

## ***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 18 (tnfn1\_pw060418p02)**

**Catalog No. NR-8052**

**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-8052 represents Plate 18 (tnfn1\_pw060418p02) 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\_pw060418p02q127 (Well C04) is not available due to quality issues. Strain tnfn1\_pw060418p02q148 (Well H06) was not available due to quality issues at the time of release of Plate 18, 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-8052 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 18 (tnfn1\_pw060418p02), NR-8052.”

### **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](http://www.cdc.gov/od/ohs/biosfty/bmbl5/bmbl5toc.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_pw060418p02q101	A01	T20	-	isochorismatase family protein	putative enzymes
tnfn1_pw060418p02q102	B01	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p02q103	C01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q104	D01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q105	E01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q106	F01	T20	-	outer membrane protein of unknown function	unknown function - novel
tnfn1_pw060418p02q107	G01	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p02q108	H01	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060418p02q109	A02	T20	-	disulfide bond formation protein, DsbB family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p02q110	B02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q111	C02	T20	pnuC	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060418p02q112	D02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q113	E02	T20	-	permease	transport
tnfn1_pw060418p02q114	F02	T20	ndh	NADH dehydrogenase	energy metabolism
tnfn1_pw060418p02q115	G02	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p02q116	H02	T20	iglC	intracellular growth locus protein C	unknown function - novel
tnfn1_pw060418p02q117	A03	T20	oppD	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060418p02q118	B03	T20	-		
tnfn1_pw060418p02q119	C03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p02q120	D03	T20	-	aspartate:alanine exchanger (AAE) family protein	transport - amino-acid
tnfn1_pw060418p02q121	E03	T20	cyoB	cytochrome bo terminal oxidase subunit I	energy metabolism
tnfn1_pw060418p02q122	F03	T20	-	bifunctional protein: 3-hydroxacyl-CoA dehydrogenase/acyl-CoA-binding protein	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p02q123	G03	T20	lepA	GTP-binding protein LepA	cell wall / LPS / capsule
tnfn1_pw060418p02q124	H03	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p02q125	A04	T20	-	serine-type D-Ala-D-Ala carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060418p02q126	B04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q127	C04	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p02q128	D04	T20	katG	peroxidase/catalase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p02q129	E04	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p02q130	F04	<KAN-2>	secA	preprotein translocase, subunit A (ATPase, RNA helicase)	motility, attachment and secretion structure
