

### ***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 2 (tnfn1\_pw060323p02)**

**Catalog No. NR-8036**

**For research use only. Not for human use.**

#### **Contributor:**

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#### **Product Description:**

A comprehensive 16508-member transposon mutant library<sup>1</sup> 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-8036 represents Plate 2 (tnfn1\_pw060323p02) 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.

*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-8036 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% CO<sub>2</sub>

##### 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 2 (tnfn1\_pw060323p02), NR-8036.”

#### **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/bmb15/bmb15toc.htm](http://www.cdc.gov/od/ohs/biosfty/bmb15/bmb15toc.htm).

#### **Disclaimers:**

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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_pw060323p02q101	A01	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p02q102	B01	T20	-	ROK family protein	putative enzymes
tnfn1_pw060323p02q103	C01	T20	asnB	asparagine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060323p02q104	D01	T20	proQ	activator of osmoprotectant transporter ProP	signal transduction and regulation
tnfn1_pw060323p02q105	E01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q106	F01	T20	recJ	single-stranded-DNA-specific exonuclease	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p02q107	G01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p02q108	H01	T20	-	glycosyl hydrolase family 3	carbohydrate metabolism - biosynthesis
tnfn1_pw060323p02q109	A02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q110	B02	T20	-	D-isomer specific 2-hydroxyacid dehydrogenase	energy metabolism
tnfn1_pw060323p02q111	C02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q112	D02	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p02q113	E02	T20	fur	ferric uptake regulation protein	signal transduction and regulation
tnfn1_pw060323p02q114	F02	T20	pdpD	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q115	G02	T20	-	10 TMS drug/metabolite exporter protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p02q116	H02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q117	A03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p02q118	B03	T20	-	methyltransferase	putative enzymes
tnfn1_pw060323p02q119	C03	T20	pilV	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p02q120	D03	T20	isfU3	isfU3	IS element
tnfn1_pw060323p02q121	E03	T20	-	predicted metal-dependent hydrolase	putative enzymes
tnfn1_pw060323p02q122	F03	T20	-	sigma54 modulation protein	translation, ribosomal structure and biogenesis
tnfn1_pw060323p02q123	G03	T20	-	disulfide bond formation protein, DsbB family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p02q124	H03	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - repair
tnfn1_pw060323p02q125	A04	T20	rplI	50S ribosomal protein L9	translation, ribosomal structure and biogenesis
tnfn1_pw060323p02q126	B04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q127	C04	T20	-	metabolite:H <sup>+</sup> symporter (MHS) family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060323p02q128	D04	T20	-	ribokinase, pfkB family	carbohydrate metabolism
tnfn1_pw060323p02q129	E04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q130	F04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q131	G04	T20	-	RND efflux transporter, AcrB/AcrD/AcrF family	transport
tnfn1_pw060323p02q132	H04	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060323p02q133	A05	T20	-	sugar porter (SP) family	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060323p02q134	B05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p02q135	C05	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060323p02q136	D05	T20	-	amino acid antiporter	transport - amino-acid
tnfn1_pw060323p02q137	E05	T20	-	AMP-binding enzyme	putative enzymes
tnfn1_pw060323p02q138	F05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q139	G05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q140	H05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q141	A06	T20	clpX	ATP-dependent Clp protease subunit X	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060323p02q142	B06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q143	C06	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p02q144	D06	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060323p02q145	E06	T20	-	RmuC family protein	putative enzymes
tnfn1_pw060323p02q146	F06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p02q147	G06	T20	adhC	Zn-dependent alcohol dehydrogenase	energy metabolism
tnfn1_pw060323p02q148	H06	T20	-	protein of unknown function	unknown function - novel

