

Article

A Genomic and Transcriptomic Overview of MATE, ABC, and MFS Transporters in *Citrus sinensis* Interaction with *Xanthomonas citri* subsp. *citri*

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Supplementary Materials

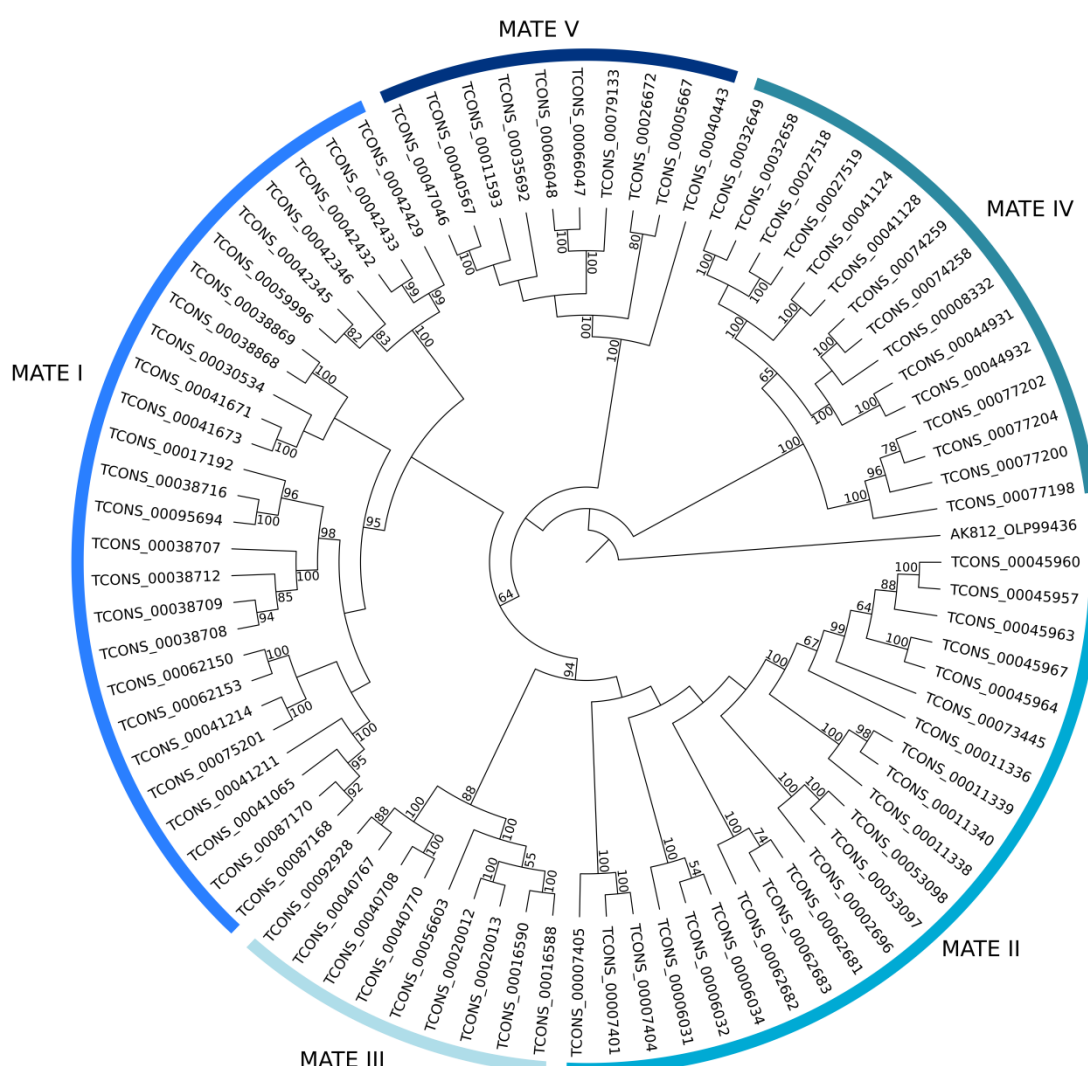
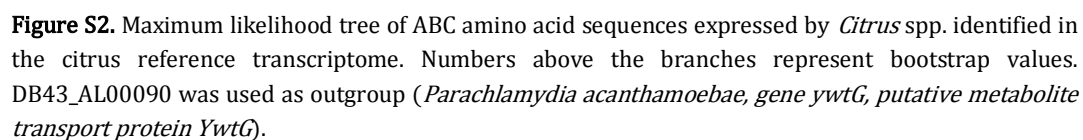


Figure S1. Maximum likelihood tree of MATE amino acid sequences expressed by *Citrus* spp. identified in the citrus reference transcriptome. Numbers above the branches represent bootstrap values. AK812_OLP99436 was used as outgroup (*Symbiodinium microadriaticum* str. CCMP2467, Gene: *slc47a1*, multidrug, and toxin extrusion protein 1).



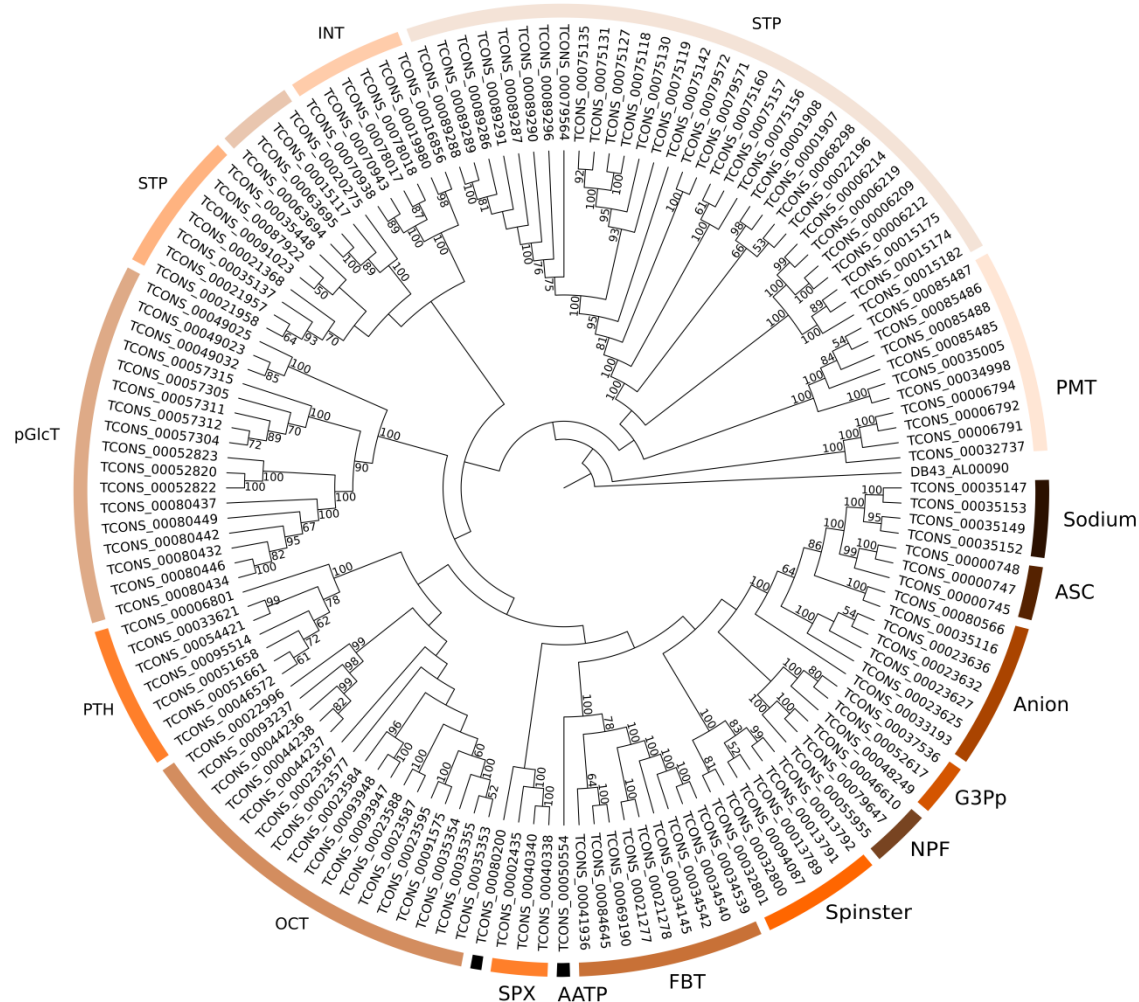


Figure S3. Maximum likelihood tree of MFS amino acid sequences expressed by *Citrus* spp. identified in the citrus reference transcriptome. Numbers above the branches represent bootstrap values. DB43_AL00090 was used as outgroup. (*Parachlamydia acanthamoebae*, gene *ywtG*, putative metabolite transport protein *YwtG*).

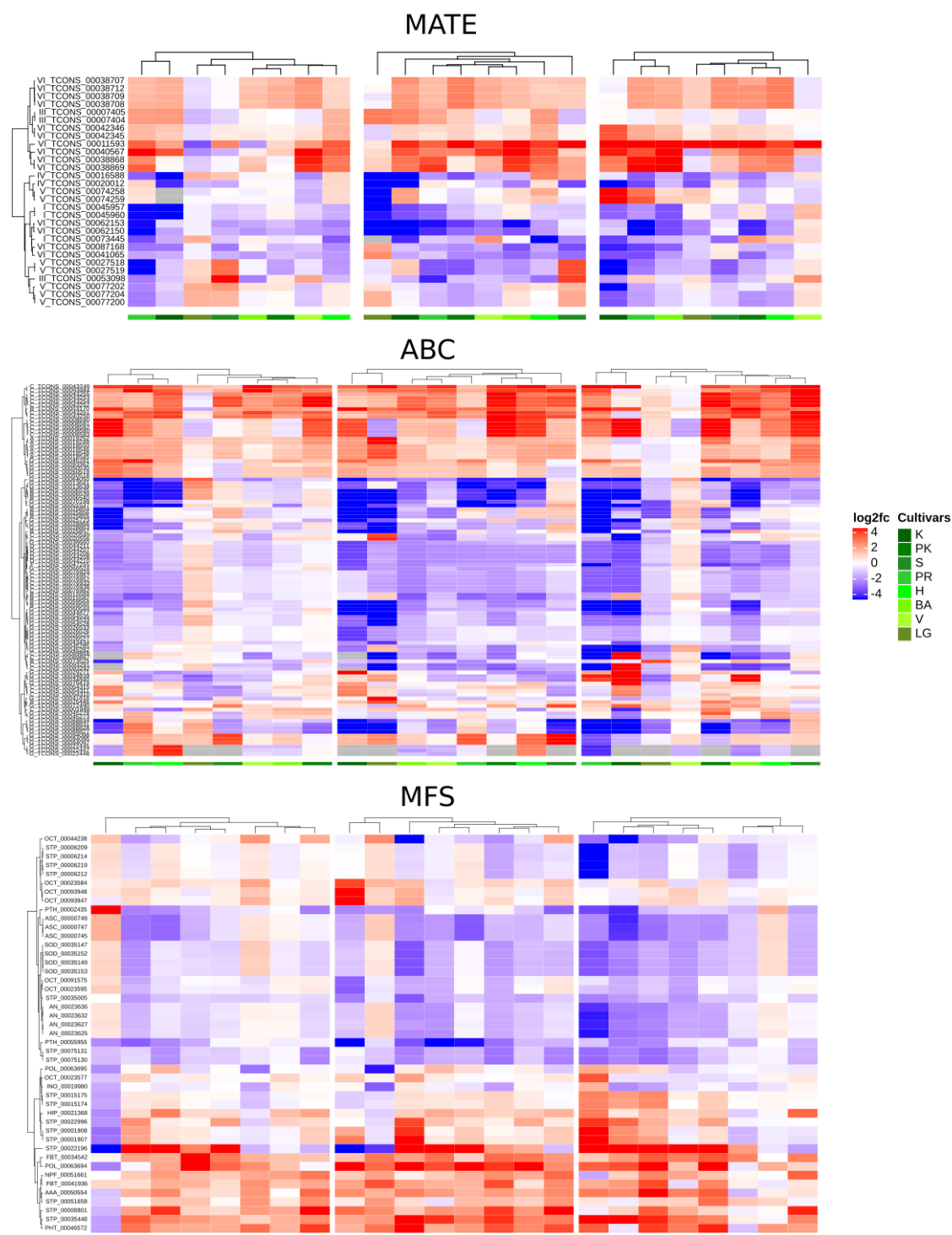


Figure S4. Clustered heatmaps of MATE, ABC, and MFS differentially expressed transcripts on at least one HAI in a species. K: 'Kumquat', PK: 'Ponkan', S: 'Satsuma', PR: 'Pera Rio', H: 'Hamlin', BA: 'Bahia', V: 'Valencia', LG: 'Galego', and HAI: Hours after bacterial inoculation. The identification of each transcript is given by the abbreviation of its respective subfamily followed by its identification number in the CRT.

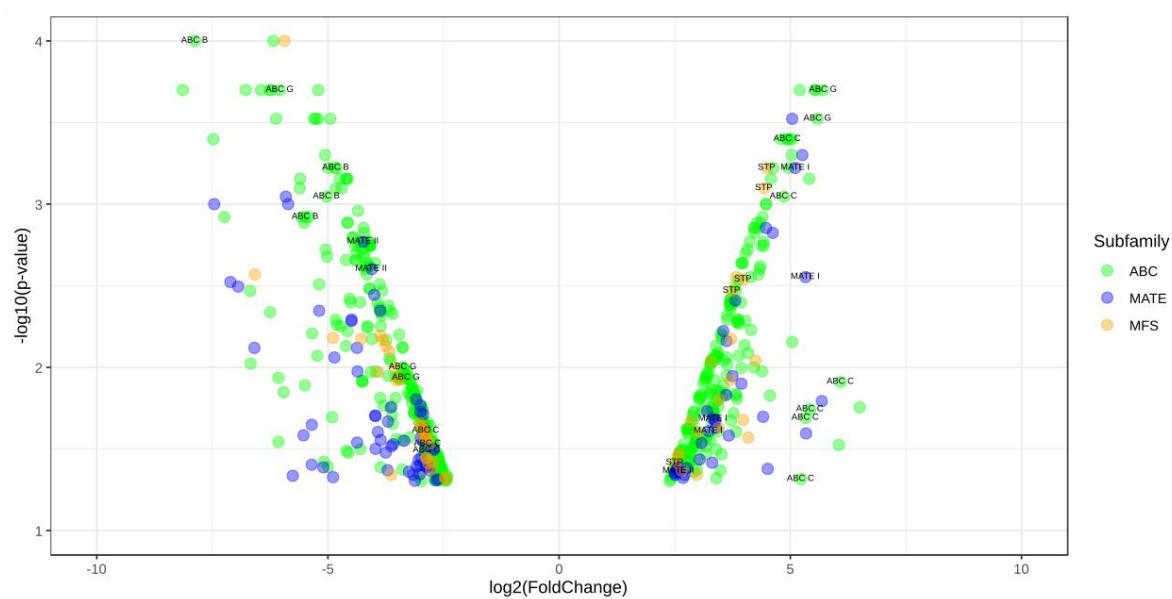


Figure S5. Volcano plot of MATE, ABC, and MFS differentially expressed transcripts. The 50 differentially expressed transcripts (Derived from the 4 MATE, 10 ABC, and 3 MFS that are potentially related to plant-defense mechanisms) associated with the plant membrane transporters gene candidates who most significantly impacted the plant defense responses under Citrus-Xac infection are annotated in the plot.