tnfn1_pw060418p02q131	G04	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q132	H04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q133	A05	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q134	B05	T17	pabA	para-aminobenzoate synthase component II	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p02q135	C05	T18	panC	pantoate-beta-alanine ligase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p02q136	D05	T18	-	peptide methionine sulfoxide reductase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p02q137	E05	T18	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p02q138	F05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p02q139	G05	T18	capC	capsule biosynthesis protein CapC	cell wall / LPS / capsule
tnfn1_pw060418p02q140	H05	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p02q141	A06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p02q142	B06	T20	-	aldo/keto reductase family protein	putative enzymes
tnfn1_pw060418p02q143	C06	T20	-	dienelactone hydrolase family protein	putative enzymes
tnfn1_pw060418p02q144	D06	T20	wrbA	trp repressor binding protein	signal transduction and regulation
tnfn1_pw060418p02q145	E06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q146	F06	T20	-	amino acid transporter (AAT) family protein	transport - amino-acid
tnfn1_pw060418p02q147	G06	T20	slt	soluble lytic murein transglycosylase	cell wall / LPS / capsule
tnfn1_pw060418p02q148	H06	T20	-	glycosyl transferase, family 8	cell wall / LPS / capsule

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

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060418p02q149	A07	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p02q150	B07	T20	-	protein of unknown function, thioesterase superfamily	unknown function - conserved
tnfn1_pw060418p02q151	C07	T20	nupC	nucleoside permease NUP family protein	transport
tnfn1_pw060418p02q152	D07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p02q153	E07	T20	gtrB	glycosyl transferase	cell wall / LPS / capsule
tnfn1_pw060418p02q154	F07	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p02q155	G07	T20	-	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060418p02q156	H07	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060418p02q157	A08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q158	B08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q159	C08	T20	ppdK	phosphoenolpyruvate synthase/pyruvate phosphate dikinase	energy metabolism
tnfn1_pw060418p02q160	D08	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p02q161	E08	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060418p02q162	F08	T20	-	DNA uptake protein, SMF family	transport
tnfn1_pw060418p02q163	G08	T20	-	heat shock protein, HSP20 family	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060418p02q164	H08	T20	-		
tnfn1_pw060418p02q165	A09	T20	pdpB	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q166	B09	T20	-	subunit of DnaJ/DnaK/GrpE: chaperone with DnaK; heat shock protein	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060418p02q167	C09	<KAN-2>	pilQ	Type IV pili secretion component	motility, attachment and secretion structure
tnfn1_pw060418p02q168	D09	T18	-	inositol monophosphatase family protein.	putative enzymes
