

Supplementary Figure 1.

a.

Functional Categories	Frequency in the genome N (%)	Frequency in our candidate list N (%)
Regulatory Proteins	195 (4.77)	53 (29.61)
Intermediary Metabolism and Respiration	923 (22.57)	39 (21.79)
Cell Wall and Cell Processes	773 (18.90)	30 (16.76)
Information Pathways	241 (5.89)	24 (13.41)
Virulence, Detoxification, Adaptation	228 (5.57)	13 (7.26)
Lipid Metabolism	247 (6.04)	15 (8.33)
Conserved Hypothetical Proteins	1081 (26.43)	5 (2.79)
PE/PPE	168 (4.11)	1 (0.56)
Stable RNAs	71 (1.74)	0 (0.00)
Insertion Sequences and Phages	147 (3.59)	0 (0.00)
Unknown	16 (0.39)	0 (0.00)
Total	4090	180

b.

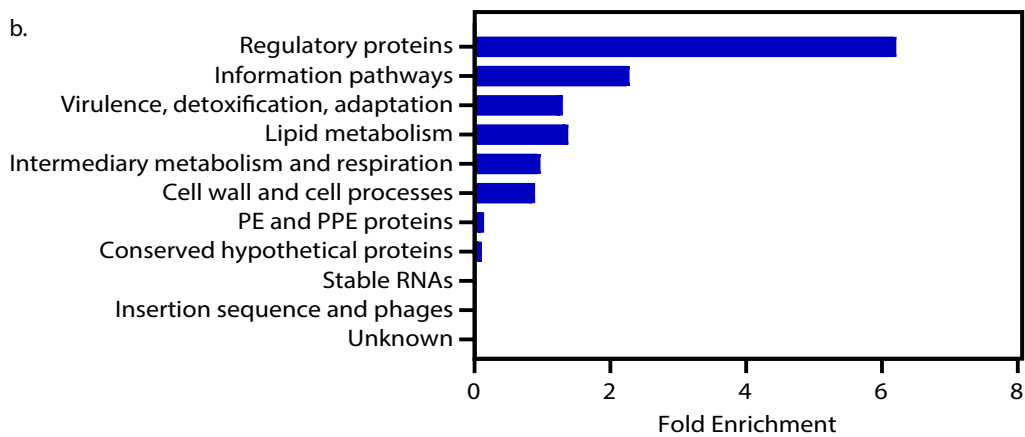
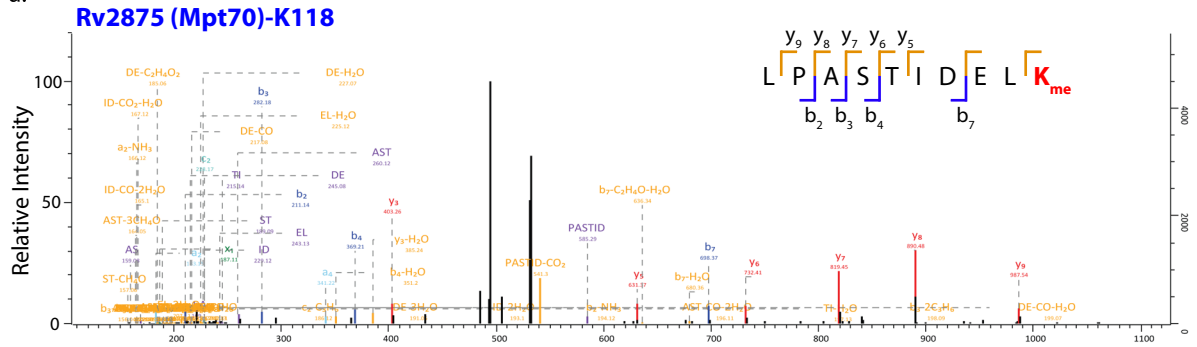


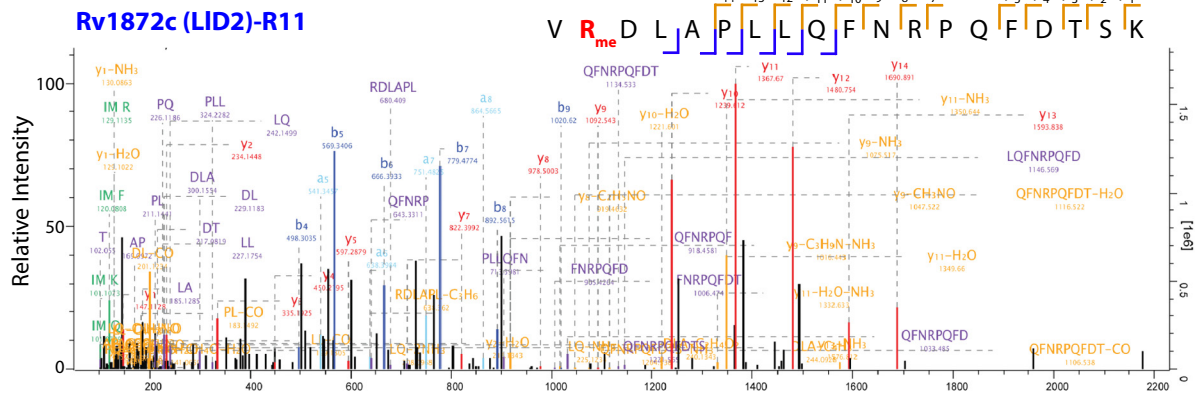
Figure S1: Functional classification of candidate protein-coding genes. **(a)** Frequency of genes in the *Mtb* proteome and in our list of 180 candidates categorized based on their functional categories. **(b)** Fold enrichment of each functional category in the list of 180 candidate proteins over that in the *Mtb* proteome.

Supplementary Figure 2a-d

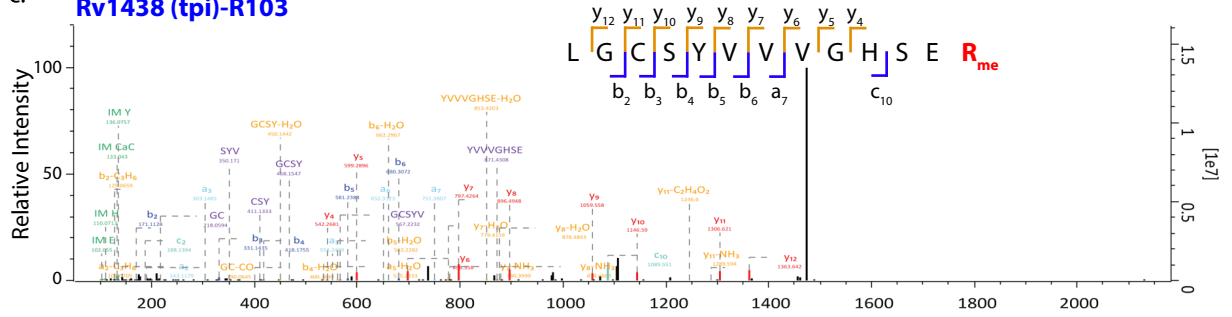
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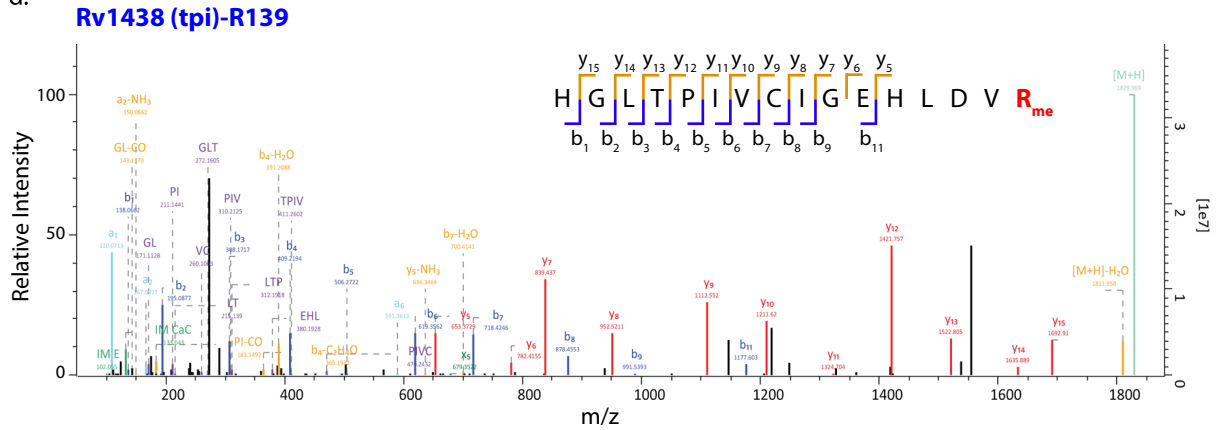
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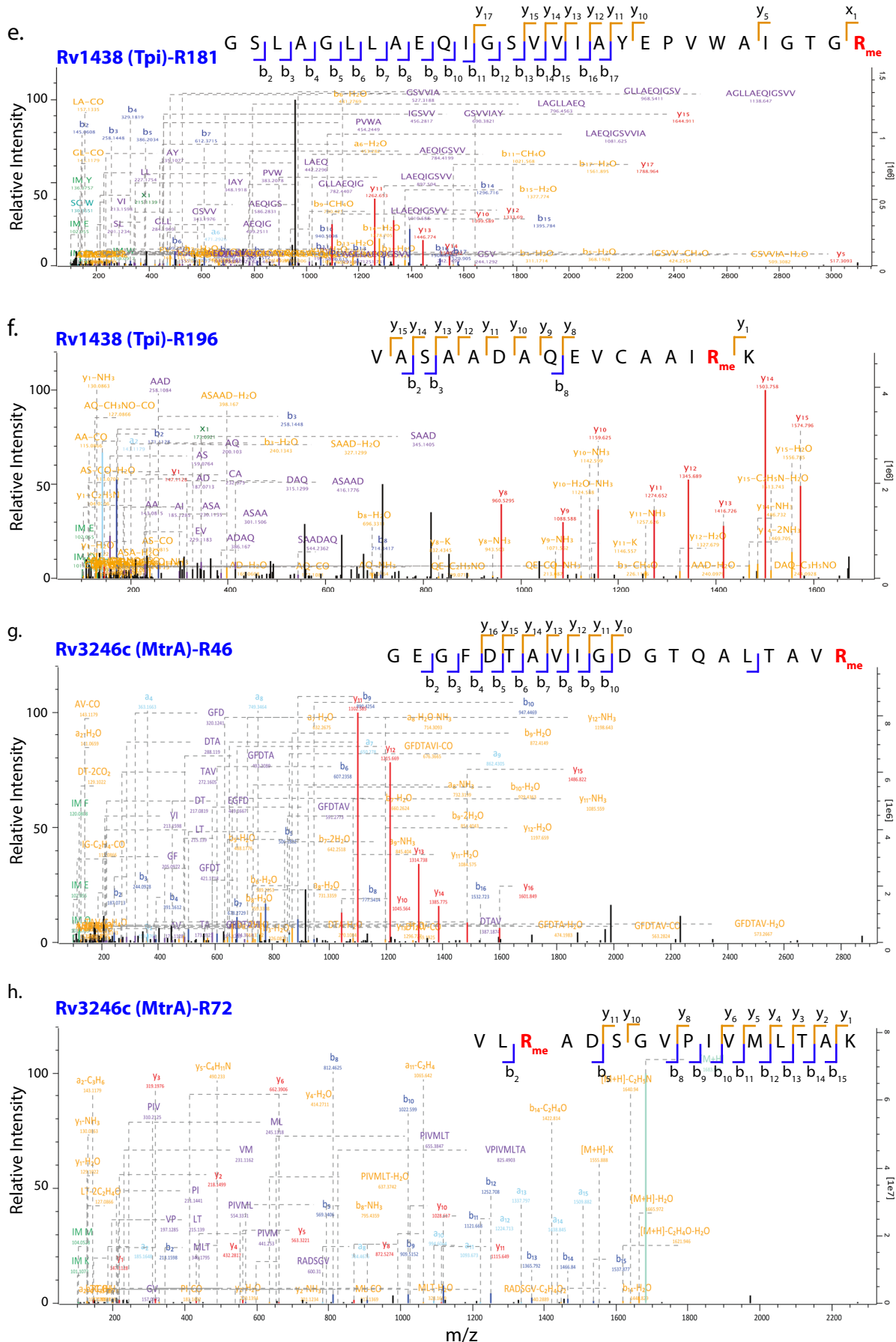
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d.

