

**Table 1. Genes induced in Mycobacterium tuberculosis H37Rv 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		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	
									mi1016	mi1020	mi1022	mi1026	mi1032	mi519	
1493	Rv0011c	-	5186	8379	1.6	0.2	0.1		1.1	1.9	1.8	1.6	1.7	1.3	1.6
2215	Rv0012	-	3368	6214	2.0	0.4	0.2	possible_cell_division_protein	1.1	1.9	2.7	1.8	1.9	2.0	1.6
1494	Rv0013	pabA	4369	7590	1.8	0.1	0.1	p-aminobenzoate_synthase_glutamine_amidotransferase	1.1	1.8	1.9	1.9	1.6	1.7	1.7
2216	Rv0014c	pknB	1718	3900	2.5	0.9	0.4	serine-threonine_protein_kinase	1.1	2.8	3.9	2.4	2.6	1.8	1.4
1495	Rv0015c	pknA	6261	14502	2.5	0.6	0.2	serine-threonine_protein_kinase	2.6	2.7	2.5	1.5	2.2	3.2	2.7
2217	Rv0016c	pbpA	3098	13675	4.9	1.1	0.4	penicillin-binding_protein	1.1	4.4	6.3	3.3	4.8	5.9	4.5
1496	Rv0017c	rodA	8441	20305	2.6	0.5	0.2	FtsW/RodA/SpovE_family	1.1	2.3	3.1	1.7	2.2	3.1	2.9
2219	Rv0020c	-	3641	7280	2.0	0.3	0.1		1.1	2.4	2.1	2.3	1.9	1.9	1.5
1499	Rv0035	fadD34	2944	4236	1.5	0.4	0.2	acyl-CoA_synthase	1.1	1.9	1.9	1.7	0.9	1.2	1.4
1202	Rv0094c	REP	5817	9737	1.8	0.4	0.2		1.1	2.1	1.7	1.1	2.3	1.6	2.0
4087	Rv0100	-	1661	3616	2.2	0.3	0.1		1.1	2.7	2.1	1.8	2.1	2.3	2.3
1977	Rv0132c	-	2286	3867	1.8	0.4	0.2	putative_oxidoreductase	1.1	1.6	2.0	2.4	1.4	1.3	nd
4863	Rv0140	-	2018	3880	1.9	0.4	0.2		1.1	2.0	1.6	2.2	2.3	1.4	nd
5585	Rv0141c	-	2892	22368	9.4	4.8	2.0		1.1	11.0	11.2	4.7	5.8	6.3	17.5
4864	Rv0142	-	3327	12720	3.9	0.9	0.4		1.1	4.3	3.6	3.1	4.2	2.9	5.3
1478	Rv0180c	-	4460	13055	3.0	0.6	0.2	probable_membrane_protein	1.1	3.7	3.3	2.8	2.1	2.7	3.1
2200	Rv0181c	-	2645	3938	1.5	0.1	0.0		1.1	1.6	1.3	1.6	1.4	1.5	1.5
243	Rv0202c	mmpL11	3301	5260	1.6	0.1	0.1	conserved_large_membrane_protein	1.1	1.7	1.7	1.7	1.5	1.4	1.5
969	Rv0251c	hsp	3615	19139	7.1	4.5	1.8	possible_heat_shock_protein	1.1	5.1	16.0	3.5	5.5	6.4	6.0
3858	Rv0280	PPE	2268	3598	1.6	0.2	0.1		2.1	1.5	1.8	1.6	1.6	1.4	1.9
2684	Rv0301	-	4097	6112	1.5	0.2	0.1		1.1	1.5	1.5	1.6	1.6	1.5	1.2
2685	Rv0303	-	3747	7183	1.9	0.3	0.1	similar_to_NADPH_dehydrogenase	1.1	2.1	2.2	2.0	1.6	2.0	1.6
1964	Rv0304c	PPE	3753	6671	1.7	0.4	0.2		2.5	1.8	1.6	2.3	1.3	1.3	1.6
1968	Rv0324	-	2001	4495	2.3	0.8	0.3	putative_transcriptional_regulator	1.1	3.0	1.3	3.4	2.3	1.4	2.6
2690	Rv0325	-	2201	3177	1.5	0.3	0.1		1.2	2.1	1.3	1.3	1.2	1.5	1.5
