

Table 2: *Mycobacterium tuberculosis* H37Rv genes repressed after a shift from 20% to 0.2% oxygen. The following microarray data are for individual interpretation. All genes in this table may not be reproducibly repressed. In addition, the table should not be seen as a complete list of all possibly repressed genes. Description of the data table details and analysis methods are described in the data analysis section.

Spot	Name	Gene	Corrected intensity		Average			Gene product	PCR	Individual array ratios (CH2/CH1)					
			Average		Corrected ratios		F			Biol. Set 1		Biol. Set 2		Biol. Set 3	
			CH1 Cye3	CH2 Cye5	CH1/CH2 Repressed	StD				SEM	mL211	mL212	mL204	mL215	mL213
2816	O-strain		115	64	1.6	0.2	0.1	hypothetical protein	1.1	0.6	0.7	0.5	0.6	0.6	0.6
2824	O-strain		90	51	1.6	0.3	0.1	hypothetical protein	2.4	0.7	0.8	0.5	0.6	0.5	0.7
4901	Rv0001	dnaA	283	184	1.8	0.8	0.3	chromosomal_replication_initiator_protein	1.1	0.2	0.4	0.8	0.8	0.5	0.6
4040	Rv0006	gyrA	174	106	1.6	0.4	0.2	DNA_gyrase_subunit_A	1.1	0.4	0.5	0.5	0.7	0.8	0.9
3319	Rv0007	-	84	48	1.6	0.4	0.2		1.1	0.6	0.7	0.5	0.4	0.8	0.8
1035	Rv0014c	pknB	236	119	1.7	0.6	0.2	serine-threonine_protein_kinase	1.1	0.5	0.5	0.4	0.4	0.8	0.9
2216	Rv0014c	pknB	359	220	1.5	0.4	0.2	serine-threonine_protein_kinase	1.1	0.5	0.6	0.5	0.6	0.9	1.0
2217	Rv0016c	pbpA	280	170	1.5	0.3	0.1	penicillin-binding_protein	1.1	0.8	0.8	0.5	0.5	0.7	0.8
1499	Rv0035	fadD34	64	45	1.5	0.3	0.1	acyl-CoA_synthase	1.1	0.6	0.8	0.8	0.8	0.5	0.6
3711	Rv0051	-	42	30	1.5	0.4	0.2	probable_membrane_protein	1.1	0.3	0.8	0.8	0.8	0.8	0.6
826	Rv0057	-	219	144	1.7	0.6	0.3		1.1	0.2	0.7	0.8	0.7	0.5	0.5
4902	Rv0058	dnaB	92	33	2.5	1.3	0.5	DNA_helicase_(contains_intein)	1.1	0.1	0.6	0.2	0.5	0.5	0.5
5624	Rv0058	dnaB	217	103	2.0	0.2	0.1	DNA_helicase_(contains_intein)	1.1	0.5	0.6	0.4	0.5	0.5	0.5
4903	Rv0059	-	117	69	1.7	0.2	0.1		1.1	0.5	0.6	0.7	0.5	0.6	0.6
5625	Rv0060	-	259	179	1.5	0.2	0.1		1.1	0.6	0.6	0.8	0.8	0.6	0.6
2020	Rv0069c	sdaA	47	29	1.5	0.3	0.1	L-serine_dehydratase_1	1.1	0.5	0.6	0.5	0.7	0.8	0.7
1348	Rv0097	-	38	26	1.5	0.4	0.2		1.1	0.4	0.7	0.5	1.0	0.8	0.7
2765	Rv0112	gca	152	108	1.5	0.2	0.1	probable_GDP-mannose_dehydratase	1.1	0.5	0.6	0.7	0.8	0.7	0.7
2044	Rv0113	gmhA	66	32	2.0	0.2	0.1	phosphoheptose_isomerase	1.1	0.5	0.6	0.5	0.5	0.4	0.5
2766	Rv0114	-	110	40	2.7	1.0	0.4	similar_to_HisB	1.1	0.2	0.6	0.3	0.4	0.4	0.4
2045	Rv0115	-	34	20	1.6	0.3	0.1	sim_to_hypos_in_antibiotic_prod_operons	1.1	0.8	0.8	0.6	0.5	0.6	0.5
5650	Rv0118c	oxcA	24	17	1.6	0.3	0.1	oxalyl-CoA_decarboxylase	1.1	0.6	0.6	0.8	0.6	0.6	nd
5080	Rv0165c	-	82	62	1.6	0.7	0.3	transcriptional_regulator_(GntR_family)	1.1	0.1	0.6	0.9	0.8	0.6	0.6
4359	Rv0166	fadD5	61	38	1.7	0.4	0.2	acyl-CoA_synthase	1.1	0.4	0.4	0.6	0.6	0.7	0.7
5081	Rv0167	-	143	90	1.7	0.2	0.1	part_of_mce1_operon	1.2	0.6	0.5	0.7	0.6	0.5	0.5
5082	Rv0169	mce1	244	139	1.8	0.4	0.2	cell_invasion_protein	1.1	0.6	0.6	0.6	0.6	0.4	0.4
4361	Rv0170	-	154	88	1.6	0.8	0.3	part_of_mce1_operon	1.1	1.0	1.0	0.5	0.5	0.3	0.4
269	Rv0171	-	329	166	1.9	0.9	0.4	part_of_mce1_operon	1.1	0.9	0.8	0.5	0.4	0.3	0.3
5083	Rv0171	-	208	114	1.8	0.6	0.3	part_of_mce1_operon	1.1	0.8	0.7	0.6	0.6	0.3	0.4
991	Rv0172	-	363	135	2.5	1.2	0.5	part_of_mce1_operon	1.1	0.7	0.6	0.4	0.4	0.2	0.2
4362	Rv0172	-	123	68	1.8	0.7	0.3	part_of_mce1_operon	1.1	0.8	0.8	0.6	0.5	0.3	0.4
270	Rv0173	lprK	342	154	2.3	1.4	0.6	part_of_mce1_operon	1.1	nd	0.9	0.4	0.5	0.2	0.2

1475Rv0174	-	376	282	1.6	0.6	0.3	part_of_mce1_operon	1.1	0.8	0.8	0.9	0.6	0.3	0.4
2198Rv0177	-	313	209	1.5	0.6	0.2		1.1	0.3	0.4	0.6	0.7	0.9	1.0
966Rv0205	-	211	160	1.5	0.4	0.1	probable_membrane_protein	1.1	0.7	0.7	0.9	0.9	0.5	0.5
5228Rv0232	-	48	31	1.6	0.7	0.3	transcriptional_regulator_(TetR/AcrR_family)	1.1	0.2	0.8	0.5	0.6	0.9	0.7
2342Rv0236c	-	31	19	1.6	0.4	0.2	possible_membrane_protein	1.1	nd	0.8	0.6	0.8	0.6	0.4
3855Rv0247c	-	146	76	1.7	0.3	0.1	probable_iron-sulphur_protein	1.1	0.6	0.7	0.4	0.5	0.6	0.7
3860Rv0284	-	565	220	1.6	0.9	0.4		1.1	1.0	1.0	0.3	0.2	0.6	0.6
