

Table 3: Genes induced in Mycobacterium tuberculosis ideR mutant compared to H37Rv 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)					
			Average	Average	CH2/CH1	StD	SEM			Biol. set 1	Biol. set 2		Biol. set 3		
			CH1 Cye3	CH2 Cye5	Induced			F	mm694	mm707	mm697	mm710	mm700	mm712	
2767	Rv0116c	-	1657	3689	2.1	0.3	0.1		1.2	1.7	2.4	2.1	2.6	1.8	2.2
4862	Rv0138	-	3317	5786	1.8	0.2	0.1		1.1	1.9	1.5	1.9	1.5	2.0	1.7
5587	Rv0145	-	1025	1939	1.9	0.1	0.1		1.1	nd	1.9	2.1	1.9	1.7	2.0
4365	Rv0190	-	572	902	1.6	0.2	0.1		1.1	1.4	1.6	1.5	1.6	1.4	1.9
3137	Rv0281	-	570	804	1.5	0.2	0.1		1.1	1.3	1.4	1.6	nd	nd	1.7
3859	Rv0282	-	718	2264	3.2	0.3	0.1		1.1	3.5	2.9	3.5	3.0	3.3	2.9
3138	Rv0283	-	370	1050	2.9	0.5	0.2		1.1	2.6	2.4	3.4	nd	3.0	3.4
3860	Rv0284	-	753	2781	3.7	0.5	0.2		1.1	4.2	3.2	4.1	3.1	4.0	3.6
3139	Rv0285	PE	520	1673	3.2	0.3	0.1		1.1	3.1	3.0	3.7	2.9	3.0	3.4
3206	Rv0286	PPE	634	2062	3.2	0.2	0.1		1.1	3.2	3.0	3.6	3.1	3.4	3.3
3140	Rv0287	-	861	4161	4.9	0.9	0.4	Ala-rich_protein	1.1	4.2	4.2	5.2	4.7	4.5	6.6
3862	Rv0288	-	1087	4554	4.2	0.1	0.0		1.1	4.0	4.2	4.2	4.2	4.3	4.2
253	Rv0289	-	505	1340	2.7	0.3	0.1		1.1	2.6	2.5	2.9	2.2	2.8	2.9
975	Rv0290	-	817	1500	1.9	0.2	0.1	unknown_hydrophobic_protein	1.1	1.8	2.0	1.8	1.6	1.9	2.0
254	Rv0291	-	458	1046	2.3	0.4	0.2	secreted_protease	1.1	2.2	2.2	2.6	1.6	2.3	2.7
976	Rv0292	-	679	1253	1.8	0.2	0.1	unknown_possible_membrane_protein	2.5	1.9	1.8	2.0	1.4	2.1	1.9
2694	Rv0333	-	1202	2296	1.9	0.1	0.0		1.1	1.8	2.0	1.9	1.9	2.0	1.9
4402	Rv0351	grpE	1640	2435	1.5	0.2	0.1	stimulates_DnaK_ATPase_activity	1.1	1.2	1.3	1.7	1.7	1.6	1.7
3151	Rv0450c	mmpL4	809	2033	2.5	0.1	0.1	conserved_large_membrane_protein	1.1	2.5	2.6	2.6	2.6	2.2	2.6
3873	Rv0451c	mmpS4	785	2861	3.6	0.6	0.3	conserved_small_membrane_protein	1.1	4.5	3.2	3.9	3.7	3.9	2.7
1540	Rv0481c	-	237	344	1.5	0.4	0.2		1.1	2.1	1.6	1.2	nd	1.1	1.6
4626	Rv0533c	fabH	532	825	1.5	0.6	0.3	b-ketoacyl-ACP_synthase_III	1.1	1.1	1.2	1.4	nd	1.2	2.6
452	Rv0587	-	805	1723	2.1	0.2	0.1	part_of_mce2_operon	1.1	2.0	2.4	2.0	2.3	1.8	2.0
3554	Rv0632c	echA3	1855	2713	1.5	0.2	0.1	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	1.3	1.3	1.4	1.4	1.5	1.9
4223	Rv0677c	mmpS5	1064	1591	1.5	0.2	0.1	conserved_small_membrane_protein	1.1	1.3	1.2	1.7	1.8	1.5	1.7
4474	Rv0766c	-	356	988	2.9	0.3	0.1	cytochrome_p-450	2.5	3.0	2.7	3.3	nd	3.0	2.6
4579	Rv0852	fadD16	387	595	1.6	0.2	0.1	acyl-CoA_synthase	1.1	1.5	1.3	1.7	1.5	1.6	1.7
