Additional File 10. Transporter distribution in hemiascomycete species

Transporters were identified through a two step process on the proteomes of *S. cerevisiae, C. glabrata, K. lactis, D. hansenii, K. pastoris, Y. lipolytica* and *A. adeninivorans*: 1) identification of protein products having at least three transmembrane domains using THMM (v2.0; http://www.cbs.dtu.dk/services/TMHMM-2.0), 2) identification of transporters by a Blastp search against the TCDB database[16].

Table S10A Transporter distribution in hemiascomycete species.

Table S10B TCDB classification of transporters of *A. adeninivorans*.

Table S10C Class of transporters amplified in *A. adeninivorans* compared to two other pre-CTG species.

Figure S10D Phylogeny of sugar porters in *A. adeninivorans* and *D. hansenii.*

Table S10A Transporter distribution in hemiascomycete species

Type	**Subfamily code TCDB**	**Species**								
		ARAD	**YALI**	**PIPA**	**DEHA**	**KLLA**	**CAGL**	**SACE**	**Total**	**TCDB Family**
α-Type Channels	1.A.1.10	**1**							1	The Voltage-gated Ion Channel (VIC) Family
	1.A.1.11	**1**	1	1	1	1	1	1	7	The Voltage-gated Ion Channel (VIC) Family
	1.A.1.5	**1**							1	The Voltage-gated Ion Channel (VIC) Family
	1.A.1.7	**1**	2			1	1	1	6	The Voltage-gated Ion Channel (VIC) Family
	1.A.11.1		1		1	1	1	1	5	The Ammonia Transporter Channel (Amt) Family
	1.A.11.2		2		2				4	The Ammonia Transporter Channel (Amt) Family
	1.A.11.3	**2**		3					5	The Ammonia Transporter Channel (Amt) Family
	1.A.15.1		1		1	1	1	1	5	The Non-selective Cation Channel-2 (NSCC2) Family
	1.A.15.2			1					1	The Non-selective Cation Channel-2 (NSCC2) Family
	1.A.16.1		1		1	1	1	1	5	The Yeast Stretch-Activated, Cation-Selective, Ca2+ Channel, Mid1 Family
	1.A.17.2	**1**							1	The Calcium-Dependent Chloride Channel (Ca-ClC) Family
	1.A.17.3			1					1	The Calcium-Dependent Chloride Channel (Ca-ClC) Family
	1.A.20.5		11		7	5	1	7	31	The BCL2/Adenovirus E1B-interacting Protein 3 (BNip3) Family
	1.A.20.Y1		1						1	The BCL2/Adenovirus E1B-interacting Protein 3 (BNip3) Family
	1.A.20.Y2		1		1				2	The BCL2/Adenovirus E1B-interacting Protein 3 (BNip3) Family
	1.A.31.Y1		1						1	The Annexin (Annexin) Family
	1.A.33.1		10		9	9	11	14	53	The Cation Channel-forming Heat Shock Protein-70 (Hsp70) Family
	1.A.35.2	**2**	3		2	2	2	3	14	The CorA Metal Ion Transporter (MIT) Family
	1.A.35.5	**1**	2		2	2	2	2	11	The CorA Metal Ion Transporter (MIT) Family
	1.A.38.1	**1**		1					2	The Golgi pH Regulator (GPHR) Family
	1.A.4.4	**3**	1	1	1	1	1	2	10	The Transient Receptor Potential Ca2+ Channel (TRP-CC) Family
	1.A.4.Y1		2						2	The Transient Receptor Potential Ca2+ Channel (TRP-CC) Family
	1.A.55.4	**1**							1	The Synaptic Vesicle-Associated Ca2+ Channel, Flower Family
	1.A.56.1	**2**							2	The Copper Transporter (Ctr) Family
	1.A.6.Y1		1		1				2	The Epithelial Na+ Channel (ENaC) Family
	1.A.6.Y2		1		1				2	The Epithelial Na+ Channel (ENaC) Family
	1.A.8.5					1	2	1	4	The Major Intrinsic Protein (MIP) Family
	1.A.8.6	**1**	1	1	1	1	2	3	10	The Major Intrinsic Protein (MIP) Family
	1.A.8.7		2	1				1	4	The Major Intrinsic Protein (MIP) Family
	1.A.X1.Y1		1		1				2	Unassigned
β-Barrel Porins	1.B.40.1	**2**							2	The Autotransporter-2 (AT-2) Family
	1.B.53.1	**1**							1	The Filamentous Phage gp3 Channel-Forming Protein (FP-gp3) Family
	1.B.8.1		1		1	1	2	2	7	The Mitochondrial and Plastid Porin (MPP) Family
	2.A.1.1	**60**	27	17	48	20	17	34	223	Sugar Porter (SP) Family
	2.A.1.11	**1**		2					3	Oxalate: Formate Antiporter (OFA) Family
	2.A.1.12	**4**	6	1	3	2		1	17	Sialate: H+ Symporter (SHS) Family
	2.A.1.13	**8**	5	3	8	12	3		39	Monocarboxylate Porter (MCP) Family (Halestrap, 2011)
	2.A.1.14	**18**	39	14	27	13	6	10	127	Anion: Cation Symporter (ACS) Family
	2.A.1.15	**1**							1	Aromatic Acid: H+ Symporter (AAHS) Family
	2.A.1.16	**6**	14	3	5	4	1	6	39	Siderophore-Iron Transporter (SIT) Family
	2.A.1.19	**1**							1	Organic Cation Transporter (OCT) Family

2.A.1.2	**39**	33	10	24	8	10	12	136	Drug: H+ Antiporter-1 (12 Spanner) (DHA1) Family
2.A.1.22	**2**							2	Vesicular Neurotransmitter Transporter (VNT) Family
2.A.1.24	**2**	1	1		1	1	1	7	Unknown Major Facilitator-1 (UMF1) Family
2.A.1.25	**1**	1	1	1	1	1	1	7	Peptide-Acetyl-Coenzyme A Transporter (PAT) Family
2.A.1.28	**1**	1						2	Feline Leukemia Virus Subgroup C Receptor (FLVCR) Family
2.A.1.3	**9**	7	2	7	6	5	10	46	Drug: H+ Antiporter-2 (14 Spanner) (DHA2) Family
2.A.1.43			1					1	The Putative Magnetosome Permease (PMP) Family
2.A.1.44	**1**		2					3	L-Amino Acid Transporter-3 (LAT3) Family (also called the SLC43 family)
2.A.1.48	**1**		3					4	Vacuolar Basic Amino Acid Transporter (V-BAAT) Family
2.A.1.58	**3**		1					4	N-Acetylglucosamine Transporter (NAG-T) Family
2.A.1.63	**1**		1					2	Unidentified Major Facilitator-12 (UMF12) Family
2.A.1.7	**2**							2	Fucose: H+ Symporter (FHS) Family
2.A.1.8	**3**							3	Nitrate/Nitrite Porter (NNP) family
2.A.1.9	**3**	5	2	3	3	2	2	20	Phosphate: H+ Symporter (PHS) Family
2.A.1.Y1		5		1	4	2	4	16	Unassigned
2.A.1.Y2		1		1			1	3	Unassigned
2.A.1.Y3		3		1				4	Unassigned
2.A.16.3			1					1	The Tellurite-resistance/Dicarboxylate Transporter (TDT) Family
2.A.16.4	**1**							1	The Telurite-resistance/Dicarboxylate Transporter (TDT) Family
2.A.16.Y1		1		3	1	1	1	7	The Telurite-resistance/Dicarboxylate Transporter (TDT) Family
2.A.17.2	**2**	7		3	1	1	1	15	The Proton-dependent Oligopeptide Transporter (POT) Family
2.A.18.4	**4**	1		3	2			10	The Amino Acid/Auxin Permease (AAAP) Family
2.A.18.5	**1**	1	1	2	1	1	1	8	The Amino Acid/Auxin Permease (AAAP) Family
2.A.18.6	**2**	2	3	3	3	3	4	20	The Amino Acid/Auxin Permease (AAAP) Family
2.A.18.7	**1**	1	2	2	2	3	2	13	The Amino Acid/Auxin Permease (AAAP) Family
2.A.18.Y1		3		1				4	The Amino Acid/Auxin Permease (AAAP) Family
2.A.19.2	**1**	2	1	1	2	2	1	10	The Ca2+:Cation Antiporter (CaCA) Family
2.A.19.4	**1**		2					3	The Ca2+:Cation Antiporter (CaCA) Family
2.A.19.7	**1**		1					2	The Ca2+:Cation Antiporter (CaCA) Family
2.A.19.Y1				1	1		1	3	The Ca2+:Cation Antiporter (CaCA) Family
2.A.2.6	**2**	1	1					4	The Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family
2.A.20.2	**1**	1	1	1	1		1	6	The Inorganic Phosphate Transporter (PiT) Family
2.A.21.6	**2**	4	5	3	3	1	1	19	The Solute:Sodium Symporter (SSS) Family
2.A.21.9	**2**							2	The Solute:Sodium Symporter (SSS) Family
2.A.29.1	**1**	3		1	1	1	3	10	The Mitochondrial Carrier (MC) Family
2.A.29.10	**1**		1	1	1	1	1	6	The Mitochondrial Carrier (MC) Family
2.A.29.12	**1**		1					2	The Mitochondrial Carrier (MC) Family
2.A.29.13		1		2	3	3	2	11	The Mitochondrial Carrier (MC) Family
2.A.29.14		1					1	2	The Mitochondrial Carrier (MC) Family
2.A.29.15		1		1	1	1	1	5	The Mitochondrial Carrier (MC) Family
2.A.29.17	**2**	2		1	1	1	1	8	The Mitochondrial Carrier (MC) Family
2.A.29.18	**3**	1		1	1	1	1	8	The Mitochondrial Carrier (MC) Family
2.A.29.2	**1**	2		2	1	2	3	11	The Mitochondrial Carrier (MC) Family
2.A.29.27	**1**							1	The Mitochondrial Carrier (MC) Family
2.A.29.4	**1**	2		2	1	1	2	9	The Mitochondrial Carrier (MC) Family