2684Rv0301	-	201	105	1.8	0.3	0.1		1.1	nd	0.8	0.5	0.5	0.5	0.5
1963Rv0302	-	54	22	2.3	0.5	0.2	transcriptional_regulator_(TetR/AcrR_family)	1.1	0.4	0.6	0.4	0.6	0.4	0.4
2685Rv0303	-	111	67	1.6	0.2	0.1	similar_to_NADPH_dehydrogenase	1.1	nd	0.7	0.6	0.7	0.6	0.5
5573Rv0315	-	300	167	1.9	0.2	0.1	probable_b-1,3-glucanase	1.2	0.5	0.5	0.6	0.5	0.5	0.5
322Rv0358	-	33	21	1.5	0.5	0.2		2.6	0.5	1.0	0.6	0.7	nd	0.6
2579Rv0362	mgtE	96	64	1.5	0.2	0.1	putative_magnesium_ion_transporter	1.1	0.7	0.8	0.7	0.7	0.5	0.6
2580Rv0364	-	86	52	1.6	0.3	0.1		1.1	0.5	0.6	0.5	0.6	0.7	0.8
3844Rv0404	fadD30	45	28	1.8	0.5	0.2	acyl-CoA_synthase	1.1	0.4	0.5	0.7	0.8	0.5	0.5
3642Rv0405	pks6	82	32	2.2	0.9	0.4	polyketide_synthase	1.1	0.6	0.8	0.3	0.4	0.3	0.3
3896Rv0422c	thiD	41	25	1.6	0.4	0.2	phosphomethylpyrimidine_kinase	1.1	0.5	0.9	0.6	0.6	0.6	0.5
4068Rv0424c	-	119	56	2.1	0.4	0.2		1.1	0.3	0.5	0.4	0.5	0.6	0.6
3351Rv0434	-	83	39	2.1	0.2	0.1		1.1	0.5	0.5	0.5	0.4	0.5	0.5
1328Rv0463	-	227	146	1.5	0.2	0.1		1.1	0.8	0.7	0.6	0.5	0.7	0.8
607Rv0464c	-	289	175	1.5	0.2	0.1		1.1	0.7	0.8	0.6	0.6	0.6	0.6
1329Rv0465c	-	137	78	1.5	0.3	0.1	transcriptional_regulator_(PbsX/Xre_family)	1.1	0.6	0.8	0.5	0.6	0.7	0.7
4212Rv0467	aceA	263	85	2.1	1.1	0.4	isocitrate_lyase	1.1	0.6	0.8	0.2	0.2	0.6	0.5
3491Rv0468	fadB2	139	79	1.6	0.3	0.1	3-hydroxyacyl-CoA_dehydrogenase	1.1	0.7	0.8	0.5	0.5	0.6	0.6
4213Rv0469	umaA1	353	189	1.9	0.3	0.1	unknown_mycolic_acid_methyltransferase	1.1	0.5	0.5	0.5	0.6	0.4	0.6
3933Rv0469	umaA2	503	282	1.9	0.3	0.1	unknown_mycolic_acid_methyltransferase	1.1	0.5	0.5	0.6	0.6	0.4	0.5
2260Rv0478	deoC	50	33	1.5	0.4	0.1	deoxyribose-phosphate_aldolase	1.1	0.4	0.8	0.8	0.7	0.7	0.6
1540Rv0481c	-	39	20	1.6	0.4	0.2		1.1	0.5	0.6	0.5	0.7	0.9	0.7
4270Rv0512	hemB	99	62	1.5	0.5	0.2	d-aminolevulinic_acid_dehydratase	1.1	0.5	0.6	0.5	0.5	1.0	0.9
3549Rv0513	-	133	93	1.5	0.6	0.3	probable_membrane_protein	1.1	0.5	0.5	0.6	0.5	1.1	1.0
4271Rv0514	-	56	26	2.1	0.9	0.4	possible_membrane_protein	1.1	0.2	0.5	0.4	0.3	0.7	0.7
1385Rv0518	-	23	16	1.5	0.3	0.1		1.1	0.4	0.7	0.9	0.6	0.6	0.6
1387Rv0522	gabP	49	29	1.5	0.4	0.2	probable_4-amino_butyrate_transporter	1.1	0.7	0.9	0.4	0.6	0.8	0.8
2464Rv0542c	menE	55	26	1.8	0.5	0.2	o-succinylbenzoic_acid-CoA_ligase_	1.1	0.6	0.8	0.4	0.4	0.6	0.4
5353Rv0556	-	109	60	1.8	0.4	0.2	possible_membrane_protein	1.1	0.4	0.7	0.5	0.5	0.5	0.7
1174Rv0586	-	42	25	1.7	0.5	0.2	transcriptional_regulator_(GntR_family)	1.3	0.3	0.8	0.6	0.7	0.5	0.6
4061Rv0588	-	170	109	1.6	0.2	0.1	part_of_mce2_operon	1.1	0.7	0.7	0.6	0.6	0.5	0.6
4060Rv0590	-	51	27	1.8	0.3	0.1	part_of_mce2_operon	1.1	0.6	0.6	0.5	0.7	0.5	0.5
3169Rv0590	-	52	36	1.5	0.3	0.1	part_of_mce2_operon	1.1	0.7	0.7	0.8	0.8	0.5	0.5
4056Rv0598c	-	86	51	1.5	0.5	0.2		1.4	0.9	0.9	0.6	0.6	0.5	0.5

451Rv0601c	-	62	47	1.6	0.5	0.2	sensor_histidine_kinase	2.1	0.3	0.6	0.9	0.7	0.8	0.6
1172Rv0602c	tcrA	108	76	1.5	0.2	0.1	two-component_response_regulator	1.4	0.5	0.7	0.8	0.8	0.6	0.7
1489Rv0668	rpoC	221	177	1.5	1.1	0.4	b'_subunit_of_RNA_polymerase	1.1	1.6	0.6	0.5	0.4	0.4	0.5
2210Rv0669c	-	158	97	1.6	0.2	0.1		1.1	0.7	0.7	0.6	0.6	0.6	0.5
4768Rv0685	tuf	354	234	1.6	0.2	0.1	elongation_factor_EF-Tu	1.1	0.5	0.5	0.7	0.7	0.7	0.7
5492Rv0690c	-	48	30	1.5	0.4	0.2		1.1	nd	0.8	0.4	0.6	0.7	0.8
5493Rv0692	-	219	162	1.5	0.2	0.1		1.1	0.5	0.8	0.8	0.7	0.6	0.7
1884Rv0693	pqqE	102	55	1.9	0.1	0.0	coenzyme_PQQ_synthesis_protein_E	1.1	0.6	0.5	0.5	0.5	0.5	0.5
2606Rv0694	lldD1	114	37	3.1	1.1	0.5	L-lactate_dehydrogenase_(cytochrome)_	1.1	0.2	0.5	0.3	0.4	0.3	0.3
1885Rv0695	-	52	19	2.7	0.8	0.3		1.1	0.3	0.6	0.4	0.4	0.3	0.4
2607Rv0696	-	56	20	2.6	1.0	0.4	glycosyltransferase	1.1	0.3	0.6	0.3	0.5	0.3	0.2
5494Rv0704	rplB	252	236	1.5	1.0	0.4	50S_ribosomal_protein_L2	1.1	0.0	0.4	1.2	1.2	0.6	0.7
4773Rv0705	rpsS	396	289	1.7	0.6	0.2	30S_ribosomal_protein_S19	1.1	0.5	0.5	0.9	0.8	0.4	0.5
5495Rv0706	rplV	121	58	2.1	0.4	0.2	50S_ribosomal_protein_L22	1.1	nd	0.6	0.5	0.5	0.4	0.4
