

**Table 1: *Mycobacterium tuberculosis* H37Rv genes induced after a shift from 20% to 0.2% oxygen.** 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		CH2/CH1	StD	SEM			Biol. Set 1		Biol. Set 2		Biol. Set 3	
			CH1	CH2						mL211	mL212	mL204	mL215	mL213	mL216
4042Rv0009	ppiA		421	688	1.5	0.4	0.1	peptidyl-prolyl_cis-trans_isomerase	1.1	1.2	1.2	1.9	1.9	1.2	1.4
2987Rv0046c	-		255	301	1.8	1.4	0.6		1.1	1.0	1.1	0.9	0.9	3.6	3.6
3709Rv0047c	-		151	221	2.3	2.1	0.9		1.1	1.0	1.0	1.0	0.8	5.7	4.1
317Rv0053	rpsF		94	162	1.6	0.5	0.2	30S_ribosomal_protein_S7	1.1	1.0	0.9	1.9	2.0	1.7	1.8
103Rv0054	ssb		124	216	1.5	0.4	0.2	single_strand_binding_protein	1.1	1.1	1.1	2.1	2.0	1.3	1.4
2016Rv0061	-		301	456	1.5	0.2	0.1	unlikely_orf	1.2	1.2	1.1	1.6	1.5	1.6	1.7
2740Rv0066c	icd2		123	184	1.6	0.5	0.2	isocitrate_dehydrogenase	1.1	2.1	2.3	1.5	1.5	1.1	1.2
5628Rv0077c	-		37	62	1.6	0.4	0.2	probable__oxidoreductase	1.1	1.5	1.4	1.9	2.2	1.4	1.2
1039Rv0079	-		23	292	13.0	3.7	1.5		1.1	17.9	7.0	13.8	15.1	12.7	11.4
5629Rv0079	-		64	359	5.4	1.7	0.7		1.2	4.5	3.7	6.5	4.1	5.5	8.1
4908Rv0080	-		36	307	8.2	2.0	0.8		1.1	7.1	6.0	8.8	7.6	11.9	8.1
5630Rv0081	-		33	137	3.8	1.2	0.5	transcriptional_regulator_(ArsR_family)	1.1	3.2	2.4	5.7	4.7	3.0	3.7
4909Rv0082	-		43	94	2.1	0.5	0.2	probable_oxidoreductase_subunit	1.1	1.9	2.3	2.7	2.4	2.0	1.3
5631Rv0083	-		47	85	1.8	0.4	0.1	probable_oxidoreductase_subunit	1.1	2.1	1.4	2.1	2.1	1.7	1.4
3176Rv0084	hycD		36	45	1.5	0.4	0.2	formate_hydrogenlyase_subunit_4	1.1	1.8	1.9	1.1	1.7	1.2	1.1
477Rv0088	-		49	72	1.6	0.9	0.4		1.1	2.5	2.4	1.7	1.9	0.5	0.6
4364Rv0188	-		106	186	1.7	0.5	0.2	putative_methyltransferase	1.1	2.4	2.3	1.8	1.5	1.2	1.2
4933Rv0196	-		84	150	1.9	0.4	0.2	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.7	1.6	1.7	1.5	2.7	1.9
5655Rv0197	-		176	354	2.1	0.7	0.3		1.1	3.1	2.6	1.4	1.3	2.2	1.9
2335Rv0211	pckA		103	184	1.9	0.2	0.1	phosphoenolpyruvate_carboxykinase_	1.1	2.2	2.0	1.8	1.7	1.7	1.8
3852Rv0241c	-		288	466	1.7	0.2	0.1		1.4	1.9	1.7	1.6	1.4	1.8	1.7
3131Rv0242c	fabG4		88	167	1.8	0.4	0.1	3-oxoacyl-[ACP]_reductase	1.1	1.5	1.4	2.0	1.7	2.3	1.9
3853Rv0243	fadA2		171	289	1.6	0.4	0.2	acetyl-CoA_C-acetyltransferase_	1.1	1.1	1.1	1.8	1.5	1.9	2.0
3132Rv0244c	fadE5		34	54	1.6	0.3	0.1	acyl-CoA_dehydrogenase_	1.1	1.5	1.5	1.4	1.3	2.2	2.0
248Rv0252	nirB		30	50	1.5	0.5	0.2	nitrite_reductase_flavoprotein	1.1	1.2	0.9	1.9	2.4	1.5	1.4
172Rv0271c	fadE6		28	63	2.6	1.0	0.4	acyl-CoA_dehydrogenase_	1.1	4.4	3.3	1.8	1.9	2.4	2.0
252Rv0275c	fadD27		159	286	1.7	0.1	0.1	acyl-CoA_synthase	1.1	1.6	1.6	1.9	1.9	1.8	1.7
4848Rv0296c	atsG		161	275	1.6	0.3	0.1	proable_arylsulfatase	1.1	1.3	1.2	1.8	1.7	2.0	1.6
1971Rv0330c	-		42	79	2.1	0.6	0.3		1.1	3.0	2.5	1.7	1.5	nd	2.0
126Rv0339c	-		51	77	1.5	0.2	0.1		1.1	1.4	1.4	1.5	1.6	2.0	1.3
5123Rv0350	dnaK		173	928	3.6	3.1	1.3	70_kD_heat_shock_protein,_chromosome_replication	1.1	2.2	1.9	8.3	6.7	1.3	1.2
4402Rv0351	grpE		116	460	2.6	2.2	0.9	stimulates_DnaK_ATPase_activity	1.1	1.1	1.1	4.9	5.7	1.2	1.3

5124Rv0352	dnaJ	159	280	1.5	0.4	0.2	acts_with_GrpE_to_stimulate_DnaK_ATPase	1.1	1.1	1.1	2.1	1.7	1.5	1.4
258Rv0368c	-	27	36	1.5	0.4	0.2		1.1	2.1	1.2	1.1	1.7	1.2	nd
3141Rv0370c	-	28	37	1.5	0.6	0.2	putative_CO_dehydrogenase_gene_cluster	1.1	2.7	1.1	1.1	1.5	1.2	1.3
3865Rv0375c	-	28	41	1.5	0.4	0.2	putative_CO_dehydrogenase_gene_cluster	1.1	2.2	1.7	1.6	1.6	1.2	0.8
260Rv0384c	clpB	61	104	1.6	0.4	0.2	heat_shock_protein	1.1	1.3	1.2	2.0	2.1	1.6	1.3
261Rv0386	-	30	40	1.5	0.4	0.2	transcriptional_regulator_(LuxR/UhpA_family)	1.1	1.6	1.3	1.1	1.2	2.1	1.7
3209Rv0410c	pknG	54	94	2.0	0.8	0.3	serine-threonine_protein_kinase	1.1	1.4	1.4	1.6	1.4	3.3	2.7
3730Rv0410c	pknG	59	91	1.7	0.7	0.3	serine-threonine_protein_kinase	1.1	1.3	1.2	1.4	1.2	2.7	2.6
458Rv0411c	glnH	278	507	2.2	0.8	0.3	putative_glutamine_binding_protein	1.1	1.9	2.0	1.6	1.5	3.2	3.2
1180Rv0412c	-	200	347	2.0	0.5	0.2	unknown_probable_membrane_protein	1.1	2.0	1.7	1.5	1.6	2.7	2.7
264Rv0440	groEL2	192	701	3.0	3.5	1.4	60_kD_chaperonin_2	1.4	0.8	0.7	7.5	7.6	0.7	0.8
