

1 **SUPPLEMENTAL MATERIAL**

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3 **Functional and genetic characterization of the Tap efflux pump in**
4 ***Mycobacterium bovis* BCG**

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6 ***Ramón-García, S. et al.***

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9 **Description:**

10 Supplemental Material contains tables with the complete list of genes
11 differentially regulated in exponential and stationary growth phase due to
12 inactivation of the Tap efflux pump.

14 **Table S1.** Genes differentially regulated in exponential growth phase due to inactivation of the Tap efflux pump.

Gene ^a	Rv number ^b	q-value ^c	Fold increase ^d	Functional category ^e
-	Rv0011c	0	1.77	Cell wall and cell processes
<i>trpG</i>	Rv0013	0	1.77	Intermediary metabolism and respiration
-	Rv0569	0	1.75	Conserved hypotheticals
-	Rv1405c	0	1.70	Intermediary metabolism and respiration
-	Rv1813c	0	1.78	Conserved hypotheticals
<i>acg</i>	Rv2032	0	1.89	Conserved hypotheticals
-	Rv3127	0	1.71	Conserved hypotheticals

15 ^aGenes were included in the Table if their q-value was ≤ 1 and the fold increase in gene expression was ≥ 1.7 .

16 ^bGenes are annotated as described by the Pasteur Institute on TUBERCULIST (<http://genolist.pasteur.fr/TubercuList/>).

17 ^cq-value indicates the false discovery rate (FDR), probability that the gene was falsely called (calculated by SAM).

18 ^dValues of increase in gene expression by microarrays experiments.

19 ^eFunctional categories as per TUBERCULIST (<http://genolist.pasteur.fr/TubercuList/>).

20 **Table S2.** Genes differentially upregulated in stationary growth phase due to inactivation of the Tap efflux pump.

Gene ^a	Rv number ^b	q-value ^c	Fold increase ^d	qPCR ^e	Functional category ^f
<i>ino1</i>	Rv0046c	0	2.47		Intermediary metabolism and respiration
-	Rv0047c	0	4.54		Conserved hypotheticals
-	Rv0249c	0	2.22		Intermediary metabolism and respiration
-	Rv0250c	0.52	2.63		Conserved hypotheticals
<i>Hsp</i>	Rv0251c	0	12.03	18.14 ± 6.17	Virulence, detoxification, adaptation
-	Rv0302	0.90	2.43		Regulatory proteins
-	Rv0331	0	2.89		Intermediary metabolism and respiration
<i>dnaK</i>	Rv0350	0	8.52	14.21 ± 0.98	Virulence, detoxification, adaptation
<i>grpE</i>	Rv0351	0	10.84		Virulence, detoxification, adaptation
<i>dnaJ1^g</i>	Rv0352	n.a.	n.a.	3.91 ± 0.82	Virulence, detoxification, adaptation
<i>hspR</i>	Rv0353	0	8.12		Virulence, detoxification, adaptation
<i>clpB</i>	Rv0384c	0	6.32		Virulence, detoxification, adaptation
<i>groEL2</i>	Rv0440	0	9.68	20.43 ± 13.50	Virulence, detoxification, adaptation
<i>mce2A</i>	Rv0589	0	2.01		Virulence, detoxification, adaptation
-	Rv0626	0	2.18		Virulence, detoxification, adaptation
-	Rv0627	0	2.12		Virulence, detoxification, adaptation
-	Rv0654	0	8.37		Intermediary metabolism and respiration
<i>mmpS5</i>	Rv0677c	0	2.23		Cell wall and cell processes
-	Rv0678	0	2.72		Conserved hypotheticals
<i>phoP</i>	Rv0757	0	2.10		Regulatory proteins
-	Rv0767c	0	2.92		Conserved hypotheticals
-	Rv0789c	0	7.58		Conserved hypotheticals
-	Rv0790c	0	11.11		Conserved hypotheticals
-	Rv0791c	0	18.08		Conserved hypotheticals
-	Rv0792c	0	7.77		Regulatory proteins

