

Supplemental information to the manuscript:

Transcriptomic analysis of a classical model of carbon catabolic regulation in *Streptomyces coelicolor*

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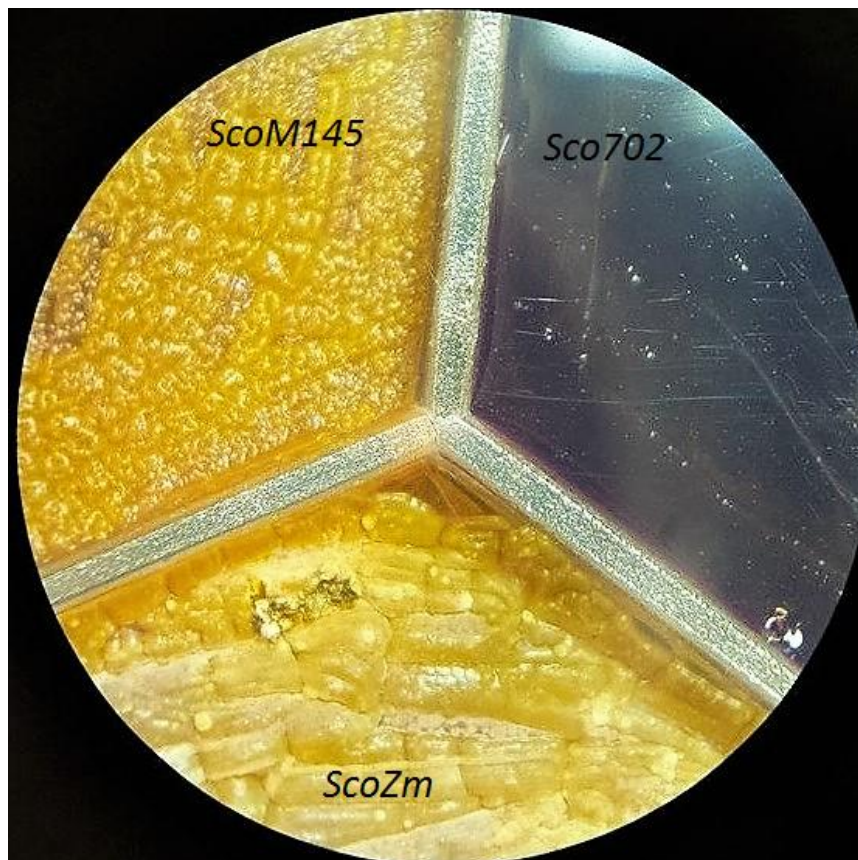


Figure S1. Qualitative visualization of Glk activity on BPG Agar medium after 48 h incubation. Strains: ScoM145, ScoZm (Δ scoglk/glk from *Z. mobilis*) and Sco702 (Δ glk).

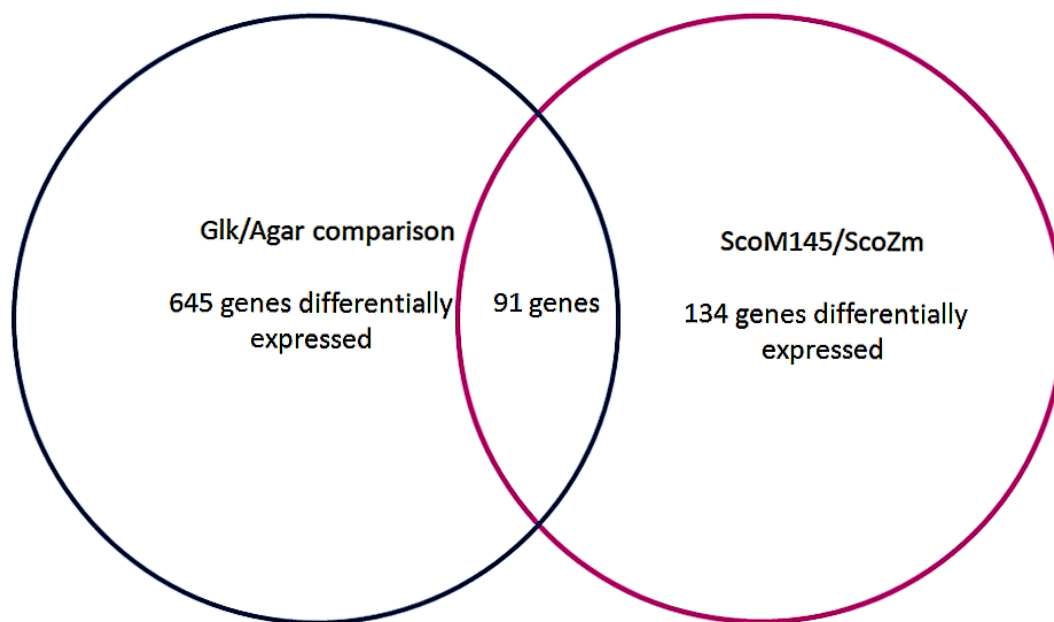


Fig. S2. Diagram summarizing the microarrays output and its intersection. In the Glc/Agar comparison, 91 differentially expressed genes were detected, while in the Glc response (ScoM145/ScoZm), 134 differentially expressed genes were identified. From the total of differentially expressed genes in *ScoM145/ScoZm*, 91 were included in Glc/Agar.

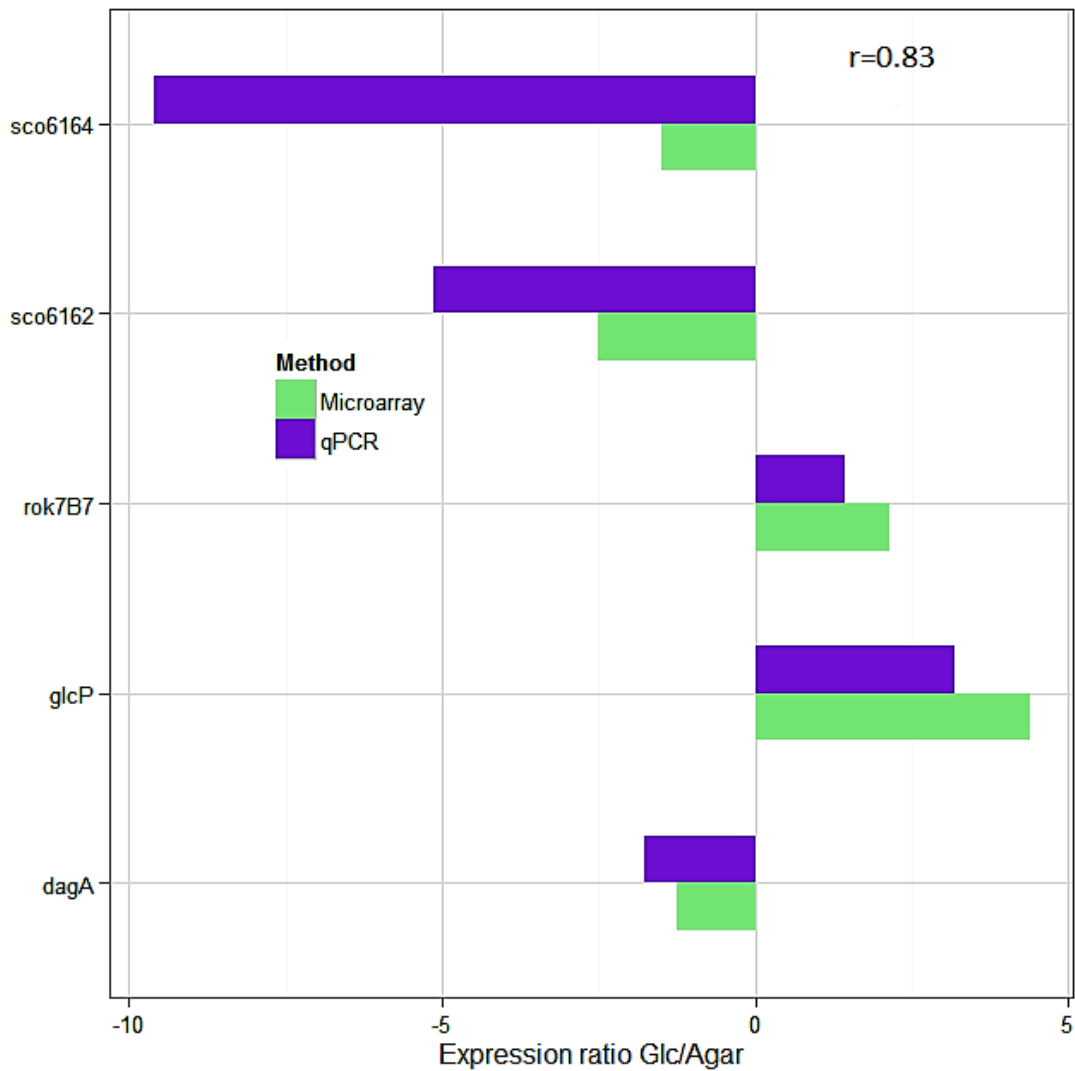


Figure S3. RT-qPCR validation of selected differentially expressed genes in Gluc/Agar (purple bars), compared to their relative transcript profile (green bars). The comparison between these conditions is indicated as ratio of Glc/Agar. Results are given as log2 ratio, thus a positive number indicates up-regulation and negative numbers down-regulation, respectively. r = Pearson correlation.

Table S1. Complete dataset of differentially expressed genes at statistically significant levels (pfp values ≤ 0.15) of *S. coelicolor* cells grown in 0.5% glucose+ 0.5% agar, relative to cells grown in 1% agar

Gene name	Rank of down-regulated genes	pfp value	Log(2) Average	GO Biological Process / Molecular Function	Product/Function
SCO0010	328	0.11104	-1.08		SCJ30.05; hypothetical protein (secreted protein); [GeneDB:SCO0010] [NCBI-GI:21218592] [NCBI-GeneID:1095439] [UniProt:Q9S1Y4]
SCO0043	306	0.09621	-1.10	metabolic process, catalytic activity	SCJ4.24c; hypothetical protein; [GeneDB:SCO0043] [NCBI-GI:21218622] [NCBI-GeneID:1095476] [UniProt:Q9S1U9]
SCO0090	336	0.11688	-1.00		SCJ11.19c; transposase; [GeneDB:SCO0090] [NCBI-GI:21218659] [NCBI-GeneID:1095518] [UniProt:Q9RI85]
SCO0108	153	0.02745	-1.23		SCJ11.37; hypothetical protein; [GeneDB:SCO0108] [NCBI-GI:21218672] [NCBI-GeneID:1095533] [UniProt:Q9RI69]
SCO0141	320	0.10703	-1.12		SCJ33.05c; calcium-binding protein; [GeneDB:SCO0141] [NCBI-GI:21218700] [NCBI-GeneID:1095565] [UniProt:Q9RIX2]
SCO0237	97	0.01175	-1.87	metabolic process, catalytic activity	SCJ9A.16; oxidoreductase; [GeneDB:SCO0237] [NCBI-GI:21218790] [NCBI-GeneID:1095661] [UniProt:Q9S1Q4]
SCO0256	143	0.02538	-1.52	metabolic process, catalytic activity	SCF20.02; short chain oxidoreductase; [GeneDB:SCO0256] [NCBI-GI:21218808] [NCBI-GeneID:1095680] [UniProt:Q9S2E4]
SCO0257	43	0.00279	-2.32	metabolic process, catalytic activity	SCF20.03; hypothetical protein; K07045; [GeneDB:SCO0257] [NCBI-GI:21218809] [NCBI-GeneID:1095681] [UniProt:Q9S2E3]
SCO0258	236	0.05818	-1.28		SCF20.04; hypothetical protein; [GeneDB:SCO0258] [NCBI-GI:21218810] [NCBI-GeneID:1095682] [UniProt:Q9S2E2]
SCO0268	72	0.00722	-1.95		SCF1.10; hypothetical protein; [GeneDB:SCO0268] [NCBI-GI:21218819] [NCBI-GeneID:1095692] [UniProt:Q9RK94]
SCO0315	66	0.00485	-1.83	metabolic process, catalytic activity	SC5G9.24c; decarboxylase; [GeneDB:SCO0315] [NCBI-GI:21218863] [NCBI-GeneID:1095739] [UniProt:Q9RL03]
SCO0381	226	0.05350	-1.22	metabolic process, catalytic activity	SCF62.07; glycosyl transferase; [GeneDB:SCO0381] [NCBI-GI:21218924] [NCBI-GeneID:1095804] [UniProt:Q9RJK7]
SCO0382	164	0.03091	-1.39	metabolic process, catalytic activity, nucleotide binding	SCF62.08; UDP-glucose/GDP-mannose family dehydrogenase (putative secreted protein) [EC:1.1.1.132]; K00066 GDPmannose 6-dehydrogenase; [GeneDB:SCO0382] [NCBI-GI:21218925] [NCBI-GeneID:1095805] [UniProt:Q9RJK6]

SCO0383	135	0.02422	-1.51	metabolic process	SCF62.09; hypothetical protein; [GeneDB:SCO0383] [NCBI-GI:21218926] [NCBI-GeneID:1095806] [UniProt:Q9RJK5]
SCO0384	359	0.13836	-0.99	metabolic process, catalytic activity, metal ion binding	SCF62.10; hypothetical protein; [GeneDB:SCO0384] [NCBI-GI:21218927] [NCBI-GeneID:1095807] [UniProt:Q9RJK4]
SCO0385	312	0.10333	-1.08	metabolic process	SCF62.11; hypothetical protein; [GeneDB:SCO0385] [NCBI-GI:21218928] [NCBI-GeneID:1095808] [UniProt:Q9RJK3]
SCO0386	299	0.09508	-1.09	metabolic process, catalytic activity, nucleotide binding	SCF62.12; putative asparagine synthetase [EC:6.3.5.4]; K01953 asparagine synthase (glutamine-hydrolysing); [GeneDB:SCO0386] [NCBI-GI:21218929] [NCBI-GeneID:1095809] [UniProt:Q9RJK2]
SCO0387	185	0.03897	-1.36	metabolic process, catalytic activity, nucleotide binding	SCF62.13; bi-domain oxidoreductase; [GeneDB:SCO0387] [NCBI-GI:21218930] [NCBI-GeneID:1095810] [UniProt:Q9RJK1]
SCO0388	339	0.11817	-1.04	metabolic process, catalytic activity	SCF62.14; hypothetical protein; [GeneDB:SCO0388] [NCBI-GI:21218931] [NCBI-GeneID:1095811] [UniProt:Q9RJK0]
SCO0389	148	0.02615	-1.46		SCF62.15; lipoprotein; [GeneDB:SCO0389] [NCBI-GI:21218932] [NCBI-GeneID:1095812] [UniProt:Q9RJJ9]
SCO0390	215	0.04865	-1.27		SCF62.16; hypothetical protein; [GeneDB:SCO0390] [NCBI-GI:21218933] [NCBI-GeneID:1095813] [UniProt:Q9RJJ8]
SCO0391	316	0.10449	-1.08	metabolic process, catalytic activity	SCF62.17; transferase; [GeneDB:SCO0391] [NCBI-GI:21218934] [NCBI-GeneID:1095814] [UniProt:Q9RJJ7]
SCO0392	103	0.01320	-1.73	metabolic process, catalytic activity	SCF62.18; methyltransferase; [GeneDB:SCO0392] [NCBI-GI:21218935] [NCBI-GeneID:1095815] [UniProt:Q9RJJ6]
SCO0393	84	0.00929	-1.83	metabolic process, catalytic activity	SCF62.19; putative transferase [EC:2.7.7.33]; K00978 glucose-1-phosphate cytidyltransferase; [GeneDB:SCO0393] [NCBI-GI:21218936] [NCBI-GeneID:1095816] [UniProt:Q9RJJ5]
SCO0394	79	0.00886	-1.86		SCF62.20; hypothetical protein; [GeneDB:SCO0394] [NCBI-GI:21218937] [NCBI-GeneID:1095817] [UniProt:Q9RJJ4]
SCO0395	69	0.00580	-1.99	metabolic process, catalytic activity	SCF62.21; epimerase/dehydratase; [GeneDB:SCO0395] [NCBI-GI:21218938] [NCBI-GeneID:1095818] [UniProt:Q9RJJ3]
SCO0396	59	0.00356	-2.16	metabolic process, catalytic activity	SCF62.22; hypothetical protein; [GeneDB:SCO0396] [NCBI-GI:21218939] [NCBI-GeneID:1095819] [UniProt:Q9RJJ2]
SCO0397	337	0.11706	-1.05		SCF62.23; integral membrane protein; [GeneDB:SCO0397] [NCBI-GI:21218940] [NCBI-GeneID:1095820] [UniProt:Q9RJJ1]
SCO0398	105	0.01343	-1.77	metabolic process,	SCF62.24; glycosyl transferase; [GeneDB:SCO0398] [NCBI-GI:21218941] [NCBI-

				catalytic activity	GeneID:1095821] [UniProt:Q9RJJ0]
SCO0399	120	0.01717	-1.72		SCF62.25; hypothetical protein; [GeneDB:SCO0399] [NCBI-GI:21218942] [NCBI-GeneID:1095822] [UniProt:Q9RJI9]
SCO0400	129	0.01907	-1.68	metabolic process, catalytic activity	SCF62.26; putative epimerase [EC:5.1.3.13]; K01790 dTDP-4-dehydrorhamnose 3.5-epimerase; [GeneDB:SCO0400] [NCBI-GI:21218943] [NCBI-GeneID:1095823] [UniProt:Q9RJI8]
SCO0401	265	0.07038	-1.23	metabolic process, catalytic activity	SCF62.27; glutamate-1-semialdehyde 2.1-aminomutase; [GeneDB:SCO0401] [NCBI-GI:21218944] [NCBI-GeneID:1095824] [UniProt:Q9RJI7]
SCO0441	295	0.08678	-1.15	metabolic process, catalytic activity	SCF51A.19; hypothetical protein; K07160; [GeneDB:SCO0441] [NCBI-GI:21218983] [NCBI-GeneID:1095864] [UniProt:Q9RL45]
SCO0572	119	0.01706	-1.81	transporter activity	SC5G5.04c; putative cytosine permease; K03457 nucleobase:cation symporter-1. NCS1 family; [GeneDB:SCO0572] [NCBI-GI:21219106] [NCBI-GeneID:1095995] [UniProt:Q93RZ8]
SCO0584	80	0.00913	-1.85	metabolic process, catalytic activity, metal ion binding	SCF55.08c; cytochrome P450; [GeneDB:SCO0584] [NCBI-GI:21219117] [NCBI-GeneID:1096007] [UniProt:Q9RJQ6]
SCO0585	60	0.00350	-2.07		cvnD11. SCF55.09c; ATP/GTP binding protein; [GeneDB:SCO0585] [NCBI-GI:21219118] [NCBI-GeneID:1096008] [UniProt:Q9RJQ5]
SCO0586	93	0.00989	-1.79		cvnC11. SCF55.10c; hypothetical protein; [GeneDB:SCO0586] [NCBI-GI:21219119] [NCBI-GeneID:1096009] [UniProt:Q9RJQ4]
SCO0587	195	0.04226	-1.34		cvnB11. SCF55.11c; hypothetical protein; [GeneDB:SCO0587] [NCBI-GI:21219120] [NCBI-GeneID:1096010] [UniProt:Q9RJQ3]
SCO0588	139	0.02446	-1.57	metabolic process, catalytic activity, nucleotide binding	cvnA11. SCF55.12c; sensor kinase; [GeneDB:SCO0588] [NCBI-GI:21219121] [NCBI-GeneID:1096011] [UniProt:Q9RJQ2]
SCO0644	39	0.00282	-2.59		SCF91.04c.; membrane protein; [GeneDB:SCO0644] [NCBI-GI:21219174] [NCBI-GeneID:1096067] [UniProt:Q9RJC0]
SCO0682	258	0.06725	-1.25	DNA Binding	SCF15.03c; hypothetical protein; [GeneDB:SCO0682] [NCBI-GI:21219211] [NCBI-GeneID:1096105] [UniProt:Q9RK34]
SCO0683	325	0.10751	-1.09		SCF15.04c; hypothetical protein; K07131; [GeneDB:SCO0683] [NCBI-GI:21219212] [NCBI-GeneID:1096106] [UniProt:Q9RK33]
SCO0684	296	0.08875	-1.12		SCF15.05c; hypothetical protein; [GeneDB:SCO0684] [NCBI-GI:21219213] [NCBI-GeneID:1096107] [UniProt:Q9RK32]
SCO0685	281	0.07972	-1.19		SCF15.06c; hypothetical protein; [GeneDB:SCO0685] [NCBI-GI:21219214] [NCBI-GeneID:1096108] [UniProt:Q9RK31]

SCO0732	99	0.01202	-1.78	metabolic process, catalytic activity	3SC5B7.10; secreted protease; [GeneDB:SCO0732] [NCBI-GI:21219257] [NCBI-GeneID:1096155] [UniProt:Q9EWT9]
SCO0746	372	0.14567	-1.03	metabolic process, catalytic activity, metal ion binding	SCF81.05; serine/threonine protein kinase (putative secreted protein); [GeneDB:SCO0746] [NCBI-GI:21219270] [NCBI-GeneID:1096169] [UniProt:Q9RJE6]
SCO0752	37	0.00297	-2.51	metabolic process, catalytic activity	salO. SCF81.11c; protease precursor; [GeneDB:SCO0752] [NCBI-GI:21219276] [NCBI-GeneID:1096175] [UniProt:Q9RJE0]
SCO0930	8	0.00000	-3.29		SCM10.18c; lipoprotein; [GeneDB:SCO0930] [NCBI-GI:21219449] [NCBI-GeneID:1096353] [UniProt:Q9RCY0]
SCO0932	220	0.05118	-1.40		SCM10.20; integral membrane protein; [GeneDB:SCO0932] [NCBI-GI:21219451] [NCBI-GeneID:1096355] [UniProt:Q9RCX8]
SCO0944	362	0.14028	-1.11		SCM10.32; hypothetical protein; [GeneDB:SCO0944] [NCBI-GI:21219463] [NCBI-GeneID:1096367] [UniProt:Q9RCW6]
SCO0955	42	0.00286	-2.27		SCM11.10c; hypothetical protein; [GeneDB:SCO0955] [NCBI-GI:21219473] [NCBI-GeneID:1096378] [UniProt:Q9RIV1]
SCO0961	253	0.06312	-1.20	metabolic process, catalytic activity, nucleotide binding	glgC. SCM11.16c; glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]; K00975 glucose-1-phosphate adenylyltransferase; [GeneDB:SCO0961] [NCBI-GI:21219479] [NCBI-GeneID:1096384] [UniProt:P72394]
SCO0992	331	0.11628	-1.11	metabolic process, catalytic activity	2SCG2.05; cysteine synthase; [GeneDB:SCO0992] [NCBI-GI:21219509] [NCBI-GeneID:1096415] [UniProt:Q9EX46]
SCO1064	371	0.14606	-0.90	transporter activity	SCG22.10c; putative sugar transport integral membrane protein; K02025 multiple sugar transport system permease protein; [GeneDB:SCO1064] [NCBI-GI:21219579] [NCBI-GeneID:1096487] [UniProt:Q9K435]
SCO1087	29	0.00138	-2.48		2SCG4.03c; putative aldolase [EC:4.1.2.5]; K01620 threonine aldolase; [GeneDB:SCO1087] [NCBI-GI:21219602] [NCBI-GeneID:1096510] [UniProt:Q9K3R1]
SCO1088	20	0.00100	-2.80	metabolic process, catalytic activity	2SCG4.04c; oxidoreductase; [GeneDB:SCO1088] [NCBI-GI:21219603] [NCBI-GeneID:1096511] [UniProt:Q9K3R0]
SCO1089	7	0.00000	-3.35		2SCG4.05c; hypothetical protein 2SCG405c; [GeneDB:SCO1089] [NCBI-GI:21219604] [NCBI-GeneID:1096512] [UniProt:Q9K3Q9]
SCO1113	330	0.11355	-0.99		2SCG38.06; hypothetical protein; [GeneDB:SCO1113] [NCBI-GI:21219627] [NCBI-GeneID:1096536] [UniProt:Q9EX13]
SCO1121	19	0.00105	-2.90		2SCG38.14; secreted protein; [GeneDB:SCO1121] [NCBI-GI:21219635] [NCBI-GeneID:1096544] [UniProt:Q9EX05]
SCO1157	137	0.02401	-1.59		cvnD3. SCG8A.11c; ATP/GTP binding protein; [GeneDB:SCO1157] [NCBI-GI:21219670] [NCBI-GeneID:1096580] [UniProt:Q9KZI8]

SCO1158	147	0.02578	-1.60		cvnC3. SCG8A.12c; hypothetical protein; [GeneDB:SCO1158] [NCBI-GI:21219671] [NCBI-GeneID:1096581] [UniProt:Q9KZI7]
SCO1159	142	0.02507	-1.59		cvnB3. SCG8A.13c; hypothetical protein; [GeneDB:SCO1159] [NCBI-GI:21219672] [NCBI-GeneID:1096582] [UniProt:Q9KZI6]
SCO1160	98	0.01163	-1.80		cvnA3. SCG8A.14c; hypothetical protein; [GeneDB:SCO1160] [NCBI-GI:21219673] [NCBI-GeneID:1096583] [UniProt:Q9KZI5]
SCO1161	150	0.02627	-1.58		SCG8A.15c; integral membrane protein; [GeneDB:SCO1161] [NCBI-GI:21219674] [NCBI-GeneID:1096584] [UniProt:Q9KZI4]
SCO1163	348	0.12328	-1.02		SCG8A.17c; hypothetical protein; [GeneDB:SCO1163] [NCBI-GI:21219676] [NCBI-GeneID:1096586] [UniProt:Q9KZI2]
SCO1174	366	0.14227	-1.04	metabolic process, catalytic activity	SCG11A.05. thcA; aldehyde dehydrogenase [EC:1.2.1.3]; K00128 aldehyde dehydrogenase (NAD+); [GeneDB:SCO1174] [NCBI-GI:21219685] [NCBI-GeneID:1096597] [UniProt:Q9RJZ6]
SCO1189	378	0.14902	-1.02		SCG11A.20; hypothetical protein; [GeneDB:SCO1189] [NCBI-GI:21219700] [NCBI-GeneID:1096612] [UniProt:Q9RJY1]
SCO1241	363	0.14080	-1.03		2SCG1.16c; hypothetical protein; [GeneDB:SCO1241] [NCBI-GI:21219750] [NCBI-GeneID:1096664] [UniProt:Q9FCC6]
SCO1294	12	0.00083	-3.04	metabolic process, catalytic activity,	SCBAC36F5.05c; cystathionine gamma-synthase; [GeneDB:SCO1294] [NCBI-GI:21219801] [NCBI-GeneID:1096717] [UniProt:Q93IX6]
SCO1328	332	0.11645	-1.15		2SCG61.10c; hypothetical protein; [GeneDB:SCO1328] [NCBI-GI:21219834] [NCBI-GeneID:1096751] [UniProt:Q9K405]
SCO1329	261	0.06969	-1.13		2SCG61.11c; hypothetical protein; [GeneDB:SCO1329] [NCBI-GI:21219835] [NCBI-GeneID:1096752] [UniProt:Q9K404]
SCO1330	239	0.05904	-1.28	metabolic process, catalytic activity	2SCG61.12c; fatty acid CoA ligase; [GeneDB:SCO1330] [NCBI-GI:21219836] [NCBI-GeneID:1096753] [UniProt:Q9K403]
SCO1356	75	0.00760	-2.14	metabolic process, transport	2SCG61.38; iron sulphur protein (secreted protein); [GeneDB:SCO1356] [NCBI-GI:21219862] [NCBI-GeneID:1096779] [UniProt:Q9K3X8]
SCO1357	15	0.00067	-3.09	metabolic process, catalytic activity, nucleotide binding	2SCG61.39; hypothetical protein; [GeneDB:SCO1357] [NCBI-GI:21219863] [NCBI-GeneID:1096780] [UniProt:Q9K3X7]
SCO1359	194	0.04216	-1.31		2SCG61.41. SC10A9.01; integral membrane protein; [GeneDB:SCO1359] [NCBI-GI:32141140] [NCBI-GeneID:1096782] [UniProt:Q8CK31]
SCO1378	319	0.10661	-1.13	metabolic process, catalytic activity	SC10A9.20c; putative glycine dehydrogenase [EC:1.4.4.2]; K00282 glycine dehydrogenase subunit 1; K00283 glycine dehydrogenase subunit 2; [GeneDB:SCO1378] [NCBI-GI:21219883] [NCBI-GeneID:1096801] [UniProt:Q9AK84]

