± 0.045	FAD dependent oxidoreductase FAD-dependent glycerol-3-phosphate dehydrogenase
1147204	1	0.251 ± 0.212	0.033 ± 0.007	0.027 ± 0.009	-
209689	1	0.137 ± 0.005	0.236 ± 0.021	0.097 ± 0.011	-
1146585	4	0.130 ± 0.052	0.283 ± 0.067	0.039 ± 0.007	-
1125366	4	0.054 ± 0.007	0.038 ± 0.005	0.044 ± 0.012	FAD dependent oxidoreductase Aromatic-ring hydroxylase Squalene epoxidase
1143198	1	0.050 ± 0.022	0.085 ± 0.049	0.055 ± 0.016	Protein of unknown function UPF0041
1144353	9	0.034 ± 0.001	0.024 ± 0.012	0.036 ± 0.001	Glycosyl transferase, family 39 EGF-like region, conserved site Lipase, active site
1143907	2	0.031 ± 0.009	0.035 ± 0.004	0.000 ± 0.000	Succinate dehydrogenase, cytochrome b subunit Succinate dehydrogenase, cytochrome b556 subunit

1179837	1	0.028 ± 0.005	0.031 ± 0.005	0.042 ± 0.006	Nucleoside phosphatase GDA1/CD39
1176655	10	0.027 ± 0.001	0.000 ± 0.000	0.004 ± 0.001	Glycosyl transferase, family 39
1184291	6	0.025 ± 0.015	0.029 ± 0.007	0.047 ± 0.016	-
1144427	1	0.024 ± 0.011	0.000 ± 0.000	0.000 ± 0.000	-
1146026	1	0.023 ± 0.002	0.031 ± 0.006	0.017 ± 0.002	-
1038150	1	0.016 ± 0.012	0.000 ± 0.000	0.000 ± 0.000	Glycosyl transferase, family 15
1144049	4	0.016 ± 0.006	0.023 ± 0.010	0.008 ± 0.002	-
1142370	2	0.015 ± 0.001	0.012 ± 0.004	0.011 ± 0.001	Mitochondrial import protein Pam17 N-acetylglucosaminyl
1084241	1	0.013 ± 0.003	0.000 ± 0.000	0.000 ± 0.000	phosphatidylinositol deacetylase
1158534	1	0.013 ± 0.004	0.000 ± 0.000	0.000 ± 0.000	Thioredoxin-like fold Copper chaperone SCO1/SenC Synthesis of cytochrome c oxidase, Sco1/Sco2
1226708	1	0.012 ± 0.000	0.000 ± 0.000	0.007 ± 0.000	Glycoside hydrolase, family 47
1090476	4	0.012 ± 0.002	0.011 ± 0.002	0.012 ± 0.000	Der1-like
1162283	2	0.011 ± 0.002	0.015 ± 0.002	0.007 ± 0.001	Protein of unknown function DUF1692
1114338	6	0.008 ± 0.000	0.021 ± 0.002	0.031 ± 0.006	-
1127980	1	0.008 ± 0.005	0.005 ± 0.000	0.009 ± 0.002	FAD-dependent pyridine nucleotide- disulphide oxidoreductase Calcium-binding EF-hand Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region
1164910	2	0.006 ± 0.000	0.009 ± 0.001	0.000 ± 0.000	-
1174618	6	0.005 ± 0.001	0.000 ± 0.000	0.007 ± 0.001	DEK C terminal Myosin head, motor region Major intrinsic protein Fungal chitin synthase RNA polymerase sigma factor 54, interaction
1100035	3	0.002 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	-
1176977	1	0.002 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	-
1164300	17	0.001 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	ABC transporter, transmembrane region, type 1

1110430	11	0.000 ± 0.000	0.009 ± 0.003	0.006 ± 0.000	Amino acid transporter, transmembrane ABC transporter, transmembrane region, type 1
1129829	4	0.000 ± 0.000	0.007 ± 0.003	0.000 ± 0.000	
1142998	1	0.000 ± 0.000	0.077 ± 0.049	0.077 ± 0.047	-
1144677	1	0.000 ± 0.000	0.131 ± 0.002	0.087 ± 0.001	-
1156944	7	0.000 ± 0.000	0.016 ± 0.005	0.014 ± 0.002	-
1148070	4	0.000 ± 0.000 ±	0.000 ± 0.000	0.007 ± 0.004	Fatty acid desaturase, type 1, N-terminal Fatty acid desaturase, type 1
1174341	8	0.000 ± 0.000	0.000 ± 0.000	0.012 ± 0.001	Phosphatidate cytidyltransferase, eukaryota Phosphatidate cytidyltransferase
1187508	8	0.000 ± 0.000	0.000 ± 0.000	0.012 ± 0.000	Cytochrome oxidase assembly
1187906	2	0.000 ± 0.000	0.000 ± 0.000	0.007 ± 0.001	Surfeit locus 1
Mitochondrial - no targeting sequence					
1182982	2	0.016 ± 0.004	0.000 ± 0.000	0.000 ± 0.000	-
1124805	1	0.009 ± 0.005	0.000 ± 0.000	0.015 ± 0.007	-
Endoplasmic reticulum (ER)					
1186974	4	0.011 ± 0.007	0.000 ± 0.000	0.000 ± 0.000	-
Golgi					
1141641	1	0.021 ± 0.005	0.000 ± 0.000	0.017 ± 0.004	Glycosyl transferase, family 15
1126561	1	0.007 ± 0.001	0.017 ± 0.001	0.009 ± 0.001	Target SNARE coiled-coil region Vesicle transport v-SNARE
Nuclear					
1144574	1	0.079 ± 0.019	0.020 ± 0.009	0.088 ± 0.016	Concanavalin A-like lectin/glucanase Legume-like lectin
Cytoplasmic					
1091575	2	0.055 ± 0.001	0.023 ± 0.003	0.030 ± 0.010	-

1161479	1	0.016 ± 0.007	0.007 ± 0.004	0.049 ± 0.008	Amidohydrolase 1
1137546	2	0.005 ± 0.003	0.000 ± 0.000	0.000 ± 0.000	Metal-dependent hydrolase, composite Metallophosphoesterase
Extracellular (secreted)					
1135869	1	0.100 ± 0.029	0.076 ± 0.042	0.071 ± 0.038	Ribosomal protein L13
1041322	1	0.012 ± 0.005	0.000 ± 0.000	0.008 ± 0.003	-
1178906	1	0.008 ± 0.004	0.000 ± 0.000	0.000 ± 0.000	-