319	Rv0326	-	1749	2840	1.7	0.3	0.1	maybe_gene_on_opposite_strand	1.1	1.7	2.4	1.5	1.4	1.5	1.8
2691	Rv0327c	-	1881	4281	2.3	0.5	0.2	cytochrome_P-450_monooxygenase	1.1	3.2	2.4	2.0	2.5	2.0	1.7
3524	Rv0332	-	2115	3443	1.6	0.2	0.1		1.1	1.9	1.5	1.9	1.5	1.4	1.5
1004	Rv0355c	PPE	4536	11504	2.6	0.4	0.2		1.1	3.0	2.5	2.0	2.6	2.5	3.0
260	Rv0384c	clpB	3163	16918	5.7	1.2	0.5	heat_shock_protein	1.1	6.8	6.2	3.6	5.0	6.7	6.0
3347	Rv0425c	ctpH	3739	5067	1.5	0.3	0.1	C-terminal_region_putative_cation-transporting_ATPase	1.4	1.3	1.5	1.2	1.6	2.1	1.2
264	Rv0440	groEL2	9819	22116	2.7	1.3	0.5	60_kD_chaperonin_2	1.4	1.9	2.3	1.5	2.0	4.8	4.0
1384	Rv0516c	-	8361	12235	1.5	0.3	0.1		1.1	1.8	1.7	1.4	1.7	1.1	1.1
4216	Rv0563	htpX	2261	4276	1.8	0.3	0.1	probable_(transmembrane)_heat_shock_protein	1.1	2.3	1.4	1.9	1.4	1.9	1.9
1332	Rv0571c	-	2194	3196	1.5	0.2	0.1		1.1	1.5	1.7	1.4	1.2	1.6	1.6
4769	Rv0687	-	2474	4937	1.9	0.3	0.1	putative_dehydrogenase_SDR_family	1.1	1.9	1.5	2.1	2.3	1.7	2.1
4227	Rv0740	-	3277	8894	2.8	0.7	0.3		1.1	2.8	3.2	1.8	3.7	2.8	2.4
622	Rv0749	-	4885	7355	1.5	0.2	0.1		1.4	1.6	1.7	1.6	1.1	1.7	1.3
1344	Rv0750	-	3865	8340	2.1	0.5	0.2		1.1	1.9	1.7	1.7	2.1	2.3	2.9
2310	Rv0759c	-	4719	9934	2.2	0.4	0.2		1.1	2.3	2.5	1.9	2.2	2.9	1.6
3509	Rv0794c	lpdB	1480	2966	2.3	0.4	0.2	dihydroipoamide_dehydrogenase	1.1	2.6	2.8	2.0	1.8	2.4	nd
1268	Rv0805	-	6632	9728	1.5	0.1	0.0		1.1	1.6	1.4	1.3	1.5	1.5	1.5
2407	Rv0816c	thiX	1453	2814	2.1	0.5	0.2	equivalent_to_M._leprae_ThiX	1.1	2.9	1.9	2.2	1.8	1.6	nd
1694	Rv0846c	-	3956	6079	1.5	0.1	0.1	similar_to_several_L-ascorbate_oxidases	1.1	1.5	1.6	1.7	1.6	1.3	1.5
2416	Rv0847	lpqS	1429	2254	1.8	0.3	0.2	lipoprotein	1.1	1.6	nd	1.5	nd	2.2	2.0
1695	Rv0848	cysM3	2881	4392	1.5	0.2	0.1	putative_cysteine_synthase	1.1	1.3	1.7	1.6	1.4	1.6	1.6
861	Rv0877	-	6061	9539	1.6	0.3	0.1		1.1	1.9	1.7	1.2	1.7	1.8	1.4
140	Rv0878c	PPE	5647	9070	1.6	0.3	0.1		1.1	1.7	1.2	1.3	2.0	1.5	1.9
1129	Rv0991c	-	3782	13920	3.9	1.5	0.6		1.1	4.6	2.9	2.0	3.6	4.0	6.5
1471	Rv1009	-	9177	15956	1.8	0.3	0.1		1.4	2.0	2.1	1.3	1.9	1.7	1.8
1149	Rv1039c	PPE	2554	4998	2.0	0.3	0.1		1.1	2.2	2.0	1.5	1.8	1.8	2.4

1147	Rv1043c	-	2504	5309	2.3	0.9	0.4		1.1	4.1	1.8	1.6	1.8	1.8	2.6
1664	Rv1057	-	2576	4342	1.6	0.2	0.1		1.1	1.9	1.5	2.0	1.6	1.3	1.5
5275	Rv1072	-	8699	14567	1.8	0.3	0.1	probable_transmembrane_protein	1.1	1.5	2.0	1.3	1.8	2.0	1.9