1324Rv0455c	-	187	300	1.5	0.4	0.2	N-term_hydrophobic_stretch	1.1	1.1	1.0	1.8	2.0	1.4	1.6
1879Rv0497	-	72	116	1.5	0.4	0.2	probable_membrane_protein	1.1	1.0	1.2	1.7	1.5	2.1	nd
1883Rv0505c	serB	155	228	1.5	0.2	0.1	probable_phosphoserine_phosphatase	1.1	1.6	1.4	1.4	1.3	1.9	1.7
325Rv0509	hemA	182	270	1.5	0.3	0.1	glutamyl-tRNA_reductase	1.1	1.4	1.2	1.5	1.4	1.8	1.9
5343Rv0524	hemL	80	102	1.5	0.5	0.2	glutamate-1-semialdehyde_aminotransferase	1.1	2.2	1.6	1.1	0.8	1.6	1.6
4622Rv0525	-	69	82	1.5	0.5	0.2		1.1	2.1	1.7	1.0	0.9	1.5	1.5
327Rv0559c	-	93	154	1.5	0.4	0.2	possible_exported	1.1	2.2	1.5	nd	1.4	1.1	1.2
1331Rv0569	-	38	563	19.3	11.2	4.6		1.1	42.0	14.5	13.6	15.3	15.0	15.5
1049Rv0569	-	19	356	17.1	3.2	1.3		1.1	15.5	14.7	23.3	15.5	16.8	16.5
610Rv0570	nrdZ	21	58	3.0	0.9	0.4	ribonucleotide_reductase_class_II	1.1	3.2	3.1	2.3	2.3	4.6	2.7
1332Rv0571c	-	24	46	2.1	0.4	0.2		1.1	nd	2.0	1.8	2.0	2.7	1.9
328Rv0572c	-	29	180	11.1	4.4	2.0		1.1	3.2	13.1	nd	12.9	13.3	13.1
611Rv0572c	-	18	91	5.0	1.4	0.6		2.6	6.6	4.2	5.8	6.4	3.8	3.5
612Rv0574c	-	18	45	2.9	0.9	0.4		1.1	2.9	2.5	1.8	2.3	4.4	3.6
4276Rv0634c	-	224	414	1.7	0.6	0.2	putative_glyoxylase_II	1.1	0.9	0.9	2.1	2.1	1.8	2.2
2929Rv0644c	mmaA2	283	421	1.5	0.3	0.1	methoxymycolic_acid_synthase_2	2.5	1.2	1.3	1.5	1.5	1.8	1.9
333Rv0651	rplJ	114	158	1.5	0.4	0.2	50S_ribosomal_protein_L10	1.1	nd	1.0	1.5	1.4	1.9	1.8
334Rv0663	atsD	48	48	1.5	0.2	0.1	proable_arylsulfatase	1.1	nd	1.2	1.6	1.8	1.6	1.3
2209Rv0670	end	65	103	1.6	0.2	0.1	endonuclease_IV_(apurinase)	1.1	1.8	1.7	1.6	1.6	1.5	1.3
3501Rv0676c	mmpL5	130	303	2.2	0.4	0.2	conserved_large_membrane_protein	1.1	2.5	2.1	2.8	2.3	1.8	1.6
4223Rv0677c	mmpS5	221	511	2.0	0.7	0.3	conserved_small_membrane_protein	1.1	1.6	1.6	3.1	2.7	1.3	1.6
614Rv0678	-	124	321	2.0	0.9	0.4		1.1	2.0	1.8	3.4	2.7	1.2	1.2
616Rv0682	rpsL	354	602	1.6	0.4	0.2	30S_ribosomal_protein_S12	1.1	1.2	1.1	1.8	1.7	2.0	2.1
283Rv0700	rpsJ	259	442	1.5	0.4	0.2	30S_ribosomal_protein_S10	1.1	1.0	0.9	1.9	1.8	1.8	1.8
5499Rv0714	rplN	339	590	1.5	0.3	0.1	50S_ribosomal_protein_L14	1.1	1.2	1.1	2.0	1.8	1.4	1.5
1890Rv0715	rplX	128	262	1.7	0.5	0.2	50S_ribosomal_protein_L24	1.1	1.4	1.4	2.5	2.0	1.3	1.6
3510Rv0796	IS6110	138	205	1.5	0.1	0.0		1.1	1.5	1.5	1.5	1.3	1.6	1.4
4233Rv0810c	-	168	282	1.6	0.4	0.2		1.1	1.5	1.5	2.0	2.1	1.0	1.2
1685Rv0815c	cysA2	233	420	1.6	0.4	0.2	thiosulfate_sulfurtransferase	1.1	1.5	1.4	2.0	2.0	1.2	1.3

1687Rv0819	-	51	72	1.5	0.3	0.1		1.1	1.9	1.5	1.4	1.3	1.4	1.2
1689Rv0823c	-	168	215	1.7	0.7	0.3	transcriptional_regulator_(NifR3/Smm1_family)	1.1	2.7	2.4	1.2	1.1	1.3	1.3
2411Rv0824c	desA1	376	636	1.9	0.7	0.3	acyl-[ACP]_desaturase_	1.1	2.8	2.4	1.8	1.9	1.1	1.2
682Rv0826	-	19	30	1.5	0.3	0.1		1.1	1.3	1.6	1.7	2.0	1.5	1.1
4573Rv0827c	-	27	55	2.0	0.6	0.2	transcriptional_regulator_(ArsR_family)	1.1	2.2	2.0	2.2	3.0	1.6	1.3
1695Rv0848	cysM3	30	42	1.5	0.3	0.1	putative_cysteine_synthase	1.1	1.6	1.5	nd	2.0	1.3	1.3
5306Rv0863	-	316	581	1.8	0.4	0.2		1.2	2.3	2.3	2.0	1.7	1.2	1.5
1697Rv0864	moaC2	93	137	1.5	0.4	0.2	molybdenum_cofactor_biosynthesis,_protein_C	1.1	2.0	1.7	nd	1.5	1.1	1.2
1701Rv0872c	PE_PGRS	99	203	1.8	0.3	0.1		1.4	2.2	1.5	2.0	1.6	2.1	1.6
3026Rv0875c	-	79	118	1.6	0.4	0.2	possible_exported_protein	1.1	1.4	1.7	1.3	1.2	2.0	2.2
3748Rv0876c	-	105	133	1.5	0.3	0.1	possible_membrane_protein	1.1	1.7	1.6	1.1	1.1	1.8	1.5
144Rv0885	-	72	206	2.5	0.8	0.3	unknown_transmembrane_protein	1.1	1.7	1.7	3.3	3.4	2.5	2.5
3570Rv0886	fprB	22	40	1.8	0.4	0.2	ferredoxin,_ferredoxin-NADP_reductase	1.1	1.2	nd	2.1	1.9	1.9	nd
866Rv0887c	-	18	30	1.5	0.6	0.3		1.1	nd	1.0	2.2	2.0	1.3	0.9
3031Rv0896	gltA2	269	412	1.6	0.4	0.1	citrate_synthase_1_	1.1	2.2	2.1	1.4	1.4	1.3	1.5
42Rv0905	echA6	136	210	1.5	0.3	0.1	enoyl-CoA_hydratase/isomerase_superfamily_(aka_eccH)	1.1	1.7	1.6	1.6	1.7	1.1	1.2
4031Rv0940c	-	64	112	1.6	0.4	0.2	probable_monooxygenase	1.1	1.7	1.4	2.1	2.0	1.3	1.1
3309Rv0941c	-	22	29	1.5	1.0	0.4		1.1	3.2	1.3	nd	1.5	0.9	0.8
1702Rv0973c	accA2	58	115	1.9	0.7	0.3	acetyl/propionyl-CoA_carboxylase,_a_subunit	1.1	2.3	0.8	2.0	2.1	2.8	1.2
