

Table 3: Genes induced 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 induced. In addition, the table should not be seen as a complete list of all possibly induced 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		CH2/CH1	StD	SEM			Biol. Set 1		Biol. Set 2		Biol. Set 3	
			CH1	CH2						mi527	mi1030	mi1028	mi1018	mi1029	mi1024
Cye3	Cye5	Induced	F												
3318Rv0005	gyrB		3660	8972	2.4	0.3	0.1	DNA_gyrase_subunit_B	1.1	2.5	2.9	2.0	2.5	2.5	2.1
4040Rv0006	gyrA		8439	12090	1.5	0.3	0.1	DNA_gyrase_subunit_A	1.1	1.3	1.6	1.4	2.1	1.5	1.3
2216Rv0014c	pknB		1955	3963	2.1	0.7	0.3	serine-threonine_protein_kinase	1.1	2.6	3.0	1.3	2.6	1.9	1.5
1495Rv0015c	pknA		6516	14151	2.2	0.4	0.2	serine-threonine_protein_kinase	2.6	2.7	2.6	1.9	2.2	2.0	1.7
2217Rv0016c	pbpA		4060	13819	3.7	1.7	0.7	penicillin-binding_protein	1.1	6.0	5.5	2.7	2.9	2.4	2.3
1496Rv0017c	rodA		8547	20410	2.6	1.2	0.5	FtsW/RodA/SpovE_family	1.1	3.9	4.2	1.8	2.2	1.7	1.6
3709Rv0047c	-		3842	7746	2.1	1.1	0.5		1.1	3.0	4.1	1.5	1.4	1.3	1.4
2016Rv0061	-		8256	14767	1.8	0.4	0.2	unlikely_orf	1.2	2.0	2.2	1.5	2.3	1.4	1.5
2739Rv0064	-		2895	4202	1.5	0.1	0.0	possible_membrane_protein	1.1	1.4	1.6	1.5	1.4	1.3	1.5
2740Rv0066c	icd2		7032	11963	1.7	0.3	0.1	isocitrate_dehydrogenase	1.1	2.2	1.9	1.6	1.5	1.6	1.5
2741Rv0068	-		1921	4777	2.6	1.7	0.7	probable_oxidoreductase	1.1	4.6	4.9	1.6	1.4	1.6	1.4
1202Rv0094c	REP		5915	8850	1.5	0.2	0.1		1.1	1.7	1.8	1.4	1.4	1.3	1.4
2042Rv0109	PE_PGRS		2378	7019	2.9	0.4	0.2		2.3	2.6	3.1	2.7	2.5	3.7	3.0
2767Rv0116c	-		3777	9659	2.6	0.8	0.3		1.2	3.7	3.5	2.3	1.7	2.5	2.1
1831Rv0121c	-		3060	4420	1.5	0.3	0.1		1.1	1.2	1.2	1.4	1.8	2.0	1.4
1977Rv0132c	-		2668	4129	1.6	0.2	0.1	putative_oxidoreductase	1.1	1.2	1.5	1.7	1.9	1.5	1.7
2699Rv0133	-		3179	4538	1.5	0.3	0.1	possible_puromycin_N-acetyltransferase	1.1	1.1	1.1	1.5	1.5	1.9	1.6
5587Rv0145	-		7147	10904	1.5	0.1	0.0		1.1	1.4	1.5	1.5	1.7	1.6	1.5
4866Rv0146	-		2771	12298	4.8	0.8	0.4		1.1	3.4	4.6	4.9	nd	5.4	5.5
4867Rv0148	-		6353	10240	1.7	0.3	0.1	steroid_dehydrogenase	1.1	1.3	1.3	1.8	1.8	1.9	1.9
5651Rv0158	-		2616	3972	1.6	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.4	1.7	1.6	1.2	1.7	1.5	1.6
2199Rv0179c	lprO		4315	6401	1.5	0.2	0.1	lipoprotein	1.1	1.5	1.5	1.2	1.9	1.6	1.4
4363Rv0186	bglS		3878	7359	1.7	0.9	0.4	b-glucosidase	1.1	3.0	2.8	1.0	1.1	1.2	1.3
4364Rv0188	-		5876	12800	2.2	0.2	0.1	putative_methyltransferase	1.1	2.1	2.1	2.2	2.6	2.3	2.1
4365Rv0190	-		7654	15675	2.1	0.4	0.2		1.1	2.5	2.4	1.7	2.4	1.6	1.9
4933Rv0196	-		2128	3746	1.7	0.8	0.3	transcriptional_regulator_(TetR/AcrR_family)	1.1	2.7	3.0	1.2	1.2	1.3	1.2
5655Rv0197	-		2306	3417	1.5	0.5	0.2		1.1	2.4	1.8	1.1	1.3	1.3	1.3
2335Rv0211	pckA		3246	16353	5.4	1.1	0.5	phosphoenolpyruvate_carboxykinase_	1.1	5.5	6.7	5.0	5.8	6.1	3.4
3129Rv0238	-		2150	4028	1.8	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2.1	2.0	1.7	1.5	2.0	1.7
3853Rv0243	fadA2		5935	10787	1.8	0.4	0.2	acetyl-CoA_C-acetyltransferase_	1.1	2.1	2.5	1.5	1.6	1.5	1.8
3132Rv0244c	fadE5		1839	7283	3.8	2.0	0.8	acyl-CoA_dehydrogenase_	1.1	6.5	6.1	2.4	2.7	2.6	2.3
969Rv0251c	hsp		3145	20575	7.2	2.6	1.1	possible_heat_shock_protein	1.1	7.3	5.9	6.1	12.4	6.3	5.2

252Rv0275c	fadD27	7879	13191	1.7	0.3	0.1	acyl-CoA_synthase	1.1	2.2	1.7	1.5	1.6	1.5	1.4
3135Rv0277c	-	4440	7555	1.6	0.7	0.3		1.1	2.5	2.6	1.2	1.2	1.0	1.2
3859Rv0282	-	3575	5633	1.7	0.3	0.1		1.1	2.0	nd	1.4	2.0	1.5	1.5
3862Rv0288	-	9341	12739	1.5	0.3	0.1		1.1	1.0	nd	1.6	1.8	1.7	1.6
4849Rv0298	-	5537	9060	1.6	0.4	0.1		1.1	1.9	2.2	1.3	1.3	1.5	1.4
1962Rv0300	-	3251	5176	1.6	0.3	0.1		1.1	1.7	2.2	1.3	1.7	1.6	1.4
2684Rv0301	-	3884	6340	1.7	0.2	0.1		1.1	1.7	2.0	1.4	1.7	1.6	1.5
1968Rv0324	-	1873	2778	1.5	0.6	0.2	putative_transcriptional_regulator	1.1	2.1	2.4	1.0	0.9	1.2	1.2
846Rv0336	-	5309	11196	2.2	0.5	0.2		1.1	1.8	2.1	2.2	2.9	2.5	1.5
1041Rv0340	-	1895	2809	1.5	0.6	0.2		1.1	1.6	2.6	1.1	1.5	1.2	1.1
260Rv0384c	clpB	3719	9768	2.6	1.2	0.5	heat_shock_protein	1.1	4.3	3.8	1.8	1.8	1.6	2.0
264Rv0440	groEL2	14714	21528	1.8	1.3	0.5	60_kD_chaperonin_2	1.4	4.0	2.8	1.1	1.0	1.0	1.0
1325Rv0457c	-	2093	3480	1.6	0.3	0.1	probable_peptidase	1.1	1.3	2.2	1.5	1.5	1.6	1.7
607Rv0464c	-	7481	12800	1.8	0.3	0.1		1.1	1.6	1.6	1.6	2.3	1.6	1.8
1329Rv0465c	-	3441	12103	3.7	0.7	0.3	transcriptional_regulator_(PbsX/Xre_family)	1.1	4.6	4.2	2.7	4.3	3.2	3.3
4212Rv0467	aceA	2033	15689	8.2	2.0	0.8	isocitrate_lyase	1.1	8.1	8.1	6.8	12.0	7.3	6.7
3491Rv0468	fadB2	2109	6135	3.1	0.6	0.3	3-hydroxyacyl-CoA_dehydrogenase	1.1	2.4	2.6	2.8	4.1	3.4	3.1
3933Rv0469	umaA2	11273	18069	1.7	0.4	0.2	unknown_mycolic_acid_methyltransferase	1.1	2.1	2.0	1.2	2.1	1.4	1.4