Porters (uniporters, symporters, antiporters)	2.A.29.5		1		1	1	2	2	7	The Mitochondrial Carrier (MC) Family
	2.A.29.6	**1**	1	1	1	1			5	The Mitochondrial Carrier (MC) Family
	2.A.29.7		3		3	2	3	2	13	The Mitochondrial Carrier (MC) Family
	2.A.29.8	**1**	1	2	1	1	1	1	8	The Mitochondrial Carrier (MC) Family
	2.A.29.9				1	1	1	1	4	The Mitochondrial Carrier (MC) Family
	2.A.29.Y1		1		1	1	1	1	5	The Mitochondrial Carrier (MC) Family
	2.A.29.Y10		1		1	1	1	1	5	The Mitochondrial Carrier (MC) Family
	2.A.29.Y11						1	1	2	The Mitochondrial Carrier (MC) Family
	2.A.29.Y12		1		1	1	1	1	5	The Mitochondrial Carrier (MC) Family
	2.A.29.Y13		1		1	1	1	1	5	The Mitochondrial Carrier (MC) Family
	2.A.29.Y14				1	1	1		3	The Mitochondrial Carrier (MC) Family
	2.A.29.Y15						1		1	The Mitochondrial Carrier (MC) Family
	2.A.29.Y16		1						1	The Mitochondrial Carrier (MC) Family
	2.A.29.Y17		1		1	1			3	The Mitochondrial Carrier (MC) Family
	2.A.29.Y18		1						1	The Mitochondrial Carrier (MC) Family
	2.A.29.Y19		2						2	The Mitochondrial Carrier (MC) Family
	2.A.29.Y2				1	1	1	1	4	The Mitochondrial Carrier (MC) Family
	2.A.29.Y20		1		1				2	The Mitochondrial Carrier (MC) Family
	2.A.29.Y21		1		2				3	The Mitochondrial Carrier (MC) Family
	2.A.29.Y22		1						1	The Mitochondrial Carrier (MC) Family
	2.A.29.Y23		1						1	The Mitochondrial Carrier (MC) Family
	2.A.29.Y3		2		2	2	2	2	10	The Mitochondrial Carrier (MC) Family
	2.A.29.Y4		1		1	1	1	2	6	The Mitochondrial Carrier (MC) Family
	2.A.29.Y5		1		1	2	1	1	6	The Mitochondrial Carrier (MC) Family
	2.A.29.Y6		1		1	1	1	1	5	The Mitochondrial Carrier (MC) Family
	2.A.29.Y7		1		2	1	1	1	6	The Mitochondrial Carrier (MC) Family
	2.A.29.Y8					1	1	1	3	The Mitochondrial Carrier (MC) Family
	2.A.3.1	**1**	2	1					4	The Amino Acid-Polyamine-Organocation (APC) Family
	2.A.3.10	**9**	14	12	24	16	14	18	107	The Amino Acid-Polyamine-Organocation (APC) Family
	2.A.3.4	**10**	9	2	6	6	2	4	39	The Amino Acid-Polyamine-Organocation (APC) Family
	2.A.3.8	**2**	5	4	3	3	3	2	22	The Amino Acid-Polyamine-Organocation (APC) Family
	2.A.30.1			1					1	The Cation-Chloride Cotransporter (CCC) Family
	2.A.30.6	**1**							1	The Cation-Chloride Cotransporter (CCC) Family
	2.A.30.7		1		1	1	1	1	5	The Cation-Chloride Cotransporter (CCC) Family
	2.A.31.3	**1**	1	1	2	1	1	1	8	The Anion Exchanger (AE) Family
	2.A.36.2	**1**	1	1	1	1	1	1	7	The Monovalent Cation: Proton Antiporter-1 (CPA1) Family
	2.A.36.4	**2**	2	1	1	1	1	1	9	The Monovalent Cation: Proton Antiporter-1 (CPA1) Family
	2.A.37.4	**1**		1	1	1	1	1	6	The Monovalent Cation: Proton Antiporter-2 (CPA2) Family
	2.A.37.Y1				2				2	The Monovalent Cation: Proton Antiporter-2 (CPA2) Family
	2.A.38.2	**2**	1	1		1	1	2	8	The K+ Transporter (Trk) Family
	2.A.39.2	**2**	2	2	3	2	4	4	19	The Nucleobase: Cation Symporter-1 (NCS1) Family
	2.A.39.3	**1**	2	2	1	2	2	3	13	The Nucleobase: Cation Symporter-1 (NCS1) Family
	2.A.39.4	**1**		1	1	2	3	3	11	The Nucleobase: Cation Symporter-1 (NCS1) Family
	2.A.4.1	**1**							1	The Cation Diffusion Facilitator (CDF) Family
	2.A.4.2	**1**	1	1	1	1	1	2	8	The Cation Diffusion Facilitator (CDF) Family

2.A.4.4	**2**	1	2	1	1	1	1	9	The Cation Diffusion Facilitator (CDF) Family
2.A.4.5	**2**		1					3	The Cation Diffusion Facilitator (CDF) Family
2.A.4.Y1		1		1	1	2	2	7	The Cation Diffusion Facilitator (CDF) Family
2.A.40.5	**1**	2	1	1	1			6	The Nucleobase: Cation Symporter-2 (NCS2) Family
2.A.41.2	**1**	2		1				4	The Concentrative Nucleoside Transporter (CNT) Family
2.A.43.1	**1**		1					2	The Lysosomal Cystine Transporter (LCT) Family
2.A.43.2			1		1	1	1	4	The Lysosomal Cystine Transporter (LCT) Family
2.A.43.3	**1**	1						2	The Lysosomal Cystine Transporter (LCT) Family
2.A.43.Y1				1				1	The Lysosomal Cystine Transporter (LCT) Family
2.A.44.2		1	1	1	1	1	1	6	The Formate-Nitrite Transporter (FNT) Family
2.A.47.2	**1**	1	1	2	2	2	3	12	The Divalent Anion: Na+ Symporter (DASS) Family
2.A.49.1	**1**		1					2	The Chloride Carrier/Channel (ClC) Family
2.A.49.2	**2**		1					3	The Chloride Carrier/Channel (ClC) Family
2.A.49.3		5		3	3	3	3	17	The Chloride Carrier/Channel (ClC) Family
2.A.5.1	**4**	4	2	3	1	2	2	18	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.5.2					1	1	1	3	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.5.4	**1**		1					2	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.5.5	**1**		1					2	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.5.7			1					1	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.5.Y1					1		1	2	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.5.Y2		1		1				2	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family
2.A.50.1	**1**	1	1	1	1	1	2	8	The Glycerol Uptake (GUP) Family
2.A.53.1	**2**	2	2	3	2	2	3	16	The Sulfate Permease (SulP) Family
2.A.53.7	**1**		1					2	The Sulfate Permease (SulP) Family
2.A.53.Y1		1		1	1	1	1	5	The Sulfate Permease (SulP) Family
2.A.54.1	**1**	1	1	1	1		1	6	The Mitochondrial Tricarboxylate Carrier (MTC) Family
2.A.55.1	**2**	2	3	3	3	3	3	19	The Metal Ion (Mn2+-iron) Transporter (Nramp) Family
2.A.57.3	**1**	1	1	1	1	1	1	7	The Equilibrative Nucleoside Transporter (ENT) Family
2.A.59.1	**1**	1	1	1	2		1	7	The Arsenical Resistance-3 (ACR3) Family
2.A.6.6	**3**	2	3	2	2	2	3	17	The Eukaryotic (Putative) Sterol Transporter (EST) Family
2.A.6.Y1		1						1	Unassigned
2.A.66.1	**2**	2	2	6	4	2	2	20	The Multi Antimicrobial Extrusion (MATE) Family
2.A.66.3	**1**	1	1		1	1	1	6	The Oligosaccharidyl-lipid Flippase (OLF) Family
2.A.67.1	**6**	17	2	4	3		2	34	The Oligopeptide Transporter (OPT) Family
2.A.67.2	**1**		1					2	The Oligopeptide Transporter (OPT) Family
2.A.67.Y1		1		1	1	1	1	5	The Oligopeptide Transporter (OPT) Family
2.A.69.3			2					2	The Auxin Efflux Carrier (AEC) Family
2.A.7.10	**1**	1	1		2		1	6	The UDP-N-Acetylglucosamine:UMP Antiporter (UAA) Family
2.A.7.11	**1**		1					2	The UDP-Galactose:UMP Antiporter (UGA) Family
2.A.7.12	**1**	1	1					3	The CMP-Sialate:CMP Antiporter (CSA) Family
2.A.7.13	**1**	1	1	1	1	1	3	9	The GDP-Mannose:GMP Antiporter (GMA) Family
2.A.7.24	**3**		3					6	The Thiamine Pyrophosphate Transporter (TPPT) Family
2.A.7.25	**2**		2					4	The NIPA Mg2+ Uptake Permease (NIPA) Family
2.A.7.3			1					1	The 10 TMS Drug/Metabolite Exporter (DME) Family
2.A.7.9	**1**	2	1	3	3	3	3	16	The Triose-phosphate Transporter (TPT) Family

	2.A.7.Y1		1		1	1	1	1	5	Unassigned
	2.A.7.Y2		1						1	Unassigned
	2.A.72.2		2						2	The K+ Uptake Permease (KUP) Family
	2.A.85.3	**4**		1					5	The Aromatic Acid Exporter (ArAE) Family
	2.A.85.4	**1**							1	The Aromatic Acid Exporter (ArAE) Family
	2.A.89.1	**1**							1	The Vacuolar Iron Transporter (VIT) Family
	2.A.9.1	**1**	1		1	1	1	1	6	The Cytochrome Oxidase Biogenesis (Oxa1) Family
	2.A.92.1	**1**		1					2	The Choline Transporter-like (CTL) Family
	2.A.93.1			1					1	The Unknown BART Superfamily-1 (UBS1) Family
	2.A.94.1	**4**		2					6	The Phosphate Permease (Pho1) Family
	2.A.96.1	**5**		5					10	The YaaH (YaaH) Family
	2.A.X1.Y1		2			2	1		5	Unassigned
	2.A.X2.Y1		1		2	1			4	Unassigned
Primary Active Transporters	3.A.1.201	**1**	3	1					5	The Multidrug Resistance Exporter (MDR) Family (ABCB)
	3.A.1.203	**2**	2		2	2	2	2	12	The Peroxysomal Fatty Acyl CoA Transporter (P-FAT) Family (ABCD)
	3.A.1.204	**3**	2	1	1	1	1	1	10	The Eye Pigment Precursor Transporter (EPP) Family (ABCG
	3.A.1.205	**5**	6	6	8	5	6	9	45	The Pleiotropic Drug Resistance (PDR) Family (ABCG)
	3.A.1.206	**1**	1	1	1	1	1	1	7	The a-Factor Sex Pheromone Exporter (STE) Family (ABCB)
	3.A.1.208	**4**	10	5	4	4	5	7	39	The Drug Conjugate Transporter (DCT) Family (ABCC)
	3.A.1.210	**1**	1	1	1	1	1	1	7	The Heavy Metal Transporter (HMT) Family
	3.A.1.211	**1**	1						2	The Cholesterol/Phospholipid/Retinal (CPR) Flippase Family
	3.A.1.212	**1**	1	1	2	2	2	2	11	The Mitochondrial Peptide Exporter (MPE) Family
	3.A.12.1	**1**							1	The Septal DNA Translocator (S-DNA-T) Family
	3.A.16.1	**2**		1					3	The Endoplasmic Reticular Retrotranslocon (ER-RT) Family
	3.A.18.1	**3**		1					4	The Nuclear mRNA Exporter (mRNA-E) Family
	3.A.2.1		7		8	10	8	12	45	The H+- or Na+-translocating F-type Family
	3.A.2.2	**5**	14	5	15	15	15	16	85	The H+- or Na+-translocating F-type Family
	3.A.3.1	**1**							1	The Na+, K+ ATPase Family
	3.A.3.10	**1**		1					2	Functionally Uncharacterized P-type ATPase Family
	3.A.3.14			1					1	Functionally Uncharacterized P-type ATPase Family
	3.A.3.15	**1**							1	Functionally Uncharacterized P-type ATPase Family
	3.A.3.2	**3**	2	2	2	2	3	2	16	The Ca2+-ATPase Family
	3.A.3.3	**2**	1	1	1	1	1	2	9	Unassigned
	3.A.3.5	**2**	2	2	2	2	1	2	13	The Cu+-, Ag+-ATPase (efflux) Family
	3.A.3.8	**5**	4	5	4	4	5	5	32	The Phospholipid Translocating P-type ATPase Family
	3.A.3.9	**1**	2	1	2	2	1	3	12	The Monovalent Alkali Cation (Na+ and K+) ATPase (efflux) Family
	3.A.3.Y1		2		3	2	2	2	11	Unassigned
	3.A.5.8	**4**	9	2	9	12	9	11	56	The General Secretory Pathway (Sec) Family
	3.A.5.9	**1**							1	The General Secretory Pathway (Sec) Family
	3.A.8.1	**1**	17		13	13	14	14	72	The Mitochondrial Protein Translocase (MPT) Family
	3.A.8.2		7		11	12	10	15	55	The Mitochondrial Protein Translocase (MPT) Family
Decarboxylation-driven transporters	3.B.1.1		2		1	1	2		6	The Na+-transporting Carboxylic Acid Decarboxylase (NaT-DC) Family

