

1 **Supplementary Information.**

2 **Text S1**

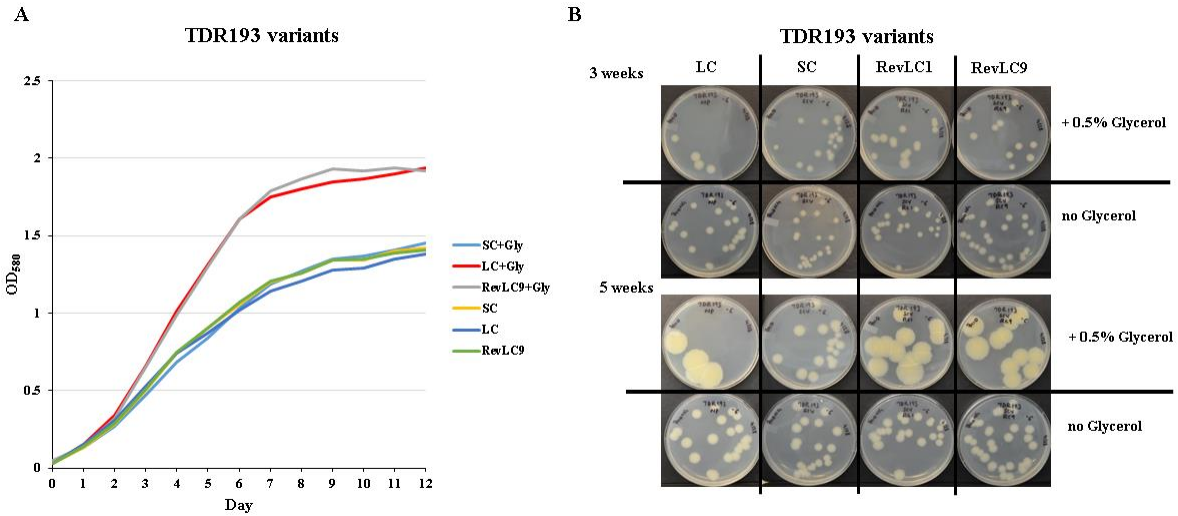
3 **Reversible drug resistance in *Mycobacterium bovis* BCG.** Previously, we had selected
4 BCG mutants resistant to pyrazinoic acid (POA)(1). Mutants with high level POA resistance
5 ($MIC_{50} \geq 496 \mu\text{g/ml}$) had missense mutations in the presumed molecular target of POA, the
6 coenzyme A biosynthetic gene *panD*, encoding aspartate decarboxylase. However, we also
7 identified POA-resistant mutants with lower MICs ($MIC_{50} = 248 \mu\text{g/ml}$). Among these were
8 strains that produced smaller colonies (BCG POA4) than the wild-type strain on media
9 containing glycerol (Fig. S3A). These SCs were found to have a C (frameshift) insertion in the
10 10C homopolymeric tract (*M. bovis glpK*, nucleotide 566 to 575) of *glpK* (BCG_3755c) (Fig.
11 S3B), compared to the BCG Pasteur 1173P2 reference sequence (GenBank ID: NC_008769.1).
12 As in the spontaneous *glpK* frameshift in *M. tuberculosis*, the BCG SCs showed increased
13 growth at sub-MIC concentrations of several antibiotics, in this case INH, EMB and RIF (Fig.
14 S3C-E). LC revertants with reconstituted *glpK* open reading frames occurred in the absence of
15 antibiotic selection, and these LCs were now fully susceptible to all antibiotics tested including
16 POA (Fig. S3F).

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18 **Supplementary Figures**

