

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 25 (tnfn1_pw060420p01)**

Catalog No. NR-8059

For research use only. Not for human use.

Contributor:

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University of Washington, Seattle, Washington

Product Description:

A comprehensive 16508-member transposon mutant library¹ of sequence-defined transposon insertion mutants of *Francisella tularensis* subsp. *novicida*, strain U112 was prepared to allow the systematic identification of virulence determinants and other factors associated with *Francisella* pathogenesis. Genes refractory to insertional inactivation helped define the genes essential for viability of the organism.

To facilitate genome-scale screening using the mutant collection, a “two-allele” single-colony purified sublibrary, made up of approximately two purified mutants per gene, was assembled.

NR-8059 represents Plate 25 (tnfn1_pw060420p01) of the “two-allele” 3050-member sublibrary. Detailed information for each mutant is shown in Tables 1-3. Information about specific clones may also be accessed through the [Francisella Tularensis Genome Research](#) homepage. **Strain tnfn1_pw060420p01q127 (Well C04) was not available due to quality issues at the time of release of Plate 25, but is now available on Plate 33 (BEI Resources NR-10484).**

Francisella tularensis subsp. *novicida*, strain U112 is excluded from Select Agent status. Please see [CDC Select Agent Program, Notification of Exclusion](#).

Material Provided:

Each well of the 96-well plate contains approximately 0.25 mL of bacterial culture in 0.7X Tryptic Soy Broth containing 0.1% L-cysteine and 10 µg/mL kanamycin supplemented with 5% glycerol.

Note: Production in the 96-well format has a potential for cross-contamination. Individual mutants should be checked by the recipient prior to use.

Packaging/Storage:

NR-8059 was packaged aseptically in 96-well plates. The product is provided frozen and should be stored at -60°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Media:

Tryptic Soy Agar containing 0.1% L-cysteine and 10 µg/mL kanamycin

Incubation:

Temperature: 37°C

Atmosphere: Aerobic with 5% CO₂

Propagation:

1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
2. Incubate the plate at 37°C for 24–48 hours.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through the NIH Biodefense and Emerging Infections Research Resources Repository, NIAID, NIH: *Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 25 (tnfn1_pw060420p01), NR-8059.”

Biosafety Level: 2

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories](#). 5th ed. Washington, DC: U.S. Government Printing Office, 2007; see www.cdc.gov/od/ohs/biosfty/bmbl5/bmbl5toc.htm.

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References:

1. Gallagher, L. A., et al. "A Comprehensive Transposon Mutant Library of *Francisella novicida*, A Bioweapon Surrogate." Proc. Natl. Acad. Sci. USA 104 (2007): 1009–1014. PubMed: 17215359.