4774Rv0707	rpsC	299	128	2.1	0.7	0.3	30S_ribosomal_protein_S3	1.1	0.7	0.6	0.4	0.4	0.3	0.3
5496Rv0708	rplP	641	225	2.3	1.0	0.4	50S_ribosomal_protein_L16	1.1	0.7	0.7	0.3	0.3	0.3	0.4
675Rv0708	rplP	272	99	2.1	0.9	0.4	50S_ribosomal_protein_L16	1.1	0.7	0.7	0.3	0.3	0.3	0.4
4775Rv0709	rpmC	258	78	2.7	1.7	0.7	50S_ribosomal_protein_L29_	1.1	0.7	0.6	0.3	0.3	0.1	0.2
1005Rv0710	rpsQ	182	46	3.2	2.1	0.9	30S_ribosomal_protein_S17	2.6	0.6	0.6	0.2	0.2	0.1	0.1
1397Rv0710	rpsQ	305	87	3.0	1.9	0.8	30S_ribosomal_protein_S17	1.4	0.6	0.6	0.3	0.2	0.1	0.2
5497Rv0710	rpsQ	47	17	2.7	0.8	0.4	30S_ribosomal_protein_S17	1.3	nd	0.6	0.4	0.3	0.3	0.3
1892Rv0719	rplF	209	179	1.6	0.8	0.3	50S_ribosomal_protein_L6	1.1	0.3	0.4	1.0	1.0	0.5	0.6
2614Rv0720	rplR	80	46	2.0	0.5	0.2	50S_ribosomal_protein_L18	1.1	0.3	0.5	0.7	0.7	0.5	0.5
1893Rv0721	rpsE	92	58	1.5	0.2	0.1	30S_ribosomal_protein_S5	1.1	0.7	0.8	0.6	0.5	0.6	0.7
2615Rv0722	rpmD	234	81	2.4	0.9	0.3	50S_ribosomal_protein_L30	1.1	0.6	0.6	0.3	0.2	0.4	0.4
1894Rv0723	rplO	216	108	1.8	0.5	0.2	50S_ribosomal_protein_L15	1.1	0.8	0.8	0.5	0.4	0.5	0.5
3506Rv0741	IS1557'	112	67	1.7	0.2	0.1	truncated_copy_of_IS1557	1.1	0.7	0.6	0.6	0.5	0.6	0.6
4229Rv0744c	-	174	112	1.5	0.2	0.1	putative_transcriptional_regulator	1.1	0.6	0.8	0.6	0.6	0.6	0.6
1926Rv0772	purD	58	32	1.6	0.7	0.3	phosphoribosylamine-glycine_ligase	1.1	0.3	1.1	0.5	0.6	0.7	0.5
2648Rv0773c	ggtA	50	28	1.7	0.3	0.1	putative_g-glutamyl_transpeptidase	1.1	0.5	0.7	0.5	0.6	0.7	0.6
5440Rv0797	IS1547	80	38	1.8	0.5	0.2		1.2	0.6	0.8	0.3	0.4	0.6	0.6
4278Rv0908	ctpE	50	29	1.5	0.5	0.2	probable_cation_transport_ATPase	1.1	0.6	0.9	0.4	0.5	0.7	0.7
1733Rv0919	-	84	52	1.5	0.9	0.4		1.2	1.3	0.4	nd	0.5	0.5	0.5
2345Rv0933	pstB	129	62	1.6	0.7	0.3	ABC_transport_component_of_phosphate_uptake	1.1	0.8	1.1	0.4	0.5	0.5	0.5
1623Rv0934	phoS1	161	90	1.8	0.3	0.1	PstS_component_of_phosphate_uptake	1.4	0.7	0.6	0.6	0.5	0.5	0.5
1001Rv0935	pstC	129	56	2.4	0.7	0.3	PstC_component_of_phosphate_uptake	1.1	0.2	0.5	0.4	0.5	0.4	0.4
1622Rv0936	pstA2	87	40	1.9	0.7	0.3	PstA_component_of_phosphate_uptake	1.4	0.9	0.7	0.4	0.4	0.4	0.4
4989Rv0937c	-	110	45	2.1	0.8	0.3		1.1	0.6	0.8	0.4	0.4	0.3	0.5
3306Rv0947c	-	44	29	1.5	0.2	0.1		1.2	0.7	0.8	0.7	0.6	0.7	0.6
4027Rv0948c	-	175	106	1.6	0.3	0.1		1.1	0.5	0.6	0.5	0.6	0.7	0.8

4026Rv0950c	-	83	47	1.7	0.2	0.1		1.1	0.6	0.7	0.6	0.5	0.5	0.5
417Rv0961	-	68	44	1.5	0.2	0.1		1.2	nd	0.7	0.6	0.6	0.7	0.7
4025Rv0964c	-	31	20	1.5	0.3	0.1		1.1	0.5	0.8	0.5	0.8	0.8	0.7
406Rv0988	-	105	49	2.0	0.3	0.1		1.1	0.5	0.6	0.4	0.5	0.4	0.5
1131Rv0995	rimJ	70	50	1.6	0.2	0.1	acetylation_of_30S_S5_subunit	1.2	0.5	0.7	0.8	0.6	0.6	0.7
4014Rv0997	-	119	50	1.8	0.9	0.4		1.1	0.9	0.9	0.3	0.5	0.3	0.3
2191Rv1006	-	339	225	1.5	0.1	0.0		1.1	0.6	0.6	0.7	0.6	0.7	0.7
2193Rv1010	ksgA	90	58	1.8	0.6	0.2	16S_rRNA_dimethyltransferase	1.1	0.2	0.6	0.7	0.6	0.7	0.6
267Rv1010	ksgA	69	48	1.6	0.3	0.1	16S_rRNA_dimethyltransferase	1.1	0.5	0.5	0.8	0.6	0.7	0.8
1150Rv1025	-	66	40	1.8	0.7	0.3		1.1	0.2	0.6	0.7	0.6	0.7	0.6
4032Rv1037c	-	278	190	1.5	0.1	0.0		1.2	0.6	0.7	0.7	0.6	0.7	0.8
1147Rv1043c	-	79	35	1.9	0.9	0.4		1.1	0.6	1.0	0.4	0.4	0.4	0.3
1145Rv1047	IS1081	243	110	2.1	0.5	0.2		1.1	0.4	0.5	0.4	0.4	0.6	0.6
3574Rv1068c	PE_PGRS	296	200	1.5	0.3	0.1		2.1	0.9	0.6	0.7	0.6	0.5	0.6
2398Rv1107c	xseB	296	169	1.7	0.2	0.1	exonuclease_VII_small_subunit	1.1	0.6	0.7	0.5	0.5	0.6	0.6
1186Rv1113	-	76	50	1.6	0.2	0.1		1.1	0.5	0.7	0.6	0.6	0.8	0.7
466Rv1116	-	55	35	1.6	0.4	0.1	questionable_ORF	1.1	0.3	0.6	0.7	0.7	0.7	0.7
3354Rv1128c	REP	69	21	2.5	1.1	0.5		1.1	0.5	0.7	0.3	0.2	0.3	0.4
4076Rv1129c	-	614	48	5.1	4.5	1.8	transcriptional_regulator_(PbsX/Xre_family)	1.1	0.4	0.4	0.0	0.1	0.1	0.1
3355Rv1130	-	444	47	4.6	3.8	1.5		1.1	0.4	0.4	0.1	0.0	0.2	0.2
4077Rv1131	gltA1	222	61	2.6	1.2	0.5	citrate_synthase_3	1.1	0.6	0.6	0.2	0.3	0.3	0.3
3356Rv1132	-	114	54	2.0	0.3	0.1	possible_transporter	1.1	0.5	0.6	0.5	0.4	0.5	0.5
1283Rv1165	-	45	22	1.9	0.6	0.3		1.1	0.2	0.7	0.4	0.5	0.6	0.6
4173Rv1181	pks4	158	62	1.8	0.7	0.3	polyketide_synthase	1.1	0.7	0.8	0.3	0.4	0.5	0.6
