

Table 2: Genes repressed in *Mycobacterium tuberculosis* H37Rv relative to a sigE mutant strain during log phase growth. The following microarray data are for individual interpretation. All genes in this table may not be reproducibly repressed. In addition, the table should not be seen as a complete list of all possibly repressed genes. Description of the data table details and analysis methods are described in the data analysis section.

Spot	Name	Gene	Corrected intensity		Average			Gene product	PCR	Individual array ratios (CH2/CH1)		
			CH1	CH2	CH1/CH2	StD	SEM			F	mi1034	mi1035
			Cye3	Cye5	Repressed							
4042	Rv0009	ppiA	12522	5956	2.1	0.7	0.4	peptidyl-prolyl_cis-trans_isomerase	1.1	0.6	0.6	0.3
2987	Rv0046c	-	15828	9090	1.7	0.2	0.1		1.1	0.7	0.5	0.6
826	Rv0057	-	9933	5880	1.7	0.1	0.1		1.1	0.6	0.6	0.6
105	Rv0058	dnaB	10472	4724	2.2	0.4	0.2	DNA_helicase_(contains_intein)	1.1	0.5	0.5	0.4
265	Rv0058	dnaB	13994	7331	1.8	0.8	0.5	DNA_helicase_(contains_intein)	2.5	0.8	0.4	0.4
2763	Rv0108c	-	13265	6514	2.0	0.7	0.4		1.2	0.7	0.4	0.4
2697	Rv0129c	fbpC2	19368	8562	2.3	0.1	0.1	antigen_85C',_mycolyltransferase	1.1	0.5	0.4	0.4
4359	Rv0166	fadD5	6816	4513	1.5	0.2	0.1	acyl-CoA_synthase	1.1	0.6	0.6	0.8
5081	Rv0167	-	8485	4442	1.9	0.4	0.2	part_of_mce1_operon	1.2	0.6	0.5	0.4
4360	Rv0168	-	7289	4723	1.5	0.2	0.1	part_of_mce1_operon	1.1	0.7	0.6	0.6
5082	Rv0169	mce1	13571	6147	2.2	0.3	0.2	cell_invasion_protein	1.1	0.5	0.4	0.4
269	Rv0171	-	19930	9718	2.1	0.3	0.2	part_of_mce1_operon	1.1	0.4	0.5	0.5
4362	Rv0172	-	11114	4933	2.3	0.6	0.3	part_of_mce1_operon	1.1	0.5	0.5	0.3
991	Rv0172	-	15920	8981	1.7	0.2	0.1	part_of_mce1_operon	1.1	0.7	0.5	0.5
270	Rv0173	lprK	16796	9489	1.7	0.3	0.2	part_of_mce1_operon	1.1	0.7	0.6	0.5
1475	Rv0174	-	19641	10327	1.9	0.2	0.1	part_of_mce1_operon	1.1	0.5	0.6	0.5
1477	Rv0178	-	13963	8429	1.7	0.1	0.1		1.1	0.6	0.7	0.6
1618	Rv0220	lipC	13710	7438	1.8	0.6	0.4	probable_esterase	1.1	0.6	0.7	0.3
5225	Rv0227c	-	18003	7139	2.5	0.7	0.4	possible_membrane_protein	1.1	0.5	0.5	0.3
3140	Rv0287	-	14473	5823	2.5	0.2	0.1	Ala-rich_protein	1.1	0.4	0.4	0.4
5573	Rv0315	-	10226	6359	1.6	0.3	0.2	probable_b-1,3-glucanase	1.2	0.8	0.6	0.5
847	Rv0338c	-	12130	7260	1.7	0.1	0.1	iron-sulfur_protein	1.1	0.7	0.6	0.5