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Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060420p01q101	A01	T18	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060420p01q102	B01	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p01q103	C01	T18	-	protein of unknown function with TPR repeat region and von Willebrand factor type A domain	unknown function - conserved
tnfn1_pw060420p01q104	D01	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p01q105	E01	T18	-	ABC-type transport system permease protein	transport
tnfn1_pw060420p01q106	F01	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p01q107	G01	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q108	H01	T18	-	metabolite:H+ symporter (MHS) family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060420p01q109	A02	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q110	B02	T18	-		
tnfn1_pw060420p01q111	C02	T18	-	outer membrane protein of unknown function	unknown function - novel
tnfn1_pw060420p01q112	D02	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q113	E02	T20	nhaA	Na ⁺ :H ⁺ antiporter	transport
tnfn1_pw060420p01q114	F02	T20	-	phage terminase, small subunit	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060420p01q115	G02	T20	fadE	Acyl-CoA dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060420p01q116	H02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q117	A03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q118	B03	T20	-	predicted hydrolase of the HAD superfamily	putative enzymes
tnfn1_pw060420p01q119	C03	T20	ostA1	organic solvent tolerance protein, OstA	cell wall / LPS / capsule
tnfn1_pw060420p01q120	D03	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p01q121	E03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q122	F03	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060420p01q123	G03	T20	asd	aspartate semialdehyde dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060420p01q124	H03	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p01q125	A04	T20	-	pseudogene: conserved hypothetical protein	pseudogene
tnfn1_pw060420p01q126	B04	T20	pilB	Type IV pili ATPase	motility, attachment and secretion structure
tnfn1_pw060420p01q127	C04	T20	-	serine-type D-Ala-D-Ala carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060420p01q128	D04	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p01q129	E04	T20	-	isochorismatase family protein	putative enzymes
tnfn1_pw060420p01q130	F04	T20	-	metal-dependent exopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060420p01q131	G04	T20	corA	divalent inorganic cation transporter	transport
tnfn1_pw060420p01q132	H04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q133	A05	T20	-	glutathione peroxidase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060420p01q134	B05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q135	C05	T20	pckA	phosphoenolpyruvate carboxykinase	energy metabolism
tnfn1_pw060420p01q136	D05	T20	-	monovalent cation:proton antiporter family protein	transport
tnfn1_pw060420p01q137	E05	T20	kdtA	3-deoxy-D-manno-octulosonic-acid transferase	fatty acids and lipids metabolism
tnfn1_pw060420p01q138	F05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q139	G05	T20	-	acid phosphatase, HAD superfamily protein	putative enzymes
tnfn1_pw060420p01q140	H05	T20	clpB	chaperone clpB	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060420p01q141	A06	T20	-	ATP binding protein	putative enzymes
tnfn1_pw060420p01q142	B06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q143	C06	T20	mdh	malate dehydrogenase	energy metabolism
tnfn1_pw060420p01q144	D06	T20	ampG	peptide-acetyl-coenzyme A transporter (PAT) family protein	transport
tnfn1_pw060420p01q145	E06	T20	-	predicted ATPase of the PP-loop superfamily	cell cycle
tnfn1_pw060420p01q146	F06	T20	fur	ferric uptake regulation protein	signal transduction and regulation
tnfn1_pw060420p01q147	G06	T20	-	AMP-binding protein	putative enzymes
tnfn1_pw060420p01q148	H06	T20	nadB	L-aspartate oxidase	cofactors, prosthetic groups, electron carriers metabolism

