

Table 4: Genes repressed in Mycobacterium tuberculosis sigH mutant 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 Induced	StD	SEM			Biol. set 1		Biol. set 2		Biol. set 3	
									mi1017	mi1021	mi1023	mi1027	mi1033	mi522	
1494	Rv0013	pabA	5692	8164	1.5	0.2	0.1	p-aminobenzoate_synthase glutamine amidotransferase	1.1	1.6	1.3	1.4	1.2	1.6	1.8
2216	Rv0014c	pknB	2358	4669	2.1	0.5	0.2	serine-threonine_protein_kinase	1.1	2.0	2.5	2.3	1.1	2.5	2.5
1495	Rv0015c	pknA	7743	14712	2.2	1.1	0.5	serine-threonine_protein_kinase	2.6	3.3	3.3	0.8	0.9	2.2	2.9
2217	Rv0016c	pbpA	4229	14463	3.7	1.4	0.6	penicillin-binding_protein	1.1	4.3	5.1	2.2	1.9	3.6	5.0
1496	Rv0017c	rodA	8948	19137	2.6	1.3	0.5	FtsW/RodA/SpovE_family	1.1	2.9	3.8	1.1	1.0	2.6	4.2
2218	Rv0018c	ppp	3402	4992	1.5	0.3	0.1	putative_phosphoprotein_phosphatase	1.2	1.7	1.5	1.9	1.1	1.5	1.4
2219	Rv0020c	-	3203	4798	1.5	0.2	0.1		1.1	1.6	1.9	1.6	1.2	1.4	1.5
5108	Rv0034	-	2283	3286	1.5	0.3	0.1		1.1	1.5	1.9	1.6	1.0	1.4	1.6
1499	Rv0035	fadD34	3297	4307	1.5	0.3	0.1	acyl-CoA_synthase	1.1	1.5	2.0	1.5	1.0	1.2	1.5
2738	Rv0062	celA	3615	6034	1.7	0.3	0.1	cellulase/endoglucanase	1.1	2.3	1.6	1.9	1.6	1.5	1.4
2741	Rv0068	-	1798	3017	1.7	0.2	0.1	probable_oxidoreductase	1.1	1.8	1.9	1.8	1.4	1.7	1.7
2020	Rv0069c	sdaA	2848	4490	1.6	0.3	0.1	L-serine_dehydratase_1	1.1	nd	1.4	2.0	1.6	1.4	1.4
3364	Rv0097	-	3459	5438	1.6	0.3	0.1		1.1	1.8	1.5	2.1	1.5	1.3	1.5
3365	Rv0099	fadD10	2310	3800	1.7	0.2	0.1	acyl-CoA_synthase	1.1	2.0	1.6	1.9	1.4	1.5	1.5
3366	Rv0101	nrp	1849	2651	1.5	0.3	0.1	unknown_non-ribosomal_peptide_synthase	1.1	1.9	1.8	1.5	1.2	1.4	1.3
1977	Rv0132c	-	2465	3811	1.6	0.4	0.2	putative_oxidoreductase	1.1	2.0	1.3	2.1	1.3	1.5	1.2
1981	Rv0152c	PE	2528	3542	1.5	0.4	0.2		1.1	2.1	1.0	1.7	1.3	1.2	1.3
2196	Rv0161	-	3121	4517	1.5	0.8	0.4	possible_oxidoreductase	2.6	1.0	nd	1.2	1.0	1.2	2.9
4357	Rv0162c	adhE	5007	7191	1.5	0.5	0.2	alcohol_dehydrogenase_(Zn)	1.1	1.8	1.7	1.0	0.9	1.8	2.0
4363	Rv0186	bgIS	4602	6715	1.5	0.4	0.2	b-glucosidase	1.1	1.8	1.6	0.8	1.2	2.0	1.8
4933	Rv0196	-	2884	4151	1.6	0.4	0.2	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.5	1.5	0.9	1.4	2.2	1.9
2340	Rv0221	-	1903	2781	1.5	0.2	0.1		1.1	1.5	1.9	1.5	1.2	1.3	1.4
969	Rv0251c	hsp	5290	9444	1.9	0.8	0.3	possible_heat_shock_protein	1.1	2.5	3.2	1.0	1.7	2.0	1.3
3858	Rv0280	PPE	3405	6429	1.9	0.3	0.1		2.1	1.9	2.0	1.4	2.0	1.9	2.4
3859	Rv0282	-	5753	10185	1.9	0.5	0.2		1.1	1.9	1.8	1.0	2.1	2.1	2.5
3138	Rv0283	-	4925	6741	1.6	0.5	0.2		1.1	1.7	1.6	0.7	1.4	2.0	2.0
1968	Rv0324	-	2010	9089	4.6	1.0	0.4	putative_transcriptional_regulator	1.1	3.9	5.4	6.0	3.3	4.2	5.0
2690	Rv0325	-	1918	4641	2.5	0.4	0.2		1.2	2.8	2.8	2.2	2.0	2.9	2.3
319	Rv0326	-	2055	8257	4.4	0.8	0.3	maybe_gene_on_opposite_strand	1.1	5.0	4.8	4.9	3.1	4.9	3.6
2691	Rv0327c	-	2205	14881	6.9	1.8	0.7	cytochrome_P-450_monooxygenase	1.1	9.9	8.4	6.3	5.6	6.1	5.4
1970	Rv0328	-	1808	4475	2.7	0.7	0.3	transcriptional_regulator_(TetR/AcrR_family)	1.1	3.2	3.1	3.1	1.5	2.5	2.6