-	Rv0793	0	6.69		Conserved hypotheticals
<i>lpqS</i>	Rv0847	0	5.10		Cell wall and cell processes
<i>cysK2</i>	Rv0848	0	4.52	10.60 ± 9.23	Intermediary metabolism and respiration
-	Rv0850	0.53	1.97		Insertion seqs and phages
-	Rv0922	0	2.06		Insertion seqs and phages
-	Rv1072	0.54	2.12		Cell wall and cell processes
-	Rv1073	0	3.72		Conserved hypotheticals
-	Rv1102c	0	2.06		Virulence, detoxification, adaptation
<i>PPE17</i>	Rv1168c	0	9.96		PE/PPE
<i>PE11</i>	Rv1169c	0	10.80		PE/PPE
-	Rv1265	0	8.68		Conserved hypotheticals
<i>cysN</i>	Rv1286	0	3.29		Intermediary metabolism and respiration
-	Rv1287	0	2.55		Conserved hypotheticals
<i>prfA</i>	Rv1299	0	2.71		Information pathways
<i>atpB</i>	Rv1304	0	2.25		Intermediary metabolism and respiration
<i>trxB1</i>	Rv1471	0	2.56	4.92 ± 1.16	Intermediary metabolism and respiration
<i>Can</i>	Rv1475c	0.97	2.50		Intermediary metabolism and respiration
<i>papA4</i>	Rv1528c	0	2.07		Lipid metabolism
<i>nadA</i>	Rv1594	0	1.97		Intermediary metabolism and respiration
<i>nadB</i>	Rv1595	0	4.39		Intermediary metabolism and respiration
-	Rv1597	0.85	3.69		Conserved hypotheticals
-	Rv1812c	0	5.78		Intermediary metabolism and respiration
-	Rv1813c	0	8.31		Conserved hypotheticals
-	Rv1839c	0	2.23		Virulence, detoxification, adaptation
-	Rv1874	1.25	3.13		Conserved hypotheticals
-	Rv1875	0.86	2.64		Conserved hypotheticals

<i>katG</i>	Rv1908c	0	2.54	3.0 ± 1.3	Virulence, detoxification, adaptation
<i>furA</i>	Rv1909c	0	4.94		Regulatory proteins
-	Rv1943c	0	2.12		Virulence, detoxification, adaptation
-	Rv1990c	0	2.03		Intermediary metabolism and respiration
<i>ctpG</i>	Rv1992c	0	3.32		Cell wall and cell processes
<i>cmtR</i>	Rv1994c	0	4.50		Regulatory proteins
-	Rv2010	0	2.34		Virulence, detoxification, adaptation
-	Rv2016	0	2.62		Conserved hypotheticals
-	Rv2020c	0	1.84		Conserved hypotheticals
-	Rv2021c	0	3.39		Regulatory proteins
-	Rv2022c	0.38	3.01		Conserved hypotheticals
-	Rv2034	0.38	6.34		Regulatory proteins
-	Rv2035	0	6.24		Conserved hypotheticals
-	Rv2036	0	3.48		Intermediary metabolism and respiration
-	Rv2052c	0.20	2.02		Conserved hypotheticals
-	Rv2053c	0.53	2.26		Cell wall and cell processes
-	Rv2103c	0.20	2.14		Virulence, detoxification, adaptation
-	Rv2104c	0	2.89		Virulence, detoxification, adaptation
<i>Mez</i>	Rv2332	0	4.01	5.16 ± 2.52	Intermediary metabolism and respiration
-	Rv2466c	0	5.78		Conserved hypotheticals
-	Rv2516c	0	3.94		Conserved hypotheticals
-	Rv2517c	0	3.17		Conserved hypotheticals
-	Rv2602	0	2.32		Virulence, detoxification, adaptation
-	Rv2617c	0	4.72		Cell wall and cell processes
-	Rv2642	0	8.59		Regulatory proteins
-	Rv2693c	0	2.56		Cell wall and cell processes
-	Rv2694c	0	3.95		Conserved hypotheticals

