

Table 5: Genes induced in *Mycobacterium tuberculosis* H37Rv sigE mutant strain (ST28) 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	Square	root N	N	Individual array ratios (CH2/CH1)					
			Average		CH2/CH1	StD	SEM						Biol. Set 1		Biol. Set 2		Biol. Set 3	
			CH1	CH2									mi1031	mi537	mi1014	mi1019	mi1025	mi609
Cye3	Cye5	Induced							F									
3318Rv0005	gyrB		3536	9562	2.9	0.5	0.2	DNA_gyrase_subunit_B	1.1	2	6	2.2	2.5	3.4	3.3	2.8	3.0	
1494Rv0013	pabA		3807	8918	2.3	0.4	0.2	p-aminobenzoate_synthase_glutamine_amidotransferase	1.1	2	6	2.8	2.4	2.1	1.5	2.5	2.2	
2216Rv0014c	pknB		2312	5877	2.7	0.8	0.3	serine-threonine_protein_kinase	1.1	2	6	2.0	2.9	2.2	4.1	2.9	2.2	
1495Rv0015c	pknA		6280	17696	2.9	0.4	0.2	serine-threonine_protein_kinase	2.6	2	6	2.5	2.6	2.9	3.6	2.6	3.1	
2217Rv0016c	pbpA		4067	22525	5.8	1.3	0.5	penicillin-binding_protein	1.1	2	6	5.8	6.9	7.2	6.3	3.6	5.3	
1496Rv0017c	rodA		7078	28757	4.2	0.7	0.3	FtsW/RodA/SpovE_family	1.1	2	6	4.4	5.1	4.4	4.0	3.2	3.8	
1497Rv0019c	-		4108	7767	1.9	0.1	0.1		1.1	2	6	1.9	1.8	1.9	2.0	2.1	1.8	
3708Rv0045c	-		2032	4070	2.0	0.4	0.2	possible_dihydrolipoamide_acetyltransferase	1.1	2	6	1.5	2.6	1.8	2.1	1.9	2.1	
2987Rv0046c	-		13913	23857	1.8	0.4	0.2		1.1	2	6	1.5	1.5	1.9	2.5	1.6	1.7	
3709Rv0047c	-		2863	10675	3.8	0.7	0.3		1.1	2	6	2.9	3.6	3.3	4.5	4.1	4.6	
265Rv0058	dnaB		13741	20665	1.5	0.2	0.1	DNA_helicase_(contains_intein)	2.5	2	6	1.5	1.4	1.5	1.5	1.2	1.8	
5625Rv0060	-		6095	10588	1.8	0.2	0.1		1.1	2	6	1.6	1.6	1.8	2.2	1.6	1.8	
2016Rv0061	-		7157	19459	2.9	0.7	0.3	unlikely_orf	1.2	2	6	1.9	2.3	3.2	4.1	3.1	2.8	
2739Rv0064	-		2595	5534	2.1	0.6	0.3	possible_membrane_protein	1.1	2	6	2.9	2.9	2.0	1.7	1.6	1.7	
2740Rv0066c	icd2		7642	14856	1.9	0.1	0.0	isocitrate_dehydrogenase	1.1	2	6	2.0	1.9	1.9	1.9	1.9	2.1	
2019Rv0067c	-		1746	3423	1.9	0.5	0.2	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	2.1	2.6	2.3	1.4	1.5	1.6	
2741Rv0068	-		1697	7165	4.6	2.1	0.9	probable_oxidoreductase	1.1	2	6	2.8	3.0	8.7	4.5	4.3	4.5	
477Rv0088	-		4254	8464	2.0	0.4	0.2		1.1	2	6	1.6	1.7	2.2	1.7	2.1	2.6	
1202Rv0094c	REP		5276	13964	2.7	0.3	0.1		1.1	2	6	3.2	2.6	2.9	2.5	2.5	2.2	
2042Rv0109	PE_PGRS		2413	6715	2.9	1.1	0.4		2.3	2	6	2.3	1.9	2.6	2.4	4.6	3.9	
2765Rv0112	gca		3222	4975	1.5	0.2	0.1	probable_GDP-mannose_dehydratase	1.1	2	6	1.7	1.7	1.6	1.3	1.3	1.6	
2767Rv0116c	-		4142	8314	2.0	0.5	0.2		1.2	2	6	1.5	1.4	2.4	1.7	2.5	2.4	
2553Rv0122	-		1887	3639	1.9	0.4	0.2		1.1	2	6	1.9	1.9	2.7	1.4	1.7	2.1	
1832Rv0123	-		2765	4130	1.6	0.3	0.1		1.1	2	6	1.2	1.5	1.9	1.5	1.9	1.5	
4866Rv0146	-		2761	14320	5.5	1.3	0.5		1.1	2	6	3.7	4.0	6.5	6.1	5.6	6.7	
5651Rv0158	-		3992	5994	1.5	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.4	2	6	1.2	1.4	1.6	1.4	1.6	1.8	
4930Rv0159c	PE		3821	5983	1.6	0.2	0.1		1.1	2	6	1.6	1.9	1.4	1.5	1.4	1.5	
3153Rv0182c	sigG		2997	5063	1.7	0.2	0.1	sigma-70_factors_ECF_subfamily_	1.1	2	6	1.7	1.9	1.7	1.5	1.5	1.6	
4363Rv0186	bglS		4849	11489	3.4	0.4	0.2	b-glucosidase	1.1	2	5	nd	2.8	3.5	3.4	4.0	3.3	
4365Rv0190	-		7060	20840	3.3	1.1	0.5		1.1	2	6	2.2	2.5	3.8	5.4	2.9	3.2	
5654Rv0195	-		1609	7926	4.5	2.7	1.1	transcriptional_regulator_(LuxR/UhpA_family)	1.1	2	6	6.7	8.7	4.1	1.9	2.4	3.0	
4933Rv0196	-		2168	6980	3.3	1.1	0.4	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	2.0	2.3	4.2	2.9	3.5	4.7	

5655Rv0197	-	2585	6558	2.4	0.7	0.3		1.1	2	6	1.6	2.1	3.5	2.0	2.7	3.0
2335Rv0211	pckA	5124	15824	3.3	1.2	0.5	phosphoenolpyruvate_carboxykinase_	1.1	2	6	1.8	1.9	4.0	4.5	3.7	3.9
1614Rv0212c	nadR	2529	3541	1.5	0.3	0.1	similar_to_E.coli_NadR	1.1	2	6	1.2	1.4	1.9	1.8	1.2	1.3
2336Rv0213c	-	3129	4579	1.5	0.1	0.0	some_similarity_to_methyltransferases	1.1	2	6	1.5	1.6	1.5	1.4	1.5	1.3
4505Rv0229c	-	3623	6230	1.7	0.2	0.1	could_be_shortened	1.1	2	6	1.8	1.6	1.6	1.8	1.5	1.9
3129Rv0238	-	2849	4615	1.6	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.6	1.4	1.6	1.4	1.6	1.9
3130Rv0240	-	2006	2925	1.5	0.1	0.0		1.1	2	6	1.6	1.5	1.4	1.4	1.4	1.3
3132Rv0244c	fadE5	3324	25559	13.6	6.7	2.8	acyl-CoA_dehydrogenase_	1.1	2	6	11.2	13.4	24.0	16.0	13.6	3.3
3854Rv0245	-	2464	4264	1.7	0.3	0.1	probable_monooxygenase	1.1	2	6	1.7	1.8	2.3	1.2	1.6	1.7
3133Rv0246	-	4377	9833	2.1	0.7	0.3	probable_membrane_transport_protein	1.1	2	6	2.9	3.0	1.7	1.8	1.5	1.8
4858Rv0256c	PPE	5837	10752	1.9	0.1	0.1		1.1	2	6	1.8	1.9	2.0	2.0	1.7	1.8
3204Rv0265c	fecB3	7491	12207	1.6	0.1	0.0	iron_transport_protein_FeIII_dicitrate_transporter	1.1	2	6	1.6	1.7	1.7	1.6	1.5	1.7
170Rv0267	narJ	5146	8213	1.6	0.2	0.1	similar_to_nitrite_extrusion_protein_2	1.1	2	6	1.7	1.7	1.6	1.4	1.4	1.8
894Rv0272c	-	7909	11655	1.5	0.4	0.1		1.1	2	6	1.9	1.8	1.2	1.2	1.1	1.7
251Rv0274	-	3215	8401	2.6	0.7	0.3	contains_extradiol_ring-cleavage_dioxygenases_sig	1.1	2	6	3.2	3.7	2.2	1.9	2.0	2.4
252Rv0275c	fadD27	7770	16112	2.1	0.4	0.2	acyl-CoA_synthase	1.1	2	6	1.8	2.9	2.1	2.0	1.7	2.1
974Rv0276	-	9702	14882	1.5	0.2	0.1		1.1	2	6	1.6	1.8	1.4	1.5	1.4	1.5
3135Rv0277c	-	4682	15358	3.3	0.3	0.1		1.1	2	6	3.3	3.9	3.3	3.3	3.2	3.0
3205Rv0279c	PE_PGRS	5326	7652	1.5	0.1	0.1		2.2	2	6	1.3	1.4	1.5	1.6	1.4	1.6
3858Rv0280	PPE	2496	5982	2.4	0.2	0.1		2.1	2	6	2.3	2.5	2.1	2.3	2.5	2.6
3859Rv0282	-	4169	12336	3.0	0.2	0.1		1.1	2	6	2.7	3.3	3.0	2.9	2.9	3.1
4849Rv0298	-	7104	13606	1.8	0.3	0.1		1.1	2	6	1.5	1.6	2.1	1.9	1.9	2.2
5571Rv0299	-	3223	4986	1.5	0.3	0.1		1.1	2	6	1.3	1.3	1.8	1.4	1.3	2.0
1962Rv0300	-	2908	5816	2.0	0.3	0.1		1.1	2	6	1.8	2.0	1.8	1.6	2.2	2.4
2684Rv0301	-	3157	7159	2.3	0.3	0.1		1.1	2	6	2.1	2.2	2.9	2.3	2.1	2.2
1963Rv0302	-	1858	3043	1.7	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.5	1.8	1.7	2.0	1.4	1.8
1968Rv0324	-	1748	4558	2.6	0.6	0.2	putative_transcriptional_regulator	1.1	2	6	1.7	2.5	2.7	2.6	3.2	3.2
2691Rv0327c	-	2036	4748	2.4	0.8	0.3	cytochrome_P-450_monooxygenase	1.1	2	6	2.5	2.1	3.9	1.9	2.0	1.8
2692Rv0329c	-	2980	4769	1.6	0.2	0.1		1.1	2	6	1.5	1.4	2.1	1.6	1.6	1.5
126Rv0339c	-	2630	4122	1.6	0.3	0.1		1.1	2	6	1.4	1.4	1.7	1.5	1.3	2.2
1041Rv0340	-	2033	3529	1.8	0.4	0.1		1.1	2	6	1.5	1.5	2.4	1.8	1.8	1.9
848Rv0340	-	2700	4246	1.6	0.3	0.1		1.1	2	6	1.3	1.4	1.8	1.9	1.5	1.9
5126Rv0355c	PPE	6211	14785	2.4	0.3	0.1		2.5	2	6	2.1	2.9	2.5	2.6	2.1	2.3
3142Rv0372c	-	4075	6695	1.7	0.2	0.1		2.5	2	6	1.6	1.4	1.7	2.0	1.7	1.8
260Rv0384c	clpB	3550	19540	5.7	1.9	0.8	heat_shock_protein	1.1	2	6	4.2	4.9	6.7	4.8	4.4	9.0
458Rv0411c	glnH	5850	10311	1.7	0.6	0.3	putative_glutamine_binding_protein	1.1	2	6	2.5	2.5	1.4	1.2	1.2	1.4
1180Rv0412c	-	5439	14022	2.5	0.8	0.3	unknown_probable_membrane_protein	1.1	2	6	3.8	3.2	2.2	2.1	2.0	2.0
462Rv0419	lpqM	4671	8699	1.9	0.2	0.1	possible_zinc_metallopeptidase_	1.1	2	6	1.7	1.7	2.3	1.6	1.9	2.1
1184Rv0420c	-	5150	8601	1.7	0.1	0.0		1.1	2	6	1.7	1.6	1.7	1.6	1.5	1.8
264Rv0440	groEL2	13759	28731	2.3	0.9	0.4	60_kD_chaperonin_2	1.4	2	6	2.9	3.9	1.9	2.2	1.5	1.7