Oxidoreduction-driven transporters	3.D.1.2		8		8				16	The H+ or Na+-translocating NADH Dehydrogenase (NDH) Family
	3.D.1.6	**1**							1	The H+ or Na+-translocating NADH Dehydrogenase (NDH) Family
	3.D.3.3		6		9	8	8	10	41	The Proton-translocating Quinol:Cytochrome c Reductase (QCR) Family
	3.D.4.4			1					1	
	3.D.4.8	**2**	7	1	10	10	7	15	52	The Proton-translocating Cytochrome Oxidase (COX) Family
Light absorption-driven transporters	3.E.1.4						3	3	6	The Ion-translocating Microbial Rhodopsin (MR) Family
	3.E.1.5	**1**							1	The Ion-translocating Microbial Rhodopsin (MR) Family
Transmembrane Electron Carriers	5.B.1.4			1					1	The Phagocyte (gp91phox) NADPH Oxidase Family
	5.B.1.5	**8**		1					9	The Phagocyte (gp91phox) NADPH Oxidase Family
	5.B.1.7	**3**		4					7	The Phagocyte (gp91phox) NADPH Oxidase Family
	5.B.2.1	**1**							1	The Eukaryotic Cytochrome b561 (Cytb561) Family
Accessory Factors Involved in Transport	8.A.13.1		1		1	1	1	1	5	The Tetratricopeptide Repeat (Tpr1) Family
	8.A.15.Y1		1				1		2	The K+ Channel Accessory Protein (KChAP) Family
	8.A.27.1	**1**							1	The Phospholipid Importer β-subunit (PLI-β) Family
	8.A.5.1		2		3	1		1	7	The Voltage-gated K+ Channel β-subunit (Kvβ) Family
	8.A.6.1		1		1	1	1	1	5	The Auxiliary Nutrient Transporter (ANT) Family
	8.A.9.1				2	2			4	The rBAT Transport Accessory Protein (rBAT) Family
	8.A.9.Y1							7	7	The rBAT Transport Accessory Protein (rBAT) Family
Incompletely Characterized Transport Systems: Recognized transporters of unknown biochemical mechanism	9.A.1.1		1		2	2	3	3	11	The Non ABC Multidrug Exporter (N-MDE) Family
	9.A.10.1	**3**	3	3	4	2	2	2	19	The Oxidase-dependent Fe2+ Transporter (OFeT) Family
	9.A.10.Y1		3		2	3	3	3	14	Unassigned
	9.A.12.1						1	2	3	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.12.2					1	1	1	3	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.12.Y1		1						1	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.12.Y2				1				1	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.12.Y3				1				1	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.12.Y4				1				1	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.12.Y5					1			1	The Peptidoglycolipid Addressing Protein (GAP) Family
	9.A.14.1	**3**		1					4	The G-protein-coupled receptor (GPCR) Family
	9.A.14.Y1		21		23	25	27	29	125	The G-protein-coupled receptor (GPCR) Family
	9.A.14.Y2		1		1	2	1	1	6	The G-protein-coupled receptor (GPCR) Family
	9.A.14.Y3		13		15	15	17	16	76	The G-protein-coupled receptor (GPCR) Family
	9.A.14.Y4		4		4	5	4	5	22	The G-protein-coupled receptor (GPCR) Family
	9.A.14.Y5		6		9	7	8	7	37	The G-protein-coupled receptor (GPCR) Family
	9.A.26.1	**5**		2	4	1	1	4	17	The Lipid-translocating Exporter (LTE) Family
	9.A.26.2		2		1	1	1	1	6	The Lipid-translocating Exporter (LTE) Family
	9.A.27.1	**1**		1					2	The Non-Classical Protein Exporter (NCPE) Family
	9.A.40.3	**2**							2	The HlyC/CorC (HCC) Family
	9.A.45.1	**1**		1					2	The Magnesium Transporter1 (MagT1) Family
	9.A.46.1	**2**		1					3	The Putative Low Affinity Ca2+ Channel (LACC) Family
	9.A.5.1		27		7	10	11	10	65	The Putative Arginine Transporter (ArgW) Family
	9.A.6.1	**3**		2					5	The ATP Exporter (ATP-E) Family

	9.A.9.1			2		1	1	1	5	The Low Affinity Fe2+ Transporter (FeT) Family
Incompletely characterized Transport Systems: Putative transport proteins	9.B.1.1	**1**				1	1	1	4	The Metal Homeostasis Protein (MHP) Family
	9.B.1.Y1		1		1				2	The Metal Homeostasis Protein (MHP) Family
	9.B.12.1				1			1	2	The (Salt or Low Temperature) Stress-induced Hydrophobic Peptide Family
	9.B.12.3	**1**	2		3	1		3	10	The (Salt or Low Temperature) Stress-induced Hydrophobic Peptide Family
	9.B.17.1		14		3	3	5	5	30	The VAMP-associated protein (VAP) Family
	9.B.17.Y1		1		4	2	3	4	14	The VAMP-associated protein (VAP) Family
	9.B.17.Y2		1		2				3	The VAMP-associated protein (VAP) Family
	9.B.19.1	**1**							1	The Mn2+ Homeostasis Protein (MnHP) Family
	9.B.2.1						1	1	2	The Ca2+ Homeostasis Protein (CHP) Family
	9.B.2.Y1				1				1	The Ca2+ Homeostasis Protein (CHP) Family
	9.B.24.3	**1**		1					2	The Outer Membrane Protein NilB/OmpU (NilB) Family
	9.B.24.Y1					1	1	1	3	The Outer Membrane Protein NilB/OmpU (NilB) Family
	9.B.24.Y2		1						1	The Outer Membrane Protein NilB/OmpU (NilB) Family
	9.B.24.Y3				1				1	The Outer Membrane Protein NilB/OmpU (NilB) Family
	9.B.26.3	**1**		1					2	The PF27 (PF27) Family
	9.B.26.Y1				1	1	1	1	4	The PF27 (PF27) Family
	9.B.26.Y2		1						1	The PF27 (PF27) Family
	9.B.32.1	**4**		1					5	The Putative Vectorial Glycosyl Polymerization (VGP) Family
	9.B.33.1		6		7	4	3	3	23	The Sensor Histidine Kinase (SHK) Family
	9.B.37.1	**2**		1					3	The Huntington-interacting Protein 14 (HIP14) Family
	9.B.37.2	**3**		3					6	The Huntington-interacting Protein 14 (HIP14) Family
	9.B.37.3			1					1	The Huntington-interacting Protein 14 (HIP14) Family
	9.B.4.Y1				1				1	The Universal Stress Protein-B (UspB) Family
	9.B.4.Y2		1			1	1		3	The Universal Stress Protein-B (UspB) Family
	9.B.4.Y3		2			1	1		4	The Universal Stress Protein-B (UspB) Family
	9.B.7.2	**1**		1					2	The Putative Sulfate Transporter (CysZ) Family
	9.B.82.1	**1**							1	Putative Heavy Metal Transporter (Rer1) Family
	Total	**430**	597	253	538	439	398	508	3163	

Table S10B TCDB classification of transporters of *A. adeninivorans*

Gene ARAD1	Nb TMH	TCDB Best Hit	TCDB class	TCDB Annotation of best hit
ARAD1C38192g	4	gnl|TC-DB|P35499	1.A.1.10	Sodium channel protein type 4 subunit alpha - *Homo sapiens* (Human).
ARAD1D08602g	21	gnl|TC-DB|P50077	1.A.1.11	Calcium-channel protein CCH1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D15510g	3	gnl|TC-DB|O54899	1.A.1.5	Brain cyclic nucleotide gated 1 - *mus musculus* (mouse).
ARAD1D15488g	10	gnl|TC-DB|P40310	1.A.1.7	Outward-rectifier potassium channel Tok1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1D14960g	11	gnl|TC-DB|P40260	1.A.11.3	Ammonium transporter mep1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1D31020g	11	gnl|TC-DB|Q59UP8	1.A.11.3	Putative uncharacterized protein MEP2 - *Candida albicans*
ARAD1C40876g	8	gnl|TC-DB|D0NGF4	1.A.17.2	Anoctamin-like protein - *Phytophthora infestans*
ARAD1D40766g	2	gnl|TC-DB|Q08269	1.A.35.2	Aluminum resistance protein 1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D30888g	3	gnl|TC-DB|P35724	1.A.35.2	Manganese resistance protein - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1A11616g	2	gnl|TC-DB|Q01926	1.A.35.5	Mitochondrial RNA splicing protein Mrs2 precursor - *Saccharomyces cerevisiae*
ARAD1D49830g	8	gnl|TC-DB|B2ZXD5	1.A.38.1	Golgi pH regulator - Cricetulus griseus
ARAD1B20526g	7	gnl|TC-DB|Q12324	1.A.4.4	Calcium channel YVC1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A02750g	8	gnl|TC-DB|Q12324	1.A.4.4	Calcium channel YVC1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C07194g	6	gnl|TC-DB|Q12324	1.A.4.4	Calcium channel YVC1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B13992g	3	gnl|TC-DB|B8N1Q6	1.A.55.4	Clathrin-coated vesicle protein, putative - *Aspergillus flavus* strain ATCC 200026
ARAD1D05984g	3	gnl|TC-DB|O94722	1.A.56.1	Copper transport protein ctr4 (Copper transporter 4) - *Schizosaccharomyces pombe*
ARAD1C44748g	3	gnl|TC-DB|A9XIK8	1.A.56.1	CTR2 long splice variant- *Colletotrichum gloeosporioides f. sp. aeschynomenes*
ARAD1D01562g	7	gnl|TC-DB|Q9C411	1.A.8.6	Aquaporin 2 - *Saccharomyces chevalieri.*
ARAD1C31372g	2	gnl|TC-DB|B3FNS7	1.B.40.1	Trimeric autotransporter adhesin - *Haemophilus sp.*
ARAD1C24640g	4	gnl|TC-DB|B3FNS7	1.B.40.1	Trimeric autotransporter adhesin - *Haemophilus sp.* 1595
ARAD1B05038g	3	gnl|TC-DB|P69169	1.B.53.1	Coat protein A - *Enterobacteria* phage f1
ARAD1D16676g	8	gnl|TC-DB|Q14770	2.A.1.1	Fructose transporter - *Homo sapiens* (human).
ARAD1C12694g	5	gnl|TC-DB|P53048	2.A.1.1	General alpha-glucoside permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D18106g	10	gnl|TC-DB|P53048	2.A.1.1	General alpha-glucoside permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D18062g	12	gnl|TC-DB|P53048	2.A.1.1	General alpha-glucoside permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C05104g	8	gnl|TC-DB|P53048	2.A.1.1	General alpha-glucoside permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D51040g	12	gnl|TC-DB|P53048	2.A.1.1	General alpha-glucoside permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D42680g	11	gnl|TC-DB|Q5A8J5	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Candida albicans*
ARAD1A14102g	12	gnl|TC-DB|Q5A8J5	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Candida albicans*
ARAD1A19954g	10	gnl|TC-DB|Q5A8J5	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Candida albicans*
ARAD1B17908g	12	gnl|TC-DB|Q5A8J5	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Candida albicans*
ARAD1D26840g	10	gnl|TC-DB|Q5A8J5	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Candida albicans*
ARAD1A06754g	11	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A08778g	12	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B10296g	10	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).