2692	Rv0329c	-	3034	4460	1.5	0.2	0.1		1.1	1.5	1.9	1.3	1.4	1.5	1.5
1971	Rv0330c	-	3088	4472	1.5	0.3	0.1		1.1	1.2	1.9	1.8	1.3	1.3	1.3
2693	Rv0331	-	5168	9421	1.9	0.3	0.1	putative_dehydrogenase	1.2	1.8	2.5	1.6	1.9	1.6	2.1
3524	Rv0332	-	3033	6305	2.2	0.3	0.1		1.1	2.1	2.3	2.0	1.7	2.7	2.3
260	Rv0384c	clpB	4407	7767	1.8	0.3	0.1	heat_shock_protein	1.1	2.0	1.8	2.2	1.7	1.4	1.6
3729	Rv0408	pta	2486	4563	1.8	0.3	0.1	phosphate_acetyltransferase	1.1	1.9	2.0	2.2	1.4	1.6	1.8
3008	Rv0409	ackA	4538	6795	1.5	0.3	0.1	acetate_kinase	1.1	1.6	1.6	1.1	1.5	1.7	1.8
985	Rv0439c	-	3999	5792	1.5	0.2	0.1	Probable_oxidoreductase	1.1	1.3	1.4	1.6	1.2	1.5	1.7
264	Rv0440	groEL2	11601	20385	2.4	1.9	0.8	60_kD_chaperonin_2	1.4	2.1	2.3	0.7	0.8	3.1	5.7
4424	Rv0485	-	4567	6800	1.5	0.3	0.1	transcriptional_regulator_(ROK_family)	1.1	1.4	1.8	0.9	1.6	1.8	1.6
1171	Rv0604	lpqO	4478	6606	1.5	0.2	0.1	lipoprotein	1.1	1.4	1.2	1.6	1.3	1.7	1.5
4776	Rv0711	atsA	3577	5113	1.5	0.3	0.1	arylsulfatase	1.1	1.3	1.8	1.6	1.7	1.1	1.3
2309	Rv0757	phoP	3320	4821	1.5	0.3	0.1	two-component_response_regulator	1.1	1.5	1.9	1.9	1.6	1.0	1.3
3431	Rv0800	pepC	2362	3613	1.5	0.1	0.1	aminopeptidase_I	1.1	1.4	1.5	1.7	1.3	1.6	1.6
682	Rv0826	-	1777	2332	1.5	0.2	0.1		1.1	1.3	1.7	1.5	nd	1.6	nd
4573	Rv0827c	-	2241	3092	1.5	0.3	0.1	transcriptional_regulator_(ArsR_family)	1.1	2.0	1.5	1.3	1.3	1.4	1.2
2415	Rv0845	-	1847	3077	1.7	0.3	0.1	sensor_histidine_kinase	1.1	1.8	1.8	1.8	1.1	1.8	1.7
1694	Rv0846c	-	4432	10102	2.4	0.6	0.2	similar_to_several_L-ascorbate_oxidases	1.1	2.8	2.3	1.5	2.0	2.8	3.0

2416	Rv0847	lpqS	1572	5476	3.6	0.9	0.4	lipoprotein	1.1	4.1	4.0	4.3	1.8	3.7	3.7
1695	Rv0848	cysM3	3660	8593	2.4	0.6	0.2	putative_cysteine_synthase	1.1	1.9	2.1	2.6	1.8	2.8	3.3
3559	Rv0913c	-	2893	4196	1.5	0.4	0.2	probable_dioxygenase	1.1	1.6	1.9	2.1	1.4	1.0	1.1
3303	Rv0965c	-	2412	3367	1.5	0.3	0.1		1.1	nd	1.4	1.9	1.1	1.7	1.3
3302	Rv0967	-	2547	4228	1.7	0.2	0.1		1.1	1.7	2.0	1.6	1.5	1.7	1.7
3301	Rv0969	ctpV	2214	3199	1.5	0.3	0.1	cation_transport_ATPase	1.1	1.3	1.8	1.8	1.2	1.4	1.4
1129	Rv0991c	-	4284	7385	1.7	0.4	0.2		1.1	1.7	1.2	2.0	1.4	1.6	2.4
3489	Rv1049	-	1640	4733	2.8	0.8	0.3	transcriptional_regulator_(MarR_family)	1.1	2.6	2.4	4.1	2.0	2.3	3.3
4211	Rv1050	-	2090	4189	2.0	0.4	0.1	probable__oxidoreductase	1.1	1.9	2.2	2.5	1.7	1.8	1.7
1661	Rv1051c	-	2384	3248	1.6	0.3	0.1		1.1	1.9	1.7	1.6	1.1	1.5	nd
3354	Rv1128c	REP	1849	4164	2.3	0.4	0.1		1.1	2.3	2.4	2.9	2.0	2.0	2.1
4076	Rv1129c	-	2314	9649	4.5	1.3	0.5	transcriptional_regulator_(PbsX/Xre_family)	1.1	7.0	3.9	4.6	4.5	3.1	3.6
3355	Rv1130	-	2480	12718	5.6	1.5	0.6		1.1	8.2	6.1	5.3	5.7	4.9	3.6
4077	Rv1131	gltA1	3408	12214	3.9	1.2	0.5	citrate_synthase_3	1.1	5.9	4.2	3.0	4.4	3.1	2.6
3455	Rv1239c	corA	2316	3446	1.5	0.2	0.1	probable_magnesium_and_cobalt_transport_protein	1.1	1.3	1.7	1.8	1.4	1.4	1.3
5540	Rv1285	cysD	2086	6427	3.4	1.0	0.4	ATP:sulphurylase_subunit_2	1.1	4.7	3.5	1.8	3.8	2.6	3.9
4819	Rv1286	cysN	4121	11142	3.1	1.2	0.5	ATP:sulphurylase_subunit_1	1.1	4.2	3.2	1.0	3.3	4.0	3.1