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060420p01q149	A07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q150	B07	T20	-	aspartate/tyrosine/aromatic aminotransferase	amino acid metabolism - biosynthesis
tnfn1_pw060420p01q151	C07	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060420p01q152	D07	T20	-	glycosyl transferase	cell wall / LPS / capsule
tnfn1_pw060420p01q153	E07	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p01q154	F07	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060420p01q155	G07	T18	pal	peptidoglycan-associated lipoprotein, OmpA family	transport - drugs / antibacterial compounds
tnfn1_pw060420p01q156	H07	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q157	A08	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p01q158	B08	<KAN-2>	fumA	fumarate hydratase, class I	energy metabolism
tnfn1_pw060420p01q159	C08	<KAN-2>	sufD	sufS activator complex, sufD subunit	post-translational modification, protein turnover, chaperones
tnfn1_pw060420p01q160	D08	<KAN-2>	ppiC	parvulin-like peptidyl-prolyl isomerase domain	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060420p01q161	E08	<KAN-2>	-	-	-
tnfn1_pw060420p01q162	F08	<KAN-2>	-	conserved membrane protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q163	G08	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q164	H08	<KAN-2>	-	-	-
tnfn1_pw060420p01q165	A09	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q166	B09	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q167	C09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p01q168	D09	T18	cscK	ROK family protein	putative enzymes
tnfn1_pw060420p01q169	E09	T18	hflC	HflK-HflC membrane protein complex, HflC	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060420p01q170	F09	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p01q171	G09	T18	-	acetyltransferase	putative enzymes
tnfn1_pw060420p01q172	H09	T18	-	conserved hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p01q173	A10	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p01q174	B10	T18	-	ABC-type transport system permease protein	transport
tnfn1_pw060420p01q175	C10	T18	lpcC	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060420p01q176	D10	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p01q177	E10	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p01q178	F10	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p01q179	G10	T20	-	GDSL-like lipolytic enzyme	fatty acids and lipids metabolism
tnfn1_pw060420p01q180	H10	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060420p01q181	A11	T20	htpX	Zn-dependent protease with chaperone function	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060420p01q182	B11	T20	phrB	deoxyribodipyrimidine photolyase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060420p01q183	C11	T20	proC	pyrroline-5-carboxylate reductase	amino acid metabolism - biosynthesis
tnfn1_pw060420p01q184	D11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p01q185	E11	T20	hemN	coproporphyrinogen III oxidase, anaerobic	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060420p01q186	F11	T20	galT	galactose-1-phosphate uridylyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060420p01q187	G11	T20	-	-	-
tnfn1_pw060420p01q188	H11	T20	-	pseudogene: Membrane Protein. Fucose permease Carbohydrate transport and metabolism	pseudogene
tnfn1_pw060420p01q189	A12	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p01q190	B12	T20	-	GDSL-like lipolytic enzyme	fatty acids and lipids metabolism
tnfn1_pw060420p01q191	C12	T20	-	potassium channel protein	transport
tnfn1_pw060420p01q192	D12	T20	hflK	HflK-HflC membrane protein complex, HflK	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060420p01q193	E12	T20	grxB	glutaredoxin 2	post-translational modification, protein turnover, chaperones
tnfn1_pw060420p01q194	F12	T20	leuA	2-isopropylmalate synthase	amino acid metabolism - biosynthesis
tnfn1_pw060420p01q195	G12	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p01q196	H12	T20	-	-	-

