Table S1. Expression indices for genes in *M. tuberculosis* during non-replicating persistence.
Entries putatively involved in respiration are highlighted.

ORF[a]	Name[a]	Functional Class[a]	Expression index[b]	Variance[c]
Rv0001	dnaA	information pathways	3.1	0.0020
Rv0009	ppiA	information pathways	4.6	0.0001
Rv0020c	Rv0020c	conserved hypotheticals	3.3	0.0001
Rv0040c	Rv0040c	conserved hypotheticals	2.6	0.0009
Rv0046c	Rv0046c	conserved hypotheticals	2.3	0.0000
Rv0056	rplI	information pathways	2.9	0.0000
Rv0068	Rv0068	intermediary metabolism and respiration	1.4	0.0010
Rv0127	Rv0127	conserved hypotheticals	1.6	0.0047
Rv0141c	Rv0141c	unknown	1.1	0.0064
Rv0144	Rv0144	regulatory proteins	1.1	0.0067
Rv0157	pntB	intermediary metabolism and respiration	3.6	0.0004
Rv0164	Rv0164	conserved hypotheticals	3.2	0.0001
Rv0165c	Rv0165c	regulatory proteins	1.1	0.0000
Rv0167	Rv0167	virulence, detoxification, adaptation	2.3	0.0054
Rv0170	Rv0170	virulence, detoxification, adaptation	3.2	0.0001
Rv0171	Rv0171	virulence, detoxification, adaptation	2.8	0.0026
Rv0172	Rv0172	virulence, detoxification, adaptation	3.3	0.0003
Rv0173	lprK	cell wall and cell processes	3.3	0.0083
Rv0174	Rv0174	virulence, detoxification, adaptation	2.8	0.0015
Rv0176	Rv0176	conserved hypotheticals	3.0	0.0000
Rv0177	Rv0177	conserved hypotheticals	1.9	0.0085
Rv0221	Rv0221	conserved hypotheticals	1.5	0.0038
Rv0222	echA1	lipid metabolism	2.6	0.0001
Rv0227c	Rv0227c	cell wall and cell processes	3.4	0.0032
Rv0232	Rv0232	regulatory proteins	2.4	0.0046
Rv0234c	gabD2	intermediary metabolism and respiration	3.2	0.0096
Rv0247c	Rv0247c	intermediary metabolism and respiration	3.2	0.0024
Rv0248c	Rv0248c	intermediary metabolism and respiration	1.8	0.0053
Rv0249c	Rv0249c	cell wall and cell processes	2.7	0.0029
Rv0257c	Rv0257c	unknown	1.3	0.0074
Rv0259c	Rv0259c	conserved hypotheticals	1.2	0.0018
Rv0265c	fecB2	cell wall and cell processes	1.2	0.0059
Rv0269c	Rv0269c	conserved hypotheticals	1.5	0.0018
Rv0281	Rv0281	conserved hypotheticals	1.2	0.0035
Rv0284	Rv0284	conserved hypotheticals	1.9	0.0010
Rv0286	PPE	PE/PPE	1.7	0.0013
Rv0287	Rv0287	regulatory proteins	1.7	0.0000
Rv0288	Rv0288	conserved hypotheticals	1.7	0.0007
Rv0290	Rv0290	cell wall and cell processes	1.1	0.0089
Rv0309	Rv0309	unknown	4.8	0.0038
Rv0331	Rv0331	intermediary metabolism and respiration	2.3	0.0065
Rv0334	rmlA	intermediary metabolism and respiration	1.3	0.0004
Rv0338c	Rv0338c	conserved hypotheticals	1.7	0.0028
Rv0341	Rv0341	conserved hypotheticals	1.7	0.0002
Rv0343	Rv0343	conserved hypotheticals	2.0	0.0075
Rv0361	Rv0361	cell wall and cell processes	1.5	0.0038
Rv0364	Rv0364	conserved hypotheticals	1.7	0.0003
Rv0379	sec	cell wall and cell processes	4.3	0.0044
Rv0413	mutT3	information pathways	1.2	0.0010