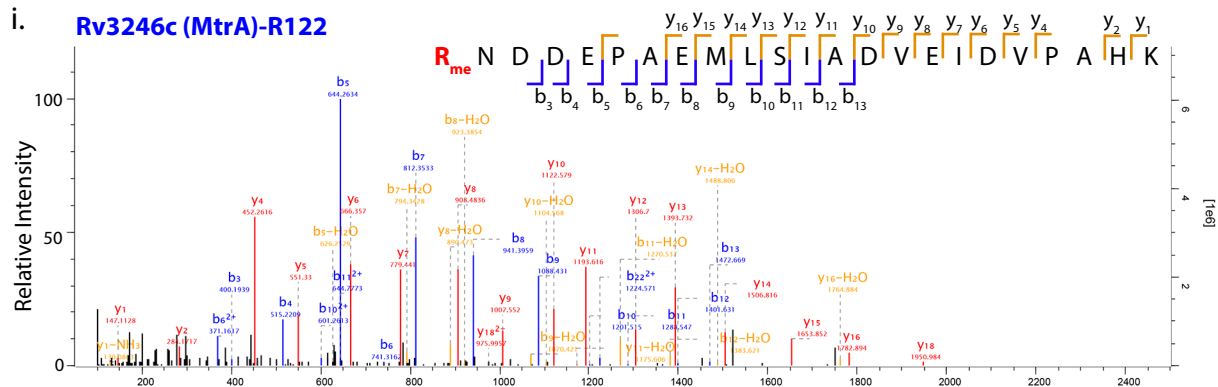


Supplementary Figure 2e-2h

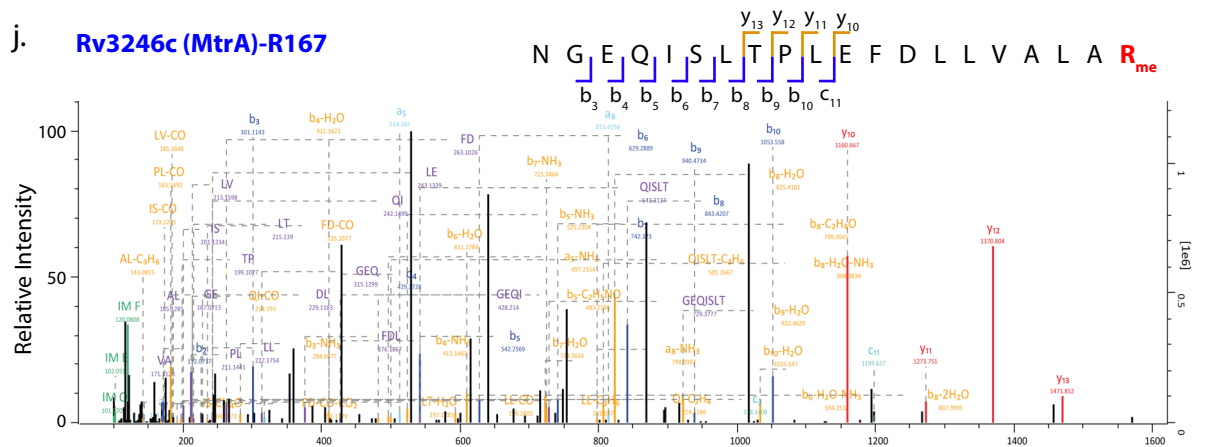


Supplementary Figure 2i-2l

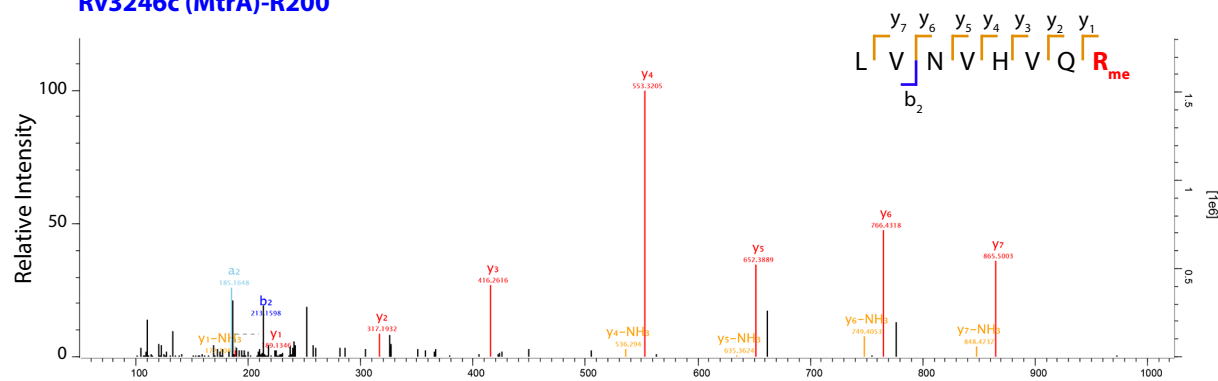
i. Rv3246c (MtrA)-R122



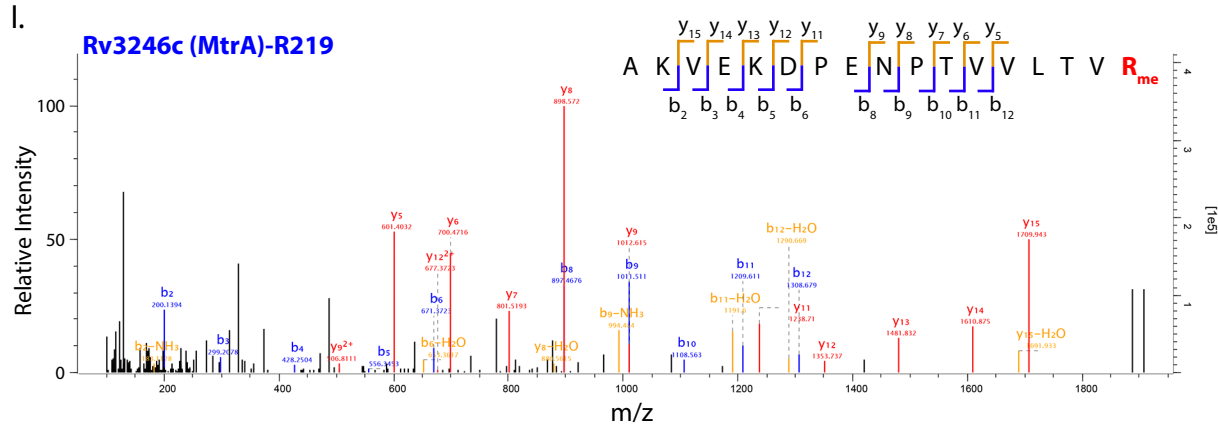
j. Rv3246c (MtrA)-R167



k. Rv3246c (MtrA)-R200

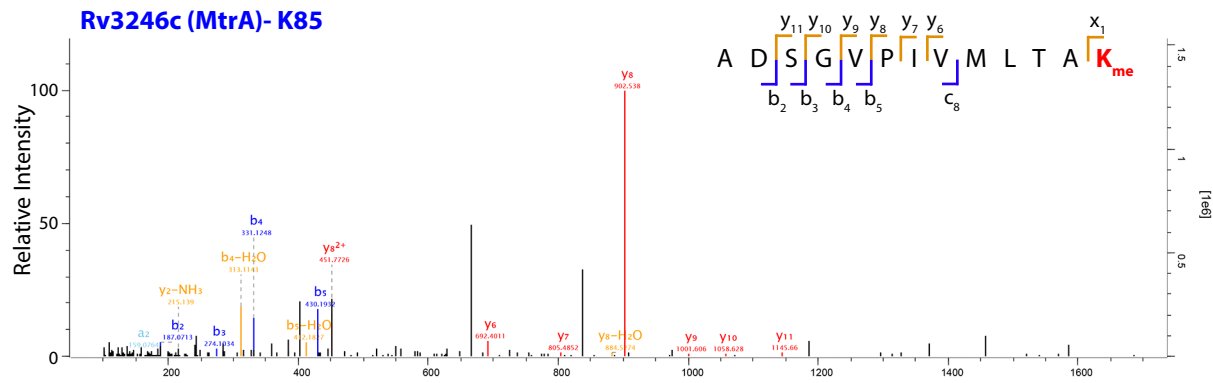


l. Rv3246c (MtrA)-R219

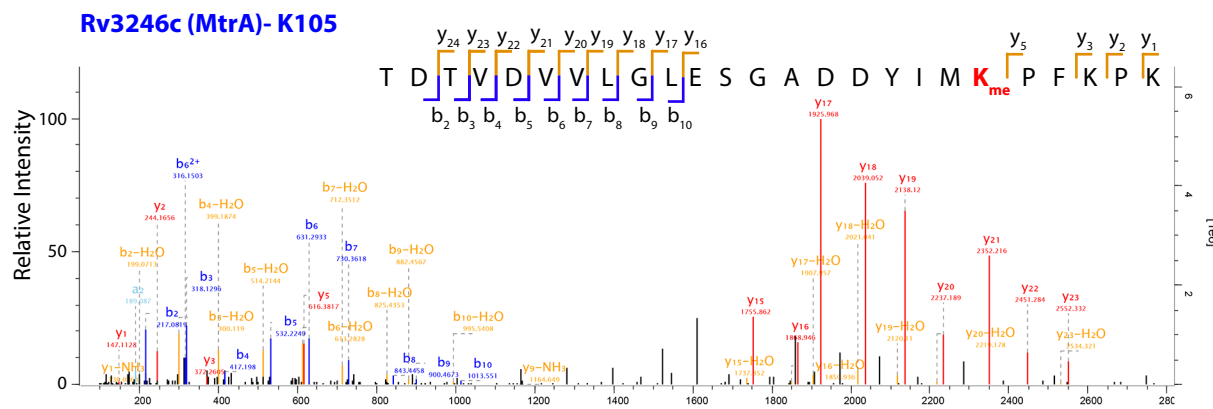


Supplementary Figure 2m-2p

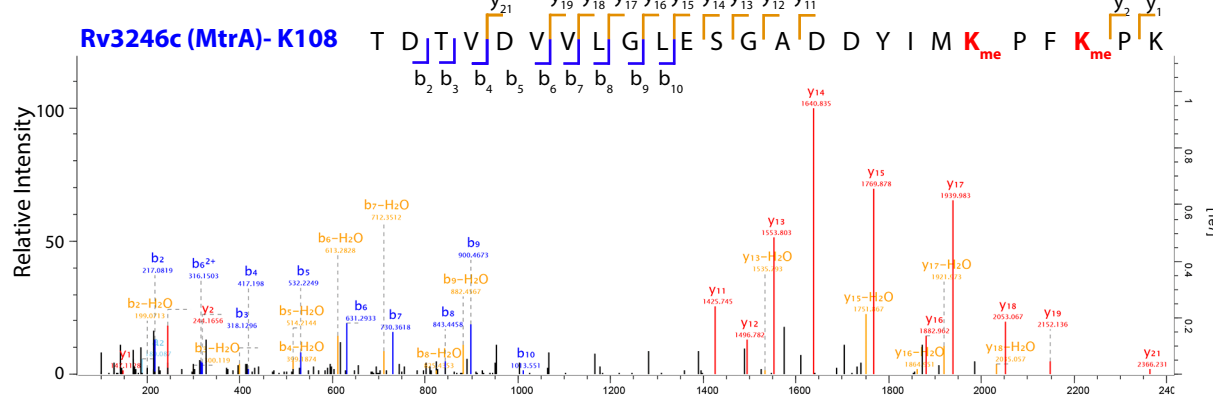
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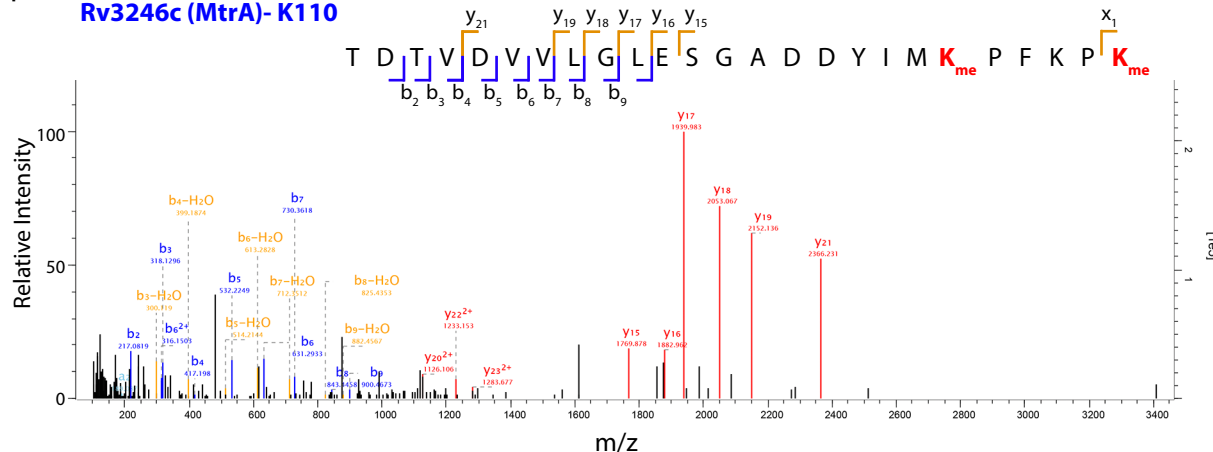
n.



o.



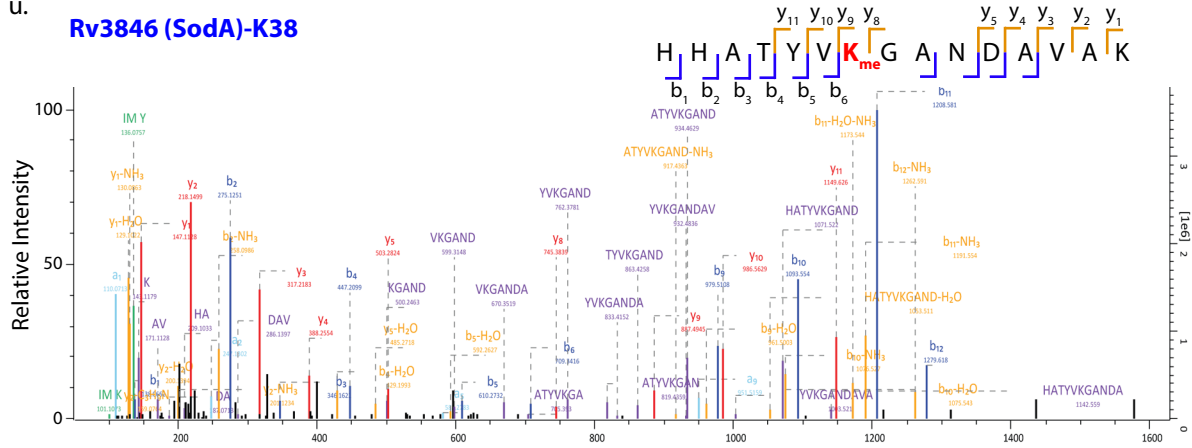
p.



Supplementary Figure 2u-2x

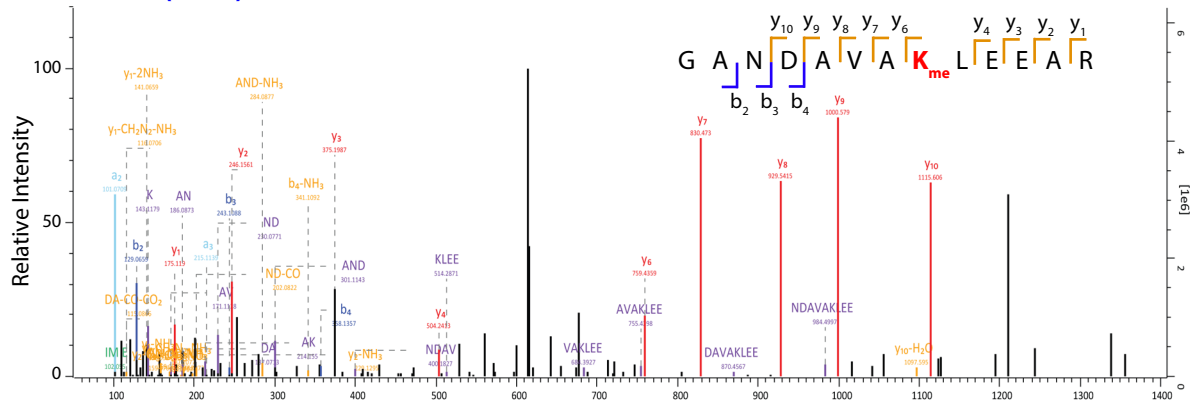
u.

Rv3846 (SodA)-K38



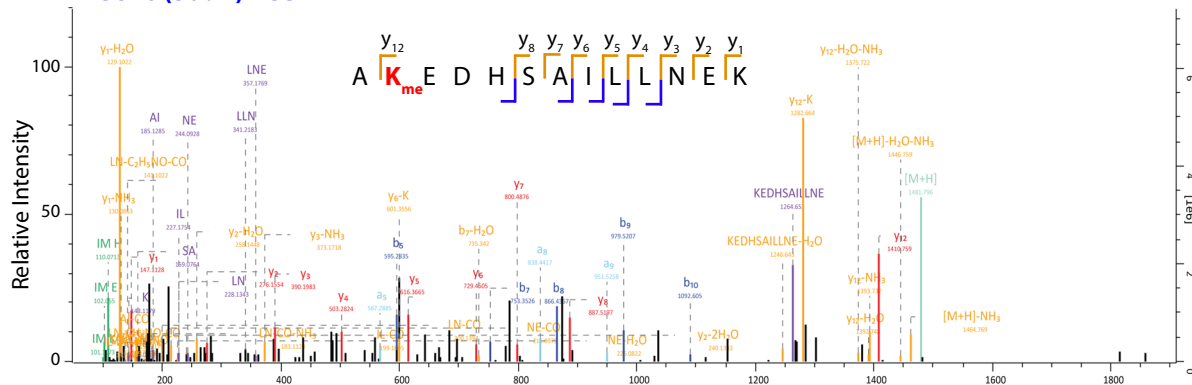
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Rv3846 (SodA)-K46



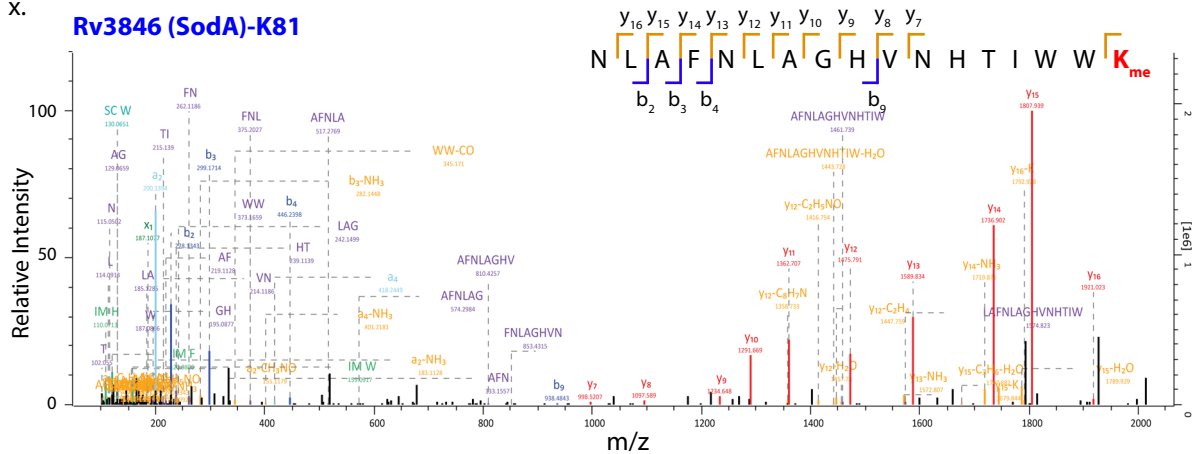
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Rv3846 (SodA)-K53



x.