ARAD1C18216g	10	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D03476g	9	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D18084g	12	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D18634g	12	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D29634g	10	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D41998g	12	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D50710g	10	gnl|TC-DB|P39932	2.A.1.1	Glycerol/H+ symportertransporter STL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B01298g	12	gnl|TC-DB|Q8NJ22	2.A.1.1	Hexose transporter (Similarity) - *Kluyveromyces lactis* (Yeast).
ARAD1B17622g	10	gnl|TC-DB|Q8NJ22	2.A.1.1	Hexose transporter (Similarity) - *Kluyveromyces lactis* (Yeast).
ARAD1D05016g	10	gnl|TC-DB|Q8NJ22	2.A.1.1	Hexose transporter (Similarity) - *Kluyveromyces lactis* (Yeast).
ARAD1B23166g	11	gnl|TC-DB|P43581	2.A.1.1	Hexose transporter HXT10 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B12496g	12	gnl|TC-DB|P49374	2.A.1.1	High-affinity glucose transporter - *Kluyveromyces lactis* (Yeast) (*Candida sphaerica*).
ARAD1B12518g	11	gnl|TC-DB|P49374	2.A.1.1	High-affinity glucose transporter - *Kluyveromyces lactis* (Yeast) (*Candida sphaerica*).
ARAD1D10362g	10	gnl|TC-DB|P49374	2.A.1.1	High-affinity glucose transporter - *Kluyveromyces lactis* (Yeast) (*Candida sphaerica*).
ARAD1B09900g	8	gnl|TC-DB|P49374	2.A.1.1	High-affinity glucose transporter - *Kluyveromyces lactis* (Yeast) (*Candida sphaerica*).
ARAD1A15246g	10	gnl|TC-DB|P49374	2.A.1.1	High-affinity glucose transporter - *Kluyveromyces lactis* (Yeast) (*Candida sphaerica*).
ARAD1D50952g	8	gnl|TC-DB|P39003	2.A.1.1	High-affinity hexose transporter HXT6 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C00242g	11	gnl|TC-DB|P07921	2.A.1.1	Lactose permease - *Kluyveromyces lactis* (Yeast).
ARAD1D12012g	12	gnl|TC-DB|P07921	2.A.1.1	Lactose permease - *Kluyveromyces lactis* (Yeast).
ARAD1A11792g	11	gnl|TC-DB|P07921	2.A.1.1	Lactose permease - *Kluyveromyces lactis* (Yeast).
ARAD1B20438g	10	gnl|TC-DB|P07921	2.A.1.1	Lactose permease - *Kluyveromyces lactis* (Yeast).
ARAD1C00264g	12	gnl|TC-DB|P15685	2.A.1.1	Maltose permease MAL6T - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D35728g	12	gnl|TC-DB|P15685	2.A.1.1	Maltose permease MAL6T - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A07150g	11	gnl|TC-DB|P15685	2.A.1.1	Maltose permease MAL6T - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D09658g	12	gnl|TC-DB|P15685	2.A.1.1	Maltose permease MAL6T - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A09746g	12	gnl|TC-DB|P15685	2.A.1.1	Maltose permease MAL6T - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C20878g	10	gnl|TC-DB|Q8J0V1	2.A.1.1	Monosaccharide transporter - *Aspergillus niger.*
ARAD1C00396g	10	gnl|TC-DB|Q8J0V1	2.A.1.1	Monosaccharide transporter - *Aspergillus niger.*
ARAD1A00572g	11	gnl|TC-DB|A0ZXK6	2.A.1.1	Monosaccharide transporter - *Geosiphon pyriformis.*
ARAD1D13442g	12	gnl|TC-DB|P30605	2.A.1.1	Myo-inositol transporter 1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C40392g	12	gnl|TC-DB|P30605	2.A.1.1	Myo-inositol transporter 1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C40678g	12	gnl|TC-DB|P30605	2.A.1.1	Myo-inositol transporter 1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C45012g	12	gnl|TC-DB|P11636	2.A.1.1	Quinate permease (Quinate transporter) - *Neurospora crassa*.
ARAD1D50622g	12	gnl|TC-DB|P11636	2.A.1.1	Quinate permease (Quinate transporter) - *Neurospora crassa*.
ARAD1C34342g	11	gnl|TC-DB|P11636	2.A.1.1	Quinate permease (Quinate transporter) - *Neurospora crassa*.
ARAD1C40326g	12	gnl|TC-DB|P11636	2.A.1.1	Quinate permease (Quinate transporter) - *Neurospora crassa*.
ARAD1C05456g	12	gnl|TC-DB|P95908	2.A.1.1	Sugar transporter (sugar transport related protein) - *Sulfolobus solfataricus*.
ARAD1B10384g	12	gnl|TC-DB|P95908	2.A.1.1	Sugar transporter (sugar transport related protein) - *Sulfolobus solfataricus*.
ARAD1C25168g	11	gnl|TC-DB|A1Z264	2.A.1.1	Sugar/H+ symporter - *Galdieria sulphuraria* GN=SPT1 PE=2 SV=1

ARAD1C40766g	11	gnl|TC-DB|A1Z264	2.A.1.1	Sugar/H+ symporter - *Galdieria sulphuraria* GN=SPT1 PE=2 SV=2
ARAD1C00440g	12	gnl|TC-DB|Q64L87	2.A.1.1	Xylose facilitator Xylhp (Fragment) - *Debaryomyces hansenii* (Yeast) *(Torulaspora hansenii*).
ARAD1C39600g	11	gnl|TC-DB|Q64L87	2.A.1.1	Xylose facilitator Xylhp (Fragment) - *Debaryomyces hansenii* (Yeast) *(Torulaspora hansenii*).
ARAD1C39094g	12	gnl|TC-DB|Q64L87	2.A.1.1	Xylose facilitator Xylhp (Fragment) - *Debaryomyces hansenii* (Yeast) *(Torulaspora hansenii*).
ARAD1D18194g	11	gnl|TC-DB|Q64L87	2.A.1.1	Xylose facilitator Xylhp (Fragment) - *Debaryomyces hansenii* (Yeast) *(Torulaspora hansenii*).
ARAD1C00220g	12	gnl|TC-DB|Q64L87	2.A.1.1	Xylose facilitator Xylhp (Fragment) - *Debaryomyces hansenii* (Yeast) *(Torulaspora hansenii*).
ARAD1D10120g	12	gnl|TC-DB|Q64L87	2.A.1.1	Xylose facilitator Xylhp (Fragment) - *Debaryomyces hansenii* (Yeast) *(Torulaspora hansenii*).
ARAD1C29898g	11	gnl|TC-DB|Q51330	2.A.1.11	Oxalate:formate antiport protein - *Oxalobacter formigenes* .
ARAD1D14168g	11	gnl|TC-DB|P36035	2.A.1.12	Carboxylic acid transporter protein homolog - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D34804g	10	gnl|TC-DB|P36035	2.A.1.12	Carboxylic acid transporter protein homolog - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D47432g	10	gnl|TC-DB|P36035	2.A.1.12	Carboxylic acid transporter protein homolog - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C08008g	11	gnl|TC-DB|P36035	2.A.1.12	Carboxylic acid transporter protein homolog - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B13464g	12	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D17842g	12	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D27170g	12	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C10824g	12	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C14718g	11	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D17292g	11	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D36124g	12	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D49390g	12	gnl|TC-DB|Q08777	2.A.1.13	Putative monocarboxylate permease YOR306c - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C00176g	9	gnl|TC-DB|P15365	2.A.1.14	Allantoate permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A13354g	12	gnl|TC-DB|P15365	2.A.1.14	Allantoate permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A19030g	12	gnl|TC-DB|P15365	2.A.1.14	Allantoate permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C20218g	10	gnl|TC-DB|P15365	2.A.1.14	Allantoate permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B22616g	10	gnl|TC-DB|P15365	2.A.1.14	Allantoate permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C11858g	12	gnl|TC-DB|P15365	2.A.1.14	Allantoate permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A16742g	11	gnl|TC-DB|P53322	2.A.1.14	High-affinity nicotinic acid transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C12562g	10	gnl|TC-DB|P53322	2.A.1.14	High-affinity nicotinic acid transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C20174g	12	gnl|TC-DB|P53322	2.A.1.14	High-affinity nicotinic acid transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D30976g	12	gnl|TC-DB|P53322	2.A.1.14	High-affinity nicotinic acid transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C04268g	12	gnl|TC-DB|P53322	2.A.1.14	High-affinity nicotinic acid transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B08778g	12	gnl|TC-DB|P53322	2.A.1.14	High-affinity nicotinic acid transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A14652g	10	gnl|TC-DB|O43000	2.A.1.14	Pantothenate transporter liz1 - *Schizosaccharomyces pombe* (Fission yeast).
ARAD1C35992g	7	gnl|TC-DB|P70786	2.A.1.14	Putative tartrate transporter - *Agrobacterium vitis* .
ARAD1B06138g	8	gnl|TC-DB|P70786	2.A.1.14	Putative tartrate transporter - *Agrobacterium vitis* .
ARAD1D08558g	12	gnl|TC-DB|P70786	2.A.1.14	Putative tartrate transporter - *Agrobacterium vitis* .
ARAD1A08228g	12	gnl|TC-DB|P53241	2.A.1.14	Vitamin H transporter (H+/biotin symporter) - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C26906g	11	gnl|TC-DB|O13880	2.A.1.14	Vitamin H transporter 1 - *Schizosaccharomyces pombe* (Fission yeast).
ARAD1D50908g	8	gnl|TC-DB|O24842	2.A.1.15	Hypothetical 47.9

ARAD1D48356g	14	gnl|TC-DB|Q08299	2.A.1.16	Ferric enterobactin transporter YOL158c - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1C11330g	13	gnl|TC-DB|P39980	2.A.1.16	Ferrioxamine B transporter YEL065W - *Saccharomyces cerevisiae*
ARAD1D51018g	13	gnl|TC-DB|P39980	2.A.1.16	Ferrioxamine B transporter YEL065W - *Saccharomyces cerevisiae*
ARAD1D11704g	13	gnl|TC-DB|P38731	2.A.1.16	Transporter of the ARN family that specifically recognizes siderophore iron chelates
ARAD1A16852g	14	gnl|TC-DB|P38724	2.A.1.16	Transporter of the ARN family that specifically recognizes siderophore iron chelates
ARAD1C34078g	14	gnl|TC-DB|P38724	2.A.1.16	Transporter of the ARN family that specifically recognizes siderophore iron chelates
ARAD1C19514g	11	gnl|TC-DB|O35956	2.A.1.19	Renal organic anion transport protein 1 - *Rattus norvegicus* (rat).
ARAD1D12672g	11	gnl|TC-DB|P28873	2.A.1.2	Benomyl/methotrexate resistance protein - *Candida albicans* (Yeast).
ARAD1D12694g	11	gnl|TC-DB|P28873	2.A.1.2	Benomyl/methotrexate resistance protein - *Candida albicans* (Yeast).
ARAD1D46156g	12	gnl|TC-DB|P32071	2.A.1.2	Cycloheximide resistance protein - *Candida maltosa* (Yeast).
ARAD1D18546g	12	gnl|TC-DB|P32071	2.A.1.2	Cycloheximide resistance protein - *Candida maltosa* (Yeast).
ARAD1D22176g	12	gnl|TC-DB|P32071	2.A.1.2	Cycloheximide resistance protein - *Candida maltosa* (Yeast).
ARAD1D27918g	10	gnl|TC-DB|P32071	2.A.1.2	Cycloheximide resistance protein - *Candida maltosa* (Yeast).
ARAD1C13860g	12	gnl|TC-DB|Q9KMQ3	2.A.1.2	Multidrug resistance protein [*Vibrio cholerae*]
ARAD1C11352g	12	gnl|TC-DB|Q9KMQ3	2.A.1.2	Multidrug resistance protein [*Vibrio cholerae*]
ARAD1A19800g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A03938g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D24970g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D27214g	10	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B15224g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A19448g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B07260g	10	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B15048g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D02772g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A19096g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D01100g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C32472g	12	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C36806g	11	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C37686g	10	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C09394g	10	gnl|TC-DB|Q07824	2.A.1.2	Polyamine transporter YLL028W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B01628g	12	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D28314g	10	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C17402g	12	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D18524g	9	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A15356g	11	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D17336g	12	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C17094g	10	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D06226g	12	gnl|TC-DB|P53389	2.A.1.2	Protein HOL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A18348g	7	gnl|TC-DB|P0A0J7	2.A.1.2	Quinolone resistance protein norA - *Staphylococcus aureus* .

