

Table 4: Genes repressed in *Mycobacterium tuberculosis* H37Rv after 90m of 0.05% SDS stress. 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)					
			Average		CH1/CH2	StD	SEM			Biol. Set 1		Biol. Set 2		Biol. Set 3	
			CH1	CH2						mi527	mi1030	mi1028	mi1018	mi1029	mi1024
			Cye3	Cye5	Repressed			F							
4901Rv0001	dnaA		6718	3622	1.8	0.1	0.1	chromosomal_replication_initiator_protein	1.1	0.5	0.6	0.5	0.6	0.6	0.6
4043Rv0010c	-		5125	3489	1.5	0.2	0.1		1.2	0.6	0.8	0.7	0.5	0.8	0.6
1035Rv0014c	pknB		7218	4434	1.6	0.4	0.1	serine-threonine_protein_kinase	1.1	0.4	0.4	0.7	0.7	0.6	0.7
314Rv0015c	pknA		6600	4382	1.5	0.3	0.1	serine-threonine_protein_kinase	1.1	0.6	0.5	0.9	0.7	0.7	0.7
4381Rv0023	-		3032	2125	1.5	0.3	0.1	putative_transcriptional_regulator	1.1	0.9	0.7	0.6	0.5	0.6	0.6
5103Rv0024	-		5244	2206	2.4	0.2	0.1	putative_p60_homologue	1.1	0.5	0.4	0.4	0.4	0.4	0.4
102Rv0040c	-		12200	8543	1.5	0.3	0.1		1.1	0.9	0.7	0.7	0.6	0.6	0.6
2985Rv0042c	-		4852	3144	1.6	0.2	0.1		1.1	0.8	0.5	0.7	0.6	0.6	0.7
826Rv0057	-		10099	5090	2.0	0.3	0.1		1.1	0.5	0.6	0.5	0.4	0.5	0.5
5624Rv0058	dnaB		8519	2288	3.6	0.4	0.2	DNA_helicase_(contains_intein)	1.1	0.2	0.3	0.3	0.3	0.3	0.3
4902Rv0058	dnaB		4926	1937	2.5	0.2	0.1	DNA_helicase_(contains_intein)	1.1	0.4	0.4	0.4	0.4	0.4	0.5
105Rv0058	dnaB		12129	6408	1.9	0.5	0.2	DNA_helicase_(contains_intein)	1.1	0.6	0.7	0.5	0.4	0.4	0.4
4903Rv0059	-		3708	2184	1.7	0.2	0.1		1.1	0.6	0.6	0.5	0.5	0.6	0.7
2742Rv0070c	glyA2		3807	2454	1.5	0.2	0.1	serine_hydroxymethyltransferase	1.1	0.7	0.8	0.6	0.6	0.6	0.6
4906Rv0076c	-		3596	2180	1.7	0.2	0.1	possible_membrane_spanning_protein	1.2	0.7	0.6	0.6	0.5	0.7	0.6
1348Rv0097	-		3583	2063	1.7	0.2	0.1		1.1	0.7	0.6	0.5	0.5	0.5	0.6
2763Rv0108c	-		12109	4949	2.5	0.5	0.2		1.2	0.3	0.4	0.5	0.3	0.4	0.5
1983Rv0156	pntAB		5033	3044	1.6	0.4	0.2	pyridine_transhydrogenase_subunit_a2	1.1	0.5	0.4	0.8	0.7	0.7	0.7
5079Rv0163	-		3191	1877	1.6	0.3	0.1	probable_dehydrogenase	1.1	0.6	0.6	0.7	0.8	0.6	0.5
3202Rv0165c	-		4225	2251	1.9	0.3	0.1	transcriptional_regulator_(GntR_family)	1.1	0.5	0.5	0.7	0.5	0.4	0.5
5080Rv0165c	-		4052	2242	1.8	0.2	0.1	transcriptional_regulator_(GntR_family)	1.1	0.5	0.7	0.5	0.5	0.5	0.6
4359Rv0166	fadD5		8000	2239	3.6	0.4	0.2	acyl-CoA_synthase	1.1	0.3	0.2	0.3	0.3	0.3	0.3
5081Rv0167	-		8924	2835	3.2	0.7	0.3	part_of_mce1_operon	1.2	0.3	0.3	0.4	0.2	0.3	0.4
990Rv0168	-		7945	2492	3.2	0.4	0.2	part_of_mce1_operon	1.1	0.3	0.3	0.4	0.3	0.3	0.4
4360Rv0168	-		8501	3135	2.8	0.3	0.1	part_of_mce1_operon	1.1	0.4	0.3	0.4	0.3	0.4	0.4
5082Rv0169	mce1		13692	3828	3.6	0.9	0.4	cell_invasion_protein	1.1	0.2	0.2	0.3	0.2	0.3	0.4
4361Rv0170	-		17226	4819	3.6	0.9	0.4	part_of_mce1_operon	1.1	0.4	0.2	0.3	0.2	0.3	0.3
269Rv0171	-		21474	6210	3.5	0.8	0.3	part_of_mce1_operon	1.1	0.3	0.2	0.4	0.2	0.2	0.3
5083Rv0171	-		12218	3740	3.3	0.4	0.2	part_of_mce1_operon	1.1	0.3	0.2	0.3	0.3	0.3	0.3
991Rv0172	-		16231	3577	4.5	0.9	0.4	part_of_mce1_operon	1.1	0.2	0.2	0.3	0.2	0.2	0.3
4362Rv0172	-		12462	4641	2.7	0.6	0.2	part_of_mce1_operon	1.1	0.5	0.3	0.4	0.3	0.4	0.4
270Rv0173	lprK		18743	3900	4.9	1.3	0.5	part_of_mce1_operon	1.1	0.2	0.1	0.3	0.2	0.2	0.3

5084Rv0173	lprK	3214	2103	1.5	0.4	0.2	part_of_mce1_operon	2.6	1.0	0.5	0.6	nd	0.7	0.6
1475Rv0174	-	18579	7786	2.3	0.9	0.4	part_of_mce1_operon	1.1	0.7	0.3	0.5	0.3	0.3	0.4
2198Rv0177	-	7964	4941	1.6	0.2	0.1		1.1	0.5	0.5	0.7	0.7	0.7	0.6
1477Rv0178	-	14129	7793	1.7	0.4	0.2		1.1	0.5	0.4	0.7	0.6	0.6	0.6
5653Rv0193c	-	2212	1544	1.5	0.2	0.1		1.1	nd	0.8	0.7	0.6	0.6	0.6
1618Rv0220	lipC	14976	9860	1.5	0.1	0.1	probable_esterase	1.1	0.6	0.7	0.7	0.6	0.6	0.7
5225Rv0227c	-	15085	10259	1.5	0.4	0.2	possible_membrane_protein	1.1	0.5	0.4	0.7	0.7	0.7	0.9