3151Rv0450c	mmpL4	6789	12046	1.7	0.7	0.3	conserved_large_membrane_protein	1.1	2	6	2.6	2.7	1.3	1.2	1.1	1.3
3873Rv0451c	mmpS4	4151	14463	3.5	1.2	0.5	conserved_small_membrane_protein	1.1	2	6	4.9	5.2	2.8	2.4	2.6	3.2
1324Rv0455c	-	13615	20942	1.6	0.2	0.1	N-term_hydrophobic_stretch	1.1	2	6	1.5	1.4	1.8	2.0	1.4	1.5
1329Rv0465c	-	4420	9018	2.1	0.7	0.3	transcriptional_regulator_(PbsX/Xre_family)	1.1	2	6	1.3	1.2	3.1	2.2	2.5	2.2
4212Rv0467	aceA	9655	13992	1.7	0.9	0.4	isocitrate_lyase	1.1	2	6	0.6	0.4	2.0	2.2	2.4	2.5
4213Rv0469	umaA1	9475	17005	1.8	0.4	0.1	unknown_mycolic_acid_methyltransferase	1.1	2	6	1.4	1.4	2.1	2.3	1.8	1.9
3933Rv0469	umaA2	13902	22862	1.7	0.3	0.1	unknown_mycolic_acid_methyltransferase	1.1	2	6	1.4	1.5	2.0	2.0	1.5	1.7
3492Rv0470c	umaA2	6882	13152	1.9	0.2	0.1	unknown_mycolic_acid_methyltransferase	1.1	2	6	1.6	1.8	1.9	2.1	1.9	2.2
3494Rv0474	-	1690	19499	11.9	2.8	1.1	transcriptional_regulator_(PbsX/Xre_family)	1.1	2	6	9.8	10.4	16.5	12.4	9.0	13.4
1537Rv0475	-	3779	16861	4.9	1.2	0.5	possible_exported_protein	1.1	2	6	4.0	3.8	6.7	6.1	4.7	4.4
2259Rv0476	-	2429	3930	1.6	0.1	0.1	unknown_hydrophobic_protein	1.1	2	6	1.4	1.7	1.7	1.6	1.5	1.8
1538Rv0477	-	2726	5346	2.0	0.4	0.2	possible_exported_protein	1.1	2	6	2.4	1.7	2.6	1.6	2.0	2.0
4423Rv0483	-	11024	15645	1.5	0.3	0.1		1.1	2	6	1.1	1.1	1.5	1.8	1.7	1.6
4424Rv0485	-	4132	13000	3.5	1.1	0.4	transcriptional_regulator_(ROK_family)	1.1	2	6	2.1	2.3	4.8	3.5	4.5	3.7
5146Rv0486	-	2402	3934	1.7	0.3	0.1		1.1	2	6	1.4	1.4	2.2	1.6	1.5	1.9
4428Rv0493c	-	4994	8550	1.6	0.3	0.1		1.2	2	6	1.7	1.5	1.3	1.4	1.8	2.1
327Rv0559c	-	7705	17562	2.4	0.5	0.2	possible_exported	1.1	2	6	1.9	3.2	2.8	2.1	1.9	2.3
1745Rv0559c	-	10077	19801	1.9	0.2	0.1	possible_exported	1.2	2	6	2.1	2.1	1.9	1.7	1.8	2.0
2467Rv0560c	-	1575	14242	9.1	1.8	0.7	methyl_transferase	1.1	2	6	9.6	9.4	12.1	7.1	8.4	7.8
3499Rv0584	-	1575	2423	1.5	0.4	0.2		1.1	2	6	1.6	2.1	1.7	1.3	1.0	1.4
1174Rv0586	-	5247	7855	1.5	0.3	0.1	transcriptional_regulator_(GntR_family)	1.3	2	6	1.9	1.5	1.7	1.2	1.3	1.3
4057Rv0596c	-	1827	3455	1.9	0.4	0.2		1.1	2	6	2.1	1.6	2.2	1.7	1.4	2.4
329Rv0598c	-	4588	8128	1.7	0.2	0.1		1.4	2	6	2.0	1.8	1.7	1.5	1.6	1.7
4056Rv0598c	-	2933	4708	1.6	0.3	0.1		1.4	2	6	2.0	1.7	1.8	1.3	1.3	1.5
447Rv0609	-	7907	11647	1.5	0.2	0.1		1.2	2	6	1.5	1.3	1.8	1.5	1.5	1.4
4053Rv0615	-	2532	4531	1.8	0.1	0.1	possible_membrane_protein	1.1	2	6	1.8	1.6	2.0	1.8	1.8	1.8
3331Rv0616c	-	1575	5208	3.1	0.8	0.3		1.1	2	6	4.2	3.5	2.9	1.8	2.6	3.6
3213Rv0616c	-	2155	4121	1.8	0.3	0.1		1.1	2	6	2.2	1.7	1.6	1.5	1.6	2.1
3889Rv0616c	-	1583	2320	1.5	0.3	0.1		1.1	2	6	1.4	1.9	1.6	1.2	1.5	1.1
4052Rv0617	-	3635	7414	2.0	0.1	0.1		1.1	2	6	2.2	2.0	2.2	1.8	1.9	2.0
3330Rv0618	galT'	6316	13693	2.3	0.3	0.1	galactose-1-phosphate_uridylyltransferase_N-term	2.1	2	6	2.2	2.0	2.3	2.7	2.3	2.0
4276Rv0634c	-	9928	14427	1.5	0.2	0.1	putative_glyoxylase_II	1.1	2	6	1.2	1.2	1.7	1.7	1.6	1.5
669Rv0638	secE	5234	12747	2.5	0.4	0.2	SecE_preprotein_translocase	1.1	2	6	2.2	2.0	2.8	2.3	2.4	3.0
3217Rv0638	secE	7031	14924	2.2	0.4	0.2	SecE_preprotein_translocase	1.1	2	6	1.6	1.9	2.5	2.3	2.4	2.6
3940Rv0641	rplA	10418	16487	1.6	0.1	0.1	50S_ribosomal_protein_L1	1.1	2	6	1.5	1.8	1.5	1.4	1.5	1.6
670Rv0641	rplA	10569	16506	1.6	0.2	0.1	50S_ribosomal_protein_L1	1.1	2	6	1.3	1.6	1.6	1.5	1.6	1.8
2929Rv0644c	mmaA2	9941	16175	1.7	0.4	0.2	methoxymycolic_acid_synthase_2	2.5	2	6	1.3	1.3	1.9	2.3	1.9	1.8
5100Rv0654	-	1947	5256	2.7	1.0	0.4	putative_dioxygenase	1.4	2	6	1.9	2.2	4.1	2.1	1.8	4.0
4222Rv0675	echA5	1712	2636	1.5	0.7	0.3	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	2	6	2.5	2.0	0.7	1.2	1.2	1.1
3501Rv0676c	mmpL5	2570	16733	6.5	0.6	0.3	conserved_large_membrane_protein	1.1	2	6	7.1	7.0	7.0	6.1	5.6	6.2

4223Rv0677c	mmpS5	2358	23423	10.0	2.2	0.9	conserved_small_membrane_protein	1.1	2	6	8.6	12.4	10.2	11.1	6.4	11.6
614Rv0678	-	3269	20143	6.4	1.7	0.7		1.1	2	6	5.5	5.7	7.1	7.7	4.0	8.7
1336Rv0679c	-	2360	9672	4.1	0.4	0.2	possible_membrane_protein	1.1	2	6	4.5	4.4	4.3	3.6	3.6	4.2
615Rv0680c	-	2655	7249	2.7	0.6	0.2	possible_membrane_protein	1.1	2	6	3.2	3.2	2.3	2.1	1.9	3.2
1337Rv0681	-	3550	6270	1.8	0.3	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.8	1.4	2.0	1.8	1.7	2.1
616Rv0682	rpsL	6574	19434	3.3	1.1	0.5	30S_ribosomal_protein_S12	1.1	2	6	2.2	2.3	3.9	4.8	2.5	4.2
1338Rv0683	rpsG	5259	11504	2.2	0.4	0.2	30S_ribosomal_protein_S7	1.1	2	6	1.9	1.7	2.6	2.3	2.1	2.8
617Rv0684	fusA	10068	16653	1.7	0.3	0.1	elongation_factor_G	1.1	2	6	1.5	1.5	1.9	1.9	1.4	2.1
4769Rv0687	-	3039	5217	1.7	0.2	0.1	putative_dehydrogenase,_SDR_family	1.1	2	6	1.5	1.8	1.8	1.8	1.5	2.0
4771Rv0691c	-	4868	9139	1.9	0.5	0.2	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.4	1.7	2.4	1.3	2.4	2.5
3892Rv0698	-	3782	8959	2.6	1.0	0.4		1.2	2	6	1.3	1.4	3.7	3.2	2.7	3.1
2608Rv0698	-	2786	4292	1.8	0.5	0.2		1.3	2	6	1.1	1.3	2.1	2.2	2.4	1.7
2610Rv0700	rpsJ	9304	12993	1.5	0.4	0.2	30S_ribosomal_protein_S10	1.1	2	6	1.0	1.0	1.8	1.9	1.4	1.8
4776Rv0711	atsA	2105	30049	17.7	10.5	4.3	arylsulfatase	1.1	2	6	9.7	10.7	37.7	20.5	14.7	12.6
5498Rv0712	-	2799	16971	7.0	2.8	1.1		1.1	2	6	3.9	7.3	11.5	5.2	5.1	8.8
1895Rv0725c	-	1728	3150	1.9	0.3	0.1		1.1	2	6	1.5	2.2	2.2	1.7	1.9	1.6
2617Rv0726c	-	4143	16946	4.0	0.5	0.2		1.1	2	6	3.7	3.6	4.7	3.8	3.7	4.6
4778Rv0727c	fucA	1719	2254	1.5	0.2	0.1	L-fucose_phosphate_aldolase	1.1	2	3	1.4	1.7	nd	nd	nd	1.5
4284Rv0743c	-	1715	2262	1.5	0.3	0.1		1.1	2	4	nd	nd	1.6	1.3	1.4	1.9
622Rv0749	-	4681	14836	3.1	0.4	0.1		1.4	2	6	3.4	3.1	3.3	2.7	2.8	3.6
4286Rv0750	-	4035	6519	1.6	0.3	0.1		2.1	2	6	1.5	1.2	2.0	1.5	1.6	1.8
1344Rv0750	-	3927	5614	1.5	0.3	0.1		1.1	2	6	1.2	1.1	1.9	1.6	1.5	1.5
624Rv0753c	mmsA	2805	6007	2.2	0.6	0.2	methylmalmonate_semialdehyde_dehydrogenase	1.1	2	6	1.5	1.7	2.9	2.1	2.5	2.8
625Rv0755c	PPE	9250	14060	1.6	0.3	0.1		1.4	2	6	1.8	1.6	1.8	1.5	1.2	1.5
632Rv0764c	-	4195	6556	1.5	0.2	0.1	possible_lanosterol_14-demethylase_cytochrome_P450	1.4	2	6	1.6	1.9	1.5	1.3	1.3	1.8
1354Rv0767c	-	2515	3701	1.5	0.5	0.2		1.1	2	6	1.9	2.1	1.6	1.0	1.2	1.1
1930Rv0781	ptrBb	7005	10745	1.6	0.2	0.1	protease_II,_b_subunit	1.1	2	6	1.3	1.3	1.6	1.7	1.9	1.6
5537Rv0788	purQ	4027	9068	2.3	0.8	0.3	phosphoribosylformylglycinamide_synthase_I	1.2	2	6	1.5	1.4	3.6	2.0	2.6	2.6
4816Rv0789c	-	2547	18860	7.5	4.0	1.6		1.2	2	6	3.2	3.6	12.6	7.5	6.3	11.6
1347Rv0791c	-	2554	4052	1.6	0.2	0.1	possible_monooxygenase	1.1	2	6	1.7	1.6	1.8	1.9	1.5	1.3
546Rv0806c	cpsY	4093	7735	1.9	0.3	0.1	probable_UDP-glucose-4-epimerase	1.1	2	6	1.7	1.7	2.4	1.7	2.1	2.1
3511Rv0809	purM	4682	8932	1.9	0.4	0.2	5'-phosphoribosyl-5-aminoimidazole_synthase	1.1	2	6	2.5	2.2	1.6	1.6	1.6	1.8
4233Rv0810c	-	5621	10471	1.9	0.2	0.1		1.1	2	6	1.7	1.8	1.9	1.7	1.8	2.2
3513Rv0813c	-	1680	3428	2.1	0.6	0.2		1.1	2	6	1.5	1.8	2.6	1.9	1.7	3.0
4235Rv0814c	sseC2	2474	4172	1.7	0.5	0.2	thiosulfate_sulfurtransferase	1.1	2	6	1.4	1.1	1.9	1.6	1.8	2.4
1685Rv0815c	cysA2	6667	29772	4.7	1.1	0.4	thiosulfate_sulfurtransferase	1.1	2	6	3.3	4.0	6.1	5.9	4.5	4.5
2408Rv0818	-	5130	7503	1.5	0.3	0.1	two-component_response_regulator	1.1	2	6	1.7	1.6	1.7	0.9	1.6	1.5
2411Rv0824c	desA1	10648	17274	1.7	0.2	0.1	acyl-[ACP]_desaturase_	1.1	2	6	1.5	1.9	1.6	1.9	1.5	1.6
682Rv0826	-	1684	7087	3.9	2.2	0.9		1.1	2	6	4.8	8.0	3.3	2.1	2.7	2.5
4573Rv0827c	-	3167	4866	1.6	0.4	0.2	transcriptional_regulator_(ArsR_family)	1.1	2	6	2.2	2.0	1.3	1.3	1.3	1.3

