

Table 3: Genes induced in Mycobacterium tuberculosis sigH mutant by diamide 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 Corrected ratios			Gene product	PCR	Individual array ratios (CH2/CH1)					
			CH1 Cye3	CH2 Cye5	CH2/CH1 Induced	StD	SEM			Biol. set 1		Biol. set 2		Biol. set 3	
								F	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
1932	Rv1288	-	2211	3334	1.6	0.3	0.1	-	1.2	1.5	1.9	1.8	1.1	1.6	1.5
2229	Rv1341	-	2050	3007	1.5	0.5	0.2	-	1.2	1.7	2.5	1.4	1.4	1.0	1.1
1299	Rv1462	-	4260	6316	1.5	0.1	0.1	-	1.1	1.6	1.6	1.6	1.3	1.3	1.5
3528	Rv1463	-	3609	5915	1.6	0.1	0.0	ABC-type_transporter	1.4	1.5	1.7	1.8	1.5	1.6	1.6
4182	Rv1464	-	3068	4890	1.6	0.2	0.1	NifS-like_protein	1.1	1.7	1.4	1.9	1.5	1.6	1.3
4183	Rv1466	-	2943	4696	1.6	0.3	0.1	-	1.1	1.8	2.0	1.9	1.4	1.4	1.3
1210	Rv1585c	-	2571	4611	1.9	0.4	0.1	phiRV1_phage_related_protein	1.1	2.2	2.3	1.9	1.5	1.7	1.7
696	Rv1585c	-	2229	3622	1.6	0.3	0.1	phiRV1_phage_related_protein	1.1	1.6	2.0	2.0	1.4	1.4	1.5
71	Rv1652	argC	3940	7500	2.1	0.7	0.3	N-acetyl-g-glutamyl-phosphate_reductase	1.1	3.3	nd	2.2	1.7	1.7	1.8
3885	Rv1653	argJ	3274	5705	1.7	0.2	0.1	glutamate_N-acetyltransferase	1.1	1.9	1.8	1.9	1.6	1.5	1.7
3164	Rv1654	argB	2299	4298	1.9	0.3	0.1	acetylglutamate_kinase	1.1	1.9	2.2	2.2	1.7	1.8	1.6
3886	Rv1655	argD	2233	4701	2.3	0.4	0.2	acetylornithine_aminotransferase	1.1	2.3	2.6	2.7	nd	1.8	2.0
2956	Rv1658	argG	4237	7275	1.8	0.3	0.1	arginosuccinate_synthase	1.4	2.0	2.1	2.0	1.6	1.5	1.5
3678	Rv1659	argH	2168	3436	1.6	0.2	0.1	arginosuccinate_lyase__	1.1	1.7	1.8	1.9	1.4	1.3	1.5
4594	Rv1673c	-	1977	2799	1.5	0.1	0.1	-	1.1	1.6	1.6	1.2	1.5	1.5	1.4
3018	Rv1766	-	2238	6193	3.0	0.6	0.3	-	1.1	2.9	2.7	2.5	2.8	nd	4.1
3740	Rv1767	-	1713	8682	5.0	1.3	0.5	-	1.1	5.6	5.1	4.0	4.0	4.3	7.3
2306	Rv1842c	-	1664	2236	1.5	0.1	0.1	possible_membrane_protein	1.1	1.5	1.7	1.3	nd	1.4	1.4
2933	Rv1908c	katG	7608	11800	1.8	0.6	0.2	catalase-peroxidase__	1.1	2.1	2.1	0.9	1.2	2.1	2.1
89	Rv1909c	furA	5482	11926	2.4	1.0	0.4	ferric_uptake_regulatory_protein	1.1	3.6	2.3	1.3	1.2	2.7	3.4
2669	Rv1989c	-	2062	4797	2.4	0.5	0.2	-	1.1	3.2	3.0	2.3	1.8	2.3	2.2
2668	Rv1991c	-	1921	3253	1.7	0.2	0.1	-	1.1	1.7	2.0	1.7	1.5	1.8	1.7
1946	Rv1992c	ctpG	3574	13785	4.2	1.9	0.8	probable_cation_transport_ATPase	1.2	4.4	5.7	1.9	1.8	5.2	6.4