3452Rv1182	papA3	159	80	1.6	0.9	0.4	PKS-associated_protein,_unknown_function	1.1	1.2	1.0	0.5	0.5	0.3	0.3
4174Rv1183	mmpL10	82	24	2.6	1.4	0.6	conserved_large_membrane_protein	1.1	0.6	0.7	0.2	0.3	0.3	0.2
3453Rv1184c	-	436	127	2.4	1.4	0.6		1.1	0.5	0.9	0.2	0.2	0.3	0.4
4175Rv1185c	fadD21	578	284	2.0	0.3	0.1	acyl-CoA_synthase	1.1	0.4	0.5	0.4	0.6	0.5	0.6
2204Rv1198	-	34	20	2.8	2.1	1.5		2.6	0.2	nd	0.6	nd	nd	nd
1483Rv1199c	IS1081	316	154	1.9	0.5	0.2		1.1	0.4	0.5	0.4	0.4	0.6	0.7
2205Rv1200	-	98	52	1.6	0.5	0.2	probable_sugar_transporter	1.1	0.7	0.9	0.5	0.4	0.5	0.5
5444Rv1225c	-	88	63	1.5	0.7	0.3		1.1	0.1	0.7	0.6	0.6	1.1	1.0
573Rv1251c	-	34	22	1.6	0.4	0.1	some_similarity_to_GTP-binding_proteins	1.1	0.4	0.6	0.7	0.7	0.9	0.5
5568Rv1254	-	42	23	1.8	0.2	0.1	acyltransferase	1.1	nd	0.5	0.5	0.6	0.6	0.6
5567Rv1256c	-	31	22	1.6	0.3	0.2	Probable_cytochrome_P-450	1.1	0.4	0.7	nd	0.6	0.7	0.7
1959Rv1265	-	56	35	1.5	0.6	0.2		1.1	1.0	0.9	0.7	0.7	0.4	0.3
1401Rv1272c	-	46	29	1.5	0.3	0.1	probable_ABC_transporter	1.1	0.5	0.9	0.6	0.7	0.7	0.6
5562Rv1280c	oppA	106	52	1.5	0.7	0.3	probable_oligopeptide_transport_protein	2.1	1.1	1.0	0.2	0.4	0.6	0.7
887Rv1282c	oppC	52	32	1.6	0.1	0.0	oligopeptide_transport_system_permease	1.1	nd	0.7	0.6	0.6	0.6	0.6
2658Rv1297	rho	393	234	1.9	0.9	0.4	transcription_termination_factor_rho	1.1	0.2	0.2	0.7	0.8	0.6	0.7

1937Rv1298	rpmE	224	181	1.5	0.7	0.3	50S_ribosomal_protein_L31	1.1	0.3	0.6	1.0	0.9	0.5	nd
2659Rv1299	prfA	474	300	1.8	0.5	0.2	peptide_chain_release_factor_1	1.2	0.5	0.4	0.7	0.7	0.4	0.5
4821Rv1302	rfe	55	30	1.6	0.5	0.2	undecaprenyl-phosphate_a-N-acetylglucosaminyltransferase	1.1	nd	0.9	0.5	0.6	0.6	0.5
5546Rv1309	atpG	498	298	1.6	0.2	0.1	ATP_synthase_g_chain	1.1	0.7	0.7	0.6	0.7	0.5	0.6
4825Rv1310	atpD	343	190	1.7	0.6	0.2	ATP_synthase_b_chain	1.1	0.9	0.8	0.6	0.5	0.4	0.4
1938Rv1312	-	119	55	2.2	0.8	0.3		1.2	0.4	0.7	0.5	0.5	0.3	0.3
2660Rv1313c	IS1557	81	47	1.7	0.3	0.1	transposase	1.1	0.5	0.6	0.6	0.7	0.6	0.6
1003Rv1316c	ogt	156	97	1.8	0.5	0.2	methylated-DNA-protein-cysteine_methyltransferase	1.1	0.6	0.5	0.8	0.7	0.4	0.4
2223Rv1317c	alkA	64	41	1.6	0.2	0.1	DNA-3-methyladenine_glycosidase_II	1.1	0.6	0.7	0.7	0.7	0.5	0.5
2224Rv1319c	-	47	28	1.5	0.2	0.1	similar_at_C-term_to_adenylate_cyclases	1.1	nd	0.7	0.5	0.6	0.7	0.8
4780Rv1387	PPE	628	397	1.5	0.5	0.2		1.1	0.4	0.6	0.6	0.5	0.9	1.0
4294Rv1440	secG	85	59	1.5	0.2	0.1	protein-export_membrane_protein_SecG	1.1	0.7	0.7	0.7	0.8	0.5	0.6
2329Rv1444c	-	132	91	1.5	0.1	0.0		1.1	0.6	0.7	0.7	0.7	0.6	0.7
575Rv1457c	-	49	24	1.9	0.4	0.2	probable_membrane_protein	1.1	0.5	0.6	0.4	0.4	0.7	0.6
1299Rv1462	-	188	99	1.5	0.5	0.2		1.1	0.8	0.8	0.5	0.3	0.9	0.7
3528Rv1463	-	128	63	1.5	0.5	0.2	ABC-type_transporter	1.4	0.7	0.8	0.4	0.4	0.8	0.8
4182Rv1464	-	81	35	1.6	0.6	0.2	NifS-like_protein	1.1	0.7	0.7	0.3	0.4	0.9	0.8
3461Rv1465	-	85	46	1.5	0.4	0.2		1.1	0.7	0.8	0.5	0.4	0.9	0.8
4183Rv1466	-	82	26	1.8	0.8	0.3		1.1	0.6	0.7	0.1	0.4	0.8	0.7
3639Rv1485	hemZ	59	37	1.7	0.4	0.2	ferrochelatase	1.1	0.4	0.8	0.6	0.5	0.7	0.6
1920Rv1490	-	59	39	1.5	0.3	0.1	unknown_putative_membrane_protein	1.1	0.5	0.6	0.6	0.7	0.8	0.8
1413Rv1502	-	204	133	1.6	0.3	0.1		1.1	0.5	0.6	0.7	0.8	0.5	0.7
4809Rv1504c	-	89	48	1.9	0.4	0.2		1.1	0.4	0.7	0.6	0.6	0.4	0.5
5531Rv1505c	-	109	42	2.5	0.7	0.3	polysialic_acid_synthesis?	1.1	0.2	0.5	0.3	0.5	0.4	0.5
4810Rv1506c	-	55	26	2.1	0.3	0.1		1.1	0.5	0.5	0.5	0.4	0.4	0.6
5532Rv1507c	-	119	75	1.6	0.2	0.1		1.1	nd	0.5	0.6	0.7	0.6	0.8
1167Rv1519	-	44	26	1.7	0.6	0.3		1.1	0.3	0.7	0.6	0.5	0.9	0.7
2922Rv1527c	pks5	57	34	1.5	0.3	0.1	polyketide_synthase	1.1	0.8	0.9	0.5	0.5	0.6	0.7
5199Rv1547	dnaE1	160	105	1.6	0.2	0.1	DNA_polymerase_III_a_subunit	1.4	0.5	0.6	0.7	0.7	0.6	0.7
4139Rv1561	-	51	32	1.6	0.3	0.1		1.1	0.5	0.8	0.7	0.7	0.6	0.5
3379Rv1567c	-	47	32	1.6	0.5	0.2		1.1	0.3	0.6	0.7	0.6	0.9	0.8
5452Rv1612	trpB	231	105	2.1	0.4	0.1	tryptophan_synthase_b_chain	1.2	0.4	0.5	0.4	0.4	0.5	0.6
4731Rv1613	trpA	393	171	2.2	0.3	0.1	tryptophan_synthase_a_chain	1.1	0.5	0.6	0.4	0.3	0.5	0.4