Table S1. Domains and motifs related to MATE, ABC, and MFS proteins used in the proteins manually verification.

Family	Accession	Name	Integrated Signatures	GO Terms
ABC	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	PF00528, cd06261, PS50928	GO:0055085,GO:0016020
	IPR002491	ABC transporter periplasmic binding domain	PF01497, PS50983	
	IPR003439	ABC transporter-like	PF00005, PS50893	GO:0005524,GO:0016887
	IPR003760	ABC transporter substrate-binding protein PnrA-like	PF02608	GO:0005886
	IPR003838	ABC transporter permease protein domain	PF02687	GO:0016020
	IPR010929	CDR ABC transporter	PF06422	GO:0005524,GO:0042626,GO:0055085,GO:0016020
				1
	IPR011527	ABC transporter type 1, transmembrane domain	PF00664, PF06472, PF13748, PS50929	GO:0005524,GO:0042626,GO:0055085,GO:0016020
				1
	IPR013563	Oligopeptide/dipeptide ABC transporter, C-terminal	TIGR01727,PF08352	GO:0000166,GO:0005524,GO:0015833
	IPR013581	Plant PDR ABC transporter associated	PF08370	
	IPR022182	ABC transporter phosphate permease PstC, N-terminal domain	PF12501	GO:0006817
	IPR032524	ABC transporter Uup, C-terminal	PF16326	GO:0003677
MATE	IPR032550	PBP-dependent ABC transporters TM subunit, N-terminal	PF16296	
	IPR040856	Glucose ABC transporter, C-terminal	PF17847	
MATE	IPR002528	Multi antimicrobial extrusion protein	PF01554,TIGR00797,PIRSF00660	GO:0015297,GO:0042910,GO:0055085,GO:0016020
			3	0
MFS	IPR036259	MFS transporter superfamily	SSF103473	
	IPR011701	Major facilitator superfamily	PF07690	GO:0022857,GO:0055085
	IPR020846	Major facilitator superfamily domain	PS50850	GO:0022857
	IPR020846	Major facilitator superfamily domain	PS50850	GO:0022857
	IPR024989	Major facilitator superfamily associated domain	PF12832	
	IPR005828	Major facilitator, sugar transporter-like	PF00083	GO:0022857,GO:0055085,GO:0016021

IPR000109	Proton-dependent oligopeptide transporter family	PTHR11654 PF00854	GO:0022857,GO:0055085,GO:0016020
IPR004768	Oligopeptide transporter	TIGR00926	GO:0035673,GO:0006857,GO:0016021
IPR004813	Oligopeptide transporter, OPT superfamily	TIGR00728,PF03169	GO:0055085
IPR004814	Oligopeptide transporter OPT	TIGR00733	
IPR004316	SWEET sugar transporter	PF03083	GO:0016021
IPR005828	Major facilitator, sugar transporter-like	PF00083	GO:0022857,GO:0055085,GO:0016021
IPR007271	Nucleotide-sugar transporter	PIRSF005799, PF04142, PTHR10231	GO:0015165,GO:0090481,GO:0000139,GO:0016021
IPR012404	Nucleotide-sugar transporter-related	PIRSF036436	GO:0016021
IPR018180	Sugar transporter SWEET1	PTHR10791:SF44, PTHR10791:SF155	GO:0051119
IPR025601	ATP-binding sugar transporter-like protein	PF13856	
IPR008509	Molybdate-anion transporter	PF05631, PTHR23516	GO:0015098,GO:0015689,GO:0016021

Table S2. Estimation of non-synonymous and synonymous substitutions mean dissimilarity for each sub-family ($\delta = d_N - d_S$ and $\omega = d_N / d_S$).

Gene families	Nei-Gojobori method	SLAC method	
	δ	<i>p</i> -Value	ω
ABC A	−10.99	1.00E−10	0.0819
ABC B	−27.98	1.00E−10	170
ABC C	−34.90	1.00E−10	202
ABC D	−8.66	1.00E−10	−*
ABC E	−	−	−
ABC F	−9.18	1.00E−10	194
ABC G	−24.24	1.00E−10	215
ABC I	−7.87	1.00E−10	112
MATE I	−23.60	1.00E−10	244
MATE II	−27.03	1.00E−10	230
MATE III	−20.86	1.00E−10	224
MATE IV	−16.31	1.00E−10	189
MATE V	−18.31	1.00E−10	0.0639
MFS Anion	−12.83	1.00E−10	145
MFS Ascorbate	−27.67	1.00E−10	146
MFS FBT	−13.85	1.00E−10	187
MFS G3Pp	−18.47	1.00E−10	86
MFS Inositol	−11.09	1.00E−10	194
MFS OTH	−	−	−
MFS PMT	−16.93	1.00E−10	−*
MFS Polyol	−25.47	1.00E−10	128
MFS PTH	−32.21	1.00E−10	0.0934
MFS Spinster	−10.06	1.00E−10	299
MFS STP	−18.54	1.00E−10	291

** SLAC can only be performed with a minimum of two sequences. In the table are reported: the average nucleotide diversity (π) of the ABC subfamilies analyzed using the Nei-Gojobori and SLAC methods and the selection ($d_N > d_S$; $d_N/d_S > 1$) or negative selection ($d_N < d_S$; $d_N/d_S < 1$). of strict-neutrality ($d_N = d_S$; $d_N/d_S = 1$) in favor of the alternative hypothesis positive probability (*p*-Value < 0.05) of rejecting the null hypothesis.

Table S3. MATE, ABC, and MFS transcripts expressed by *Citrus* spp., molecular weight, isoelectric point, sequence length, subcellular localization, and putative gene name from *C. sinensis*.

Transcript	Molecular Weigh	Isoelectric Point	Sequence Length	Sublocalization	Annotation	Subfamily	Putative Gene
TCONS_00095694	11907.7	4.1957	111	chloroplast	DTX_14	MATE I	Cs2g13500
TCONS_00087170	27328.3	4.5576	244	plasma membrane	DTX_8	MATE I	Cs6g18200
TCONS_00087168	20442.3	8.3374	183	E.R.	DTX_8	MATE I	Cs6g18200
TCONS_00075201	49998.5	8.6245	461	plasma membrane	DTX_12	MATE I	Cs2g31280
TCONS_00062153	31277.8	8.6791	287	vacuole	DTX_14	MATE I	Cs5g20110_m
TCONS_00062150	49446.9	8.9154	454	plasma membrane	DTX_14	MATE I	Cs5g19630
TCONS_00059996	10086.6	6.7034	92	E.R.	DTX_19	MATE I	Cs1g07550
TCONS_00042433	56145.1	8.2104	506	plasma membrane	DTX_19	MATE I	Cs1g07550
TCONS_00042432	34605.6	9.2806	309	plasma membrane	DTX_19	MATE I	Cs1g07550
TCONS_00042429	19791.2	7.9528	179	vacuole	DTX_19	MATE I	Cs1g07550
TCONS_00042346	52550.9	6.6813	481	plasma membrane	DTX_19	MATE I	Cs1g07540
TCONS_00042345	40783	6.4827	371	E.R.	DTX_19	MATE I	Cs1g07540
TCONS_00041673	36382.5	8.3743	328	plasma membrane	DTX_16	MATE I	orange1.1t00013
TCONS_00041671	58872.5	7.8564	538	plasma membrane	DTX_16	MATE I	orange1.1t00013
TCONS_00041214	28026.8	8.5859	256	plasma membrane	DTX_12	MATE I	Cs6g18160
TCONS_00041211	56198.5	7.1551	513	plasma membrane	DTX_8	MATE I	Cs6g18150
TCONS_00041065	24054.1	8.2445	223	vacuole	DTX_8	MATE I	Cs6g18200
TCONS_00038869	54635.3	7.7156	502	plasma membrane	DTX_16	MATE I	Cs2g13530
TCONS_00038868	41382.3	8.2776	375	plasma membrane	DTX_16	MATE I	Cs2g13530
TCONS_00038716	54731.5	5.0645	500	plasma membrane	DTX_14	MATE I	Cs2g13500
TCONS_00038712	35180.5	5.2449	320	plasma membrane	DTX_12	MATE I	Cs2g13510
TCONS_00038709	50403.4	7.9799	461	plasma membrane	DTX_12	MATE I	Cs2g13510
TCONS_00038708	54657.3	8.1167	502	plasma membrane	DTX_12	MATE I	Cs2g13510
TCONS_00038707	27145.1	6.8017	244	plasma membrane	DTX_12	MATE I	Cs2g13510
TCONS_00030534	52006.4	7.9821	476	plasma membrane	DTX_16	MATE I	Cs5g06100
TCONS_00017192	27457.8	4.5817	250	plasma membrane	DTX_14	MATE I	Cs2g13501_m
TCONS_00073445	52576.4	6.5865	476	plasma membrane	DTX_27	MATE II	Cs5g21940
TCONS_00062683	55735.5	5.2952	507	plasma membrane	DTX_33	MATE II	Cs5g28190
TCONS_00062682	57912.2	7.837	525	plasma membrane	DTX_33	MATE II	Cs5g28190
TCONS_00062681	30391.1	7.1433	278	vacuole	DTX_33	MATE II	Cs5g28190
TCONS_00053098	55726.9	6.7161	509	plasma membrane	DTX_35	MATE II	Cs9g19420
TCONS_00053097	52762.7	8.5186	482	plasma membrane	DTX_35	MATE II	Cs9g19430
TCONS_00045967	54929.9	6.3298	499	plasma membrane	DTX_27	MATE II	Cs1g20120
TCONS_00045964	37222	5.2667	335	E.R.	DTX_27	MATE II	Cs1g20120
TCONS_00045963	27335.1	7.9173	244	plasma membrane	DTX_27	MATE II	Cs1g20120
TCONS_00045960	54381.5	8.216	499	plasma membrane	DTX_27	MATE II	Cs1g20130
TCONS_00045957	37170	7.8896	338	plasma membrane	DTX_27	MATE II	Cs1g20130
TCONS_00011340	53151	6.4797	487	plasma membrane	DTX_27	MATE II	Cs3g17660

TCONS_00011339	36043.5	7.4298	323	plasma membrane	DTX_27	MATE II	Cs3g17660
TCONS_00011338	19623.3	7.1645	183	vacuole	DTX_27	MATE II	Cs3g17660
TCONS_00011336	56101	7.9652	512	plasma membrane	DTX_27	MATE II	Cs3g17670
TCONS_00007405	51604.6	10.1562	464	plasma membrane	DTX_29	MATE II	Cs7g09190
TCONS_00007404	57249.7	6.969	527	plasma membrane	DTX_29	MATE II	Cs7g09190
TCONS_00007401	37381.2	6.8374	341	plasma membrane	DTX_29	MATE II	Cs7g09190
TCONS_00006034	43126.5	7.8135	398	vacuole	DTX_33	MATE II	Cs3g24330
TCONS_00006032	25481.8	8.4818	230	vacuole	DTX_33	MATE II	Cs3g24330
TCONS_00006031	18326.5	6.8755	173	vacuole	DTX_33	MATE II	Cs3g24330
TCONS_00002696	57273	5.4118	524	plasma membrane	DTX_34	MATE II	orange1.1t00390
TCONS_00092928	33423.7	8.6776	303	vacuole	DTX_41	MATE III	Cs2g15080
TCONS_00056603	59547.2	8.1005	547	plasma membrane	DTX_40	MATE III	Cs2g21460
TCONS_00040770	23853	6.4396	219	E.R.	DTX_41	MATE III	Cs2g15080
TCONS_00040767	55481.7	7.5818	505	plasma membrane	DTX_41	MATE III	Cs2g15120
TCONS_00040708	28640.7	7.2885	257	vacuole	DTX_41	MATE III	Cs2g15610
TCONS_00020013	27074.2	5.6849	252	vacuole	DTX_40	MATE III	Cs2g08000
TCONS_00020012	54024.1	7.6783	501	plasma membrane	DTX_40	MATE III	Cs2g08000
TCONS_00016590	23209.7	9.9123	215	vacuole	DTX_40	MATE III	Cs2g03200
TCONS_00016588	56297.2	6.0341	519	plasma membrane	DTX_40	MATE III	Cs2g03220
TCONS_00077204	60550.5	8.6079	557	chloroplast	DTX_46	MATE IV	Cs8g08470
TCONS_00077202	28053.4	7.6464	257	chloroplast	DTX_46	MATE IV	Cs8g08470
TCONS_00077200	43554.2	8.5898	398	plasma membrane	DTX_46	MATE IV	Cs8g08470
TCONS_00077198	59496.7	7.7824	548	plasma membrane	DTX_46	MATE IV	Cs8g08480
TCONS_00074259	40292.9	9.7167	375	plasma membrane	DTX_42	MATE IV	orange1.1t03403
TCONS_00074258	58134.8	7.4094	538	plasma membrane	DTX_42	MATE IV	orange1.1t03403
TCONS_00044932	57227.2	7.8844	535	plasma membrane	DTX_42	MATE IV	Cs2g30270
TCONS_00044931	31956.1	5.1502	299	plasma membrane	DTX_42	MATE IV	Cs2g30270
TCONS_00041128	29661.1	10.5478	279	chloroplast	DTX_44	MATE IV	Cs6g09270
TCONS_00041124	44027.1	10.24	413	chloroplast	DTX_44	MATE IV	Cs6g09270
TCONS_00032658	30083.9	10.0467	282	plasma membrane	DTX_45	MATE IV	Cs8g01660
TCONS_00032649	63766.5	9.2068	602	plasma membrane	DTX_45	MATE IV	Cs8g01660
TCONS_00027519	35806.2	10.3576	330	chloroplast	DTX_45	MATE IV	Cs1g26350
TCONS_00027518	65503.2	9.2159	611	E.R.	DTX_45	MATE IV	Cs1g26350
TCONS_00008332	26412.6	10.2381	246	plasma membrane	DTX_43	MATE IV	Cs1g26350
TCONS_00079133	50154	7.6444	465	vacuole	DTX_53	MATE V	Cs7g16290_m
TCONS_00066048	53856.7	8.5624	496	plasma membrane	DTX_53	MATE V	Cs6g09880
TCONS_00066047	36822.5	8.4209	337	plasma membrane	DTX_53	MATE V	Cs6g09880
TCONS_00047046	57180.6	7.7634	525	plasma membrane	DTX_49	MATE V	Cs9g16870
TCONS_00040567	56054.2	7.4348	513	plasma membrane	DTX_49	MATE V	Cs5g10270
TCONS_00040443	58872.7	8.3841	543	plasma membrane	DTX_56	MATE V	Cs5g09710
TCONS_00035692	57003.4	8.0683	531	plasma membrane	DTX_51	MATE V	Cs4g15415_m
TCONS_00026672	54470.4	8.2021	501	plasma membrane	DTX_55	MATE V	Cs9g04120
TCONS_00011593	61807.3	7.8303	586	plasma membrane	DTX_48	MATE V	Cs3g16650
TCONS_00005667	37133	6.4647	336	plasma membrane	DTX_54	MATE V	Cs3g22600

