

### ***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 21 (tnfn1\_pw060419p01)**

**Catalog No. NR-8055**

**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-8055 represents Plate 21 (tnfn1\_pw060419p01) 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-8055 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 21 (tnfn1\_pw060419p01), NR-8055.”

#### **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_pw060419p01q101	A01	T18			
tnfn1_pw060419p01q102	B01	<KAN-2>	wbtP	galactosyl transferase	cell wall / LPS / capsule
tnfn1_pw060419p01q103	C01	T18	secG	preprotein translocase, subunit G, membrane protein	motility, attachment and secretion structure
tnfn1_pw060419p01q104	D01	T20	-	amino acid-polyamine-organocation family protein	transport - amino-acid
tnfn1_pw060419p01q105	E01	T18	-	hypothetical protein	hypothetical - conserved
tnfn1_pw060419p01q106	F01	T18	ribH	riboflavin synthase beta-chain	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p01q107	G01	T18	-	flavodoxin, related to tryptophan repressor binding protein	putative enzymes
tnfn1_pw060419p01q108	H01	T18	-	RimI-like acetyltransferase	putative enzymes
tnfn1_pw060419p01q109	A02	T18	recF	RecFOR complex, RecF component	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060419p01q110	B02	T18	-	membrane fusion protein	motility, attachment and secretion structure
tnfn1_pw060419p01q111	C02	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p01q112	D02	T18	kdpE	two-component response regulator	signal transduction and regulation
tnfn1_pw060419p01q113	E02	T18	-		
tnfn1_pw060419p01q114	F02	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p01q115	G02	T18	-	NADPH-dependent FMN reductase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p01q116	H02	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q117	A03	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q118	B03	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p01q119	C03	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q120	D03	T18	-	prophage maintenance system killer protein (DOC)	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060419p01q121	E03	T18	yqhD	Fe-dependent alcohol dehydrogenase	energy metabolism
tnfn1_pw060419p01q122	F03	T18	trpE	anthranilate synthase component I	amino acid metabolism - biosynthesis
tnfn1_pw060419p01q123	G03	T20	-	glutamate:GABA antiporter (APC family) protein	transport - amino-acid
tnfn1_pw060419p01q124	H03	T20	dnaK	chaperone, heat shock protein, HSP 70 family	post-translational modification, protein turnover, chaperones
tnfn1_pw060419p01q125	A04	T20	-	protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q126	B04	T20	cyoA	cytochrome bo terminal oxidase subunit II	energy metabolism
tnfn1_pw060419p01q127	C04	T20	-	pyridoxine/pyridoxal 5-phosphate biosynthesis protein	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p01q128	D04	T20	lysA	diaminopimelate decarboxylase	amino acid metabolism - biosynthesis
tnfn1_pw060419p01q129	E04	T20	cydB	cytochrome bd-I terminal oxidase subunit II	energy metabolism