4213Rv0469	umaA1	8905	13854	1.6	0.4	0.2	unknown_mycolic_acid_methyltransferase	1.1	2.2	2.0	1.3	1.8	1.3	1.3
3494Rv0474	-	2081	7582	3.4	2.8	1.1	transcriptional_regulator_(PbsX/Xre_family)	1.1	5.8	8.0	1.5	2.0	1.8	1.5
1537Rv0475	-	4826	10334	2.1	0.9	0.4	possible_exported_protein	1.1	3.5	2.8	1.4	1.5	1.4	1.8
2259Rv0476	-	2489	3892	1.6	0.3	0.1	unknown_hydrophobic_protein	1.1	1.7	2.0	1.5	1.3	1.7	1.2
4423Rv0483	-	8402	14116	1.8	0.4	0.2		1.1	1.3	1.4	1.7	2.1	2.0	2.4
4424Rv0485	-	3645	9196	2.6	0.5	0.2	transcriptional_regulator_(ROK_family)	1.1	2.4	3.5	2.1	2.7	2.6	2.2
4428Rv0493c	-	4929	7700	1.6	0.3	0.1		1.2	2.0	1.7	1.5	1.3	1.7	1.3
662Rv0515	-	4149	8485	2.1	0.3	0.1		1.1	1.7	1.8	2.0	2.5	2.3	2.2
1384Rv0516c	-	4704	16242	3.7	1.2	0.5		1.1	4.1	2.9	3.4	5.9	3.5	2.7
326Rv0530	-	5617	9821	1.9	0.5	0.2		1.1	1.3	1.3	2.1	2.2	2.1	2.2
4628Rv0549c	-	1780	2570	1.6	0.4	0.2		1.1	2.0	1.9	1.2	nd	nd	1.3
5350Rv0550c	-	1931	3047	1.6	0.1	0.0		1.2	1.8	1.7	1.5	1.6	1.5	1.5
327Rv0559c	-	7843	13705	1.7	0.3	0.1	possible_exported	1.1	2.2	1.8	1.5	1.5	1.6	1.4
1745Rv0559c	-	9088	13810	1.5	0.2	0.1	possible_exported	1.2	1.6	1.8	1.3	1.4	1.4	1.5
2467Rv0560c	-	1629	6885	4.2	2.6	1.1	methyl_transferase	1.1	6.8	8.1	1.7	3.4	2.2	3.0
4216Rv0563	htpX	2247	9134	4.1	1.2	0.5	probable_(transmembrane)_heat_shock_protein	1.1	5.1	5.9	3.7	3.8	3.2	2.9
450Rv0603	-	3163	4976	1.6	0.3	0.1		2.1	2.1	1.7	1.4	1.4	1.5	1.4
4054Rv0613c	-	5952	9163	1.6	0.2	0.1		2.1	1.4	1.4	1.5	1.8	1.6	1.6
4053Rv0615	-	2912	4466	1.5	0.2	0.1	possible_membrane_protein	1.1	1.5	1.6	1.4	1.3	1.5	1.8
3331Rv0616c	-	2194	2703	1.7	0.8	0.5		1.1	2.2	2.0	nd	nd	nd	0.8
669Rv0638	secE	5532	10676	2.0	0.3	0.1	SecE_preprotein_translocase	1.1	2.5	1.6	1.9	2.0	1.9	1.9
3217Rv0638	secE	6659	12905	1.9	0.3	0.1	SecE_preprotein_translocase	1.1	2.5	2.0	1.8	1.8	1.9	1.6

1391Rv0639	nusG	8777	12739	1.5	0.1	0.0	transcription_antitermination_protein	1.1	1.6	1.3	1.5	1.5	1.5	1.4
3940Rv0641	rplA	9119	14438	1.6	0.2	0.1	50S_ribosomal_protein_L1	1.1	1.3	1.3	1.6	1.9	1.8	1.8
670Rv0641	rplA	9981	14674	1.5	0.3	0.1	50S_ribosomal_protein_L1	1.1	1.5	1.1	1.5	1.8	1.8	1.4
5100Rv0654	-	2590	3800	1.6	0.6	0.2	putative_dioxygenase	1.4	2.5	1.7	1.0	1.7	1.2	1.2
3501Rv0676c	mmpL5	2606	11641	4.6	0.9	0.4	conserved_large_membrane_protein	1.1	4.9	5.4	4.8	5.0	4.6	2.8
4223Rv0677c	mmpS5	2710	13697	5.4	1.6	0.7	conserved_small_membrane_protein	1.1	6.1	7.9	4.1	5.9	4.5	3.6
614Rv0678	-	2776	14943	5.5	1.2	0.5		1.1	7.3	5.5	4.5	6.4	4.6	4.5
1336Rv0679c	-	2576	5482	2.3	0.7	0.3	possible_membrane_protein	1.1	3.0	3.1	1.4	2.3	1.7	2.0
1337Rv0681	-	3497	5159	1.5	0.3	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.8	1.9	1.2	1.4	1.3	1.4
616Rv0682	rpsL	8363	12839	1.6	0.6	0.2	30S_ribosomal_protein_S12	1.1	2.6	1.8	1.1	1.2	1.3	1.3
3892Rv0698	-	3044	4392	1.5	0.3	0.1		1.2	1.9	1.6	1.3	1.7	1.2	1.4
4776Rv0711	atsA	2967	25438	10.1	4.5	1.8	arylsulfatase	1.1	6.8	8.1	7.5	16.5	15.1	6.5
5498Rv0712	-	3306	13709	4.4	1.0	0.4		1.1	4.8	5.2	3.4	5.9	3.6	3.8
2617Rv0726c	-	4266	10957	2.8	0.9	0.4		1.1	4.2	3.6	2.0	2.8	1.9	2.1
3507Rv0743c	-	2209	3290	1.5	0.2	0.1		2.5	1.8	1.7	1.2	1.4	1.3	1.3
4285Rv0747	PE_PGERS	6370	12477	2.0	0.4	0.2		2.5	2.2	2.8	1.6	1.9	1.7	1.7
622Rv0749	-	4648	7046	1.5	0.6	0.2		1.4	1.9	2.4	1.0	1.1	1.2	1.1
1344Rv0750	-	3842	6239	1.7	0.4	0.2		1.1	2.3	2.0	1.4	1.2	1.5	1.6
4286Rv0750	-	4187	6611	1.6	0.4	0.2		2.1	2.1	2.1	1.3	1.5	1.3	1.4
2309Rv0757	phoP	3555	6066	1.7	0.4	0.2	two-component_response_regulator	1.1	2.1	2.1	1.4	1.2	1.6	1.5
5537Rv0788	purQ	3601	7444	2.1	0.4	0.2	phosphoribosylformylglycinamide_synthase_I	1.2	1.7	1.8	2.1	2.2	1.9	2.8
4816Rv0789c	-	2823	17459	6.6	1.8	0.7		1.2	4.5	6.7	6.2	9.1	8.1	5.0
4233Rv0810c	-	5954	8388	1.5	0.5	0.2		1.1	2.2	2.0	1.1	1.2	1.1	1.2
4235Rv0814c	sseC2	2296	3665	1.6	0.3	0.1	thiosulfate_sulfurtransferase	1.1	1.9	2.1	1.2	1.4	1.6	1.4
1685Rv0815c	cysA2	8979	19669	2.3	0.8	0.3	thiosulfate_sulfurtransferase	1.1	3.2	3.3	1.6	2.1	1.9	1.5
2409Rv0820	phoT	3647	5341	1.5	0.3	0.1	phosphate_transport_system_ABC_transporter	1.1	1.2	1.4	1.8	1.7	1.8	1.3
1688Rv0821c	phoY2	3781	5714	1.5	0.1	0.0	phosphate_transport_system_regulator	1.1	1.5	1.5	1.7	1.5	1.7	1.4
5296Rv0830	-	2246	7416	3.3	1.7	0.7		1.1	6.2	4.6	1.9	2.5	2.7	2.3
1694Rv0846c	-	5350	10468	2.5	1.9	0.8	similar_to_several_L-ascorbate_oxidases	1.1	4.0	5.6	1.5	1.6	0.8	1.4
2416Rv0847	lpqS	1777	4440	2.5	1.8	0.7	lipoprotein	1.1	5.0	4.7	1.1	1.1	1.5	1.7
1695Rv0848	cysM3	3097	8798	2.7	1.3	0.5	putative_cysteine_synthase	1.1	3.9	4.7	2.0	2.0	1.6	2.1
5304Rv0859	fadA	5168	15271	3.3	0.7	0.3	b_oxidation_complex,_b_subunit_(acetyl-CoA_C-acetyltransferase)	1.1	2.7	3.7	nd	4.2	2.7	2.9
4583Rv0860	fadB	5643	15535	2.8	0.2	0.1	b_oxidation_complex,_a_subunit_(multiple_activities)	1.1	3.1	2.8	2.5	2.8	2.5	2.9