ARAD1D31416g	11	gnl|TC-DB|Q5JAK9	2.A.1.2	TetA(41) - *Serratia marcescens* GN=tetA(41) PE=4 SV=1
ARAD1A13112g	9	gnl|TC-DB|B2YGG2	2.A.1.2	Tetracycline resistance protein [*Micrococcus sp*. SMCC G887]
ARAD1C21626g	11	gnl|TC-DB|P02982	2.A.1.2	Tetracycline resistance protein, class A (TETA(A)) - *Escherichia coli.*
ARAD1C33044g	12	gnl|TC-DB|P38227	2.A.1.2	Uncharacterized transporter YBR043C - *Saccharomyces cerevisiae*
ARAD1A18260g	12	gnl|TC-DB|P38125	2.A.1.2	Uncharacterized transporter YBR180W - *Saccharomyces cerevisiae*
ARAD1D36146g	11	gnl|TC-DB|P40474	2.A.1.2	Uncharacterized transporter YIL121W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B13662g	10	gnl|TC-DB|P40474	2.A.1.2	Uncharacterized transporter YIL121W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D02948g	11	gnl|TC-DB|Q02563	2.A.1.22	Synaptic vesicle protein 2 (SV2) - *Rattus norvegicus* (Rat).
ARAD1C35530g	10	gnl|TC-DB|Q02563	2.A.1.22	Synaptic vesicle protein 2 (SV2) - *Rattus norvegicus* (Rat).
ARAD1D35860g	10	gnl|TC-DB|P25568	2.A.1.24	Hypothetical 58.8
ARAD1C23496g	10	gnl|TC-DB|P25568	2.A.1.24	Hypothetical 58.8
ARAD1D28864g	8	gnl|TC-DB|O00400	2.A.1.25	Acetyl-coenzyme A transporter - *Homo sapiens* (human).
ARAD1B19778g	12	gnl|TC-DB|Q8CE47	2.A.1.28	Major facilitator superfamily domain-containing protein 7 - *Mus musculus* (Mouse).
ARAD1D20108g	14	gnl|TC-DB|P13090	2.A.1.3	Aminotriazole resistance protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D01320g	12	gnl|TC-DB|P13090	2.A.1.3	Aminotriazole resistance protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B22836g	14	gnl|TC-DB|P13090	2.A.1.3	Aminotriazole resistance protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C13750g	10	gnl|TC-DB|P32369	2.A.1.3	Bile acid transporter - *Eubacterium sp.* (strain VPI 12708).
ARAD1B14916g	14	gnl|TC-DB|Q9ZGB6	2.A.1.3	Drug resistance transporter LanJ [*Streptomyces cyanogenus*]
ARAD1B04334g	14	gnl|TC-DB|Q9ZGB6	2.A.1.3	Drug resistance transporter LanJ [*Streptomyces cyanogenus*]
ARAD1D20680g	14	gnl|TC-DB|P42670	2.A.1.3	Puromycin resistance protein pur8 - *Streptomyces lipmanii* (*Streptomyces alboniger*).
ARAD1D14058g	13	gnl|TC-DB|O69070	2.A.1.3	Tetracycline efflux protein - *Streptomyces rimosus*.
ARAD1B22814g	14	gnl|TC-DB|O32182	2.A.1.3	Uncharacterized MFS-type transporter yusP - *Bacillus subtilis*
ARAD1D40678g	11	gnl|TC-DB|O75387	2.A.1.44	Large neutral amino acids transporter small subunit 3 - *Homo sapiens* (Human).
ARAD1C44066g	13	gnl|TC-DB|Q09752	2.A.1.48	Multidrug resistance protein fnx1 - *Schizosaccharomyces pombe* (Fission yeast).
ARAD1C21362g	12	gnl|TC-DB|Q5A7S4	2.A.1.58	Putative uncharacterized protein - *Candida albicans* (Yeast).
ARAD1D00946g	11	gnl|TC-DB|Q5A7S4	2.A.1.58	Putative uncharacterized protein - *Candida albicans* (Yeast).
ARAD1D31658g	10	gnl|TC-DB|Q5A7S4	2.A.1.58	Putative uncharacterized protein - *Candida albicans* (Yeast).
ARAD1D03124g	9	gnl|TC-DB|Q467Y6	2.A.1.63	Transport protein - Methanosarcina barkeri (strain Fusaro / DSM 804).
ARAD1C16346g	12	gnl|TC-DB|Q07W00	2.A.1.7	Major facilitator superfamily MFS_1 - *Shewanella frigidimarina* (strain NCIMB 400).
ARAD1B04554g	12	gnl|TC-DB|Q07W00	2.A.1.7	Major facilitator superfamily MFS_1 - *Shewanella frigidimarina* (strain NCIMB 400).
ARAD1C19250g	10	gnl|TC-DB|P22152	2.A.1.8	Nitrate transporter (Nitrate permease) - *Emericella nidulans* (Aspergillus nidulans).
ARAD1C27632g	9	gnl|TC-DB|P22152	2.A.1.8	Nitrate transporter (Nitrate permease) - *Emericella nidulans* (Aspergillus nidulans).
ARAD1C19206g	8	gnl|TC-DB|P22152	2.A.1.8	Nitrate transporter (Nitrate permease) - *Emericella nidulans* (Aspergillus nidulans).
ARAD1D22352g	10	gnl|TC-DB|Q01MW8	2.A.1.9	Probable inorganic phosphate transporter 1-4 - *Oryza sativa subsp. indica*
ARAD1A19360g	9	gnl|TC-DB|Q01MW8	2.A.1.9	Probable inorganic phosphate transporter 1-4 - *Oryza sativa subsp. indica*
ARAD1D45606g	8	gnl|TC-DB|Q01MW8	2.A.1.9	Probable inorganic phosphate transporter 1-4 - *Oryza sativa subsp. indica*
ARAD1A09416g	8	gnl|TC-DB|A2QYD7	2.A.16.4	Plasma membrane free sulphite efflux pump Ssu1p - *Aspergillus niger*.
ARAD1D03740g	11	gnl|TC-DB|P32901	2.A.17.2	Peptide transporter Ptr2 (peptide permease Ptr2) - *Saccharomyces cerevisiae*
ARAD1C43318g	11	gnl|TC-DB|P32901	2.A.17.2	Peptide transporter Ptr2 (peptide permease Ptr2) - *Saccharomyces cerevisiae*

ARAD1A19910g	11	gnl|TC-DB|Q6IT47	2.A.18.4	Aromatic and neutral aliphatic amino acid permease - *Penicillium chrysogenum*
ARAD1D06270g	9	gnl|TC-DB|Q6IT47	2.A.18.4	Aromatic and neutral aliphatic amino acid permease - *Penicillium chrysogenum*
ARAD1A14564g	11	gnl|TC-DB|Q6IT47	2.A.18.4	Aromatic and neutral aliphatic amino acid permease - *Penicillium chrysogenum*
ARAD1D29084g	11	gnl|TC-DB|P38680	2.A.18.4	N amino acid transport system protein (Methyltryptophan resistance) - *Neurospora crassa* .
ARAD1A06578g	11	gnl|TC-DB|P47082	2.A.18.5	Hypothetical 65.3
ARAD1C44528g	11	gnl|TC-DB|Q91XR7	2.A.18.6	Amino acid transporter system N2 - *Rattus norvegicus* (Rat).
ARAD1B21538g	10	gnl|TC-DB|P40074	2.A.18.6	Hypothetical 48.8
ARAD1D35376g	11	gnl|TC-DB|P36062	2.A.18.7	Hypothetical 75.5
ARAD1B22440g	11	gnl|TC-DB|Q99385	2.A.19.2	Vacuolar H+/Ca++ exchanger YDL128W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D46904g	11	gnl|TC-DB|Q6J4K2	2.A.19.4	Sodium/potassium/calcium exchanger 6 - *Homo sapiens*
ARAD1D30162g	13	gnl|TC-DB|P42839	2.A.19.7	Putative cation exchanger YNL321W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B10142g	12	gnl|TC-DB|O14091	2.A.2.6	Hypothetical 61.7
ARAD1C07238g	12	gnl|TC-DB|O14091	2.A.2.6	Hypothetical 61.7
ARAD1D06468g	9	gnl|TC-DB|P15710	2.A.20.2	Phosphate-repressible phosphate permease - *Neurospora crassa.*
ARAD1B12386g	11	gnl|TC-DB|P33413	2.A.21.6	Urea active transporter - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1D16852g	15	gnl|TC-DB|P33413	2.A.21.6	Urea active transporter - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1D41294g	3	gnl|TC-DB|Q93N33	2.A.21.9	Proline sensor PrlS - *Aeromonas hydrophila.*
ARAD1C09284g	3	gnl|TC-DB|Q93N33	2.A.21.9	Proline sensor PrlS - *Aeromonas hydrophila.*
ARAD1B19668g	3	gnl|TC-DB|P18239	2.A.29.1	ADP,ATP carrier protein 2 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D08272g	3	gnl|TC-DB|Q9H2D1	2.A.29.10	Folate transporter/carrier - *Homo sapiens* (human).
ARAD1D13002g	2	gnl|TC-DB|Q01888	2.A.29.12	Mitochondrial solute carrier protein homolog - *Bos taurus*
ARAD1B21252g	4	gnl|TC-DB|Q06497	2.A.29.17	Similar to mitochondrial ADP/ATP carrier protein - *Saccharomyces cerevisiae*
ARAD1C04466g	3	gnl|TC-DB|Q06497	2.A.29.17	Similar to mitochondrial ADP/ATP carrier protein - *Saccharomyces cerevisiae*
ARAD1B10318g	3	gnl|TC-DB|Q94AG6	2.A.29.18	Putative mitochondrial carrier protein - *Arabidopsis thaliana* (Mouse-ear cress).
ARAD1D34716g	2	gnl|TC-DB|P38921	2.A.29.18	Putative mitochondrial carrier protein PET8 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A09922g	4	gnl|TC-DB|P38921	2.A.29.18	Putative mitochondrial carrier protein PET8 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D29282g	2	gnl|TC-DB|Q99297	2.A.29.2	Putative mitochondrial carrier YOR222W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B01958g	4	gnl|TC-DB|P40556	2.A.29.27	Putative mitochondrial carrier YIL006W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C33572g	2	gnl|TC-DB|P40035	2.A.29.4	Mitochondrial phosphate carrier protein 2 - *Saccharomyces cerevisiae*
ARAD1C39270g	6	gnl|TC-DB|Q00319	2.A.29.6	Peroxisomal membrane protein PMP47B - *Candida boidinii* (Yeast).
ARAD1A10912g	3	gnl|TC-DB|O43772	2.A.29.8	Mitochondrial carnitine/acylcarnitine carrier protein - *Homo sapiens* (Human).
ARAD1D36080g	11	gnl|TC-DB|P25737	2.A.3.1	Lysine-specific permease - *Escherichia coli* .
ARAD1D09482g	12	gnl|TC-DB|P04817	2.A.3.10	Arginine permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A00550g	11	gnl|TC-DB|P53388	2.A.3.10	Dicarboxylic amino acid permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A11946g	12	gnl|TC-DB|P43548	2.A.3.10	General amino acid permease AGP3 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D17600g	11	gnl|TC-DB|P19145	2.A.3.10	General amino-acid permease GAP1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A19228g	12	gnl|TC-DB|P19145	2.A.3.10	General amino-acid permease GAP1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C04070g	12	gnl|TC-DB|P19145	2.A.3.10	General amino-acid permease GAP1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A02376g	11	gnl|TC-DB|P15380	2.A.3.10	Proline-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).

