

Table S1 Pathological scoring of murine spleens infected by *B. melitensis* M28 and its derivatives. Scores were given by at least two pathologists in a blinded manner, and range from 0 to 3: 0, normal (no pathology, similar/equivalent to the uninfected group); 1, mild pathological change; 2, moderate pathological change; 3, severe pathological change.

	Uninfected	M28	M28ΔtatA	M28ΔtatA pBBRtatA
White pulp to red pulp ratio	~1:1	Markedly reduced, (2-3)	No change, (0)	Reduced, (1)
Average lymphoid follicles per field	~10	Reduced, (2)	No change, (0)	Reduced, (2)
Size of follicles	Normal	Reduced, (1)	Minimal change, (0-1)	Reduced, (2)
Marginal zone depletion	Normal	Increased, (2)	Minimal to moderately increased, (1)	Markedly increased, (3)
Extramedullary hematopoiesis	Minimal	Moderately increased, (2)	Minimal, (0-1)	Moderately increased, (2)
Granulomas	Absent	Frequent, (3)	Absent, (0)	Frequent, (2-3)
Brucella immunoreactivities	Absent	Frequent, (3)	Rare, (1)	Frequent, (2-3)

Table S2 Putative Tat-substrates predicted by TAT-P.

M28 locus tag	Product	Note
_locus_tag_BM28_RS00045_	ABC transporter substrate-binding protein	Four yes Found RRHFM as Tat motif starting at pos. 8
_locus_tag_BM28_RS00235_	hypothetical protein	Three yes Found RRRFL as Tat motif starting at pos. 10
_locus_tag_BM28_RS00330_	hypothetical protein	Four yes Found RRMVT as Tat motif starting at pos. 10
_locus_tag_BM28_RS00655_	L,D-transpeptidase	Three yes Found RRQVV as Tat motif starting at pos. 56
_locus_tag_BM28_RS01600_	CAP domain-containing protein	Five yes Found RRGFL as Tat motif starting at pos. 11
_locus_tag_BM28_RS01755_	twin-arginine translocation signal domain-containing protein	Five yes Found RRSFL as Tat motif starting at pos. 7
_locus_tag_BM28_RS02425_	DsbA family protein	Four yes Found RRHVI as Tat motif starting at pos. 7
_locus_tag_BM28_RS02635_	ABC transporter substrate-binding protein	Three yes Found RRNLM as Tat motif starting at pos. 2
_locus_tag_BM28_RS02950_	hypothetical protein	Four yes Found RRKAL as Tat motif starting at pos. 73
_locus_tag_BM28_RS03675_	murein L,D-transpeptidase	Five yes Found RRRFL as Tat motif starting at pos. 15
_locus_tag_BM28_RS04380_	M48 family peptidase	Four yes Found RRIFV as Tat motif starting at pos. 95
_locus_tag_BM28_RS05450_	L,D-transpeptidase	Five yes Found RRILL as Tat motif starting at pos. 4
_locus_tag_BM28_RS05715_	TAXI family TRAP transporter solute-binding subunit_	Four yes Found RRLAV as Tat motif starting at pos. 8
_locus_tag_BM28_RS05780_	50S ribosomal protein L17	Four yes Found RRQAI as Tat motif starting at pos. 63
_locus_tag_BM28_RS10140_	apolipoprotein N-acyltransferase	Five yes Found RRLLL as Tat motif starting at pos. 65
_locus_tag_BM28_RS11540_	nitrous-oxide reductase	Five yes~ Found RRQLL as Tat motif starting at pos. 12
_locus_tag_BM28_RS11570_	thiamine biosynthesis protein ApbE	Five yes~ Found RRRVL as Tat motif starting at pos. 5
_locus_tag_BM28_RS12380_	ABC transporter substrate-binding protein	Five yes Found RRQAL as Tat motif starting at pos. 30
_locus_tag_BM28_RS12730_	hypothetical protein	Five yes Found RRAVM as Tat motif starting at pos. 13
_locus_tag_BM28_RS13455_	multicopper oxidase CueO	Five yes Found RRRL as Tat motif starting at pos. 6
_locus_tag_BM28_RS13760_	Hint domain-containing protein	Five yes Found RRHFL as Tat motif starting at pos. 15
_locus_tag_BM28_RS13965_	extracellular solute-binding protein	Four yes Found RRQAL as Tat motif starting at pos. 5
_locus_tag_BM28_RS14670_	MetQ_NlpA family ABC transporter	Five yes