4400	Rv0347	-	13124	5603	2.3	0.3	0.2		1.1	0.5	0.4	0.4
3931	Rv0415	-	7009	3710	1.5	0.7	0.4		1.1	0.5	1.0	0.5
1324	Rv0455c	-	13651	7020	1.9	0.2	0.1	N-term_hydrophobic_stretch	1.1	0.6	0.5	0.5
607	Rv0464c	-	9025	5986	1.5	0.4	0.2		1.1	0.9	0.6	0.5
1392	Rv0642c	mmaA4	16211	10988	1.5	0.4	0.2	methoxymycolic_acid_synthase_4	1.1	0.9	0.5	0.6
765	Rv0649	fabD2	17386	8192	2.1	0.4	0.2	malonyl_CoA-[ACP]_transacylase	1.4	0.6	0.5	0.4
617	Rv0684	fusA	12665	6525	1.8	0.8	0.5	elongation_factor_G	1.1	0.8	0.5	0.4
4768	Rv0685	tuf	16067	5811	2.7	0.6	0.3	elongation_factor_EF-Tu	1.1	0.4	0.4	0.3
2610	Rv0700	rpsJ	12893	6306	2.0	0.1	0.1	30S_ribosomal_protein_S10	1.1	0.5	0.5	0.5
2611	Rv0702	rpID	13181	5185	2.5	0.3	0.2	50S_ribosomal_protein_L4	1.1	0.4	0.4	0.4

5496Rv0708	rplP	15683	6984	2.2	0.2	0.1	50S_ribosomal_protein_L16	1.1	0.4	0.5	0.4
1341Rv0732	secY	12443	5976	2.0	0.6	0.3	SecY_subunit_of_preprotein_translocase	1.4	0.6	0.4	0.4
625Rv0755c	PPE	11272	6508	1.6	0.7	0.4		1.4	0.9	0.6	0.4
4471Rv0760c	-	9619	4965	2.0	0.2	0.2		1.2	0.5	nd	0.5
5306Rv0863	-	15854	5979	2.6	0.3	0.2		1.2	0.4	0.4	0.3
3027Rv0888	-	12590	6476	1.8	0.8	0.4	possible_membrane_protein	1.2	0.9	0.5	0.4
3031Rv0896	gltA2	16858	9187	1.8	0.1	0.1	citrate_synthase_1_	1.1	0.6	0.5	0.5
1143Rv0952	sucD	14693	7949	1.8	0.3	0.2	succinyl-CoA_synthase_a_chain	1.1	0.6	0.6	0.5
1142Rv0954	-	10949	7078	1.5	0.1	0.1	cell_envelope_antigen	1.1	0.6	0.7	0.6
2917Rv1013	pks16	11261	7226	1.5	0.3	0.1	polyketide_synthase_	1.1	0.8	0.6	0.6
1154Rv1017c	prsA	13032	6877	1.9	0.3	0.2	ribose-phosphate_pyrophosphokinase	1.4	0.7	0.5	0.5
4032Rv1037c	-	12109	5704	2.1	0.2	0.1		1.2	0.5	0.5	0.4
3310Rv1038c	-	12544	7155	1.7	0.4	0.2		1.1	0.7	0.6	0.5
424Rv1046c	-	9346	5456	1.7	0.3	0.2		1.2	0.7	0.5	0.6
5275Rv1072	-	16558	10563	1.6	0.2	0.1	probable_transmembrane_protein	1.1	0.6	0.7	0.6
4639Rv1078	pra	15312	6541	2.3	0.3	0.2		2.5	0.5	0.4	0.4
4558Rv1094	desA2	11237	7266	1.5	0.6	0.4	acyl-[ACP]_desaturase	1.1	1.0	0.5	0.5
3581Rv1174c	-	16709	6729	2.4	0.7	0.4		1.1	0.5	0.5	0.3
4171Rv1177	fdxC	12565	7799	1.5	0.6	0.3	ferredoxin_4Fe-4S	1.1	0.6	0.9	0.5
3451Rv1180	pks3	4456	2892	1.6	0.3	0.2	polyketide_synthase	1.1	0.5	0.7	0.7
3452Rv1182	papA3	11311	6738	1.7	0.3	0.2	PKS-associated_protein,_unknown_function	1.1	0.5	0.6	0.7