1701Rv0872c	PE_PGERS	7622	11464	1.6	0.2	0.1		1.4	1.6	1.4	1.5	1.8	1.7	1.4
2423Rv0873	fadE10	4510	7576	1.7	0.3	0.1	acyl-CoA_dehydrogenase_	1.1	1.5	1.6	1.6	1.6	2.2	1.8
3025Rv0873	fadE10	6057	8866	1.6	0.4	0.2	acyl-CoA_dehydrogenase_	1.1	1.4	1.1	1.9	1.9	1.8	1.2
484Rv0903c	-	4803	6957	1.5	0.1	0.1	two-component_response_regulator	1.1	1.4	1.4	1.5	1.3	1.6	1.6
485Rv0906	-	4241	6947	1.7	0.1	0.1	probable_membrane_protein	1.1	1.5	1.6	1.6	1.8	1.6	1.9
4031Rv0940c	-	3940	6515	1.7	0.6	0.2	probable_monooxygenase	1.1	2.4	2.4	1.2	1.3	1.2	1.5
3302Rv0967	-	2416	3959	1.6	0.5	0.2		1.1	2.3	2.1	1.4	1.6	1.2	1.0

4021Rv0972c	fadE12	1965	3416	1.8	0.1	0.1	acyl-CoA_dehydrogenase_	1.1	1.8	1.5	1.7	2.0	1.7	1.8
1702Rv0973c	accA2	2352	4651	2.1	0.5	0.2	acetyl/propionyl-CoA_carboxylase,_a_subunit	1.1	2.0	1.8	1.9	3.1	2.1	1.9
2424Rv0974c	accD2	1643	2204	1.5	0.4	0.2	acetyl/propionyl-CoA_carboxylase,_b_subunit	1.1	nd	1.4	1.2	2.1	1.3	1.6
4585Rv0975c	fadE13	1887	3138	1.6	0.1	0.1	acyl-CoA_dehydrogenase	1.1	1.7	1.7	1.8	1.6	1.5	1.5
5307Rv0976c	-	2044	3197	1.6	0.2	0.1		1.4	1.4	1.6	1.6	2.0	1.7	1.4
4588Rv0981	-	4441	15487	3.5	0.4	0.2	two-component_response_regulator	1.1	3.3	3.3	3.7	4.2	3.1	3.6
5310Rv0982	-	3955	12869	3.5	0.8	0.3	sensor_histidine_kinase	1.1	2.6	2.7	3.3	4.6	3.7	3.9
4589Rv0983	-	4710	16682	3.9	1.2	0.5	probable_serine_protease	1.1	3.2	2.8	3.1	4.8	5.9	3.9
5311Rv0984	moaB2	4665	14974	3.3	0.4	0.2	molybdenum_cofactor_biosynthesis,_protein_B	1.1	3.0	3.2	2.8	3.8	3.4	3.8
1408Rv0985c	mscL	4172	7863	1.9	0.4	0.2	highly_similar_to_large-conductance_mechanosensitive_channels	1.1	2.6	2.2	1.5	1.7	1.9	1.8
1129Rv0991c	-	4564	8159	1.8	1.0	0.4		1.1	3.3	2.6	1.2	1.0	1.3	1.3
4014Rv0997	-	3261	16142	5.5	1.9	0.8		1.1	4.3	5.8	4.3	9.2	5.1	4.3
3293Rv0998	-	3805	5710	1.7	0.4	0.2		1.1	2.0	1.6	1.5	2.2	1.7	1.0
3433Rv1037c	-	7704	12537	1.6	0.2	0.1		1.1	1.7	1.6	1.6	1.5	1.9	1.5
424Rv1046c	-	7542	11673	1.6	0.3	0.1		1.2	2.2	1.7	1.2	1.6	1.2	1.5
1145Rv1047	IS1081	4627	11581	2.5	0.4	0.2		1.1	3.2	2.7	2.4	2.2	2.0	2.5
4210Rv1048c	-	1619	2236	1.6	0.4	0.2		1.1	1.9	1.9	nd	nd	1.4	1.0
2383Rv1052	-	1979	2890	1.5	0.3	0.1		1.1	1.9	1.3	1.3	1.2	1.5	1.5
1662Rv1053c	-	2831	4437	1.6	0.3	0.1		1.1	1.7	1.9	1.4	1.9	nd	1.2
2385Rv1056	-	1751	2730	1.7	0.5	0.2		1.1	1.9	1.6	1.1	2.6	1.4	1.5
1664Rv1057	-	2983	19854	7.1	2.0	0.8		1.1	5.9	6.1	6.7	9.7	9.6	4.9
2386Rv1058	fadD14	2552	4666	1.9	0.5	0.2	acyl-CoA_synthase	1.1	2.7	2.4	1.5	1.7	1.6	1.3
5275Rv1072	-	7921	20753	2.8	0.9	0.4	probable_transmembrane_protein	1.1	3.0	3.5	2.0	4.3	2.2	2.2
4554Rv1073	-	5111	12280	2.4	0.4	0.1		1.1	2.5	3.0	2.3	2.1	2.0	2.4
646Rv1080c	greA	3936	9145	2.3	1.0	0.4	transcription_elongation_factor_G	1.1	3.9	3.2	1.8	1.6	1.9	1.8
1669Rv1080c	greA	5889	13293	2.3	0.3	0.1	transcription_elongation_factor_G	2.5	2.2	2.8	1.9	2.4	2.2	2.0
1670Rv1082	-	5359	8971	1.7	0.2	0.1	similar_to_S._lincolnsis_lmbE	1.4	1.4	1.7	1.9	1.9	1.7	1.7
3575Rv1086	-	3195	4805	1.6	0.3	0.1	similar_to_UPF0015_family_from_Streptomyces_fradiae	1.1	1.2	1.3	1.7	1.8	1.6	1.9
1672Rv1086	-	2911	4221	1.5	0.2	0.1		1.1	1.3	1.4	1.6	1.6	1.5	1.5
5279Rv1093	glyA	4223	6089	1.5	0.4	0.1	serine_hydroxymethyltransferase	1.1	0.9	1.2	1.5	1.7	1.7	1.8
1674Rv1102c	-	4651	7625	1.6	0.1	0.0		1.1	1.8	1.7	1.7	1.5	1.5	1.6
1414Rv1103c	-	5835	8810	1.6	0.4	0.2		1.1	2.3	1.9	1.3	1.3	1.3	1.4
1188Rv1117	-	4761	7458	1.6	0.1	0.0		1.1	1.4	1.5	1.6	1.5	1.7	1.6
4076Rv1129c	-	1929	9522	5.5	1.7	0.7	transcriptional_regulator_(PbsX/Xre_family)	1.1	6.0	3.9	2.9	7.3	6.7	6.3
3355Rv1130	-	1886	12382	7.7	3.6	1.5		1.1	4.6	6.4	6.4	14.8	7.7	6.4
4077Rv1131	gltA1	2560	12726	5.3	1.5	0.6	citrate_synthase_3	1.1	3.1	4.0	6.0	6.7	6.8	5.2
4728Rv1152	-	3854	8016	2.1	0.3	0.1	transcriptional_regulator_(GntR_family)	1.1	2.2	2.4	1.7	1.9	2.2	2.2
5450Rv1153c	omt	2701	4602	1.7	0.2	0.1	PKS_o-methyltransferase	1.1	1.8	2.0	1.6	1.5	1.6	1.6
1845Rv1162	narH	6290	9974	1.5	0.2	0.1	nitrate_reductase_b_chain	1.1	1.7	1.8	1.5	1.2	1.6	1.4
563Rv1168c	PPE	2319	12359	5.4	0.6	0.3		1.1	5.2	5.4	4.8	6.3	6.0	4.7

1285Rv1169c	PE	2348	12720	5.7	1.9	0.8		1.1	8.0	7.7	4.0	6.3	3.6	4.6
3448Rv1174c	-	4803	9901	2.1	0.5	0.2		1.2	2.7	2.8	1.8	2.2	1.9	1.4
3581Rv1174c	-	11264	19151	1.8	0.6	0.2		1.1	2.9	1.9	1.4	1.9	1.6	1.2
4171Rv1177	fdxC	9217	13348	1.6	0.5	0.2	ferredoxin_4Fe-4S	1.1	2.3	2.2	1.1	1.6	1.3	1.1
5090Rv1194c	-	5198	7904	1.5	0.2	0.1		1.1	1.4	1.4	1.4	1.8	1.6	1.8
1481Rv1195	PE	2818	14806	5.3	0.3	0.1		1.1	5.8	5.2	5.4	5.1	4.8	5.3
2203Rv1196	PPE	6817	14434	2.1	0.4	0.2		1.1	2.7	2.5	1.9	2.2	2.0	1.6
1483Rv1199c	IS1081	7567	23032	3.2	0.7	0.3		1.1	2.4	3.0	2.9	4.6	3.3	3.3
3656Rv1221	sigE	5081	26128	5.4	1.3	0.5	ECF_subfamily_sigma_subunit	1.1	4.5	6.2	4.7	7.7	5.1	4.1
