

### ***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 4 (tnfn1\_pw060323p04)**

**Catalog No. NR-8038**

**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 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-8038 represents Plate 4 (tnfn1\_pw060323p04) 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-8038 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 4 (tnfn1\_pw060323p04), NR-8038.”

#### **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_pw060323p04q101	A01	<KAN-2>	-	30S ribosomal protein S21	translation, ribosomal structure and biogenesis
tnfn1_pw060323p04q102	B01	<KAN-2>	pcp	pyrrolidone carboxylate peptidase	post-translational modification, protein turnover, chaperones
tnfn1_pw060323p04q103	C01	<KAN-2>	wbtQ	aminotransferase	putative enzymes
tnfn1_pw060323p04q104	D01	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q105	E01	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q106	F01	T18	rbsK	ribokinase, pfkB family	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q107	G01	T20	tig	trigger factor (TF) protein (peptidyl-prolyl cis/trans isomerase)	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p04q108	H01	T18	fkpB	FKBP-type peptidyl-prolyl cis-trans isomerase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p04q109	A02	T20	-	asparaginase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q110	B02	T20	nuoC	NADH dehydrogenase I, C subunit	energy metabolism
tnfn1_pw060323p04q111	C02	T20	uvrB	excinuclease ABC, subunit B	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p04q112	D02	T20	mutM	formamidopyrimidine-DNA glycosylase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p04q113	E02	T20	-	predicted ATPase of the PP-loop superfamily	cell cycle
tnfn1_pw060323p04q114	F02	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060323p04q115	G02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p04q116	H02	T20	leuB	3-isopropylmalate dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060323p04q117	A03	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p04q118	B03	T20	-	transcriptional regulator, ArsR family	signal transduction and regulation
tnfn1_pw060323p04q119	C03	T20	purN	phosphoribosylglycinamide formyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060323p04q120	D03	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p04q121	E03	T20	glnA	glutamine synthetase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q122	F03	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p04q123	G03	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060323p04q124	H03	T20	gpsA	glycerol-3-phosphate-dehydrogenase-[NAD+]	fatty acids and lipids metabolism
tnfn1_pw060323p04q125	A04	T20	-	galactose mutarotase	carbohydrate metabolism - biosynthesis
tnfn1_pw060323p04q126	B04	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p04q127	C04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p04q128	D04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q129	E04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q130	F04	T20	-	DNA/RNA endonuclease G	nucleotides and nucleosides metabolism