3031	Rv0896	glTA2	1544	2623	1.7	0.1	0.1	citrate_synthase_1_	1.1	1.8	1.5	1.6	1.7	1.9	1.8
4557	Rv1092c	coaA	694	1055	1.5	0.1	0.0	pantothenate_kinase	1.4	1.5	1.5	1.6	1.5	1.4	1.6
3355	Rv1130	-	245	450	1.8	0.2	0.1		1.1	2.0	1.9	2.1	1.8	1.9	1.4
1840	Rv1140	-	529	779	1.5	0.1	0.1		1.1	1.4	1.4	1.6	1.4	1.7	1.3
3581	Rv1174c	-	1418	2081	1.5	0.1	0.1		1.1	1.5	1.3	1.4	1.4	1.5	1.7
4371	Rv1211	-	651	980	1.5	0.1	0.1		1.1	1.4	1.4	1.7	nd	1.6	1.6
3656	Rv1221	sigE	1532	2842	1.9	0.3	0.1	ECF_subfamily_sigma_subunit	1.1	2.2	1.7	1.5	1.7	2.1	2.0
1399	Rv1233c	-	5217	7646	1.5	0.2	0.1	hydrophobic_protein	1.4	1.4	1.1	1.5	1.4	1.8	1.6
4740	Rv1342c	pks14	235	374	1.5	0.1	0.1	polyketide_synthase_(chalcone_synthase-like)	1.1	1.4	1.7	1.5	1.5	1.3	nd
5462	Rv1343c	-	455	958	2.1	0.2	0.1		1.1	2.2	1.7	2.1	2.0	2.3	2.2
4741	Rv1344	-	319	1002	3.2	0.4	0.1	possible_acyl_carrier_protein	1.1	3.4	3.1	3.4	2.7	2.9	3.6
5463	Rv1345	fadD33	375	1046	2.7	0.5	0.2	acyl-CoA_synthase	1.1	2.5	2.5	2.3	3.4	2.4	3.1
49	Rv1346	fadE14	220	722	3.3	0.5	0.2	acyl-CoA_dehydrogenase_	1.1	2.7	3.6	4.0	2.8	3.3	3.3
771	Rv1347c	-	228	1465	6.4	0.5	0.2	possible_aminoglycoside_6'-N-acetyltransferase	1.1	6.2	6.5	6.5	6.4	7.3	5.7
50	Rv1348	-	218	1148	5.3	1.0	0.4	heavy_metal_tolerance_protein	1.1	4.3	6.9	5.8	4.6	5.3	4.8
3878	Rv1349	-	229	1051	4.6	0.7	0.3	probable_membrane_protein	1.1	5.7	4.1	5.2	4.2	4.7	3.8
51	Rv1350	fabG2	225	327	1.5	0.3	0.1	3-oxoacyl-[ACP]_reductase	1.1	1.0	1.6	1.7	1.3	1.4	1.7
773	Rv1351	-	367	677	1.8	0.2	0.1		1.1	2.1	1.9	2.0	1.7	1.9	1.6
4288	Rv1351	-	545	880	1.6	0.1	0.0		1.1	1.7	1.7	1.6	1.5	1.6	1.5
4780	Rv1387	PPE	2018	3634	1.8	0.3	0.1		1.1	1.6	1.5	2.0	2.1	2.0	1.8
4786	Rv1411c	lprG	1564	2261	1.5	0.1	0.0	lipoprotein	1.1	1.4	1.4	1.4	1.5	1.6	1.5
5510	Rv1415	ribA2	1184	1895	1.6	0.1	0.1	probable_GTP_cyclohydrolase_II	1.1	1.3	1.6	1.6	1.6	1.6	1.7
3328	Rv1518	-	242	397	1.6	0.1	0.0	involved_in_exopolysaccharide_synthesis	1.1	1.6	nd	1.7	1.8	1.5	1.6
1167	Rv1519	-	309	915	2.9	0.3	0.1		1.1	3.3	2.9	2.8	2.5	3.4	2.8

445	Rv1520	-	573	884	1.6	0.1	0.1	glycosyltransferase	1.1	1.4	1.6	1.5	1.8	1.6	1.4
3372	Rv1594	nadA	1389	2265	1.6	0.1	0.1	quinolinate_synthase	2.5	1.5	1.6	1.6	1.5	1.8	1.9
4467	Rv1854c	ndh	734	1062	1.5	0.1	0.1	probable_NADH_dehydrogenase	1.4	1.4	1.6	1.5	nd	1.3	1.6
4879	Rv1938	ephB	1208	1814	1.5	0.1	0.0	probable_epoxide_hydrolase	1.1	1.6	1.4	1.4	1.5	1.6	1.5