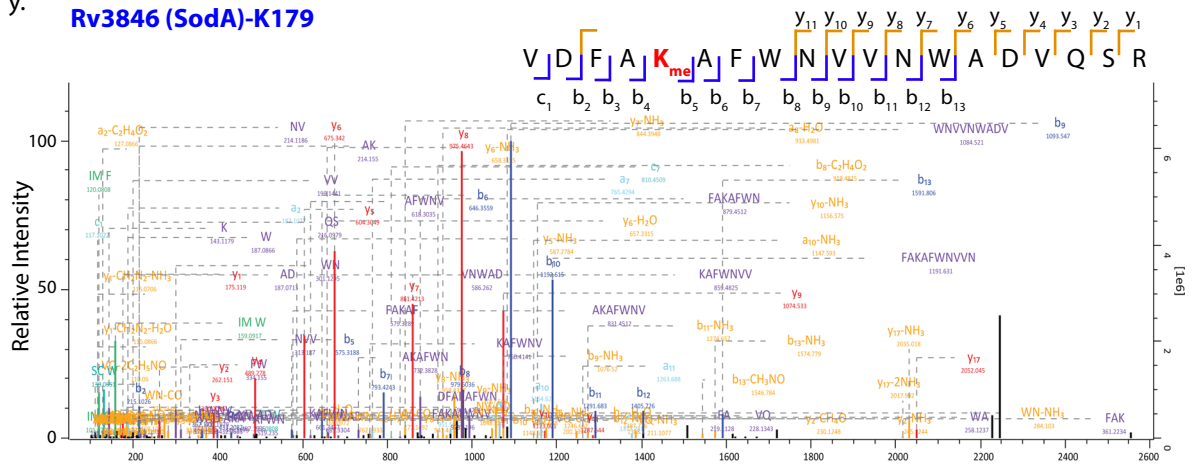
Rv3846 (SodA)-K81



Supplementary Figure 2y-2ab

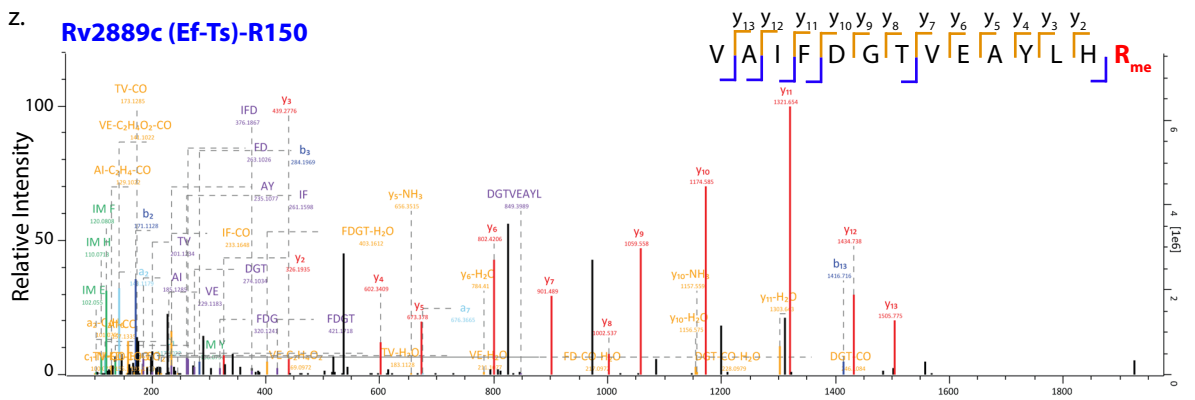
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Rv3846 (SodA)-K179



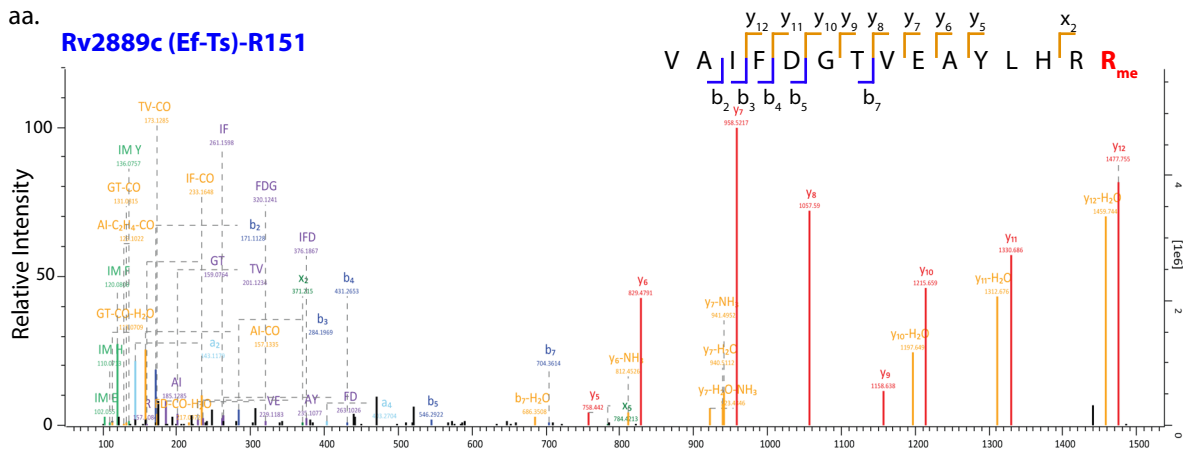
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Rv289c (Ef-Ts)-R150



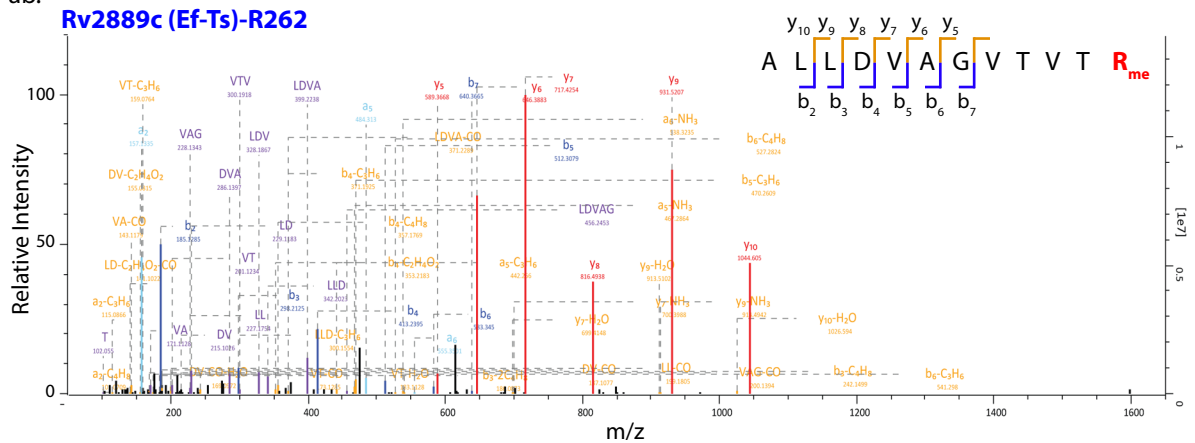
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Rv289c (Ef-Ts)-R151



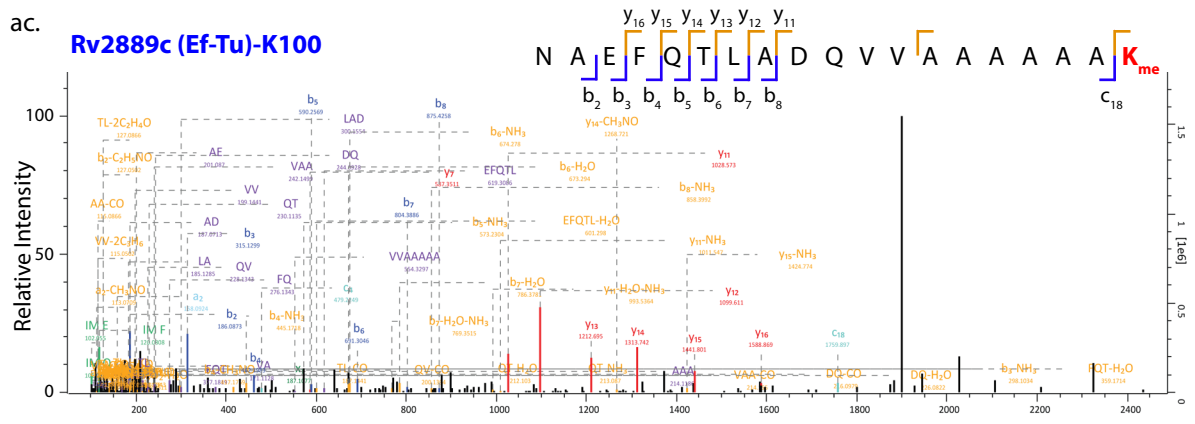
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Rv289c (Ef-Ts)-R262

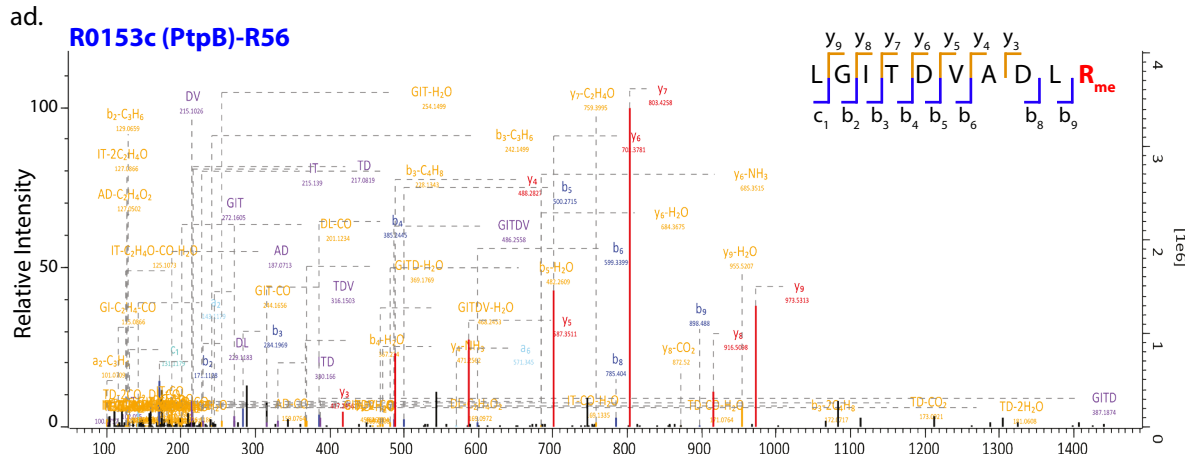


Supplementary Figure 2ac-2af

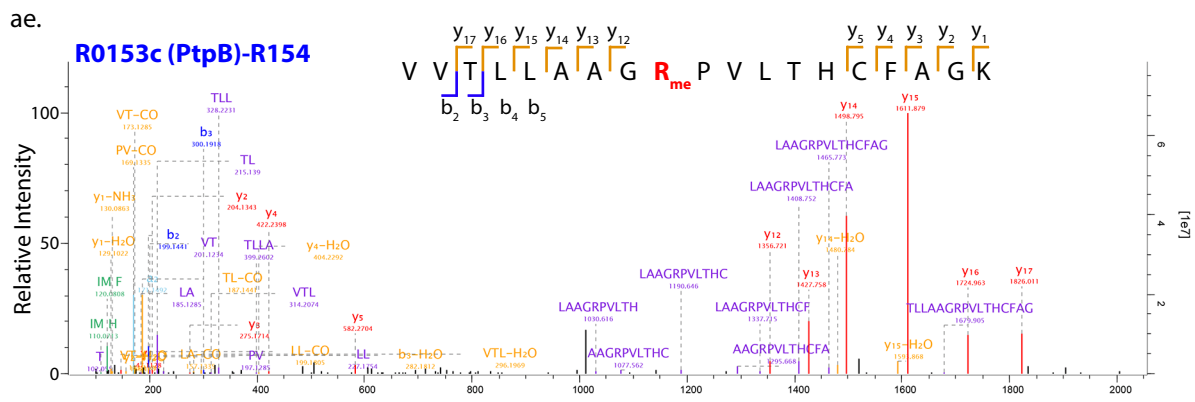
ac.



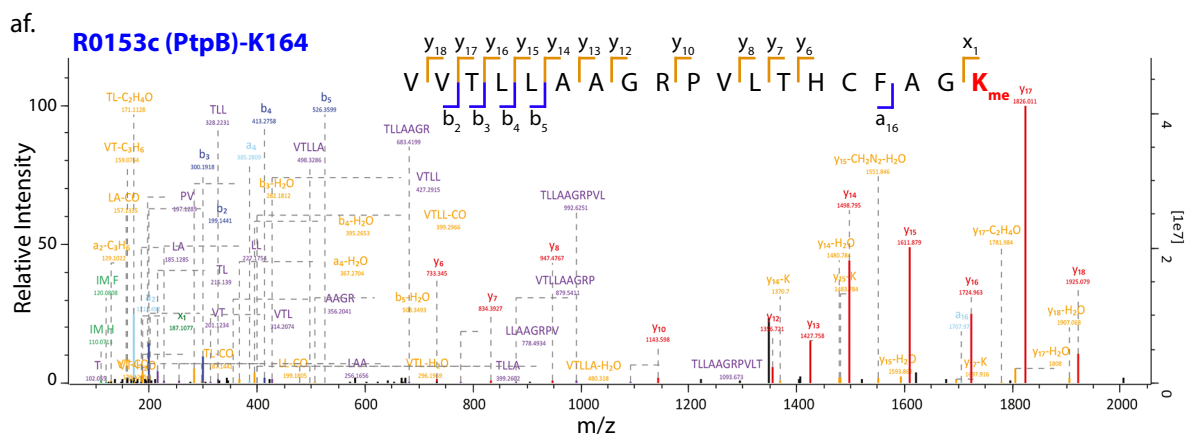
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ae.



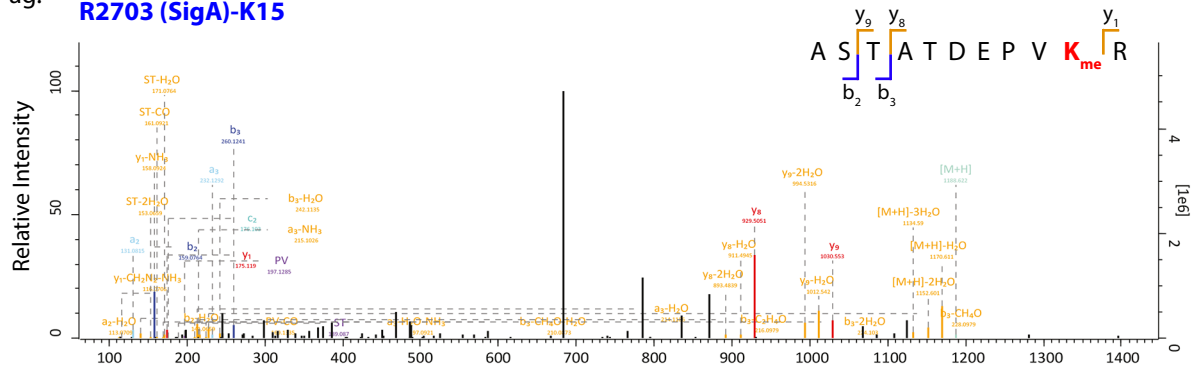
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Supplementary Figure 2ag-2aj

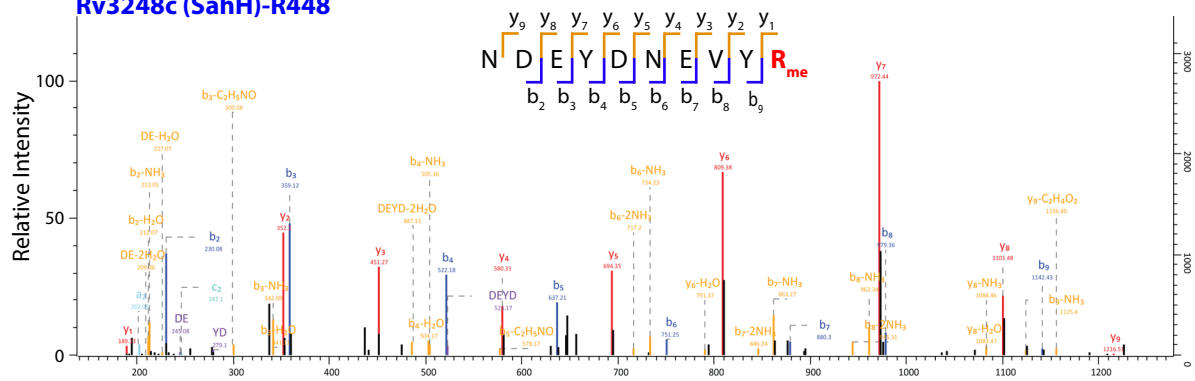
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R2703 (SigA)-K15



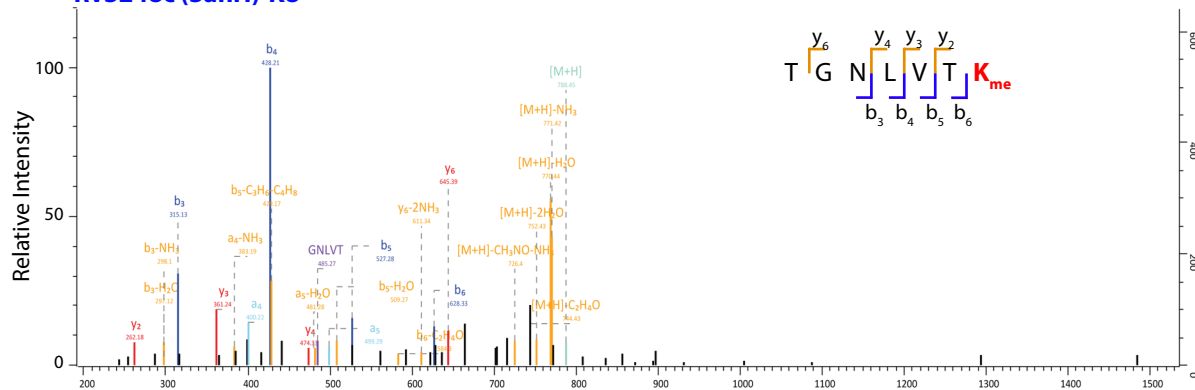
ah.

