

Table 6: Genes repressed in Mycobacterium tuberculosis ideR complemented mutant compared to H37Rv 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		CH2/CH1	StD	SEM			Biol. set 1		Biol. set 2		Biol. set 3	
			CH1 Cye3	CH2 Cye5						Repressed	mm708	mm715	mm698	mm711	mm713
102	Rv0040c	-	1010	653	1.5	0.2	0.1		1.1	0.6	0.8	0.6	0.6	0.7	0.6
826	Rv0057	-	1380	931	1.5	0.2	0.1		1.1	0.7	0.6	0.6	0.7	0.8	0.6
5624	Rv0058	dnaB	1193	786	1.5	0.1	0.1	DNA_helicase_(contains_intein)	1.1	0.6	0.7	0.6	0.6	0.8	0.6
1976	Rv0130	-	939	574	1.6	0.2	0.1		1.1	0.6	0.5	0.7	0.6	0.7	0.5
5572	Rv0313	-	1451	917	1.6	0.2	0.1		1.1	0.6	0.6	0.7	0.6	0.6	0.8
5123	Rv0350	dnaK	3785	1829	2.0	0.4	0.1	70_kD_heat_shock_protein,_chromosome_replication	1.1	0.5	0.5	0.5	0.5	0.6	0.4
4402	Rv0351	grpE	2292	1148	2.0	0.2	0.1	stimulates_DnaK_ATPase_activity	1.1	0.5	0.5	0.5	0.5	0.6	0.5
264	Rv0440	groEL2	4153	1954	2.1	0.3	0.1	60_kD_chaperonin_2	1.4	0.5	0.5	0.5	0.5	0.5	0.4
4051	Rv0619	galT	436	253	1.7	0.5	0.2	galactose-1-phosphate_uridylyltransferase_C-term	1.1	0.4	0.4	0.7	0.7	0.4	0.8
1055	Rv0652	rplL	583	341	1.7	0.1	0.0	50S_ribosomal_protein_L7/L12	1.1	0.6	0.6	0.5	0.6	0.6	0.6
672	Rv0652	rplL	656	429	1.5	0.1	0.0	50S_ribosomal_protein_L7/L12	1.1	0.6	0.7	0.6	0.7	0.6	0.6
2474	Rv0653c	-	380	240	1.5	0.3	0.1	putative_transcriptional_regulator	2.1	0.6	0.8	0.6	0.6	0.5	0.8
5495	Rv0706	rplV	977	616	1.6	0.2	0.1	50S_ribosomal_protein_L22	1.1	0.6	0.7	0.6	0.7	0.6	0.8
4774	Rv0707	rpsC	2291	1415	1.6	0.2	0.1	30S_ribosomal_protein_S3	1.1	0.7	0.7	0.5	0.6	nd	0.6
5496	Rv0708	rplP	3003	1598	1.9	0.2	0.1	50S_ribosomal_protein_L16	1.1	0.5	0.6	0.5	0.6	0.6	0.5
4775	Rv0709	rpmC	2115	1403	1.5	0.1	0.1	50S_ribosomal_protein_L29_	1.1	0.7	0.8	0.6	0.7	0.7	0.6
1397	Rv0710	rpsQ	1903	1179	1.6	0.1	0.0	30S_ribosomal_protein_S17	1.4	0.7	0.6	0.6	0.6	0.6	0.6
2615	Rv0722	rpmD	1610	929	1.7	0.2	0.1	50S_ribosomal_protein_L30	1.1	0.6	0.6	0.6	0.6	0.6	0.5
1894	Rv0723	rplO	1353	907	1.5	0.1	0.0	50S_ribosomal_protein_L15	1.1	0.6	0.7	0.7	0.6	0.7	0.6
484	Rv0903c	-	777	529	1.5	0.1	0.1	two-component_response_regulator	1.1	0.6	0.7	0.7	0.7	0.7	0.7
3292	Rv0996	-	587	381	1.5	0.3	0.1		1.1	0.6	0.6	0.7	0.6	nd	0.9
4038	Rv1013	pks16	1541	870	1.7	0.2	0.1	polyketide_synthase_	1.2	0.6	0.6	0.5	0.4	0.6	0.6
1002	Rv1036c	IS1560	658	444	1.5	0.1	0.0		1.1	0.7	0.6	0.7	0.7	0.7	0.8
