

**Table 1: Genes induced in Mycobacterium tuberculosis H37Rv by low iron** 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		Average Corrected ratios			Gene product	PCR F	Individual array ratios (CH2/CH1)					
			CH1 Cye3	CH2 Cye5	CH2/CH1 Induced	StD	SEM			Biol. set 1		Biol. set 2		Biol. set 3	
									mm693	mm706	mm696	mm709	mm699	mm702	
4901	Rv0001	dnaA	1100	1808	1.6	0.1	0.0	chromosomal_replication_initiator_protein	1.1	1.7	1.4	1.7	1.6	1.7	1.6
2763	Rv0108c	-	1238	1960	1.6	0.2	0.1		1.2	1.3	1.5	1.8	1.7	1.9	1.5
2767	Rv0116c	-	1096	2530	2.3	0.3	0.1		1.2	2.1	2.8	2.1	2.2	2.4	2.0
5587	Rv0145	-	779	1507	2.0	0.5	0.2		1.1	nd	2.8	2.0	1.6	1.6	1.8
4359	Rv0166	fadD5	627	947	1.5	0.1	0.1	acyl-CoA_synthase	1.1	1.6	1.4	1.5	1.6	1.3	1.4
1619	Rv0233	nrdB	629	1117	1.8	0.1	0.0	ribonucleoside-diphosphate_reductase_B2_(eukaryotic-like)	1.1	1.7	1.8	1.9	1.7	1.6	1.9
892	Rv0268c	-	946	1500	1.6	0.2	0.1		1.1	1.9	1.3	1.6	1.4	1.8	1.5
974	Rv0276	-	1311	1910	1.5	0.2	0.1		1.1	1.3	1.2	1.5	1.4	1.8	1.5
3205	Rv0279c	PE_PGRS	911	2065	2.2	0.2	0.1		2.2	2.2	2.0	2.3	2.6	1.9	2.4
3859	Rv0282	-	645	2575	3.9	0.5	0.2		1.1	4.5	3.5	4.3	3.8	3.2	4.0
3138	Rv0283	-	400	1207	2.9	0.6	0.3		1.1	3.7	2.5	3.1	2.7	2.0	3.5
3860	Rv0284	-	756	3175	4.1	0.6	0.2		1.1	4.8	3.2	4.5	4.0	3.8	4.4
3139	Rv0285	PE	608	1834	3.0	0.5	0.2		1.1	2.9	2.5	3.3	3.3	2.3	3.5
3206	Rv0286	PPE	595	2429	4.0	0.8	0.3		1.1	4.0	3.3	4.2	4.2	3.1	5.3
3140	Rv0287	-	879	3590	4.0	0.6	0.2	Ala-rich_protein	1.1	3.8	3.4	4.2	4.3	3.5	5.0
3862	Rv0288	-	998	3524	3.5	0.4	0.2		1.1	3.1	3.0	3.8	4.0	3.4	3.7
253	Rv0289	-	544	1639	3.2	0.6	0.2		1.1	2.7	2.2	3.6	3.0	3.6	3.8
975	Rv0290	-	896	1801	2.0	0.2	0.1	unknown_hydrophobic_protein	1.1	1.9	1.7	2.1	2.1	2.1	2.2
254	Rv0291	-	466	1369	3.0	0.3	0.1	secreted_protease	1.1	3.3	2.5	3.1	2.7	2.9	3.3
976	Rv0292	-	660	1790	2.7	0.3	0.1	unknown_possible_membrane_protein	2.5	3.0	2.2	2.8	2.5	2.9	2.7
255	Rv0293c	-	453	664	1.5	0.1	0.0		1.1	1.5	1.2	1.5	1.6	1.5	1.6
2694	Rv0333	-	881	1817	2.1	0.1	0.1		1.1	1.9	2.2	2.1	2.0	2.1	2.1
1857	Rv0361	-	681	1083	1.6	0.1	0.0	possible_membrane_protein	1.1	1.6	1.5	1.6	1.5	1.7	1.6
1182	Rv0416	-	337	516	1.5	0.1	0.1		1.1	1.5	1.5	1.7	1.4	1.6	1.3
3896	Rv0422c	thiD	437	919	2.2	1.1	0.4	phosphomethylpyrimidine_kinase	1.1	1.4	4.3	1.5	1.8	2.3	2.2