Transcript	Molecular Weigh	Isoelectric Point	Sequence Length	Sublocalization	Subfamily	Putative Gene
TCONS_00068851	188525,17	7,0271	1695	plasma membrane	ABC A	orange1.1t02318
TCONS_00068849	205029,33	7,8267	1841	plasma membrane	ABC A	orange1.1t02318
TCONS_00019252	78376,39	7,2099	706	plasma membrane	ABC A	Cs5g04120
TCONS_00019248	53839,28	5,2737	483	plasma membrane	ABC A	Cs5g04120
TCONS_00018550	70976,26	8,4755	637	plasma membrane	ABC A	Cs5g04110
TCONS_00018548	65454,57	7,1179	589	plasma membrane	ABC A	Cs5g04110
TCONS_00018546	106798,08	8,0549	956	plasma membrane	ABC A	Cs5g04110
TCONS_00018545	101276,4	7,2179	908	plasma membrane	ABC A	Cs5g04110
TCONS_00095146	51233,21	7,3486	478	plasma membrane	ABC B	Cs2g04080
TCONS_00091259	76008,04	7,8674	703	plasma membrane	ABC B	Cs9g01170
TCONS_00087281	124578,86	7,0244	1139	plasma membrane	ABC B	Cs9g11040
TCONS_00073525	171667,2	9,2634	1560	plasma membrane	ABC B	Cs1g16850
TCONS_00062200	148975,56	8,3082	1359	plasma membrane	ABC B	orange1.1t00937
TCONS_00059892	137715,87	9,0217	1255	plasma membrane	ABC B	Cs4g11230
TCONS_00059566	99686,33	8,6588	903	plasma membrane	ABC B	Cs3g09820
TCONS_00059564	142127,25	8,645	1292	plasma membrane	ABC B	Cs3g09820
TCONS_00056253	77986,37	9,6879	702	plasma membrane	ABC B	Cs1g08880
TCONS_00056251	81372,51	10,0389	731	plasma membrane	ABC B	Cs1g08880
TCONS_00055909	79846,69	8,3853	709	plasma membrane	ABC B	Cs2g27440
TCONS_00055908	46192,76	7,4341	407	mitochondria	ABC B	Cs2g27440
TCONS_00055903	76001,21	8,5797	677	plasma membrane	ABC B	Cs2g27440
TCONS_00055897	52723,24	9,3561	467	plasma membrane	ABC B	Cs2g27440
TCONS_00046918	86191,02	9,387	791	plasma membrane	ABC B	Cs9g16780
TCONS_00036985	64853,55	8,4383	611	plasma membrane	ABC B	Cs5g12150
TCONS_00036980	68987,4	8,6972	647	plasma membrane	ABC B	Cs5g12150
TCONS_00035639	134759,42	9,172	1230	plasma membrane	ABC B	Cs4g15420
TCONS_00033725	46021,68	9,9774	412	chloroplast	ABC B	Cs7g28610

TCONS_00033443	144915,27	7,2087	1303	plasma membrane	ABC B	Cs7g28610
TCONS_00033441	82815,6	5,4403	747	plasma membrane	ABC B	Cs7g28610
TCONS_00028662	63740,34	8,6188	582	plasma membrane	ABC B	Cs6g14480
TCONS_00028659	64880,75	9,341	592	plasma membrane	ABC B	Cs6g14480
TCONS_00028658	17715,28	7,1293	160	cytosol	ABC B	Cs6g14480
TCONS_00026583	133450,29	7,2295	1236	plasma membrane	ABC B	Cs9g01170_a
TCONS_00025857	136076,59	7,5088	1247	plasma membrane	ABC B	Cs6g20290
TCONS_00025856	112925,74	8,4603	1027	plasma membrane	ABC B	Cs6g20280
TCONS_00025855	73470,79	8,2938	668	vacuole	ABC B	Cs6g20270
TCONS_00025854	71274,68	7,2363	647	plasma membrane	ABC B	Cs6g20270
TCONS_00025446	136438,12	8,5551	1253	plasma membrane	ABC B	Cs6g21110
TCONS_00015585	68155,5	7,0146	632	plasma membrane	ABC B	Cs2g04070
TCONS_00015584	144638,8	8,1973	1332	plasma membrane	ABC B	Cs2g04080
TCONS_00015582	91599,66	9,194	837	plasma membrane	ABC B	Cs2g04080
TCONS_00007410	37102,54	10,0755	326	plasma membrane	ABC B	Cs7g09160
TCONS_00007407	96751,66	9,7628	854	plasma membrane	ABC B	Cs7g09160
TCONS_00007278	133938,42	9,0203	1224	plasma membrane	ABC B	Cs7g09730
TCONS_00006540	85588,31	7,1752	789	plasma membrane	ABC B	Cs3g26380
TCONS_00006539	136639,36	8,4429	1260	plasma membrane	ABC B	Cs3g26380
TCONS_00006535	88318,42	7,5953	819	plasma membrane	ABC B	Cs3g26380
TCONS_00003170	140125,78	6,6978	1299	plasma membrane	ABC B	orange1.1t01769_a
TCONS_00093484	56051,65	6,1313	508	plasma membrane	ABC C	Cs4g09150
TCONS_00093292	19006,58	10,4364	161	plasma membrane	ABC C	Cs1g18450
TCONS_00093291	21974,13	9,6543	191	plasma membrane	ABC C	Cs1g18450
TCONS_00089868	61573,8	8,5267	555	chloroplast	ABC C	Cs1g18450
TCONS_00089867	37479,06	7,5084	332	nucleus	ABC C	Cs1g18450
TCONS_00076962	160756,62	6,6066	1433	plasma membrane	ABC C	orange1.1t02765
TCONS_00076957	164017,51	6,6624	1465	plasma membrane	ABC C	orange1.1t02765

TCONS_00076952	110325,28	6,7756	980	plasma membrane	ABC C	orange1.1t02765
TCONS_00076938	94373,23	7,9232	835	plasma membrane	ABC C	orange1.1t02765
TCONS_00076933	59151,17	6,8578	530	plasma membrane	ABC C	orange1.1t02765
TCONS_00076929	30369,87	7,6572	273	chloroplast	ABC C	orange1.1t02765
TCONS_00054315	137138,23	8,3994	1234	plasma membrane	ABC C	Cs9g18660
TCONS_00054311	165306,37	8,1658	1485	plasma membrane	ABC C	Cs9g18660
TCONS_00054310	99858,66	8,8131	895	plasma membrane	ABC C	Cs9g18660
TCONS_00046220	149463,19	7,5066	1343	plasma membrane	ABC C	Cs5g28990
TCONS_00044886	129092,47	7,5305	1156	plasma membrane	ABC C	Cs1g13700
TCONS_00044885	61122,26	8,0095	547	plasma membrane	ABC C	Cs4g09140
TCONS_00043255	165906,5	6,5071	1496	plasma membrane	ABC C	Cs4g09120
TCONS_00043254	166553,59	7,1469	1495	plasma membrane	ABC C	Cs4g09130
TCONS_00043253	98197,19	5,9232	885	plasma membrane	ABC C	Cs4g09130
TCONS_00043252	163674,91	7,1965	1469	plasma membrane	ABC C	Cs1g13720
TCONS_00043251	145109,16	6,4705	1300	nucleus	ABC C	Cs4g09140
TCONS_00043250	47502,63	5,656	425	chloroplast	ABC C	Cs4g09140
TCONS_00043249	56270,37	9,0061	501	plasma membrane	ABC C	Cs4g09150
TCONS_00037840	164345,38	8,7054	1475	plasma membrane	ABC C	Cs1g18460
TCONS_00020564	127020,95	5,5519	1142	plasma membrane	ABC C	Cs2g09550
TCONS_00020560	183757,62	6,5966	1635	plasma membrane	ABC C	Cs2g09550
TCONS_00020556	147399,58	9,2353	1307	plasma membrane	ABC C	Cs2g09560
TCONS_00020549	61168,52	9,6605	543	plasma membrane	ABC C	Cs7g32530
TCONS_00019595	141203,84	6,6556	1261	plasma membrane	ABC C	Cs5g02710
TCONS_00019594	89232,09	6,1392	799	plasma membrane	ABC C	Cs5g02710
TCONS_00008590	87945,08	9,2257	781	plasma membrane	ABC C	Cs7g10200
TCONS_00008583	165591,13	8,4506	1472	plasma membrane	ABC C	Cs7g10200
TCONS_00008582	99974,37	6,9255	893	plasma membrane	ABC C	Cs7g10200
TCONS_00008581	87533,28	8,4347	779	plasma membrane	ABC C	Cs7g10200

TCONS_00008580	162302,14	8,4242	1444	plasma membrane	ABC C	Cs7g10200
TCONS_00003487	90298,15	6,2127	807	plasma membrane	ABC C	Cs5g33060
TCONS_00003486	169310,85	7,6464	1513	plasma membrane	ABC C	Cs5g33060
TCONS_00003485	48814,36	7,1194	435	chloroplast	ABC C	Cs5g33060
TCONS_00001949	168678,36	7,849	1514	plasma membrane	ABC C	Cs1g02710
TCONS_00053511	57332,25	9,1375	513	cytosol	ABC D	Cs1g01510
TCONS_00053505	155020,14	9,3954	1384	plasma membrane	ABC D	Cs1g01510
TCONS_00053498	96849,32	7,3367	865	cytosol	ABC D	Cs1g01510
TCONS_00044211	88875,29	7,4742	788	chloroplast	ABC D	orange1.1t03223
TCONS_00044210	35136,86	7,4169	314	nucl_plas	ABC D	orange1.1t03223
TCONS_00044208	53120,39	6,0318	472	chloroplast	ABC D	orange1.1t03223
TCONS_00044207	58140,61	9,0197	510	peroxissome	ABC D	orange1.1t03223
TCONS_00044206	59869,57	5,4323	532	E.R.	ABC D	orange1.1t03223
TCONS_00025710	72131,23	7,9791	639	chloroplast_mitochondrial	ABC E	Cs6g19410
TCONS_00025709	37972,64	6,2521	335	cytosol	ABC E	Cs6g19410
TCONS_00057828	14732,98	10,6387	134	nucleus	ABC F	Cs9g09560
TCONS_00057755	17521,35	8,1524	158	golgi	ABC F	Cs1g13980
TCONS_00050492	83228,16	6,2344	747	cytosol	ABC F	Cs1g13980
TCONS_00047255	79816,03	7,9346	708	chloroplast	ABC F	orange1.1t04404
TCONS_00046735	66209,91	6,6092	593	cytosol	ABC F	Cs8g15910
TCONS_00018973	29364,85	8,145	266	mitochondria	ABC F	Cs5g01810
TCONS_00018972	12084,95	10,238	114	chloroplast	ABC F	Cs5g01810
TCONS_00094098	41685,77	6,4893	369	plasma membrane	ABC G	orange1.1t01993
TCONS_00094097	29178,53	7,8791	255	plasma membrane	ABC G	orange1.1t01993
TCONS_00094095	45512,18	6,8219	401	plasma membrane	ABC G	orange1.1t01993
TCONS_00089385	15598,15	5,5119	149	vacuole	ABC G	Cs1g01420
TCONS_00087505	26682,38	6,9439	233	plasma membrane	ABC G	Cs6g01131_a
TCONS_00087325	41403,15	5,8926	363	E.R.	ABC G	Cs6g01330

TCONS_00085441	132593,43	7,8679	1174	plasma membrane	ABC G	Cs5g13760
TCONS_00085440	18175,52	6,887	159	vacuole	ABC G	Cs5g13760
TCONS_00084950	86749,31	6,5015	775	plasma membrane	ABC G	Cs6g01330
TCONS_00084948	137934,65	6,5931	1218	plasma membrane	ABC G	Cs6g01330
TCONS_00084947	141227,66	6,6279	1247	plasma membrane	ABC G	Cs6g01330
TCONS_00083379	66930,45	9,2959	604	plasma membrane	ABC G	orange1.1t02544
TCONS_00082842	42303,44	9,0279	364	plasma membrane	ABC G	Cs6g02250
TCONS_00082841	17329,96	9,9551	149	nucleus	ABC G	Cs6g02250
TCONS_00082558	93748,86	9,3593	829	plasma membrane	ABC G	Cs1g13620
TCONS_00082557	58835,62	7,0814	521	cytosol	ABC G	Cs1g13620
TCONS_00081251	165085,24	8,2034	1458	plasma membrane	ABC G	Cs6g02210
TCONS_00080820	26350,81	9,8679	231	cytosol	ABC G	Cs6g02250
TCONS_00079758	46775,38	6,8769	422	plasma membrane	ABC G	Cs6g02250
TCONS_00079420	29858,47	9,0717	263	vacuole	ABC G	Cs6g05320
TCONS_00079419	81275,02	8,0374	737	plasma membrane	ABC G	Cs6g05280
TCONS_00079418	72483,81	8,092	651	plasma membrane	ABC G	Cs6g05270
TCONS_00076442	149230,7	7,7144	1326	plasma membrane	ABC G	Cs1g18920
TCONS_00076441	148195,03	7,9792	1311	plasma membrane	ABC G	Cs1g18930
TCONS_00076439	144892,13	7,7566	1283	plasma membrane	ABC G	Cs1g18930
TCONS_00076436	30907,98	10,1429	265	cytosol	ABC G	?
TCONS_00076220	144152,63	8,9493	1280	plasma membrane	ABC G	Cs5g13760
TCONS_00074289	95598,55	7,8067	846	plasma membrane	ABC G	Cs6g01130_a
TCONS_00072490	124041,34	8,8628	1111	plasma membrane	ABC G	Cs7g24870
TCONS_00071185	166799,14	8	1472	plasma membrane	ABC G	orange1.1t01531
TCONS_00070199	66615,51	8,7726	592	plasma membrane	ABC G	Cs6g05270
TCONS_00068834	13370,37	10,9972	122	cytosol	ABC G	orange1.1t02321_a
TCONS_00068831	37862,85	7,9148	330	plasma membrane	ABC G	orange1.1t02321
TCONS_00068828	41946,33	8,0557	376	mitochondria	ABC G	orange1.1t02321