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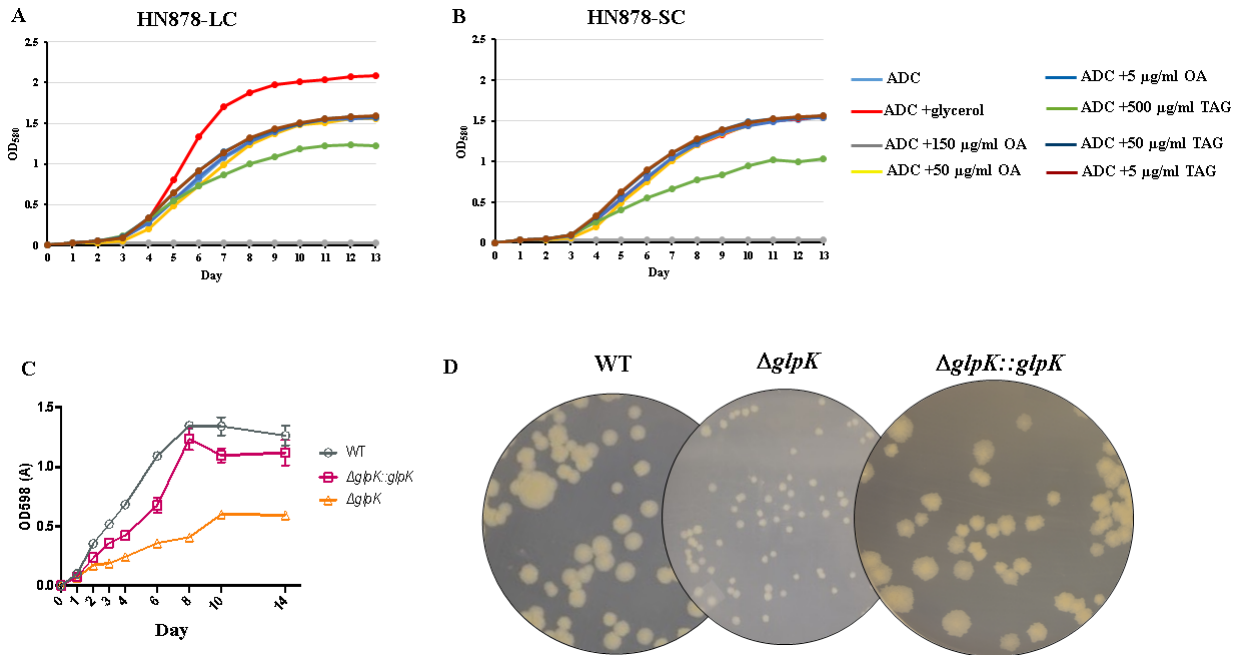
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22 **Fig. S1. Growth kinetics of *M. tuberculosis* small and large colonies in the presence of**
23 **glycerol. (A)** TDR193 variants were grown in 7H9 + OADC (Oleic acid-Albumin-NaCl-
24 Dextrose-Catalase) containing or not-containing glycerol. Growth of each strain was followed by
25 measuring optical density at 580nm (OD₅₈₀). A representative graph of three independent
26 experiments is shown. **(B)** The cultures were plated on 7H10 + OADC media containing or not-
27 containing glycerol and incubated at 37°C for 5 weeks. Colony sizes were visualized at 3 and 5
28 weeks. A representative growth on 7H10 agar medium of three independent experiments is
29 shown. LC: TDR193-LC (large colony); SC: TDR193-SC (small colony); RevLC1: TDR193-
30 SC-RevLC1 (revertant large-colony #1); RevLC9: TDR193-SC-RevLC9 (revertant large-colony
31 #9); + Gly: with 1% glycerol.

