

Table 4: 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 repressed. In addition, the table should not be seen as a complete list of all possibly repressed 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 Repressed	StD	SEM			Biol. set 1		Biol. set 2		Biol. set 3	
										mm694	mm707	mm697	mm710	mm700	mm712
4042	Rv0009	ppiA	3970	1341	3.0	0.3	0.1	peptidyl-prolyl_cis-trans_isomerase	1.1	0.4	0.3	0.3	0.4	0.4	0.3
4043	Rv0010c	-	660	345	1.9	0.2	0.1		1.2	0.5	0.5	0.4	0.6	0.5	0.5
1203	Rv0096	PPE	800	434	1.9	0.2	0.1		1.1	0.6	0.5	0.5	0.6	0.5	0.5
626	Rv0096	PPE	1045	562	1.8	0.2	0.1		1.1	0.6	0.6	0.5	0.6	0.5	0.5
1348	Rv0097	-	4742	2822	1.7	0.2	0.1		1.1	0.6	0.7	0.5	0.7	0.6	0.6
4086	Rv0098	-	2478	1596	1.6	0.1	0.0		1.1	0.7	0.7	0.6	0.7	0.7	0.6
3365	Rv0099	fadD10	1707	1049	1.6	0.1	0.0	acyl-CoA_synthase	1.1	0.6	0.6	0.6	0.6	0.6	0.6
4087	Rv0100	-	1143	719	1.6	0.3	0.1		1.1	0.6	0.6	0.6	0.8	0.6	0.6
125	Rv0337c	aspC	731	476	1.5	0.2	0.1	aspartate_aminotransferase	1.1	0.6	0.6	0.6	0.8	0.6	0.7
847	Rv0338c	-	2170	897	2.4	0.4	0.1	iron-sulfur_protein	1.1	0.4	0.4	0.4	0.5	0.4	0.4
665	Rv0521c	-	386	247	1.5	0.4	0.2		1.1	0.6	1.0	0.6	0.6	0.6	0.5
1049	Rv0569	-	768	460	1.7	0.1	0.0		1.1	0.6	0.6	0.5	0.6	0.6	0.6
4051	Rv0619	galT	554	238	2.3	0.3	0.1	galactose-1-phosphate_uridyltransferase_C-term	1.1	0.5	0.4	0.4	0.4	0.4	0.4
620	Rv0745	-	313	212	1.5	0.4	0.2		1.2	nd	1.0	0.6	0.7	0.7	0.4
1690	Rv0825c	-	341	222	1.5	0.3	0.2		1.1	0.7	0.9	nd	0.6	0.6	0.5
4038	Rv1013	pks16	1785	1013	1.8	0.2	0.1	polyketide_synthase_	1.2	0.6	0.5	0.6	0.6	0.6	0.5
4171	Rv1177	fdxC	2292	1432	1.6	0.4	0.1	ferredoxin_4Fe-4S	1.1	0.6	0.6	0.6	0.6	0.9	0.6
1481	Rv1195	PE	428	277	1.6	0.2	0.1		1.1	0.6	0.7	0.6	0.6	0.6	0.8
1593	Rv1552	frdA	307	196	1.5	0.4	0.2	fumarate_reductase_flavoprotein_subunit	1.1	0.8	0.9	0.6	0.6	0.6	0.5
2314	Rv1553	frdB	244	196	1.5	0.1	0.1	fumarate_reductase_iron_sulphur_protein	2.6	nd	nd	nd	0.7	nd	0.6
391	Rv1726	-	426	229	1.9	0.1	0.1	6-hydroxy-d-nicotine_oxidase_	1.1	0.6	0.6	0.5	0.6	0.6	0.5
3998	Rv1733c	-	676	418	1.6	0.3	0.1	possible_membrane_protein	1.1	0.5	0.6	0.5	0.7	0.6	0.8
3279	Rv1738	-	3261	1844	1.8	0.3	0.1		1.1	0.4	0.5	0.5	0.7	0.6	0.7