tnfn1_pw060419p01q130	F04	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p01q131	G04	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060419p01q132	H04	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p01q133	A05	T20	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060419p01q134	B05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q135	C05	T20	-	magnesium chelatase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p01q136	D05	T20	gidB	glucose-inhibited cell division protein	cell wall / LPS / capsule
tnfn1_pw060419p01q137	E05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q138	F05	T20	cphB	cyanophycinase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p01q139	G05	T20	-	kinase-like protein	putative enzymes
tnfn1_pw060419p01q140	H05	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p01q141	A06	T20	iglB	intracellular growth locus protein B	unknown function - conserved
tnfn1_pw060419p01q142	B06	T20	galP2	galactose-proton symporter, major facilitator superfamily (MFS) transport protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060419p01q143	C06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q144	D06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p01q145	E06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q146	F06	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060419p01q147	G06	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p01q148	H06	T20			

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Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060419p01q149	A07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q150	B07	T20	kdpD	two component regulator, sensor histidine kinase kdpD	signal transduction and regulation
tnfn1_pw060419p01q151	C07	T20	-	serine permease	transport - amino-acid
tnfn1_pw060419p01q152	D07	T20	-	arsenite-antimonite (ArsB) efflux family protein	transport
tnfn1_pw060419p01q153	E07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q154	F07	T20	-		
tnfn1_pw060419p01q155	G07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q156	H07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q157	A08	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q158	B08	T18	pal	peptidoglycan-associated lipoprotein, OmpA family	transport - drugs / antibacterial compounds
tnfn1_pw060419p01q159	C08	T18	-	beta-fructofuranosidase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060419p01q160	D08	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q161	E08	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q162	F08	<KAN-2>	grpE	chaperone GrpE (heat shock protein). Hsp70/Hsc70 protein regulator activity	post-translational modification, protein turnover, chaperones
tnfn1_pw060419p01q163	G08	T18	appC	cytochrome bd-II terminal oxidase subunit I	energy metabolism
tnfn1_pw060419p01q164	H08	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q165	A09	<KAN-2>	-	manganese/Zinc/Iron chelate uptake transporter family protein	transport
tnfn1_pw060419p01q166	B09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q167	C09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q168	D09	T18	cdd	cytidine deaminase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p01q169	E09	T20	-	tRNA-methyltransferase MiaB protein	translation, ribosomal structure and biogenesis