32

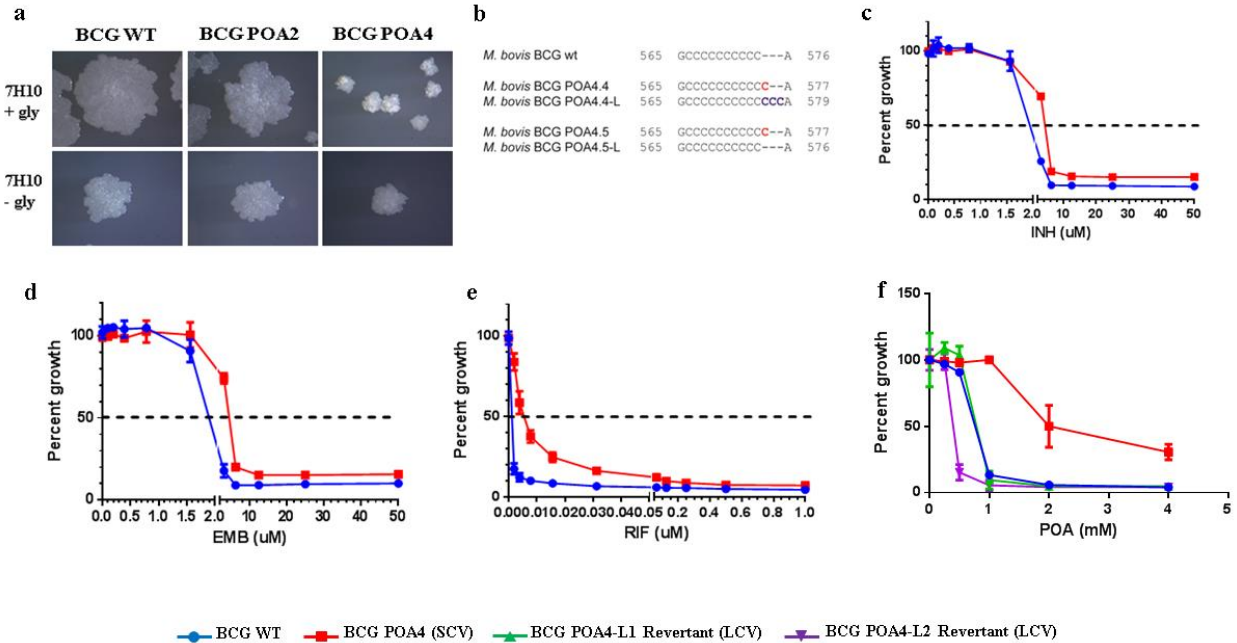


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35 **Fig. S2. Growth kinetics of *M. tuberculosis* small and large colonies in the presence of**
 36 **various carbon sources and antibiotics. (A) HN878-LC and (B) HN878-SC were grown in**
 37 **7H9 + ADC (Albumin-NaCl-Dextrose-Catalase) medium supplemented with various carbon**
 38 **sources, glycerol (trihydroxy sugar alcohol), OA (oleic acid, free fatty acid), or TAG (glyceryl**
 39 **trioleate, triglyceride derived from glycerol and three units of oleic acid). (C) Slow growth of**
 40 **H37Rv $\Delta glpK$ compared to wild type (WT) and complement strain ($\Delta glpK::glpK$) in 7H9**
 41 **supplemented with oleic acid-Albumin-NaCl-Dextrose-Catalase and 0.5% glycerol. (D) The**
 42 **H37Rv $\Delta glpK$ mutant showed a small colony phenotype on 7H10 medium supplemented with**
 43 **0.5% glycerol compared to WT and complement $\Delta glpK::glpK$.**

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Fig. S3. *M. bovis* BCG small colony variants and drug susceptibility. (A) Colony morphology of POA-resistant *panD* mutant BCG POA2 and POA-resistant *glpK* mutant BCG POA4 in comparison with BCG wild-type (WT) on 7H10 agar with 0.5% glycerol and without glycerol (gly). Bacteria were grown at 37°C for 4 weeks. Isolation and characterization of *panD* mutant BCG POA2 and *glpK* mutant BCG POA4 has been described previously(1): BCG POA2 harbors a missense mutation Leu132Arg (T395G) in *panD* and BCG POA4 harbors +1 frameshift mutations in *glpK* (Ins567C) and *mas* (Ins4999G) respectively. (B) *glpK* slippage site sequences of WT *M. bovis* BCG and various mutant strains. BCG POA4.4 and POA 4.5 harbor +1 frameshifted *glpK* with 1 C (indicated in red) inserted while their LC variants BCG POA4.4-L harbor doublet C insertions (indicated in blue) and BCG POA4.5-L display a 1 C deletion in *glpK* as compared to their respective parent strains. In addition, POA4.4-L and POA4.5-L harbor *panD* missense mutations (Δ 417/418A/T and A62G/His21Arg, respectively), conferring POA resistance. Differential susceptibility of BCG variants to (C) INH, (D) EMB, (E) RIF, and (F) POA was determined by percent growth using OD₆₀₀ measurement, compared to no treated control.

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63 **Supplementary Tables**64 **Table S1. Resistance profile and the *glpK* 7C homopolymeric tract genotypes of clinical *M.***
65 ***tuberculosis* isolates.**

TDR strain (s)	Genotype of 7C homopolymeric tract	Resistance
5; 17; 22; 41; 63; 64; 77; 95; 146; 163; 180; 182; 213	WT	---
1; 34	WT	RIF
52; 83	WT	INH
94; 126; 128	WT	EMB
10; 28; 51; 76; 119; 129	WT	RIF; INH
218	WT	RIF; EMB
42; 93; 104; 105; 120; 121; 123; 144	WT	INH; EMB
7; 11; 13; 19; 21; 50; 56; 58; 59; 67; 69; 70; 72; 73; 74; 87; 101; 106; 111; 114; 115; 117; 122; 124; 133; 135; 150; 151; 154; 155; 162; 168; 176	WT	RIF; INH; EMB
80	InsC	---
148	InsC	RIF; INH
6; 31; 89; 100; 116; 152; 175; 216	InsC	RIF; INH; EMB
29; 33; 81	WT and InsC	---
12; 18	WT and InsC	RIF
143	WT and InsC	EMB
86; 189	WT and InsC	RIF; INH
85; 132	WT and InsC	INH; EMB
32; 65; 71; 99; 113; 196	WT and InsC	RIF; INH; EMB

66 WT, wild-type; InsC, insertion of C; RIF, rifampicin, INH, isoniazid; EMB, ethambutol

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68 **Table S2. Mutations in homopolymeric tracts were identified in whole-genome shotgun**
69 **contigs of clinical *M. tuberculosis* isolates and complete genome sequences of reference**
70 **strains.**