3453Rv1184c	-	8143	4672	1.7	0.3	0.2		1.1	0.7	0.5	0.6
1482Rv1197	-	21897	7589	2.9	0.2	0.1		1.1	0.4	0.3	0.3
570Rv1233c	-	8136	4093	1.9	0.5	0.3	hydrophobic_protein	1.1	0.7	0.4	0.4
1399Rv1233c	-	15714	8056	1.9	0.3	0.2	hydrophobic_protein	1.4	0.6	0.5	0.4
2658Rv1297	rho	14739	7574	1.9	0.4	0.2	transcription_termination_factor_rho	1.1	0.4	0.6	0.5
2659Rv1299	prfA	10277	6074	1.6	0.5	0.3	peptide_chain_release_factor_1	1.2	0.5	0.8	0.5
4822Rv1304	atpB	18558	9122	2.0	0.4	0.2	ATP_synthase_a_chain	1.1	0.6	0.5	0.4
4823Rv1306	atpF	18001	8533	2.1	0.2	0.1	ATP_synthase_b_chain	1.1	0.5	0.4	0.4
5546Rv1309	atpG	11555	6792	1.7	0.4	0.3	ATP_synthase_g_chain	1.1	0.5	0.7	nd
4825Rv1310	atpD	15836	7957	1.9	0.6	0.3	ATP_synthase_b_chain	1.1	0.7	0.5	0.4
4780Rv1387	PPE	14624	7309	2.0	0.2	0.1		1.1	0.6	0.5	0.5
5502Rv1388	mlHF	11025	5213	2.1	0.6	0.4	integration_host_factor	1.1	0.5	0.6	0.3
2619Rv1398c	-	14972	5686	2.6	0.4	0.3		1.1	0.4	0.4	0.3
2571Rv1626	-	14950	7409	2.0	0.2	0.1	two-component_response_regulator	1.1	0.5	0.5	0.5
5458Rv1636	-	13715	6375	2.1	0.4	0.2		1.1	0.5	0.5	0.4
2953Rv1641	infC	17248	6929	2.5	0.2	0.1	initiation_factor_IF-3	1.1	0.4	0.4	0.4
68Rv1646	PE	12603	7166	1.7	0.5	0.3		1.1	0.8	0.5	0.5
387Rv1718	-	12600	5756	2.1	0.7	0.4		2.5	0.6	0.5	0.3
3279Rv1738	-	11790	6248	1.9	0.4	0.2		1.1	0.5	0.7	0.5

3011Rv1744c	-	11769	6449	1.7	0.8	0.4		2.5	0.9	0.5	0.4
5712Rv1792	-?	20160	9337	2.2	0.4	0.2	but_in-frame_stop_codon:_pseudogene?	1.1	0.4	0.6	0.4
5658Rv1793	-	13923	8244	1.6	0.1	0.1		1.1	0.6	0.6	nd
5132Rv1826	gcvH	12446	6024	2.1	1.0	0.6	glycine_cleavage_system_H_protein	1.1	0.7	0.3	0.4
4410Rv1827	-	10785	6268	2.0	0.3	0.2		1.1	0.5	nd	0.4
4467Rv1854c	ndh	8671	5646	1.5	0.5	0.3	probable_NADH_dehydrogenase	1.4	0.6	0.9	0.5
4464Rv1872c	lldD2	10960	6915	1.5	0.5	0.3	L-lactate_dehydrogenase	1.1	0.9	0.6	0.5
95Rv1884c	-	17465	7995	2.2	0.2	0.1		1.1	0.5	0.4	0.5
816Rv1885c	-	16843	6410	2.6	0.8	0.5		1.1	0.5	0.4	0.3
94Rv1886c	fbpB	18548	7981	2.3	0.3	0.2	antigen_85B,_mycolyltransferase	1.1	0.4	0.5	0.4
2719Rv1925	fadD31	21943	10352	2.1	0.4	0.2	acyl-CoA_synthase	1.1	0.5	0.5	0.4
4834Rv1980c	mpt64	19514	9073	2.1	0.3	0.2	secreted_immunogenic_protein_Mpb64/Mpt64	1.1	0.6	0.4	0.4
2670Rv1987	-	11358	6319	1.7	0.4	0.3	probable_secreted_protein	1.3	0.7	0.6	0.4