tnfn1_pw060419p01q170	F09	T20	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060419p01q171	G09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q172	H09	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q173	A10	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p01q174	B10	T20	-	VacJ like lipoprotein	cell wall / LPS / capsule
tnfn1_pw060419p01q175	C10	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060419p01q176	D10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q177	E10	T20	perM	PerM family protein	transport
tnfn1_pw060419p01q178	F10	T20	relA	GDP pyrophosphokinase/GTP pyrophosphokinase	other metabolism - biosynthesis
tnfn1_pw060419p01q179	G10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p01q180	H10	T20	ostA2	organic solvent tolerance protein OstA	cell wall / LPS / capsule
tnfn1_pw060419p01q181	A11	T20	mreA	FAD binding family protein	energy metabolism
tnfn1_pw060419p01q182	B11	T20	cysN	sulfate adenylate transferase, subunit 1	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p01q183	C11	T20	acs	acyl-coenzyme A synthetase/AMP-(fatty) acid ligases	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p01q184	D11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q185	E11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q186	F11	T20	-	ROK family protein	putative enzymes
tnfn1_pw060419p01q187	G11	T20	-	glycosyl transferase, group 2	cell wall / LPS / capsule
tnfn1_pw060419p01q188	H11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p01q189	A12	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060419p01q190	B12	T20	purF	amidophosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060419p01q191	C12	T20	gloB	hydroxyacylglutathione hydrolase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p01q192	D12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p01q193	E12	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p01q194	F12	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060419p01q195	G12	T20	-	disulfide bond formation protein DsbB family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p01q196	H12	T20	-	Type IV pili, pilus assembly protein	motility, attachment and secretion structure

**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_pw060419p01q101	A01	C	818486	F	intergenic					
tnfn1_pw060419p01q102	B01	C	1509510	R	FTN_1429	1509260	1509886	R	209	377(627)
tnfn1_pw060419p01q103	C01	C	1741101	R	FTN_1630	1740964	1741314	R	117	214(351)
tnfn1_pw060419p01q104	D01	C	1620558	R	FTN_1523	1620541	1621251	F	237	18(711)
tnfn1_pw060419p01q105	E01	C	663547	F	FTN_0630	663345	663686	F	114	203(342)
tnfn1_pw060419p01q106	F01	C	122684	F	FTN_0111	122336	122776	R	147	93(441)
tnfn1_pw060419p01q107	G01	C	1353092	R	FTN_1280	1352702	1353265	R	188	174(564)
tnfn1_pw060419p01q108	H01	C	166396	F	FTN_0153	166021	166443	R	141	48(423)
tnfn1_pw060419p01q109	A02	C	786819	R	FTN_0734	786285	787331	R	349	513(1047)
tnfn1_pw060419p01q110	B02	C	774284	R	FTN_0718	773937	774791	R	285	508(855)
tnfn1_pw060419p01q111	C02	C	911875	R	FTN_0857	911588	912034	F	149	288(447)
tnfn1_pw060419p01q112	D02	C	1838394	F	FTN_1714	1837876	1838559	R	228	166(684)
tnfn1_pw060419p01q113	E02	C	1000198	R	intergenic					
tnfn1_pw060419p01q114	F02	C	570667	R	FTN_0544	570050	570853	R	268	187(804)
tnfn1_pw060419p01q115	G02	C	475383	R	FTN_0471	475227	475760	R	178	378(534)
tnfn1_pw060419p01q116	H02	C	1636141	R	FTN_1537	1635781	1636650	R	290	510(870)