3346	Rv0423c	thiC	779	1292	1.6	0.1	0.0	thiamine_synthesis_pyrimidine_moiety	1.1	1.7	1.6	1.7	1.6	1.5	1.7
3210	Rv0425c	ctpH	493	730	1.5	0.1	0.0	C-terminal_region_putative_cation-transporting_ATPase	1.1	1.5	1.5	1.5	1.5	1.2	1.5
3151	Rv0450c	mmpL4	827	1793	2.1	0.3	0.1	conserved_large_membrane_protein	1.1	2.1	2.0	2.1	2.5	1.6	2.2
3873	Rv0451c	mmpS4	659	2086	3.1	0.4	0.2	conserved_small_membrane_protein	1.1	3.3	3.0	3.3	3.5	2.4	3.0
1328	Rv0463	-	1403	2305	1.6	0.2	0.1		1.1	1.6	1.3	1.7	1.5	1.8	1.7
607	Rv0464c	-	1340	3006	2.2	0.2	0.1		1.1	2.3	1.9	2.5	2.1	2.4	2.3
1329	Rv0465c	-	1013	4424	4.3	0.7	0.3	transcriptional_regulator_(PbsX/Xre_family)	1.1	4.1	3.8	5.1	3.5	5.1	4.4
4212	Rv0467	aceA	540	1908	3.5	0.4	0.2	isocitrate_lyase	1.1	3.8	2.9	3.9	3.4	3.1	3.7
3491	Rv0468	fadB2	676	1105	1.6	0.1	0.0	3-hydroxyacyl-CoA_dehydrogenase	1.1	1.7	1.5	1.7	1.6	1.4	1.7
1540	Rv0481c	-	230	413	1.8	0.3	0.1		1.1	2.2	1.8	1.5	1.9	1.4	1.7
3649	Rv0503c	cmaA2	764	1151	1.5	0.1	0.1	cyclopropane_mycolic_acid_synthase_2	1.1	1.6	1.6	1.4	1.6	1.5	1.3
452	Rv0587	-	667	1520	2.2	0.2	0.1	part_of_mce2_operon	1.1	2.1	2.6	2.0	2.2	2.5	2.1
3501	Rv0676c	mmpL5	624	1702	2.8	0.2	0.1	conserved_large_membrane_protein	1.1	2.8	2.7	3.1	2.7	nd	2.6
4223	Rv0677c	mmpS5	894	2893	3.2	0.3	0.1	conserved_small_membrane_protein	1.1	3.1	2.8	3.6	3.7	3.0	3.0
614	Rv0678	-	621	1480	2.4	0.5	0.2		1.1	2.2	1.8	3.3	2.7	2.0	2.6
4771	Rv0691c	-	498	921	1.8	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.8	1.4	2.0	1.8	1.9	2.0
5493	Rv0692	-	840	2341	2.7	0.2	0.1		1.1	3.1	2.6	2.8	2.7	2.7	2.6
1884	Rv0693	pqqE	460	1178	2.5	0.3	0.1	coenzyme_PQQ_synthase_protein_E	1.1	2.9	2.2	2.7	2.5	2.2	2.8
2606	Rv0694	lldD1	492	1137	2.3	0.2	0.1	L-lactate_dehydrogenase_(cytochrome_)	1.1	2.2	2.2	2.7	2.3	2.4	2.2
1885	Rv0695	-	384	722	1.9	0.2	0.1		1.1	1.8	1.7	2.1	2.0	1.7	2.0
2607	Rv0696	-	740	1206	1.6	0.2	0.1	glycosyltransferase	1.1	1.5	1.5	1.9	1.6	1.7	1.6
4776	Rv0711	atsA	507	967	1.9	0.1	0.0	arylsulfatase	1.1	1.9	1.9	1.8	2.1	1.8	1.9
4474	Rv0766c	-	455	1520	3.3	0.4	0.2	cytochrome_p-450	2.5	3.7	2.6	3.5	3.0	3.4	3.6
1689	Rv0823c	-	555	846	1.5	0.3	0.1	transcriptional_regulator_(NifR3/Smm1_family)	1.1	1.6	1.3	1.9	1.5	1.1	1.8
5300	Rv0839	-	371	687	1.8	0.1	0.0		1.1	1.9	1.8	1.8	1.8	1.9	1.9