TCONS_00068827	76953,72	8,2362	683	plasma membrane	ABC G	orange1.1t02321
TCONS_00068615	68722,2	9,2709	612	plasma membrane	ABC G	Cs7g24870_a
TCONS_00064966	49804,12	8,8014	449	golgi	ABC G	orange1.1t00127_a
TCONS_00064965	25345,04	7,3462	223	plasma membrane	ABC G	orange1.1t01996
TCONS_00064050	73309,61	8,6615	648	plasma membrane	ABC G	Cs1g09530
TCONS_00061978	148436,35	7,7382	1314	plasma membrane	ABC G	Cs1g15710
TCONS_00054535	55518,6	9,4559	493	plasma membrane	ABC G	Cs5g17290
TCONS_00054533	54966,21	8,2126	500	cytosol	ABC G	Cs5g17290
TCONS_00054528	79707,16	8,6803	715	plasma membrane	ABC G	Cs5g17290
TCONS_00053514	67987,7	6,2911	604	cytosol	ABC G	Cs1g01500
TCONS_00053513	37178,16	6,849	329	cytosol	ABC G	Cs1g01500
TCONS_00053089	67472,76	9,1039	605	plasma membrane	ABC G	Cs9g18660_a
TCONS_00050546	101744,58	9,5249	899	plasma membrane	ABC G	Cs1g13620
TCONS_00050545	164163,46	8,8657	1455	plasma membrane	ABC G	Cs1g13620
TCONS_00050544	160180,46	8,1096	1425	plasma membrane	ABC G	Cs1g13640
TCONS_00050541	159978,23	8,6815	1412	plasma membrane	ABC G	Cs1g13650
TCONS_00050539	148567,09	8,8585	1315	plasma membrane	ABC G	Cs1g13660
TCONS_00050538	162306,23	7,3781	1436	plasma membrane	ABC G	Cs1g13680
TCONS_00050536	163592,29	7,9602	1446	plasma membrane	ABC G	Cs1g13690
TCONS_00050535	162134,52	8,3761	1435	plasma membrane	ABC G	Cs1g13700
TCONS_00050532	164929,9	8,1443	1459	plasma membrane	ABC G	Cs1g13710
TCONS_00050530	111391,01	8,5203	993	plasma membrane	ABC G	Cs1g13720
TCONS_00050519	165990,72	8,3549	1469	plasma membrane	ABC G	Cs4g09130
TCONS_00050518	72409,85	7,2202	640	plasma membrane	ABC G	Cs1g13720
TCONS_00050517	150420,48	8,3174	1332	plasma membrane	ABC G	Cs1g13730
TCONS_00048605	76380,14	9,2969	674	plasma membrane	ABC G	Cs4g08300
TCONS_00046720	123969,03	8,822	1118	plasma membrane	ABC G	Cs8g16110
TCONS_00046616	80359,31	8,9366	723	plasma membrane	ABC G	Cs8g15960

TCONS_00046613	53455,62	8,9756	487	plasma membrane	ABC G	Cs8g15960
TCONS_00046612	77511	9,1194	697	plasma membrane	ABC G	Cs8g15960
TCONS_00046041	43833,54	8,0435	396	nucleus	ABC G	Cs1g19860
TCONS_00045285	164392,97	8,8255	1458	plasma membrane	ABC G	Cs6g15300
TCONS_00045282	110790,16	8,918	988	plasma membrane	ABC G	Cs6g15280
TCONS_00045281	159327,4	7,339	1403	plasma membrane	ABC G	orange1.1t01531
TCONS_00045278	100677,11	7,2409	889	plasma membrane	ABC G	Cs6g01330_a
TCONS_00045273	158528,42	7,0977	1403	plasma membrane	ABC G	Cs6g15300
TCONS_00044877	77939,37	9,6856	697	plasma membrane	ABC G	Cs2g30650
TCONS_00044875	73989,92	9,3344	661	plasma membrane	ABC G	Cs2g30650_a
TCONS_00044636	71045,37	7,8188	627	plasma membrane	ABC G	Cs5g08870
TCONS_00041816	94991,58	9,531	846	plasma membrane	ABC G	orange1.1t00127
TCONS_00040706	69007,7	9,431	610	plasma membrane	ABC G	Cs2g13730_a
TCONS_00038660	68983,76	9,1971	622	chloroplast	ABC G	Cs2g13730
TCONS_00034840	159924,72	9,1767	1427	plasma membrane	ABC G	Cs8g16470
TCONS_00034839	94000,45	9,4414	836	plasma membrane	ABC G	Cs8g16470
TCONS_00033842	45799,06	8,5341	406	plasma membrane	ABC G	Cs7g28610_a
TCONS_00033503	58962,31	9,9116	525	plasma membrane	ABC G	Cs7g28090
TCONS_00029271	77528,86	8,7514	698	golgi	ABC G	Cs7g12620
TCONS_00028866	85084,45	9,3389	772	plasma membrane	ABC G	?
TCONS_00028863	54444,1	8,2338	490	plasma membrane	ABC G	?
TCONS_00027801	60334,67	7,243	531	plasma membrane	ABC G	Cs1g20770_a
TCONS_00026533	122293,91	7,9901	1086	plasma membrane	ABC G	Cs9g01400
TCONS_00026527	45575,32	8,0846	397	cytosol	ABC G	Cs9g01400
TCONS_00026526	25722,7	10,3057	224	cytosol	ABC G	Cs9g01400
TCONS_00026525	119657,27	7,0831	1051	plasma membrane	ABC G	Cs9g01400
TCONS_00025723	70994,53	9,0574	637	plasma membrane	ABC G	Cs6g19470
TCONS_00024640	140163,24	8,5262	1250	plasma membrane	ABC G	Cs8g16470

TCONS_00022448	57413,25	8,6982	520	plasma membrane	ABC G	Cs1g06780
TCONS_00022447	35552,84	8,0065	309	plasma membrane	ABC G	Cs1g06780
TCONS_00022445	38000,1	8,3426	345	chloroplast	ABC G	Cs1g06780
TCONS_00021082	45553,87	10,0202	413	chloroplast	ABC G	Cs2g04080_a
TCONS_00014556	72039,37	9,8131	646	plasma membrane	ABC G	Cs1g20770
TCONS_00013641	161335,96	9,1147	1422	plasma membrane	ABC G	Cs4g17100
TCONS_00013639	101491,62	9,3168	893	plasma membrane	ABC G	Cs4g17100
TCONS_00012028	162300,73	7,0452	1436	plasma membrane	ABC G	Cs4g20440
TCONS_00005376	27256,27	7,9397	243	plasma membrane	ABC G	Cs3g21080
TCONS_00004136	75199,05	9,0489	679	plasma membrane	ABC G	Cs3g22340
TCONS_00001537	44936,87	7,1453	399	cytosol	ABC G	Cs5g33740
TCONS_00001499	22256,97	9,7118	198	nucleus	ABC G	orange1.1t01659
TCONS_00094695	16011,68	6,7221	146	cytosol	ABC I	Cs4g04420
TCONS_00080497	54738	7,0896	497	chloroplast	ABC I	Cs7g22890
TCONS_00067965	36406,82	6,9638	332	chloroplast	ABC I	Cs7g23800
TCONS_00067934	45051,76	4,3434	394	cytosol	ABC I	Cs7g23530
TCONS_00067050	23654,66	5,5354	199	chloroplast	ABC I	Cs5g33740_a
TCONS_00066524	87011,44	5,8905	791	plasma membrane	ABC I	Cs9g11110
TCONS_00064800	29884,54	7,4136	273	chloroplast	ABC I	Cs1g09070
TCONS_00064799	19497,76	9,619	177	chloroplast	ABC I	Cs1g09070
TCONS_00063142	39195,32	8,494	349	cytosol	ABC I	Cs6g06520
TCONS_00048155	27477,28	10,4245	245	chloroplast	ABC I	Cs4g01550
TCONS_00046520	32993,69	6,3034	294	nucleus	ABC I	Cs5g29600
TCONS_00046519	23299,67	5,9505	201	cytosol	ABC I	Cs5g29600
TCONS_00043579	22787,67	10,0709	206	vacuole	ABC I	Cs4g04420_a
TCONS_00043434	34979,9	7,246	317	plasma membrane	ABC I	Cs4g04420
TCONS_00040108	33348,38	9,8604	304	chloroplast	ABC I	Cs2g25590
TCONS_00040105	18404,9	10,7889	168	chloroplast	ABC I	Cs2g25590

TCONS_00034495	32847,23	10,5325	291	E.R.	ABC I	Cs7g09160_a
TCONS_00020726	62921,7	5,439	565	chloroplast	ABC I	Cs2g07970
TCONS_00001230	67732,03	4,9734	614	chloroplast	ABC I	orange1.1t01791

Transcript	Molecular		Sequence		Annotation	Subfamily	Putative Gene
	Weigh	Isoelectric Point	Lenght	Sublocalization			
TCONS_00050554	64111.66	10.0865	584	plasma membrane	Plastidic ATP/ADP	AATP	Cs1g13530
TCONS_00080566	47904.98	8.7492	442	plasma membrane	Anion	Anion	Cs6g07670
TCONS_00035116	58078.05	10.0500	533	chloroplast	Anion	Anion	Cs8g19810
TCONS_00033193	53111.68	6.6901	489	plasma membrane	Anion	Anion	Cs8g01190
TCONS_00023636	58006.20	9.4607	526	plasma membrane	Anion	Anion	Cs4g05170
TCONS_00023632	80151.32	5.1906	747	plasma membrane	Anion	Anion	Cs4g05170
TCONS_00023627	76808.37	5.3881	715	cytosol	Anion	Anion	Cs4g05170
TCONS_00023625	53190.22	4.8059	495	vacuole	Anion	Anion	Cs4g05170
TCONS_00000748	44855.05	9.5612	412	plasma membrane	Ascorbate	ASC	orange1.1t00376
TCONS_00000747	69186.39	9.2324	620	plasma membrane	Ascorbate	ASC	orange1.1t00376
TCONS_00000745	54291.40	9.6342	490	plasma membrane	Ascorbate	ASC	orange1.1t00376
TCONS_00084645	62349.91	10.0206	574	plasma membrane	Folate-Biopterin	FBT	Cs5g35030
TCONS_00069190	44647.85	9.4466	411	vacuole	Folate-Biopterin	FBT	Cs7g15410
TCONS_00041936	55065.03	10.2587	496	plasma membrane	Folate-Biopterin	FBT	Cs4g10690
TCONS_00034542	56388.42	7.7881	511	plasma membrane	Folate-Biopterin	FBT	Cs7g06530
TCONS_00034540	54750.77	8.7188	492	plasma membrane	Folate-Biopterin	FBT	Cs7g06540
TCONS_00034539	53060.91	8.6966	476	plasma membrane	Folate-Biopterin	FBT	Cs7g06540
TCONS_00034145	54711.45	5.2402	499	plasma membrane	Folate-Biopterin	FBT	Cs7g06580
TCONS_00021278	40658.16	4.9001	379	plasma membrane	Folate-Biopterin	FBT	Cs9g07150
TCONS_00021277	61865.69	8.2114	569	plasma membrane	Folate-Biopterin	FBT	Cs9g07150
TCONS_00052617	57942.40	9.2053	538	plasma membrane	Glycerol-3-phosphate	G3Pp	Cs5g07940
TCONS_00048249	54218.49	7.0189	499	plasma membrane	Glycerol-3-phosphate	G3Pp	Cs4g01150

TCONS_00037536	59172.52	9.0540	547	plasma membrane	Glycerol-3-phosphate	G3Pp	Cs9g14660
TCONS_00078018	54928.07	5.0839	511	plasma membrane	Inositol	INT	orange1.1t03682
TCONS_00078017	35324.40	5.7519	323	vacuole	Inositol	INT	orange1.1t03682
TCONS_00070943	24612.76	7.1867	227	plasma membrane	Inositol	INT	orange1.1t03682
TCONS_00070938	19476.51	5.5685	177	chloroplast	Inositol	INT	Cs7g20530
TCONS_00019980	63731.35	9.2529	586	plasma membrane	Inositol	INT	Cs2g08110
TCONS_00016856	62789.41	8.2940	581	plasma membrane	Inositol	INT	Cs2g02060
TCONS_00079647	57487.21	9.3174	530	plasma membrane	Nitrate	NPF	orange1.1t02415
TCONS_00055955	57942.40	9.2053	538	plasma membrane	Nitrate	NPF	Cs2g27650
TCONS_00046610	53994.25	6.4793	493	plasma membrane	Nitrate	NPF	Cs8g16000
TCONS_00093948	11507.44	4.2497	105	cytosol	Organic Cation/carnitine	OCT	Cs4g04930
TCONS_00093947	20449.15	5.0770	189	vacuole	Organic Cation/carnitine	OCT	Cs4g04930
TCONS_00093237	46214.88	9.7904	422	vacuole	Organic Cation/carnitine	OCT	Cs1g18890
TCONS_00091575	52470.82	8.5248	489	plasma membrane	Organic Cation/carnitine	OCT	Cs4g04960
TCONS_00044238	38710.20	4.7590	352	plasma membrane	Organic Cation/carnitine	OCT	orange1.1t03244
TCONS_00044237	49867.44	9.2545	457	plasma membrane	Organic Cation/carnitine	OCT	orange1.1t03245
TCONS_00044236	51921.51	8.7318	473	plasma membrane	Organic Cation/carnitine	OCT	orange1.1t03244
TCONS_00035355	50281.97	9.8426	460	plasma membrane	Organic Cation/carnitine	OCT	Cs8g20990
TCONS_00035354	78531.72	5.0690	736	plasma membrane	Organic Cation/carnitine	OCT	Cs8g20990
TCONS_00035353	46687.91	9.1259	427	plasma membrane	Organic Cation/carnitine	OCT	Cs8g20990
TCONS_00023595	65079.63	9.2476	584	vacuole	Organic Cation/carnitine	OCT	Cs4g04960
TCONS_00023588	69186.39	9.2324	620	plasma membrane	Organic Cation/carnitine	OCT	Cs4g04940
TCONS_00023587	46584.12	9.3293	413	plasma membrane	Organic Cation/carnitine	OCT	Cs4g04940
TCONS_00023584	78745.00	6.6601	704	plasma membrane	Organic Cation/carnitine	OCT	Cs4g04930
TCONS_00023577	70058.08	5.9581	619	vacuole	Organic Cation/carnitine	OCT	Cs4g04920
TCONS_00023567	27538.92	8.6440	255	vacuole	Organic Cation/carnitine	OCT	Cs4g04910
TCONS_00022996	58555.62	7.6381	539	plasma membrane	Organic Cation/carnitine	OCT	Cs4g12030
TCONS_00085488	25587.50	10.4829	231	plasma membrane	D-xylose-proton	Other	Cs5g24870