5296Rv0830	-	2429	18777	8.2	2.8	1.1		1.1	2	6	4.5	10.2	11.6	6.5	6.4	9.9
4578Rv0837c	-	1894	2966	1.6	0.2	0.1		1.1	2	6	1.5	1.7	1.5	1.8	1.3	1.7
1691Rv0840c	-	1647	4412	2.5	1.5	0.6	probable_proline_iminopeptidase	1.1	2	6	4.0	4.7	2.3	1.1	1.4	1.5
2413Rv0841c	-	1575	4771	2.8	1.3	0.5		1.1	2	6	4.8	3.9	2.3	1.7	2.4	1.6
1694Rv0846c	-	3825	11864	3.1	0.3	0.1	similar_to_several_L-ascorbate_oxidases	1.1	2	6	3.4	3.3	3.2	2.8	2.7	2.9
2416Rv0847	lpqS	1591	5820	3.6	0.5	0.2	lipoprotein	1.1	2	6	3.5	3.0	4.0	3.0	4.1	4.2
1695Rv0848	cysM3	2871	10170	3.5	0.6	0.2	putative_cysteine_synthase	1.1	2	6	3.4	2.8	4.2	2.8	3.8	4.0
5304Rv0859	fadA	6466	20077	3.4	1.0	0.4	b_oxidation_complex,_b_subunit	1.1	2	6	2.0	2.7	4.5	4.2	3.0	3.9
4583Rv0860	fadB	6801	21190	3.2	0.4	0.2	b_oxidation_complex,_a_subunit_(multiple_activities)	1.1	2	6	2.4	3.5	3.6	3.1	3.3	3.3
144Rv0885	-	6739	12385	1.9	0.6	0.3	unknown_transmembrane_protein	1.1	2	6	1.1	1.2	2.6	2.2	2.2	2.4
3029Rv0892	-	3205	4666	1.5	0.2	0.1	putative_monooxygenase	1.1	2	6	1.4	1.2	1.8	1.6	1.6	1.5
4283Rv0918	-	2351	3325	1.5	0.2	0.1		1.1	2	5	1.3	nd	1.7	1.4	1.3	1.6
1734Rv0921	IS1535	2611	5660	2.1	0.5	0.2	resolvase	1.1	2	6	2.0	1.6	2.2	1.6	2.2	2.9
2460Rv0930	pstA1	2948	5120	1.6	0.8	0.3	PstA_component_of_phosphate_uptake	1.1	2	6	2.6	2.7	1.2	1.3	1.0	1.1
1624Rv0932c	pstS	15288	27163	1.8	0.3	0.1	PstS_component_of_phosphate_uptake	1.1	2	6	1.6	2.2	2.0	2.0	1.6	1.6
4031Rv0940c	-	3842	11191	2.9	0.1	0.1	probable_monooxygenase	1.1	2	6	2.8	2.7	2.8	2.9	2.9	3.1
3306Rv0947c	-	1682	2608	1.5	0.2	0.1		1.2	2	6	1.4	1.7	1.8	1.2	1.4	1.8
4027Rv0948c	-	2942	7213	2.5	0.7	0.3		1.1	2	6	1.9	1.7	3.2	2.2	3.0	3.1
3302Rv0967	-	2200	3514	1.6	0.2	0.1		1.1	2	6	1.4	1.4	1.9	1.4	1.8	1.8
4021Rv0972c	fadE12	1751	4838	2.6	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	2	6	3.3	3.4	2.9	1.4	2.1	2.7
1702Rv0973c	accA2	1844	7688	4.0	1.4	0.6	acetyl/propionyl-CoA_carboxylase,_a_subunit	1.1	2	6	5.4	5.7	3.7	2.2	2.9	4.0
3299Rv0973c	accA2	2228	3868	1.7	0.5	0.2	acetyl/propionyl-CoA_carboxylase,_a_subunit	1.3	2	6	1.6	2.8	1.3	1.4	1.5	1.7
2424Rv0974c	accD2	1588	3291	2.2	0.5	0.2	acetyl/propionyl-CoA_carboxylase,_b_subunit	1.1	2	6	1.9	2.3	3.1	2.1	1.8	1.7
4585Rv0975c	fadE13	1909	5009	2.5	0.9	0.4	acyl-CoA_dehydrogenase	1.1	2	6	3.2	3.7	1.9	1.5	1.9	2.7
5307Rv0976c	-	2238	6189	2.7	0.5	0.2		1.4	2	6	2.7	3.5	2.8	2.1	2.2	3.0
4588Rv0981	-	6329	12557	2.0	0.4	0.2	two-component_response_regulator	1.1	2	6	1.7	1.4	2.1	2.2	2.4	2.3
4589Rv0983	-	6815	16980	2.6	0.8	0.3	probable_serine_protease	1.1	2	6	1.6	1.6	3.4	3.2	3.1	2.9
5311Rv0984	moaB2	6484	10811	1.7	0.5	0.2	molybdenum_cofactor_biosynthesis,_protein_B	1.1	2	6	1.1	1.3	1.5	1.6	2.0	2.4
1408Rv0985c	mscL	4675	8860	1.9	0.2	0.1	highly_similar_to_large-conductance_	1.1	2	6	1.8	1.9	2.1	1.6	1.8	2.1
407Rv0990c	-	3910	6371	1.6	0.3	0.1		1.1	2	6	1.6	1.8	1.5	1.2	1.6	1.9
1129Rv0991c	-	3433	13262	4.2	1.7	0.7		1.1	2	6	3.6	3.4	5.5	2.7	2.9	7.0
3292Rv0996	-	4778	10323	2.2	0.3	0.1		1.1	2	6	2.0	1.8	2.7	2.4	2.1	2.3
4014Rv0997	-	5386	23368	4.6	1.0	0.4		1.1	2	6	3.2	4.1	5.0	6.2	3.9	4.8
3293Rv0998	-	3680	8018	2.5	0.9	0.4		1.1	2	6	1.6	1.3	3.4	2.8	2.2	3.6
3294Rv1000	-	2826	4179	1.6	0.3	0.1		1.1	2	6	1.2	1.4	2.2	1.6	1.5	1.5
1155Rv1015c	rplY	5649	10240	1.9	0.7	0.3	50S_ribosomal_protein_L25	1.1	2	6	1.1	1.0	2.9	2.0	2.0	2.3
3433Rv1037c	-	9308	15844	1.7	0.3	0.1		1.1	2	6	1.3	1.5	1.9	1.9	1.9	1.8
3310Rv1038c	-	10021	15714	1.6	0.2	0.1		1.1	2	6	1.3	1.6	1.8	2.0	1.6	1.5
1146Rv1045	-	2919	6251	2.1	0.4	0.2		1.1	2	6	2.2	2.4	2.4	1.6	1.6	2.5
424Rv1046c	-	7970	17187	2.4	0.7	0.3		1.2	2	6	2.0	2.0	3.5	2.7	1.5	2.4

1145Rv1047	IS1081	5170	14950	3.0	0.7	0.3		1.1	2	6	2.6	2.3	4.2	2.6	2.8	3.4
4210Rv1048c	-	1597	8254	5.5	2.5	1.0		1.1	2	6	4.6	2.7	10.1	4.6	4.8	6.3
423Rv1048c	-	3843	7224	1.9	0.4	0.1		1.1	2	6	1.6	1.6	2.2	1.5	1.7	2.4
1662Rv1053c	-	2559	4785	1.8	0.2	0.1		1.1	2	6	1.9	1.8	2.0	1.5	1.7	2.0
1664Rv1057	-	4045	13572	3.8	1.8	0.8		1.1	2	5	1.9	1.9	5.2	nd	4.1	5.8
646Rv1080c	greA	4792	13338	2.9	0.8	0.3	transcription_elongation_factor_G	1.1	2	6	1.9	2.1	3.5	2.6	3.4	3.8
1669Rv1080c	greA	6954	15867	2.6	0.8	0.3	transcription_elongation_factor_G	2.5	2	6	1.6	1.6	3.3	3.0	2.7	3.4
1670Rv1082	-	5776	9032	1.6	0.1	0.0	similar_to_S._lincolnensis_ImbE	1.4	2	6	1.7	1.5	1.6	1.4	1.6	1.6
2395Rv1101c	-	1983	3150	1.6	0.3	0.1	putative_membrane_protein	1.1	2	6	1.6	2.0	1.2	1.5	1.5	1.6
692Rv1101c	-	2045	3124	1.5	0.2	0.1	putative_membrane_protein	1.1	2	6	1.7	1.7	1.5	1.3	1.3	1.5
1674Rv1102c	-	4533	9906	2.1	0.3	0.1		1.1	2	6	2.5	2.5	2.1	1.7	1.9	2.1
1414Rv1103c	-	6156	11539	1.9	0.2	0.1		1.1	2	6	2.1	2.0	2.0	1.7	1.7	1.8
3354Rv1128c	REP	1910	3027	1.6	0.2	0.1		1.1	2	6	1.5	1.9	1.7	1.8	1.4	1.5
4076Rv1129c	-	3293	5413	2.0	0.8	0.3	transcriptional_regulator_(PbsX/Xre_family)	1.1	2	6	1.0	1.0	2.4	2.2	2.2	3.2
3355Rv1130	-	5248	7982	1.9	0.8	0.3		1.1	2	6	0.9	0.9	2.4	2.6	2.3	2.2
4727Rv1150	IS-like	4201	6393	1.6	0.5	0.2		1.1	2	5	1.9	2.3	nd	1.4	1.2	1.3
4728Rv1152	-	4949	8225	1.7	0.1	0.1	transcriptional_regulator_(GntR_family)	1.1	2	5	1.6	1.5	nd	1.8	1.9	1.7
5450Rv1153c	omt	2655	5450	2.0	0.4	0.2	PKS_o-methyltransferase	1.1	2	6	2.0	2.2	2.6	1.4	2.1	1.8
2564Rv1157c	-	2561	3880	1.5	0.2	0.1		2.6	2	6	1.8	1.5	1.4	1.1	1.4	1.4
1845Rv1162	narH	6360	10286	1.5	0.3	0.1	nitrate_reductase_b_chain	1.1	2	6	1.9	1.9	1.1	1.2	1.4	1.5
563Rv1168c	PPE	2410	12959	5.7	1.1	0.4		1.1	2	6	5.4	4.1	6.8	5.2	5.6	7.0
1285Rv1169c	PE	1796	18809	11.4	4.5	1.8		1.1	2	6	7.2	9.3	19.0	12.9	7.3	12.7
4302Rv1171	-	1692	2674	1.5	0.3	0.1	hydrophobic_protein	1.1	2	6	2.1	1.6	1.6	1.1	1.3	1.4
565Rv1172c	PE	4541	8778	1.9	0.2	0.1		1.1	2	6	2.1	1.9	1.6	1.5	2.0	2.1
3448Rv1174c	-	6382	11173	2.3	0.7	0.3		1.2	2	5	1.5	1.5	2.9	2.7	2.7	nd
3581Rv1174c	-	12890	23490	1.9	0.4	0.2		1.1	2	6	1.3	1.9	1.8	2.5	1.7	2.2
4171Rv1177	fdxC	8226	17983	2.3	0.4	0.2	ferredoxin_4Fe-4S	1.1	2	6	1.7	2.4	2.0	3.0	2.3	2.5
643Rv1187	rocA	2420	4472	1.9	0.4	0.2	pyrroline-5-carboxylate_dehydrogenase	1.1	2	6	1.4	1.6	2.6	1.8	2.1	2.1
1481Rv1195	PE	2708	20075	9.2	4.2	1.7		1.1	2	6	4.5	4.6	14.9	12.4	8.6	10.2
2203Rv1196	PPE	6885	14887	2.3	0.7	0.3		1.1	2	6	1.5	1.5	3.3	2.4	2.2	3.0
1483Rv1199c	IS1081	7837	27218	4.0	1.3	0.5		1.1	2	6	2.1	3.1	5.6	4.9	4.1	4.3
4373Rv1216c	-	5739	12514	2.1	0.3	0.1		1.1	2	6	2.5	2.2	1.8	1.8	2.0	2.2
5095Rv1217c	-	2592	4666	1.8	0.4	0.1	probable_integral_membrane_protein	1.1	2	6	1.3	2.0	2.2	1.6	2.0	2.0
5441Rv1218c	-	3270	9172	2.9	0.8	0.3	probable_ABC_transmembrane_transport_protein	1.1	2	6	2.0	2.1	3.9	2.9	3.1	3.7
4720Rv1219c	-	1752	5467	3.2	1.2	0.5	putative_transcriptional_regulator	1.1	2	6	1.7	2.5	4.4	3.0	2.6	4.9
3656Rv1221	sigE	10011	32243	3.5	0.9	0.4	ECF_subfamily_sigma_subunit	1.1	2	6	2.7	3.6	4.2	5.0	3.1	2.6
3458Rv1245c	-	2435	3727	1.6	0.4	0.1	putative_dehydrogenase	1.1	2	6	1.1	1.3	2.0	1.3	1.9	1.8
4818Rv1284	-	4877	13036	2.6	0.5	0.2		1.1	2	6	1.9	2.2	3.2	2.7	2.9	3.0
5540Rv1285	cysD	1781	12980	8.0	3.2	1.3	ATP:sulphurylase_subunit_2	1.1	2	6	4.5	4.4	12.3	8.9	7.3	10.4
4819Rv1286	cysN	2966	19783	6.9	2.0	0.8	ATP:sulphurylase_subunit_1	1.1	2	6	4.3	5.1	9.5	8.5	6.4	7.4