5453Rv1614	lgt	537	192	2.5	0.4	0.2	prolipoprotein_diacylglyceryl_transferase	1.1	0.4	0.5	0.3	0.3	0.4	0.4
2574Rv1632c	-	75	30	2.3	0.6	0.3		1.2	0.4	0.7	0.4	0.3	0.4	0.4
3674Rv1640c	lysX	237	98	2.3	0.9	0.4	C-term_lysyl-tRNA_synthase	2.1	0.6	0.6	0.5	0.6	0.2	0.2
67Rv1645c	-	105	70	1.6	0.2	0.1		1.1	0.6	0.7	0.7	0.6	0.5	0.6
3584Rv1656	argF	93	60	1.5	0.2	0.1	ornithine_carbamoyltransferase	2.4	0.8	0.7	0.7	0.5	0.6	0.6
4005Rv1682	-	32	20	1.6	0.4	0.2	probable_coiled-coil_structural_protein	1.1	0.4	0.7	0.7	0.7	0.5	0.5
1125Rv1698	-	119	65	1.6	0.8	0.3		1.1	0.9	1.0	0.5	0.6	0.3	0.3

404Rv1711	-	102	72	1.6	0.5	0.2		1.1	0.4	0.4	0.7	0.7	0.8	0.8
405Rv1713	-	53	28	2.0	0.7	0.3	probable_GTP-binding_protein_YPHC_BACSU	1.1	0.2	0.5	0.5	0.5	0.7	0.6
386Rv1716	-	46	21	2.3	0.4	0.2		1.2	0.3	0.5	0.5	0.4	0.5	0.4
994Rv1716	-	38	20	1.9	0.4	0.2		1.3	0.4	0.6	0.5	0.6	0.5	0.5
3997Rv1731	gabD1	27	17	2.0	0.8	0.3	succinate-semialdehyde_dehydrogenase	1.1	0.2	0.6	nd	0.7	0.5	0.4
397Rv1751	-	129	85	1.5	0.9	0.4	possible_hydroxylase	1.1	0.1	0.6	0.6	0.4	1.1	1.2
4236Rv1753c	PPE	119	56	1.8	0.5	0.2		1.1	0.7	0.7	0.3	0.5	0.5	0.6
1119Rv1753c	PPE	37	22	1.7	0.2	0.1		1.1	nd	0.6	0.6	0.7	0.6	0.6
5712Rv1792		848	570	1.5	0.2	0.1		1.1	0.6	0.6	0.7	0.6	0.7	0.9
5660Rv1797	-	140	63	1.8	0.6	0.2		1.1	0.6	0.8	0.3	0.4	0.6	0.6
4939Rv1798	-	177	104	1.6	0.2	0.1	CBXX/CFQX_family	1.1	0.7	0.7	0.6	0.5	0.6	0.6
2246Rv1822	pgsA2	85	47	1.9	0.6	0.3	CDP-diacylglycerol-glycerol-3-phosphate_phosphatidyltransferase	1.1	0.2	0.7	0.5	0.6	0.6	0.6
3221Rv1870c	-	301	138	2.2	0.8	0.3		1.1	0.6	0.6	0.5	0.5	0.2	0.3
3695Rv1903	-	74	48	1.6	0.3	0.1	unknown_membrane_protein	1.1	0.6	0.8	0.7	0.7	0.5	0.6
2779Rv1918c	PPE	98	64	1.6	0.1	0.1		1.2	0.6	0.6	0.7	0.6	0.6	0.7
2718Rv1927	-	60	39	1.7	0.4	0.2		1.1	nd	0.8	0.6	0.6	0.5	0.5
1992Rv1936	-	133	83	1.5	0.4	0.2	similar_alkanal_monooxygenase_alpha_chain	1.1	0.8	0.9	0.6	0.7	0.5	0.5
5601Rv1937	-	41	29	1.5	0.2	0.1	similar_to_ring-hydroxylating_dioxygenases	1.1	0.6	0.8	nd	0.6	0.7	0.6
5598Rv1943c	-	120	69	1.6	0.7	0.3		1.1	0.2	0.6	0.5	0.6	0.8	1.0
2713Rv1949c	-	64	35	1.7	0.2	0.1		1.1	0.5	0.6	0.5	0.5	0.6	0.6
2805Rv1970	lprM	75	44	1.7	0.2	0.1	part_of_mce3_operon	1.4	0.5	0.7	0.6	0.7	0.5	0.5
5556Rv1979c	-	166	130	1.5	0.6	0.3	unknown_permease	1.1	0.3	0.6	1.0	1.1	0.5	0.7
2664Rv2009	-	129	89	1.5	0.3	0.1		1.1	0.7	0.9	0.7	0.8	0.5	0.5
1942Rv2010	-	64	40	1.6	0.3	0.1		1.1	0.6	0.9	0.7	0.7	0.5	0.5
2663Rv2011c	-	33	22	1.5	0.4	0.2		1.4	0.5	0.9	nd	nd	0.6	0.6
1757Rv2047c	-	32	22	1.6	0.3	0.2		1.1	0.8	0.6	nd	0.6	0.5	0.6
5293Rv2048c	pks12	582	302	1.9	0.5	0.2	polyketide_synthase_(erythronolide_synthase-like)	1.1	0.6	0.7	0.6	0.4	0.4	0.4
2024Rv2062c	cobN	22	17	1.6	0.4	0.2	cobalt_insertion_	1.1	0.4	nd	nd	0.8	0.6	0.7
2481Rv2081c	-	145	83	1.6	0.2	0.1		1.1	0.6	0.7	0.5	0.5	0.7	0.6
5208Rv2081c	-	247	158	1.5	0.2	0.1		1.1	0.6	0.7	0.6	0.5	0.7	0.8
5164Rv2129c	-	70	38	1.6	0.3	0.1	putative_oxidoreductase	1.1	nd	0.7	0.4	0.6	0.7	0.7
4911Rv2174	-	125	75	1.8	0.3	0.1	_probable_membrane_protein	1.3	0.6	0.6	0.7	0.4	0.5	nd
5634Rv2177c	IS1558	38	25	1.6	0.2	0.1		1.1	nd	0.7	nd	0.6	0.5	0.6
2752Rv2189c	-	106	56	1.8	0.3	0.1		1.1	nd	0.7	0.5	0.6	0.5	0.5
509Rv2227	-	84	55	1.5	0.2	0.1		1.1	nd	0.7	0.6	0.8	0.6	0.7
952Rv2248	-	179	93	2.1	0.2	0.1		1.1	0.5	0.5	0.6	0.4	0.4	0.5
2915Rv2248	-	76	46	1.8	0.2	0.1		1.1	0.5	0.6	0.6	0.6	0.5	nd
5638Rv2257c	-	75	47	1.5	0.4	0.2		1.1	0.7	0.9	0.6	0.6	0.6	0.5
4917Rv2258c	-	49	29	1.8	0.5	0.2	putative_transcriptional_regulator	1.1	0.2	0.7	0.6	0.5	0.6	0.6
4115Rv2273	-	60	27	2.0	0.4	0.1		1.1	0.4	0.6	0.4	0.5	0.5	0.5

3392Rv2276	-	197	121	1.8	0.3	0.1	Probable_cytochrome_P-450	1.1	0.5	0.5	0.7	0.7	0.5	0.5
4113Rv2277c	-	54	32	1.6	0.4	0.2	possible_glycerolphosphodiesterase	1.1	0.8	0.9	0.5	0.6	0.5	0.5
1225Rv2289	cdh	175	104	1.6	0.3	0.1	CDP-diacylglycerol_phosphatidylhydrolase	1.1	0.7	0.8	0.6	0.6	0.5	0.6
5372Rv2335	cysE	69	42	1.8	0.6	0.2	serine_acetyltransferase	1.1	0.2	0.7	0.6	0.6	0.6	0.6
4509Rv2336	-	71	41	1.7	0.2	0.1		1.1	0.6	0.7	0.5	0.6	0.6	0.7