tnfn1_pw060419p01q117	A03	C	192450	R	FTN_0175	191251	192873	F	541	1200(1623)
tnfn1_pw060419p01q118	B03	C	1295182	R	FTN_1224	1294574	1295269	R	232	88(696)
tnfn1_pw060419p01q119	C03	C	1462661	R	FTN_1382	1462421	1462831	R	137	171(411)
tnfn1_pw060419p01q120	D03	C	1580633	F	FTN_1488	1579953	1580906	R	318	274(954)
tnfn1_pw060419p01q121	E03	C	1045208	R	FTN_0989	1044415	1045569	R	385	362(1155)
tnfn1_pw060419p01q122	F03	C	1906506	R	FTN_1778	1905885	1907426	R	514	921(1542)
tnfn1_pw060419p01q123	G03	C	1625884	R	FTN_1529	1625383	1626783	R	467	900(1401)
tnfn1_pw060419p01q124	H03	C	1357356	R	FTN_1284	1356205	1358130	R	642	775(1926)
tnfn1_pw060419p01q125	A04	C	1389010	F	FTN_1316	1388629	1389249	F	207	382(621)
tnfn1_pw060419p01q126	B04	U	217222	R	FTN_0195	216593	217492	F	300	630(900)
tnfn1_pw060419p01q127	C04	U	634500	R	FTN_0601	634045	634905	F	287	456(861)
tnfn1_pw060419p01q128	D04	C	1627946	F	FTN_1530	1626798	1627979	R	394	34(1182)
tnfn1_pw060419p01q129	E04	C	210479	R	FTN_0192	209805	210995	R	397	517(1191)
tnfn1_pw060419p01q130	F04	U	1504595	F	FTN_1424	1503994	1505283	R	430	689(1290)
tnfn1_pw060419p01q131	G04	C	1883819	R	FTN_1755	1883615	1884871	F	419	205(1257)
tnfn1_pw060419p01q132	H04	C	1015077	R	FTN_0960	1014799	1015527	R	243	451(729)
tnfn1_pw060419p01q133	A05	C	1074628	F	FTN_1014	1074014	1074643	R	210	16(630)
tnfn1_pw060419p01q134	B05	U	92080	F	FTN_0081	91627	92358	R	244	279(732)
tnfn1_pw060419p01q135	C05	C	1779969	R	FTN_1665	1778927	1780432	R	502	464(1506)
tnfn1_pw060419p01q136	D05	U	109241	F	FTN_0098	109204	109818	F	205	38(615)
tnfn1_pw060419p01q137	E05	C	798012	F	FTN_0744	797981	798376	F	132	32(396)
tnfn1_pw060419p01q138	F05	C	1279202	R	FTN_1209	1278824	1279639	R	272	438(816)
tnfn1_pw060419p01q139	G05	C	893451	R	FTN_0836	893030	893530	R	167	80(501)
tnfn1_pw060419p01q140	H05	C	837406	R	FTN_0779	836764	838143	F	460	643(1380)
tnfn1_pw060419p01q141	A06	C	1398665	F	FTN_1323	1397638	1399155	R	506	491(1518)
tnfn1_pw060419p01q142	B06	U	732726	F	FTN_0688	731758	733149	F	464	969(1392)
tnfn1_pw060419p01q143	C06	C	1414939	R	FTN_1334	1414639	1415139	F	167	301(501)
tnfn1_pw060419p01q144	D06	C	319606	R	FTN_0309	318501	320303	F	601	1106(1803)
tnfn1_pw060419p01q145	E06	C	371994	F	FTN_0368	371729	372250	F	174	266(522)
tnfn1_pw060419p01q146	F06	C	105515	R	FTN_0094	105129	106073	R	315	559(945)
tnfn1_pw060419p01q147	G06	C	1902009	R	FTN_1771	1901829	1902239	R	137	231(411)
tnfn1_pw060419p01q148	H06	U	171109	R	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 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_pw060419p01q149	A07	C	1631330	R	FTN_1533	1630614	1631801	F	396	717(1188)
tnfn1_pw060419p01q150	B07	U	1839738	R	FTN_1715	1838604	1841282	R	893	1545(2679)
tnfn1_pw060419p01q151	C07	C	193720	F	FTN_0176	193022	194287	F	422	699(1266)
tnfn1_pw060419p01q152	D07	C	384242	R	FTN_0382	383357	384592	F	412	886(1236)
tnfn1_pw060419p01q153	E07	C	997781	R	FTN_0936	997186	998415	F	410	596(1230)
tnfn1_pw060419p01q154	F07	C	323964	F	intergenic					
tnfn1_pw060419p01q155	G07	C	1613008	F	FTN_1517	1612827	1613456	F	210	182(630)
tnfn1_pw060419p01q156	H07	C	1457836	R	FTN_1378	1457390	1457926	F	179	447(537)
tnfn1_pw060419p01q157	A08	C	681795	F	FTN_0643	681664	682170	F	169	132(507)
tnfn1_pw060419p01q158	B08	C	360297	R	FTN_0357	360228	360848	F	207	70(621)