465	Rv1114	-	2095	3007	1.6	0.3	0.1		1.1	1.9	1.8	1.5	nd	1.4	1.2
3355	Rv1130	-	1660	4979	2.9	0.7	0.3		1.1	3.6	2.5	2.7	2.0	2.8	3.8
4077	Rv1131	gltA1	2630	6352	2.5	0.4	0.2	citrate_synthase_3	1.1	2.9	2.8	2.0	2.1	2.2	2.7
2559	Rv1135c	PPE	5128	8961	1.8	0.3	0.1		1.1	2.3	1.6	1.7	1.8	1.5	1.6
3656	Rv1221	sigE	4764	26684	5.8	1.2	0.5	ECF_subfamily_sigma_subunit	1.1	5.6	7.6	4.6	6.9	5.7	4.6
4721	Rv1222	-	5823	11792	2.1	0.3	0.1		1.1	1.8	2.1	1.7	2.1	2.7	2.0
5443	Rv1223	htrA	4842	7731	1.6	0.1	0.1	serine_protease	1.1	1.5	1.4	1.8	1.5	1.5	1.7
4722	Rv1224	-	2838	4173	1.5	0.1	0.0		1.1	1.4	1.3	1.6	1.5	1.4	1.6
4844	Rv1259	-	2350	4134	1.7	0.3	0.1		1.1	1.3	1.3	1.9	2.0	1.8	1.9
5540	Rv1285	cysD	1922	7465	3.8	0.9	0.4	ATP_sulphurylase_subunit_2	1.1	5.6	3.6	3.8	3.4	3.0	3.3
4819	Rv1286	cysN	2603	10461	4.0	0.5	0.2	ATP_sulphurylase_subunit_1	1.1	4.7	3.5	3.6	4.0	3.7	4.4
1932	Rv1288	-	2255	3277	1.5	0.2	0.1		1.2	1.6	1.5	1.8	1.3	1.4	1.2
1937	Rv1298	rpmE	4804	9033	1.8	0.2	0.1	50S_ribosomal_protein_L31	1.1	1.8	1.8	1.8	1.7	1.8	2.2
2659	Rv1299	prfA	8179	14851	1.9	0.3	0.1	peptide_chain_release_factor_1	1.2	1.9	2.3	1.3	1.8	2.1	2.0
4820	Rv1300	hemK	5650	8793	1.6	0.1	0.1	protoporphyrinogen_oxidase	1.1	1.5	1.6	1.7	1.7	1.5	1.3
5112	Rv1331	-	2697	4099	1.6	0.2	0.1		1.3	1.3	1.9	1.4	1.5	1.5	1.7
4391	Rv1332	-	5005	8630	1.8	0.3	0.1	putative_transcriptional_regulator	1.1	1.8	2.0	1.3	nd	2.0	1.8
5113	Rv1333	-	1492	3509	2.3	0.7	0.3	probable_hydrolase	1.1	2.0	1.9	1.8	2.2	2.1	3.7
4392	Rv1334	-	3867	12185	3.6	1.2	0.5		1.1	5.3	4.5	2.4	nd	3.3	2.7
5114	Rv1335	-	2080	10814	5.1	1.0	0.4		1.1	5.9	3.9	5.5	5.3	3.8	5.9
1505	Rv1336	cysM	4087	14490	3.7	0.8	0.3	cysteine_synthase_B	1.1	5.0	3.8	2.6	3.6	3.5	3.6
5459	Rv1337	-	2882	11632	4.1	1.3	0.5		1.1	5.1	6.0	3.6	4.2	2.1	3.8
4738	Rv1338	murl	2227	7708	3.3	0.8	0.3	glutamate_racemase	1.1	4.5	2.3	3.9	2.9	3.1	3.3
5460	Rv1339	-	4812	8690	1.8	0.2	0.1		1.1	1.8	1.6	1.9	1.7	2.1	1.8
4739	Rv1340	rphA	4238	6557	1.6	0.1	0.0	ribonuclease_PH	1.1	1.5	1.6	1.6	1.4	1.6	1.7
3661	Rv1363c	-	2231	3209	1.5	0.3	0.1		1.1	1.4	2.0	1.5	1.6	1.3	1.2
4242	Rv1450c	PE_PGERS	2603	4153	1.6	0.1	0.1		2.6	1.5	1.6	1.8	1.5	1.4	1.6
3520	Rv1452c	PE_PGERS	2419	4723	1.9	0.3	0.1		2.6	1.9	1.7	2.3	1.7	1.6	2.0
577	Rv1461	-	7669	13099	1.8	0.3	0.1		1.4	1.8	2.2	1.3	1.7	1.8	1.8