2424Rv0974c	accD2	18	35	1.7	0.6	0.3	acetyl/propionyl-CoA_carboxylase,_b_subunit	1.1	nd	0.8	2.4	1.6	2.1	1.4
1129Rv0991c	-	38	95	2.0	1.2	0.5		1.1	1.1	1.6	3.7	3.4	1.2	1.1
3293Rv0998	-	71	121	1.6	0.3	0.1		1.1	1.3	1.2	2.0	1.7	1.8	1.3
1470Rv1007c	metS	74	147	2.1	1.4	0.6	methionyl-tRNA_synthase	1.1	4.9	1.2	1.4	1.2	2.1	2.0
2917Rv1013	pks16	227	774	3.6	1.9	0.8	polyketide_synthase_	1.1	1.7	1.6	3.3	3.1	5.6	6.1
4038Rv1013	pks16	142	234	1.6	0.6	0.3	polyketide_synthase_	1.2	1.0	1.0	1.7	1.2	2.5	2.3
3316Rv1014c	pth	85	188	2.0	0.4	0.2	peptidyl-tRNA_hydrolase	1.1	1.7	2.3	2.4	1.9	2.2	1.3
1155Rv1015c	rplY	138	275	1.8	0.4	0.2	50S_ribosomal_protein_L25	1.1	1.3	1.3	2.2	2.3	1.7	2.1
1149Rv1039c	PPE	39	61	1.5	0.4	0.2		1.1	nd	0.9	1.8	1.8	1.2	1.5
2387Rv1060	-	60	109	1.7	0.3	0.1		1.1	1.3	1.3	2.0	1.9	1.9	1.6
4549Rv1063c	-	119	195	1.7	0.3	0.1		1.1	1.7	1.6	1.5	1.4	2.1	1.9
2389Rv1076	lipU	61	98	1.7	0.4	0.2	probable_esterase	1.1	2.1	2.3	1.4	1.5	1.8	1.3
1668Rv1077	cysM2	55	82	1.5	0.1	0.0	cystathionine_b-synthase	1.1	1.6	1.5	1.4	1.5	1.7	1.5
4639Rv1078	pra	286	386	1.5	0.3	0.1		2.5	1.2	1.2	1.3	1.3	1.7	2.0
4558Rv1094	desA2	373	825	2.2	0.7	0.3	acyl-[ACP]_desaturase	1.1	2.7	2.8	2.5	2.5	1.2	1.5
4728Rv1152	-	62	109	1.6	0.3	0.1	transcriptional_regulator_(GntR_family)	1.1	1.6	1.5	2.1	1.6	1.5	1.4
1842Rv1156	-	268	361	1.5	0.2	0.1		1.1	1.7	1.7	1.2	1.2	1.4	1.6
2566Rv1161	narG	153	256	1.7	0.1	0.0	nitrate_reductase_a_subunit	2.5	1.8	1.6	1.6	1.5	1.8	1.8
3155Rv1162	narH	159	253	1.6	0.2	0.1	nitrate_reductase_b_chain	1.1	1.6	1.4	1.7	1.4	1.6	1.8
565Rv1172c	PE	144	256	1.8	0.5	0.2		1.1	nd	1.1	1.9	1.6	2.2	2.1
3581Rv1174c	-	439	781	1.5	0.5	0.2		1.1	1.1	1.1	2.3	1.8	1.3	1.3

4171Rv1177	fdxC	296	572	1.9	0.7	0.3	ferredoxin_4Fe-4S	1.1	2.5	2.5	2.2	2.1	1.0	1.2
4371Rv1211	-	97	163	1.6	0.6	0.2		1.1	1.2	1.8	1.7	2.7	1.2	1.3
3526Rv1229c	mrp	87	125	1.5	0.4	0.2	similar_to_MRP/NBP35_ATP-binding_proteins	1.1	1.4	1.3	1.3	1.1	2.1	1.8
3458Rv1245c	-	53	108	1.9	0.3	0.1	putative_dehydrogenase	1.1	1.5	1.5	2.2	2.0	2.2	2.0
2681Rv1264	-	156	407	2.6	0.2	0.1	similar_to_adenylate_cyclases	1.4	2.6	2.7	2.7	2.8	2.2	2.6
4818Rv1284	-	41	78	1.8	0.3	0.1		1.1	1.7	1.6	2.0	2.0	2.1	1.4
5540Rv1285	cysD	24	49	1.8	1.0	0.4	ATP:sulphurylase_subunit_2	1.1	1.3	1.2	2.7	3.3	1.2	1.1
4819Rv1286	cysN	49	121	2.1	1.2	0.5	ATP:sulphurylase_subunit_1	1.1	1.3	1.4	3.5	3.6	1.7	0.9
135Rv1369c	IS6110	130	200	1.5	0.1	0.1		1.1	1.6	1.3	1.5	1.5	1.5	1.8
3022Rv1379	pyrR	40	88	2.5	1.7	0.7	regulatory_protein_pyrimidine_biosynthesis	1.1	0.9	1.2	2.1	1.8	5.1	4.0
3744Rv1380	pyrB	23	57	2.9	2.0	0.8	aspartate_carbamoyltransferase_	1.1	1.2	1.6	1.8	1.9	5.9	4.9
683Rv1381	pyrC	77	107	1.5	0.6	0.3	dihydroorotase	1.1	1.0	1.1	1.2	1.1	2.2	2.4
3745Rv1382	-	39	68	2.3	1.7	0.7		1.1	1.4	1.6	1.1	1.2	5.3	3.4
5503Rv1390	-	230	411	1.6	0.4	0.2		1.1	1.5	1.5	2.0	2.2	1.1	1.4
2622Rv1404	-	97	171	1.7	0.2	0.1	transcriptional_regulator_(MarR_family)	1.1	1.9	1.5	1.8	1.7	1.6	1.8
684Rv1405c	-	22	41	1.7	0.6	0.3	similar_to_phosphatidylethanolamine_N-methyltransferase	1.1	2.0	1.6	2.4	2.4	1.0	1.0
4786Rv1411c	lprG	265	394	1.5	0.1	0.1	lipoprotein	1.1	1.6	1.4	1.5	1.3	1.6	1.6
3521Rv1443c	-	37	59	1.6	0.5	0.2		1.1	2.5	1.5	1.7	1.6	1.3	1.1
2643Rv1493	mutB	87	156	1.7	0.6	0.3	methylmalonyl-CoA_mutase,_a_subunit	1.1	0.8	0.9	2.0	1.8	2.3	2.2
1922Rv1494	-	53	91	1.5	0.5	0.2		1.1	0.8	0.9	2.0	1.9	1.8	1.7
2644Rv1495	-	64	97	1.6	0.4	0.2		1.1	nd	1.0	1.4	1.6	2.1	1.8
4481Rv1540	-	98	138	1.7	0.7	0.3	yabO/yceC/yfil_family	1.1	2.6	2.4	1.2	1.0	1.4	1.4
1591Rv1556	-	21	32	1.6	0.2	0.1	putative_transcriptional_regulator	1.1	1.7	nd	1.6	1.5	1.7	1.3
1214Rv1576c	-	39	72	1.7	0.9	0.4	phiRV1_phage_related_protein	1.1	nd	0.8	2.2	3.0	1.3	1.1
489Rv1584c	-	56	107	1.5	0.6	0.3	phiRV1_phage_related_protein	1.2	nd	0.9	2.4	1.7	1.4	1.3
3374Rv1590	-	41	52	1.5	0.4	0.2		1.1	0.8	nd	1.3	1.7	1.9	1.6
3373Rv1592c	-	186	743	3.4	0.8	0.3		1.1	2.7	2.4	4.5	3.4	3.7	3.7
4094Rv1593c	-	78	172	2.0	0.4	0.2		1.1	1.6	1.6	2.5	2.2	1.9	2.4
3372Rv1594	nadA	166	321	1.9	0.1	0.1	quinolinate_synthase	2.5	2.0	1.8	2.0	1.8	1.8	1.8
4093Rv1595	nadB	120	212	1.7	0.4	0.2	L-aspartate_oxidase	1.1	1.4	1.2	1.9	1.2	2.1	2.0