Rv0419	lpqM	cell wall and cell processes	1.4	0.0025
Rv0424c	Rv0424c	unknown	2.0	0.0012
Rv0425c	ctpH	cell wall and cell processes	2.4	0.0006
Rv0430	Rv0430	unknown	5.5	0.0068
Rv0432	sodC	virulence, detoxification, adaptation	3.0	0.0002
Rv0433	Rv0433	conserved hypotheticals	4.7	0.0030
Rv0434	Rv0434	conserved hypotheticals	1.0	0.0039
Rv0440	groEL2	virulence, detoxification, adaptation	2.1	0.0033
Rv0447c	ufaA1	lipid metabolism	3.0	0.0056
Rv0448c	Rv0448c	conserved hypotheticals	1.6	0.0017
Rv0462	Rv0462	intermediary metabolism and respiration	1.8	0.0070
Rv0464c	Rv0464c	conserved hypotheticals	2.3	0.0046
Rv0466	Rv0466	conserved hypotheticals	3.0	0.0000
Rv0469	umaA1	lipid metabolism	5.7	0.0065
Rv0470c	umaA2	lipid metabolism	1.5	0.0000
Rv0479c	Rv0479c	cell wall and cell processes	2.8	0.0003
Rv0485	Rv0485	regulatory proteins	2.4	0.0106
Rv0489	gpm	intermediary metabolism and respiration	3.4	0.0007
Rv0501	galE1	intermediary metabolism and respiration	3.7	0.0023
Rv0502	Rv0502	conserved hypotheticals	1.1	0.0003
Rv0503c	cmaA2	lipid metabolism	2.5	0.0026
Rv0510	hemC	intermediary metabolism and respiration	2.1	0.0002
Rv0523c	Rv0523c	conserved hypotheticals	1.2	0.0011
Rv0532	PE_PGRS	PE/PPE	1.2	0.0076
Rv0545c	pitA	cell wall and cell processes	2.2	0.0052
Rv0554	bpoC	virulence, detoxification, adaptation	7.2	0.0031
Rv0561c	Rv0561c	intermediary metabolism and respiration	1.3	0.0090
Rv0578c	PE_PGRS	PE/PPE	1.3	0.0003
Rv0608	Rv0608	conserved hypotheticals	1.9	0.0042
Rv0613c	Rv0613c	unknown	4.7	0.0023
Rv0620	galK	intermediary metabolism and respiration	1.7	0.0004
Rv0627	Rv0627	conserved hypotheticals	1.6	0.0007
Rv0632c	echA3	lipid metabolism	2.4	0.0011
Rv0636	Rv0636	unknown	2.0	0.0069
Rv0637	Rv0637	conserved hypotheticals	4.0	0.0047
Rv0642c	mmaA4	lipid metabolism	5.0	0.0008
Rv0643c	mmaA3	lipid metabolism	4.5	0.0028
Rv0655	Rv0655	cell wall and cell processes	1.4	0.0012
Rv0667	rpoB	information pathways	1.1	0.0097
Rv0679c	Rv0679c	cell wall and cell processes	1.7	0.0103
Rv0682	rpsL	information pathways	2.5	0.0023
Rv0685	tuf	information pathways	2.2	0.0002
Rv0692	Rv0692	unknown	8.6	0.0000
Rv0693	pqqE	intermediary metabolism and respiration	12.8	0.0057
Rv0700	rpsJ	information pathways	2.0	0.0059
Rv0701	rplC	information pathways	1.2	0.0073
Rv0702	rplD	information pathways	2.4	0.0035
Rv0703	rplW	information pathways	2.9	0.0016
Rv0704	rplB	information pathways	1.8	0.0054
Rv0705	rpsS	information pathways	1.5	0.0020
Rv0710	rpsQ	information pathways	4.2	0.0017
Rv0711	atsA	intermediary metabolism and respiration	1.2	0.0068
Rv0714	rplN	information pathways	2.4	0.0001

Rv0715	rplX	information pathways	2.1	0.0028
Rv0716	rplE	information pathways	3.1	0.0000
Rv0717	rpsN	information pathways	4.7	0.0015
Rv0719	rplF	information pathways	3.9	0.0006
Rv0721	rpsE	information pathways	1.1	0.0004
Rv0731c	Rv0731c	conserved hypotheticals	1.3	0.0000
Rv0732	secY	cell wall and cell processes	3.5	0.0041
Rv0733	adk	intermediary metabolism and respiration	4.2	0.0036
Rv0741	Rv0741	insertion seqs and phages	1.2	0.0003
Rv0748	Rv0748	conserved hypotheticals	1.6	0.0033
Rv0755c	PPE	PE/PPE	1.4	0.0106
Rv0759c	Rv0759c	conserved hypotheticals	2.4	0.0019
Rv0760c	Rv0760c	conserved hypotheticals	4.6	0.0039
Rv0761c	adhB	intermediary metabolism and respiration	4.5	0.0105
Rv0809	purM	intermediary metabolism and respiration	3.1	0.0000
Rv0814c	sseC2	intermediary metabolism and respiration	4.1	0.0015
Rv0815c	cysA2	intermediary metabolism and respiration	4.3	0.0000
Rv0831c	Rv0831c	conserved hypotheticals	2.5	0.0016
Rv0857	Rv0857	conserved hypotheticals	3.0	0.0000
Rv0863	Rv0863	conserved hypotheticals	2.7	0.0003
Rv0896	gltA2	intermediary metabolism and respiration	2.9	0.0000
Rv0905	echA6	lipid metabolism	2.6	0.0032
Rv0909	Rv0909	unknown	1.8	0.0032
Rv0925c	Rv0925c	unknown	4.6	0.0039
Rv0931c	pknD	regulatory proteins	1.1	0.0027
Rv0932c	pstS	cell wall and cell processes	1.3	0.0064
Rv0934	phoS1	cell wall and cell processes	3.3	0.0030
Rv0951	sucC	intermediary metabolism and respiration	5.0	0.0042
Rv0952	sucD	intermediary metabolism and respiration	3.4	0.0016
Rv1013	pks16	lipid metabolism	2.5	0.0000
Rv1031	kdpC	cell wall and cell processes	2.1	0.0085
Rv1074c	fadA3	lipid metabolism	1.2	0.0008
Rv1076	lipU	intermediary metabolism and respiration	3.0	0.0042
Rv1078	pra	conserved hypotheticals	4.3	0.0019
Rv1083	Rv1083	conserved hypotheticals	1.9	0.0009
Rv1091	PE_PGRS	PE/PPE	1.3	0.0000
Rv1093	glyA	intermediary metabolism and respiration	1.4	0.0036
Rv1096	Rv1096	intermediary metabolism and respiration	2.6	0.0084
Rv1097c	Rv1097c	cell wall and cell processes	1.5	0.0001
Rv1103c	Rv1103c	unknown	1.1	0.0014
Rv1107c	xseB	intermediary metabolism and respiration	2.5	0.0009
Rv1109c	Rv1109c	unknown	1.4	0.0023
Rv1113	Rv1113	unknown	1.2	0.0076
Rv1119c	Rv1119c	unknown	1.5	0.0007
Rv1125	Rv1125	unknown	1.0	0.0072
Rv1129c	Rv1129c	regulatory proteins	1.5	0.0023
Rv1140	Rv1140	conserved hypotheticals	1.4	0.0004
Rv1142c	echA10	lipid metabolism	1.0	0.0012
Rv1155	Rv1155	unknown	1.1	0.0034
Rv1157c	Rv1157c	conserved hypotheticals	2.0	0.0000
Rv1172c	PE	PE/PPE	2.0	0.0002
Rv1177	fdxC	intermediary metabolism and respiration	1.9	0.0036
Rv1182	papA3	lipid metabolism	1.3	0.0033