Gene or intergenic	Gene coordinates	Homopolymeric tract coordinates (#N)	Number of mutants identified in NCBI database	Mutations in reference strains
Rv0759c- Rv0760c	853825-854157 854267-854686	854253-854261 (9C)	>5	CDC1551; CCDC5079; CCDC5180; F11; KZN1435; KZN4207; KZN605 (Δ C); K (Δ CC)
PPE13	976872-978203	976898-976906 (9G)	>5	F11; KZN1435; KZN4207; KZN605 (InsC); K (Δ C)
pknA	17467-18762	17897-17904 (8G)	0	None
PPE13	976872-978203	976890-976897 (8T)	>5	None
wag22	1989833-1992577	1992324-1992331 (8C)	>5	CDC1551 (Δ C)
Rv2081c	2338065-2338505	2338195-2338202 (8C)	>5	F11; CCDC5180 (InsC); K (Δ C); KZN605; KZN4207 (Ins12C); KZN1435 (InsCs and other mutations)
lppZ	3364709-3365830	3364856-3364863 (8C)	1	None
dnaA-dnaN	1-1524 2052-3260	1553-1559 (7A)	2	None
bioF2	34295-36610	36471-36477 (7C)	>5	KZN1435; KZN4207; KZN605 (InsC)
Rv0064	68620-71559	71454-71460 (7C)	0	None
ctpA	100583-102868	101500-101506 (7G)	3	None
Rv0161	100583-102868	101500-101506 (7G)	>5	CDC1551 (InsC) (the insertion is confirmed by Sanger sequencing)
mmpL11	238392-241292	238808-238814 (7C)	0	None
htdX	289812-290654	290164-290170 (7T)	0	None

vapC2-Rv0302	364044-364469 364605-365237	364499-364505 (7G)	>5	None
PPE6	372820-375711	373027-373033 (7A)	Indel mutants	None
lpqK	477327-478556	478228-478234 (7T)	1	None
Rv0497	587377-588309	587729-587735 (7C)	0	None
PE_PGRS6	622793-624577	623675-623681 (7G)	5	None
menC	644490-645470	644505-644511 (7C)	1	None
mce2D	690501-692027	691888-691894 (7C)	>5	None
lldD1-Rv0695	793335-794525 794715-795470	794673-794679 (7A)	4	None
Rv0698	798833-799444	799137-799143 (7C)	>5	None
PE_PGRS10	838451-840856	839546-839552 (7G)	0	None
Rv0774c	867440-868351	868161-868167 (7G)	3	None
Rv0805	898831-899787	898906-898912 (7G)	3	None
mshD-phoT	911736-912683 912726-913502	912695-912701 (7C)	2	None
Rv0822c	914257-916311	914502-914508 (7A)	2	None
PE_PGRS13	925361-927610	926306-926312 (7G) 927020-927026 (7G)	4 0	None
PE_PGRS14	927837-930485	928286-928292 (7C) 929018-929024 (7C)	>5 5	None
PE_PGRS15	968424-970244	969734-969740 (7C)	>5	None
Rv0897c	1000808-1002415	1002283-1002289 (7C)	>5	None
Rv0920c-Rv0921	1025497-1026816 1027104-1027685	1026917-1026923 (7G)	>5	None
Rv0954	1065127-1066038	1066021-1066027 (7G)	3	None
PE_PGRS16	1090373-1093144	1091981-1091987 (7G)	>5	CCDC5180 (Δ GG)
Rv0987	1102542-1105109	1104574-1104580 (7T)	3	None
Rv1048c	1171038-1172153	1171552-1171558 (7T)	2	None
pra	1203313-1204035	1203484-1203490 (7G)	0	None
Rv1190	1332980-1333858	1333662-1333668 (7G)	>5	CCDC5180; CCDC5079 (InsG)

PE_PGRS23	1384989-1386677	1386011-1386017 (7C)	4	None
Rv1303	1459766-1460251	1459830-1459836 (7T)	0	None
PE_PGRS24	1488154-1489965	1488558-1488564 (7C)	1	None
Rv1373	1546012-1546992	1546466-1546472 (7C)	>5	None
PE_PGRS25	1572127-1573857	1572681-1572687 (7C) 1573161-1573167 (7C)	>5 1	KZN605; KZN1435; KZN4207 (Δ G) None
PE_PGRS26	1618209-1619784	1619016-1619022 (7G)	>5	None
PE_PGRS27	1630638-1634627	1632350-1632356 (7C)	>5	None
PE_PGRS29	1655609-1656721	1655830-1655836 (7C)	>5	None
mutB	1684005-1686257	1685260-1685266 (7G)	4	None
Rv1509	1700212-1701093	1700416-1700422 (7G)	>5	None
Rv1526c	1720780-1722060	1721428-1721435 (7A)	0	None
pks5-papA4	1722083-1728409 1728953-1729450	1728581-1728588 (7A)	3	CCDC5079 (Δ A)
lspA	1742244-1742852	1742298-1742304 (7G)	0	None
frdB	1759435-1760178	1760165-1760171 (7G)	>5	None
Rv1590	1791334-1791573	1791451-1791457 (7C)	1	None
Rv1634	1839168-1840583	1839756-1839762 (7G)	0	CCDC5180; CCDC5079; K (the fourth G of the sequence is mutated to C)
lysX-infC	1848517-1852035 1852273-1852878	1852177-1852183 (7T)	0	K (Δ T)
infC	1852273-1852878	1852336-1852342 (7G)	0	None
Rv1648-pheS	1857731-1858537 1858733-1859758	1858709-1858715 (7C)	0	None
pheT	1859758-1862253	1860940-1860946 (7G)	0	None
PE_PGRS30	1862347-1865382	1864038-1864044 (7C) 1864138-1864144 (7C)	0 2	None
argD	1868723-1869925	1868796-1868802 (7C)	0	None
wag22	1989833-1992577	1990552-1990558 (7C)	>5	None
PE_PGRS31	2000614-2002470	2001790-2001796 (7G)	>5	None