4579	Rv0852	fadD16	407	812	2.0	0.3	0.1	acyl-CoA_synthase	1.1	1.9	1.5	1.9	2.3	2.3	2.1

140	Rv0878c	PPE	396	630	1.6	0.1	0.0			1.1	1.7	1.4	1.7	1.5	1.7	1.6
144	Rv0885	-	491	909	1.9	0.2	0.1	unknown_transmembrane_protein		1.1	1.8	1.6	2.0	1.9	2.0	1.9
4588	Rv0981	-	547	937	1.7	0.2	0.1	two-component_response_regulator		1.1	1.9	1.3	1.6	1.6	1.7	2.0
3310	Rv1038c	-	3960	5979	1.5	0.1	0.0			1.1	1.4	1.5	1.6	1.5	1.6	1.6
563	Rv1168c	PPE	442	891	2.0	0.2	0.1			1.1	2.1	1.9	2.3	1.8	2.0	2.0
1285	Rv1169c	PE	441	977	2.2	0.2	0.1			1.1	2.0	2.2	2.5	2.2	2.2	2.2
3581	Rv1174c	-	1311	2151	1.6	0.1	0.0			1.1	1.7	1.6	1.6	1.5	1.7	1.7
3448	Rv1174c	-	651	1009	1.5	0.1	0.1			1.2	1.6	1.3	1.6	1.5	1.4	1.6
3452	Rv1182	papA3	1859	3247	1.7	0.1	0.0	PKS-associated_protein_unknown_function		1.1	1.8	1.6	1.8	1.9	1.7	1.7
4174	Rv1183	mmpL10	949	1536	1.6	0.1	0.0	conserved_large_membrane_protein		1.1	1.8	1.6	1.6	1.6	1.5	1.5
3453	Rv1184c	-	2153	4770	2.2	0.1	0.0			1.1	2.4	2.1	2.2	2.1	2.1	2.2
4175	Rv1185c	fadD21	2549	3773	1.5	0.1	0.0	acyl-CoA_synthase		1.1	1.5	1.4	1.4	1.6	1.5	1.4
643	Rv1187	rocA	365	537	1.5	0.3	0.1	pyroline-5-carboxylate_dehydrogenase		1.1	1.2	1.4	1.9	1.4	1.4	1.8
1481	Rv1195	PE	398	871	2.2	0.2	0.1			1.1	2.0	1.9	2.4	2.3	2.5	2.2
2203	Rv1196	PPE	1520	2249	1.5	0.2	0.1			1.1	1.3	1.2	1.6	1.6	1.6	1.4
1482	Rv1197	-	4039	7170	1.8	0.1	0.0			1.1	1.7	1.7	1.8	1.9	1.8	1.7
1483	Rv1199c	IS1081	895	1352	1.5	0.1	0.0			1.1	1.5	1.3	1.6	1.6	1.6	1.5
3656	Rv1221	sigE	1226	2603	2.2	0.3	0.1	ECF_subfamily_sigma_subunit		1.1	1.8	1.9	2.0	2.3	2.6	2.4
3117	Rv1341	-	340	637	1.8	0.2	0.1			1.1	2.1	2.0	1.8	1.8	1.5	1.9
4740	Rv1342c	pkc14	231	484	2.0	0.5	0.2	polyketide_synthase_(chalcone_synthase-like)		1.1	2.4	2.0	2.2	2.1	1.2	2.2
5462	Rv1343c	-	413	1058	2.5	0.5	0.2			1.1	2.8	1.9	2.5	2.0	3.0	2.9
4741	Rv1344	-	333	1346	3.9	0.6	0.3	possible_acyl_carrier_protein		1.1	4.8	3.8	3.9	3.9	2.8	4.1
5463	Rv1345	fadD33	295	996	3.4	0.4	0.2	acyl-CoA_synthase		1.1	3.9	3.0	3.5	2.9	3.9	3.3
49	Rv1346	fadE14	227	1116	4.9	0.9	0.4	acyl-CoA_dehydrogenase_		1.1	5.4	4.6	4.2	4.3	6.5	4.6
771	Rv1347c	-	226	1767	7.9	1.7	0.7	possible_aminoglycoside_6'-N-acetyltransferase		1.1	6.6	5.8	9.3	7.5	10.3	7.9
50	Rv1348	-	1124	1122	5.1	0.7	0.3	heavy_metal_tolerance_protein		1.1	5.1	5.8	4.7	4.2	6.0	4.6