tnfn1_pw060419p01q159	C08	C	68787	R	FTN_0058	67916	69628	R	571	842(1713)
tnfn1_pw060419p01q160	D08	U	28448	F	FTN_0027	28044	28592	F	183	405(549)
tnfn1_pw060419p01q161	E08	C	1445692	R	FTN_1362	1445486	1445869	R	128	178(384)
tnfn1_pw060419p01q162	F08	C	1358625	R	FTN_1285	1358234	1358818	R	195	194(585)
tnfn1_pw060419p01q163	G08	C	1729892	R	FTN_1619	1728955	1730328	F	458	938(1374)
tnfn1_pw060419p01q164	H08	C	603900	R	FTN_0576	603499	604158	F	220	402(660)
tnfn1_pw060419p01q165	A09	C	200588	R	FTN_0183	200205	201119	R	305	532(915)
tnfn1_pw060419p01q166	B09	C	237307	F	FTN_0215	237281	237943	F	221	27(663)
tnfn1_pw060419p01q167	C09	C	341589	R	FTN_0336	341568	341762	F	65	22(195)
tnfn1_pw060419p01q168	D09	C	691087	F	FTN_0651	691035	691433	R	133	347(399)
tnfn1_pw060419p01q169	E09	C	361764	F	FTN_0358	360958	362274	F	439	807(1317)
tnfn1_pw060419p01q170	F09	C	1065618	F	FTN_1006	1065118	1066374	R	419	757(1257)
tnfn1_pw060419p01q171	G09	C	541508	R	FTN_0521	541170	541526	F	119	339(357)
tnfn1_pw060419p01q172	H09	C	1103123	F	FTN_1044	1102531	1104324	R	598	1202(1794)
tnfn1_pw060419p01q173	A10	C	208025	F	FTN_0190	207626	208801	R	392	777(1176)
tnfn1_pw060419p01q174	B10	C	1232560	F	FTN_1160	1231701	1232618	R	306	59(918)
tnfn1_pw060419p01q175	C10	C	1038449	R	FTN_0984	1037817	1039706	R	630	1258(1890)
tnfn1_pw060419p01q176	D10	C	48322	R	FTN_0043	47436	48965	F	510	887(1530)
tnfn1_pw060419p01q177	E10	C	596889	F	FTN_0570	596517	597620	R	368	732(1104)
tnfn1_pw060419p01q178	F10	C	1615535	F	FTN_1518	1614441	1616447	R	669	913(2007)
tnfn1_pw060419p01q179	G10	C	454658	R	FTN_0452	454529	455929	F	467	130(1401)
tnfn1_pw060419p01q180	H10	C	759267	F	FTN_0713	757653	760250	R	866	984(2598)
tnfn1_pw060419p01q181	A11	C	1333842	F	FTN_1262	1333174	1334967	R	598	1126(1794)
tnfn1_pw060419p01q182	B11	C	984776	F	FTN_0927	984277	985686	R	470	911(1410)
tnfn1_pw060419p01q183	C11	C	783300	R	FTN_0730	782807	784741	F	645	494(1935)
tnfn1_pw060419p01q184	D11	C	1465639	F	FTN_1387	1465519	1465962	F	148	121(444)
tnfn1_pw060419p01q185	E11	C	1465649	F	FTN_1387	1465519	1465962	F	148	131(444)
tnfn1_pw060419p01q186	F11	C	649387	F	FTN_0618	649296	650240	F	315	92(945)
tnfn1_pw060419p01q187	G11	C	571313	F	FTN_0545	570952	571905	F	318	362(954)
tnfn1_pw060419p01q188	H11	C	1476093	R	FTN_1397	1473445	1477344	R	1300	1252(3900)
tnfn1_pw060419p01q189	A12	C	881204	R	FTN_0824	881019	882230	R	404	1027(1212)
tnfn1_pw060419p01q190	B12	C	1821942	R	FTN_1700	1820537	1822024	R	496	83(1488)
tnfn1_pw060419p01q191	C12	C	1450290	R	FTN_1370	1450037	1450792	R	252	503(756)
tnfn1_pw060419p01q192	D12	C	1022019	R	FTN_0966	1021590	1022996	R	469	978(1407)
tnfn1_pw060419p01q193	E12	C	1439192	R	FTN_1358	1439009	1439578	R	190	387(570)
tnfn1_pw060419p01q194	F12	C	1245615	F	FTN_1173	1244658	1245932	R	425	318(1275)
tnfn1_pw060419p01q195	G12	C	1372219	F	FTN_1303	1372091	1372657	F	189	129(567)
tnfn1_pw060419p01q196	H12	C	413981	F	FTN_0414	413585	414019	R	145	39(435)

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_pw060419p01q101	A01	EXACT(0)	121	119	96	30	EXACT(0)	200	166	55
tnfn1_pw060419p01q102	B01	EXACT(0)	122	119	95	30	EXACT(0)	200	187	55
tnfn1_pw060419p01q103	C01	EXACT(0)	121	112	96	26	EXACT(0)	200	177	42
tnfn1_pw060419p01q104	D01	EXACT(0)	156	153	122	35	EXACT(0)	200	175	55