4721Rv1222	-	7151	10340	1.5	0.3	0.1		1.1	1.3	1.7	1.3	1.9	1.5	1.2
1294Rv1250	-	2717	4031	1.5	0.2	0.1	probable_drug_efflux_protein	1.1	1.6	1.8	1.4	1.4	1.4	1.4
1959Rv1265	-	2938	6304	2.2	0.6	0.2		1.1	2.1	3.2	2.1	2.1	1.7	1.7
5540Rv1285	cysD	1955	13685	7.8	2.6	1.1	ATP:sulphurylase_subunit_2	1.1	8.3	10.0	5.4	11.5	5.4	6.0
4819Rv1286	cysN	2906	19766	7.3	2.0	0.8	ATP:sulphurylase_subunit_1	1.1	5.6	7.6	5.0	10.7	7.9	7.2
1935Rv1294	thrA	5121	7638	1.6	0.3	0.1	homoserine_dehydrogenase	1.1	1.2	1.3	1.7	1.8	1.5	1.9
5111Rv1329c	dinG	2117	6488	3.2	0.8	0.3	probable_ATP-dependent_helicase	1.1	3.0	2.4	3.1	4.7	2.8	3.4
1507Rv1340	rphA	6152	9472	1.6	0.2	0.1	ribonuclease_PH	1.1	1.5	1.2	1.6	1.6	1.8	1.7
773Rv1351	-	4178	6658	1.6	0.1	0.0		1.1	1.5	1.4	1.6	1.6	1.7	1.7
54Rv1356c	-	4780	10356	2.1	0.6	0.3		1.1	3.3	2.4	1.8	1.8	1.7	1.8
3659Rv1359	-	2412	3731	1.6	0.2	0.1	putative_transcriptional_regulator	1.1	1.7	1.6	1.4	1.6	1.8	1.3
2940Rv1364c	rsbU	2385	4091	1.8	0.2	0.1	SigB_regulation_protein_	1.1	1.7	2.0	1.8	1.8	1.9	1.3
138Rv1375	-	5247	9450	1.7	0.5	0.2		1.1	2.5	2.2	1.4	1.3	1.2	1.6
5503Rv1390	-	6563	10023	1.6	0.6	0.2		1.1	2.1	2.5	1.1	1.5	1.2	1.3
5504Rv1392	metK	3006	7909	2.5	0.9	0.4	S-adenosylmethionine_synthase	1.1	3.5	3.3	1.1	2.3	2.4	2.4
1897Rv1397c	-	3313	6811	1.9	0.6	0.2		1.1	2.6	2.7	1.9	1.4	1.5	1.5
1900Rv1403c	-	3146	6582	2.0	0.9	0.4	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	3.4	2.9	1.2	1.6	1.4	1.6
2622Rv1404	-	5331	11148	2.1	0.8	0.3	transcriptional_regulator_(MarR_family)	1.1	3.6	2.5	1.6	1.7	1.7	1.8
1901Rv1405c	-	2034	6331	3.1	2.0	0.8	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	5.6	5.7	1.6	2.3	1.4	2.1
684Rv1405c	-	1747	4776	2.7	2.0	0.8	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	3.4	6.4	1.3	1.8	1.8	1.3
5507Rv1410c	-	7615	10833	1.6	0.4	0.2	probable_drug_efflux_protein	1.1	1.1	1.2	1.4	2.1	1.8	1.7
2330Rv1442	bisC	5154	9140	1.8	0.3	0.1	biotin_sulfoxide_reductase	1.4	1.6	1.7	1.8	1.5	2.4	1.9
577Rv1461	-	7374	16427	2.3	0.2	0.1		1.4	2.4	2.2	2.2	2.4	2.5	1.8
1299Rv1462	-	4116	8308	2.0	0.3	0.1		1.1	2.3	2.3	1.7	2.2	2.0	1.8
3528Rv1463	-	2822	6853	2.4	0.4	0.2	ABC-type_transporter	1.4	2.8	2.7	2.3	2.6	2.4	1.8
4182Rv1464	-	2589	5366	2.1	0.2	0.1	NifS-like_protein	1.1	2.1	1.9	1.9	2.4	2.0	2.2
4183Rv1466	-	2723	5113	1.9	0.2	0.1		1.1	1.6	1.6	2.0	2.0	2.0	2.1
1637Rv1475c	acn	7750	15428	2.1	0.3	0.1	aconitate_hydratase	1.1	1.9	1.8	2.2	2.7	2.1	1.7
1639Rv1479	moxR	11829	16773	1.5	0.2	0.1	transcriptional_regulator,_MoxR_homologue	1.1	1.5	1.3	1.5	1.9	1.4	1.2
2361Rv1480	-	2799	4054	1.5	0.3	0.1		1.1	1.3	1.1	1.5	1.6	2.1	1.6
2643Rv1493	mutB	3889	6267	1.6	0.1	0.1	methylmalonyl-CoA_mutase,_a_subunit	1.1	1.6	1.8	1.4	1.7	1.6	1.6

1704Rv1528c	papA4	2342	3298	1.5	0.6	0.2	PKS-associated_protein,_unknown_function	1.1	1.6	2.5	1.0	1.5	1.0	1.1
3849Rv1535	-	6366	17279	2.9	0.8	0.3		1.1	4.1	3.6	2.1	3.2	2.5	2.1
999Rv1536	ileS	3432	15587	5.0	2.4	1.0	isoleucyl-tRNA_synthase	1.1	9.5	5.8	3.5	4.0	4.1	3.2
1595Rv1536	ileS	4992	14305	2.9	0.4	0.2	isoleucyl-tRNA_synthase	1.1	3.2	3.4	2.3	3.2	2.5	2.7
3128Rv1536	ileS	6395	15954	2.5	0.3	0.1	isoleucyl-tRNA_synthase	1.1	2.9	2.9	2.0	2.4	2.4	2.3
2312Rv1557	mmpL6	2289	4104	1.8	0.4	0.2	conserved_large_membrane_protein	1.1	1.9	2.6	1.5	2.0	1.7	1.4
493Rv1575	-	2023	3060	1.5	0.4	0.2	phiRV1_phage_related_protein	2.1	2.0	2.1	1.2	1.7	1.1	1.2
1214Rv1576c	-	2427	4584	1.9	0.3	0.1	phiRV1_phage_related_protein	1.1	2.1	2.3	1.9	1.5	1.7	1.6
492Rv1577c	-	2174	4531	2.0	0.9	0.4	phiRV1_possible_prohead_protease	1.1	3.2	3.1	1.5	1.8	1.3	1.3
1417Rv1584c	-	2227	4967	2.3	1.3	0.5	phiRV1_phage_related_protein	1.1	4.4	3.4	1.3	1.2	1.7	1.4
489Rv1584c	-	2953	6402	2.1	1.1	0.5	phiRV1_phage_related_protein	1.2	3.8	3.4	1.6	1.2	1.3	1.4
1210Rv1585c	-	2542	4415	1.8	0.7	0.3	phiRV1_phage_related_protein	1.1	2.4	2.9	1.4	1.3	1.4	1.4
696Rv1585c	-	1925	3230	1.7	0.5	0.2	phiRV1_phage_related_protein	1.1	2.2	2.3	1.4	1.1	1.6	1.2
488Rv1586c	-	6693	9978	1.5	0.3	0.1	phiRV1_integrase	1.1	1.8	1.8	1.2	1.3	1.3	1.4
4094Rv1593c	-	5786	9705	1.7	0.5	0.2		1.1	2.2	2.6	1.2	1.5	1.4	1.5
3372Rv1594	nadA	5389	14268	2.7	0.4	0.1	quinolinate_synthase	2.5	2.7	3.1	2.4	2.6	3.0	2.2
4093Rv1595	nadB	4609	11352	2.6	0.5	0.2	L-aspartate_oxidase	1.1	2.4	3.0	2.3	3.3	2.6	1.9
3371Rv1596	nadC	4367	9232	2.2	0.5	0.2	nicotinate-nucleotide_pyrophosphatase	1.4	2.4	2.5	1.7	2.4	2.8	1.5
1208Rv1601	hisB	5277	8015	1.6	0.2	0.1	imidazole_glycerol-phosphate_dehydratase	1.1	1.6	1.7	1.3	1.7	1.4	1.5
3275Rv1730c	-	2658	3914	1.5	0.3	0.1	probable_penicillin_binding_protein	1.1	2.0	1.2	1.4	1.8	1.4	1.1
133Rv1772	-	5532	10430	1.9	0.2	0.1		1.1	2.2	1.8	1.7	1.6	2.1	1.8
2048Rv1779c	-	3082	4618	1.6	0.2	0.1	possible_integral_membrane_protein	1.1	1.2	1.7	1.5	1.8	1.8	1.5