1299	Rv1462	-	3737	6026	1.6	0.2	0.1		1.1	1.9	1.4	1.7	1.5	1.3	1.7
4182	Rv1464	-	2398	3441	1.5	0.2	0.1	NifS-like_protein	1.1	1.4	1.9	1.4	1.6	1.3	1.2
3461	Rv1465	-	1644	2485	1.6	0.3	0.1		1.1	1.7	2.1	1.5	1.3	1.5	1.4
4183	Rv1466	-	2563	4006	1.6	0.2	0.1		1.1	1.4	1.9	1.7	1.6	1.6	1.4
3463	Rv1469	ctpD	2799	5569	2.0	0.3	0.1	probable_cadmium-transporting_ATPase	1.1	1.7	1.9	2.4	2.0	1.7	2.0
4185	Rv1470	trxA	2161	4398	2.1	0.3	0.1	thioredoxin	1.1	2.6	2.3	2.0	2.0	1.6	1.9
3464	Rv1471	trxB	1429	6689	5.4	0.9	0.4	thioredoxin_reductase	1.1	6.0	6.0	6.3	4.4	4.3	nd
4186	Rv1472	echA12	3260	13622	4.3	0.7	0.3	enoyl-CoA_hydratase/isomerase_superfamily	1.1	4.3	4.5	3.3	3.7	4.7	5.3
3465	Rv1473	-	2000	4126	2.2	0.4	0.2	ABC_transporter_possible_in_EF-3_subfamily	1.1	1.9	1.9	2.5	1.8	2.6	nd
1704	Rv1528c	papA4	1569	13276	8.7	1.0	0.4	PKS-associated_protein_unknown_function	1.1	9.0	10.6	8.1	8.0	7.9	8.6
973	Rv1529	fadD24	2367	3359	1.5	0.2	0.1	acyl-CoA_synthase	1.1	1.7	1.3	1.5	1.1	1.5	1.6
3375	Rv1588c	REP	2273	3780	1.8	0.5	0.2		1.1	1.6	2.4	2.0	1.9	1.9	1.0
789	Rv1645c	-	4753	12542	2.7	0.5	0.2		1.1	2.8	3.2	2.0	3.4	2.6	2.4
67	Rv1645c	-	3844	9860	2.6	0.3	0.1		1.1	3.0	2.5	2.0	2.8	2.7	2.7
4593	Rv1671	-	3287	3659	1.5	0.2	0.1	similar_to_many_mercuric_transport_proteins	1.1	1.6	1.3	1.3	nd	1.7	1.7
4594	Rv1673c	-	3779	6611	2.8	0.8	0.4		1.1	4.1	2.5	2.6	nd	3.0	1.8
3289	Rv1705c	PPE	2704	4038	1.5	0.2	0.1		1.1	1.3	1.8	1.5	1.3	1.6	1.6
995	Rv1718	-	2524	4546	1.8	0.2	0.1		1.1	1.8	1.6	1.9	1.5	1.8	2.1
1110	Rv1721c	-	2377	4133	1.8	0.3	0.1		1.1	2.3	1.8	1.4	1.9	1.5	1.7
3018	Rv1766	-	2247	4649	2.1	0.2	0.1		1.1	1.9	2.3	2.0	2.0	1.9	2.2
3740	Rv1767	-	1429	4831	3.3	0.8	0.3		1.1	3.5	2.5	2.6	4.5	2.7	4.1
2250	Rv1814	-	3047	4433	1.5	0.4	0.2	possible_C-5_sterol_desaturase	1.1	1.5	2.3	1.7	1.4	1.4	1.1
2308	Rv1838c	-	1970	3127	1.8	0.5	0.2		1.4	1.7	2.8	1.7	1.5	1.4	nd
2244	Rv1838c	-	2593	2994	1.5	0.5	0.2		1.1	1.1	2.3	1.4	1.5	1.1	nd
2982	Rv1874	-	2058	5611	2.7	0.4	0.2		1.1	3.1	2.3	2.5	2.3	2.7	3.3
3703	Rv1875	-	2667	6351	2.5	0.5	0.2		1.1	3.0	2.3	1.8	3.1	2.4	2.1

89	Rv1909c	furA	5350	7719	1.5	0.2	0.1	ferric_uptake_regulatory_protein	1.1	1.7	1.4	1.3	1.5	1.3	1.6
85	Rv1917c	PPE	5675	8379	1.5	0.2	0.1		1.4	1.5	1.5	1.5	1.7	1.2	1.4
5554	Rv1983	PE_PGRS	4006	6933	1.7	0.3	0.1		1.2	1.8	1.7	1.9	2.0	1.3	1.3
2669	Rv1989c	-	2310	3476	1.5	0.2	0.1		1.1	1.7	1.6	1.6	1.3	1.5	1.4