ARAD1B00352g	11	gnl|TC-DB|P15380	2.A.3.10	Proline-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D24222g	11	gnl|TC-DB|Q03770	2.A.3.10	Putative amino-acid permease SSY1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D20878g	12	gnl|TC-DB|Q9Y860	2.A.3.4	GABA permease - *Emericella nidulans* (*Aspergillus nidulans*).
ARAD1D20900g	10	gnl|TC-DB|Q9Y860	2.A.3.4	GABA permease - *Emericella nidulans* (*Aspergillus nidulans*).
ARAD1D49984g	11	gnl|TC-DB|Q9Y860	2.A.3.4	GABA permease - *Emericella nidulans* (*Aspergillus nidulans*).
ARAD1D12584g	12	gnl|TC-DB|Q9Y860	2.A.3.4	GABA permease - *Emericella nidulans* (*Aspergillus nidulans*).
ARAD1D04268g	12	gnl|TC-DB|P32837	2.A.3.4	GABA-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D15884g	12	gnl|TC-DB|P32837	2.A.3.4	GABA-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B20746g	12	gnl|TC-DB|P32837	2.A.3.4	GABA-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D45210g	12	gnl|TC-DB|P32837	2.A.3.4	GABA-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C11814g	12	gnl|TC-DB|P32837	2.A.3.4	GABA-specific permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D08074g	12	gnl|TC-DB|Q9UT18	2.A.3.4	Uncharacterized amino-acid permease C9.10
ARAD1A06600g	10	gnl|TC-DB|P82252	2.A.3.8	B(0,+)-type amino acid transporter 1 - *Rattus norvegicus* (Rat).
ARAD1D28292g	12	gnl|TC-DB|P50276	2.A.3.8	High affinity methionine permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C23914g	9	gnl|TC-DB|O22526	2.A.30.6	Cation-chloride co-transporter - *Nicotiana tabacum* (common tobacco).
ARAD1C19030g	12	gnl|TC-DB|P53838	2.A.31.3	Boron efflux transporter - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C09856g	10	gnl|TC-DB|Q04121	2.A.36.2	Mitochondrial NA(+)/H(+) exchanger - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C36938g	10	gnl|TC-DB|Q9P937	2.A.36.4	Na+/H+ antiporter Cnh1 - *Candida albicans* (Yeast).
ARAD1D28578g	10	gnl|TC-DB|Q9P937	2.A.36.4	Na+/H+ antiporter Cnh1 - *Candida albicans* (Yeast).
ARAD1D02706g	12	gnl|TC-DB|P40309	2.A.37.4	Hypothetical 97.1
ARAD1C44154g	6	gnl|TC-DB|Q6BYD8	2.A.38.2	DhTRK1 protein - *Debaryomyces hansenii* (Yeast) (*Torulaspora hansenii*).
ARAD1B15598g	6	gnl|TC-DB|Q6BYD8	2.A.38.2	DhTRK1 protein - *Debaryomyces hansenii* (Yeast) (*Torulaspora hansenii*).
ARAD1D48642g	12	gnl|TC-DB|Q708J7	2.A.39.2	Putative purine-cytosine permease - *Candida albicans* (Yeast).
ARAD1B03256g	12	gnl|TC-DB|P53099	2.A.39.2	Tpn1 64.5
ARAD1A06402g	12	gnl|TC-DB|Q04895	2.A.39.3	Allantoin permease (allantoin transport protein) - *Saccharomyces cerevisiae*
ARAD1C22902g	12	gnl|TC-DB|Q05998	2.A.39.4	Thiamine transporter -*Saccharomyces cerevisiae* (baker's yeast).
ARAD1D24618g	3	gnl|TC-DB|O07084	2.A.4.1	Cation transport protein YRDO - *Bacillus subtilis.*
ARAD1A12342g	6	gnl|TC-DB|P32798	2.A.4.2	Cobalt uptake protein Cot1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1C14410g	6	gnl|TC-DB|P53735	2.A.4.4	Hypothetical 82.5
ARAD1B10802g	12	gnl|TC-DB|Q03455	2.A.4.4	Protein ZRG17 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A14586g	5	gnl|TC-DB|A4ZUV2	2.A.4.5	Mn-specific cation diffusion facilitator transporter - *Populus trichocarpa*
ARAD1A08580g	5	gnl|TC-DB|A4ZUV2	2.A.4.5	Mn-specific cation diffusion facilitator transporter - *Populus trichocarpa*
ARAD1D20966g	12	gnl|TC-DB|P48777	2.A.40.5	Purine permease - *Emericella nidulans* (*aspergillus nidulans*).
ARAD1D46244g	12	gnl|TC-DB|Q874I3	2.A.41.2	H+/nucleoside cotransporter - *Candida albicans* (Yeast).
ARAD1C07480g	5	gnl|TC-DB|O60931	2.A.43.1	Cystinosin - *Homo sapiens* (Human).
ARAD1D24464g	4	gnl|TC-DB|Q60441	2.A.43.3	Mannose-P-dolichol utilization defect 1 protein - *Cricetulus griseus*
ARAD1C43098g	12	gnl|TC-DB|P27514	2.A.47.2	Uncharacterized transporter YNR013C - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D30404g	10	gnl|TC-DB|A7LKG1	2.A.49.1	CLC voltage-gated chloride channel - *Fusarium oxysporum f. sp. lycopersici* .
ARAD1D47938g	9	gnl|TC-DB|Q9GKE7	2.A.49.2	Outwardly rectifying chloride channel - *Sus scrofa* (Pig).

ARAD1B05742g	9	gnl|TC-DB|Q9GKE7	2.A.49.2	Outwardly rectifying chloride channel - *Sus scrofa* (Pig).
ARAD1D26268g	7	gnl|TC-DB|P32804	2.A.5.1	Zinc transporter ZRT1 Protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D26290g	7	gnl|TC-DB|P32804	2.A.5.1	Zinc transporter ZRT1 Protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A06138g	7	gnl|TC-DB|P32804	2.A.5.1	Zinc transporter ZRT1 Protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A07678g	7	gnl|TC-DB|P32804	2.A.5.1	Zinc transporter ZRT1 Protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C28468g	4	gnl|TC-DB|P40544	2.A.5.4	Zinc transporter YKE4 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C06380g	7	gnl|TC-DB|P0A8H3	2.A.5.5	Zinc transporter zupT - *Escherichia coli* .
ARAD1C19338g	11	gnl|TC-DB|P53154	2.A.50.1	Hypothetical 65.3
ARAD1B18326g	9	gnl|TC-DB|P38359	2.A.53.1	Sulfate transporter 1 (high-affinity) - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1B08954g	9	gnl|TC-DB|Q9SAY1	2.A.53.1	Sulfate transporter 1.1
ARAD1B20284g	11	gnl|TC-DB|Q09764	2.A.53.7	Hypothetical protein C24H6.11c in chromosome I - *Schizosaccharomyces pombe*
ARAD1D30580g	4	gnl|TC-DB|Q63965	2.A.54.1	Tricarboxylate carrier (fragment) - *Rattus norvegicus* (rat).
ARAD1C27698g	11	gnl|TC-DB|P38778	2.A.55.1	Transporter protein Smf1/Esp1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1C06358g	11	gnl|TC-DB|P38925	2.A.55.1	Transporter protein Smf1/Esp1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1D09812g	11	gnl|TC-DB|P31381	2.A.57.3	Nucleoside transporter Fun26 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1D45496g	10	gnl|TC-DB|P45946	2.A.59.1	Hypothetical protein yqcL - *Bacillus subtilis* .
ARAD1D41008g	6	gnl|TC-DB|P04035	2.A.6.6	3-hydroxy-3-methylglutaryl-coenzyme A reductase - *Homo sapiens* (human).
ARAD1D13640g	12	gnl|TC-DB|Q12200	2.A.6.6	Hypothetical 132.6
ARAD1D41470g	8	gnl|TC-DB|P97260	2.A.6.6	SREBP cleavage activating protein - *Cricetulus griseus* (Chinese hamster).
ARAD1D09042g	12	gnl|TC-DB|P38767	2.A.66.1	Hypothetical 64.2
ARAD1D22022g	10	gnl|TC-DB|P38767	2.A.66.1	Hypothetical 64.2
ARAD1D11110g	10	gnl|TC-DB|P38206	2.A.66.3	Nuclear division RFT1 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A01166g	15	gnl|TC-DB|O14411	2.A.67.1	OPT1P - *Candida albicans* (Yeast).
ARAD1B01254g	13	gnl|TC-DB|Q06593	2.A.67.1	Hypothetical Protein HRD799 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B14564g	12	gnl|TC-DB|Q06593	2.A.67.1	Hypothetical Protein HRD799 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B01540g	11	gnl|TC-DB|Q06593	2.A.67.1	Hypothetical Protein HRD799 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C10934g	14	gnl|TC-DB|Q06593	2.A.67.1	Hypothetical Protein HRD799 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D42988g	12	gnl|TC-DB|O14031	2.A.67.1	Uncharacterized oligopeptide transporter C29B12.10c - *Schizosaccharomyces pombe*
ARAD1C13178g	13	gnl|TC-DB|Q54EF1	2.A.67.2	Putative uncharacterized protein - *Dictyostelium discoideum*
ARAD1D28072g	9	gnl|TC-DB|Q00974	2.A.7.10	UDP N-acetylglucosamine transporter - *Kluyveromyces lactis* (Yeast).
ARAD1C27478g	10	gnl|TC-DB|O64503	2.A.7.11	Expressed protein - *Arabidopsis thaliana* (Mouse-ear cress).
ARAD1C40700g	7	gnl|TC-DB|O16658	2.A.7.12	Putative uncharacterized protein - *Caenorhabditis elegans* .
ARAD1D08646g	9	gnl|TC-DB|Q96WN8	2.A.7.13	Golgi GDP-mannose transporter - *Candida albicans* (Yeast).
ARAD1D04576g	10	gnl|TC-DB|Q9SFT8	2.A.7.24	Putative integral membrane protein - *Arabidopsis thaliana* (Mouse-ear cress).
ARAD1A13882g	8	gnl|TC-DB|Q04083	2.A.7.24	Thiamine-repressible mitochondrial transport protein THI74 - *Saccharomyces cerevisiae*
ARAD1B20196g	10	gnl|TC-DB|Q04083	2.A.7.24	Thiamine-repressible mitochondrial transport protein THI74 - *Saccharomyces cerevisiae*
ARAD1B21626g	8	gnl|TC-DB|Q9LIR9	2.A.7.25	Gb|AAF34307.1
ARAD1C42988g	9	gnl|TC-DB|Q7RWT8	2.A.7.25	Putative uncharacterized protein - *Neurospora crassa* .
ARAD1B17006g	8	gnl|TC-DB|P22215	2.A.7.9	SLY41 protein - *Saccharomyces cerevisiae* (Baker's yeast).

