

Figure S1. Reproducibility between the biological replicates (MXA and MXB) for mixed cultures. Correlations for RPKM values were plotted once assigned to M8 (upper panel), with a $R = 0.9956$, or M31 (lower panel) with $R = 1$.

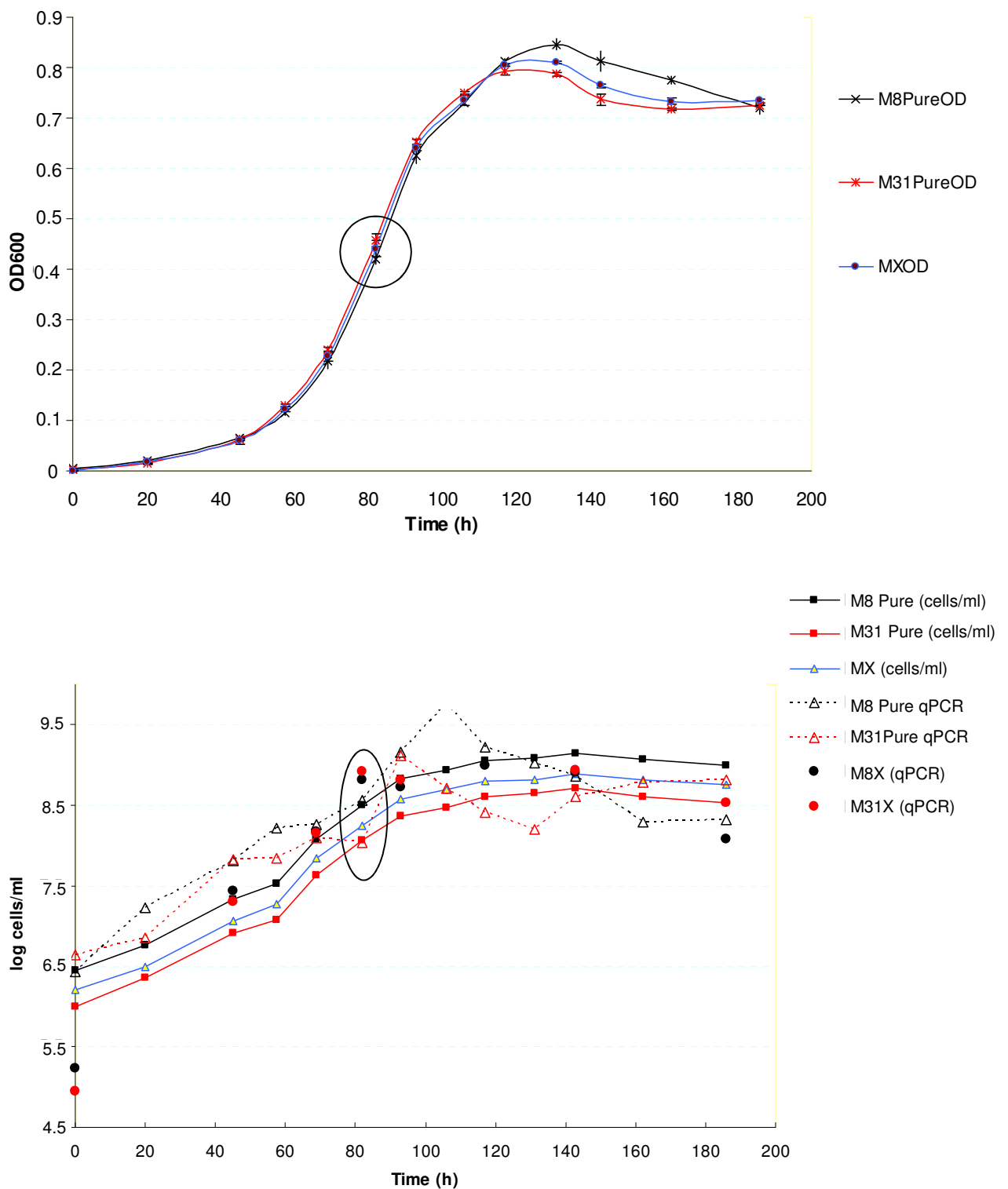
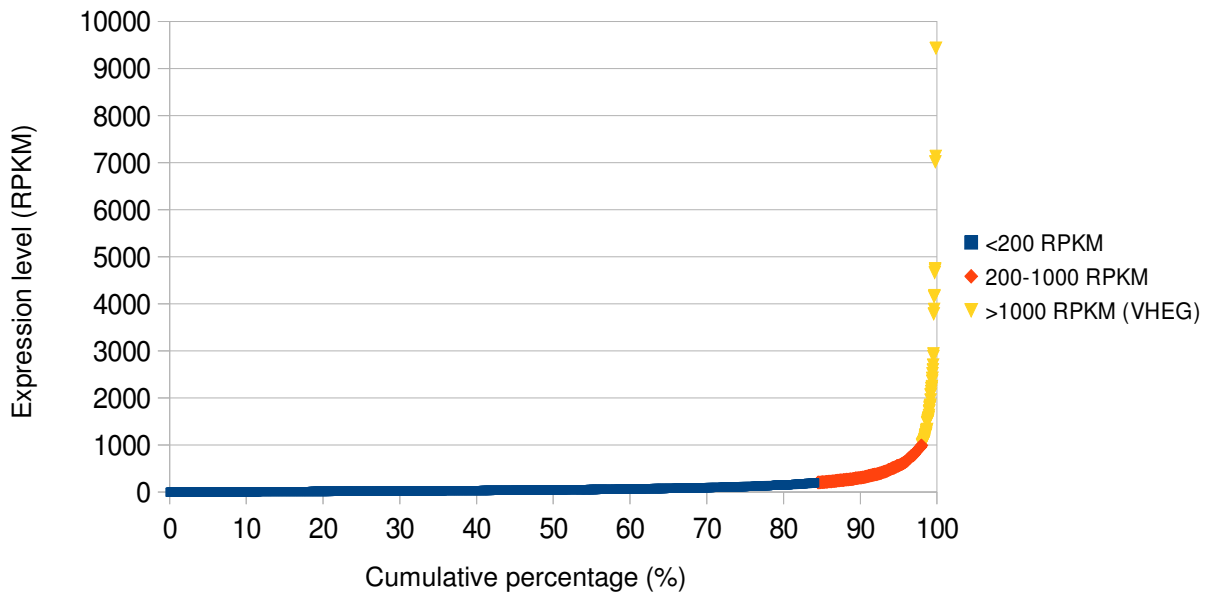


Figure S2. Growth curves for pure cultures of M8 (blue) and M31 (red). In the upper figure lines represent OD reads for pure and mixed cultures, as indicated in the insert. The bottom figure show log cells/ml values for M8 and M31 cultures measured by quantitative PCR (black and red dots for mixed and triangles for pure cultures) and DAPI (continuous lines). Circled the point selected for sequencing.