1935Rv1294	thrA	5986	8795	1.5	0.2	0.1	homoserine_dehydrogenase	1.1	2	6	1.8	1.4	1.6	1.4	1.3	1.3
1937Rv1298	rpmE	5443	11285	2.2	0.5	0.2	50S_ribosomal_protein_L31	1.1	2	6	2.1	2.2	2.4	1.4	2.8	2.3
2659Rv1299	prfA	7320	15098	2.1	0.3	0.1	peptide_chain_release_factor_1	1.2	2	6	1.9	1.8	1.9	2.5	1.9	2.5
3565Rv1303	-	6011	8981	1.5	0.4	0.2		1.1	2	6	1.7	2.2	1.4	1.2	1.1	1.4
2225Rv1321	-	3870	7015	1.8	0.3	0.1		1.1	2	6	2.2	2.0	1.5	1.5	2.1	1.5
5111Rv1329c	dinG	1669	2716	1.7	0.5	0.2	probable_ATP-dependent_helicase	1.1	2	6	1.3	1.3	2.7	1.3	1.6	1.9
51Rv1350	fabG2	3101	6421	2.0	0.4	0.2	3-oxoacyl-[ACP]_reductase	1.1	2	6	1.9	2.1	2.4	1.6	1.7	2.5
4288Rv1351	-	2278	3732	1.6	0.3	0.1		1.1	2	6	1.6	1.2	2.0	1.6	1.5	1.8
773Rv1351	-	4445	7051	1.6	0.1	0.1		1.1	2	6	1.7	1.6	1.7	1.7	1.5	1.4
53Rv1354c	-	3152	4691	1.5	0.2	0.1		1.1	2	6	1.5	1.7	1.6	1.3	1.3	1.4
54Rv1356c	-	5890	14322	2.5	0.4	0.2		1.1	2	6	2.0	2.4	3.1	2.2	2.3	2.9
3659Rv1359	-	1980	3770	1.8	0.5	0.2	putative_transcriptional_regulator	1.1	2	6	1.7	2.2	1.9	1.3	1.4	2.5
137Rv1373	-	2653	9382	3.3	1.3	0.5	slight_similarity_to_sulfotransferases	1.1	2	6	5.0	4.9	2.7	2.6	2.1	2.7
138Rv1375	-	5546	13733	2.6	0.6	0.2		1.1	2	6	2.1	2.1	3.6	3.0	2.3	2.7
4780Rv1387	PPE	14034	21028	1.6	0.2	0.1		1.1	2	6	1.5	1.6	1.5	2.0	1.3	1.4
5503Rv1390	-	5156	14486	2.9	0.5	0.2		1.1	2	6	2.3	2.9	3.7	3.0	2.6	3.0
5504Rv1392	metK	3126	12462	4.0	0.8	0.3	S-adenosylmethionine_synthase	1.1	2	6	3.3	3.7	5.4	3.9	3.3	4.5
1897Rv1397c	-	2910	10442	3.7	0.6	0.3		1.1	2	6	4.5	4.1	3.7	3.7	3.1	2.8
2619Rv1398c	-	11997	18054	1.5	0.2	0.1		1.1	2	6	1.5	1.5	1.4	1.9	1.4	1.5
2621Rv1402	priA	1971	3201	1.6	0.2	0.1	putative_primosomal_protein_n'(replication_factor_Y)	1.1	2	6	1.7	1.6	2.0	1.3	1.5	1.6
1900Rv1403c	-	3876	13057	3.5	0.6	0.3	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	2	6	3.3	3.1	4.4	3.3	4.1	2.8
2622Rv1404	-	5996	15654	2.8	0.9	0.4	transcriptional_regulator_(MarR_family)	1.1	2	6	1.8	2.1	3.9	2.9	2.4	3.7
684Rv1405c	-	1728	12816	7.4	2.0	0.8	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	2	6	6.9	9.4	7.9	3.8	8.8	7.7
1901Rv1405c	-	2073	11898	5.9	0.8	0.3	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	2	6	5.6	6.8	6.9	5.3	6.0	4.8
5510Rv1415	ribA2	5301	9244	1.7	0.3	0.1	probable_GTP_cyclohydrolase_II	1.1	2	6	1.7	1.5	1.8	1.2	1.9	2.1
819Rv1419	-	7128	12940	1.9	0.2	0.1		1.1	2	6	1.9	2.0	2.2	1.8	1.6	1.7
2330Rv1442	bisC	5576	8087	1.5	0.2	0.1	biotin_sulfoxide_reductase	1.4	2	6	1.2	1.3	1.5	1.6	1.8	1.5
1298Rv1460	-	1983	3257	1.6	0.2	0.1	putative_transcriptional_regulator	2.6	2	6	1.7	1.7	1.7	1.1	1.6	1.7
577Rv1461	-	7431	23974	3.3	0.6	0.3		1.4	2	6	3.2	2.6	3.7	3.9	2.5	3.8
1299Rv1462	-	3644	9651	2.8	0.7	0.3		1.1	2	6	2.8	2.0	3.9	2.6	2.1	3.2
3528Rv1463	-	3040	9036	2.9	0.7	0.3	ABC-type_transporter	1.4	2	6	2.4	3.1	2.7	2.1	2.9	4.1
4182Rv1464	-	2432	5932	2.4	0.3	0.1	NifS-like_protein	1.1	2	6	2.5	2.2	2.9	1.9	2.4	2.5
4183Rv1466	-	2913	4259	1.5	0.1	0.1		1.1	2	6	1.3	1.4	1.6	1.6	1.6	1.5
3462Rv1467c	fadE15	3895	6844	2.0	0.5	0.2	acyl-CoA_dehydrogenase_	1.1	2	6	2.5	1.9	2.4	2.1	2.2	1.2
1637Rv1475c	acn	8634	13300	1.6	0.3	0.1	aconitate_hydratase	1.1	2	6	1.3	1.1	1.8	1.6	1.9	1.7
1921Rv1492	mutA	1926	3585	1.8	0.4	0.2	methylmalonyl-CoA_mutase,_b_subunit	1.1	2	6	2.0	2.5	2.0	1.4	1.4	1.6
3640Rv1492	mutA	1919	2772	1.5	0.3	0.1	methylmalonyl-CoA_mutase,_b_subunit	1.1	2	6	1.6	1.7	1.9	1.1	1.3	1.1
2643Rv1493	mutB	4282	9870	2.3	0.3	0.1	methylmalonyl-CoA_mutase,_a_subunit	1.1	2	6	2.5	2.7	2.2	2.1	2.0	2.1
2647Rv1501	-	6717	10005	1.5	0.2	0.1		1.1	2	6	1.7	1.5	1.4	1.3	1.3	1.5
3644Rv1526c	-	1945	2920	1.5	0.1	0.1	possible_rhamnosyl/glycosyl_transferase	1.2	2	6	1.5	1.7	1.5	1.5	1.4	1.4

1704Rv1528c	papA4	1839	2823	1.6	0.2	0.1	PKS-associated_protein,_unknown_function	1.1	2	5	1.4	1.7	1.9	nd	1.4	1.7
3126Rv1532c	-	2590	4351	1.7	0.3	0.1		1.1	2	6	1.2	1.4	2.0	1.8	1.8	2.1
3849Rv1535	-	5538	14185	2.9	1.6	0.7		1.1	2	6	0.8	0.9	4.3	3.5	3.4	4.4
999Rv1536	ileS	3026	17182	6.6	3.5	1.4	isoleucyl-tRNA_synthase	1.1	2	6	2.0	2.9	10.7	7.9	6.7	9.1
1595Rv1536	ileS	3464	13183	4.2	1.6	0.6	isoleucyl-tRNA_synthase	1.1	2	6	2.4	2.3	6.2	5.4	4.5	4.4
3128Rv1536	ileS	5756	17034	3.1	0.9	0.4	isoleucyl-tRNA_synthase	1.1	2	6	2.1	1.9	3.5	3.6	3.9	3.5
2312Rv1557	mmpL6	1970	4786	2.4	0.4	0.1	conserved_large_membrane_protein	1.1	2	6	1.8	2.5	2.3	2.6	2.8	2.6
1215Rv1574	-	4163	6282	1.5	0.1	0.0	phiRV1_phage_related_protein	2.6	2	6	1.6	1.4	1.6	1.6	1.5	1.5
493Rv1575	-	2653	6710	2.6	0.5	0.2	phiRV1_phage_related_protein	2.1	2	6	2.5	2.8	3.4	2.2	2.6	2.2
695Rv1575	-	1982	3867	1.9	0.3	0.1	phiRV1_phage_related_protein	1.4	2	6	2.2	2.0	1.8	1.6	2.3	1.6
4238Rv1575	-	1585	2742	1.7	0.3	0.1	phiRV1_phage_related_protein	2.1	2	6	1.8	1.5	2.1	1.4	1.7	1.9
1214Rv1576c	-	2676	9730	3.5	0.7	0.3	phiRV1_phage_related_protein	1.1	2	6	4.5	3.6	3.9	2.4	3.4	3.4
492Rv1577c	-	2300	10599	4.5	1.2	0.5	phiRV1_possible_prohead_protease	1.1	2	6	5.1	5.7	5.8	3.0	3.9	3.7
1211Rv1582c	-	2142	4053	1.9	0.3	0.1	phiRV1_phage_related_protein	1.1	2	6	2.0	1.8	2.3	2.1	1.7	1.6
1417Rv1584c	-	2412	9382	3.9	0.7	0.3	phiRV1_phage_related_protein	1.1	2	6	3.7	3.2	5.0	3.2	4.0	4.6
489Rv1584c	-	4001	12101	3.4	1.2	0.5	phiRV1_phage_related_protein	1.2	2	6	2.6	2.5	5.6	3.1	3.7	2.8
1210Rv1585c	-	2207	10910	4.9	0.8	0.3	phiRV1_phage_related_protein	1.1	2	6	5.2	4.7	6.5	4.3	4.3	4.5
696Rv1585c	-	2132	8580	4.0	0.9	0.4	phiRV1_phage_related_protein	1.1	2	6	4.5	4.3	3.9	2.3	3.9	4.9
488Rv1586c	-	8503	16473	2.0	0.3	0.1	phiRV1_integrase	1.1	2	6	2.2	1.5	2.2	2.5	1.9	1.9
4097Rv1587c	REP	2529	4997	1.9	0.3	0.1		1.1	2	6	2.4	1.7	2.1	1.8	1.8	1.7
3375Rv1588c	REP	3367	6695	2.0	0.2	0.1		1.1	2	6	2.1	2.0	1.7	2.1	1.8	2.0
3373Rv1592c	-	2225	9351	4.1	1.4	0.6		1.1	2	6	5.4	5.9	3.3	2.3	3.5	4.2
4094Rv1593c	-	4988	12567	2.5	0.3	0.1		1.1	2	6	3.1	2.6	2.1	2.3	2.6	2.4
3372Rv1594	nadA	5685	17080	3.1	0.5	0.2	quinolinate_synthase	2.5	2	6	2.8	2.5	3.3	3.9	3.4	2.8
4093Rv1595	nadB	5213	10535	2.0	0.2	0.1	L-aspartate_oxidase	1.1	2	6	2.0	1.8	1.9	1.7	2.3	2.2
3371Rv1596	nadC	4565	8625	1.9	0.2	0.1	nicotinate-nucleotide_pyrophosphatase	1.4	2	6	1.8	1.8	2.1	1.8	2.3	1.8
1208Rv1601	hisB	6449	12571	2.0	0.2	0.1	imidazole_glycerol-phosphate_dehydratase	1.1	2	6	2.0	1.7	2.1	2.0	1.7	2.2
2572Rv1628c	-	5704	10298	1.8	0.2	0.1		1.2	2	6	1.8	2.0	1.8	1.6	1.8	1.7
2953Rv1641	infC	13189	21453	1.7	0.3	0.1	initiation_factor_IF-3	1.1	2	6	1.7	2.1	1.5	2.0	1.5	1.4
3675Rv1642	rpml	4956	10270	2.1	0.3	0.1	50S_ribosomal_protein_L35	1.1	2	6	2.3	2.5	1.7	1.9	1.9	2.0
2954Rv1643	rpIT	4510	9801	2.1	0.1	0.0	50S_ribosomal_protein_L20	1.1	2	6	2.1	2.1	2.0	2.1	2.3	2.3
67Rv1645c	-	4643	7698	1.6	0.3	0.1		1.1	2	6	2.0	2.0	1.6	1.2	1.3	1.5
2919Rv1663	pkS17	3386	5152	1.5	0.1	0.0	polyketide_synthase_	1.1	2	6	1.6	1.4	1.7	1.4	1.4	1.5
4005Rv1682	-	1664	4123	2.3	0.8	0.3	probable_coiled-coil_structural_protein	1.1	2	6	3.3	3.0	2.7	1.4	1.7	1.8
3289Rv1705c	PPE	2901	4307	1.6	0.3	0.1		1.1	2	6	1.2	1.4	2.2	1.7	1.6	1.5
1110Rv1721c	-	2843	4639	1.6	0.3	0.1		1.1	2	6	1.7	1.8	2.0	1.1	1.6	1.5
1113Rv1727	-	6533	11270	1.7	0.1	0.1		1.4	2	6	1.9	1.7	1.7	1.7	1.5	1.7
3275Rv1730c	-	2116	5942	2.9	0.6	0.2	probable_penicillin_binding_protein	1.1	2	6	2.2	2.7	3.6	3.2	2.4	3.5
3280Rv1774	-	2029	3046	1.6	0.5	0.2	putative_oxidoreductase_with_FAD-binding_site_	1.1	2	6	1.3	1.5	2.6	1.7	1.5	1.3
2771Rv1782	-	5077	7855	1.5	0.2	0.1		1.1	2	6	1.8	1.7	1.5	1.4	1.4	1.5