SCO1411	91	0.00923	-1.96	transporter activity	SC6D7.28c; transmembrane transport protein; [GeneDB:SCO1411] [NCBI-GI:21219914] [NCBI-GeneID:1096837] [UniProt:Q9RKX0]
SCO1412	55	0.00327	-2.24		SC6D7.27c; hypothetical protein; [GeneDB:SCO1412] [NCBI-GI:21219915] [NCBI-GeneID:1096838] [UniProt:Q9RKX1]
SCO1427	315	0.10432	-1.15		SC6D7.12c; hypothetical protein; [GeneDB:SCO1427] [NCBI-GI:21219930] [NCBI-GeneID:1096853] [UniProt:Q9RKY6]
SCO1428	121	0.01711	-1.73	metabolic process, catalytic activity, nucleotide binding	acd; acyl-CoA dehydrogenase [EC:1.3.99.-]; K00257; [GeneDB:SCO1428] [NCBI-GI:21219931] [NCBI-GeneID:1096854] [UniProt:Q9RKY7]
SCO1474	373	0.14552	-1.03		SCL6.31; hypothetical protein; [GeneDB:SCO1474] [NCBI-GI:21219976] [NCBI-GeneID:1096900] [UniProt:Q9L0Y5]
SCO1541	175	0.03680	-1.45		SCL2.31; regulator; [GeneDB:SCO1541] [NCBI-GI:21220041] [NCBI-GeneID:1096967] [UniProt:Q9L268]
SCO1563	65	0.00462	-2.00	metabolic process, DNA binding	SCL11.19c; acetyltransferase; [GeneDB:SCO1563] [NCBI-GI:21220062] [NCBI-GeneID:1096994] [UniProt:Q9L1B9]
SCO1573	18	0.00111	-2.96	metabolic process, catalytic activity	SCL24.09; oxidoreductase (membrane protein); [GeneDB:SCO1573] [NCBI-GI:21220071] [NCBI-GeneID:1097004] [UniProt:Q9L1A8]
SCO1574	216	0.04926	-1.33		SCL24.10; hypothetical protein; [GeneDB:SCO1574] [NCBI-GI:21220072] [NCBI-GeneID:1097005] [UniProt:Q9L1A7]
SCO1575	96	0.01010	-1.80	cell organization and biogenesis, metabolic process	SCL24.11; putative thiamine biosynthesis lipoprotein precursor; K03734 thiamine biosynthesis lipoprotein; [GeneDB:SCO1575] [NCBI-GI:21220073] [NCBI-GeneID:1097006] [UniProt:Q9L1A6]
SCO1590	346	0.12283	-1.03	metabolic process	SCI35.12c; secreted protein; [GeneDB:SCO1590] [NCBI-GI:21220087] [NCBI-GeneID:1097021] [UniProt:O88050]
SCO1626	157	0.02911	-1.63	metabolic process, catalytic activity, metal ion binding	SCI41.09c; cytochrome P450; [GeneDB:SCO1626] [NCBI-GI:21220122] [NCBI-GeneID:1097057] [UniProt:Q9RJ75]
SCO1627	85	0.00918	-1.91		cvnD9. SCI41.10c; ATP-GTP binding protein; [GeneDB:SCO1627] [NCBI-GI:21220123] [NCBI-GeneID:1097058] [UniProt:Q9RJ74]
SCO1628	172	0.03227	-1.55		cvnC9. SCI41.11c; hypothetical protein; [GeneDB:SCO1628] [NCBI-GI:21220124] [NCBI-GeneID:1097059] [UniProt:Q9RJ73]
SCO1629	108	0.01676	-1.78		cvnB9. SCI41.12c; hypothetical protein; [GeneDB:SCO1629] [NCBI-GI:21220125] [NCBI-GeneID:1097060] [UniProt:Q9RJ72]

SCO1630	127	0.01874	-1.78		cvnA9. SCI41.13c; integral membrane protein; [GeneDB:SCO1630] [NCBI-GI:21220126] [NCBI-GeneID:1097061] [UniProt:Q9RJ71]
SCO1660	367	0.14253	-0.98	metabolic process, catalytic activity	glpK. SCI52.02; putative glycerol kinase [EC:2.7.1.30]; K00864 glycerol kinase; [GeneDB:SCO1660] [NCBI-GI:21220156] [NCBI-GeneID:1097091] [UniProt:Q9ADA7]
SCO1699	243	0.05922	-1.27	metabolic process, regulation of biological process, DNA Binding	SCI30A.20c; transcriptional regulator; [GeneDB:SCO1699] [NCBI-GI:21220194] [NCBI-GeneID:1097130] [UniProt:Q9S253]
SCO1700	177	0.03712	-1.45		SCI30A.21c; hypothetical protein; [GeneDB:SCO1700] [NCBI-GI:21220195] [NCBI-GeneID:1097131] [UniProt:Q9S252]
SCO1705	227	0.05335	-1.22	metabolic process, catalytic activity, metal ion binding	SCI30A.26c; alcohol dehydrogenase (zinc-binding); [GeneDB:SCO1705] [NCBI-GI:21220200] [NCBI-GeneID:1097136] [UniProt:Q9S247]
SCO1706	200	0.04320	-1.29	metabolic process, catalytic activity	SCI30A.27c; putative aldehyde dehydrogenase [EC:1.2.1.3]; K00128 aldehyde dehydrogenase (NAD+); [GeneDB:SCO1706] [NCBI-GI:21220201] [NCBI-GeneID:1097137] [UniProt:Q9S246]
SCO1722	377	0.14878	-0.96		SCI11.11c; hypothetical protein; [GeneDB:SCO1722] [NCBI-GI:21220216] [NCBI-GeneID:1097153] [UniProt:Q9S2A8]
SCO1773	32	0.00125	-2.46	metabolic process, catalytic activity	SCI51.13c; putative L-alanine dehydrogenase [EC:1.4.1.1]; K00259 alanine dehydrogenase; [GeneDB:SCO1773] [NCBI-GI:21220265] [NCBI-GeneID:1097204] [UniProt:Q9S227]
SCO1810	250	0.06288	-1.22		SCI28.04c; hypothetical protein; [GeneDB:SCO1810] [NCBI-GI:21220300] [NCBI-GeneID:1097244] [UniProt:Q9S279]
SCO1823	107	0.01589	-1.63		SCI8.08c; integral membrane protein; [GeneDB:SCO1823] [NCBI-GI:21220312] [NCBI-GeneID:1097257] [UniProt:Q9RJ45]
SCO1860	178	0.03713	-1.57		SCI39.07c; secreted protein; [GeneDB:SCO1860] [NCBI-GI:21220348] [NCBI-GeneID:1097294] [UniProt:Q93RW6]
SCO1903	217	0.05120	-1.23	stimulus response	SCI7.21; transport associated protein; [GeneDB:SCO1903] [NCBI-GI:21220390] [NCBI-GeneID:1097337] [UniProt:Q9X9W9]
SCO2016	384	0.15010	-0.94	metabolic process, catalytic activity	SC7H2.30c; monooxygenase; [GeneDB:SCO2016] [NCBI-GI:21220498] [NCBI-GeneID:1097450] [UniProt:Q9S217]
SCO2113	256	0.06652	-1.36	catalytic activity, metal ion binding	bfr. SC6E10.07; putative bacterioferritin; K03594 bacterioferritin; [GeneDB:SCO2113] [NCBI-GI:21220591] [NCBI-GeneID:1097547] [UniProt:Q9S2N0]
SCO2207	35	0.00171	-2.48		SC10B7.02; hypothetical secreted protein; [GeneDB:SCO2207] [NCBI-GI:21220679] [NCBI-GeneID:1097640] [UniProt:Q9X955]
SCO2209	203	0.04365	-1.33	metabolic process,	SC10B7.04; transcriptional regulator; [GeneDB:SCO2209] [NCBI-GI:21220681]

				regulation of biological process	[NCBI-GeneID:1097642] [UniProt:Q9X957]
SCO2217	4	0.00000	-3.91		SC10B7.12; secreted protein; [GeneDB:SCO2217] [NCBI-GI:21220689] [NCBI-GeneID:1097650] [UniProt:Q9KZ20]
SCO2218	68	0.00559	-2.15		SC10B7.13c; lipoprotein; [GeneDB:SCO2218] [NCBI-GI:21220690] [NCBI-GeneID:1097651] [UniProt:Q9KZ19]
SCO2229	327	0.11064	-1.03	transporter activity	malG. SC10B7.24c; putative maltose permease; K10110 maltose/maltodextrin transport system permease protein; [GeneDB:SCO2229] [NCBI-GI:21220701] [NCBI-GeneID:1097662] [UniProt:Q9KZ08]
SCO2230	311	0.10122	-1.06	transporter activity	malF. SC10B7.25c; putative maltose permease; K10109 maltose/maltodextrin transport system permease protein; [GeneDB:SCO2230] [NCBI-GI:21220702] [NCBI-GeneID:1097663] [UniProt:Q9KZ07]
SCO2408	88	0.00932	-1.91	metabolic process, catalytic activity	SC4A7.36; aminotransferase; [GeneDB:SCO2408] [NCBI-GI:21220875] [NCBI-GeneID:1097842] [UniProt:Q9RDM9]
SCO2494	23	0.00130	-2.71	metabolic process, catalytic activity, nucleotide binding	SC7A8.33c; putative pyruvate phosphate dikinase [EC:2.7.9.1]; K01006 pyruvate.orthophosphate dikinase; [GeneDB:SCO2494] [NCBI-GI:21220957] [NCBI-GeneID:1097928] [UniProt:Q9L2C5]
SCO2495	50	0.00280	-2.34		SC7A8.34. SCC82.01; hypothetical protein; [GeneDB:SCO2495] [NCBI-GI:32141171] [NCBI-GeneID:1097929] [UniProt:Q8CJZ4]
SCO2529	78	0.00859	-1.82	metabolic process, catalytic activity	SCC117.02; metalloprotease [EC:3.4.24.-]; K01417; [GeneDB:SCO2529] [NCBI-GI:21220989] [NCBI-GeneID:1097963] [UniProt:Q9L2L8]
SCO2530	83	0.00928	-1.80		SCC117.03; hypothetical protein; [GeneDB:SCO2530] [NCBI-GI:21220990] [NCBI-GeneID:1097964] [UniProt:Q9L2L7]
SCO2560	297	0.08923	-1.15	metabolic process, catalytic activity, nucleotide binding	SCC77.27c; hypothetical protein; [GeneDB:SCO2560] [NCBI-GI:21221019] [NCBI-GeneID:1097994] [UniProt:Q9RDD1]
SCO2572	262	0.06966	-1.22		SCC123.10; integral membrane protein; [GeneDB:SCO2572] [NCBI-GI:21221031] [NCBI-GeneID:1098006] [UniProt:Q9RDL4]
SCO2573	134	0.02366	-1.60	metabolic process, catalytic activity, metal ion binding	SCC123.11; oxidoreductase; [GeneDB:SCO2573] [NCBI-GI:21221032] [NCBI-GeneID:1098007] [UniProt:Q9RDL3]
SCO2717	361	0.13920	-1.13		SCC46.02c; small membrane protein; [GeneDB:SCO2717] [NCBI-GI:21221171] [NCBI-GeneID:1098151] [UniProt:Q9L1J9]
SCO2718	240	0.05892	-1.20		SCC46.03c; secreted protein; [GeneDB:SCO2718] [NCBI-GI:21221172] [NCBI-GeneID:1098152] [UniProt:Q9L1J8]

SCO2719	292	0.08421	-1.07		SCC46.04; secreted protein; [GeneDB:SCO2719] [NCBI-GI:21221173] [NCBI-GeneID:1098153] [UniProt:Q9L1J7]
SCO2726	62	0.00387	-2.06	metabolic process, catalytic activity	msdA. SCC46.11c; methylmalonic acid semialdehyde dehydrogenase [EC:1.2.1.27]; K00140 methylmalonate-semialdehyde dehydrogenase; [GeneDB:SCO2726] [NCBI-GI:21221180] [NCBI-GeneID:1098160] [UniProt:Q9L1J1]
SCO2727	140	0.02507	-1.59		SCC46.12c; hypothetical protein; [GeneDB:SCO2727] [NCBI-GI:21221181] [NCBI-GeneID:1098161] [UniProt:Q9L1J0]
SCO2770	357	0.13555	-0.95	metabolic process, catalytic activity, metal ion binding	SCC105.01c. SCC57A.41c. speB; agmatinase [EC:3.5.3.11]; K01480 agmatinase; [GeneDB:SCO2770] [NCBI-GI:32141181] [NCBI-GeneID:1098204] [UniProt:Q8CJY5]
SCO2774	280	0.07911	-1.12	metabolic process, catalytic activity, nucleotide binding	acdH2. SCC105.05c; acyl-CoA dehydrogenase [EC:1.3.99.3]; K00249 acyl-CoA dehydrogenase; [GeneDB:SCO2774] [NCBI-GI:21221225] [NCBI-GeneID:1098208] [UniProt:Q9L079]
SCO2776	22	0.00091	-2.83		accD1. SCC105.07; acetyl/propionyl CoA carboxylase. beta subunit [EC:6.4.1.3]; K01966 propionyl-CoA carboxylase beta chain; [GeneDB:SCO2776] [NCBI-GI:21221227] [NCBI-GeneID:1098210] [UniProt:Q9L077]
SCO2777	158	0.02918	-1.48	metabolic process, catalytic activity, metal ion binding	accC. SCC105.08; acetyl/propionyl CoA carboxylase alpha subunit [EC:6.3.4.14]; K01946 biotin carboxylase; [GeneDB:SCO2777] [NCBI-GI:21221228] [NCBI-GeneID:1098211] [UniProt:Q9L076]
SCO2778	34	0.00147	-2.61		hmgL. SCC105.09; hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]; K01640 hydroxymethylglutaryl-CoA lyase; [GeneDB:SCO2778] [NCBI-GI:21221229] [NCBI-GeneID:1098212] [UniProt:Q9L075]
SCO2779	3	0.00000	-3.90	metabolic process, catalytic activity, nucleotide binding	acdH. SCC105.10; acyl-CoA dehydrogenase; [GeneDB:SCO2779] [NCBI-GI:21221230] [NCBI-GeneID:1098213] [UniProt:Q9XCG6]
SCO2788	95	0.00989	-1.81		SCC105.19; hypothetical protein; [GeneDB:SCO2788] [NCBI-GI:21221239] [NCBI-GeneID:1098222] [UniProt:Q9L066]
SCO2789	100	0.01250	-1.85	metabolic process, catalytic activity	glmS2. SCC105.20; glucosamine-fructose-6-phosphate aminotransferase [EC:2.6.1.16]; K00820 glucosamine--fructose-6-phosphate aminotransferase (isomerizing); [GeneDB:SCO2789] [NCBI-GI:21221240] [NCBI-GeneID:1098223] [UniProt:Q9L065]
SCO2805	114	0.01632	-1.67		2SCC13.13; hypothetical protein; [GeneDB:SCO2805] [NCBI-GI:21221256] [NCBI-GeneID:1098239] [UniProt:Q9F3H6]
SCO2822	294	0.08673	-1.11	metabolic process,	SCBAC17F8.13c; decarboxylase; [GeneDB:SCO2822] [NCBI-GI:21221272] [NCBI-

				catalytic activity	GeneID:1098256] [UniProt:Q93J75]
SCO2823	279	0.07849	-1.11	metabolic process, catalytic activity	SCBAC17F8.14c; decarboxylase; [GeneDB:SCO2823] [NCBI-GI:21221273] [NCBI-GeneID:1098257] [UniProt:Q93J74]
SCO2826	228	0.05338	-1.30		SCBAC17F8.17; hypothetical protein; [GeneDB:SCO2826] [NCBI-GI:21221276] [NCBI-GeneID:1098260] [UniProt:Q93J71]
SCO2883	355	0.13251	-0.98	metabolic process, catalytic activity, metal ion binding	SCE6.20; cytochrome P450; [GeneDB:SCO2883] [NCBI-GI:21221332] [NCBI-GeneID:1098317] [UniProt:Q9KZR8]
SCO2953	161	0.02975	-1.48		SCE59.12c; hypothetical protein; [GeneDB:SCO2953] [NCBI-GI:21221398] [NCBI-GeneID:1098386] [UniProt:Q9L1U2]
SCO2954	28	0.00143	-2.60	metabolic process, regulation of biological process, DNA binding	SCE59.13c; putative RNA polymerase sigma factor; K03088 RNA polymerase sigma-70 factor. ECF subfamily; [GeneDB:SCO2954] [NCBI-GI:21221399] [NCBI-GeneID:1098387] [UniProt:Q9L1U1]
SCO2976	56	0.00357	-2.16		SCE50.04c; hypothetical protein; [GeneDB:SCO2976] [NCBI-GI:21221420] [NCBI-GeneID:1098409] [UniProt:Q9L059]
SCO2977	183	0.03874	-1.42		SCE50.05; hypothetical protein; [GeneDB:SCO2977] [NCBI-GI:21221421] [NCBI-GeneID:1098410] [UniProt:Q9L058]
SCO2979	254	0.06323	-1.24	transporter activity	SCE50.07; putative integral membrane transport protein; K10233 alpha-glucoside transport system permease protein; [GeneDB:SCO2979] [NCBI-GI:21221423] [NCBI-GeneID:1098412] [UniProt:Q9L056]
SCO2980	231	0.05398	-1.27	transporter activity	SCE50.08; putative integral membrane transport protein; K10234 alpha-glucoside transport system permease protein; [GeneDB:SCO2980] [NCBI-GI:21221424] [NCBI-GeneID:1098413] [UniProt:Q9L055]
SCO2999	40	0.00300	-2.22	metabolic process, catalytic activity	SCE33.01c. SCE99.06c; hypothetical protein; [GeneDB:SCO2999] [NCBI-GI:32141188] [NCBI-GeneID:1098432] [UniProt:Q8CJY0]
SCO3051	64	0.00406	-2.20	metabolic process, catalytic activity, nucleotide binding	fadE. SCBAC19G2.06c; acyl-CoA dehydrogenase [EC:1.3.99.-]; K00257; [GeneDB:SCO3051] [NCBI-GI:21221493] [NCBI-GeneID:1098484] [UniProt:Q7AKM9]
SCO3112	235	0.05511	-1.31		SCE41.21c; hypothetical protein; [GeneDB:SCO3112] [NCBI-GI:21221551] [NCBI-GeneID:1098546] [UniProt:Q9F2N8]
SCO3134	266	0.07034	-1.20	cell communication, metabolic process, DNA binding	SCE66.13c; two-component system response regulator; [GeneDB:SCO3134] [NCBI-GI:21221572] [NCBI-GeneID:1098568] [UniProt:Q9K3T0]

SCO3263	369	0.14268	-1.64		SCE39.13c; hypothetical protein; [GeneDB:SCO3263] [NCBI-GI:21221696] [NCBI-GeneID:1098697] [UniProt:Q9X8D6]
SCO3265	349	0.12307	-1.85		SCE39.15c; hypothetical protein; [GeneDB:SCO3265] [NCBI-GI:21221698] [NCBI-GeneID:1098699] [UniProt:Q9X8D8]
SCO3266	271	0.07111	-1.93		SCE39.16c; hypothetical protein; [GeneDB:SCO3266] [NCBI-GI:21221699] [NCBI-GeneID:1098700] [UniProt:Q9X8D9]
SCO3268	263	0.06981	-1.97		SCE39.18c; secreted protein; [GeneDB:SCO3268] [NCBI-GI:21221701] [NCBI-GeneID:1098702] [UniProt:Q9X8E1]
SCO3288	144	0.02521	-1.70		SCE15.05; integral membrane protein; [GeneDB:SCO3288] [NCBI-GI:21221720] [NCBI-GeneID:1098722] [UniProt:Q9X880]
SCO3289	89	0.00933	-2.02		SCE15.06; large membrane protein; [GeneDB:SCO3289] [NCBI-GI:21221721] [NCBI-GeneID:1098723] [UniProt:Q9X881]
SCO3290	141	0.02511	-1.77		SCE15.07; hypothetical protein; [GeneDB:SCO3290] [NCBI-GI:21221722] [NCBI-GeneID:1098724] [UniProt:Q9X882]
SCO3323	210	0.04610	-1.37	metabolic process, DNA binding	SCE68.21; putative RNA polymerase sigma factor; K03088 RNA polymerase sigma-70 factor.ECF subfamily; [GeneDB:SCO3323] [NCBI-GI:21221754] [NCBI-GeneID:1098757] [UniProt:Q9WX11]
SCO3328	181	0.03801	-1.34	metabolic process, DNA binding	SCE68.26c; hypothetical protein; [GeneDB:SCO3328] [NCBI-GI:21221759] [NCBI-GeneID:1098762] [UniProt:Q9WX06]
SCO3362	57	0.00351	-2.11	transporter activity	SCE94.13; hypothetical protein; [GeneDB:SCO3362] [NCBI-GI:21221791] [NCBI-GeneID:1098799] [UniProt:Q9X8L9]
SCO3365	188	0.04064	-1.31	metabolic process, DNA binding	SCE94.16c; hypothetical protein; [GeneDB:SCO3365] [NCBI-GI:21221794] [NCBI-GeneID:1098802] [UniProt:Q9X8M2]
SCO3471	169	0.03207	-1.24	metabolic process, catalytic activity	dagA. SCE65.07c; extracellular agarase precursor [EC:3.2.1.81]; K01219 agarase; [GeneDB:SCO3471] [NCBI-GI:21221895] [NCBI-GeneID:1098908] [UniProt:P07883]
SCO3472	128	0.01875	-1.82	metabolic process, DNA binding	SCE65.08c; transposase remnant; [GeneDB:SCO3472] [NCBI-GI:21221896] [NCBI-GeneID:1098909] [UniProt:Q9RKG5]
SCO3473	71	0.00732	-2.23		SCE65.09c; putative aldolase [EC:4.1.2.14 4.1.3.16]; K01625 2-dehydro-3-deoxyphosphogluconate aldolase; K01650 4-hydroxy-2-oxoglutarate aldolase; [GeneDB:SCO3473] [NCBI-GI:21221897] [NCBI-GeneID:1098910] [UniProt:Q9RKG4]
SCO3474	92	0.00913	-2.07		SCE65.10c; sugar kinase; [GeneDB:SCO3474] [NCBI-GI:21221898] [NCBI-GeneID:1098911] [UniProt:Q9RKG3]
SCO3475	67	0.00507	-2.24	metabolic process,	SCE65.11c; putative galactonate dehydratase protein [EC:4.2.1.6]; K01684

				catalytic activity	galactonate dehydratase; [GeneDB:SCO3475] [NCBI-GI:21221899] [NCBI-GeneID:1098912] [UniProt:Q9RKG2]
SCO3476	49	0.00286	-2.50		SCE65.12c; putative short-chain dehydrogenase [EC:1.1.1.125]; K00065 2-deoxy-D-gluconate 3-dehydrogenase; [GeneDB:SCO3476] [NCBI-GI:21221900] [NCBI-GeneID:1098913] [UniProt:Q9RKG1]
SCO3477	48	0.00271	-2.52	metabolic process, catalytic activity, metal ion binding	SCE65.13c; dehydrogenase; [GeneDB:SCO3477] [NCBI-GI:21221901] [NCBI-GeneID:1098914] [UniProt:Q9RKG0]
SCO3478	45	0.00267	-2.53		SCE65.14c; dehydrogenase; [GeneDB:SCO3478] [NCBI-GI:21221902] [NCBI-GeneID:1098915] [UniProt:Q9RKF9]
SCO3479	52	0.00327	-2.46	metabolic process, catalytic activity	SCE65.15c; putative beta-galactosidase [EC:3.2.1.23]; K01190 beta-galactosidase; [GeneDB:SCO3479] [NCBI-GI:21221903] [NCBI-GeneID:1098916] [UniProt:Q9RKF8]
SCO3480	38	0.00289	-2.55	metabolic process, catalytic activity, metal ion binding	SCE65.16c; putative racemase [EC:5.1.2.2]; K01781 mandelate racemase; [GeneDB:SCO3480] [NCBI-GI:21221904] [NCBI-GeneID:1098917] [UniProt:Q9RKF7]
SCO3481	51	0.00333	-2.43	metabolic process, catalytic activity	SCE65.17c; hypothetical protein; [GeneDB:SCO3481] [NCBI-GI:21221905] [NCBI-GeneID:1098918] [UniProt:Q9RKF6]
SCO3482	41	0.00293	-2.56	transporter activity	SCE65.18c; putative sugar-permease; K02026 multiple sugar transport system permease protein; [GeneDB:SCO3482] [NCBI-GI:21221906] [NCBI-GeneID:1098919] [UniProt:Q9RKF5]
SCO3483	14	0.00071	-3.09	transporter activity	SCE65.19c; putative integral membrane transport protein; K02025 multiple sugar transport system permease protein; [GeneDB:SCO3483] [NCBI-GI:21221907] [NCBI-GeneID:1098920] [UniProt:Q9RKF4]
SCO3484	25	0.00160	-2.85	transporter activity	SCE65.20c; putative secreted sugar-binding protein; K02027 multiple sugar transport system substrate-binding protein; [GeneDB:SCO3484] [NCBI-GI:21221908] [NCBI-GeneID:1098921] [UniProt:Q9RKF3]
SCO3486	149	0.02638	-1.51	metabolic process, catalytic activity, metal ion binding	SCE65.22; putative aldehyde dehydrogenase [EC:1.2.1.22]; K00138 lactaldehyde dehydrogenase; [GeneDB:SCO3486] [NCBI-GI:21221910] [NCBI-GeneID:1098923] [UniProt:Q9RKF1]
SCO3487	26	0.00154	-2.79		SCE65.23; hydrolase; [GeneDB:SCO3487] [NCBI-GI:21221911] [NCBI-GeneID:1098924] [UniProt:Q9RKF0]
SCO3527	192	0.04135	-1.23		SCE2.08; hypothetical protein; [GeneDB:SCO3527] [NCBI-GI:21221948] [NCBI-GeneID:1098963] [UniProt:Q9X8A3]