Rv1778c	2012081-2012530	2012424-2012430 (7G)	2	None
PPE28	2039453-2041420	2041242-2041248 (7T)	2	None
gcvB	2075877-2078702	2076160-2076166 (7C)	1	None
apa	2107736-2108713	2107941-2107947 (7C)	4	None
Rv1894c	2140739-2141869	2141409-2141415 (7G)	>5	None
Rv1990A-mazF6	2233881-2234216 2234305-2234649	2234248-2234254 (7G)	>5	None
ppm1	2308131-2310755	2308554-2308560 (7C)	0	None
Rv2082	2338709-2340874	2339949-2339955 (7C)	>5	CCDC5180 (InsC)
ansP1	2388616-2390085	2389157-2389163 (7T)	0	None
ftsZ	2408385-2409524	2409194-2409200 (7C) 2409514-2409520 (7G)	0 0	None
Rv2177c-aroG	2439282-2439947 2440332-2441720	2440188-2440194 (7G)	>5	KZN605; KZN1435; KZN4207 (Δ G)
Rv2186c	2447605-2447994	2447670-2447676 (7T)	0	None
Rv2204c	2468931-2469287	2469149-2469156 (7C)	0	None
Rv2209	2473400-2474938	2473737-2473743 (7T)	5	None
Rv2240c	2511690-2512280	2512238-2512244 (7C)	4	None
fabD	2516787-2517695	2517590-2517596 (7C)	0	None
Rv2248	2522360-2523175	2522482-2522488 (7G)	>5	None
Rv2264c	2536572-2538350	2536626-2536632 (7G)	>5	K (InsG); CCDC5079; CCDC5180 (InsA between the third and fourth Gs)
Rv2293c-Rv2294	2564292-2565032 2565327-2566550	2565159-2565166 (7T)	3	None
htpG	2570059-2572002	2571312-2571318 (7C)	2	None
PPE40	2637688-2639535	2639268-2639274 (7C)	5	None
hemN	2682015-2683142	2682917-2682923 (7C)	>5	None
PE_PGRS41	2692799-2693884	2693195-2693201 (7G)	5	None
gdh	2777388-2782262	2779013-2779019 (7C)	0	None
PE_PGRS42	2795301-2797385	2796132-2796138 (7C)	>5	F11 (InsG)

PE_PGRS43	2801254-2806236	2804943-2804949 (7C)	>5	None
nusB	2858254-2858724	2858259-2858265 (7C)	0	None
lppB	2867124-2867786	2867738-2867744 (7C)	>5	None
Rv2561	2881409-2881702	2881583-2881589 (7T)	Indel mutants	None
PE_PGRS46	2960105-2962441	2960945-2960951 (7C)	>5	CCDC5079 (InsC)
Rv2652c- Rv2653c	2975928-2976554 2976586-2976909	2976559-2976565 (7C)	>5	None
dxs1	2998052-2999968	2999852-2999858 (7C)	0	None
dxs1-Rv2683	2998052-2999968 3000112-3000609	2999989-2999995 (7C)	4	None
Rv2762c	3072637-3073056	3072706-3072712 (7C)	>5	None
rpsO	3093479-3093748	3093723-3093729 (7T)	2	None
Rv2803	3111822-3112289	3112278-3112284 (7C)	>5	None
PE_PGRS48	3162268-3164115	3163651-3163657 (7G)	>5	K (the fifth G of the sequence is mutated to C)
ppsA	3245445-3251075	3248309-3248315 (7C)	0	KZN1435 (InsC)
ppsC	3255685-3262251	3258352-3258358 (7C) 3258369-3258375 (7C)	0 2	None
Rv2955c	3307580-3308545	3308314-3308320 (7G)	>5	None
PPE46	3376939-3378243	3377347-3377353 (7C)	5	None
PPE47	3379376-3380452	3379784-3379790 (7C)	0	None
lipR	3449997-3450923	3450183-3450189 (7C)	>5	None
Rv3143	3509654-3510055	3509817-3509823 (7G)	1	None
aofH	3538505-3539851	3539140-3539146 (7G)	>5	None
Rv3192	3559563-3560024	3559991-3559997 (7C)	>5	None
Rv3205c	3581627-3582505	3582012-3582018 (7G)	1	None
Rv3225c	3601016-3602440	3602344-3602350 (7C)	>5	None
Rv3256c	3636275-3637315	3636334-3636340 (7C)	2	None
PE_PGRS50	3738158-3742774	3741964-3741970 (7C)	0	None
PE_PGRS50- Rv3346c	3738158-3742774 3743198-3743455	3742992-3742998 (7G)	>5	None