Rv3248c (SahH)-R448



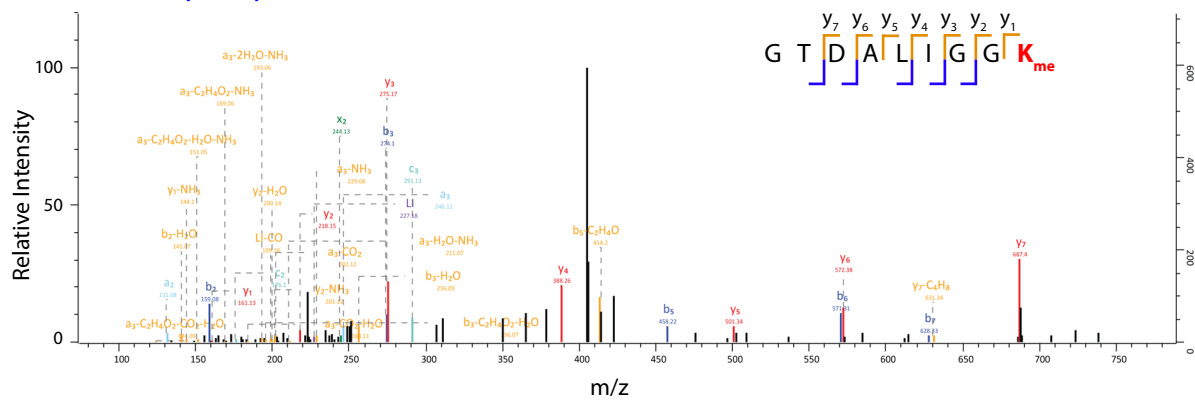
ai.

Rv3248c (SahH)-K8



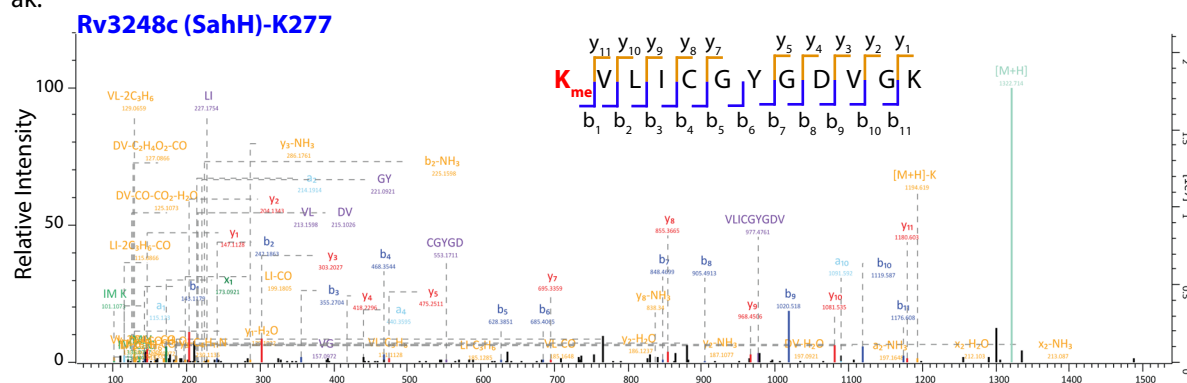
aj.

Rv3248c (SahH)-K276



Supplementary Figure 2ak-2al

ak.



al.

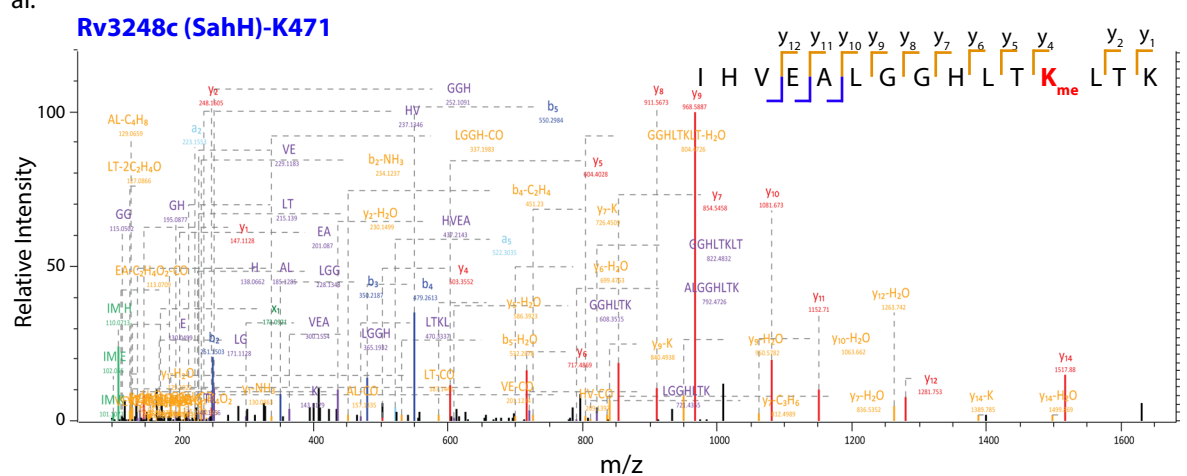


Figure S2: Mass spectra of methylated peptides. *Mtb* proteins purified from *Msm* were subjected to mass spectrometry for the identification of methylation sites. **(2a)** Mass spectrum of Mpt70 (*rv2875*). **(2b)** Mass spectrum of LldD2 (*rv1872c*). **(2c-2f)** Mass spectrum of Tpi (*rv1438*). **(2g-2I) & (2m-2S)** Mass spectrum of MtrA (*rv3246c*). **(2t-2y)** Mass spectrum of SodA (*rv3846*). **(2z-2ac)** Mass spectrum of Ef-Ts (*rv2889c*). **(2ad-2af)** Mass spectrum of PtpB (*rv0153c*). **(2ag)** Mass spectrum of SigA (*rv2703*). **(2ah-2al)** Mass spectrum of SahH (*rv3248c*). Each spectrum represents different methylation site at arginine or lysine residue.

Supplementary Figure 3

OmpR -MQENYKILVVDDDMRLRALLERYLTEQGFQVRSVANAEQMDRLLTRESFHLMVLDLMLP
MtrA MDTMRQRILVVDDDDASLAEMLTIVLRGEGFDTAVIGDGTQALTAVRELRPDLVLLDLMLP
.:***** * :* * :**:. :.. * : . .*:*****

OmpR GEDGLSICRRLRSQSNPMPIIMVTAKGEEVDRIVGLEIGADDYIPKPFNPPELLARIRAV
MtrA GMNGIDVCRVLRADS-GVPIVMLTAKTDTVDVVLGLES GADDYIMKPFKPKELVARVRAR
* :*:.:** **:* :**:*:** : ** :*** ***** **:*:**:****

OmpR LRRQANELPGAPSQEEAVIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREP
MtrA LRRNDDEPAE-----MLSIADVEIDVPAHKVTRNGEQISLTPLEFDLLVALARKPRQV
***: :* :.....: : : *.* : ** ** :* ** . :**:

OmpR LSRDKLMNLRGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTVWGLGYVFPDGSKA
MtrA FTRDVLLEQVWGYRHPADTRLVNVHVQRLRAKVEKDPENPTVVLTVRGVGYKAGPP----
:** * : . * .: * * :**:.*** **:** :* : ** *:** *

Figure S3: Sequence alignment of *E. coli* OmpR and *Mtb* MtrA. Three key MtrA methylated residues studied here are marked in red and DNA recognition helix is underlined.

Supplementary Figure 4

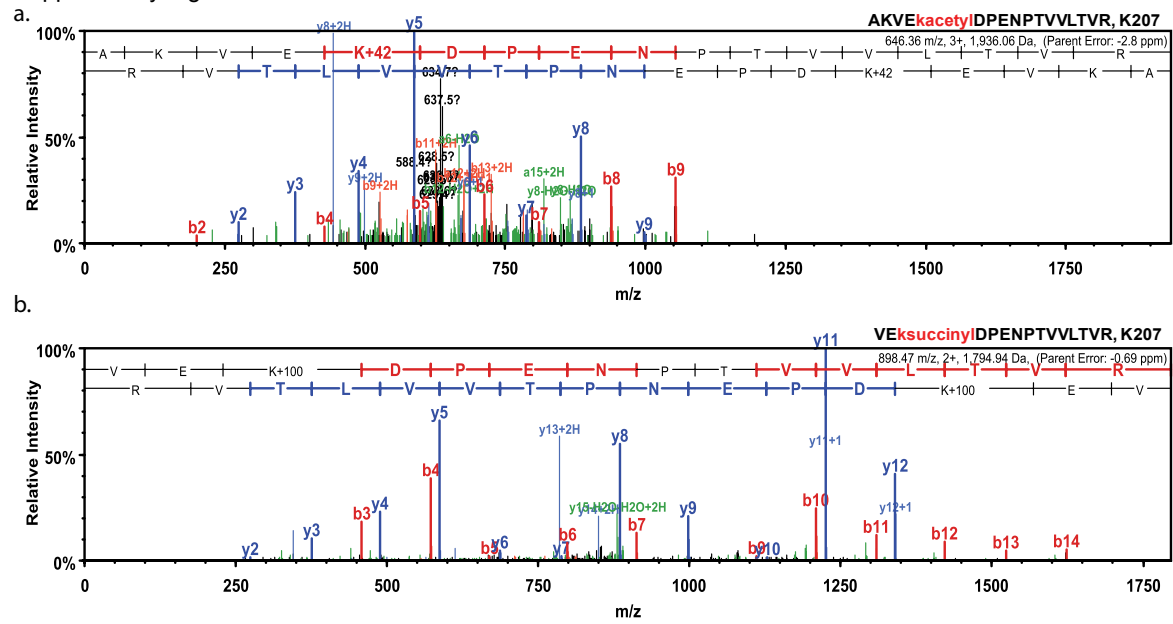


Figure S4: Mass spectra of acetylated and succinylated peptides. *Mtb* MtrA purified from *Msm* was subjected to mass-spectrometry for the identification of **(a)** acetylation and **(b)** succinylation sites; and the peptide spectra are shown.

Table S1: Details of 180 candidate protein-coding genes. Cells in green color shows methylated proteins identified in the study. Cell in light pink color shows the protein for which methylation was not detected by mass spectrometer. Cells in indigo color represents proteins that were purified but not detected as methylated by western blot.

Table S2: Methylation sites identified by mass spectrometry.

Table S3: The table shows mass spectrometric signal defined by the type of identification- either by “MS/MS” or by “match between run event (matching)”. The fold change in signal intensities are shown relative to those in MtrA.

Table S1: List of the selected proteins.							
*Y (Essential for <i>in vitro</i> growth); C (Essential during growth on cholesterol); I (Essential during infection); and N (Non-essential).							
**Purification status is shown by Y (Yes) or N (No).							
Gene name	Protein name	Functional category	Essentiality *	Purified **	GO Molecular Function	GO Cellular compartment	GO Biological Process
Rv0153c	Phosphotyrosine protein phosphatase PTPB (PTPase)	Regulatory proteins	C	Y	protein tyrosine phosphatase activity	cytoplasm	
Rv1438	Triosephosphate isomerase (TIM) (TPI)	Intermediate metabolism and respiration	Y	Y	triose-phosphate isomerase activity	cytosol; extracellular region; plasma membrane	gluconeogenesis; glyceraldehyde-3-phosphate biosynthetic process; glycerol catabolic process; glycolytic process; growth; pentose-phosphate shunt
Rv1872c	Putative L-lactate dehydrogenase, LldD2	Intermediate metabolism and respiration	N	Y	FMN binding; oxidoreductase activity	cell wall; plasma membrane	
Rv2703	RNA polymerase sigma factor SigA (Sigma-A)	Information pathways	Y	Y	DNA binding; sigma factor activity; transcription factor activity, sequence-specific DNA binding	cell wall; cytoplasm; plasma membrane	growth; pathogenesis; response to water; transcription initiation from bacterial-type RNA polymerase promoter
Rv2875	Immunogenic protein Mpt70	Cell wall and cell processes	N	Y		extracellular region; extracellular space; outer membrane-bounded periplasmic space	
Rv2889c	Elongation factor Ts (EF-Ts)	Information pathways	Y	Y	translation elongation factor activity	cell wall; cytosol; plasma membrane	growth
Rv3246c	DNA-binding response regulator MtrA	Regulatory proteins	I	Y	DNA binding; metal ion binding	cytoplasm; plasma membrane	growth of symbiont in host; phosphorelay signal transduction system; positive regulation of transcription, DNA-templated; protein phosphorylation; transcription, DNA-templated
Rv3248c	S-adenosyl-L-homocysteine	Intermediate	Y	Y	adenosylhomocysteine activity; NAD+	cell wall; cytosol; extracellular region;	adenosine metabolic process; adhesion of symbiont to host cell; entry of bacterium into

	(AdoHcyase)	and respiration					one-carbon metabolic process; S-adenosylhomocysteine catabolic process; S-adenosylmethionine cycle
Rv3846	Superoxide dismutase [Fe], SodA	Virulence, detoxification, adaptation	Y	Y	iron ion binding; superoxide dismutase activity	cytosol; extracellular region; periplasmic space; plasma membrane	evasion or tolerance by symbiont of host-produced reactive oxygen species; pathogenesis; response to oxidative stress
Rv0694	Possible L-lactate dehydrogenase (cytochrome) LldD1	Intermediate metabolism and respiration	C	Y	FMN binding; oxidoreductase activity	plasma membrane	
Rv0009	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (Cyclophilin) (Rotamase A)	Information pathways	C	Y	peptidyl-prolyl cis-trans isomerase activity	cell wall; cytosol; extracellular region; plasma membrane	protein folding; response to iron ion
Rv0053	30S ribosomal protein S6, Rpsf	Information pathways	Y	Y	small ribosomal subunit rRNA binding; structural constituent of ribosome	cell wall; cytosolic small ribosomal subunit; plasma membrane	translation
Rv0089	Uncharacterized methyltransferase Rv0089	Intermediate metabolism and respiration	N	Y	S-adenosylmethionine-dependent methyltransferase activity	cell wall; cytoplasm	methylation
Rv0129c	Diacylglycerol acyltransferase/mycolytransferase Ag85C (DGAT) (Acyl-CoA:diacylglycerol acyltransferase) (Antigen 85 complex C) (85C) (Ag85C) (Fibronectin-binding protein C) (Fbps C)	Lipid metabolism	N	Y	diacylglycerol O-acyltransferase activity; transferase activity, transferring acyl groups other than amino-acyl groups; trehalose O-mycolytransferase activity	cell wall; extracellular region	glycolipid biosynthetic process; lipid transport; mycolate cell wall layer assembly; response to antibiotic
Rv0166	Deoxyrib...	Regulatory	N	Y	DNA binding		