tnfn1_pw060323p04q131	G04	T20	frgA	siderophore biosynthesis protein	other metabolism - biosynthesis
tnfn1_pw060323p04q132	H04	T20	-	pseudogene: hypothetical protein	pseudogene
tnfn1_pw060323p04q133	A05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p04q134	B05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p04q135	C05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q136	D05	T20	-	D-isomer specific 2-hydroxyacid dehydrogenase	energy metabolism
tnfn1_pw060323p04q137	E05	T20	deoB	phosphopentomutase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q138	F05	T20	-	EAL and a GDEF domain	signal transduction and regulation
tnfn1_pw060323p04q139	G05	T20	rliD	ribosomal large subunit pseudouridine synthase D	translation, ribosomal structure and biogenesis
tnfn1_pw060323p04q140	H05	T20	pilB	type IV pili ATPase	motility, attachment and secretion structure
tnfn1_pw060323p04q141	A06	T20	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060323p04q142	B06	T20	-	heat shock protein, HSP20 family	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060323p04q143	C06	T20	gltB	glutamate synthase domain 2	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q144	D06	T20	-	sterol desaturase	fatty acids and lipids metabolism
tnfn1_pw060323p04q145	E06	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p04q146	F06	T20	secB1	preprotein translocase, subunit B	motility, attachment and secretion structure
tnfn1_pw060323p04q147	G06	T20	-	pseudogene: hypothetical protein, fragment	pseudogene
tnfn1_pw060323p04q148	H06	T20	-	membrane protein of unknown function	unknown function - conserved

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

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p04q149	A07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q150	B07	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p04q151	C07	T20	-	ATPase, AAA family, related to the helicase subunit of the Holliday junction resolvase	DNA replication, recombination, modification and repair
tnfn1_pw060323p04q152	D07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p04q153	E07	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060323p04q154	F07	T20	-	acid phosphatase	fatty acids and lipids metabolism
tnfn1_pw060323p04q155	G07	T20	-	pseudogene: type I restriction-modification system, subunit M (methyltransferase)	pseudogene
tnfn1_pw060323p04q156	H07	T20	recB	ATP-dependent exoDNase (exonuclease V) beta subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p04q157	A08	T20	-	HIT family protein	putative enzymes
tnfn1_pw060323p04q158	B08	T20	dtl	D-tyrosyl-tRNA(Tyr) deacylase	translation, ribosomal structure and biogenesis
tnfn1_pw060323p04q159	C08	T20	tmpT	thiopurine S-methyltransferase	putative enzymes