Rv1185c	fadD21	lipid metabolism	2.0	0.0065
Rv1192	Rv1192	unknown	1.0	0.0015
Rv1194c	Rv1194c	conserved hypotheticals	1.2	0.0057
Rv1196	PPE	PE/PPE	3.4	0.0001
Rv1197	Rv1197	conserved hypotheticals	1.1	0.0101
Rv1201c	Rv1201c	conserved hypotheticals	3.1	0.0024
Rv1211	Rv1211	conserved hypotheticals	1.2	0.0003
Rv1215c	Rv1215c	conserved hypotheticals	3.8	0.0006
Rv1233c	Rv1233c	unknown	4.0	0.0015
Rv1234	Rv1234	unknown	1.0	0.0080
Rv1240	mdh	intermediary metabolism and respiration	2.5	0.0002
Rv1249c	Rv1249c	cell wall and cell processes	2.4	0.0049
Rv1261c	Rv1261c	conserved hypotheticals	2.0	0.0027
Rv1270c	lprA	cell wall and cell processes	3.2	0.0015
Rv1274	lprB	cell wall and cell processes	1.7	0.0038
Rv1277	Rv1277	unknown	2.2	0.0009
Rv1293	lysA	intermediary metabolism and respiration	1.4	0.0039
Rv1295	thrC	intermediary metabolism and respiration	3.1	0.0004
Rv1304	atpB	intermediary metabolism and respiration	14.8	0.0099
Rv1305	atpE	intermediary metabolism and respiration	3.8	0.0006
Rv1306	atpF	intermediary metabolism and respiration	11.1	0.0023
Rv1307	atpH	intermediary metabolism and respiration	4.9	0.0011
Rv1308	atpA	intermediary metabolism and respiration	8.4	0.0041
Rv1309	atpG	intermediary metabolism and respiration	5.4	0.0008
Rv1310	atpD	intermediary metabolism and respiration	5.6	0.0068
Rv1311	atpC	intermediary metabolism and respiration	4.0	0.0000
Rv1312	Rv1312	conserved hypotheticals	3.5	0.0035
Rv1324	Rv1324	unknown	2.4	0.0001
Rv1340	rphA	intermediary metabolism and respiration	2.6	0.0051
Rv1342c	pks14	lipid metabolism	3.2	0.0009
Rv1361c	PPE	PE/PPE	6.2	0.0028
Rv1379	pyrR	regulatory proteins	3.2	0.0003
Rv1391	dfp	intermediary metabolism and respiration	1.3	0.0045
Rv1392	metK	intermediary metabolism and respiration	1.1	0.0005
Rv1395	Rv1395	regulatory proteins	1.4	0.0002
Rv1410c	Rv1410c	cell wall and cell processes	1.6	0.0004
Rv1411c	lprG	cell wall and cell processes	1.6	0.0018
Rv1415	ribA2	intermediary metabolism and respiration	2.7	0.0006
Rv1418	lprH	cell wall and cell processes	1.1	0.0037
Rv1423	Rv1423	regulatory proteins	3.3	0.0042
Rv1424c	Rv1424c	cell wall and cell processes	1.1	0.0023
Rv1425	Rv1425	conserved hypotheticals	2.0	0.0010
Rv1435c	Rv1435c	conserved hypotheticals	5.5	0.0039
Rv1436	gap	intermediary metabolism and respiration	2.8	0.0074
Rv1445c	devB	intermediary metabolism and respiration	1.2	0.0017
Rv1448c	tal	intermediary metabolism and respiration	4.5	0.0042
Rv1449c	tkt	intermediary metabolism and respiration	1.2	0.0088
Rv1451	ctaB	intermediary metabolism and respiration	1.1	0.0102
Rv1469	ctpD	cell wall and cell processes	1.4	0.0013
Rv1475c	acn	intermediary metabolism and respiration	2.5	0.0005
Rv1479	moxR	regulatory proteins	1.1	0.0021
Rv1499	Rv1499	unknown	1.6	0.0002
Rv1515c	Rv1515c	conserved hypotheticals	2.0	0.0014