1208Rv1601	hisB	197	311	1.6	0.1	0.1	imidazole_glycerol-phosphate_dehydratase	1.1	1.6	1.4	1.5	1.7	1.6	1.8
2572Rv1628c	-	91	162	1.5	0.5	0.2		1.2	1.1	1.1	2.1	2.1	1.3	1.4
3284Rv1683	-	53	87	1.6	0.5	0.2	possible_acyl-CoA_synthase	1.1	1.1	1.2	1.6	1.4	2.4	1.8
3289Rv1705c	PPE	58	95	1.6	0.4	0.2		1.1	1.1	1.2	1.7	1.7	2.1	1.6
3290Rv1707	-	84	109	1.6	0.9	0.4	probable_sulphate_permease	1.1	0.9	1.0	1.0	1.1	3.1	2.4
3276Rv1732c	-	125	224	1.6	0.4	0.2		1.1	1.2	1.1	2.0	1.7	1.9	1.7
3998Rv1733c	-	23	417	15.5	6.1	2.5	possible_membrane_protein	1.1	10.3	9.5	25.4	12.2	18.2	17.5
3277Rv1734c	-	18	89	5.1	2.6	1.1		1.1	2.8	4.2	4.0	3.5	9.7	6.6
3999Rv1735c	-	22	37	2.2	0.5	0.2		1.1	2.1	1.8	nd	1.9	2.9	2.2
3278Rv1736c	narX	56	165	3.3	0.8	0.3	fused_nitrate_reductase	2.5	3.8	3.0	2.5	2.3	4.3	3.6

1057Rv1737c	narK2	19	252	12.5	3.2	1.3	nitrite_extrusion_protein_	1.1	13.5	9.1	13.1	8.5	16.9	14.1
4000Rv1737c	narK2	57	101	1.8	0.4	0.2	nitrite_extrusion_protein_	1.3	1.5	1.6	1.9	1.3	2.2	2.2
3279Rv1738	-	22	1169	50.4	19.1	7.8		1.1	36.2	20.1	73.1	61.7	57.6	53.7
4001Rv1739c	-	21	82	4.1	1.1	0.4	possible_sulphate_transporter	1.1	4.4	2.2	3.6	4.7	5.0	4.6
3014Rv1749c	-	66	115	1.7	0.5	0.2	possible_integral_membrane_protein	1.1	1.1	1.3	1.8	1.6	2.4	2.1
131Rv1756c	IS6110	161	248	1.5	0.1	0.0		1.1	1.5	1.5	1.5	1.7	1.6	1.5
3017Rv1764	IS6110	130	196	1.5	0.1	0.0		1.1	1.5	1.4	1.5	1.5	1.6	1.6
2776Rv1805c	-	45	71	1.5	0.2	0.1	unlikely_orf	1.1	1.4	1.5	1.8	1.6	1.4	1.2
3693Rv1812c	-	29	54	2.0	1.2	0.5	probable_dehydrogenase	1.1	1.2	1.2	1.4	1.5	4.3	2.6
2971Rv1813c	-	29	312	12.8	6.3	2.6		1.1	7.3	8.5	8.1	12.1	23.0	17.8
4411Rv1813c	-	45	326	12.6	5.5	2.2		1.1	11.4	9.8	4.9	12.4	20.9	16.1
1528Rv1815	-	92	159	1.5	0.2	0.1		1.1	1.6	1.5	1.9	1.6	1.2	1.3
4408Rv1831	-	170	391	2.2	0.2	0.1		1.1	2.1	2.0	2.5	2.3	2.1	2.0
5189Rv1853	ureD	70	89	1.5	0.4	0.2	urease_accessory_protein	1.1	nd	2.3	1.4	1.5	1.4	1.1
5188Rv1855c	-	75	122	1.5	0.2	0.1	probable_monooxygenase_	1.1	1.6	1.3	1.8	1.5	1.5	1.6
4466Rv1856c	-	56	96	1.8	1.0	0.4	short-chain_dehydrogenase/reductase_family	1.1	0.7	0.8	1.8	1.7	3.0	2.7
2301Rv1865c	-	72	198	2.4	0.6	0.2	Short-chain_alcohol_dehydrogenase	1.4	2.0	1.7	3.2	2.9	2.4	2.3
95Rv1884c	-	447	969	1.9	0.6	0.2		1.1	1.8	1.6	2.6	2.6	1.2	1.4
91Rv1892	-	29	48	1.8	0.2	0.1		1.1	2.0	2.0	1.7	1.6	nd	nd
3943Rv1893	-	22	35	1.7	0.7	0.3		1.1	2.9	1.9	1.5	1.5	1.3	1.1
3700Rv1893	-	33	53	1.5	0.4	0.2		1.1	1.8	2.0	1.6	1.7	1.4	0.8
2978Rv1894c	-	57	124	2.0	0.4	0.2	some_similarity_to_dioxygenases	1.1	1.9	1.9	2.5	2.2	1.9	1.3
3697Rv1899c	lppD	260	426	1.5	0.2	0.1	lipoprotein	1.1	1.7	1.4	1.8	1.4	1.5	1.4
86Rv1915	aceAa	98	147	1.5	0.1	0.0	isocitrate_lyase,_a_module	1.1	1.4	1.4	1.5	1.5	1.7	1.7
1988Rv1956	-	51	93	1.9	0.3	0.1	putative_transcriptional_regulator	1.1	2.3	2.1	1.8	1.8	1.6	1.5
2669Rv1989c	-	36	67	1.6	0.6	0.3		1.1	nd	1.2	2.5	1.8	1.2	1.1
2668Rv1991c	-	20	38	1.8	0.7	0.3		1.1	nd	1.6	2.7	2.1	1.2	1.1
1946Rv1992c	ctpG	44	146	2.5	1.2	0.5	probable_cation_transport_ATPase	1.2	1.6	1.4	4.4	3.7	2.1	1.9
2667Rv1993c	-	40	102	2.1	1.0	0.4		1.1	2.3	1.2	3.3	3.2	1.4	1.3
2666Rv1995	-	18	43	2.0	0.9	0.4		1.3	nd	1.1	3.5	2.1	1.5	1.7
1944Rv1996	-	18	249	13.7	3.2	1.3		1.2	17.3	10.5	14.2	10.2	17.4	12.4
5553Rv1997	ctpF	33	259	9.7	7.1	2.9	probable_cation_transport_ATPase_	2.6	23.8	5.1	7.8	4.7	7.9	9.2
4831Rv1997	ctpF	50	201	4.4	1.5	0.6	probable_cation_transport_ATPase_	1.1	3.8	3.9	3.6	2.9	7.1	5.1
5552Rv1998c	-	27	158	8.6	8.8	3.6		1.1	26.4	5.3	6.0	2.8	5.6	5.3
4828Rv2003c	-	27	246	12.3	7.5	3.1		1.1	16.5	8.6	4.8	5.1	24.2	14.7
5549Rv2003c	-	22	148	8.4	5.1	2.1		1.1	14.8	5.1	4.5	2.7	13.7	9.6
4827Rv2004c	-	204	395	2.1	0.5	0.2		1.1	1.9	1.9	1.8	1.7	2.8	2.6
5548Rv2005c	-	43	434	9.2	2.9	1.2		1.1	9.0	5.7	13.0	6.7	8.7	12.4
4826Rv2006	otsB	22	68	4.0	2.2	0.9	trehalose-6-phosphate_phosphatase	1.1	7.2	2.7	2.3	2.0	6.1	3.5
2665Rv2007c	fdxA	64	1252	24.1	11.9	4.9	ferredoxin	1.1	47.4	16.3	17.8	23.1	16.3	23.6

4566Rv2025c	-	45	101	1.9	0.9	0.4	possible_membrane_protein	1.1	1.7	1.8	2.8	3.3	1.2	0.9
2401Rv2028c	-	40	136	3.5	1.2	0.5		1.1	3.8	2.5	3.2	2.9	5.8	3.0