Cumulative frequency curve. *S. ruber* M8, pure cultures



Cumulative frequency curve. *S. ruber* M31, pure cultures

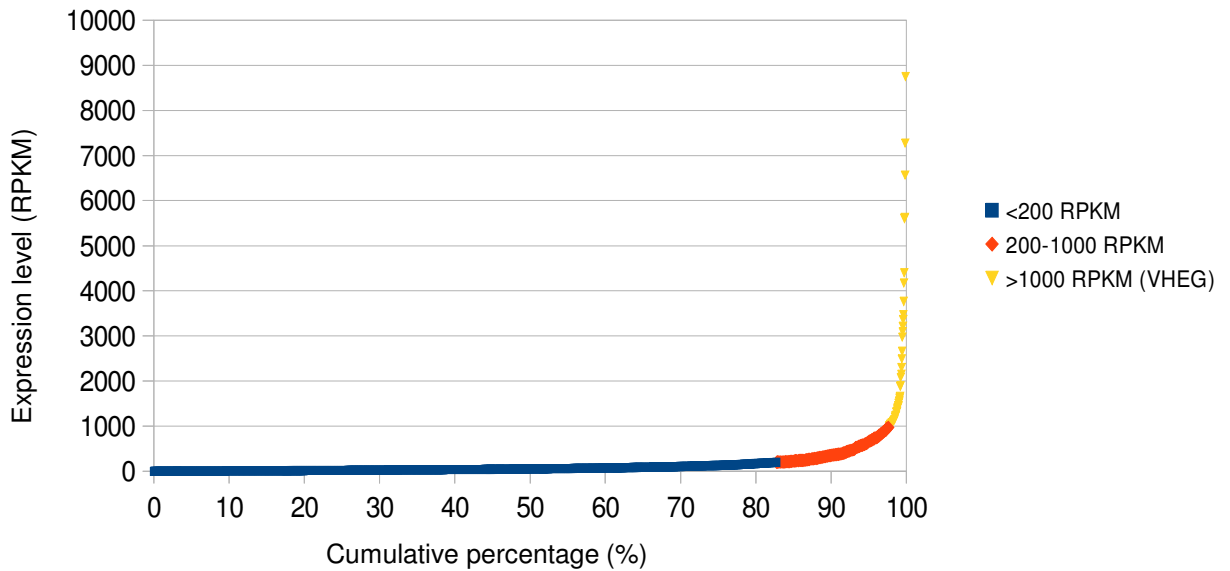
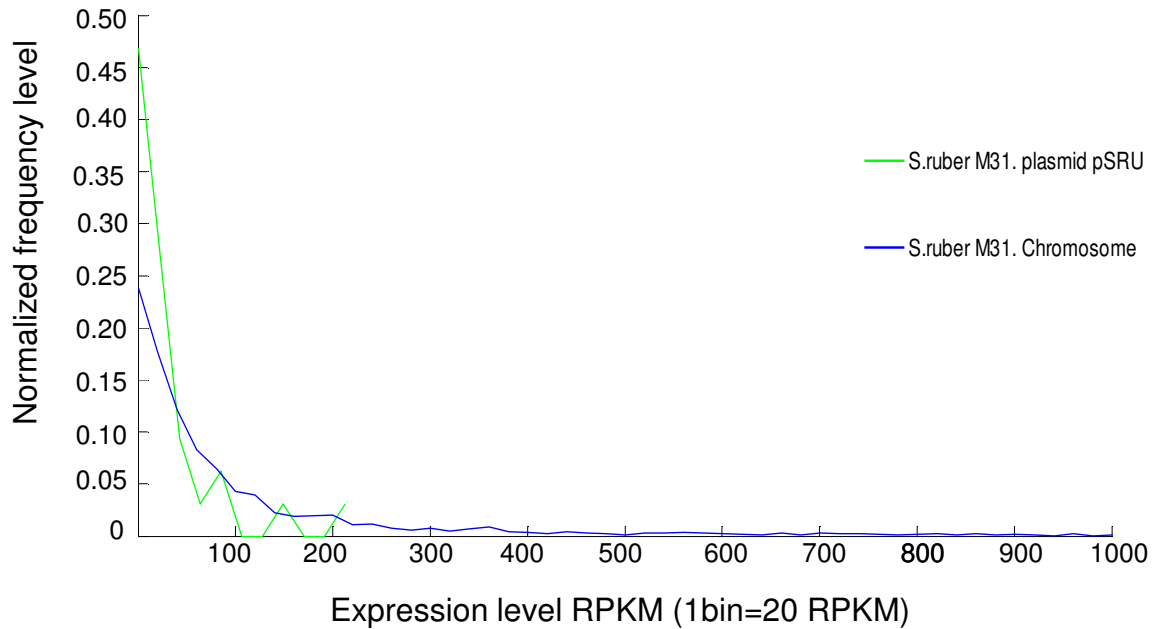


Figure S3. RPKM transcription levels for M8 (upper panel) and M31 (lower panel) genes in pure cultures. Cumulative curves represents the percentage of genes with transcription levels between 0-200 RPKM (blue), 200-1000 RPKM (orange) and above 1000 RPKM (yellow).