2667	Rv1993c	-	2747	12290	4.7	1.4	0.6	-	1.1	5.2	5.2	2.2	4.3	6.5	4.8
1945	Rv1994c	-	3388	8035	2.4	0.7	0.3	transcriptional_regulator_(MerR_family)	1.2	2.2	1.8	2.0	2.4	2.2	3.9
2666	Rv1995	-	1900	3376	1.8	0.3	0.1	-	1.3	1.8	2.0	1.9	1.2	1.9	2.0
5283	Rv2016	-	3536	5770	1.6	0.3	0.1	-	1.1	1.9	1.4	1.8	1.9	1.4	1.4
4566	Rv2025c	-	2380	5199	2.3	0.5	0.2	possible_membrane_protein	1.1	2.8	2.5	2.5	1.6	2.6	1.9
5578	Rv2056c	rpsN2	3004	4300	1.5	0.2	0.1	30S_ribosomal_protein_S14	1.1	1.7	1.6	1.5	1.3	1.5	1.3
4856	Rv2057c	rpmG	3514	5523	1.6	0.3	0.1	50S_ribosomal_protein_L33	1.2	1.9	1.4	1.1	1.6	2.0	1.8
1973	Rv2059	-	2733	4751	1.8	0.4	0.2	-	1.1	1.4	1.7	2.3	1.2	2.0	2.1
1556	Rv2123	PPE	2597	4505	1.9	0.5	0.2	-	1.1	1.7	2.7	2.1	1.6	1.2	2.4
3834	Rv2242	-	2290	3420	1.5	0.4	0.1	unknown__poss__regulatory_protein?	1.1	1.3	2.0	1.9	1.3	1.3	1.1
2753	Rv2251	-	1779	2788	1.6	0.2	0.1	-	1.1	2.0	1.5	1.8	1.6	1.4	1.4
2032	Rv2252	-	3483	5758	1.6	0.2	0.1	-	1.1	1.6	1.7	1.9	1.4	1.6	1.7
2931	Rv2359	furB	3679	5668	1.5	0.2	0.1	ferric_uptake_regulatory_protein	1.1	1.4	1.5	1.7	1.4	1.5	1.7
1552	Rv2385	lipK	2246	4120	1.9	0.4	0.1	probable_acetyl-hydrolase	1.1	2.0	1.8	2.0	1.6	1.5	2.5
2273	Rv2386c	trpE2	2164	4743	2.4	0.7	0.3	anthranilate_synthase_component_I	1.1	3.2	2.4	2.5	1.3	2.0	3.2
5154	Rv2400c	subI	2486	3910	1.5	0.2	0.1	sulphate_binding_precursor	1.1	1.2	1.5	1.4	1.4	1.8	1.8
831	Rv2579	linB	4068	5976	1.5	0.2	0.1	1,3,4,6-tetrachloro-1,4-cyclohexadiene_hydrolase	1.1	1.5	1.5	1.5	1.1	1.4	1.9
1474	Rv2601	speE	3604	5245	1.5	0.2	0.1	spermidine_synthase	1.1	1.4	1.6	1.2	1.3	1.7	1.8

521	Rv2638	-	3893	6136	1.6	0.3	0.1		1.1	2.1	1.8	1.9	1.4	1.3	1.3
1243	Rv2639c	-	2360	3573	1.5	0.1	0.1		1.1	1.7	1.6	1.5	1.4	1.4	1.7
522	Rv2640c	-	2415	4041	1.7	0.3	0.1	transcriptional_regulator_(ArsR_family)	1.1	1.8	1.7	2.1	1.4	1.3	2.0
1244	Rv2641	-	2664	17731	7.3	3.7	1.5		1.1	10.2	12.6	3.3	4.2	5.1	8.4
1245	Rv2643	arsC	1764	3107	1.8	0.3	0.1	probable_arsenical_pump	1.1	2.1	2.1	1.8	1.4	1.5	2.0
3088	Rv2780	ald	6064	10149	1.8	0.6	0.2	L-alanine_dehydrogenase	1.1	1.9	2.0	0.8	1.5	2.2	2.3
3686	Rv2820c	-	4191	5828	1.5	0.3	0.1		1.1	1.5	2.1	1.4	1.2	1.4	1.3
2964	Rv2821c	-	6867	10304	1.6	0.4	0.2		1.1	1.8	2.2	0.9	1.5	1.5	1.5
3685	Rv2822c	-	5428	7884	1.5	0.3	0.1		1.1	1.6	2.1	1.1	1.6	1.3	1.5