2981	Rv1876	bfrA	1031	394	2.6	0.2	0.1	bacterioferritin	1.1	0.3	0.4	0.4	0.4	0.4	0.4
1944	Rv1996	-	935	478	1.9	0.2	0.1		1.2	0.5	0.6	0.4	0.6	0.5	0.6
5553	Rv1997	ctpF	644	379	1.7	0.1	0.0	probable_cation_transport_ATPase_	2.6	0.6	0.6	0.6	0.6	0.7	0.6
2665	Rv2007c	fdxA	1921	1251	1.5	0.5	0.2	ferredoxin	1.1	0.5	0.4	0.6	0.7	0.9	0.8
1682	Rv2033c	-	663	395	1.7	0.3	0.1		2.6	0.7	0.7	0.6	0.5	0.5	0.5
3946	Rv2034	-	318	219	1.5	0.3	0.1	transcriptional_regulator_(ArsR_family)	1.1	0.8	nd	0.7	0.8	0.5	0.6
5205	Rv2075c	-	445	307	1.5	0.1	0.0		1.1	0.7	0.7	0.7	0.8	0.6	0.7
3836	Rv2245	kasA	1264	852	1.5	0.1	0.0	b-ketoacyl-ACP_synthase_(meromycolate_extension)	1.1	0.7	0.6	0.6	0.7	0.7	0.7
5231	Rv2337c	-	519	336	1.6	0.1	0.0		1.1	0.6	0.7	0.6	0.7	0.6	0.7
1517	Rv2611c	-	381	226	1.6	0.3	0.1		1.1	0.6	0.8	0.7	0.7	0.5	0.5
3646	Rv2935	ppsE	695	442	1.6	0.1	0.0	phenolphthiocerol_synthase_(pksF)	1.4	0.7	0.7	0.6	0.7	0.6	0.6
2729	Rv3042c	serB2	1137	786	1.5	0.2	0.1	C-term_similar_to_phosphoserine_phosphatase	1.1	0.8	0.5	0.7	0.7	0.8	0.7
5618	Rv3084	lipR	511	345	1.5	0.1	0.0	probable_acetyl-hydrolase	1.1	0.6	0.7	0.7	0.7	0.7	0.7
5481	Rv3108	-	628	434	1.5	0.2	0.1		1.1	0.8	0.7	0.6	0.7	0.6	0.6
2594	Rv3110	moaB	363	235	1.5	0.2	0.1	molybdenum_cofactor_biosynthesis_protein_B	1.1	0.6	0.8	0.7	0.6	0.6	0.6
2497	Rv3112	moaD	320	203	1.7	0.3	0.1	molybdopterin_converting_factor_subunit_1	1.1	0.7	nd	0.7	0.6	0.5	0.5
5484	Rv3126c	-	1086	513	2.1	0.3	0.1		1.1	0.4	0.4	0.4	0.5	0.5	0.6
4763	Rv3127	-	1080	711	1.5	0.3	0.1		1.1	0.5	0.5	0.7	0.7	0.7	0.8
3841	Rv3129	-	486	316	1.6	0.3	0.1		1.1	0.5	0.5	0.6	0.7	0.7	0.8
1776	Rv3130c	-	1187	592	2.0	0.3	0.1		1.1	0.5	0.4	0.5	0.5	0.6	0.6
993	Rv3145	nuoA	728	469	1.5	0.2	0.1	NADH_dehydrogenase_chain_A	1.1	0.7	0.6	0.6	0.6	0.7	0.6
581	Rv3165c	-	266	198	1.5	0.2	0.1		1.1	nd	nd	0.7	0.8	0.7	0.6
5682	Rv3801c	fadD32	2012	1328	1.5	0.1	0.1	acyl-CoA_synthase	1.1	0.6	0.7	0.7	0.6	0.6	0.8
5140	Rv3841	bfrB	5525	1294	4.3	0.7	0.3	bacterioferritin	1.1	0.2	0.2	0.2	0.3	0.2	0.2
2128	Rv3842c	glpQ1	903	526	1.7	0.1	0.1	glycerophosphoryl_diester_phosphodiesterase	1.1	0.6	0.6	0.6	0.6	0.6	0.5