**Table 1 - Transposon Type and Mutated Gene**

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p02q149	A07	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060323p02q150	B07	T20	-	aspartate aminotransferase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p02q151	C07	T20	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	translation, ribosomal structure and biogenesis
tnfn1_pw060323p02q152	D07	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p02q153	E07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q154	F07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p02q155	G07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q156	H07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q157	A08	T20	-	pseudogene: hypothetical membrane protein, fragment	pseudogene
tnfn1_pw060323p02q158	B08	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p02q159	C08	<KAN-2>	-	lipase/esterase	fatty acids and lipids metabolism
tnfn1_pw060323p02q160	D08	<KAN-2>	-	lipase/esterase	fatty acids and lipids metabolism
tnfn1_pw060323p02q161	E08	<KAN-2>	cyoE	heme O synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p02q162	F08	<KAN-2>	sspA	stringent starvation protein A	signal transduction and regulation
tnfn1_pw060323p02q163	G08	<KAN-2>	smpB	SsrA (tmRNA)-binding protein	translation, ribosomal structure and biogenesis
tnfn1_pw060323p02q164	H08	<KAN-2>	rplY	50S ribosomal protein L25	translation, ribosomal structure and biogenesis
tnfn1_pw060323p02q165	A09	T18	-	DNA uptake protein, SMF family	transport
tnfn1_pw060323p02q166	B09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q167	C09	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p02q168	D09	T18	wzb	low molecular weight (LMW) phosphotyrosine protein phosphatase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p02q169	E09	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q170	F09	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p02q171	G09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q172	H09	T18	-	licB-like transmembrane protein	putative enzymes
tnfn1_pw060323p02q173	A10	T18	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060323p02q174	B10	T18	nth	endonuclease III	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p02q175	C10	T20	cspC	cold shock protein, DNA-binding	signal transduction and regulation
tnfn1_pw060323p02q176	D10	T20	sdaC	serine permease	transport - amino-acid
tnfn1_pw060323p02q177	E10	T20	pheA	prephenate dehydratase	amino acid metabolism - biosynthesis
tnfn1_pw060323p02q178	F10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q179	G10	T20	-	type I restriction-modification system, subunit M (methyltransferase)	DNA replication, recombination, modification and repair - repair
tnfn1_pw060323p02q180	H10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q181	A11	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q182	B11	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p02q183	C11	T20	-	arsenite-antimonite (ArsB) efflux family protein	transport
tnfn1_pw060323p02q184	D11	T20	pta	phosphate acetyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p02q185	E11	T20	-	dGTP triphosphohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060323p02q186	F11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p02q187	G11	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p02q188	H11	T20	pilM	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p02q189	A12	T20	-	phage integrase	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060323p02q190	B12	T20	-	MutT/nudix family protein	putative enzymes
tnfn1_pw060323p02q191	C12	T20	-	allophanate hydrolase subunit 2	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p02q192	D12	T20	-	lipoprotein of unknown function	unknown function - novel
tnfn1_pw060323p02q193	E12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p02q194	F12	T20	sbcB	exodeoxyribonuclease I	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p02q195	G12	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p02q196	H12	T20	-	conserved hypothetical membrane protein	hypothetical - conserved