1680Rv2029c	pfkB	24	264	12.2	5.6	2.3	phosphofructokinase_II	1.1	5.9	9.3	9.2	10.5	19.7	18.7
2402Rv2030c	-	19	211	10.6	3.5	1.4		1.1	10.7	6.4	11.8	7.8	16.6	10.4
1681Rv2031c	hspX	42	612	14.6	3.0	1.2	14kD_antigen,_heat_shock_protein_Hsp20_family	1.1	10.6	11.2	15.1	16.4	17.2	17.3
2403Rv2032	-	22	1032	45.2	16.5	6.7		1.1	37.2	19.3	56.5	38.6	64.2	55.2
1683Rv2035	-	53	95	1.7	0.3	0.1		1.1	2.0	1.3	1.8	2.0	1.7	1.5
2405Rv2036	-	48	78	1.6	0.3	0.1	similar_to_lincomycin_production_genes	1.1	1.2	1.4	1.7	1.8	1.8	1.4
5290Rv2042c	-	70	82	1.5	1.2	0.5		1.1	3.9	1.6	1.1	0.9	1.0	0.8
648Rv2043c	pncA	63	94	1.5	0.1	0.1	pyrazinamide_resistance/sensitivity	1.1	1.8	1.6	1.5	1.3	1.5	1.4
4569Rv2043c	pncA	83	123	1.5	0.1	0.0	pyrazinamide_resistance/sensitivity	1.1	1.6	1.5	1.5	1.5	1.4	1.4
5206Rv2077c	-	101	153	1.7	0.7	0.3		1.1	3.1	1.2	1.8	1.5	1.1	1.3
4438Rv2111c	-	305	485	1.5	0.2	0.1		1.1	1.6	1.5	1.7	1.6	1.1	1.2
5171Rv2161c	-	147	287	2.0	0.3	0.1	similar_to_alkanal_monooxygenase_beta_chain	2.5	2.4	1.9	1.8	1.6	2.1	2.4
4449Rv2162c	PE_PGRS	165	249	1.6	0.2	0.1		2.5	1.6	1.7	1.4	1.2	1.8	1.7
4447Rv2166c	-	346	537	1.5	0.2	0.1		1.1	1.6	1.6	1.7	1.4	1.2	1.3
4915Rv2182c	-	152	235	1.5	0.2	0.1		1.1	1.5	1.4	1.7	1.7	1.3	1.5
4637Rv2188c	-	84	135	1.6	0.3	0.1		1.4	1.5	1.5	1.7	1.3	1.9	1.9
434Rv2193	ctaE	333	587	1.8	0.4	0.2	cytochrome_c_oxidase_polypeptide_III	1.1	nd	1.5	1.8	1.4	1.8	2.4
506Rv2220	glnA1	265	767	2.4	1.2	0.5	glutamine_synthase_class_I	1.1	1.1	1.2	3.8	3.8	2.2	2.2
1163Rv2220	glnA1	378	1058	2.4	1.1	0.5	glutamine_synthase_class_I	2.5	1.4	1.3	3.2	4.2	2.0	2.2
508Rv2224c	-	66	86	1.5	0.3	0.1	probable_exported_protease	1.1	1.8	1.8	1.0	1.7	1.3	1.2
636Rv2232	-	38	59	1.5	0.3	0.1		1.1	1.3	1.3	1.9	1.6	1.5	1.1
3394Rv2233	-	31	46	1.6	0.2	0.1		1.1	1.5	1.6	1.4	1.5	2.0	1.4
4116Rv2234	ptpA	38	55	1.5	0.3	0.1	low_molecular_weight_protein-tyrosine-phosphatase	1.1	2.1	1.6	1.4	1.3	1.5	1.3
3395Rv2235	-	43	63	1.5	0.1	0.1		1.1	1.6	1.4	1.4	1.4	1.6	1.7
751Rv2241	aceE	171	188	1.6	1.0	0.4	pyruvate_dehydrogenase_E1_component	1.1	3.5	1.5	1.0	1.1	1.1	1.2
3113Rv2243	fabD	151	392	2.6	0.7	0.3	malonyl_CoA-[ACP]_transacylase	1.1	2.1	1.9	2.6	2.2	3.4	3.3
3398Rv2243	fabD	209	513	2.5	0.6	0.2	malonyl_CoA-[ACP]_transacylase	1.1	2.2	1.8	2.4	2.0	3.2	3.1
752Rv2243	fabD	206	452	2.3	0.4	0.2	malonyl_CoA-[ACP]_transacylase	1.1	2.5	1.7	2.2	1.9	2.4	3.0
3835Rv2243	fabD	373	679	1.8	0.2	0.1	malonyl_CoA-[ACP]_transacylase	1.1	1.9	1.7	1.8	1.5	2.0	2.0
3114Rv2244	acpM	711	1644	2.2	0.3	0.1	acyl_carrier_protein_(meromycolate_extension)	1.1	1.9	2.0	2.4	2.1	2.4	2.7
4120Rv2244	acpM	521	948	1.8	0.2	0.1	acyl_carrier_protein_(meromycolate_extension)	1.1	1.5	1.5	1.9	1.9	1.7	2.0
2288Rv2269c	-	23	39	1.5	0.3	0.2	questionable_orf,	1.1	nd	1.3	2.0	1.8	1.4	1.2
3390Rv2280	-	43	99	2.4	0.6	0.2	similar_to_D-lactate_dehydrogenase	1.1	3.1	2.5	2.2	1.6	3.0	2.1
885Rv2312	-	35	56	1.5	0.4	0.2		1.2	nd	1.1	2.0	1.7	1.2	1.4
4511Rv2340c	PE	48	94	1.7	1.1	0.4		1.1	3.9	1.2	1.2	1.1	1.5	1.4
1564Rv2357c	glyS	189	289	1.6	0.2	0.1	glycyl-tRNA_synthase	2.6	2.1	1.4	1.4	1.6	1.6	1.7
2931Rv2359	furB	44	73	1.6	0.3	0.1	ferric_uptake_regulatory_protein	1.1	1.8	2.1	1.4	1.6	1.4	1.5
1544Rv2412	rpsT	155	330	2.3	0.7	0.3	30S_ribosomal_protein_S20	1.1	1.4	1.4	2.3	2.8	2.8	2.9

3654Rv2428	ahpC	226	1114	4.2	1.3	0.5	alkyl_hydroperoxide_reductase	1.1	3.8	3.2	5.7	6.0	3.1	3.2
25Rv2438c	-	71	105	1.6	0.3	0.1		1.1	2.0	1.8	1.3	1.6	1.4	1.6
513Rv2442c	rplU	221	377	1.5	0.5	0.2	50S_ribosomal_protein_L21	1.1	1.0	1.1	1.9	2.2	1.4	1.5
2364Rv2450c	-	139	243	1.6	0.4	0.2		1.1	1.1	1.2	1.8	1.5	2.2	1.8
5248Rv2454c	-	128	204	1.5	0.3	0.1	oxidoreductase_beta_subunit	1.1	1.1	1.1	1.7	1.4	1.7	1.9
4527Rv2455c	-	120	204	2.0	0.3	0.1	probable_oxidoreductase_alpha_subunit	1.1	2.0	2.1	1.5	1.6	2.1	2.4
4532Rv2477c	-	162	209	1.5	0.4	0.2	ABC-transporter_ATP_binding_protein	1.1	1.3	1.3	1.2	1.2	1.8	2.1
4533Rv2479c	IS6110	160	251	1.6	0.1	0.0		1.1	1.5	1.5	1.6	1.5	1.6	1.7
5257Rv2484c	-	113	169	1.5	0.2	0.1		1.1	1.7	1.4	1.5	1.2	1.5	1.5
2958Rv2495c	pdhC	51	97	1.6	0.7	0.3	dihydrolipoamide_acetyltransferase	1.1	0.9	1.0	2.3	2.4	1.4	1.2