2054Rv1804c	-	1575	2873	1.9	0.4	0.1		1.2	2	6	1.5	1.7	2.4	1.8	1.6	2.3
2776Rv1805c	-	2663	6726	2.8	1.5	0.6	unlikely_orf	1.1	2	6	1.1	1.2	4.1	3.0	2.7	4.6
2055Rv1806	PE	1575	5521	3.8	2.3	0.9		1.1	2	6	1.1	1.3	5.2	4.6	3.6	7.0
2777Rv1807	PPE	3860	9781	2.6	1.3	0.5		1.1	2	6	1.0	1.1	3.2	2.9	3.1	4.2
2056Rv1808	PPE	3991	7585	1.9	0.3	0.1		1.1	2	6	1.6	1.6	2.2	1.8	2.0	2.5
2778Rv1809	PPE	2684	4833	1.8	0.7	0.3		1.1	2	6	0.8	0.9	2.3	2.1	2.2	2.3
1527Rv1817	-	2844	4501	1.5	0.4	0.2	flavoprotein	1.1	2	6	1.9	2.0	1.6	1.0	1.3	1.3
4408Rv1831	-	8397	12834	1.6	0.3	0.1		1.1	2	6	1.2	1.3	2.1	1.9	1.7	1.6
4466Rv1856c	-	5989	12426	2.3	0.6	0.3	short-chain_dehydrogenase/reductase_family	1.1	2	6	1.4	1.7	2.2	2.5	3.1	2.6
2301Rv1865c	-	1896	3484	1.9	0.4	0.2	Short-chain_alcohol_dehydrogenase	1.4	2	5	1.7	2.5	nd	1.6	1.7	1.7
2983Rv1872c	lldD2	11042	18438	1.8	0.3	0.1	L-lactate_dehydrogenase	1.1	2	6	1.3	1.5	2.1	2.1	2.0	1.6
3703Rv1875	-	2629	4786	1.8	0.4	0.2		1.1	2	6	2.0	2.4	1.8	1.3	1.7	1.6
2981Rv1876	bfrA	4099	6209	1.5	0.2	0.1	bacterioferritin	1.1	2	6	1.7	1.8	1.4	1.4	1.3	1.5
93Rv1888c	-	8211	15849	2.0	0.4	0.2	unknown_hydrophobic_protein	1.1	2	6	1.6	1.6	2.7	2.1	1.9	2.2
91Rv1892	-	6178	9945	1.6	0.2	0.1		1.1	2	6	1.9	1.9	1.6	1.3	1.4	1.4
2978Rv1894c	-	3214	13649	4.2	0.4	0.2	some_similarity_to_dioxygenases	1.1	2	6	4.3	4.3	4.1	3.5	4.7	4.3
2976Rv1898	-	3809	6580	1.7	0.2	0.1		1.1	2	6	1.9	1.9	1.6	1.6	1.6	1.6
89Rv1909c	furA	5357	8492	1.5	0.3	0.1	ferric_uptake_regulatory_protein	1.1	2	6	1.7	1.8	1.6	1.0	1.3	1.6
1996Rv1928c	-	2475	5456	2.1	0.7	0.3	short-chain_alcohol_dehydrogenase_family	1.1	2	6	2.9	3.1	1.9	1.8	1.7	1.5
2717Rv1929c	-	3771	7623	2.0	0.6	0.2		1.1	2	6	2.9	2.1	2.1	1.2	1.6	1.8
4877Rv1942c	-	2042	3087	1.5	0.3	0.1		1.1	2	6	1.2	1.4	1.1	1.7	1.4	2.0
4874Rv1948c	-	2443	4308	1.7	0.4	0.2		1.1	2	6	2.3	2.1	1.7	1.5	1.4	1.4
2710Rv1955	-	2446	4064	1.7	0.3	0.1		1.1	2	6	1.6	1.5	2.1	1.2	1.5	2.1
1986Rv1960c	-	2094	3578	1.7	0.2	0.1		1.1	2	6	1.4	1.7	1.9	1.8	1.8	1.7
5555Rv1981c	nrdf	7676	19568	2.5	0.5	0.2	ribonucleotide_reductase_small_subunit	1.1	2	6	2.8	3.5	2.3	2.0	2.3	2.3
4833Rv1982c	-	4029	8305	2.0	0.4	0.2		2.6	2	6	2.2	2.5	1.7	1.5	2.1	2.0
1949Rv1986	-	1898	2565	1.5	0.2	0.1	membrane_protein,_LYSE/YGGA_family	1.1	2	5	nd	1.4	1.9	1.5	1.3	1.4
2669Rv1989c	-	2867	9818	3.9	1.4	0.6		1.1	2	6	5.1	4.3	5.8	2.8	3.1	2.2
1947Rv1990c	-	3600	9627	2.8	0.5	0.2	putative_transcriptional_regulator	1.1	2	6	3.0	2.4	3.6	2.5	2.8	2.3
2668Rv1991c	-	1862	3645	2.0	0.4	0.2		1.1	2	6	1.8	1.7	2.7	1.8	1.7	2.1
1946Rv1992c	ctpG	2609	10642	4.1	0.3	0.1	probable_cation_transport_ATPase	1.2	2	6	4.2	4.2	3.6	4.5	3.8	4.1
2667Rv1993c	-	2873	9283	3.3	0.7	0.3		1.1	2	6	3.7	3.0	4.4	3.1	3.5	2.4
1945Rv1994c	-	2963	5721	1.9	0.3	0.1	transcriptional_regulator_(MerR_family)	1.2	2	6	2.0	2.2	1.6	1.6	2.2	1.7
2666Rv1995	-	2068	3613	1.8	0.4	0.2		1.3	2	6	1.5	1.5	2.4	1.4	1.8	1.9
1943Rv2008c	-	1722	2798	1.7	0.5	0.2		1.1	2	6	1.3	2.2	2.3	1.3	1.3	1.5
2664Rv2009	-	2941	7421	2.5	0.2	0.1		1.1	2	6	2.6	2.7	2.7	2.1	2.3	2.5
1942Rv2010	-	2704	7288	2.5	0.6	0.3		1.1	2	6	3.2	3.4	1.8	2.2	2.1	2.6
2663Rv2011c	-	1699	6907	4.0	1.0	0.4		1.4	2	6	4.9	5.5	4.0	3.5	2.7	3.6
1941Rv2012	-	1670	7254	4.1	1.0	0.4		1.1	2	6	4.2	5.0	3.0	3.0	4.0	5.5
2662Rv2013	IS1607	1791	2954	1.7	0.3	0.1	transposase	1.1	2	6	1.4	1.9	1.9	1.7	1.8	1.3

1940Rv2014	IS1607	3930	6667	1.7	0.2	0.1	transposase	1.1	2	6	1.8	1.5	1.5	1.8	1.9	1.7
961Rv2014	IS1607	3372	5076	1.5	0.2	0.1	transposase	1.1	2	6	1.6	1.5	1.8	1.3	1.4	1.6
5283Rv2016	-	2838	20640	7.8	2.2	0.9		1.1	2	6	4.8	6.6	10.8	9.3	6.7	8.4
4562Rv2017	-	4806	18667	4.6	1.7	0.7	putative_transcriptional_regulator_(PbsX/Xre_family)	1.1	2	6	2.4	4.1	6.8	6.5	4.1	3.5
5284Rv2018	-	3202	5010	1.6	0.2	0.1		1.1	2	6	1.3	1.6	1.8	1.8	1.5	1.7
4566Rv2025c	-	2521	5107	2.0	0.6	0.3	possible_membrane_protein	1.1	2	6	2.6	2.8	1.6	1.4	1.5	1.8
3946Rv2034	-	2783	4417	1.7	0.6	0.3	transcriptional_regulator_(ArsR_family)	1.1	2	6	1.1	1.8	2.5	1.0	1.5	2.4
1683Rv2035	-	2185	7799	3.6	0.8	0.3		1.1	2	6	3.0	3.3	4.7	3.2	2.9	4.4
2405Rv2036	-	2605	6062	2.4	0.4	0.2	similar_to_lincomycin_production_genes	1.1	2	6	2.0	2.4	2.5	3.1	2.0	2.7
5294Rv2050	-	3472	9711	2.8	0.7	0.3		1.1	2	6	2.2	2.6	3.4	1.9	2.9	3.6
3845Rv2053c	-	2604	4097	1.6	0.2	0.1		1.1	2	6	1.5	1.5	1.6	1.6	1.4	2.0
5206Rv2077c	-	4627	11679	2.4	0.5	0.2		1.1	2	6	2.7	3.2	2.1	2.0	2.0	2.5
2323Rv2086	IS1556	1575	3594	2.2	0.4	0.2	putative_transposase	1.1	2	5	1.9	2.4	nd	2.3	2.7	1.8
1602Rv2087	IS1556	1995	5716	2.9	0.5	0.2	putative_transposase	1.1	2	6	3.1	2.3	3.2	2.2	3.0	3.6
5211Rv2098c	PE_PGRS	2466	3727	1.5	0.2	0.1		2.6	2	6	1.4	1.6	1.4	1.2	1.5	1.8
2747Rv2104c	-	2332	4008	1.7	0.2	0.1		1.1	2	6	1.5	1.6	1.8	1.7	1.6	2.1
5159Rv2110c	prcB	6135	9853	1.6	0.2	0.1	proteasome_b-type_subunit_2	1.1	2	6	1.6	1.8	1.5	1.3	1.5	1.6
1556Rv2123	PPE	1813	7036	3.5	2.3	0.9		1.1	2	6	5.6	7.1	2.5	1.7	1.7	2.3
2278Rv2124c	metH	2866	4640	1.7	0.3	0.1	5-methyltetrahydrofolate-homocysteine_methyltransferase	2.5	2	6	1.4	1.2	2.0	1.8	1.8	1.8
4790Rv2142c	-	3041	5306	1.8	0.2	0.1		1.1	2	6	1.8	1.8	1.9	2.2	1.5	1.6
2625Rv2151c	ftsQ	2731	4947	1.8	0.5	0.2	ingrowth_of_wall_at_septum	1.1	2	6	2.5	2.2	1.4	1.6	1.6	1.3
5170Rv2163c	pbpB	8694	13842	1.6	0.1	0.0	penicillin-binding_protein_2	2.5	2	6	1.6	1.8	1.5	1.6	1.6	1.4
5169Rv2165c	-	5627	10557	1.9	0.1	0.1		1.1	2	6	1.8	2.0	1.9	1.8	2.0	1.7
4447Rv2166c	-	12015	32890	3.0	1.0	0.4		1.1	2	6	2.1	2.0	3.8	4.2	3.6	2.6
2748Rv2169c	-	2999	4563	1.5	0.4	0.2		1.1	2	6	1.2	1.0	2.0	1.5	1.6	2.1
4910Rv2172c	-	3343	8364	2.5	0.3	0.1		1.2	2	6	2.1	2.8	2.8	2.1	2.5	2.7
4915Rv2182c	-	7362	13882	1.9	0.2	0.1		1.1	2	6	1.6	1.9	1.8	2.1	2.0	2.0
750Rv2225	panB	10517	20488	2.0	0.5	0.2	3-methyl-2-oxobutanoate_hydroxymethyltransferase	1.4	2	6	1.6	1.5	2.7	2.6	1.8	2.1
4916Rv2256c	-	5747	11404	2.0	0.4	0.2		1.1	2	6	1.5	1.6	1.9	2.1	2.6	2.3
2288Rv2269c	-	1630	2664	1.7	0.5	0.2	questionable_orf,	1.1	2	6	1.2	1.8	2.5	1.7	1.7	1.4
3768Rv2322c	rocD1	1618	2804	1.7	0.2	0.1	ornithine_aminotransferase	1.1	2	6	1.7	1.7	1.8	1.5	1.6	2.1
3767Rv2324	-	1763	2780	1.6	0.3	0.1	transcriptional_regulator_(Lrp/AsnC_family)	1.2	2	6	1.3	1.7	2.0	1.3	1.4	1.9
882Rv2330c	lppP	3006	4729	1.6	0.1	0.0	lipoprotein	1.1	2	6	1.5	1.6	1.8	1.5	1.5	1.6
2348Rv2347c	-	13910	22057	1.6	0.3	0.1		1.1	2	6	1.3	1.5	1.6	2.0	1.5	1.9
2282Rv2365c	-	3901	5939	1.5	0.2	0.1		2.5	2	6	1.4	1.8	1.6	1.6	1.4	1.4
770Rv2373c	dnaJ2	5574	9291	1.7	0.1	0.1	DnaJ_homologue	1.1	2	6	1.7	1.9	1.6	1.7	1.6	1.6
471Rv2380c	mbtE	2443	4005	1.7	0.2	0.1	mycobactin/exochelin_synthesis_(lysine_ligation)	1.1	2	6	1.7	1.6	2.1	1.5	1.6	1.5
1192Rv2381c	mbtD	2491	3706	1.5	0.3	0.1	mycobactin/exochelin_synthesis_(polyketide_synthase)	1.1	2	6	1.3	1.4	2.0	1.4	1.6	1.4
4079Rv2383c	mbtB	1730	2694	1.5	0.2	0.1	mycobactin/exochelin_synthesis_(serine/threonine_ligation)	1.1	2	6	1.6	1.5	1.9	1.2	1.4	1.6
2273Rv2386c	trpE2	1812	4370	2.5	0.7	0.3	anthranilate_synthase_component_I	1.1	2	6	2.4	3.4	3.3	2.0	2.1	1.5

1550Rv2389c	-	3302	8746	2.4	0.9	0.4		1.1	2	6	3.6	3.5	2.2	1.3	2.1	1.9
2271Rv2390c	-	3158	7263	2.4	0.5	0.2		1.1	2	6	2.2	2.8	3.1	2.5	1.9	2.0
1549Rv2391	nirA	4789	19123	4.0	0.3	0.1	probable_nitrite_reductase/sulphite_reductase	1.1	2	6	3.9	4.3	4.3	4.2	3.6	4.0
2270Rv2392	cysH	3447	10415	3.0	0.6	0.3	3'-phosphoadenylylsulfate_(PAPS)_reductase	1.1	2	6	3.4	4.1	2.3	3.0	2.9	2.6
1548Rv2393	-	5652	10558	1.8	0.3	0.1		1.1	2	6	2.4	2.0	1.5	1.7	1.7	1.5
2269Rv2394	ggxB	2739	5003	1.8	0.5	0.2	g_-glutamyltranspeptidase_precursor	1.1	2	6	1.8	2.7	1.5	2.1	1.4	1.4
5154Rv2400c	subI	1727	4087	2.4	1.0	0.4	sulphate_binding_precursor	1.1	2	6	1.5	1.6	3.9	2.1	2.3	3.4
4122Rv2430c	PPE	5128	11668	2.4	0.6	0.2		1.1	2	6	1.8	1.7	3.0	2.9	2.3	2.8
3400Rv2431c	PE	2106	7279	4.1	0.9	0.4		1.1	2	5	2.6	nd	4.0	4.4	4.2	5.2
1239Rv2432c	-	2805	4764	1.7	0.3	0.1		1.1	2	6	2.2	1.9	1.8	1.4	1.6	1.3
1235Rv2441c	rpmA	10856	14350	1.5	0.6	0.2	50S_ribosomal_protein_L27	1.1	2	6	0.8	0.6	2.0	1.8	1.6	1.9
513Rv2442c	rplU	8520	14368	1.9	1.0	0.4	50S_ribosomal_protein_L21	1.1	2	6	0.8	0.8	3.1	2.5	1.7	2.6
512Rv2444c	rne	6870	12527	1.9	0.3	0.1	similar_at_C-term_to_ribonuclease_E	1.1	2	6	2.2	1.6	2.3	2.0	1.5	1.8
1766Rv2444c	rne	5322	9046	1.7	0.1	0.0	similar_at_C-term_to_ribonuclease_E	1.1	2	6	1.8	1.8	1.6	1.5	1.7	1.7
2366Rv2466c	-	1765	3938	2.2	0.5	0.2		1.1	2	6	1.6	2.0	2.6	1.8	2.9	2.5
2369Rv2472	-	3779	8833	2.4	0.2	0.1		1.1	2	6	2.3	2.4	2.7	2.6	2.0	2.4
2958Rv2495c	pdhC	3326	5835	1.8	0.2	0.1	dihydrolipoamide_acetyltransferase	1.1	2	6	1.6	1.8	1.8	1.6	2.0	1.8
3680Rv2496c	pdhB	3423	6466	1.9	0.2	0.1	pyruvate_dehydrogenase_E1_component_b_subunit	1.4	2	6	1.7	1.8	1.9	1.9	2.2	2.0
2959Rv2497c	pdhA	3744	13009	3.5	0.8	0.3	pyruvate_dehydrogenase_E1_component_a_subunit	1.1	2	6	3.1	4.3	4.1	2.0	3.4	3.9
2960Rv2499c	-	2938	4645	1.5	0.3	0.1	putative_aldehyde_dehydrogenase	1.1	2	6	1.5	2.1	1.6	1.0	1.4	1.5
3682Rv2500c	fadE19	2391	4878	2.0	0.1	0.1	acyl-CoA_dehydrogenase_(aka_mmgC)	1.1	2	6	2.0	2.2	2.0	1.8	2.0	2.1
28Rv2501c	accA1	3368	11501	3.5	0.9	0.4	acetyl/propionyl-CoA_carboxylase,_a_subunit	1.1	2	6	3.2	3.3	5.0	2.6	2.9	4.1
749Rv2502c	accD1	2646	6026	2.4	0.4	0.2	acetyl/propionyl-CoA_carboxylase,_b_subunit	1.1	2	6	1.8	2.2	2.4	2.6	2.4	2.9
1132Rv2503c	scoB	10287	15898	1.6	0.3	0.1	3-oxo_acid:CoA_transferase,_b_subunit	2.5	2	6	1.3	1.2	1.8	1.7	1.4	1.9
411Rv2504c	scoA	6571	13549	2.2	0.6	0.3	3-oxo_acid:CoA_transferase,_a_subunit	1.1	2	6	1.6	1.5	2.9	2.8	1.9	2.6
412Rv2506	-	3351	6010	1.9	0.3	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.4	1.7	2.1	1.9	2.0	2.1
415Rv2512c	IS1081	6088	15121	3.0	1.1	0.5		1.1	2	6	1.8	1.6	4.6	3.7	2.7	3.3
1137Rv2513	-	3382	6917	2.0	0.9	0.4		1.1	2	5	3.3	2.8	1.5	nd	1.2	1.4
1653Rv2516c	-	1905	16324	9.0	2.2	0.9		1.1	2	6	8.0	7.5	13.3	8.9	7.4	9.0
2375Rv2517c	-	2152	11106	5.3	0.8	0.3	questionable	1.1	2	6	5.3	5.1	4.9	6.4	4.3	6.1
1868Rv2526	-	3023	5568	1.8	0.2	0.1		1.1	2	6	1.8	2.0	1.8	1.6	2.1	1.7
2589Rv2527	-	4153	10276	2.4	0.2	0.1		1.1	2	6	2.5	2.8	2.4	2.2	2.2	2.6
4750Rv2539c	aroK	2383	3276	1.5	0.3	0.1	shikimate_kinase_I	1.1	2	6	1.2	1.3	2.0	1.4	1.5	1.4
2489Rv2541	-	2475	3738	1.5	0.2	0.1		1.1	2	6	1.7	1.2	1.8	1.4	1.6	1.4
3717Rv2583c	relA	3425	5180	1.5	0.3	0.1	(p)ppGpp_synthase_I	1.1	2	6	1.5	1.7	1.0	1.4	1.7	1.4
3714Rv2589	gabT	2762	4510	1.6	0.4	0.2	4-aminobutyrate_aminotransferase	1.1	2	6	1.7	2.0	0.9	1.9	1.3	1.6
2992Rv2590	fadD9	3462	13632	3.9	0.3	0.1	acyl-CoA_synthase	1.1	2	6	3.9	4.1	4.3	3.4	3.9	3.8
1474Rv2601	speE	3299	5003	1.6	0.2	0.1	spermidine_synthase	1.1	2	6	1.5	1.5	1.9	1.3	1.6	1.5
2195Rv2602	-	2844	4204	1.5	0.2	0.1		1.1	2	6	1.3	1.4	1.8	1.4	1.6	1.5
3341Rv2620c	-	1775	2626	1.5	0.2	0.1		1.1	2	6	1.2	1.5	1.6	1.7	1.4	1.7