2665Rv2007c	fdxA	11085	6897	1.5	0.6	0.3	ferredoxin	1.1	0.6	0.9	0.5
1681Rv2031c	hspX	8902	5353	1.7	0.3	0.1	14kD_antigen,_heat_shock_protein_Hsp20_family	1.1	0.5	0.6	0.7
1604Rv2091c	-	17001	9728	1.7	0.6	0.3	potential_transmembrane_region	1.1	0.8	0.6	0.4
4438Rv2111c	-	8551	4016	2.1	0.2	0.1		1.1	0.5	nd	0.5
2750Rv2185c	-	14857	6467	2.3	0.3	0.2		1.1	0.5	0.5	0.4
434Rv2193	ctaE	19021	8018	2.4	0.2	0.1	cytochrome_c_oxidase_polypeptide_III	1.1	0.5	0.4	0.4
435Rv2195	qcrA	13839	5512	2.5	0.4	0.2	Rieske_iron-sulphur_component_of_ubiQ-cytB_reductase	1.1	0.4	0.4	0.3
1157Rv2196	qcrB	15618	6415	2.4	0.4	0.2	cytochrome_b_component_of_ubiQ-cytB_reductase	1.1	0.4	0.4	0.3
1161Rv2204c	-	18311	6743	2.7	0.3	0.2	hesB/yadR/yfhF_family_YADR_ECOLI	1.1	0.4	0.3	0.4
3327Rv2215	sucB	9668	5246	1.8	0.1	0.0	dihydrolipoamide_succinyltransferase	2.1	0.6	0.6	0.5
506Rv2220	glnA1	19062	6497	2.9	0.6	0.4	glutamine_synthase_class_I	1.1	0.3	0.4	0.3
1163Rv2220	glnA1	20431	8721	2.3	0.6	0.3	glutamine_synthase_class_I	2.5	0.5	0.5	0.3
751Rv2241	aceE	13295	5325	2.5	0.7	0.4	pyruvate_dehydrogenase_E1_component	1.1	0.5	0.5	0.3
752Rv2243	fabD	17473	7789	2.2	0.4	0.2	malonyl_CoA-[ACP]_transacylase	1.1	0.5	0.5	0.4
3398Rv2243	fabD	9844	5348	1.8	0.5	0.3	malonyl_CoA-[ACP]_transacylase	1.1	0.8	0.5	0.4
3113Rv2243	fabD	8252	5187	1.5	0.3	0.2	malonyl_CoA-[ACP]_transacylase	1.1	0.8	0.5	0.6
3114Rv2244	acpM	22107	6770	3.2	0.2	0.1	acyl_carrier_protein_(meromycolate_extension)	1.1	0.3	0.3	0.3
4120Rv2244	acpM	15784	8470	1.8	0.4	0.2	acyl_carrier_protein_(meromycolate_extension)	1.1	0.7	0.6	0.4
3838Rv2246	kasB	15823	9562	1.6	0.1	0.1	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.7	0.6	0.6
2287Rv2271	-	10411	5868	1.7	0.4	0.2		1.1	0.7	0.5	0.5
162Rv2327	-	12278	7027	1.7	0.7	0.4		1.4	0.9	0.5	0.4
1626Rv2346c	-	22480	9552	2.3	0.6	0.3		1.1	0.4	0.5	0.4
2348Rv2347c	-	20476	11347	1.8	0.5	0.3		1.1	0.7	0.5	0.5
1360Rv2348c	-	19628	7148	2.7	0.2	0.1		1.1	0.4	0.4	0.3
1627Rv2348c	-	21503	10644	1.9	0.6	0.3		1.4	0.7	0.5	0.4
1235Rv2441c	rpmA	13616	7698	1.7	0.5	0.3	50S_ribosomal_protein_L27	1.1	0.8	0.5	0.5
4528Rv2457c	clpX	15068	7120	2.1	0.3	0.2	ATP-dependent_Clp_protease_ATP-binding_subunit_ClpX	1.1	0.5	0.4	0.5