TCONS_00085487	56188.34	8.5209	523	plasma membrane	D-xylose-proton	Other	Cs5g24870
TCONS_00085486	27290.24	8.9826	252	plasma membrane	D-xylose-proton	Other	Cs5g24870
TCONS_00085485	28525.64	7.0525	259	endoplasmic reticulum	D-xylose-proton	Other	Cs5g24870
TCONS_00035153	58563.74	7.8722	539	plasma membrane	Sodium-dependent Phosphate	Other	Cs8g19980
TCONS_00035152	29663.34	9.4923	268	plasma membrane	Sodium-dependent Phosphate	Other	Cs8g19980
TCONS_00035149	56898.38	8.7905	519	plasma membrane	Sodium-dependent Phosphate	Other	Cs8g19980
TCONS_00035147	28856.39	9.1738	265	endoplasmic reticulum	Sodium-dependent Phosphate	Other	Cs8g19980
TCONS_00035005	60537.00	9.8988	559	chloroplast	D-xylose-proton	Other	Cs8g18970
TCONS_00034998	49308.64	9.2279	458	plasma membrane	D-xylose-proton	Other	Cs8g18970
TCONS_00080449	25266.33	8.6770	234	plasma membrane	Plastidic Glucose	pGlcT	Cs4g16110
TCONS_00080446	34604.22	6.7392	316	chloroplast	Plastidic Glucose	pGlcT	Cs4g16110
TCONS_00080442	54588.16	8.4681	504	endoplasmic reticulum	Plastidic Glucose	pGlcT	Cs4g16110
TCONS_00080437	39948.48	8.6022	364	plasma membrane	Plastidic Glucose	pGlcT	Cs4g16110
TCONS_00080434	59681.48	7.4355	547	plasma membrane	Plastidic Glucose	pGlcT	Cs4g16110
TCONS_00080432	57482.92	7.3998	526	plasma membrane	Plastidic Glucose	pGlcT	Cs4g16110
TCONS_00057315	32360.57	4.6924	299	plasma membrane	Plastidic Glucose	pGlcT	Cs2g20710
TCONS_00057312	59681.48	7.4355	547	plasma membrane	Plastidic Glucose	pGlcT	Cs2g20710
TCONS_00057311	60456.87	8.5433	558	plasma membrane	Plastidic Glucose	pGlcT	Cs2g20710
TCONS_00057305	26365.00	8.0920	243	plasma membrane	Plastidic Glucose	pGlcT	Cs2g20710
TCONS_00057304	40797.39	7.8636	372	plasma membrane	Plastidic Glucose	pGlcT	Cs2g20710
TCONS_00052823	67072.51	10.1052	622	plasma membrane	Plastidic Glucose	pGlcT	Cs1g15250
TCONS_00052822	44326.31	9.9976	420	plasma membrane	Plastidic Glucose	pGlcT	Cs1g15250
TCONS_00052820	42249.51	9.2611	401	plasma membrane	Plastidic Glucose	pGlcT	Cs1g15250
TCONS_00049032	67072.51	10.1052	622	plasma membrane	Plastidic Glucose	pGlcT	Cs6g18490
TCONS_00049025	59172.52	9.0540	547	chloroplast	Plastidic Glucose	pGlcT	Cs6g18490
TCONS_00049023	56360.41	8.9078	514	plasma membrane	Plastidic Glucose	pGlcT	Cs6g18490
TCONS_00063695	57461.27	7.7683	535	plasma membrane	Polyol	PMT	Cs4g15780
TCONS_00063694	58621.50	9.2732	541	plasma membrane	Polyol	PMT	Cs4g15770

TCONS_00032737	78531.72	5.0690	736	plasma membrane	Monosaccharide-sensing	PMT	Cs8g01220
TCONS_00020275	55711.14	5.9938	519	plasma membrane	Polyol	PMT	Cs2g06380
TCONS_00015117	31335.97	10.3404	285	plasma membrane	Polyol	PMT	Cs1g23890
TCONS_00006794	80151.32	5.1906	747	plasma membrane	Monosaccharide-sensing	PMT	Cs3g27610
TCONS_00006792	57576.63	5.2352	525	plasma membrane	Monosaccharide-sensing	PMT	Cs3g27610
TCONS_00006791	56239.69	7.2794	509	vacuole	Monosaccharide-sensing	PMT	Cs3g27610
TCONS_00095514	37362.12	6.4038	338	plasma membrane	Phosphate	PTH	Cs8g06780
TCONS_00054421	59451.34	8.1361	534	plasma membrane	Inorganic Phosphate	PTH	Cs9g18560
TCONS_00051661	56655.36	9.6122	520	plasma membrane	Phosphate	PTH	Cs9g10540
TCONS_00051658	57030.88	9.0777	519	plasma membrane	Inorganic Phosphate	PTH	Cs9g10530
TCONS_00046572	59253.94	8.9326	542	plasma membrane	Inorganic Phosphate	PTH	Cs5g29860
TCONS_00033621	44188.37	8.0427	402	plasma membrane	Inorganic Phosphate	PTH	Cs7g29450
TCONS_00006801	59714.57	8.7491	538	plasma membrane	Phosphate	PTH	Cs3g27660
TCONS_00040340	70058.08	5.9581	619	plasma membrane	SPX Domain	PTH5	Cs5g10180
TCONS_00002435	78745.00	6.6601	704	plasma membrane	SPX Domain	PTH5	orange1.1t00286
TCONS_00040338	35145.90	8.1386	324	plasma membrane	SPX Domain	PTH8	Cs5g10180
TCONS_00094087	17718.65	5.6301	162	plasma membrane	Sphingolipid	Spinster	Cs8g03150
TCONS_00080200	36297.97	6.9506	329	plasma membrane	Spinster	Spinster	Cs1g01440
TCONS_00032801	39484.82	9.8127	358	plasma membrane	Sphingolipid	Spinster	Cs8g03150
TCONS_00032800	31663.76	9.2530	283	plasma membrane	Sphingolipid	Spinster	Cs8g03150
TCONS_00013792	55268.53	6.0920	511	plasma membrane	Sphingolipid	Spinster	Cs1g20960
TCONS_00013791	59854.78	6.0936	555	plasma membrane	Sphingolipid	Spinster	Cs1g20960
TCONS_00013789	43218.56	7.8872	402	plasma membrane	Sphingolipid	Spinster	Cs1g20960
TCONS_00091023	56188.34	8.5209	523	plasma membrane	Sugar	STP	Cs7g13670
TCONS_00089296	32378.30	4.7276	305	vacuole	ERD6-like	STP	Cs3g12510
TCONS_00089291	24114.36	6.2618	224	vacuole	ERD6-like	STP	Cs3g12510
TCONS_00089290	15851.97	9.4787	141	vacuole	ERD6-like	STP	Cs3g12510
TCONS_00089289	15826.60	10.1332	140	vacuole	ERD6-like	STP	Cs3g12490

TCONS_00089288	14512.28	10.3399	127	vacuole	ERD6-like	STP	Cs3g12490
TCONS_00089287	17976.93	4.1788	170	vacuole	ERD6-like	STP	Cs3g12510
TCONS_00089286	10553.12	3.6463	106	extracellular space	ERD6-like	STP	Cs3g12500
TCONS_00087922	39182.79	4.9863	364	vacuole	Sugar	STP	orange1.1t03853
TCONS_00079572	37886.64	8.5662	343	plasma membrane	ERD6-like	STP	Cs3g12480
TCONS_00079571	35426.84	8.7952	323	plasma membrane	ERD6-like	STP	Cs3g12410
TCONS_00079564	33506.96	4.6451	312	plasma membrane	ERD6-like	STP	Cs3g12420
TCONS_00075160	35354.20	5.1028	335	vacuole	ERD6-like	STP	Cs3g12540
TCONS_00075157	51904.03	6.4758	488	vacuole	ERD6-like	STP	Cs3g12540
TCONS_00075156	26943.60	7.1075	249	chloroplast	ERD6-like	STP	Cs3g12540
TCONS_00075142	9660.60	7.1045	87	cytosol	ERD6-like	STP	Cs3g12510
TCONS_00075135	21854.92	9.5502	198	vacuole	ERD6-like	STP	Cs3g12510
TCONS_00075131	21252.06	8.6742	193	vacuole	ERD6-like	STP	Cs3g12510
TCONS_00075130	24761.96	6.6831	226	plasma membrane	ERD6-like	STP	Cs3g12520
TCONS_00075127	40277.71	9.2776	366	plasma membrane	ERD6-like	STP	Cs3g12520
TCONS_00075119	19638.09	9.3633	174	plasma membrane	ERD6-like	STP	Cs3g12510
TCONS_00075118	38016.95	8.8851	345	plasma membrane	ERD6-like	STP	Cs3g12520
TCONS_00068298	34159.84	9.2197	308	plasma membrane	ERD6-like	STP	Cs9g05220
TCONS_00035448	56360.41	8.9078	514	plasma membrane	Sugar	STP	orange1.1t03833
TCONS_00035137	49901.46	6.8871	458	plasma membrane	Sugar	STP	Cs8g19880
TCONS_00022196	38754.00	9.5455	355	plasma membrane	ERD6-like	STP	Cs9g05220
TCONS_00021958	47871.04	10.4165	435	plasma membrane	Sugar	STP	Cs9g06590
TCONS_00021957	57487.21	9.3174	530	plasma membrane	Sugar	STP	Cs9g06600
TCONS_00021368	58006.20	9.4607	526	plasma membrane	Sugar	STP	Cs9g06620
TCONS_00015182	37001.28	8.2215	339	plasma membrane	ERD6-like	STP	Cs1g24180
TCONS_00015175	53131.24	8.4353	490	plasma membrane	ERD6-like	STP	Cs1g24180
TCONS_00015174	26326.06	9.4997	242	plasma membrane	ERD6-like	STP	Cs1g24180
TCONS_00006219	55197.80	9.0178	506	plasma membrane	ERD6-like	STP	Cs3g24900

TCONS_00006214	25287.62	9.0791	230	plasma membrane	ERD6-like	STP	Cs3g24900
TCONS_00006212	34157.52	8.2489	316	plasma membrane	ERD6-like	STP	Cs3g24900
TCONS_00006209	34835.72	6.3963	321	plasma membrane	ERD6-like	STP	Cs3g24900
TCONS_00001908	14411.12	7.0042	133	vacuole	ERD6-like	STP	Cs5g32070
TCONS_00001907	54498.57	7.7054	506	plasma membrane	ERD6-like	STP	Cs5g32060

Table S4. MATE, ABC, and MFS expressed genes by *Citrus* spp., including gene duplication status, number of putative isoforms produced, and the annotation.

Gene ID	Duplication Status	Isoforms	Subfamily
Cs2g13500_m	Dispersed	1	MATE I
Cs2g31280	Dispersed	1	MATE I
Cs3g16650	Dispersed	1	MATE I
Cs5g06100	Dispersed	1	MATE I
Cs5g19630	Dispersed	1	MATE I
Cs5g20110_m	Dispersed	1	MATE I
Cs6g18150	WGD	1	MATE I
Cs2g13500	WGD	2	MATE I
orange1t00013	Singleton	2	MATE I
Cs6g18160	Tandem	1	MATE I
Cs1g07540	Tandem	2	MATE I
Cs2g13530	Tandem	2	MATE I
Cs6g18200	Tandem	3	MATE I
Cs1g07550	Tandem	4	MATE I
Cs2g13510	Tandem	4	MATE I
Cs5g21940	Dispersed	1	MATE II
Cs3g17670	WGD	1	MATE II
Cs1g20120	WGD	3	MATE II
Cs3g17660	WGD	3	MATE II
Cs1g20130	Tandem	2	MATE II
Cs3g24330	Dispersed	3	MATE II
Cs5g28190	Dispersed	3	MATE II
orange1t00390	Singleton	1	MATE II
Cs9g19420	Tandem	1	MATE II
Cs9g19430	Tandem	1	MATE II
Cs7g09190	Tandem	3	MATE II
Cs2g15610	Dispersed	1	MATE III
Cs2g08000	Dispersed	2	MATE III
Cs2g03200	WGD	1	MATE III
Cs2g21460	WGD	1	MATE III
Cs2g03220	Tandem	1	MATE III
Cs2g15120	Tandem	1	MATE III
Cs2g15080	Tandem	2	MATE III
Cs6g09270	Dispersed	2	MATE IV
Cs2g30270	WGD	2	MATE IV
Cs8g01660	WGD	2	MATE IV
Cs1g26350	WGD	3	MATE IV
orange1t03403	Singleton	2	MATE IV
Cs8g08480	Tandem	1	MATE IV
Cs8g08470	Tandem	3	MATE IV
Cs3g22600	Dispersed	1	MATE V

Cs4g15415_m	Dispersed	1	MATE V
Cs5g09710	Dispersed	1	MATE V
Cs9g04120	Dispersed	1	MATE V
Cs5g10270	WGD	1	MATE V
Cs7g16290_m	WGD	1	MATE V
Cs9g16870	WGD	1	MATE V
Cs6g09880	WGD	2	MATE V
Cs5g04110	Tandem	4	ABC A
Cs5g04120	Tandem	2	ABC A
orange1t02318	Singleton	2	ABC A
Cs1g08880	Dispersed	2	ABC B
Cs1g16850	Dispersed	1	ABC B
Cs2g04070	Tandem	1	ABC B
Cs2g04080	Tandem	3	ABC B
Cs2g04080_a	WGD	1	ABC B
Cs2g27440	WGD	4	ABC B
Cs3g09820	Tandem	1	ABC B
Cs3g26380	Singleton	3	ABC B
Cs4g11230	Dispersed	1	ABC B
Cs4g15420	Tandem	1	ABC B
Cs5g12150	Dispersed	2	ABC B
Cs6g06520	Dispersed	1	ABC B
Cs6g14480	Singleton	3	ABC B
Cs6g19410	Singleton	2	ABC B
Cs6g20270	Tandem	2	ABC B
Cs6g20280	Tandem	1	ABC B
Cs6g20290	Tandem	1	ABC B
Cs6g21110	Dispersed	1	ABC B
Cs7g09160	WGD	2	ABC B
Cs7g09730	Dispersed	1	ABC B
Cs7g28610	Dispersed	3	ABC B
Cs9g01170	Tandem	1	ABC B
Cs9g01170_a	Tandem	1	ABC B
Cs9g11040	Dispersed	1	ABC B
Cs9g16780	Dispersed	1	ABC B
orange1t00937	Singleton	1	ABC B
orange1t01769_a	Dispersed	1	ABC B
Cs1g02710	Dispersed	1	ABC C
Cs1g13700	Tandem	2	ABC C
Cs1g13720	Tandem	1	ABC C
Cs1g18450	Tandem	4	ABC C
Cs1g18460	Tandem	1	ABC C
Cs2g09550	Tandem	2	ABC C

Cs2g09560	Tandem	1	ABC C
Cs4g09120	Tandem	1	ABC C
Cs4g09130	Tandem	3	ABC C
Cs4g09140	Tandem	3	ABC C
Cs4g09150	Tandem	2	ABC C
Cs5g02710	WGD	2	ABC C
Cs5g28990	Dispersed	1	ABC C
Cs5g33060	Dispersed	3	ABC C
Cs7g10200	Dispersed	5	ABC C
Cs7g32530	Dispersed	1	ABC C
Cs9g18660	Tandem	3	ABC C
orange1t02765	Singleton	6	ABC C
Cs1g01510	Dispersed	3	ABC D
orange1t03223	Singleton	5	ABC D
Cs1g13980	Dispersed	2	ABC F
Cs5g01810	Dispersed	2	ABC F
Cs8g15910	Dispersed	1	ABC F
Cs9g09560	Dispersed	1	ABC F
orange1t04404	Singleton	1	ABC F
Cs1g09530	Dispersed	1	ABC G
Cs1g15710	Dispersed	1	ABC G
Cs1g20770	Dispersed	1	ABC G
Cs1g20770_a	Dispersed	1	ABC G
Cs2g13730	Dispersed	1	ABC G
Cs2g13730_a	Dispersed	1	ABC G
Cs3g21080	Dispersed	1	ABC G
Cs3g22340	Dispersed	1	ABC G
Cs4g08300	Dispersed	1	ABC G
Cs4g20440	Dispersed	1	ABC G
Cs5g08870	Dispersed	1	ABC G
Cs5g33740	Dispersed	1	ABC G
Cs1g13620	Tandem	4	ABC G
Cs1g13690	Tandem	1	ABC G
Cs5g17290	Dispersed	3	ABC G
Cs6g05320	Tandem	1	ABC G
Cs6g01130_a	Tandem	1	ABC G
Cs7g28090	Dispersed	1	ABC G
Cs1g13720	Tandem	3	ABC G
Cs6g01131_a	Tandem	1	ABC G
orange1t01659	Singleton	1	ABC G
Cs1g13680	Tandem	1	ABC G
Cs1g01420	WGD	1	ABC G
Cs6g15280	Tandem	1	ABC G