S. ruber M31 replicons. Normalized expression frequency histogram



S. ruber M8 replicons. Normalized expression frequency histogram

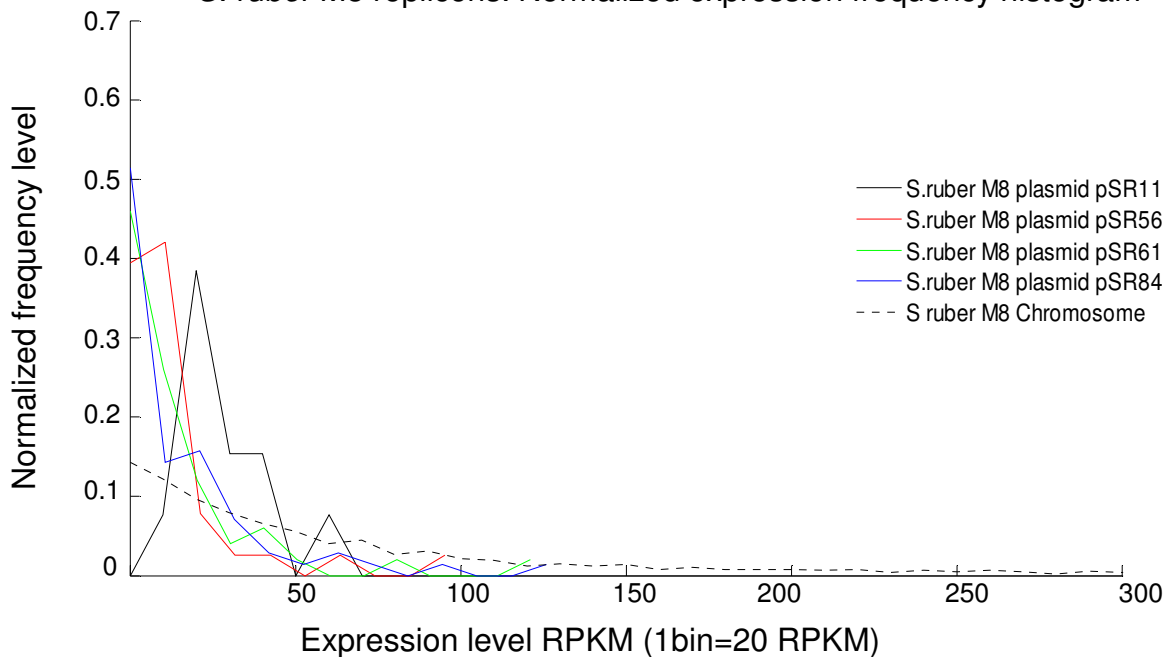
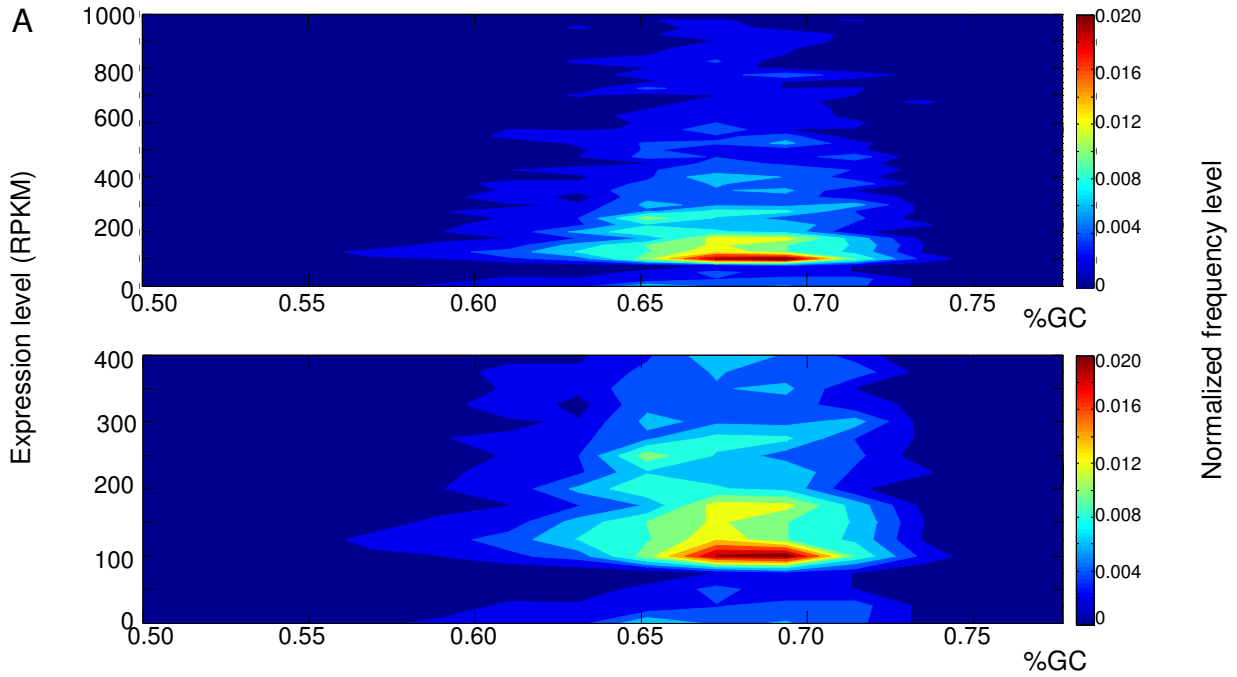


Figure S4. Normalized gene distribution for M31 (upper figure) and M8 (bottom figure) based on their expression level (RPKM). All the replicons were represented in both cases.