tnfn1_pw060323p04q160	D08	T20	rluC	ribosomal large subunit pseudouridine synthase C	translation, ribosomal structure and biogenesis
tnfn1_pw060323p04q161	E08	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p04q162	F08	T20	aspC	aspartate aminotransferase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q163	G08	T20	pnuC	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060323p04q164	H08	T20	-	AMP-binding protein	putative enzymes
tnfn1_pw060323p04q165	A09	T20	hpt	hypoxanthine-guanine phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060323p04q166	B09	T20	glnA	glutamine synthetase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q167	C09	T20	-	S-adenosylmethionine-dependent methyltransferase	putative enzymes
tnfn1_pw060323p04q168	D09	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p04q169	E09	T20	-	cholyglycine hydrolase family protein	cell wall / LPS / capsule
tnfn1_pw060323p04q170	F09	T20	aspC	aspartate aminotransferase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q171	G09	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p04q172	H09	<KAN-2>	deoD	purine nucleoside phosphorylase	nucleotides and nucleosides metabolism
tnfn1_pw060323p04q173	A10	<KAN-2>	rplS	50S ribosomal protein L19	translation, ribosomal structure and biogenesis
tnfn1_pw060323p04q174	B10	T18	yrbl	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	fatty acids and lipids metabolism
tnfn1_pw060323p04q175	C10	<KAN-2>	panD	aspartate 1-decarboxylase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p04q176	D10	<KAN-2>	pyrF	orotidine-5'-phosphate decarboxylase	nucleotides and nucleosides metabolism
tnfn1_pw060323p04q177	E10	<KAN-2>	cphB	cyanophycinase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p04q178	F10	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q179	G10	<KAN-2>	putA	bifunctional proline dehydrogenase, pyrroline-5-carboxylate dehydrogenase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p04q180	H10	<KAN-2>	-	X-prolyl aminopeptidase 2	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p04q181	A11	<KAN-2>	-	transcriptional regulator, IclR family	signal transduction and regulation
tnfn1_pw060323p04q182	B11	<KAN-2>	-	glycoprotease family protein	post-translational modification, protein turnover, chaperones
tnfn1_pw060323p04q183	C11	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p04q184	D11	<KAN-2>	-	DNA-directed RNA polymerase, alpha subunit/40 kD subunit	transcription
tnfn1_pw060323p04q185	E11	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p04q186	F11	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q187	G11	<KAN-2>	fopA	OmpA family protein	cell wall / LPS / capsule
tnfn1_pw060323p04q188	H11	<KAN-2>	-	protein of unknown function	unknown function - conserved
tnfn1_pw060323p04q189	A12	T18	pilT	Type IV pili nucleotide-binding protein	motility, attachment and secretion structure
tnfn1_pw060323p04q190	B12	T18	-	phosphosugar binding protein	cell wall / LPS / capsule