tnfn1_pw060419p01q105	E01	EXACT(0)	122	119	98	31	EXACT(0)	129	125	32
tnfn1_pw060419p01q106	F01	EXACT(0)	122	109	86	26	EXACT(0)	200	186	54
tnfn1_pw060419p01q107	G01	EXACT(0)	123	106	92	26	EXACT(0)	200	192	56
tnfn1_pw060419p01q108	H01	EXACT(0)	122	105	73	24	EXACT(0)	200	186	54
tnfn1_pw060419p01q109	A02	EXACT(0)	124	120	109	31	EXACT(0)	200	188	56
tnfn1_pw060419p01q110	B02	EXACT(0)	123	120	110	30	EXACT(0)	200	194	50
tnfn1_pw060419p01q111	C02	EXACT(0)	124	109	62	21	EXACT(0)	200	181	46
tnfn1_pw060419p01q112	D02	EXACT(0)	121	112	93	26	EXACT(0)	200	191	50
tnfn1_pw060419p01q113	E02	EXACT(0)	124	120	104	29	EXACT(0)	200	188	38
tnfn1_pw060419p01q114	F02	EXACT(0)	121	112	96	36	EXACT(0)	200	187	35
tnfn1_pw060419p01q115	G02	EXACT(0)	123	112	64	20	EXACT(0)	200	185	54
tnfn1_pw060419p01q116	H02	EXACT(0)	123	120	98	29	EXACT(0)	200	184	45
tnfn1_pw060419p01q117	A03	EXACT(0)	122	106	85	24	EXACT(0)	200	182	49
tnfn1_pw060419p01q118	B03	EXACT(0)	125	120	106	31	EXACT(0)	145	134	51
tnfn1_pw060419p01q119	C03	EXACT(0)	122	112	104	32	EXACT(0)	200	189	50
tnfn1_pw060419p01q120	D03	EXACT(0)	121	112	90	33	EXACT(0)	200	184	49
tnfn1_pw060419p01q121	E03	EXACT(0)	122	83	56	17	EXACT(0)	200	192	44
tnfn1_pw060419p01q122	F03	EXACT(0)	123	120	105	28	EXACT(0)	200	189	50
tnfn1_pw060419p01q123	G03	EXACT(0)	159	153	144	40	EXACT(0)	200	182	41
tnfn1_pw060419p01q124	H03	EXACT(0)	158	153	126	30	EXACT(0)	200	193	43
tnfn1_pw060419p01q125	A04	EXACT(0)	157	153	134	38	EXACT(0)	151	138	55
tnfn1_pw060419p01q126	B04	EXACT(0)	156	145	124	39	EXACT(0)	200	196	59
tnfn1_pw060419p01q127	C04	EXACT(0)	155	145	134	42	EXACT(0)	200	190	57
tnfn1_pw060419p01q128	D04	EXACT(0)	158	152	125	34	EXACT(0)	200	183	54
tnfn1_pw060419p01q129	E04	EXACT(0)	158	153	136	38	EXACT(0)	200	189	52
tnfn1_pw060419p01q130	F04	EXACT(0)	155	145	110	28	EXACT(0)	200	179	61
tnfn1_pw060419p01q131	G04	EXACT(0)	158	153	127	38	EXACT(0)	200	188	55
tnfn1_pw060419p01q132	H04	EXACT(0)	157	152	133	38	EXACT(0)	198	187	52
tnfn1_pw060419p01q133	A05	EXACT(0)	157	152	102	21	EXACT(0)	200	190	51
tnfn1_pw060419p01q134	B05	EXACT(0)	155	145	129	44	EXACT(0)	200	190	55
tnfn1_pw060419p01q135	C05	EXACT(0)	157	152	124	39	EXACT(0)	200	192	49
tnfn1_pw060419p01q136	D05	EXACT(0)	155	144	138	42	EXACT(0)	200	191	62
tnfn1_pw060419p01q137	E05	EXACT(0)	161	155	144	41	EXACT(0)	200	123	30
tnfn1_pw060419p01q138	F05	EXACT(0)	155	153	138	40	EXACT(0)	199	191	44
tnfn1_pw060419p01q139	G05	EXACT(0)	158	153	130	40	EXACT(0)	200	158	32
tnfn1_pw060419p01q140	H05	EXACT(0)	157	153	134	37	EXACT(0)	200	191	59
tnfn1_pw060419p01q141	A06	EXACT(0)	157	145	104	23	EXACT(0)	200	185	59
tnfn1_pw060419p01q142	B06	EXACT(0)	159	153	139	42	EXACT(0)	200	185	63
tnfn1_pw060419p01q143	C06	EXACT(0)	156	142	102	18	EXACT(0)	200	187	37
tnfn1_pw060419p01q144	D06	EXACT(0)	158	153	136	31	EXACT(0)	200	195	58
tnfn1_pw060419p01q145	E06	EXACT(0)	154	145	126	42	EXACT(0)	200	187	52
tnfn1_pw060419p01q146	F06	EXACT(0)	157	153	130	32	EXACT(0)	200	189	51
tnfn1_pw060419p01q147	G06	EXACT(0)	155	145	134	43	EXACT(0)	57	56	37
tnfn1_pw060419p01q148	H06	EXACT(0)	157	151	138	36	EXACT(0)	200	182	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_pw060419p01q149	A07	EXACT(0)	156	154	132	39	EXACT(0)	200	192	58