M8 Pure culture. Relation between %GC and expression values



M31 Pure culture. Relation between %GC and expression values

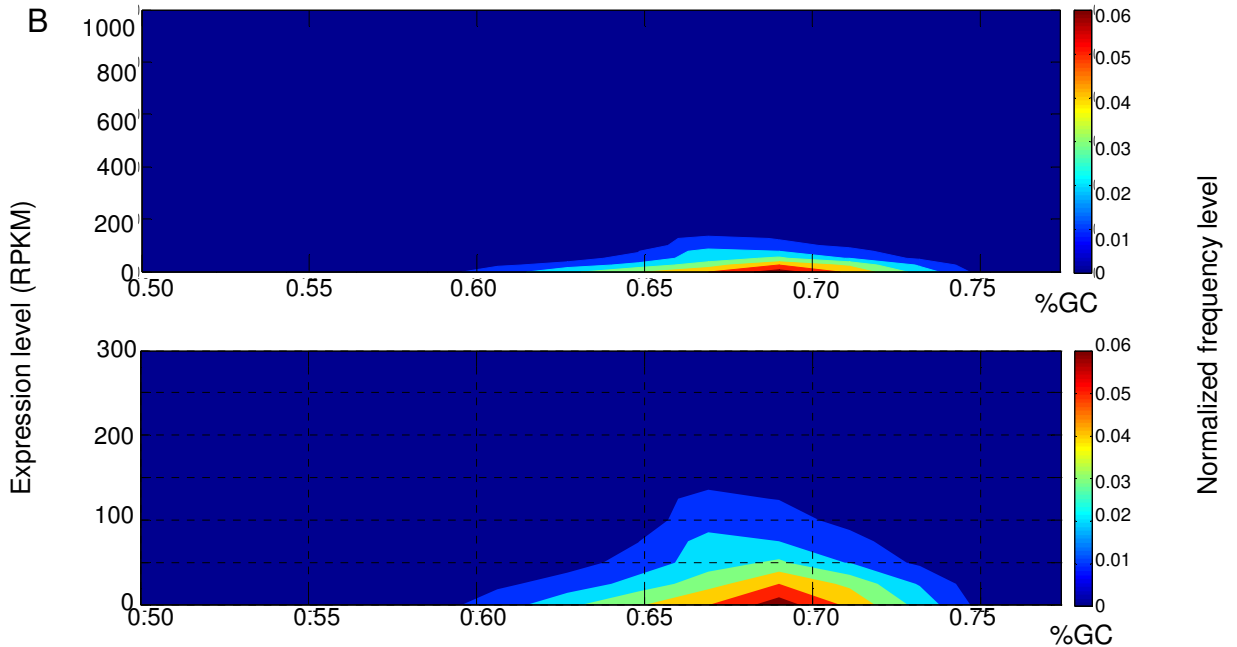


Figure S5. Normalized gene distribution for M8 (A) and M31 (B) based on their % GC and RPKM expression levels. For each strain, genes with expression values below 300 RPKM are shown in bottom panels.

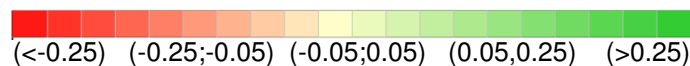
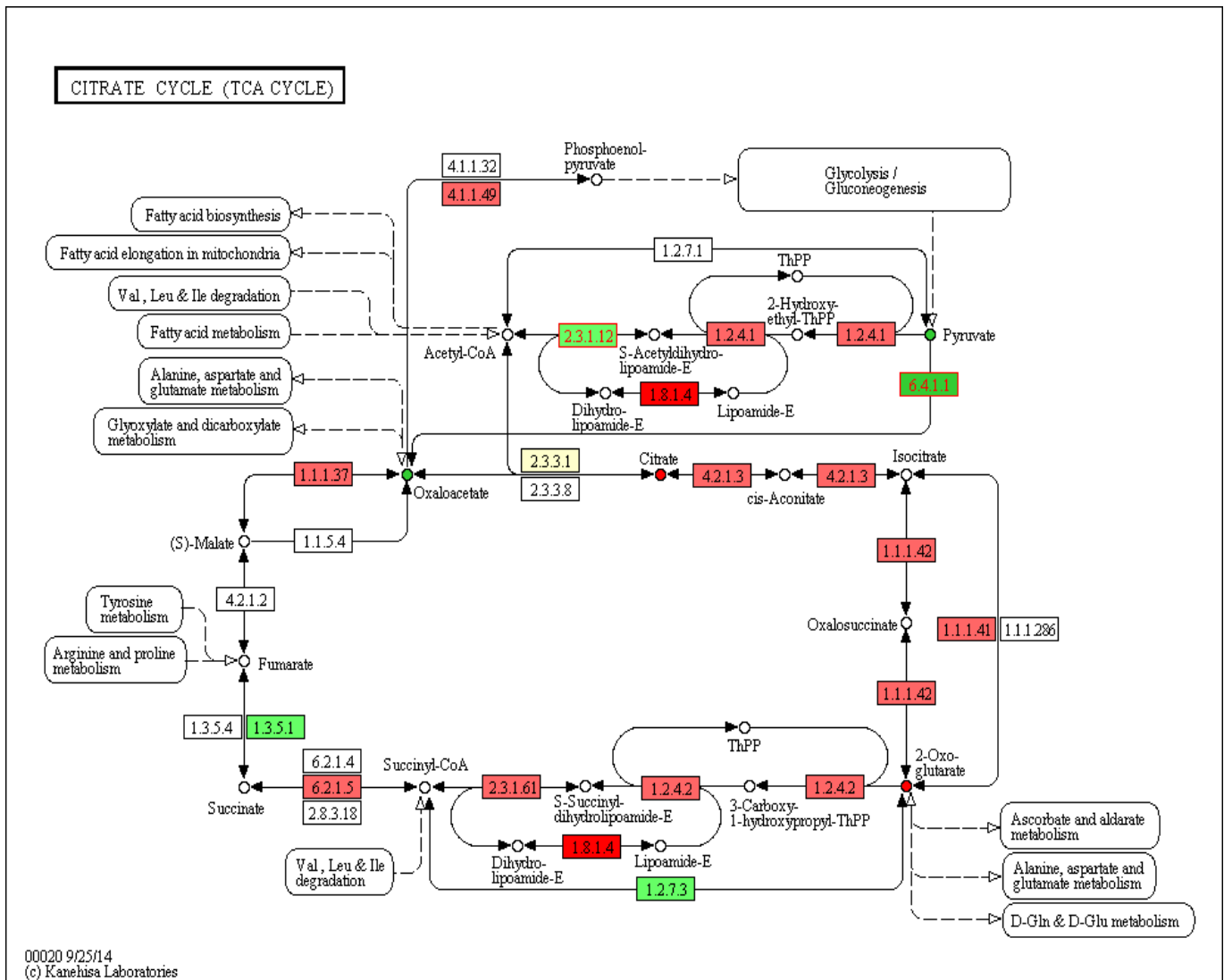


Figure S6. M31 citrate cycle (TCA cycle) KEGG map (sru:00020) showing the differential expression changes (log₂ fold change) of *S. ruber* M31 mean a percentage color gradient. The green boxes represent genes that increase their expression and the reds that decrease it. In red letters the genes that change its expression significantly (SRU_828 = 6.4.1. 1; (SRU_1969 = 2.3.1. 12). The circles show the increases (green) or decreases (red) of intermediate metabolites based on the genes expression levels that encode the enzymes that produce them.