Rv1517	Rv1517	conserved hypotheticals	1.0	0.0025
Rv1527c	pks5	lipid metabolism	1.5	0.0001
Rv1576c	Rv1576c	insertion seqs and phages	1.3	0.0000
Rv1584c	Rv1584c	insertion seqs and phages	1.2	0.0009
Rv1591	Rv1591	conserved hypotheticals	2.5	0.0012
Rv1594	nadA	intermediary metabolism and respiration	5.0	0.0009
Rv1595	nadB	intermediary metabolism and respiration	3.5	0.0000
Rv1611	trpC	intermediary metabolism and respiration	3.5	0.0025
Rv1613	trpA	intermediary metabolism and respiration	2.8	0.0002
Rv1623c	appC	intermediary metabolism and respiration	3.5	0.0000
Rv1626	Rv1626	regulatory proteins	3.6	0.0008
Rv1630	rpsA	information pathways	1.9	0.0018
Rv1643	rplT	information pathways	1.1	0.0004
Rv1676	Rv1676	intermediary metabolism and respiration	1.5	0.0005
Rv1677	dsbF	cell wall and cell processes	5.0	0.0038
Rv1694	tlyA	virulence, detoxification, adaptation	1.3	0.0023
Rv1697	Rv1697	conserved hypotheticals	4.8	0.0001
Rv1698	Rv1698	conserved hypotheticals	5.8	0.0090
Rv1700	Rv1700	conserved hypotheticals	2.1	0.0036
Rv1703c	Rv1703c	intermediary metabolism and respiration	2.7	0.0000
Rv1731	gabD1	intermediary metabolism and respiration	3.2	0.0009
Rv1743	pknE	regulatory proteins	1.5	0.0002
Rv1747	Rv1747	cell wall and cell processes	4.7	0.0014
Rv1748	Rv1748	unknown	1.4	0.0001
Rv1749c	Rv1749c	cell wall and cell processes	3.4	0.0012
Rv1753c	PPE	PE/PPE	2.3	0.0076
Rv1770	Rv1770	conserved hypotheticals	1.4	0.0004
Rv1778c	Rv1778c	unknown	1.1	0.0049
Rv1798	Rv1798	conserved hypotheticals	1.3	0.0015
Rv1807	PPE	PE/PPE	2.5	0.0000
Rv1809	PPE	PE/PPE	1.3	0.0093
Rv1810	Rv1810	conserved hypotheticals	1.7	0.0046
Rv1816	Rv1816	regulatory proteins	1.9	0.0041
Rv1821	secA2	cell wall and cell processes	1.3	0.0029
Rv1837c	glcB	intermediary metabolism and respiration	2.2	0.0083
Rv1843c	guaB1	intermediary metabolism and respiration	1.2	0.0092
Rv1862	adhA	intermediary metabolism and respiration	1.0	0.0086
Rv1876	bfrA	intermediary metabolism and respiration	2.1	0.0049
Rv1883c	Rv1883c	conserved hypotheticals	1.5	0.0001
Rv1884c	Rv1884c	conserved hypotheticals	7.1	0.0081
Rv1887	Rv1887	unknown	1.8	0.0007
Rv1903	Rv1903	cell wall and cell processes	1.4	0.0031
Rv1904	Rv1904	conserved hypotheticals	1.1	0.0050
Rv1906c	Rv1906c	conserved hypotheticals	1.5	0.0026
Rv1909c	furA	regulatory proteins	1.5	0.0007
Rv1916	aceAb	intermediary metabolism and respiration	1.0	0.0053
Rv1934c	fadE17	lipid metabolism	2.1	0.0004
Rv1947	Rv1947	unknown	4.9	0.0032
Rv1987	Rv1987	cell wall and cell processes	4.8	0.0003
Rv2056c	rpsN2	information pathways	1.7	0.0016
Rv2061c	Rv2061c	unknown	3.9	0.0021
Rv2066	cobI	intermediary metabolism and respiration	1.4	0.0004
Rv2071c	cobM	intermediary metabolism and respiration	2.5	0.0056