1946	Rv1992c	ctpG	2622	11155	4.3	1.2	0.5	probable_cation_transport_ATPase	1.2	4.1	5.4	4.7	2.3	3.9	5.4
2667	Rv1993c	-	2842	10385	3.8	0.5	0.2		1.1	3.5	4.4	3.1	4.1	3.6	3.8
1945	Rv1994c	-	2829	4944	1.8	0.4	0.2	transcriptional_regulator_(MerR_family)	1.2	2.0	2.1	2.3	1.5	1.1	1.8
2666	Rv1995	-	1945	2499	1.6	0.9	0.4		1.3	1.1	3.4	1.3	1.1	1.3	1.3
1940	Rv2014	IS1607	3470	7210	2.1	0.6	0.2	transposase	1.1	1.9	2.9	2.6	1.4	1.8	2.2
5294	Rv2050	-	3673	8097	2.2	0.4	0.2		1.1	2.2	1.4	2.1	2.4	2.1	2.8
2744	Rv2052c	-	1798	3778	2.2	0.5	0.2		1.1	2.2	2.3	1.6	1.8	2.0	3.1
3845	Rv2053c	-	2867	4829	1.7	0.3	0.1		1.1	1.6	1.6	1.5	1.7	1.8	2.2
1973	Rv2059	-	2027	2980	1.5	0.2	0.1		1.1	1.6	1.8	1.4	1.4	1.2	1.8
4440	Rv2115c	-	6289	9821	1.6	0.2	0.1	ATPase_of_AAA-family	1.1	1.8	1.6	1.5	nd	1.4	1.5
1557	Rv2125	-	4267	9823	2.4	0.5	0.2		1.4	2.5	2.7	2.2	2.2	1.6	3.1
1160	Rv2202c	cbhK	6340	11859	1.9	0.3	0.1	carbohydrate_kinase	1.1	2.4	1.7	1.4	1.9	2.0	1.9
439	Rv2203	-	5999	12300	2.2	0.4	0.2		1.1	2.3	2.6	1.3	2.4	2.0	2.2
1161	Rv2204c	-	12792	27394	2.5	1.0	0.4	hesB/yadR/yfhF_family_YADR_ECOLI	1.1	3.1	4.2	1.5	2.4	1.8	1.7
30	Rv2242	-	3948	7512	1.9	0.3	0.1	unknown_poss_regulatory_protein?	1.1	2.3	1.7	1.5	1.8	1.9	2.1
1223	Rv2293c	-	2449	3620	1.6	0.3	0.1		1.1	1.9	1.9	1.2	1.6	1.5	1.6
3387	Rv2298	-	1933	2764	1.5	0.2	0.1		1.1	1.5	2.0	1.3	1.4	1.6	1.3
881	Rv2332	mez	2283	4574	2.0	0.4	0.2	probable_malate_oxidoreductase	1.1	2.4	1.8	1.6	2.7	1.8	1.9
4445	Rv2372c	-	3073	5362	1.7	0.1	0.0		1.1	1.8	1.7	1.8	nd	1.6	1.7
770	Rv2373c	dnaJ2	5346	10085	1.9	0.3	0.1	DnaJ_homologue	1.1	2.1	2.0	1.4	2.0	1.9	2.2
1549	Rv2391	nirA	9113	13608	1.6	0.2	0.1	probable_nitrite_reductase/sulphite_reductase	1.1	1.8	1.9	1.3	1.5	1.4	1.5
2270	Rv2392	cysH	5011	8544	1.7	0.2	0.1	3'-phosphoadenylylsulfate_(PAPS)_reductase	1.1	1.8	1.6	1.9	1.8	1.8	1.3
1548	Rv2393	-	7400	12178	1.7	0.2	0.1		1.1	2.0	1.8	1.4	1.8	1.5	1.6
2269	Rv2394	ggdB	3695	5725	1.6	0.2	0.1	g_glutamyltranspeptidase_precursor	1.1	1.5	1.6	1.7	1.5	1.8	1.4
4434	Rv2397c	cysA	3200	9569	3.3	0.7	0.3	sulphate_transport_ATP-binding_protein_	1.1	3.9	3.9	2.4	nd	2.9	3.3
5155	Rv2398c	cysW	1530	9628	6.3	1.9	0.8	sulphate_transport_system_permease_protein	1.1	9.7	5.5	5.2	5.3	4.8	7.6
4433	Rv2399c	cysT	4435	13091	3.0	0.8	0.3	sulphate_transport_system_permease_protein	1.1	3.9	3.3	1.9	nd	2.9	2.8