tnfn1_pw060418p02q169	E09	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q170	F09	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p02q171	G09	T20	nhaA	Na+:H+ antiporter	transport
tnfn1_pw060418p02q172	H09	T20	-		
tnfn1_pw060418p02q173	A10	T18	-	Zn-dependent peptidase, M16 family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p02q174	B10	T20	-	subunit of DnaJ/DnaK/GrpE: chaperone with DnaK; heat shock protein	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060418p02q175	C10	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p02q176	D10	<KAN-2>	-	acetyltransferase	putative enzymes
tnfn1_pw060418p02q177	E10	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q178	F10	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060418p02q179	G10	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p02q180	H10	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p02q181	A11	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060418p02q182	B11	<KAN-2>	-	drug:H+ antiporter-1 (DHA2) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p02q183	C11	T20	-	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	transport
tnfn1_pw060418p02q184	D11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p02q185	E11	T20	mfd	transcription-repair coupling factor	transcription
tnfn1_pw060418p02q186	F11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q187	G11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p02q188	H11	T20	-	rhodanese-related sulfurtransferase	other metabolism - biosynthesis
tnfn1_pw060418p02q189	A12	T20	dctA	C4-dicarboxylate transport protein	transport
tnfn1_pw060418p02q190	B12	T20	-	DedA family protein	putative enzymes
tnfn1_pw060418p02q191	C12	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060418p02q192	D12	T20	-	protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q193	E12	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p02q194	F12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p02q195	G12	T20	aroE	shikimate 5-dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060418p02q196	H12	T20	-	delta 9 acyl-lipid fatty acid desaturase	fatty acids and lipids 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_pw060418p02q101	A01	C	1159159	F	FTN_1097	1158946	1159515	R	190	357(570)
tnfn1_pw060418p02q102	B01	C	1647533	R	FTN_1549	1646760	1647938	F	393	774(1179)
tnfn1_pw060418p02q103	C01	C	1465041	R	FTN_1386	1464785	1465294	F	170	257(510)
tnfn1_pw060418p02q104	D01	C	297065	F	FTN_0290	296739	297281	F	181	327(543)
tnfn1_pw060418p02q105	E01	C	1421966	F	FTN_1343	1421385	1422068	R	228	103(684)
tnfn1_pw060418p02q106	F01	C	627014	F	FTN_0595	625825	627738	F	638	1190(1914)
tnfn1_pw060418p02q107	G01	C	570332	R	FTN_0544	570050	570853	R	268	522(804)
tnfn1_pw060418p02q108	H01	C	1893296	F	FTN_1763	1892635	1893852	F	406	662(1218)
tnfn1_pw060418p02q109	A02	C	1455051	R	FTN_1376	1454884	1455417	F	178	168(534)
tnfn1_pw060418p02q110	B02	C	32412	R	FTN_0032	32208	32831	R	208	420(624)
tnfn1_pw060418p02q111	C02	C	1869736	R	FTN_1742	1869321	1870028	R	236	293(708)
tnfn1_pw060418p02q112	D02	U	1812969	F	FTN_1695	1812953	1813585	F	211	17(633)