3684	Rv2824c	-	2324	3532	1.6	0.2	0.1		1.2	1.7	1.8	1.1	1.5	1.7	1.6
1574	Rv2963	-	3557	8777	2.5	0.4	0.2	integral_membrane_protein	1.1	2.4	2.7	2.5	2.0	2.2	3.2
5381	Rv2964	purU	2776	4204	1.6	0.3	0.1	formyltetrahydrofolate_deformylase	1.1	1.5	1.5	1.4	1.3	2.0	1.9
1656	Rv2990c	-	4743	8725	1.9	0.4	0.2		1.1	2.1	1.9	1.3	1.7	2.1	2.4
3895	Rv3061c	fadE22	1596	2286	1.6	0.3	0.2	acyl-CoA_dehydrogenase_	1.1	1.9	1.7	1.9	nd	1.3	1.1
1010	Rv3080c	pknK	1652	2227	1.6	0.2	0.1	serine-threonine_protein_kinase	1.1	1.6	1.6	1.3	nd	1.8	nd
5617	Rv3082c	virS	2148	4033	1.8	0.4	0.2	putative_virulence_regulating_protein_(AraC/XylS_family)	1.1	1.8	1.5	2.5	1.5	1.7	1.9
3467	Rv3173c	-	3606	6025	1.8	0.6	0.2	transcriptional_regulator_(TetR/AcrR_family)	1.1	2.0	1.8	1.0	1.3	2.4	2.3
4189	Rv3174	-	1597	3774	2.4	0.4	0.1	putative_oxidoreductase	1.1	2.4	2.7	2.6	1.7	2.4	2.6
4190	Rv3176c	lipS	1664	5822	3.5	1.0	0.4	probable_esterase/lipase	1.1	3.0	3.9	3.5	2.4	3.0	5.2
3469	Rv3177	-	2029	5231	2.5	0.6	0.2	probable_non-heme_haloperoxidase	1.4	2.8	2.3	2.4	1.7	2.7	3.4
4191	Rv3178	-	1679	4415	2.7	0.6	0.2		1.1	2.5	3.3	3.1	1.9	2.1	3.3
3790	Rv3270	ctpC	3931	6572	1.6	0.3	0.1	cation_transport_ATPase	1.1	1.4	1.6	1.7	1.3	1.8	1.9
2502	Rv3293	aldB	2672	3892	1.5	0.3	0.1	aldehyde_dehydrogenase	1.1	1.4	1.5	2.1	1.3	1.2	1.2
601	Rv3334	-	3206	8697	3.0	0.9	0.4	transcriptional_regulator_(MerR_family)	1.1	3.7	4.3	1.9	2.5	2.4	3.1
537	Rv3402c	-	3380	6619	2.1	0.3	0.1	possible_involved_in_LPS_synthesis	1.1	2.3	2.5	2.3	1.5	1.9	1.9
1258	Rv3403c	-	3996	6837	1.7	0.2	0.1		1.1	1.6	2.0	1.6	1.4	1.9	1.9
1750	Rv3417c	groEL1	7984	12429	2.1	1.4	0.6	60_kD_chaperonin_1	1.1	1.8	1.7	0.7	1.0	3.4	4.2
3418	Rv3418c	groES	8443	18214	2.8	2.0	0.8	10_kD_chaperone	1.1	2.1	2.2	1.0	1.0	5.8	4.8
3436	Rv3601c	panD	3672	5282	1.5	0.1	0.1	aspartate_1-decarboxylase	1.1	1.5	1.7	1.4	1.5	1.4	1.3
5330	Rv3706c	-	7537	9907	1.5	0.5	0.2		1.1	1.6	1.7	0.6	1.3	2.0	1.6
1509	Rv3769	-	6516	10137	1.6	0.2	0.1	possible_coiled-coil_protein	1.1	1.7	1.9	1.7	1.4	1.4	1.6
2231	Rv3770c	-	2486	3984	1.8	0.4	0.2		1.1	2.0	2.2	2.2	1.4	1.4	1.4
5144	Rv3833	-	3122	6847	2.6	0.6	0.3	transcriptional_regulator_(AraC/XylS_family)	1.1	2.8	3.2	2.8	1.5	2.9	2.2
5141	Rv3839	-	2605	5332	2.3	0.6	0.2		1.1	2.3	3.0	2.6	1.4	2.1	2.5