4506Rv0231	fadE4	7816	4389	1.8	0.1	0.1	acyl-CoA_dehydrogenase_	1.1	0.5	0.5	0.6	0.6	0.6	0.6
1619Rv0233	nrdB	12178	8301	1.5	0.4	0.2	ribonucleoside-diphosphate_reductase_B2_(eukaryotic-like)_	1.1	0.9	0.9	0.6	0.5	0.5	0.5
967Rv0236c	-	4021	2591	1.6	0.2	0.1	possible_membrane_protein	1.1	0.5	0.7	0.6	0.7	0.8	0.6
4851Rv0314c	-	6554	4236	1.5	0.1	0.1	unknown_hydrophobic_protein	1.1	0.6	0.6	0.7	0.7	0.7	0.7
5573Rv0315	-	10670	3295	3.3	0.8	0.3	probable_b-1,3-glucanase	1.2	0.2	0.3	0.4	0.3	0.4	0.4
5576Rv0321	dcd	4284	2888	1.5	0.2	0.1	deoxycytidine_triphosphate_deaminase	1.1	0.6	0.7	0.6	0.7	0.7	0.8
5123Rv0350	dnaK	6377	3602	1.7	0.4	0.2	70_kD_heat_shock_protein,_chromosome_replication	1.1	0.4	0.4	0.6	0.7	0.7	0.7
2578Rv0360c	-	3177	1786	1.8	0.1	0.0		1.1	0.6	0.6	0.6	0.5	0.6	0.5
1046Rv0379	sec	6056	3450	1.7	0.3	0.1	probable_transport_protein_SecE/Sec61-_g_family	1.1	0.4	0.5	0.6	0.7	0.6	0.6
5560Rv0402c	mmpL1	3249	2064	1.6	0.1	0.1	conserved_large_membrane_protein	1.1	0.7	0.7	0.6	0.7	0.6	0.6
4071Rv0430	-	5719	3391	1.7	0.3	0.1		1.1	0.7	0.8	0.5	0.6	0.6	0.5
3870Rv0445c	sigK	3166	2158	1.5	0.2	0.1	ECF-type_sigma_factor	1.1	0.5	0.6	0.7	0.8	0.7	0.8
3649Rv0503c	cmaA2	8468	4531	1.9	0.2	0.1	cyclopropane_mycolic_acid_synthase_2	1.1	0.5	0.5	0.6	0.5	0.5	0.6
608Rv0566c	-	4408	2288	1.9	0.3	0.1		1.4	0.4	0.5	0.7	0.5	0.5	0.5
1331Rv0569	-	6994	3005	2.3	0.1	0.1		1.1	0.5	0.5	0.5	0.4	0.4	0.4
1049Rv0569	-	3771	2231	1.7	0.1	0.0		1.1	0.6	0.6	0.6	0.6	0.5	0.6
328Rv0572c	-	4746	2622	1.8	0.1	0.1		1.1	0.6	0.5	0.6	0.6	0.5	0.5
1335Rv0577	-	5356	3647	1.5	0.1	0.1		1.1	0.7	0.6	0.6	0.6	0.7	0.8
4220Rv0583c	lpqN	7067	4063	1.7	0.4	0.1		1.1	0.6	0.8	0.5	0.5	0.5	0.6
4061Rv0588	-	10090	4477	2.3	0.3	0.1	part_of_mce2_operon	1.1	0.4	0.4	0.5	0.4	0.5	0.5
331Rv0642c	mmaA4	10168	5981	1.7	0.1	0.0	methoxymycolic_acid_synthase_4	1.1	0.6	0.6	0.6	0.6	0.5	0.6
1392Rv0642c	mmaA4	15780	10641	1.5	0.1	0.0	methoxymycolic_acid_synthase_4	1.1	0.7	0.7	0.6	0.7	0.6	0.7
3650Rv0643c	mmaA3	6940	4785	1.5	0.2	0.1	methoxymycolic_acid_synthase_3	1.1	0.8	0.7	0.6	0.7	0.6	0.8
333Rv0651	rplJ	6855	4625	1.5	0.1	0.0	50S_ribosomal_protein_L10	1.1	0.7	0.6	0.7	0.7	0.6	0.7
672Rv0652	rplL	9179	4598	2.0	0.3	0.1	50S_ribosomal_protein_L7/L12	1.1	0.4	0.5	0.6	0.5	0.5	0.6
1055Rv0652	rplL	5769	3164	1.8	0.3	0.1	50S_ribosomal_protein_L7/L12	1.1	0.4	0.5	0.6	0.6	0.6	0.6
4378Rv0655	-	18475	8888	2.0	0.8	0.3	ABC_transporter	1.1	0.9	0.5	0.4	0.4	0.4	0.4
1488Rv0669c	-	6352	4280	1.5	0.3	0.1		1.1	0.6	0.4	0.8	0.7	0.8	0.8
335Rv0672	fadE8	5541	3447	1.6	0.1	0.0	acyl-CoA_dehydrogenase_(aka_aidB)	1.1	0.6	0.6	0.7	0.7	0.6	0.6
5710Rv0673	-	3437	2267	1.5	0.2	0.1	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	0.5	0.7	0.7	0.7	0.6	0.7
5491Rv0688	-	4446	2962	1.5	0.1	0.1	putative_oxidoreductase	1.1	0.6	0.6	0.6	0.7	0.7	0.8
5493Rv0692	-	7380	3177	2.3	0.5	0.2		1.1	0.3	0.4	0.5	0.4	0.5	0.5
1884Rv0693	pqqE	3886	1897	1.8	0.7	0.3	coenzyme_PQQ_synthesis_protein_E	1.1	0.3	0.3	0.7	0.7	0.5	0.8

2606Rv0694	lldD1	6346	2611	2.4	0.6	0.3	L-lactate_dehydrogenase_(cytochrome)_	1.1	0.3	0.3	0.6	0.3	0.4	0.5
1885Rv0695	-	3867	1985	1.9	0.4	0.2		1.1	0.4	0.5	0.6	0.4	0.5	0.7
2607Rv0696	-	5667	2254	2.6	0.3	0.1	glycosyltransferase	1.1	0.4	0.4	0.5	0.3	0.4	0.4
4774Rv0707	rpsC	12054	8044	1.5	0.3	0.1	30S_ribosomal_protein_S3	1.1	0.7	0.5	0.8	0.8	0.8	0.4
2613Rv0718	rpsH	10374	6971	1.5	0.4	0.1	30S_ribosomal_protein_S8	1.1	0.4	0.5	0.8	0.7	0.8	0.9
1892Rv0719	rplF	8334	5178	1.6	0.3	0.1	50S_ribosomal_protein_L6	1.1	0.4	0.5	0.7	0.6	0.7	0.8
2615Rv0722	rpmD	9269	6628	1.5	0.4	0.2	50S_ribosomal_protein_L30	1.1	0.4	0.5	0.8	0.7	0.8	0.9
4471Rv0760c	-	12553	7891	1.6	0.3	0.1		1.2	0.6	0.5	0.7	0.5	0.7	0.7