3878	Rv1349	-	227	1013	4.3	1.2	0.5	probable_membrane_protein		1.1	5.0	2.8	5.5	4.3	2.9	5.5
51	Rv1350	fabG2	243	363	1.5	0.2	0.1	3-oxoacyl-[ACP]_reductase		1.1	nd	1.7	1.2	1.5	1.8	1.4
773	Rv1351	-	376	633	1.7	0.2	0.1			1.1	1.7	1.3	1.8	nd	1.9	1.6
52	Rv1352	-	523	854	1.6	0.2	0.1			1.1	1.6	nd	1.7	1.3	1.8	1.7
3567	Rv1352	-	629	956	1.5	0.2	0.1			1.1	1.8	1.4	1.5	1.4	1.2	1.7
4783	Rv1393c	-	654	1637	2.4	0.3	0.1	FAD-containing_monooxygenase		1.1	2.9	2.1	2.7	2.3	2.4	2.2
5505	Rv1394c	-	516	886	1.7	0.2	0.1	possible_cytochrome_p450		1.1	2.0	1.5	1.8	1.6	1.7	1.6
5510	Rv1415	ribA2	774	1309	1.6	0.2	0.1	probable_GTP_cyclohydrolase_II		1.1	1.6	2.0	1.5	1.6	1.5	1.7
577	Rv1461	-	988	4725	4.7	0.4	0.2			1.4	4.5	4.5	4.4	5.4	4.7	4.8
1299	Rv1462	-	607	2017	3.4	0.6	0.3			1.1	2.8	2.8	4.0	nd	4.1	3.4
3528	Rv1463	-	589	1993	3.3	0.5	0.2	ABC-type_transporter		1.4	3.4	2.4	3.5	3.2	3.3	4.1
4182	Rv1464	-	406	1182	3.0	0.3	0.1	NifS-like_protein		1.1	3.4	2.8	3.1	2.6	nd	3.1
3461	Rv1465	-	412	1049	2.6	0.5	0.2			1.1	2.8	nd	2.6	2.7	1.7	3.0
4183	Rv1466	-	452	1449	3.2	0.6	0.2			1.1	3.1	2.5	3.4	4.1	2.8	3.1
3328	Rv1518	-	232	321	1.5	0.1	0.0	involved_in_exopolysaccharide_synthesis		1.1	1.4	1.4	1.5	1.6	nd	1.4
1167	Rv1519	-	298	1103	3.7	0.4	0.2			1.1	3.4	3.6	4.4	3.2	4.0	3.5
445	Rv1520	-	628	1315	2.1	0.2	0.1	glycosyltransferase		1.1	2.1	1.9	2.3	nd	2.1	1.9
3849	Rv1535	-	652	1069	1.6	0.2	0.1			1.1	2.0	1.5	1.8	1.5	1.4	1.6
488	Rv1586c	-	1468	2194	1.5	0.1	0.1	phiRV1_integrase		1.1	1.5	1.3	1.5	1.4	1.7	1.5
1848	Rv1623c	appC	1067	1778	1.5	0.2	0.1	cytochrome_bd-II_oxidase_subunit_I		1.4	1.4	1.2	1.7	1.8	1.4	1.5
2952	Rv1639c	-	1493	3014	2.0	0.2	0.1			1.1	2.1	1.7	2.2	2.0	1.9	2.1
3221	Rv1870c	-	577	1216	2.1	0.2	0.1			1.1	2.2	1.9	2.3	1.9	1.8	2.2
5186	Rv1871c	-	1406	2204	1.5	0.1	0.1			1.1	1.6	1.4	1.4	1.7	1.7	1.5
2983	Rv1872c	lldD2	2040	3702	1.8	0.2	0.1	L-lactate_dehydrogenase		1.1	2.0	1.7	1.8	1.5	1.8	2.0
3703	Rv1875	-	437	639	1.5	0.2	0.1			1.1	1.8	1.5	1.5	1.2	1.5	1.4
2973	Rv1904	-	517	878	1.6	0.3	0.1			1.1	1.8	1.5	1.8	1.6	1.1	2.0
812	Rv1905c	aao	453	652	1.5	0.2	0.1	D-amino_acid_oxidase		1.1	1.4	1.2	1.5	nd	1.7	1.4
5602	Rv1923	lipD	288	546	1.9	0.2	0.1	probable_esterase		1.1	2.1	2.2	1.7	1.6	1.9	1.9