tnfn1_pw060323p04q191	C12	T18	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p04q192	D12	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p04q193	E12	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p04q194	F12	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p04q195	G12	T18	cspA	cold shock protein, DNA-binding	transcription
tnfn1_pw060323p04q196	H12	T18	bioC	biotin synthesis protein BioC	cofactors, prosthetic groups, electron carriers metabolism

**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_pw060323p04q101	A01	C	493751	R	FTN_0487	493677	493871	R	65	121(195)
tnfn1_pw060323p04q102	B01	C	231730	F	FTN_0211	231598	232263	F	222	133(666)
tnfn1_pw060323p04q103	C01	C	1510880	R	FTN_1430	1509879	1510991	R	371	112(1113)
tnfn1_pw060323p04q104	D01	C	976907	F	FTN_0918	976636	977244	F	203	272(609)
tnfn1_pw060323p04q105	E01	C	974393	R	FTN_0915	974276	974719	R	148	327(444)
tnfn1_pw060323p04q106	F01	C	1896540	R	FTN_1767	1896135	1897052	R	306	513(918)
tnfn1_pw060323p04q107	G01	U	1118757	R	FTN_1058	1117803	1119116	R	438	360(1314)
tnfn1_pw060323p04q108	H01	C	353861	F	FTN_0347	353592	354053	F	154	270(462)
tnfn1_pw060323p04q109	A02	U	617414	F	FTN_0588	616823	617740	R	306	327(918)
tnfn1_pw060323p04q110	B02	C	1793691	R	FTN_1678	1793680	1794321	R	214	631(642)
tnfn1_pw060323p04q111	C02	C	1248904	F	FTN_1176	1247657	1249660	R	668	757(2004)
tnfn1_pw060323p04q112	D02	C	635986	R	FTN_0603	635462	636283	R	274	298(822)
tnfn1_pw060323p04q113	E02	C	1235321	F	FTN_1165	1235224	1235982	F	253	98(759)
tnfn1_pw060323p04q114	F02	C	1632610	F	FTN_1535	1632461	1633282	F	274	150(822)
tnfn1_pw060323p04q115	G02	C	1029788	R	FTN_0975	1029173	1030660	F	496	616(1488)
tnfn1_pw060323p04q116	H02	C	70177	F	FTN_0059	69707	70783	R	359	607(1077)
tnfn1_pw060323p04q117	A03	C	1423959	F	FTN_1345	1423503	1424552	F	350	457(1050)
tnfn1_pw060323p04q118	B03	C	395272	F	FTN_0395	395071	395433	R	121	162(363)
tnfn1_pw060323p04q119	C03	C	421033	R	FTN_0421	420678	421250	F	191	356(573)
tnfn1_pw060323p04q120	D03	C	1607515	R	FTN_1511	1607392	1608612	F	407	124(1221)
tnfn1_pw060323p04q121	E03	C	189062	R	FTN_0172	188353	189387	R	345	326(1035)
tnfn1_pw060323p04q122	F03	C	319013	F	FTN_0309	318501	320303	F	601	513(1803)
tnfn1_pw060323p04q123	G03	C	1288079	R	FTN_1217	1286888	1288573	R	562	495(1686)
tnfn1_pw060323p04q124	H03	U	396980	F	FTN_0397	396549	397544	F	332	432(996)
tnfn1_pw060323p04q125	A04	C	1815122	R	FTN_1697	1814406	1815263	R	286	142(858)
tnfn1_pw060323p04q126	B04	C	557377	F	FTN_0535	556910	558133	F	408	468(1224)
tnfn1_pw060323p04q127	C04	C	13581	R	FTN_0016	13110	13781	R	224	201(672)
tnfn1_pw060323p04q128	D04	C	797915	F	intergenic					
tnfn1_pw060323p04q129	E04	C	457692	F	FTN_0454	457266	458279	F	338	427(1014)
tnfn1_pw060323p04q130	F04	C	1135931	R	FTN_1073	1135198	1136259	R	354	329(1062)
tnfn1_pw060323p04q131	G04	C	1796350	F	FTN_1682	1796074	1797990	F	639	277(1917)
tnfn1_pw060323p04q132	H04	C	852070	F	FTN_0794	851999	852079	R	27	10(81)