-	Rv2743c	0	2.12		Cell wall and cell processes
<i>35kd_ag</i>	Rv2744c	0	3.43		Conserved hypotheticals
-	Rv2837c	0	3.56		Conserved hypotheticals
<i>rbfA</i>	Rv2838c	0.79	1.83		Information pathways
<i>infB</i>	Rv2839c	0	2.46		Information pathways
-	Rv2865	0	3.82		Virulence, detoxification, adaptation
-	Rv2912c	0	6.81		Regulatory proteins
-	Rv2913c	0	24.75		Intermediary metabolism and respiration
-	Rv2949c	0.38	2.10		Conserved hypotheticals
<i>nrdE</i>	Rv3051c	0	3.00		Information pathways
<i>nrdI</i>	Rv3052c	0	4.07		Information pathways
<i>nrdH</i>	Rv3053c	0	4.30		Information pathways
-	Rv3122	0	1.99		Conserved hypotheticals
-	Rv3160c	0	2.86		Regulatory proteins
-	Rv3182	0.20	3.16		Conserved hypotheticals
-	Rv3269	0	7.03		Virulence, detoxification, adaptation
-	Rv3272	0	3.34		Virulence, detoxification, adaptation
-	Rv3334	0.38	1.97		Regulatory proteins
<i>groEL1</i>	Rv3417c	0	7.51	17.55 ± 11.64	Virulence, detoxification, adaptation
<i>groES</i>	Rv3418c	0	6.35		Virulence, detoxification, adaptation
<i>ispF</i>	Rv3581c	0	2.91		Intermediary metabolism and respiration
-	Rv3833	0	2.57		Regulatory proteins
<i>bfrB</i>	Rv3841	0	3.14		Intermediary metabolism and respiration
<i>whiB6</i>	Rv3862c	0	6.00	4.39 ± 0.93	Regulatory proteins
-	Rv3863	0	2.68		Conserved hypotheticals
-	Rv3864	0	5.48		Conserved hypotheticals
-	Rv3865	0	2.16		Conserved hypotheticals

-	Rv3866	0	2.44	Conserved hypotheticals
-	Rv3880c	0	2.27	Conserved hypotheticals
-	Rv3881c	0	2.09	Conserved hypotheticals
<i>trxC</i>	Rv3914	0	3.31	Intermediary metabolism and respiration

21 ^aGenes were included in the Table if their q-value was ≤ 1 (unless included as part of an operon) and the fold increase in
 22 gene expression was ≥ 1.7 .

23 ^bGenes are annotated as described by the Pasteur Institute on TUBERCULIST (<http://genolist.pasteur.fr/TubercuList/>).

24 ^cq-value indicates the false discovery rate (FDR), probability that the gene was falsely called (calculated by SAM).

25 ^dValues of increase in gene expression by microarrays experiments.

26 ^eData represent mean values of two biological independent experiments performed in duplicate. Standard deviation in
 27 shown.

28 ^fFunctional categories as per TUBERCULIST (<http://genolist.pasteur.fr/TubercuList/>).

29 ^gThis gene was included in the table based on the results obtained by RT-PCR, since no data were obtained from the
 30 DNA microarrays experiments.

31 n.a., not available.

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33 **Table S3.** Genes differentially downregulated in stationary growth phase due to inactivation of the Tap efflux pump.