5c	transcriptional regulatory protein Mce1R (Probably GntR-family)	proteins			transcription factor activity, sequence-specific DNA binding		immune response; negative regulation of symbiont transcription in response to host; transcription, DNA-templated
Rv035 1	Protein GrpE (HSP-70 cofactor)	Virulence, detoxification, adaptation	Y	Y	adenyl-nucleotide exchange factor activity; unfolded protein binding	cell wall; cytoplasm	cellular response to starvation; growth; protein folding
Rv035 2	Chaperone protein DnaJ 1	Virulence, detoxification, adaptation	N	Y	ATP binding; zinc ion binding	cell wall; cytoplasm; plasma membrane	DNA replication; growth; protein folding; regulation of gene expression; response to heat
Rv038 3c	Possible conserved secreted protein	Cell wall and cell processes	Y	Y		cell wall; integral component of membrane; plasma membrane	growth
Rv041 0c	Serine/threonine-protein kinase PknG	Regulatory proteins	Y	Y	ATP binding; protein serine/threonine kinase activity	cytosol; plasma membrane	avoidance of host defenses; glutamate catabolic process; glutamine catabolic process; growth; modulation by symbiont of host phagocytosis; modulation by symbiont of host signal transduction pathway; negative regulation of cytolysis by symbiont of host cells; pathogenesis; positive regulation by symbiont of defense-related host reactive oxygen species production; protein autophosphorylation; response to antibiotic
Rv046 7	Isocitrate lyase (ICL) (Isocitrase)	Intermediary metabolism and respiration	Y	Y	isocitrate lyase activity; metal ion binding; methylisocitrate lyase activity; transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	cytosol; plasma membrane	cellular response to hypoxia; glyoxylate cycle; isocitrate metabolic process; maintenance of symbiont tolerance to host environment; pathogenesis; response to acetate; response to acid chemical; response to fatty acid; response to host immune response; tricarboxylic acid cycle
Rv047 0c	Cyclopropane mycolic acid synthase 3 (CMAS) (Cyclopropane-fatty-acyl-phospholipid	Lipid metabolism	I	Y	cyclopropane-fatty-acyl-phospholipid synthase activity		active evasion of host immune response; modulation by symbiont of host innate immune response; mycolic acid biosynthetic process; pathogenesis; S-adenosylmethionine metabolic process

	synthase) (CFA synthase) (Mycolic acid methyltransferase) (MA-MT) (S-adenosylmethionine-dependent methyltransferase) (AdoMet-MT) (SAM-MT)						
Rv0490	Sensor-like histidine kinase senX3	Regulatory proteins	I	Y	ATP binding; phosphorelay sensor kinase activity	extracellular region; integral component of membrane; intracellular; plasma membrane	pathogenesis; peptidyl-histidine phosphorylation; protein autophosphorylation
Rv0491	Sensory transduction protein regX3	Regulatory proteins	N	Y	DNA binding	intracellular	pathogenesis; phosphorelay signal transduction system; regulation of fatty acid metabolic process; regulation of phosphate metabolic process; regulation of response to stress; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv0600c	Sensor histidine kinase component HK1	Regulatory proteins	N	Y	ATP binding; phosphorelay response regulator activity; protein histidine kinase activity; protein kinase activity	intracellular	negative regulation of phosphorelay signal transduction system
Rv0644c	Cyclopropane mycolic acid synthase MmaA2 (CMAS) (Cyclopropane-fatty-acyl-phospholipid synthase) (CFA synthase) (Mycolic acid methyltransferase) (MA-MT) (S-adenosylmethionine-dependent	Lipid metabolism	N	Y	cyclopropane-fatty-acyl-phospholipid synthase activity; methyltransferase activity	cell wall; cytoplasm; plasma membrane	mycolic acid biosynthetic process

	methyltransferase) (AdoMet-MT) (SAM-MT)						
Rv0685	Elongation factor Tu (EF-Tu)	Information pathways	Y	Y	GTPase activity; GTP binding; translation elongation factor activity	cell wall; cytosol; plasma membrane	growth; response to hypoxia; response to iron ion; translational elongation
Rv0703	50S ribosomal protein L23, RplW	Information pathways	Y	Y	nucleotide binding; rRNA binding; structural constituent of ribosome	cytosol; cytosolic large ribosomal subunit; plasma membrane	growth; ribosomal large subunit assembly; translation
Rv0705	30S ribosomal protein S19, RpsS	Information pathways	Y	Y	rRNA binding; structural constituent of ribosome	cytosolic small ribosomal subunit; plasma membrane	growth; ribosomal small subunit assembly; translation
Rv0706	50S ribosomal protein L22, RplV	Information pathways	Y	Y	rRNA binding; structural constituent of ribosome	cell wall; cytosolic large ribosomal subunit	growth; translation
Rv0733	Adenylate kinase (AK) (ATP-AMP transphosphorylase) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase)	Intermediate metabolism and respiration	N	Y	adenylate kinase activity; ATP binding; nucleoside diphosphate kinase activity	cell wall; cytosol; plasma membrane	AMP salvage; nucleoside diphosphate metabolic process; nucleoside monophosphate metabolic process; nucleoside triphosphate metabolic process; purine nucleobase metabolic process
Rv0758	ATP-binding protein (Possible two component system response sensor kinase membrane associated PhoR)	Regulatory proteins	N	Y	ATP binding; phosphorelay sensor kinase activity	integral component of membrane; intracellular	
Rv0814c	Uncharacterized protein Rv0814c, SseC2	Intermediate metabolism and respiration	N	Y		cell wall; plasma membrane	
Rv0844c	Probable transcriptional regulatory protein	Regulatory proteins	N	Y	DNA binding		phosphorelay signal transduction system; regulation of transcription, DNA-templated;

Rv086 7c	Resuscitation-promoting factor RpfA	Cell wall and cell processes	N	Y	hydrolase activity	extracellular region	negative regulation of gene expression; pathogenesis; positive regulation of growth rate
Rv093 1c	Serine/threonine-protein kinase PknD	Regulatory proteins	N	Y	ATP binding; manganese ion binding; protein kinase activity; protein serine/threonine kinase activity	cell wall; cytosol; extracellular region; integral component of plasma membrane; plasma membrane	cellular response to phosphate starvation; negative regulation of catalytic activity; negative regulation of fatty acid biosynthetic process; negative regulation of protein binding; pathogenesis; positive regulation of catalytic activity
Rv101 5c	50S ribosomal protein L25 (General stress protein CTC), RplY	Information pathways	Y	Y	5S rRNA binding; structural constituent of ribosome	cytosol; ribosome	translation
Rv103 3c	Transcriptional regulator (Two component transcriptional regulator TrcR)	Regulatory proteins	N	Y	DNA binding	intracellular	phosphorelay signal transduction system; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv107 9	Cystathionine gamma-synthase (CGS) (O-succinylhomoserine (thiol)-lyase), MetB	Intermediate metabolism and respiration	I	Y	cystathionine gamma-lyase activity; cystathionine gamma-synthase activity; pyridoxal phosphate binding	cytoplasm; cytosol; plasma membrane	cysteine biosynthetic process via cystathionine; L-methionine biosynthetic process from L-homoserine via cystathionine; sulfur amino acid metabolic process; transsulfuration
Rv115 1c	NAD-dependent protein deacylase (Regulatory protein SIR2 homolog)	Regulatory proteins	N	Y	NAD+ binding; NAD+ nucleosidase activity; NAD-dependent protein deacetylase activity; protein-malonyllysine demalonylase activity; protein-succinyllysine desuccinylase activity; transferase activity; zinc ion binding	cell wall; cytoplasm	DNA repair; protein auto-ADP-ribosylation; protein deacetylation
Rv122 1	Alternative RNA polymerase sigma factor SigE	Information pathways	N	Y	DNA binding; sigma factor activity; transcription factor activity, sequence-specific DNA binding	cytoplasm	DNA-templated transcription, initiation; growth of symbiont in host cell; pathogenesis; regulation of chaperone-mediated protein complex assembly; response to heat; response to heat immune response; response to

							hydrogen peroxide; response to xenobiotic stimulus
Rv1240	Malate dehydrogenase, Mdh	Intermediary metabolism and respiration	N	Y	L-malate dehydrogenase activity	cell wall; cytosol; plasma membrane	carbohydrate metabolic process; malate metabolic process; NADH metabolic process; oxaloacetate metabolic process; tricarboxylic acid cycle
Rv1267c	Transcriptional regulatory protein EmbR	Regulatory proteins	N	Y	ATPase activity; DNA binding; GTPase activity	cell wall; intracellular; plasma membrane	phosphorelay signal transduction system; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv1392	S-adenosylmethionine synthase (AdoMet synthase) (MAT) (Methionine adenosyltransferase), MetK	Intermediary metabolism and respiration	Y	Y	ATP binding; magnesium ion binding; methionine adenosyltransferase activity	cell wall; cytosol; plasma membrane	growth; one-carbon metabolic process; S-adenosylmethionine biosynthetic process
Rv1436	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (NAD-dependent glyceraldehyde-3-phosphate dehydrogenase)	Intermediary metabolism and respiration	Y	Y	glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity; NAD binding; NADP binding	cell wall; cytosol; extracellular region; plasma membrane	glucose metabolic process; glycolytic process; growth
Rv1437	Phosphoglycerate kinase, Pgk	Intermediary metabolism and respiration	Y	Y	ATP binding; phosphoglycerate kinase activity	cytoplasm; extracellular region; plasma membrane	glycolytic process; growth
Rv1617	Pyruvate kinase (PK) PykA	Intermediary metabolism and respiration	Y	Y	ATP binding; kinase activity; magnesium ion binding; potassium ion binding; pyruvate kinase activity	cytosol; plasma membrane	growth
Rv1626	Probable transcriptional regulatory protein pdaR	Regulatory proteins	C	Y	RNA binding	cell wall; intracellular; plasma membrane	growth; phosphorelay signal transduction system; transcription, DNA-templated; transcription antitermination

4	(cytidine-2'-O)-methyltransferase TlyA (16S rRNA (cytidine1409-2'-O)-methyltransferase) (23S rRNA (cytidine1920-2'-O)-methyltransferase) (Hemolysin)	detoxification, adaptation			methyltransferase activity	cytoplasm; extracellular region; host cell plasma membrane; membrane	pathogenesis; rRNA methylation
Rv1747	ABC transporter ATP-binding/permease protein Rv1747	Cell wall and cell processes	N	Y	ATPase activity, coupled to transmembrane movement of substances; ATP binding	cell wall; cytosol; integral component of membrane; plasma membrane	
Rv1827	Glycogen accumulation regulator GarA	Conserved hypotheticals	Y	Y	identical protein binding	cell wall; extracellular region; plasma membrane	negative regulation of glycolytic process; protein autophosphorylation; regulation of cellular respiration
Rv1932	Probable thiol peroxidase, Tpx	Virulence, detoxification, adaptation	N	Y	disulfide oxidoreductase activity; peroxidase activity; peroxiredoxin activity; thioredoxin peroxidase activity	cell wall; cytosol; extracellular region	cell redox homeostasis; evasion or tolerance by symbiont of host-produced nitric oxide; oxidation-reduction process; pathogenesis; response to nitrosative stress; response to oxidative stress
Rv1984c	Probable cutinase Rv1984c	Cell wall and cell processes	N	Y	acylglycerol lipase activity; carboxylic ester hydrolase activity; short-chain carboxylesterase activity	cell wall; extracellular region	medium-chain fatty acid catabolic process; monoacylglycerol catabolic process; short-chain fatty acid catabolic process
Rv2068c	Beta-lactamase (Ambler class A beta-lactamase)	Intermediate metabolism and respiration	N	Y	beta-lactamase activity; cephalosporinase activity; penicillinase activity	extracellular region; periplasmic space; plasma membrane	beta-lactam antibiotic catabolic process; response to antibiotic
Rv2112c	Deamidase of Pup, Dop	Intermediate metabolism and	N	Y	ATP binding; hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds in		modification-dependent protein catabolic process; pathogenesis; proteasomal protein catabolic process; protein regulation

		respiration			linear amides; metal ion binding; peptidase activity		
Rv2234	Probable low molecular weight protein-tyrosine-phosphatase (PTPase)	Regulatory proteins	N	Y	protein tyrosine phosphatase activity	extracellular region; host cell endosome; plasma membrane	modification by symbiont of host morphology or physiology via secreted substance; negative regulation by symbiont of host cell-mediated immune response; pathogenesis; protein dephosphorylation
Rv2244	Meromycolate extension acyl carrier protein (ACP)	Lipid metabolism	Y	Y	ACP phosphopantetheine attachment site binding involved in fatty acid biosynthetic process; acyl binding	cell wall; cytosol; plasma membrane	acyl-CoA metabolic process; growth
Rv2445c	Nucleoside diphosphate kinase (NDK) (NDKA) (NDP kinase) (Nucleoside-2-P kinase)	Intermediary metabolism and respiration	N	Y	ATP binding; metal ion binding; nuclease activity; nucleoside diphosphate kinase activity	cytoplasm; extracellular region; host cell nucleus; intracellular; plasma membrane	CTP biosynthetic process; GTP biosynthetic process; nucleic acid phosphodiester bond hydrolysis; nucleoside triphosphate biosynthetic process; protein autophosphorylation; purine nucleotide metabolic process; pyrimidine nucleotide metabolic process; UTP biosynthetic process
Rv2582	Probable peptidyl-prolyl cis-trans isomerase B (PPIase B) (Rotamase B)	Information pathways	Y	Y	peptidyl-prolyl cis-trans isomerase activity	integral component of plasma membrane; plasma membrane	growth; protein folding
Rv2611c	Phosphatidylinositol mannoside acyltransferase (PIM acyltransferase)	Lipid metabolism	Y	Y	transferase activity, transferring acyl groups	integral component of membrane; plasma membrane	growth; phosphatidylinositol metabolic process
Rv2711	Iron-dependent repressor IdeR	Regulatory proteins	Y	Y	cadmium ion binding; cobalt ion binding; DNA binding; ferrous iron binding; iron ion binding; manganese ion binding; nickel cation binding; transcription factor activity, sequence-specific DNA binding; zinc ion	cell wall; cytoplasm; plasma membrane	growth; negative regulation of transcription, DNA-templated; regulation of transcription, DNA-templated; response to oxidative stress; siderophore biosynthetic process from catechol; transcription, DNA-templated

					binding		
Rv2956	Conserved protein	Conserved hypotheticals	N	Y	O-methyltransferase activity		
Rv3082c	HTH-type transcriptional regulator VirS (Virulence-regulating protein)	Virulence, detoxification, adaptation	N	Y	core promoter proximal region sequence-specific DNA binding; transcription factor activity, sequence-specific DNA binding	cytosol	cellular response to acidic pH; pathogenesis; positive regulation of transcription, DNA-templated; transcription, DNA-templated
Rv3143	Uncharacterized response regulatory protein Rv3143	Regulatory proteins	N	Y		cell wall; intracellular	phosphorelay signal transduction system
Rv3220c	Probable sensor histidine kinase pdtaS	Regulatory proteins	N	Y	ATP binding; phosphorelay sensor kinase activity; protein kinase activity	intracellular	phosphorelay signal transduction system; protein autophosphorylation
Rv3249c	Possible transcriptional regulatory protein (Probably TetR-family)	Regulatory proteins	N	Y	DNA binding		regulation of transcription, DNA-templated; transcription, DNA-templated
Rv3366	Putative tRNA (cytidine(34)-2'-O)-methyltransferase (tRNA (cytidine/uridine-2'-O)-methyltransferase), SpoU	Information pathways	N	Y	methyltransferase activity; RNA binding; S-adenosylmethionine-dependent methyltransferase activity; tRNA methyltransferase activity	cytoplasm	wobble position cytosine ribose methylation; wobble position uridine ribose methylation
Rv3418c	10 kDa chaperonin (10 kDa antigen) (BCG-A heat shock protein) (GroES protein) (Protein Cpn10)	Virulence, detoxification, adaptation	Y	Y	ATP binding; chaperone binding; metal ion binding; unfolded protein binding	cell wall; cytosol; extracellular region; GroEL-GroES complex; plasma membrane	cellular response to heat; chaperone mediated protein folding requiring cofactor; growth; regulation of transcription, DNA-templated; response to antibiotic; response to heat; response to unfolded protein