ARAD1D06908g	9	gnl|TC-DB|Q10495	2.A.85.3	Hypothetical 111.4
ARAD1D23386g	7	gnl|TC-DB|Q10495	2.A.85.3	Hypothetical 111.4
ARAD1C21824g	8	gnl|TC-DB|Q10495	2.A.85.3	Hypothetical 111.4
ARAD1C39710g	10	gnl|TC-DB|Q10495	2.A.85.3	Hypothetical 111.4
ARAD1A17996g	2	gnl|TC-DB|Q25771	2.A.85.4	Asparagine-rich antigen (clone 25c4) (fragment) - *Plasmodium falciparum.*
ARAD1A06820g	3	gnl|TC-DB|P47818	2.A.89.1	Protein CCC1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B01188g	4	gnl|TC-DB|P39952	2.A.9.1	Cytochrome oxidase biogenesis protein Oxa1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1C39754g	10	gnl|TC-DB|Q8BY89	2.A.92.1	Choline transporter-like protein 2 - *Mus musculus* (Mouse).
ARAD1B15180g	3	gnl|TC-DB|B0WNM	2.A.94.1	Xenotropic and polytropic murine leukemia virus receptor xpr1 - *Culex quinquefasciatus*
ARAD1C31768g	4	gnl|TC-DB|B0WNM	2.A.94.1	Xenotropic and polytropic murine leukemia virus receptor xpr1 - *Culex quinquefasciatus*
ARAD1C23254g	6	gnl|TC-DB|B0WNM	2.A.94.1	Xenotropic and polytropic murine leukemia virus receptor xpr1 - *Culex quinquefasciatus*
ARAD1D46134g	3	gnl|TC-DB|B0WNM	2.A.94.1	Xenotropic and polytropic murine leukemia virus receptor xpr1 - *Culex quinquefasciatus*
ARAD1A09152g	6	gnl|TC-DB|P25613	2.A.96.1	Uncharacterized protein YCR010C - *Saccharomyces cerevisiae* GN=YCR010C
ARAD1A17248g	6	gnl|TC-DB|P25613	2.A.96.1	Uncharacterized protein YCR010C - *Saccharomyces cerevisiae* GN=YCR010C
ARAD1D43692g	5	gnl|TC-DB|P25613	2.A.96.1	Uncharacterized protein YCR010C - *Saccharomyces cerevisiae* GN=YCR010C
ARAD1A01188g	5	gnl|TC-DB|P25613	2.A.96.1	Uncharacterized protein YCR010C - *Saccharomyces cerevisiae* GN=YCR010C
ARAD1A01276g	6	gnl|TC-DB|P25613	2.A.96.1	Uncharacterized protein YCR010C - *Saccharomyces cerevisiae* GN=YCR010C
ARAD1A15114g	12	gnl|TC-DB|P08183	3.A.1.201	Multidrug resistance protein 1 (P-glycoprotein 1) - *Homo sapiens* (Human).
ARAD1C40040g	2	gnl|TC-DB|P33897	3.A.1.203	Adrenoleukodystrophy protein (ALDP) - *Homo sapiens* (Human).
ARAD1C11440g	3	gnl|TC-DB|P33897	3.A.1.203	Adrenoleukodystrophy protein (ALDP) - *Homo sapiens* (Human).
ARAD1C37202g	7	gnl|TC-DB|A8WEV1	3.A.1.204	ABC transporter ABCG6 - *Leishmania donovani* .
ARAD1D38104g	11	gnl|TC-DB|Q9H221	3.A.1.204	ATP-binding cassette sub-family G member 8 (Sterolin-2) - *Homo sapiens* (Human).
ARAD1A14146g	6	gnl|TC-DB|Q9C8K2	3.A.1.204	ATP-dependent transmembrane transporter - *Arabidopsis thaliana*
ARAD1C43582g	12	gnl|TC-DB|P43071	3.A.1.205	Multidrug resistance protein CDR1 - *Candida albicans* (Yeast).
ARAD1D07634g	13	gnl|TC-DB|P43071	3.A.1.205	Multidrug resistance protein CDR1 - *Candida albicans* (Yeast).
ARAD1A12298g	10	gnl|TC-DB|P32568	3.A.1.205	SNQ2 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D20724g	12	gnl|TC-DB|P32568	3.A.1.205	SNQ2 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B20988g	12	gnl|TC-DB|P32568	3.A.1.205	SNQ2 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D37796g	12	gnl|TC-DB|P12866	3.A.1.206	Mating factor A secretion protein STE6 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C02970g	16	gnl|TC-DB|P32386	3.A.1.208	ATP-dependent bile acid permease - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D22132g	16	gnl|TC-DB|P39109	3.A.1.208	Metal resistance protein YCF1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D25124g	14	gnl|TC-DB|P39109	3.A.1.208	Metal resistance protein YCF1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A18106g	10	gnl|TC-DB|P53049	3.A.1.208	Oligomycin resistance ATP-dependent permease YOR1 - *Saccharomyces cerevisiae*
ARAD1D05544g	5	gnl|TC-DB|P40416	3.A.1.210	Mitochondrial transporter ATM1 precursor - Saccharomyces cerevisiae (Baker's yeast).
ARAD1B18150g	14	gnl|TC-DB|P78363	3.A.1.211	Retinal-specific ATP-binding cassette transporter - *Homo sapiens* (Human).
ARAD1C13288g	5	gnl|TC-DB|P33310	3.A.1.212	ATP-dependent permease MDL1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A07766g	4	gnl|TC-DB|P46889	3.A.12.1	Cell division protein ftsK - *Escherichia coli* .
ARAD1D37180g	2	gnl|TC-DB|P25694	3.A.16.1	Cell division control protein 48 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C38610g	4	gnl|TC-DB|Q9BUN8	3.A.16.1	Transitional endoplasmic reticulum ATPase (TER ATPase) - *Homo sapiens* (Human).

ARAD1C16214g	4	gnl|TC-DB|Q9UKV3	3.A.18.1	Apoptotic chromatin condensation inducer in the nucleus - *Homo sapiens* (Human).
ARAD1C11704g	3	gnl|TC-DB|Q8IYB3	3.A.18.1	Eukaryotic initiation factor 4A-III - *Homo sapiens* (Human).
ARAD1A10296g	4	gnl|TC-DB|Q8IYB3	3.A.18.1	Serine/arginine repetitive matrix protein 1 - *Homo sapiens* (Human).
ARAD1C03278g	4	gnl|TC-DB|P32842	3.A.2.2	Vacuolar ATP synthase subunit b - *Saccharomyces cerevisiae*
ARAD1C30008g	4	gnl|TC-DB|P25515	3.A.2.2	Vacuolar ATP synthase subunit b - *Saccharomyces cerevisiae*
ARAD1C38280g	5	gnl|TC-DB|P23968	3.A.2.2	Vacuolar ATP synthase subunit b - *Saccharomyces cerevisiae*
ARAD1D18832g	7	gnl|TC-DB|P32563	3.A.2.2	Vacuolar ATP synthase subunit b - *Saccharomyces cerevisiae*
ARAD1B14322g	6	gnl|TC-DB|P32563	3.A.2.2	Vacuolar ATP synthase subunit b - *Saccharomyces cerevisiae*
ARAD1D35706g	10	gnl|TC-DB|P50993	3.A.3.1	Sodium/potassium-transporting ATPase subunit alpha-2 - *Homo sapiens*
ARAD1B19404g	7	gnl|TC-DB|P39986	3.A.3.10	Probable cation-transporting ATPase 1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D44946g	10	gnl|TC-DB|Q54X63	3.A.3.15	Cation-transporting ATPase - *Dictyostelium discoideum* AX4.
ARAD1D42218g	8	gnl|TC-DB|P13586	3.A.3.2	Calcium-transporting ATPase 1 - *Saccharomyces cerevisiae* (baker's yeast).
ARAD1A06798g	7	gnl|TC-DB|P54678	3.A.3.2	Probable calcium-transporting ATPase PAT1 - *Dictyostelium discoideum* (Slime mold).
ARAD1C10296g	8	gnl|TC-DB|P16615	3.A.3.2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2
ARAD1C39468g	10	gnl|TC-DB|P07038	3.A.3.3	Plasma membrane ATPase (EC 3.6.3.6) (proton pump) - *Neurospora crassa* .
ARAD1C41800g	9	gnl|TC-DB|P07038	3.A.3.3	Plasma membrane ATPase (EC 3.6.3.6) (proton pump) - *Neurospora crassa* .
ARAD1D15114g	8	gnl|TC-DB|Q9UVL6	3.A.3.5	Copper resistance-associated P-type ATPase - *Candida albicans* (Yeast).
ARAD1D04444g	8	gnl|TC-DB|P38995	3.A.3.5	Copper-transporting ATPase - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D36564g	7	gnl|TC-DB|P39524	3.A.3.8	Potential phospholipid-transporting ATPase 1 - *Saccharomyces cerevisiae*
ARAD1C23694g	5	gnl|TC-DB|P39524	3.A.3.8	Potential phospholipid-transporting ATPase 1 - *Saccharomyces cerevisiae*
ARAD1C07084g	10	gnl|TC-DB|P32660	3.A.3.8	Probable phospholipid-transporting ATPase DNF1 - *Saccharomyces cerevisiae*
ARAD1D11220g	10	gnl|TC-DB|P32660	3.A.3.8	Probable phospholipid-transporting ATPase DNF1 - *Saccharomyces cerevisiae*
ARAD1D01364g	7	gnl|TC-DB|Q9XIE6	3.A.3.8	Putative phospholipid-transporting ATPase 3 - *Arabidopsis thaliana* (Mouse-ear cress).
ARAD1D26796g	10	gnl|TC-DB|O13398	3.A.3.9	P-type ATPase 2 - *Debaryomyces occidentalis* (Yeast) (*Schwanniomyces occidentalis*).
ARAD1D33770g	8	gnl|TC-DB|P32915	3.A.5.8	Signal recognition particle receptor alpha subunit homolog - *Saccharomyces cerevisiae*
ARAD1D17028g	2	gnl|TC-DB|P21825_I	3.A.5.8	Translocation protein (NPL1 protein) - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A16566g	3	gnl|TC-DB|P14906	3.A.5.8	Translocation protein SEC66 (HSS1 protein) - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1B03894g	8	gnl|TC-DB|P32915	3.A.5.8	Translocation protein SEC72 (P23) - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D01958g	3	gnl|TC-DB|Q9UGP8	3.A.5.9	Signal recognition particle 68 kDa protein (SRP68) - *Homo sapiens* (Human).
ARAD1C41646g	3	gnl|TC-DB|P39515	3.A.8.1	Mitochondrial import inner membrane translocase subunit TIM22 - *Saccharomyces cerevisiae*
ARAD1D14542g	4	gnl|TC-DB|P25710	3.D.1.6	NADH:ubiquinone oxidoreductase 14kD subunit - *Neurospora crassa* .
ARAD1B03476g	5	gnl|TC-DB|P21592	3.D.4.8	Cytochrome c oxidase polypeptide VII (EC 1.9.3.1) - *Saccharomyces cerevisiae*
ARAD1C15598g	2	gnl|TC-DB|P53266	3.D.4.8	SHY1 protein - i (Baker's yeast).
ARAD1D36212g	7	gnl|TC-DB|O74631	3.E.1.5	Protein FDD123 (CVHSP30/1) - *Coriolus versicolor* .
ARAD1C06138g	7	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1D37862g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1D26136g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1C28952g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1D38060g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*