tnfn1_pw060418p02q113	E02	C	346692	R	FTN_0342	346275	347585	R	437	894(1311)
tnfn1_pw060418p02q114	F02	U	969689	F	FTN_0912	969311	970570	R	420	882(1260)
tnfn1_pw060418p02q115	G02	C	1771053	F	FTN_1657	1770083	1771378	R	432	326(1296)
tnfn1_pw060418p02q116	H02	C	1397212	F	FTN_1322	1396992	1397618	R	209	407(627)
tnfn1_pw060418p02q117	A03	C	1688796	R	FTN_1590	1688316	1689281	R	322	486(966)
tnfn1_pw060418p02q118	B03	C	817294	F	intergenic					
tnfn1_pw060418p02q119	C03	C	1719655	R	FTN_1612	1719296	1719874	F	193	360(579)
tnfn1_pw060418p02q120	D03	U	349923	F	FTN_0344	349254	350966	R	571	1044(1713)
tnfn1_pw060418p02q121	E03	C	218939	F	FTN_0196	217534	219561	F	676	1406(2028)
tnfn1_pw060418p02q122	F03	U	1526680	R	FTN_1438	1525003	1527696	F	898	1678(2694)
tnfn1_pw060418p02q123	G03	C	118616	R	FTN_0107	117842	119623	F	594	775(1782)
tnfn1_pw060418p02q124	H03	C	186683	F	FTN_0170	185849	186718	R	290	36(870)
tnfn1_pw060418p02q125	A04	C	975544	F	FTN_0917	975232	976632	F	467	313(1401)
tnfn1_pw060418p02q126	B04	C	601067	R	FTN_0573	600640	601452	R	271	386(813)
tnfn1_pw060418p02q127	C04	C	1652762	R	FTN_1554	1651824	1653341	F	506	939(1518)
tnfn1_pw060418p02q128	D04	U	667143	R	FTN_0633	666386	668602	R	739	1460(2217)
tnfn1_pw060418p02q129	E04	C	1025909	F	FTN_0970	1025702	1025914	R	71	6(213)
tnfn1_pw060418p02q130	F04	C	717225	F	FTN_0672	714516	717233	F	906	2710(2718)
tnfn1_pw060418p02q131	G04	C	977106	F	FTN_0918	976636	977244	F	203	471(609)
tnfn1_pw060418p02q132	H04	C	1332505	R	FTN_1261	1331640	1333124	F	495	866(1485)
tnfn1_pw060418p02q133	A05	C	1154567	R	FTN_1093	1154519	1155004	R	162	438(486)
tnfn1_pw060418p02q134	B05	C	880472	F	FTN_0823	880461	881012	F	184	12(552)
tnfn1_pw060418p02q135	C05	C	1432060	F	FTN_1353	1431659	1432441	F	261	402(783)
tnfn1_pw060418p02q136	D05	C	1902895	F	FTN_1772	1902247	1902933	R	229	39(687)
tnfn1_pw060418p02q137	E05	C	66925	R	FTN_0057	66665	67894	R	410	970(1230)
tnfn1_pw060418p02q138	F05	C	1025909	F	FTN_0970	1025702	1025914	R	71	6(213)
tnfn1_pw060418p02q139	G05	C	1274459	F	FTN_1200	1274037	1274498	R	154	40(462)
tnfn1_pw060418p02q140	H05	C	1801192	F	FTN_1685	1800523	1801710	F	396	670(1188)
tnfn1_pw060418p02q141	A06	U	402245	F	FTN_0403	402038	402688	R	217	444(651)
tnfn1_pw060418p02q142	B06	C	884265	R	FTN_0826	883402	884463	R	354	199(1062)
tnfn1_pw060418p02q143	C06	C	198082	R	FTN_0180	197925	198641	R	239	560(717)
tnfn1_pw060418p02q144	D06	C	203183	R	FTN_0186	203016	203609	R	198	427(594)
tnfn1_pw060418p02q145	E06	U	1078569	F	FTN_1020	1078395	1079204	R	270	636(810)
tnfn1_pw060418p02q146	F06	C	913539	F	FTN_0860	912967	914316	R	450	778(1350)
tnfn1_pw060418p02q147	G06	C	501789	F	FTN_0496	501311	503284	F	658	479(1974)
tnfn1_pw060418p02q148	H06	C	1324223	R	FTN_1255	1323964	1324851	F	296	260(888)

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_pw060418p02q149	A07	C	1033049	F	FTN_0979	1032719	1033228	R	170	180(510)
tnfn1_pw060418p02q150	B07	C	820517	R	FTN_0763	820263	820709	F	149	255(447)
tnfn1_pw060418p02q151	C07	C	1699970	R	FTN_1599	1699890	1701089	R	400	1120(1200)
tnfn1_pw060418p02q152	D07	C	750173	R	FTN_0706	750173	750673	F	167	1(501)
tnfn1_pw060418p02q153	E07	C	1481792	R	FTN_1403	1481150	1482091	F	314	643(942)