tnfn1_pw060419p01q150	B07	EXACT(0)	156	114	102	36	EXACT(0)	200	191	61
tnfn1_pw060419p01q151	C07	EXACT(0)	156	145	131	42	EXACT(0)	200	189	53
tnfn1_pw060419p01q152	D07	EXACT(0)	155	145	110	29	EXACT(0)	200	183	52
tnfn1_pw060419p01q153	E07	EXACT(0)	157	145	104	24	EXACT(0)	200	174	53
tnfn1_pw060419p01q154	F07	EXACT(0)	155	145	90	19	EXACT(0)	200	153	29
tnfn1_pw060419p01q155	G07	EXACT(0)	155	139	131	43	EXACT(0)	200	189	49
tnfn1_pw060419p01q156	H07	EXACT(0)	158	145	133	36	EXACT(0)	111	108	48
tnfn1_pw060419p01q157	A08	EXACT(0)	121	112	83	24	EXACT(0)	200	187	52
tnfn1_pw060419p01q158	B08	EXACT(0)	124	119	108	34	EXACT(0)	198	166	43
tnfn1_pw060419p01q159	C08	EXACT(0)	123	120	93	22	EXACT(0)	200	175	41
tnfn1_pw060419p01q160	D08	EXACT(0)	123	119	98	28	EXACT(0)	200	186	49
tnfn1_pw060419p01q161	E08	EXACT(0)	123	73	66	29	EXACT(0)	174	160	48
tnfn1_pw060419p01q162	F08	EXACT(0)	112	113	98	41	EXACT(0)	200	189	54
tnfn1_pw060419p01q163	G08	EXACT(0)	121	112	96	29	EXACT(0)	200	187	39
tnfn1_pw060419p01q164	H08	EXACT(0)	123	120	75	24	EXACT(0)	200	191	55
tnfn1_pw060419p01q165	A09	EXACT(0)	116	112	62	25	EXACT(0)	200	126	38
tnfn1_pw060419p01q166	B09	EXACT(0)	121	106	70	22	EXACT(0)	200	166	35
tnfn1_pw060419p01q167	C09	EXACT(0)	123	120	99	32	EXACT(0)	200	184	53
tnfn1_pw060419p01q168	D09	EXACT(0)	121	85	67	21	EXACT(0)	200	193	48
tnfn1_pw060419p01q169	E09	EXACT(0)	157	145	123	35	EXACT(0)	200	196	49
tnfn1_pw060419p01q170	F09	EXACT(0)	157	142	131	31	EXACT(0)	200	177	65
tnfn1_pw060419p01q171	G09	EXACT(0)	156	145	131	36	EXACT(0)	200	191	56
tnfn1_pw060419p01q172	H09	EXACT(0)	155	139	134	52	EXACT(0)	200	180	52
tnfn1_pw060419p01q173	A10	EXACT(0)	155	145	110	32	EXACT(0)	200	182	55
tnfn1_pw060419p01q174	B10	EXACT(0)	157	116	112	42	EXACT(0)	200	168	47
tnfn1_pw060419p01q175	C10	EXACT(0)	156	145	124	34	EXACT(0)	200	194	51
tnfn1_pw060419p01q176	D10	EXACT(0)	156	145	140	50	EXACT(0)	200	159	46
tnfn1_pw060419p01q177	E10	EXACT(0)	155	118	100	25	EXACT(0)	200	187	45
tnfn1_pw060419p01q178	F10	EXACT(0)	156	153	127	35	EXACT(0)	200	191	54
tnfn1_pw060419p01q179	G10	EXACT(0)	155	145	112	33	EXACT(0)	200	182	39
tnfn1_pw060419p01q180	H10	EXACT(0)	156	139	127	42	EXACT(0)	200	189	61
tnfn1_pw060419p01q181	A11	EXACT(0)	155	145	123	35	EXACT(0)	200	192	54
tnfn1_pw060419p01q182	B11	EXACT(0)	158	152	134	36	EXACT(0)	200	194	56
tnfn1_pw060419p01q183	C11	EXACT(0)	159	153	143	45	EXACT(0)	200	195	58
tnfn1_pw060419p01q184	D11	EXACT(0)	156	145	125	43	EXACT(0)	200	190	62
tnfn1_pw060419p01q185	E11	EXACT(0)	154	87	43	12	EXACT(0)	200	190	41
tnfn1_pw060419p01q186	F11	EXACT(0)	155	146	132	39	EXACT(0)	200	185	57
tnfn1_pw060419p01q187	G11	EXACT(0)	155	136	84	20	EXACT(0)	200	194	48
tnfn1_pw060419p01q188	H11	EXACT(0)	158	153	147	42	EXACT(0)	200	169	53
tnfn1_pw060419p01q189	A12	EXACT(0)	156	88	71	16	EXACT(0)	200	179	48
tnfn1_pw060419p01q190	B12	EXACT(0)	156	142	131	40	EXACT(0)	200	195	53
tnfn1_pw060419p01q191	C12	EXACT(0)	155	152	137	52	EXACT(0)	200	157	45
tnfn1_pw060419p01q192	D12	EXACT(0)	158	153	129	37	EXACT(0)	200	187	58
tnfn1_pw060419p01q193	E12	EXACT(0)	158	153	129	37	EXACT(0)	200	187	58
tnfn1_pw060419p01q194	F12	EXACT(0)	153	153	137	39	EXACT(0)	200	193	56
tnfn1_pw060419p01q195	G12	EXACT(0)	157	145	122	34	EXACT(0)	200	191	47
tnfn1_pw060419p01q196	H12	EXACT(0)	156	152	130	34	EXACT(0)	192	170	51