SUPPLEMENTAL TABLE 1. BLAST comparison of putative protein-coding genes of strains Fx1, U112, and 3523

Strain	3523 (1854 CDS)			Fx1 (1819 CDS)			U112 (1821 CDS)		
	BBH	UH	NH	BBH	UH	NH	BBH	UH	NH
3523	-	-	-	1623	55	176	1616	59	179
Fx1	1623	51	145	-	-	-	1672	48	99
U112	1616	75	130	1672	55	94	-	-	-

CDS: protein-coding sequences

BBH: (bidirectional best hits) indicates highly similar genes, most likely orthologs

UH: (unidirectional hits) indicates less similar genes, or gene fragments

NH: (no hits) indicates genes without a significant match in the other strain

SUPPLEMENTAL TABLE 2. Comparison of the *wbt* gene clusters of strains Schu S4, 3523, Fx1, and U112

F. tularensis strain Schu S4 Locus tag (protein)	*F. novicida*-like strain 3523 Locus tag (protein, % identity[1])	*F. novicida*-like strain Fx1 Locus tag (protein, % identity[1])	*F. novicida* strain U112 Locus tag (protein, % identity[1])	Annotation
FTT_1447c (494 aa)	FN3523_1475 (495 aa, 88%)	FNFX1_1451 (494 aa, 96%)	FTN_1417 (494 aa, 99%)	ManB: Phosphomannomutase
FTT_1448c (468 aa)	FN3523_1476 (468 aa, 95%)	FNFX1_1452 (468 aa, 97%)	FTN_1418 (468 aa, 97%)	ManC: Mannose-1-phosphate guanylyltransferase/ mannose-6-phosphate isomerase
ISFtu1/IS630 (126 aa)[2]	None	None	None	Transposase
FTT_1450c (348 aa)	FN3523_1477 (333 aa, 94%)	FNFX1_1453 (339 aa, 98%)	FTN_1420c (85 aa)[2]	WbtM: dTDP-D-glucose 4,6-dehydratase

None	None	None	ISFtu3/IS1016 (233 aa)[2]	Transposase
None	None	FNFX1_1454 (121 aa)	None	Hypothetical protein
FTT_1451c (294 aa)	FN3523_1478 (293 aa, 96%)	FNFX1_1455 (299 aa, 97%)	None	WbtL: Glucose-1-phosphate thymidylyltransferase
None	FN3523_1479 (417 aa)	FNFX1_1456 (413 aa, 38%)	FTN_1420 (415 aa, 45%)	WzxE: O antigen flippase
FTT_1452c (286 aa)	None	None	None	WbtK: Glycosyltransferase
FTT_1453c (495 aa)	None	None	None	WzxE: O-antigen flippase[3]
FTT_1454c (241 aa)	None	None	None	WbtJ: Hypothetical protein
FTT_1455c (360 aa)	None	None	None	WbtI: Sugar transamine/ perosamine synthetase
None	FN3523_1480 (505 aa)	None	None	Aminotransferase

None	FN3523_1481 (84 aa)	None	None	Hypothetical protein
None	FN3523_1482 (402 aa)	None	None	Hypothetical protein
None	FN3523_1483 (132 aa)	None	None	WblP protein
None	FN3523_1484 (353 aa)	None	None	Hypothetical protein
None	None	FNFX1_1457 (294 aa)	None	Acyltransferase 3
None	None	FNFX1_1458 (370 aa)	None	TDP-4-oxo-6-deoxy-D-glucose transaminase
None	None	FNFX1_1459 (188 aa)	None	O-acetyltransferase
None	None	FNFX1_1460 (422 aa)	None	Glycosyl transferase, group 1
FTT_1456c (628 aa)	FN3523_1485 (621 aa, 68%)	None	FTN_1421 (630 aa, 98%)	WbtH: Glutamine amidotransferase
None	FN3523_1486 (389 aa)	None	None	UDP-glucose 6-dehydrogenase
None	FN3523_1487 (378 aa)	None	None	Glycosyl transferase, group 1

None	FN3523_1488 (325 aa)	FNFX1_1461 (332 aa, 65%)	None	Hypothetical protein
None	FN3523_1489 (369 aa)	FNFX1_1462 (369 aa, 96%)	None	UDP-N-acetylglucosamine 2-epimerase
None	FN3523_1490 (364 aa)	FNFX1_1463 (364 aa, 96%)	None	NAD-dependent epimerase/ dehydratase
None	FN3523_1491 (331 aa)	FNFX1_1464 (334 aa, 96%)	None	Putative epimerase/ dehydratase
None	FN3523_1492 (403 aa)	None	None	Glycosyltransferase
None	FN3523_1493 (343 aa)	None	None	Conserved hypothetical protein
None	FN3523_1494 (319 aa)	None	None	Aminotransferase
None	None	None	FTN_1422 (370 aa)	WbtN: Glycosyl transferase, group 1