5193Rv0761c	adhB	10202	5181	2.0	0.4	0.2	zinc-containing_alcohol_dehydrogenase	1.1	0.4	0.3	0.5	0.5	0.6	0.6
5440Rv0797	IS1547	3612	2467	1.5	0.2	0.1		1.2	0.5	0.6	0.8	nd	0.7	0.8
4718Rv0798c	-	8690	5052	1.7	0.4	0.2	similar_to_bacteriocins	1.1	0.5	0.4	0.7	0.7	0.7	0.7
4580Rv0854	-	8940	5528	1.6	0.3	0.1		1.1	0.8	0.6	0.6	0.5	0.6	0.6
2420Rv0867c	-	3557	2256	1.6	0.2	0.1	probable_exported_protein	2.5	0.5	0.6	0.6	0.6	0.7	0.7
1699Rv0868c	moaD2	3158	1977	1.6	0.3	0.1	molybdopterin_converting_factor_subunit_1	1.1	0.5	0.4	0.8	0.6	0.7	0.7
864Rv0882	-	3496	2367	1.5	0.1	0.1	unknown_hydrophobic_protein	1.1	0.7	0.7	0.7	0.6	0.7	0.6
143Rv0883c	-	12158	6522	1.9	0.3	0.1		1.1	0.6	0.6	0.5	0.4	0.5	0.5
3027Rv0888	-	12339	6290	2.0	0.4	0.1	possible_membrane_protein	1.2	0.6	0.4	0.6	0.4	0.4	0.6
1736Rv0925c	-	6576	4253	1.6	0.1	0.0		1.1	0.7	0.6	0.7	0.6	0.6	0.7
2345Rv0933	pstB	3692	2460	1.5	0.2	0.1	ABC_transport_component_of_phosphate_uptake	1.1	0.6	0.7	0.8	0.6	0.8	0.6
1623Rv0934	phoS1	17177	5941	2.9	0.8	0.3	PstS_component_of_phosphate_uptake	1.4	0.3	0.2	0.4	0.4	0.4	0.4
1001Rv0935	pstC	9311	3521	2.7	0.8	0.3	PstC_component_of_phosphate_uptake	1.1	0.2	0.3	0.5	0.4	0.4	0.5
4026Rv0950c	-	7621	2720	2.8	0.2	0.1		1.1	0.3	0.3	0.4	0.4	0.4	0.3
417Rv0961	-	6385	3717	1.7	0.1	0.0		1.2	0.6	0.6	0.6	0.5	0.6	0.6
5312Rv0986	-	3866	1907	2.0	0.6	0.2	Probable_ABC_transporter	1.1	0.6	0.7	0.3	0.3	0.5	0.5
1703Rv0987	-	5193	2849	1.9	0.2	0.1	potential_integral_membrane_protein	1.4	0.6	0.5	0.6	0.5	0.5	0.6
406Rv0988	-	6390	2792	2.3	0.3	0.1		1.1	0.5	0.4	0.5	0.3	0.4	0.5
1130Rv0993	galU	7251	4722	1.6	0.1	0.1	UTP-glucose-1-phosphate_uridylyltransferase	1.1	0.7	0.7	0.6	0.5	0.7	0.7
267Rv1010	ksgA	3389	1745	1.9	0.3	0.1	16S_rRNA_dimethyltransferase	1.1	0.4	0.4	0.7	0.5	0.6	0.6
2193Rv1010	ksgA	3913	2538	1.5	0.4	0.1	16S_rRNA_dimethyltransferase	1.1	0.6	0.5	0.9	0.6	0.8	0.6
2917Rv1013	pks16	11780	4711	2.5	1.5	0.6	polyketide_synthase_	1.1	0.8	0.6	0.3	0.2	0.3	0.2
4038Rv1013	pks16	8317	3281	2.4	1.0	0.4	polyketide_synthase_	1.2	0.5	0.7	0.3	0.3	0.3	0.3
4034Rv1033c	-	3048	2075	1.5	0.2	0.1	two-component_response_regulator	1.1	0.7	0.8	0.7	0.7	0.6	0.6
5280Rv1095	phoH2	5926	3074	2.0	0.3	0.1	PhoH-like_protein	1.1	0.4	0.5	0.5	0.5	0.5	0.7
2398Rv1107c	xseB	4365	2920	1.5	0.4	0.2	exonuclease_VII_small_subunit	1.1	0.5	0.4	0.8	0.8	0.8	0.8
1843Rv1158c	-	7544	5046	1.5	0.1	0.1		1.2	0.6	0.8	0.7	0.6	0.7	0.6
4174Rv1183	mmpL10	4124	2812	1.5	0.2	0.1	conserved_large_membrane_protein	1.1	0.5	0.6	0.7	0.6	0.8	0.8
3453Rv1184c	-	7192	4290	1.6	0.4	0.2		1.1	0.5	0.4	0.7	0.7	0.7	0.7
1484Rv1201c	-	9706	6337	1.5	0.3	0.1		1.1	0.6	0.5	0.8	0.7	0.8	0.7
3154Rv1206	fadD6	4310	2673	1.5	0.3	0.1	acyl-CoA_synthase	1.4	0.5	0.4	0.8	0.7	0.7	0.8
3582Rv1220c	-	4607	3001	1.5	0.2	0.1	probable_methyltransferase	1.1	0.6	0.6	0.7	0.7	0.7	0.7

4248Rv1230c	-	3425	1971	1.8	0.1	0.1	possible_membrane_protein	1.1	0.6	0.6	0.5	nd	0.6	0.5
4177Rv1240	mdh	7627	4378	1.7	0.1	0.0	malate_dehydrogenase	1.1	0.5	0.6	0.6	0.6	0.6	0.6
3456Rv1241	-	3485	1608	2.1	0.3	0.1		1.1	0.3	0.5	0.5	0.5	0.5	0.5
573Rv1251c	-	3548	1980	1.8	0.2	0.1	some_similarity_to_GTP-binding_proteins	1.1	0.5	0.5	0.6	0.5	0.6	0.5
4244Rv1252c	lprE	5375	2127	2.5	0.3	0.1	lipoprotein	1.1	0.5	0.4	0.4	0.3	0.4	0.4
5569Rv1252c	lprE	6489	2622	2.4	0.5	0.2	lipoprotein	1.1	0.4	0.6	0.3	0.3	0.4	0.4
2678Rv1270c	lprA	9064	5829	1.5	0.4	0.1	lipoprotein	1.1	0.9	0.8	0.6	0.5	0.5	0.6
4841Rv1279	-	6706	4330	1.5	0.2	0.1	probable_choline_dehydrogenase	2.1	0.6	0.6	0.6	0.7	0.7	0.7
5544Rv1305	atpE	11284	7467	1.5	0.3	0.1	ATP_synthase_c_chain	1.1	0.5	0.6	0.7	0.8	0.7	0.7
5545Rv1307	atpH	13486	8693	1.5	0.4	0.2	ATP_synthase_d_chain	1.1	0.4	0.4	0.7	0.8	0.7	0.8