	substrate-binding protein	Found RRAGL as Tat motif starting at pos. 12
_locus_tag_BM28_RS14815_	protein-methionine-sulfoxide reductase catalytic subunit MsrP	Five yes Found RREFM as Tat motif starting at pos. 28
_locus_tag_BM28_RS14970_	50S ribosomal protein L34	Three yes Found RRHGF as Tat motif starting at pos. 14
_locus_tag_BM28_RS15630_	D-xylose ABC transporter substrate-binding protein	Four yes Found RRNFL as Tat motif starting at pos. 3
_locus_tag_BM28_RS00220_	SH3 domain-containing protein	Four yes
_locus_tag_BM28_RS00240_	hypothetical protein	Five yes
_locus_tag_BM28_RS00310_	lytic transglycosylase domain-containing protein	Four yes
_locus_tag_BM28_RS00345_	invasion associated locus B family protein	Three yes
_locus_tag_BM28_RS16010_	hypothetical protein	Three yes
_locus_tag_BM28_RS00740_	organic solvent tolerance protein OstA	Five yes
_locus_tag_BM28_RS16050_	hypothetical protein	Five yes
_locus_tag_BM28_RS00840_	YraN family protein	Three yes
_locus_tag_BM28_RS00885_	BA14K family protein_	Five yes
_locus_tag_BM28_RS00945_	sigma-54-dependent Fis family transcriptional regulator	Four yes
_locus_tag_BM28_RS01135_	SDR family oxidoreductase	Four yes
_locus_tag_BM28_RS01500_	esterase	Four yes
_locus_tag_BM28_RS01515_	multidrug efflux RND transporter periplasmic adaptor subunit BepD	Five yes
_locus_tag_BM28_RS01730_	invasion associated locus B family protein	Five yes
_locus_tag_BM28_RS01770_	hypothetical protein	Four yes
_locus_tag_BM28_RS01860_	DsbA family protein	Five yes
_locus_tag_BM28_RS01890_	peptide antibiotic transporter SbmA	Three yes
_locus_tag_BM28_RS02075_	enoyl-_acyl-carrier-protein_ reductase FabI	Four yes
_locus_tag_BM28_RS02140_	DUF937 domain-containing protein	Four yes
_locus_tag_BM28_RS02250_	3-oxoacyl-_acyl-carrier-protein_ reductase	Three yes
_locus_tag_BM28_RS16245_	hypothetical protein	Three yes
_locus_tag_BM28_RS02285_	invasion associated locus B family protein	Five yes
_locus_tag_BM28_RS02290_	cytochrome c oxidase subunit II	Four yes
_locus_tag_BM28_RS02360_	sensor domain-containing phosphodiesterase	Four yes
_locus_tag_BM28_RS02460_	DUF1499 domain-containing protein	Three yes
_locus_tag_BM28_RS16315_	hypothetical protein	Three yes
_locus_tag_BM28_RS02645_	Gfo_Idh_MocA family oxidoreductase	Three yes
_locus_tag_BM28_RS02810_	DUF1491 family protein	Three yes
_locus_tag_BM28_RS16335_	phage tail assembly chaperone	Five yes
_locus_tag_BM28_RS02960_	cytochrome c biogenesis protein CcmE	Three yes
_locus_tag_BM28_RS02975_	DegQ family serine endoprotease	Three yes
_locus_tag_BM28_RS03075_	hypothetical protein	Five yes

_locus_tag_BM28_RS03080_	DUF423 domain-containing protein	Four yes
_locus_tag_BM28_RS03205_	GTPase Era	Three yes
_locus_tag_BM28_RS03350_	META domain-containing protein	Four yes
_locus_tag_BM28_RS03390_	ribonuclease T_2	Three yes
_locus_tag_BM28_RS03395_	phage portal protein	Four yes
_locus_tag_BM28_RS03415_	DUF992 domain-containing protein	Four yes
_locus_tag_BM28_RS03445_	hypothetical protein	Four yes
_locus_tag_BM28_RS03450_	SDR family oxidoreductase	Five yes
_locus_tag_BM28_RS03570_	hypothetical protein	Four yes
_locus_tag_BM28_RS03660_	enoyl-CoA hydratase_isomerase family protein	Three yes
_locus_tag_BM28_RS03715_	outer membrane protein assembly factor BamE	Four yes
_locus_tag_BM28_RS03760_	undecaprenyl-phosphate glucose phosphotransferase	Three yes
_locus_tag_BM28_RS03770_	polysaccharide export protein	Four yes
_locus_tag_BM28_RS03850_	hypothetical protein_	Four yes
_locus_tag_BM28_RS03915_	NADH-quinone oxidoreductase subunit Nuol	Three yes
_locus_tag_BM28_RS03970_	lipoprotein-releasing ABC transporter permease subunit	Four yes
_locus_tag_BM28_RS04075_	VOC family protein	Four yes
_locus_tag_BM28_RS04270_	hypothetical protein	Five yes
_locus_tag_BM28_RS16460_	hypothetical protein	Three yes
_locus_tag_BM28_RS04570_	transporter substrate-binding domain-containing protein	Three yes
_locus_tag_BM28_RS04580_	molybdenum cofactor guanylyltransferase	Five yes
_locus_tag_BM28_RS04605_	hypothetical protein	Five yes
_locus_tag_BM28_RS04670_	hypothetical protein	Three yes
_locus_tag_BM28_RS04755_	septal ring lytic transglycosylase RlpA family protein	Three yes
_locus_tag_BM28_RS04760_	D-alanyl-D-alanine carboxypeptidase	Four yes
_locus_tag_BM28_RS04800_	DMT family transporter	Four yes
_locus_tag_BM28_RS04850_	glutathione-disulfide reductase	Four yes
_locus_tag_BM28_RS16540_	D-alanyl-D-alanine carboxypeptidase_ _pseudo	Five yes
_locus_tag_BM28_RS16590_	hypothetical protein	Three yes
_locus_tag_BM28_RS05445_	CTP synthase	Three yes
_locus_tag_BM28_RS05455_	preprotein translocase subunit SecG	Three yes
_locus_tag_BM28_RS05540_	outer membrane protein assembly factor BamA	Five yes
_locus_tag_BM28_RS05585_	DUF1849 family protein	Five yes
_locus_tag_BM28_RS05615_	ATP-dependent Clp protease adapter ClpS	Three yes
_locus_tag_BM28_RS05760_	OmpA family protein	Three yes
_locus_tag_BM28_RS05810_	50S ribosomal protein L15	Three yes
_locus_tag_BM28_RS06100_	hypothetical protein	Four yes