tnfn1_pw060323p04q133	A05	C	1597063	R	FTN_1502	1596730	1597764	R	345	702(1035)
tnfn1_pw060323p04q134	B05	C	999540	R	FTN_0938	999438	999626	R	63	87(189)
tnfn1_pw060323p04q135	C05	C	1273800	F	FTN_1199	1272824	1274032	R	403	233(1209)
tnfn1_pw060323p04q136	D05	C	1886307	R	FTN_1757	1885735	1886715	R	327	409(981)
tnfn1_pw060323p04q137	E05	C	1703845	R	FTN_1602	1703024	1704265	R	414	421(1242)
tnfn1_pw060323p04q138	F05	C	461564	R	FTN_0456	461255	463570	F	772	310(2316)
tnfn1_pw060323p04q139	G05	C	1336316	R	FTN_1264	1335988	1336983	F	332	329(996)
tnfn1_pw060323p04q140	H05	C	1179701	F	FTN_1115	1178703	1180478	F	592	999(1776)
tnfn1_pw060323p04q141	A06	C	310563	R	FTN_0301	310260	311564	F	435	304(1305)
tnfn1_pw060323p04q142	B06	C	1900128	F	FTN_1769	1899948	1900373	F	142	181(426)
tnfn1_pw060323p04q143	C06	C	1443492	F	FTN_1360	1442839	1444422	R	528	931(1584)
tnfn1_pw060323p04q144	D06	C	404326	R	FTN_0406	403941	404729	F	263	386(789)
tnfn1_pw060323p04q145	E06	C	29619	R	FTN_0028	28714	29763	R	350	145(1050)
tnfn1_pw060323p04q146	F06	C	131759	F	FTN_0121	131668	132114	F	149	92(447)
tnfn1_pw060323p04q147	G06	C	1890173	F	FTN_1761	1889997	1890802	R	268.6	630(806)
tnfn1_pw060323p04q148	H06	C	920509	F	FTN_0868	920419	920994	F	192	91(576)

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_pw060323p04q149	A07	C	423079	R	FTN_0424	422962	423312	R	117	234(351)
tnfn1_pw060323p04q150	B07	C	1717938	R	FTN_1611	1717771	1719048	F	426	168(1278)
tnfn1_pw060323p04q151	C07	C	1490572	F	FTN_1413	1489726	1490961	R	412	390(1236)
tnfn1_pw060323p04q152	D07	C	1475007	F	FTN_1397	1473445	1477344	R	1300	2338(3900)
tnfn1_pw060323p04q153	E07	C	1013203	R	FTN_0957	1012691	1013299	R	203	97(609)
tnfn1_pw060323p04q154	F07	C	101847	F	FTN_0990	101004	102545	R	514	699(1542)
tnfn1_pw060323p04q155	G07	C	291220	F	FTN_0283	289901	291434	F	511.3	1320(1534)
tnfn1_pw060323p04q156	H07	C	1435806	F	FTN_1357	1435327	1438974	R	1216	3169(3648)
tnfn1_pw060323p04q157	A08	C	727851	F	FTN_0684	727685	728077	F	131	167(393)
tnfn1_pw060323p04q158	B08	C	66291	R	FTN_0056	65954	66388	R	145	98(435)
tnfn1_pw060323p04q159	C08	C	24396	F	FTN_0023	24071	24748	R	226	353(678)
tnfn1_pw060323p04q160	D08	C	1768840	F	FTN_1655	1768091	1769017	R	309	178(927)
tnfn1_pw060323p04q161	E08	U	376743	F	FTN_0375	376636	377250	F	205	108(615)
tnfn1_pw060323p04q162	F08	C	1853718	F	FTN_1725	1852730	1853917	R	396	200(1188)
tnfn1_pw060323p04q163	G08	C	1869930	F	FTN_1742	1869321	1870028	R	236	99(708)
tnfn1_pw060323p04q164	H08	C	636964	F	FTN_0604	636377	638473	F	699	588(2097)
tnfn1_pw060323p04q165	A09	C	197569	R	FTN_0179	197370	197900	F	177	200(531)
tnfn1_pw060323p04q166	B09	C	189062	R	FTN_0172	188353	189387	R	345	326(1035)
tnfn1_pw060323p04q167	C09	C	1479091	R	FTN_1400	1478681	1479367	R	229	277(687)
tnfn1_pw060323p04q168	D09	C	742545	F	FTN_0699	742065	743228	F	388	481(1164)
tnfn1_pw060323p04q169	E09	C	1320614	R	FTN_1252	1320488	1321630	F	381	127(1143)
tnfn1_pw060323p04q170	F09	C	1853718	F	FTN_1725	1852730	1853917	R	396	200(1188)