FTT_1457c (366 aa)	None	None	FTN_1423 (362 aa, 90%)	WbtG: Glycosyl transferase, group 1
None	None	None	FTN_1424 (430 aa)	Hypothetical protein
FTT_1458c (409 aa)	None	None	None	Membrane protein/O-antigen protein
FTT_1459c (323 aa)	None	None	FTN_1425 (324 aa, 99%)	WbtF: NAD dependent epimerase
FTT_1460c (436 aa)	None	None	FTN_1426 (436 aa, 99%)	WbtE: UDP-glucose/ GDP-mannose dehydrogenase
FTT_1461c (363 aa)	None	None	FTN_1427 (363 aa, 87%)	WbtD: Glycosyl transferase, group 1
None	None	None	FTN_1428 (203 aa)	WbtO: Acyltransferase
None	None	FNFX1_1465 (407 aa)	None	Glycosyl transferase, group 1

FTT_1462c (263 aa)	None	FNFX1_1466 (263 aa, 95%)	None	WbtC: UDP-glucose 4-epimerase
FTT_1463c (205 aa)	None	FNFX1_1467 (143 aa, 99%)	None	WbtB: Galactosyl transferase
None	FN3523_1495 (366 aa)	None	FTN_1429 (209 aa, 76%)	WbtP: Galactosyl transferase
None	FN3523_1496 (371 aa)	None	FTN_1430 (371 aa, 93%)	WbtQ: Aminotransferase
FTT_1464c (578 aa)	FN3523_1497 (581 aa, 92%)	FNFX1_1468 (522 aa, 98%)	FTN_1431 (578 aa, 99%)	WbtA: dTDP-glucose 4,6-dehydratase
ISFtu1/IS630 (126 aa)[2]	None	None	None	Transposase

[1] Identity percentages to protein in column 1 or 2, when present

[2] These features are not annotated in the published genomes of strains Schu S4 and U112

[3] FTT_1453c has 20% identity to FNFX1_1456 but is unrelated to FN3523_1479 and FTN_1420 at the amino acid level

SUPPLEMENTAL TABLE 3. Comparison of the *psl* gene clusters of strains 3523, Fx1, and Schu S4

F. novicida-like strain 3523 Locus tag (protein)	*F. novicida*-like strain Fx1[1] Locus tag (protein, % identity[3])	*F. tularensis* strain Schu S4[2] Locus tag (protein, % identity[3])	Annotation
None	FNFX1_1255 (315 aa)	None	Transposase
FN3523_1275 (220 aa)	FNFX1_1256 (220 aa, 95%)	FTT_0800 (220 aa, 95%)	HAD family hydrolase
FN3523_1276 (337 aa)	FNFX1_1257 (337 aa, 91%)	FTT_0799 (337 aa, 92%)	Glycosytransferase
FN3523_1277 (330 aa)	FNFX1_1258 (335 aa, 90%)	FTT_0798 (335 aa, 90%)	Glycosyltransferase
None	FNFX1_1259 (318 aa)	FTT_0797 (319 aa, 97%)	Glycosyltransferase
FN3523_1278 (269 aa)	None	None	Glycosyltransferase
FN3523_1279 (319 aa)	None	None	GDP-L-fucose synthetase
FN3523_1280 (372 aa)	None	None	GDP-mannose-4,6-dehydratase
FN3523_1281 (413 aa)	None	None	Glycosyltransferase
FN3523_1282 (275 aa)	None	None	Methyltransferase
FN3523_1283 (243 aa)	None	None	Methyltransferase
FN3523_1284 (300 aa)	None	None	Sugar transferase

FN3523_1285 (387 aa)	None	None	UDP-glucose 6-dehydrogenase
FN3523_1286 (217 aa)	None	None	Hypothetical protein
FN3523_1287 (273 aa)	None	None	Methyltransferase
FN3523_1288 (432 aa)	None	None	Polysaccharide biosynthesis protein
None	FNFX1_1260 (386 aa)	None	KpsC: Capsule polysaccharide export protein
None	FNFX1_1261 (247 aa)	None	Hypothetical protein
None	None	FTT_0796 (253 aa)	Conserved hypothetical protein
None	None	FTT_0795 (227 aa)	Methyltransferase domain family
None	None	FTT_0794 (428 aa)	Conserved hypothetical protein
None	FNFX1_1262 (562 aa)	FTT_0793 (560 aa, 97%)	ABC transporter ATP-binding protein
FN3523_1289 (371 aa)	FNFX1_1263 (423 aa, 79%)	FTT_0792 (409 aa, 84)	WejK: Glycosyltransferase
FN3523_1290 (339 aa)	FNFX1_1264 (339 aa, 95%)	FTT_0791 (339 aa, 82%)	GalE: UDP-glucose 4-epimerase
FN3523_1291 (417 aa)	FNFX1_1265 (417 aa, 90%)	FTT_0790 (464 aa, 90%)	Sugar transferase

[1] The *psl* gene clusters of strains Fx1 and U112 have identical chromosomal arrangements

[2] The *psl* gene clusters in *F. tularensis* strains Schu S4, WY96-3418, and FSC198 have identical chromosomal arrangements

[3] Identity percentages to protein in column 1 or 2, when present