_locus_tag_BM28_RS06105_	hypothetical protein	Three yes
_locus_tag_BM28_RS06140_	porin family protein	Four yes
_locus_tag_BM28_RS06170_	hypothetical protein	Four yes
_locus_tag_BM28_RS06220_	cobalt-precorrin-6A reductase	Four yes
_locus_tag_BM28_RS06595_	potassium transporter Kup	Three yes
_locus_tag_BM28_RS06640_	DegQ family serine endoprotease	Five yes
_locus_tag_BM28_RS06795_	cell division protein FtsQ_DivIB	Three yes
_locus_tag_BM28_RS06820_	putative lipid II flippase FtsW	Three yes
_locus_tag_BM28_RS06865_	lytic transglycosylase domain-containing protein	Three yes
_locus_tag_BM28_RS06890_	lytic murein transglycosylase	Five yes
_locus_tag_BM28_RS06975_	linear amide C-N hydrolase_	Four yes
_locus_tag_BM28_RS07015_	SIMPL domain-containing protein	Four yes
_locus_tag_BM28_RS07020_	hypothetical protein	Five yes
_locus_tag_BM28_RS07080_	ABC transporter ATP-binding protein_permease	Three yes
_locus_tag_BM28_RS07145_	DUF1176 domain-containing protein	Four yes
_locus_tag_BM28_RS07150_	DMT family transporter	Four yes
_locus_tag_BM28_RS07315_	cytochrome c1	Four yes
_locus_tag_BM28_RS07345_	hypothetical protein	Four yes
_locus_tag_BM28_RS07385_	DUF1285 domain-containing protein	Five yes
_locus_tag_BM28_RS07480_	choline ABC transporter substrate-binding protein	Five yes
_locus_tag_BM28_RS07660_	SDR family oxidoreductase	Three yes
_locus_tag_BM28_RS07710_	D-threitol dehydrogenase_ _pseudo	Three yes
_locus_tag_BM28_RS07725_	sugar ABC transporter ATP-binding protein	Three yes
_locus_tag_BM28_RS07900_	tonB-system energizer ExbB	Five yes
_locus_tag_BM28_RS07915_	phosphodiester glycosidase family protein	Five yes
_locus_tag_BM28_RS07935_	efflux RND transporter periplasmic adaptor subunit	Three yes
_locus_tag_BM28_RS08010_	phosphoglucosamine mutase	Three yes
_locus_tag_BM28_RS08050_	protein TolR	Three yes
_locus_tag_BM28_RS08160_	5-formyltetrahydrofolate cyclo-ligase	Three yes
_locus_tag_BM28_RS07660_	SDR family oxidoreductase	Three yes
_locus_tag_BM28_RS08290_	glycine zipper 2TM domain-containing protein	Four yes
_locus_tag_BM28_RS08305_	thiamine_thiamine pyrophosphate ABC transporter permease ThiP	Three yes
_locus_tag_BM28_RS08325_	RNA polymerase factor sigma-32	Four yes
_locus_tag_BM28_RS08380_	3-hydroxybutyrate dehydrogenase	Three yes
_locus_tag_BM28_RS08290_	glycine zipper 2TM domain-containing protein	Four yes
_locus_tag_BM28_RS08455_	F0F1 ATP synthase subunit beta	Three yes
_locus_tag_BM28_RS08545_	MFS transporter_ _pseudo_true	Four yes
_locus_tag_BM28_RS08550_	NAD-glutamate dehydrogenase	Five yes
_locus_tag_BM28_RS08585_	lytic murein transglycosylase	Four yes

_locus_tag_BM28_RS08630_	S41 family peptidase	Four yes
_locus_tag_BM28_RS08915_	ammonium transporter	Four yes
_locus_tag_BM28_RS09105_	_protein_hypothetical	Three yes
_locus_tag_BM28_RS09390_	_protein_hypothetical	Five yes
_locus_tag_BM28_RS09400_	outer membrane lipoprotein carrier protein LolA	Five yes
_locus_tag_BM28_RS09450_	membrane protein	Four yes
_locus_tag_BM28_RS16950_	_protein_hypothetical	Three yes
_locus_tag_BM28_RS09595_	3-ketoacyl-ACP reductase	Four yes
_locus_tag_BM28_RS09600_	GMC family oxidoreductase	Four yes
_locus_tag_BM28_RS16970_	_protein_hypothetical	Three yes
_locus_tag_BM28_RS09765_	DUF1402 family protein	Five yes
_locus_tag_BM28_RS09860_	two-component sensor histidine kinase	Five yes
_locus_tag_BM28_RS09875_	double-strand break repair protein AddB	Four yes
_locus_tag_BM28_RS09925_	M48 family peptidase	Three yes
_locus_tag_BM28_RS10040_	_protein_hypothetical	Five yes
_locus_tag_BM28_RS10235_	_protein_hypothetical	Three yes
_locus_tag_BM28_RS10280_	_protein_hypothetical	Three yes
_locus_tag_BM28_RS10610	lytic murein transglycosylase	Three yes
_locus_tag_BM28_RS10675	DUF882 domain-containing protein	Five yes
_locus_tag_BM28_RS10985	flagellar basal body P-ring formation protein FlgA	Four yes
_locus_tag_BM28_RS11005	flagellar basal body protein FlhL	Five yes
_locus_tag_BM28_RS11065	autotransporter outer membrane beta-barrel domain-containing protein	Four yes
_locus_tag_BM28_RS11225	insulinase family protein	Three yes
_locus_tag_BM28_RS11470_	nitrite reductase, copper-containing	Five yes
_locus_tag_BM28_RS11590_	ABC transporter substrate-binding protein	Five yes
_locus_tag_BM28_RS11760_	DUF3597 domain-containing protein	Five yes
_locus_tag_BM28_RS11800_	hypothetical protein	Four yes
_locus_tag_BM28_RS11875_	peptidase S58 family protein	Five yes
_locus_tag_BM28_RS11945_	cupredoxin domain-containing protein	Three yes
_locus_tag_BM28_RS12075_	peptide ABC transporter substrate-binding protein	Four yes
_locus_tag_BM28_RS12150_	putative colanic acid biosynthesis acetyltransferase	Four yes
_locus_tag_BM28_RS12200_	glutamate-1-semialdehyde 2,1-aminomutase	Four yes
_locus_tag_BM28_RS12220_	dTDP-4-dehydrorhamnose 3,5-epimerase	Three yes
_locus_tag_BM28_RS12330_	YeeE_YedE family protein	Three yes
_locus_tag_BM28_RS17210_	hypothetical protein	Three yes
_locus_tag_BM28_RS12725_	DUF995 domain-containing protein	Five yes
_locus_tag_BM28_RS17245_	hypothetical protein	Four yes
_locus_tag_BM28_RS12780_	hypothetical protein	Five yes
_locus_tag_BM28_RS12865_	invasion associated locus B family protein	Four yes
_locus_tag_BM28_RS12870_	_ABC transporter substrate-binding	Four yes

