

Table 2: Genes repressed in Mycobacterium tuberculosis H37Rv by low iron 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		Average Corrected ratios			Gene product	PCR F	Individual array ratios (CH2/CH1)					
			CH1 Cye3	CH2 Cye5	CH2/CH1 Repressed	StD	SEM			Biol. set 1 mm693	mm706	Biol. set 2 mm696	mm709	Biol. set 3 mm699	mm702
4042	Rv0009	ppiA	3614	1353	2.7	0.1	0.1	peptidyl-prolyl_cis-trans_isomerase	1.1	0.4	0.4	0.3	0.4	0.4	0.4
3321	Rv0010c	-	636	338	1.8	0.2	0.1		1.1	0.5	0.6	0.5	0.5	0.6	0.5
1976	Rv0130	-	773	502	1.5	0.2	0.1		1.1	0.6	0.5	0.7	0.7	0.7	0.6
2698	Rv0131c	fadE1	1233	754	1.6	0.2	0.1	acyl-CoA_dehydrogenase_	1.1	0.5	0.5	0.6	0.6	0.7	0.6
247	Rv0250c	-	1718	1155	1.5	0.1	0.1	unlikely_orf	1.1	0.6	0.6	0.7	0.7	0.8	0.7
125	Rv0337c	aspC	807	508	1.6	0.2	0.1	aspartate_aminotransferase	1.1	0.6	0.7	0.6	0.7	0.7	0.6
847	Rv0338c	-	2039	736	2.8	0.2	0.1	iron-sulfur_protein	1.1	0.4	0.4	0.3	0.4	0.4	0.3
4071	Rv0430	-	2044	1398	1.5	0.1	0.0		1.1	nd	0.6	0.7	0.7	0.7	0.7
665	Rv0521c	-	405	266	1.5	0.3	0.1		1.1	0.5	0.8	0.8	0.8	0.6	0.7
5344	Rv0526	-	462	316	1.5	0.1	0.0	some_similarity_to_thioredoxin	1.1	0.7	0.7	0.7	0.6	0.7	0.7
5354	Rv0558	ubiE	1058	722	1.5	0.1	0.0	ubiquinone/menaquinone_biosynthesis_methyltransferase	1.1	0.7	0.6	0.7	0.7	0.7	0.7
1746	Rv0561c	-	323	210	1.5	0.3	0.1	similar_to_squalene_monooxygenase	1.1	0.5	0.7	0.7	0.7	0.5	0.9
4051	Rv0619	galT	474	224	2.1	0.5	0.2	galactose-1-phosphate_uridylyltransferase_C-term	1.1	0.5	0.7	0.6	0.4	0.4	0.4
3554	Rv0632c	echA3	2119	1303	1.6	0.2	0.1	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	0.6	0.5	0.7	0.6	0.6	0.7
5495	Rv0706	rplV	983	627	1.6	0.1	0.0	50S_ribosomal_protein_L22	1.1	0.6	0.6	0.6	0.6	0.6	0.7
1397	Rv0710	rpsQ	1920	1319	1.5	0.1	0.1	30S_ribosomal_protein_S17	1.4	0.7	0.8	0.7	nd	0.6	0.6
5440	Rv0797	IS1547	402	276	1.5	0.2	0.1		1.2	0.8	0.7	0.7	0.6	0.6	0.7
4078	Rv1133c	metE	916	597	1.5	0.1	0.0	5-methyltetrahydropteroyltrylglutamate-homocysteine_methyl	1.1	0.6	0.6	0.7	0.7	0.7	0.7
4171	Rv1177	fdxC	1796	964	1.9	0.1	0.0	ferredoxin_4Fe-4S	1.1	0.6	0.5	0.5	0.5	0.6	0.6
4177	Rv1240	mdh	792	544	1.5	0.1	0.0	malate_dehydrogenase	1.1	0.7	0.7	0.7	0.7	0.7	0.6
4244	Rv1252c	lprE	1115	699	1.6	0.1	0.0	lipoprotein	1.1	0.6	0.7	0.6	0.6	0.6	0.7
2654	Rv1289	-	607	403	1.5	0.2	0.1		1.1	0.6	0.7	0.6	0.8	0.7	0.6
5544	Rv1305	atpE	2721	1727	1.6	0.1	0.1	ATP_synthase_c_chain	1.1	0.6	0.6	0.7	0.7	0.7	0.6