guaB2	3829930-3831519	3830214-3830220 (7C)	0	None
Rv3413c	3832146-3833045	3832357-3832363 (7G)	>5	None
rpsK	3879273-3879692	3879675-3879681 (7T)	1	None
PE_PGRS53	3926569-3930714	3927679-3927685 (7G)	0	None
fadE33	4005247-4006203	4005251-4005257 (7C)	0	None
aspB	4006200-4007366	4007272-4007278 (7G)	3	None
Rv3577	4019262-4020128	4019547-4019553 (7G)	>5	None
lpqE-radA	4025830-4026378 4026444-4027886	4026423-4026429 (7C)	>5	None
Rv3603c	4045207-4046118	4045485-4045491 (7C)	2	None
espA-ephA	4055197-4056375 4057733-4058701	4056481-4056487 (7T)	1	None
PE_PGRS61	4093940-4094527	4094054-4094060 (7G)	1	None
B11	4099386-4099478	4099403-4099409 (7G)	>5	None
ponA2	4121916-4124348	4123559-4123565 (7C)	1	None
glpK	4138202-4139755	4139184-4139190 (7C)	>5	None
fadE35	4251085-4252866	4251294-4251300 (7G)	5	CCDC5079; CCDC5180; K (the fourth G of the sequence is mutated to C)
pks13	4255945-4261146	4258501-4258507 (7G)	0	None
pks2	4293225-4299605	4298221-4298227 (7G)	>5	None
Rv3835	4309047-4310396	4310176-4310182 (7C)	>5	None
Rv3848-espR	4322326-4323234 4323499-4323897	4323355-4323361 (7G)	>5	CDC1551 (the first G of the sequence is mutated to C)
hns	4325074-4325478	4325206-4325212 (7A)	5	None
Rv3860	4336777-4337949	4337821-4337827 (7G)	>5	None
eccD1	4355007-4356542	4355864-4355870 (7G)	1	None
espK	4357593-4359782	4358980-4358986 (7G)	>5	None
Rv3910	4396597-4400151	4398671-4398677 (7C)	0	None

71 CDC1551 (GenBank ID: AE000516.2), CCDC5079 (GenBank ID: CP002884.1), CCDC5180
72 (GenBank ID: CP001642.1), F11 (GenBank ID: CP000717.1), KZN605 (GenBank ID:

73 CP001976.1), KZN1435 (GenBank ID: CP001658.1), KZN4207 (GenBank ID: CP001662.1)
74 and K (GenBank ID: CP007803.1).
75

76 **Table S3. BioSample accession numbers for genomes and transcriptomes analyzed in this**
77 **study.**

Accession	Strain	Method	Biological replicate	Medium
SAMN09517834	TDR193-LC	WGS	1	N/A
SAMN09517835	TDR193-SC	WGS	1	N/A
SAMN09517836	TDR193-SC-RevC1	WGS	1	N/A
SAMN09517837	TDR193-SC-RevC9	WGS	1	N/A
SAMN09517838	C71-LC	WGS	1	N/A
SAMN09517839	C71-SC	WGS	1	N/A
SAMN09517840	C71-SC-RevC1	WGS	1	N/A
SAMN09517841	HN878-XM4-LC1	WGS	1	N/A
SAMN09517842	HN878-XM4-LC2	WGS	1	N/A
SAMN09517843	HN878-XM4-LC3	WGS	1	N/A
SAMN09517844	HN878-XM4-SC4	WGS	1	N/A
SAMN09517845	HN878-XM4-SC5	WGS	1	N/A
SAMN09517846	HN878-XM4-SC6	WGS	1	N/A
SAMN10742622	HN878-SC	WGS	1	N/A
SAMN09517865	TDR193-SC-RevC9	RNAseq	1	7H9
SAMN09517866	TDR193-SC-RevC9	RNAseq	2	7H9
SAMN09517867	TDR193-SC-RevC9	RNAseq	3	7H9
SAMN09517868	TDR193-SC	RNAseq	1	7H9
SAMN09517869	TDR193-SC	RNAseq	2	7H9
SAMN09517870	TDR193-SC	RNAseq	3	7H9
SAMN09517871	TDR193-SC-RevC9	RNAseq	1	7H9 with glycerol
SAMN09517872	TDR193-SC-RevC9	RNAseq	2	7H9 with glycerol
SAMN09517873	TDR193-SC-RevC9	RNAseq	3	7H9 with glycerol
SAMN09517874	TDR193-SC	RNAseq	1	7H9 with glycerol