Gene ^a	Rv number ^b	q-value ^c	Fold decrease ^d	qPCR ^e	Functional category ^f
-	Rv0043c	0	0.48		Regulatory proteins
-	Rv0079	0	0.49		Conserved hypotheticals
-	Rv0080	0.38	0.59		Conserved hypotheticals
<i>fbpC</i>	Rv0129c	0	0.56		Lipid metabolism
<i>mce1E</i>	Rv0173	0.55	0.51		Cell wall and cell processes
-	Rv0188	0	0.50		Cell wall and cell processes
-	Rv0373c	0	0.22		Intermediary metabolism and respiration
-	Rv0374c	0.86	0.42		Intermediary metabolism and respiration
<i>galE2</i>	Rv0501	0	0.44	0.50 ± 0.17	Intermediary metabolism and respiration
<i>fadB</i>	Rv0860	0	0.38		Lipid metabolism
<i>PE_PGRS15</i>	Rv0872c	0	0.40		PE/PPE
<i>metS</i>	Rv1007c	0.84	0.57		Information pathways
<i>esxJ</i>	Rv1038c	0.95	0.45		Cell wall and cell processes
<i>sigE</i>	Rv1221	0	0.37		Information pathways
<i>eccB5</i>	Rv1782 ^g	n.a.	n.a.	0.43 ± 1.38	Cell wall and cell processes
<i>eccCb5</i>	Rv1784	0	0.44	0.36 ± 0.27	Cell wall and cell processes
<i>PPE26</i>	Rv1789 ^g	n.a.	n.a.	0.31 ± 0.11	PE/PPE
<i>esxM</i>	Rv1792	0.51	0.44	0.13 ± 0.01	Cell wall and cell processes
<i>esxN</i>	Rv1793 ^g	n.a.	n.a.	0.28 ± 0.02	Cell wall and cell processes
<i>mycP5</i>	Rv1796	0	0.42		Intermediary metabolism and respiration
-	Rv1797	0	0.53		Cell wall and cell processes
<i>eccA5</i>	Rv1798 ^g	n.a.	n.a.	0.39 ± 0.12	Cell wall and cell processes
<i>Ndh</i>	Rv1854c	0	0.49		Intermediary metabolism and respiration
-	Rv1862	0.51	0.57		Intermediary metabolism and respiration

<i>ahpE</i>	Rv2238c	0.92	0.48		Virulence, detoxification, adaptation
-	Rv2405	0	0.54		Conserved hypotheticals
-	Rv2418c	0	0.49		Conserved hypotheticals
-	Rv2621c	0	0.42		Regulatory proteins
-	Rv2721c	0.20	0.41		Cell wall and cell processes
<i>Rip</i>	Rv2869c	0.54	0.59		Cell wall and cell processes
<i>mpt70</i>	Rv2875	0	0.36		Cell wall and cell processes
<i>adhC</i>	Rv3045	0	0.40		Intermediary metabolism and respiration
<i>nuoJ</i>	Rv3154	0.20	0.51		Intermediary metabolism and respiration
-	Rv3222c	0	0.55		Conserved hypotheticals
<i>sugI</i>	Rv3331	0	0.12	0.01 ± 0.00	Cell wall and cell processes
<i>nagA</i>	Rv3332	0.38	0.38		Cell wall and cell processes
<i>esxU</i>	Rv3445c	0	0.30		Cell wall and cell processes
<i>Crp</i>	Rv3676	0	0.45		Regulatory proteins
<i>Asd</i>	Rv3708c	0.55	0.41		Intermediary metabolism and respiration
<i>proX</i>	Rv3759c	0	0.51		Virulence, detoxification, adaptation

34 ^aGenes were included in the Table if their q-value was ≤ 1 (unless it was included as part of an operon) and the fold
35 decrease in gene expression was ≤ 0.7 .

36 ^bGenes are annotated as described by the Pasteur Institute on TUBERCULIST (<http://genolist.pasteur.fr/TubercuList/>).

37 ^cq-value indicates the false discovery rate (FDR), probability that the gene was falsely called (calculated by SAM).

38 ^dValues of decrease in gene expression by microarrays experiments.

39 ^eData represent mean values of two biological independent experiments performed in duplicate. Standard deviation in
40 shown.

41 ^fFunctional categories as per TUBERCULIST (<http://genolist.pasteur.fr/TubercuList/>).

- 42 ⁹This gene was included in the table based on the results obtained by RT-PCR, since no data were obtained from the
43 DNA microarrays experiments.
44 n.a., not availabl