2771Rv1782	-	5469	9399	1.7	0.2	0.1		1.1	1.4	1.8	1.7	1.9	2.0	1.7
2050Rv1783	-	6072	9732	1.7	0.4	0.1		1.1	1.2	1.3	1.8	2.1	1.9	1.7
2772Rv1784	-	11175	15869	1.5	0.2	0.1		1.1	1.4	1.3	1.5	1.9	1.4	1.4
2054Rv1804c	-	1956	3437	1.8	0.6	0.3		1.2	2.2	2.8	1.2	1.6	1.2	1.6
2776Rv1805c	-	3827	8748	2.5	0.9	0.4		1.1	4.0	3.2	1.9	2.0	1.9	1.8
2055Rv1806	PE	1793	7247	4.0	1.8	0.7		1.1	7.0	5.1	2.4	3.7	3.4	2.3
2777Rv1807	PPE	4391	12706	3.0	0.8	0.3		1.1	4.5	3.4	2.3	2.7	2.6	2.5
2056Rv1808	PPE	3994	8576	2.1	0.4	0.2		1.1	2.5	2.7	1.9	2.1	1.9	1.7
2778Rv1809	PPE	3290	9539	3.0	0.4	0.1		1.1	3.5	3.0	2.9	3.2	2.5	2.8
3694Rv1810	-	3106	4523	1.5	0.3	0.1	All_secreted_proteins?	1.1	1.4	1.2	1.4	2.0	1.8	1.4
1525Rv1821	secA2	8214	11490	1.5	0.3	0.1	SecA,_preprotein_translocase_subunit	1.1	1.2	1.1	1.7	1.6	1.5	1.7
4408Rv1831	-	6823	11111	1.6	0.2	0.1		1.1	1.7	1.9	1.4	1.7	1.5	1.5
2308Rv1838c	-	2003	3246	1.7	0.3	0.1		1.4	1.6	2.0	1.3	2.1	1.5	1.6
5188Rv1855c	-	4353	6823	1.6	0.3	0.1	probable_monooxygenase_	1.1	1.3	1.4	1.6	2.0	1.7	1.8
2978Rv1894c	-	3550	7451	2.2	1.3	0.5	some_similarity_to_dioxygenases	1.1	4.4	3.0	1.3	1.5	1.4	1.4
5597Rv1945	REP	3745	5443	1.5	0.4	0.2		1.1	0.9	1.3	1.5	2.0	1.7	1.8
4719Rv1977	-	3641	5756	1.6	0.3	0.1	probable_zinc_metallopeptidase	1.1	1.7	2.1	1.3	1.8	1.4	1.5
2669Rv1989c	-	2569	3893	1.6	0.7	0.3		1.1	2.3	2.4	1.0	nd	1.1	1.1

1947Rv1990c	-	4098	6793	1.6	0.5	0.2	putative_transcriptional_regulator	1.1	2.0	2.5	1.3	1.5	1.3	1.3
1946Rv1992c	ctpG	2635	5121	1.9	0.8	0.3	probable_cation_transport_ATPase	1.2	2.6	3.3	1.2	1.6	1.4	1.3
2667Rv1993c	-	3278	5466	1.7	0.6	0.2		1.1	2.0	2.6	1.5	1.1	1.3	1.5
2664Rv2009	-	2353	4149	1.8	0.3	0.1		1.1	2.1	2.1	1.7	2.1	1.4	1.5
1940Rv2014	IS1607	4182	5689	1.5	0.4	0.2	transposase	1.1	1.0	1.3	1.5	2.1	1.3	1.5
5283Rv2016	-	2734	6919	2.7	0.9	0.4		1.1	3.8	3.8	2.0	2.7	1.9	1.9
4562Rv2017	-	4446	10829	2.4	0.4	0.2	putative_transcriptional_regulator_(PbsX/Xre_family)	1.1	3.2	2.5	2.0	2.3	2.2	2.3
2405Rv2036	-	2381	3475	1.5	0.3	0.1	similar_to_lincomycin_production_genes	1.1	1.6	2.0	1.3	1.4	1.3	1.2
648Rv2043c	pncA	5231	7796	1.5	0.2	0.1	pyrazinamide_resistance/sensitivity	1.1	1.4	1.2	1.5	1.6	1.6	1.8
5294Rv2050	-	3651	13494	3.8	0.9	0.4		1.1	5.1	4.5	2.9	3.2	3.5	3.5
2744Rv2052c	-	1711	4241	2.5	0.4	0.2		1.1	2.2	2.2	2.3	2.8	3.2	2.5
3845Rv2053c	-	2719	6985	2.8	0.1	0.1		1.1	2.8	nd	2.6	2.9	2.9	2.6
5206Rv2077c	-	4282	6335	1.5	0.4	0.2		1.1	2.0	2.0	1.2	1.3	1.3	1.3
5159Rv2110c	prcB	4812	9435	2.0	0.2	0.1	proteasome_b-type_subunit_2	1.1	1.9	2.1	1.7	2.1	1.9	2.3
4440Rv2115c	-	5874	13834	2.5	0.5	0.2	ATPase_of_AAA-family	1.1	1.8	1.9	2.7	3.0	2.8	2.9
2278Rv2124c	metH	3073	7894	2.6	0.4	0.2	5-methyltetrahydrofolate-homocysteine_methyltransferase	2.5	2.4	2.7	2.5	3.3	2.5	2.4
4447Rv2166c	-	10953	17490	1.6	0.4	0.2		1.1	2.0	2.3	1.4	1.5	1.4	1.1
2748Rv2169c	-	3972	6976	1.8	0.5	0.2		1.1	2.5	2.4	1.5	1.5	1.5	1.6
4910Rv2172c	-	3402	7916	2.3	0.2	0.1		1.2	2.6	2.6	2.2	2.2	2.3	2.1
4915Rv2182c	-	7391	13388	1.8	0.4	0.2		1.1	1.9	2.6	1.4	1.8	1.6	1.8
1160Rv2202c	cbhK	7390	10925	1.5	0.1	0.0	carbohydrate_kinase	1.1	1.3	1.5	1.4	1.4	1.5	1.6
508Rv2224c	-	3819	8282	2.2	0.2	0.1	probable_exported_protease	1.1	2.0	2.2	2.1	2.0	2.2	2.5
750Rv2225	panB	8649	16389	1.9	0.3	0.1	3-methyl-2-oxobutanoate_hydroxymethyltransferase	1.4	2.5	2.0	1.5	2.0	1.6	1.8
4916Rv2256c	-	4750	9613	2.0	0.3	0.1		1.1	2.1	2.5	1.8	1.8	1.8	2.0
2347Rv2345	-	3657	5408	1.5	0.3	0.1	precursor_of_probable_membrane_protein	1.1	1.2	1.2	1.4	1.8	1.8	1.6
770Rv2373c	dnaJ2	5125	8850	1.7	0.2	0.1	DnaJ_homologue	1.1	1.6	1.6	2.0	1.6	1.8	1.9
1549Rv2391	nirA	7744	16148	2.1	0.2	0.1	probable_nitrite_reductase/sulphite_reductase	1.1	2.0	2.1	2.0	2.4	1.9	2.2
2270Rv2392	cysH	4845	8892	1.9	0.2	0.1	3'-phosphoadenylylsulfate_(PAPS)_reductase	1.1	1.7	2.1	1.6	2.0	2.0	1.8
2932Rv2429	ahpD	6339	9133	1.6	0.4	0.2	member_of_AhpC/TSA_family	1.1	1.2	1.0	1.9	1.9	1.8	1.7
4122Rv2430c	PPE	5253	7859	1.5	0.2	0.1		1.1	1.3	1.3	1.5	1.6	1.5	1.8
3400Rv2431c	PE	1754	3011	1.9	0.4	0.2		1.1	nd	2.6	1.5	1.9	1.6	1.7
513Rv2442c	rplU	7217	10588	1.5	0.6	0.3	50S_ribosomal_protein_L21	1.1	2.8	1.6	1.3	1.3	1.2	1.1
512Rv2444c	rne	5556	9757	1.7	0.2	0.1	similar_at_C-term_to_ribonuclease_E	1.1	2.2	1.7	1.7	1.5	1.6	1.9
1766Rv2444c	rne	6068	9863	1.7	0.3	0.1	similar_at_C-term_to_ribonuclease_E	1.1	1.3	1.4	1.7	2.2	1.8	1.9
5251Rv2460c	clpP2	7650	14991	2.1	0.6	0.2	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	1.8	1.8	1.7	3.2	1.8	2.2
4530Rv2461c	clpP	8488	16083	2.0	0.4	0.2	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	1.6	1.6	1.8	2.6	1.9	2.2
2958Rv2495c	pdhC	3410	6828	2.0	0.2	0.1	dihydrolipoamide_acetyltransferase	1.1	1.9	2.1	1.9	2.3	2.1	2.0