3c	dehydrogenase FadE29 (ACAD) (3-oxo-23,24-bisnorchol-4-en-22-oyl-CoA dehydrogenase beta subunit) (3-oxo-4-pregnene-20-carboxyl-CoA dehydrogenase beta subunit)	metabolism			dehydrogenase activity; electron carrier activity; FAD binding; fatty-acyl-CoA binding; flavin adenine dinucleotide binding; oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor		oxidation using acyl-CoA dehydrogenase; growth of symbiont in host; lipid homeostasis; pathogenesis
Rv3597c	Iron-regulated H-NS-like protein Lsr2	Information pathways	Y	Y	DNA binding	cell wall; cytosol; nucleoid; plasma membrane	cellular response to oxygen levels; DNA protection; growth; pathogenesis; regulation of transcription, DNA-templated; response to hydrogen peroxide; response to iron ion; transcription, DNA-templated
Rv3676	CRP-like cAMP-activated global transcriptional regulator (cAMP receptor protein) (CRP) (cAMP regulatory protein)	Regulatory proteins	N	Y	cAMP binding; DNA binding; transcription factor activity, sequence-specific DNA binding	cell wall; plasma membrane	growth; negative regulation of transcription, DNA-templated; pathogenesis; positive regulation of transcription, DNA-templated; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv3874	ESAT-6-like protein EsxB (10 kDa culture filtrate antigen CFP-10) (CFP-10) (Secreted antigenic protein MTSA-10)	Cell wall and cell processes	N	Y	host cell surface binding	cell wall; extracellular region; host cell endoplasmic reticulum; host cell surface; plasma membrane	pathogenesis; protein secretion by the type VII secretion system
Rv3875	6 kDa early secretory antigenic target (ESAT-6), EsxA	Cell wall and cell processes	N	Y	host cell surface binding; protein homodimerization activity	cell wall; cytoplasm; extracellular region; host cell endoplasmic reticulum; host cell plasma membrane; host cell surface; integral component	modulation by symbiont of host signal transduction pathway; negative regulation by symbiont of host cell-mediated immune response; pathogenesis; protein secretion by the type VII secretion system

						of membrane; plasma membrane	
Rv001 4c	Serine/threonine- protein kinase PknB	Regulatory proteins	Y	N	ATP binding; identical protein binding; manganese ion binding; protein kinase activity; protein serine/threonine kinase activity	cell wall; integral component of membrane; plasma membrane	growth; negative regulation of catalytic activity; negative regulation of fatty acid biosynthetic process; negative regulation of protein binding; pathogenesis; positive regulation of catalytic activity; positive regulation of DNA binding; protein autophosphorylation; regulation of cell shape; regulation of transferase activity; response to host immune response
Rv001 5c	Serine/threonine- protein kinase PknA	Regulatory proteins	Y	N	ATP binding; protein kinase activity; protein serine/threonine kinase activity	cytosol; extracellular region; integral component of membrane; plasma membrane	growth; negative regulation of catalytic activity; negative regulation of fatty acid biosynthetic process; negative regulation of lipid biosynthetic process; pathogenesis; positive regulation of catalytic activity; positive regulation of DNA binding; protein autophosphorylation; protein phosphorylation; regulation of cell shape
Rv001 6c	Penicillin-binding protein A (PBPA)	Cell wall and cell processes	N	N	penicillin binding; transferase activity	cell septum; cytosol; integral component of membrane; plasma membrane	cell wall assembly; peptidoglycan biosynthetic process; regulation of cell shape
Rv001 7c	Uncharacterized FtsW-like protein, RodA	Cell wall and cell processes	I	N		integral component of membrane; plasma membrane	cell cycle; cell division; positive regulation by symbiont of host immune response
Rv001 8c	PP2C-family Ser/Thr phosphatase (Mycobacterial Ser/Thr phosphatase) (Mstp) (Possible serine/threonine phosphatase Ppp)	Regulatory proteins	N	N	magnesium ion binding; manganese ion binding; phosphoprotein phosphatase activity; phosphoserine phosphatase activity; protein serine/threonine phosphatase activity	cell wall; integral component of membrane; integral component of plasma membrane	negative regulation of catalytic activity; negative regulation of DNA binding; negative regulation of protein kinase activity; positive regulation of catalytic activity; protein dephosphorylation
Rv002 4	Putative secreted protein P60- related protein	Virulence, detoxificati on, adaptation	N	N		plasma membrane	
Rv005	Single stranded	Information	Y	N	single stranded DNA	plasma membrane	

4	DNA-binding protein (SSB)	n pathways			binding	plasma membrane	DNA replication; response to antibiotic
Rv0091	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase (MTA/SAH nucleosidase) (MTAN) (5'-methylthioadenosine nucleosidase) (MTA nucleosidase) (S-adenosylhomocysteine nucleosidase) (AdoHcy nucleosidase) (SAH nucleosidase) (SRH nucleosidase)	Intermediary metabolism and respiration	N	N	adenosylhomocysteine nucleosidase activity	cytoplasm	L-methionine biosynthetic process from methylthioadenosine; nucleoside metabolic process
Rv0195	LuxR family transcriptional regulator (Possible two component transcriptional regulatory protein)	Regulatory proteins	N	N	DNA binding	cytoplasm	regulation of transcription, DNA-templated; transcription, DNA-templated
Rv0206c	Trehalose monomycolate exporter MmpL3 (TMM exporter MmpL3)	Cell wall and cell processes	Y	N		cell wall; extracellular region; integral component of plasma membrane	Actinobacterium-type cell wall biogenesis; cell wall organization; growth; lipopolysaccharide transport
Rv0228	Probable integral membrane acyltransferase	Intermediary metabolism and respiration	Y	N	transferase activity, transferring acyl groups other than amino-acyl groups	integral component of membrane; membrane	growth; lipopolysaccharide biosynthetic process
Rv0260c	Bifunctional phosphorelay system	Regulatory proteins	N	N	DNA binding; phosphorelay system III	cell wall; intracellular	phosphorelay signal transduction system; regulation of gene expression; regulation of

	-III synthetase/response regulator domain protein (Possible transcriptional regulatory protein)				synthase activity		transcription, DNA-templated; tetrapyrrole biosynthetic process
Rv0278c	Uncharacterized PE-PGRS family protein PE_PGRS3	PE/PPE	N	N			
Rv0287	ESAT-6-like protein EsxG (Conserved protein TB9.8)	Cell wall and cell processes	N	N		extracellular region	pathogenesis
Rv0350	Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein)	Virulence, detoxification, adaptation	Y	N	ATP binding	bacterial extracellular vesicle; capsule; cell surface; cell wall; cytosol; extracellular region; plasma membrane	cellular response to superoxide; growth; protein autophosphorylation; protein folding; response to antibiotic; response to copper ion; response to heat
Rv0363c	Fructose-bisphosphate aldolase (FBP aldolase) (FBPA) (Fructose-1,6-bisphosphate aldolase)	Intermediate metabolism and respiration	Y	N	fructose-bisphosphate aldolase activity; zinc ion binding	cell wall; cytosol; extracellular region; plasma membrane	gluconeogenesis; glycolytic process
Rv0409	Acetate kinase (Acetokinase)	Intermediate metabolism and respiration	N	N	acetate kinase activity; ATP binding; magnesium ion binding	cytoplasm	acetyl-CoA biosynthetic process; organic acid metabolic process
Rv0411c	ABC transporter substrate-binding protein (Probable glutamine-binding lipoprotein GlnH (GlnB))	Cell wall and cell processes	Y	N		extracellular region	growth

Rv0440	60 kDa chaperonin 2 (65 kDa antigen) (Antigen A) (Cell wall protein A) (GroEL protein 2) (Heat shock protein 65) (Protein Cpn60-2)	Virulence, detoxification, adaptation	Y	N	ATP binding	cell wall; cytosol; extracellular region; plasma membrane	adhesion of symbiont to host; growth; protein refolding; response to heat; response to hypoxia
Rv0475	Heparin-binding hemagglutinin (Adhesin), HbhA	Cell wall and cell processes	N	N	heparin binding; identical protein binding	cell surface; cell wall; cytosol; plasma membrane	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules; pathogenesis; positive regulation by symbiont of host receptor-mediated endocytosis
Rv0601c	Sensor histidine kinase component HK2	Regulatory proteins	N	N	phosphorelay sensor kinase activity; protein homodimerization activity; protein kinase activity	integral component of membrane; intracellular; plasma membrane	negative regulation of phosphorelay signal transduction system
Rv0602c	Transcriptional regulatory protein TcrA	Regulatory proteins	N	N	DNA binding; phosphorelay response regulator activity	cytoplasm; plasma membrane	negative regulation of phosphorelay signal transduction system; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv0677c	Siderophore export accessory protein MmpS5	Cell wall and cell processes	N	N		extracellular region; integral component of membrane; plasma membrane	pathogenesis
Rv0702	50S ribosomal protein L4, RplD	Information pathways	Y	N	RNA binding; rRNA binding; structural constituent of ribosome	cytosol; cytosolic ribosome; plasma membrane	growth; translation
Rv0710	30S ribosomal protein S17, RpsQ	Information pathways	Y	N	rRNA binding; structural constituent of ribosome	cytosolic small ribosomal subunit; plasma membrane	growth; translation
Rv0757	Possible two component system response transcriptional positive regulator PhoP	Regulatory proteins	Y	N	DNA binding	intracellular; plasma membrane	glycolipid biosynthetic process; negative regulation of transcription, DNA-templated; pathogenesis; phosphorelay signal transduction system; positive regulation of gene expression; positive regulation of lipid biosynthetic process; positive regulation of transcription, DNA-templated; protein secretion by the type VII secretion system; response to oxidative stress; transcription, DNA-templated

Rv0815c	Putative thiosulfate sulfurtransferase CysA2 (Rhodanese-like protein)	Intermediate metabolism and respiration	N	N	thiosulfate sulfurtransferase activity	cell wall; cytosol; plasma membrane	
Rv0818	Transcriptional regulatory protein	Regulatory proteins	N	N	DNA binding	intracellular; plasma membrane	nitrate assimilation; phosphorelay signal transduction system; positive regulation of transcription, DNA-templated; regulation of fatty acid metabolic process; regulation of gene expression; transcription, DNA-templated
Rv0845	Probable sensor histidine kinase NarS	Regulatory proteins	N	N	protein histidine kinase activity	integral component of membrane; intracellular; plasma membrane	phosphorelay signal transduction system
Rv0902c	Sensor-type histidine kinase PrrB	Regulatory proteins	Y	N	ATP binding; phosphorelay sensor kinase activity; protein kinase activity	cell wall; integral component of plasma membrane; intracellular	growth involved in symbiotic interaction; protein autophosphorylation
Rv0903c	Transcriptional regulatory protein PrrA	Regulatory proteins	Y	N	calcium ion binding; DNA binding; magnesium ion binding	cytosol; plasma membrane	growth involved in symbiotic interaction; phosphorelay signal transduction system; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv0929	Phosphate-transport integral membrane ABC transporter PstC2	Cell wall and cell processes	I	N	ATPase-coupled phosphate ion transmembrane transporter activity; inorganic phosphate transmembrane transporter activity	integral component of plasma membrane	growth of symbiont in host
Rv0930	Probable phosphate-transport integral membrane ABC transporter PstA1	Cell wall and cell processes	I	N	ATPase-coupled phosphate ion transmembrane transporter activity; inorganic phosphate transmembrane transporter activity	integral component of plasma membrane	growth of symbiont in host
Rv0946c	Glucose-6-phosphate isomerase (GPI)	Intermediate metabolism and	Y	N	glucose-6-phosphate isomerase activity	cytoplasm; plasma membrane	glucose-6-phosphate isomerase activity; growth

	isomerase) (PGI) (Phosphohexose isomerase) (PHI)	respiration					
Rv098 1	Mycobacterial persistence regulator MRPA	Regulatory proteins	N	N	DNA binding	cell wall; cytoplasm; plasma membrane	negative regulation of transcription, DNA- templated; pathogenesis; phosphorelay signal transduction system; positive regulation of transcription, DNA-templated; regulation of chaperone-mediated protein complex assembly; regulation of transcription, DNA-templated; response to stress; transcription, DNA- templated
Rv098 2	Two component sensor kinase MprB	Regulatory proteins	Y	N	ATP binding; kinase activity; phosphoprotein phosphatase activity; phosphorelay sensor kinase activity	extracellular region; integral component of membrane; intracellular; plasma membrane	growth; pathogenesis; peptidyl-histidine phosphorylation; phosphorelay signal transduction system
Rv099 5	GCN5 family acetyltransferase (Ribosomal- protein-alanine acetyltransferase RimJ (Acetylating enzyme for N- terminal of ribosomal protein S5))	Informatio n pathways	N	N	N-acetyltransferase activity	cytoplasm	N-terminal protein amino acid acetylation
Rv099 8	Acetyltransferase Pat (GCN5-like enzyme) (GCN5- related N- acetyltransferase) (GNAT) (Protein acetyltransferase) (Pat)	Conserved hypothetical s	N	N	acetyltransferase activity; cAMP binding; metal ion binding; N- acetyltransferase activity; transferase activity, transferring acyl groups	cytoplasm	
Rv102 3	Enolase (2- phospho-D- glycerate hydro- lyase) (2- phosphoglycerate dehydratase)	Intermediar y metabolism and respiration	Y	N	magnesium ion binding; phosphopyruvate hydratase activity	cell surface; cell wall; extracellular region; phosphopyruvate hydratase complex; plasma membrane	glycolytic process; growth

Rv102 7c	Transcriptional regulatory protein KdpE	Regulatory proteins	I	N	DNA binding	cytoplasm	growth; phosphorelay signal transduction system; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv102 8c	Sensor protein KdpD	Regulatory proteins	N	N	ATP binding; phosphorelay sensor kinase activity	cytoplasm; integral component of membrane; plasma membrane	response to stress
Rv103 2c	Histidine kinase (Two component sensor histidine kinase TrcS)	Regulatory proteins	N	N	ATP binding; calcium ion binding; manganese ion binding; phosphorelay sensor kinase activity; protein kinase activity	integral component of membrane; intracellular	protein autophosphorylation
Rv107 7	Putative cystathionine beta-synthase Rv1077 (Beta-thionase) (Serine sulfhydrase)	Intermediary metabolism and respiration	N	N	cystathionine beta-synthase activity; cysteine synthase activity; pyridoxal phosphate binding	cell wall; cytoplasm; extracellular region; plasma membrane	cysteine biosynthetic process from serine; cysteine biosynthetic process via cystathionine
Rv114 6	Probable conserved transmembrane transport protein MmpL13b	Cell wall and cell processes	N	N		integral component of membrane	positive regulation by symbiont of host immune response
Rv117 4c	Low molecular weight T-cell antigen (Low molecular weight T-cell antigen TB8.4)	Cell wall and cell processes	N	N	heme binding	cell wall; extracellular region	dormancy exit of symbiont in host
Rv119 7	ESAT-6-like protein EsxK	Cell wall and cell processes	N	N		extracellular region	
Rv119 8	ESAT-6-like protein EsxL	Cell wall and cell processes	N	N		cell wall; extracellular region; plasma membrane	pathogenesis
Rv126 6c	Serine/threonine-protein kinase PknH	Regulatory proteins	N	N	ATP binding; protein kinase activity; protein serine/threonine kinase activity	cell wall; integral component of	negative regulation of catalytic activity; negative regulation of growth; positive regulation of catalytic activity; positive regulation of DNA binding; positive regulation of transcription,

							regulation of lipid biosynthetic process; response to host immune response
Rv1312	Conserved hypothetical secreted protein	Cell wall and cell processes	N	N		integral component of membrane	
Rv1318c	Possible adenylate cyclase (ATP pyrophosphatase) (adenylyl cyclase)	Intermediate metabolism and respiration	N	N	adenylate cyclase activity; signal transducer activity	cytosol; integral component of membrane; plasma membrane	cAMP biosynthetic process; intracellular signal transduction; signal transduction
Rv1319c	Possible adenylate cyclase (ATP pyrophosphatase) (adenylyl cyclase)	Intermediate metabolism and respiration	N	N	adenylate cyclase activity; signal transducer activity	extracellular region; integral component of membrane; intracellular; plasma membrane	cAMP biosynthetic process; intracellular signal transduction; signal transduction
Rv1388	Putative integration host factor MihF	Information pathways	N	N		cell wall; cytosol; plasma membrane	growth
Rv1448c	Transaldolase	Intermediate metabolism and respiration	N	N	sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity	cytosol; extracellular region	carbohydrate metabolic process; growth; pentose-phosphate shunt
Rv1456c	Membrane protein (Probable unidentified antibiotic-transport integral membrane ABC transporter)	Cell wall and cell processes	Y	N	oxidoreductase activity, acting on the CH-CH group of donors	integral component of membrane	growth; heme a biosynthetic process
Rv1642	50S ribosomal protein L35, RpmI	Information pathways	N	N	structural constituent of ribosome	cytosolic large ribosomal subunit	translation
Rv1643	50S ribosomal protein L20, RplT	Information pathways	Y	N	rRNA binding; structural constituent of ribosome	cytosolic large ribosomal subunit; plasma membrane	ribosomal large subunit assembly; translation
Rv1743	Serine/threonine-protein kinase PknE	Regulatory proteins	N	N	ATP binding; protein kinase activity; protein serine/threonine kinase	extracellular region; integral component of membrane;	negative regulation of catalytic activity; negative regulation of fatty acid biosynthetic process; pathogenesis; positive regulation of catalytic

