

Supplementary Table 2. Virulence factor matches in Virulence Factor DataBase (VFDB) and protein identity determine through BLASTp.

Virulence Factor Class	Annotation from <i>D. congolensis</i> genomes	Gene	Species	Identity %	Accession #
Adherence	GroEL chaperonin	<i>groEL</i>	<i>M. tuberculosis</i>	72	CNF16026.1
	Streptococcal plasmin receptor/	<i>plr/gapA</i>	<i>Str. pneumoniae</i>	65	CKE63244.1
Iron uptake	ABC transporter	<i>fagA</i>	<i>M. tuberculosis</i>	51	CNK55089.1
	Iron siderophore ABC transporter	<i>fagD</i>	<i>Mycobacterium sp</i> LNNU 331112	38	WP_149359153.1
	Exochelin	<i>fxbA</i>	<i>M. smegmatis</i>	50	WP_029104465.1
	Exochelin	<i>fxuB</i>	<i>Corynebacteriales</i>	61	WP_064906802.1
	Iron/manganese transport	<i>sitA</i>	<i>Mycobacteraceae</i>	73	WP_019511651.1
		<i>sitB</i>	<i>Mycobacterium sp</i> LNNU 331112	61	WP_149359937.1
	Mycobactin (Mycobacterium)	<i>mbtH</i>	<i>Mycobacteriaceae</i>	64	WP_046283878.1
	Antranilate synthase component 1	<i>mbtI</i>	<i>M. sp</i> LNNU 331112	57	WP_149360889.1
	ABC transporter	<i>irtA</i>	<i>M. sp.</i> OK889	45	TDR65420.1
Regulation	Diphtheria toxin repressor DtxR	<i>IdeR</i>	<i>M. tuberculosis</i>	54	CNI59779.1
	(p)ppGpp synthesis and hydrolysis	<i>relA</i>	<i>M. tuberculosis</i>	53	CNF85191.1
	Response regulator transcription factor	<i>(devR/dosR)</i>	<i>Mycobacterium sp.</i>	52	SBS74131.1
	Response regulator transcription factor	<i>phoP</i>	<i>M. tuberculosis</i>	66	CNE26216.1
		<i>phosR</i>	<i>M. pseudoshottsii</i> JCM 15466	43	GAQ32061.1
	Response regulator transcription factor	<i>(regX3)</i>	<i>M. tuberculosis</i>	74	CNE05134.1
	RNA polymerase Sigma factor	<i>sigA</i>	<i>M. tuberculosis</i>	90	CNI09155.1
	RNA polymerase Sigma factor E	<i>sigE</i>	<i>M. tuberculosis</i>	72	CND44553.1
	RNA polymerase Sigma H (sigma-24)	<i>sigH</i>	<i>M. tuberculosis</i>	74	CNG47707.1
	WhiB family transcription regulator 3	<i>whib3</i>	<i>Mycobacterium sp.</i> 1245111.1	61	WP_067342063.1
Toxin	Phospholipase D	<i>pld</i>	<i>C. ulcerans</i>	59	WP_029975046.1
Acid resistance	Urease	<i>ureB</i>	<i>M. tuberculosis</i>	61	WP_057332578.1
	Urease	<i>ureG</i>	<i>Mycobacteria sp.</i> NAZ190054	64	WP_067957749.1
Amino acid and purine metabolism	Diaminopimelate decarboxylase	<i>lysA</i>	<i>M. leprae</i>	52	Q50140.2
	Purine synthesis	<i>purC</i>	<i>M. tuberculosis</i>	54	CNJ22485.1
	Tryptophan synthesis	<i>trpD</i>	<i>M. leprae</i>	52	WP_010907993.1
	type I glutamate ligase	<i>glnA1</i>	<i>M. leprae</i>	61	WP_010908444.1
Anti-apoptosis factor	NuoG(Mycobacterium)	<i>nuoG</i>	<i>M. avium</i>	61	WP_084050036.1
Antiphagocytosis	Nucleotide sugar dehydrogenase	<i>fgd</i>	<i>M. tuberculosis</i>	68	REN02080.1
		<i>gnd</i>	<i>Mycobacterium sp.</i> 3519A	60	WP_101946767.1
Cell surface components	Trehalose-recycling ABC transporter	<i>sugA</i>	<i>M. tuberculosis</i>	55	CND65206.1
	Carbohydrate ABC transporter permease	<i>sugB</i>	<i>M. tuberculosis</i>	63	CND65175.1
	Trehalose import ATP-binding protein	<i>sugC</i>	<i>M. tuberculosis</i>	62	CND65145.1
Copper uptake	Copper exporter	<i>ctpV</i>	<i>M. sp</i> D16Q16	52	WP_139360043.1
Endotoxin	O-antigen biosynthesis aminotransferase	<i>bplF</i>	<i>B. bronchiseptica</i>	53	WP_033453820.1
Immune evasion					

	Capsule (Staphylococcus)	<i>cap5G</i>	<i>S. aureus</i>	51	HAR5208460.1
	Exopolysaccharide (Haemophilus)	<i>pgi</i>	<i>M. noviomagense</i>	61	WP_083087194.1
	polysaccharide biosynthesis protein	<i>gna</i>	<i>Acinetobacter sp.</i> YH12025	56	WP_180175575.1
Motility and export apparatus	Flagellar	<i>fliP</i>	<i>Austwickia sp.</i>	67	OOS02820.1
Others	O-antigen (Yersinia)				
	Glucose-1-phosphate cytidyltransferase	<i>ddhA</i>	<i>Y. enterocolitica</i>	63	WP_174847827.1
	GDP-L-fucose synthase	<i>wcaG</i>	<i>Y. pseudotuberculosis</i>	54	AKA21002.1
Phagosome arresting	Nucleoside diphosphate kinase (Mycobacterium)	<i>ndk</i>	<i>M. goodnae</i>	61	WP_180914471.1
Protease	Proteasome-associated proteins	<i>mpa</i>	<i>M. tuberculosis</i>	53	CNF79738.1
	Zn++ metallophrotease (peptide m13)	<i>Zmp1</i>	<i>M. Leprae</i>	53	SRX92647.1
Secretion system	Mxi-Spa TTSS effectors controlled by MxiE (Shigella)	<i>lhgO</i>	<i>Mycobacterium sp.</i> MS1601	54	WP_083736669.1
	T6SS-II	<i>clpB</i>	<i>M. tuberculosis</i>	68	CNH94644.1
Stress adaptation	Iron-co-factored SOD (Mycobacterium)	<i>sodA</i>	<i>M. avium</i>	64	WP_062889796.1
Nutritional virulence	Pyrimidine biosynthesis	<i>carB</i>	<i>M. tuberculosis</i>	74	CNE60285.1