Table S1. M8 (Gene ID SRM_) and M31 (Gene ID SRU_) genes with transcription below the detection threshold in pure culture. In blue, strain specific genes. In green, genes “untranscribed” both in M8 and M31. I: Island; CR: conserved region; HP: Hypothetical protein; CHP: Conserved hypothetical protein.

GeneID	Location	Function	GeneID	Location	Function
SRM_00004		HP	SRM_00807	I2	HP
SRM_00141		HP	SRM_00808	I2	HP
SRM_00142		CHP	SRM_01218		HP
SRM_00143		HP	SRM_01405		HP
SRM_00152		HP	SRM_01571		CHP
SRM_00202		HP	SRM_01654		HP
SRM_00204		HP	SRM_01683		HP
SRM_00239	I1	HP	SRM_01760		CHP
SRM_00318	I1	HP	SRM_01835		HP
SRM_00328	I1	HP	SRM_01949		HP
SRM_00332	I1	HP	SRM_02101		HP
SRM_00376		HP	SRM_02231		HP
SRM_00401		HP	SRM_02302	CR	HP
SRM_00479		HP	SRM_02491	CR	
SRM_00536		HP	SRM_02677		CHP
SRM_00670		HP	SRM_02688		HP
SRM_00686	I2	transposase	SRM_02978		HP
SRM_00756	I2	HP	PSR_56034	PSR56	HP
SRM_00765	I2	HP	PSR_61015	PSR61	HP
SRM_00775	I2	HP	PSR_61026	PSR61	HP
SRM_00784	I2	HP	PSR_61031	PSR61	HP
SRM_00799	I2	transposase	PSR_84007	PSR84	HP
SRM_00875		HP	PSR_84047	PSR84	HP
SRM_01016		HP	PSR_84058	PSR84	HP
SRM_01047		CHP	PSR_84061	PSR84	HP
SRM_01074		HP	PSR_84063	PSR84	HP
SRM_01130		HP	PSR_84067	PSR84	HP
SRM_01182		HP			
SRU_0013		HP	SRU_0863	I3	CHP
SRU_0125		CHP	SRU_1104	I3	HP
SRU_0181	I1	HP	SRU_1107	I3	HP
SRU_0186	I1	HP	SRU_1376		CHP
SRU_0187	I1	Transcription regulator	SRU_1406		HP
SRU_0212	I1	CHP	SRU_1562		CHP
SRU_0214	I1	CHP	SRU_1834		HP
SRU_0215	I1	CHP	SRU_2021	CR	HP
SRU_0217	I1	HP	SRU_2339		HP
SRU_0250	I1	HP	SRU_2394		sensor kinase protein rcsC

SRU_0263	I1	HP	SRU_2457	CHP
SRU_0284		HP	SRU_2465	HP
SRU_0578		HP	SRU_2634	HP
SRU_0593	I2	HP	SRU_2862	
SRU_0625	I2	HP	SRU_p0008	tyrosine recombinase XerD

Table S2. Genes with expression above 1000 RPKM (VHEG: “Very highly expressed genes”). Pink: M8 VHEG. Blue: M31 VHEG.

Gene ID	RPKM	Annotation	Location ^a	Ortholog.
SRM_00001	27298	hypothetical protein		M8 specific
SRM_00036	1054	50S ribosomal protein L13		SRU_0038
SRM_00088	3787	conserved hypothetical protein		SRU_0081
SRM_00272	2882	hypothetical protein	I1	M8 specific
SRM_00392	1807	hypothetical protein		M8 specific
SRM_00393	1324	cytochrome c oxidase subunit II		SRU_0313
SRM_00452	2360	hypothetical protein		SRU_0375
SRM_00460	7131	AsnC family transcriptional regulator		SRU_0384
SRM_00461	2700	glutamine synthetase		SRU_0385
SRM_00512	2080	hypothetical protein		SRU_0435
SRM_00590	1483	TonB protein		SRU_0510
SRM_00689	1216	Chain length determinant protein		SRU_0594
SRM_00690	1079	Phage integrase family protein	I2	SRU_0595
SRM_00691	1155	UDP-glucose 6-dehydrogenase	I2	M8 specific
SRM_00692	2198	hypothetical protein	I2	M8 specific
SRM_00700	1062	acyl-[acyl-carrier-protein]--UDP-N-	I2	SRU_0606
SRM_00846	1205	succinyl-CoA synthetase, alpha subunit		SRU_0670
SRM_01098	1833	PKD repeat protein		SRU_0906
SRM_01105	2142	ATP synthase subunit C		SRU_0912
SRM_01159	7018	cold-shock DNA-binding protein		SRU_0966
SRM_01223	2420	hypothetical protein		M8 specific
SRM_01230	1238	30S ribosomal protein S12		SRU_1030
SRM_01245	1502	30S ribosomal protein S17		SRU_1044
SRM_01262	1542	50S ribosomal protein L17		SRU_1061
SRM_01290	69145	hypothetical protein		M8 specific
SRM_01319	1005	adenosylhomocysteinase		SRU_1139
SRM_01343	9430	50S ribosomal protein L31		SRU_1162
SRM_01355	4175	30S ribosomal protein S21		M8 specific
SRM_01510	1188	ATP-dependent Clp protease, ATPase subunit		SRU_1317
SRM_01511	1071	iron-sulfur cluster assembly accessory protein		SRU_1318
SRM_01611	3883	50S ribosomal protein L27		SRU_1419
SRM_01612	1525	50S ribosomal protein L21		SRU_1420
SRM_01670	1331	Aconitate hydratase		SRU_1477
SRM_01698	1478	Xanthorhodopsin		SRU_1500
SRM_01735	1026	hypothetical protein		SRU_1536
SRM_01789	1569	Azurin		SRU_1590
SRM_01798	1716	hypothetical protein		M8 specific
SRM_01885	1032	MotA/TolQ/ExbB proton channel		SRU_1681
SRM_01935	2210	superoxide dismutase		SRU_1724
SRM_01939	1281	cold-shock protein		SRU_1727
SRM_01942	10023	hypothetical protein		SRU_1731
SRM_01970	1042	DNA-directed RNA polymerase subunit beta'		SRU_1757
SRM_01972	2596	50S ribosomal protein L7/L12		SRU_1759
SRM_01986	1308	30S ribosomal protein S15		SRU_1774
SRM_01995	1724	conserved hypothetical protein		SRU_1783
SRM_01999	1629	30S ribosomal protein S1		SRU_1787
SRM_02130	1023	hypothetical protein		SRU_1919
SRM_02344	4749	10 kDa chaperonin	CR	SRU_2121