	protein	
_locus_tag_BM28_RS17250_	hypothetical protein	Four yes
_locus_tag_BM28_RS12930_	BA14K family protein	Three yes
_locus_tag_BM28_RS13140_	amidohydrolase	Three yes
_locus_tag_BM28_RS13240_	sn-glycerol-3-phosphate ABC transporter substrate-binding protein UgpB	Four yes
_locus_tag_BM28_RS13320_	siderophore ABC transporter substrate-binding protein	Four yes
_locus_tag_BM28_RS13365_	Ppx_GppA family phosphatase	Three yes
_locus_tag_BM28_RS13370_	RlmE family RNA methyltransferase	Four yes
_locus_tag_BM28_RS13460_	hypothetical protein	Three yes
_locus_tag_BM28_RS13535_	ABC transporter substrate-binding protein	Four yes
_locus_tag_BM28_RS17285_	hypothetical protein	Four yes
_locus_tag_BM28_RS13595_	BA14K family protein	Four yes
_locus_tag_BM28_RS13605_	glycine betaine ABC transporter substrate-binding protein	Four yes
_locus_tag_BM28_RS13645_	SDR family oxidoreductase	Five yes
_locus_tag_BM28_RS13740_	glutamine synthetase	Three yes
_locus_tag_BM28_RS13785_	glucose 1-dehydrogenase	Five yes
_locus_tag_BM28_RS13935_	nickel ABC transporter, nickel_metallophore periplasmic binding protein	Four yes
_locus_tag_BM28_RS14085_	hypothetical protein	Three yes
_locus_tag_BM28_RS14340_	thioredoxin	Five yes
_locus_tag_BM28_RS14465_	FdhF_YdeP family oxidoreductase	Four yes
_locus_tag_BM28_RS14735_	hypothetical protein	Four yes
_locus_tag_BM28_RS14765_	SDR family oxidoreductase	Four yes
_locus_tag_BM28_RS14850_	ABC transporter substrate-binding protein	Five yes
_locus_tag_BM28_RS14865_	TonB-dependent copper receptor	Five yes
_locus_tag_BM28_RS15010_	transglutaminase	Five yes
_locus_tag_BM28_RS15080_	SDR family oxidoreductase	Three yes
_locus_tag_BM28_RS15085_	penicillin-insensitive murein endopeptidase	Four yes
_locus_tag_BM28_RS15175_	bifunctional demethylmenaquinone methyltransferase_2-methoxy-6-polypren yl-1,4-benzoquinol methylase UbiE	Four yes
_locus_tag_BM28_RS15375_	ABC transporter substrate-binding protein	Four yes
_locus_tag_BM28_RS15720_	APC family permease	Five yes
_locus_tag_BM28_RS17515_	hypothetical protein	Three yes~

Table S3 Putative TAT-substrates predicted by TAT-FIND.

M28 locus tag	Product
[locus_tag=BM28_RS00235]	[protein=hypothetical]
[locus_tag=BM28_RS01600]	CAP domain-containing protein
[locus_tag=BM28_RS02275]	guanylate kinase
[locus_tag=BM28_RS02740]	L,D-transpeptidase
[locus_tag=BM28_RS07325]	ubiquinol-cytochrome c reductase iron-sulfur subunit
[locus_tag=BM28_RS01755]	twin-arginine translocation signal domain-containing protein
[locus_tag=BM28_RS03675]	murein L,D-transpeptidase
[locus_tag=BM28_RS00010]	DNA polymerase III subunit beta
[locus_tag=BM28_RS11540]	nitrous-oxide reductase
[locus_tag=BM28_RS11570]	thiamine biosynthesis protein ApbE
[locus_tag=BM28_RS17000]	BMP family ABC transporter substrate-binding protein
[locus_tag=BM28_RS13845]	ABC transporter substrate-binding protein
[locus_tag=BM28_RS11470]	nitrite reductase, copper-containing
[locus_tag=BM28_RS10730]	DUF1007 family protein
[locus_tag=BM28_RS10375]	twin-arginine translocation signal domain-containing protein
[locus_tag=BM28_RS15800]	aliphatic sulfonate ABC transporter substrate-binding protein
[locus_tag=BM28_RS11465]	lipase
[locus_tag=BM28_RS12110]	LPS biosynthesis protein
[locus_tag=BM28_RS13455]	multicopper oxidase CueO
[locus_tag=BM28_RS13965]	extracellular solute-binding protein
[locus_tag=BM28_RS14815]	protein-methionine-sulfoxide reductase catalytic subunit MsrP
[locus_tag=BM28_RS12380]	ABC transporter substrate-binding protein
[locus_tag=BM28_RS11590]	ABC transporter substrate-binding protein
[locus_tag=BM28_RS13140]	amidohydrolase
[locus_tag=BM28_RS15630]	D-xylose ABC transporter substrate-binding protein

Table S4 Putative TAT-substrates predicted by PRED-TAT.