1684	Rv2037c	-	454	990	2.1	0.3	0.1	probable_transmembrane_protein	1.1	2.2	nd	2.3	2.1	1.7	2.3
4567	Rv2039c	-	428	763	1.8	0.2	0.1	probable_sugar_transporter	1.1	1.7	2.0	1.9	nd	1.7	2.0
1604	Rv2091c	-	1506	2184	1.5	0.1	0.0	potential_transmembrane_region	1.1	1.4	nd	1.5	1.5	1.5	1.5
4489	Rv2097c	-	1481	2468	1.7	0.1	0.1		1.1	1.5	1.6	1.7	nd	1.6	1.8
1555	Rv2121c	hisG	423	642	1.5	0.2	0.1	ATP_phosphoribosyltransferase	1.1	1.4	1.6	1.7	1.6	1.3	1.5
2277	Rv2122c	hisI	276	682	2.5	0.4	0.1	phosphoribosyl-AMP_cyclohydrolase	1.1	2.7	2.0	2.6	2.4	3.0	2.2
1556	Rv2123	PPE	228	2261	10.1	3.9	1.6		1.1	8.6	7.2	17.1	6.6	11.7	9.5
4447	Rv2166c	-	912	1430	1.6	0.3	0.1		1.1	1.5	1.4	1.7	nd	1.6	2.0
3392	Rv2276	-	828	1248	1.5	0.1	0.1	Probable_cytochrome_P-450	1.1	1.7	1.7	1.4	1.4	1.5	1.4
4444	Rv2377c	mbtH	264	1453	5.6	1.5	0.6	mycobactin/exochelin_synthase_	1.1	4.6	6.8	7.3	5.5	6.3	3.4
5165	Rv2378c	mbtG	317	1470	4.7	0.8	0.3	mycobactin/exochelin_synthase_(lysine_hydroxylase)	1.1	5.6	5.0	5.0	3.6	5.1	3.7
47	Rv2379c	mbtF	218	529	2.4	0.4	0.2	mycobactin/exochelin_synthase_(lysine_ligation)	1.1	1.9	2.9	2.6	2.6	2.0	2.7
471	Rv2380c	mbtE	235	1253	5.4	1.1	0.4	mycobactin/exochelin_synthase_(lysine_ligation)	1.1	4.3	6.8	6.3	5.2	5.8	4.0
1192	Rv2381c	mbtD	341	2547	7.5	0.9	0.4	mycobactin/exochelin_synthase_(polyketide_synthase)	1.1	8.7	7.5	7.2	5.9	8.0	7.6
470	Rv2382c	mbtC	320	1073	3.6	0.8	0.3	mycobactin/exochelin_synthase	1.1	3.3	3.8	4.8	4.3	2.7	2.9
4079	Rv2383c	mbtB	336	1310	3.9	0.8	0.3	mycobactin/exochelin_synthase_(serine/threonine_ligation)	1.1	4.7	3.0	4.3	3.0	4.7	3.4
2274	Rv2384	mbtA	225	395	1.8	0.2	0.1	mycobactin/exochelin_synthase_(salicylate-AMP_ligase)	1.1	2.1	1.9	1.7	1.6	1.8	1.4
1552	Rv2385	lipK	231	750	3.2	0.6	0.2	probable_acetyl-hydrolase	1.1	3.2	2.7	4.4	3.0	3.3	2.7
2273	Rv2386c	trpE2	277	2493	9.3	1.8	0.7	anthranilate_synthase_component_I	1.1	10.8	6.7	9.9	7.9	11.5	8.7
3654	Rv2428	ahpC	1031	2450	2.4	0.2	0.1	alkyl_hydroperoxide_reductase	1.1	2.1	2.2	2.4	2.4	2.7	2.5
2932	Rv2429	ahpD	759	1818	2.1	0.5	0.2	member_of_AhpC/TSA_family	1.1	1.7	1.6	2.1	2.9	2.1	2.4
4122	Rv2430c	PPE	1048	1679	1.6	0.2	0.1		1.1	1.8	1.7	1.3	1.5	1.5	1.7
3400	Rv2431c	PE	458	755	1.6	0.1	0.1		1.1	1.5	1.9	1.6	1.6	1.6	1.7
4530	Rv2461c	clpP	915	1345	1.5	0.2	0.1	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	1.3	1.3	1.7	nd	1.6	1.6
4532	Rv2477c	-	883	1427	1.6	0.2	0.1	ABC-transporter_ATP_binding_protein	1.1	1.4	1.6	1.6	nd	1.5	1.9