Table 2 - Sequencing and Insertion Location

Strain Name	Well	Sequence confirmation (C, Confirmed; U, unconfirmed)	Effective Genome Position of Insertion	Direction of insertion (F, forward relative to genome; R, reverse)	Locus Tag	ORF left end	ORF right end	Direction of ORF (F, forward relative to genome; R, reverse)	Length of ORF (codons)	Effective position of insertion in ORF [nucleotide of insertion(length of ORF in nucleotides)]
tnfn1_pw060420p01q101	A01	C	1810208	F	FTN_1693	1809633	1811171	R	513	964(1539)
tnfn1_pw060420p01q102	B01	C	752860	F	FTN_0709	752359	753102	F	248	502(744)
tnfn1_pw060420p01q103	C01	C	229723	R	FTN_0209	229107	229973	F	289	617(867)
tnfn1_pw060420p01q104	D01	C	311715	R	FTN_0302	311638	311982	F	115	78(345)
tnfn1_pw060420p01q105	E01	C	335354	F	FTN_0327	335057	335818	R	254	465(762)
tnfn1_pw060420p01q106	F01	C	816729	R	FTN_0760	816310	816897	F	196	420(588)
tnfn1_pw060420p01q107	G01	C	330501	F	FTN_0320	330339	331079	R	247	579(741)
tnfn1_pw060420p01q108	H01	C	139947	F	FTN_0128	139163	140368	F	402	785(1206)
tnfn1_pw060420p01q109	A02	C	1448306	F	FTN_1367	1447268	1448899	R	544	594(1632)
tnfn1_pw060420p01q110	B02	C	1847711	R	intergenic					
tnfn1_pw060420p01q111	C02	C	1112544	F	FTN_1053	1111641	1113071	R	477	528(1431)
tnfn1_pw060420p01q112	D02	C	1534580	F	FTN_1445	1533937	1534848	R	304	269(912)
tnfn1_pw060420p01q113	E02	C	1881401	R	FTN_1752	1880874	1882022	R	383	622(1149)
tnfn1_pw060420p01q114	F02	C	9794	R	FTN_0010	9375	9806	R	144	13(432)
tnfn1_pw060420p01q115	G02	C	1523667	R	FTN_1437	1522690	1524927	F	746	978(2238)
tnfn1_pw060420p01q116	H02	C	543783	R	FTN_0523	543248	544063	F	272	536(816)
tnfn1_pw060420p01q117	A03	C	1645171	R	FTN_1547	1644749	1645384	F	212	423(636)
tnfn1_pw060420p01q118	B03	C	92439	F	FTN_0082	92435	92995	F	187	5(561)
tnfn1_pw060420p01q119	C03	C	584934	F	FTN_0558	583164	585767	F	868	1771(2604)
tnfn1_pw060420p01q120	D03	C	742828	F	FTN_0699	742065	743228	F	388	764(1164)
tnfn1_pw060420p01q121	E03	C	1641361	F	FTN_1543	1640934	1641398	F	155	428(465)
tnfn1_pw060420p01q122	F03	C	1343829	R	FTN_1272	1342876	1344357	F	494	954(1482)
tnfn1_pw060420p01q123	G03	C	544738	F	FTN_0524	544119	545216	R	366	479(1098)
tnfn1_pw060420p01q124	H03	C	900397	R	FTN_0844	900355	900618	R	88	222(264)
tnfn1_pw060420p01q125	A04	C	378710	F	FTN_0377	378265	379017	F	251	446(753)
tnfn1_pw060420p01q126	B04	C	1179096	R	FTN_1115	1178703	1180478	F	592	394(1776)
tnfn1_pw060420p01q127	C04	U	670284	F	FTN_0635	669592	670983	R	464	700(1392)
tnfn1_pw060420p01q128	D04	C	816169	F	FTN_0759	816036	816326	F	97	134(291)
tnfn1_pw060420p01q129	E04	C	1074787	R	FTN_1015	1074646	1075146	R	167	360(501)
tnfn1_pw060420p01q130	F04	C	1019915	F	FTN_0965	1019741	1021147	F	469	175(1407)
tnfn1_pw060420p01q131	G04	C	6424	R	FTN_0005	5832	6800	F	323	593(969)
tnfn1_pw060420p01q132	H04	C	1737232	F	FTN_1624	1736861	1737736	R	292	505(876)
tnfn1_pw060420p01q133	A05	C	741893	R	FTN_0698	741553	742020	F	156	341(468)
tnfn1_pw060420p01q134	B05	C	1165366	F	FTN_1103	1164647	1165492	R	282	127(846)
tnfn1_pw060420p01q135	C05	C	565438	R	FTN_0540	564807	566396	F	530	632(1590)
tnfn1_pw060420p01q136	D05	U	1072797	F	FTN_1013	1072741	1073913	R	391	1117(1173)
tnfn1_pw060420p01q137	E05	U	1557777	F	FTN_1469	1557427	1558719	F	431	351(1293)
tnfn1_pw060420p01q138	F05	C	400046	R	FTN_0400	399470	400237	R	256	192(768)
tnfn1_pw060420p01q139	G05	C	1654585	R	FTN_1556	1654346	1654927	R	194	343(582)
tnfn1_pw060420p01q140	H05	C	1870848	R	FTN_1743	1870244	1872820	F	859	605(2577)
tnfn1_pw060420p01q141	A06	C	1182236	F	FTN_1117	1181802	1182965	R	388	730(1164)
tnfn1_pw060420p01q142	B06	C	62265	F	FTN_0052	61717	63777	F	687	549(2061)
tnfn1_pw060420p01q143	C06	C	1033888	R	FTN_0980	1033379	1034335	F	319	510(957)
tnfn1_pw060420p01q144	D06	C	1753903	F	FTN_1641	1753261	1754523	F	421	643(1263)
tnfn1_pw060420p01q145	E06	C	978160	R	FTN_0920	977672	978472	F	267	489(801)
tnfn1_pw060420p01q146	F06	C	1795653	F	FTN_1681	1795398	1795817	F	140	256(420)
tnfn1_pw060420p01q147	G06	C	637749	R	FTN_0604	636377	638473	F	699	1373(2097)
tnfn1_pw060420p01q148	H06	U	738532	R	FTN_0694	737909	739393	F	495	624(1485)