tnfn1_pw060323p04q171	G09	C	1445742	R	FTN_1362	1445486	1445869	R	128	128(384)
tnfn1_pw060323p04q172	H09	C	712390	F	FTN_0669	712184	712903	F	240	207(720)
tnfn1_pw060323p04q173	A10	C	1656976	R	FTN_1559	1656947	1657291	R	115	316(345)
tnfn1_pw060323p04q174	B10	C	961839	R	FTN_0905	961628	962173	R	182	335(546)
tnfn1_pw060323p04q175	C10	C	1432574	F	FTN_1354	1432438	1432770	F	111	137(333)
tnfn1_pw060323p04q176	D10	C	37525	F	FTN_0035	37218	37859	F	214	308(642)
tnfn1_pw060323p04q177	E10	C	1279347	R	FTN_1209	1278824	1279639	R	272	293(816)
tnfn1_pw060323p04q178	F10	C	1537201	R	FTN_1447	1536391	1537371	R	327	171(981)
tnfn1_pw060323p04q179	G10	C	1196712	R	FTN_1131	1194416	1198477	R	1354	1766(4062)
tnfn1_pw060323p04q180	H10	C	1136711	R	FTN_1074	1136360	1138117	R	586	1407(1758)
tnfn1_pw060323p04q181	A11	C	775387	F	FTN_0720	775195	775908	F	238	193(714)
tnfn1_pw060323p04q182	B11	C	1213615	R	FTN_1148	1213587	1214222	R	212	608(636)
tnfn1_pw060323p04q183	C11	C	1464865	F	FTN_1386	1464785	1465294	F	170	81(510)
tnfn1_pw060323p04q184	D11	C	1488954	R	FTN_1412	1488682	1489635	R	318	682(954)
tnfn1_pw060323p04q185	E11	C	840818	F	FTN_0782	840650	841222	F	191	169(573)
tnfn1_pw060323p04q186	F11	C	1086047	R	FTN_1029	1085576	1086232	R	219	186(657)
tnfn1_pw060323p04q187	G11	C	808639	F	FTN_0756	808202	809377	F	392	438(1176)
tnfn1_pw060323p04q188	H11	C	1091722	F	FTN_1036	1091504	1091932	F	143	219(429)
tnfn1_pw060323p04q189	A12	C	1733427	F	FTN_1622	1732820	1733845	R	342	419(1026)
tnfn1_pw060323p04q190	B12	C	1143547	F	FTN_1080	1142674	1143699	R	342	153(1026)
tnfn1_pw060323p04q191	C12	C	606886	F	FTN_0578	606155	607375	F	407	732(1221)
tnfn1_pw060323p04q192	D12	C	445653	F	FTN_0445	445344	446786	F	481	310(1443)
tnfn1_pw060323p04q193	E12	C	379175	R	FTN_0378	379010	380461	F	484	166(1452)
tnfn1_pw060323p04q194	F12	C	1079400	F	FTN_1021	1079294	1079827	F	178	107(534)
tnfn1_pw060323p04q195	G12	C	778458	F	FTN_0723	778322	778522	R	67	65(201)
tnfn1_pw060323p04q196	H12	U	870726	R	FTN_0813	870029	870763	R	245	38(735)

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_pw060323p04q101	A01	EXACT(0)	122	113	97	27	EXACT(0)	200	190	53
tnfn1_pw060323p04q102	B01	EXACT(0)	122	125	102	30	EXACT(0)	200	194	54
tnfn1_pw060323p04q103	C01	EXACT(0)	123	119	103	28	EXACT(0)	200	195	49
tnfn1_pw060323p04q104	D01	EXACT(0)	121	120	107	48	EXACT(0)	200	170	56
tnfn1_pw060323p04q105	E01	EXACT(0)	122	96	73	23	EXACT(0)	200	191	39
tnfn1_pw060323p04q106	F01	EXACT(0)	122	105	87	28	EXACT(0)	200	178	39
tnfn1_pw060323p04q107	G01	EXACT(0)	156	152	130	37	EXACT(0)	200	187	58
tnfn1_pw060323p04q108	H01	EXACT(0)	124	119	103	24	EXACT(0)	200	187	51
tnfn1_pw060323p04q109	A02	EXACT(0)	157	145	129	42	EXACT(0)	106	100	59
tnfn1_pw060323p04q110	B02	EXACT(0)	156	146	127	41	EXACT(0)	163	152	48
tnfn1_pw060323p04q111	C02	EXACT(0)	156	146	138	41	EXACT(0)	200	194	51
tnfn1_pw060323p04q112	D02	EXACT(0)	158	151	131	36	EXACT(0)	200	188	57
tnfn1_pw060323p04q113	E02	EXACT(0)	155	151	127	39	EXACT(0)	200	192	56