							phosphorylation; response to nitrosative stress
Rv174 6	Serine/threonine- protein kinase PknF	Regulatory proteins	N	N	ATP binding; protein kinase activity; protein serine/threonine kinase activity	cytosol; integral component of plasma membrane	barrier septum assembly; negative regulation of catalytic activity; negative regulation of lipid biosynthetic process; positive regulation of catalytic activity; regulation of cell growth; regulation of glucose transport
Rv179 3	ESAT-6-like protein EsxN	Cell wall and cell processes	N	N		extracellular region; plasma membrane	
Rv188 4c	Resuscitation- promoting factor RpfC	Cell wall and cell processes	N	N	hydrolase activity	extracellular region	negative regulation of gene expression; pathogenesis; positive regulation of gene expression; positive regulation of growth rate
Rv190 8c	Catalase- peroxidase (CP) (Peroxidase/catala se), KatG	Virulence, detoxificati on, adaptation	N	N	catalase activity; heme binding; metal ion binding; NADH binding; NADPH binding; oxidoreductase activity, acting on a heme group of donors, nitrogenous group as acceptor; peroxidase activity	cell wall; cytosol; extracellular region; plasma membrane	cellular response to hydrogen peroxide; evasion or tolerance by symbiont of host-produced reactive oxygen species; hydrogen peroxide catabolic process; pathogenesis; response to antibiotic; response to oxidative stress
Rv191 5	Putative isocitrate lyase subunit A (ICL) (Isocitrase) (Isocitratase)	Intermediar y metabolism and respiration	I	N	isocitrate lyase activity; methylisocitrate lyase activity; transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	cytoplasm	glyoxylate cycle; isocitrate metabolic process
Rv191 6	Putative isocitrate lyase subunit B (ICL) (Isocitrase) (Isocitratase)	Intermediar y metabolism and respiration	I	N	isocitrate lyase activity; transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	cytoplasm	glyoxylate cycle
Rv202 7c	Hypoxia sensor histidine kinase response regulator DosT	Regulatory proteins	N	N	ATP binding; calcium ion binding; carbon monoxide binding; heme binding; magnesium ion	cytoplasm; integral component of	detection of hypoxia; protein

					binding; oxygen binding; oxygen sensor activity; phosphorelay sensor kinase activity; protein histidine kinase activity; protein kinase activity		
Rv2048c	Polyketide synthase Pks12	Lipid metabolism	I+C	N	oxidoreductase activity; phosphopantetheine binding; transferase activity	plasma membrane	
Rv2088	Serine/threonine-protein kinase PknJ	Regulatory proteins	N	N	ATP binding; cobalt ion binding; nickel cation binding; protein serine/threonine kinase activity	integral component of membrane; plasma membrane	protein autophosphorylation; regulation of energy homeostasis
Rv2111c	Prokaryotic ubiquitin-like protein Pup (Bacterial ubiquitin-like modifier)	Intermediary metabolism and respiration	Y	N	protein tag		growth; modification-dependent protein catabolic process; proteasomal protein catabolic process; protein pupylation
Rv2145c	Cell wall synthesis protein Wag31 (Antigen 84)	Cell wall and cell processes	Y	N		cell pole; cell wall; cytoplasm; plasma membrane	cell cycle; cell division; growth; peptidoglycan-based cell wall biogenesis; protein stabilization; regulation of cell shape
Rv2150c	Cell division protein FtsZ	Cell wall and cell processes	Y	N	GTPase activity; GTP binding; magnesium ion binding	cell division site; cytoplasm; plasma membrane	barrier septum assembly; cell cycle; FtsZ-dependent cytokinesis; growth; protein polymerization
Rv2176	Serine/threonine-protein kinase PknL	Regulatory proteins	N	N	ATP binding; protein kinase activity; protein serine/threonine kinase activity	integral component of membrane; plasma membrane	negative regulation of fatty acid biosynthetic process; peptidyl-threonine phosphorylation; protein autophosphorylation
Rv2202c	Adenosine kinase (AK)	Intermediary metabolism and respiration	Y	N	adenosine kinase activity; ATP binding; carbohydrate kinase activity; dGTP binding; GTP binding; magnesium ion binding	cytoplasm; plasma membrane	AMP salvage; carbohydrate phosphorylation
Rv2232	Uncharacterized protein Rv2232, PkA	Regulatory proteins	N	N	magnesium ion binding; phosphatase activity		

					tyrosine kinase activity		
Rv224 3	Malonyl CoA-acyl carrier protein transacylase (MCT)	Lipid metabolism	Y	N	[acyl-carrier-protein] S-malonyltransferase activity	fatty acid synthase complex	fatty acid biosynthetic process
Rv224 5	3-oxoacyl-[acyl-carrier-protein] synthase 1 (Beta-ketoacyl-ACP synthase 1) (KAS 1)	Lipid metabolism	Y	N	3-oxoacyl-[acyl-carrier-protein] synthase activity	cell wall; cytosol; plasma membrane	fatty acid elongation; fatty acid elongation, saturated fatty acid; growth
Rv224 6	3-oxoacyl-[acyl-carrier-protein] synthase 2 (Beta-ketoacyl-ACP synthase 2) (KAS 2)	Lipid metabolism	N	N	3-oxoacyl-[acyl-carrier-protein] synthase activity	cell wall; cytoplasm; plasma membrane	fatty acid elongation; growth; mycolic acid biosynthetic process; response to hypoxia
Rv236 4c	GTPase Era	Intermediate metabolism and respiration	Y	N	GTPase activity; GTP binding; ribosomal small subunit binding; rRNA binding; small ribosomal subunit rRNA binding	cytosol; plasma membrane	growth; ribosomal small subunit assembly
Rv237 6c	Low molecular weight antigen MTB12 (CFP-2) (Low molecular weight protein antigen 2)	Cell wall and cell processes	N	N		cell wall; extracellular region	
Rv241 6c	Enhanced intracellular survival protein, Eis	Virulence, detoxification, adaptation	Y	N	aminoglycoside N-acetyltransferase activity	cytoplasm	aminoglycoside antibiotic catabolic process; growth of symbiont in host cell; growth of symbiont in host organelle; modulation by symbiont of defense-related host reactive oxygen species production; modulation by symbiont of host innate immune response; modulation by symbiont of host programmed cell death; positive regulation by symbiont of host inflammatory response
Rv262 2	Methyltransferase (Possible	Intermediate	N	N	S-adenosylmethionine-dependent		

	(Methylase))	and respiration			activity		
Rv2710	RNA polymerase sigma factor SigB	Information pathways	Y	N	DNA binding; RNA polymerase core enzyme binding; sigma factor activity; transcription factor activity, sequence-specific DNA binding	cytosol; plasma membrane	DNA-templated transcription, initiation; growth; positive regulation of transcription, DNA-templated; regulation of fatty acid metabolic process; regulation of protein secretion; response to heat; response to hypoxia; response to xenobiotic stimulus
Rv2884	Probable transcriptional regulatory protein	Regulatory proteins	N	N	DNA binding	intracellular	phosphorelay signal transduction system; regulation of transcription, DNA-templated
Rv2914c	Serine/threonine-protein kinase PknI	Regulatory proteins	C	N	ATP binding; manganese ion binding; protein kinase activity; protein serine/threonine kinase activity	cytosol; integral component of membrane; plasma membrane	pathogenesis; peptidyl-serine phosphorylation; peptidyl-threonine phosphorylation; protein autophosphorylation; regulation of growth rate
Rv2938	Probable doxorubicin resistance ABC transporter permease protein DrrC	Cell wall and cell processes	I	N	efflux transmembrane transporter activity	cell wall; extracellular region; integral component of plasma membrane	antibiotic transport; daunorubicin transport; doxorubicin transport; growth of symbiont in host cell; response to antibiotic; response to host immune response; transmembrane transport
Rv2952	Phthiotriol/phosphothiotriol dimycocerosates methyltransferase	Intermediate metabolism and respiration	N	N	O-methyltransferase activity; S-adenosylmethionine-dependent methyltransferase activity	cytoplasm; plasma membrane	DIM/DIP cell wall layer assembly; lipid metabolic process
Rv2954c	Uncharacterized protein (Methyltransferase)	Conserved hypotheticals	N	N	O-methyltransferase activity; S-adenosylmethionine-dependent methyltransferase activity	cytoplasm	
Rv2955c	Conserved protein (Methyltransferase)	Conserved hypotheticals	N	N	O-methyltransferase activity	cell wall; cytosol; plasma membrane	

9c	methyltransferase	y metabolism and respiration			activity		DIM/DIP cell wall layer assembly; lipid biosynthetic process
Rv2986c	DNA-binding protein HU homolog (21 kDa laminin-2-binding protein) (28 kDa iron-regulated protein) (Irep-28) (Histone-like protein) (Hlp)	Information pathways	Y	N	damaged DNA binding; double-stranded DNA binding; supercoiled DNA binding	cell wall; extracellular region; plasma membrane	cellular response to iron ion starvation; chromosome condensation; DNA protection; growth; nucleoid organization
Rv3004	Low molecular weight protein antigen 6 (CFP-6)	Cell wall and cell processes	N	N		extracellular region	
Rv3080c	Serine/threonine-protein kinase PknK (Protein kinase K)	Regulatory proteins	N	N	ATP binding; identical protein binding; metal ion binding; protein kinase activity; protein serine/threonine kinase activity	cell wall; cytosol; extracellular region; plasma membrane	pathogenesis; protein autophosphorylation; regulation of sequence-specific DNA binding transcription factor activity
Rv3132c	Redox sensor histidine kinase response regulator DevS	Regulatory proteins	Y	N	ATP binding; carbon monoxide binding; heme binding; magnesium ion binding; nitric oxide binding; oxygen binding; oxygen sensor activity; phosphorelay sensor kinase activity; protein kinase activity	cell wall; cytoplasm; integral component of membrane; plasma membrane	detection of hypoxia; detection of redox state; growth; protein autophosphorylation; response to redox state
Rv3133c	Transcriptional regulatory protein DevR (DosR)	Regulatory proteins	I	N	DNA binding; transcription factor activity, sequence-specific DNA binding	cell wall; cytosol; extracellular space; host cell cytoplasmic vesicle; host cell endosome lumen; plasma membrane	dormancy process; pathogenesis; phosphorelay signal transduction system; positive regulation of transcription, DNA-templated; regulation of fatty acid metabolic process; regulation of response to stress; response to hypoxia; transcription, DNA-templated
Rv3232c	Polyphosphate kinase 2	Intermediate	N	N	GTP binding; polyphosphate kinase	plasma membrane	growth of symbiont in host organelle; GTP biosynthetic process, protein

	(Polyphosphate kinase Ppk2 (Polyphosphoric acid kinase))	metabolism and respiration			activity		autophosphorylation; regulation of nucleotide biosynthetic process
Rv324 4c	Lipoprotein LpqB	Cell wall and cell processes	Y	N		cell wall; extracellular region; plasma membrane	growth
Rv324 5c	Sensor histidine kinase MtrB	Regulatory proteins	Y	N	ATP binding; phosphorelay sensor kinase activity	cytosol; integral component of membrane; plasma membrane	growth
Rv324 7c	Thymidylate kinase (Thymidine monophosphate kinase) (dTMP kinase) (TMPK)	Intermediary metabolism and respiration	Y	N	ATP binding; GTP binding; magnesium ion binding; protein homodimerization activity; thymidylate kinase activity; uridylate kinase activity	cytoplasm	dTDP biosynthetic process; dTTP biosynthetic process; dUDP biosynthetic process; TMP metabolic process
Rv331 3c	Adenosine deaminase (Adenosine aminohydrolase)	Intermediary metabolism and respiration	N	N	adenosine deaminase activity; zinc ion binding	cytosol	adenosine catabolic process; hypoxanthine salvage; inosine biosynthetic process; nucleotide metabolic process; purine ribonucleoside monophosphate biosynthetic process
Rv341 4c	ECF RNA polymerase sigma factor SigD (Alternative RNA polymerase sigma factor SigD)	Information pathways	N	N	DNA binding; sigma factor activity; transcription factor activity, sequence-specific DNA binding	cytoplasm	DNA-templated transcription, initiation; pathogenesis; regulation of fatty acid metabolic process; regulation of protein secretion; response to heat
Rv341 7c	60 kDa chaperonin 1 (GroEL protein 1) (Protein Cpn60-1)	Virulence, detoxification, adaptation	N	N	ATP binding; single-stranded DNA binding	bacterial nucleoid; cell surface; cell wall; cytoplasm; plasma membrane	DNA protection; growth; nucleoid organization; protein refolding; response to heat
Rv345 9c	30S ribosomal protein S11	Information pathways	Y	N	mRNA 5'-UTR binding; small ribosomal subunit rRNA binding; structural constituent of ribosome	cytosolic small ribosomal subunit; plasma membrane	growth; maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA); ribosomal small subunit assembly; translation
Rv354 4c	Probable acyl-CoA oxidase 1	Lipid metabolism	N	N	FAD binding; oxidoreductase activity		cholesterol catabolic process; fatty acid beta-oxidation

	dehydrogenase FadE28				acting on the CH-CH group of donors		growth of symbiont in host; pathogenesis; response to pH
Rv356 0c	Acyl-CoA dehydrogenase (Probable acyl- CoA dehydrogenase FadE30)	Lipid metabolism	I+C	N	acyl-CoA dehydrogenase activity; electron carrier activity; fatty-acyl-CoA binding; flavin adenine dinucleotide binding; oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	plasma membrane	fatty acid beta-oxidation using acyl-CoA dehydrogenase; lipid homeostasis
Rv356 2	Acyl-CoA dehydrogenase (Probable acyl- CoA dehydrogenase FadE31)	Lipid metabolism	N	N	acyl-CoA dehydrogenase activity; electron carrier activity; fatty-acyl-CoA binding; flavin adenine dinucleotide binding; oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	plasma membrane	fatty acid beta-oxidation using acyl-CoA dehydrogenase; lipid homeostasis
Rv356 3	Probable acyl- CoA dehydrogenase FadE32	Lipid metabolism	I+C	N	acyl-CoA dehydrogenase activity; electron carrier activity; fatty-acyl-CoA binding; flavin adenine dinucleotide binding; oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	cytoplasm	fatty acid beta-oxidation using acyl-CoA dehydrogenase; lipid homeostasis
Rv356 4	Acyl-CoA dehydrogenase (Probable acyl- CoA dehydrogenase FadE33)	Lipid metabolism	C	N	acyl-CoA dehydrogenase activity; electron carrier activity; fatty-acyl-CoA binding; flavin adenine dinucleotide binding; oxidoreductase activity, acting on the CH-CH group of donors, with a	cytoplasm	fatty acid beta-oxidation using acyl-CoA dehydrogenase; lipid homeostasis

					flavin as acceptor		
Rv376 4c	Probable sensor histidine kinase TcrY	Regulatory proteins	N	N	ATPase activity; ATP binding; calcium ion binding; magnesium ion binding; phosphorelay sensor kinase activity; protein homodimerization activity	cytosol; integral component of membrane; plasma membrane	protein autophosphorylation
Rv376 5c	Probable transcriptional regulatory protein TcrX	Regulatory proteins	N	N	DNA binding	cytoplasm	cellular response to iron ion starvation; phosphorelay signal transduction system; regulation of transcription, DNA-templated; transcription, DNA-templated
Rv386 3	Uncharacterized protein	Regulatory proteins	Y	N	DNA binding	cell wall; plasma membrane	

Table S1: Details of 180 candidate protein-coding genes. Cells in green color shows methylated proteins identified in the study. Cell in light pink color shows the protein for which methylation was not detected by mass spectrometer. Cells in indigo color represents proteins that were purified but not detected as methylated by western blot.