4062Rv2621c	-	1862	3026	1.6	0.3	0.1	putative_transcriptional_regulator	2.1	2	6	1.5	1.3	2.0	1.4	1.4	2.0
1179Rv2622	-	5893	9994	1.7	0.1	0.0	similar_to_SAM-dependent_methyltransferase	1.1	2	6	1.7	1.8	1.7	1.5	1.7	1.7
454Rv2629	-	3727	10416	2.7	0.7	0.3		1.1	2	6	3.2	3.7	2.6	1.9	2.3	2.5
3406Rv2644c	-	2060	2942	1.5	0.3	0.1		1.1	2	6	1.2	1.5	2.0	1.4	1.4	1.3
4130Rv2650c	-	2043	4112	2.0	0.5	0.2	phiRV2_phage_related_protein	1.1	2	6	2.5	2.6	2.1	1.3	1.5	1.8
3409Rv2651c	-	5303	9524	2.8	1.1	0.4	phiRV2_prohead_protease	1.1	2	6	3.2	4.5	3.0	1.2	2.4	2.8
4131Rv2652c	-	1767	6913	4.3	2.3	0.9	phiRV2_phage_related_protein	1.1	2	6	3.1	2.0	8.5	2.7	4.4	4.8
4133Rv2656c	-	2970	5408	1.9	0.4	0.2	phiRV2_phage_related_protein	1.1	2	6	1.6	1.4	2.5	1.6	2.0	2.0
524Rv2657c	-	6498	14085	2.2	0.3	0.1	similar_to_gp36_of_mycobacteriophage_L5_	1.1	2	6	2.4	2.0	2.5	1.8	2.1	2.2
1246Rv2658c	-	7937	16571	2.1	0.1	0.0	phiRV2_phage_related_protein	1.4	2	6	2.1	1.9	2.2	2.1	2.2	2.2
525Rv2659c	-	4538	13971	3.1	0.5	0.2	phiRV2_integrase	1.1	2	6	3.7	3.3	3.4	2.6	3.0	2.6
1247Rv2660c	-	4376	21636	5.1	1.1	0.5		1.1	2	6	4.5	3.7	6.3	5.9	4.2	6.1
526Rv2661c	-	2329	5166	2.2	0.3	0.1		1.1	2	6	2.7	2.3	2.4	2.2	1.8	2.1
1248Rv2662	-	2887	4587	1.5	0.3	0.1		1.1	2	6	1.7	1.9	1.9	1.3	1.4	1.2
527Rv2663	-	4861	7805	1.6	0.3	0.1		1.1	2	6	1.9	1.3	1.9	1.5	1.4	1.8
528Rv2665	-	5293	13149	2.5	0.4	0.2		1.1	2	6	2.4	2.1	3.0	2.3	2.5	3.0
1250Rv2666	IS1081'	2854	12623	4.6	0.9	0.4		1.1	2	6	4.0	3.3	5.9	5.1	4.8	4.5
56Rv2685	arsB	2496	3759	1.5	0.4	0.1	probable_arsenical_pump	1.1	2	6	1.7	2.0	1.6	1.2	1.1	1.2
778Rv2686c	-	3282	8929	2.7	0.6	0.2	possible_membrane_protein	1.1	2	6	2.2	3.0	3.4	1.9	2.6	3.1
998Rv2687c	-	1771	4083	2.3	0.6	0.2		1.1	2	6	1.7	2.5	3.0	1.8	2.1	2.9
779Rv2688c	-	3539	13789	3.9	0.9	0.4	similar_to_transport_ATP-binding_proteins	1.1	2	6	3.3	4.6	4.9	2.4	3.8	4.4
2934Rv2710	sigB	4119	5921	1.5	0.2	0.1	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	2	6	1.3	1.3	1.6	1.5	1.6	1.5
2491Rv2724c	fadE20	2041	11040	5.9	2.1	0.9	acyl-CoA_dehydrogenase_	1.1	2	6	3.1	3.7	8.4	5.8	6.5	7.8
4743Rv2724c	fadE20	4435	13045	3.6	1.4	0.6	acyl-CoA_dehydrogenase_	1.2	2	6	2.0	2.3	5.7	4.5	4.0	2.9
5606Rv2739c	-	6492	14389	2.2	0.4	0.2	glycosyltransferase	2.2	2	6	2.0	2.8	2.5	1.8	2.2	2.0
3086Rv2764c	thyA	7085	12492	1.8	0.1	0.0	thymidylate_synthase	1.1	2	6	1.8	1.8	1.9	1.8	1.8	1.7
926Rv2777c	-	3534	7015	2.0	0.3	0.1		1.1	2	6	1.7	1.7	2.3	2.0	2.2	2.1
3088Rv2780	ald	5307	12852	2.6	0.9	0.4	L-alanine_dehydrogenase	1.1	2	6	1.4	1.4	3.4	3.2	3.2	3.1
3090Rv2784c	lppU	6329	11709	1.8	0.1	0.1	lipoprotein	2.5	2	6	2.0	1.7	1.7	1.7	1.8	2.0
3812Rv2785c	rpsO	8186	20513	2.6	0.5	0.2	30S_ribosomal_protein_S15	1.1	2	6	2.1	3.2	2.7	3.3	2.0	2.5
206Rv2792c	IS1602	12718	18600	1.5	0.2	0.1	resolvase	2.2	2	6	1.5	1.4	1.5	1.8	1.3	1.5
207Rv2794c	-	4228	8283	2.1	0.4	0.1	possible_4'-phosphopantetheine_transferase_	2.3	2	6	1.7	1.7	2.5	2.2	2.5	2.0
804Rv2809	-	4315	7180	1.7	0.2	0.1		1.1	2	6	1.4	1.7	2.0	1.6	1.5	2.0
2961Rv2827c	-	5404	13939	2.7	0.3	0.1		2.5	2	6	2.7	2.4	2.5	3.0	3.1	2.3
799Rv2830c	-	6665	12192	1.9	0.3	0.1	similar_to_phage_P1_phd_gene	1.1	2	6	1.4	1.6	2.1	2.0	1.8	2.2
2494Rv2830c	-	1836	2809	1.6	0.3	0.1	similar_to_phage_P1_phd_gene	1.1	2	6	1.3	1.6	2.2	1.3	1.5	1.6
795Rv2838c	rbfA	9893	17118	1.7	0.5	0.2	ribosome-binding_factor_A	1.2	2	6	1.2	1.2	2.3	1.8	1.8	2.2
73Rv2839c	infB	10552	14284	1.5	0.5	0.2	initiation_factor_IF-2_	1.1	2	6	0.9	0.9	2.0	1.7	1.7	1.6
5487Rv2840c	-	11367	18524	1.6	0.4	0.2	similar_to_NUSA/INFB	1.1	2	6	1.1	1.2	2.1	1.9	1.8	1.7
2496Rv2871	-	3241	4482	1.6	0.5	0.2		1.1	2	6	1.2	1.7	2.1	0.9	1.8	1.7

1908Rv2871	-	4603	6917	1.5	0.2	0.1		1.2	2	6	1.5	1.6	1.6	1.3	1.7	1.3
2630Rv2872	-	2373	4913	2.1	0.6	0.3		1.1	2	6	1.5	1.6	2.8	1.7	2.0	2.9
1747Rv2873	mpt83	2859	9966	3.5	0.6	0.2	surface_lipoprotein_Mpt83	1.1	2	6	2.8	2.8	4.1	3.5	3.8	4.1
2632Rv2878c	mpt53	2121	5677	2.6	0.4	0.2	secreted_protein_Mpt53	1.1	2	6	3.1	2.9	2.9	2.1	2.2	2.7
1351Rv2879c	-	4442	8635	1.9	0.3	0.1		1.1	2	6	1.9	1.9	2.2	1.5	1.9	2.2
1911Rv2879c	-	3818	7109	1.8	0.2	0.1		1.2	2	6	2.0	1.8	1.5	1.9	1.9	2.0
630Rv2879c	-	6375	10651	1.7	0.1	0.1		1.1	2	6	1.8	1.5	1.7	1.5	1.6	1.8
5519Rv2887	-	6263	10051	1.6	0.1	0.1	transcriptional_regulator_(MarR_family)	1.1	2	6	1.5	1.4	1.7	1.5	1.6	1.8
4799Rv2890c	rpsB	10383	19857	1.9	0.2	0.1	30S_ribosomal_protein_S2	1.4	2	6	1.8	1.6	2.1	2.0	1.9	2.1
1918Rv2904c	rpIS	5826	13047	2.3	0.3	0.1	50S_ribosomal_protein_L19	1.1	2	6	1.9	1.9	2.6	2.2	2.2	2.8
2641Rv2907c	rimM	3818	5699	1.5	0.4	0.2	16S_rRNA_processing_protein	1.1	2	6	1.2	1.0	1.8	1.1	1.7	2.1
4803Rv2909c	rpsP	8382	13989	1.7	0.5	0.2	30S_ribosomal_protein_S16	1.1	2	6	1.0	1.1	2.1	2.0	1.9	2.2
1352Rv2909c	rpsP	5355	7716	1.5	0.4	0.2	30S_ribosomal_protein_S16	1.1	2	6	0.9	1.0	1.8	1.9	1.7	1.8
1217Rv2919c	glnB	4120	6099	1.5	0.2	0.1	nitrogen_regulatory_protein	1.1	2	6	1.7	1.6	1.3	1.4	1.4	1.3
496Rv2920c	amt	2027	2888	1.5	0.2	0.1	putative_ammonium_transporter	1.1	2	6	1.6	1.4	1.7	1.6	1.3	1.2
1220Rv2925c	rnc	8073	12441	1.6	0.2	0.1	RNAse_III	1.4	2	6	1.5	1.4	1.5	1.8	1.6	1.7
755Rv2930	fadD26	6632	20648	3.2	0.7	0.3	acyl-CoA_synthase	1.1	2	6	2.9	2.5	4.5	3.1	2.7	3.7
1574Rv2963	-	2960	11583	3.8	1.0	0.4	integral_membrane_protein	1.1	2	6	4.1	4.9	3.6	2.2	3.0	4.8
5180Rv2971	-	6027	13119	2.1	0.3	0.1	oxidoreductase_of_Aldo/keto_reductase_family	1.1	2	6	1.7	2.0	2.1	2.2	2.2	2.6
1656Rv2990c	-	2556	9116	3.5	0.7	0.3		1.1	2	6	3.2	2.7	4.2	2.8	4.0	4.3
4251Rv3002c	ivN	2789	4626	1.7	0.1	0.0	acetolactate_synthase_I_small_subunit	1.1	2	6	1.5	1.6	1.7	1.8	1.5	1.8
4544Rv3002c	ivN	4977	7529	1.5	0.3	0.1	acetolactate_synthase_I_small_subunit	1.1	2	6	1.5	1.6	1.6	1.5	1.0	1.6
5266Rv3003c	ivB	3279	7165	2.2	0.3	0.1	acetolactate_synthase_I_large_subunit_	1.3	2	6	1.9	1.9	2.7	2.2	2.3	2.4
4886Rv3023c	IS1081	5277	15107	2.9	0.4	0.2		1.4	2	6	2.7	2.4	2.6	3.3	3.3	3.2
4661Rv3045	adhC	12780	20936	1.7	0.5	0.2	alcohol_dehydrogenase	1.1	2	6	1.2	1.2	2.1	2.4	1.7	1.8
4893Rv3049c	-	4155	6748	1.5	0.6	0.2	Probable_monooxygenase	1.1	2	6	2.1	2.4	1.1	1.3	1.1	1.2
5615Rv3050c	-	7982	11894	1.5	0.2	0.1	putative_transcriptional_regulator	1.3	2	6	1.4	1.8	1.3	1.4	1.5	1.6
3007Rv3051c	nrdE	5286	13240	2.6	0.2	0.1	ribonucleoside_diphosphate_reductase_a_chain	1.3	2	6	2.5	2.5	2.9	2.6	2.7	2.2
4894Rv3051c	nrdE	14066	25963	1.9	0.4	0.2	ribonucleoside_diphosphate_reductase_a_chain	1.1	2	6	1.8	2.6	1.8	2.1	1.6	1.6
3728Rv3052c	nrdI	3971	13819	3.4	1.0	0.4	NrdI/YgaO/YmaA_family	1.1	2	6	4.1	4.8	2.7	2.0	3.2	3.5
3006Rv3053c	nrdH	7423	18092	2.7	0.8	0.3	glutaredoxin_electron_transport_component_of_NrdEF_system	1.1	2	6	1.9	3.9	3.0	3.3	2.0	2.1
120Rv3060c	-	5169	13420	2.6	0.4	0.1	transcriptional_regulator_(GntR_family)	1.1	2	6	3.0	2.5	3.2	2.3	2.4	2.5
3895Rv3061c	fadE22	1685	7659	4.4	1.5	0.6	acyl-CoA_dehydrogenase_	1.1	2	6	5.6	5.5	5.7	2.1	3.3	4.6
119Rv3062	ligB	5709	11305	1.9	0.6	0.3	DNA_ligase	1.1	2	6	2.4	3.0	1.7	1.4	1.5	1.6
118Rv3065	emrE	2485	10775	4.4	1.2	0.5	resistance_to_ethidium_bromide	1.1	2	6	3.9	5.7	5.7	2.9	3.5	4.5
117Rv3066	-	3378	10533	3.2	1.0	0.4	putative_transcriptional_regulator	1.1	2	6	3.6	4.5	4.0	2.0	2.7	2.4
839Rv3066	-	2349	6462	2.7	0.7	0.3	putative_transcriptional_regulator	1.3	2	6	2.7	4.1	2.6	2.0	2.5	2.4
3894Rv3066	-	1603	4154	2.6	0.8	0.3	putative_transcriptional_regulator	1.1	2	6	3.0	2.3	3.9	1.9	2.0	2.6
838Rv3067	-	4495	8078	1.8	0.2	0.1		1.1	2	6	1.8	2.1	1.7	1.9	1.6	1.6
4895Rv3081	-	2172	4180	1.9	0.3	0.1		1.1	2	6	2.1	2.3	1.6	1.7	1.7	1.8