4824Rv1308	atpA	12173	7692	1.5	0.4	0.1	ATP_synthase_a_chain	1.1	0.5	0.4	0.8	0.8	0.8	0.6
4825Rv1310	atpD	15532	9940	1.5	0.3	0.1	ATP_synthase_b_chain	1.1	0.5	0.4	0.8	0.8	0.7	0.7
856Rv1368	lprF	6208	3956	1.6	0.1	0.0	lipoprotein	1.1	0.6	0.7	0.7	0.6	0.7	0.6
4499Rv1425	-	4369	3041	1.5	0.2	0.1		1.1	0.6	0.7	0.8	0.6	0.7	0.7
4294Rv1440	secG	4621	2859	1.6	0.1	0.0	protein-export_membrane_protein_SecG	1.1	0.6	0.6	0.6	0.6	0.6	0.6
1753Rv1480	-	7355	2311	3.0	1.0	0.4		1.1	0.3	0.2	0.5	0.3	0.4	0.4
1413Rv1502	-	11540	7735	1.5	0.2	0.1		1.1	0.6	0.6	0.6	0.8	0.7	0.7
4808Rv1502	-	6805	4518	1.5	0.2	0.1		2.6	0.5	0.6	0.7	0.8	0.7	0.8
5531Rv1505c	-	3033	1990	1.5	0.2	0.1	polysialic_acid_synthesis?	1.1	0.6	0.8	0.6	0.8	0.6	0.7
5532Rv1507c	-	5678	3362	1.7	0.2	0.1		1.1	0.6	0.6	0.5	0.6	0.5	0.7
843Rv1515c	-	6580	3935	1.7	0.4	0.2		1.1	0.4	0.5	0.7	0.5	0.8	0.6
5199Rv1547	dnaE1	8476	4313	2.0	0.2	0.1	DNA_polymerase_III,_a_subunit	1.4	0.5	0.4	0.5	0.5	0.5	0.6
4092Rv1597	-	7886	4405	1.8	0.2	0.1		1.4	0.6	0.6	0.5	0.6	0.5	0.5
4730Rv1611	trpC	9053	5845	1.5	0.4	0.1	indole-3-glycerol_phosphate_synthase	1.1	0.5	0.4	0.7	0.7	0.8	0.8
5452Rv1612	trpB	7645	3793	1.9	0.6	0.2	tryptophan_synthase_b_chain	1.2	0.3	0.4	0.6	0.6	0.6	0.6
4731Rv1613	trpA	10076	4792	2.0	0.7	0.3	tryptophan_synthase_a_chain	1.1	0.3	0.3	0.6	0.6	0.6	0.6
5453Rv1614	lgt	11115	5473	2.0	0.5	0.2	prolipoprotein_diacylglyceryl_transferase	1.1	0.3	0.5	0.6	0.6	0.5	0.6
2952Rv1639c	-	12371	7536	1.6	0.3	0.1		1.1	0.6	0.4	0.6	0.7	0.6	0.7
5318Rv1678	-	5377	2932	1.8	0.3	0.1	probably_integral_membrane_protein	1.1	0.4	0.6	0.5	0.6	0.6	0.6
4004Rv1680	-	3537	2334	1.5	0.1	0.1		1.1	0.6	0.7	0.7	0.6	0.7	0.7
403Rv1697	-	9137	5072	1.8	0.1	0.0		1.1	0.6	0.5	0.6	0.5	0.6	0.6
1125Rv1698	-	6397	4155	1.5	0.2	0.1		1.1	0.6	0.6	0.7	0.6	0.7	0.7
4010Rv1704c	cycA	4464	3050	1.5	0.2	0.1	transport_of_D-alanine,_D-serine_and_glycine	1.1	0.6	0.6	0.7	0.7	0.7	0.7
3998Rv1733c	-	3525	2313	1.5	0.3	0.1	possible_membrane_protein	1.1	0.8	0.9	0.6	0.5	0.6	0.6
3279Rv1738	-	12021	3735	3.2	0.7	0.3		1.1	0.3	0.2	0.3	0.3	0.3	0.4
397Rv1751	-	8340	5180	1.5	0.4	0.2	possible_hydroxylase	1.1	0.4	0.5	0.9	0.7	0.8	0.7
1528Rv1815	-	6729	4355	1.6	0.2	0.1		1.1	0.7	0.6	0.7	0.6	0.6	0.6
1523Rv1825	-	4791	3091	1.5	0.3	0.1		1.1	0.6	0.5	0.9	0.6	0.7	0.7
3941Rv1826	gcvH	5745	3155	1.8	0.1	0.0	glycine_cleavage_system_H_protein	1.1	0.6	0.6	0.6	0.6	0.5	0.5
5132Rv1826	gcvH	10962	6947	1.6	0.2	0.1	glycine_cleavage_system_H_protein	1.1	0.6	0.6	0.8	0.6	0.6	0.6

5130Rv1830	-	4449	3107	1.5	0.1	0.1		1.1	0.8	0.7	0.6	0.6	0.7	0.7
3942Rv1860	modD	8160	4198	1.9	0.3	0.1	precursor_of_Apa_(45/47_kD_secreted_protein)	1.4	0.6	0.6	0.5	0.5	0.4	0.5
1582Rv1860	modD	8767	5241	1.8	0.8	0.3	precursor_of_Apa_(45/47_kD_secreted_protein)	1.3	1.1	0.5	0.5	0.4	0.4	0.5
3221Rv1870c	-	4216	2810	1.5	0.2	0.1		1.1	0.6	0.5	0.7	0.7	nd	0.7
816Rv1885c	-	14609	5876	2.5	0.6	0.3		1.1	0.3	0.5	0.5	0.3	0.4	0.4
94Rv1886c	fbpB	20169	12279	1.7	0.4	0.2	antigen_85B,_mycolyltransferase	1.1	0.7	0.7	0.5	0.4	0.5	0.7
2779Rv1918c	PPE	8398	3806	2.2	0.3	0.1		1.2	0.4	0.6	0.4	0.4	0.4	0.5
2709Rv1957	-	5913	3296	1.8	0.2	0.1		1.1	0.7	0.6	0.5	0.5	0.5	0.5
5553Rv1997	ctpF	2806	1788	1.6	0.2	0.1	probable_cation_transport_ATPase_	2.6	0.6	0.8	0.7	0.5	0.6	0.6
5548Rv2005c	-	4604	2851	1.6	0.1	0.0		1.1	0.6	0.6	0.6	0.6	0.6	0.6
2665Rv2007c	fdxA	10372	4868	2.2	0.2	0.1	ferredoxin	1.1	0.4	0.5	0.5	0.4	0.4	0.5
4564Rv2021c	-	3932	2723	1.5	0.1	0.1	putative_transcriptional_regulator	1.1	0.6	0.6	0.7	0.6	0.7	0.8
1681Rv2031c	hspX	10501	2819	3.8	0.5	0.2	14kD_antigen,_heat_shock_protein_Hsp20_family	1.1	0.2	0.3	0.3	0.3	0.3	0.3
2403Rv2032	-	3968	1736	2.2	0.4	0.2		1.1	0.4	0.6	0.4	0.5	0.4	0.4