5231Rv2337c	-	37	25	1.5	0.2	0.1		1.1	nd	0.7	0.7	0.8	0.6	0.6
5232Rv2339	mmpL9	62	34	1.7	0.3	0.1	conserved_large_membrane_protein	1.1	nd	0.5	0.5	0.5	0.7	0.7
5166Rv2375	-	267	199	1.5	0.3	0.1		1.1	0.5	0.6	0.8	0.7	0.7	0.7
2269Rv2394	ggtB	123	89	1.5	0.3	0.1	g_-glutamyltranspeptidase_precursor	1.1	0.6	0.8	0.8	0.8	0.5	0.6
5155Rv2398c	cysW	68	54	1.5	0.5	0.2	sulphate_transport_system_permease_protein	1.1	0.5	0.8	0.9	0.9	0.5	0.4
1238Rv2434c	-	60	36	1.7	0.3	0.1	probable_membrane_protein	1.1	0.4	0.8	0.6	0.5	0.6	0.7
516Rv2435c	-	78	43	1.8	0.3	0.1	similar_to_adenylate/guanylate_cyclases	1.1	0.5	0.5	0.5	0.7	0.5	0.6
1234Rv2443	dctA	156	96	1.6	0.4	0.2	C4-dicarboxylate_transport_protein	1.1	0.4	0.7	0.6	0.7	0.6	0.7
415Rv2512c	IS1081	346	149	2.2	0.8	0.3		1.1	0.3	0.4	0.4	0.3	0.6	0.7
5260Rv2523c	acpS	71	45	1.7	0.3	0.1	CoA:apo-[ACP]_pantethienephosphotransferase	1.1	0.4	0.6	0.7	0.5	0.6	0.7
1866Rv2530c	-	59	25	2.0	0.8	0.3		1.1	0.7	0.7	0.4	0.5	0.3	0.3
5470Rv2543	lppA	86	56	1.5	0.2	0.1	lipoprotein	1.1	0.6	0.7	0.6	0.8	0.6	0.7
4748Rv2544	lppB	94	64	1.5	0.2	0.1	lipoprotein	1.1	0.6	0.8	0.7	0.6	0.6	0.6
1863Rv2550c	-	25	18	1.5	0.4	0.2		1.1	0.4	0.9	0.7	0.7	nd	0.6
3716Rv2585c	-	114	59	1.8	0.2	0.1		1.1	0.5	0.7	0.5	0.5	0.5	0.6
2992Rv2590	fadD9	68	45	1.5	0.3	0.1	acyl-CoA_synthase	1.1	0.8	0.7	0.7	0.7	0.5	0.5
1250Rv2666	IS1081'	188	74	2.6	0.9	0.4		1.1	0.2	0.3	0.4	0.4	0.5	0.5
5465Rv2725c	hflX	90	64	1.5	0.3	0.1	GTP-binding_protein	1.1	0.4	0.6	0.7	0.7	0.9	0.8
2582Rv2735c	-	37	21	1.6	0.2	0.1		1.1	nd	0.7	0.5	0.7	0.6	0.6
74Rv2837c	-	148	95	1.5	0.2	0.1		1.1	0.7	0.7	0.6	0.5	0.7	0.7
1193Rv2856	nicT	67	45	1.6	0.5	0.2	probable_nickel_transport_protein	1.1	0.2	0.6	0.7	0.8	0.7	0.7
2638Rv2901c	-	213	134	1.6	0.1	0.0		1.1	0.6	0.6	0.6	0.7	0.5	0.6
1917Rv2902c	rnhB	69	46	1.6	0.4	0.1	ribonuclease_HII	1.1	0.4	0.7	0.7	0.6	0.7	0.7
1919Rv2906c	trmD	67	39	1.6	0.3	0.1	tRNA_(guanine-N1)-methyltransferase	1.1	nd	0.8	0.6	0.6	0.6	0.5
756Rv2931	ppsA	1220	342	2.4	1.2	0.5	phenolphthiocerol_synthesis_(pksB)	1.1	0.4	0.6	0.2	0.2	0.6	0.6
35Rv2932	ppsB	232	83	2.1	0.8	0.3	phenolphthiocerol_synthesis_(pksC)	1.1	0.6	0.7	0.3	0.3	0.5	0.5
5263Rv2932	ppsB	388	150	1.7	0.7	0.3	phenolphthiocerol_synthesis_(pksC)	1.1	0.8	0.8	0.2	0.4	0.7	0.7
3645Rv2933	ppsC	154	73	1.5	0.6	0.2	phenolphthiocerol_synthesis_(pksD)	1.1	0.7	0.9	0.2	0.8	0.7	0.5
37Rv2936	drrA	80	45	1.6	0.3	0.1	similar_daunorubicin_resistance_ABC-transporter_	1.2	0.7	0.8	0.5	0.5	0.7	0.6
5380Rv2936	drrA	409	238	1.5	0.3	0.1	similar_daunorubicin_resistance_ABC-transporter_	1.4	0.8	0.8	0.5	0.4	0.7	0.8
759Rv2937	drrB	277	143	1.7	0.3	0.1	similar_daunorubicin_resistance_transmembrane_protein	1.1	0.5	0.6	0.5	0.5	0.6	0.7
760Rv2939	papA5	324	150	2.3	1.0	0.4	PKS-associated_protein,_unknown_function	1.1	0.1	0.6	0.4	0.5	0.5	0.6
3842Rv2940c	mas	236	96	1.9	0.9	0.3	mycocerosic_acid_synthase	1.1	0.8	0.8	0.3	0.3	0.4	0.4
39Rv2940c	mas	287	167	1.5	0.3	0.1	mycocerosic_acid_synthase	2.5	0.9	0.8	0.5	0.7	0.6	0.6
4083Rv2944	IS1533	35	24	1.5	0.4	0.2		1.1	0.6	0.9	nd	0.8	0.6	0.5

40Rv2945c	lppX	164	66	2.3	0.6	0.3	lipoprotein	1.1	0.5	0.6	0.4	0.4	0.3	0.3
762Rv2946c	pks1	136	58	1.9	0.6	0.3	polyketide_synthase	1.1	nd	0.7	0.4	0.3	0.7	0.5
41Rv2947c	pks15	458	111	3.1	1.3	0.5	polyketide_synthase_	1.1	0.5	0.5	0.2	0.2	0.2	0.3
763Rv2948c	fadD22	505	102	3.8	1.5	0.6	acyl-CoA_synthase	1.1	0.3	0.4	0.2	0.2	0.2	0.2
960Rv2949c	-	437	196	2.6	0.6	0.3		1.1	nd	0.4	0.5	0.4	0.3	0.4
5185Rv2951c	-	186	100	1.9	0.2	0.1	putative_oxidoreductase	1.1	0.4	0.6	0.6	0.6	0.5	0.5
4463Rv2952	-	278	168	1.6	0.1	0.0	glycosyltransferase	1.1	0.7	0.6	0.6	0.5	0.6	0.6
5184Rv2953	-	145	73	1.9	0.6	0.3		1.1	0.4	0.9	0.5	0.5	0.4	0.5
5181Rv2957	-	313	237	1.8	0.5	0.2	similarity_to_glycosyltransferases	1.1	0.5	0.6	0.8	nd	0.4	0.4
766Rv2965c	kdtB	46	22	1.9	0.3	0.1	lipopolysaccharide_core_biosynthesis_protein	1.1	nd	0.6	0.4	0.6	0.6	0.6
1573Rv2966c	-	33	26	1.5	0.4	0.1		1.1	0.4	0.7	0.9	0.8	0.7	0.5
5268Rv3007c	-	101	63	1.6	0.3	0.1		1.1	nd	0.8	0.6	0.6	0.5	0.6