Rv2074	Rv2074	unknown	2.3	0.0017
Rv2080	lppJ	cell wall and cell processes	2.2	0.0022
Rv2093c	Rv2093c	cell wall and cell processes	1.3	0.0066
Rv2109c	prcA	intermediary metabolism and respiration	1.2	0.0020
Rv2119	Rv2119	conserved hypotheticals	1.2	0.0068
Rv2127	ansP	cell wall and cell processes	6.6	0.0038
Rv2128	Rv2128	unknown	2.5	0.0014
Rv2138	lppL	cell wall and cell processes	2.2	0.0013
Rv2141c	dapE2	intermediary metabolism and respiration	1.3	0.0020
Rv2145c	wag31	cell wall and cell processes	1.8	0.0089
Rv2147c	Rv2147c	unknown	3.1	0.0048
Rv2160c	Rv2160c	unknown	1.8	0.0004
Rv2165c	Rv2165c	conserved hypotheticals	2.5	0.0044
Rv2171	lppM	cell wall and cell processes	2.7	0.0000
Rv2175c	Rv2175c	regulatory proteins	1.5	0.0010
Rv2181	Rv2181	cell wall and cell processes	1.5	0.0024
Rv2185c	Rv2185c	conserved hypotheticals	3.1	0.0001
Rv2187	fadD15	lipid metabolism	2.0	0.0001
Rv2190c	Rv2190c	virulence, detoxification, adaptation	8.3	0.0059
Rv2191	Rv2191	information pathways	2.1	0.0040
Rv2193	ctaE	intermediary metabolism and respiration	5.6	0.0076
Rv2194	qcrC	intermediary metabolism and respiration	5.4	0.0013
Rv2195	qcrA	intermediary metabolism and respiration	7.6	0.0001
Rv2196	qcrB	intermediary metabolism and respiration	5.5	0.0021
Rv2199c	Rv2199c	cell wall and cell processes	2.4	0.0009
Rv2200c	ctaC	intermediary metabolism and respiration	5.6	0.0014
Rv2209	Rv2209	cell wall and cell processes	2.1	0.0059
Rv2239c	Rv2239c	unknown	1.5	0.0004
Rv2241	aceE	intermediary metabolism and respiration	1.1	0.0001
Rv2245	kasA	lipid metabolism	1.7	0.0051
Rv2259	adhE2	intermediary metabolism and respiration	1.5	0.0044
Rv2269c	Rv2269c	unknown	1.6	0.0004
Rv2271	Rv2271	unknown	6.0	0.0076
Rv2275	Rv2275	unknown	1.1	0.0021
Rv2283	Rv2283	unknown	2.1	0.0048
Rv2291	sseB	intermediary metabolism and respiration	1.9	0.0053
Rv2309c	Rv2309c	insertion seqs and phages	2.5	0.0059
Rv2328	PE	PE/PPE	1.6	0.0003
Rv2334	cysK	intermediary metabolism and respiration	1.6	0.0060
Rv2335	cysE	intermediary metabolism and respiration	1.4	0.0001
Rv2339	mmpL9	cell wall and cell processes	3.2	0.0001
Rv2348c	Rv2348c	unknown	2.8	0.0005
Rv2370c	Rv2370c	conserved hypotheticals	2.1	0.0082
Rv2375	Rv2375	unknown	1.0	0.0001
Rv2376c	Rv2376c	conserved hypotheticals	3.0	0.0001
Rv2391	nirA	intermediary metabolism and respiration	4.2	0.0004
Rv2392	cysH	intermediary metabolism and respiration	2.3	0.0005
Rv2421c	Rv2421c	conserved hypotheticals	1.7	0.0021
Rv2428	ahpC	virulence, detoxification, adaptation	3.3	0.0000
Rv2431c	PE	PE/PPE	2.2	0.0062
Rv2442c	rplU	information pathways	1.7	0.0014
Rv2457c	clpX	intermediary metabolism and respiration	1.5	0.0003
Rv2459	Rv2459	cell wall and cell processes	2.9	0.0009

Rv2461c	clpP	intermediary metabolism and respiration	1.2	0.0052
Rv2465c	rpi	intermediary metabolism and respiration	1.3	0.0003
Rv2467	pepD	intermediary metabolism and respiration	2.2	0.0027
Rv2477c	Rv2477c	cell wall and cell processes	2.1	0.0029
Rv2493	Rv2493	conserved hypotheticals	2.1	0.0035
Rv2500c	fadE19	lipid metabolism	1.5	0.0000
Rv2503c	scoB	lipid metabolism	1.3	0.0023
Rv2516c	Rv2516c	unknown	2.3	0.0060
Rv2590	fadD9	lipid metabolism	1.3	0.0042
Rv2607	pdxH	intermediary metabolism and respiration	1.7	0.0016
Rv2673	Rv2673	cell wall and cell processes	1.6	0.0009
Rv2706c	Rv2706c	unknown	1.6	0.0000
Rv2794c	Rv2794c	conserved hypotheticals	3.1	0.0000
Rv2813	Rv2813	cell wall and cell processes	2.0	0.0042
Rv2843	Rv2843	unknown	1.7	0.0000
Rv2850c	Rv2850c	intermediary metabolism and respiration	1.1	0.0028
Rv2883c	pyrH	intermediary metabolism and respiration	3.6	0.0007
Rv2899c	fdhD	intermediary metabolism and respiration	1.5	0.0001
Rv2900c	fdhF	intermediary metabolism and respiration	1.3	0.0022
Rv2908c	Rv2908c	conserved hypotheticals	2.1	0.0024
Rv2909c	rpsP	information pathways	1.9	0.0032
Rv2914c	pknI	regulatory proteins	1.1	0.0012
Rv2919c	glnB	regulatory proteins	1.0	0.0028
Rv2927c	Rv2927c	conserved hypotheticals	9.2	0.0016
Rv2928	tesA	lipid metabolism	5.3	0.0021
Rv2929	Rv2929	unknown	3.1	0.0017
Rv2930	fadD26	lipid metabolism	1.1	0.0082
Rv2937	drrB	cell wall and cell processes	2.1	0.0002
Rv2950c	fadD29	lipid metabolism	1.5	0.0010
Rv2954c	Rv2954c	unknown	1.1	0.0063
Rv2956	Rv2956	conserved hypotheticals	3.4	0.0024
Rv2958c	Rv2958c	intermediary metabolism and respiration	1.3	0.0015
Rv2982c	gpdA2	lipid metabolism	1.2	0.0011
Rv2994	Rv2994	cell wall and cell processes	2.5	0.0068
Rv3028c	fixB	intermediary metabolism and respiration	1.2	0.0099
Rv3029c	fixA	intermediary metabolism and respiration	1.9	0.0023
Rv3043c	ctaD	intermediary metabolism and respiration	1.2	0.0003
Rv3044	fecB	cell wall and cell processes	1.1	0.0012
Rv3101c	ftsX	cell wall and cell processes	1.5	0.0036
Rv3117	cysA3	intermediary metabolism and respiration	3.9	0.0006
Rv3118	sseC	intermediary metabolism and respiration	3.5	0.0002
Rv3147	nuoC	intermediary metabolism and respiration	2.4	0.0008
Rv3148	nuoD	intermediary metabolism and respiration	2.2	0.0015
Rv3150	nuoF	intermediary metabolism and respiration	1.3	0.0075
Rv3151	nuoG	intermediary metabolism and respiration	3.6	0.0010
Rv3155	nuoK	intermediary metabolism and respiration	1.7	0.0053
Rv3157	nuoM	intermediary metabolism and respiration	1.6	0.0086
Rv3193c	Rv3193c	cell wall and cell processes	2.2	0.0006
Rv3205c	Rv3205c	unknown	1.4	0.0018
Rv3207c	Rv3207c	unknown	1.6	0.0017
Rv3209	Rv3209	conserved hypotheticals	4.5	0.0013
Rv3211	rhlE	information pathways	1.0	0.0000
Rv3213c	Rv3213c	cell wall and cell processes	3.3	0.0002