3680Rv2496c	pdhB	3516	7768	2.2	0.2	0.1	pyruvate_dehydrogenase_E1_component_b_subunit	1.4	2.1	2.1	1.9	2.3	2.3	2.6
2959Rv2497c	pdhA	4164	11813	2.8	0.6	0.2	pyruvate_dehydrogenase_E1_component_a_subunit	1.1	3.1	3.8	2.4	2.4	2.9	2.2
415Rv2512c	IS1081	5001	12554	2.6	0.6	0.2		1.1	3.1	2.5	2.2	3.5	2.1	2.2

1653Rv2516c	-	2675	4967	1.7	1.0	0.4		1.1	3.1	2.7	1.1	1.0	1.0	1.1
2375Rv2517c	-	2431	4869	1.9	1.4	0.6	questionable	1.1	3.4	3.9	0.9	1.1	1.0	1.2
1654Rv2518c	lppS	4151	6028	1.5	0.2	0.1	lipoprotein	1.1	1.5	1.7	1.4	1.5	1.3	1.3
1868Rv2526	-	3114	5062	1.6	0.5	0.2		1.1	2.1	2.3	1.2	1.4	1.3	1.3
2589Rv2527	-	4402	8420	1.9	0.4	0.2		1.1	2.7	2.0	1.6	1.7	1.6	1.9
3717Rv2583c	relA	4249	6461	1.5	0.1	0.0	(p)ppGpp_synthase_I	1.1	1.4	1.4	1.5	1.6	1.5	1.7
2994Rv2586c	secF	10663	15150	1.5	0.2	0.1	protein-export_membrane_protein	1.1	1.2	1.3	1.4	1.8	1.7	1.6
2992Rv2590	fadD9	3802	10700	2.8	0.4	0.1	acyl-CoA_synthase	1.1	2.8	3.4	2.6	3.1	2.4	2.6
2195Rv2602	-	2552	4528	1.8	0.2	0.1		1.1	2.1	1.6	1.8	1.7	2.0	1.6
4062Rv2621c	-	2038	2944	1.5	0.1	0.1	putative_transcriptional_regulator	2.1	1.6	1.4	1.4	1.7	1.4	1.3
3409Rv2651c	-	2219	3338	1.5	0.6	0.2	phiRV2_prohead_protease	1.1	2.0	2.4	1.1	1.5	1.2	1.1
4131Rv2652c	-	2043	3748	1.8	0.7	0.3	phiRV2_phage_related_protein	1.1	2.8	2.6	1.3	1.5	1.3	1.3
4133Rv2656c	-	3133	4627	1.5	0.4	0.2	phiRV2_phage_related_protein	1.1	2.0	1.9	1.2	1.2	1.2	1.3
524Rv2657c	-	6146	9239	1.5	0.6	0.2	similar_to_gp36_of_mycobacteriophage_L5_	1.1	2.2	2.2	1.1	1.0	1.1	1.2
1246Rv2658c	-	6796	10964	1.6	0.4	0.1	phiRV2_phage_related_protein	1.4	1.9	2.2	1.5	1.4	1.4	1.4
525Rv2659c	-	3745	6521	1.7	0.7	0.3	phiRV2_integrase	1.1	2.6	2.7	1.2	1.2	1.4	1.3
1247Rv2660c	-	4561	11861	3.1	2.4	1.0		1.1	6.9	5.3	1.5	1.8	1.3	1.7
528Rv2665	-	3834	6919	1.8	0.7	0.3		1.1	2.6	2.6	1.1	1.4	1.5	1.4
1250Rv2666	IS1081'	2777	9593	3.5	0.4	0.1		1.1	3.5	3.9	3.8	3.2	3.1	3.2
778Rv2686c	-	2996	8120	2.8	0.4	0.2	possible_membrane_protein	1.1	3.6	2.5	2.4	2.7	2.5	3.0
998Rv2687c	-	1897	3062	1.6	0.4	0.1		1.1	1.5	2.1	1.6	1.5	2.0	1.2
779Rv2688c	-	3682	10715	3.0	1.2	0.5	similar_to_transport_ATP-binding_proteins	1.1	5.2	3.8	2.2	2.3	2.2	2.4
3881Rv2694c	-	1981	4394	2.5	0.4	0.2		1.1	2.9	nd	2.1	3.0	2.3	2.3
782Rv2694c	-	4577	7640	1.8	0.6	0.2		1.3	2.9	1.8	1.6	1.6	1.4	1.5
3655Rv2703	sigA	7395	12313	1.7	0.2	0.1	RNA_polymerase_sigma_factor_(aka_MysA,_RpoV)	1.1	1.5	1.5	1.7	2.0	1.8	1.7
2948Rv2706c	-	5746	10368	1.9	0.3	0.1		1.1	1.8	1.8	1.7	2.6	1.8	1.6
2934Rv2710	sigB	4743	25672	6.5	3.0	1.2	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	5.5	4.6	4.5	7.3	12.3	4.6
3653Rv2711	ideR	6342	15462	2.5	0.5	0.2	iron_dependent_repressor,_IdeR	1.1	2.8	3.3	1.9	2.5	2.4	2.0
62Rv2711	ideR	7753	14379	1.9	0.1	0.1	iron_dependent_repressor,_IdeR	1.1	1.8	1.8	1.7	1.9	2.0	2.0
2491Rv2724c	fadE20	2157	6938	3.3	1.0	0.4	acyl-CoA_dehydrogenase_	1.1	4.9	4.2	2.7	2.7	2.9	2.3
4743Rv2724c	fadE20	4329	10537	2.5	0.2	0.1	acyl-CoA_dehydrogenase_	1.2	2.6	2.7	2.0	2.6	2.3	2.6
915Rv2743c	-	2327	6461	2.9	0.4	0.2		1.1	2.8	2.9	2.5	3.6	2.8	2.4
194Rv2744c	35kd_ag	7251	18707	2.6	0.4	0.2	35-kd_antigen	1.1	3.0	2.9	2.1	2.9	2.5	2.2
916Rv2745c	-	4964	13184	2.7	0.3	0.1	putative_transcriptional_regulator	1.4	2.7	2.6	2.3	3.2	2.9	2.5
918Rv2749	-	2293	3886	1.7	0.3	0.1	questionable	1.1	1.5	1.9	1.8	2.1	1.5	1.5
920Rv2753c	dapA	5631	10404	1.9	0.3	0.1	dihydrodipicolinate_synthase	1.1	1.4	1.7	2.1	2.1	2.0	2.1
3812Rv2785c	rpsO	8541	12819	1.5	0.4	0.2	30S_ribosomal_protein_S15	1.1	2.1	2.1	1.1	1.5	1.3	1.2
207Rv2794c	-	4766	9460	2.0	0.5	0.2	possible_4'-phosphopantetheine_transferase_	2.3	3.0	1.6	1.9	1.6	1.8	2.0
2961Rv2827c	-	4950	7565	1.5	0.3	0.1		2.5	1.6	2.1	1.1	1.7	1.3	1.4
799Rv2830c	-	5219	8148	1.5	0.4	0.2	similar_to_phage_P1_phd_gene	1.1	1.9	2.1	1.3	1.1	1.4	1.3

74Rv2837c	-	6056	10564	1.8	0.2	0.1		1.1	1.8	1.6	1.6	1.9	1.6	2.0
795Rv2838c	rbfA	7837	17307	2.3	0.5	0.2	ribosome-binding_factor_A	1.2	3.2	2.0	1.9	2.5	1.8	2.2
73Rv2839c	infB	6866	15187	2.2	0.2	0.1	initiation_factor_IF-2_	1.1	2.2	2.2	2.1	2.7	2.3	2.0
5487Rv2840c	-	10214	16771	1.8	0.5	0.2	similar_to_NUSA/INFB	1.1	2.1	2.0	1.3	2.5	1.3	1.4
4765Rv2841c	nusA	3998	6948	1.9	0.4	0.2	transcription_termination_factor	1.1	1.4	1.7	1.8	2.5	2.0	1.9
4082Rv2842c	-	2542	4404	1.8	0.3	0.1		1.1	1.7	1.6	1.7	2.3	1.9	1.6
3817Rv2865	-	3762	5812	1.6	0.2	0.1		1.1	1.5	1.4	1.5	2.0	1.4	1.7
3097Rv2868c	gcpE	6437	9410	1.5	0.3	0.1	essential_gene_of_unknown_function	1.1	1.3	1.2	1.7	1.9	1.6	1.5
1908Rv2871	-	3496	5289	1.5	0.3	0.1		1.2	1.7	1.6	1.4	1.8	1.4	1.1
1747Rv2873	mpt83	2853	5039	1.8	0.5	0.2	surface_lipoprotein_Mpt83	1.1	2.3	2.4	1.3	1.8	1.6	1.4
5519Rv2887	-	4422	6669	1.5	0.2	0.1	transcriptional_regulator_(MarR_family)	1.1	1.7	1.9	1.3	1.6	1.5	1.4