Cs6g01330_a	Tandem	1	ABC G
Cs7g24870	WGD	1	ABC G
orange1t01996	Singleton	1	ABC G
Cs9g01400	WGD	4	ABC G
Cs6g05280	Tandem	1	ABC G
Cs1g18930	Tandem	2	ABC G
Cs6g05270	Tandem	2	ABC G
Cs1g13660	Tandem	2	ABC G
Cs7g28610_a	Dispersed	1	ABC G
orange1t02544	Singleton	1	ABC G
Cs2g30650	Tandem	1	ABC G
Cs7g24870_a	Dispersed	1	ABC G
Cs7g12620	Dispersed	1	ABC G
Cs8g15960	Dispersed	3	ABC G
Cs1g13710	Tandem	1	ABC G
Cs1g18920	Tandem	1	ABC G
Cs9g18660_a	Dispersed	1	ABC G
orange1t00127	Singleton	1	ABC G
Cs1g06780	WGD	3	ABC G
Cs1g13650	Tandem	1	ABC G
orange1t01531	Singleton	2	ABC G
orange1t01993	Singleton	3	ABC G
orange1t00127_a	Dispersed	1	ABC G
Cs6g02210	WGD	1	ABC G
orange1t02321_a	Dispersed	1	ABC G
Cs1g19860	Tandem	1	ABC G
Cs8g16470	Dispersed	3	ABC G
Cs1g13730	Tandem	1	ABC G
Cs6g02250	Tandem	4	ABC G
orange1t02321	Singleton	3	ABC G
Cs1g13640	Tandem	1	ABC G
Cs1g01500	Dispersed	2	ABC G
Cs4g17100	Dispersed	2	ABC G
Cs6g15300	Tandem	2	ABC G
Cs8g16110	WGD	1	ABC G
Cs5g13760	Dispersed	3	ABC G
Cs6g19470	Dispersed	1	ABC G
Cs2g30650_a	Tandem	1	ABC G
Cs6g01330	Tandem	4	ABC G
Cs9g11110	Dispersed	1	ABC I
Cs4g01550	Dispersed	1	ABC I
Cs1g09070	Dispersed	2	ABC I
Cs2g25590	Dispersed	2	ABC I

Cs4g04420	Dispersed	2	ABC I
Cs5g29600	Dispersed	2	ABC I
Cs4g16980	WGD	1	ABC I
Cs7g23530	WGD	1	ABC I
Cs7g23800	Singleton	1	ABC I
orange1t01791	Singleton	1	ABC I
Cs5g33740_a	Tandem	1	ABC I
Cs4g04420_a	Dispersed	1	ABC I
Cs7g09160_a	Tandem	1	ABC I
Cs2g07970	Dispersed	1	ABC I
Cs7g22890	Dispersed	1	ABC I
Cs1g13530	Singleton	1	AATP
Cs4g05170	Dispersed	4	Anion
Cs6g07670	WGD	1	Anion
Cs8g01190	Dispersed	1	Anion
Cs8g19810	WGD	1	Anion
orange1.1t00376	Singleton	3	ASC
Cs4g10690	Dispersed	1	FBT
Cs5g35030	Dispersed	1	FBT
Cs7g06530	Tandem	1	FBT
Cs7g06540	Tandem	2	FBT
Cs7g06580	Tandem	1	FBT
Cs7g15410	Dispersed	1	FBT
Cs9g07150	Dispersed	2	FBT
Cs4g01150	Dispersed	1	G3Pp
Cs5g07940	Dispersed	1	G3Pp
Cs9g14660	Dispersed	1	G3Pp
Cs2g02060	Dispersed	1	INT
Cs2g08110	Dispersed	1	INT
Cs7g20530	Dispersed	1	INT
orange1.1t03682	Singleton	3	INT
Cs2g27650	WGD	1	NPF
Cs8g16000	Tandem	1	NPF
orange1.1t02415	Singleton	1	NPF
Cs1g18890	Dispersed	1	OCT
Cs4g04910	Tandem	1	OCT
Cs4g04920	Tandem	1	OCT
Cs4g04930	Tandem	3	OCT
Cs4g04940	Tandem	2	OCT
Cs4g04960	Tandem	2	OCT
Cs4g12030	Dispersed	1	OCT
Cs8g20990	Dispersed	3	OCT
orange1.1t03244	Singleton	2	OCT
orange1.1t03245	Singleton	1	OCT

Cs5g24870	Dispersed	4	Other
Cs8g18970	Dispersed	2	Other
Cs8g19980	Dispersed	4	Other
Cs1g15250	WGD	3	pGlcT
Cs2g20710	Dispersed	5	pGlcT
Cs4g16110	WGD	6	pGlcT
Cs6g18490	Dispersed	3	pGlcT
Cs1g23890	Dispersed	1	PMT
Cs2g06380	Dispersed	1	PMT
Cs3g27610	WGD	3	PMT
Cs4g15770	Tandem	1	PMT
Cs4g15780	Tandem	1	PMT
Cs8g01220	WGD	1	PMT
Cs3g27660	Dispersed	1	PTH
Cs5g29860	WGD	1	PTH
Cs7g29450	Dispersed	1	PTH
Cs8g06780	Dispersed	1	PTH
Cs9g10530	WGD	1	PTH
Cs9g10540	Tandem	1	PTH
Cs9g18560	Dispersed	1	PTH
Cs5g10180	Singleton	2	PTH5
orange1.1t00286	Singleton	1	PTH5
Cs1g01440	Tandem	1	Spinster
Cs1g20960	WGD	3	Spinster
Cs8g03150	WGD	3	Spinster
Cs1g24180	WGD	3	STP
Cs3g12410	WGD	1	STP
Cs3g12420	Tandem	1	STP
Cs3g12480	Tandem	1	STP
Cs3g12490	Tandem	2	STP
Cs3g12500	Tandem	1	STP
Cs3g12510	Tandem	8	STP
Cs3g12520	Tandem	3	STP
Cs3g12540	WGD	3	STP
Cs3g24900	WGD	4	STP
Cs5g32060	Tandem	1	STP
Cs5g32070	Tandem	1	STP
Cs7g13670	Dispersed	1	STP
Cs8g19880	Dispersed	1	STP
Cs9g05220	Dispersed	2	STP
Cs9g06590	Tandem	1	STP
Cs9g06600	Tandem	1	STP
Cs9g06620	Tandem	1	STP
orange1.1t03833	Singleton	1	STP
orange1.1t03853	Singleton	1	STP

Table S5. MATE, ABC, and MFS differentially expressed, Log₂FC values according to the time points after bacterial inoculation (HAI) and species, *p*-value, and annotation.

Transcript ID	Log ₂ FC	HAI	<i>p</i> -value	Subfamily
TCONS_00087169	-3.86	K72	0.03	MATE I
TCONS_00087168	-3.25	PR72	0.04	MATE I
TCONS_00087168	-3.75	K72	0.03	MATE I
TCONS_00077204	-2.88	K72	0.03	MATE IV
TCONS_00077202	-4.37	K72	0.01	MATE IV
TCONS_00077200	-2.93	K72	0.03	MATE IV
TCONS_00074259	5.68	K72	0.02	MATE IV
TCONS_00074258	-5.53	LG48	0.03	MATE IV
TCONS_00074258	4.41	K72	0.02	MATE IV
TCONS_00073445	-5.76	H48	0.05	MATE II
TCONS_00062153	-3.12	BA72	0.05	MATE I
TCONS_00062153	-3.35	PK48	0.03	MATE I
TCONS_00062153	-3.70	PK72	0.02	MATE I
TCONS_00062153	-3.92	PR48	0.02	MATE I
TCONS_00062153	-3.97	BA48	0.03	MATE I
TCONS_00062153	-4.86	PR72	0.01	MATE I
TCONS_00062153	-6.59	LG48	0.01	MATE I
TCONS_00062150	-3.08	BA72	0.04	MATE I
TCONS_00062150	-3.59	PR48	0.03	MATE I
TCONS_00062150	-3.64	PK72	0.02	MATE I
TCONS_00062150	-4.36	PR72	0.01	MATE I
TCONS_00062150	-4.37	PR24	0.03	MATE I
TCONS_00062150	-5.10	K48	0.04	MATE I
TCONS_00062150	-6.94	LG48	0.00	MATE I
TCONS_00053098	-3.71	PR48	0.04	MATE II
TCONS_00045960	-2.72	K72	0.03	MATE II
TCONS_00045960	-2.94	BA72	0.02	MATE II
TCONS_00045960	-3.00	K48	0.02	MATE II
TCONS_00045960	-3.87	LG48	0.00	MATE II
TCONS_00045960	-3.97	PR24	0.02	MATE II
TCONS_00045960	-4.05	K24	0.00	MATE II
TCONS_00045957	-2.66	PR48	0.05	MATE II
TCONS_00045957	-2.71	K72	0.03	MATE II
TCONS_00045957	-3.00	BA72	0.02	MATE II
TCONS_00045957	-3.09	K48	0.02	MATE II
TCONS_00045957	-3.98	PR24	0.02	MATE II
TCONS_00045957	-4.00	LG48	0.00	MATE II
TCONS_00045957	-4.23	K24	0.00	MATE II
TCONS_00042346	3.33	K72	0.02	MATE I
TCONS_00042345	3.23	K72	0.02	MATE I
TCONS_00041065	-2.63	PK72	0.05	MATE I

TCONS_00041065	-3.01	K72	0.04	MATE I
TCONS_00041065	-3.04	PR72	0.04	MATE I
TCONS_00040567	4.51	BA48	0.04	MATE I
TCONS_00040567	5.34	BA72	0.03	MATE I
TCONS_00038869	2.71	K48	0.05	MATE I
TCONS_00038869	3.61	BA48	0.01	MATE I
TCONS_00038869	3.67	PR48	0.03	MATE I
TCONS_00038869	5.26	BA72	0.00	MATE I
TCONS_00038869	5.33	PR72	0.00	MATE I
TCONS_00038868	2.68	K72	0.05	MATE I
TCONS_00038868	2.76	K48	0.04	MATE I
TCONS_00038868	3.04	H48	0.04	MATE I
TCONS_00038868	3.31	PR48	0.04	MATE I
TCONS_00038868	3.75	BA48	0.01	MATE I
TCONS_00038868	3.94	PR72	0.01	MATE I
TCONS_00038868	5.11	BA72	0.00	MATE I
TCONS_00038712	2.51	PK48	0.05	MATE I
TCONS_00038712	2.58	H72	0.04	MATE I
TCONS_00038709	2.54	PK48	0.04	MATE I
TCONS_00038709	2.55	H72	0.04	MATE I
TCONS_00038708	2.54	H72	0.04	MATE I
TCONS_00038708	2.55	PK48	0.04	MATE I
TCONS_00038707	2.50	PK48	0.04	MATE I
TCONS_00038707	2.51	H72	0.04	MATE I
TCONS_00027519	-2.80	S72	0.04	MATE IV
TCONS_00027519	-2.88	PR48	0.04	MATE IV
TCONS_00027519	-2.93	PK48	0.02	MATE IV
TCONS_00027519	-4.49	K72	0.01	MATE IV
TCONS_00027519	-5.86	PR24	0.00	MATE IV
TCONS_00027519	3.37	S48	0.02	MATE IV
TCONS_00027518	-2.84	S72	0.04	MATE IV
TCONS_00027518	-2.87	PR48	0.04	MATE IV
TCONS_00027518	-2.91	PK48	0.02	MATE IV
TCONS_00027518	-4.49	K72	0.01	MATE IV
TCONS_00027518	-5.91	PR24	0.00	MATE IV
TCONS_00027518	3.38	S48	0.02	MATE IV
TCONS_00020012	-2.98	LG72	0.04	MATE III
TCONS_00020012	-3.16	S48	0.05	MATE III
TCONS_00020012	-3.63	K24	0.03	MATE III
TCONS_00020012	-4.89	K72	0.05	MATE III
TCONS_00020012	-5.19	LG48	0.00	MATE III
TCONS_00020012	-5.35	K48	0.02	MATE III
TCONS_00016588	-3.01	PK48	0.05	MATE III

TCONS_00016588	-5.35	LG48	0.04	MATE III
TCONS_00016588	-7.11	K48	0.00	MATE III
TCONS_00016588	-7.46	K24	0.00	MATE III
TCONS_00011593	-2.99	LG24	0.03	MATE I
TCONS_00011593	3.08	PR48	0.03	MATE I
TCONS_00011593	3.20	H24	0.02	MATE I
TCONS_00011593	3.39	V48	0.02	MATE I
TCONS_00011593	3.55	H72	0.01	MATE I
TCONS_00011593	3.62	H48	0.01	MATE I
TCONS_00011593	3.81	K48	0.00	MATE I
TCONS_00011593	4.47	PR72	0.00	MATE I
TCONS_00011593	4.62	S48	0.00	MATE I
TCONS_00011593	5.04	PK72	0.00	MATE I
TCONS_00007405	2.59	LG48	0.04	MATE II
TCONS_00007404	2.59	LG48	0.04	MATE II
TCONS_00094098	-2.99	PR72	0.0235	ABC G
TCONS_00094098	2.89	H48	0.0197	ABC G
TCONS_00094098	3.17	PR48	0.0175	ABC G
TCONS_00094098	3.62	S24	0.0112	ABC G
TCONS_00094098	4.31	S48	0.0027	ABC G
TCONS_00094097	-3.04	PR72	0.0212	ABC G
TCONS_00094097	2.92	H48	0.0186	ABC G
TCONS_00094097	3.26	PR48	0.0144	ABC G
TCONS_00094097	3.34	S24	0.0187	ABC G
TCONS_00094097	4.34	S48	0.0025	ABC G
TCONS_00094095	-2.94	PR72	0.0257	ABC G
TCONS_00094095	2.91	H48	0.0189	ABC G
TCONS_00094095	3.26	PR48	0.0146	ABC G
TCONS_00094095	3.42	S24	0.0160	ABC G
TCONS_00094095	4.35	S48	0.0024	ABC G
TCONS_00093484	3.18	H24	0.0340	ABC C
TCONS_00093484	3.33	H72	0.0183	ABC C
TCONS_00093484	3.49	PR72	0.0429	ABC C
TCONS_00093484	3.59	H48	0.0144	ABC C
TCONS_00093484	3.64	PK48	0.0096	ABC C
TCONS_00093484	3.83	S48	0.0149	ABC C
TCONS_00093484	4.09	S72	0.0082	ABC C
TCONS_00093484	4.39	PR24	0.0106	ABC C
TCONS_00093484	6.50	V24	0.0176	ABC C
TCONS_00093292	-4.91	PR72	0.0202	ABC C
TCONS_00093292	-6.07	LG48	0.0287	ABC C
TCONS_00093292	5.23	K72	0.0484	ABC C
TCONS_00093291	-3.39	BA72	0.0423	ABC C
TCONS_00093291	-5.23	PR72	0.0085	ABC C