The Effective Genome Position of Insertion indicates the effective insertion position that is most likely to be functionally relevant in light of the 9-bp Tn5 target-site duplication and the direction of transcription of the predicted gene of insertion. E.g., for genes oriented to the right, the value reported indicates the genomic position of the nucleotide immediately adjacent to the left end of the insertion element when accounting for the 9-bp target site duplication.

Table 2 - Sequencing and Insertion Location

Strain Name	Well	Sequence confirmation (C, Confirmed; U, unconfirmed)	Effective Genome Position of Insertion	Direction of insertion (F, forward relative to genome; R, reverse)	Locus Tag	ORF left end	ORF right end	Direction of ORF (F, forward relative to genome; R, reverse)	Length of ORF (codons)	Effective position of insertion in ORF [nucleotide of insertion(length of ORF in nucleotides)]
tnfn1_pw060420p01q149	A07	C	45211	F	FTN_0041	44369	46582	R	738	1372(2214)
tnfn1_pw060420p01q150	B07	C	408826	R	FTN_0410	407870	409057	R	396	232(1188)
tnfn1_pw060420p01q151	C07	C	800562	R	FTN_0747	800413	802020	F	536	150(1608)
tnfn1_pw060420p01q152	D07	U	456128	F	FTN_0453	455936	457249	F	438	193(1314)
tnfn1_pw060420p01q153	E07	U	1546812	F	FTN_1458	1546487	1546990	F	168	326(504)
tnfn1_pw060420p01q154	F07	U	1740502	F	FTN_1628	1739841	1740791	R	317	290(951)
tnfn1_pw060420p01q155	G07	C	360606	R	FTN_0357	360228	360848	F	207	379(621)
tnfn1_pw060420p01q156	H07	C	1016060	R	FTN_0962	1015900	1016691	R	264	632(792)
tnfn1_pw060420p01q157	A08	C	1000053	R	FTN_0939	1000022	1000177	R	52	125(156)
tnfn1_pw060420p01q158	B08	C	343253	F	FTN_0337	342333	343844	F	504	921(1512)
tnfn1_pw060420p01q159	C08	C	909601	F	FTN_0853	908463	909605	F	381	1139(1143)
tnfn1_pw060420p01q160	D08	C	733444	F	FTN_0689	733247	733522	F	92	198(276)
tnfn1_pw060420p01q161	E08	C	485586	F	intergenic					
tnfn1_pw060420p01q162	F08	C	1341416	R	FTN_1270	1341158	1341841	R	228	426(684)
tnfn1_pw060420p01q163	G08	C	1199213	F	FTN_1133	1198995	1199375	F	127	219(381)
tnfn1_pw060420p01q164	H08	C	209770	R	intergenic					
tnfn1_pw060420p01q165	A09	C	1530929	R	FTN_1442	1530875	1531099	R	75	171(225)
tnfn1_pw060420p01q166	B09	C	392523	F	FTN_0393	391849	392901	F	351	675(1053)