5251Rv2460c	clpP2	11552	7110	1.6	0.5	0.3	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	0.9	0.6	0.5
4536Rv2485c	lipQ	4929	2423	2.0	0.4	0.2	probable_carboxylesterase	1.1	0.6	0.4	0.5
1134Rv2507	-	10272	5839	1.7	0.2	0.1	probable_membrane_spanning_protein	1.3	0.6	0.5	0.6
415Rv2512c	IS1081	8204	4258	1.9	0.3	0.1		1.1	0.5	0.5	0.6
31Rv2524c	fas	12238	6827	1.8	0.1	0.1	fatty_acid_synthase	1.1	0.6	0.5	0.6
112Rv2574	-	9024	5972	1.5	0.3	0.2		1.1	0.9	0.6	0.6
1177Rv2626c	-	8024	5348	1.5	0.1	0.1		1.1	0.6	0.7	0.6
518Rv2632c	-	12316	7203	1.7	0.2	0.1		1.1	0.6	0.6	0.5
1240Rv2633c	-	18384	9127	2.0	0.3	0.2		1.1	0.6	0.4	0.5
4135Rv2672	-	15342	7697	1.9	0.6	0.3	putative_exported_protease	1.1	0.6	0.7	0.4
61Rv2708c	-	14682	7080	2.1	0.2	0.1		2.5	0.5	0.5	0.4
2934Rv2710	sigB	13364	3786	3.5	0.4	0.2	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	0.2	0.3	0.3
786Rv2716	-	14090	7208	1.9	0.2	0.1		1.1	0.6	0.5	0.5
206Rv2792c	IS1602	14843	6011	2.4	0.5	0.3	resolvase	2.2	0.4	0.5	0.3
796Rv2836c	dinF	16105	8641	1.7	1.1	0.6	DNA-damage-inducible_protein_F	2.5	1.0	0.5	0.3
32Rv2927c	-	15630	7044	2.2	0.3	0.2		1.1	0.4	0.5	0.5
4658Rv2927c	-	13452	6739	2.0	0.1	0.1		1.1	0.5	0.5	0.5
754Rv2928	tesA	16804	9767	1.7	0.3	0.1	thioesterase	1.1	0.6	0.7	0.5
39Rv2940c	mas	12297	6381	1.9	0.2	0.1	mycocerosic_acid_synthase	2.5	0.5	0.5	0.6
761Rv2941	fadD28	14850	8170	1.8	0.0	0.0	acyl-CoA_synthase	1.1	0.5	0.6	0.6
41Rv2947c	pks15	15365	6512	2.3	0.2	0.1	polyketide_synthase_	1.1	0.5	0.4	0.4
44Rv2950c	fadD29	21619	9984	2.2	0.2	0.1	acyl-CoA_synthase	1.1	0.4	0.5	0.4
1569Rv2986c	hupB	16226	7672	2.1	0.4	0.2	DNA-binding_protein_II_	1.1	0.4	0.6	0.4
2597Rv3116	moeB	9723	6390	1.5	0.4	0.2	molybdopterin_biosynthesis	1.1	0.9	0.5	0.6
3036Rv3130c	-	5894	3394	1.8	0.3	0.2		2.6	0.5	0.5	0.7
1776Rv3130c	-	5147	3376	1.6	0.1	0.1		1.1	0.6	0.6	0.7
543Rv3205c	-	13889	6908	2.0	0.6	0.4		2.5	0.7	0.5	0.4
4146Rv3219	whiB1	18440	8994	2.0	0.2	0.1	WhiB_transcriptional_activator_homologue	1.1	0.5	0.5	0.4
1262Rv3224	-	16495	7423	2.2	0.5	0.3	putative_oxidoreductases	1.1	0.6	0.5	0.3
3541Rv3229c	desA3	5820	3458	1.5	0.4	0.3	acyl-[ACP]_desaturase	1.1	0.9	0.6	0.5
907Rv3280	accD5	17218	9005	1.9	0.3	0.2	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	0.6	0.5	0.5
4246Rv3281	-	12105	7333	1.5	0.7	0.4		2.5	0.6	1.0	0.4
