1 SUPPLEMENTARY MATERIAL

Supplementary Figure S1

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3 А 10000 2000 4000 8000 4 DraIII DraIII Τ. 5 probe I HpaI HpaI ClaI probe I fgdl pks6 ackA pknG Rv0412c glnH pta Rv0406c 6 7 С В WT ND1 WT ND1 5.7 kb 1.2 kb 0.8 kb 1.3 kb 8 9 10 D 4000 6000 8000 2000 10000 L 11 PstI PstI PstI Γ Т probe II 12 HindⅢ KpnI HindIII probe II pks6 ackA pknG Rv0412c fgdl 4

pta

RV0406c

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glnH









used to validate the Δpta mutant (ND7): *Dra* III digestion and *Hind* III-*Kpn* I double digestion. E) Southern blot showing the result of the *Dra* III digestion. F) Southern blot showing the results of the *Hpa* I-*Cla* I double digestion. G) Explains the strategy used to validate the Δacs mutant (ND9): the *Age* I digestion. H) Southern blot showing the result of the *Age* I digestion. For further details see method section.

38 METHOD

Verification of $\triangle ackA$, $\triangle pta$ and $\triangle acs$ knock-out mutants in *Mtb* by Southern Blot 39 analysis. To analyze the knock-out mutants for gene deletion by allelic exchange, different 40 DNA probes were generated by PCR from chromosomal DNA of Mtb H37Rv. To amplify a 41 42 501 bp probe corresponding to the sequence downstream of the ackA gene the following primers were used: 5'-caccggttgcgcaagtac-3', and 5'-gcaccaaccacatcctcg-3'. The 621 bp 43 probe corresponding to the sequence upstream of the *pta* gene was amplified by the following 44 primers: 5'-ggctttcgccaccatggg-3', and 5'-ttcgacggcttcgtcggg-3'. The primer 45 pair 5'-gcggtgatcagcagcttg-3', and 5'-cacatccgtgagtgagtc-3' was used to design a DNA probe to 46 47 analyze the Δacs mutant. The PCR products were labelled with digoxigenin dUTP (Roche Applied Science) and were used to detect the size change in fragments of digested genomic 48 DNA in the wild type and the mutant strains. Pst I-digestion of chromosomal DNA produced 49 50 a 1,235 bp fragment in the wild type, and an 861 bp fragment in the $\Delta ackA$ mutant. Double digestion of genomic DNA by Hind III and Kpn I produced a 1,294 bp fragment in the wild 51 type and a 5,681 bp fragment in the $\Delta ackA$ mutant. Dra III digested chromosomal DNA 52 produced a 3,593 bp fragment in the wild type and a 1,973 bp fragment in the Δpta mutant. 53 The *Hpa* I and *Cla* I digestion produced a 2,761 bp fragment in the wild type and a 3,331 bp 54 55 fragment in the Δpta mutant. Age I digested chromosomal DNA produced a 2,524 bp fragment in the wild type and a 1,627 bp fragment in the Δacs mutant. For detection, the 56 fragments were separated by agarose gel electrophoresis, transferred to a nylonmembrane, and 57

hybridized with the respective probe. Southern blotting and DNA hybridization wereperformed according to the manufacturer's instructions (Roche Applied Science).

61 Supplementary Figure S2



Figure S2: Growth of *Mtb* wild type strain on different carbon substrates. *Mtb* H37Rv was grown for 10 days in standing culture tubes in a standard growth medium containing 7H9 broth supplemented with 0.5% AS and 0.05% tween 80 (red squares). To analyze the impact of the carbon source on growth, different substrates were added to the standard medium (black squares) and growth was followed by measuring OD_{600} . Growth on standard medium with and without additional carbon source was compared for each substrate. Data represents the mean of three independent experiments, error bars indicate the SD.



Figure S3: Impact of a defined basic medium on growth and acetate secretion in the *Mtb* wild type strain. *Mtb* H37Rv was grown for 10 days in standing cultures. The 7H9 based medium contained 0.5% AS of a fatty acid free albumin and 0.05% tyloxapol. The medium was supplemented with different carbon substrates and acetate secretion (A) and growth (B) were detected at indicated time points. To analyze the effect of carbon supplementation, growth of *Mtb* on the basic medium (red squares) was compared to growth in the presence of

- 80 the respective carbon source (black squares). Data shows one representative of two
- 81 independent experiments.