1994	Rv1932	tpx	781	1204	1.5	0.1	0.0	thiol_peroxidase		1.1	1.6	1.4	1.6	1.6	1.4	1.5
1947	Rv1990c	-	598	883	1.5	0.2	0.1	putative_transcriptional_regulator		1.1	1.4	1.2	1.7	1.6	1.5	1.5
1684	Rv2037c	-	547	1239	2.4	0.3	0.1	probable_transmembrane_protein		1.1	2.4	2.7	2.3	2.0	2.7	2.5
4567	Rv2039c	-	511	1060	2.0	0.3	0.1	probable_sugar_transporter		1.1	2.0	2.4	1.4	2.0	2.3	2.0

2936	Rv2069	sigC	524	824	1.5	0.1	0.0	ECF_subfamily_sigma_subunit	1.1	1.6	1.6	1.5	1.6	1.3	1.7
1555	Rv2121c	hisG	416	670	1.6	0.2	0.1	ATP_phosphoribosyltransferase	1.1	1.6	1.6	1.8	1.7	1.3	1.6
2277	Rv2122c	hisI	241	754	3.1	0.3	0.1	phosphoribosyl-AMP_cyclohydrolase	1.1	2.6	3.1	3.4	3.3	3.3	3.2
1556	Rv2123	PPE	220	2243	10.1	2.1	0.9		1.1	11.3	7.8	12.2	8.8	7.9	12.4
4646	Rv2159c	-	2069	3340	1.6	0.1	0.1		1.4	1.7	1.4	1.6	1.5	1.8	1.7
4450	Rv2160c	-	444	674	1.5	0.1	0.0	Function:_unknown_improbable	1.1	1.6	1.4	1.5	1.5	1.5	1.6
4915	Rv2182c	-	692	1029	1.5	0.1	0.0		1.1	1.5	1.5	1.4	1.6	1.5	1.5
2914	Rv2246	kasB	835	1240	1.5	0.1	0.1	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	1.4	1.3	1.7	1.5	1.5	1.5
230	Rv2247	accD6	966	1436	1.5	0.1	0.1	acetyl/propionyl_CoA_carboxylase_b_subunit	1.4	1.5	1.3	1.5	1.7	1.5	1.4
2915	Rv2248	-	343	487	1.5	0.1	0.1		1.1	1.6	1.6	1.4	1.4	nd	1.3
4509	Rv2336	-	561	862	1.5	0.1	0.1		1.1	1.7	1.6	1.4	1.6	1.3	1.5
1626	Rv2346c	-	3215	5187	1.6	0.2	0.1		1.1	1.5	1.4	1.9	1.7	1.6	1.7
2348	Rv2347c	-	3676	5624	1.5	0.1	0.0		1.1	1.4	1.5	1.6	1.6	1.6	1.5
1627	Rv2348c	-	2587	4237	1.7	0.2	0.1		1.4	1.5	1.4	1.8	1.7	1.7	1.7
2931	Rv2359	furB	356	590	1.6	0.3	0.1	ferric_uptake_regulatory_protein	1.1	1.7	1.7	1.6	1.9	1.0	1.7
1559	Rv2368c	phoH	566	841	1.5	0.1	0.1	ATP-binding_pho_regulon_component	1.1	1.6	1.3	1.5	1.4	1.6	1.6
4444	Rv2377c	mbtH	249	1384	5.4	1.9	0.8	mycobactin/exochelin_synthase_	1.1	7.0	5.1	5.5	5.6	1.9	7.2
5165	Rv2378c	mbtG	286	1592	5.5	1.5	0.6	mycobactin/exochelin_synthase_(lysine_hydroxylase)	1.1	7.9	3.4	5.9	4.5	5.9	5.4
47	Rv2379c	mbtF	220	774	3.6	0.7	0.3	mycobactin/exochelin_synthase_(lysine_ligation)	1.1	3.3	4.5	2.4	3.3	4.2	3.8
471	Rv2380c	mbtE	252	1808	7.1	0.9	0.4	mycobactin/exochelin_synthase_(lysine_ligation)	1.1	7.8	5.9	8.4	6.7	7.4	6.6
1192	Rv2381c	mbtD	309	3033	9.9	1.8	0.7	mycobactin/exochelin_synthase_(polyketide_synthase)	1.1	9.7	7.9	11.5	8.7	12.5	9.1