SRM_02345	4666	60 kDa chaperonin	CR	SRU_2122
SRM_02401	1006	TonB-dependent receptor	CR	SRU_2178
SRM_02404	2243	hypothetical protein	CR	M8 specific
SRM_02405	1219	outer membrane protein	CR	SRU_2181
SRM_02406	1789	TonB-dependent receptor	CR	SRU_2182
SRM_02434	4719	peptidyl-prolyl cis-trans isomerase	CR	SRU_2208
SRM_02598	1960	conserved hypothetical protein		SRU_2378
SRM_02647	1123	ATP synthase beta chain		SRU_2429
SRM_02648	1101	ATP synthase subunit epsilon		SRU_2430
SRM_02671	11771	cold-shock protein		SRU_2449
SRM_02965	4151	acyl carrier protein		SRU_2754
SRM_03020	2518	50S ribosomal protein L35		SRU_2804
SRM_03021	1592	50S ribosomal protein L20		SRU_2805
SRM_03022	1851	hypothetical protein		M8 specific
SRM_03086	2065	conserved hypothetical protein		SRU_2870
PSR_11013	2937	hypothetical protein containing Lambda repressor-like, DNA-binding domain	PSR11	M8 specific
M8ncRNA1	6616	SAM (RF00162)SAM riboswitch (S box leader)	688232pb-688349pb	M31ncRNA1
M8ncRNA2	378643	TmRNA (RF00023) transfer-messenger RNA	1459257pb-1459625pb	M31ncRNA2
M8ncRNA3	3611	TPP (RF00059) TPP riboswitch (THI element)	1510121pb-1510199pb	M31ncRNA3
SRU_0021	1152	ribosomal protein L28		SRM_00022
SRU_0081	3219	conserved hypothetical protein		SRM_00088
SRU_0237	1454	chaperonin GroEL	I1	SRM_00297
SRU_0313	1062	cytochrome c oxidase subunit II		SRM_00393
SRU_0375	1419	hypothetical protein		SRM_00452
SRU_0384	8756	putative AsnC-family transcriptional regulator		SRM_00460
SRU_0385	3098	glutamine synthetase, type I		SRM_00461
SRU_0394	1142	NADH-quinone oxidoreductase chain b		SRM_00470
SRU_0435	2151	conserved hypothetical protein		SRM_00512
SRU_0510	2083	TonB		SRM_00590
SRU_0594	1212	Chain length determinant protein	I2	SRM_00689
SRU_0595	1144	Phage integrase family protein	I2	SRM_00690
SRU_0596	1244	UDP-glucose dehydrogenase	I2	M31 specific
SRU_0598	1001	ABC transporter, multidrug efflux family	I2	M31 specific
SRU_0599	1047	NDP-sugar dehydrogenase, putative	I2	SRM_00718
SRU_0600	1095	nucleoside-diphosphate-sugar epimerase	I2	M31 specific
SRU_0601	1262	perosamine synthetase , putative	I2	SRM_00695
SRU_0670	1428	succinyl-CoA synthetase, alpha subunit		SRM_00846
SRU_0729	1076	bioY family protein		SRM_00907
SRU_0867	4175	hypothetical protein		SRM_01051
SRU_0906	2304	conserved protein		SRM_01098
SRU_0912	2494	ATP synthase F0, C subunit		SRM_01105
SRU_0966	12252	'Cold-shock' DNA-binding domain, putative		SRM_01159
SRU_1035	1083	ribosomal protein L3		SRM_01236
SRU_1044	1553	30S ribosomal protein S17		SRM_01245
SRU_1046	1015	ribosomal protein L24		SRM_01247
SRU_1057	1014	ribosomal protein S13p/S18e		SRM_01258
SRU_1061	1125	ribosomal protein L17		SRM_01262
SRU_1139	1094	adenosylhomocysteinase		SRM_01319
SRU_1162	7278	ribosomal protein L31		SRM_01343
SRU_1305	1080	osmotically inducible protein C		SRM_01497