M28 locus tag	Product	Note
BM28_RS00045	ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site
BM28_RS00235	hypothetical protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 38
BM28_RS01600	CAP domain-containing protein]	Tat signal peptide predicted. Most likely cleavage site: 1 - 34
BM28_RS01755	twin-arginine translocation signal domain-containing protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 34
BM28_RS01860	DsbA family protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 27
BM28_RS02425	DsbA family protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 29
BM28_RS02740	L,D-transpeptidase	Tat signal peptide predicted. Most likely cleavage site: 1 - 29
BM28_RS03245	TIGR02301 family protein]	Tat signal peptide predicted. Most likely cleavage site: 1 - 27
BM28_RS03675	murein L,D-transpeptidase	Tat signal peptide predicted. Most likely cleavage site: 1 - 40
BM28_RS05225	LysR family transcriptional regulator]	Tat signal peptide predicted. Most likely cleavage site: 1 - 31
BM28_RS05375	Bifunctional 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase/2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Tat signal peptide predicted. Most likely cleavage site: 1 - 55
BM28_RS06600	pyridoxine 5'-phosphate synthase	Tat signal peptide predicted. Most likely cleavage site: 1 - 38
BM28_RS06975	linear amide C-N hydrolase	Tat signal peptide predicted. Most likely cleavage site: 1 - 36
BM28_RS07325	ubiquinol-cytochrome c reductase iron-sulfur subunit	Tat signal peptide predicted. Most likely cleavage site: 1 - 48
BM28_RS08305	thiamine/thiamine pyrophosphate ABC transporter permease ThiP	Tat signal peptide predicted. Most likely cleavage site: 1 - 40
BM28_RS08910	DNA translocase FtsK	Tat signal peptide predicted. Most likely cleavage site: 1 - 63
BM28_RS17000	BMP family ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 32
BM28_RS10375	twin-arginine translocation signal domain-containing protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 29
BM28_RS11465	Lipase	Tat signal peptide predicted. Most likely cleavage site: 1 - 25
BM28_RS11470	nitrite reductase, copper-containing	Tat signal peptide predicted. Most likely cleavage site: 1 - 42
BM28_RS11540	nitrous-oxide reductase	Tat signal peptide predicted. Most likely cleavage site: 1 - 44
BM28_RS11570	thiamine biosynthesis protein ApbE	Tat signal peptide predicted. Most likely cleavage site: 1 - 27

BM28_RS11590	ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 28
BM28_RS11875	peptidase S58 family protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 27
BM28_RS12110	LPS biosynthesis protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 51
BM28_RS12380	ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 52
BM28_RS12550	thiol reductant ABC exporter subunit CydD	Tat signal peptide predicted. Most likely cleavage site: 1 - 57
BM28_RS12730	hypothetical protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 37
BM28_RS13140	Amidohydrolase	Tat signal peptide predicted. Most likely cleavage site: 1 - 39
BM28_RS13455	multicopper oxidase CueO	Tat signal peptide predicted. Most likely cleavage site: 1 - 29
BM28_RS13760	Hint domain-containing protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 44
BM28_RS13845	ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 30
BM28_RS13965	extracellular solute-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 25
BM28_RS14670	MetQ/NlpA family ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 37
BM28_RS14815	protein-methionine-sulfoxide reductase catalytic subunit MsrP	Tat signal peptide predicted. Most likely cleavage site: 1 - 49
BM28_RS15630	D-xylose ABC transporter substrate-binding protein	Tat signal peptide predicted. Most likely cleavage site: 1 - 28

Table S5 Comparisons of Tat substrates between *B. melitensis* M28 and other bacterial species.

Tat substrates in <i>B. melitensis</i> M28	<i>E. coli</i>		<i>Y. pstb</i> ^b		<i>P. aeruginosa</i>		<i>S. coelicolor</i>		<i>M. loti</i> ^c	
	Homologous substrate	Identity	Homologous substrate	Identity	Homologous substrate	Identity	Homologous substrate	Identity	Homologous substrate	Identity
Substrate/solute-binding protein										
A0009	/ ^a	/	/	/	/	/	SCO7677	21%	mll5493	54%
A0376	/	/	/	/	/	/	/	/	mlr5166	55%
B0279	/	/	/	/	/	/	/	/	mll9181	23%
B0446	/	/	/	/	/	/	/	/	mlr6082	29%
B0520	/	/	/	/	/	/	/	/	/	/
B0754	/	/	/	/	/	/	SCO7677	27%	mlr3395	74%
B0779	/	/	/	/	/	/	/	/	/	/
B0934	/	/	/	/	/	/	/	/	mll4794	62%
Oxidoreductases										
A0396	/	/	/	/	/	/	/	/	mlr7525	25%
B0019	YedY	36%	/	/	PA4692	33%	/	/	mlr0879	63%
B0251	/	/	/	/	PA2065	27%	/	/	mll3586	27%
B0672	CueO	40%	PRK10965	39%	PA3768	28%	/	/	mll3586	33%
B0965	YedY	55%	PRK05363	54%	PA4692	51%	/	/	mlr0879	36%
Cell envelope biosynthesis										
A0577	/	/	/	/	/	/	/	/	mll1519	60%
A0773	/	/	/	/	/	/	/	/	mlr8397	62%
A1479	/	/	/	/	/	/	/	/	/	/
B0388	/	/	/	/	/	/	/	/	/	/
Others										
A0340	/	/	/	/	/	/	/	/	mll8234	44%
B0340	/	/	/	/	/	/	/	/	/	/
B0737	/	/	/	/	/	/	/	/	/	/
RS03245	/	/	/	/	/	/	/	/	/	/
B0249	/	/	/	/	/	/	/	/	/	/
B0604	/	/	/	/	/	/	/	/	/	/

a. "/" indicates that no homolog exist in that organism based on a BLASTP search of amino acid sequences.

b and c. Substrates of these bacteria were predicted by bioinformatics, but not verified experimentally.

Table S6 Strains and plasmids used in this study.