1918Rv2904c	rplS	6677	10801	1.6	0.2	0.1	50S_ribosomal_protein_L19	1.1	1.9	1.6	1.4	1.7	1.6	1.6
494Rv2916c	ffh	3611	5574	1.6	0.2	0.1	signal_recognition_particle_protein	1.1	1.3	1.5	1.5	1.8	1.6	1.6
1220Rv2925c	inc	6605	10438	1.6	0.1	0.1	RNase_III	1.4	1.5	1.8	1.6	1.5	1.6	1.5
755Rv2930	fadD26	5617	19274	3.5	0.5	0.2	acyl-CoA_synthase	1.1	4.5	3.5	3.1	3.6	3.0	3.2
34Rv2931	ppsA	4944	10366	2.2	0.4	0.2	phenolphthiocerol_synthase_(pksB)	1.1	1.8	1.6	2.3	2.5	2.6	2.2
756Rv2931	ppsA	4970	9834	2.0	0.3	0.1	phenolphthiocerol_synthase_(pksB)	1.1	1.5	1.6	2.2	2.3	2.1	2.2
35Rv2932	ppsB	3478	5301	1.6	0.3	0.1	phenolphthiocerol_synthase_(pksC)	1.1	1.4	1.2	1.6	1.5	1.9	1.8
3645Rv2933	ppsC	2934	4554	1.6	0.3	0.1	phenolphthiocerol_synthase_(pksD)	1.1	1.2	1.2	1.6	1.7	1.9	1.8
4542Rv2933	ppsC	3094	4522	1.6	0.3	0.1	phenolphthiocerol_synthase_(pksD)	1.1	1.2	1.1	1.7	1.9	1.6	1.9
3842Rv2940c	mas	4103	5729	1.6	0.5	0.2	mycocerosic_acid_synthase	1.1	1.1	nd	1.8	2.2	1.1	1.6
761Rv2941	fadD28	12899	18900	1.5	0.2	0.1	acyl-CoA_synthase	1.1	1.7	1.3	1.4	1.7	1.3	1.4
1574Rv2963	-	3397	8055	2.1	1.3	0.6	integral_membrane_protein	1.1	3.4	4.2	1.3	1.5	1.2	1.1
2293Rv2969c	-	6444	9072	1.5	0.3	0.1	possible_transmembrane_domain	1.1	1.1	1.3	1.7	1.7	1.6	1.4
1571Rv2970c	lipN	5516	8418	1.5	0.1	0.0	probable_lipase/esterase	1.1	1.4	1.5	1.6	1.6	1.6	1.6
5180Rv2971	-	5116	9052	1.8	0.2	0.1	oxidoreductase_of_Aldo/keto_reductase_family	1.1	2.0	1.9	1.4	2.0	1.7	1.9
1656Rv2990c	-	3014	5361	1.7	0.8	0.3		1.1	2.6	2.8	1.1	1.3	1.1	1.3
5266Rv3003c	ilvB	3138	4953	1.6	0.3	0.1	acetolactate_synthase_I_large_subunit_	1.3	2.2	1.6	1.3	1.8	1.4	1.4
4546Rv3006	lppZ	10520	15225	1.5	0.2	0.1		1.1	1.3	1.4	1.5	1.7	nd	1.5
4886Rv3023c	IS1081	4512	11701	2.6	0.2	0.1		1.4	2.5	2.9	2.4	2.9	2.6	2.5
2726Rv3036c	-	5162	8019	1.6	0.1	0.0	probable_secreted_protein	1.2	1.5	1.6	1.5	1.7	1.6	1.5
4661Rv3045	adhC	11441	18645	1.7	0.2	0.1	alcohol_dehydrogenase	1.1	1.8	1.5	1.5	2.0	1.6	1.6
3007Rv3051c	nrdE	5472	9679	1.7	0.4	0.1	ribonucleoside_diphosphate_reductase_a_chain	1.3	2.4	1.7	1.5	1.6	1.7	1.5
4894Rv3051c	nrdE	13326	20486	1.6	0.2	0.1	ribonucleoside_diphosphate_reductase_a_chain	1.1	1.5	1.7	1.3	1.7	1.4	1.6
3728Rv3052c	nrdI	4402	9760	2.2	0.7	0.3	NrdI/YgaO/YmaA_family	1.1	2.6	3.4	1.7	1.8	1.9	1.8
3006Rv3053c	nrdH	8666	13973	1.6	0.5	0.2	glutaredoxin_electron_transport_component_of_NrdEF_system	1.1	2.6	1.8	1.3	1.6	1.4	1.2
118Rv3065	emrE	2720	4276	1.5	0.7	0.3	resistance_to_ethidium_bromide	1.1	2.8	1.9	1.0	1.2	1.0	1.2
2593Rv3095	-	4067	6774	1.6	0.2	0.1	putative_transcriptional_regulator	1.1	1.8	1.9	1.5	1.5	1.5	1.7
5480Rv3105c	prfB	3358	5193	1.5	0.1	0.1	peptide_chain_release_factor_2	1.1	1.4	1.4	1.6	1.5	1.6	1.8
1875Rv3115	IS1081	3210	10689	3.3	0.3	0.1		1.1	3.5	3.6	3.2	3.2	2.8	3.6

1876Rv3117	cysA3	7666	16011	2.2	0.9	0.4	thiosulfate_sulfurtransferase	1.1	2.8	3.8	1.5	2.1	1.6	1.5
2598Rv3118	sseC	4002	5912	1.5	0.3	0.1	thiosulfate_sulfurtransferase	1.1	1.9	1.8	1.2	1.4	1.4	1.4
3111Rv3138	pflA	2368	4614	2.0	0.4	0.2	similar_to_pyruvate_lyase_activating_protein	1.1	1.9	2.5	1.5	nd	2.2	1.9
150Rv3138	pflA	4779	7661	1.6	0.2	0.1	similar_to_pyruvate_lyase_activating_protein	1.1	1.9	1.6	1.5	1.5	1.5	1.4
3647Rv3139	fadE24	3430	14147	4.2	1.0	0.4	acyl-CoA_dehydrogenase_	1.1	4.0	6.1	3.6	3.7	4.6	3.3
950Rv3139	fadE24	4093	12060	3.0	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	3.7	4.0	2.5	2.4	2.4	2.8
228Rv3139	fadE24	5389	15118	2.9	0.4	0.1	acyl-CoA_dehydrogenase_	2.1	3.4	2.4	2.7	2.7	2.8	3.2
272Rv3139	fadE24	4991	12788	2.6	0.2	0.1	acyl-CoA_dehydrogenase_	1.1	2.4	2.6	2.5	2.5	2.6	2.9
949Rv3139	fadE24	2298	5020	2.2	0.3	0.1	acyl-CoA_dehydrogenase_	1.1	2.4	2.5	1.7	2.0	2.3	2.3
948Rv3140	fadE23	3751	13006	3.5	0.4	0.2	acyl-CoA_dehydrogenase_	1.1	3.8	3.5	3.1	3.4	4.1	3.0
227Rv3140	fadE23	4069	12868	3.3	0.5	0.2	acyl-CoA_dehydrogenase_	1.1	4.0	2.6	2.9	3.4	3.2	3.4
2925Rv3140	fadE23	5549	16579	3.2	0.9	0.4	acyl-CoA_dehydrogenase_	1.1	2.8	2.7	3.0	4.9	3.5	2.5
226Rv3140	fadE23	5186	15131	3.1	0.6	0.2	acyl-CoA_dehydrogenase_	1.1	3.6	2.2	2.8	3.6	2.9	3.3
579Rv3161c	-	3053	8560	2.6	1.2	0.5	putative_dioxygenases	1.1	4.7	3.5	2.1	1.8	1.7	1.9
3467Rv3173c	-	2711	5794	2.5	1.1	0.5	transcriptional_regulator_(TetR/AcrR_family)	1.1	3.0	4.4	2.0	2.6	1.9	1.2
4193Rv3182	-	1619	1968	1.6	0.5	0.4		1.1	2.0	1.3	nd	nd	nd	nd
3473Rv3197	-	3442	5599	1.7	0.3	0.1	probable_ABC_transporter	1.1	1.6	1.3	1.8	2.0	2.0	1.3
3428Rv3211	rhIE	7370	12716	1.7	0.2	0.1	probable_ATP-dependent_RNA_helicase	1.1	1.7	1.7	1.6	2.1	1.7	1.7
4263Rv3230c	-	4905	8815	2.0	0.7	0.3	similar_to_various_oxygenases	1.1	2.8	2.8	1.4	1.6	1.4	1.6
1380Rv3240c	secA	6108	12448	2.2	0.7	0.3	SecA,_preprotein_translocase_subunit	1.1	3.4	2.6	1.5	2.0	1.7	1.8