5502	Rv1388	mlHF	3069	2054	1.5	0.2	0.1	integration_host_factor	1.1	0.6	0.6	0.6	0.8	0.8	0.7
1612	Rv1435c	-	882	604	1.5	0.1	0.1	Pro-_Gly_Val-rich_protein	1.1	0.6	0.6	0.7	0.7	0.6	0.8
2425	Rv1527c	pks5	276	199	1.5	0.2	0.1	polyketide_synthase	2.6	0.7	nd	0.7	0.7	0.5	0.7
1593	Rv1552	frdA	339	202	1.6	0.3	0.1	fumarate_reductase_flavoprotein_subunit	1.1	0.5	0.7	0.7	0.7	0.4	0.6
1708	Rv1608c	bcpB	853	591	1.5	0.2	0.1	probable_bacterioferritin_comigratory_protein	1.1	0.7	0.7	0.7	0.7	0.5	0.8
5452	Rv1612	trpB	1161	794	1.5	0.2	0.1	tryptophan_synthase_b_chain	1.2	0.7	0.6	0.7	0.6	0.7	0.7
5453	Rv1614	lgt	1683	1054	1.6	0.2	0.1	prolipoprotein_diacylglyceryl_transferase	1.1	0.7	0.5	0.7	0.5	0.7	0.6
391	Rv1726	-	460	241	1.9	0.3	0.1	6-hydroxy-d-nicotine_oxidase_	1.1	0.6	0.6	0.5	0.4	0.6	0.5
5127	Rv1836c	-	501	340	1.5	0.1	0.0		1.1	0.7	0.8	0.6	0.7	0.7	0.7
2981	Rv1876	bfrA	959	447	2.1	0.3	0.1	bacterioferritin	1.1	0.4	0.4	0.5	0.5	0.6	0.5
2933	Rv1908c	katG	660	388	1.7	0.2	0.1	catalase-peroxidase_	1.1	0.5	0.6	0.6	0.6	0.6	0.7
4879	Rv1938	ephB	1475	988	1.5	0.1	0.0	probable_epoxide_hydrolase	1.1	0.7	0.7	0.6	0.7	nd	0.7
5598	Rv1943c	-	898	516	1.7	0.1	0.0		1.1	0.5	0.6	0.6	0.6	0.6	0.6
2665	Rv2007c	fdxA	1670	1095	1.5	0.1	0.1	ferredoxin	1.1	0.7	0.6	0.7	0.6	0.7	0.6
1682	Rv2033c	-	703	395	1.7	0.5	0.2		2.6	0.5	0.6	0.7	0.8	0.3	0.7
636	Rv2232	-	477	315	1.5	0.2	0.1		1.1	0.6	0.6	0.7	0.7	0.6	0.8
3392	Rv2276	-	818	513	1.6	0.2	0.1	Probable_cytochrome_P-450	1.1	0.7	0.8	0.5	0.6	0.7	0.6
3390	Rv2280	-	663	433	1.5	0.1	0.1	similar_to_D-lactate_dehydrogenase	1.1	0.6	0.8	0.6	0.6	0.7	0.6
2472	Rv2351c	plcA	777	523	1.5	0.1	0.1	phospholipase_C_precursor	1.1	0.6	0.8	0.6	0.7	0.7	0.6
5259	Rv2521	bcp	877	589	1.5	0.2	0.1	bacterioferritin_comigratory_protein	1.1	0.7	0.6	0.7	0.6	0.7	0.8
1868	Rv2526	-	390	252	1.6	0.1	0.1		1.1	0.6	0.6	0.7	0.7	0.7	0.6
2589	Rv2527	-	680	464	1.5	0.2	0.1		1.1	0.6	0.6	0.7	0.6	0.8	0.8
2585	Rv2549c	-	419	264	1.6	0.1	0.0		1.1	0.7	0.6	0.7	0.6	0.7	0.7
1863	Rv2550c	-	511	255	2.0	0.2	0.1		1.1	0.5	0.4	nd	0.5	0.5	0.5
1517	Rv2611c	-	444	252	1.7	0.3	0.1		1.1	0.5	0.6	0.7	0.7	0.4	0.7
1771	Rv2792c	IS1602	391	259	1.5	0.4	0.2	resolvase	1.1	0.6	0.8	0.8	0.7	0.4	0.9
32	Rv2927c	-	1919	1232	1.6	0.1	0.0		1.1	0.6	0.6	0.6	0.6	0.7	0.6
1659	Rv2996c	serA	543	364	1.5	0.2	0.1	D-3-phosphoglycerate_dehydrogenase	1.1	0.7	0.6	0.7	0.7	0.6	0.8