2936Rv2069	sigC	12822	7793	1.7	0.2	0.1	ECF_subfamily_sigma_subunit	1.1	0.7	0.5	0.6	0.6	0.6	0.6
4483Rv2074	-	9995	5610	1.8	0.3	0.1		1.1	0.5	0.5	0.7	0.5	0.6	0.6
5205Rv2075c	-	2994	2096	1.5	0.3	0.1		1.1	0.6	1.0	0.7	0.6	0.6	0.7
5209Rv2083	-	3985	2383	1.6	0.4	0.2		1.1	0.4	0.5	0.6	0.7	0.9	0.7
4635Rv2101	helZ	4943	3231	1.5	0.2	0.1	probable_helicase,_Snf2/Rad54_family	1.1	0.6	0.6	0.8	0.6	0.7	0.7
5158Rv2108	PPE	5677	2828	2.0	0.3	0.1		1.1	0.6	0.6	0.4	0.5	0.4	0.5
4442Rv2128	-	4971	3189	1.5	0.1	0.1	unknown_hydrophobic_protein	1.1	0.6	0.6	0.7	0.6	0.7	0.7
4791Rv2140c	-	5952	3899	1.5	0.3	0.1		1.1	0.5	0.5	0.8	0.8	0.8	0.7
2627Rv2147c	-	11771	7302	1.6	0.2	0.1		1.1	0.7	0.7	0.6	0.5	0.5	0.6
4450Rv2160c	-	6021	4122	1.5	0.1	0.1	Function:_unknown,_improbable	1.1	0.7	0.7	0.7	0.7	0.6	0.6
3705Rv2190c	-	9609	3298	2.9	0.5	0.2	putative_p60_homologue	1.1	0.3	0.3	0.4	0.4	0.4	0.4
438Rv2201	asnB	6122	4178	1.5	0.2	0.1	asparagine_synthase_B	1.1	0.7	0.6	0.8	0.6	0.7	0.7
4118Rv2238c	ahpE	7576	3921	1.9	0.2	0.1	member_of_AhpC/TSA_family	1.1	0.4	0.5	0.5	0.5	0.5	0.6
5370Rv2241	aceE	4374	2885	1.5	0.3	0.1	pyruvate_dehydrogenase_E1_component	1.1	0.5	0.6	0.7	0.8	0.7	0.8
3398Rv2243	fabD	10882	2309	4.7	2.5	1.0	malonyl_CoA-[ACP]_transacylase	1.1	0.4	0.3	0.2	0.1	0.2	0.1
3113Rv2243	fabD	8158	1986	4.1	1.6	0.6	malonyl_CoA-[ACP]_transacylase	1.1	0.3	0.4	0.2	0.1	0.2	0.2
3835Rv2243	fabD	10430	2497	3.7	1.9	0.8	malonyl_CoA-[ACP]_transacylase	1.1	0.4	0.5	0.2	0.2	0.2	0.2
752Rv2243	fabD	16980	5801	2.9	1.4	0.6	malonyl_CoA-[ACP]_transacylase	1.1	0.4	0.6	0.3	0.2	0.3	0.2
4120Rv2244	acpM	15431	2744	5.6	2.9	1.2	acyl_carrier_protein_(meromycolate_extension)	1.1	0.2	0.3	0.1	0.1	0.2	0.2
3114Rv2244	acpM	24726	6914	3.4	2.8	1.1	acyl_carrier_protein_(meromycolate_extension)	1.1	0.7	0.5	0.1	0.1	0.1	0.2
3836Rv2245	kasA	6592	1704	3.7	1.1	0.5	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.3	0.4	0.2	0.2	0.3	0.2
3635Rv2245	kasA	7520	2449	3.2	0.7	0.3	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.4	0.4	0.4	0.2	0.3	0.3
3115Rv2245	kasA	4903	1927	2.6	0.5	0.2	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.4	0.4	0.4	0.2	0.4	0.5
3116Rv2246	kasB	8323	2440	3.5	0.9	0.4	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.4	0.4	0.3	0.2	0.2	0.2
3838Rv2246	kasB	15345	4300	3.5	1.0	0.4	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.4	0.4	0.3	0.2	0.2	0.3
2914Rv2246	kasB	13028	3910	3.4	1.3	0.5	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.5	0.4	0.3	0.2	0.3	0.2

3837Rv2246	kasB	7621	2248	3.3	0.9	0.4	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.4	0.4	0.3	0.2	0.3	0.3
229Rv2247	accD6	5962	2074	3.0	0.6	0.2	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	0.4	0.3	0.4	0.3	0.4	0.3
951Rv2247	accD6	9239	3248	2.9	0.7	0.3	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	0.3	0.4	0.4	0.2	0.4	0.3
230Rv2247	accD6	11286	4503	2.6	0.6	0.3	acetyl/propionyl_CoA_carboxylase_b_subunit	1.4	0.5	0.5	0.4	0.3	0.3	0.3
3636Rv2247	accD6	5775	2975	1.9	0.4	0.2	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	0.4	0.6	0.6	0.4	0.6	0.5
952Rv2248	-	4775	1797	2.5	0.8	0.3		1.1	0.6	0.4	0.4	0.2	0.4	0.3
2915Rv2248	-	3984	2294	1.8	0.5	0.2		1.1	0.7	0.5	0.7	0.3	0.7	0.4
5638Rv2257c	-	2544	1645	1.5	0.2	0.1		1.1	0.6	0.6	0.6	0.8	0.7	0.7
4917Rv2258c	-	5210	3248	1.5	0.3	0.1	putative_transcriptional_regulator	1.1	0.5	0.5	0.7	0.8	0.7	0.7
3392Rv2276	-	4627	2932	1.5	0.3	0.1	Probable_cytochrome_P-450	1.1	0.5	0.4	0.8	0.7	0.8	0.7
504Rv2288	-	10643	4792	2.2	0.2	0.1		1.1	0.4	0.4	0.5	0.4	0.5	0.5
1225Rv2289	cdh	13764	5127	2.7	0.4	0.2	CDP-diacylglycerol_phosphatidylhydrolase	1.1	0.3	0.3	0.4	0.3	0.4	0.5
3385Rv2301	-	2866	1968	1.5	0.2	0.1	probable_cutinase	1.1	0.7	0.6	0.7	0.5	0.8	0.7