4078	Rv1133c	metE	848	519	1.6	0.2	0.1	5-methyltetrahydropteroyltriglutamate-homocysteine_methyl	1.1	0.6	0.7	0.6	0.5	0.6	0.7
5448	Rv1149	IS-like	1615	937	1.7	0.1	0.0		1.1	0.6	0.6	0.6	0.5	0.6	0.6
4728	Rv1152	-	454	309	1.5	0.2	0.1	transcriptional_regulator_(GntR_family)	1.1	0.7	0.7	0.8	0.6	0.6	0.7
1843	Rv1158c	-	612	363	1.6	0.2	0.1		1.2	0.6	0.7	0.5	0.6	0.6	0.7
1399	Rv1233c	-	5327	2957	1.8	0.2	0.1	hydrophobic_protein	1.4	0.6	0.6	0.5	0.5	0.6	0.6
4177	Rv1240	mdh	828	556	1.5	0.1	0.1	malate_dehydrogenase	1.1	0.6	0.8	0.7	0.6	nd	0.7
4244	Rv1252c	lprE	995	564	1.7	0.2	0.1	lipoprotein	1.1	0.6	0.7	0.5	0.5	0.5	0.6
5569	Rv1252c	lprE	1114	676	1.6	0.2	0.1	lipoprotein	1.1	0.5	0.6	0.6	0.6	0.6	0.7

4780	Rv1387	PPE	2247	1008	2.2	0.2	0.1			1.1	0.4	0.5	0.4	0.4	0.5	0.4
5502	Rv1388	miHF	3569	1825	1.9	0.2	0.1	integration_host_factor		1.1	0.6	0.6	0.4	0.5	0.5	0.5
2334	Rv1434	-	645	419	1.6	0.1	0.1	improbable		1.1	0.7	0.6	0.6	0.6	0.6	0.7
2360	Rv1478	-	803	539	1.5	0.1	0.0	putative_exported_p60_protein_homologue		1.1	0.6	0.7	0.7	0.6	0.6	0.7
3849	Rv1535	-	768	522	1.5	0.2	0.1			1.1	0.8	0.7	0.7	0.5	0.7	0.7
4101	Rv1566c	-	941	567	1.6	0.2	0.1	putative_exported_p60_protein_homologue		1.1	0.6	0.6	0.6	0.5	0.7	0.7
1121	Rv1690	lprJ	802	424	1.9	0.3	0.1	lipoprotein		1.1	0.6	0.4	0.5	0.5	0.7	0.5
391	Rv1726	-	388	245	1.6	0.2	0.1	6-hydroxy-d-nicotine_oxidase_		1.1	0.6	nd	0.7	0.7	0.5	0.6
5127	Rv1836c	-	479	322	1.5	0.1	0.0			1.1	0.7	0.6	0.7	0.7	0.6	0.7
5598	Rv1943c	-	887	590	1.5	0.2	0.1			1.1	0.6	0.8	0.6	0.6	0.7	0.8
3945	Rv1987	-	2139	1452	1.5	0.2	0.1	probable_secreted_protein		1.1	0.8	0.7	0.6	0.6	0.8	0.6
2627	Rv2147c	-	1993	1313	1.5	0.2	0.1			1.1	0.7	0.7	0.6	0.6	0.8	0.6
4120	Rv2244	acpM	5049	3047	1.8	0.4	0.2	acyl_carrier_protein_(meromycolate_extension)		1.1	0.7	nd	0.5	0.5	nd	0.5
5252	Rv2462c	tig	1269	825	1.5	0.2	0.1	chaperone_protein_similar_to_trigger_factor		1.1	0.7	0.8	0.5	0.7	0.7	0.6
1643	Rv2463	lipP	735	369	2.0	0.3	0.1	probable_esterase		1.1	0.4	0.6	0.5	0.5	0.4	0.5
2590	Rv2525c	-	678	453	1.5	0.1	0.1			1.1	0.7	0.6	0.7	0.7	0.6	0.6
2589	Rv2527	-	581	367	1.6	0.1	0.0			1.1	0.7	0.6	0.6	0.7	0.7	0.6
1863	Rv2550c	-	454	248	1.8	0.2	0.1			1.1	0.4	0.5	0.6	0.6	0.5	0.6
2581	Rv2721c	-	572	368	1.6	0.1	0.0			1.1	0.6	0.6	0.7	0.6	0.7	0.6
4884	Rv2738c	-	2592	1316	1.8	0.5	0.2			1.1	0.7	0.7	0.3	0.4	0.5	0.6