SCO3540	354	0.12972	-1.00		SCH5.02c. slpD; proteinase (secreted protein); [GeneDB:SCO3540] [NCBI-GI:21221959] [NCBI-GeneID:1098976] [UniProt:Q7AKL3]
SCO3603	308	0.09789	-1.03	transporter activity	SC66T3.14c; putative Na(+)/H(+) antiporter; K03316 monovalent cation:H+ antiporter. CPA1 family; [GeneDB:SCO3603] [NCBI-GI:21222019] [NCBI-GeneID:1099039] [UniProt:Q9XAJ9]
SCO3604	356	0.13399	-1.02		SC66T3.15c; hypothetical protein; [GeneDB:SCO3604] [NCBI-GI:21222020] [NCBI-GeneID:1099040] [UniProt:Q9XAJ8]
SCO3622	212	0.04811	-1.30	metabolic process, catalytic activity	SC66T3.33; hypothetical protein; [GeneDB:SCO3622] [NCBI-GI:21222038] [NCBI-GeneID:1099058] [UniProt:Q9XAI0]
SCO3656	269	0.07086	-1.20		SCH10.34c; hypothetical protein; [GeneDB:SCO3656] [NCBI-GI:21222071] [NCBI-GeneID:1099092] [UniProt:Q9X8S3]
SCO3713	191	0.04099	-1.36		SCH35.11; hypothetical protein; [GeneDB:SCO3713] [NCBI-GI:21222126] [NCBI-GeneID:1099149] [UniProt:Q9X8Z5]
SCO3714	264	0.06970	-1.25		SCH35.10; putative transposase; K07496 putative transposase; [GeneDB:SCO3714] [NCBI-GI:21222127] [NCBI-GeneID:1099150] [UniProt:Q9X8Z6]
SCO3800	229	0.05332	-1.21	metabolic process, catalytic activity, nucleotide binding	SCAC2.08. SCGD3.01; putative acyl-CoA dehydrogenase [EC:1.3.99.-]; K00257; [GeneDB:SCO3800] [NCBI-GI:32141216] [NCBI-GeneID:1099236] [UniProt:Q8CJV6]
SCO3816	360	0.13917	-0.99	metabolic process, DNA binding	bkdB1. SCGD3.17c; putative branched-chain alpha keto acid dehydrogenase E1 beta subunit [EC:1.2.4.1]; K00162 pyruvate dehydrogenase E1 component. beta subunit; [GeneDB:SCO3816] [NCBI-GI:21222226] [NCBI-GeneID:1099252] [UniProt:Q9XA61]
SCO3817	208	0.04500	-1.33	metabolic process, catalytic activity	bkdA1. SCGD3.18c; putative branched-chain alpha keto acid dehydrogenase E1 alpha subunit [EC:1.2.4.1]; K00161 pyruvate dehydrogenase E1 component. alpha subunit; [GeneDB:SCO3817] [NCBI-GI:21222227] [NCBI-GeneID:1099253] [UniProt:Q9XA60]
SCO3835	252	0.06278	-1.20	metabolic process, catalytic activity	SCH69.05; dehydrogenase; [GeneDB:SCO3835] [NCBI-GI:21222244] [NCBI-GeneID:1099271] [UniProt:Q9XA29]
SCO3933	102	0.01333	-1.78	metabolic process, transport	SCQ11.16; regulatory protein; [GeneDB:SCO3933] [NCBI-GI:21222339] [NCBI-GeneID:1099369] [UniProt:Q9X9T5]
SCO3982	131	0.02145	-2.19		SCBAC25E3.19; hypothetical protein; [GeneDB:SCO3982] [NCBI-GI:21222386] [NCBI-GeneID:1099418] [UniProt:Q93J25]

SCO3983	189	0.04074	-2.10		SCBAC25E3.20; hypothetical protein; [GeneDB:SCO3983] [NCBI-GI:21222387] [NCBI-GeneID:1099419] [UniProt:Q93J24]
SCO3986	163	0.03055	-2.17	metabolic process, regulation of biological process, response to stimulus, DNA Binding	SCBAC25E3.23; GntR-family transcriptional regulator; [GeneDB:SCO3986] [NCBI-GI:21222390] [NCBI-GeneID:1099422] [UniProt:Q93J21]
SCO3987	184	0.03864	-1.97		SCBAC25E3.24; hypothetical protein; [GeneDB:SCO3987] [NCBI-GI:21222391] [NCBI-GeneID:1099423] [UniProt:Q93J20]
SCO3988	207	0.04483	-1.63		SCBAC25E3.25; hypothetical protein; [GeneDB:SCO3988] [NCBI-GI:21222392] [NCBI-GeneID:1099424] [UniProt:Q93J19]
SCO4053	290	0.08297	-1.20	metabolic process, regulation of biological process, response to stimulus, DNA Binding	2SCD60.19; putative transport integral membrane protein; K07156; K07245 putative copper resistance protein D; [GeneDB:SCO4053] [NCBI-GI:21222456] [NCBI-GeneID:1099489] [UniProt:Q9AK64]
SCO4089	171	0.03228	-1.39	metabolic process, catalytic activity	SCD25.25c. vdh; valine dehydrogenase [EC:1.4.1.-]; K00271; [GeneDB:SCO4089] [NCBI-GI:21222491] [NCBI-GeneID:1099526] [UniProt:Q06539]
SCO4122	343	0.12020	-1.03	metabolic process, regulation of biological process, response to stimulus, DNA Binding stimulus response	SCD72A.08; MarR-family transcriptional regulator; [GeneDB:SCO4122] [NCBI-GI:21222521] [NCBI-GeneID:1099559] [UniProt:Q9KYE8]
SCO4187	111	0.01658	-1.62		2SCD46.01c. SCD66.24c; hypothetical protein; [GeneDB:SCO4187] [NCBI-GI:32141229] [NCBI-GeneID:1099627] [UniProt:Q8CJU4]
SCO4189	117	0.01615	-1.87		2SCD46.03c; hypothetical protein; [GeneDB:SCO4189] [NCBI-GI:21222585] [NCBI-GeneID:1099629] [UniProt:Q7AKJ8]
SCO4301	344	0.12320	-0.99	metabolic process, regulation of biological process, response to stimulus, DNA Binding stimulus response	SCD95A.34c; DNA-binding protein; [GeneDB:SCO4301] [NCBI-GI:21222694] [NCBI-GeneID:1099741] [UniProt:Q9KXU0]
SCO4412	267	0.07019	-1.20		SC6F11.10; regulatory protein; [GeneDB:SCO4412] [NCBI-GI:21222801] [NCBI-GeneID:1099852] [UniProt:Q9F376]
SCO4458	221	0.05109	-1.26		SCD6.36c. SCD65.01c; lipoprotein; [GeneDB:SCO4458] [NCBI-GI:32141237] [NCBI-

					GeneID:1099898] [UniProt:Q8CJT7]
SCO4561	318	0.10635	-1.11		SCD16A.22; NLP/P60 family protein; [GeneDB:SCO4561] [NCBI-GI:21222944] [NCBI-GeneID:1100001] [UniProt:Q9XAQ3]
SCO4562	225	0.05320	-1.29	metabolic process, catalytic activity	nuoA. SCD16A.21c; NADH dehydrogenase I chain A [EC:1.6.5.3]; K00330 NADH dehydrogenase I chain A; [GeneDB:SCO4562] [NCBI-GI:21222945] [NCBI-GeneID:1100002] [UniProt:Q9XAQ4]
SCO4563	167	0.03192	-1.48	metabolic process, catalytic activity, metal ion binding	nuoB. SCD16A.20c; NADH dehydrogenase I chain B [EC:1.6.5.3]; K00331 NADH dehydrogenase I chain B; [GeneDB:SCO4563] [NCBI-GI:21222946] [NCBI-GeneID:1100003] [UniProt:Q9XAQ5]
SCO4564	145	0.02586	-1.60	catalytic activity, metal ion binding	nuoC. SCD16A.19c; NADH dehydrogenase I chain C [EC:1.6.5.3]; K00332 NADH dehydrogenase I chain C; [GeneDB:SCO4564] [NCBI-GI:21222947] [NCBI-GeneID:1100004] [UniProt:Q9XAQ6]
SCO4565	101	0.01257	-1.89	catalytic activity, metal ion binding	nuoD. SCD16A.18c; NADH dehydrogenase I chain D [EC:1.6.5.3]; K00333 NADH dehydrogenase I chain D; [GeneDB:SCO4565] [NCBI-GI:21222948] [NCBI-GeneID:1100005] [UniProt:Q9XAQ7]
SCO4566	125	0.01888	-1.77	metabolic process, catalytic activity, nucleotide binding	nuoE. SCD16A.17c; NADH dehydrogenase I chain E [EC:1.6.5.3]; K00334 NADH dehydrogenase I chain E; [GeneDB:SCO4566] [NCBI-GI:21222949] [NCBI-GeneID:1100006] [UniProt:Q9XAQ8]
SCO4567	110	0.01673	-1.81	metabolic process, catalytic activity, metal ion binding	nuoF. SCD16A.16c; NADH dehydrogenase I chain F [EC:1.6.5.3]; K00335 NADH dehydrogenase I chain F; [GeneDB:SCO4567] [NCBI-GI:21222950] [NCBI-GeneID:1100007]
SCO4568	176	0.03682	-1.46	metabolic process, catalytic activity, metal ion binding	nuoG. SCD16A.15c; NADH dehydrogenase I chain G [EC:1.6.5.3]; K00336 NADH dehydrogenase I chain G; [GeneDB:SCO4568] [NCBI-GI:21222951] [NCBI-GeneID:1100008]
SCO4569	112	0.01643	-1.82	metabolic process, catalytic activity	nuoH. SCD16A.14c; NADH dehydrogenase I chain H [EC:1.6.5.3]; K00337 NADH dehydrogenase I chain H; [GeneDB:SCO4569] [NCBI-GI:21222952] [NCBI-GeneID:1100009] [UniProt:Q9XAR1]
SCO4570	94	0.01000	-2.00	metabolic process, catalytic activity, metal	nuoI. SCD16A.13c; NADH dehydrogenase I chain I [EC:1.6.5.3]; K00338 NADH dehydrogenase I chain I; [GeneDB:SCO4570] [NCBI-GI:21222953] [NCBI-

				ion binding	GeneID:1100010] [UniProt:Q9XAR2]
SCO4571	90	0.00933	-1.98	metabolic process, catalytic activity	nuoJ. SCD16A.12c; NADH dehydrogenase I chain J [EC:1.6.5.3]; K00339 NADH dehydrogenase I chain J; [GeneDB:SCO4571] [NCBI-GI:21222954] [NCBI-GeneID:1100011] [UniProt:Q9XAR3]
SCO4572	77	0.00870	-2.04	catalytic activity,metal ion binding	nuoK. SCD16A.11c; NADH dehydrogenase I chain K [EC:1.6.5.3]; K00340 NADH dehydrogenase I chain K; [GeneDB:SCO4572] [NCBI-GI:21222955] [NCBI-GeneID:1100012] [UniProt:Q9XAR4]
SCO4573	179	0.03782	-1.46	metabolic process, catalytic activity	nuoL. SCD16A.10c; NADH dehydrogenase I chain L [EC:1.6.5.3]; K00341 NADH dehydrogenase I chain L; [GeneDB:SCO4573] [NCBI-GI:21222956] [NCBI-GeneID:1100013]
SCO4574	58	0.00362	-2.21	metabolic process, catalytic activity	nuoM. SCD16A.09c; NADH dehydrogenase I chain M [EC:1.6.5.3]; K00342 NADH dehydrogenase I chain M; [GeneDB:SCO4574] [NCBI-GI:21222957] [NCBI-GeneID:1100014] [UniProt:Q9XAR6]
SCO4575	170	0.03212	-1.47	catalytic activity,metal ion binding	nuoN. SCD16A.08c; NADH dehydrogenase I chain N [EC:1.6.5.3]; K00343 NADH dehydrogenase I chain N; [GeneDB:SCO4575] [NCBI-GI:21222958] [NCBI-GeneID:1100015] [UniProt:Q9XAR7]
SCO4581	282	0.07965	-1.25	metabolic process, catalytic activity	SCD16A.02c; hypothetical protein; K07024; [GeneDB:SCO4581] [NCBI-GI:21222964] [NCBI-GeneID:1100021] [UniProt:Q9XAS3]
SCO4675	276	0.07743	-1.17		SCD40A.21c; hypothetical protein; [GeneDB:SCO4675] [NCBI-GI:21223056] [NCBI-GeneID:1100116] [UniProt:Q9L0J0]
SCO4676	222	0.05108	-1.24		SCD31.01c. SCD40A.22c; hypothetical protein; [GeneDB:SCO4676] [NCBI-GI:32141244] [NCBI-GeneID:1100117] [UniProt:Q8CJT0]
SCO4677	116	0.01629	-1.66		SCD31.02c; regulatory protein; [GeneDB:SCO4677] [NCBI-GI:21223057] [NCBI-GeneID:1100118] [UniProt:Q9L0G5]
SCO4789	219	0.05114	-1.32		SCD63.21; integral membrane protein; [GeneDB:SCO4789] [NCBI-GI:21223168] [NCBI-GeneID:1100230] [UniProt:Q9L0G8]
SCO4790	232	0.05504	-1.24		SCD63.22c. SCD63A.01c; integral membrane protein; [GeneDB:SCO4790] [NCBI-GI:32141246] [NCBI-GeneID:1100231] [UniProt:Q8CJS9]
SCO4793	124	0.01863	-1.67		SCD63A.04c; NPL/P60 family secreted protein; [GeneDB:SCO4793] [NCBI-GI:21223171] [NCBI-GeneID:1100234] [UniProt:Q9KY71]
SCO4799	196	0.04240	-1.37	metabolic process,	SCD63A.10c; secreted lipase; [GeneDB:SCO4799] [NCBI-GI:21223177] [NCBI-

				catalytic activity	GeneID:1100240] [UniProt:Q9KY65]
SCO4800	104	0.01317	-1.73	metabolic process, catalytic activity, metal ion binding	icmB. SCD63A.11; isobutyryl CoA mutase. small subunit [EC:5.4.99.2]; K01849 methylmalonyl-CoA mutase.C-terminal domain; [GeneDB:SCO4800] [NCBI-GI:21223178] [NCBI-GeneID:1100241] [UniProt:Q9KY64]
SCO4894	270	0.07085	-1.13		2SCK8.20c; hypothetical protein 2SCK820c; [GeneDB:SCO4894] [NCBI-GI:21223268] [NCBI-GeneID:1100335] [UniProt:Q9AK32]
SCO4920	251	0.06295	-1.26	metabolic process, regulation of biological process, DNA Binding	SCK13.12; DeoR-family transcriptional regulator; [GeneDB:SCO4920] [NCBI-GI:21223294] [NCBI-GeneID:1100361] [UniProt:Q9AD80]
SCO4930	130	0.02008	-1.63	metabolic process, catalytic activity	SCK13.22; putative enoyl-CoA hydratase [EC:4.2.1.17]; K01692 enoyl-CoA hydratase; [GeneDB:SCO4930] [NCBI-GI:21223304] [NCBI-GeneID:1100371] [UniProt:Q9EWW0]
SCO4974	310	0.10126	-1.05	metabolic process, catalytic activity, metal ion binding	2SCK31.34; deaminase; [GeneDB:SCO4974] [NCBI-GI:21223347] [NCBI-GeneID:1100415] [UniProt:Q9ADJ9]
SCO4979	24	0.00125	-2.61	metabolic process, catalytic activity	2SCK36.02; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]; K01596 phosphoenolpyruvate carboxykinase (GTP); [GeneDB:SCO4979] [NCBI-GI:21223352] [NCBI-GeneID:1100420] [UniProt:Q93JL5]
SCO5028	122	0.01820	-1.65		SCK7.01; putative ATP-binding protein; K07175 PhoH-like ATPase; [GeneDB:SCO5028] [NCBI-GI:21223401] [NCBI-GeneID:1100469] [UniProt:Q9FBP8]
SCO5047	285	0.08105	-1.17		SCK7.20c; fructose-1.6-bisphosphatase II / sedoheptulose-1.7-bisphosphatase [EC:3.1.3.11]; K02446 fructose-1.6-bisphosphatase II; [GeneDB:SCO5047] [NCBI-GI:21223420] [NCBI-GeneID:1100488] [UniProt:Q9FBN2]
SCO5054	204	0.04422	-1.30		SCK7.27; hypothetical protein; [GeneDB:SCO5054] [NCBI-GI:21223427] [NCBI-GeneID:1100495] [UniProt:Q9FBM5]
SCO5071	54	0.00333	-2.44		SCBAC20F6.14c; hydroxylacyl-CoA dehydrogenase; [GeneDB:SCO5071] [NCBI-GI:21223443] [NCBI-GeneID:1100512] [UniProt:Q53925]
SCO5072	323	0.10768	-1.13	metabolic process, catalytic activity, nucleotide binding	SCBAC20F6.15; hydroxylacyl-CoA dehydrogenase [EC:1.1.1.-]; K05556 hydroxylacyl-CoA dehydrogenase; [GeneDB:SCO5072] [NCBI-GI:21223444] [NCBI-GeneID:1100513] [UniProt:Q53926]
SCO5073	255	0.06329	-1.21	metabolic process, catalytic activity, metal	SCBAC20F6.16; putative oxidoreductase [EC:1.6.5.5]; K00344 NADPH2:quinone reductase; [GeneDB:SCO5073] [NCBI-GI:21223445] [NCBI-GeneID:1100514]

				ion binding	[UniProt:Q53927]
SCO5074	82	0.00902	-1.88		SCBAC20F6.17; dehydratase; [GeneDB:SCO5074] [NCBI-GI:21223446] [NCBI-GeneID:1100515] [UniProt:Q9ADD7]
SCO5079	113	0.01628	-1.62	metabolic process, catalytic activity	actVA4. SCBAC28G1.05; hypothetical protein; [GeneDB:SCO5079] [NCBI-GI:21223450] [NCBI-GeneID:1100520] [UniProt:Q53906]
SCO5080	201	0.04348	-1.29	metabolic process, catalytic activity, nucleotide binding	actVA5. SCBAC28G1.06; hydrolase; [GeneDB:SCO5080] [NCBI-GI:21223451] [NCBI-GeneID:1100521] [UniProt:Q53907]
SCO5081	180	0.03811	-1.35		actVA6. SCBAC28G1.07; hypothetical protein; [GeneDB:SCO5081] [NCBI-GI:21223452] [NCBI-GeneID:1100522] [UniProt:Q53908]
SCO5086	123	0.01837	-1.62	metabolic process, catalytic activity	actIII. SCBAC28G1.12c; ketoacyl reductase [EC:1.3.1.-]; K00224; [GeneDB:SCO5086] [NCBI-GI:21223457] [NCBI-GeneID:1100527] [UniProt:P16544]
SCO5089	70	0.00714	-2.06	metabolic process	actIORF3. SCBAC28G1.15; actinorhodin polyketide synthase acyl carrier protein; K05553 3-oxoacyl-ACP synthase acyl carrier protein; [GeneDB:SCO5089] [NCBI-GI:21223460] [NCBI-GeneID:1100530] [UniProt:Q02054]
SCO5112	173	0.03474	-1.57	transporter activity	bldKA. SCBAC31E11.08; BldKA. ABC transport system integral membrane protein; [GeneDB:SCO5112] [NCBI-GI:21223483] [NCBI-GeneID:1100553] [UniProt:Q93IU3]
SCO5113	205	0.04473	-1.43	transporter activity	bldKB. SCBAC31E11.09; BldKB. putative ABC transport system lipoprotein; K02035 peptide/nickel transport system substrate-binding protein; [GeneDB:SCO5113] [NCBI-GI:21223484] [NCBI-GeneID:1100554] [UniProt:Q93IU2]
SCO5114	193	0.04197	-1.51	transporter activity	bldKC. SCBAC31E11.10; BldKC. putative ABC transport system integral membrane protein; K02033 peptide/nickel transport system permease protein; [GeneDB:SCO5114] [NCBI-GI:21223485] [NCBI-GeneID:1100555] [UniProt:Q93IU1]
SCO5115	268	0.07007	-1.32	transporter activity	bldKD. SCBAC31E11.11; BldKD. putative ABC transporter intracellular ATPase subunit; K02031 peptide/nickel transport system ATP-binding protein; [GeneDB:SCO5115] [NCBI-GI:21223486] [NCBI-GeneID:1100556] [UniProt:Q93IU0]
SCO5116	257	0.06681	-1.34	metabolic process, transport	bldKE. SC9E12.01. SCBAC31E11.12; putative peptide transport system ATP-binding subunit; K02032 peptide/nickel transport system ATP-binding protein; [GeneDB:SCO5116] [NCBI-GI:32141254] [NCBI-GeneID:1100557] [UniProt:Q8CJS2]

SCO5117	224	0.05223	-1.23	transport	SC9E12.02; putative peptide transport system secreted peptide-binding protein; K02035 peptide/nickel transport system substrate-binding protein; [GeneDB:SCO5117] [NCBI-GI:21223487] [NCBI-GeneID:1100558] [UniProt:Q9F353]
SCO5125	335	0.11719	-0.99	DNA Binding	SC9E12.10c; hypothetical protein; [GeneDB:SCO5125] [NCBI-GI:21223495] [NCBI-GeneID:1100566] [UniProt:Q9F345]
SCO5174	162	0.02963	-1.48	metabolic process, catalytic activity	SCP8.37; transferase; [GeneDB:SCO5174] [NCBI-GI:21223543] [NCBI-GeneID:1100615] [UniProt:Q9FBI5]
SCO5175	151	0.02629	-1.51		SCP8.38; integral membrane protein; [GeneDB:SCO5175] [NCBI-GI:21223544] [NCBI-GeneID:1100616] [UniProt:Q9FBI4]
SCO5176	155	0.02858	-1.50	metabolic process, catalytic activity	SCP8.39; reductase; [GeneDB:SCO5176] [NCBI-GI:21223545] [NCBI-GeneID:1100617] [UniProt:Q9FBI3]
SCO5177	159	0.02937	-1.48		2SC3B6.01; hypothetical protein 2SC3B601; [GeneDB:SCO5177] [NCBI-GI:21223546] [NCBI-GeneID:1100618] [UniProt:Q9FCL1]
SCO5254	47	0.00277	-2.34	metabolic process, catalytic activity, metal ion binding	2SC7G11.16c. sodN; superoxide dismutase [EC:1.15.1.1]; K00518 superoxide dismutase; [GeneDB:SCO5254] [NCBI-GI:21223621] [NCBI-GeneID:1100695] [UniProt:P80735]
SCO5311	46	0.00261	-2.35		SC6G9.22; secreted protein; [GeneDB:SCO5311] [NCBI-GI:21223674] [NCBI-GeneID:1100751] [UniProt:Q9XAG0]
SCO5350	260	0.06827	-1.23		SCBAC5H2.19; hypothetical protein; [GeneDB:SCO5350] [NCBI-GI:21223711] [NCBI-GeneID:1100790] [UniProt:Q9ADB8]
SCO5385	351	0.12544	-0.99	metabolic process, catalytic activity, nucleotide binding	2SC6G5.29; putative 3-hydroxybutyryl-coA dehydrogenase [EC:1.1.1.157]; K00074 3-hydroxybutyryl-CoA dehydrogenase; [GeneDB:SCO5385] [NCBI-GI:21223745] [NCBI-GeneID:1100825] [UniProt:Q9K4C6]
SCO5390	248	0.06246	-1.28	metabolic process, catalytic activity	2SC6G5.34c; alkanal monooxygenase (luciferase); [GeneDB:SCO5390] [NCBI-GI:21223750] [NCBI-GeneID:1100830] [UniProt:Q9K4C1]
SCO5398	309	0.09835	-1.07		SC8F4.02c; hypothetical protein; [GeneDB:SCO5398] [NCBI-GI:21223758] [NCBI-GeneID:1100838] [UniProt:Q9L2C2]
SCO5399	61	0.00393	-2.02	metabolic process, catalytic activity	SC8F4.03; probable acetoacetyl-coA thiolase [EC:2.3.1.9]; K00626 acetyl-CoA C-acetyltransferase; [GeneDB:SCO5399] [NCBI-GI:21223759] [NCBI-GeneID:1100839] [UniProt:Q9L2C1]
SCO5400	118	0.01653	-1.67	cell organization and biogenesis, metabolic	SC8F4.04; putative transport system kinase [EC:2.7.-.-]; K07588 LAO/AO transport system kinase; [GeneDB:SCO5400] [NCBI-GI:21223760] [NCBI-GeneID:1100840] [UniProt:Q9L2C0]

				process, transport	
SCO5415	33	0.00152	-2.47	metabolic process, DNA binding	icmA. SC8F4.19; isobutyryl-CoA mutase A [EC:5.4.99.2]; K01848 methylmalonyl-CoA mutase. N-terminal domain; [GeneDB:SCO5415] [NCBI-GI:21223775] [NCBI-GeneID:1100855] [UniProt:Q9X949]
SCO5420	324	0.10769	-1.03		SC8F4.24; cholesterol esterase; [GeneDB:SCO5420] [NCBI-GI:21223780] [NCBI-GeneID:1100860] [UniProt:Q9L2A2]
SCO5421	300	0.09483	-1.11		SC8F4.25; integral membrane protein; [GeneDB:SCO5421] [NCBI-GI:21223781] [NCBI-GeneID:1100861] [UniProt:Q9L2A1]
SCO5442	321	0.10766	-1.12	metabolic process, catalytic activity	SC6A11.18c; trehalose synthase; [GeneDB:SCO5442] [NCBI-GI:21223801] [NCBI-GeneID:1100882] [UniProt:Q9L1K3]
SCO5443	382	0.14990	-0.94	metabolic process, catalytic activity	pep1A; putative alpha-amylase [EC:3.2.1.-]; K01238; [GeneDB:SCO5443] [NCBI-GI:21223802] [NCBI-GeneID:1100883] [UniProt:Q9L1K2]
SCO5444	301	0.09571	-1.18	metabolic process, catalytic activity	glgP. SC3D11.01. SC6A11.20; putative glycogen phosphorylase [EC:2.4.1.1]; K00688 starch phosphorylase; [GeneDB:SCO5444] [NCBI-GI:32141263] [NCBI-GeneID:1100884] [UniProt:Q8CJR4]
SCO5447	109	0.01688	-1.64	metabolic process, catalytic activity, metal ion binding	SC3D11.04c; neutral zinc metalloprotease; [GeneDB:SCO5447] [NCBI-GI:21223805] [NCBI-GeneID:1100887] [UniProt:Q9L1F8]
SCO5459	302	0.09629	-1.08	metabolic process, catalytic activity	SC3D11.16; enoyl-coA hydratase; [GeneDB:SCO5459] [NCBI-GI:21223817] [NCBI-GeneID:1100899] [UniProt:Q9L1E6]
SCO5466	197	0.04284	-1.28	metabolic process, catalytic activity	SC3D11.23c; hydrolase; [GeneDB:SCO5466] [NCBI-GI:21223824] [NCBI-GeneID:1100906] [UniProt:Q9L1D9]
SCO5476	313	0.10447	-1.07	transporter activity	SC2A11.10; oligopeptide transport integral membrane protein; K02034 peptide/nickel transport system permease protein; [GeneDB:SCO5476] [NCBI-GI:21223833] [NCBI-GeneID:1100916] [UniProt:O86571]
SCO5477	284	0.08039	-1.11	transporter activity	SC2A11.11; putative oligopeptide-binding lipoprotein; K02035 peptide/nickel transport system substrate-binding protein; [GeneDB:SCO5477] [NCBI-GI:21223834] [NCBI-GeneID:1100917] [UniProt:O86572]
SCO5478	199	0.04256	-1.30	transporter activity	SC2A11.12; oligopeptide transport system integral membrane protein; K02033 peptide/nickel transport system permease protein; [GeneDB:SCO5478] [NCBI-GI:21223835] [NCBI-GeneID:1100918] [UniProt:O86573]