TCONS_00093291	−6.67	LG48	0.0095	ABC C
TCONS_00093291	6.09	K72	0.0123	ABC C
TCONS_00089868	−2.98	BA72	0.0499	ABC C
TCONS_00089868	−4.83	PR72	0.0051	ABC C
TCONS_00089868	−5.05	PK72	0.0019	ABC C
TCONS_00089868	−6.07	LG48	0.0116	ABC C
TCONS_00089868	5.33	K72	0.0204	ABC C
TCONS_00089867	−3.40	BA72	0.0280	ABC C
TCONS_00089867	−4.81	PR72	0.0055	ABC C
TCONS_00089867	−5.02	PK72	0.0021	ABC C
TCONS_00089867	−5.96	LG48	0.0142	ABC C
TCONS_00089867	5.43	K72	0.0181	ABC C
TCONS_00079419	4.48	K72	0.0010	ABC G
TCONS_00076962	−2.81	PR72	0.0354	ABC C
TCONS_00076962	−2.88	K72	0.0245	ABC C
TCONS_00076957	−2.79	PR72	0.0368	ABC C
TCONS_00076957	−2.87	K72	0.0249	ABC C
TCONS_00076952	−2.81	PR72	0.0353	ABC C
TCONS_00076952	−2.90	K72	0.0232	ABC C
TCONS_00076938	−2.83	K72	0.0264	ABC C
TCONS_00076938	−2.86	PR72	0.0323	ABC C
TCONS_00076933	−2.81	PR72	0.0358	ABC C
TCONS_00076933	−2.87	K72	0.0250	ABC C
TCONS_00076929	−2.78	PR72	0.0405	ABC C
TCONS_00076929	−2.84	K72	0.0295	ABC C
TCONS_00073525	3.40	LG72	0.0479	ABC B
TCONS_00072490	3.11	K72	0.0264	ABC G
TCONS_00072490	3.44	S48	0.0246	ABC G
TCONS_00070199	−4.56	PR48	0.0334	ABC G
TCONS_00068834	−3.54	H72	0.0154	ABC G
TCONS_00068834	−4.61	S48	0.0074	ABC G
TCONS_00068834	−5.00	K48	0.0408	ABC G
TCONS_00068834	−5.09	K72	0.0378	ABC G
TCONS_00068834	−5.42	PR72	0.0012	ABC G
TCONS_00068831	−2.44	PK24	0.0473	ABC G
TCONS_00068831	−2.52	LG72	0.0449	ABC G
TCONS_00068831	−2.72	H72	0.0285	ABC G
TCONS_00068831	−3.33	K24	0.0112	ABC G
TCONS_00068831	−3.86	S48	0.0056	ABC G
TCONS_00068831	−4.30	LG48	0.0040	ABC G
TCONS_00068831	−4.35	PK72	0.0011	ABC G
TCONS_00068831	−6.04	K72	0.0002	ABC G
TCONS_00068828	−2.53	H72	0.0414	ABC G
TCONS_00068828	−2.56	LG72	0.0435	ABC G
TCONS_00068828	−2.72	PK24	0.0303	ABC G

TCONS_00068828	−3.27	K24	0.0143	ABC G
TCONS_00068828	−3.67	S48	0.0088	ABC G
TCONS_00068828	−4.51	LG48	0.0040	ABC G
TCONS_00068828	−4.60	PK72	0.0007	ABC G
TCONS_00068828	−6.23	K72	0.0002	ABC G
TCONS_00068827	−2.51	H72	0.0429	ABC G
TCONS_00068827	−2.56	LG72	0.0432	ABC G
TCONS_00068827	−2.72	PK24	0.0297	ABC G
TCONS_00068827	−3.18	K24	0.0166	ABC G
TCONS_00068827	−3.65	S48	0.0091	ABC G
TCONS_00068827	−4.53	LG48	0.0038	ABC G
TCONS_00068827	−4.61	PK72	0.0007	ABC G
TCONS_00068827	−6.26	K72	0.0002	ABC G
TCONS_00066524	−2.77	K72	0.0300	ABC I
TCONS_00066524	−2.92	K48	0.0226	ABC I
TCONS_00064050	−2.97	H72	0.0396	ABC G
TCONS_00064050	−3.24	BA72	0.0269	ABC G
TCONS_00064050	−3.62	H48	0.0173	ABC G
TCONS_00064050	−3.70	PK48	0.0113	ABC G
TCONS_00064050	−3.80	PR48	0.0172	ABC G
TCONS_00064050	−4.05	PK72	0.0067	ABC G
TCONS_00064050	−5.19	PR72	0.0031	ABC G
TCONS_00064050	−5.34	PR24	0.0062	ABC G
TCONS_00064050	−6.68	K72	0.0034	ABC G
TCONS_00064050	−7.24	K48	0.0012	ABC G
TCONS_00064050	−7.48	K24	0.0004	ABC G
TCONS_00059566	−2.66	K24	0.0361	ABC B
TCONS_00059566	−3.88	BA72	0.0031	ABC B
TCONS_00059566	−4.10	PR72	0.0033	ABC B
TCONS_00059566	−4.38	LG48	0.0020	ABC B
TCONS_00059566	−4.45	K72	0.0016	ABC B
TCONS_00059566	−5.30	K48	0.0003	ABC B
TCONS_00059564	−2.69	K24	0.0339	ABC B
TCONS_00059564	−3.83	BA72	0.0034	ABC B
TCONS_00059564	−4.10	PR72	0.0033	ABC B
TCONS_00059564	−4.42	LG48	0.0018	ABC B
TCONS_00059564	−4.47	K72	0.0016	ABC B
TCONS_00059564	−5.06	K48	0.0005	ABC B
TCONS_00054535	−2.55	K48	0.0411	ABC G
TCONS_00054535	−2.71	K72	0.0315	ABC G
TCONS_00054535	−4.14	LG48	0.0023	ABC G
TCONS_00054533	−2.45	K72	0.0494	ABC G
TCONS_00054533	−2.60	K48	0.0377	ABC G
TCONS_00054533	−4.12	LG48	0.0024	ABC G
TCONS_00054528	−2.45	K72	0.0494	ABC G

TCONS_00054528	−2.59	K48	0.0379	ABC G
TCONS_00054528	−4.12	LG48	0.0024	ABC G
TCONS_00054315	2.44	K24	0.0452	ABC C
TCONS_00054315	2.48	K48	0.0427	ABC C
TCONS_00054311	2.39	K24	0.0498	ABC C
TCONS_00054311	2.47	K72	0.0439	ABC C
TCONS_00054311	2.52	K48	0.0399	ABC C
TCONS_00054310	2.41	K24	0.0484	ABC C
TCONS_00054310	2.61	K48	0.0349	ABC C
TCONS_00054310	2.61	K72	0.0348	ABC C
TCONS_00050544	−3.60	BA72	0.0047	ABC G
TCONS_00050544	−3.98	K48	0.0023	ABC G
TCONS_00050544	−4.21	PR72	0.0021	ABC G
TCONS_00050544	−4.57	LG48	0.0007	ABC G
TCONS_00050544	−4.95	K72	0.0003	ABC G
TCONS_00050530	2.77	K24	0.0238	ABC G
TCONS_00050519	2.76	K24	0.0241	ABC G
TCONS_00050518	2.77	K24	0.0238	ABC G
TCONS_00047255	−2.79	BA72	0.0230	ABC F
TCONS_00047255	−2.84	K72	0.0218	ABC F
TCONS_00047255	−3.07	K48	0.0139	ABC F
TCONS_00047255	−3.46	PK72	0.0063	ABC F
TCONS_00047255	−4.25	PR72	0.0019	ABC F
TCONS_00045285	−3.87	PR72	0.0154	ABC G
TCONS_00045282	−4.07	PR72	0.0107	ABC G
TCONS_00045281	3.03	K48	0.0157	ABC G
TCONS_00045281	3.11	PR72	0.0182	ABC G
TCONS_00045281	3.26	K24	0.0098	ABC G
TCONS_00045281	3.30	PK72	0.0090	ABC G
TCONS_00045281	3.39	BA72	0.0074	ABC G
TCONS_00045281	4.03	PR24	0.0052	ABC G
TCONS_00045278	3.12	PK72	0.0125	ABC G
TCONS_00045273	−2.43	K72	0.0460	ABC G
TCONS_00044877	−2.59	K24	0.0384	ABC G
TCONS_00044877	−2.95	BA72	0.0183	ABC G
TCONS_00044877	−3.40	PR72	0.0118	ABC G
TCONS_00044877	−4.34	K72	0.0018	ABC G
TCONS_00044877	−6.18	LG48	0.0001	ABC G
TCONS_00044211	−2.72	PR72	0.0401	ABC D
TCONS_00044211	−2.99	K72	0.0199	ABC D
TCONS_00044211	−3.28	K48	0.0113	ABC D
TCONS_00044210	−2.60	PR72	0.0490	ABC D
TCONS_00044210	−2.63	PK72	0.0344	ABC D
TCONS_00044210	−3.02	K72	0.0186	ABC D
TCONS_00044210	−3.16	K48	0.0140	ABC D

TCONS_00044208	−2.46	K24	0.0484	ABC D
TCONS_00044208	−2.65	PR72	0.0450	ABC D
TCONS_00044208	−2.65	PK72	0.0332	ABC D
TCONS_00044208	−3.15	K72	0.0146	ABC D
TCONS_00044208	−3.20	K48	0.0128	ABC D
TCONS_00044207	−2.59	PR72	0.0495	ABC D
TCONS_00044207	−2.62	PK72	0.0353	ABC D
TCONS_00044207	−3.02	K72	0.0184	ABC D
TCONS_00044207	−3.18	K48	0.0135	ABC D
TCONS_00044206	−2.60	PK72	0.0360	ABC D
TCONS_00044206	−2.61	PR72	0.0479	ABC D
TCONS_00044206	−3.09	K72	0.0160	ABC D
TCONS_00044206	−3.22	K48	0.0121	ABC D
TCONS_00043434	−3.05	K72	0.0470	ABC I
TCONS_00043255	3.22	PK24	0.0262	ABC C
TCONS_00043255	3.28	BA72	0.0278	ABC C
TCONS_00043255	3.40	H24	0.0318	ABC C
TCONS_00043255	3.94	PK72	0.0101	ABC C
TCONS_00043255	4.01	PK48	0.0073	ABC C
TCONS_00043255	4.21	S72	0.0100	ABC C
TCONS_00043254	2.57	BA24	0.0380	ABC C
TCONS_00043254	2.62	H72	0.0328	ABC C
TCONS_00043254	2.89	H24	0.0309	ABC C
TCONS_00043254	2.97	BA48	0.0277	ABC C
TCONS_00043254	3.05	H48	0.0147	ABC C
TCONS_00043254	3.20	BA72	0.0108	ABC C
TCONS_00043254	3.34	S24	0.0194	ABC C
TCONS_00043254	3.34	S48	0.0168	ABC C
TCONS_00043254	3.95	PK48	0.0023	ABC C
TCONS_00043254	4.03	PK24	0.0020	ABC C
TCONS_00043254	4.22	PK72	0.0014	ABC C
TCONS_00043254	4.42	S72	0.0017	ABC C
TCONS_00043253	2.69	H72	0.0296	ABC C
TCONS_00043253	2.96	BA48	0.0289	ABC C
TCONS_00043253	2.96	H24	0.0278	ABC C
TCONS_00043253	3.04	H48	0.0154	ABC C
TCONS_00043253	3.44	S24	0.0175	ABC C
TCONS_00043253	3.46	S48	0.0141	ABC C
TCONS_00043253	3.50	BA72	0.0062	ABC C
TCONS_00043253	3.88	PK72	0.0029	ABC C
TCONS_00043253	3.98	PK48	0.0023	ABC C
TCONS_00043253	4.08	PK24	0.0019	ABC C
TCONS_00043253	4.43	S72	0.0018	ABC C
TCONS_00043252	2.61	H72	0.0332	ABC C
TCONS_00043252	2.67	BA24	0.0321	ABC C

TCONS_00043252	2.89	H24	0.0310	ABC C
TCONS_00043252	2.95	BA48	0.0288	ABC C
TCONS_00043252	3.03	H48	0.0152	ABC C
TCONS_00043252	3.16	BA72	0.0116	ABC C
TCONS_00043252	3.32	S48	0.0175	ABC C
TCONS_00043252	3.34	S24	0.0196	ABC C
TCONS_00043252	3.94	PK48	0.0023	ABC C
TCONS_00043252	4.12	PK24	0.0017	ABC C
TCONS_00043252	4.22	PK72	0.0014	ABC C
TCONS_00043252	4.38	S72	0.0018	ABC C
TCONS_00043251	2.48	BA24	0.0452	ABC C
TCONS_00043251	2.65	PR72	0.0417	ABC C
TCONS_00043251	2.98	S48	0.0311	ABC C
TCONS_00043251	3.17	PK72	0.0116	ABC C
TCONS_00043251	3.19	PK24	0.0112	ABC C
TCONS_00043251	3.30	PR24	0.0214	ABC C
TCONS_00043251	3.31	V48	0.0192	ABC C
TCONS_00043251	3.55	V24	0.0130	ABC C
TCONS_00043251	3.56	H24	0.0091	ABC C
TCONS_00043251	3.71	H48	0.0038	ABC C
TCONS_00043251	3.80	BA72	0.0032	ABC C
TCONS_00043251	4.80	PK48	0.0004	ABC C
TCONS_00043251	5.03	S72	0.0005	ABC C
TCONS_00043250	2.49	H72	0.0438	ABC C
TCONS_00043250	2.61	PK72	0.0360	ABC C
TCONS_00043250	2.83	PK24	0.0239	ABC C
TCONS_00043250	2.98	V24	0.0424	ABC C
TCONS_00043250	3.17	V48	0.0279	ABC C
TCONS_00043250	3.17	PR24	0.0304	ABC C
TCONS_00043250	3.42	S48	0.0157	ABC C
TCONS_00043250	3.62	H24	0.0087	ABC C
TCONS_00043250	3.71	H48	0.0044	ABC C
TCONS_00043250	3.72	BA72	0.0042	ABC C
TCONS_00043250	4.63	PK48	0.0006	ABC C
TCONS_00043250	4.96	S72	0.0006	ABC C
TCONS_00043249	2.99	PK24	0.0369	ABC C
TCONS_00043249	3.51	PK72	0.0341	ABC C
TCONS_00043249	3.77	PK48	0.0191	ABC C
TCONS_00043249	3.83	H72	0.0248	ABC C
TCONS_00043249	4.56	H48	0.0149	ABC C
TCONS_00043249	5.04	S72	0.0070	ABC C
TCONS_00041816	6.05	LG48	0.0299	ABC G
TCONS_00038660	−2.42	BA72	0.0476	ABC G
TCONS_00038660	−3.24	K72	0.0118	ABC G
TCONS_00038660	−3.29	K48	0.0105	ABC G