Strains and plasmids	Description	Source or reference
Strains		
<i>B.melitensis</i> M28	Parental strain;smooth phenotype	Our lab stock
ΔtatA	Deletion strain for <i>tatA</i> gene, km ^r	This study
ΔA0009	Deletion strain for A0009 gene, km ^r	This study
ΔA0340	Deletion strain for A0340 gene, km ^r	This study
ΔA0376	Deletion strain for A0376 gene, km ^r	This study
ΔA0396	Deletion strain for A0396 gene, km ^r	This study
ΔA0577	Deletion strain for A0577 gene, km ^r	This study
ΔRS03245	Deletion strain for RS03245 gene, km ^r	This study
ΔA0773	Deletion strain for A0773 gene, km ^r	This study
ΔA1479	Deletion strain for A1479 gene, km ^r	This study
ΔB0019	Deletion strain for B0019 gene, km ^r	This study
ΔB0249	Deletion strain for B0249 gene, km ^r	This study
ΔB0251	Deletion strain for B0251 gene, km ^r	This study
ΔB0279	Deletion strain for B0279 gene, km ^r	This study
ΔB0340	Deletion strain for B0340 gene, km ^r	This study
ΔB0446	Deletion strain for B0446 gene, km ^r	This study
ΔB0520	Deletion strain for B0520 gene, km ^r	This study
ΔB0604	Deletion strain for B0604 gene, km ^r	This study
ΔB0672	Deletion strain for B0672 gene, km ^r	This study
ΔB0737	Deletion strain for B0737 gene, km ^r	This study
ΔB0754	Deletion strain for B0754 gene, km ^r	This study
ΔB0779	Deletion strain for B0779 gene, km ^r	This study
ΔB0934	Deletion strain for B0934 gene, km ^r	This study
ΔB0965	Deletion strain for B0965 gene, km ^r	This study
ΔB1133	Deletion strain for B1133 gene, km ^r	This study
M28ΔtatApBBRtatA	ΔtatA strain carrying the plasmid pBBR-tatA, Amp ^r	This study
E.coli strains		
DH5α	F ⁻ Φ80lacZΔM15 Δ(lacZYA-argF) U169 <i>recA1 endA1 hsdR17</i> (rk ⁻ , mk ⁺) <i>phoA</i> supE44 <i>thi-1 gyrA96 relA1 λ-</i>	Invitrogen
MC 4100	F ⁻ Δlac U169 <i>araD139 rpsL150 relA1 ptsFrbs flb5301</i>	Our lab stock
MC4100ΔssamiAC	as MC4100, <i>amiA</i> Δ2–33, <i>amiC</i> Δ2–32	This study
MC4100ΔtatC	deletion strain for <i>tatC</i> gene	This study
Plasmid		
pSP72	suicide vector, Amp ^r	[1]
pBBR1MCS4	Broad-host range cloning vector;Amp ^r	[2]
pSP72-Ptat	pT7.5-similar vectorallowing constitutive expression under the control of the <i>Brucella tat</i> promoter or inducible expression from the upstream T7promoter (Amp ^r)	This study
pssAmiA-AmiAH	ssAmiA fused to mature AmiA carrying a C-terminal hexa histidine tag in pSP72-Ptat	This study
pssA0009-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by BM28_ A0009 signal peptide	This study
pss A0340-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study

	BM28_A0340signal peptide	
pss A0376-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A0376signal peptide	
pss A0396-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A0396signal peptide	
pss A0577-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A0577signal peptide	
pssRS03245-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_RS03245signal peptide	
pss A0773-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A0773signal peptide	
pss A1479-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A1479signal peptide	
pss B0019-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0019signal peptide	
pss B0249-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0249signal peptide	
pss B0251-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0251signal peptide	
pss B0279-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0279signal peptide	
pss B0340-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0340signal peptide	
pss B0388-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0388signal peptide	
pss B0446-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0446signal peptide	
pss B0520-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0520signal peptide	
pss B0604-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0604signal peptide	
pss B0672-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0672signal peptide	
pss B0737-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0737signal peptide	
pss B0754-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0754signal peptide	
pss B0779-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0779signal peptide	
pss B0934-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0934signal peptide	
pss B0965-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B0965signal peptide	
pss B1133-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_B1133signal peptide	
pss A0515-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A0515signal peptide	
pss A1551-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by	This study
	BM28_A1551signal peptide	

pss A1757-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by BM28_A1757signal peptide	This study
pss A1724-AmiAH	As pssAmiA-AmiAH but where AmiA signal peptide has beenreplaced by BM28_A1724signal peptide	This study

Table S7 Primers used in this study

Primer	Nucleotide sequence(5' -3')	Purpose of use
A0889-HA1-F	caggtcgactctagaggatccCCTCGCCGGTGACGCTTG	Amplification of upstream
A0889-HA1-R	ATTATTCCTCTCAGTGCCGCC	homologous arm
A0889-Km-F	gcggcactgagaggaataaTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
A0889-Km-R	ccggaaggaTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
A0889-HA2-F	agttcttctgaTCCTTCCGGGATGAACTGC	Amplification of
A0889-HA2-R	tctgatatcatcgaattcCTGTTTTGCGAAAGCAAAGCA	downstream homologous arm
TatA-COM-F	cgctctagaactagtgatccAATTGCGCGGCGCAGGGC	Amplification of <i>tatA</i> and its
TatA-COM-R	gataagcttgatcgaattcTCAGGACTTGGTGGTCTTCTTGA	promoter region
A0577-HA1-F	caggtcgactctagaggatccGCTTATAGCGATTTCTGGAAACTG	Amplification of upstream
A0577-HA1-R	gcggatacatattgaaATGAAAACCAAGATTGATGATGGG	homologous arm
A0577-Km-F	catTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
A0577-Km-R	cctactgcctaaacTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
A0577-HA2-F	tctgaGTTTAGGGCAGTAGGGCTGTAGG	Amplification of
A0577-HA2-R	tctgatatcatcgaattcGTCGGCATCTATTTCGTCACG	downstream homologous arm
A0396-HA1-F	caggtcgactctagaggatccGGACCGATGCTCACGTTTTTC	Amplification of upstream
A0396-HA1-R	gaaGAGCTTTCTCCTTTGCCCGA	homologous arm
A0396-Km-F	ggcaaaggagaaagctcTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
A0396-Km-R	atcccaggaTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
A0396-HA2-F	ttcttctgaTCCTGCGGGATAAAAGGGC	Amplification of
A0396-HA2-R	tctgatatcatcgaattcCAGGTGCGCAGGATTATCGC	downstream homologous arm
A0773-HA1-F	caggtcgactctagaggatccTGGAGGCTCTCCAGCTTGTC	Amplification of upstream
A0773-HA1-R	TTGATTAACGTCCCAAAAGGCT	homologous arm
A0773-Km-F	cctttgggacgttaatacaTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
A0773-Km-R	gacgcaaTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
A0773-HA2-F	cgagttcttctgaTTGCGTCAAAAACCACTGTT	Amplification of
A0773-HA2-R	tctgatatcatcgaattcAATAGGCCGTGCCGCCTG	downstream homologous arm
B0249-HA1-F	caggtcgactctagaggatccCCAGGTGCGGATAAAGGATATG	Amplification of upstream
B0249-HA1-R	ttgaaCCTGTCTGTTTCGGCAGCA	homologous arm