470	Rv2382c	mbtC	226	1208	5.3	0.4	0.2	mycobactin/exochelin_synthase	1.1	5.1	5.2	5.1	5.2	6.2	5.4
4079	Rv2383c	mbtB	292	1591	5.4	0.8	0.3	mycobactin/exochelin_synthase_(serine/threonine_ligation)	1.1	6.3	4.2	6.3	5.1	5.0	5.5
3357	Rv2384	mbtA	591	1146	1.9	0.3	0.1	mycobactin/exochelin_synthase_(salicylate-AMP_ligase)	1.1	2.1	1.5	2.2	1.8	1.7	2.1
1552	Rv2385	lipK	244	888	3.6	0.6	0.2	probable_acetyl-hydrolase	1.1	3.7	3.2	4.2	3.7	2.8	4.3
2273	Rv2386c	trpE2	249	2109	8.6	1.8	0.7	anthranilate_synthase_component_I	1.1	8.2	5.4	9.8	10.6	8.4	9.0
1549	Rv2391	nirA	958	1626	1.7	0.2	0.1	probable_nitrite_reductase/sulphite_reductase	1.1	1.8	1.5	1.6	2.0	1.5	1.7
2270	Rv2392	cysH	1027	1794	1.8	0.1	0.1	3'-phosphoadenylylsulfate_(PAPS)_reductase	1.1	1.6	1.8	1.7	1.7	2.0	1.7
1548	Rv2393	-	699	1006	1.5	0.2	0.1		1.1	1.6	1.1	1.6	1.3	1.6	1.5
3654	Rv2428	ahpC	917	2403	2.6	0.4	0.2	alkyl_hydroperoxide_reductase	1.1	2.1	2.2	2.6	3.0	2.9	3.0
2932	Rv2429	ahpD	484	885	1.8	0.2	0.1	member_of_AhpC/TSA_family	1.1	1.8	1.8	1.9	1.7	1.6	2.2
5247	Rv2452c	-	328	472	1.5	0.2	0.1		1.1	1.4	1.3	1.4	1.6	nd	1.7
4526	Rv2453c	-	291	435	1.5	0.2	0.1		1.1	1.8	nd	1.2	1.4	1.3	1.6
5248	Rv2454c	-	801	1251	1.6	0.2	0.1	oxidoreductase_beta_subunit	1.1	1.5	1.2	1.6	1.6	1.7	1.7
4527	Rv2455c	-	828	1306	1.6	0.1	0.0	probable_oxidoreductase_alpha_subunit	1.1	1.6	1.6	1.4	1.6	1.6	1.7
4528	Rv2457c	clpX	2212	3457	1.6	0.2	0.1	ATP-dependent_Clp_protease_ATP-binding_subunit_ClpX	1.1	1.4	1.6	1.3	1.9	1.7	1.6
4529	Rv2459	-	692	1042	1.5	0.1	0.0	probable_drug_efflux_protein	1.1	1.6	1.4	1.4	1.6	1.5	1.5
2372	Rv2490c	PE_PGRS	1300	1931	1.5	0.2	0.1		2.5	1.5	1.4	1.6	1.7	1.4	1.3
415	Rv2512c	IS1081	438	701	1.5	0.1	0.1		1.1	1.6	1.4	1.7	nd	1.6	1.4
2992	Rv2590	fadD9	639	1076	1.7	0.1	0.0	acyl-CoA_synthase	1.1	1.7	1.5	1.7	1.8	1.5	1.7
3341	Rv2620c	-	269	519	1.9	0.3	0.1		1.1	2.2	1.7	2.2	1.9	1.3	2.0
4062	Rv2621c	-	358	864	2.4	0.3	0.1	putative_transcriptional_regulator	2.1	2.2	2.3	2.4	2.9	2.2	2.3
454	Rv2629	-	547	1043	1.9	0.1	0.1		1.1	2.0	1.8	1.9	1.8	2.0	1.8
518	Rv2632c	-	1061	2138	2.0	0.2	0.1		1.1	2.0	1.7	2.1	2.1	2.2	2.0
1240	Rv2633c	-	2378	3849	1.6	0.1	0.0		1.1	1.6	1.6	1.7	1.6	1.7	1.5
2934	Rv2710	sigB	1206	2306	2.0	0.2	0.1	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	1.7	1.8	2.0	2.0	2.1	2.2
