

Table 2. Genes repressed in Mycobacterium tuberculosis H37Rv by diamide 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		Biol. set 2		Biol. set 3	
									mi1016	mi1020	mi1022	mi1026	mi1032	mi519	
2738	Rv0062	celA	4315	2143	1.9	0.4	0.1	cellulase/endoglucanase	1.1	0.4	0.6	0.5	0.5	0.6	0.4
5573	Rv0315	-	10668	6218	1.7	0.3	0.1	probable_b-1,3-glucanase	1.2	0.5	0.5	0.7	0.5	0.7	0.6
5343	Rv0524	hemL	3973	2667	1.5	0.2	0.1	glutamate-1-semialdehyde_aminotransferase	1.1	0.5	0.7	0.7	0.8	0.7	0.5
608	Rv0566c	-	4077	2714	1.5	0.2	0.1		1.4	0.6	0.6	0.8	0.6	0.8	0.6
5493	Rv0692	-	6414	4306	1.5	0.2	0.1		1.1	0.6	0.7	0.8	0.6	0.7	0.7
3562	Rv0734	map'	3616	2715	1.5	0.4	0.2	probable_methionine_aminopeptidase	1.1	0.7	nd	0.8	0.6	0.9	0.4
5193	Rv0761c	adhB	7758	5034	1.5	0.1	0.1	zinc-containing_alcohol_dehydrogenase	1.1	0.5	0.7	0.7	0.7	0.7	0.7
4233	Rv0810c	-	5261	3613	1.5	0.2	0.1		1.1	0.7	0.7	0.8	0.7	0.6	0.6
1623	Rv0934	phoS1	15530	10853	1.5	0.3	0.1	PstS_component_of_phosphate_uptake	1.4	0.6	0.6	0.9	0.6	0.7	0.8
1001	Rv0935	pstC	8630	5622	1.5	0.1	0.0	PstC_component_of_phosphate_uptake	1.1	0.6	0.7	0.6	0.7	0.7	0.6
4026	Rv0950c	-	7395	5035	1.5	0.1	0.1		1.1	0.7	0.6	0.7	0.6	0.7	0.8
4038	Rv1013	pks16	7042	4434	1.6	0.3	0.1	polyketide_synthase_	1.2	0.5	0.5	0.7	0.6	0.8	0.7
4558	Rv1094	desA2	12904	7679	1.6	0.3	0.1	acyl-[ACP]_desaturase	1.1	0.5	0.5	0.8	nd	0.6	0.7
1481	Rv1195	PE	4700	2401	1.9	0.4	0.2		1.1	0.3	0.6	0.5	0.5	0.6	0.6
1483	Rv1199c	IS1081	11072	7791	1.5	0.3	0.1		1.1	0.6	0.5	0.8	0.9	0.6	0.7
4177	Rv1240	mdh	7459	4236	1.7	0.3	0.1	malate_dehydrogenase	1.1	0.6	0.5	0.6	0.4	0.7	0.7
2678	Rv1270c	lprA	8613	5661	1.5	0.2	0.1	lipoprotein	1.1	0.6	0.7	0.7	0.7	0.6	0.6
4824	Rv1308	atpA	10646	7112	1.5	0.2	0.1	ATP_synthase_a_chain	1.1	0.5	0.7	0.8	0.6	0.8	0.6
4781	Rv1389	gmk	5749	3642	1.6	0.3	0.1	putative_guanylate_kinase	1.1	0.5	0.6	0.6	0.7	0.9	0.7
3572	Rv1436	gap	7424	4918	1.5	0.2	0.1	glyceraldehyde_3-phosphate_dehydrogenase	1.1	0.5	0.7	0.8	0.7	0.7	0.6
1748	Rv1484	inhA	5627	3578	1.6	0.2	0.1	enoyl-[ACP]_reductase	1.1	0.5	0.7	0.7	0.6	0.6	0.6
4301	Rv1559	ilvA	4270	2938	1.5	0.2	0.1	threonine_deaminase	2.1	0.7	0.7	0.8	0.5	0.8	0.7
5452	Rv1612	trpB	7504	4578	1.8	0.3	0.1	tryptophan_synthase_b_chain	1.2	0.6	0.5	0.6	0.5	0.5	0.7
5453	Rv1614	lgt	9475	6483	1.6	0.3	0.1	prolipoprotein_diacylglyceryl_transferase	1.1	0.9	0.6	0.7	0.6	0.4	0.6
2777	Rv1807	PPE	4370	2797	1.5	0.3	0.1		1.1	0.6	0.8	0.5	0.8	0.7	0.8
4940	Rv1919c	-	6964	4588	1.5	0.2	0.1	weak_similarity_to_pollen_antigens	1.1	0.6	0.7	0.6	0.8	0.7	0.6
1948	Rv1988	-	2123	1640	1.5	0.4	0.2	possible_rRNAmethyltransferase	2.6	nd	0.7	nd	nd	0.5	0.9
2665	Rv2007c	fdxA	10458	7007	1.5	0.2	0.1	ferredoxin	1.1	0.6	0.5	0.7	0.6	0.7	0.8