B0249-Km-F	gccgaaacagacaggTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0249-Km-R	cgcagcgttTCAGAAGAACTCGTCAAGAAGGC	
B0249-HA2-F	agttcttctgaAACGCTGCGCTCAGCCAA	Amplification of downstream homologous arm
B0249-HA2-R	tctgatatcatc gatgaattcAATCGTCTGATGCACGACC	
B0019-HA1-F	caggtcgactctagaggatccGACAATTGATTTACCGCCAGCG	Amplification of upstream homologous arm
B0019-HA1-R	ttgaaGATTGTTTTCTCCGTCTTTTCGTCC	
B0019-Km-F	gacggagaacaatcTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0019-Km-R	gatccggtacTCAGAAGAACTCGTCAAGAAGGC	
B0019-HA2-F	gttcttctgaGTACCGGATCGGGCGGCT	Amplification of downstream homologous arm
B0019-HA2-R	tctgatatcatc gatgaattcACGCTTATCGGGCAAGCC	
B0279-HA1-F	caggtcgactctagaggatccGTTTCTGGCGCAGCTCGG	Amplification of upstream homologous arm
B0279-HA1-R	tttgaGGTTTCCTCCTACGATATTGTCCG	
B0279-Km-F	cgtaggaggaaccTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0279-Km-R	tggaccggaTCAGAAGAACTCGTCAAGAAGGC	
B0279-HA2-F	agttcttctgaTCCGGTCCAGCTTCAAAACC	Amplification of downstream homologous arm
B0279-HA2-R	tctgatatcatc gatgaattcTCATGATCGCCAATTTCCG	
A1479-HA1-F	caggtcgactctagaggatccACTTCAAGGCCTGCCTTCAAC	Amplification of upstream homologous arm
A1479-HA1-R	aGATGACCTCATTCATCCGCAA	
A1479-Km-F	gcgatgaatgaggtcatcTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
A1479-Km-R	atggtcgcTCAGAAGAACTCGTCAAGAAGGC	
A1479-HA2-F	agttcttctgaGGCGACCATGAAAAAGGCG	Amplification of downstream homologous arm
A1479-HA2-R	tctgatatcatc gatgaattcAGGCAAAATCACCAGCACGC	
B0779-HA1-F	caggtcgactctagaggatccATGAAACTGCGCCTGCTCAA	Amplification of upstream homologous arm
B0779-HA1-R	tttgaGTTCTGACCTCCCGTCATATC	
B0779-Km-F	ggggaggtcagaacTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0779-Km-R	cggtttgTCAGAAGAACTCGTCAAGAAGGC	
B0779-HA2-F	cgagttcttctgaCAAACCGTAAACGGCCAAG	Amplification of downstream homologous arm
B0779-HA2-R	tctgatatcatc gatgaattcGATTGCGATATCCATAAATTCG	
A0376-HA1-F	caggtcgactctagaggatccATCAACGGTCGCCTCAACC	Amplification of upstream homologous arm
A0376-HA1-R	atttgaGTCTCTCCTCCTCAATATATGTTGTTTT	

A0376-Km-F	gaggaggagagacTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
A0376-Km-R	gaaactTCAGAAGAAGGCTCGTCAAGAAGGC	
A0376-HA2-F	cgagttctctgaACGTTTCAACACTTGATTGGAACA	Amplification of downstream homologous arm
A0376-HA2-R	tctgatatcatcgaattcAAGGCACGTTACGCGATATCG	
B0251-HA1-F	caggctgactctagaggatccGTGTGAATGCGCATGTGCAA	Amplification of upstream homologous arm
B0251-HA1-R	gaaCGTTTCTCTCTTTGCGATAGG	
B0251-Km-F	cgcaaaggagagaaacgTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0251-Km-R	cgcTCAGAAGAAGGCTCGTCAAGAAGGC	
B0251-HA2-F	ttgacgagttctctgaGCGCCCGTGAACAGGGG	Amplification of downstream homologous arm
B0251-HA2-R	tctgatatcatcgaattcCAGGTTTGGCTCCATTC	
B0446-HA1-F	caggctgactctagaggatccCTTCCGGCGCTTCTTTCTTA	Amplification of upstream homologous arm
B0446-HA1-R	ttgaaTTCGCGTGCAGATCCCA	
B0446-Km-F	gatctgcaccgggaaTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0446-Km-R	tgccagagagTCAGAAGAAGGCTCGTCAAGAAGGC	
B0446-HA2-F	gttctctgaCTCTCTGGCATGATGGGGC	Amplification of downstream homologous arm
B0446-HA2-R	tctgatatcatcgaattcCATGGCTTCTTACGCATCA	
B0604-HA1-F	caggctgactctagaggatccCAATTCGGATATACAAAATCGCA	Amplification of upstream homologous arm
B0604-HA1-R	tatttgaaGGGAGACACCCCAATAITTTG	
B0604-Km-F	ggggtgtctcccTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0604-Km-R	aaggctcggTCAGAAGAAGGCTCGTCAAGAAGGC	
B0604-HA2-F	gttctctgaCCGAAGCCTTCTCATGCAAA	Amplification of downstream homologous arm
B0604-HA2-R	tctgatatcatcgaattcCGAAAACGTTGCCGAGGA	
A0009-HA1-F	caggctgactctagaggatccAGTACAAGCGCATCAACAGCTATT	Amplification of upstream homologous arm
A0009-HA1-R	ttgaaTCTCGTTCAGGCTCATGCA	
A0009-Km-F	gaggcctgaacgagaTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
A0009-Km-R	ccggtaaTCAGAAGAAGGCTCGTCAAGAAGGC	
A0009-HA2-F	cgagttctctgaTTACCGGAAAGTGGCGATCC	Amplification of downstream homologous arm
A0009-HA2-R	tctgatatcatcgaattcTCATCTGCGGAAATCGG	
A0340-HA1-F	caggctgactctagaggatccATCCATCCTGCTCATCCCCT	Amplification of upstream