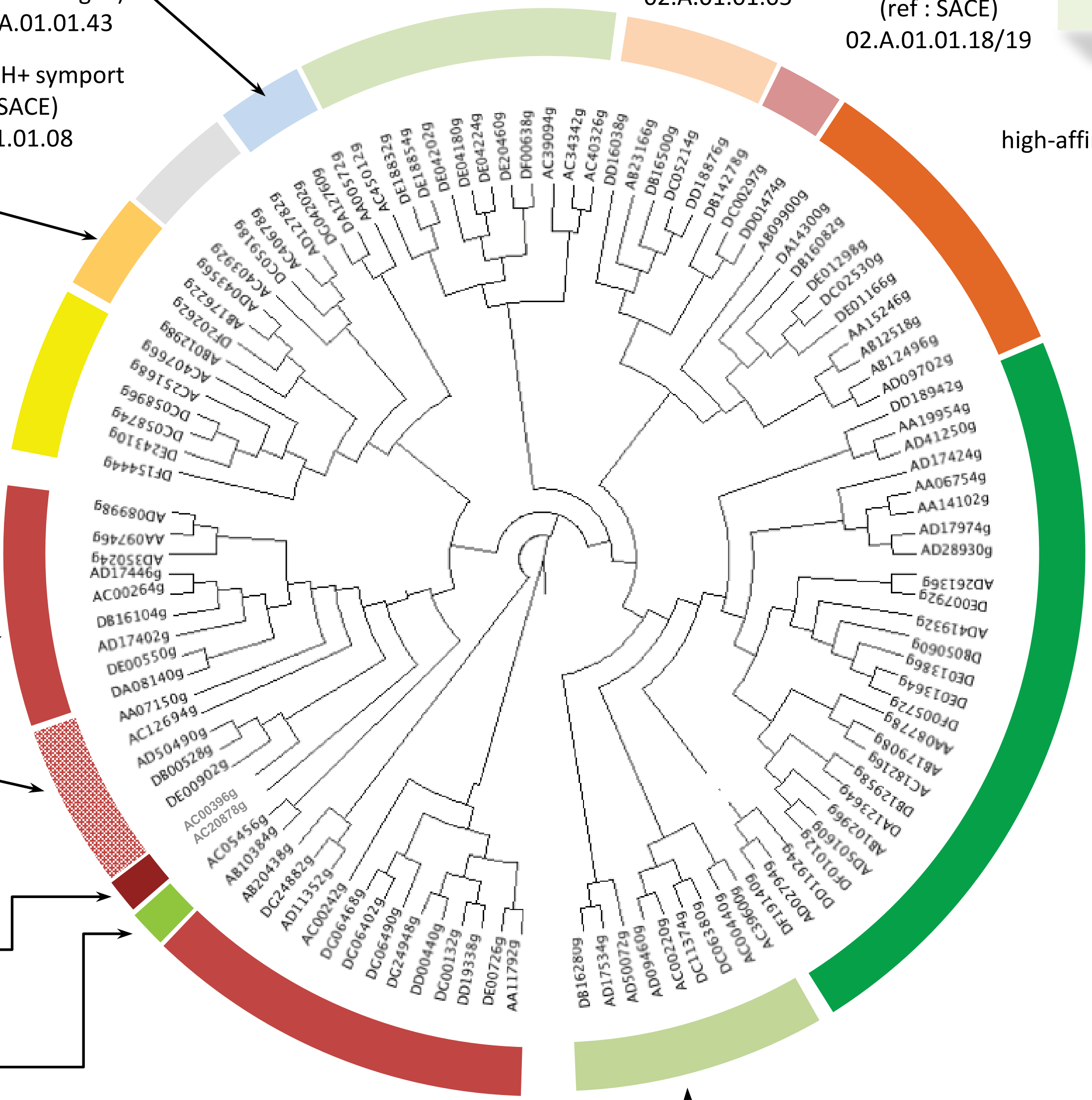
ARAD1D04136g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1B03432g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1D50996g	6	gnl|TC-DB|P32791	5.B.1.5	Ferric reductase transmembrane component 1 precursor - *Saccharomyces cerevisiae*
ARAD1A00264g	7	gnl|TC-DB|Q12473	5.B.1.7	Ferric reductase transmembrane component 6 - *Saccharomyces cerevisiae*
ARAD1A00286g	7	gnl|TC-DB|Q12473	5.B.1.7	Ferric reductase transmembrane component 6 - *Saccharomyces cerevisiae*
ARAD1D40370g	8	gnl|TC-DB|Q12473	5.B.1.7	Ferric reductase transmembrane component 6 - *Saccharomyces cerevisiae*
ARAD1D25784g	6	gnl|TC-DB|Q9WUE3	5.B.2.1	101F6 protein (Tumor suppressor region 10) - *Mus musculus* (Mouse).
ARAD1B20570g	2	gnl|TC-DB|P25656	8.A.27.1	Cell division control protein 50 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A13288g	7	gnl|TC-DB|Q9P8U8	9.A.10.1	High-affinity iron permease CaFTR2 - *Candida albicans* (Yeast).
ARAD1A02970g	7	gnl|TC-DB|Q9P8U8	9.A.10.1	High-affinity iron permease CaFTR2 - *Candida albicans* (Yeast).
ARAD1A02992g	7	gnl|TC-DB|Q9P8U8	9.A.10.1	High-affinity iron permease CaFTR2 - *Candida albicans* (Yeast).
ARAD1C27610g	3	gnl|TC-DB|P39685	9.A.14.1	Nucleoporin GLE1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C28028g	2	gnl|TC-DB|Q12445	9.A.14.1	Nucleoporin GLE2 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C08932g	3	gnl|TC-DB|Q02455	9.A.14.1	Protein MLP1 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C19316g	7	gnl|TC-DB|P53047	9.A.26.1	RTA1 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1A19184g	7	gnl|TC-DB|Q08417	9.A.26.1	*S.cerevisiae* chromosome XV reading frame ORF YOR049c - *Saccharomyces cerevisiae*
ARAD1D27698g	8	gnl|TC-DB|Q08417	9.A.26.1	*S.cerevisiae* chromosome XV reading frame ORF YOR049c - *Saccharomyces cerevisiae*
ARAD1D02684g	7	gnl|TC-DB|P40100	9.A.26.1	Uncharacterized protein YER185W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C44088g	7	gnl|TC-DB|P40100	9.A.26.1	Uncharacterized protein YER185W - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D13090g	4	gnl|TC-DB|Q12207	9.A.27.1	Non-classical export protein 2 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D20526g	4	gnl|TC-DB|Q3TWN3	9.A.40.3	Metal transporter CNNM2 - *Mus musculus* (Mouse).
ARAD1D41734g	5	gnl|TC-DB|Q3TWN3	9.A.40.3	Metal transporter CNNM2 - *Mus musculus* (Mouse).
ARAD1A06556g	4	gnl|TC-DB|Q13454	9.A.45.1	Tumor suppressor candidate 3 - *Homo sapiens* GN=TUSC3 PE=2 SV=1
ARAD1D32538g	4	gnl|TC-DB|P38224	9.A.46.1	Factor-induced gene 1 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D27258g	4	gnl|TC-DB|P38224	9.A.46.1	Factor-induced gene 1 protein - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C21450g	16	gnl|TC-DB|P36051	9.A.6.1	GPI-anchor biosynthetic protein MCD4 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C06490g	10	gnl|TC-DB|P36051	9.A.6.1	GPI-anchor biosynthetic protein MCD4 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C05786g	16	gnl|TC-DB|P36051	9.A.6.1	GPI-anchor biosynthetic protein MCD4 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D06204g	2	gnl|TC-DB|P38356	9.B.1.1	Metal homeostasis protein BSD2 - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1C09966g	2	gnl|TC-DB|P14359	9.B.12.3	Hypothetical 15.2
ARAD1C00968g	7	gnl|TC-DB|Q12067_	9.B.19.1	Metal homeostasis protein ATX2 - *Saccharomyces cerevisiae* (Bakers yeast).
ARAD1B19118g	7	gnl|TC-DB|Q63863	9.B.24.3	NMDA receptor glutamate-binding subunit - *Rattus sp.*
ARAD1D19052g	4	gnl|TC-DB|Q10320	9.B.26.3	Hypothetical 31.3
ARAD1D36058g	4	gnl|TC-DB|P0C0H0	9.B.32.1	Hyaluronan synthase - *Streptococcus pyogenes.*
ARAD1C38104g	6	gnl|TC-DB|P0C0H0	9.B.32.1	Hyaluronan synthase - *Streptococcus pyogenes* .
ARAD1C37862g	7	gnl|TC-DB|Q54066	9.B.32.1	Poly-beta-1,6-N-acetyl-D-glucosamine synthase ICAA - *Staphylococcus epidermidis.*
ARAD1C38126g	6	gnl|TC-DB|Q54066	9.B.32.1	Poly-beta-1,6-N-acetyl-D-glucosamine synthase ICAA - *Staphylococcus epidermidis.*
ARAD1D48466g	5	gnl|TC-DB|Q8IUH5	9.B.37.1	Palmitoyltransferase ZDHHC17 - *Homo sapiens*
ARAD1C41690g	5	gnl|TC-DB|Q8IUH5	9.B.37.1	Palmitoyltransferase ZDHHC17 - *Homo sapiens*

ARAD1C27368g	4	gnl|TC-DB|Q8R173	9.B.37.2	Palmitoyltransferase ZDHHC3 - *Mus musculus*
ARAD1D07326g	4	gnl|TC-DB|Q8R173	9.B.37.2	Palmitoyltransferase ZDHHC3 - *Mus musculus*
ARAD1B07040g	4	gnl|TC-DB|Q8R173	9.B.37.2	Palmitoyltransferase ZDHHC3 - *Mus musculus*
ARAD1D07568g	4	gnl|TC-DB|P31379	9.B.7.2	Uncharacterized membrane protein YAL018C - *Saccharomyces cerevisiae* (Baker's yeast).
ARAD1D17952g	3	gnl|TC-DB|P25560	9.B.82.1	Protein RER1 involved in retention of membrane proteins - *Saccharomyces cerevisiae*

Table S10C Class of transporters amplified in *A. adeninivorans* compared to two other pre-CTG species

ID-TCDB	ARAD	PIPA	YALI	ACRONYM	FAMILY NAME
01.A.01.10	1	none	none	VIC	Voltage-sensitive Na+Channel
02.A.01.01	60	17	24	SP	Sugar Porter
02.A.01.08	3	none	none	NPP	Nitrate/Nitrite Porter
02.A.01.19	1	none	none	AAHS	Aromatic Acid:H^+ Symporter
02.A.01.15	1	none	none	OCS	Organic Cation Transporter
02.A.01.58	3	1	1	NAG-T	N-Acetylglucosamine Transporter
02.A.29.17	1	none	none	MC	Peroxisomal ATP/ADP/AMP Antiporter,
02.A.29.18	1	none	none	MC	Mitochondrial S-adenosylmethionine Carrier,
02.A.29.27	1	none	none	MC	Mitochondrial NAD^+ Transporter,
03.A.01.204	3	none	1	ABCG	Eye Pigment Precursor Transporter
03.A.12.01	1	none	none	S-DNA-T	Septal DNA Translocator
03.D.01.06.	1	none	none	NDH	Animal H^+-translocating NADH Dehydrogenase Complex
09.A.40.03	2	none	none	HCC	HlyC/CorC Family (HemolysinC/Co2+-resistance Protein)
09.A.46.01	2	none	1	LACC	Putative Low Affinity Ca^{2+} Channel Family

S10D Sugar porters from ARAD & DEHA



quinate:H+ symport
(ref : CAAL)
02.A.01.01.07

glucose
uniport
(ref : SACE)
02.A.01.01.05

glucose sensor
(ref : SACE)
02.A.01.01.18/19

high-affinity glucose transporter
(ref : KLLA)
02.A.01.01.39

glycerol:H+ symport
(ref : SACE)
02.A.01.01.38

xylose:H+ symport - (ref : CAAL) –02.A.01.01.40

lactose:H+ symport
(ref : KLLA)
02.A.01.01.09

sugar porter
(ref : Archae)
02.A.01.01.15

monosaccharide:H+ symport
(ref : *Aspergilus*)
02.A.01.01.57

maltose:H+ symport
(ref : SACE)
02.A.01.01.10
02.A.01.01.11

sugar/polyol porter
(ref : Red Algae)
02.A.01.01.69

fructose:H+ symport
(ref : KLLA)
02.A.01.01.33

myoinositol:H+ symport
(ref : SACE)
02.A.01.01.08

monosaccharide:H+ symport
(ref : Red Algae)
02.A.01.01.43