

Figure S1: Schematic of the shikimate pathway and additional terminal pathways leading to the aromatic compounds. PEP: phosphoenolpyruvate; E4: D-erythrose 4-phosphate; *aroG*: gene encoding DAHP synthase; DAHP: 3-deoxy-d-arabino-heptulosonate-7-phosphate; *aroB*: gene encoding DHQ synthase; DHQ: 3-dehydroquininate; *aroD*: gene encoding DHQ dehydratase; DHS: 3-dehydroshikimate; *aroE*: gene encoding SKH dehydrogenase (SDH); SKH: shikimate; *aroK*: gene encoding SKH kinase; S3P: shikimate- 3-phosphate; *aroA*: gene encoding EPSP synthase; EPSP: 5-enolpyruvylshikimate-3-phosphate; *aroF*: gene encoding chorismate synthase.

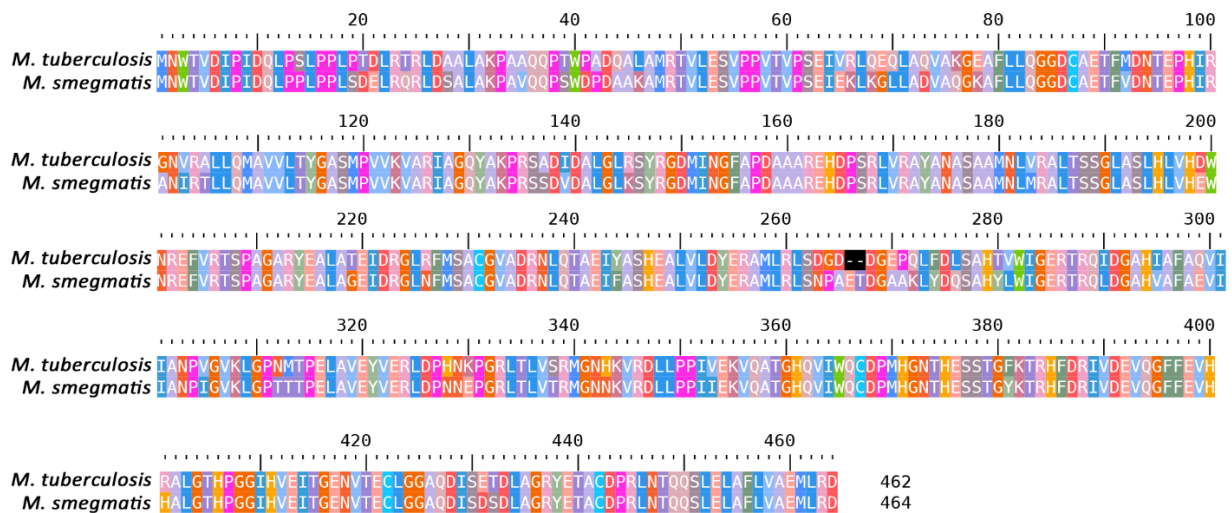


Figure S2: Pairwise alignment of *aroG* from *M. tuberculosis* and MSMEG_4244 from *M. smegmatis*. Identity: 405/464 (87.3%). Similarity: 436/464 (94.0%). Gaps: 2/464 (0.4%). Alignment parameters: Matrix: EBLOSUM62; Gap penalty: 10.0; Extend penalty: 0.5.