SRU_1317	1131	ATP-dependent Clp protease, ATPase subunit		SRM_01510
SRU_1318	1200	iron-sulfur cluster assembly accessory protein,		SRM_01511
SRU_1367	1080	ribosomal protein L9		SRM_01562
SRU_1419	3475	ribosomal protein L27		SRM_01611
SRU_1477	1520	aconitate hydratase, putative		SRM_01670
SRU_1500	1230	xanthorhodopsin		SRM_01698
SRU_1563	3368	putative cold shock-like protein cspG		M31 specific
SRU_1590	1325	auracyanin A precursor		SRM_01789
SRU_1681	1034	MotA/TolQ/ExbB proton channel family protein		SRM_01885
SRU_1724	1074	Mn-superoxide dismutase		SRM_01935
SRU_1727	1576	conserved domain protein		SRM_01939
SRU_1731	10618	histone H1-like protein		SRM_01942
SRU_1757	1035	DNA-directed RNA polymerase, beta' subunit		SRM_01970
SRU_1759	2979	ribosomal protein L7/L12		SRM_01972
SRU_1774	1318	ribosomal protein S15		SRM_01986
SRU_1783	1336	conserved hypothetical protein		SRM_01995
SRU_1787	1663	ribosomal protein S1, putative		SRM_01999
SRU_1898	1069	putative regulatory protein, FmdB family		SRM_02108
SRU_1919	1048	conserved hypothetical protein		SRM_02130
SRU_2121	3768	chaperonin, 10 kDa	CR	SRM_02344
SRU_2122	5605	chaperonin GroEL	CR	SRM_02345
SRU_2176	1270	fasciclin domain protein	CR	SRM_02399
SRU_2178	1425	putative outer membrane protein, probably	CR	SRM_02401
SRU_2181	1898	putative outer membrane protein probably	CR	SRM_02405
SRU_2182	2660	putative outer membrane protein probably	CR	SRM_02406
SRU_2208	4404	peptidyl-prolyl cis-trans isomerase, FKBP-type	CR	SRM_02434
SRU_2362	1518	tetratricopeptide repeat domain protein		SRM_02581
SRU_2378	1883	conserved hypothetical protein		SRM_02598
SRU_2449	6566	conserved domain protein		SRM_02671
SRU_2754	5634	acyl carrier protein		SRM_02965
SRU_2781	1113	oxidoreductase, putative		SRM_02995
SRU_2792	1389	hypothetical HIT-like protein slr1234		SRM_03009
SRU_2805	1626	ribosomal protein L20		SRM_03021
SRU_2870	2096	conserved hypothetical protein		SRM_03086
M31ncRNA1	19416	SAM (RF00162)SAM riboswitch (S box leader)	648791pb- 648908pb	M8ncRNA1
M31ncRNA2	787545	TmRNA (RF00023) transfer-messenger RNA	1401829pb- 1402196pb	M8ncRNA2
M31ncRNA3	5095	TPP (RF00059) TPP riboswitch (THI element)	1450683pb- 1450760pb	M8ncRNA3

^aI: Island; CR: Conserved region

Table S3. Expression level differences between paralogous genes. 205 gene duplication events, 182 pre-M8/M31 divergence (1) and 23 post-M8/M31 divergence and detected in M8 strain (0), and genes involved are shown in the table. An average of Log2 fold change value was obtained in order to estimate expression level differences, 1.31 ± 1.26 and 2.5 ± 2.13 for duplication events accounted after (0; orange) and before (1; yellow) M8 and M31 strains divergence respectively.

1= Paralogs M8+M31 0= Paralogs M8 Strain specific	Gene ID	Absolute value (log2Foldchange)
1	SRM_00129	0.0173
0	SRM_00261; SRM_00259	0.0246
1	SRM_02262	0.0265
1	SRM_02262; SRM_02974	0.0265
0	SRM_00213; SRM_00270	0.0295
0	SRM_00270; SRM_00213	0.0295
1	SRM_02656	0.1200
1	SRM_01444	0.1297
1	SRM_02509	0.1312
1	SRM_02509	0.1312
0	SRM_00221; SRM_03003	0.1354
0	SRM_0789; SRM_00832	0.1582
1	SRM_00925	0.1651
1	SRM_00232; SRM_0077	0.1656
1	SRM_01359; SRM_02708	0.1934
1	SRM_00231; SRM_01776	0.2189
1	SRM_00129; SRM_00342	0.2230
1	SRM_00220	0.2361
1	SRM_01838; SRM_02731	0.2568
1	SRM_01954; SRM_02906	0.2916
0	SRM_00685; SRM_01408	0.2947
1	SRM_00409; SRM_00553	0.2947
1	SRM_01305; SRM_01306	0.2947
1	SRM_00468; SRM_02549	0.2961
1	SRM_00880; SRM_02030	0.3486
0	SRM_00627; SRM_00832	0.3518
1	SRM_00167; SRM_00961; SRM_01947	0.4449
1	SRM_00301; SRM_02935	0.4604
1	SRM_02733	0.4798
1	SRM_02733	0.4798
1	SRM_00322; SRM_01443; SRM_01749	0.4805
0	SRM_00073; SRM_01073; SRM_02614	0.4852
0	SRM_01073; SRM_00073; SRM_02614	0.4852
1	SRM_02989	0.4900
1	SRM_00972; SRM_00973	0.4908
1	SRM_02694	0.5403
1	SRM_01020; SRM_01422	0.5523
1	SRM_00546; SRM_01101	0.5531
0	SRM_01932; SRM_01930	0.5811
1	SRM_00349; SRM_01219; SRM_01366	0.6070

1	SRM_00235; SRM_00335	0.6449
1	SRM_00080; SRM_00113; SRM_02547	0.6449
1	SRM_00322; SRM_01284; SRM_01749	0.6612
1	SRM_00305; SRM_02932	0.6868
1	SRM_01666; SRM_01674	0.7007
1	SRM_01159; SRM_02671	0.7460
1	SRM_00221; SRM_01378; SRM_01407; SRM_03003	0.7826
1	SRM_00221; SRM_00686; SRM_01378; SRM_01407; SRM_03003	0.7826
1	SRM_00118; SRM_01294	0.7942
0	SRM_00286; SRM_00275	0.8155
1	SRM_01450; SRM_01726	0.8844
1	SRM_01450; SRM_01726	0.8844
1	SRM_01036; SRM_01734	0.9243
1	SRM_00200; SRM_01017	0.9311
1	SRM_02695	0.9752
1	SRM_03004	1.0121
1	SRM_02402	1.0439
1	SRM_01585; SRM_01586	1.0513
1	SRM_00072; SRM_01075	1.0522
1	SRM_00197; SRM_02947	1.0605
0	SRM_00783; SRM_00736; SRM_00735	1.0660
1	SRM_00230; SRM_00243; SRM_00749	1.0977
1	SRM_01276; SRM_01961	1.0979
1	SRM_01276; SRM_01961	1.0979
1	SRM_01644	1.1098
1	SRM_00383; SRM_00495	1.1269
1	SRM_00370; SRM_00371	1.1521
1	SRM_00181; SRM_00192	1.1870
1	SRM_01264; SRM_01572	1.2349
0	SRM_00736; SRM_00747; SRM_00831	1.2580
1	SRM_02736	1.3319
1	SRM_01304; SRM_01645	1.3517
1	SRM_01228; SRM_01782	1.4008
1	SRM_00891; SRM_01320	1.4458
1	SRM_00293; SRM_00477	1.4646
1	SRM_00171	1.4947
1	SRM_01506; SRM_02201; SRM_02206; SRM_02207	1.5955
1	SRM_02650	1.6394
1	SRM_02650	1.6394
1	SRM_00164; SRM_02855	1.6482
1	SRM_00224; SRM_02476;	1.6629
1	SRM_00864; SRM_02102	1.6778
1	SRM_00432; SRM_02241	1.7030
0	SRM_00216; SRM_03002	1.7033
1	SRM_00751; SRM_01491	1.7078
1	SRM_00116	1.7090
1	SRM_01208; SRM_01209	1.7429
1	SRM_00159; SRM_00879	1.7819
1	SRM_01838	1.8226
1	SRM_00434; SRM_03056	1.8322
1	SRM_02848	1.8333
1	SRM_00185; SRM_02669	1.8806
1	SRM_02300	1.9126
1	SRM_00478; SRM_01071	1.9518