tnfn1_pw060418p02q154	F07	C	919520	F	FTN_0866	919330	919911	F	194	191(582)
tnfn1_pw060418p02q155	G07	C	388351	F	FTN_0389	388044	388991	R	316	641(948)
tnfn1_pw060418p02q156	H07	U	1170653	R	FTN_1108	1169873	1171081	F	403	781(1209)
tnfn1_pw060418p02q157	A08	C	1240826	F	FTN_1170	1240289	1242037	R	583	1212(1749)
tnfn1_pw060418p02q158	B08	C	59810	R	FTN_0050	59569	61089	F	507	242(1521)
tnfn1_pw060418p02q159	C08	C	76463	F	FTN_0064	75648	78278	R	877	1816(2631)
tnfn1_pw060418p02q160	D08	C	1069353	R	FTN_1010	1069039	1070319	F	427	315(1281)
tnfn1_pw060418p02q161	E08	C	1209669	R	FTN_1143	1207355	1210072	R	906	404(2718)
tnfn1_pw060418p02q162	F08	C	351611	F	FTN_0345	351044	352147	R	368	537(1104)
tnfn1_pw060418p02q163	G08	C	1900033	R	FTN_1769	1899948	1900373	F	142	86(426)
tnfn1_pw060418p02q164	H08	C	1462852	F	intergenic					
tnfn1_pw060418p02q165	A09	C	1382943	R	FTN_1310	1380761	1384039	F	1093	2183(3279)
tnfn1_pw060418p02q166	B09	C	1619651	F	FTN_1522	1619418	1620341	R	308	691(924)
tnfn1_pw060418p02q167	C09	C	1202660	R	FTN_1137	1201461	1203242	R	594	583(1782)
tnfn1_pw060418p02q168	D09	C	1425219	R	FTN_1346	1424642	1425427	F	262	578(786)
tnfn1_pw060418p02q169	E09	C	807215	R	FTN_0753	806791	807339	F	183	425(549)
tnfn1_pw060418p02q170	F09	C	999577	R	FTN_0938	999438	999626	R	63	50(189)
tnfn1_pw060418p02q171	G09	C	1881916	F	FTN_1752	1880874	1882022	R	383	107(1149)
tnfn1_pw060418p02q172	H09	C	853122	R	intergenic					
tnfn1_pw060418p02q173	A10	C	695466	R	FTN_0656	694302	695522	R	407	57(1221)
tnfn1_pw060418p02q174	B10	C	1619651	F	FTN_1522	1619418	1620341	R	308	691(924)
tnfn1_pw060418p02q175	C10	C	773697	R	FTN_0717	772243	773937	R	565	241(1695)
tnfn1_pw060418p02q176	D10	C	1426871	R	FTN_1348	1426691	1427179	R	163	309(489)
tnfn1_pw060418p02q177	E10	C	1140408	R	FTN_1077	1140193	1140936	F	248	216(744)
tnfn1_pw060418p02q178	F10	C	1634381	F	FTN_1536	1633310	1634656	R	449	276(1347)
tnfn1_pw060418p02q179	G10	C	1199631	R	FTN_1134	1199448	1199690	R	81	60(243)
tnfn1_pw060418p02q180	H10	C	1472328	F	FTN_1395	1471775	1472776	R	334	449(1002)
tnfn1_pw060418p02q181	A11	C	889339	R	FTN_0832	888904	890442	R	513	1104(1539)
tnfn1_pw060418p02q182	B11	U	1347530	F	FTN_1275	1347139	1348665	F	509	392(1527)
tnfn1_pw060418p02q183	C11	C	163325	F	FTN_0151	163057	163836	R	260	512(780)
tnfn1_pw060418p02q184	D11	C	1611188	R	FTN_1514	1610738	1611460	F	241	451(723)
tnfn1_pw060418p02q185	E11	C	1095733	R	FTN_1039	1094041	1097463	F	1141	1693(3423)
tnfn1_pw060418p02q186	F11	C	1538356	R	FTN_1448	1537385	1538812	R	476	457(1428)
tnfn1_pw060418p02q187	G11	U	631259	R	FTN_0599	630525	631322	R	266	64(798)
tnfn1_pw060418p02q188	H11	C	1470149	R	FTN_1392	1469819	1470334	R	172	186(516)
tnfn1_pw060418p02q189	A12	U	677480	R	FTN_0640	676608	677855	F	416	873(1248)
tnfn1_pw060418p02q190	B12	U	1309357	R	FTN_1242	1308961	1309605	F	215	397(645)
tnfn1_pw060418p02q191	C12	C	1152019	F	FTN_1090	1151656	1152243	R	196	225(588)
tnfn1_pw060418p02q192	D12	C	43573	R	FTN_0040	41096	44347	R	1084	775(3252)
tnfn1_pw060418p02q193	E12	C	1798365	F	FTN_1683	1798000	1799259	F	420	366(1260)
tnfn1_pw060418p02q194	F12	C	423064	F	FTN_0424	422962	423312	R	117	249(351)
tnfn1_pw060418p02q195	G12	U	88763	R	FTN_0078	88548	89318	F	257	216(771)
