

Table S1: Summary of known virulence genes of *Trueperella pyogenes* detected in *Treuperella abortisuis* strain KKAHC01

Virulence factor	Related gene	NCBI accession number for reference gene	Percentage Identity	Start and end Position in <i>T. abortisuis</i> strain KKAHC01 genome (bp)
Neuraminidase H	<i>nanH</i>	KX462010.1	72.96	2380527 - 2381958
Neuraminidase P	<i>nanP</i>	KX462011.1	76.26	1747934 - 1749988

Table S2: List of virulence related genes predicted in *Trueperella abortusis* strain KKAHC01 by VFAnalyzer (1)

Virulence factor class	Virulence factors	Related genes	Bacterial species and NCBI GenBank accession number related to reference virulence genes	Hits in <i>Trueperella abortusis</i> strain KKAHC01 genome	
				Start and end position (bp)	Strand
Amino acid and purine metabolism	Glutamine synthesis	<i>glnA1</i>	<i>Mycobacterium abscessus</i> (YP_006520757)	851042 - 852460	plus
			<i>Mycobacterium tuberculosis</i> (YP_005360830)	856155 - 857489	minus
	Leucine synthesis	<i>leuD</i>	<i>Mycobacterium smegmatis</i> (YP_886728)	390167 - 390823	plus
	Lysine synthesis	<i>lysA</i>	<i>Mycobacterium smegmatis</i> (YP_007294361)	96592 - 97905	plus
Anaerobic respiration	Nitrate reductase	<i>narG</i>	<i>Mycobacterium canettii</i> (YP_007287068)	2292917 - 2296609	plus
		<i>narH</i>	<i>Mycobacterium gilvum</i> (YP_004076091)	2296609 - 2298129	plus
		<i>narI</i>	<i>Mycobacterium smegmatis</i> (YP_889383)	2298782 - 2299549	plus
Anti-apoptosis factor	NuoG	<i>nuoG</i>	<i>Mycobacterium smegmatis</i> (YP_007291351)	25055 - 27631	plus
Cell surface components	GPL locus	<i>rmlA</i>	<i>Mycobacterium tuberculosis</i> (NP_214848.1)	1383894 - 1384760	plus
	Trehalose-recycling ABC transporter	<i>sugC</i>	<i>Mycobacterium sp.</i> (YP_641141)	1689575 - 1690756	plus
Iron uptake	ABC transporter	<i>irtA</i>	<i>Mycobacterium tuberculosis</i> (NP_215864);	598274 - 599929	plus
	ABC-type heme transporter	<i>hmuU</i>	<i>Corynebacterium efficiens</i> (NP_737304)	2259788 - 2261575	plus
Lipid and fatty acid metabolism	Pantothenate synthesis	<i>panC</i>	<i>Mycobacterium gilvum</i> (YP_001132694)	1562491 - 1563441	minus
		<i>panD</i>	<i>Mycobacterium gilvum</i> (YP_001132695)	2537333 - 2538133	plus
Phagosome arresting	Nucleoside diphosphate kinase	<i>ndk</i>	<i>Mycobacterium canettii</i> (YP_007269154)	2538145 - 2538558	plus
	Proteasome-associated proteins	<i>mpa</i>	<i>Mycobacterium intracellulare</i> (YP_005337929)	1031345 - 1031758	minus
Protease	Zn ⁺⁺ metalloprotease	<i>zmp1</i>	<i>Mycobacterium gilvum</i> (YP_004074832)	630473 - 632119	plus
	(p)ppGpp synthesis and hydrolysis	<i>relA</i>	<i>Mycobacterium gilvum</i> (YP_004077605)	265560 - 267557	minus
Regulation	PhoP/R	<i>phoP</i>	<i>Mycobacterium avium</i> (YP_879977)	762977 - 765274	minus
	RegX3	<i>regX3</i>	<i>Mycobacterium gilvum</i> (YP_001131366)	1627317 - 1628060	plus
	Sigma H	<i>sigH</i>	<i>Mycobacterium sp.</i> (YP_004524191)	2159888 - 2160568	plus
	WhiB3	<i>whiB3</i>	<i>Mycobacterium tuberculosis</i> (YP_005309652)	63652 - 64257	plus
Secretion system	T6SS-II		<i>Klebsiella oxytoca</i> (YP_005015987.1)	1258635 - 1258937	plus
Stress adaptation	Iron-cofactored SOD	<i>sodA</i>	<i>Mycobacterium sp.</i> (YP_642204)	2335966 - 2338602	plus
Adherence	SpaH-type pili	<i>srtD</i>	<i>Corynebacterium diphtheriae</i> (NP_940532)	837426 - 838040	plus
				1331555 - 1332433	minus
Antiphagocytosis	Capsule	<i>gnd</i>	<i>Klebsiella pneumoniae</i> (YP_001336147.1)	1927012 - 1927887	minus
	Capsule	<i>rmlB</i>	<i>Streptococcus mutans</i> (NP_721810)	1757407 - 1758882	plus
Immune evasion	Exopolysaccharide	<i>pgi</i>	<i>Haemophilus influenzae</i> (YP_001290850)	1418576 - 1419571	plus
	Polysaccharide capsule	<i>galE3</i>	<i>Bacillus cereus</i> (YP_002341326.1)	1213875 - 1215527	minus
				557612 - 558655	minus

References: 1. Liu B, Zheng D, Zhou S, Chen L, Yang J. VFDB 2022 : a general classification scheme for bacterial virulence factors. Nucleic Acids Res. 2022;50(November 2021):912–7.