**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_pw060323p02q101	A01	C	753902	R	FTN_0710	753221	756328	F	1036	682(3108)
tnfn1_pw060323p02q102	B01	C	648705	F	FTN_0617	648331	649293	F	321	375(963)
tnfn1_pw060323p02q103	C01	C	996119	F	FTN_0935	995336	997186	F	617	784(1851)
tnfn1_pw060323p02q104	D01	C	296191	F	FTN_0289	296016	296714	F	233	176(699)
tnfn1_pw060323p02q105	E01	C	1862806	R	FTN_1736	1862687	1863082	F	132	120(396)
tnfn1_pw060323p02q106	F01	C	595540	F	FTN_0569	594781	596520	R	580	981(1740)
tnfn1_pw060323p02q107	G01	U	992353	F	FTN_0931	991793	992749	F	319	561(957)
tnfn1_pw060323p02q108	H01	C	863831	F	FTN_0806	862723	864387	R	555	557(1665)
tnfn1_pw060323p02q109	A02	C	146043	R	FTN_0132	145235	146200	R	322	158(966)
tnfn1_pw060323p02q110	B02	C	1846779	R	FTN_1719	1846033	1847178	R	382	400(1146)
tnfn1_pw060323p02q111	C02	C	146043	R	FTN_0132	145235	146200	R	322	158(966)
tnfn1_pw060323p02q112	D02	U	499961	F	FTN_0494	499405	500001	R	199	41(597)
tnfn1_pw060323p02q113	E02	U	1795568	F	FTN_1681	1795398	1795817	F	140	171(420)
tnfn1_pw060323p02q114	F02	C	1402305	F	FTN_1325	1399806	1403540	R	1245	1236(3735)
tnfn1_pw060323p02q115	G02	C	1619008	R	FTN_1521	1618541	1619422	F	294	468(882)
tnfn1_pw060323p02q116	H02	C	26439	F	FTN_0025	26213	26797	R	195	359(585)
tnfn1_pw060323p02q117	A03	C	93417	R	FTN_0083	93070	93825	F	252	348(756)
tnfn1_pw060323p02q118	B03	C	1229294	R	FTN_1158	1229066	1229818	F	251	229(753)
tnfn1_pw060323p02q119	C03	C	412980	R	FTN_0413	412120	413349	R	410	370(1230)
tnfn1_pw060323p02q120	D03	C	1717230	F	-	1716927	1717650	R	241.3	421(724)
tnfn1_pw060323p02q121	E03	C	803611	F	FTN_0749	802977	803642	F	222	635(666)
tnfn1_pw060323p02q122	F03	C	1366369	R	FTN_1296	1366367	1366660	R	98	292(294)
tnfn1_pw060323p02q123	G03	C	1455051	R	FTN_1376	1454884	1455417	F	178	168(534)
tnfn1_pw060323p02q124	H03	C	1223789	F	FTN_1155	1222624	1224969	R	782	1181(2346)