161Rv2329c	narK1	8111	4888	1.6	0.3	0.1	probable_nitrite_extrusion_protein	1.1	0.5	0.5	0.7	0.7	0.7	0.7
4509Rv2336	-	6268	2702	2.3	0.5	0.2		1.1	0.6	0.5	0.4	0.4	0.3	0.4
5231Rv2337c	-	3203	1937	1.6	0.2	0.1		1.1	0.5	0.7	0.6	0.6	0.6	0.6
5232Rv2339	mmpL9	3275	2087	1.5	0.2	0.1	conserved_large_membrane_protein	1.1	0.6	0.6	0.6	0.8	0.7	0.7
1628Rv2350c	plcB	4451	2596	1.7	0.1	0.1	phospholipase_C_precursor	1.1	0.5	0.6	0.7	0.6	0.6	0.6
5355Rv2357c	glyS	7417	4903	1.5	0.1	0.1	glycyl-tRNA_synthase	1.1	0.6	0.6	0.6	0.7	0.7	0.8
5166Rv2375	-	10234	6146	1.7	0.2	0.1		1.1	0.6	0.7	0.6	0.5	0.5	0.6
4429Rv2406c	-	6361	3730	1.7	0.2	0.1		1.4	0.7	0.6	0.6	0.5	0.5	0.5
4529Rv2459	-	5626	2672	2.1	0.4	0.1	probable_drug_efflux_protein	1.1	0.4	0.4	0.5	0.5	0.6	0.5
1646Rv2469c	-	3569	2285	1.6	0.1	0.0		1.1	0.6	0.6	0.7	0.6	0.7	0.7
2370Rv2474c	-	2317	1689	1.5	0.3	0.2		1.1	0.5	0.5	nd	0.8	nd	0.8
4536Rv2485c	lipQ	5785	1962	2.9	0.6	0.2	probable_carboxylesterase	1.1	0.3	0.5	0.3	0.3	0.3	0.3
414Rv2510c	-	2843	1999	1.5	0.3	0.1		1.1	0.6	0.7	0.8	0.5	0.8	0.7
1863Rv2550c	-	3973	2255	1.8	0.3	0.1		1.1	0.5	0.5	0.7	0.5	0.6	0.6
5593Rv2557	-	9575	4974	1.9	0.3	0.1		1.1	0.6	0.7	0.5	0.4	0.5	0.5
5591Rv2561	-	2901	1932	1.5	0.2	0.1		1.1	0.5	0.6	0.8	0.6	0.7	0.7
5590Rv2563	-	3613	2044	1.8	0.2	0.1	possible_membrane_protein	1.1	0.5	0.7	0.6	0.5	0.5	0.6
4868Rv2564	glnQ	8265	4653	1.8	0.3	0.1	probable_ATP-binding_transport_protein	1.1	0.5	0.4	0.6	0.6	0.6	0.6
2996Rv2582	ppiB	8503	4549	1.8	0.3	0.1	peptidyl-prolyl_cis-trans_isomerase	1.1	0.4	0.4	0.6	0.6	0.6	0.6
4991Rv2600	-	7219	2770	2.6	0.5	0.2		1.1	0.3	0.3	0.4	0.4	0.4	0.4
958Rv2600	-	6197	2821	2.3	0.4	0.2		1.1	0.3	0.5	0.5	0.4	0.5	0.4
1177Rv2626c	-	7460	3579	2.0	0.5	0.2		1.1	0.7	0.5	0.4	0.4	0.4	0.5
518Rv2632c	-	12738	8049	1.6	0.4	0.2		1.1	0.8	0.8	0.6	0.4	0.6	0.5
1240Rv2633c	-	16388	6679	2.5	0.5	0.2		1.1	0.4	0.5	0.4	0.3	0.4	0.5
4541Rv2680	-	3805	2515	1.5	0.2	0.1		1.1	0.5	0.6	0.8	0.8	0.6	0.7
64Rv2715	-	10365	6750	1.5	0.3	0.1	2-hydroxymuconic_semialdehyde_hydrolase	1.1	0.5	0.5	0.8	0.6	0.8	0.8
786Rv2716	-	11977	7565	1.6	0.2	0.1		1.1	0.5	0.7	0.8	0.6	0.7	0.6

2581Rv2721c	-	4600	2797	1.7	0.1	0.1		1.1	0.6	0.6	0.6	0.5	0.7	0.6
3162Rv2721c	-	6050	3727	1.6	0.3	0.1		1.1	0.5	0.5	0.7	0.7	0.7	0.7
4885Rv2740	-	3067	1805	1.7	0.2	0.1		1.1	0.6	0.6	0.7	0.5	0.5	0.6
3087Rv2778c	-	5066	3129	1.6	0.2	0.1		1.1	0.6	0.5	0.6	0.8	0.7	0.6
79Rv2816c	-	14713	7839	1.9	0.3	0.1		1.1	0.6	0.6	0.6	0.4	0.4	0.5
3688Rv2817c	-	7475	3720	2.0	0.4	0.2		1.1	0.4	0.5	0.6	0.5	0.5	0.6
4080Rv2846c	efpA	10328	7072	1.5	0.4	0.1	putative_efflux_protein	1.1	0.8	1.0	0.6	0.5	0.6	0.7
210Rv2858c	aldC	3864	2652	1.5	0.3	0.1	aldehyde_dehydrogenase_phenylacetaldehyde_	1.1	0.6	0.5	0.9	0.5	0.8	0.8
3095Rv2864c	-	2556	1690	1.5	0.2	0.1	probable_penicillin_binding_protein	2.6	0.6	0.7	0.7	0.8	0.6	0.8
40Rv2945c	lppX	10108	4761	2.1	0.5	0.2	lipoprotein	1.1	0.4	0.3	0.6	0.5	0.5	0.6
41Rv2947c	pks15	16382	10803	1.5	0.3	0.1	polyketide_synthase_	1.1	0.6	0.5	0.8	0.7	0.7	0.8
4463Rv2952	-	7306	3856	1.9	0.4	0.1	glycosyltransferase	1.1	0.4	0.4	0.6	0.6	0.6	0.6
5184Rv2953	-	3348	1943	1.6	0.3	0.1		1.1	0.4	0.6	0.6	0.7	0.6	0.7
4462Rv2954c	-	7813	5025	1.5	0.2	0.1		1.1	0.6	0.6	0.7	0.8	0.6	0.7
2298Rv2959c	-	4820	2780	1.7	0.6	0.3	some_similarity_to_methyltransferases	1.1	0.9	0.8	0.4	0.5	0.4	0.5
4659Rv2960c	-	3669	2359	1.6	0.3	0.1		1.1	0.8	0.7	0.6	0.5	0.6	0.6
1657Rv2992c	gltS	5988	3719	1.5	0.4	0.2	glutamyl-tRNA_synthase	1.1	0.5	0.4	0.9	0.8	0.7	0.7
5267Rv3005c	-	4329	2287	1.8	0.2	0.1		1.1	0.5	0.5	0.5	0.6	0.6	0.5
3003Rv3058c	-	7698	5293	1.5	0.3	0.1	putative_transcriptional_regulator	1.1	0.9	0.5	0.7	0.7	0.5	0.7
4896Rv3083	-	4644	2169	2.1	0.3	0.1	probable_monooxygenase	1.1	0.3	0.5	0.5	0.5	0.5	0.5