SCO5479	329	0.11179	-1.06	metabolic process, transport	SC2A11.13; oligopeptide ABC transporter ATP-binding protein; K02031 peptide/nickel transport system ATP-binding protein; [GeneDB:SCO5479] [NCBI-GI:21223836] [NCBI-GeneID:1100919] [UniProt:O86574]
SCO5480	303	0.09604	-1.10	metabolic process, transport	SC2A11.14; oligopeptide ABC transporter ATP-binding protein; K02032 peptide/nickel transport system ATP-binding protein; [GeneDB:SCO5480] [NCBI-GI:21223837] [NCBI-GeneID:1100920] [UniProt:O86575]
SCO5511	322	0.10748	-1.05	transporter activity	SC8D9.23; membrane associated phosphodiesterase; [GeneDB:SCO5511] [NCBI-GI:21223867] [NCBI-GeneID:1100951] [UniProt:Q9Z568]
SCO5629	249	0.06249	-1.32	stimulus response	SC6A9.38; ATP/GTP-binding protein; [GeneDB:SCO5629] [NCBI-GI:21223984] [NCBI-GeneID:1101070] [UniProt:O86768]
SCO5644	182	0.03808	-1.38		SC6A9.23c; hypothetical protein; [GeneDB:SCO5644] [NCBI-GI:21223995] [NCBI-GeneID:1101083] [UniProt:O86755]
SCO5658	81	0.00901	-1.84		SC6A9.09c; polyamine-binding lipoprotein; [GeneDB:SCO5658] [NCBI-GI:21224009] [NCBI-GeneID:1101097] [UniProt:O86741]
SCO5667	305	0.09570	-1.10	transporter activity	SC8B7.11c; putative ABC-transporter polyamine-binding lipoprotein; K02055 spermidine/putrescine transport system substrate-binding protein; [GeneDB:SCO5667] [NCBI-GI:21224017] [NCBI-GeneID:1101106] [UniProt:O86832]
SCO5676	13	0.00077	-2.96	metabolic process, catalytic activity	gabT; putative 4-aminobutyrate aminotransferase [EC:2.6.1.19]; K00823 4-aminobutyrate aminotransferase; [GeneDB:SCO5676] [NCBI-GI:21224026] [NCBI-GeneID:1101115] [UniProt:O86823]
SCO5679	63	0.00397	-1.98	metabolic process, catalytic activity	SC5H4.03; putative aldehyde dehydrogenase [EC:1.2.1.3]; K00128 aldehyde dehydrogenase (NAD+); [GeneDB:SCO5679] [NCBI-GI:21224028] [NCBI-GeneID:1101118] [UniProt:Q9KYT6]
SCO5784	304	0.09586	-1.07	cell communication, metabolic process, regulation of biological process, response to stimulus, DNA binding	SC4H2.05; two-component sensor; [GeneDB:SCO5784] [NCBI-GI:21224129] [NCBI-GeneID:1101226] [UniProt:O69960]
SCO5785	237	0.05827	-1.26	cell communication, metabolic process,	SC4H2.06; two-component regulator; [GeneDB:SCO5785] [NCBI-GI:21224130] [NCBI-GeneID:1101227] [UniProt:O69961]

				regulation of biological process, response to stimulus, DNA binding stimulus response	
SCO5811	347	0.12303	-1.01	metabolic process, catalytic activity, DNA binding	SC4H2.32; transcriptional regulator; [GeneDB:SCO5811] [NCBI-GI:32141274] [NCBI-GeneID:1101253] [UniProt:Q8CJQ4]
SCO5819	247	0.06267	-1.23	cell communication, metabolic process, regulation of biological process, response to stimulus, DNA binding	sporulation transcription factor. WhiH; [GeneDB:SCO5819] [NCBI-GI:21224163] [NCBI-GeneID:1101261] [UniProt:O50536]
SCO5879	340	0.11809	-1.05	metabolic process, catalytic activity, nucleotide binding	redW; acyl-CoA dehydrogenase RedW; [GeneDB:SCO5879] [NCBI-GI:21224222] [NCBI-GeneID:1101321] [UniProt:O54143]
SCO5880	152	0.02638	-1.50		redY; RedY protein; [GeneDB:SCO5880] [NCBI-GI:21224223] [NCBI-GeneID:1101322] [UniProt:O54144]
SCO5884	278	0.07878	-1.20		SC3F7.04c; hypothetical protein; [GeneDB:SCO5884] [NCBI-GI:21224226] [NCBI-GeneID:1101326] [UniProt:O54147]
SCO5885	21	0.00095	-2.90		SC3F7.05c; hypothetical protein; [GeneDB:SCO5885] [NCBI-GI:21224227] [NCBI-GeneID:1101327] [UniProt:O54148]
SCO5886	272	0.07147	-1.24	metabolic process, catalytic activity	redR. SC3F7.06c; 3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]; K09458 3-oxoacyl-[acyl-carrier-protein] synthase II; [GeneDB:SCO5886] [NCBI-GI:21224228] [NCBI-GeneID:1101328] [UniProt:O54149]
SCO5887	246	0.06276	-1.31		redQ. SC3F7.07c; acyl carrier protein; K02078 acyl carrier protein; [GeneDB:SCO5887] [NCBI-GI:21224229] [NCBI-GeneID:1101329] [UniProt:O54150]
SCO5888	345	0.12290	-1.10	metabolic process, catalytic activity	redP. SC3F7.08; 3-oxoacyl-[acyl-carrier-protein] synthase [EC:2.3.1.180]; K00648 3-oxoacyl-[acyl-carrier-protein] synthase III; [GeneDB:SCO5888] [NCBI-GI:21224230] [NCBI-GeneID:1101330] [UniProt:O54151]
SCO5889	27	0.00148	-2.75		redO. SC3F7.09; hypothetical protein; [GeneDB:SCO5889] [NCBI-GI:21224231] [NCBI-GeneID:1101331] [UniProt:O54152]
SCO5890	187	0.03973	-1.50	metabolic process, catalytic activity	redN. SC3F7.10; 8-amino-7-oxononanoate synthase; [GeneDB:SCO5890] [NCBI-GI:21224232] [NCBI-GeneID:1101332] [UniProt:O54153]
SCO5891	233	0.05494	-1.31	metabolic process,	redM. St3F7.11; peptide synthase; [GeneDB:SCO5891] [NCBI-GI:21224233] [NCBI-

				catalytic activity, nucleotide binding	GeneID:1101333] [UniProt:O54154]
SCO5893	168	0.03185	-1.53	metabolic process, catalytic activity	redK. SC3F7.13; oxidoreductase; [GeneDB:SCO5893] [NCBI-GI:21224235] [NCBI- GeneID:1101335] [UniProt:O54156]
SCO5894	277	0.07791	-1.12	metabolic process, catalytic activity	redJ. SC3F7.14; thioesterase; [GeneDB:SCO5894] [NCBI-GI:21224236] [NCBI- GeneID:1101336] [UniProt:O54157]
SCO5895	166	0.03084	-1.50	metabolic process, catalytic activity	redI. SC3F7.15; methyltransferase; [GeneDB:SCO5895] [NCBI-GI:21224237] [NCBI- GeneID:1101337] [UniProt:O54158]
SCO5896	198	0.04263	-1.43	metabolic process, catalytic activity, nucleotide binding	redH. SC10A5.01. SC3F7.16; phosphoenolpyruvate-utilizing enzyme [EC:2.7.9.2]; K01007 pyruvate.water dikinase; [GeneDB:SCO5896] [NCBI-GI:32141277] [NCBI- GeneID:1101338] [UniProt:Q8CJQ2]
SCO5897	87	0.00931	-1.97	metabolic process, catalytic activity	redG. SC10A5.02; oxidase; [GeneDB:SCO5897] [NCBI-GI:21224238] [NCBI- GeneID:1101339] [UniProt:O54095]
SCO5898	283	0.07943	-1.17	metabolic process, catalytic activity	redF. SC10A5.03; probable membrane protein; [GeneDB:SCO5898] [NCBI- GI:21224239] [NCBI-GeneID:1101340] [UniProt:O54096]
SCO5932	376	0.14896	-1.04	metabolic process, catalytic activity	abfB; arabinofuranosidase [EC:3.2.1.55]; K01209 alpha-N-arabinofuranosidase; [GeneDB:SCO5932] [NCBI-GI:21224270] [NCBI-GeneID:1101374] [UniProt:O54161]
SCO5965	234	0.05521	-1.53		SC7H1.35; integral membrane protein; [GeneDB:SCO5965] [NCBI-GI:21224303] [NCBI-GeneID:1101407] [UniProt:O54194]
SCO5993	146	0.02589	-1.48		StBAC16H6.28; hypothetical protein; [GeneDB:SCO5993] [NCBI-GI:21224330] [NCBI-GeneID:1101435] [UniProt:Q93JD4]
SCO6026	213	0.04826	-1.24	metabolic process, catalytic activity	SC1C3.14c; fatty acid oxidation complex alpha-subunit; [GeneDB:SCO6026] [NCBI- GI:21224358] [NCBI-GeneID:1101467] [UniProt:O69856]
SCO6027	211	0.04725	-1.23	metabolic process, catalytic activity	SC1C3.15c; acetyl-coa acetyltransferase (thiolase); [GeneDB:SCO6027] [NCBI- GI:21224359] [NCBI-GeneID:1101468] [UniProt:O69857]
SCO6155	334	0.11713	-1.06	metabolic process, catalytic activity, metal ion binding	SC1A9.19; pyruvate dehydrogenase [EC:1.2.2.2]; K00156 pyruvate dehydrogenase (cytochrome); [GeneDB:SCO6155] [NCBI-GI:21224481] [NCBI-GeneID:1101596] [UniProt:Q9ZBT3]
SCO6160	6	0.00000	-3.46	transporter activity	SC1A9.24c; putative SecDF protein-export membrane protein; K03072 preprotein translocase SecD subunit; K03074 preprotein translocase SecF subunit; [GeneDB:SCO6160] [NCBI-GI:21224486] [NCBI-GeneID:1101601] [UniProt:Q9ZBS8]
SCO6161	16	0.00125	-2.87		SC1A9.25c; secreted protein; [GeneDB:SCO6161] [NCBI-GI:21224487] [NCBI- GeneID:1101602] [UniProt:Q9ZBS7]
SCO6162	36	0.00250	-2.50	cell communication,	SC1A9.26c; two-component system response regulator; [GeneDB:SCO6162] [NCBI-

				metabolic process, regulation of biological process, response to stimulus, DNA binding stimulus response	GI:21224488] [NCBI-GeneID:1101603] [UniProt:Q9ZBS6]
SCO6163	76	0.00789	-2.09	metabolic process, regulation of biological process, response to stimulus, DNA binding	SC1A9.27c; sensor kinase; [GeneDB:SCO6163] [NCBI-GI:21224489] [NCBI-GeneID:1101604] [UniProt:Q9ZBS5]
SCO6164	1	0.00000	-5.26		SC1A9.28c; putative DnaK suppressor protein; K06204 DnaK suppressor protein; [GeneDB:SCO6164] [NCBI-GI:21224490] [NCBI-GeneID:1101605] [UniProt:Q9ZBS4]
SCO6165	11	0.00000	-3.07		SC1A9.29c. SC6C5.01; hypothetical protein; [GeneDB:SCO6165] [NCBI-GI:32141289] [NCBI-GeneID:1101606] [UniProt:Q8CJP0]
SCO6166	5	0.00000	-3.64		SC6C5.02; hypothetical protein; [GeneDB:SCO6166] [NCBI-GI:21224491] [NCBI-GeneID:1101607] [UniProt:Q9ZBP3]
SCO6167	30	0.00133	-2.56		SC6C5.03; proline rich protein (membrane protein); [GeneDB:SCO6167] [NCBI-GI:21224492] [NCBI-GeneID:1101608] [UniProt:Q9ZBP2]
SCO6173	368	0.14245	-0.97	transporter activity	SC6C5.09; putative permease SC6C5.09; K06901 putative MFS transporter. AGZA family. xanthine/uracil permease; [GeneDB:SCO6173] [NCBI-GI:21224498] [NCBI-GeneID:1101614] [UniProt:Q9ZBN6]
SCO6205	364	0.14184	-1.00	metabolic process, catalytic activity	SC2G5.26c; putative dehydrogenase [EC:1.1.1.60]; K00042 2-hydroxy-3-oxopropionate reductase; [GeneDB:SCO6205] [NCBI-GI:21224529] [NCBI-GeneID:1101646] [UniProt:Q9Z597]
SCO6206	350	0.12386	-1.05	metabolic process, DNA binding	SC2G5.27c; putative oxidoreductase [EC:5.3.1.22]; K01816 hydroxypyruvate isomerase; [GeneDB:SCO6206] [NCBI-GI:21224530] [NCBI-GeneID:1101647] [UniProt:Q9Z596]
SCO6243	259	0.06776	-1.22	metabolic process, catalytic activity	aceB1. SCAH10.08c; malate synthase [EC:2.3.3.9]; K01638 malate synthase; [GeneDB:SCO6243] [NCBI-GI:21224564] [NCBI-GeneID:1101684] [UniProt:Q9RKU9]
SCO6375	206	0.04481	-1.26		SC4A2.11c; secreted protein; [GeneDB:SCO6375] [NCBI-GI:21224687] [NCBI-GeneID:1101816] [UniProt:O86667]
SCO6393	375	0.14891	-1.04	DNA Binding	SC3C8.12; transposase; [GeneDB:SCO6393] [NCBI-GI:21224705] [NCBI-GeneID:1101834] [UniProt:O69924]
SCO6414	156	0.02904	-1.47	metabolic process,	SC1A6.03; hypothetical protein; [GeneDB:SCO6414] [NCBI-GI:21224721] [NCBI-

				catalytic activity	GeneID:1101853] [UniProt:O69808]
SCO6416	314	0.10427	-1.07	metabolic process, catalytic activity	SC1A6.05; oxidoreductase; [GeneDB:SCO6416] [NCBI-GI:21224723] [NCBI-GeneID:1101855] [UniProt:O69810]
SCO6417	244	0.06045	-1.29	transporter activity	SC1A6.06; putative integral membrane transporter; K03457 nucleobase:cation symporter-1. NCS1 family; [GeneDB:SCO6417] [NCBI-GI:21224724] [NCBI-GeneID:1101856] [UniProt:O69811]
SCO6423	154	0.02799	-1.48	metabolic process, catalytic activity	SC1A6.12c; putative lipoate-protein ligase [EC:2.7.7.63]; K03800 lipoate-protein ligase A; [GeneDB:SCO6423] [NCBI-GI:21224730] [NCBI-GeneID:1101862] [UniProt:O69817]
SCO6424	44	0.00273	-2.44	response to stimulus	SC1A6.13c; two-component system sensor protein; [GeneDB:SCO6424] [NCBI-GI:21224731] [NCBI-GeneID:1101863] [UniProt:O69818]
SCO6469	352	0.12636	-1.01	metabolic process, catalytic activity	SC9C7.05c; putative acyl-CoA dehydrogenase [EC:1.3.99.-]; K00257; [GeneDB:SCO6469] [NCBI-GI:21224773] [NCBI-GeneID:1101908] [UniProt:Q9ZBK5]
SCO6470	333	0.11676	-1.06	metabolic process, catalytic activity	SC9C7.06c; hypothetical protein; [GeneDB:SCO6470] [NCBI-GI:21224774] [NCBI-GeneID:1101909] [UniProt:Q9ZBK4]
SCO6472	74	0.00743	-1.82	metabolic process, catalytic activity, metal ion binding	SC9C7.08c; coenzyme B12-dependent mutase [EC:5.4.99.2]; K01848 methylmalonyl-CoA mutase.N-terminal domain; K01849 methylmalonyl-CoA mutase.C-terminal domain; [GeneDB:SCO6472] [NCBI-GI:21224776] [NCBI-GeneID:1101911] [UniProt:Q9ZBK2]
SCO6473	31	0.00129	-2.44	metabolic process, catalytic activity	SC9C7.09c; crotonyl CoA reductase; [GeneDB:SCO6473] [NCBI-GI:21224777] [NCBI-GeneID:1101912] [UniProt:Q9ZBK1]
SCO6475	358	0.13827	-1.01	metabolic process, catalytic activity, nucleotide binding	SC9C7.11c; oxidoreductase; [GeneDB:SCO6475] [NCBI-GI:21224779] [NCBI-GeneID:1101914] [UniProt:Q9ZBJ9]
SCO6629	136	0.02419	-1.52	DNA binding	SC4G2.03; hypothetical protein; [GeneDB:SCO6629] [NCBI-GI:21224926] [NCBI-GeneID:1102068] [UniProt:O86676]
SCO6641	291	0.08368	-1.16		SC4G2.15c; hypothetical protein; [GeneDB:SCO6641] [NCBI-GI:21224938] [NCBI-GeneID:1102080] [UniProt:O86687]
SCO6647	53	0.00321	-2.22	metabolic process, catalytic activity	SC4G2.21c; integral membrane protein; [GeneDB:SCO6647] [NCBI-GI:21224944] [NCBI-GeneID:1102086] [UniProt:O86693]
SCO6650	2	0.00000	-4.13		SC4G2.24; hypothetical protein; [GeneDB:SCO6650] [NCBI-GI:21224947] [NCBI-GeneID:1102089] [UniProt:O86696]
SCO6651	9	0.00000	-3.14	metabolic process, catalytic activity	SC4G2.25. SC5A7.01; glycosyl transferase; [GeneDB:SCO6651] [NCBI-GI:32141310] [NCBI-GeneID:1102090] [UniProt:Q8CJM1]

SCO6652	17	0.00118	-3.03		SC5A7.02; hypothetical protein; [GeneDB:SCO6652] [NCBI-GI:21224948] [NCBI-GeneID:1102091] [UniProt:O88008]
SCO6653	73	0.00712	-2.09		SC5A7.03; hypothetical protein; [GeneDB:SCO6653] [NCBI-GI:21224949] [NCBI-GeneID:1102092] [UniProt:O88009]
SCO6655	10	0.00000	-3.14	metabolic process, catalytic activity, metal ion binding	ribA2. SC5A7.05; GTP cyclohydrolase II [EC:3.5.4.25]; K01497 GTP cyclohydrolase II; [GeneDB:SCO6655] [NCBI-GI:21224951] [NCBI-GeneID:1102094] [UniProt:O88011]
SCO6749	138	0.02435	-1.58		SC5F2A.32; hypothetical protein; [GeneDB:SCO6749] [NCBI-GI:21225043] [NCBI-GeneID:1102188] [UniProt:Q9X7Q5]
SCO6794	286	0.08213	-1.22		cvnA7. SC1A2.03; membrane protein; [GeneDB:SCO6794] [NCBI-GI:21225087] [NCBI-GeneID:1102233] [UniProt:Q9L238]
SCO6795	160	0.02931	-1.56		cvnB7. SC1A2.04; hypothetical protein; [GeneDB:SCO6795] [NCBI-GI:21225088] [NCBI-GeneID:1102234] [UniProt:Q9L237]
SCO6796	186	0.03919	-1.45		cvnC7. SC1A2.05; hypothetical protein; [GeneDB:SCO6796] [NCBI-GI:21225089] [NCBI-GeneID:1102235] [UniProt:Q9L236]
SCO6797	115	0.01626	-1.74		cvnD7. SC1A2.06; ATP/GTP binding protein; [GeneDB:SCO6797] [NCBI-GI:21225090] [NCBI-GeneID:1102236] [UniProt:Q9L235]
SCO6798	190	0.04100	-1.47		SC1A2.07; hypothetical protein; [GeneDB:SCO6798] [NCBI-GI:21225091] [NCBI-GeneID:1102237] [UniProt:Q9L234]
SCO6885	275	0.07462	-1.33	metabolic process, regulation of biological process, DNA binding, catalytic activity	SC7F9.37; putative DNA methylase [EC:2.1.1.72]; K07319 putative adenine-specific DNA-methyltransferase; [GeneDB:SCO6885] [NCBI-GI:21225176] [NCBI-GeneID:1102324] [UniProt:Q9L1N0]
SCO6906	274	0.07471	-1.16		SC1B2.12c; hypothetical protein; [GeneDB:SCO6906] [NCBI-GI:21225196] [NCBI-GeneID:1102345] [UniProt:Q9KYC4]
SCO6919	293	0.08539	-1.12		SC1B2.25c; hypothetical protein; [GeneDB:SCO6919] [NCBI-GI:21225207] [NCBI-GeneID:1102357] [UniProt:Q9KYB4]
SCO6941	209	0.04483	-1.39		cvnC8. SC1G8.13c; hypothetical protein; [GeneDB:SCO6941] [NCBI-GI:21225228] [NCBI-GeneID:1102379] [UniProt:Q9KYK0]
SCO6982	317	0.10420	-1.09		SC8F11.08; lolE protein; K03335 myo-inositol catabolism protein lolE; [GeneDB:SCO6982] [NCBI-GI:21225268] [NCBI-GeneID:1102420] [UniProt:Q9KZH0]
SCO6992	133	0.02353	-1.60	metabolic process, catalytic activity, metal ion binding	absR1. SC8F11.18c; regulatory protein; [GeneDB:SCO6992] [NCBI-GI:21225278] [NCBI-GeneID:1102430] [UniProt:Q9RGD7]
SCO7040	287	0.08345	-1.34	metabolic process,	gap2. SC4G1.06c; glyceraldehyde-3-phosphate dehydrogenase;

				catalytic activity, nucleotide binding	[GeneDB:SCO7040] [NCBI-GI:21225323] [NCBI-GeneID:1102478] [UniProt:Q9FC43]
SCO7079	370	0.14432	-0.99		SC3A4.05; pseudogene; [GeneDB:SCO7079] [NCBI-GeneID:1102517]
SCO7095	174	0.03500	-1.46	metabolic process, catalytic activity	SC3A4.21c; hydrolase; [GeneDB:SCO7095] [NCBI-GI:21225377] [NCBI-GeneID:1102533] [UniProt:Q9KZ37]
SCO7130	273	0.07341	-1.22		SC4B10.31; hypothetical protein; [GeneDB:SCO7130] [NCBI-GI:21225412] [NCBI-GeneID:1102568] [UniProt:Q9FC56]
SCO7131	288	0.08347	-1.08	metabolic process, catalytic activity, metal ion binding	SC4B10.32; lipase; [GeneDB:SCO7131] [NCBI-GI:21225413] [NCBI-GeneID:1102569] [UniProt:Q9FC55]
SCO7189	338	0.11737	-1.17		SC8A11.17c; hypothetical protein; [GeneDB:SCO7189] [NCBI-GI:21225468] [NCBI-GeneID:1102627] [UniProt:Q9FBZ3]
SCO7190	86	0.00942	-1.81	metabolic process, catalytic activity	SC8A11.18; hypothetical protein; [GeneDB:SCO7190] [NCBI-GI:21225469] [NCBI-GeneID:1102628] [UniProt:Q9FBZ2]
SCO7197	132	0.02182	-1.61	transporter activity	SC8A11.25c; amino acid transport integral membrane protein; [GeneDB:SCO7197] [NCBI-GI:21225476] [NCBI-GeneID:1102635] [UniProt:Q9FBY5]
SCO7208	341	0.11792	-1.01		SC2H12.07c; hypothetical protein; [GeneDB:SCO7208] [NCBI-GI:21225485] [NCBI-GeneID:1102646] [UniProt:Q9K477]
SCO7226	202	0.04337	-1.26		SC2H12.25; integral membrane protein; [GeneDB:SCO7226] [NCBI-GI:21225503] [NCBI-GeneID:1102664] [UniProt:Q9K459]
SCO7253	298	0.09010	-1.14	cell communication, metabolic process, stimulus response	SC5H1.39; hypothetical protein; [GeneDB:SCO7253] [NCBI-GI:21225530] [NCBI-GeneID:1102691] [UniProt:Q9X7U6]
SCO7271	383	0.14950	-0.99		SC5H1.21c; ion channel subunit; [GeneDB:SCO7271] [NCBI-GI:21225548] [NCBI-GeneID:1102709] [UniProt:Q9X7S9]
SCO7291	230	0.05348	-1.28	metabolic process, catalytic activity	SC5F8.01c. SC5H1.01; serine/threonine protein kinase; [GeneDB:SCO7291] [NCBI-GI:32141327] [NCBI-GeneID:1102729] [UniProt:Q8CJK5]
SCO7336	326	0.10908	-1.36		pepA. SC4G10.15c; hypothetical protein; [GeneDB:SCO7336] [NCBI-GI:21225611] [NCBI-GeneID:1102774] [UniProt:O54206]
SCO7337	289	0.08325	-1.12		pepA2. SC4G10.16; hypothetical protein; [GeneDB:SCO7337] [NCBI-GI:21225612] [NCBI-GeneID:1102775] [UniProt:O54205]

SCO7408	307	0.09687	-1.16	transporter activity	SC6D11.04c; probable solute-binding lipoprotein.; K02027 multiple sugar transport system substrate-binding protein; [GeneDB:SCO7408] [NCBI-GI:21225678] [NCBI-GeneID:1102846] [UniProt:Q9L151]
SCO7472	214	0.04879	-1.27		paaB. SCBAC17A6.05; putative phenylacetic acid degradation protein PaaB; K02610 phenylacetic acid degradation protein; [GeneDB:SCO7472] [NCBI-GI:21225740] [NCBI-GeneID:1102910] [UniProt:Q93JC4]
SCO7473	353	0.13006	-1.01		paaC. SCBAC17A6.06; putative phenylacetic acid degradation protein PaaC; K02611 phenylacetic acid degradation protein; [GeneDB:SCO7473] [NCBI-GI:21225741] [NCBI-GeneID:1102911] [UniProt:Q93JC3]
SCO7474	342	0.11906	-1.01		paaD. SCBAC17A6.07; putative phenylacetic acid degradation protein PaaD; K02612 phenylacetic acid degradation protein; [GeneDB:SCO7474] [NCBI-GI:21225742] [NCBI-GeneID:1102912] [UniProt:Q93JC2]
SCO7475	365	0.14233	-0.95	metabolic process, response to stimulus	SCBAC17A6.08; putative phenylacetic acid degradation NADH oxidoreductase PaaE; K02613 phenylacetic acid degradation NADH oxidoreductase; [GeneDB:SCO7475] [NCBI-GI:21225743] [NCBI-GeneID:1102913] [UniProt:Q93JC1]
SCO7524	374	0.14626	-0.96		SCBAC25F8.16; hypothetical protein; [GeneDB:SCO7524] [NCBI-GI:21225790] [NCBI-GeneID:1102962] [UniProt:Q93IZ6]
SCO7573	126	0.01889	-1.86	metabolic process, regulation of biological process	SC5F1.27c; anti-sigma factor antagonist; [GeneDB:SCO7573] [NCBI-GI:21225837] [NCBI-GeneID:1103011] [UniProt:Q9F3A2]
SCO7612	106	0.01387	-1.75		SC2H2.10c; hypothetical protein; [GeneDB:SCO7612] [NCBI-GI:21225874] [NCBI-GeneID:1103050] [UniProt:Q9F3E5]
SCO7643	238	0.05908	-1.56		SC10F4.16; hypothetical protein; [GeneDB:SCO7643] [NCBI-GI:21225904] [NCBI-GeneID:1103081] [UniProt:Q9F3P4]
SCO7700	223	0.05224	-1.26	metabolic process, catalytic activity, metal ion binding	SC1A4.08. SCBAC12C8.01; cyclase; [GeneDB:SCO7700] [NCBI-GI:32141341] [NCBI-GeneID:1103138] [UniProt:Q9F1Y6]
SCO7701	245	0.06147	-1.33	metabolic process, catalytic activity	SCBAC12C8.02; methyltransferase; [GeneDB:SCO7701] [NCBI-GI:21225960] [NCBI-GeneID:1103139] [UniProt:Q9F1Y5]
SCO7726	165	0.03079	-1.46	metabolic process, catalytic activity	SC8D11.17; hydrolase; [GeneDB:SCO7726] [NCBI-GI:21225985] [NCBI-GeneID:1103164] [UniProt:Q9AK02]
SCO7727	218	0.05119	-1.25	metabolic process, regulation of biological process	SC8D11.18c; MarR-family regulatory protein; [GeneDB:SCO7727] [NCBI-GI:21225986] [NCBI-GeneID:1103165] [UniProt:Q9AK01]