tnfn1_pw060323p02q125	A04	C	1007312	F	FTN_0949	1006996	1007448	R	151	137(453)
tnfn1_pw060323p02q126	B04	C	1352230	F	FTN_1279	1352177	1352596	F	140	54(420)
tnfn1_pw060323p02q127	C04	C	139640	R	FTN_0128	139163	140368	F	402	478(1206)
tnfn1_pw060323p02q128	D04	C	1280057	R	FTN_1210	1279841	1280944	F	368	217(1104)
tnfn1_pw060323p02q129	E04	C	1639766	R	intergenic					
tnfn1_pw060323p02q130	F04	C	91934	R	FTN_0081	91627	92358	R	244	425(732)
tnfn1_pw060323p02q131	G04	C	1715466	F	FTN_1610	1713789	1716899	F	1037	1678(3111)
tnfn1_pw060323p02q132	H04	C	993455	R	FTN_0932	992752	994548	F	599	704(1797)
tnfn1_pw060323p02q133	A05	C	1142263	F	FTN_1079	1141288	1142637	R	450	375(1350)
tnfn1_pw060323p02q134	B05	C	48037	F	FTN_0043	47436	48965	F	510	602(1530)
tnfn1_pw060323p02q135	C05	C	1151997	F	FTN_1090	1151656	1152243	R	196	247(588)
tnfn1_pw060323p02q136	D05	C	903767	R	FTN_0848	902798	904216	R	473	450(1419)
tnfn1_pw060323p02q137	E05	C	878005	F	FTN_0821	877333	878700	F	456	673(1368)
tnfn1_pw060323p02q138	F05	C	950655	R	FTN_0895	950585	950917	R	111	263(333)
tnfn1_pw060323p02q139	G05	C	1079926	F	FTN_1022	1079866	1080159	F	98	61(294)
tnfn1_pw060323p02q140	H05	C	950655	R	FTN_0895	950585	950917	R	111	263(333)
tnfn1_pw060323p02q141	A06	C	1117073	R	FTN_1056	1115895	1117145	R	417	73(1251)
tnfn1_pw060323p02q142	B06	C	1390127	R	FTN_1317	1389274	1390422	F	383	854(1149)
tnfn1_pw060323p02q143	C06	C	1602828	R	FTN_1507	1602509	1603009	R	167	182(501)
tnfn1_pw060323p02q144	D06	C	1046843	F	FTN_0990	1045587	1048394	R	936	1552(2808)
tnfn1_pw060323p02q145	E06	C	1081661	R	FTN_1024	1080823	1082235	R	471	575(1413)
tnfn1_pw060323p02q146	F06	C	505003	F	FTN_0498	504268	505494	F	409	736(1227)
tnfn1_pw060323p02q147	G06	C	406949	F	FTN_0409	406706	407815	F	370	244(1110)
tnfn1_pw060323p02q148	H06	C	798642	R	FTN_0745	798391	799095	F	235	252(705)