tnfn1_pw060420p01q167	C09	C	850205	R	FTN_0792	849966	850385	R	140	181(420)
tnfn1_pw060420p01q168	D09	C	684414	F	FTN_0646	683745	684641	R	299	228(897)
tnfn1_pw060420p01q169	E09	C	1105579	F	FTN_1047	1105546	1106469	R	308	891(924)
tnfn1_pw060420p01q170	F09	C	463945	F	FTN_0457	463591	464247	F	219	355(657)
tnfn1_pw060420p01q171	G09	C	324201	R	FTN_0313	323976	324464	F	163	226(489)
tnfn1_pw060420p01q172	H09	C	1466960	R	FTN_1389	1466621	1467367	R	249	408(747)
tnfn1_pw060420p01q173	A10	C	615425	F	FTN_0586	615044	615559	F	172	382(516)
tnfn1_pw060420p01q174	B10	C	1338043	F	FTN_1266	1337851	1338948	F	366	193(1098)
tnfn1_pw060420p01q175	C10	C	1322096	F	FTN_1253	1321637	1322698	R	354	603(1062)
tnfn1_pw060420p01q176	D10	C	1624068	R	FTN_1527	1623669	1624385	R	239	318(717)
tnfn1_pw060420p01q177	E10	C	1395580	R	FTN_1320	1395199	1395762	F	188	382(564)
tnfn1_pw060420p01q178	F10	C	1631926	F	FTN_1534	1631854	1632321	F	156	73(468)
tnfn1_pw060420p01q179	G10	C	950328	R	FTN_0894	949934	950560	R	209	233(627)
tnfn1_pw060420p01q180	H10	C	108873	F	FTN_0097	107902	109104	R	401	232(1203)
tnfn1_pw060420p01q181	A11	C	390107	R	FTN_0390	389099	390163	R	355	57(1065)
tnfn1_pw060420p01q182	B11	U	1185013	F	FTN_1121	1184715	1186106	F	464	299(1392)
tnfn1_pw060420p01q183	C11	C	1556339	F	FTN_1467	1555816	1556637	R	274	299(822)
tnfn1_pw060420p01q184	D11	C	52249	R	FTN_0046	50758	53733	F	992	1492(2976)
tnfn1_pw060420p01q185	E11	C	1738414	R	FTN_1626	1738188	1739327	F	380	227(1140)
tnfn1_pw060420p01q186	F11	C	729755	R	FTN_0686	729231	730253	R	341	499(1023)
tnfn1_pw060420p01q187	G11	C	709944	R	intergenic					
tnfn1_pw060420p01q188	H11	C	1405896	R	FTN_1327	1404933	1406114	F	394	964(1182)
tnfn1_pw060420p01q189	A12	C	1718484	F	FTN_1611	1717771	1719048	F	426	714(1278)
tnfn1_pw060420p01q190	B12	C	1803677	R	FTN_1687	1803376	1804866	F	497	302(1491)
tnfn1_pw060420p01q191	C12	C	1058365	R	FTN_0998	1057851	1059008	F	386	515(1158)
tnfn1_pw060420p01q192	D12	C	1107330	R	FTN_1048	1106474	1107538	R	355	209(1065)
tnfn1_pw060420p01q193	E12	C	1089643	R	FTN_1033	1089601	1090242	F	214	43(642)
tnfn1_pw060420p01q194	F12	C	73989	R	FTN_0062	72771	74348	R	526	360(1578)
tnfn1_pw060420p01q195	G12	C	368374	R	FTN_0365	368251	369006	F	252	124(756)
tnfn1_pw060420p01q196	H12	C	299276	F	intergenic					