Rv3224	*Rv3224*	intermediary metabolism and respiration	1.2	0.0007
Rv3246c	*mtrA*	regulatory proteins	2.1	0.0063
Rv3260c	*whiB2*	regulatory proteins	5.2	0.0021
Rv3281	*Rv3281*	conserved hypotheticals	2.5	0.0011
Rv3285	*accA3*	lipid metabolism	1.2	0.0065
Rv3307	*deoD*	intermediary metabolism and respiration	2.1	0.0005
Rv3320c	*Rv3320c*	conserved hypotheticals	1.7	0.0001
Rv3334	*Rv3334*	regulatory proteins	2.0	0.0060
Rv3356c	*folD*	intermediary metabolism and respiration	1.0	0.0001
Rv3376	*Rv3376*	conserved hypotheticals	2.5	0.0040
Rv3377c	*Rv3377c*	intermediary metabolism and respiration	1.7	0.0000
Rv3387	*Rv3387*	insertion seqs and phages	1.9	0.0039
Rv3390	*lpqD*	cell wall and cell processes	2.3	0.0002
Rv3408	*Rv3408*	conserved hypotheticals	1.0	0.0067
Rv3409c	*choD*	lipid metabolism	1.4	0.0044
Rv3413c	*Rv3413c*	unknown	1.1	0.0071
Rv3414c	*sigD*	information pathways	4.7	0.0032
Rv3418c	*groES*	virulence, detoxification, adaptation	3.0	0.0018
Rv3425	*PPE*	PE/PPE	1.4	0.0002
Rv3429	*PPE*	PE/PPE	1.6	0.0001
Rv3443c	*rplM*	information pathways	1.2	0.0102
Rv3465	*rmlC*	intermediary metabolism and respiration	1.3	0.0073
Rv3476c	*kgtP*	cell wall and cell processes	1.7	0.0001
Rv3477	*PE*	PE/PPE	1.4	0.0031
Rv3478	*PPE*	PE/PPE	4.4	0.0000
Rv3495c	*lprN*	cell wall and cell processes	4.8	0.0055
Rv3497c	*Rv3497c*	virulence, detoxification, adaptation	5.9	0.0033
Rv3522	*Rv3522*	regulatory proteins	1.7	0.0053
Rv3524	*Rv3524*	cell wall and cell processes	1.7	0.0048
Rv3528c	*Rv3528c*	unknown	3.6	0.0001
Rv3569c	*Rv3569c*	intermediary metabolism and respiration	1.5	0.0003
Rv3597c	*lsr2*	conserved hypotheticals	1.5	0.0006
Rv3624c	*hpt*	intermediary metabolism and respiration	3.5	0.0001
Rv3635	*Rv3635*	cell wall and cell processes	2.0	0.0008
Rv3648c	*cspA*	virulence, detoxification, adaptation	4.9	0.0043
Rv3669	*Rv3669*	unknown	2.1	0.0097
Rv3673c	*Rv3673c*	intermediary metabolism and respiration	1.7	0.0001
Rv3679	*Rv3679*	cell wall and cell processes	3.4	0.0068
Rv3682	*ponA'*	cell wall and cell processes	2.0	0.0008
Rv3688c	*Rv3688c*	conserved hypotheticals	1.4	0.0039
Rv3694c	*Rv3694c*	conserved hypotheticals	2.6	0.0064
Rv3715c	*recR*	information pathways	1.2	0.0008
Rv3720	*Rv3720*	lipid metabolism	1.1	0.0017
Rv3725	*Rv3725*	intermediary metabolism and respiration	1.6	0.0026
Rv3747	*Rv3747*	conserved hypotheticals	1.3	0.0025
Rv3749c	*Rv3749c*	unknown	2.7	0.0017
Rv3755c	*Rv3755c*	unknown	1.1	0.0053
Rv3757c	*proW*	virulence, detoxification, adaptation	2.7	0.0071
Rv3760	*Rv3760*	conserved hypotheticals	1.0	0.0021
Rv3763	*Rv3763*	cell wall and cell processes	3.2	0.0004
Rv3771c	*Rv3771c*	conserved hypotheticals	1.8	0.0021
Rv3775	*lipE*	intermediary metabolism and respiration	2.1	0.0019
Rv3779	*Rv3779*	cell wall and cell processes	2.0	0.0010
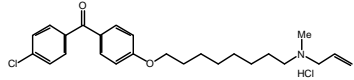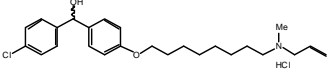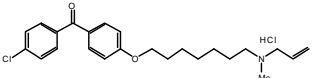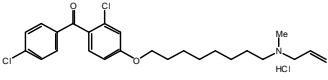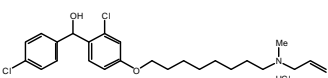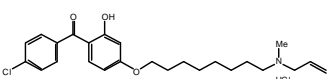
Rv3795	*embB*	cell wall and cell processes	2.6	0.0000
Rv3803c	*fbpC1*	lipid metabolism	1.1	0.0093
Rv3804c	*fbpA*	lipid metabolism	3.6	0.0003
Rv3806c	*Rv3806c*	cell wall and cell processes	2.1	0.0043
Rv3809c	*glf*	cell wall and cell processes	1.2	0.0015
Rv3810	*pirG*	cell wall and cell processes	4.4	0.0094
Rv3815c	*Rv3815c*	intermediary metabolism and respiration	2.1	0.0036
Rv3823c	*mmpL8*	cell wall and cell processes	1.1	0.0011
Rv3824c	*papA1*	lipid metabolism	1.3	0.0004
Rv3846	*sodA*	virulence, detoxification, adaptation	1.5	0.0056
Rv3853	*Rv3853*	intermediary metabolism and respiration	1.7	0.0068
Rv3864	*Rv3864*	conserved hypotheticals	1.2	0.0047
Rv3882c	*Rv3882c*	conserved hypotheticals	1.2	0.0020
Rv3920c	*Rv3920c*	conserved hypotheticals	1.1	0.0080
Rv3921c	*Rv3921c*	cell wall and cell processes	1.1	0.0007