3680Rv2496c	pdhB	59	93	1.5	0.2	0.1	pyruvate_dehydrogenase_E1_component_b_subunit	1.4	1.3	1.5	1.8	1.6	1.4	1.2
2959Rv2497c	pdhA	125	204	1.5	0.2	0.1	pyruvate_dehydrogenase_E1_component_a_subunit	1.1	1.8	1.7	1.5	1.4	1.5	1.4
411Rv2504c	scoA	127	192	1.7	0.2	0.1	3-oxo_acid:CoA_transferase_a_subunit	1.1	nd	1.3	1.7	1.7	2.0	1.8
412Rv2506	-	36	45	1.7	0.9	0.4	transcriptional_regulator_(TetR/AcrR_family)	1.1	nd	0.8	1.0	3.1	2.2	1.6
1654Rv2518c	lppS	55	81	1.5	0.2	0.1	lipoprotein	1.1	1.8	1.7	1.5	1.4	1.3	1.5
4537Rv2520c	-	108	224	1.8	0.5	0.2		1.1	1.2	1.1	2.4	2.1	1.8	1.8
3119Rv2532c	-	257	417	1.7	0.3	0.1	secreted?	1.4	1.6	1.5	1.6	1.4	1.9	2.1
111Rv2576c	-	147	282	1.9	0.2	0.1		1.1	2.1	1.9	2.0	1.9	1.9	1.6
109Rv2580c	hisS	59	84	1.6	0.4	0.2	histidyl-tRNA_synthase	1.1	2.1	2.0	1.1	1.2	1.9	1.5
3718Rv2581c	-	149	204	1.5	0.3	0.1	putative_glyoxylase_II	1.1	1.4	1.4	1.2	1.2	1.7	1.8
2996Rv2582	ppiB	109	145	1.5	0.6	0.2	peptidyl-prolyl_cis-trans_isomerase	1.1	0.9	1.0	1.2	1.4	2.4	2.0
1768Rv2583c	relA	51	75	1.6	0.2	0.1	(p)ppGpp_synthase_I	1.1	1.6	1.5	1.4	1.4	1.8	1.8
3717Rv2583c	relA	76	86	1.5	0.5	0.2	(p)ppGpp_synthase_I	1.1	2.2	2.1	0.9	1.0	1.3	1.4
2241Rv2606c	-	83	114	1.5	0.2	0.1	Similar_to_G1209317_ethylene-inducible_protein	1.1	1.9	1.5	1.4	1.2	1.5	1.5
3340Rv2621c	-	35	53	1.5	0.3	0.1	putative_transcriptional_regulator	1.1	1.2	nd	1.6	1.3	2.0	1.6
457Rv2623	-	32	200	7.3	2.5	1.0		1.1	10.1	9.8	5.9	4.0	8.8	5.6
1178Rv2624c	-	18	309	19.7	8.6	3.5		1.1	37.1	17.3	16.2	15.3	16.0	16.0
456Rv2625c	-	49	300	6.9	3.3	1.3		1.1	13.0	5.2	5.0	3.8	7.7	6.7
1177Rv2626c	-	32	1266	40.6	8.0	3.3		1.1	42.9	26.8	39.9	47.6	37.6	48.7
455Rv2627c	-	18	194	11.9	3.0	1.2		1.1	16.8	11.7	9.9	9.2	14.2	9.6
1176Rv2628	-	51	248	5.2	1.3	0.5		1.1	7.4	5.2	4.3	3.6	5.0	5.7
454Rv2629	-	75	510	7.4	1.4	0.6		1.1	9.1	6.6	5.8	6.2	8.8	8.0
1175Rv2630	-	31	127	4.2	1.1	0.4		1.1	2.9	3.8	4.3	3.7	4.4	6.1
4127Rv2631	-	55	88	1.6	0.2	0.1		1.1	1.4	1.4	1.5	1.4	2.0	1.7
3408Rv2649	IS6110	112	174	1.6	0.2	0.1		1.1	1.7	1.4	1.6	1.4	1.8	1.5
4131Rv2652c	-	31	73	2.2	1.0	0.4	phiRV2_phage_related_protein	1.1	1.5	1.2	3.7	3.1	1.8	1.7
524Rv2657c	-	111	198	1.5	0.4	0.2	similar_to_gp36_of_mycobacteriophage_L5_	1.1	1.0	1.0	2.1	1.6	1.6	1.7
525Rv2659c	-	33	148	4.1	1.7	0.7	phiRV2_integrase	1.1	4.1	2.8	6.1	6.2	2.9	2.3
1247Rv2660c	-	75	236	2.8	1.9	0.8		1.1	1.5	1.4	4.7	5.6	1.7	1.9
3667Rv2700	-	86	136	1.5	0.2	0.1		1.1	1.2	1.3	1.7	1.5	1.8	1.3

2948Rv2706c	-	107	164	1.5	0.6	0.2		1.1	1.9	2.0	2.0	1.5	0.7	0.8
62Rv2711	ideR	88	124	1.5	0.1	0.0	iron_dependent_repressor,_IdeR	1.1	1.6	1.5	1.3	1.6	1.4	1.4
4884Rv2738c	-	385	603	1.7	0.8	0.3		1.1	1.2	1.0	1.4	1.4	2.8	2.7
196Rv2748c	ftsK	202	337	1.8	0.3	0.1	chromosome_partitioning	1.1	2.3	2.0	1.5	1.5	1.8	1.9
197Rv2750	-	147	228	1.5	0.1	0.1	putative_dehydrogenase	1.1	1.4	1.3	1.6	1.5	1.5	1.7
920Rv2753c	dapA	304	451	1.5	0.3	0.1	dihydrodipicolinate_synthase	1.1	1.5	1.4	1.4	1.2	2.0	1.6
3084Rv2760c	-	72	162	2.2	0.2	0.1		1.4	2.2	2.2	2.3	2.0	2.0	2.5
3086Rv2764c	thyA	141	211	1.5	0.3	0.1	thymidylate_synthase	1.1	1.2	1.2	1.5	1.5	1.6	1.9
203Rv2774c	-	172	270	1.6	0.1	0.1		1.1	1.6	1.4	1.6	1.5	1.6	1.8
3088Rv2780	ald	87	904	9.8	10.2	4.2	L-alanine_dehydrogenase	1.1	4.1	4.1	22.4	23.3	2.1	2.4
3810Rv2781c	-	114	464	2.9	2.5	1.0	probable_oxidoreductase	1.4	1.6	1.6	7.0	4.9	1.2	1.0
80Rv2814c	IS6110	113	183	1.5	0.2	0.1		1.1	1.5	1.3	1.7	1.7	1.5	1.6
79Rv2816c	-	152	188	1.5	1.0	0.4		1.1	0.7	0.6	1.1	1.1	2.2	3.2
799Rv2830c	-	63	136	1.9	0.7	0.3	similar_to_phage_P1_phd_gene	1.1	1.5	1.2	2.8	2.7	1.6	1.4
2494Rv2830c	-	19	33	1.6	0.4	0.1	similar_to_phage_P1_phd_gene	1.1	1.7	1.3	1.9	2.1	1.5	1.2
1747Rv2873	mpt83	51	111	1.8	0.6	0.2	surface_lipoprotein_Mpt83	1.1	1.4	1.4	2.6	2.6	1.7	1.4
2631Rv2876	-	168	281	1.5	0.3	0.1		1.1	1.2	1.2	1.9	1.7	1.5	1.7
4799Rv2890c	rpsB	255	434	1.6	0.4	0.2	30S_ribosomal_protein_S2	1.4	1.0	1.0	1.8	1.8	1.9	1.9
4803Rv2909c	rpsP	234	405	1.5	0.4	0.2	30S_ribosomal_protein_S16	1.1	1.1	1.0	1.9	1.6	1.8	1.6
496Rv2920c	amt	20	37	1.7	0.7	0.3	putative_ammonium_transporter	1.1	1.5	1.3	2.2	2.6	nd	0.8