4886Rv3023c	IS1081	433	237	1.6	0.4	0.1		1.4	0.7	0.7	0.5	0.4	0.7	0.7
5612Rv3032	-	51	28	1.6	0.3	0.1		1.1	0.6	0.8	0.5	0.6	0.8	0.7
4892Rv3047c	-	54	36	1.6	0.6	0.3		1.2	0.7	0.6	0.9	0.9	0.3	0.3
5383Rv3047c	-	56	42	1.5	0.5	0.2		1.1	0.4	0.8	1.0	0.8	0.5	0.6
4896Rv3083	-	57	24	2.3	0.7	0.3	probable_monooxygenase	1.1	0.5	0.7	0.4	0.4	0.3	0.3
5618Rv3084	lipR	32	18	2.2	0.6	0.3	probable_acetyl-hydrolase	1.1	0.3	0.7	nd	0.4	0.4	0.5
5619Rv3086	adhD	63	39	1.5	0.3	0.1	zinc-containing_alcohol_dehydrogenase	2.6	0.7	0.8	0.6	0.5	0.7	0.7
2592Rv3093c	-	48	29	1.5	0.6	0.2		1.1	0.4	0.6	0.5	0.5	1.1	0.9
2593Rv3095	-	173	99	1.7	0.9	0.4	putative_transcriptional_regulator	1.1	0.3	0.4	0.4	0.4	1.0	1.0
4754Rv3096	-	106	72	1.5	0.2	0.1	unknown_glycosyl_hydrolase,_secreted?	1.1	0.7	0.6	0.7	0.6	0.8	0.8
1875Rv3115	IS1081	166	77	2.0	0.4	0.2		1.1	0.4	0.5	0.4	0.4	0.6	0.6
1877Rv3119	moaE	71	48	1.5	0.3	0.1	molybdopterin-converting_factor_subunit_2	1.1	0.4	0.7	0.7	0.6	0.7	0.8
4760Rv3121	-	66	48	1.5	0.2	0.1	probable_cytochrome_p450	1.1	0.6	0.8	0.8	0.7	0.6	0.7
871Rv3142c	-	141	96	1.6	0.3	0.1		1.1	0.6	0.7	0.7	0.8	0.5	0.5
993Rv3145	nuoA	94	54	1.5	0.4	0.2	NADH_dehydrogenase_chain_A	1.1	0.7	0.6	0.5	0.5	0.8	0.9
869Rv3146	nuoB	155	98	1.5	0.2	0.1	NADH_dehydrogenase_chain_B	1.1	0.5	0.6	0.6	0.6	0.8	0.8
868Rv3148	nuoD	100	40	2.3	1.0	0.4	NADH_dehydrogenase_chain_D	1.1	0.1	0.5	0.3	0.4	0.6	0.6
146Rv3149	nuoE	53	31	1.6	0.4	0.2	NADH_dehydrogenase_chain_E	1.1	0.9	0.7	0.6	0.6	0.6	0.4
867Rv3150	nuoF	96	57	1.6	0.4	0.2	NADH_dehydrogenase_chain_F	1.1	nd	0.9	0.6	0.4	0.6	0.6
5559Rv3152	nuoH	218	56	3.4	2.0	0.8	NADH_dehydrogenase_chain_H	1.1	0.1	0.6	0.2	0.3	0.3	0.3
4837Rv3153	nuoI	238	121	1.8	0.7	0.3	NADH_dehydrogenase_chain_I	1.1	0.8	0.9	0.5	0.5	0.4	0.3
5558Rv3154	nuoJ	272	139	1.8	0.3	0.1	NADH_dehydrogenase_chain_J	1.4	0.6	0.7	0.5	0.6	0.4	0.5
4836Rv3155	nuoK	294	170	1.6	0.4	0.2	NADH_dehydrogenase_chain_K	1.1	0.8	0.8	0.6	0.4	0.4	0.6
5557Rv3156	nuoL	222	109	1.9	0.6	0.2	NADH_dehydrogenase_chain_L	1.1	0.6	0.8	0.5	0.5	0.4	0.4
4835Rv3157	nuoM	213	114	1.8	0.5	0.2	NADH_dehydrogenase_chain_M	1.1	0.7	0.7	0.6	0.4	0.4	0.4
2478Rv3157	nuoM	158	101	1.5	0.4	0.2	NADH_dehydrogenase_chain_M	1.1	0.8	0.8	0.7	0.8	0.4	0.4
3850Rv3158	nuoN	163	94	1.7	0.6	0.3	NADH_dehydrogenase_chain_N	1.1	0.8	0.8	0.7	0.5	0.4	0.3
578Rv3159c	PPE	141	65	2.3	0.4	0.2		1.4	0.4	0.5	0.5	0.5	0.3	0.4

1300Rv3160c	-	52	35	1.6	0.4	0.2	putative_transcriptional_regulator	1.1	0.3	0.6	0.8	0.7	0.7	0.7
1304Rv3168	-	63	42	1.5	0.3	0.1		1.1	0.5	0.7	0.6	0.6	0.8	0.8
3470Rv3179	-	30	19	1.5	0.3	0.1		1.1	nd	0.8	0.6	0.7	0.7	0.5
4262Rv3228	-	27	19	1.5	0.4	0.2		1.1	0.6	0.9	nd	0.8	0.5	0.5
3541Rv3229c	desA3	120	58	2.2	1.3	0.5	acyl-[ACP]_desaturase	1.1	0.6	0.5	0.7	0.8	0.1	0.1
3542Rv3231c	-	31	20	1.5	0.7	0.3		1.1	0.6	1.1	nd	0.7	0.4	0.4
4264Rv3232c	pvdS	97	41	2.1	0.6	0.3	alternative_sigma_factor_for_siderophore_production	1.1	0.5	0.6	0.2	0.4	0.5	0.6
3543Rv3233c	-	78	54	1.5	0.2	0.1		1.1	0.6	0.6	0.7	0.6	0.8	0.8
1378Rv3236c	kefB	63	42	1.5	0.1	0.1	probable_glutathione-regulated_potassium-efflux_protein	1.1	0.6	0.8	0.7	0.7	0.6	0.7
658Rv3239c	-	610	1044	1.6	0.0	0.0	possible_antibiotic_efflux_proteins	1.1	nd	nd	nd	nd	0.6	0.6
3545Rv3249c	-	274	78	3.0	1.5	0.6	transcriptional_regulator_(TetR/AcrR_family)	1.1	0.5	0.5	0.4	0.3	0.1	0.1
4267Rv3250c	rubB	320	55	4.4	2.8	1.2	rubredoxin_B	1.1	0.4	0.4	0.2	0.2	0.1	0.1
3546Rv3251c	rubA	219	33	4.5	3.4	1.4	rubredoxin_A	1.1	0.4	0.4	0.2	0.2	0.1	0.1
4268Rv3252c	-	296	52	4.9	2.3	1.0	possible_alkane-1_monooxygenase	1.1	0.2	0.3	0.1	0.2	0.1	0.3
3547Rv3253c	-	30	18	1.6	0.7	0.3	probable_cationic_amino_acid_transport	1.1	0.6	nd	0.7	1.0	0.3	0.4
4269Rv3254	-	29	20	1.7	0.3	0.1	slight_similarity_to_squalene_monooxygenases	1.1	0.5	0.8	nd	0.5	0.5	0.6
906Rv3278c	-	294	191	1.5	0.2	0.1		1.1	0.5	0.6	0.6	0.7	0.6	0.8
4246Rv3281	-	429	241	1.6	0.2	0.1		2.5	0.7	0.7	0.5	0.6	0.6	0.7
908Rv3282	-	88	43	2.2	0.5	0.2		1.1	0.2	0.5	0.5	0.6	0.4	0.5
911Rv3299c	atsB	54	39	1.5	0.2	0.1	proable_arylsulfatase	1.1	0.6	0.8	0.7	0.7	0.7	0.6