[a]ORF, gene and functional class as described http://genolist.pasteur.fr/TubercuList/

[b]expression index = $\dfrac{\text{expression intensity of RvXXXX in NRP/mean channel expression intensity in NRP}}{\text{expression intensity of RvXXXX in growing cultures/mean channel intensity in growing cultures}}$

[c]variance ANOVA calculated from independent biological replicates

Table S2. Structures of aminoalkoxydiphenylmethane derivatives.

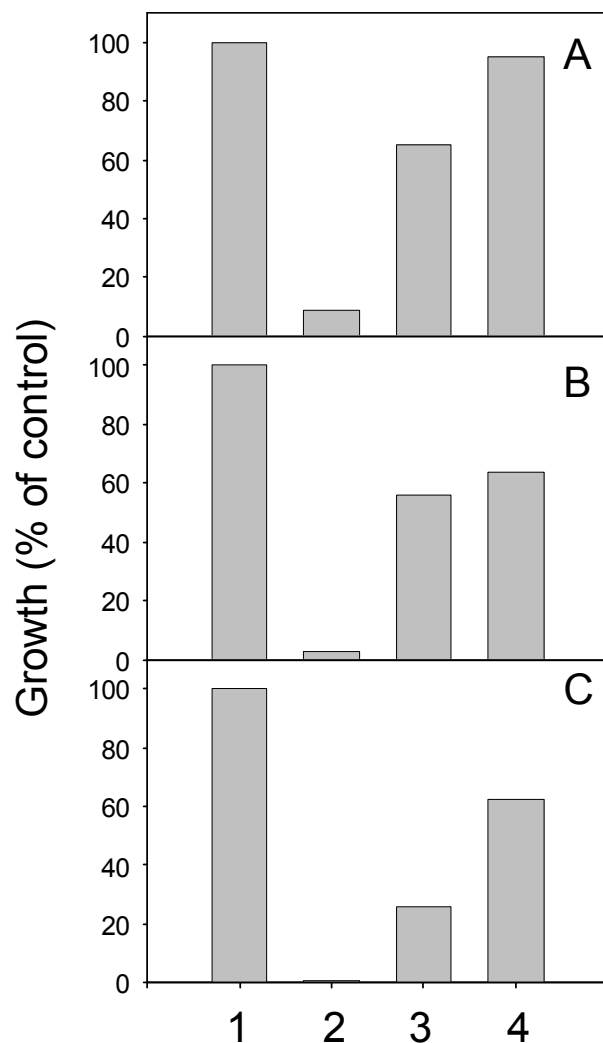| Compound	Structure
CSU-11	
CSU-12	
CSU-13	
CSU-17	
CSU-18	
CSU-20	

Fig. S1. Rescue of bacterial growth and oxygen consumption by menaquinone (Vitamin K2) or phylloquinone (Vitamin K1). *M. smegmatis* was cultured in the presence of 10 (Panel A), 20 (Panel B), or 40 μM (Panel C) Ro 48-8071. Lane 1: control (no Ro 48-8071); Lane 2: no supplementation; Lane 3: medium supplemented with 400 μM vitamin K1; Lane 4: medium supplemented with 400 μM Vitamin K2. Mid-log phase cultures (OD_{600} of 0.5-0.8) grown in 7H9 medium (supplemented with oleic acid, albumin, dextrose and 0.05% Tween 80) were diluted 1:100 and dispensed into 48 well plates and treated with the indicated concentrations of Ro 48-8071 and vitamin K1 or K2.
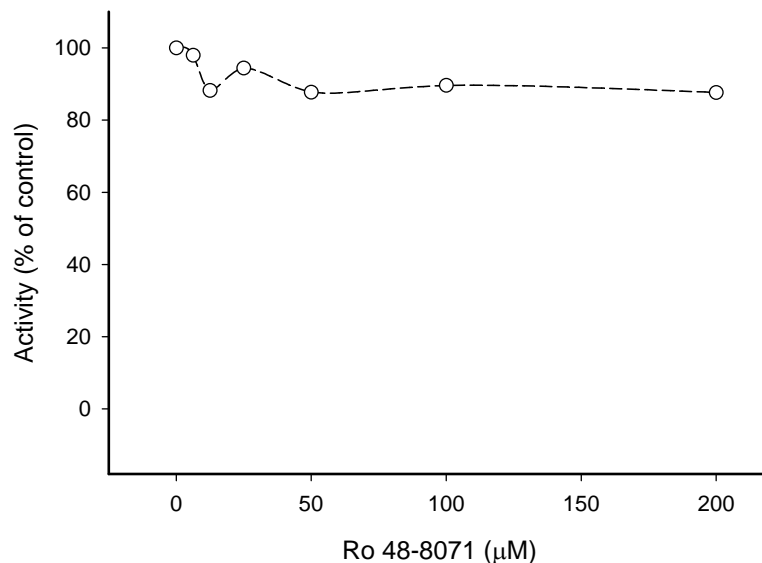
Fig. S2. The effect of Ro 48-8071 on total prenyl diphosphate activity in membranes