The Effective Genome Position of Insertion indicates the effective insertion position that is most likely to be functionally relevant in light of the 9-bp Tn5 target-site duplication and the direction of transcription of the predicted gene of insertion. E.g., for genes oriented to the right, the value reported indicates the genomic position of the nucleotide immediately adjacent to the left end of the insertion element when accounting for the 9-bp target site duplication.

Table 3 - Sequence Mapping Quality Metrics

Strain Name	Well	Junction information	Position in sequence read of last vector nucleotide	Length of match to transposon	Transposon match score	Average phred score for transposon match	Genome position information	Length of match to genome	Genome match score	Average phred score for genome match
tnfn1_pw060420p01q101	A01	EXACT(0)	123	110	102	31	EXACT(0)	200	176	30
tnfn1_pw060420p01q102	B01	EXACT(0)	121	106	83	33	EXACT(0)	200	177	50
tnfn1_pw060420p01q103	C01	EXACT(0)	122	120	96	29	EXACT(0)	200	150	56
tnfn1_pw060420p01q104	D01	EXACT(0)	124	109	70	20	EXACT(0)	200	185	54
tnfn1_pw060420p01q105	E01	EXACT(0)	121	106	95	33	EXACT(0)	200	196	55
tnfn1_pw060420p01q106	F01	EXACT(0)	123	119	92	32	EXACT(0)	200	188	48
tnfn1_pw060420p01q107	G01	EXACT(0)	124	109	93	23	EXACT(0)	200	174	44
tnfn1_pw060420p01q108	H01	EXACT(0)	126	119	93	23	EXACT(0)	200	191	52
tnfn1_pw060420p01q109	A02	EXACT(0)	124	119	108	30	EXACT(0)	200	156	46
tnfn1_pw060420p01q110	B02	EXACT(0)	123	112	92	28	EXACT(0)	200	198	50
tnfn1_pw060420p01q111	C02	EXACT(0)	124	119	103	33	EXACT(0)	200	181	49
tnfn1_pw060420p01q112	D02	EXACT(0)	123	119	100	28	EXACT(0)	200	191	54
tnfn1_pw060420p01q113	E02	EXACT(0)	157	142	100	25	EXACT(0)	200	192	43
tnfn1_pw060420p01q114	F02	EXACT(0)	156	145	134	45	EXACT(0)	200	186	66
tnfn1_pw060420p01q115	G02	EXACT(0)	155	145	113	35	EXACT(0)	200	198	56
tnfn1_pw060420p01q116	H02	EXACT(0)	157	152	143	42	EXACT(0)	200	191	60
tnfn1_pw060420p01q117	A03	EXACT(0)	157	145	138	44	EXACT(0)	200	185	59
tnfn1_pw060420p01q118	B03	EXACT(0)	157	152	135	45	EXACT(0)	200	194	65
tnfn1_pw060420p01q119	C03	EXACT(0)	158	153	142	40	EXACT(0)	200	189	60
tnfn1_pw060420p01q120	D03	EXACT(0)	159	152	133	38	EXACT(0)	200	192	58
tnfn1_pw060420p01q121	E03	EXACT(0)	157	142	108	33	EXACT(0)	200	188	55
tnfn1_pw060420p01q122	F03	EXACT(0)	154	145	113	35	EXACT(0)	200	190	54
tnfn1_pw060420p01q123	G03	EXACT(0)	156	152	133	37	EXACT(0)	200	194	51
tnfn1_pw060420p01q124	H03	EXACT(0)	155	145	126	43	EXACT(0)	200	180	56
tnfn1_pw060420p01q125	A04	EXACT(0)	158	151	143	44	EXACT(0)	200	193	60
tnfn1_pw060420p01q126	B04	EXACT(0)	154	138	101	28	EXACT(0)	200	169	34
tnfn1_pw060420p01q127	C04	EXACT(0)	152	142	109	31	EXACT(0)	190	177	41
tnfn1_pw060420p01q128	D04	EXACT(0)	157	145	122	39	EXACT(0)	200	185	64
tnfn1_pw060420p01q129	E04	EXACT(0)	159	151	136	44	EXACT(0)	200	163	45
tnfn1_pw060420p01q130	F04	EXACT(0)	159	153	139	37	EXACT(0)	200	197	52
tnfn1_pw060420p01q131	G04	EXACT(0)	156	145	134	47	EXACT(0)	200	184	60
tnfn1_pw060420p01q132	H04	EXACT(0)	158	152	141	43	EXACT(0)	200	191	59
tnfn1_pw060420p01q133	A05	EXACT(0)	158	151	140	42	EXACT(0)	200	192	56
tnfn1_pw060420p01q134	B05	EXACT(0)	160	157	144	36	EXACT(0)	193	177	50
tnfn1_pw060420p01q135	C05	EXACT(0)	157	145	136	32	EXACT(0)	200	191	52
tnfn1_pw060420p01q136	D05	EXACT(0)	157	152	139	48	EXACT(0)	200	186	64
tnfn1_pw060420p01q137	E05	EXACT(0)	157	152	139	47	EXACT(0)	200	168	30
tnfn1_pw060420p01q138	F05	EXACT(0)	157	145	126	28	EXACT(0)	200	180	50
tnfn1_pw060420p01q139	G05	EXACT(0)	158	152	134	37	EXACT(0)	200	184	50
tnfn1_pw060420p01q140	H05	EXACT(0)	156	145	100	22	EXACT(0)	200	186	55
tnfn1_pw060420p01q141	A06	EXACT(0)	159	152	133	37	EXACT(0)	200	197	54
tnfn1_pw060420p01q142	B06	EXACT(0)	156	116	89	30	EXACT(0)	182	165	51
tnfn1_pw060420p01q143	C06	EXACT(0)	159	153	127	27	EXACT(0)	200	191	53
tnfn1_pw060420p01q144	D06	EXACT(0)	157	145	116	31	EXACT(0)	200	184	58
tnfn1_pw060420p01q145	E06	EXACT(0)	157	145	136	44	EXACT(0)	200	165	44
tnfn1_pw060420p01q146	F06	EXACT(0)	156	145	119	32	EXACT(0)	200	193	50
tnfn1_pw060420p01q147	G06	EXACT(0)	158	152	141	40	EXACT(0)	200	191	55
tnfn1_pw060420p01q148	H06	EXACT(0)	157	145	142	46	EXACT(0)	200	186	62