2499Rv3240c	secA	2782	5820	2.1	0.4	0.2	SecA,_preprotein_translocase_subunit	1.1	2.4	2.7	1.6	1.8	2.2	1.8
2501Rv3290c	lat	1876	4511	2.4	1.2	0.5	lysine-e_aminotransferase	1.1	3.7	4.1	1.5	1.4	1.9	1.8
3794Rv3290c	lat	2540	4814	1.9	0.8	0.3	lysine-e_aminotransferase	1.1	2.6	3.2	1.4	1.5	1.5	1.3
601Rv3334	-	3009	5762	1.9	1.2	0.5	transcriptional_regulator_(MerR_family)	1.1	3.1	3.8	1.1	1.2	1.1	1.2
3826Rv3367	PE_PGRS	3266	5498	1.7	0.5	0.2		2.1	2.5	nd	1.4	1.7	1.4	1.5
1277Rv3371	-	2122	3471	1.6	0.2	0.1		1.1	2.0	1.8	1.5	1.5	1.3	1.6
4145Rv3405c	-	4261	7413	1.8	0.1	0.1	putative_transcriptional_regulator	1.1	1.8	1.9	1.6	1.9	1.6	1.8
3423Rv3406	-	5020	16438	3.4	0.7	0.3	putative_dioxygenase	1.4	2.3	4.1	3.8	3.7	4.0	2.7
3418Rv3418c	groES	10234	17599	2.3	1.7	0.7	10_kD_chaperone	1.1	4.4	4.8	1.2	1.4	1.1	1.1
533Rv3424c	-	2918	6528	2.2	0.6	0.2		1.1	3.1	2.5	1.6	2.2	1.6	2.2
1254Rv3425	PPE	5179	7891	1.5	0.5	0.2		1.1	2.0	2.2	1.4	1.2	1.1	1.3
190Rv3429	PPE	5263	8260	1.5	0.4	0.2		1.1	2.1	1.9	1.1	1.2	1.2	1.2
3900Rv3461c	rpmJ	8974	14514	1.7	0.4	0.1	50S_ribosomal_protein_L36	1.1	2.1	2.1	1.3	1.8	1.4	1.4
3903Rv3467	REP	3876	5658	1.5	0.2	0.1		1.1	1.6	1.8	1.2	1.6	1.4	1.4
2037Rv3503c	fdxD	5046	9120	1.8	0.4	0.2	probable_ferredoxin	1.1	2.5	2.0	1.4	1.5	1.4	1.7
4925Rv3515c	fadD19	2007	3124	1.5	0.3	0.1	acyl-CoA_synthase	1.1	1.9	1.8	1.3	1.2	1.6	1.3
5649Rv3520c	-	2831	4431	1.6	0.2	0.1	probable_coenzyme_F420-dependent_enzyme	1.1	1.7	1.7	1.3	1.7	1.5	1.7
157Rv3526	-	4441	9057	2.0	0.9	0.4	putative_phthalate_oxygenase	1.1	3.2	3.1	1.3	1.2	1.5	1.5
3041Rv3534c	-	2779	3994	1.5	0.4	0.2	4-hydroxy-2-oxovalerate_aldolase	1.1	1.9	2.2	1.2	1.5	1.2	1.1
3761Rv3537	-	1703	3509	2.0	0.6	0.2	3-oxosteroid_1-dehydrogenase	1.1	2.8	2.6	1.7	1.6	1.8	1.5

3039 Rv3538	ufaA2	2247	3639	1.6	0.3	0.1	unknown_fatty_acid_methyltransferase	1.1	2.1	1.5	1.3	1.7	1.5	1.6
896 Rv3557c	-	2993	4422	1.5	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.8	1.7	1.3	1.5	1.3	1.2
902 Rv3581c	-	4607	6759	1.5	0.1	0.0	YGBB/_YACN	1.1	1.5	1.5	1.3	1.6	1.4	1.5
4160 Rv3596c	clpC	8329	13569	1.7	0.3	0.1	ATP-dependent_Clp_protease	2.1	2.0	1.7	1.4	1.9	1.5	1.4
3438 Rv3597c	lsr2	6385	9461	1.5	0.4	0.2		1.1	2.0	1.9	1.0	1.3	1.3	1.4
5007 Rv3603c	-	2400	4768	2.0	0.7	0.3		1.1	3.0	3.0	1.4	1.6	1.6	1.6
550 Rv3609c	folE	3494	5642	1.6	0.2	0.1	GTP_cyclohydrolase_I_	1.1	1.5	1.4	1.6	1.8	1.7	1.8
1271 Rv3610c	ftsH	5484	10543	2.0	0.3	0.1	inner_membrane_protein,_chaperone	1.1	2.5	2.1	1.7	1.9	1.8	1.7
1027 Rv3642c	-	7318	11124	1.5	0.0	0.0		1.1	1.5	1.5	1.5	1.6	1.5	1.6
304 Rv3645	-	4354	8517	2.0	0.2	0.1	probable_transmembrane_protein	1.1	2.0	1.8	1.8	2.0	1.9	2.3
5330 Rv3706c	-	8818	12617	1.5	0.4	0.2		1.1	1.1	1.2	1.4	2.2	1.4	1.7
2444 Rv3710	leuA	2929	5451	1.9	0.2	0.1	2-isopropylmalate_synthase	1.4	1.9	1.9	1.7	1.8	2.2	1.9
4610 Rv3722c	-	6141	9717	1.6	0.3	0.2		1.1	1.9	2.0	1.4	1.4	nd	1.2
2796 Rv3765c	-	3558	8199	2.5	0.7	0.3	two-component_response_regulator	1.1	1.5	1.9	2.2	3.3	3.2	2.7
2075 Rv3766	-	2747	6757	2.5	0.2	0.1		1.1	2.7	2.5	2.2	2.6	2.4	2.4
2797 Rv3767c	-	2854	9036	3.3	1.2	0.5		1.1	2.1	2.1	3.0	5.2	3.6	4.0
1509 Rv3769	-	5805	9130	1.6	0.1	0.0	possible_coiled-coil_protein	1.1	1.6	1.4	1.6	1.7	1.5	1.7
4397 Rv3782	rfbE	3824	6670	1.7	0.1	0.0	similar_to_rhamnosyl_transferase	1.1	1.8	1.7	1.7	1.7	1.6	1.8
1511 Rv3786c	-	3594	5951	1.6	0.4	0.1		1.1	2.0	2.1	1.6	1.2	1.5	1.3
2236 Rv3796	atsH	2336	3595	1.5	0.1	0.0	proable_arylsulfatase	1.1	1.6	1.6	1.5	1.5	1.6	1.4
4961 Rv3802c	-	5667	10495	1.9	0.2	0.1		1.1	1.7	1.9	2.0	2.1	1.9	1.5
890 Rv3824c	papA1	7714	12349	1.6	0.2	0.1	PKS-associated_protein,_unknown_function_	1.1	1.6	1.6	1.4	2.0	1.6	1.6
5142 Rv3837c	-	4189	6334	1.5	0.2	0.1	putative_phosphoglycerate_mutase	1.1	1.3	1.3	1.6	1.7	1.7	1.6
5139 Rv3843c	-	4191	6904	1.7	0.2	0.1	probable_membrane_protein	1.1	1.5	1.5	1.6	1.8	1.7	2.0
1533 Rv3848	-	3138	4834	1.5	0.3	0.1	probable_membrane_protein	1.1	1.7	2.0	1.3	1.5	1.4	1.3
2252 Rv3853	menG	2580	5037	1.9	0.9	0.4	S-adenosylmethionine:2-demethylmenaquinone_	1.1	2.5	3.4	1.2	1.3	1.6	1.2
1530 Rv3854c	-	4521	15838	3.6	1.2	0.5	probable_monooxygenase	1.1	5.8	3.6	2.7	3.7	3.0	2.8
2251 Rv3855	-	1851	6615	3.4	1.8	0.7	putative_transcriptional_regulator	1.1	4.5	6.5	1.9	2.3	2.4	2.6
5137 Rv3859c	gltB	5374	8290	1.6	0.2	0.1	ferredoxin-dependent_glutamate_synthase	1.4	1.4	1.4	1.5	1.8	1.9	1.7
4971 Rv3866	-	8708	13949	1.6	0.1	0.0		1.1	1.5	1.7	1.5	1.6	1.7	1.7
2800 Rv3867	-	5111	8676	1.7	0.3	0.1		1.1	2.0	2.1	1.5	1.6	1.5	1.6
2081 Rv3872	PE	2320	4205	1.8	0.6	0.2		1.1	2.7	2.4	1.3	1.8	1.4	1.3
2803 Rv3873	PPE	3905	6487	1.6	0.4	0.2		1.1	2.0	1.9	1.5	1.0	1.5	1.8
2129 Rv3879c	-	2997	5891	2.0	0.1	0.0	N-terminus_is_repetitive_and_highly_Proline-rich	1.1	2.0	1.9	nd	2.0	2.1	2.2