isolated from *M. tuberculosis*. Prenyl diphosphate synthase activity was assayed

essentially as previously published (Crick,D.C., Schulbach,M.C., Zink,E.E., Macchia,M.,

Barontini,S., Besra,G.S., and Brennan,P.J. (2000) Polyprenyl phosphate biosynthesis in

Mycobacterium tuberculosis and *Mycobacterium smegmatis. J Bacteriol* **182**: 5771-

5778). Reaction mixtures containing 50 mM MOPS (pH 7.9), 5 mM phosphatase

inhibitor cocktail (Roche), 5 mM MgCl2, 2.5 mM dithiothreitol, 0.3% Triton X-100, 100 µM

farnesyl diphosphate, 30 µM [^{14}C]isopentenyl diphosphate, and 100 µg of

M. tuberculosis membrane protein in a final volume of 200 µl were incubated at 37°C for

60 min. The reaction was stopped by the addition of 1 ml of water saturated with NaCl

and radiolabeled products (prenyl diphosphates) were extracted with n-butanol saturated

with water. An aliquot of the extract was taken and newly synthesized products were

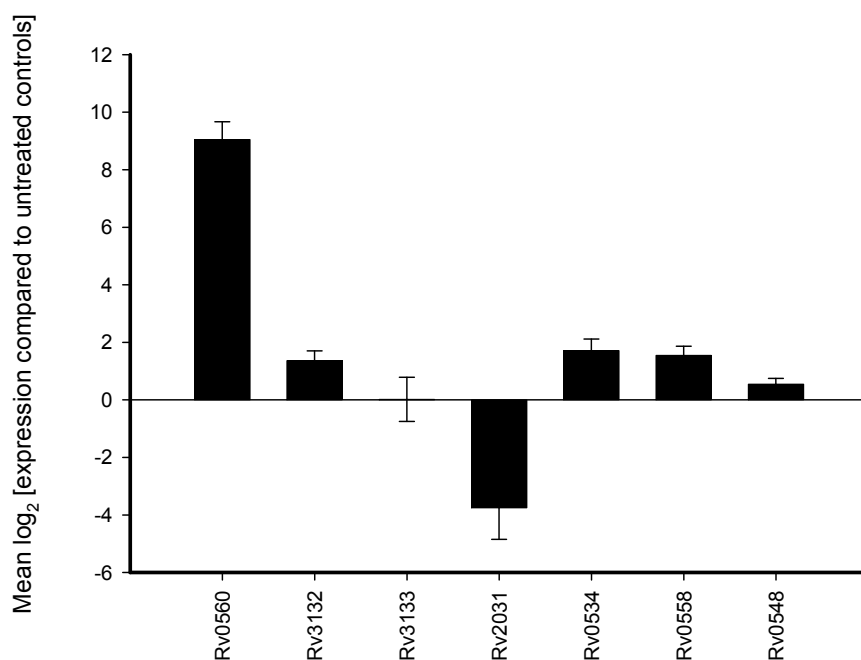quantitated by liquid scintillation spectrometry.

Fig. S3. Quantitative real-time PCR analysis of selected genes in response to treatment with Ro 48-8071. *M. tuberculosis* (H37Rv) was grown to early log phase and subsequently diluted to an OD_{600} of 0.1 OD at 600nm in 7H9 medium containing OADC and some cultures were treated with 50 µM Ro 48-8071 for 6 h at 37 ºC.   Total RNA was isolated as described in Methods and cDNA was generated using the SuperScript™ III First-Strand Synthesis System for RT-PCR (Invitrogen). Primer sequences were designed using the Primer3-web interface. QRT-PCR was performed with an iCycler iQ real-time PCR detection system (Bio-Rad Laboratories) using Platinum® SYBR® Green qPCR SuperMix UDG (Invitrogen).   All reactions were performed in triplicate on independent total RNA preparations. Performance of each primer-set was evaluated using genomic DNA to establish specific amplification characteristics. The number of targets in each sample for each gene corresponding to the threshold cycle for each PCR was determined based on the specific standard curves generated for each primer set.

The relative number of transcripts for each gene was determined from standard curves established for each primer set by linear regression of data obtained using 100 ng, 10 ng, and 1 ng of *M. tuberculosis* (H37Rv) genomic DNA. Amplification results were visualized and analyzed using BioRad iCycler software and results for each gene was determined relative to paired untreated control. Data are average values +/- SD from three independent biological samples.