3722	Rv3075c	-	803	472	1.7	0.2	0.1			1.1	0.5	0.8	0.6	0.6	0.6	0.5
993	Rv3145	nuoA	771	444	1.7	0.3	0.1	NADH_dehydrogenase_chain_A		1.1	0.5	0.8	0.6	0.5	0.6	0.6
869	Rv3146	nuoB	1488	821	1.8	0.1	0.1	NADH_dehydrogenase_chain_B		1.1	0.5	0.5	0.5	0.6	0.6	0.5
147	Rv3147	nuoC	744	475	1.6	0.2	0.1	NADH_dehydrogenase_chain_C		1.1	0.7	0.5	0.7	0.6	0.7	0.7
868	Rv3148	nuoD	1172	680	1.7	0.2	0.1	NADH_dehydrogenase_chain_D		1.1	0.5	0.7	0.6	0.6	0.6	0.5
867	Rv3150	nuoF	799	526	1.5	0.2	0.1	NADH_dehydrogenase_chain_F		1.1	0.6	0.8	0.6	0.7	0.8	0.6
5559	Rv3152	nuoH	1408	786	1.8	0.1	0.0	NADH_dehydrogenase_chain_H		1.1	0.6	0.6	0.5	0.6	0.6	0.6
4837	Rv3153	nuoI	1362	865	1.6	0.1	0.1	NADH_dehydrogenase_chain_I		1.1	0.6	0.6	0.6	0.6	0.7	0.6
4836	Rv3155	nuoK	1936	1204	1.6	0.2	0.1	NADH_dehydrogenase_chain_K		1.1	0.7	0.6	0.6	0.6	0.7	0.6
5557	Rv3156	nuoL	2264	1337	1.7	0.2	0.1	NADH_dehydrogenase_chain_L		1.1	0.6	0.5	0.6	0.6	0.6	0.7
4835	Rv3157	nuoM	895	558	1.6	0.1	0.1	NADH_dehydrogenase_chain_M		1.1	0.7	0.5	0.6	0.6	0.7	0.6
3850	Rv3158	nuoN	1014	618	1.6	0.1	0.1	NADH_dehydrogenase_chain_N		1.1	0.6	0.7	0.6	0.6	0.6	0.6
1383	Rv3246c	mtrA	1964	987	2.0	0.3	0.1	two-component_response_regulator		1.1	0.4	0.4	0.6	0.6	0.6	0.5
2500	Rv3258c	-	1053	665	1.7	0.1	0.1			1.1	0.5	nd	0.6	0.6	0.6	0.6
3482	Rv3320c	-	515	359	1.5	0.0	0.0			1.1	0.7	nd	0.7	0.7	0.7	0.7
555	Rv3370c	dnaE2	522	356	1.5	0.1	0.0	DNA_polymerase_III_a_chain		1.1	0.6	0.7	0.7	0.7	0.8	0.7
642	Rv3394c	-	253	199	1.7	0.2	0.2			2.6	0.7	nd	nd	nd	0.5	nd
4254	Rv3587c	-	1519	961	1.6	0.1	0.0			1.1	0.6	0.6	0.6	0.6	0.7	0.6
1709	Rv3659c	trbB	285	199	1.5	0.5	0.2	similar_to_conjugal_transfer_proteins		1.1	0.6	0.9	nd	nd	0.4	0.9
1723	Rv3711c	dnaQ	547	295	1.8	0.4	0.2	DNA_polymerase_III_e_chain		1.1	0.5	0.6	0.7	0.6	0.3	0.6
1724	Rv3713	cobQ2	432	261	1.6	0.4	0.2	possible_cobryric_acid_synthase		1.1	0.5	0.8	0.6	0.7	0.4	0.7
1725	Rv3715c	recR	602	375	1.6	0.4	0.2	RecBC-Independent_process_of_DNA_repair		1.1	0.6	0.6	0.7	0.7	0.3	0.7
1726	Rv3718c	-	503	288	1.7	0.4	0.2			1.1	nd	0.6	0.6	0.7	0.4	0.7
5140	Rv3841	bfrB	5013	434	11.5	1.8	0.7	bacterioferritin		1.1	0.1	0.1	0.1	0.1	0.1	0.1
2128	Rv3842c	glpQ1	876	392	2.3	0.5	0.2	glycerophosphoryl_diester_phosphodiesterase		1.1	0.4	0.3	0.5	0.5	0.5	0.5
289	Rv3846	sodA	805	528	1.5	0.2	0.1	superoxide_dismutase		1.1	0.6	0.7	0.6	0.8	0.7	0.6