tnfn1_pw060323p04q114	F02	EXACT(0)	156	153	129	37	EXACT(0)	200	190	51
tnfn1_pw060323p04q115	G02	EXACT(0)	157	152	114	30	EXACT(0)	200	191	54
tnfn1_pw060323p04q116	H02	EXACT(0)	155	152	131	39	EXACT(0)	200	191	55
tnfn1_pw060323p04q117	A03	EXACT(0)	156	151	121	35	EXACT(0)	200	191	43
tnfn1_pw060323p04q118	B03	EXACT(0)	155	145	120	40	EXACT(0)	200	187	60
tnfn1_pw060323p04q119	C03	EXACT(0)	154	139	125	42	EXACT(0)	200	193	57
tnfn1_pw060323p04q120	D03	EXACT(0)	155	146	124	35	EXACT(0)	190	173	54
tnfn1_pw060323p04q121	E03	EXACT(0)	157	151	128	35	EXACT(0)	200	198	49
tnfn1_pw060323p04q122	F03	EXACT(0)	156	146	127	41	EXACT(0)	200	184	53
tnfn1_pw060323p04q123	G03	EXACT(0)	155	153	127	37	EXACT(0)	200	182	52
tnfn1_pw060323p04q124	H03	EXACT(0)	154	145	129	49	EXACT(0)	200	169	48
tnfn1_pw060323p04q125	A04	EXACT(0)	154	145	120	38	EXACT(0)	200	192	54
tnfn1_pw060323p04q126	B04	EXACT(0)	156	151	118	36	EXACT(0)	200	186	58
tnfn1_pw060323p04q127	C04	EXACT(0)	157	152	132	38	EXACT(0)	200	172	52
tnfn1_pw060323p04q128	D04	EXACT(0)	157	153	134	40	EXACT(0)	167	156	46
tnfn1_pw060323p04q129	E04	EXACT(0)	155	145	126	41	EXACT(0)	200	183	46
tnfn1_pw060323p04q130	F04	EXACT(0)	155	146	124	41	EXACT(0)	200	193	58
tnfn1_pw060323p04q131	G04	EXACT(0)	158	152	129	38	EXACT(0)	200	183	58
tnfn1_pw060323p04q132	H04	EXACT(0)	158	151	119	33	EXACT(0)	200	124	40
tnfn1_pw060323p04q133	A05	EXACT(0)	156	145	122	37	EXACT(0)	200	160	39
tnfn1_pw060323p04q134	B05	EXACT(0)	156	153	132	37	EXACT(0)	201	100	28
tnfn1_pw060323p04q135	C05	EXACT(0)	156	151	127	41	EXACT(0)	200	191	57
tnfn1_pw060323p04q136	D05	EXACT(0)	155	145	123	37	EXACT(0)	200	189	56
tnfn1_pw060323p04q137	E05	EXACT(0)	158	153	132	35	EXACT(0)	200	195	52
tnfn1_pw060323p04q138	F05	EXACT(0)	156	153	132	36	EXACT(0)	200	167	44
tnfn1_pw060323p04q139	G05	EXACT(0)	155	151	127	40	EXACT(0)	200	191	52
tnfn1_pw060323p04q140	H05	EXACT(0)	156	151	130	35	EXACT(0)	200	191	50
tnfn1_pw060323p04q141	A06	EXACT(0)	157	153	125	33	EXACT(0)	200	195	55
tnfn1_pw060323p04q142	B06	EXACT(0)	156	152	125	37	EXACT(0)	200	183	56
tnfn1_pw060323p04q143	C06	EXACT(0)	155	145	129	40	EXACT(0)	200	198	56
tnfn1_pw060323p04q144	D06	EXACT(0)	155	152	131	39	EXACT(0)	200	189	51
tnfn1_pw060323p04q145	E06	EXACT(0)	156	152	131	40	EXACT(0)	200	190	57
tnfn1_pw060323p04q146	F06	EXACT(0)	156	152	133	35	EXACT(0)	200	196	55
tnfn1_pw060323p04q147	G06	EXACT(0)	155	145	128	32	EXACT(0)	200	191	54
tnfn1_pw060323p04q148	H06	EXACT(0)	155	145	113	33	EXACT(0)	200	185	56

**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_pw060323p04q149	A07	EXACT(0)	155	145	120	38	EXACT(0)	200	187	55
tnfn1_pw060323p04q150	B07	EXACT(0)	155	151	130	37	EXACT(0)	200	184	49
tnfn1_pw060323p04q151	C07	EXACT(0)	155	145	132	41	EXACT(0)	200	183	53
tnfn1_pw060323p04q152	D07	EXACT(0)	153	152	106	32	EXACT(0)	200	183	55
tnfn1_pw060323p04q153	E07	EXACT(0)	157	152	125	32	EXACT(0)	200	187	53
tnfn1_pw060323p04q154	F07	EXACT(0)	155	145	123	38	EXACT(0)	200	196	53