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_pw060323p02q149	A07	C	1634011	F	FTN_1536	1633310	1634656	R	449	646(1347)
tnfn1_pw060323p02q150	B07	C	1212220	R	FTN_1146	1211574	1212764	R	397	545(1191)
tnfn1_pw060323p02q151	C07	C	1303193	R	FTN_1234	1302512	1303525	R	338	333(1014)
tnfn1_pw060323p02q152	D07	C	1093416	F	FTN_1038	1093310	1093993	F	228	107(684)
tnfn1_pw060323p02q153	E07	C	371861	F	FTN_0368	371729	372250	F	174	133(522)
tnfn1_pw060323p02q154	F07	C	494555	R	FTN_0489	494328	494654	R	109	100(327)
tnfn1_pw060323p02q155	G07	C	1322976	F	FTN_1254	1322868	1323953	F	362	109(1086)
tnfn1_pw060323p02q156	H07	C	1322976	F	FTN_1254	1322868	1323953	F	362	109(1086)
tnfn1_pw060323p02q157	A08	C	1459603	F	FTN_1379	1457975	1459691	R	572.3	89(1717)
tnfn1_pw060323p02q158	B08	C	87349	F	FTN_0074	87173	87418	R	82	70(246)
tnfn1_pw060323p02q159	C08	C	875581	R	FTN_0818	874701	875618	R	306	38(918)
tnfn1_pw060323p02q160	D08	C	875581	R	FTN_0818	874701	875618	R	306	38(918)
tnfn1_pw060323p02q161	E08	C	221025	F	FTN_0199	220528	221373	F	282	498(846)
tnfn1_pw060323p02q162	F08	C	575437	F	FTN_0549	574840	575469	F	210	598(630)
tnfn1_pw060323p02q163	G08	C	1235178	F	FTN_1164	1234750	1235220	F	157	429(471)
tnfn1_pw060323p02q164	H08	C	1066479	R	FTN_1007	1066473	1066760	R	96	282(288)
tnfn1_pw060323p02q165	A09	C	351083	F	FTN_0345	351044	352147	R	368	1065(1104)
tnfn1_pw060323p02q166	B09	C	40337	F	FTN_0037	40006	40347	R	114	11(342)
tnfn1_pw060323p02q167	C09	C	391999	R	FTN_0393	391849	392901	F	351	151(1053)
tnfn1_pw060323p02q168	D09	C	1105371	F	FTN_1046	1105060	1105542	R	161	172(483)
tnfn1_pw060323p02q169	E09	C	1685652	R	FTN_1587	1685390	1685998	R	203	347(609)
tnfn1_pw060323p02q170	F09	C	397793	F	FTN_0398	397551	398084	R	178	292(534)
tnfn1_pw060323p02q171	G09	C	27140	R	FTN_0026	27076	27327	F	84	65(252)
tnfn1_pw060323p02q172	H09	C	1653776	F	FTN_1555	1653462	1654343	F	294	315(882)
tnfn1_pw060323p02q173	A10	C	112145	F	FTN_0101	111569	112462	R	298	318(894)
tnfn1_pw060323p02q174	B10	C	1091038	R	FTN_1035	1090869	1091504	F	212	170(636)
tnfn1_pw060323p02q175	C10	C	494000	R	FTN_0488	493874	494074	R	67	75(201)
tnfn1_pw060323p02q176	D10	C	16741	R	FTN_0018	15688	16908	R	407	168(1221)
tnfn1_pw060323p02q177	E10	C	802429	R	FTN_0748	802109	802948	F	280	321(840)
tnfn1_pw060323p02q178	F10	C	244971	F	FTN_0222	244745	245710	F	322	227(966)
tnfn1_pw060323p02q179	G10	C	1219012	R	FTN_1152	1218102	1219547	R	482	536(1446)
tnfn1_pw060323p02q180	H10	C	311758	R	FTN_0302	311638	311982	F	115	121(345)
tnfn1_pw060323p02q181	A11	C	191659	F	FTN_0175	191251	192873	F	541	409(1623)
tnfn1_pw060323p02q182	B11	C	376195	F	FTN_0374	376108	376314	F	69	88(207)
tnfn1_pw060323p02q183	C11	C	384242	F	FTN_0382	383357	384592	F	412	886(1236)
tnfn1_pw060323p02q184	D11	C	136284	R	FTN_0126	135582	137675	F	698	703(2094)
tnfn1_pw060323p02q185	E11	C	666145	F	FTN_0632	664957	666279	R	441	135(1323)
tnfn1_pw060323p02q186	F11	C	1757039	R	FTN_1644	1755794	1758634	R	947	1596(2841)
tnfn1_pw060323p02q187	G11	C	151085	R	FTN_0138	151080	151694	F	205	6(615)
tnfn1_pw060323p02q188	H11	C	1205553	R	FTN_1141	1205009	1206010	R	334	458(1002)
tnfn1_pw060323p02q189	A12	C	14837	F	FTN_0017	13789	15027	R	413	191(1239)
tnfn1_pw060323p02q190	B12	C	344628	R	FTN_0338	344391	345035	F	215	238(645)
tnfn1_pw060323p02q191	C12	C	100405	R	FTN_0089	100182	100991	F	270	224(810)
tnfn1_pw060323p02q192	D12	C	426168	F	FTN_0427	425944	426390	F	149	225(447)
tnfn1_pw060323p02q193	E12	C	283186	F	FTN_0275	282485	283540	F	352	702(1056)
tnfn1_pw060323p02q194	F12	C	1250675	F	FTN_1177	1249665	1251110	R	482	436(1446)
tnfn1_pw060323p02q195	G12	C	747055	R	FTN_0703	746848	747417	F	190	208(570)
tnfn1_pw060323p02q196	H12	U	693534	R	FTN_0654	693039	693686	R	216	153(648)