1681	Rv2031c	hspX	7329	5076	1.5	0.1	0.0	14kD_antigen_heat_shock_protein_Hsp20_family	1.1	0.6	0.6	0.8	0.7	0.7	0.7
4049	Rv2216	-	5750	3735	1.5	0.2	0.1		1.1	0.6	0.8	0.6	0.6	0.8	0.6
3835	Rv2243	fabD	8123	4769	1.6	0.3	0.1	malonyl_CoA-[ACP]_transacylase	1.1	0.4	0.6	0.6	0.6	0.8	0.8
4120	Rv2244	acpM	12524	5949	2.2	0.5	0.2	acyl_carrier_protein_(meromycolate_extension)	1.1	0.5	0.3	0.5	0.4	0.6	0.5
3836	Rv2245	kasA	6690	2647	2.3	0.7	0.3	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.3	0.4	0.4	0.3	0.7	0.5
3838	Rv2246	kasB	11791	7104	1.7	0.2	0.1	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.6	0.6	0.6	0.7	0.7	0.4
229	Rv2247	accD6	6281	3013	2.1	0.9	0.4	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	0.2	0.4	0.3	0.5	0.7	0.8
952	Rv2248	-	5027	2723	1.7	0.4	0.2		1.1	0.4	0.5	0.5	0.6	0.8	0.7
3392	Rv2276	-	3650	1763	1.9	0.4	0.2	Probable_cytochrome_P-450	1.1	0.3	0.6	0.6	0.6	0.6	0.4
415	Rv2512c	IS1081	8830	5934	1.5	0.1	0.1		1.1	0.8	0.6	0.7	0.7	0.7	0.6
5259	Rv2521	bcp	4415	2858	1.5	0.2	0.1	bacterioferritin_comigratory_protein	1.1	0.5	0.7	0.6	0.6	0.8	0.8
1177	Rv2626c	-	6689	4075	1.5	0.4	0.2		1.1	0.5	0.5	0.5	0.6	0.9	0.9
210	Rv2858c	aldC	3538	2372	1.5	0.4	0.1	aldehyde_dehydrogenase_phenylacetaldehyde_	1.1	0.4	0.7	0.5	0.7	0.7	0.9
5185	Rv2951c	-	6121	4202	1.5	0.3	0.1	putative_oxidoreductase	1.1	0.9	0.6	0.5	0.6	0.7	0.7
4463	Rv2952	-	6740	4446	1.5	0.3	0.1	glycosyltransferase	1.1	0.5	0.6	0.8	nd	0.8	0.7
5182	Rv2956	-	6243	4087	1.5	0.3	0.1		1.1	0.6	0.9	0.7	0.8	0.6	0.5
5265	Rv3001c	ilvC	6216	3405	1.7	0.4	0.2	ketol-acid_reductoisomerase	1.1	0.4	0.6	0.5	0.6	0.7	0.7
4251	Rv3002c	ilvN	2557	1640	1.6	0.2	0.1	acetolactate_synthase_l_small_subunit	1.1	0.6	nd	0.8	0.6	0.7	0.6
5484	Rv3126c	-	3286	2237	1.5	0.2	0.1		1.1	0.7	0.7	0.8	0.5	0.7	0.7
3068	Rv3269	-	7518	3808	1.9	0.4	0.2	probable_heat_shock_protein	1.1	0.4	0.5	0.4	0.5	0.7	0.6
1313	Rv3304	-	3918	2611	1.5	0.2	0.1		1.1	0.6	0.7	0.7	0.7	0.8	0.6
3800	Rv3442c	rpsI	6369	4053	1.5	0.2	0.1	30S_ribosomal_protein_S9	2.5	0.5	0.7	0.7	0.6	0.8	0.7
1025	Rv3646c	topA	8365	5060	1.6	0.2	0.1	DNA_topoisomerase	1.1	0.6	0.6	0.6	0.5	0.7	0.6

5322	Rv3678c	-	6635	4233	1.5	0.3	0.1	transcriptional_regulator_(LysR_family)	1.1	0.5	0.8	0.6	0.7	0.8	0.5
5338	Rv3747	-	3486	2343	1.5	0.3	0.1		1.1	0.4	0.7	0.8	0.7	0.8	0.5
4617	Rv3748	-	8666	5461	1.5	0.3	0.1		1.4	0.6	0.7	0.5	nd	0.8	0.7
2795	Rv3763	lpqH	9671	6388	1.5	0.2	0.1	19_kD	1.1	0.7	0.6	0.8	0.7	0.6	0.6
1011	Rv3774	echA21	10023	6493	1.5	0.1	0.1	enoyl-CoA_hydratase/isomerase_superfamily	1.1	0.6	0.6	0.7	0.6	0.7	0.6
4962	Rv3804c	fbpA	9804	6612	1.6	0.4	0.2	antigen_85A_mycolytransferase	1.1	0.3	0.6	0.8	0.6	0.7	0.7