SCO7786	241	0.05913	-1.23		SC5E9.34c; hypothetical protein; [GeneDB:SCO7786] [NCBI-GI:21226037] [NCBI-GeneID:1103223] [UniProt:Q9EWK7]
SCO7837	242	0.05905	-1.31		SC8E7.34c; membrane protein; [GeneDB:SCO7837] [NCBI-GI:21226086] [NCBI-GeneID:1103275] [UniProt:Q9S1Y4]
Gene	Rank of up-regulated genes	pfp value	Log(2) Average	GO Biological Process / Molecular Function	Product/Function
SCO0074	165	0.06436	1.28		SCJ11.03; hypothetical protein; [GeneDB:SCO0074] [NCBI-GI:21218648] [NCBI-GeneID:1095505] [UniProt:Q9RIA1]
SCO0140	131	0.04305	1.49	metabolic process, regulation of biological process, DNA binding, nucleotide binding	SCJ33.04; MerR-family transcriptional regulator; [GeneDB:SCO0140] [NCBI-GI:21218699] [NCBI-GeneID:1095564] [UniProt:Q9RIX3]
SCO0171	249	0.14510	0.95	metabolic process, catalytic activity, metal ion binding	SCJ1.20; nicotinate phosphoribosyltransferase [EC:2.4.2.11]; K00763 nicotinate phosphoribosyltransferase; [GeneDB:SCO0171] [NCBI-GI:21218728] [NCBI-GeneID:1095595] [UniProt:Q9RIZ4]
SCO0231	146	0.05226	1.32	metabolic process, structural molecule activity	SCJ9A.10c; small hydrophobic hypothetical protein; [GeneDB:SCO0231] [NCBI-GI:21218784] [NCBI-GeneID:1095655] [UniProt:Q9S1R0]
SCO0446	194	0.09897	1.33		SCF51A.24c; hypothetical protein; [GeneDB:SCO0446] [NCBI-GI:21218988] [NCBI-GeneID:1095869] [UniProt:Q9RL40]
SCO0472	256	0.14766	1.02		SCF76.12c; secreted protein; [GeneDB:SCO0472] [NCBI-GI:21219012] [NCBI-GeneID:1095895] [UniProt:Q9RJG2]
SCO0476	105	0.02524	1.47	metabolic process, catalytic activity	SCF76.16; ABC transport protein. ATP-binding subunit; K02074 zinc/manganese transport system ATP-binding protein; [GeneDB:SCO0476] [NCBI-GI:21219016] [NCBI-GeneID:1095899] [UniProt:Q9RJF8]
SCO0489	51	0.00549	1.91		SCF34.08c; hypothetical protein; K05375 MbtH protein; [GeneDB:SCO0489] [NCBI-GI:21219027] [NCBI-GeneID:1095912] [UniProt:Q9RK17]
SCO0498	139	0.04885	1.39	metabolic process, catalytic activity	SCF34.17c; putative peptide monooxygenase [EC:1.13.12.-]; K00468; [GeneDB:SCO0498] [NCBI-GI:21219036] [NCBI-GeneID:1095921] [UniProt:Q9RK08]
SCO0499	252	0.14464	1.07		SCF34.18; formyltransferase; [GeneDB:SCO0499] [NCBI-GI:21219037] [NCBI-GeneID:1095922] [UniProt:Q9RK07]
SCO0694	250	0.14480	1.03		SCF42.04; hypothetical protein; [GeneDB:SCO0694] [NCBI-GI:21219222] [NCBI-GeneID:1096117] [UniProt:Q9L2K9]

SCO0715	181	0.08193	1.15		SCF42.25c; hypothetical protein; [GeneDB:SCO0715] [NCBI-GI:21219241] [NCBI-GeneID:1096138] [UniProt:Q9L2J4]
SCO0859	158	0.05911	1.35		SCM2.12c; membrane protein; [GeneDB:SCO0859] [NCBI-GI:21219380] [NCBI-GeneID:1096282] [UniProt:Q9RCV2]
SCO0860	61	0.00885	1.91	metabolic process, catalytic activity, transport, metal ion binding	SCM2.13c; probable cation-transporting ATPase [EC:3.6.3.-]; K01552; [GeneDB:SCO0860] [NCBI-GI:21219381] [NCBI-GeneID:1096283] [UniProt:Q9RCV1]
SCO0861	12	0.00083	3.03		SCM2.14c; secreted protein; [GeneDB:SCO0861] [NCBI-GI:21219382] [NCBI-GeneID:1096284] [UniProt:Q9RCV0]
SCO0862	74	0.01149	1.84		SCM2.15c; integral membrane protein; [GeneDB:SCO0862] [NCBI-GI:21219383] [NCBI-GeneID:1096285] [UniProt:Q9RCU9]
SCO0863	37	0.00324	2.31		SCM2.16c; integral membrane protein; [GeneDB:SCO0863] [NCBI-GI:21219384] [NCBI-GeneID:1096286] [UniProt:Q9RCU8]
SCO0865	64	0.01094	1.84		SCM2.18c; integral-membrane protein; [GeneDB:SCO0865] [NCBI-GI:21219386] [NCBI-GeneID:1096288] [UniProt:Q9RCU6]
SCO0866	118	0.03280	1.56	metabolic process, regulation of biological process, DNA binding	SCM2.19c; probable ECF-family sigma factor; K03088 RNA polymerase sigma-70 factor. ECF subfamily; [GeneDB:SCO0866] [NCBI-GI:21219387] [NCBI-GeneID:1096289] [UniProt:Q9RCU5]
SCO0867	172	0.06936	1.23		SCM2.20c; integral-membrane protein; [GeneDB:SCO0867] [NCBI-GI:21219388] [NCBI-GeneID:1096290] [UniProt:Q9RCU4]
SCO0888	63	0.01063	1.77	metabolic process, catalytic activity	SCM1.21; secreted protein; [GeneDB:SCO0888] [NCBI-GI:21219408] [NCBI-GeneID:1096311] [UniProt:Q9RD22]
SCO0922	221	0.11615	1.23		SCM10.10c; putative reductase iron-sulfur protein [EC:1.3.99.1]; K00240 succinate dehydrogenase iron-sulfur protein; [GeneDB:SCO0922] [NCBI-GI:21219441] [NCBI-GeneID:1096345] [UniProt:Q9RCY8]
SCO0923	137	0.04730	1.42		SCM10.11c; putative reductase flavoprotein subunit [EC:1.3.99.1]; K00239 succinate dehydrogenase flavoprotein subunit; [GeneDB:SCO0923] [NCBI-GI:21219442] [NCBI-GeneID:1096346] [UniProt:Q9RCY7]
SCO0924	84	0.01619	1.66	metabolic process, catalytic activity	SCM10.12c; putative cytochrome B subunit [EC:1.3.99.1]; K00241 succinate dehydrogenase cytochrome b-556 subunit; [GeneDB:SCO0924] [NCBI-GI:21219443] [NCBI-GeneID:1096347] [UniProt:Q9RCY6]
SCO0958	186	0.08559	1.13	metabolic process, catalytic activity	SCM11.13c; hypothetical protein; [GeneDB:SCO0958] [NCBI-GI:21219476] [NCBI-GeneID:1096381] [UniProt:Q9RIU8]
SCO0973	206	0.10757	1.16		SCM11.28; integral membrane protein; [GeneDB:SCO0973] [NCBI-GI:21219491]

					[NCBI-GeneID:1096396] [UniProt:Q9RIT4]
SCO0988	232	0.12754	1.09	metabolic process, catalytic activity	2SCG2.01; acetyltransferase; [GeneDB:SCO0988] [NCBI-GI:21219505] [NCBI-GeneID:1096411] [UniProt:Q8R5N4]
SCO0999	50	0.00500	1.98	metabolic process, catalytic activity, metal ion binding	2SCG2.12c. sodF2; superoxide dismutase [EC:1.15.1.1]; K00518 superoxide dismutase; [GeneDB:SCO0999] [NCBI-GI:21219516] [NCBI-GeneID:1096422] [UniProt:Q9X469]
SCO1033	243	0.13519	1.11		SCG20A.13c; hypothetical protein; [GeneDB:SCO1033] [NCBI-GI:21219549] [NCBI-GeneID:1096456] [UniProt:Q9K3M7]
SCO1067	185	0.08476	1.18		SCG22.13; integral membrane transport protein; [GeneDB:SCO1067] [NCBI-GI:21219582] [NCBI-GeneID:1096490] [UniProt:Q9K432]
SCO1138	81	0.01333	1.68		2SCG38.31; putative tricarboxylic transport membrane protein; K07795 putative tricarboxylic transport membrane protein; [GeneDB:SCO1138] [NCBI-GI:21219652] [NCBI-GeneID:1096561] [UniProt:Q9EWY8]
SCO1139	119	0.03294	1.42		2SCG38.32; integral membrane protein; [GeneDB:SCO1139] [NCBI-GI:21219653] [NCBI-GeneID:1096562] [UniProt:Q9EWY7]
SCO1140	151	0.05556	1.29		2SCG38.33; putative integral membrane protein; K07793 putative tricarboxylic transport membrane protein; [GeneDB:SCO1140] [NCBI-GI:21219654] [NCBI-GeneID:1096563] [UniProt:Q9EWY6]
SCO1250	33	0.00303	2.17	metabolic process, catalytic activity	2SCG1.25; acetyltransferase; [GeneDB:SCO1250] [NCBI-GI:21219759] [NCBI-GeneID:1096673] [UniProt:Q9FCB7]
SCO1364	115	0.03035	1.43	metabolic process	SC10A9.06c; hypothetical protein; [GeneDB:SCO1364] [NCBI-GI:21219869] [NCBI-GeneID:1096787] [UniProt:Q9AK98]
SCO1523	208	0.11111	1.18		SCL2.13c; pyridoxine biosynthesis protein [EC:4.-.-.-]; K06215 pyridoxine biosynthesis protein; [GeneDB:SCO1523] [NCBI-GI:21220023] [NCBI-GeneID:1096949] [UniProt:Q9L286]
SCO1550	219	0.11288	1.14		SCL11.06c; small membrane protein; [GeneDB:SCO1550] [NCBI-GI:21220049] [NCBI-GeneID:1096981] [UniProt:Q9L1D2]
SCO1658	236	0.13038	1.11	metabolic process, regulation of biological process, DNA binding	gylR. SCI46.03; glycerol operon regulatory protein; [GeneDB:SCO1658] [NCBI-GI:21220154] [NCBI-GeneID:1097089] [UniProt:P15360]
SCO1679	40	0.00300	1.98	metabolic process, catalytic activity, nucleotide binding	SCI52.21; putative gluconokinase [EC:2.7.1.12]; K00851 gluconokinase; [GeneDB:SCO1679] [NCBI-GI:21220175] [NCBI-GeneID:1097110] [UniProt:Q9AD88]
SCO1680	36	0.00333	1.99	metabolic process, catalytic activity	SCI30A.01. SCI52.22; putative gluconate permease; K03299 gluconate:H+ symporter. GntP family; [GeneDB:SCO1680] [NCBI-GI:32141150] [NCBI-

					GeneID:1097111] [UniProt:Q8CK22]
SCO1713	73	0.01164	1.76		SCI11.02c; hypothetical protein; [GeneDB:SCO1713] [NCBI-GI:21220207] [NCBI-GeneID:1097144] [UniProt:Q9S2B7]
SCO1714	238	0.13013	1.05		SCI11.03c; secreted protein; [GeneDB:SCO1714] [NCBI-GI:21220208] [NCBI-GeneID:1097145] [UniProt:Q9S2B6]
SCO1715	193	0.09715	1.13	metabolic process, catalytic activity	hgd. SCI11.04; putative homogentisate 1.2-dioxygenase [EC:1.13.11.5]; K00451 homogentisate 1.2-dioxygenase; [GeneDB:SCO1715] [NCBI-GI:21220209] [NCBI-GeneID:1097146] [UniProt:Q9S2B5]
SCO1792	128	0.04211	1.31	metabolic process, response to stimulus, DNA binding, catalytic activity	SCI51.32c; putative 3-methyladenine DNA glycosylase [EC:3.2.2.-]; K03652 3-methyladenine DNA glycosylase; [GeneDB:SCO1792] [NCBI-GI:21220284] [NCBI-GeneID:1097226] [UniProt:Q9S208]
SCO1947	68	0.01162	1.67		gap1. SCC54.07c; glyceraldehyde-3-phosphate dehydrogenase [EC:1.2.1.12]; K00134 glyceraldehyde 3-phosphate dehydrogenase; [GeneDB:SCO1947] [NCBI-GI:21220432] [NCBI-GeneID:1097381] [UniProt:Q9Z518]
SCO2014	46	0.00457	1.89	metabolic process, catalytic activity, metal ion binding	pyk1. SC7H2.28c; pyruvate kinase [EC:2.7.1.40]; K00873 pyruvate kinase; [GeneDB:SCO2014] [NCBI-GI:21220496] [NCBI-GeneID:1097448] [UniProt:Q9S2I9]
SCO2019	176	0.07773	1.25	metabolic process	SC7H2.33c; putative chorismate mutase [EC:5.4.99.5]; K04092 chorismate mutase; [GeneDB:SCO2019] [NCBI-GI:21220501] [NCBI-GeneID:1097453] [UniProt:Q9S2I4]
SCO2025	11	0.00091	2.96	metabolic process, catalytic activity, nucleotide binding	gltD. SC3A3.03c; putative glutamate synthase small subunit [EC:1.4.1.13]; K00266 glutamate synthase (NADPH) small chain; [GeneDB:SCO2025] [NCBI-GI:21220506] [NCBI-GeneID:1097459] [UniProt:Q9S2Z0]
SCO2026	9	0.00111	3.09	metabolic process, catalytic activity, protein binding	gltB. SC3A3.04c; putative glutamate synthase large subunit [EC:1.4.1.13]; K00265 glutamate synthase (NADPH) large chain; [GeneDB:SCO2026] [NCBI-GI:21220507] [NCBI-GeneID:1097460] [UniProt:Q9S2Y9]
SCO2114	242	0.13570	1.07		SC6E10.08c; hypothetical protein; [GeneDB:SCO2114] [NCBI-GI:21220592] [NCBI-GeneID:1097548] [UniProt:Q9S2M9]
SCO2146	49	0.00510	2.14	metabolic process, catalytic activity	SC6G10.19c; aminotransferase; [GeneDB:SCO2146] [NCBI-GI:21220623] [NCBI-GeneID:1097580] [UniProt:Q9X805]
SCO2164	136	0.04441	1.29		SC5F7.37c. St6G10A.02c; putative integral membrane efflux protein; K03296 hydrophobic/amphiphilic exporter-1 (mainly G- bacteria). HAE1 family; [GeneDB:SCO2164] [NCBI-GI:32141159] [NCBI-GeneID:1097597] [UniProt:Q8CK05]
SCO2210	226	0.12000	1.10	metabolic process, catalytic activity,	glnI. SC10B7.05; glutamine synthetase [EC:6.3.1.2]; K01915 glutamine synthetase; [GeneDB:SCO2210] [NCBI-GI:21220682] [NCBI-GeneID:1097643] [UniProt:Q9X958]

				nucleotide binding	
SCO2305	52	0.00577	2.03	metabolic process, catalytic activity, nucleotide binding	SCC30.13; putative ABC transporter ATP-binding subunit; K09687 antibiotic transport system ATP-binding protein; [GeneDB:SCO2305] [NCBI-GI:21220774] [NCBI-GeneID:1097739] [UniProt:Q9L008]
SCO2306	17	0.00059	2.62		SCC30.14; putative ABC transporter integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO2306] [NCBI-GI:21220775] [NCBI-GeneID:1097740] [UniProt:Q9L007]
SCO2307	195	0.10405	1.22	cell communication, metabolic process, nucleotide binding, signal transducer	SCC30.15; two-component sensor kinase; [GeneDB:SCO2307] [NCBI-GI:21220776] [NCBI-GeneID:1097741] [UniProt:Q9L006]
SCO2346	35	0.00314	1.99	metabolic process, catalytic activity	SCC8A.04c; putative hydrolase [EC:3.1.3.-]; K01112; [GeneDB:SCO2346] [NCBI-GI:21220814] [NCBI-GeneID:1097780] [UniProt:Q9KY44]
SCO2383	178	0.08146	1.17		SC4A7.11; secreted protein; [GeneDB:SCO2383] [NCBI-GI:21220850] [NCBI-GeneID:1097817] [UniProt:Q9RDQ1]
SCO2463	132	0.04371	1.51	metabolic process, catalytic activity, nucleotide binding, transporter activity	SC7A8.02; putative ABC transporter; K06147 ATP-binding cassette. subfamily B. bacterial; [GeneDB:SCO2463] [NCBI-GI:21220926] [NCBI-GeneID:1097897] [UniProt:Q9L2F3]
SCO2464	254	0.14713	1.20	metabolic process, catalytic activity, nucleotide binding, transporter activity	SC7A8.03; putative ABC transporter; K06147 ATP-binding cassette. subfamily B. bacterial; [GeneDB:SCO2464] [NCBI-GI:21220927] [NCBI-GeneID:1097898] [UniProt:Q9L2F2]
SCO2489	190	0.09111	1.16	metabolic process, regulation of biological process, DNA binding	SC7A8.28; TetR-family transcriptional regulator; [GeneDB:SCO2489] [NCBI-GI:21220952] [NCBI-GeneID:1097923] [UniProt:Q9L2D0]
SCO2505	100	0.02400	1.48		SCC121.08; putative ABC-transporter metal-binding lipoprotein; K09815 zinc transport system substrate-binding protein; [GeneDB:SCO2505] [NCBI-GI:21220966] [NCBI-GeneID:1097939] [UniProt:Q9L2H8]
SCO2528	39	0.00308	2.29	metabolic process, catalytic activity	leuA. SCC121.31c; 2-isopropylmalate synthase [EC:2.3.3.13]; K01649 2-isopropylmalate synthase; [GeneDB:SCO2528] [NCBI-GI:32141173] [NCBI-GeneID:1097962] [UniProt:O31046]
SCO2591	91	0.02033	1.52		SCC88.02; secreted protein; [GeneDB:SCO2591] [NCBI-GI:21221049] [NCBI-GeneID:1098025] [UniProt:Q9L1I5]
SCO2633	21	0.00190	2.42	metabolic process,	SC8E4A.03. sodF; superoxide dismutase [Fe-Zn] [EC:1.15.1.1]; K00518 superoxide

				catalytic activity, metal ion binding	dismutase; [GeneDB:SCO2633] [NCBI-GI:21221090] [NCBI-GeneID:1098067] [UniProt:O51917]
SCO2683	134	0.04358	1.41	metabolic process, DNA binding	SCC61A.04c; single-strand DNA-binding protein; [GeneDB:SCO2683] [NCBI-GI:21221138] [NCBI-GeneID:1098117] [UniProt:Q9KYI9]
SCO2722	200	0.10665	1.16		SCC46.07c; putative integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO2722] [NCBI-GI:21221176] [NCBI-GeneID:1098156] [UniProt:Q9L1J4]
SCO2762	216	0.11213	1.14		SCC57A.33c; secreted protein; [GeneDB:SCO2762] [NCBI-GI:21221214] [NCBI-GeneID:1098196] [UniProt:Q9RDG6]
SCO2784	121	0.03421	1.37		SCC105.15; acetyltransferase; [GeneDB:SCO2784] [NCBI-GI:21221235] [NCBI-GeneID:1098218] [UniProt:Q9L070]
SCO2839	95	0.02000	1.73		SCE20.13c; lipoprotein; [GeneDB:SCO2839] [NCBI-GI:21221289] [NCBI-GeneID:1098273] [UniProt:Q9RDB2]
SCO2861	207	0.10768	1.28		SCE20.35.; hypothetical protein; [GeneDB:SCO2861] [NCBI-GI:21221311] [NCBI-GeneID:1098295] [UniProt:Q9RD90]
SCO2907	202	0.10688	1.07		SCE19A.07; putative PTS transmembrane component [EC:2.7.1.69]; K02803 PTS system. N-acetylglucosamine-specific IIB component; K02804 PTS system. N-acetylglucosamine-specific IIC component; [GeneDB:SCO2907] [NCBI-GI:21221354] [NCBI-GeneID:1098340] [UniProt:Q9S2H4]
SCO2935	233	0.12760	1.07	metabolic process, DNA binding	SCE19A.35c; transcriptional regulator; [GeneDB:SCO2935] [NCBI-GI:21221382] [NCBI-GeneID:1098368] [UniProt:Q9R3R2]
SCO2950	201	0.10741	1.08	cell organization and biogenesis, metabolic process, DNA binding	hup. SCE59.09c; DNA-binding protein Hu (hs1); [GeneDB:SCO2950] [NCBI-GI:21221395] [NCBI-GeneID:1098383] [UniProt:P0A3H5]
SCO3035	253	0.14735	0.97	metabolic process, catalytic activity, metal ion binding	SCE34.16; hypothetical protein; [GeneDB:SCO3035] [NCBI-GI:21221478] [NCBI-GeneID:1098468] [UniProt:Q9KZL0]
SCO3074	223	0.11834	1.07		SCE25.15c; integral membrane protein; [GeneDB:SCO3074] [NCBI-GI:21221515] [NCBI-GeneID:1098507] [UniProt:Q9KZ74]
SCO3089	26	0.00269	2.47	metabolic process, catalytic activity, nucleotide binding	SCE25.30; putative ABC transporter ATP-binding protein; K02003; [GeneDB:SCO3089] [NCBI-GI:21221529] [NCBI-GeneID:1098523] [UniProt:Q9KZ60]
SCO3090	31	0.00290	2.37		SCE25.31; putative ABC transporter integral membrane protein; K02004; [GeneDB:SCO3090] [NCBI-GI:21221530] [NCBI-GeneID:1098524] [UniProt:Q9KZ59]
SCO3091	168	0.06506	1.32		SCE25.32c; cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]; K00574

					cyclopropane-fatty-acyl-phospholipid synthase; [GeneDB:SCO3091] [NCBI-GI:21221531] [NCBI-GeneID:1098525] [UniProt:Q9KZ58]
SCO3096	169	0.06645	1.21	metabolic process, catalytic activity, metal ion binding	eno. SCE41.05c; enolase [EC:4.2.1.11]; K01689 enolase; [GeneDB:SCO3096] [NCBI-GI:21221535] [NCBI-GeneID:1098530] [UniProt:Q9F2Q3]
SCO3111	114	0.03035	1.55	metabolic process, catalytic activity, nucleotide binding	SCE41.20c; putative ABC transport system ATP-binding protein; K02003; [GeneDB:SCO3111] [NCBI-GI:21221550] [NCBI-GeneID:1098545] [UniProt:Q9F2N9]
SCO3151	78	0.01321	1.81	metabolic process, catalytic activity	SCE87.02c; putative deoxyribonuclease [EC:3.1.21.-]; K03424 Mg-dependent DNase; [GeneDB:SCO3151] [NCBI-GI:21221588] [NCBI-GeneID:1098585] [UniProt:Q9RKD6]
SCO3152	5	0.00000	3.59		SCE87.03c; hypothetical protein; [GeneDB:SCO3152] [NCBI-GI:21221589] [NCBI-GeneID:1098586] [UniProt:Q9RKD5]
SCO3185	239	0.13226	1.08		SCE22.02; putative Na ⁺ /H ⁺ antiporter; K03316 monovalent cation:H ⁺ antiporter. CPA1 family; [GeneDB:SCO3185] [NCBI-GI:21221620] [NCBI-GeneID:1098619] [UniProt:Q9KYW0]
SCO3306	210	0.11048	1.08	metabolic process, catalytic activity,	SCE68.04c; aminotransferase; [GeneDB:SCO3306] [NCBI-GI:21221737] [NCBI-GeneID:1098740] [UniProt:Q9WX27]
SCO3332	154	0.05838	1.35		SCE68.30c; hypothetical protein; [GeneDB:SCO3332] [NCBI-GI:21221763] [NCBI-GeneID:1098766] [UniProt:Q9WX02]
SCO3338	164	0.06384	1.19		SCE7.05c; putative integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO3338] [NCBI-GI:21221768] [NCBI-GeneID:1098775] [UniProt:Q9X8G2]
SCO3345	89	0.01989	1.69	metabolic process, catalytic activity,	SCE7.12c; dihydroxy acid dehydratase [EC:4.2.1.9]; K01687 dihydroxy-acid dehydratase; [GeneDB:SCO3345] [NCBI-GI:21221775] [NCBI-GeneID:1098782] [UniProt:O69198]
SCO3361	258	0.15050	1.01		SCE94.12c; AsnC-family transcriptional regulator; [GeneDB:SCO3361] [NCBI-GI:21221790] [NCBI-GeneID:1098798] [UniProt:Q9ZEP1]
SCO3375	222	0.11685	1.06		SCE94.26c; Lsr2-like protein; [GeneDB:SCO3375] [NCBI-GI:21221804] [NCBI-GeneID:1098812] [UniProt:Q9X8N1]
SCO3390	98	0.02082	1.70		SCE126.08c; two component sensor kinase; [GeneDB:SCO3390] [NCBI-GI:21221818] [NCBI-GeneID:1098827] [UniProt:Q9X851]
SCO3423	231	0.12688	1.05		SCE9.30; regulator; [GeneDB:SCO3423] [NCBI-GI:21221850] [NCBI-GeneID:1098860] [UniProt:Q9X8K2]
SCO3427	28	0.00250	2.27	metabolic process,	rpmE. SCE9.34c; putative 50S ribosomal protein L31; K02909 large subunit

				structural molecule activity	ribosomal protein L31; [GeneDB:SCO3427] [NCBI-GI:21221854] [NCBI-GeneID:1098864] [UniProt:Q9X8K6]
SCO3429	174	0.07149	1.28	metabolic process, structural molecule activity	rpmB. SCE9.36; putative 50S ribosomal protein L28; K02902 large subunit ribosomal protein L28; [GeneDB:SCO3429] [NCBI-GI:21221856] [NCBI-GeneID:1098866] [UniProt:Q9X8K8]
SCO3649	215	0.11121	1.11		fba. SCH10.27c; putative fructose 1.6-bisphosphate aldolase [EC:4.1.2.13]; K01624 fructose-bisphosphate aldolase. class II; [GeneDB:SCO3649] [NCBI-GI:21222064] [NCBI-GeneID:1099085] [UniProt:Q9X8R6]
SCO3704	167	0.06431	1.34		SCH35.20c; putative substrate-binding transport protein; K02020 molybdate transport system substrate-binding protein; [GeneDB:SCO3704] [NCBI-GI:21222117] [NCBI-GeneID:1099140] [UniProt:Q9X8Y6]
SCO3705	159	0.05987	1.38		SCH35.19c; putative ABC transporter membrane subunit; K02018 molybdate transport system permease protein; [GeneDB:SCO3705] [NCBI-GI:21222118] [NCBI-GeneID:1099141] [UniProt:Q9X8Y7]
SCO3712	150	0.05413	1.30	metabolic process, catalytic activity,	SCH35.12c; hydrolase; [GeneDB:SCO3712] [NCBI-GI:21222125] [NCBI-GeneID:1099148] [UniProt:Q9X8Z4]
SCO3717	241	0.13618	1.12	metabolic process, catalytic activity, metal ion binding	SCH35.07; putative cation transport system component [EC:3.6.3.12]; K01547 K+-transporting ATPase ATPase B chain; [GeneDB:SCO3717] [NCBI-GI:21222130] [NCBI-GeneID:1099153] [UniProt:Q9X8Z9]
SCO3718	92	0.02011	1.67	metabolic process, catalytic activity, nucleotide binding, transporter activity	SCH35.06; putative cation transport system component [EC:3.6.3.12]; K01546 K+-transporting ATPase ATPase A chain; [GeneDB:SCO3718] [NCBI-GI:21222131] [NCBI-GeneID:1099154] [UniProt:Q9X900]
SCO3719	60	0.00900	1.89		SCH35.05; small membrane protein; [GeneDB:SCO3719] [NCBI-GI:21222132] [NCBI-GeneID:1099155] [UniProt:Q9X901]
SCO3724	101	0.02426	1.45		SCH22A.02c; hypothetical protein; [GeneDB:SCO3724] [NCBI-GI:21222136] [NCBI-GeneID:1099160] [UniProt:Q9L0Y0]
SCO3793	198	0.10520	1.14		SCAC2.01; hypothetical protein; [GeneDB:SCO3793] [NCBI-GI:21222204] [NCBI-GeneID:1099229] [UniProt:Q9F325]
SCO3810	217	0.11226	1.00	metabolic process, regulation of biological process, DNA binding	SCGD3.11c; GntR-family transcriptional regulator; [GeneDB:SCO3810] [NCBI-GI:21222220] [NCBI-GeneID:1099246] [UniProt:Q9XA67]
SCO3877	234	0.12731	1.02	metabolic process, catalytic activity, nucleotide binding	SCH18.14c; putative 6-phosphogluconate dehydrogenase [EC:1.1.1.44]; K00033 6-phosphogluconate dehydrogenase; [GeneDB:SCO3877] [NCBI-GI:21222285] [NCBI-GeneID:1099313] [UniProt:Q53917]