1236	Rv2439c	proB	6480	13192	2.1	0.3	0.1	glutamate_5-kinase_	1.3	2.3	2.0	1.5	2.2	2.3	2.1
5247	Rv2452c	-	1631	3579	2.1	0.4	0.2		1.1	2.3	1.5	2.0	2.6	2.0	2.3
4526	Rv2453c	-	2530	6222	2.6	0.5	0.2		1.1	2.6	2.3	2.4	nd	2.2	3.4
5248	Rv2454c	-	3019	10072	3.4	0.4	0.2	oxidoreductase_beta_subunit	1.1	3.6	3.8	2.8	3.5	3.0	3.9
5251	Rv2460c	clpP2	6274	11451	1.9	0.3	0.1	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	2.0	2.1	1.4	2.2	1.7	1.8
4530	Rv2461c	clpP	8038	13182	1.7	0.3	0.1	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	2.0	2.0	1.3	nd	1.7	1.7
1644	Rv2465c	rpi	3742	12338	3.4	0.6	0.3	phosphopentose__isomerase	1.1	4.0	2.7	2.6	3.4	4.1	3.5
2366	Rv2466c	-	1476	13881	10.0	2.6	1.0		1.1	13.0	11.0	6.1	9.3	8.6	12.2
2374	Rv2494	-	1668	2137	1.5	0.2	0.1		1.1	nd	1.8	1.4	1.3	1.5	nd
2958	Rv2495c	pdhC	3456	6353	1.8	0.3	0.1	dihydropyrimidinase	1.1	1.8	1.6	2.3	1.6	1.8	1.8
3680	Rv2496c	pdhB	3580	6003	1.7	0.3	0.1	pyruvate_dehydrogenase_E1_component_b_subunit	1.4	2.1	2.0	1.6	1.7	1.7	1.4
2959	Rv2497c	pdhA	3669	8519	2.3	0.4	0.2	pyruvate_dehydrogenase_E1_component_a_subunit	1.1	2.3	1.6	2.6	2.2	2.5	2.5
3716	Rv2585c	-	2477	3856	1.6	0.1	0.0		1.1	1.6	nd	1.5	1.6	1.7	1.6
1474	Rv2601	speE	3563	7442	2.1	0.5	0.2	spermidine_synthase	1.1	2.7	1.8	1.9	1.5	2.1	2.6
2195	Rv2602	-	2878	6302	2.2	0.5	0.2		1.1	2.2	2.8	2.5	1.7	1.5	2.3
3891	Rv2615c	PE	4976	9891	2.1	0.5	0.2		2.3	2.0	2.4	1.4	2.3	1.7	2.7
1244	Rv2641	-	3667	14282	4.1	1.2	0.5		1.1	5.3	3.9	2.4	3.7	3.8	5.6
3881	Rv2694c	-	1593	2535	1.6	0.3	0.1		1.1	1.7	1.4	1.9	1.9	1.3	nd
3666	Rv2698	-	2903	9120	3.4	0.9	0.3		1.1	3.6	5.0	3.0	3.3	3.1	2.5
2945	Rv2699c	-	2287	7936	3.6	0.6	0.2		1.1	4.3	3.4	4.2	3.4	2.7	3.4
2948	Rv2706c	-	3760	12828	3.6	0.8	0.3		1.1	4.8	4.1	2.6	3.0	3.3	3.6
3670	Rv2707	-	3359	7902	2.4	0.3	0.1		1.1	2.5	2.2	2.9	2.1	2.4	2.0
2934	Rv2710	sigB	9057	22350	2.6	0.5	0.2	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	2.3	3.3	2.2	2.6	3.1	2.2
4744	Rv2726c	dapF	2760	5764	2.0	0.4	0.2	diaminopimelate_epimerase	1.1	2.3	1.7	2.6	2.3	1.7	1.5
915	Rv2743c	-	2696	4473	1.7	0.2	0.1		1.1	1.9	1.6	1.5	1.7	1.8	1.4
194	Rv2744c	35kd_ag	8814	16737	2.0	0.4	0.2	35-kd_antigen	1.1	1.9	2.1	1.3	2.4	2.0	2.4
916	Rv2745c	-	6577	10783	1.7	0.2	0.1	putative_transcriptional_regulator	1.4	1.7	1.7	1.3	1.9	1.9	1.6

200	Rv2768c	PPE	2046	3512	1.8	0.4	0.2			1.1	2.3	2.3	1.7	1.4	1.5	1.6