A0340-HA1-R	tgaaTGGCTGACTGTATCTGATGTATCGC	homologous arm
A0340-Km-F	cagatacagtcagccaTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
A0340-Km-R	cgaaacTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
A0340-HA2-F	cgagttctctgaGGTTTCGTTTCTCCTGACAGGTT	Amplification of
A0340-HA2-R	tctgatatcatcgatgaattcCAAGTTCCAGTCCCAGAACGAT	downstream homologous arm
A0965-HA1-F	caggtcgactctagaggatccCCAAATCTTCGTGGCAAGCG	Amplification of upstream
A0965-HA1-R	atttgaaGGGGCGTTCTCACTTCTTTTC	homologous arm
A0965-Km-F	gtgagaacgccccTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
A0965-Km-R	gccatgTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
A0965-HA2-F	acgagttctctgaCATGGCGGCGCAACC	Amplification of
A0965-HA2-R	tctgatatcatcgatgaattcGGTTCCTGTTTCAATAGAACCGC	downstream homologous arm
B0672-HA1-F	caggtcgactctagaggatccTGCCGATCATGCTTGCCG	Amplification of upstream
B0672-HA1-R	ttgaaGATAAGTCTCCAGACAATAATCGTCATT	homologous arm
B0672-Km-F	gtctggagacttateTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
B0672-Km-R	gccttgctcTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
B0672-HA2-F	agttctctgaGAGCAAGGCCCGATGCGC	Amplification of
B0672-HA2-R	tctgatatcatcgatgaattcACCACTAGAAATTGGGCATGGC	downstream homologous arm
B0754-HA1-F	caggtcgactctagaggatccGCAAGGCGCATGAAATTGA	Amplification of upstream
B0754-HA1-R	tatttgaaGCTTACCGCCCCAATTTTCT	homologous arm
B0754-Km-F	ggggcgtaagcTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
B0754-Km-R	ccggttgcttcaTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
B0754-HA2-F	tcttctgaTGAAGCAACCGGATTGATTGT	Amplification of
B0754-HA2-R	tctgatatcatcgatgaattcCAGCATGGAAGCAGCCTGC	downstream homologous arm
RS03245-HA1-F	caggtcgactctagaggatccACCGCAAGAATGGCGAG	Amplification of upstream
RS03245-HA1-R	ttgaaTCATCAACCTCTTGCTTGAACG	homologous arm
RS03245-Km-F	gcaagaggttgatgTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan
RS03245-Km-R	ggTCAGAAGAACTCGTCAAGAAGGC	Resistance Gene
RS03245-HA2-F	cttgacgagttctctgaCCATTCATTCCTTGTGCGG	Amplification of
RS03245-HA2-R	tctgatatcatcgatgaattcCTGTGCGAAATCCCGGTGAA	downstream homologous arm

B0340-HA1-F	caggtcgactctagaggatccACCAATGGCCTCGTACTTTCCG	Amplification of upstream homologous arm
B0340-HA1-R	tttgaaGAACGATCCTCCCCCGATC	
B0340-Km-F	ggggaggatcgttcTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0340-Km-R	gtggTCAGAAGAAGCTCGTCAAGAAGGC	
B0340-HA2-F	tgacgagttcttctgaCCACGCGCCCAGCCGACG	Amplification of downstream homologous arm
B0340-HA2-R	tctgatatcatc gatgaattcCAATGCCTCGGTATCGACCG	
B0737-HA1-F	caggtcgactctagaggatccTGCATCAATATTTGGTATGCGC	Amplification of upstream homologous arm
B0737-HA1-R	gaaAAATCCCTCCGCTCTTCCG	
B0737-Km-F	gaagagcggaggatTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0737-Km-R	ccccggttcagaatgatTCAGAAGAAGCTCGTCAAGAAGGC	
B0737-HA2-F	gaATCATTCTGAAACCGGGGTCG	Amplification of downstream homologous arm
B0737-HA2-R	tctgatatcatc gatgaattcTCCTCATCTCGCGCTGTC	
B0520-HA1-F	caggtcgactctagaggatccACGTGCAACAATGTGCGCGC	Amplification of upstream homologous arm
B0520-HA1-R	ttgaaGACATGCCTCCTGTCTTCTTGTATG	
B0520-Km-F	gacaggaggcatgtcTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0520-Km-R	ccggttcgatttttaTCAGAAGAAGCTCGTCAAGAAGGC	
B0520-HA2-F	ctgaTAAAAATGCGAACCGGCTTG	Amplification of downstream homologous arm
B0520-HA2-R	tctgatatcatc gatgaattcTGGATTGATCGGCGGCTG	
B0934-HA1-F	caggtcgactctagaggatccTGCGAATCTGCAATATCATGTGC	Amplification of upstream homologous arm
B0934-HA1-R	gaaTTTTTGTTTCCTTGCTGTAGAATTCT	
B0934-Km-F	cagcaaggaacaaaaTTCAAATATGTATCCGCTCATGAGA	Amplification of Kan Resistance Gene
B0934-Km-R	gggatgaTCAGAAGAAGCTCGTCAAGAAGGC	
B0934-HA2-F	cgagttcttctgaTCATCCCCAAAACAGAAAGTCC	Amplification of downstream homologous arm
B0934-HA2-R	tctgatatcatc gatgaattcTGGAACACCATGCCAATGC	
Qpcr-16s-F	CCGACGGCTAACATTTCATCG	Housekeeping gene
Qpcr-16s-R	CATTACTGACGCTGAGGTGC	
Qpcr-tatB-F	CAACGAGTTTCGCCATCAATTC	Detection of transcription level of tatB in M28 Δ tatA
Qpcr-tatB-R	TCAAGGCTTCTGGCTTCATC	
Qpcr-tatC-F	CTTGCCGACGATCCTTCTTTA	Detection of transcription level of tatC in M28 Δ tatA
Qpcr-tatC-R	GGTGGAGGAAGCGTTGTTAT	

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