1	SRM_00885; SRM_02685	1.9663
1	SRM_01455	1.9876
1	SRM_00296; SRM_00627; SRM_00832; SRM_01317	2.0276
0	SRM_00296; SRM_01317	2.0276
1	SRM_00216; SRM_00685; SRM_01377; SRM_01408; SRM_03002	2.0278
1	SRM_00222; SRM_02478	2.0431
0	SRM_02107; SRM_00794; SRM_00787; SRM_00795	2.0645
1	SRM_00229; SRM_01775	2.2107
1	SRM_00926; SRM_03073	2.2329
1	SRM_00291; SRM_00820	2.4000
1	SRM_00292; SRM_00551	2.4307
0	SRM_02145; SRM_00817	2.4469
1	SRM_00164	2.5168
1	SRM_02263	2.5605
1	SRM_01838	2.5605
1	SRM_00200; SRM_01838	2.7033
1	SRM_01338; SRM_02609	2.7342
1	SRM_01338	2.7342
1	SRM_02474	2.7413
1	SRM_01667; SRM_02064	2.7550
1	SRM_00798; SRM_02957	2.7897
1	SRM_00435; SRM_01712	2.8115
1	SRM_00335	2.8429
1	SRM_00198	2.8754
1	SRM_00351; SRM_02155	2.9545
1	SRM_00351; SRM_02155	2.9545
1	SRM_00792; SRM_00937; SRM_02135; SRM_02850;	2.9663
1	SRM_00404; SRM_00415	2.9900
0	SRM_0793; SRM_02851	3.0115
1	SRM_00475; SRM_00844	3.0492
1	SRM_02725	3.0605
1	SRM_01954	3.1082
1	SRM_00247; SRM_00716	3.1216
1	SRM_00310; SRM_00929; SRM_01620	3.1245
1	SRM_01359	3.1476
1	SRM_00094; SRM_00150; SRM_00169	3.1561
1	SRM_01336	3.2071
1	SRM_00750; SRM_00810	3.2623
1	SRM_02465	3.2815
1	SRM_02171; SRM_02555; SRM_02579	3.2990
1	SRM_02171	3.2990
1	SRM_02171	3.2990
0	SRM_00251; SRM_00693	3.3166
0	SRM_02410; SRM_00220	3.3362
1	SRM_00745; SRM_00833	3.3386
1	SRM_00383; SRM_02602	3.3647
1	SRM_00819; SRM_02923	3.4656
1	SRM_00223; SRM_02360; SRM_02477	3.6470
1	SRM_00165	3.6796
1	SRM_01430	3.6986
1	SRM_01464; SRM_01682	3.7152
1	SRM_01464; SRM_01682	3.7152
1	SRM_00547; SRM_02652	3.8041
1	SRM_00356; SRM_01514	3.8456

1	SRM_02061	3.8536
1	SRM_00435; SRM_00446	3.8655
0	SRM_00228; SRM_00733	3.9360
1	SRM_00093; SRM_01057; SRM_02263; SRM_02612	3.9836
1	SRM_00549; SRM_01015; SRM_02226	4.0012
1	SRM_01014; SRM_01081; SRM_01091; SRM_01092	4.0087
1	SRM_00691; SRM_02917	4.1720
	SRM_00167; SRM_00961; SRM_01947; SRM_00853; SRM_00980; SRM_01507; SRM_01508; SRM_01948; SRM_02204	4.3709
1	SRM_00302	4.4304
1	SRM_00715; SRM_00802; SRM_00818	4.5593
1	SRM_00561; SRM_01959	4.9932
1	SRM_00317; SRM_01325	5.0824
1	SRM_00316;	5.1316
1	SRM_00129; SRM_02127; SRM_02128	5.1368
1	SRM_00340; SRM_01328	5.3633
1	SRM_00690; SRM_00735; SRM_00833;	5.3929
1	SRM_00690; SRM_00735; SRM_00784	5.3929
1	SRM_00186; SRM_00194	5.8964
1	SRM_00690; SRM_00735; SRM_00833	6.4589
	SRM_00101; SRM_00412; SRM_00433; SRM_00549; SRM_01015; SRM_01017; SRM_02226	6.5000
1	SRM_00101	6.5000
1	SRM_00338; SRM_00590	6.5267
1	SRM_00101	6.8795
1	SRM_02403	7.5403
1	SRM_02435	7.7904
1	SRM_00161; SRM_01460	7.8309
1	SRM_00161; SRM_01460	7.8309
1	SRM_00315; SRM_01798	7.9594
1	SRM_00050; SRM_00285; SRM_01098; SRM_03074	9.1698
1	SRM_00088; SRM_00573	9.9783
1	SRM_00297	10.1071
1	SRM_02934	
1	SRM_00381	
1	SRM_00489	
1	SRM_00503; SRM_00510; SRM_00511	
1	SRM_00221; SRM_00686; SRM_01378; SRM_01407	
1	SRM_00765	
1	SRM_00780	
1	SRM_00781	
1	SRM_00806	
1	SRM_00809	
1	SRM_01015	
1	SRM_01195	
1	SRM_01491	
1	SRM_01506	
1	SRM_02201	
1		
1	SRM_01682	
1	SRM_01684	
1	SRM_02092	
1	SRM_02141	
1		

1	
1	SRM_02671
1	SRM_02685
1	SRM_02701
1	SRM_02916
0	SRM_00686; SRM_01407
0	SRM_0784; SRM_00735