194	Rv2744c	35kd_ag	620	881	1.5	0.2	0.1	35-kd_antigen	1.1	1.3	1.3	1.3	1.6	1.7	1.6
3813	Rv2787	-	383	483	1.5	1.2	0.5		1.1	0.9	1.5	3.8	0.8	0.9	0.8
207	Rv2794c	-	585	1606	2.7	0.2	0.1	possible_4'-phosphopantetheine_transferase_	2.3	2.7	2.4	2.9	2.7	2.9	2.9
79	Rv2816c	-	1113	1962	1.8	0.1	0.1		1.1	1.7	1.7	1.8	2.0	1.7	1.6
3688	Rv2817c	-	1040	1793	1.7	0.2	0.1		1.1	1.9	1.9	1.8	1.7	1.6	1.5
755	Rv2930	fadD26	884	1568	1.7	0.3	0.1	acyl-CoA_synthase	1.1	1.7	1.4	1.9	1.6	2.2	1.5
756	Rv2931	ppsA	830	1450	1.7	0.3	0.1	phenolphthiocerol_synthase_(pksB)	1.1	1.9	1.4	2.0	1.4	1.9	1.6
1655	Rv2988c	leuC	278	438	1.6	0.1	0.0	3-isopropylmalate_dehydratase_large_subunit	1.1	1.5	1.6	1.6	1.7	nd	1.7
2377	Rv2989	-	669	1039	1.5	0.1	0.1	transcriptional_regulator_(IcIR_family)	1.1	1.5	1.4	1.8	1.6	1.5	1.5
4546	Rv3006	lppZ	1362	2112	1.6	0.1	0.0		1.1	1.6	1.6	1.4	1.4	1.7	1.6
4548	Rv3010c	pfkA	428	822	1.9	0.2	0.1	phosphofructokinase_I	1.1	1.8	2.0	1.6	1.9	2.0	2.0
2723	Rv3019c	-	394	765	1.9	0.2	0.1	similar_to_Esat6	1.1	2.1	1.5	1.9	1.9	2.1	1.9

2002	Rv3020c	PE	332	624	1.9	0.3	0.1		1.1	2.0	1.4	1.9	1.7	1.9	2.2
4893	Rv3049c	-	731	1189	1.6	0.2	0.1	Probable_monoxygenase	1.1	1.9	1.5	1.6	1.5	1.5	1.5
2593	Rv3095	-	1214	2701	2.0	0.5	0.2	putative_transcriptional_regulator	1.1	1.2	2.6	2.5	1.6	1.9	2.4
227	Rv3140	fadE23	780	1387	1.8	0.2	0.1	acyl-CoA_dehydrogenase_	1.1	1.5	1.7	1.5	2.0	2.1	1.7
145	Rv3151	nuoG	259	377	1.5	0.1	0.0	NADH_dehydrogenase_chain_G	2.6	1.4	1.3	1.6	1.4	1.5	1.4
579	Rv3161c	-	738	1298	1.7	0.3	0.1	putative_dioxygenases	1.1	1.5	1.5	1.9	2.2	1.7	1.7
4191	Rv3178	-	780	2162	2.6	0.6	0.2		1.1	2.1	3.6	1.9	2.7	2.7	2.5
4262	Rv3228	-	358	610	1.7	0.2	0.1		1.1	1.8	1.6	2.0	1.8	1.3	1.6
3541	Rv3229c	desA3	1002	4513	5.0	2.7	1.1	acyl-[ACP]_desaturase	1.1	3.4	2.8	8.4	8.6	3.3	3.7
4263	Rv3230c	-	1090	2750	2.5	0.5	0.2	similar_to_various_oxygenases	1.1	2.3	1.9	3.1	3.1	2.2	2.6
3545	Rv3249c	-	693	1056	1.5	0.1	0.0	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.7	1.5	1.6	1.4	1.4	1.5
211	Rv3346c	-	374	585	1.6	0.2	0.1		1.1	1.7	1.4	1.4	1.4	1.8	1.7
937	Rv3354	-	613	933	1.5	0.3	0.1		1.1	1.8	1.4	1.5	1.2	1.9	1.5
216	Rv3355c	-	501	786	1.6	0.2	0.1		1.1	1.7	1.3	1.5	1.4	1.7	1.9
3447	Rv3390	lpqD	809	1228	1.5	0.1	0.1	lipoprotein	1.1	1.7	1.3	1.5	1.5	1.5	1.6