tnfn1_pw060323p04q155	G07	EXACT(0)	158	153	138	36	EXACT(0)	200	177	41
tnfn1_pw060323p04q156	H07	EXACT(0)	157	153	130	36	EXACT(0)	200	172	47
tnfn1_pw060323p04q157	A08	EXACT(0)	156	153	126	37	EXACT(0)	200	189	57
tnfn1_pw060323p04q158	B08	EXACT(0)	155	151	124	36	EXACT(0)	200	190	55
tnfn1_pw060323p04q159	C08	EXACT(0)	154	145	132	41	EXACT(0)	200	181	52
tnfn1_pw060323p04q160	D08	EXACT(0)	155	153	126	36	EXACT(0)	200	145	43
tnfn1_pw060323p04q161	E08	EXACT(0)	156	145	106	22	EXACT(0)	200	185	53
tnfn1_pw060323p04q162	F08	EXACT(0)	155	145	126	43	EXACT(0)	200	191	55
tnfn1_pw060323p04q163	G08	EXACT(0)	155	152	111	30	EXACT(0)	200	186	54
tnfn1_pw060323p04q164	H08	EXACT(0)	156	152	117	33	EXACT(0)	200	195	51
tnfn1_pw060323p04q165	A09	EXACT(0)	156	152	118	34	EXACT(0)	200	189	54
tnfn1_pw060323p04q166	B09	EXACT(0)	156	152	130	37	EXACT(0)	200	198	52
tnfn1_pw060323p04q167	C09	EXACT(0)	155	152	131	43	EXACT(0)	200	192	58
tnfn1_pw060323p04q168	D09	EXACT(0)	155	152	134	40	EXACT(0)	200	190	54
tnfn1_pw060323p04q169	E09	EXACT(0)	157	151	138	40	EXACT(0)	200	173	42
tnfn1_pw060323p04q170	F09	EXACT(0)	155	152	131	41	EXACT(0)	200	191	53
tnfn1_pw060323p04q171	G09	EXACT(0)	123	119	79	22	EXACT(0)	200	178	51
tnfn1_pw060323p04q172	H09	EXACT(0)	122	119	109	48	EXACT(0)	200	183	65
tnfn1_pw060323p04q173	A10	EXACT(0)	121	120	105	41	EXACT(0)	200	189	62
tnfn1_pw060323p04q174	B10	EXACT(0)	132	103	65	13	EXACT(0)	200	183	29
tnfn1_pw060323p04q175	C10	EXACT(0)	122	121	106	48	EXACT(0)	200	194	64
tnfn1_pw060323p04q176	D10	EXACT(0)	120	112	81	24	EXACT(0)	200	194	52
tnfn1_pw060323p04q177	E10	EXACT(0)	123	126	100	32	EXACT(0)	200	197	50
tnfn1_pw060323p04q178	F10	EXACT(0)	122	125	96	31	EXACT(0)	200	191	53
tnfn1_pw060323p04q179	G10	EXACT(0)	122	125	93	21	EXACT(0)	200	189	52
tnfn1_pw060323p04q180	H10	EXACT(0)	121	112	90	31	EXACT(0)	200	194	55
tnfn1_pw060323p04q181	A11	EXACT(0)	122	113	97	27	EXACT(0)	200	186	52
tnfn1_pw060323p04q182	B11	EXACT(0)	121	120	105	49	EXACT(0)	198	167	45
tnfn1_pw060323p04q183	C11	EXACT(0)	122	125	99	31	EXACT(0)	200	191	56
tnfn1_pw060323p04q184	D11	EXACT(0)	122	119	77	23	EXACT(0)	200	183	52
tnfn1_pw060323p04q185	E11	EXACT(0)	123	121	110	47	EXACT(0)	199	169	57
tnfn1_pw060323p04q186	F11	EXACT(0)	122	120	99	27	EXACT(0)	200	191	48
tnfn1_pw060323p04q187	G11	EXACT(0)	122	118	94	30	EXACT(0)	200	168	44
tnfn1_pw060323p04q188	H11	EXACT(0)	121	120	110	47	EXACT(0)	199	173	56
tnfn1_pw060323p04q189	A12	EXACT(0)	123	120	104	28	EXACT(0)	200	160	47
tnfn1_pw060323p04q190	B12	EXACT(0)	122	106	62	21	EXACT(0)	200	186	47
tnfn1_pw060323p04q191	C12	EXACT(0)	124	120	104	33	EXACT(0)	200	183	46
tnfn1_pw060323p04q192	D12	EXACT(0)	124	120	98	24	EXACT(0)	200	195	53
tnfn1_pw060323p04q193	E12	EXACT(0)	125	120	97	23	EXACT(0)	200	191	49
tnfn1_pw060323p04q194	F12	EXACT(0)	124	119	88	25	EXACT(0)	200	190	53
tnfn1_pw060323p04q195	G12	EXACT(0)	133	81	34	17	ESTIMATE(6)	194	177	41
tnfn1_pw060323p04q196	H12	EXACT(0)	123	105	96	29	EXACT(0)	200	186	51