2632	Rv2878c	mpt53	2366	3675	1.6	0.2	0.1	secreted_protein_Mpt53		1.1	1.6	1.8	1.6	1.6	1.3	1.4
2638	Rv2901c	-	6141	9021	1.5	0.2	0.1			1.1	1.7	1.6	1.7	1.5	1.1	1.3
1919	Rv2906c	trmD	2824	6034	2.3	0.8	0.3	tRNA_(guanine-N1)-methyltransferase		1.1	3.2	1.5	2.8	2.6	1.3	2.5
759	Rv2937	drbB	6415	10130	1.6	0.2	0.1	similar_daunorubicin_resistance_transmembrane_protein		1.1	1.5	1.5	1.3	1.8	1.5	1.7
1656	Rv2990c	-	2850	4769	1.7	0.1	0.0			1.1	1.8	1.5	1.8	1.6	1.6	1.7
2722	Rv3017c	-	1979	3880	1.9	0.1	0.0			1.1	2.0	1.7	2.1	1.9	1.9	2.0
2726	Rv3036c	-	5181	8726	1.7	0.2	0.1	probable_secreted_protein		1.2	1.9	1.7	1.7	1.7	1.6	1.5
4894	Rv3051c	nrdE	10181	15007	1.5	0.4	0.2	ribonucleoside_diphosphate_reductase_a_chain		1.1	1.5	1.9	1.3	2.1	1.4	1.1
3728	Rv3052c	nrdI	4197	7138	1.7	0.2	0.1	NrdI/YgaO/YmaA_family		1.1	1.5	1.6	1.6	1.9	1.5	2.0
3006	Rv3053c	nrdH	9076	12694	1.5	0.2	0.1	glutaredoxin_electron_transport_component_of_NrdEF_syst		1.1	1.6	1.7	1.1	1.5	1.6	1.3
3727	Rv3054c	-	1824	7129	4.0	1.1	0.4			1.1	4.1	3.7	3.7	4.1	2.6	6.0
2598	Rv3118	sseC	4595	6791	1.5	0.2	0.1	thiosulfate_sulfurtransferase		1.1	1.4	1.3	1.5	1.3	1.6	1.7
1877	Rv3119	moaE	4692	10135	2.2	0.4	0.2	molybdopterin-converting_factor_subunit_2		1.1	2.4	2.8	1.9	2.3	1.8	2.2
2599	Rv3120	-	5804	8660	1.5	0.2	0.1	Slight_similarity_to_methyltransferases		1.1	1.9	1.5	1.4	1.3	1.6	1.6
1301	Rv3162c	-	6414	10219	1.6	0.2	0.1	probable_membrane_protein		1.4	1.7	1.7	1.4	1.7	1.3	1.7
1264	Rv3206c	moeZ	4610	20152	4.6	0.9	0.4	probably_involved_in_molybdopterin_biosynthesis		1.1	5.4	5.2	2.8	4.8	4.4	4.7
1263	Rv3221c	-	7272	13268	1.9	0.4	0.2	possible_biotin_carboxyl_carrier		1.1	1.9	1.8	1.3	1.7	2.4	2.4
541	Rv3222c	-	3095	14241	5.0	1.9	0.8			1.1	7.8	4.5	2.7	3.6	4.7	6.6
3657	Rv3223c	sigH	3233	19154	6.3	1.6	0.7	ECF_subfamily_sigma_subunit		1.1	7.3	9.2	4.9	5.9	5.7	4.9
2502	Rv3293	aldB	2332	4127	1.8	0.3	0.1	aldehyde_dehydrogenase		1.1	1.5	1.5	2.2	1.9	1.4	2.0
601	Rv3334	-	2619	4236	1.6	0.2	0.1	transcriptional_regulator_(MerR_family)		1.1	1.6	nd	1.9	1.3	1.5	1.7
3487	Rv3343c	PPE	4321	8241	1.9	0.2	0.1			1.4	1.9	2.0	2.1	1.9	1.6	1.8
933	Rv3347c	PPE	4577	9129	2.1	0.4	0.2			1.1	2.2	2.8	1.9	1.9	2.0	1.8
935	Rv3350c	PPE	2163	4186	2.0	0.4	0.2			1.1	2.1	2.5	2.2	1.4	1.6	2.1
537	Rv3402c	-	2825	6602	2.3	0.5	0.2	possible_involved_in_LPS_synthesis		1.1	3.0	2.5	2.6	1.8	1.7	2.1