SCO3888	113	0.02982	1.42	metabolic process, catalytic activity,	StH24.10; hypothetical protein; [GeneDB:SCO3888] [NCBI-GI:21222295] [NCBI-GeneID:1099324] [UniProt:Q9R3S2]
SCO3899	93	0.02011	1.59		SCH24.21c; myo-inositol-1-phosphate synthase [EC:5.5.1.4]; K01858 myo-inositol-1-phosphate synthase; [GeneDB:SCO3899] [NCBI-GI:21222306] [NCBI-GeneID:1099335] [UniProt:Q9X8T5]
SCO3900	102	0.02441	1.54		SCH24.22c; hypothetical protein; [GeneDB:SCO3900] [NCBI-GI:21222307] [NCBI-GeneID:1099336] [UniProt:Q9X8T6]
SCO3910	157	0.05904	1.27		SCH24.32c; hypothetical protein; [GeneDB:SCO3910] [NCBI-GI:21222317] [NCBI-GeneID:1099346] [UniProt:Q9X8U6]
SCO3918	261	0.15215	1.19	metabolic process, catalytic activity	SCH24.40c. SCQ11.01c; hypothetical protein; [GeneDB:SCO3918] [NCBI-GI:32141220] [NCBI-GeneID:1099354] [UniProt:Q8CJV3]
SCO3943	191	0.09063	1.14	metabolic process, regulation of biological process, DNA binding	rstP. SCD78.10c; transcriptional regulator; [GeneDB:SCO3943] [NCBI-GI:21222348] [NCBI-GeneID:1099379] [UniProt:O87640]
SCO3956	147	0.05211	1.34	metabolic process, catalytic activity, nucleotide binding	SCD78.23; putative ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-binding protein; [GeneDB:SCO3956] [NCBI-GI:21222361] [NCBI-GeneID:1099392] [UniProt:Q9ZBX6]
SCO3957	153	0.05758	1.31		SCD78.24; possible integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO3957] [NCBI-GI:21222362] [NCBI-GeneID:1099393] [UniProt:Q9ZBX5]
SCO3958	183	0.08421	1.21	metabolic process, catalytic activity, nucleotide binding	SCD78.25; ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-binding protein; [GeneDB:SCO3958] [NCBI-GI:21222363] [NCBI-GeneID:1099394] [UniProt:Q9ZBX4]
SCO3959	135	0.04444	1.41		SCD78.26; possible integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO3959] [NCBI-GI:21222364] [NCBI-GeneID:1099395] [UniProt:Q9ZBX3]
SCO3967	140	0.04857	1.38		SCBAC25E3.04c; conserved hypothetical membrane protein; K07040; [GeneDB:SCO3967] [NCBI-GI:21222371] [NCBI-GeneID:1099403] [UniProt:Q93J39]
SCO3968	189	0.08952	1.21		SCBAC25E3.05c; integral membrane protein; [GeneDB:SCO3968] [NCBI-GI:21222372] [NCBI-GeneID:1099404] [UniProt:Q93J38]
SCO3993	260	0.15200	1.06		SCBAC25E3.30c; hypothetical protein; [GeneDB:SCO3993] [NCBI-GI:21222396] [NCBI-GeneID:1099429] [UniProt:Q93J15]
SCO4005	47	0.00447	2.10	metabolic process, regulation of biological process, DNA binding	2SC10A7.09; RNA polymerase sigma factor; [GeneDB:SCO4005] [NCBI-GI:21222408] [NCBI-GeneID:1099441] [UniProt:Q9ADQ0]

SCO4020	156	0.05827	1.24	cell communication, metabolic process regulation, DNA binding, signal transducer activity	2SC10A7.24; putative two component system response regulator; K02483 two-component system. OmpR family. response regulator; [GeneDB:SCO4020] [NCBI-GI:21222423] [NCBI-GeneID:1099456] [UniProt:Q9ADN7]
SCO4021	182	0.08236	1.16	cell communication, metabolic process regulation, DNA binding, signal transducer activity	2SC10A7.25; putative two component system histidine kinase [EC:2.7.13.3]; K02484 two-component system. OmpR family. sensor kinase; [GeneDB:SCO4021] [NCBI-GI:21222424] [NCBI-GeneID:1099457] [UniProt:Q9ADN6]
SCO4054	214	0.11098	1.17		2SCD60.20; integral membrane protein; [GeneDB:SCO4054] [NCBI-GI:21222457] [NCBI-GeneID:1099490] [UniProt:Q9AK63]
SCO4157	235	0.12736	1.14	metabolic process, catalytic activity	SCD84.24c; protease; [GeneDB:SCO4157] [NCBI-GI:21222555] [NCBI-GeneID:1099597] [UniProt:Q9KZU4]
SCO4158	175	0.07303	1.17	metabolic process, regulation of biological process, DNA binding	SCD84.25c; putative LacI-family regulatory protein; [GeneDB:SCO4158] [NCBI-GI:21222556] [NCBI-GeneID:1099598] [UniProt:Q05954]
SCO4159	38	0.00316	2.03	cell communication, metabolic process regulation, DNA binding, signal transducer activity	glnR. SCD84.26c; transcriptional regulatory protein; [GeneDB:SCO4159] [NCBI-GI:21222557] [NCBI-GeneID:1099599] [UniProt:Q05943]
SCO4244	213	0.11061	1.13		SCD8A.17c; hypothetical protein; [GeneDB:SCO4244] [NCBI-GI:21222639] [NCBI-GeneID:1099684] [UniProt:Q9L0P7]
SCO4245	177	0.07768	1.27	metabolic process, metal ion binding	SCD8A.18c; hypothetical protein; K06903; [GeneDB:SCO4245] [NCBI-GI:21222640] [NCBI-GeneID:1099685] [UniProt:Q9L0P6]
SCO4246	143	0.05140	1.38		SCD8A.19c; hypothetical protein; [GeneDB:SCO4246] [NCBI-GI:21222641] [NCBI-GeneID:1099686] [UniProt:Q9L0P5]
SCO4247	77	0.01169	1.81	metabolic process	SCD8A.20c; hypothetical protein; [GeneDB:SCO4247] [NCBI-GI:21222642] [NCBI-GeneID:1099687] [UniProt:Q9L0P4]
SCO4248	54	0.00648	1.94		SCD8A.21c; hypothetical protein; [GeneDB:SCO4248] [NCBI-GI:21222643] [NCBI-GeneID:1099688] [UniProt:Q9L0P3]
SCO4251	32	0.00313	2.14		SCD8A.24c; secreted protein; [GeneDB:SCO4251] [NCBI-GI:21222646] [NCBI-GeneID:1099691] [UniProt:Q9L0P0]
SCO4252	56	0.00679	1.93		SCD8A.25c; hypothetical protein; [GeneDB:SCO4252] [NCBI-GI:21222647] [NCBI-

					GeneID:1099692] [UniProt:Q9L0N9]
SCO4253	42	0.00381	1.99		SCD8A.26c; hypothetical protein; K06907; [GeneDB:SCO4253] [NCBI-GI:21222648] [NCBI-GeneID:1099693] [UniProt:Q9L0N8]
SCO4256	109	0.02688	1.56		SCD8A.29; hydrolytic protein; [GeneDB:SCO4256] [NCBI-GI:21222651] [NCBI-GeneID:1099696] [UniProt:Q9L0N5]
SCO4257	96	0.02010	1.60		SCD8A.30; hydrolytic protein; [GeneDB:SCO4257] [NCBI-GI:21222652] [NCBI-GeneID:1099697] [UniProt:Q9L0N4]
SCO4258	88	0.01920	1.68		SCD8A.31; hydrolytic protein; [GeneDB:SCO4258] [NCBI-GI:21222653] [NCBI-GeneID:1099698] [UniProt:Q9L0N3]
SCO4259	192	0.09651	1.14		SCD8A.32c; AAA family ATPase; [GeneDB:SCO4259] [NCBI-GI:21222654] [NCBI-GeneID:1099699] [UniProt:Q9L0N2]
SCO4260	67	0.01179	1.68		SCD49.01c. SCD8A.33c; hypothetical protein; [GeneDB:SCO4260] [NCBI-GI:32141231] [NCBI-GeneID:1099700] [UniProt:Q8CJU2]
SCO4261	124	0.03839	1.39	metabolic process, regulation of biological process, DNA binding	SCD49.02c; response regulator; [GeneDB:SCO4261] [NCBI-GI:21222655] [NCBI-GeneID:1099701] [UniProt:Q9K4F1]
SCO4289	125	0.03824	1.38		SCD95A.22; secreted protein; [GeneDB:SCO4289] [NCBI-GI:21222682] [NCBI-GeneID:1099729] [UniProt:Q9KXV2]
SCO4293	10	0.00100	3.15		SCD95A.26; putative threonine synthase [EC:4.2.3.1]; K01733 threonine synthase; [GeneDB:SCO4293] [NCBI-GI:21222686] [NCBI-GeneID:1099733] [UniProt:Q9KXU8]
SCO4294	15	0.00067	2.62		SCD95A.27; hypothetical protein; [GeneDB:SCO4294] [NCBI-GI:21222687] [NCBI-GeneID:1099734] [UniProt:Q9KXU7]
SCO4366	130	0.04300	1.45	metabolic process, catalytic activity	SCD19.21c; putative phosphoserine aminotransferase [EC:2.6.1.52]; K00831 phosphoserine aminotransferase; [GeneDB:SCO4366] [NCBI-GI:21222757] [NCBI-GeneID:1099806] [UniProt:Q9F2Y1]
SCO4368	59	0.00831	1.96	metabolic process, catalytic activity	SCD19.23c; lipase (secreted protein); [GeneDB:SCO4368] [NCBI-GI:21222759] [NCBI-GeneID:1099808] [UniProt:Q9F2X9]
SCO4464	94	0.02000	1.50	metabolic process, catalytic activity	SCD65.07c; hydrolase; [GeneDB:SCO4464] [NCBI-GI:21222851] [NCBI-GeneID:1099904] [UniProt:Q9F2S5]
SCO4471	229	0.12358	1.10		SCD65.14; secreted protein; [GeneDB:SCO4471] [NCBI-GI:21222858] [NCBI-GeneID:1099911] [UniProt:Q9F2R8]
SCO4495	211	0.11104	1.13		SCD35.02; putative DNA polymerase related protein [EC:2.7.7.7]; K02334 DNA polymerase bacteriophage-type; [GeneDB:SCO4495] [NCBI-GI:21222880] [NCBI-GeneID:1099935] [UniProt:Q9L0U9]

SCO4584	227	0.11960	1.13		SCD20.02; hypothetical protein; [GeneDB:SCO4584] [NCBI-GI:21222967] [NCBI-GeneID:1100024] [UniProt:Q9F2X7]
SCO4640	209	0.11062	1.11	metabolic process, regulation of biological process, DNA binding	SCD82.11; TetR-family transcriptional regulator; [GeneDB:SCO4640] [NCBI-GI:21223022] [NCBI-GeneID:1100081] [UniProt:Q9L0M0]
SCO4657	259	0.15035	0.98	metabolic process, catalytic activity	SCD40A.03c; integral membrane protein; [GeneDB:SCO4657] [NCBI-GI:21223038] [NCBI-GeneID:1100098] [UniProt:Q9L0K6]
SCO4683	85	0.01600	1.57	metabolic process, catalytic activity	gdhA. SCD31.08; NADP-specific glutamate dehydrogenase [EC:1.4.1.4]; K00262 glutamate dehydrogenase (NADP+); [GeneDB:SCO4683] [NCBI-GI:21223063] [NCBI-GeneID:1100124] [UniProt:Q9L0F9]
SCO4762	228	0.12026	1.04	metabolic process, nucleotide binding protein, protein binding	groEL1; 60 kD chaperonin cpn60; K04077 chaperonin GroEL; [GeneDB:SCO4762] [NCBI-GI:21223141] [NCBI-GeneID:1100203] [UniProt:P40171]
SCO4850	251	0.14434	1.06	metabolic process, regulation of biological process, DNA binding	SC5G8.18c; TetR-family transcriptional regulator; [GeneDB:SCO4850] [NCBI-GI:21223226] [NCBI-GeneID:1100291] [UniProt:Q9KZ96]
SCO4851	25	0.00200	2.35		SC5G8.19c; hypothetical protein; [GeneDB:SCO4851] [NCBI-GI:21223227] [NCBI-GeneID:1100292] [UniProt:Q9KZ95]
SCO4852	41	0.00390	2.23		SC5G8.20c; integral membrane protein; [GeneDB:SCO4852] [NCBI-GI:21223228] [NCBI-GeneID:1100293] [UniProt:Q9KZ94]
SCO4904	170	0.06671	1.20		2SCK8.30c; integral membrane protein; [GeneDB:SCO4904] [NCBI-GI:21223278] [NCBI-GeneID:1100345] [UniProt:Q9AK22]
SCO4943	248	0.14327	1.05		2SCK31.03; oxidoreductase; [GeneDB:SCO4943] [NCBI-GI:21223316] [NCBI-GeneID:1100384] [UniProt:Q9EWW3]
SCO4945	110	0.02664	1.51	metabolic process, catalytic activity, metal ion binding	2SCK31.05; putative dehydrogenase [EC:1.1.1.2]; K00002 alcohol dehydrogenase (NADP+); [GeneDB:SCO4945] [NCBI-GI:21223318] [NCBI-GeneID:1100386] [UniProt:Q9EWF1]
SCO4947	187	0.08529	0.98	metabolic process, catalytic activity, metal ion binding	2SCK31.07. narG3; nitrate reductase alpha chain NarG3 [EC:1.7.99.4]; K00370 nitrate reductase 1. alpha subunit; [GeneDB:SCO4947] [NCBI-GI:21223320] [NCBI-GeneID:1100388] [UniProt:Q9EWF3]
SCO4954	199	0.10508	1.09		2SCK31.14c; hypothetical protein 2SCK3114c; [GeneDB:SCO4954] [NCBI-GI:21223327] [NCBI-GeneID:1100395] [UniProt:Q9ADK6]
SCO4955	152	0.05776	1.25		2SCK31.15c; ATP/GTP-binding protein; [GeneDB:SCO4955] [NCBI-GI:21223328] [NCBI-GeneID:1100396] [UniProt:Q9ADK5]
SCO5031	142	0.05063	1.28	metabolic process,	ahpD. SCK7.04c; alkyl hydroperoxide reductase system hypothetical protein; K04756

				response to stimulus, catalytic activity	alkyl hydroperoxide reductase subunit D; [GeneDB:SCO5031] [NCBI-GI:21223404] [NCBI-GeneID:1100472] [UniProt:Q7AKI6]
SCO5032	123	0.03659	1.41	metabolic process, antioxidant activity, catalytic activity,	ahpC. SCK7.05c; alkyl hydroperoxide reductase [EC:1.11.1.15]; K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C); [GeneDB:SCO5032] [NCBI-GI:21223405] [NCBI-GeneID:1100473] [UniProt:Q9FBP5]
SCO5129	141	0.04943	1.41	metabolic process, catalytic activity, nucleotide binding	SC9E12.14; putative ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-binding protein; [GeneDB:SCO5129] [NCBI-GI:21223499] [NCBI-GeneID:1100570] [UniProt:Q9F341]
SCO5162	122	0.03467	1.38		SCP8.25; putative integral membrane protein; K05595 multiple antibiotic resistance protein; [GeneDB:SCO5162] [NCBI-GI:21223531] [NCBI-GeneID:1100603] [UniProt:Q9FBJ6]
SCO5229	171	0.06977	1.18		SC7E4.26c; putative permease; K03307 solute:Na ⁺ symporter. SSS family; [GeneDB:SCO5229] [NCBI-GI:21223597] [NCBI-GeneID:1100670] [UniProt:Q9K494]
SCO5230	133	0.04346	1.31		SC7E4.27c; integral membrane protein; [GeneDB:SCO5230] [NCBI-GI:21223598] [NCBI-GeneID:1100671] [UniProt:Q9K493]
SCO5257	82	0.01524	1.65	metabolic process, catalytic activity	2SC7G11.19. metZ; methyltransferase; [GeneDB:SCO5257] [NCBI-GI:21223624] [NCBI-GeneID:1100698] [UniProt:Q9F3K8]
SCO5258	126	0.04143	1.34	metabolic process, catalytic activity, nucleotide binding	2SC7G11.20c. atrC; ATP-binding protein [EC:3.6.3.21]; K02028 polar amino acid transport system ATP-binding protein; [GeneDB:SCO5258] [NCBI-GI:21223625] [NCBI-GeneID:1100699] [UniProt:Q9F3K7]
SCO5285	255	0.14773	0.94	metabolic process, response o stimulus, DNA binding	lon. SCCB12.09; ATP-dependent protease [EC:3.4.21.53]; K01338 ATP-dependent Lon protease; [GeneDB:SCO5285] [NCBI-GI:21223651] [NCBI-GeneID:1100726] [UniProt:Q9EVK2]
SCO5299	104	0.02529	1.49		SC6G9.34; hypothetical protein; [GeneDB:SCO5299] [NCBI-GI:21223662] [NCBI-GeneID:1100739] [UniProt:Q9XAE8]
SCO5300	53	0.00604	2.06		SC6G9.33; hypothetical protein; [GeneDB:SCO5300] [NCBI-GI:21223663] [NCBI-GeneID:1100740] [UniProt:Q9XAE9]
SCO5379	220	0.11641	1.03	metabolic process, regulation of biological process	2SC6G5.23; hypothetical protein; [GeneDB:SCO5379] [NCBI-GI:21223739] [NCBI-GeneID:1100819] [UniProt:Q9K4D2]
SCO5413	247	0.13883	1.07	metabolic process, regulation of biological process, DNA binding	SC8F4.17; MarR-transcriptional regulator; [GeneDB:SCO5413] [NCBI-GI:21223773] [NCBI-GeneID:1100853] [UniProt:Q9L2A7]
SCO5423	16	0.00063	2.50	metabolic process, catalytic activity, metal	pyk2. SC8F4.27c; pyruvate kinase [EC:2.7.1.40]; K00873 pyruvate kinase; [GeneDB:SCO5423] [NCBI-GI:21223783] [NCBI-GeneID:1100863] [UniProt:Q9L299]

				ion binding	
SCO5468	218	0.11179	1.11		SC2A11.02c; transmembrane transport protein; [GeneDB:SCO5468] [NCBI-GI:21223825] [NCBI-GeneID:1100908] [UniProt:O86563]
SCO5512	127	0.04181	1.41	metabolic process, catalytic activity, metal ion binding, nucleotide binding	ilvB. SC8D9.24; acetolactate synthase large subunit [EC:2.2.1.6]; K01652 acetolactate synthase large subunit; [GeneDB:SCO5512] [NCBI-GI:21223868] [NCBI-GeneID:1100952] [UniProt:Q9Z567]
SCO5513	90	0.01989	1.60		ilvN. SC8D9.25; acetolactate synthase small subunit [EC:2.2.1.6]; K01653 acetolactate synthase small subunit; [GeneDB:SCO5513] [NCBI-GI:21223869] [NCBI-GeneID:1100953] [UniProt:Q9Z566]
SCO5514	225	0.12004	1.09	metabolic process, catalytic activity	ilvC. SC8D9.26; acetolactate synthase small subunit [EC:1.1.1.86]; K00053 ketol-acid reductoisomerase; [GeneDB:SCO5514] [NCBI-GI:21223870] [NCBI-GeneID:1100954] [UniProt:Q9Z565]
SCO5515	76	0.01171	1.70	metabolic process, catalytic activity, nucleotide binding	SC8D9.27. serA; probable D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]; K00058 D-3-phosphoglycerate dehydrogenase; [GeneDB:SCO5515] [NCBI-GI:21223871] [NCBI-GeneID:1100955] [UniProt:Q9Z564]
SCO5521	4	0.00000	3.34		SC1C2.02; hypothetical protein; [GeneDB:SCO5521] [NCBI-GI:21223876] [NCBI-GeneID:1100961] [UniProt:O86503]
SCO5522	7	0.00143	3.20	metabolic process, catalytic activity, nucleotide binding	leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]; K00052 3-isopropylmalate dehydrogenase; [GeneDB:SCO5522] [NCBI-GI:21223877] [NCBI-GeneID:1100962] [UniProt:O86504]
SCO5552	129	0.04194	1.34	metabolic process, regulation of biological process, DNA binding	SC1C2.33c; regulator; [GeneDB:SCO5552] [NCBI-GI:21223907] [NCBI-GeneID:1100992] [UniProt:O86533]
SCO5553	69	0.01159	1.94	metabolic process, catalytic activity, metal ion binding	leuC; 3-isopropylmalate dehydratase large subunit [EC:4.2.1.33]; K01703 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit; [GeneDB:SCO5553] [NCBI-GI:21223908] [NCBI-GeneID:1100993] [UniProt:O86534]
SCO5554	24	0.00208	2.46	metabolic process, catalytic activity	leuD; 3-isopropylmalate dehydratase small subunit [EC:4.2.1.33]; K01704 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit; [GeneDB:SCO5554] [NCBI-GI:21223909] [NCBI-GeneID:1100994] [UniProt:O86535]
SCO5578	2	0.00000	4.38		SC7A1.22; putative sugar transporter; K08139 MFS transporter. SP family. sugar:H+ symporter; [GeneDB:SCO5578] [NCBI-GI:21223934] [NCBI-GeneID:1101019] [UniProt:Q9ZBQ1]
SCO5583	144	0.05257	1.37		SC7A1.27; ammonium transporter; K03320 ammonium transporter. Amt family; [GeneDB:SCO5583] [NCBI-GI:21223939] [NCBI-GeneID:1101024] [UniProt:Q9ZBP6]

SCO5638	43	0.00419	2.15		SC6A9.29; integral membrane protein; [GeneDB:SCO5638] [NCBI-GI:21223989] [NCBI-GeneID:1101077] [UniProt:O86761]
SCO5640	108	0.02667	1.44		SC6A9.27; hypothetical protein; [GeneDB:SCO5640] [NCBI-GI:21223991] [NCBI-GeneID:1101079] [UniProt:O86759]
SCO5771	246	0.13858	1.15		SC4H8.10c; hypothetical protein; [GeneDB:SCO5771] [NCBI-GI:21224117] [NCBI-GeneID:1101213] [UniProt:O50489]
SCO5774	18	0.00111	2.41		gluD; glutamate permease; K10007 glutamate transport system permease protein; [GeneDB:SCO5774] [NCBI-GI:21224120] [NCBI-GeneID:1101216] [UniProt:O50492]
SCO5775	29	0.00241	2.17		gluC; glutamate permease; K10006 glutamate transport system permease protein; [GeneDB:SCO5775] [NCBI-GI:21224121] [NCBI-GeneID:1101217] [UniProt:O50493]
SCO5776	34	0.00294	2.15		gluB; glutamate binding protein; K10005 glutamate transport system substrate-binding protein; [GeneDB:SCO5776] [NCBI-GI:21224122] [NCBI-GeneID:1101218] [UniProt:O50494]
SCO5777	57	0.00754	1.89		gluA; glutamate uptake system ATP-binding protein [EC:3.6.3.-]; K10008 glutamate transport system ATP-binding protein; [GeneDB:SCO5777] [NCBI-GI:21224123] [NCBI-GeneID:1101219] [UniProt:O50495]
SCO5810	205	0.10785	1.07		SC4H2.31c; transmembrane efflux protein; [GeneDB:SCO5810] [NCBI-GI:21224155] [NCBI-GeneID:1101252] [UniProt:O69986]
SCO5830	197	0.10477	1.12		hypothetical protein; [GeneDB:SCO5830] [NCBI-GI:21224174] [NCBI-GeneID:1101272] [UniProt:O70006]
SCO5929	149	0.05409	1.26	metabolic process, catalytic activity	SC10A5.34c; oxidoreductase; [GeneDB:SCO5929] [NCBI-GI:21224268] [NCBI-GeneID:1101371] [UniProt:O54125]
SCO5982	80	0.01350	1.62		StBAC16H6.17c; regulator; K02616 phenylacetic acid degradation operon negative regulatory protein; [GeneDB:SCO5982] [NCBI-GI:21224319] [NCBI-GeneID:1101424] [UniProt:Q93JE5]
SCO6008	27	0.00259	2.14		SC7B7.05; probable transcriptional repressor protein; [GeneDB:SCO6008] [NCBI-GI:21224343] [NCBI-GeneID:1101450] [UniProt:O50502]
SCO6009	8	0.00125	3.23		SC7B7.06; solute-binding protein; K02058 simple sugar transport system substrate-binding protein; [GeneDB:SCO6009] [NCBI-GI:21224344] [NCBI-GeneID:1101451] [UniProt:O50503]
SCO6010	3	0.00000	3.58	metabolic process, catalytic activity, nucleotide binding	SC7B7.07; probable ABC-transport system ATP binding protein [EC:3.6.3.17]; K02056 simple sugar transport system ATP-binding protein; [GeneDB:SCO6010] [NCBI-GI:21224345] [NCBI-GeneID:1101452] [UniProt:O50504]
SCO6011	6	0.00000	3.31		SC7B7.08; probable ABC-type transmembrane transport protein; K02057 simple sugar transport system permease protein; [GeneDB:SCO6011] [NCBI-GI:21224346]

					[NCBI-GeneID:1101453] [UniProt:O50505]
SCO6044	244	0.13811	1.01		SC1B5.04c; integral membrane protein; [GeneDB:SCO6044] [NCBI-GI:21224375] [NCBI-GeneID:1101485] [UniProt:O69832]
SCO6109	173	0.06942	1.20	metabolic process, catalytic activity	SCBAC1A6.33; secreted hydrolase; [GeneDB:SCO6109] [NCBI-GI:21224438] [NCBI-GeneID:1101550] [UniProt:Q9ADF4]
SCO6124	240	0.13254	1.15		SC9B2.11; hypothetical protein; [GeneDB:SCO6124] [NCBI-GI:21224451] [NCBI-GeneID:1101565] [UniProt:Q9Z548]
SCO6272	120	0.03408	1.22	metabolic process, catalytic activity, nucleotide binding	SC2C4.02; secreted FAD-binding protein; [GeneDB:SCO6272] [NCBI-GI:21224592] [NCBI-GeneID:1101713] [UniProt:Q9EX55]
SCO6273	179	0.08123	0.92	metabolic process, catalytic activity	SC2C4.03c; type I polyketide synthase; [GeneDB:SCO6273] [NCBI-GI:21224593] [NCBI-GeneID:1101714] [UniProt:Q9EX54]
SCO6274	155	0.05813	0.94	metabolic process, catalytic activity	SC2C4.04c; type I polyketide synthase; [GeneDB:SCO6274] [NCBI-GI:21224594] [NCBI-GeneID:1101715] [UniProt:Q9EX53]
SCO6275	203	0.10714	0.85	metabolic process, catalytic activity	SC1G7.01c. SC2C4.05c; type I polyketide synthase; [GeneDB:SCO6275] [NCBI-GI:32141295] [NCBI-GeneID:1101716] [UniProt:Q8CJN6]
SCO6276	103	0.02485	0.66		SC1G7.02; secreted protein; [GeneDB:SCO6276] [NCBI-GI:21224595] [NCBI-GeneID:1101717] [UniProt:Q93S13]
SCO6277	111	0.02748	0.62	metabolic process, catalytic activity	SC1G7.03; epoxide hydrolase; [GeneDB:SCO6277] [NCBI-GI:21224596] [NCBI-GeneID:1101718] [UniProt:Q93S12]
SCO6278	75	0.01173	1.09		SC1G7.04; putative integral membrane transport protein; K08167 MFS transporter. DHA2 family. methyl viologen resistance protein SmvA; [GeneDB:SCO6278] [NCBI-GI:21224597] [NCBI-GeneID:1101719] [UniProt:Q93S11]
SCO6279	48	0.00521	1.03		SC1G7.05; diaminobutyrate-pyruvate aminotransferase; [GeneDB:SCO6279] [NCBI-GI:21224598] [NCBI-GeneID:1101720] [UniProt:Q93S10]
SCO6282	66	0.01167	0.94	metabolic process, catalytic activity	SC1G7.08c; 3-oxoacyl-[acyl-carrier protein] reductase; [GeneDB:SCO6282] [NCBI-GI:21224601] [NCBI-GeneID:1101723] [UniProt:Q93S07]
SCO6283	107	0.02477	1.13		SC1G7.09; hypothetical protein; [GeneDB:SCO6283] [NCBI-GI:21224602] [NCBI-GeneID:1101724] [UniProt:Q93S06]
SCO6284	230	0.12743	0.78		SC1G7.10; putative decarboxylase [EC:4.1.1.41]; K01604 methylmalonyl-CoA decarboxylase alpha chain; [GeneDB:SCO6284] [NCBI-GI:21224603] [NCBI-GeneID:1101725] [UniProt:Q93S05]
SCO6285	163	0.06423	0.94		SC1G7.11; hypothetical protein; [GeneDB:SCO6285] [NCBI-GI:21224604] [NCBI-GeneID:1101726] [UniProt:Q93S04]