1317Rv3312c	-	53	28	1.7	0.5	0.2		1.1	0.6	0.9	0.5	0.6	0.5	0.5
3482Rv3320c	-	134	83	1.5	0.4	0.2		1.1	1.0	0.8	0.6	0.6	0.5	0.6
1321Rv3331	sugI	74	46	1.5	0.2	0.1	probable_sugar_transport_protein	1.1	0.7	0.8	0.6	0.6	0.7	0.6
3488Rv3345c	PE_PGRS	34	26	1.5	0.2	0.1		2.6	0.6	nd	0.9	0.6	0.6	0.7
1280Rv3377c	-	122	57	2.1	0.3	0.1	similar_to_many_cyclases_involved_in_steroid_biosynthesis	1.1	0.5	0.5	0.5	0.6	0.4	0.5
4165Rv3383c	idsB	93	34	2.3	0.7	0.3	transfergeranyl,_similar_geranyl_pyrophosphate_synthase	1.1	0.5	0.6	0.3	0.5	0.3	0.3
1261Rv3395c	-	30	21	1.6	0.2	0.1		1.1	0.6	0.6	0.8	nd	0.6	0.6
1258Rv3403c	-	83	54	1.5	0.2	0.1		1.1	0.6	0.7	0.6	0.6	0.8	0.8
293Rv3454	-	72	35	1.6	0.1	0.0	some_similarity_to_proline_permeases	1.3	nd	0.7	0.6	0.6	0.6	0.7
1020Rv3477	PE	152	136	1.5	0.9	0.4		1.1	0.2	0.3	0.7	0.6	1.0	1.1
1021Rv3479	-	256	101	2.2	0.8	0.3		1.1	0.2	0.7	0.3	0.4	0.5	0.5
3906Rv3485c	-	108	40	2.0	1.3	0.6	short-chain_alcohol_dehydrogenase_family	1.1	nd	1.1	0.3	0.5	0.3	0.3
3188Rv3492c	-	52	28	1.8	0.2	0.1		1.1	0.7	0.5	0.5	0.6	0.5	0.6
4158Rv3600c	-	105	28	2.3	0.9	0.4		1.1	0.6	0.5	0.1	0.4	0.5	0.5
3436Rv3601c	panD	202	86	2.0	0.7	0.3	aspartate_1-decarboxylase	1.1	0.5	0.8	0.4	0.4	0.4	0.4
5728Rv3602c	panC	38	23	1.6	0.4	0.2	pantoate-b-alanine_ligase	1.1	0.4	0.8	0.7	0.4	0.7	0.7
5007Rv3603c	-	154	84	1.6	0.4	0.2		1.1	0.7	0.9	0.5	0.4	0.6	0.6
5729Rv3611	-	40	27	1.7	0.5	0.2		2.5	0.3	0.5	nd	0.7	0.7	0.7
4154Rv3620c	-	726	480	1.5	0.2	0.1		1.1	0.6	0.6	0.6	0.7	0.7	0.8
303Rv3647c	-	158	111	1.5	0.4	0.2		1.2	0.5	0.5	0.8	0.5	0.9	0.8

5730Rv3648c	cspA	317	169	1.8	0.5	0.2	cold_shock_protein,_transcriptional_regulator	1.1	0.5	0.5	0.5	0.5	0.5	0.9
5011Rv3662c	-	102	65	1.6	0.2	0.1		1.1	0.5	0.6	0.7	0.6	0.6	0.8
5330Rv3706c	-	274	139	1.7	0.4	0.2		1.1	0.7	0.7	0.5	0.4	0.6	0.8
5334Rv3727	-	201	58	3.3	1.1	0.4	similar_to_phytoene_dehydrogenase_precursor	1.1	0.2	0.5	0.3	0.3	0.2	0.3
5335Rv3729	-	72	48	1.6	0.5	0.2	probable_transferase	1.1	0.2	0.7	0.7	0.6	0.7	0.8
5339Rv3749c	-	121	82	1.6	0.3	0.1		1.1	0.6	0.6	0.8	0.8	0.5	0.6
5119Rv3783	-	163	105	1.5	0.2	0.1	integral_membrane_protein,_ABC-2_SUBFAMILY	1.1	0.5	0.7	0.6	0.6	0.7	0.7
767Rv3793	embC	80	46	1.6	0.3	0.1	involved_in_arabinogalactan_synthesis	1.1	nd	0.7	0.5	0.5	0.7	0.7
768Rv3795	embB	52	32	1.7	0.3	0.2	involved_in_arabinogalactan_synthesis	1.1	nd	0.8	0.6	0.5	0.6	0.5
5692Rv3796	atsH	75	35	2.1	0.6	0.2	proable_arylsulfatase	1.1	0.3	0.7	0.4	0.6	0.4	0.5
2236Rv3796	atsH	61	36	1.8	0.7	0.3	proable_arylsulfatase	1.1	0.5	1.0	0.7	0.6	0.3	0.4
5680Rv3798	IS1557	52	31	1.8	0.7	0.3	transposase	1.1	0.2	0.7	0.7	0.6	0.6	0.6
3773Rv3822	-	380	255	1.5	0.3	0.1		1.1	0.6	0.8	0.8	0.7	0.5	0.6
890Rv3824c	papA1	130	66	2.2	1.0	0.4	PKS-associated_protein,_unknown_function_	1.1	0.3	0.8	0.6	0.5	0.3	0.3
168Rv3825c	pks2	83	61	1.6	0.6	0.2	polyketide_synthase	1.1	0.9	0.4	0.8	0.7	0.4	0.6
889Rv3826	fadD23	66	46	1.5	0.1	0.0	acyl-CoA_synthase	1.3	nd	0.7	0.7	0.7	0.6	0.6
2254Rv3849	-	107	62	1.7	0.2	0.1		1.1	0.6	0.7	0.6	0.5	0.5	0.6
2801Rv3869	-	465	213	2.0	0.6	0.2		1.1	0.7	0.7	0.5	0.4	0.4	0.4
2080Rv3870	-	190	104	1.8	0.5	0.2		1.1	0.6	0.7	0.6	0.7	0.3	0.4
3538Rv3884c	-	50	26	1.9	0.3	0.1	CBXX/CFQX_family	1.1	0.5	0.7	0.5	0.5	0.5	0.6
1377Rv3885c	-	39	21	1.7	0.3	0.1		1.1	nd	0.7	0.4	0.6	0.6	0.6
1034Rv3909	-	33	20	1.5	0.3	0.2		1.2	nd	0.9	0.5	0.5	0.7	0.7
2015Rv3917c	parA	130	73	1.7	0.3	0.1	chromosome_partitioning;_DNA_binding	1.1	0.8	0.7	0.6	0.6	0.5	0.5
2737Rv3918c	parB	600	234	2.2	0.5	0.2	possibly_involved_in_chromosome_partitioning	1.1	0.6	0.6	0.4	0.4	0.4	0.4
4898Rv3919c	gid	273	104	2.6	0.4	0.1	glucose_inhibited_division_protein_B	1.1	0.4	0.5	0.4	0.3	0.4	0.4
5620Rv3920c	-	633	189	3.6	0.8	0.3		1.1	0.2	0.3	0.3	0.4	0.2	0.2
4899Rv3921c	-	495	242	2.5	1.0	0.4	unknown_membrane_protein	1.1	0.2	0.2	0.6	0.5	0.4	0.5
5621Rv3922c	-	431	237	2.0	0.6	0.3	possible_hemolysin	1.1	0.3	0.4	0.6	0.6	nd	0.6
4900Rv3923c	mpaA	232	187	1.5	0.5	0.2	ribonuclease_P_protein_component	1.1	0.3	0.5	1.0	0.8	0.6	0.6