2593Rv3095	-	4568	8015	1.8	0.5	0.2	putative_transcriptional_regulator	1.1	2	6	1.4	1.2	2.6	1.6	2.0	2.1
5481Rv3108	-	2653	4024	1.5	0.2	0.1		1.1	2	6	1.7	1.4	1.7	1.1	1.4	1.5
2596Rv3114	-	1736	3857	2.1	1.0	0.4		1.1	2	6	2.9	3.8	1.9	1.1	1.5	1.4
1875Rv3115	IS1081	3282	13229	4.0	0.5	0.2		1.1	2	6	3.4	4.1	3.7	3.4	4.7	4.5
1876Rv3117	cysA3	7541	27677	3.9	1.1	0.4	thiosulfate_sulfurtransferase	1.1	2	6	2.9	2.8	4.6	5.5	3.2	4.4
2598Rv3118	sseC	4116	6238	1.5	0.5	0.2	thiosulfate_sulfurtransferase	1.1	2	6	1.1	1.0	1.9	1.3	1.8	2.2
5483Rv3124	-	2360	4061	1.7	0.4	0.2	transcriptional_regulator_(AfsR/DndI/RedD_family)	1.1	2	6	2.2	2.2	1.5	1.2	1.4	1.5
950Rv3139	fadE24	4694	9958	2.3	1.1	0.4	acyl-CoA_dehydrogenase_	1.1	2	6	1.0	0.9	3.4	2.5	2.8	3.2
3647Rv3139	fadE24	4507	9307	2.3	0.9	0.4	acyl-CoA_dehydrogenase_	1.1	2	6	1.0	1.1	2.6	2.7	3.1	3.0
228Rv3139	fadE24	7109	13635	2.2	0.9	0.4	acyl-CoA_dehydrogenase_	2.1	2	6	1.0	1.1	3.0	2.5	2.4	3.0
272Rv3139	fadE24	8163	16348	2.0	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	2	6	1.2	1.2	2.5	2.0	1.8	3.0
227Rv3140	fadE23	5893	9864	1.9	0.9	0.3	acyl-CoA_dehydrogenase_	1.1	2	6	0.9	0.9	2.6	2.4	2.2	2.8
2925Rv3140	fadE23	6851	11492	1.9	0.8	0.3	acyl-CoA_dehydrogenase_	1.1	2	6	0.9	1.0	2.6	2.3	2.5	2.2
226Rv3140	fadE23	8011	12027	1.8	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	2	6	1.0	0.9	2.5	2.3	1.8	2.3
948Rv3140	fadE23	5410	8559	1.8	0.8	0.3	acyl-CoA_dehydrogenase_	1.1	2	6	0.8	0.8	2.4	2.1	2.0	2.4
578Rv3159c	PPE	4177	10333	2.4	1.2	0.5		1.4	2	6	4.3	3.6	1.9	1.5	1.7	1.5
1300Rv3160c	-	1812	7121	3.9	1.1	0.4	putative_transcriptional_regulator	1.1	2	6	4.0	5.4	4.4	2.1	3.4	3.9
579Rv3161c	-	3339	18439	5.6	0.6	0.2	putative_dioxygenases	1.1	2	6	6.1	5.3	6.3	5.9	4.7	5.4
4188Rv3172c	-	2105	4650	2.2	0.3	0.1	unlikely_orf	1.1	2	6	2.5	2.0	2.6	1.9	2.2	1.9
3467Rv3173c	-	2174	7424	3.6	0.8	0.3	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	2.5	2.7	4.3	4.1	4.0	4.0
4193Rv3182	-	1666	3606	2.1	0.8	0.3		1.1	2	6	1.9	2.2	2.9	1.2	1.1	3.1
584Rv3183	-	1594	2701	1.6	0.4	0.2	putative_transcriptional_regulator	1.1	2	6	1.5	1.9	1.3	1.3	1.5	2.4
1308Rv3188	-	1599	1951	1.5	0.2	0.1		1.1	2	4	nd	1.6	1.8	1.3	1.3	nd
1264Rv3206c	moeZ	6149	10515	1.7	0.2	0.1	probably_involved_in_molybdopterin_biosynthesis	1.1	2	6	1.7	1.5	2.0	1.9	1.7	1.5
4151Rv3208	-	3794	5652	1.5	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.6	1.4	1.7	1.3	1.5	1.4
3428Rv3211	rhIE	7559	14788	2.0	0.2	0.1	probable_ATP-dependent_RNA_helicase	1.1	2	6	1.8	2.2	1.8	2.2	2.0	2.0
3657Rv3223c	sigH	5086	8481	1.7	0.2	0.1	ECF_subfamily_sigma_subunit	1.1	2	6	1.4	1.6	1.7	1.7	2.0	1.7
1380Rv3240c	secA	6637	12217	1.9	0.3	0.1	SecA,_preprotein_translocase_subunit	1.1	2	6	1.6	1.4	2.2	2.2	1.9	2.1
2499Rv3240c	secA	2379	3951	1.7	0.1	0.1	SecA,_preprotein_translocase_subunit	1.1	2	6	1.5	1.6	1.9	1.5	1.8	1.7
1778Rv3245c	mtrB	3872	6086	1.6	0.2	0.1	sensor_histidine_kinase	1.1	2	6	1.4	1.4	1.9	1.5	1.7	1.8
661Rv3245c	mtrB	5956	9132	1.5	0.1	0.1	sensor_histidine_kinase	1.1	2	6	1.4	1.4	1.6	1.5	1.7	1.7
4199Rv3259	-	3696	5823	1.5	0.4	0.2		1.1	2	6	1.3	1.3	1.6	1.0	1.6	2.1
590Rv3260c	whiB2	7475	13191	1.8	0.2	0.1	WhiB_transcriptional_activator_homologue	1.1	2	6	1.5	1.8	2.1	2.0	1.7	1.8
3068Rv3269	-	7588	15056	2.1	0.4	0.2	probable_heat_shock_protein	1.1	2	6	1.4	1.8	2.1	2.2	2.4	2.5
3790Rv3270	ctpC	3879	8792	2.2	0.4	0.1	cation_transport_ATPase	1.1	2	6	2.3	2.8	1.9	1.9	2.4	2.1
184Rv3277	-	9994	14036	1.5	0.3	0.1		1.1	2	6	1.2	1.0	1.7	1.7	1.5	1.7
2501Rv3290c	lat	2004	9146	4.6	1.1	0.5	lysine-e_aminotransferase	1.1	2	6	4.0	5.1	3.9	3.0	5.9	5.5
3794Rv3290c	lat	2526	7993	3.2	0.3	0.1	lysine-e_aminotransferase	1.1	2	6	3.2	2.7	3.3	3.3	3.7	3.1
601Rv3334	-	3039	10154	3.5	1.1	0.4	transcriptional_regulator_(MerR_family)	1.1	2	6	2.1	2.4	4.5	3.3	3.9	4.7
1323Rv3335c	-	3149	4272	1.5	0.5	0.2		1.1	2	6	1.1	1.1	1.9	2.1	1.6	1.0

5356Rv3340	metC	2751	4082	1.5	0.3	0.1	cystathionine_b-lyase	1.1	2	6	1.2	1.2	1.9	1.5	1.7	1.5
933Rv3347c	PPE	5666	8669	1.5	0.3	0.1		1.1	2	6	1.9	1.9	1.5	1.3	1.1	1.5
3826Rv3367	PE_PGRS	3951	8806	2.2	0.2	0.1		2.1	2	6	2.1	1.9	2.2	2.3	2.2	2.6
1279Rv3375	amiD	5619	9798	1.8	0.2	0.1	probable_amidase	1.4	2	6	1.7	1.5	1.8	1.8	1.8	2.0
558Rv3376	-	10088	14165	1.5	0.3	0.1		1.1	2	6	1.1	1.2	1.9	1.8	1.3	1.7
3443Rv3382c	lytB	2110	3755	1.8	0.3	0.1	LytB_protein_homologue	1.1	2	6	1.9	2.1	2.1	1.6	1.3	1.7
4166Rv3385c	-	2210	4004	1.8	0.2	0.1		1.1	2	6	1.7	1.8	1.6	1.6	1.7	2.1
2927Rv3392c	cmaA1	5496	8477	1.6	0.3	0.1	cyclopropane_mycolic_acid_synthase_1	1.1	2	6	1.4	1.2	1.9	1.6	1.8	1.8
3648Rv3397c	phyA	2201	4250	2.0	0.2	0.1	phytoene_synthase	1.1	2	6	1.8	1.9	2.2	2.0	2.0	1.8
1260Rv3399	-	5603	7987	1.5	0.2	0.1		1.1	2	6	1.2	1.2	1.6	1.5	1.6	1.6
538Rv3400	-	6354	9430	1.7	0.4	0.2	probable_b-phosphoglucomutase	1.1	2	5	1.3	1.3	2.1	1.9	2.0	nd
537Rv3402c	-	2728	6928	2.5	0.4	0.2	possible_involved_in_LPS_synthesis	1.1	2	6	2.7	3.1	2.6	2.1	2.0	2.2
1258Rv3403c	-	3505	8436	2.3	0.8	0.3		1.1	2	6	3.2	3.4	1.9	1.9	1.7	1.8
4145Rv3405c	-	4256	8986	2.1	0.4	0.2	putative_transcriptional_regulator	1.1	2	6	1.8	1.7	2.5	2.1	1.9	2.7
3423Rv3406	-	5744	19935	3.8	1.1	0.4	putative_dioxygenase	1.4	2	6	3.5	1.8	5.0	3.8	3.8	4.6
4144Rv3407	-	11348	20410	1.8	0.2	0.1		1.1	2	6	1.7	2.1	1.9	1.8	1.6	1.9
3422Rv3408	-	13117	25089	2.1	0.4	0.2		1.1	2	6	2.0	2.4	2.0	2.7	1.7	1.5
1750Rv3417c	groEL1	8829	18010	2.1	0.6	0.2	60_kD_chaperonin_1	1.1	2	6	2.8	2.8	1.7	1.9	1.9	1.6
3418Rv3418c	groES	10992	27406	3.4	1.9	0.8	10_kD_chaperone	1.1	2	6	4.9	6.4	2.1	3.2	1.7	1.8
535Rv3420c	rimI	7188	10719	1.5	0.2	0.1	ribosomal_protein_S18_acetyltransferase	1.1	2	6	1.4	1.2	1.8	1.7	1.6	1.4
1255Rv3423c	alr	3954	8145	2.1	0.1	0.1	alanine_racemase	1.1	2	6	2.0	1.9	2.3	2.1	2.1	2.2
533Rv3424c	-	3109	14232	4.8	0.8	0.3		1.1	2	6	3.9	5.2	6.3	4.5	4.6	4.3
1254Rv3425	PPE	6268	14896	2.4	0.4	0.1		1.1	2	6	3.0	2.1	2.6	2.0	2.3	2.1
532Rv3426	PPE	3526	7861	2.2	0.2	0.1		1.1	2	6	2.7	2.2	2.3	2.1	2.1	2.0
1253Rv3427c	IS1532	7213	13027	1.8	0.4	0.2		1.1	2	6	2.5	1.7	1.9	1.5	1.8	1.2
190Rv3429	PPE	6096	17281	2.9	0.6	0.2		1.1	2	6	3.4	2.8	3.7	2.2	2.5	2.6
1013Rv3451	-	3005	5248	1.8	0.2	0.1	probable_cutinase	1.1	2	6	1.5	1.6	1.8	1.8	1.9	2.0
293Rv3454	-	1765	4487	2.3	0.7	0.3	some_similarity_to_proline_permeases	1.3	2	6	3.1	3.0	2.1	1.4	1.5	2.7
1015Rv3455c	truA	3912	8591	2.1	0.3	0.1	probable_pseudouridylate_synthase	1.1	2	6	2.2	2.6	2.2	1.9	1.8	2.1
294Rv3456c	rplQ	10069	14784	1.5	0.2	0.1	50S_ribosomal_protein_L17	1.1	2	6	1.4	1.8	1.5	1.4	1.4	1.4
1016Rv3457c	rpoA	10956	20440	1.9	0.1	0.1	a_subunit_of_RNA_polymerase	1.1	2	6	2.0	1.9	1.8	1.9	1.6	1.9
3899Rv3459c	rpsK	6866	12336	1.8	0.3	0.1	30S_ribosomal_protein_S11	1.1	2	6	2.2	2.3	1.5	1.7	1.6	1.7
3178Rv3460c	rpsM	10960	19435	1.9	0.3	0.1	30S_ribosomal_protein_S13	1.1	2	6	1.6	2.2	2.1	2.2	1.7	1.5
3900Rv3461c	rpmJ	7069	18179	2.7	0.5	0.2	50S_ribosomal_protein_L36	1.1	2	6	2.3	3.4	2.8	3.0	2.0	2.7
3179Rv3462c	infA	15232	24700	1.7	0.3	0.1	initiation_factor_IF-1	1.1	2	6	1.5	1.7	1.7	2.2	1.4	1.5
3181Rv3466	REP	4876	9764	1.9	0.3	0.1		1.1	2	6	2.4	1.9	1.6	1.8	1.6	2.1
3903Rv3467	REP	3798	10727	2.8	0.7	0.3		1.1	2	6	3.5	3.9	2.3	2.5	2.1	2.5
2037Rv3503c	fdxD	4831	10171	2.2	0.3	0.1	probable_ferredoxin	1.1	2	6	2.0	1.8	2.5	2.1	2.4	2.3
4925Rv3515c	fadD19	2362	4695	1.9	0.2	0.1	acyl-CoA_synthase	1.1	2	6	1.9	1.8	2.2	1.7	1.9	2.3
5647Rv3516	echA19	2000	4458	2.3	0.5	0.2	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	2	6	1.7	2.5	2.7	2.0	1.9	2.8