499Rv2926c	-	142	232	1.5	0.2	0.1		1.1	1.7	1.6	1.8	1.4	1.5	1.3
32Rv2927c	-	252	423	1.7	0.2	0.1		1.1	1.9	1.9	1.6	2.0	1.3	1.5
4658Rv2927c	-	166	263	1.6	0.3	0.1		1.1	2.0	1.9	1.5	1.4	1.3	1.6
1574Rv2963	-	53	80	1.5	0.3	0.1	integral_membrane_protein	1.1	1.1	1.4	1.6	1.7	1.9	1.4
2377Rv2989	-	214	383	1.5	0.8	0.3	transcriptional_regulator_(IcIR_family)	1.1	1.3	1.2	2.7	2.4	0.8	0.8
4547Rv3008	-	165	234	1.5	0.2	0.1		2.5	1.4	1.3	1.4	1.2	1.6	1.8
1998Rv3012c	gatC	44	80	1.8	0.9	0.4	glu-tRNA-gln_amidotransferase,_subunit_C_	1.1	0.8	1.1	1.8	1.8	3.3	2.2
4889Rv3029c	fixA	180	293	1.7	0.7	0.3	electron_transfer_flavoprotein_b_subunit	1.1	1.1	1.0	1.6	1.6	2.3	2.7
3001Rv3074	-	40	70	1.8	0.3	0.1		1.1	1.9	1.9	1.6	1.3	2.3	1.7
1876Rv3117	cysA3	210	386	1.5	0.4	0.2	thiosulfate_sulfurtransferase	1.1	1.4	1.4	2.2	1.9	1.0	1.2
4762Rv3125c	PPE	178	271	1.5	0.2	0.1		1.4	1.2	1.2	1.5	1.4	1.8	1.8
5484Rv3126c	-	22	534	22.7	8.6	3.5		1.1	34.2	15.4	33.0	19.1	16.2	18.6
4763Rv3127	-	24	824	36.0	16.2	6.6		1.1	64.0	18.5	37.5	21.6	39.6	34.7
4764Rv3128c	-	18	302	17.5	6.7	2.7		1.1	22.9	8.1	15.9	14.7	27.2	16.2
5485Rv3128c	-	41	469	12.9	5.6	2.3		1.1	23.9	11.1	11.4	7.6	11.0	12.3
3841Rv3129	-	18	413	24.5	7.0	2.9		1.1	37.6	21.7	22.9	16.8	25.4	22.7
5486Rv3129	-	18	312	17.5	6.2	2.5		1.1	29.6	13.5	18.4	14.1	16.1	13.5
1776Rv3130c	-	40	373	14.0	6.7	2.7		1.1	2.6	13.9	22.6	13.1	13.6	18.1
3036Rv3130c	-	18	192	9.8	2.4	1.0		2.6	12.2	8.3	13.3	8.7	8.5	7.7
3757Rv3131	-	63	323	4.6	1.1	0.5		1.1	3.3	3.6	5.9	4.1	5.7	5.2



3035Rv3132c	-	28	214	9.8	4.0	1.6	sensor_histidine_kinase	1.1	10.7	9.1	5.8	5.6	16.1	11.8
3756Rv3133c	-	23	266	11.9	4.2	1.7	two-component_response_regulator	1.1	7.8	10.0	10.4	9.0	18.1	16.2
3034Rv3134c	-	23	273	11.5	2.6	1.1		1.1	8.0	11.1	13.4	10.8	10.1	15.4
3033Rv3136	PPE	312	526	1.8	1.0	0.4		1.1	0.8	0.7	1.7	1.5	3.1	2.9
3647Rv3139	fadE24	126	258	2.1	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	3.2	2.6	2.2	2.1	1.4	1.3
228Rv3139	fadE24	109	224	2.1	0.6	0.3	acyl-CoA_dehydrogenase_	2.1	3.1	2.5	2.1	1.9	1.5	1.4
949Rv3139	fadE24	45	73	2.1	1.4	0.6	acyl-CoA_dehydrogenase_	1.1	4.7	2.3	1.7	1.5	1.2	1.0
950Rv3139	fadE24	116	241	2.0	0.5	0.2	acyl-CoA_dehydrogenase_	1.1	2.3	2.1	2.4	2.2	1.2	1.5
272Rv3139	fadE24	152	279	1.8	0.4	0.2	acyl-CoA_dehydrogenase_	1.1	2.5	2.1	1.9	1.7	1.4	1.4
2925Rv3140	fadE23	116	250	1.9	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	2.5	2.2	2.6	2.3	1.1	1.0
948Rv3140	fadE23	123	236	1.8	0.8	0.3	acyl-CoA_dehydrogenase_	1.1	2.5	2.1	2.3	2.3	0.9	0.9
226Rv3140	fadE23	100	193	1.7	0.7	0.3	acyl-CoA_dehydrogenase_	1.1	1.9	1.7	2.6	2.2	0.9	0.9
3467Rv3173c	-	79	181	2.1	0.3	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.9	1.6	2.6	2.0	2.4	1.9
1308Rv3188	-	21	26	1.5	0.7	0.3		1.1	1.5	1.0	nd	2.7	1.1	1.1
3068Rv3269	-	50	254	3.7	3.3	1.4	probable_heat_shock_protein	1.1	2.2	2.1	8.3	7.5	0.9	1.1
3790Rv3270	ctpC	45	135	2.5	2.0	0.8	cation_transport_ATPase	1.1	1.4	1.4	5.0	5.1	1.1	1.0
181Rv3271c	-	88	292	2.1	1.9	0.8		1.1	0.8	0.7	5.2	4.0	1.1	1.0
3070Rv3285	accA3	50	74	1.5	0.5	0.2	acetyl/propionyl_CoA_carboxylase_a_subunit	1.1	1.2	1.0	1.4	1.5	2.2	1.9
3792Rv3286c	sigF	58	109	1.6	0.4	0.2	ECF_subfamily_sigma_subunit	1.1	1.4	1.3	2.1	2.2	1.5	1.5
3793Rv3288c	-	49	70	1.5	0.2	0.1		1.1	1.1	1.4	1.4	1.5	1.8	1.6
2501Rv3290c	lat	52	155	3.1	1.5	0.6	lysine-e_aminotransferase	1.1	1.3	1.2	4.7	4.2	3.7	3.7
3794Rv3290c	lat	72	167	2.1	0.8	0.3	lysine-e_aminotransferase	1.1	1.2	1.2	3.0	2.7	2.5	2.3
1780Rv3291c	-	46	78	1.7	0.5	0.2	transcriptional_regulator_(Lrp/AsnC_family)	1.1	1.0	1.2	1.7	2.0	2.3	1.9
3074Rv3293	aldB	26	42	1.6	0.3	0.1	aldehyde_dehydrogenase	1.1	1.7	1.2	1.4	2.1	1.9	1.5
4206Rv3337	-	67	126	1.7	0.5	0.2		2.5	1.2	1.2	2.6	1.4	1.8	1.8
3485Rv3338	-	48	115	2.2	0.7	0.3		1.1	1.5	1.6	2.5	1.9	3.5	2.2
5356Rv3340	metC	161	618	2.8	1.6	0.7	cystathionine_b-lyase	1.1	1.0	0.9	5.1	4.0	2.9	2.6
3822Rv3360	-	59	89	1.6	0.5	0.2	possible_ABC_transporter	1.1	1.3	1.5	1.3	1.2	2.4	1.9
3826Rv3367	PE_PGRS	94	165	1.8	0.6	0.3		2.1	2.8	2.2	1.8	1.6	1.3	1.2
1281Rv3379c	-	93	139	1.6	0.2	0.1	unknown_transketolase,_interrupted_by_IS6110	1.1	1.8	1.5	1.4	1.7	1.6	1.4
