

Table 1: Genes induced in *Mycobacterium tuberculosis* H37Rv relative to a *sigE* mutant strain during log phase growth. 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			Gene product	PCR	Individual array ratios (CH2/CH1)		
			Average		Corrected ratios		F			mi1034	mi1035	mi1036
			CH1 Cye3	CH2 Cye5	CH2/CH1 Induced	StD						
5104Rv0026	-		3095	4897	1.5	0.2	0.1		1.1	1.3	1.7	1.6
2335Rv0211	pckA		4719	9096	2.1	0.7	0.4	phosphoenolpyruvate_carboxykinase_	1.1	2.8	1.7	1.6
320Rv0341	-		2159	3353	1.6	0.3	0.2		1.1	1.9	1.4	1.5
1858Rv0363c	fba		4364	6585	1.5	0.2	0.1	fructose_bisphosphate_aldolase	1.1	1.7	1.3	1.6
3729Rv0408	pta		1855	2553	1.5	0.3	0.2	phosphate_acetyltransferase	1.1	1.8	1.5	1.1
4212Rv0467	aceA		2574	7554	3.1	1.0	0.6	isocitrate_lyase	1.1	3.0	4.2	2.2
3491Rv0468	fadB2		2593	4619	1.8	0.2	0.1	3-hydroxyacyl-CoA_dehydrogenase	1.1	2.0	1.7	1.7
5148Rv0490	senX3		4186	6129	1.5	0.2	0.1	sensor_histidine_kinase	1.1	1.2	1.6	1.5
1878Rv0495c	-		3427	5728	1.7	0.2	0.1		1.1	1.7	1.5	1.8
5343Rv0524	hemL		3421	5377	1.7	0.3	0.2	glutamate-1-semialdehyde_aminotransferase	1.1	2.1	1.6	1.5
3335Rv0597c	-		2725	3941	1.5	0.1	0.1		1.1	1.5	1.6	1.3
1884Rv0693	pqqE		3488	5420	1.6	0.1	0.1	coenzyme_PQQ_synthesis_protein_E	1.1	1.6	1.7	1.4
2606Rv0694	lldD1		5531	8430	1.6	0.3	0.2	L-lactate_dehydrogenase_(cytochrome)_	1.1	1.2	1.9	1.6
2408Rv0818	-		2671	3628	1.5	0.3	0.2	two-component_response_regulator	1.1	1.8	1.6	1.2
4574Rv0829	IS1605'		3489	5610	1.6	0.2	0.1	probable_transposase_fragment	1.1	1.7	1.4	1.7
485Rv0906	-		4306	6349	1.5	0.1	0.0	probable_membrane_protein	1.1	1.5	1.5	1.4
3846Rv0931c	pknD		3897	5621	1.5	0.1	0.1	serine-threonine_protein_kinase	1.1	1.6	1.3	1.5
5310Rv0982	-		4285	6150	1.5	0.5	0.3	sensor_histidine_kinase	1.1	1.0	1.9	1.6
4014Rv0997	-		5063	9093	1.8	0.4	0.3		1.1	2.0	2.1	1.3
4076Rv1129c	-		1996	4382	2.4	1.0	0.6	transcriptional_regulator_(PbsX/Xre_family)	1.1	3.4	1.5	2.3
3355Rv1130	-		1757	6823	3.8	0.8	0.4		1.1	3.0	3.9	4.5
4077Rv1131	gltA1		2728	7842	3.0	1.1	0.6	citrate_synthase_3	1.1	4.2	2.1	2.8
3746Rv1384	carB		2645	3929	1.6	0.2	0.1	carbamoyl-phosphate_synthase_subunit	1.1	1.8	1.6	1.3
3375Rv1588c	REP		2881	4644	1.6	0.0	0.0		1.1	1.6	1.6	1.6
2430Rv1609	trpE		3514	5808	1.7	0.0	0.0	anthranilate_synthase_component_I	1.1	1.7	1.7	1.6
1528Rv1815	-		5333	8673	1.6	0.5	0.3		1.1	1.1	1.6	2.2
2249Rv1816	-		2610	3834	1.5	0.1	0.1	putative_transcriptional_regulator	1.1	1.5	1.3	1.6
2718Rv1927	-		2274	3169	1.5	0.3	0.1		1.1	1.5	1.7	1.2
1994Rv1932	tpx		3807	7032	1.9	0.3	0.2	thiol_peroxidase	1.1	1.6	2.2	1.8
3390Rv2280	-		2638	4236	1.7	0.3	0.2	similar_to_D-lactate_dehydrogenase	1.1	1.6	2.0	1.5
2932Rv2429	ahpD		5099	7844	1.5	0.2	0.1	member_of_AhpC/TSA_family	1.1	1.7	1.3	1.6
1652Rv2493	-		2524	3963	1.5	0.1	0.1		1.1	1.4	1.6	1.6

5259 Rv2521	bcp	5157	7497	1.5	0.3	0.2	bacterioferritin_comigratory_protein	1.1	1.1	1.7	1.5
5260 Rv2523c	acpS	2507	4566	1.8	0.4	0.2	CoA:apo-[ACP]_pantethienephosphotransferase	1.1	1.4	2.0	2.1
3360 Rv2843	-	2268	3725	1.6	0.2	0.1		1.1	1.4	1.8	1.7
2380 Rv2995c	leuB	6418	9387	1.5	0.2	0.1	3-isopropylmalate_dehydrogenase	1.1	1.3	1.5	1.6
5267 Rv3005c	-	3719	5270	1.5	0.2	0.1		1.1	1.7	1.5	1.2
2592 Rv3093c	-	3257	4827	1.5	0.3	0.2		1.1	1.2	1.7	1.6
1871 Rv3094c	-	2448	3561	1.5	0.0	0.0		1.1	1.4	1.5	1.5
228 Rv3139	fadE24	4899	7143	1.5	0.1	0.0	acyl-CoA_dehydrogenase_	2.1	1.4	1.5	1.5
3068 Rv3269	-	5602	9887	1.8	0.2	0.1	probable_heat_shock_protein	1.1	1.8	1.5	2.0
3434 Rv3617	ephA	2128	3259	1.6	0.2	0.1	probable_epoxide_hydrolase	1.1	1.7	1.5	1.4
1530 Rv3854c	-	4839	7529	1.5	0.2	0.1	probable_monooxygenase	1.1	1.5	1.4	1.7