5649Rv3520c	-	4059	6148	1.5	0.1	0.1	probable_coenzyme_F420-dependent_enzyme	1.1	2	6	1.4	1.5	1.4	1.5	1.3	1.7
157Rv3526	-	3661	14665	4.0	0.6	0.3	putative_phthalate_oxygenase	1.1	2	6	3.8	3.5	4.9	3.3	3.8	4.5
3043Rv3530c	-	1824	3821	2.1	0.6	0.3	probable_cis-diol_dehydrogenase	1.1	2	5	2.9	2.4	2.0	nd	1.4	1.8
3764Rv3531c	-	3946	5716	1.5	0.2	0.1		1.1	2	6	1.2	1.5	1.6	1.8	1.5	1.5
3041Rv3534c	-	2754	8453	2.9	0.5	0.2	4-hydroxy-2-oxovalerate_aldolase	1.1	2	6	3.3	3.1	3.0	2.0	3.0	3.2
3762Rv3535c	-	1704	4733	2.7	0.6	0.2	acetaldehyde_dehydrogenase	1.1	2	6	3.4	2.7	2.1	2.2	2.3	3.3
3040Rv3536c	-	1940	4579	2.3	0.4	0.2	aromatic__hydrocarbon_degradation	1.1	2	6	2.1	2.8	2.1	2.1	2.1	2.8
3761Rv3537	-	1793	6521	3.7	0.8	0.3	3-oxosteroid_1-dehydrogenase	1.1	2	6	3.0	3.1	4.8	2.8	3.9	4.5
3039Rv3538	ufaA2	1934	6127	3.1	0.5	0.2	unknown_fatty_acid_methyltransferase	1.1	2	6	3.2	3.6	3.0	2.7	2.3	3.6
875Rv3545c	-	6647	9870	1.5	0.2	0.1	cytochrome_p450	1.3	2	6	1.8	1.4	1.3	1.3	1.4	1.6
151Rv3550	echA20	2410	3589	1.6	0.3	0.1	enoyl-CoA_hydratase/isomerase_superfamily	1.1	2	6	1.2	1.3	1.9	1.5	1.7	1.8
174Rv3556c	fadA6	6313	10691	1.7	0.1	0.1	acetyl-CoA_C-acetyltransferase	1.1	2	6	1.7	1.7	1.8	1.5	1.5	1.8
896Rv3557c	-	3386	8108	2.5	0.7	0.3	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.8	1.8	3.2	2.6	2.3	3.6
175Rv3570c	-	5248	15606	3.1	0.5	0.2	putative_oxidoreductase	1.1	2	6	2.6	3.2	4.0	3.1	2.5	3.0
897Rv3571	-	3473	5345	1.6	0.2	0.1	electron_transfer_component_of_monooxygenase	1.1	2	6	1.5	1.3	1.9	1.5	1.4	1.8
177Rv3574	-	2837	5383	1.9	0.3	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	1.9	1.7	2.3	1.6	1.6	2.2
3063Rv3582c	-	4425	11840	2.6	0.3	0.1		1.1	2	6	2.9	2.5	2.5	2.1	2.4	3.0
3785Rv3583c	-	7586	15696	2.0	0.4	0.1	putative_transcriptional_regulator	1.1	2	6	2.1	2.7	1.6	1.9	1.8	2.2
3438Rv3597c	Isr2	7086	13601	1.9	0.1	0.0		1.1	2	6	1.8	2.0	1.8	1.9	2.0	2.0
5007Rv3603c	-	2894	11022	4.0	1.5	0.6		1.1	2	6	2.3	2.3	5.2	3.6	5.1	5.6
553Rv3603c	-	4367	6811	1.6	0.3	0.1		2.6	2	6	1.4	1.4	2.0	1.4	1.6	1.7
1271Rv3610c	ftsH	7600	11227	1.6	0.3	0.1	inner_membrane_protein,_chaperone	1.1	2	6	1.2	1.1	1.8	1.7	1.8	1.8
4156Rv3616c	-	7199	11901	1.6	0.2	0.1		1.1	2	6	2.0	1.6	1.5	1.4	1.7	1.6
311Rv3619c	-	11569	16143	1.5	0.3	0.1		1.1	2	6	1.1	1.3	1.8	1.8	1.3	1.5
1032Rv3620c	-	14347	21935	1.6	0.2	0.1		1.1	2	6	1.2	1.4	1.7	1.8	1.4	1.7
306Rv3641c	fic	2434	4239	1.7	0.4	0.2	possible_cell_division_protein	1.1	2	6	2.4	1.9	1.5	1.4	1.4	1.5
305Rv3643	-	3435	5579	1.6	0.2	0.1		1.1	2	6	1.5	1.3	1.9	1.6	1.6	2.0
304Rv3645	-	5683	7997	1.6	0.4	0.2	probable_transmembrane_protein	1.1	2	6	1.1	1.0	2.1	1.7	1.8	1.7
301Rv3651	-	5653	8229	1.5	0.3	0.1		1.1	2	6	1.2	1.1	1.7	1.6	1.6	1.7
4602Rv3681c	whiB4	3663	6652	1.8	0.6	0.2	WhiB_transcriptional_activator_homologue	1.1	2	6	2.5	2.6	1.3	1.3	1.4	1.5
2444Rv3710	leuA	2905	8989	3.1	0.3	0.1	2-isopropylmalate_synthase	1.4	2	6	2.7	3.1	3.5	2.9	3.2	3.2
4610Rv3722c	-	8152	16084	2.0	0.3	0.1		1.1	2	6	1.7	1.5	2.2	2.2	2.1	2.3
5332Rv3723	-	5085	7772	1.5	0.1	0.1		1.1	2	6	1.5	1.7	1.4	1.5	1.4	1.7
4611Rv3724	-	3006	7290	2.3	0.3	0.1	probable_cutinase_precursor	1.1	2	6	2.5	2.5	1.9	2.3	2.1	2.7
2452Rv3739c	PPE	4388	6892	1.6	0.2	0.1		1.4	2	6	1.7	1.8	1.2	1.5	1.5	1.7
5340Rv3751	-	2346	3481	1.6	0.2	0.1	putative_integrase	1.1	2	5	1.5	1.7	1.8	nd	1.4	1.4
2075Rv3766	-	2152	4854	2.4	0.6	0.2		1.1	2	6	1.7	1.6	3.3	2.4	2.6	2.5
1509Rv3769	-	5502	8829	1.5	0.4	0.1	possible_coiled-coil_protein	1.1	2	6	1.9	2.1	1.4	1.3	1.4	1.1
4397Rv3782	rfbE	5516	9524	1.9	0.4	0.2	similar_to_rhamnosyl_transferase	1.1	2	6	1.4	2.0	1.8	2.5	1.8	1.7
1511Rv3786c	-	2958	4930	1.7	0.2	0.1		1.1	2	6	1.8	1.9	1.8	1.3	1.7	1.4

4958Rv3797	fadE35	2257	3321	1.5	0.4	0.1	acyl-CoA_dehydrogenase_	1.1	2	6	1.0	1.2	1.6	1.4	1.6	2.0
5682Rv3801c	fadD32	5387	16942	3.1	1.1	0.5	acyl-CoA_synthase	1.1	2	6	3.3	5.3	2.3	2.4	2.7	2.7
890Rv3824c	papA1	6360	9696	1.6	0.5	0.2	PKS-associated_protein,_unknown_function_	1.1	2	6	2.2	2.2	1.4	1.1	1.2	1.3
5144Rv3833	-	2171	4138	1.9	0.2	0.1	transcriptional_regulator_(AraC/XylS_family)	1.1	2	6	2.0	1.8	2.2	1.9	1.6	2.0
1533Rv3848	-	3508	4763	1.6	0.6	0.2	probable_membrane_protein	1.1	2	6	1.2	1.2	1.7	2.7	1.6	1.2
2252Rv3853	menG	2456	12555	5.5	1.3	0.5	S-adenosylmethionine:2-demethylmenaquinone_	1.1	2	6	4.2	4.8	7.2	6.4	6.5	4.1
1530Rv3854c	-	2516	29760	13.9	5.7	2.3	probable_monooxygenase	1.1	2	6	8.2	11.9	23.6	17.6	12.5	9.9
2251Rv3855	-	1917	15281	8.5	2.0	0.8	putative_transcriptional_regulator	1.1	2	6	5.5	7.3	11.2	8.7	8.4	10.2
1529Rv3856c	-	3227	5155	1.6	0.3	0.1		1.1	2	6	1.8	1.9	1.4	1.8	1.6	1.2
5138Rv3857c	-	3636	5804	1.5	0.4	0.2		1.1	2	6	1.7	1.9	0.8	1.2	1.5	1.7
5136Rv3861	-	1606	5003	2.9	0.7	0.3		1.1	2	6	3.2	3.6	2.2	2.1	2.6	3.9
4414Rv3862c	-	8228	17958	2.4	1.0	0.4		1.1	2	6	4.0	2.0	2.0	1.0	2.9	2.8
5135Rv3863	-	4092	7125	1.7	0.1	0.1		1.1	2	6	1.9	1.9	1.7	1.6	1.7	1.5
2850Rv3863	-	2812	4413	1.5	0.3	0.1		1.1	2	6	1.8	1.5	1.7	1.0	1.4	1.9
4413Rv3864	-	9670	18018	1.9	0.3	0.1		1.1	2	6	1.7	1.7	2.1	2.5	1.9	1.8
4971Rv3866	-	9565	15556	1.6	0.3	0.1		1.1	2	6	1.7	2.2	1.3	1.5	1.6	1.5
2800Rv3867	-	3852	7566	1.9	0.3	0.1		1.1	2	6	2.4	2.2	1.9	1.6	1.8	1.7
2081Rv3872	PE	2008	7807	4.0	0.7	0.3		1.1	2	6	3.0	3.2	4.4	3.9	4.3	4.9
2803Rv3873	PPE	3576	10408	2.8	0.8	0.3		1.1	2	6	3.4	2.4	2.9	1.5	3.5	3.4
5686Rv3875	esat6	17014	24967	1.5	0.3	0.1	early_secretory_antigen_target	1.1	2	6	1.3	1.6	1.7	2.0	1.4	1.3
4966Rv3878	-	7255	13354	1.8	0.2	0.1		1.1	2	6	1.8	2.1	1.7	1.7	1.7	2.0
2129Rv3879c	-	2634	5496	2.1	0.3	0.1	N-terminus_is_repetitive_and_highly_Proline-rich	1.1	2	6	2.3	2.2	2.3	1.7	1.9	2.1
2014Rv3915	cwIM	3652	6920	1.9	0.2	0.1	hydrolase	1.1	2	6	1.8	2.0	1.8	1.5	1.9	2.1
2736Rv3916c	-	4089	10562	2.5	0.7	0.3		1.1	2	6	3.4	3.1	2.7	1.7	2.0	2.0
5622Rv3924c	rpmH	10476	15049	1.6	0.6	0.2	50S_ribosomal_protein_L34	1.1	2	6	0.9	0.9	2.1	2.2	1.7	1.6