537	Rv3402c	-	321	3108	9.7	2.5	1.0	possible_involved_in_LPS_synthesis	1.1	11.4	6.7	12.9	6.9	9.4	10.9
1258	Rv3403c	-	514	2757	5.6	1.0	0.4		1.1	6.2	7.0	5.9	4.2	5.4	4.6
1020	Rv3477	PE	1861	2729	1.5	0.1	0.0		1.1	1.3	1.4	1.5	1.5	1.7	1.4
1021	Rv3479	-	1184	2406	2.0	0.1	0.1		1.1	2.0	2.0	2.1	1.9	2.3	1.9
3185	Rv3486	-	717	1064	1.5	0.2	0.1		1.1	1.8	1.4	1.5	1.2	1.3	1.5
3186	Rv3487c	lipF	824	1447	1.6	0.3	0.1	probable_esterase	1.1	2.1	1.6	1.6	1.7	1.4	1.5
175	Rv3570c	-	492	756	1.5	0.1	0.0	putative_oxidoreductase	1.1	1.5	1.4	1.6	1.6	1.6	1.6
176	Rv3572	-	527	845	1.6	0.2	0.1		1.1	1.5	1.4	1.6	1.6	1.9	1.7
278	Rv3611	-	432	681	1.6	0.1	0.1		2.6	1.7	1.6	1.6	1.5	1.4	1.7
1270	Rv3612c	-	1144	1767	1.6	0.1	0.1		1.1	1.6	1.6	1.5	1.4	1.8	1.5
548	Rv3613c	-	1329	2443	1.8	0.2	0.1		1.1	2.0	1.6	1.9	1.6	2.1	1.7
4157	Rv3614c	-	2373	4874	2.1	0.1	0.1		1.1	2.1	2.2	2.0	2.0	2.0	1.9
3435	Rv3615c	-	2625	4869	1.9	0.3	0.1		1.2	1.6	1.6	2.0	2.1	2.2	1.9
4156	Rv3616c	-	2896	5126	1.8	0.3	0.1		1.1	1.4	1.4	1.9	2.1	1.9	1.9
311	Rv3619c	-	1593	2456	1.6	0.2	0.1		1.1	1.5	1.2	1.8	1.6	1.8	1.7
1032	Rv3620c	-	2122	3175	1.5	0.1	0.0		1.1	1.4	1.5	1.5	1.5	1.7	1.4
5011	Rv3662c	-	1178	2089	1.7	0.1	0.1		1.1	1.8	1.5	1.9	1.8	1.7	1.7
1718	Rv3689	-	1500	2459	1.6	0.2	0.1	hydrophobic_highly_Proline_rich_N-terminus	2.5	1.9	1.5	1.7	1.5	1.5	1.7
2074	Rv3764c	-	557	841	1.5	0.1	0.1	sensor_histidine_kinase	1.1	1.5	1.3	1.6	1.5	1.4	1.7
3773	Rv3822	-	2816	5888	2.1	0.2	0.1		1.1	2.2	1.7	2.1	2.1	2.2	2.2
3051	Rv3823c	mmpL8	225	360	1.7	0.3	0.2	conserved_large_membrane_protein	1.1	1.7	1.1	2.0	1.9	nd	1.8
890	Rv3824c	papA1	1520	2906	1.9	0.2	0.1	PKS-associated_protein_unknown_function_	1.1	2.0	1.6	2.0	2.0	1.9	1.9
168	Rv3825c	pkx2	722	1250	1.7	0.1	0.0	polyketide_synthase	1.1	1.8	1.9	1.8	1.7	1.7	1.6
5141	Rv3839	-	258	5233	19.3	7.0	2.8		1.1	28.4	10.1	24.7	13.9	16.5	22.4
4419	Rv3840	-	325	868	2.6	0.5	0.2	putative_transcriptional_regulator	1.1	3.4	2.4	2.7	2.7	2.0	2.6
1530	Rv3854c	-	519	2314	4.4	0.4	0.2	probable_monoxygenase	1.1	4.6	3.9	4.6	4.4	4.1	5.0
2251	Rv3855	-	343	548	1.6	0.1	0.1	putative_transcriptional_regulator	1.1	1.5	1.6	1.8	1.5	1.8	1.6
5622	Rv3924c	rpmH	1648	2557	1.6	0.1	0.0	50S_ribosomal_protein_L34	1.1	1.5	1.4	1.6	1.5	1.7	1.7