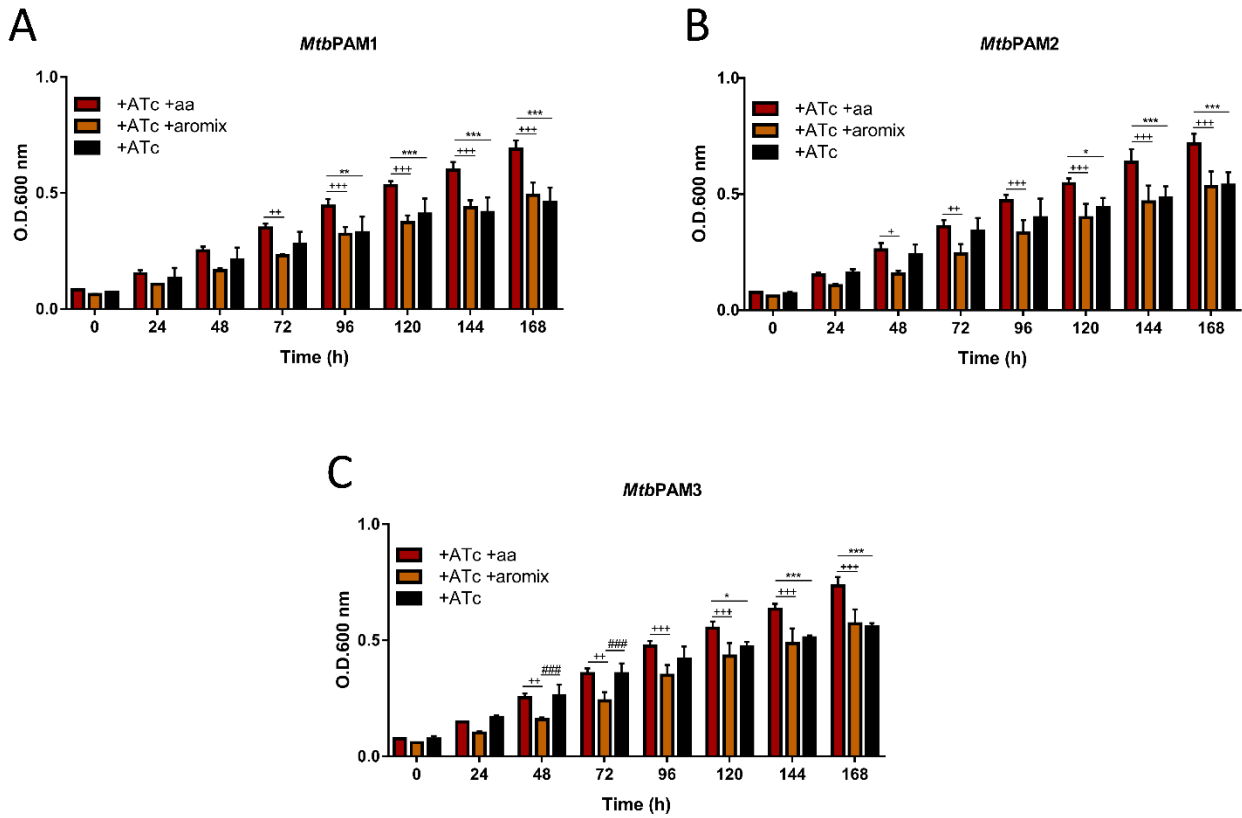


Figure S3: Comparative effect of *aroG* silencing on *M. tuberculosis*. Comparison of *aroG*-silencing cultures growth in presence of ATc 100ug/mL in medium supplemented with amino acids or aromix knockdown directed to PAM1 (A), PAM2 (B) or PAM3 (C). Mean \pm standard deviation from biological and technical duplicates. For *=P value <0.03, **=P value <0.002 and ***=P value <0.001.

Table S1 - qQT-PCR primers and probes used in this study.

Target	Primer Forward	Primer Reverse	Probe
Rv2178c	5'ctacagaccgccgaaatctatg 3'	5' gtgcggacaggtcaaaca 3'	/56-FAM/catgttgag/ Zen/gtgtccgacggtga/3IABkFQ/
MSMEG_4244	5' ggtacaagaccaggcacttc 3'	5' cgagacattcggtgacgttt 3'	/56-FAM/tcgacgagg/ Zen/tgcagggcttt/3IABkFQ/
SigA (<i>M. tuberculosis</i>)	5' catggtcgaggtgatcaacaa 3'	5' gggatgatgccatctctttgg 3'	/56-FAM/cattcaacg/ Zen/cgagctgctgca/3IABkFQ/
SigA (<i>M. smegmatis</i>)	5' cgagaagttcgactacaccaag 3'	5' ccatgtgcaccgggatac 3'	/56-FAM/tggcgtagg/Zen/ tcgagaactttagc/3IABkFQ/
inhA	5' gcattcgattgggtcatgc 3'	5' atacgaatacggagatgtg 3'	56-FAM/atgggcatc/Zen/aaccgt tcttca/3IABkFQ/
mmpL3	5' ctggtaacgctggtgatgaa 3'	5' ggcaggtattctcgctgatac 3'	/56-FAM/tggtggtga/Zen/tggtgct gctgat/3IABkFQ/

Table S2 – Essentiality and vulnerability of *aro* genes from *M. tuberculosis* and *M. smegmatis*.

<i>M. tuberculosis</i>				<i>M. smegmatis</i>			
gene	Rv number	Essentiality ¹	VI ²	gene	MSMEG number	Essentiality ³	VI ²
<i>aroG</i>	Rv2178c	essential	-13.36	<i>aroG</i>	MSMEG_4244	uncertain	-0.2
<i>aroB</i>	Rv2538c	essential	-9.2	<i>aroB</i>	MSMEG_3033	uncertain	-4.93
<i>aroD</i>	Rv2537c	essential	-5.92	<i>aroQ</i>	MSMEG_1922	uncertain	-3.52
				<i>aroQ</i>	MSMEG_2532	uncertain	0.11
<i>aroE</i>	Rv2552c	NonEssential	-9.01	<i>aroE</i>	MSMEG_3028	uncertain	-4.02
<i>aroK</i>	Rv2539c	Essential	-10.16	<i>aroK</i>	MSMEG_0453	uncertain	0.24
				<i>aroK</i>	MSMEG_3031	uncertain	-7.18
<i>aroA</i>	Rv3227	Essential	-9.00	<i>aroA</i>	MSMEG_1890	uncertain	-7.56
<i>aroF/aroC</i>	Rv2540c	Essential	-11.38	<i>aroC</i>	MSMEG_3030	uncertain	-9.05

¹TnSeq essentiality predictions for *M. tuberculosis* taken from DeJesus et al. 2017 (PMID: 28096490).

²VI: Vulnerability Index. Vulnerability predictions taken from Bosch & DeJesus et al. Cell. 2021 (PMID: 34297925).

³TnSeq essentiality predictions for *M. smegmatis* taken from Dragset et al. 2019 (PMID: 31388080). Data obtained from <https://pebble.rockefeller.edu>.