599Rv3330	-	8762	5647	1.5	0.7	0.4	probable_penicillin_binding_protein	1.1	1.0	0.5	0.5
1322Rv3333c	-	13141	8195	1.5	0.6	0.3	proline_rich	2.5	0.9	0.5	0.5
558Rv3376	-	8057	4956	1.6	0.3	0.2		1.1	0.7	0.6	0.6
3422Rv3408	-	15005	8896	1.6	0.4	0.2		1.1	0.8	0.5	0.6
3418Rv3418c	groES	15002	7977	1.7	0.6	0.3	10_kD_chaperone	1.1	0.8	0.6	0.4
4667Rv3433c	-	21905	11932	1.8	0.4	0.2		2.5	0.7	0.6	0.4
3079Rv3443c	rpIM	14362	9226	1.5	0.6	0.3	50S_ribosomal_protein_L13	1.1	0.5	0.9	0.5
3179Rv3462c	infA	16828	7442	2.2	0.8	0.4	initiation_factor_IF-1	1.1	0.4	0.6	0.4

1020Rv3477	PE	17108	8136	2.1	0.3	0.2		1.1	0.5	0.4	0.5
158Rv3524	-	9364	6056	1.5	0.5	0.3	possible_membrane_sensor_protein	1.1	0.6	0.5	0.9
4157Rv3614c	-	14452	5847	2.6	0.7	0.4		1.1	0.3	0.4	0.5
3435Rv3615c	-	17425	7471	2.4	0.6	0.3		1.2	0.3	0.5	0.4
4156Rv3616c	-	19149	6583	3.0	0.5	0.3		1.1	0.3	0.3	0.4
311Rv3619c	-	12868	7948	1.6	0.4	0.2		1.1	0.8	0.5	0.6
4154Rv3620c	-	18149	8871	2.0	0.2	0.1		1.1	0.5	0.5	0.4
1032Rv3620c	-	20683	10431	1.9	0.6	0.3		1.1	0.7	0.5	0.4
5730Rv3648c	cspA	16566	6693	2.5	0.3	0.2	cold_shock_protein,_transcriptional_regulator	1.1	0.4	0.5	0.3
1024Rv3648c	cspA	3782	2355	1.6	0.2	0.1	cold_shock_protein,_transcriptional_regulator	2.6	0.6	0.6	0.7
4602Rv3681c	whiB4	3853	1938	1.7	0.8	0.5	WhiB_transcriptional_activator_homologue	1.1	0.7	0.3	0.8
5330Rv3706c	-	11160	6063	1.8	0.5	0.3		1.1	0.7	0.5	0.5
4393Rv3773c	-	13826	6630	2.0	0.3	0.2		1.1	0.6	0.5	0.4
224Rv3804c	fbpA	13861	6736	1.9	0.8	0.5	antigen_85A,_mycolyltransferase	1.1	0.8	0.4	0.4
3773Rv3822	-	15356	8211	1.9	0.5	0.3		1.1	0.5	0.7	0.4
890Rv3824c	papA1	10522	5855	1.8	0.2	0.1	PKS-associated_protein,_unknown_function_	1.1	0.6	0.5	0.6
5140Rv3841	bfrB	13211	7648	1.6	0.5	0.3	bacterioferritin	1.1	0.8	0.5	0.5
289Rv3846	sodA	17572	7212	2.4	0.2	0.1	superoxide_dismutase	1.1	0.4	0.4	0.4
1531Rv3852	hns	13835	7432	1.9	0.1	0.1	HU-histone_protein	2.5	0.6	0.5	0.6
5134Rv3865	-	12495	6165	2.0	0.5	0.3		1.1	0.7	0.4	0.4
4964Rv3874	-	20692	7547	2.7	0.3	0.2		1.1	0.4	0.4	0.3
5686Rv3875	esat6	18006	8678	2.1	0.3	0.2	early_secretory_antigen_target	1.1	0.5	0.6	0.4
1374Rv3891c	-	8819	5433	1.6	0.3	0.2		1.1	0.6	0.8	0.5
2735Rv3914	trxC	14407	7463	1.9	0.6	0.3	thioredoxin	1.1	0.6	0.6	0.4
3478		8538	4850	1.8	0.1	0.1		1.1	0.5	0.5	0.6