TCONS_00034840	−2.63	LG72	0.0470	ABC G
TCONS_00034840	3.52	PR72	0.0151	ABC G
TCONS_00034840	5.53	BA72	0.0002	ABC G
TCONS_00034840	5.59	K72	0.0003	ABC G
TCONS_00034839	−2.65	LG72	0.0458	ABC G
TCONS_00034839	3.88	PR72	0.0085	ABC G
TCONS_00034839	5.55	BA72	0.0002	ABC G
TCONS_00034839	5.71	K72	0.0002	ABC G
TCONS_00029271	4.15	K48	0.0059	ABC G
TCONS_00029271	5.41	K72	0.0007	ABC G
TCONS_00028866	−2.77	BA72	0.0263	ABC G
TCONS_00028866	−2.94	K72	0.0234	ABC G
TCONS_00028866	−2.97	K48	0.0213	ABC G
TCONS_00028866	−4.83	PR72	0.0008	ABC G
TCONS_00028866	−5.27	K24	0.0003	ABC G
TCONS_00028863	−2.73	BA72	0.0290	ABC G
TCONS_00028863	−2.93	K48	0.0238	ABC G
TCONS_00028863	−3.23	K72	0.0146	ABC G
TCONS_00028863	−4.99	PR72	0.0006	ABC G
TCONS_00028863	−5.21	K24	0.0003	ABC G
TCONS_00026533	−3.31	K48	0.0116	ABC G
TCONS_00026527	−3.38	K48	0.0100	ABC G
TCONS_00026526	−3.36	K48	0.0104	ABC G
TCONS_00026525	−3.37	K48	0.0101	ABC G
TCONS_00025857	−3.53	PK72	0.0114	ABC B
TCONS_00025857	−4.58	LG48	0.0060	ABC B
TCONS_00025857	−5.60	PR72	0.0007	ABC B
TCONS_00025857	−6.25	K48	0.0046	ABC B
TCONS_00025856	−2.77	PK72	0.0282	ABC B
TCONS_00025856	−2.99	LG72	0.0206	ABC B
TCONS_00025856	−4.61	K24	0.0022	ABC B
TCONS_00025856	−6.12	K48	0.0003	ABC B
TCONS_00025855	−2.93	PK72	0.0218	ABC B
TCONS_00025855	−3.05	LG72	0.0193	ABC B
TCONS_00025855	−4.15	K24	0.0057	ABC B
TCONS_00025855	−5.48	K48	0.0012	ABC B
TCONS_00025854	−3.14	LG72	0.0186	ABC B
TCONS_00025854	−3.20	PK72	0.0152	ABC B
TCONS_00025854	−4.14	K24	0.0056	ABC B
TCONS_00025854	−6.45	LG48	0.0002	ABC B
TCONS_00025854	−7.87	K48	0.0001	ABC B
TCONS_00025723	−3.96	K24	0.0106	ABC G
TCONS_00025723	−5.61	PR72	0.0008	ABC G
TCONS_00025723	−6.78	K48	0.0002	ABC G
TCONS_00025723	−8.14	K72	0.0002	ABC G

TCONS_00025446	2.58	PK72	0.0423	ABC B
TCONS_00025446	3.36	LG48	0.0120	ABC B
TCONS_00022448	−3.52	PR72	0.0275	ABC G
TCONS_00022448	3.72	H24	0.0212	ABC G
TCONS_00022447	−3.60	PR72	0.0222	ABC G
TCONS_00022447	3.85	H24	0.0156	ABC G
TCONS_00022445	−3.61	PR72	0.0196	ABC G
TCONS_00022445	3.82	H24	0.0146	ABC G
TCONS_00020556	−5.21	K72	0.0002	ABC C
TCONS_00020556	3.77	LG48	0.0040	ABC C
TCONS_00020549	−4.74	K72	0.0007	ABC C
TCONS_00020549	3.43	LG48	0.0085	ABC C
TCONS_00019252	2.79	PK72	0.0251	ABC A
TCONS_00019252	4.22	LG48	0.0015	ABC A
TCONS_00019248	2.79	PK72	0.0254	ABC A
TCONS_00019248	4.28	LG48	0.0013	ABC A
TCONS_00018550	2.75	S72	0.0417	ABC A
TCONS_00018550	3.09	LG48	0.0149	ABC A
TCONS_00018548	2.80	S72	0.0378	ABC A
TCONS_00018548	3.35	LG48	0.0088	ABC A
TCONS_00018546	2.81	S72	0.0371	ABC A
TCONS_00018546	3.32	LG48	0.0091	ABC A
TCONS_00018545	2.80	S72	0.0376	ABC A
TCONS_00018545	3.37	LG48	0.0084	ABC A
TCONS_00015584	−2.70	PR48	0.0482	ABC B
TCONS_00015584	−2.91	BA48	0.0332	ABC B
TCONS_00015584	−2.92	H48	0.0223	ABC B
TCONS_00015582	−2.69	PR48	0.0493	ABC B
TCONS_00015582	−2.90	BA48	0.0338	ABC B
TCONS_00015582	−2.91	H48	0.0228	ABC B
TCONS_00013641	−2.62	K24	0.0368	ABC G
TCONS_00013641	−2.90	BA48	0.0295	ABC G
TCONS_00013641	−2.90	K48	0.0223	ABC G
TCONS_00013641	−3.09	K72	0.0165	ABC G
TCONS_00013641	−3.13	PR72	0.0193	ABC G
TCONS_00013641	−3.38	PK48	0.0076	ABC G
TCONS_00013641	−3.66	BA72	0.0045	ABC G
TCONS_00013641	−3.84	H24	0.0048	ABC G
TCONS_00013641	−4.21	H48	0.0015	ABC G
TCONS_00013641	−4.58	PR48	0.0013	ABC G
TCONS_00013641	−5.51	PR24	0.0013	ABC G
TCONS_00013639	−2.57	K24	0.0400	ABC G
TCONS_00013639	−2.87	BA48	0.0308	ABC G
TCONS_00013639	−2.87	K48	0.0233	ABC G
TCONS_00013639	−3.09	K72	0.0162	ABC G

TCONS_00013639	−3.14	PR72	0.0190	ABC G
TCONS_00013639	−3.39	PK48	0.0075	ABC G
TCONS_00013639	−3.69	BA72	0.0042	ABC G
TCONS_00013639	−3.86	H24	0.0046	ABC G
TCONS_00013639	−4.23	H48	0.0014	ABC G
TCONS_00013639	−4.57	PR48	0.0013	ABC G
TCONS_00013639	−5.57	PR24	0.0012	ABC G
TCONS_00008590	2.88	H72	0.0219	ABC C
TCONS_00008590	3.29	K48	0.0139	ABC C
TCONS_00008590	3.47	PR72	0.0140	ABC C
TCONS_00008590	3.52	H48	0.0064	ABC C
TCONS_00008590	3.63	PK24	0.0051	ABC C
TCONS_00008590	3.90	S72	0.0054	ABC C
TCONS_00008590	4.14	K72	0.0028	ABC C
TCONS_00008590	4.86	K24	0.0009	ABC C
TCONS_00008583	2.58	H72	0.0353	ABC C
TCONS_00008583	2.84	PR72	0.0324	ABC C
TCONS_00008583	3.28	PK24	0.0093	ABC C
TCONS_00008583	3.38	K48	0.0090	ABC C
TCONS_00008583	3.68	H48	0.0041	ABC C
TCONS_00008583	3.85	S72	0.0053	ABC C
TCONS_00008583	4.47	K72	0.0010	ABC C
TCONS_00008583	4.94	K24	0.0004	ABC C
TCONS_00008582	2.53	H72	0.0382	ABC C
TCONS_00008582	2.82	PR72	0.0333	ABC C
TCONS_00008582	3.28	PK24	0.0094	ABC C
TCONS_00008582	3.44	K48	0.0081	ABC C
TCONS_00008582	3.71	H48	0.0039	ABC C
TCONS_00008582	3.87	S72	0.0051	ABC C
TCONS_00008582	4.35	K72	0.0013	ABC C
TCONS_00008582	4.98	K24	0.0004	ABC C
TCONS_00008581	2.62	H72	0.0329	ABC C
TCONS_00008581	2.99	PR72	0.0253	ABC C
TCONS_00008581	3.29	PK24	0.0091	ABC C
TCONS_00008581	3.42	K48	0.0086	ABC C
TCONS_00008581	3.72	H48	0.0038	ABC C
TCONS_00008581	3.87	S72	0.0051	ABC C
TCONS_00008581	4.33	K72	0.0014	ABC C
TCONS_00008581	4.93	K24	0.0004	ABC C
TCONS_00008580	2.60	H72	0.0339	ABC C
TCONS_00008580	2.83	PR72	0.0326	ABC C
TCONS_00008580	3.28	PK24	0.0094	ABC C
TCONS_00008580	3.41	K48	0.0086	ABC C
TCONS_00008580	3.69	H48	0.0041	ABC C
TCONS_00008580	3.85	S72	0.0053	ABC C

TCONS_00008580	4.40	K72	0.0012	ABC C
TCONS_00008580	5.04	K24	0.0004	ABC C
TCONS_00006540	−2.77	BA48	0.0367	ABC B
TCONS_00006540	−2.97	H48	0.0176	ABC B
TCONS_00006540	−3.16	K24	0.0135	ABC B
TCONS_00006540	−3.46	PR48	0.0117	ABC B
TCONS_00006540	−3.89	H24	0.0043	ABC B
TCONS_00006540	−4.08	PK48	0.0018	ABC B
TCONS_00006540	−4.12	BA72	0.0017	ABC B
TCONS_00006540	−4.21	PR72	0.0024	ABC B
TCONS_00006540	−4.26	PR24	0.0121	ABC B
TCONS_00006540	−4.30	K72	0.0017	ABC B
TCONS_00006540	−4.40	LG48	0.0022	ABC B
TCONS_00006540	−4.82	K48	0.0006	ABC B
TCONS_00006539	−2.78	BA48	0.0363	ABC B
TCONS_00006539	−2.99	H48	0.0171	ABC B
TCONS_00006539	−3.13	K24	0.0144	ABC B
TCONS_00006539	−3.47	PR48	0.0114	ABC B
TCONS_00006539	−3.88	H24	0.0044	ABC B
TCONS_00006539	−4.09	PK48	0.0018	ABC B
TCONS_00006539	−4.12	BA72	0.0017	ABC B
TCONS_00006539	−4.20	PR72	0.0025	ABC B
TCONS_00006539	−4.26	PR24	0.0121	ABC B
TCONS_00006539	−4.31	K72	0.0017	ABC B
TCONS_00006539	−4.40	LG48	0.0022	ABC B
TCONS_00006539	−4.84	K48	0.0006	ABC B
TCONS_00006535	−2.76	BA48	0.0380	ABC B
TCONS_00006535	−2.96	H48	0.0182	ABC B
TCONS_00006535	−3.11	K24	0.0149	ABC B
TCONS_00006535	−3.47	PR48	0.0115	ABC B
TCONS_00006535	−3.93	H24	0.0040	ABC B
TCONS_00006535	−4.09	PK48	0.0018	ABC B
TCONS_00006535	−4.09	BA72	0.0018	ABC B
TCONS_00006535	−4.16	PR72	0.0027	ABC B
TCONS_00006535	−4.22	K72	0.0020	ABC B
TCONS_00006535	−4.25	PR24	0.0123	ABC B
TCONS_00006535	−4.70	K48	0.0008	ABC B
TCONS_00006535	−5.02	LG48	0.0009	ABC B
TCONS_00003170	2.68	H48	0.0320	ABC B
TCONS_00003170	2.72	PR48	0.0419	ABC B
TCONS_00003170	2.80	S72	0.0378	ABC B
TCONS_00003170	2.88	LG48	0.0211	ABC B
TCONS_00003170	2.92	V48	0.0438	ABC B
TCONS_00003170	2.95	H24	0.0288	ABC B
TCONS_00003170	3.17	H72	0.0122	ABC B

TCONS_00003170	3.23	PK72	0.0110	ABC B
TCONS_00003170	3.39	BA48	0.0138	ABC B
TCONS_00003170	3.51	K72	0.0067	ABC B
TCONS_00003170	3.63	PK48	0.0048	ABC B
TCONS_00003170	3.82	K24	0.0034	ABC B
TCONS_00003170	3.93	PR72	0.0040	ABC B
TCONS_00003170	4.58	K48	0.0007	ABC B
TCONS_00003170	5.20	BA72	0.0002	ABC B
TCONS_00001949	−3.74	K72	0.0068	ABC C
TCONS_00001949	2.52	PK72	0.0461	ABC C
TCONS_00001537	−3.86	BA72	0.0409	ABC G
TCONS_00001537	−4.30	PR48	0.0317	ABC G
TCONS_00001537	−4.60	H24	0.0324	ABC G
TCONS_00001537	−4.72	PK48	0.0056	ABC G
TCONS_00001537	−5.50	PR72	0.0129	ABC G
TCONS_00093948	3.98	LG48	0,02	OCT
TCONS_00093947	4.25	LG48	0,01	OCT
TCONS_00091575	-2.72	LG48	0,04	OCT
TCONS_00055955	-4.89	LG48	0,01	NPF
TCONS_00055955	-5.94	PK48	0,00	NPF
TCONS_00055955	-3.91	PR48	0,01	NPF
TCONS_00044238	-6.58	K48	0,00	OCT
TCONS_00044238	-4.28	PR72	0,01	OCT
TCONS_00035448	3.72	BA48	0,01	STP
TCONS_00035448	3.83	BA72	0,00	STP
TCONS_00035448	2.56	H48	0,04	STP
TCONS_00035448	2.51	H72	0,04	STP
TCONS_00035448	4.50	K48	0,00	STP
TCONS_00035448	4.44	K72	0,00	STP
TCONS_00035448	3.74	PK48	0,00	STP
TCONS_00035448	2.84	PK72	0,02	STP
TCONS_00035448	2.65	PR48	0,04	STP
TCONS_00035448	3.99	PR72	0,00	STP
TCONS_00035153	-2.95	K48	0,02	Other
TCONS_00035153	-2.87	K72	0,03	Other
TCONS_00035152	-2.95	K48	0,02	Other
TCONS_00035152	-3.02	K72	0,02	Other
TCONS_00035149	-2.93	K48	0,02	Other
TCONS_00035149	-2.87	K72	0,03	Other
TCONS_00035147	-2.91	K48	0,03	Other
TCONS_00035147	-2.91	K72	0,03	Other
TCONS_00034998	-2.78	K48	0,03	D-xylose-proton
TCONS_00023636	-3.52	K72	0,01	Anion
TCONS_00023632	-3.81	K72	0,01	Anion

TCONS_00023627	-3.75	K72	0,01	Anion
TCONS_00023625	-3.87	K72	0,01	Anion
TCONS_00023595	-2.77	LG48	0,04	OCT
TCONS_00023584	3.46	LG48	0,02	OCT
TCONS_00023577	3.28	K72	0,01	OCT
TCONS_00022996	3.45	K48	0,02	OCT
TCONS_00022996	3.70	K72	0,01	OCT
TCONS_00022996	2.98	PR72	0,05	OCT
TCONS_00021368	2.60	K72	0,03	STP
TCONS_00021368	3.01	S72	0,02	STP
TCONS_00002435	4.09	LG24	0,03	PTH5
TCONS_00002435	-3.63	PR72	0,05	PTH5
TCONS_00000748	-2.83	PR48	0,04	ASC
TCONS_00000748	-3.67	PR72	0,01	ASC
TCONS_00000747	-2.47	BA72	0,05	ASC
TCONS_00000747	-2.87	PR48	0,04	ASC
TCONS_00000747	-3.55	PR72	0,01	ASC
TCONS_00000745	-2.45	BA72	0,05	ASC
TCONS_00000745	-2.87	PR48	0,04	ASC
TCONS_00000745	-3.45	PR72	0,01	ASC