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_pw060323p02q101	A01	EXACT(0)	155	153	131	39	EXACT(0)	175	126	28
tnfn1_pw060323p02q102	B01	EXACT(0)	157	152	136	41	EXACT(0)	200	176	41
tnfn1_pw060323p02q103	C01	EXACT(0)	157	146	120	38	EXACT(0)	200	189	56
tnfn1_pw060323p02q104	D01	EXACT(0)	156	153	129	39	EXACT(0)	200	189	55
tnfn1_pw060323p02q105	E01	EXACT(0)	156	153	122	36	EXACT(0)	200	194	57
tnfn1_pw060323p02q106	F01	EXACT(0)	157	153	131	35	EXACT(0)	170	162	55
tnfn1_pw060323p02q107	G01	EXACT(0)	157	152	124	42	EXACT(0)	200	185	61
tnfn1_pw060323p02q108	H01	EXACT(0)	157	153	121	33	EXACT(0)	200	190	53
tnfn1_pw060323p02q109	A02	EXACT(0)	157	151	129	35	EXACT(0)	200	185	57
tnfn1_pw060323p02q110	B02	EXACT(0)	156	153	129	40	EXACT(0)	200	191	59
tnfn1_pw060323p02q111	C02	EXACT(0)	156	146	123	35	EXACT(0)	200	185	58
tnfn1_pw060323p02q112	D02	EXACT(0)	156	152	128	43	EXACT(0)	200	184	67
tnfn1_pw060323p02q113	E02	EXACT(0)	154	145	126	50	EXACT(0)	199	187	57
tnfn1_pw060323p02q114	F02	EXACT(0)	156	153	126	38	EXACT(0)	200	185	58
tnfn1_pw060323p02q115	G02	EXACT(0)	155	153	124	38	EXACT(0)	200	192	51
tnfn1_pw060323p02q116	H02	EXACT(0)	156	145	128	37	EXACT(0)	200	173	48
tnfn1_pw060323p02q117	A03	EXACT(0)	156	153	129	39	EXACT(0)	118	104	53
tnfn1_pw060323p02q118	B03	EXACT(0)	156	150	120	33	EXACT(0)	200	191	55
tnfn1_pw060323p02q119	C03	EXACT(0)	157	146	129	40	EXACT(0)	200	195	55
tnfn1_pw060323p02q120	D03	EXACT(0)	155	145	123	39	EXACT(0)	200	192	54
tnfn1_pw060323p02q121	E03	EXACT(0)	156	146	127	40	EXACT(0)	198	186	52
tnfn1_pw060323p02q122	F03	EXACT(0)	155	145	123	38	EXACT(0)	200	182	52
tnfn1_pw060323p02q123	G03	EXACT(0)	157	151	128	32	EXACT(0)	200	188	56
tnfn1_pw060323p02q124	H03	EXACT(0)	156	153	126	39	EXACT(0)	200	195	58
tnfn1_pw060323p02q125	A04	EXACT(0)	155	144	124	34	EXACT(0)	200	169	45
tnfn1_pw060323p02q126	B04	EXACT(0)	155	145	123	39	EXACT(0)	200	183	44
tnfn1_pw060323p02q127	C04	EXACT(0)	157	153	130	37	EXACT(0)	143	127	33
tnfn1_pw060323p02q128	D04	EXACT(0)	155	145	126	39	EXACT(0)	200	193	49
tnfn1_pw060323p02q129	E04	EXACT(0)	156	152	131	42	EXACT(0)	199	187	54
tnfn1_pw060323p02q130	F04	EXACT(0)	156	151	118	35	EXACT(0)	200	191	59
tnfn1_pw060323p02q131	G04	EXACT(0)	156	152	121	35	EXACT(0)	200	194	54
tnfn1_pw060323p02q132	H04	EXACT(0)	155	152	126	38	EXACT(0)	200	182	55
tnfn1_pw060323p02q133	A05	EXACT(0)	156	142	100	31	EXACT(0)	166	70	27
tnfn1_pw060323p02q134	B05	EXACT(0)	154	150	121	39	EXACT(0)	55	46	23
tnfn1_pw060323p02q135	C05	EXACT(0)	156	146	121	39	EXACT(0)	201	123	40
tnfn1_pw060323p02q136	D05	EXACT(0)	156	150	123	38	EXACT(0)	200	189	55
tnfn1_pw060323p02q137	E05	EXACT(0)	156	152	128	38	EXACT(0)	200	192	43
tnfn1_pw060323p02q138	F05	EXACT(0)	155	151	118	30	EXACT(0)	200	184	54
tnfn1_pw060323p02q139	G05	EXACT(0)	156	153	132	41	EXACT(0)	76	75	56
tnfn1_pw060323p02q140	H05	EXACT(0)	155	153	122	33	EXACT(0)	200	181	56
tnfn1_pw060323p02q141	A06	EXACT(0)	156	152	125	40	EXACT(0)	200	186	53
tnfn1_pw060323p02q142	B06	EXACT(0)	156	153	129	38	EXACT(0)	200	185	54
tnfn1_pw060323p02q143	C06	EXACT(0)	155	145	117	32	EXACT(0)	200	187	52
tnfn1_pw060323p02q144	D06	EXACT(0)	156	152	133	38	EXACT(0)	200	190	54
tnfn1_pw060323p02q145	E06	EXACT(0)	155	145	129	40	EXACT(0)	200	193	51
tnfn1_pw060323p02q146	F06	EXACT(0)	155	152	116	33	EXACT(0)	200	188	56
tnfn1_pw060323p02q147	G06	EXACT(0)	155	146	127	41	EXACT(0)	200	196	57
tnfn1_pw060323p02q148	H06	EXACT(0)	156	150	126	36	EXACT(0)	200	186	58