4897Rv3085	-	2686	1847	1.5	0.2	0.1	short_chain_alcohol_dehydrogenase	1.1	0.6	0.6	0.8	0.7	0.7	nd
5619Rv3086	adhD	3121	1630	1.8	0.4	0.2	zinc-containing_alcohol_dehydrogenase	2.6	0.4	0.5	0.6	0.7	0.6	0.6
1877Rv3119	moaE	5761	3819	1.5	0.3	0.1	molybdopterin-converting_factor_subunit_2	1.1	0.5	0.5	0.8	0.7	0.7	0.8
5484Rv3126c	-	3471	1939	1.8	0.2	0.1		1.1	0.6	0.7	0.5	0.6	0.5	0.5
3841Rv3129	-	2549	1695	1.6	0.3	0.1		1.1	0.7	nd	0.6	0.5	0.8	0.6
3036Rv3130c	-	6542	2429	2.7	0.5	0.2		2.6	0.3	0.4	0.4	0.3	0.4	0.4
1776Rv3130c	-	7363	2871	2.5	0.4	0.2		1.1	0.3	0.3	0.4	0.5	0.4	0.4
3757Rv3131	-	5726	3562	1.6	0.2	0.1		1.1	0.7	0.7	0.5	0.6	0.6	0.6
149Rv3143	-	7211	4427	1.6	0.3	0.1	putative_sensory_transduction_protein	1.1	0.5	0.5	0.8	0.6	0.7	0.7
993Rv3145	nuoA	4370	2637	1.7	0.3	0.1	NADH_dehydrogenase_chain_A	1.1	0.4	0.6	0.7	0.6	0.7	0.7
869Rv3146	nuoB	7887	3770	2.1	0.5	0.2	NADH_dehydrogenase_chain_B	1.1	0.3	0.5	0.6	0.4	0.6	0.5
147Rv3147	nuoC	9592	4609	2.1	0.4	0.1	NADH_dehydrogenase_chain_C	1.1	0.4	0.4	0.6	0.5	0.5	0.6
868Rv3148	nuoD	8383	3464	2.4	0.7	0.3	NADH_dehydrogenase_chain_D	1.1	0.2	0.3	0.5	0.4	0.5	0.5
146Rv3149	nuoE	6479	3906	1.6	0.2	0.1	NADH_dehydrogenase_chain_E	1.1	0.6	0.5	0.7	0.5	0.6	0.7
867Rv3150	nuoF	6874	3378	2.0	0.5	0.2	NADH_dehydrogenase_chain_F	1.1	0.3	0.5	0.5	0.5	0.6	0.6
5559Rv3152	nuoH	8917	2912	3.0	0.9	0.4	NADH_dehydrogenase_chain_H	1.1	0.2	0.2	0.4	0.4	0.4	0.4
4837Rv3153	nuoI	11177	4002	2.7	0.6	0.3	NADH_dehydrogenase_chain_I	1.1	0.2	0.3	0.4	0.4	0.4	0.4
4836Rv3155	nuoK	14228	4625	3.1	0.6	0.3	NADH_dehydrogenase_chain_K	1.1	0.3	0.2	0.4	0.3	0.4	0.4
5557Rv3156	nuoL	8782	4593	1.9	0.3	0.1	NADH_dehydrogenase_chain_L	1.1	0.4	0.6	0.6	0.6	0.5	0.5
4835Rv3157	nuoM	11973	5023	2.3	0.5	0.2	NADH_dehydrogenase_chain_M	1.1	0.3	0.4	0.5	0.4	0.5	0.5

2478Rv3157	nuoM	4511	3043	1.5	0.2	0.1	NADH_dehydrogenase_chain_M	1.1	0.6	0.9	0.7	0.7	0.6	0.7
3850Rv3158	nuoN	7363	3118	2.3	0.4	0.2	NADH_dehydrogenase_chain_N	1.1	0.3	0.4	0.4	0.4	0.5	0.5
1304Rv3168	-	3048	2016	1.5	0.3	0.1		1.1	0.8	0.8	0.7	0.6	0.6	0.6
583Rv3169	-	4302	2377	1.8	0.2	0.1		1.1	0.6	0.6	0.6	0.5	0.5	0.5
1777Rv3199c	-	5502	3071	1.8	0.3	0.1		1.1	0.5	0.4	0.6	0.6	0.6	0.6
1262Rv3224	-	14081	9296	1.6	0.3	0.1	putative_oxidoreductases	1.1	0.5	0.6	0.7	0.5	0.7	0.8
4264Rv3232c	pvdS	4432	2567	1.7	0.3	0.1	alternative_sigma_factor_for_siderophore_production	1.1	0.4	0.6	0.6	0.7	0.6	0.6
3543Rv3233c	-	3181	1975	1.6	0.3	0.1		1.1	0.5	0.5	0.8	0.6	0.7	0.8
4267Rv3250c	rubB	5117	2792	1.8	0.3	0.1	rubredoxin_B	1.1	0.4	0.5	0.6	0.5	0.6	0.6
4246Rv3281	-	11745	7239	1.7	0.5	0.2		2.5	0.4	0.4	0.7	0.6	0.7	0.8
186Rv3281	-	12019	7095	1.7	0.3	0.1		2.4	0.5	0.5	0.7	0.7	0.6	0.7
3070Rv3285	accA3	6357	3987	1.6	0.1	0.0	acetyl/propionyl_CoA_carboxylase_a_subunit	1.1	0.7	0.6	0.6	0.6	0.7	0.6
3795Rv3292	-	3268	2211	1.5	0.2	0.1		1.1	0.5	0.6	0.8	0.7	0.8	0.7
187Rv3295	-	10054	5811	1.7	0.1	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	0.6	0.6	0.5	0.5	0.6	0.6
1316Rv3310	-	4623	2842	1.6	0.2	0.1	probable_acid_phosphatase	1.1	0.7	0.6	0.7	0.5	0.6	0.6
1280Rv3377c	-	4877	3329	1.5	0.3	0.1	similar_to_many_cyclases_involved_in_steroid_biosynthesis	1.1	0.5	0.6	0.8	0.7	0.8	0.8
3447Rv3390	lpqD	7127	3581	2.0	0.7	0.3	lipoprotein	1.1	0.7	0.6	0.4	0.4	0.4	0.4
1020Rv3477	PE	15886	3326	4.9	1.1	0.4		1.1	0.2	0.2	0.3	0.1	0.2	0.2
1021Rv3479	-	9483	3221	2.9	0.4	0.2		1.1	0.3	0.4	0.4	0.3	0.3	0.3
300Rv3480c	-	8731	5160	1.7	0.2	0.1		1.1	0.5	0.5	0.7	0.6	0.6	0.7
3186Rv3487c	lipF	7957	4904	1.6	0.4	0.1	probable_esterase	1.1	0.4	0.5	0.7	0.7	0.8	0.8
3188Rv3492c	-	4053	2154	1.8	0.3	0.1		1.1	0.4	0.5	0.5	0.5	0.7	0.6
2118Rv3493c	-	2964	1884	1.5	0.3	0.1		1.1	0.5	0.5	0.8	0.6	0.7	0.8