SCO6320	161	0.06348	1.26		SCIF3.22c; transport integral membrane protein; [GeneDB:SCO6320] [NCBI-GI:21224636] [NCBI-GeneID:1101761] [UniProt:Q93RS4]
SCO6429	44	0.00432	2.00		SC1A6.18; hypothetical protein; [GeneDB:SCO6429] [NCBI-GI:21224736] [NCBI-GeneID:1101868] [UniProt:O69823]
SCO6430	184	0.08451	1.18		SC1A6.19; hypothetical protein; [GeneDB:SCO6430] [NCBI-GI:21224737] [NCBI-GeneID:1101869] [UniProt:O69824]
SCO6431	86	0.01872	1.74		SC1A6.20; peptide synthase; [GeneDB:SCO6431] [NCBI-GI:21224738] [NCBI-GeneID:1101870] [UniProt:O69825]
SCO6433	20	0.00200	2.54		SC1A6.22; hypothetical protein; K06995; [GeneDB:SCO6433] [NCBI-GI:21224740] [NCBI-GeneID:1101872] [UniProt:O69827]
SCO6434	83	0.01566	1.85	metabolic process, catalytic activity	SC1A6.23. SC9B5.01; oxidoreductase; [GeneDB:SCO6434] [NCBI-GI:32141301] [NCBI-GeneID:1101873] [UniProt:Q8CJN0]
SCO6435	70	0.01143	1.97	metabolic process, regulation of biological process	SC9B5.02; hypothetical protein; [GeneDB:SCO6435] [NCBI-GI:21224741] [NCBI-GeneID:1101874] [UniProt:Q9ZBH8]
SCO6436	58	0.00828	2.04	metabolic process, catalytic activity	SC9B5.03; tRNA synthetase; [GeneDB:SCO6436] [NCBI-GI:21224742] [NCBI-GeneID:1101875] [UniProt:Q9ZBH7]
SCO6437	116	0.03017	1.55		SC9B5.04; hypothetical protein; [GeneDB:SCO6437] [NCBI-GI:21224743] [NCBI-GeneID:1101876] [UniProt:Q9ZBH6]
SCO6438	55	0.00691	2.00		SC9B5.05; diaminopimelate decarboxylase [EC:4.1.1.20]; K01586 diaminopimelate decarboxylase; [GeneDB:SCO6438] [NCBI-GI:21224744] [NCBI-GeneID:1101877] [UniProt:Q9ZBH5]
SCO6451	145	0.05248	1.30		SC9B5.18; putative substrate binding protein; K02035 peptide/nickel transport system substrate-binding protein; [GeneDB:SCO6451] [NCBI-GI:21224757] [NCBI-GeneID:1101890] [UniProt:Q9ZBG2]
SCO6452	117	0.03085	1.40		SC9B5.19; putative transport permease protein; K02033 peptide/nickel transport system permease protein; [GeneDB:SCO6452] [NCBI-GI:21224758] [NCBI-GeneID:1101891] [UniProt:Q9ZBG1]
SCO6453	160	0.06338	1.20		SC9B5.20; putative transport permease protein; K02034 peptide/nickel transport system permease protein; [GeneDB:SCO6453] [NCBI-GI:21224759] [NCBI-GeneID:1101892] [UniProt:Q9ZBG0]
SCO6509	13	0.00077	2.79		SC1E6.18c; hydrophobic protein; [GeneDB:SCO6509] [NCBI-GI:21224812] [NCBI-GeneID:1101948] [UniProt:Q9ZC04]
SCO6510	22	0.00182	2.39	metabolic process, catalytic activity	SC1E6.19c; hypothetical protein; [GeneDB:SCO6510] [NCBI-GI:21224813] [NCBI-GeneID:1101949] [UniProt:Q9ZC03]

SCO6658	138	0.04833	1.28	metabolic process, catalytic activity, nucleotide binding	SC5A7.08c; 6-phosphogluconate dehydrogenase [EC:1.1.1.44]; K00033 6-phosphogluconate dehydrogenase; [GeneDB:SCO6658] [NCBI-GI:21224954] [NCBI-GeneID:1102097] [UniProt:O88014]
SCO6659	212	0.11104	1.10	metabolic process, catalytic activity	pgi. SC5A7.09c; glucose-6-phosphate isomerase [EC:5.3.1.9]; K01810 glucose-6-phosphate isomerase; [GeneDB:SCO6659] [NCBI-GI:21224955] [NCBI-GeneID:1102098] [UniProt:O88015]
SCO6660	99	0.02141	1.49		SC5A7.10c; hypothetical protein; [GeneDB:SCO6660] [NCBI-GI:21224956] [NCBI-GeneID:1102099] [UniProt:O88016]
SCO6661	106	0.02500	1.44	metabolic process, catalytic activity, nucleotide binding	SC5A7.11c. zwf; glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]; K00036 glucose-6-phosphate 1-dehydrogenase; [GeneDB:SCO6661] [NCBI-GI:21224957] [NCBI-GeneID:1102100] [UniProt:O88017]
SCO6662	30	0.00267	2.11	metabolic process, catalytic activity, nucleotide binding	tal1; transaldolase [EC:2.2.1.2]; K00616 transaldolase; [GeneDB:SCO6662] [NCBI-GI:21224958] [NCBI-GeneID:1102101] [UniProt:O88018]
SCO6663	97	0.01990	1.53	metabolic process, catalytic activity	tktB; transketolase B [EC:2.2.1.1]; K00615 transketolase; [GeneDB:SCO6663] [NCBI-GI:21224959] [NCBI-GeneID:1102102] [UniProt:O88019]
SCO6990	72	0.01139	1.77		SC8F11.16c; putative membrane transport protein.; K03453 bile acid:Na ⁺ symporter. BASS family; [GeneDB:SCO6990] [NCBI-GI:21225276] [NCBI-GeneID:1102428] [UniProt:Q9KZG2]
SCO7047	188	0.08846	1.17		SC4G1.13; undecaprenyl-diphosphatase [EC:3.6.1.27]; K06153 undecaprenyl-diphosphatase; [GeneDB:SCO7047] [NCBI-GI:21225330] [NCBI-GeneID:1102485] [UniProt:Q9FC36]
SCO7153	1	0.00000	4.48		SC9A4.15; putative sugar transporter; K08139 MFS transporter. SP family. sugar:H ⁺ symporter; [GeneDB:SCO7153] [NCBI-GI:21225433] [NCBI-GeneID:1102591] [UniProt:Q9ZBQ1]
SCO7154	257	0.15058	1.02	metabolic process, catalytic activity	ilvC2. SC9A4.16c; ketol-acid reductoisomerase [EC:1.1.1.86]; K00053 ketol-acid reductoisomerase; [GeneDB:SCO7154] [NCBI-GI:21225434] [NCBI-GeneID:1102592] [UniProt:Q9FBT8]
SCO7199	62	0.01000	1.68		SC1D2.02c; membrane protein; [GeneDB:SCO7199] [NCBI-GI:21225477] [NCBI-GeneID:1102637] [UniProt:Q9K448]
SCO7200	87	0.01851	1.80	metabolic process, catalytic activity	SC1D2.03c; hypothetical protein; [GeneDB:SCO7200] [NCBI-GI:21225478] [NCBI-GeneID:1102638] [UniProt:Q9K447]
SCO7399	204	0.10706	1.15		SC10G8.27c; binding-protein-dependent transport lipoprotein; [GeneDB:SCO7399] [NCBI-GI:21225670] [NCBI-GeneID:1102837] [UniProt:Q9L178]
SCO7400	245	0.13882	1.06	metabolic process,	SC10G8.28c; putative ABC-transport protein. ATP-binding component. [EC:3.6.3.34];

				catalytic activity, nucleotide binding	K02013 iron complex transport system ATP-binding protein; [GeneDB:SCO7400] [NCBI-GI:21225671] [NCBI-GeneID:1102838] [UniProt:Q9L177]
SCO7417	224	0.12054	1.12		SC6D11.13c; putative cytochrome P450-family protein. [EC:1.14.-.-]; K00517; [GeneDB:SCO7417] [NCBI-GI:21225687] [NCBI-GeneID:1102855] [UniProt:Q9L142]
SCO7424	45	0.00444	1.91	metabolic process, regulation of biological process, DNA binding	SC6D11.20; MarR-family transcriptional regulator; [GeneDB:SCO7424] [NCBI-GI:21225694] [NCBI-GeneID:1102862] [UniProt:Q9L135]
SCO7428	196	0.10500	1.13		hmpA1; flavohemoprotein [EC:1.14.12.17]; K05916 nitric oxide dioxygenase; [GeneDB:SCO7428] [NCBI-GI:21225698] [NCBI-GeneID:1102866] [UniProt:Q9L131]
SCO7459	71	0.01127	1.78	metabolic process, catalytic activity, nucleotide binding	SC5C11.16c; putative ABC transport protein.ATP-binding component. [EC:3.6.3.34]; K02013 iron complex transport system ATP-binding protein; [GeneDB:SCO7459] [NCBI-GI:21225728] [NCBI-GeneID:1102897] [UniProt:Q9L156]
SCO7462	162	0.06364	1.22		SCBAC14E8.02c; putative integral membrane protein; K07090; [GeneDB:SCO7462] [NCBI-GI:21225731] [NCBI-GeneID:1102900] [UniProt:Q9ADJ7]
SCO7463	79	0.01316	1.60	metabolic process, catalytic activity, nucleotide binding	cvnA13. SCBAC14E8.03; sensor histidine kinase; [GeneDB:SCO7463] [NCBI-GI:21225732] [NCBI-GeneID:1102901] [UniProt:Q9ADJ6]
SCO7464	65	0.01154	1.70		cvnB13. SCBAC14E8.04; hypothetical protein; [GeneDB:SCO7464] [NCBI-GI:21225733] [NCBI-GeneID:1102902] [UniProt:Q9ADJ5]
SCO7465	148	0.05378	1.25		cvnC13. SCBAC14E8.05; hypothetical protein; [GeneDB:SCO7465] [NCBI-GI:21225734] [NCBI-GeneID:1102903] [UniProt:Q9ADJ4]
SCO7510	112	0.02902	1.45		cypH. SCBAC25F8.02c; peptidyl-prolyl cis-trans isomerase [EC:5.2.1.8]; K01802 peptidylprolyl isomerase; [GeneDB:SCO7510] [NCBI-GI:21225776] [NCBI-GeneID:1102948] [UniProt:Q93J09]
SCO7511	23	0.00217	2.25	metabolic process, catalytic activity, nucleotide binding	gap2. SCBAC25F8.03c; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]; K00134 glyceraldehyde 3-phosphate dehydrogenase; [GeneDB:SCO7511] [NCBI-GI:21225777] [NCBI-GeneID:1102949] [UniProt:Q93J08]
SCO7544	180	0.08128	1.19		SC8G12.20; putative ABC-transport protein. membrane component.; K02050 sulfonate/nitrate/taurine transport system permease protein; [GeneDB:SCO7544] [NCBI-GI:21225809] [NCBI-GeneID:1102982] [UniProt:Q9KYY5]
SCO7676	14	0.00071	2.87		SC4C2.11; ferredoxin; [GeneDB:SCO7676] [NCBI-GI:21225936] [NCBI-GeneID:1103114] [UniProt:Q9EWQ1]
SCO7695	166	0.06470	1.24		SC1A4.03c; hypothetical protein; [GeneDB:SCO7695] [NCBI-GI:21225955] [NCBI-GeneID:1103133] [UniProt:Q9EX60]
SCO7756	19	0.00105	2.56		SC5E9.04; hypothetical protein; [GeneDB:SCO7756] [NCBI-GI:21226012] [NCBI-

					GeneID:1103194] [UniProt:Q9EWN1]
SCO7799	237	0.13000	1.05		SC10B8A.09c; transposase; [GeneDB:SCO7799] [NCBI-GI:21226051] [NCBI-GeneID:1103237] [UniProt:Q9FCL5]

Table S2. Complete dataset of differentially expressed genes at statistically significant levels (pfp values ≤ 0.15) in the *ScoM145* wild type strain relative to the *ScoZm* mutant.

Gene name	Rank of down-regulated genes	pfp value	Log(2) Average	GO Biological Process / Molecular Function	Product/Function
SCO0138	28	0.06464	-2.21	metabolic process, catalytic activity	SCJ33.02; short chain dehydrogenase; [GeneDB:SCO0138] [NCBI-GI:21218697] [NCBI-GeneID:1095562] [UniProt:Q9RIX5]
SCO0555	15	0.06800	-1.96	metabolic process, catalytic activity, metal ion binding	SCF73.02c; membrane-bound oxidoreductase; [GeneDB:SCO0555] [NCBI-GI:21219089] [NCBI-GeneID:1095978] [UniProt:Q9RJ14]
SCO0556	6	0.01667	-2.96		SCF73.03c; hypothetical protein; [GeneDB:SCO0556] [NCBI-GI:21219090] [NCBI-GeneID:1095979] [UniProt:Q9RJ13]
SCO1087	44	0.14136	-1.14	metabolic process, catalytic activity	2SCG4.03c; putative aldolase [EC:4.1.2.5]; K01620 threonine aldolase; [GeneDB:SCO1087] [NCBI-GI:21219602] [NCBI-GeneID:1096510] [UniProt:Q9K3R1]
SCO1088	48	0.13979	-1.14	metabolic process, catalytic activity	2SCG4.04c; oxidoreductase; [GeneDB:SCO1088] [NCBI-GI:21219603] [NCBI-GeneID:1096511] [UniProt:Q9K3R0]
SCO1089	12	0.07667	-1.46		2SCG4.05c; hypothetical protein 2SCG405c; [GeneDB:SCO1089] [NCBI-GI:21219604] [NCBI-GeneID:1096512] [UniProt:Q9K3Q9]
SCO1570	16	0.06500	-1.48	metabolic process, catalytic activity	argH. SCL24.06c; argininosuccinate lyase [EC:4.3.2.1]; K01755 argininosuccinate lyase; [GeneDB:SCO1570] [NCBI-GI:21220068] [NCBI-GeneID:1097001] [UniProt:Q9L1B1]
SCO1576	11	0.05636	-1.55	metabolic process, regulation of biological process, DNA binding	argR. SCL24.12c; arginine repressor; K03402 transcriptional regulator of arginine metabolism; [GeneDB:SCO1576] [NCBI-GI:21220074] [NCBI-GeneID:1097007] [UniProt:Q9L1A5]
SCO1577	10	0.05000	-1.57	metabolic process, catalytic activity	argD. SCL24.13c; acetonitrile aminotransferase [EC:2.6.1.11]; K00818 acetylornithine aminotransferase; [GeneDB:SCO1577] [NCBI-GI:21220075] [NCBI-GeneID:1097008] [UniProt:Q9L1A4]
SCO1578	8	0.01875	-1.72	metabolic process, catalytic activity, nucleotide binding	argB. SCL24.14c; acetylglutamate kinase [EC:2.7.2.8]; K00930 acetylglutamate kinase; [GeneDB:SCO1578] [NCBI-GI:21220076] [NCBI-GeneID:1097009] [UniProt:Q9L1A3]
SCO1579	29	0.06828	-1.40	metabolic process, catalytic activity	argJ. SCL24.15c; putative glutamate N-acetyltransferase [EC:2.3.1.1 2.3.1.35]; K00620 amino-acid N-acetyltransferase; K00642 glutamate N-acetyltransferase; [GeneDB:SCO1579] [NCBI-

					GI:32141148] [NCBI-GeneID:1097010] [UniProt:Q8CK24]
SCO1580	14	0.07143	-1.50	metabolic process, catalytic activity, nucleotide binding, protein binding	argC; N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]; K00145 N-acetyl-gamma-glutamyl-phosphate reductase; [GeneDB:SCO1580] [NCBI-GI:21220077] [NCBI-GeneID:1097011] [UniProt:P54895]
SCO1815	45	0.14400	-1.21	metabolic process, catalytic activity, nucleotide binding	fabG. SCI28.09c; probable 3-oxacyl-(acyl-carrier-protein) reductase [EC:1.1.1.100]; K00059 3-oxoacyl-[acyl-carrier protein] reductase; [GeneDB:SCO1815] [NCBI-GI:21220305] [NCBI-GeneID:1097249] [UniProt:Q9S274]
SCO2296	30	0.06700	-1.69		SCC30.04; integral membrane protein; [GeneDB:SCO2296] [NCBI-GI:21220765] [NCBI-GeneID:1097730] [UniProt:Q9L017]
SCO2463	31	0.07194	-1.58	metabolic process, catalytic activity, nucleotide binding, transporter activity	SC7A8.02; putative ABC transporter; K06147 ATP-binding cassette. subfamily B. bacterial; [GeneDB:SCO2463] [NCBI-GI:21220926] [NCBI-GeneID:1097897] [UniProt:Q9L2F3]
SCO2464	27	0.06444	-1.67	metabolic process, catalytic activity, nucleotide binding, transporter activity	SC7A8.03; putative ABC transporter; K06147 ATP-binding cassette. subfamily B. bacterial; [GeneDB:SCO2464] [NCBI-GI:21220927] [NCBI-GeneID:1097898] [UniProt:Q9L2F2]
SCO2776	42	0.13548	-2.00	metabolic process, catalytic activity	accD1. SCC105.07; acetyl/propionyl CoA carboxylase. beta subunit [EC:6.4.1.3]; K01966 propionyl-CoA carboxylase beta chain; [GeneDB:SCO2776] [NCBI-GI:21221227] [NCBI-GeneID:1098210] [UniProt:Q9L077]
SCO2778	47	0.14277	-1.86	metabolic process, catalytic activity	hmgL. SCC105.09; hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]; K01640 hydroxymethylglutaryl-CoA lyase; [GeneDB:SCO2778] [NCBI-GI:21221229] [NCBI-GeneID:1098212] [UniProt:Q9L075]
SCO2779	9	0.04111	-2.71	metabolic process, catalytic activity, nucleotide binding	acdH. SCC105.10; acyl-CoA dehydrogenase; [GeneDB:SCO2779] [NCBI-GI:21221230] [NCBI-GeneID:1098213] [UniProt:Q9XCG6]
SCO3138	3	0.02333	-1.86	metabolic process, catalytic activity, metal ion binding	galT. SCE66.17c; galactose-1-phosphate uridylyltransferase [EC:2.7.7.10]; K00964 galactose-1-phosphate uridylyltransferase; [GeneDB:SCO3138] [NCBI-GI:21221576] [NCBI-GeneID:1098572] [UniProt:Q9K3S6]
SCO3411	49	0.14939	-1.30		SCE9.18c; possible membrane protein; K03975 membrane-associated protein; [GeneDB:SCO3411] [NCBI-GI:21221838] [NCBI-GeneID:1098848] [UniProt:Q9X8J1]
SCO3413	1	0.00000	-3.35	metabolic process, DNA binding, nucleotide binding	SCE9.20. tipA; transcriptional regulator; [GeneDB:SCO3413] [NCBI-GI:21221840] [NCBI-GeneID:1098850] [UniProt:P0A4T8]

SCO3472	2	0.00500	-2.22	metabolic process, DNA binding, catalytic activity	SCE65.08c; transposase remnant; [GeneDB:SCO3472] [NCBI-GI:21221896] [NCBI-GeneID:1098909] [UniProt:Q9RKG5]
SCO3473	34	0.07853	-1.23	metabolic process, catalytic activity	SCE65.09c; putative aldolase [EC:4.1.2.14 4.1.3.16]; K01625 2-dehydro-3-deoxyphosphogluconate aldolase; K01650 4-hydroxy-2-oxoglutarate aldolase; [GeneDB:SCO3473] [NCBI-GI:21221897] [NCBI-GeneID:1098910] [UniProt:Q9RKG4]
SCO3474	24	0.06917	-1.73	metabolic process, catalytic activity	SCE65.10c; sugar kinase; [GeneDB:SCO3474] [NCBI-GI:21221898] [NCBI-GeneID:1098911] [UniProt:Q9RKG3]
SCO3475	26	0.06615	-1.84	metabolic process, catalytic activity	SCE65.11c; putative galactonate dehydratase protein [EC:4.2.1.6]; K01684 galactonate dehydratase; [GeneDB:SCO3475] [NCBI-GI:21221899] [NCBI-GeneID:1098912] [UniProt:Q9RKG2]
SCO3476	25	0.06840	-1.77	metabolic process, catalytic activity	SCE65.12c; putative short-chain dehydrogenase [EC:1.1.1.125]; K00065 2-deoxy-D-gluconate 3-dehydrogenase; [GeneDB:SCO3476] [NCBI-GI:21221900] [NCBI-GeneID:1098913] [UniProt:Q9RKG1]
SCO3477	33	0.07273	-1.79	metabolic process, catalytic activity, metal ion binding	SCE65.13c; dehydrogenase; [GeneDB:SCO3477] [NCBI-GI:21221901] [NCBI-GeneID:1098914] [UniProt:Q9RKG0]
SCO3478	37	0.12432	-1.72	metabolic process, catalytic activity	SCE65.14c; dehydrogenase; [GeneDB:SCO3478] [NCBI-GI:21221902] [NCBI-GeneID:1098915] [UniProt:Q9RKF9]
SCO3480	43	0.14047	-1.45	metabolic process, catalytic activity	SCE65.16c; putative racemase [EC:5.1.2.2]; K01781 mandelate racemase; [GeneDB:SCO3480] [NCBI-GI:21221904] [NCBI-GeneID:1098917] [UniProt:Q9RKF7]
SCO3481	40	0.12925	-1.36	metabolic process, catalytic activity	SCE65.17c; hypothetical protein; [GeneDB:SCO3481] [NCBI-GI:21221905] [NCBI-GeneID:1098918] [UniProt:Q9RKF6]
SCO3483	13	0.07615	-1.70	transporter activity	SCE65.19c; putative integral membrane transport protein; K02025 multiple sugar transport system permease protein; [GeneDB:SCO3483] [NCBI-GI:21221907] [NCBI-GeneID:1098920] [UniProt:Q9RKF4]
SCO3484	23	0.07174	-1.55		SCE65.20c; putative secreted sugar-binding protein; K02027 multiple sugar transport system substrate-binding protein; [GeneDB:SCO3484] [NCBI-GI:21221908] [NCBI-GeneID:1098921] [UniProt:Q9RKF3]
SCO3487	17	0.06353	-1.74	metabolic process, catalytic activity	SCE65.23; hydrolase; [GeneDB:SCO3487] [NCBI-GI:21221911] [NCBI-GeneID:1098924] [UniProt:Q9RKF0]
SCO5025	5	0.01400	-3.16	metabolic process, regulation of biological process, DNA binding,	SCK15.27; transcriptional regulator; [GeneDB:SCO5025] [NCBI-GI:21223398] [NCBI-GeneID:1100466] [UniProt:Q9KY77]

				nucleotide binding	
SCO5026	21	0.06286	-2.49	metabolic process, catalytic activity	SCK15.28; hypothetical protein; [GeneDB:SCO5026] [NCBI-GI:21223399] [NCBI-GenelD:1100467] [UniProt:Q9KY76]
SCO5367	39	0.13205	-0.97		2SC6G5.11. atpB; ATP synthase A chain [EC:3.6.3.14]; K02108 F-type H ⁺ -transporting ATPase a chain; [GeneDB:SCO5367] [NCBI-GI:21223727] [NCBI-GenelD:1100807] [UniProt:Q9K4D8]
SCO5536	18	0.06111	-1.59		SC1C2.17; hypothetical protein; [GeneDB:SCO5536] [NCBI-GI:21223891] [NCBI-GenelD:1100976] [UniProt:O86518]
SCO5676	35	0.08829	-1.27	metabolic process, catalytic activity	gabT; putative 4-aminobutyrate aminotransferase [EC:2.6.1.19]; K00823 4-aminobutyrate aminotransferase; [GeneDB:SCO5676] [NCBI-GI:21224026] [NCBI-GenelD:1101115] [UniProt:O86823]
SCO5839	46	0.14217	-1.16		SC9B10.06; hypothetical protein; [GeneDB:SCO5839] [NCBI-GI:21224183] [NCBI-GenelD:1101281] [UniProt:O50513]
SCO5976	32	0.06969	-1.34		arcB. StBAC16H6.11; ornithine carbamoyltransferase [EC:2.1.3.3]; K00611 ornithine carbamoyltransferase; [GeneDB:SCO5976] [NCBI-GI:21224313] [NCBI-GenelD:1101418] [UniProt:Q93JF1]
SCO6164	36	0.10833	-1.51		SC1A9.28c; putative DnaK suppressor protein; K06204 DnaK suppressor protein; [GeneDB:SCO6164] [NCBI-GI:21224490] [NCBI-GenelD:1101605] [UniProt:Q9ZBS4]
SCO6266	20	0.06350	-2.00		SCAH10.31. scbA; ScbA protein; [GeneDB:SCO6266] [NCBI-GI:21224587] [NCBI-GenelD:1101707] [UniProt:O86851]
SCO7036	4	0.01750	-1.84	metabolic process, catalytic activity, nucleotide binding	argG. SC4G1.02; argininosuccinate synthase [EC:6.3.4.5]; K01940 argininosuccinate synthase; [GeneDB:SCO7036] [NCBI-GI:21225319] [NCBI-GenelD:1102474] [UniProt:P24532]
SCO7262	22	0.07364	-1.51		SC5H1.30c; hypothetical protein; [GeneDB:SCO7262] [NCBI-GI:21225539] [NCBI-GenelD:1102700] [UniProt:Q9X7T7]
SCO7530	41	0.13220	-1.69	metabolic process, regulation of biological process, DNA binding, nucleotide binding	SC8G12.06c; regulatory protein; [GeneDB:SCO7530] [NCBI-GI:21225795] [NCBI-GenelD:1102968] [UniProt:Q9KYZ9]
SCO7586	7	0.02143	-2.78	metabolic process, catalytic activity, nucleotide binding	SC5F1.40; oxidoreductase; [GeneDB:SCO7586] [NCBI-GI:21225850] [NCBI-GenelD:1103024] [UniProt:Q9F389]
SCO7587	38	0.12237	-1.39		SC5F1.41; integral membrane protein; [GeneDB:SCO7587] [NCBI-GI:21225851] [NCBI-GenelD:1103025] [UniProt:Q9F388]