1750	Rv3417c	groEL1	7574	13410	2.0	0.6	0.3	60_kD_chaperonin_1		1.1	1.5	1.5	1.4	1.7	2.8	2.8
3418	Rv3418c	groES	7374	17603	3.1	1.4	0.6	10_kD_chaperone		1.1	1.8	3.4	1.8	2.5	5.6	3.2
1013	Rv3451	-	2749	4103	1.5	0.2	0.1	probable_cutinase		1.1	1.6	1.6	1.6	1.5	1.6	1.1
3900	Rv3461c	rpmJ	6094	14090	2.3	0.3	0.1	50S_ribosomal_protein_L36		1.1	2.4	2.5	2.0	2.9	2.2	2.1
3179	Rv3462c	infA	11447	17808	1.6	0.3	0.1	initiation_factor_IF-1		1.1	1.7	2.1	nd	1.5	1.2	1.5
3901	Rv3463	-	1644	17634	11.6	3.9	1.6	probable_neuraminidase		1.1	15.4	11.8	8.7	12.9	5.3	15.3
3180	Rv3464	rmlB	5224	13261	2.7	0.2	0.1	dTDP-glucose_4,6-dehydratase		1.1	2.9	2.8	nd	2.6	2.4	2.5
3902	Rv3465	rmlC	2086	7831	3.9	0.9	0.4	dTDP-4-dehydrothamnose_3,5-epimerase		1.1	4.9	4.6	3.7	3.9	2.4	4.0
3181	Rv3466	REP	2949	4786	1.8	0.2	0.1			1.1	1.8	2.0	nd	1.8	1.5	1.7
3903	Rv3467	REP	2898	5509	1.9	0.2	0.1			1.1	1.8	1.6	1.8	2.3	1.7	2.0
3533	Rv3588c	-	2654	3751	1.5	0.4	0.1	putative_carbonic_anhydrase		1.1	1.4	1.9	1.7	1.7	1.0	1.1
4160	Rv3596c	clpC	8140	12575	1.5	0.1	0.0	ATP-dependent_Clp_protease		2.1	1.6	1.6	1.5	1.3	1.5	1.6
278	Rv3611	-	3714	6913	1.9	0.3	0.1			2.6	2.3	2.2	1.6	1.6	1.9	1.7
3915	Rv3630	-	1817	2666	1.5	0.4	0.2	unknown_membrane_protein		1.1	1.5	2.1	1.7	1.6	1.2	0.9
5330	Rv3706c	-	6483	9536	1.5	0.3	0.1			1.1	1.4	1.8	1.4	1.9	1.1	1.2
2450	Rv3735	-	1435	2124	1.5	0.2	0.1	similar_to_gp		1.1	1.8	1.5	1.6	1.5	1.2	1.3
3773	Rv3822	-	9264	13221	1.5	0.3	0.1			1.1	1.4	1.8	1.7	1.7	1.1	1.1
168	Rv3825c	pkS2	6949	11467	1.7	0.4	0.1	polyketide_synthase		1.1	2.2	2.1	1.3	1.6	1.5	1.7
1536	Rv3830c	-	3623	5443	1.6	0.4	0.1	transcriptional_regulator_(TetR/AcrR_family)		1.1	1.6	1.9	1.8	1.4	0.9	1.8
2257	Rv3831	-	2563	5337	2.1	0.4	0.2			1.1	1.8	2.1	2.4	1.5	2.5	2.6
5144	Rv3833	-	1913	2942	1.5	0.1	0.1	transcriptional_regulator_(AraC/XylS_family)		1.1	1.6	1.6	1.6	1.4	1.3	1.6
5142	Rv3837c	-	3240	5155	1.6	0.2	0.1	putative_phosphoglycerate_mutase		1.1	1.4	1.4	1.7	1.7	1.4	1.7
2012	Rv3911	sigM	1821	2532	1.5	0.3	0.1	probable_sigma_factor_similar_to_SigE		1.1	1.8	1.5	1.8	1.2	1.2	nd
2013	Rv3913	trxB2	1975	16199	8.5	1.8	0.7	thioredoxin_reductase		1.1	11.3	8.1	7.8	6.9	6.9	10.0
2735	Rv3914	trxC	4040	20727	5.8	2.2	0.9	thioredoxin		1.1	5.7	10.0	3.6	4.9	5.8	4.9
2014	Rv3915	cwIM	4030	7145	1.7	0.3	0.1	hydrolase		1.1	2.0	1.5	1.9	1.5	1.5	1.9