4921Rv3495c	lprN	5236	3334	1.5	0.2	0.1	part_of_mce4_operon	1.1	0.6	0.6	0.7	0.6	0.6	0.8
5643Rv3496c	-	6303	3691	1.7	0.2	0.1	part_of_mce4_operon	1.1	0.5	0.6	0.6	0.7	0.6	0.6
2034Rv3497c	-	4153	2686	1.5	0.2	0.1	part_of_mce4_operon	1.1	0.6	0.6	0.7	0.7	0.7	0.7
2035Rv3499c	mce4	5759	3485	1.6	0.2	0.1	cell_invasion_protein	1.1	0.6	0.5	0.7	0.7	0.6	0.7
2757Rv3500c	-	3760	2588	1.5	0.1	0.0	part_of_mce4_operon	1.1	0.6	0.7	0.7	0.6	0.7	0.7
173Rv3554	fdxB	4535	2291	2.0	0.3	0.1	ferredoxin	1.1	0.5	0.4	0.6	0.4	0.5	0.5
176Rv3572	-	6778	4438	1.5	0.2	0.1		1.1	0.7	0.7	0.7	0.5	0.6	0.6
4254Rv3587c	-	8410	4688	1.9	0.4	0.2		1.1	0.6	0.6	0.5	0.3	0.5	0.7
4159Rv3598c	lysS	5305	3052	1.8	0.2	0.1	lysyl-tRNA_synthase	1.1	0.5	0.5	0.6	0.5	0.6	0.6
548Rv3613c	-	11529	6821	1.7	0.2	0.1		1.1	0.7	0.7	0.6	0.5	0.5	0.5
4157Rv3614c	-	14040	7783	1.8	0.5	0.2		1.1	0.7	0.8	0.5	0.3	0.5	0.5
3435Rv3615c	-	16883	10450	1.6	0.5	0.2		1.2	0.8	0.9	0.5	0.4	0.5	0.6
4156Rv3616c	-	15427	8995	1.6	1.1	0.4		1.1	1.2	1.2	0.4	0.3	0.4	0.4
309Rv3623	lpqG	3924	2379	1.7	0.2	0.1		1.1	0.7	0.5	0.6	0.6	0.6	0.6
1030Rv3624c	hpt	4374	2961	1.5	0.1	0.1	probable_hypoxanthine-guanine_phosphoribosyltransferase	1.1	0.6	0.6	0.7	0.7	0.7	0.7
3192Rv3633	-	6938	4201	1.7	0.2	0.1		1.1	0.6	0.6	0.7	0.5	0.6	0.6
5730Rv3648c	cspA	15937	8922	1.8	0.4	0.2	cold_shock_protein,_transcriptional_regulator	1.1	0.4	0.5	0.6	0.4	0.6	0.7

5011Rv3662c	-	5013	2379	2.1	0.4	0.2		1.1	0.4	0.5	0.5	0.4	0.5	0.6
4597Rv3671c	-	5274	3539	1.5	0.3	0.1	probable_serine_protease	1.1	0.6	0.5	0.8	0.6	0.8	0.8
5323Rv3680	-	10268	6738	1.5	0.2	0.1	probable_anion_transporter	1.1	0.5	0.6	0.7	0.8	0.7	0.7
1719Rv3691	-	4219	2817	1.5	0.3	0.1		1.1	0.6	0.5	0.8	0.8	0.8	0.8
2441Rv3692	moxR2	4061	2235	1.8	0.3	0.1	transcriptional_regulator,_MoxR_homologue	1.1	0.5	0.4	0.7	0.6	0.6	0.5
2847Rv3705c	-	2630	1608	1.7	0.2	0.1		1.1	0.6	0.7	nd	0.7	0.5	0.5
4608Rv3705c	-	3340	2244	1.6	0.3	0.1		1.1	0.7	0.7	0.7	0.5	nd	0.6
1723Rv3711c	dnaQ	4612	2776	1.6	0.2	0.1	DNA_polymerase_III_e_chain	1.1	0.6	0.5	0.6	0.6	0.7	0.7
1724Rv3713	cobQ2	4012	2127	1.8	0.4	0.2	possible_cobyric_acid_synthase	1.1	0.6	0.4	0.6	0.6	0.7	0.5
5334Rv3727	-	5099	2334	2.2	0.2	0.1	similar_to_phytoene_dehydrogenase_precursor	1.1	0.4	0.5	0.4	0.4	0.4	0.5
5338Rv3747	-	5889	4127	1.5	0.2	0.1		1.1	0.8	0.6	0.6	0.6	0.6	0.7
4617Rv3748	-	7089	4443	1.6	0.2	0.1		1.4	0.5	0.6	0.7	0.6	0.7	0.7
5339Rv3749c	-	4897	2659	1.9	0.2	0.1		1.1	0.6	0.5	0.5	0.5	0.5	0.6
4618Rv3750c	-	13470	8362	1.6	0.2	0.1	excisionase	1.1	0.8	0.6	0.6	0.5	0.5	0.7
5341Rv3753c	-	3984	2569	1.5	0.1	0.0		1.1	0.6	0.6	0.6	0.7	0.7	0.7
2795Rv3763	lpqH	10885	3865	2.8	0.4	0.1	19_kD	1.1	0.3	0.4	0.4	0.3	0.4	0.4
2074Rv3764c	-	5334	2627	1.9	0.5	0.2	sensor_histidine_kinase	1.1	0.4	0.4	0.6	0.6	0.7	0.6
1011Rv3774	echA21	8215	5337	1.5	0.4	0.2	enoyl-CoA_hydratase/isomerase_superfamily	1.1	0.4	0.5	0.8	0.6	0.8	0.9
4394Rv3776	-	3745	2509	1.5	0.2	0.1		1.1	0.7	0.5	0.7	0.6	0.8	0.7
5117Rv3779	-	3786	2429	1.6	0.1	0.0	unknown_membrane_protein	1.1	0.7	0.6	0.7	0.7	0.6	0.6
46Rv3794	embA	9108	5112	1.7	0.5	0.2	involved_in_arabinogalactan_synthesis	1.1	0.5	0.3	0.7	0.6	0.7	0.7
4959Rv3799c	accD4	13262	7806	1.7	0.3	0.1	acetyl/propionyl_CoA_carboxylase_b_subunit	1.4	0.5	0.5	0.6	0.6	0.6	0.7
2799Rv3811	csp	5553	3685	1.5	0.1	0.0	secreted_protein	1.1	0.6	0.8	0.7	0.7	0.7	0.6
3773Rv3822	-	12654	8174	1.5	0.2	0.1		1.1	0.8	0.7	0.6	0.7	0.5	0.7
289Rv3846	sodA	17646	11969	1.5	0.1	0.1	superoxide_dismutase	1.1	0.6	0.7	0.7	0.6	0.6	0.8
5620Rv3920c	-	10207	6744	1.5	0.5	0.2		1.1	0.4	0.4	0.8	0.8	0.8	0.9
4899Rv3921c	-	10858	7139	1.5	0.4	0.1	unknown_membrane_protein	1.1	0.5	0.5	0.7	0.8	0.7	0.9
5621Rv3922c	-	8800	5843	1.5	0.3	0.1	possible_hemolysin	1.1	0.5	0.5	0.7	0.9	0.7	0.8