1219	Rv2923c	-	636	422	1.5	0.2	0.1			1.1	0.6	0.7	0.6	0.6	0.7	0.8
32	Rv2927c	-	1781	1090	1.6	0.3	0.1			1.1	0.7	0.7	0.5	0.5	0.8	0.5
3646	Rv2935	ppsE	630	385	1.6	0.2	0.1	phenolphthiocerol_synthesis_(pksF)		1.4	0.7	0.6	0.6	0.6	0.6	0.5
1569	Rv2986c	hupB	2684	1528	1.7	0.3	0.1	DNA-binding_protein_II_		1.1	0.6	0.6	0.6	0.6	0.7	0.4
5264	Rv2987c	leuD	559	319	1.7	0.3	0.1	3-isopropylmalate_dehydratase_small_subunit		1.1	0.5	0.8	0.5	0.5	0.5	0.7
3033	Rv3136	PPE	1184	693	1.6	0.2	0.1			1.1	0.7	0.7	0.5	0.5	0.7	0.6
1383	Rv3246c	mtrA	1856	861	2.2	0.2	0.1	two-component_response_regulator		1.1	0.5	0.5	0.5	0.4	0.5	0.4
2500	Rv3258c	-	1041	555	1.9	0.3	0.1			1.1	0.6	0.5	0.6	0.4	0.4	0.7
3477	Rv3258c	-	1132	622	1.8	0.4	0.1			1.1	0.6	0.5	0.6	0.4	0.5	0.7
590	Rv3260c	whiB2	1400	954	1.5	0.1	0.0	WhiB_transcriptional_activator_homologue		1.1	0.8	0.7	0.7	0.6	0.7	0.6
3067	Rv3267	-	686	453	1.5	0.2	0.1			1.1	0.6	0.8	0.6	0.6	0.7	0.7
555	Rv3370c	dnaE2	498	302	1.7	0.2	0.1	DNA_polymerase_III_a_chain		1.1	0.5	0.6	0.6	0.7	0.5	0.7
4168	Rv3389c	-	1292	825	1.5	0.2	0.1	putative_dehydrogenase		1.4	0.6	0.6	0.8	nd	0.7	0.6
4144	Rv3407	-	3333	2139	1.6	0.3	0.1			1.1	0.7	0.6	0.5	0.6	0.8	0.6
4141	Rv3413c	-	753	506	1.5	0.1	0.0			1.1	0.6	0.6	0.7	0.7	0.7	0.7
3658	Rv3414c	sigD	829	541	1.6	0.1	0.1	ECF_subfamily_sigma_subunit		1.1	0.7	0.6	0.6	0.6	0.7	nd
1750	Rv3417c	groEL1	1419	898	1.6	0.2	0.1	60_kD_chaperonin_1		1.1	0.6	0.7	0.7	0.7	0.6	0.5

3418	Rv3418c	groES	10482	5817	1.9	0.4	0.2	10_kD_chaperone	1.1	0.5	0.5	0.5	0.6	0.7	0.4
4254	Rv3587c	-	1479	877	1.7	0.2	0.1		1.1	0.6	0.7	0.6	0.5	0.7	0.6
5330	Rv3706c	-	1628	1049	1.5	0.2	0.1		1.1	0.6	0.7	0.5	0.7	0.7	0.7
1723	Rv3711c	dnaQ	469	297	1.6	0.5	0.2	DNA_polymerase_III_e_chain	1.1	0.4	0.7	0.8	0.7	0.4	0.8
5681	Rv3800c	pks13	930	629	1.5	0.1	0.0	polyketide_synthase	1.1	0.6	0.7	0.6	0.7	0.8	0.7
2077	Rv3810	pirG	2813	1720	1.6	0.2	0.1	cell_surface_protein_precursor_(Erp_protein)	1.1	0.7	0.7	0.5	0.6	0.7	0.6
2799	Rv3811	csp	1151	787	1.5	0.2	0.1	secreted_protein	1.1	0.9	0.7	0.6	0.7	nd	0.6
5140	Rv3841	bfrB	3303	852	3.8	0.6	0.3	bacterioferritin	1.1	0.3	0.3	0.2	0.3	nd	0.2
2128	Rv3842c	glpQ1	788	457	1.7	0.1	0.0	glycerophosphoryl_diester_phosphodiesterase	1.1	0.6	0.6	0.6	0.6	0.6	0.5
653	Rv3890c	-	845	534	1.6	0.2	0.1		1.1	0.5	0.7	0.7	0.7	0.7	0.6
2735	Rv3914	trxC	1916	1128	1.7	0.3	0.1	thioredoxin	1.1	0.7	0.5	0.5	0.7	0.8	0.5