SAMN09517875	TDR193-SC	RNAseq	2	7H9 with glycerol
SAMN09517876	TDR193-SC	RNAseq	3	7H9 with glycerol
SAMN10742623	HN878-SC	RNAseq	1	7H9
SAMN10742624	HN878-SC	RNAseq	2	7H9
SAMN10742625	HN878-SC	RNAseq	3	7H9
SAMN10742626	HN878-SC	RNAseq	1	7H9 with glycerol
SAMN10742627	HN878-SC	RNAseq	2	7H9 with glycerol
SAMN10742628	HN878-SC	RNAseq	3	7H9 with glycerol
SAMN10742629	HN878-LC	RNAseq	1	7H9
SAMN10742630	HN878-LC	RNAseq	2	7H9
SAMN10742631	HN878-LC	RNAseq	3	7H9
SAMN10742632	HN878-LC	RNAseq	1	7H9 with glycerol
SAMN10742633	HN878-LC	RNAseq	2	7H9 with glycerol
SAMN10742634	HN878-LC	RNAseq	3	7H9 with glycerol

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79

80 **RNaseq Supplementary Information (RNaseq SI)**

81

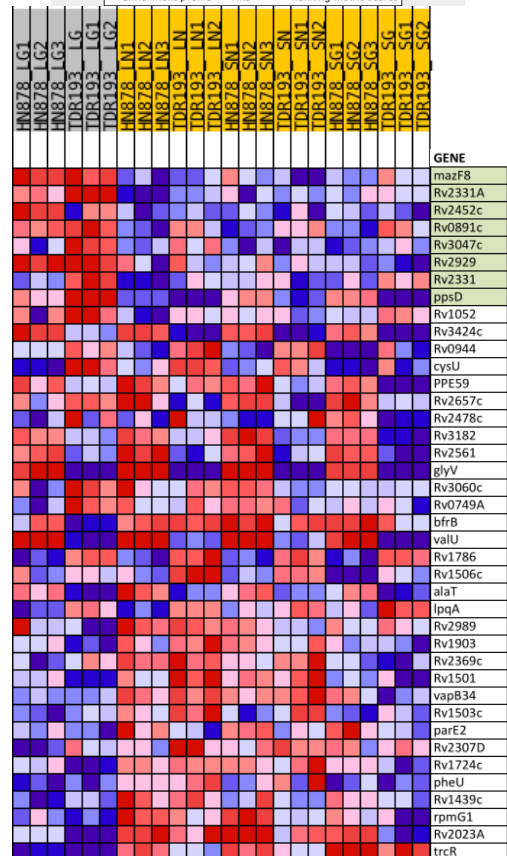
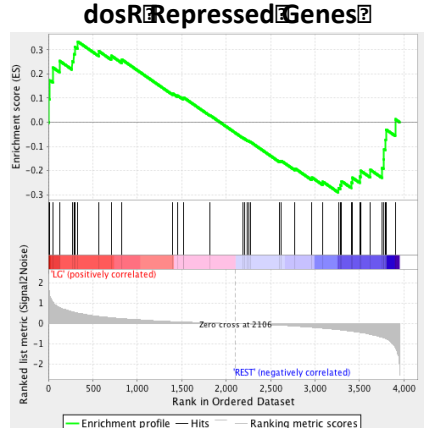
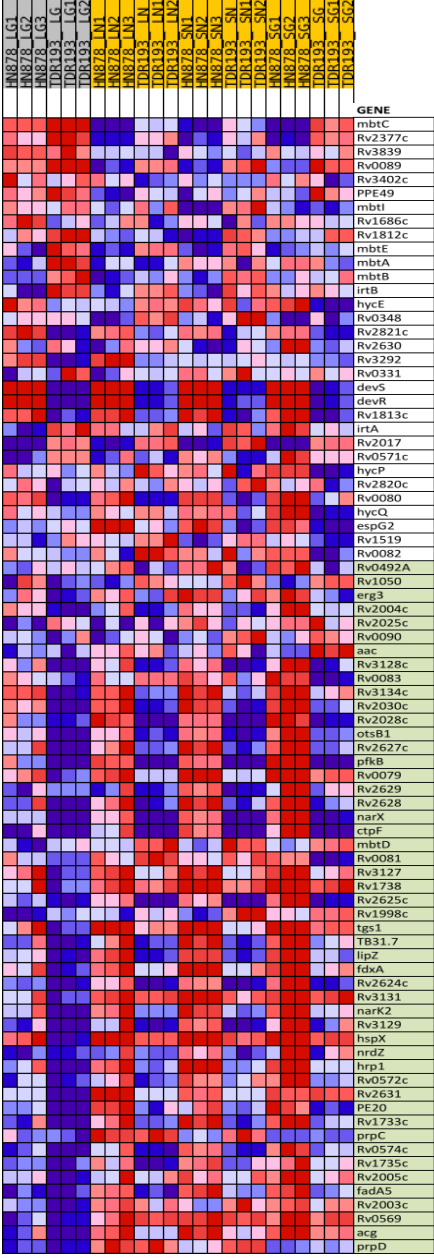
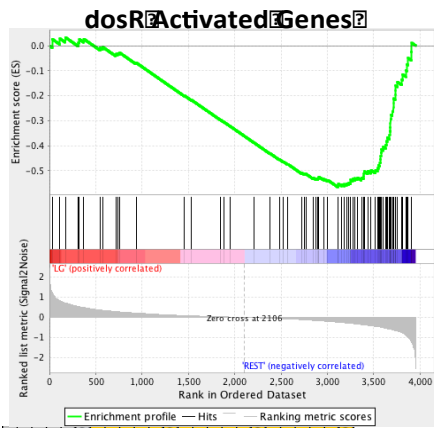
82 **GSEA Enrichment: Regulons**