Table S2: Methylated peptides identified by mass spectrometry.

Gene	Number of sites on protein	Position within protein	Localization probability	Score diff	PE P	Score	Delta score	Number of Methyl (KR)	Amino acid	Sequence window	Peptide window coverage	Methyl (KR) Probabilities	Methyl (KR) Score diffs	Position in peptide	Charge	Mass error [ppm]	Intensity
Rv015 3c	3	56	1.00	121.90	1.66 E-03	121.9	77.581	1	R	RATLRR LGITDV ADLRSS REVAR RGPGR VPD	XXXXXXXXPPPP PPPPXXXXXXXX XXXXXXXXXX	LGITDVADLR(1)	LGITDVADLR(1 21.9)	10	2	-0.37539	4.21E+07
Rv015 3c	3	154	0.82	6.71	5.47 E-03	47.68	44.534	1	R	AQRAL HRVVT LLAAG RPVLTH CFAGK DRTGF	XXXXXXXXPPPP PPPPPPPPPP PPPPPPPPPP PPPPPPPPPP PPPPPPPPPP PPPPPPPPPP	VVTLAAGR(0.824)PVLTHCFAGK(0.1 76)	VVTLAAGR(6.7 1)PVLTHCFAG K(-6.71)	9	4	0.60576	2.92E+08
Rv015 3c	3	164	0.90	9.39	3.68 E-14	125.45	123.34	1	K	LLAAG RPVLTH CFAGK DRTGF VVALVL EAVG	PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP	VVTLAAGR(0.103)PVLTHCFAGK(0.8 97)	VVTLAAGR(- 9.39)PVLTHCFA GK(9.39)	19	3	-0.19039	1.67E+08
Rv1438	4	103	1.00	90.41	1.14 E-06	90.412	82.002	1	R	LAKLGCS YVVVGH SERRTYH NEDDAL VAAKA	XXXXXXXXPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP	LGCSYVVVGHSER(1)	LGCSYVVVGHSER (90.41)	13	2	0.11294	0.00E+00
Rv1438	4	139	1.00	96.21	4.12 E-06	96.208	89.076	1	R	HGLTPIV CIGEHLD VREAGN HVAHNI EQLRG	PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	HGLTPIVCIGEHLDV R(1)	HGLTPIVCIGEHL DVR(96.21)	16	3	0.37472	9.44E+08
Rv1438	4	181	1.00	118.64	3.11 E-24	118.63	117.9	1	R	SVVIAYE PVWAIG TGRVASA ADAQEV CAAIR	PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	GSLAGLLAEQIGSVVI AYEPVWAIGTGR(1)	GSLAGLLAEQIGS VVIAYEPVWAIGT GR(118.63)	28	3	0.23633	9.39E+06
Rv1438	4	196	0.56	1.02	1.42 E-05	87.519	73.818	1	R	RVASAA DAQEVC AAIRKEL ASLSPRI ADTV	XXXXXXXXPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	VASAADAQEVCAAIR (0.559)K(0.441)	VASAADAQEVCA AIR(1.02)K(-1.02)	15	3	0.17231	7.17E+07
Rv1872c	1	11	0.99	23.08	1.01 E-03	63.706	60.56	1	R	—MA VNRRVP RVRDLAP LLQFNRP QFDI	XXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXX	VR(0.995)DLAPLLQFN R(0.005)PQFDTSK	VR(23.08)DLAPLLQ FNR(- 23.08)PQFDTSK(- 36.58)	2	4	0.47703	2.10E+07
Rv2703	1	15	0.85	7.41	2.93 E-02	40.496	21.54	1	K	_MAATK ASTATDE PVKRTAT KSPAASA SGAK	XXXXXXXXPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	ASTATDEPVK(0.846)R (0.154)	ASTATDEPVK(7.41)R(-7.41)	10	2	-0.0037856	4.26E+07
Rv2875	1	118	1.00	96.34	7.98 E-04	96.342	58.998	1	K	NAAFSKL PASTIDE LKTINSL LTSILTY HVV	XXXXXXXXPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	LPASTIDELK(1)	LPASTIDELK(96.34)	10	2	0.33379	2.51E+05
Rv2889c	4	100	1.00	58.12	7.36 E-03	58.123	50.038	1	K	FQTLAD QVAAA AAAKPA DVDALK GASIGD K	PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	NAEFQTLADQVVAA AAAAK(1)	NAEFQTLADQVV AAAAAK(58.12)	19	2	1.0924	1.56E+07
Rv2889c	4	150	1.00	95.26	9.41 E-05	95.264	92.296	1	R	RRVAIFD GTVEAY LHRRSAD IPPAVGV	XXXXXXXXPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP PPPPPPPPPPPPPP	VAIHFGTVEAYLHR(1)	VAIHFGTVEAYLH R(95.26)	14	3	-0.44689	1.08E+08

Rv2889c	4	151	0.58	1.39	5.07 E-08	116.51	89.739	1	R	RVAIFDG TVEAYL HRRSADL PPAVGVL VEYR	XPPPPPPPPPPPP PXXXXXXXXXXXX XXXXX	VAFIDGTVEAYLHR(0 421)R(0.579)	VAFIDGTVEAYLH R(-1.39)R(1.39)	15	4	-0.515	1.84E+0 8
Rv2889c	4	262	1.00	81.9 2	6.84 E-03	81.92	48.831	1	R	KTVKAL LDVAGV TVTRFVR FEVGQA	XXXXPPPPPPPPPP PXXXXXXXXXXXX XXXXX	ALLDVAGVTVTR(1)	ALLDVAGVTVTR(81.92)	12	2	-0.31422	9.02E+0 7
Rv3246c	13	46	1.00	101. 92	6.81 E-09	101.92	89.033	1	R	DTAVIG DGTQAL TAVREL PDLVLLD LMLPG	PPPPPPPPPPPPPP PXXXXXXXXXXXX XXXXX	GEGFDTAVIGDGTQ ALTAVR(1)	GEGFDTAVIGDGTQ ALTAVR(101.92)	20	2	0.37687	6.33E+0 7
Rv3246c	13	72	1.00	74.7 9	8.23 E-04	82.877	70.385	1	R	LMLPGM NGIDVC RVLRAVS GVPIVML TAKTD	XXXXXXXXXXXXXX XPPPPPPPPPPPP PPPPX	VLR(1)ADSGVPIVMLT AK	VLR(74.79)ADSGVP IVMLTAK(-74.79)	3	2	-0.1078	2.84E+0 8
Rv3246c	13	85	1.00	41.6 2	1.69 E-03	67.997	63.481	1	K	VLRADS GVPIVML TAKTDT VDVVLG LESAD	XXXXPPPPPPPPPP PXXXXXXXXXXXX XXXXX	ADSGVPIVMLTAK(1)	ADSGVPIVMLTAK (41.62)	13	2	0.98921	2.70E+0 8
Rv3246c	13	105	0.85	6.70	2.19 E-45	165.1	155.7	1,2	K	DVVLGL ESGADD YIMKPK PKELVAR VRARL	PPPPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP XXX	TDTVDDVVLGLES GADDYIMK(0.85)PFK(0.8 5)PK(0.299)	TDTVDDVVLGLES GADDYIMK(6.7)PF K(6.7)PK(6.7)	20	4	0.58761	8.73E+0 8
Rv3246c	13	108	0.85	6.70	2.19 E-45	128.88	127.21	2	K	LGLES DDYIMK PFKPKEL VARVAR RLRRN	PPPPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP XXXX	TDTVDDVVLGLES GADDYIMK(0.85)PFK(0.8 5)PK(0.299)	TDTVDDVVLGLES GADDYIMK(6.7)PF K(6.7)PK(6.7)	23	4	0.58761	7.59E+0 8
Rv3246c	13	110	0.74	1.55	5.28 E-12	88.872	85.75	2	K	LESAD DYIMKPK KPKELV ARVRARL RRNDD	PPPPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP XXXX	TDTVDDVVLGLES GADDYIMK(0.63)PFK(0.6 3)PK(0.741)	TDTVDDVVLGLES GADDYIMK(0)PFK (0)PK(1.55)	25	3	0.47793	1.41E+0 8
Rv3246c	13	122	1.00	127. 78	9.00 E-34	162.11	157.8	1	R	FKPKELV ARVRARL RRNDD PAEMLSI ADVE	XXXXXXXXXXXXXX XPPPPPPPPPPPP PPPPPPPPPPPP PPPPP	R(1)NDDEPAEMLSIA DVEIDVPAHK	R(127.78)NDDEPA EMLSIA DVEIDV PAHK(-127.78)	1	4	-0.77349	5.98E+0 8
Rv3246c	13	144	1.00	101. 36	1.98 E-58	207.17	206.06	1	K	EMLSIAD VEIDVPA HKVTRN GEQISLT PLEF	PPPPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP XXXX	RNDDEPAEMLSIA DVEIDVPAHK(1)	R(- 101.36)NDDEPAE MLSIA DVEIDV PAHK(101.36)	23	4	-0.67454	2.11E+0 9
Rv3246c	13	167	1.00	56.0 2	5.85 E-19	143.46	139.38	1	R	ISLTPLF DLLVALA RKPRQV FTRDVL EQV	PPPPPPPPPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP XXXX	NGEQISLTPLF DLLVALAR(1)	NGEQISLTPLF DLLVALAR(56.02)	20	3	-1.2252	1.40E+0 8
Rv3246c	13	200	1.00	65.2 5	9.71 E-03	79.469	61.649	1	R	YRHPAD TRLVNV HVQRLR AKVEKD PENPTVV	XXXXXXXXPPPPPP PPPPPPPPPPPP PPPPPPPPPPPP XXXXXX	LVNVHVQR(1)	LVNVHVQR(65.25)	8	2	-0.13874	2.30E+0 8
Rv3246c	13	204	1.00	94.9 4	1.03 E-19	149.47	146.56	1,2	K	ADTRLV NVHVQR LRAKVE KDPENP TVVLTVR	XXXXXXXXXXXXXX XPPPPPPPPPPPP PPPPPPPPPPPP PPPPP	AK(1)VEK(1)DPENPT VTVR	AK(94.94)VEK(95.2) DPENPTVTVR(- 94.94)	2	4	-0.23266	5.58E+0 8
Rv3246c	13	207	1.00	90.5 7	7.82 E-25	185.26	176.26	1,2	K	RLVNVH VQRLRA KVEKDP ENPTVVL TVRGGV	XXXXXXXXXXXXXP PPPPPPPPPPPPPP PPPPPPPPPPPP PXXXX	VEK(1)DPENPTVTVR	VEK(90.57)DPENP TVVLTVR(-90.57)	3	3	0.35713	2.64E+0 9
Rv3246c	13	219	1.00	93.6 1	1.49 E-10	109.72	107.79	1	R	KVEKDP ENPTVVL TVRGGV VKAGDP	PPPPPPPPPPPPPP PXXXXXXXXXXXX XXXXX	DPENPTVTVR(1)	DPENPTVTVR(93.61)	12	2	0.84151	1.53E+0 8

Rv3248c	5	8	1.00	60.44	1.63E-02	60.436	38.665	1	K	MTGNLV TKNSLTP DVRNGI DFKI	XXXXXXXXXXPP PPPPXXXXXXXX XXXXXXX	TGNLVTK(1)	TGNLVTK(60.44)	7	1	-0.24929	2.40E+05
Rv3248c	5	276	1.00	61.78	7.06E-03	61.78	41.081	1	K	LIDGINR GTDALIG GKKVLIC YGDVVG KGCA	XXXXXXXXPPPP PPPPPPPPPP XXXXXX	GTDALIGGK(1)	GTDALIGGK(61.78)	9	2	0.032999	0.00E+00
Rv3248c	5	277	1.00	64.49	2.96E-03	67.136	55.217	1	K	IDGINRG TDALIGG KKVLICG YGDVVG GCAE	XXXXXXXXXXXX PPPPPPPPPP PXXXX	K(1)VLICGYDVGK	K(64.49)VLICGYDVGK(-64.49)	1	2	0.11205	2.46E+08
Rv3248c	5	448	1.00	199.80	1.05E-68	199.8	199.8	1	R	IELWTK NDEYDN EVYRLPK HLDEKV ARIHVE	XXXXXPPPPPP PPPPPPPPPP XXXXXX	NDEYDNEVYR(1)	NDEYDNEVYR(199.8)	10	2	0.22627	9.98E+05
Rv3248c	5	471	1.00	90.61	4.41E-06	95.822	88.765	1	K	KVARIHV EALGGH LTKLTKE QAEYLG VDVEG	XXXXPPPPPPPP PPPPPPPPPP XXXX	IHVEALGGHLTK(1)	IHVEALGGHLTK(90.61)	12	2	1.3323	3.40E+08
Rv3846	6	38	1.00	95.36	6.04E-27	166.03	162.83	1	K	QINELH HSKHHA TYVKG NDAVAK LEEARK	XXXXXXXXXXPP PPPPPPPPPP XXXXXX	HHATYVK(1)GANDAVAK	HHATYVK(95.36)GANDAVAK(-95.36)	7	3	0.33384	1.27E+08
Rv3846	6	46	1.00	26.09	2.06E-02	56.569	43.292	1	K	KHHATY VKGAND AVAKLE EARAKE DHSAILL	XXXXXXXXPPPP PPPPPPPPPP XXXXXX	GANDAVAK(0.998)LEEAR(0.002)	GANDAVAK(26.09)LEEAR(-26.09)	8	3	-0.9437	1.19E+08
Rv3846	6	53	1.00	71.63	8.50E-04	91.307	69.532	1	K	KGANDA VAKLEE ARAKED HSAILLN EKNLAF	XXXXXXXXXX XXPPPPPPPP PXXXX	AK(1)EDHSAILLNEK	AK(71.63)EDHSAILLNEK(-71.63)	2	3	1.6193	1.31E+08
Rv3846	6	81	1.00	88.39	3.12E-06	88.385	81.149	1	K	LAFNLA GHVNHT IWWKNL SPNGGD KPTGEL A	PPPPPPPPPP PPPPPPPPPP XXXX	NLAFNLAGHVNHTIWWK(1)	NLAFNLAGHVNHTIWWK(88.39)	17	3	-0.16001	4.21E+08
Rv3846	6	110	0.58	1.38	2.80E-18	99.536	95.414	1	R	LAAAAD AFGSFD KFRAQF HAAATT VQSGW	PPPPPPPPPP PPPPPPPPPP XXXX	NLSPNGGDKPTGELAAAADAFGSFDK(0.421)FR(0.579)	NLSPNGGDK(-63.49)PTGELAAAADAFGSFDK(-1.38)FR(1.38)	29	4	0.017534	3.98E+07
Rv3846	6	179	1.00	135.69	3.09E-42	183.22	169.9	1	K	HAFYLQ YKNVKV DFAKAF WNVVN WADVQS RY	XXXXXXXXXX PPPPPPPPPP PPPX	VDFAK(1)AFWNVVNWADVQSR	VDFAK(135.69)AFWNVVNWADVQSR(-135.69)	5	2	-0.27803	6.36E+07

Table S3: The table shows mass spectrometric signal defined by the type of identification- either by “MS/MS” or by “match between run event (matching)”. The fold change in signal intensities are shown relative to those in MtrA.

Amino acid position	Identification type				Fold change over WT		
	WT	MtrA-R122M	MtrA-K207M	MtrA-K204M	MtrA-R122M	MtrA-K207M	MtrA-K204M
K85	MS/MS	matching	MS/MS		0.334	0.463	0.000
K105	matching	matching	MS/MS	MS/MS	0.054	0.000	0.211
K108	matching	matching	MS/MS	MS/MS	0.054	0.240	0.060
K110	matching	matching	MS/MS	MS/MS	0.048	0.240	0.058
R122	MS/MS	MS/MS	MS/MS	MS/MS	0.022	0.103	0.243
K144	MS/MS	MS/MS	MS/MS	MS/MS	0.047	0.181	0.235
R200	MS/MS	MS/MS	MS/MS		0.339	0.530	0.000
K204	MS/MS	MS/MS			0.020	0.000	0.000
K207	MS/MS	MS/MS	matching		0.503	0.004	0.000
R219	MS/MS	MS/MS		matching	0.331	0.000	0.009