**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_pw060323p02q149	A07	EXACT(0)	156	146	125	34	EXACT(0)	200	187	52
tnfn1_pw060323p02q150	B07	EXACT(0)	156	153	129	38	EXACT(0)	200	190	56
tnfn1_pw060323p02q151	C07	EXACT(0)	155	146	130	40	EXACT(0)	200	194	55
tnfn1_pw060323p02q152	D07	EXACT(0)	154	136	125	45	EXACT(0)	200	191	53
tnfn1_pw060323p02q153	E07	EXACT(0)	156	153	129	48	EXACT(0)	59	55	54
tnfn1_pw060323p02q154	F07	EXACT(0)	155	153	132	39	EXACT(0)	200	182	58
tnfn1_pw060323p02q155	G07	EXACT(0)	155	153	135	41	EXACT(0)	200	186	56
tnfn1_pw060323p02q156	H07	EXACT(0)	154	150	115	35	EXACT(0)	200	186	54
tnfn1_pw060323p02q157	A08	EXACT(0)	157	151	135	42	EXACT(0)	200	177	56
tnfn1_pw060323p02q158	B08	EXACT(0)	156	151	127	41	EXACT(0)	200	192	54
tnfn1_pw060323p02q159	C08	EXACT(0)	122	119	98	26	EXACT(0)	200	190	55
tnfn1_pw060323p02q160	D08	EXACT(0)	122	118	97	26	EXACT(0)	200	190	54
tnfn1_pw060323p02q161	E08	EXACT(0)	121	118	97	30	EXACT(0)	200	187	52
tnfn1_pw060323p02q162	F08	EXACT(0)	122	120	93	26	EXACT(0)	200	191	49
tnfn1_pw060323p02q163	G08	EXACT(0)	123	106	49	31	EXACT(0)	200	192	59
tnfn1_pw060323p02q164	H08	EXACT(0)	121	112	87	25	EXACT(0)	173	146	50
tnfn1_pw060323p02q165	A09	EXACT(0)	123	120	66	21	ESTIMATE(2)	198	176	53
tnfn1_pw060323p02q166	B09	EXACT(0)	124	119	106	35	EXACT(0)	200	183	54
tnfn1_pw060323p02q167	C09	EXACT(0)	123	117	87	24	EXACT(0)	200	192	56
tnfn1_pw060323p02q168	D09	EXACT(0)	122	112	99	36	EXACT(0)	200	162	43
tnfn1_pw060323p02q169	E09	EXACT(0)	122	118	100	34	EXACT(0)	200	194	51
tnfn1_pw060323p02q170	F09	EXACT(0)	124	120	104	32	EXACT(0)	115	109	50
tnfn1_pw060323p02q171	G09	EXACT(0)	123	112	47	14	ESTIMATE(8)	192	173	37
tnfn1_pw060323p02q172	H09	EXACT(0)	123	119	96	27	EXACT(0)	200	187	51
tnfn1_pw060323p02q173	A10	EXACT(0)	122	113	97	30	EXACT(0)	200	187	57
tnfn1_pw060323p02q174	B10	EXACT(0)	122	119	101	29	EXACT(0)	200	184	51
tnfn1_pw060323p02q175	C10	EXACT(0)	155	146	130	39	EXACT(0)	162	154	53
tnfn1_pw060323p02q176	D10	EXACT(0)	156	150	123	34	EXACT(0)	200	187	53
tnfn1_pw060323p02q177	E10	EXACT(0)	156	152	131	43	EXACT(0)	201	143	45
tnfn1_pw060323p02q178	F10	EXACT(0)	157	152	126	36	EXACT(0)	200	196	53
tnfn1_pw060323p02q179	G10	EXACT(0)	155	152	125	39	EXACT(0)	200	197	52
tnfn1_pw060323p02q180	H10	EXACT(0)	155	78	64	18	EXACT(0)	200	187	47
tnfn1_pw060323p02q181	A11	EXACT(0)	155	145	120	36	EXACT(0)	200	194	45
tnfn1_pw060323p02q182	B11	EXACT(0)	157	152	136	41	EXACT(0)	200	190	55
tnfn1_pw060323p02q183	C11	EXACT(0)	158	151	140	39	EXACT(0)	200	192	54
tnfn1_pw060323p02q184	D11	EXACT(0)	154	145	126	37	EXACT(0)	200	190	56
tnfn1_pw060323p02q185	E11	EXACT(0)	156	152	124	39	EXACT(0)	200	184	57
tnfn1_pw060323p02q186	F11	EXACT(0)	156	152	125	40	EXACT(0)	200	190	57
tnfn1_pw060323p02q187	G11	EXACT(0)	156	152	118	33	EXACT(0)	200	172	57
tnfn1_pw060323p02q188	H11	EXACT(0)	155	142	88	25	EXACT(0)	139	132	44
tnfn1_pw060323p02q189	A12	EXACT(0)	155	142	108	31	EXACT(0)	200	172	48
tnfn1_pw060323p02q190	B12	EXACT(0)	157	145	108	33	EXACT(0)	200	186	54
tnfn1_pw060323p02q191	C12	EXACT(0)	157	152	129	36	EXACT(0)	150	148	54
tnfn1_pw060323p02q192	D12	EXACT(0)	155	153	122	34	EXACT(0)	200	193	57
tnfn1_pw060323p02q193	E12	EXACT(0)	157	152	144	37	EXACT(0)	200	195	51
tnfn1_pw060323p02q194	F12	EXACT(0)	157	153	134	39	EXACT(0)	200	186	56
tnfn1_pw060323p02q195	G12	EXACT(0)	156	152	128	40	EXACT(0)	200	184	56
tnfn1_pw060323p02q196	H12	EXACT(0)	156	151	135	46	EXACT(0)	200	184	65