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REGULATOR	TARGET		SET	SIZE	ES	NES	Regulon		Fisher's		LeadingEdge			Analysis	
	GENE	ES					Activity	NOM	Combined	RANK	Tags	List	Signal		Weighted
							Change	Score	p-val	p-val	AT	MAX			Signal
Rv3133c (dosR)	Repressed	40	0.33	0.82	-1.07	0.73	0.73	0.55	330	20%	8%	22%	58%		
	Activated	82	-0.57	-1.19	0.30	0.30	0.55	840	61%	21%	76%				
Rv3574 (kstR)	Repressed	60	-0.54	-1.51	1.49	0.05	0.05	0.01	980	57%	25%	74%	66%		
	Activated	13	0.60	1.38	0.03	0.03	0.01	57	31%	1%	31%				
Rv1395	Repressed	20	-0.49	-1.04	1.08	0.48	0.48	0.38	1087	50%	27%	69%	60%		
	Activated	12	0.50	1.14	0.26	0.26	0.38	222	42%	6%	44%				
Rv1219c	Repressed	39	-0.34	-1.13	1.34	0.24	0.24	0.00	418	18%	11%	20%	43%		
	Activated	41	0.72	1.54	0.00	0.00	0.00	387	59%	10%	64%				
Rv1994c (cmtR)	Repressed	29	-0.39	-1.06	1.17	0.40	0.40	0.12	527	28%	13%	32%	42%		
	Activated	15	0.68	1.39	0.06	0.06	0.12	516	53%	13%	61%				
Rv1990c	Repressed	64	-0.33	-0.97	1.09	0.53	0.53	0.07	507	19%	13%	21%	32%		
	Activated	25	0.74	1.40	0.03	0.03	0.07	273	56%	7%	60%				
Rv2250c	Repressed	59	0.53	1.47	-1.46	0.02	0.02	0.00	749	42%	19%	51%	53%		
	Activated	37	-0.58	-1.43	0.03	0.03	0.00	764	46%	19%	56%				
Rv3058c	Repressed	121	0.47	1.23	-1.28	0.22	0.22	0.12	723	40%	18%	48%	51%		
	Activated	131	-0.57	-1.32	0.11	0.11	0.12	576	47%	15%	54%				
Rv0324	Repressed	125	0.31	1.06	-1.25	0.33	0.33	0.06	523	20%	13%	22%	37%		
	Activated	120	-0.59	-1.44	0.04	0.04	0.06	551	47%	14%	53%				
Rv3765c (tcrX)	Repressed	36	0.46	0.90	-1.02	0.64	0.64	0.52	611	39%	15%	46%	51%		
	Activated	55	-0.42	-1.11	0.30	0.30	0.52	782	44%	20%	54%				
Rv0576	Repressed	242	-0.42	-1.33	1.33	0.05	0.05	0.02	855	40%	22%	49%	49%		
	Activated	23	0.56	1.39	0.06	0.06	0.02	691	39%	17%	47%				
Rv2034	Repressed	37	-0.51	-1.40	1.38	0.07	0.07	0.03	908	35%	23%	45%	45%		
	Activated	26	0.58	1.35	0.08	0.08	0.03	376	42%	10%	46%				
Rv3223c (sigH)	Repressed	254	0.48	1.47	-1.42	0.02	0.02	0.01	594	31%	15%	34%	36%		
	Activated	88	-0.44	-1.28	0.08	0.08	0.01	608	36%	15%	42%				
Rv0047c	Repressed	33	0.35	1.14	-1.28	0.25	0.25	0.06	451	18%	11%	20%	30%		
	Activated	30	-0.61	-1.44	0.04	0.04	0.06	387	37%	10%	40%				

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- 90 1. Gopal P, *et al.* (2016) Pyrazinamide Resistance Is Caused by Two Distinct Mechanisms:
91 Prevention of Coenzyme A Depletion and Loss of Virulence Factor Synthesis. *ACS Infectious*
92 *Diseases* 2(9):616-626.

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