SCO7698	19	0.06579	-2.39	metabolic process, regulation of biological process, DNA binding, nucleotide binding	SC1A4.06c; MerR-family transcriptional regulator; [GeneDB:SCO7698] [NCBI-GI:21225958] [NCBI-GeneID:1103136] [UniProt:Q9EX58]
Gene name	Rank of up-regulated genes	pfp value	Log(2)	GO Biological Process / Molecular Function	Product/Function
SCO0016	68	0.10735	2.28		SCJ30.12; hypothetical protein; [GeneDB:SCO0016] [NCBI-GI:21218598] [NCBI-GeneID:1095450] [UniProt:Q9S1X7]
SCO0090	58	0.08345	1.62		SCJ11.19c; transposase; [GeneDB:SCO0090] [NCBI-GI:21218659] [NCBI-GeneID:1095518] [UniProt:Q9RI85]
SCO0489	36	0.04861	1.43		SCF34.08c; hypothetical protein; K05375 MbtH protein; [GeneDB:SCO0489] [NCBI-GI:21219027] [NCBI-GeneID:1095912] [UniProt:Q9RK17]
SCO0498	41	0.05122	1.27	metabolic process, catalytic activity	SCF34.17c; putative peptide monooxygenase [EC:1.13.12.-]; K00468; [GeneDB:SCO0498] [NCBI-GI:21219036] [NCBI-GeneID:1095921] [UniProt:Q9RK08]
SCO0861	65	0.09815	1.90		SCM2.14c; secreted protein; [GeneDB:SCO0861] [NCBI-GI:21219382] [NCBI-GeneID:1096284] [UniProt:Q9RCV0]
SCO0863	84	0.15250	1.64		SCM2.16c; integral membrane protein; [GeneDB:SCO0863] [NCBI-GI:21219384] [NCBI-GeneID:1096286] [UniProt:Q9RCU8]
SCO0973	66	0.09970	1.67	transporter activity	SCM11.28; integral membrane protein; [GeneDB:SCO0973] [NCBI-GI:21219491] [NCBI-GeneID:1096396] [UniProt:Q9RIT4]
SCO1550	69	0.10696	1.34		SCL11.06c; small membrane protein; [GeneDB:SCO1550] [NCBI-GI:21220049] [NCBI-GeneID:1096981] [UniProt:Q9L1D2]
SCO1713	45	0.05422	1.80		SCI11.02c; hypothetical protein; [GeneDB:SCO1713] [NCBI-GI:21220207] [NCBI-GeneID:1097144] [UniProt:Q9S2B7]
SCO2126	74	0.10730	2.03	metabolic process, catalytic activity, nucleotide binding	glk. SC6E10.20c; glucokinase [EC:2.7.1.2]; K00845 glucokinase; [GeneDB:SCO2126] [NCBI-GI:21220604] [NCBI-GeneID:1097560] [UniProt:P0A4E1]
SCO2306	83	0.14361	1.68	transporter activity, catalytic activity, nucleotide binding	SCC30.14; putative ABC transporter integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO2306] [NCBI-GI:21220775] [NCBI-GeneID:1097740] [UniProt:Q9L007]

SCO2513	35	0.04714	1.81		SCC121.16; hypothetical protein; [GeneDB:SCO2513] [NCBI-GI:21220974] [NCBI-GeneID:1097947] [UniProt:Q9L2H0]
SCO2528	72	0.10667	1.86	metabolic process, catalytic activity,	leuA. SCC121.31c; 2-isopropylmalate synthase [EC:2.3.3.13]; K01649 2-isopropylmalate synthase; [GeneDB:SCO2528] [NCBI-GI:32141173] [NCBI-GeneID:1097962] [UniProt:O31046]
SCO2839	37	0.04784	1.81		SCE20.13c; lipoprotein; [GeneDB:SCO2839] [NCBI-GI:21221289] [NCBI-GeneID:1098273] [UniProt:Q9RDB2]
SCO2930	59	0.08763	1.53	transporter activity	SCE19A.30; putative permease membrane component; K05846 osmoprotectant transport system permease protein; [GeneDB:SCO2930] [NCBI-GI:21221377] [NCBI-GeneID:1098363] [UniProt:Q9S2F1]
SCO2986	47	0.05681	1.72	response to stimulus	SCE50.14c; hypothetical protein; [GeneDB:SCO2986] [NCBI-GI:21221430] [NCBI-GeneID:1098419] [UniProt:Q9L049]
SCO3089	34	0.04588	2.05		SCE25.30; putative ABC transporter ATP-binding protein; K02003; [GeneDB:SCO3089] [NCBI-GI:21221529] [NCBI-GeneID:1098523] [UniProt:Q9KZ60]
SCO3090	56	0.08179	1.62		SCE25.31; putative ABC transporter integral membrane protein; K02004; [GeneDB:SCO3090] [NCBI-GI:21221530] [NCBI-GeneID:1098524] [UniProt:Q9KZ59]
SCO3111	43	0.05395	1.87	metabolic process, catalytic activity, nucleotide binding	SCE41.20c; putative ABC transport system ATP-binding protein; K02003; [GeneDB:SCO3111] [NCBI-GI:21221550] [NCBI-GeneID:1098545] [UniProt:Q9F2N9]
SCO3152	39	0.05154	2.43		SCE87.03c; hypothetical protein; [GeneDB:SCO3152] [NCBI-GI:21221589] [NCBI-GeneID:1098586] [UniProt:Q9RKD5]
SCO3263	16	0.01938	3.25		SCE39.13c; hypothetical protein; [GeneDB:SCO3263] [NCBI-GI:21221696] [NCBI-GeneID:1098697] [UniProt:Q9X8D6]
SCO3264	38	0.05079	2.50	metabolic process, regulation of biological process, DNA binding	SCE39.14c; GntR-family regulator; [GeneDB:SCO3264] [NCBI-GI:21221697] [NCBI-GeneID:1098698] [UniProt:Q9X8D7]
SCO3265	7	0.00571	3.46		SCE39.15c; hypothetical protein; [GeneDB:SCO3265] [NCBI-GI:21221698] [NCBI-GeneID:1098699] [UniProt:Q9X8D8]
SCO3266	26	0.03615	2.77	metabolic process, catalytic activity, transporter activity	SCE39.16c; hypothetical protein; [GeneDB:SCO3266] [NCBI-GI:21221699] [NCBI-GeneID:1098700] [UniProt:Q9X8D9]
SCO3268	2	0.00500	3.74		SCE39.18c; secreted protein; [GeneDB:SCO3268] [NCBI-GI:21221701] [NCBI-GeneID:1098702] [UniProt:Q9X8E1]
SCO3390	77	0.12857	1.58	metabolic process, catalytic activity,	SCE126.08c; two component sensor kinase; [GeneDB:SCO3390] [NCBI-GI:21221818] [NCBI-GeneID:1098827] [UniProt:Q9X851]

				nucleotide binding, receptor activity	
SCO3717	49	0.06327	1.65	metabolic process, catalytic activity, transporter activity	SCH35.07; putative cation transport system component [EC:3.6.3.12]; K01547 K+-transporting ATPase ATPase B chain; [GeneDB:SCO3717] [NCBI-GI:21222130] [NCBI-GeneID:1099153] [UniProt:Q9X8Z9]
SCO3719	23	0.03478	2.20	metabolic process, catalytic activity, transporter activity	SCH35.05; small membrane protein; [GeneDB:SCO3719] [NCBI-GI:21222132] [NCBI-GeneID:1099155] [UniProt:Q9X901]
SCO3918	55	0.08309	1.59	metabolic process, catalytic activity	SCH24.40c. SCQ11.01c; hypothetical protein; [GeneDB:SCO3918] [NCBI-GI:32141220] [NCBI-GeneID:1099354] [UniProt:Q8CJV3]
SCO3956	19	0.02526	2.02	metabolic process, catalytic activity, nucleotide binding	SCD78.23; putative ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-binding protein; [GeneDB:SCO3956] [NCBI-GI:21222361] [NCBI-GeneID:1099392] [UniProt:Q9ZBX6]
SCO3957	32	0.04281	1.79		SCD78.24; possible integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO3957] [NCBI-GI:21222362] [NCBI-GeneID:1099393] [UniProt:Q9ZBX5]
SCO3958	42	0.05024	1.61	metabolic process, catalytic activity,, nucleotide binding	SCD78.25; ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-binding protein; [GeneDB:SCO3958] [NCBI-GI:21222363] [NCBI-GeneID:1099394] [UniProt:Q9ZBX4]
SCO3959	61	0.08885	1.55		SCD78.26; possible integral membrane protein; K01992 ABC-2 type transport system permease protein; [GeneDB:SCO3959] [NCBI-GI:21222364] [NCBI-GeneID:1099395] [UniProt:Q9ZBX3]
SCO3967	52	0.07750	1.67		SCBAC25E3.04c; conserved hypothetical membrane protein; K07040; [GeneDB:SCO3967] [NCBI-GI:21222371] [NCBI-GeneID:1099403] [UniProt:Q93J39]
SCO3982	3	0.00333	3.96		SCBAC25E3.19; hypothetical protein; [GeneDB:SCO3982] [NCBI-GI:21222386] [NCBI-GeneID:1099418] [UniProt:Q93J25]
SCO3983	15	0.01533	3.48		SCBAC25E3.20; hypothetical protein; [GeneDB:SCO3983] [NCBI-GI:21222387] [NCBI-GeneID:1099419] [UniProt:Q93J24]
SCO3985	48	0.06229	2.29		SCBAC25E3.22; hypothetical protein; [GeneDB:SCO3985] [NCBI-GI:21222389] [NCBI-GeneID:1099421] [UniProt:Q93J22]
SCO3986	8	0.00750	3.77	metabolic process, regulation of biological process, DNA binding	SCBAC25E3.23; GntR-family transcriptional regulator; [GeneDB:SCO3986] [NCBI-GI:21222390] [NCBI-GeneID:1099422] [UniProt:Q93J21]
SCO3987	14	0.01571	3.36		SCBAC25E3.24; hypothetical protein; [GeneDB:SCO3987] [NCBI-GI:21222391] [NCBI-GeneID:1099423] [UniProt:Q93J20]
SCO3988	30	0.04467	2.47		SCBAC25E3.25; hypothetical protein; [GeneDB:SCO3988] [NCBI-GI:21222392] [NCBI-

					GeneID:1099424] [UniProt:Q93J19]
SCO4004	6	0.00500	2.99		2SC10A7.08c; small membrane protein; [GeneDB:SCO4004] [NCBI-GI:21222407] [NCBI-GenelD:1099440] [UniProt:Q9ADQ1]
SCO4005	13	0.01538	2.90	metabolic process, regulation of biological process, DNA binding	2SC10A7.09; RNA polymerase sigma factor; [GeneDB:SCO4005] [NCBI-GI:21222408] [NCBI-GenelD:1099441] [UniProt:Q9ADQ0]
SCO4054	75	0.11027	1.45		2SCD60.20; integral membrane protein; [GeneDB:SCO4054] [NCBI-GI:21222457] [NCBI-GenelD:1099490] [UniProt:Q9AK63]
SCO4173	70	0.10857	1.87		SCD66.10c; hypothetical protein; [GeneDB:SCO4173] [NCBI-GI:21222570] [NCBI-GenelD:1099613] [UniProt:Q9K4G5]
SCO4174	11	0.01455	3.70		SCD66.11c; integral membrane protein; [GeneDB:SCO4174] [NCBI-GI:21222571] [NCBI-GenelD:1099614] [UniProt:Q9K4G4]
SCO4175	79	0.13608	1.75		SCD66.12c; hypothetical protein; [GeneDB:SCO4175] [NCBI-GI:21222572] [NCBI-GenelD:1099615] [UniProt:Q9K4G3]
SCO4261	54	0.08111	1.56	metabolic process, regulation of biological process, DNA binding	SCD49.02c; response regulator; [GeneDB:SCO4261] [NCBI-GI:21222655] [NCBI-GenelD:1099701] [UniProt:Q9K4F1]
SCO4293	78	0.13269	1.74	metabolic process, catalytic activity	SCD95A.26; putative threonine synthase [EC:4.2.3.1]; K01733 threonine synthase; [GeneDB:SCO4293] [NCBI-GI:21222686] [NCBI-GenelD:1099733] [UniProt:Q9KXU8]
SCO4317	53	0.07717	1.79		SCD95A.50; hypothetical protein; [GeneDB:SCO4317] [NCBI-GI:21222710] [NCBI-GenelD:1099757] [UniProt:Q9KXS4]
SCO4368	57	0.08368	1.77	metabolic process, catalytic activity	SCD19.23c; lipase (secreted protein); [GeneDB:SCO4368] [NCBI-GI:21222759] [NCBI-GenelD:1099808] [UniProt:Q9F2X9]
SCO4851	18	0.02111	2.19		SC5G8.19c; hypothetical protein; [GeneDB:SCO4851] [NCBI-GI:21223227] [NCBI-GenelD:1100292] [UniProt:Q9KZ95]
SCO4852	5	0.00600	2.77		SC5G8.20c; integral membrane protein; [GeneDB:SCO4852] [NCBI-GI:21223228] [NCBI-GenelD:1100293] [UniProt:Q9KZ94]
SCO4903	31	0.04323	1.98		2SCK8.29c; hypothetical protein; [GeneDB:SCO4903] [NCBI-GI:21223277] [NCBI-GenelD:1100344] [UniProt:Q9AK23]
SCO4947	80	0.13813	1.23	metabolic process, catalytic activity, metal ion binding	2SCK31.07. narG3; nitrate reductase alpha chain NarG3 [EC:1.7.99.4]; K00370 nitrate reductase 1. alpha subunit; [GeneDB:SCO4947] [NCBI-GI:21223320] [NCBI-GenelD:1100388] [UniProt:Q9EWF3]

SCO4950	85	0.15294	1.24	metabolic process, catalytic activity	2SCK31.10. narI3; nitrate reductase gamma chain NarI3; [GeneDB:SCO4950] [NCBI-GI:21223323] [NCBI-GeneID:1100391] [UniProt:Q9EWF6]
SCO5285	73	0.10562	1.50	metabolic process, response to stimulus, DNA binding, catalytic activity	lon. SCCB12.09; ATP-dependent protease [EC:3.4.21.53]; K01338 ATP-dependent Lon protease; [GeneDB:SCO5285] [NCBI-GI:21223651] [NCBI-GeneID:1100726] [UniProt:Q9EVK2]
SCO5521	1	0.01000	3.17		SC1C2.02; hypothetical protein; [GeneDB:SCO5521] [NCBI-GI:21223876] [NCBI-GeneID:1100961] [UniProt:O86503]
SCO5774	33	0.04273	2.04	transporter activity	gluD; glutamate permease; K10007 glutamate transport system permease protein; [GeneDB:SCO5774] [NCBI-GI:21224120] [NCBI-GeneID:1101216] [UniProt:O50492]
SCO5775	63	0.08746	1.68	transporter activity	gluC; glutamate permease; K10006 glutamate transport system permease protein; [GeneDB:SCO5775] [NCBI-GI:21224121] [NCBI-GeneID:1101217] [UniProt:O50493]
SCO5776	20	0.02800	2.18	transporter activity	gluB; glutamate binding protein; K10005 glutamate transport system substrate-binding protein; [GeneDB:SCO5776] [NCBI-GI:21224122] [NCBI-GeneID:1101218] [UniProt:O50494]
SCO5777	62	0.08742	1.77	metabolic process, catalytic activity, nucleotide binding	gluA; glutamate uptake system ATP-binding protein [EC:3.6.3.-]; K10008 glutamate transport system ATP-binding protein; [GeneDB:SCO5777] [NCBI-GI:21224123] [NCBI-GeneID:1101219] [UniProt:O50495]
SCO6268	64	0.09375	1.56	cell communication, metabolic process, regulation of biological process, nucleotide binding	SCAH10.33c; histidine kinase; [GeneDB:SCO6268] [NCBI-GI:21224589] [NCBI-GeneID:1101709] [UniProt:Q9RKS6]
SCO6272	21	0.02667	1.66	metabolic process, catalytic activity, nucleotide binding	SC2C4.02; secreted FAD-binding protein; [GeneDB:SCO6272] [NCBI-GI:21224592] [NCBI-GeneID:1101713] [UniProt:Q9EX55]
SCO6273	46	0.05609	1.70	metabolic process, catalytic activity	SC2C4.03c; type I polyketide synthase; [GeneDB:SCO6273] [NCBI-GI:21224593] [NCBI-GeneID:1101714] [UniProt:Q9EX54]
SCO6274	44	0.05545	1.59	metabolic process, catalytic activity	SC2C4.04c; type I polyketide synthase; [GeneDB:SCO6274] [NCBI-GI:21224594] [NCBI-GeneID:1101715] [UniProt:Q9EX53]
SCO6275	67	0.10746	1.41	metabolic process, catalytic activity	SC1G7.01c. SC2C4.05c; type I polyketide synthase; [GeneDB:SCO6275] [NCBI-GI:32141295] [NCBI-GeneID:1101716] [UniProt:Q8CJN6]
SCO6276	17	0.02118	1.57		SC1G7.02; secreted protein; [GeneDB:SCO6276] [NCBI-GI:21224595] [NCBI-GeneID:1101717] [UniProt:Q93S13]

SCO6277	27	0.03481	1.47	metabolic process, catalytic activity	SC1G7.03; epoxide hydrolase; [GeneDB:SCO6277] [NCBI-GI:21224596] [NCBI-GenelD:1101718] [UniProt:Q93S12]
SCO6278	24	0.03458	1.94	transport	SC1G7.04; putative integral membrane transport protein; K08167 MFS transporter. DHA2 family. methyl viologen resistance protein SmvA; [GeneDB:SCO6278] [NCBI-GI:21224597] [NCBI-GenelD:1101719] [UniProt:Q93S11]
SCO6279	12	0.01333	1.85	metabolic process, catalytic activity	SC1G7.05; diaminobutyrate-pyruvate aminotransferase; [GeneDB:SCO6279] [NCBI-GI:21224598] [NCBI-GenelD:1101720] [UniProt:Q93S10]
SCO6282	9	0.01000	2.19	metabolic process, catalytic activity	SC1G7.08c; 3-oxoacyl-[acyl-carrier protein] reductase; [GeneDB:SCO6282] [NCBI-GI:21224601] [NCBI-GenelD:1101723] [UniProt:Q93S07]
SCO6283	50	0.06740	1.44		SC1G7.09; hypothetical protein; [GeneDB:SCO6283] [NCBI-GI:21224602] [NCBI-GenelD:1101724] [UniProt:Q93S06]
SCO6285	82	0.14220	1.52		SC1G7.11; hypothetical protein; [GeneDB:SCO6285] [NCBI-GI:21224604] [NCBI-GenelD:1101726] [UniProt:Q93S04]
SCO6288	81	0.13901	1.00	cell communication, metabolic process, regulation of biological process, DNA binding, signal transducer activity	SC1G7.14. SCBAC8D1.01; regulatory protein; [GeneDB:SCO6288] [NCBI-GI:21224607] [NCBI-GenelD:1101729] [UniProt:Q93RY4]
SCO6429	25	0.03600	1.94		SC1A6.18; hypothetical protein; [GeneDB:SCO6429] [NCBI-GI:21224736] [NCBI-GenelD:1101868] [UniProt:O69823]
SCO6431	29	0.04379	1.85	metabolic process, catalytic activity	SC1A6.20; peptide synthase; [GeneDB:SCO6431] [NCBI-GI:21224738] [NCBI-GenelD:1101870] [UniProt:O69825]
SCO6433	10	0.00900	2.37		SC1A6.22; hypothetical protein; K06995; [GeneDB:SCO6433] [NCBI-GI:21224740] [NCBI-GenelD:1101872] [UniProt:O69827]
SCO6434	51	0.07765	1.63	metabolic process, catalytic activity	SC1A6.23. SC9B5.01; oxidoreductase; [GeneDB:SCO6434] [NCBI-GI:32141301] [NCBI-GenelD:1101873] [UniProt:Q8CJN0]
SCO6435	22	0.02591	2.00	metabolic process, regulation of biological process	SC9B5.02; hypothetical protein; [GeneDB:SCO6435] [NCBI-GI:21224741] [NCBI-GenelD:1101874] [UniProt:Q9ZBH8]
SCO6436	28	0.03893	1.96	metabolic process, catalytic activity, nucleotide binding	SC9B5.03; tRNA synthetase; [GeneDB:SCO6436] [NCBI-GI:21224742] [NCBI-GenelD:1101875] [UniProt:Q9ZBH7]

SCO6509	60	0.08633	1.88		SC1E6.18c; hydrophobic protein; [GeneDB:SCO6509] [NCBI-GI:21224812] [NCBI-GeneID:1101948] [UniProt:Q9ZC04]
SCO7399	76	0.12987	1.20		SC10G8.27c; binding-protein-dependent transport lipoprotein; [GeneDB:SCO7399] [NCBI-GI:21225670] [NCBI-GeneID:1102837] [UniProt:Q9L178]
SCO7643	71	0.10789	1.36		SC10F4.16; hypothetical protein; [GeneDB:SCO7643] [NCBI-GI:21225904] [NCBI-GeneID:1103081] [UniProt:Q9F3P4]
SCO7676	4	0.00500	3.17	metal ion binding	SC4C2.11; ferredoxin; [GeneDB:SCO7676] [NCBI-GI:21225936] [NCBI-GeneID:1103114] [UniProt:Q9EWQ1]
SCO7799	40	0.05200	1.92		SC10B8A.09c; transposase; [GeneDB:SCO7799] [NCBI-GI:21226051] [NCBI-GeneID:1103237] [UniProt:Q9FCL5]

Table S3. Differentially expressed genes shared between Glc/Agar and *ScoM145/ScoZm* comparisons

Gene name	Product	Function
<i>SCO0090</i>		Transposase
<i>SCO0489</i>		Hypothetical protein
<i>SCO0498</i>		Putative peptide monooxygenase [EC:1.13.12.-]
<i>SCO0861</i>		Secreted protein
<i>SCO0863</i>		Integral membrane protein
<i>SCO0973</i>		Integral membrane protein
<i>SCO1087</i>		Putative aldolase [EC:4.1.2.5]
<i>SCO1088</i>		Oxidoreductase
<i>SCO1089</i>		Hypothetical protein 2SCG405c
<i>SCO1550</i>		Small membrane protein
<i>SCO1713</i>		Hypothetical protein
<i>SCO2306</i>		Putative ABC transporter integral membrane protein
<i>SCO2463</i>		Putative ABC transporter
<i>SCO2464</i>		Putative ABC transporter
<i>SCO2528</i>	leuA. SCC121.31c	2-Isopropylmalate synthase [EC:2.3.3.13]
<i>SCO2776</i>	accD1. SCC105.07	Acetyl/propionyl CoA carboxylase. beta subunit [EC:6.4.1.3]
<i>SCO2778</i>	hmgL. SCC105.09	Hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]
<i>SCO2779</i>	acdH. SCC105.10	Acyl-CoA dehydrogenase
<i>SCO2839</i>		Lipoprotein
<i>SCO3089</i>		Putative ABC transporter ATP-binding protein
<i>SCO3090</i>		Putative ABC transporter integral membrane protein

SCO3111		Putative ABC transport system ATP-binding protein
SCO3152		Hypothetical protein
SCO3263		Hypothetical protein
SCO3265		Hypothetical protein
SCO3266		Hypothetical protein
SCO3268		Secreted protein
SCO3390		Two component sensor kinase
SCO3472		Transposase remnant
SCO3473		Putative aldolase [EC:4.1.2.14 4.1.3.16]
SCO3474		Sugar kinase
SCO3475		Putative galactonate dehydratase protein [EC:4.2.1.6]
SCO3476		Putative short-chain dehydrogenase [EC:1.1.1.125]
SCO3477		Dehydrogenase
SCO3478		Dehydrogenase
SCO3480		Putative racemase [EC:5.1.2.2]
SCO3481		Hypothetical protein
SCO3483		Putative integral membrane transport protein
SCO3484		Putative secreted sugar-binding protein
SCO3487		Hydrolase
SCO3717		Putative cation transport system component [EC:3.6.3.12]
SCO3719		Small membrane protein
SCO3918		Hypothetical protein
SCO3956		Putative ABC transporter ATP-binding protein
SCO3957		Possible integral membrane protein
SCO3958		ABC transporter ATP-binding protein
SCO3959		Possible integral membrane protein

SCO3967		Conserved hypothetical membrane protein
SCO3982		Hypothetical protein
SCO3983		Hypothetical protein
SCO3986		GntR-family transcriptional regulator
SCO3987		Hypothetical protein
SCO3988		Hypothetical protein
SCO4005		RNA polymerase sigma factor
SCO4054		Integral membrane protein
SCO4261		Response regulator
SCO4293		Putative threonine synthase [EC:4.2.3.1]
SCO4368		Lipase (secreted protein)
SCO4851		Hypothetical protein
SCO4852		Integral membrane protein
SCO4947		Nitrate reductase alpha chain NarG3 [EC:1.7.99.4]
SCO5285		ATP-dependent protease [EC:3.4.21.53]
SCO5521		Hypothetical protein
SCO5676	gabT	Putative 4-aminobutyrate aminotransferase [EC:2.6.1.19]
SCO5774	gluD	Glutamate permease
SCO5775	gluC	Glutamate permease
SCO5776	gluB	Glutamate binding protein
SCO5777	gluA	Glutamate uptake system ATP-binding protein [EC:3.6.3.-]
SCO6164		Putative DnaK suppressor protein
SCO6272		Secreted FAD-binding protein
SCO6273		Type I polyketide synthase
SCO6274		Type I polyketide synthase
SCO6275		Type I polyketide synthase

SCO6276		Secreted protein
SCO6277		Epoxide hydrolase
SCO6278		Putative integral membrane transport protein
SCO6279		Diaminobutyrate-pyruvate aminotransferase
SCO6282		3-Oxoacyl-[acyl-carrier protein] reductase
SCO6283		Hypothetical protein
SCO6285		Hypothetical protein
SCO6429		Hypothetical protein
SCO6431		Peptide synthase
SCO6433		Hypothetical protein
SCO6434		Oxidoreductase
SCO6435		Hypothetical protein
SCO6436		tRNA synthetase
SCO6509		Hydrophobic protein
SCO7399		Binding-protein-dependent transport lipoprotein
SCO7643		Hypothetical protein
SCO7676		Ferredoxin
SCO7799		Transposase

Table S4. Oligonucleotides used in this study

Name	Target	Sequence 5'-3'
<i>glk</i> fwd-large		ttagcggggctcgaccgaactgagggattcatgggactcattccggggatccgtcgacc
<i>glk</i> rev-large		cgggtgagcgcagctcccggagtcgggaagtgatcgtcatgtaggctggagctgcttc
<i>glk</i> out-fwd		gtcgaaccacaggaacgccgtggaccac
<i>glk</i> out-rev		gagcgccgggagggatgttccatgccgtcaa
<i>glk1</i>	<i>glk</i>	[23]
<i>glk2</i>	<i>glk</i>	[23]
SCO5373 fwd qpcr	<i>atpd</i>	tggtcttcggtcagatgga
SCO5373 rev qpcr	<i>atpd</i>	cggaagatgttgatgaaga
SCO3878 fwd qpcr	<i>dnan</i>	ctcaaccgcaccttctg
SCO3878 rev qpcr	<i>dnan</i>	aggacttgtaggcctcgt
SCO5769 fwd qpcr	<i>reca</i>	ggagatcgagggcgagat
SCO5769 rev qpcr	<i>reca</i>	gtggtcttgactggttgag
SCO6008 fwd qpcr	<i>rok7b7</i>	cgaaatcgggcacatcac
SCO6008 rev qpcr	<i>rok7b7</i>	aggagcggaagcacatag

SCO6162 fwd qpcr	SCO6162	atcgccgagatcctcttcat
SCO6162 rev qpcr	SCO6162	gtaccgggtcagctcca
SCO5578 fwd qpcr	<i>glcp</i>	gcagttcgtcggcatcaa
SCO5578 rev qpcr	<i>glcp</i>	cgtcgtgaacgagtagaagaac
SCO6164 fwd qpcr	SCO6164	gcgtcaccagcttcag
SCO6164 rev qpcr	SCO6164	tcgtcgatctccttgagca
SCO3471 fwd qpcr	<i>daga</i>	ttcactgaactggcgagaag
SCO3471 rev qpcr	<i>daga</i>	tggaatccattccgaagaagag
SCO4729 fwd qpcr	<i>rpoa</i>	aagggcaagctggagatg
SCO4729 rev qpcr	<i>rpoa</i>	tgagaaccggcgagtaga
SCO3873 fwd qpcr	<i>gyra</i>	gcgaagatcaccgagtacaac
SCO3873 rev qpcr	<i>gyra</i>	tacgggatcagcttggtctt
SCO5820 fwd qpcr	<i>hrdb</i>	ggagaagttcgactacaccaag
SCO5820 rev qpcr	<i>hrdb</i>	ccatgtgcaccgggatac