411	Rv2504c	scoA	534	759	1.5	0.2	0.1	3-oxo_acid:CoA_transferase_a_subunit	1.1	1.4	1.3	1.4	1.9	1.4	1.3
2993	Rv2588c	-	860	1257	1.5	0.2	0.1		1.1	1.4	1.3	1.4	1.5	1.7	1.6
454	Rv2629	-	516	858	1.7	0.1	0.0		1.1	1.7	1.7	1.5	1.7	1.6	1.7
2934	Rv2710	sigB	1221	3079	2.6	0.6	0.2	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	2.0	2.0	2.5	2.7	3.0	3.4
62	Rv2711	ideR	718	1140	1.6	0.2	0.1	iron_dependent_repressor_IdeR	1.1	1.3	1.5	1.6	1.8	1.5	1.9
197	Rv2750	-	480	707	1.5	0.1	0.0	putative_dehydrogenase	1.1	1.5	1.5	1.5	1.4	1.4	1.5
4658	Rv2927c	-	842	1378	1.6	0.2	0.1		1.1	1.4	1.6	1.6	nd	1.5	2.0
4542	Rv2933	ppsC	321	460	1.5	0.1	0.1	phenolphthiocerol_synthase_(pksD)	1.1	1.4	1.5	1.6	nd	nd	1.7
39	Rv2940c	mas	854	1482	1.7	0.4	0.1	mycocerosic_acid_synthase	2.5	1.7	1.5	1.4	2.4	1.5	1.9
41	Rv2947c	pks15	1292	1908	1.5	0.2	0.1	polyketide_synthase_	1.1	1.8	1.6	1.4	1.3	1.3	1.5
4548	Rv3010c	pfkA	361	629	1.9	0.2	0.1	phosphofructokinase_I	1.1	1.8	2.0	2.1	nd	1.7	1.6
2723	Rv3019c	-	438	903	2.0	0.3	0.1	similar_to_Esat6	1.1	2.4	1.4	1.9	2.1	2.2	1.8
2002	Rv3020c	PE	340	609	1.8	0.2	0.1		1.1	1.8	1.4	2.0	1.7	2.0	1.8
4894	Rv3051c	nrdE	2157	3310	1.5	0.1	0.0	ribonucleoside_diphosphate_reductase_a_chain	1.1	1.5	1.5	1.5	1.7	1.6	1.4
227	Rv3140	fadE23	627	1137	1.8	0.2	0.1	acyl-CoA_dehydrogenase_	1.1	1.6	2.1	1.7	1.9	1.5	1.7
4191	Rv3178	-	1073	2450	2.1	0.4	0.2		1.1	1.7	2.6	1.8	2.4	1.9	2.3
3541	Rv3229c	desA3	1372	1623	1.5	1.1	0.5	acyl-[ACP]_desaturase	1.1	0.4	0.4	2.9	2.9	1.3	1.2
3069	Rv3283	sseA	1113	1676	1.5	0.1	0.0	thiosulfate_sulfurtransferase	1.1	1.4	1.4	1.5	1.5	1.5	1.7
537	Rv3402c	-	298	1539	5.1	1.0	0.4	possible_involved_in_LPS_synthase	1.1	4.3	5.5	6.5	4.1	5.9	4.4
1258	Rv3403c	-	648	1930	3.0	0.3	0.1		1.1	3.4	3.2	2.9	2.7	3.0	2.5
3179	Rv3462c	infA	2278	3693	1.6	0.2	0.1	initiation_factor_IF-1	1.1	1.4	1.7	1.4	1.6	1.4	1.9
3181	Rv3466	REP	407	599	1.5	0.2	0.1		1.1	1.3	1.4	1.6	1.5	1.3	1.7
158	Rv3524	-	794	1226	1.6	0.2	0.1	possible_membrane_sensor_protein	1.1	1.5	1.2	1.8	1.4	1.9	1.5
4420	Rv3838c	pheA	306	472	1.5	0.3	0.1	prephenate_dehydratase	1.1	1.6	1.4	1.9	1.2	1.5	1.5
5141	Rv3839	-	320	4456	14.1	3.7	1.5		1.1	18.5	11.5	17.1	11.8	16.6	9.3
4419	Rv3840	-	256	1512	6.7	0.5	0.2	putative_transcriptional_regulator	1.1	7.1	nd	7.4	6.3	6.1	6.6
4412	Rv3866	-	617	954	1.5	0.5	0.2		2.1	1.3	1.0	2.4	nd	1.2	1.4
4964	Rv3874	-	5585	9151	1.6	0.2	0.1		1.1	1.4	1.6	1.5	1.8	1.6	1.8