3442Rv3380c	IS6110	126	189	1.5	0.1	0.0		1.1	1.7	1.5	1.5	1.4	1.6	1.6
1750Rv3417c	groEL1	60	108	1.6	0.6	0.2	60_kD_chaperonin_1	1.1	1.1	1.5	2.5	2.1	1.2	1.1
3418Rv3418c	groES	184	582	2.5	2.5	1.0	10_kD_chaperone	1.1	1.1	0.9	5.7	5.6	0.7	0.8
535Rv3420c	rimI	173	287	1.5	0.5	0.2	ribosomal_protein_S18_acetyltransferase	1.1	0.9	0.9	1.7	1.9	1.8	1.9
3079Rv3443c	rplM	292	465	1.6	0.5	0.2	50S_ribosomal_protein_L13	1.1	1.1	1.1	1.7	1.4	2.0	2.2
1013Rv3451	-	68	107	1.5	0.3	0.1	probable_cutinase	1.1	1.4	1.3	1.7	2.0	1.6	1.2
3179Rv3462c	infA	170	285	1.7	0.6	0.2	initiation_factor_IF-1	1.1	1.1	1.1	1.8	1.4	2.3	2.5
300Rv3480c	-	110	185	1.9	0.5	0.2		1.1	2.3	2.0	1.3	1.4	2.4	2.2
3184Rv3484	cpsA	258	368	1.5	0.2	0.1	cpsA,CpsA_:_Q50160	1.1	1.6	1.4	1.4	1.2	1.6	1.6
2758Rv3502c	-	18	20	1.5	0.5	0.2	putative_dehydrogenase	1.1	1.8	1.8	nd	nd	1.6	0.8

2037 Rv3503c	fdxD	18	29	1.7	0.3	0.1	probable_ferredoxin	1.1	2.0	1.8	1.4	2.1	1.7	1.3
4925 Rv3515c	fadD19	48	84	1.7	0.4	0.2	acyl-CoA_synthase	1.1	1.4	1.3	1.8	2.2	2.0	1.4
5647 Rv3516	echA19	56	86	1.5	0.3	0.1	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	1.2	1.1	1.6	1.8	1.8	1.5
157 Rv3526	-	42	86	2.0	0.5	0.2	putative_phthalate_oxygenase	1.1	1.8	1.3	2.3	2.6	2.1	1.7
3762 Rv3535c	-	18	29	1.5	0.4	0.2	acetaldehyde_dehydrogenase	1.1	1.8	1.8	1.9	1.4	1.3	0.8
3040 Rv3536c	-	20	31	1.5	0.2	0.1	aromatic_hydrocarbon_degradation	1.1	1.6	1.4	1.6	1.8	1.5	1.2
3039 Rv3538	ufaA2	31	78	2.5	0.7	0.3	unknown_fatty_acid_methyltransferase	1.1	2.1	2.4	2.8	3.6	2.1	1.8
155 Rv3542c	-	38	64	1.6	0.8	0.3		1.1	0.6	0.6	1.8	2.2	2.2	2.2
876 Rv3543c	fadE29	32	61	1.9	0.5	0.2	acyl-CoA_dehydrogenase_	1.1	1.3	1.4	2.1	2.7	2.1	1.9
873 Rv3549c	-	166	252	1.5	0.1	0.0	short-chain_alcohol_dehydrogenase_family	1.4	1.6	1.5	1.5	1.4	1.5	1.6
175 Rv3570c	-	89	166	1.9	0.5	0.2	putative_oxidoreductase	1.1	1.4	1.2	1.9	2.2	2.4	2.4
176 Rv3572	-	53	94	1.6	0.3	0.1		1.1	2.1	1.4	1.9	1.7	1.4	1.3
177 Rv3574	-	23	38	1.6	0.2	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	1.6	1.5	1.9	1.8	1.3	1.3
649 Rv3584	lpqE	125	220	1.6	0.4	0.2	lipoprotein	1.1	1.1	1.0	1.9	2.0	1.8	1.8
4157 Rv3614c	-	140	378	2.1	2.1	0.8		1.1	0.8	0.8	5.5	4.0	0.8	0.9
3435 Rv3615c	-	137	661	3.7	3.6	1.5		1.2	1.1	1.1	8.9	7.7	1.5	1.7
4156 Rv3616c	-	99	349	2.9	2.6	1.1		1.1	1.1	1.1	6.8	5.8	1.2	1.4
5008 Rv3617	ephA	63	127	1.5	0.5	0.2	probable_epoxide_hydrolase	1.1	1.7	1.0	1.3	1.5	1.3	2.5
1029 Rv3626c	-	75	118	1.7	0.4	0.2		1.1	1.6	2.1	1.3	1.3	2.0	2.1
1713 Rv3667	acs	70	100	1.6	0.3	0.1	acetyl-CoA_synthase	1.1	1.7	1.7	1.3	1.1	1.9	1.8
4610 Rv3722c	-	183	289	1.6	0.1	0.1		1.1	1.6	1.6	1.6	1.4	1.6	1.8
2454 Rv3743c	-	18	23	1.7	0.6	0.3	probable_cation-transporting_ATPase	1.1	2.0	2.2	nd	1.8	nd	0.8
1509 Rv3769	-	97	152	1.5	0.1	0.0	possible_coiled-coil_protein	1.1	1.4	1.4	1.6	1.5	1.5	1.5
4394 Rv3776	-	90	131	1.6	0.4	0.2		1.1	1.9	1.9	1.1	1.2	1.7	1.8
1513 Rv3790	-	112	167	1.5	0.6	0.2	putative_oxidoreductase	1.1	2.1	0.9	0.9	1.1	2.0	1.9
5682 Rv3801c	fadD32	273	600	2.0	0.5	0.2	acyl-CoA_synthase	1.1	1.5	1.4	2.5	1.8	2.2	2.5
2077 Rv3810	pirG	245	407	1.5	0.5	0.2	cell_surface_protein_precursor_(Erp_protein)	1.1	1.0	0.8	1.8	1.5	2.1	2.1
5140 Rv3841	bfrB	93	914	8.9	3.3	1.4	bacterioferritin	1.1	8.3	7.3	14.3	11.3	5.6	6.4
2128 Rv3842c	glpQ1	26	215	7.6	1.7	0.7	glycerophosphoryl_diester_phosphodiesterase	1.1	8.5	6.6	9.6	8.9	5.7	5.9
4418 Rv3842c	glpQ1	36	87	2.2	0.3	0.1	glycerophosphoryl_diester_phosphodiesterase	2.6	2.2	2.0	2.7	2.0	2.0	2.2
5139 Rv3843c	-	85	159	1.7	0.5	0.2	probable_membrane_protein	1.1	1.1	1.2	2.1	2.2	1.9	1.6
2252 Rv3853	menG	52	153	3.1	1.6	0.7	S-adenosylmethionine:2-demethylmenaquinone_	1.1	5.2	3.6	4.2	3.0	1.2	1.1
1530 Rv3854c	-	72	311	7.0	6.6	2.7	probable_monooxygenase	1.1	18.2	11.9	4.1	4.6	1.7	1.8
2251 Rv3855	-	68	155	2.2	0.7	0.3	putative_transcriptional_regulator	1.1	1.8	2.5	3.1	3.0	1.4	1.6
1529 Rv3856c	-	89	128	1.6	0.4	0.1		1.1	1.7	1.4	1.2	1.3	2.1	1.9
5138 Rv3857c	-	166	237	1.5	0.3	0.1		1.1	1.4	1.3	1.3	1.3	1.8	2.0
3195 Rv3908	-	94	342	4.0	1.5	0.6		1.1	2.4	2.6	3.3	5.9	4.4	5.7