Table 3 - Sequence Mapping Quality Metrics

Strain Name	Well	Junction information	Position in sequence read of last vector nucleotide	Length of match to transposon	Transposon match score	Average phred score for transposon match	Genome position information	Length of match to genome	Genome match score	Average phred score for genome match
tnfn1_pw060420p01q149	A07	EXACT(0)	155	144	115	38	EXACT(0)	200	186	48
tnfn1_pw060420p01q150	B07	EXACT(0)	158	152	125	33	EXACT(0)	200	195	58
tnfn1_pw060420p01q151	C07	EXACT(0)	157	153	140	43	EXACT(0)	200	190	51
tnfn1_pw060420p01q152	D07	EXACT(0)	156	144	133	46	EXACT(0)	200	189	64
tnfn1_pw060420p01q153	E07	EXACT(0)	159	152	143	43	EXACT(0)	200	167	43
tnfn1_pw060420p01q154	F07	EXACT(0)	156	151	138	39	EXACT(0)	200	185	62
tnfn1_pw060420p01q155	G07	EXACT(0)	122	112	75	19	EXACT(0)	200	189	48
tnfn1_pw060420p01q156	H07	EXACT(0)	121	111	85	23	EXACT(0)	200	189	52
tnfn1_pw060420p01q157	A08	EXACT(0)	117	112	97	29	EXACT(0)	200	180	48
tnfn1_pw060420p01q158	B08	EXACT(0)	123	120	98	27	EXACT(0)	200	190	47
tnfn1_pw060420p01q159	C08	EXACT(0)	118	112	107	39	EXACT(0)	200	180	56
tnfn1_pw060420p01q160	D08	EXACT(0)	114	112	97	39	EXACT(0)	200	184	53
tnfn1_pw060420p01q161	E08	EXACT(0)	113	112	89	30	EXACT(0)	200	140	35
tnfn1_pw060420p01q162	F08	EXACT(0)	122	117	96	33	EXACT(0)	200	186	45
tnfn1_pw060420p01q163	G08	EXACT(0)	122	106	91	30	EXACT(0)	200	170	43
tnfn1_pw060420p01q164	H08	EXACT(0)	114	103	88	36	EXACT(0)	200	171	32
tnfn1_pw060420p01q165	A09	EXACT(0)	118	112	107	36	EXACT(0)	200	173	52
tnfn1_pw060420p01q166	B09	EXACT(0)	123	111	87	23	EXACT(0)	196	187	51
tnfn1_pw060420p01q167	C09	EXACT(0)	123	83	49	18	EXACT(0)	200	160	35
tnfn1_pw060420p01q168	D09	EXACT(0)	123	110	93	28	EXACT(0)	200	192	35
tnfn1_pw060420p01q169	E09	EXACT(0)	124	109	70	19	EXACT(0)	200	190	48
tnfn1_pw060420p01q170	F09	EXACT(0)	125	119	105	32	EXACT(0)	200	190	57
tnfn1_pw060420p01q171	G09	EXACT(0)	125	120	93	21	EXACT(0)	200	183	44
tnfn1_pw060420p01q172	H09	EXACT(0)	122	115	67	19	EXACT(0)	200	192	47
tnfn1_pw060420p01q173	A10	EXACT(0)	123	83	26	12	EXACT(0)	200	172	24
tnfn1_pw060420p01q174	B10	EXACT(0)	122	117	87	27	EXACT(0)	200	186	51
tnfn1_pw060420p01q175	C10	EXACT(0)	123	120	99	30	EXACT(0)	200	191	45
tnfn1_pw060420p01q176	D10	EXACT(0)	121	112	84	22	EXACT(0)	200	191	44
tnfn1_pw060420p01q177	E10	EXACT(0)	122	109	82	26	EXACT(0)	200	180	56
tnfn1_pw060420p01q178	F10	EXACT(0)	125	119	99	24	EXACT(0)	200	187	52
tnfn1_pw060420p01q179	G10	EXACT(0)	154	145	87	19	EXACT(0)	200	192	51
tnfn1_pw060420p01q180	H10	EXACT(0)	155	138	108	35	EXACT(0)	124	120	38
tnfn1_pw060420p01q181	A11	EXACT(0)	157	142	112	26	EXACT(0)	200	190	50
tnfn1_pw060420p01q182	B11	EXACT(0)	157	87	81	36	EXACT(0)	200	173	39
tnfn1_pw060420p01q183	C11	EXACT(0)	158	145	116	29	EXACT(0)	200	183	56
tnfn1_pw060420p01q184	D11	EXACT(0)	156	153	122	33	EXACT(0)	200	185	56
tnfn1_pw060420p01q185	E11	EXACT(0)	157	145	108	25	EXACT(0)	200	177	45
tnfn1_pw060420p01q186	F11	EXACT(0)	154	144	112	34	EXACT(0)	200	190	55
tnfn1_pw060420p01q187	G11	EXACT(0)	155	145	111	25	EXACT(0)	200	175	51
tnfn1_pw060420p01q188	H11	EXACT(0)	156	145	117	31	EXACT(0)	200	185	57
tnfn1_pw060420p01q189	A12	EXACT(0)	158	157	115	25	EXACT(0)	200	193	55
tnfn1_pw060420p01q190	B12	EXACT(0)	156	145	115	34	EXACT(0)	200	183	64
tnfn1_pw060420p01q191	C12	EXACT(0)	155	116	101	38	EXACT(0)	200	179	49
tnfn1_pw060420p01q192	D12	EXACT(0)	156	153	118	34	EXACT(0)	200	189	49
tnfn1_pw060420p01q193	E12	EXACT(0)	156	145	116	31	EXACT(0)	200	171	58
tnfn1_pw060420p01q194	F12	EXACT(0)	158	152	135	45	EXACT(0)	200	173	56
tnfn1_pw060420p01q195	G12	EXACT(0)	155	139	113	29	EXACT(0)	200	187	45
tnfn1_pw060420p01q196	H12	EXACT(0)	157	151	138	42	EXACT(0)	200	177	51