tnfn1_pw060418p02q196	H12	C	1548176	F	FTN_1460	1547752	1548579	F	276	425(828)

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_pw060418p02q101	A01	EXACT(0)	156	152	130	37	EXACT(0)	200	194	56
tnfn1_pw060418p02q102	B01	EXACT(0)	157	151	134	40	EXACT(0)	200	185	46
tnfn1_pw060418p02q103	C01	EXACT(0)	155	154	135	44	EXACT(0)	200	193	58
tnfn1_pw060418p02q104	D01	EXACT(0)	158	145	108	30	EXACT(0)	200	188	57
tnfn1_pw060418p02q105	E01	EXACT(0)	157	152	135	35	EXACT(0)	162	152	54
tnfn1_pw060418p02q106	F01	EXACT(0)	156	145	105	39	EXACT(0)	200	186	57
tnfn1_pw060418p02q107	G01	EXACT(0)	157	153	136	36	EXACT(0)	200	189	55
tnfn1_pw060418p02q108	H01	EXACT(0)	156	145	130	44	EXACT(0)	200	185	41
tnfn1_pw060418p02q109	A02	EXACT(0)	158	142	123	35	EXACT(0)	200	188	58
tnfn1_pw060418p02q110	B02	EXACT(0)	156	153	134	40	EXACT(0)	200	192	55
tnfn1_pw060418p02q111	C02	EXACT(0)	156	152	136	40	EXACT(0)	200	184	51
tnfn1_pw060418p02q112	D02	EXACT(0)	158	145	132	49	EXACT(0)	200	193	66
tnfn1_pw060418p02q113	E02	EXACT(0)	155	138	132	42	EXACT(0)	200	190	47
tnfn1_pw060418p02q114	F02	EXACT(0)	154	144	109	34	EXACT(0)	200	180	40
tnfn1_pw060418p02q115	G02	EXACT(0)	159	153	135	37	EXACT(0)	200	182	57
tnfn1_pw060418p02q116	H02	EXACT(0)	156	152	133	44	EXACT(0)	182	165	51
tnfn1_pw060418p02q117	A03	EXACT(0)	158	153	142	39	EXACT(0)	200	186	35
tnfn1_pw060418p02q118	B03	EXACT(0)	158	152	138	38	EXACT(0)	200	192	52
tnfn1_pw060418p02q119	C03	EXACT(0)	155	145	129	48	EXACT(0)	200	152	41
tnfn1_pw060418p02q120	D03	EXACT(0)	155	152	128	43	EXACT(0)	200	179	58
tnfn1_pw060418p02q121	E03	EXACT(0)	156	142	125	39	EXACT(0)	200	191	52
tnfn1_pw060418p02q122	F03	EXACT(0)	157	153	134	44	EXACT(0)	200	194	63
tnfn1_pw060418p02q123	G03	EXACT(0)	156	152	130	43	EXACT(0)	200	195	55
tnfn1_pw060418p02q124	H03	EXACT(0)	159	153	135	42	EXACT(0)	199	186	53
tnfn1_pw060418p02q125	A04	EXACT(0)	156	152	133	46	EXACT(0)	178	168	46
tnfn1_pw060418p02q126	B04	EXACT(0)	155	145	125	39	EXACT(0)	200	197	55
tnfn1_pw060418p02q127	C04	EXACT(0)	157	148	137	40	EXACT(0)	200	185	64
tnfn1_pw060418p02q128	D04	EXACT(0)	158	153	142	46	EXACT(0)	199	189	57
tnfn1_pw060418p02q129	E04	EXACT(0)	122	81	75	24	EXACT(0)	80	75	38
tnfn1_pw060418p02q130	F04	EXACT(0)	123	121	80	21	EXACT(0)	200	181	46
tnfn1_pw060418p02q131	G04	EXACT(0)	123	112	72	22	EXACT(0)	200	190	53
tnfn1_pw060418p02q132	H04	EXACT(0)	156	139	124	36	EXACT(0)	200	181	55
tnfn1_pw060418p02q133	A05	EXACT(0)	122	120	104	37	EXACT(0)	200	190	53
tnfn1_pw060418p02q134	B05	EXACT(0)	122	119	91	28	EXACT(0)	200	192	54
tnfn1_pw060418p02q135	C05	EXACT(0)	124	120	78	22	EXACT(0)	200	185	49
tnfn1_pw060418p02q136	D05	EXACT(0)	123	120	107	32	EXACT(0)	200	171	52
tnfn1_pw060418p02q137	E05	EXACT(0)	123	119	109	34	EXACT(0)	171	165	51
tnfn1_pw060418p02q138	F05	EXACT(0)	121	105	94	37	EXACT(0)	200	138	38
tnfn1_pw060418p02q139	G05	EXACT(0)	121	119	98	34	EXACT(0)	200	186	57
tnfn1_pw060418p02q140	H05	EXACT(0)	156	153	132	43	EXACT(0)	137	135	54
tnfn1_pw060418p02q141	A06	EXACT(0)	155	138	117	38	EXACT(0)	200	185	60
tnfn1_pw060418p02q142	B06	EXACT(0)	155	153	126	38	EXACT(0)	200	190	57
tnfn1_pw060418p02q143	C06	EXACT(0)	155	144	127	38	EXACT(0)	200	186	56
tnfn1_pw060418p02q144	D06	EXACT(0)	157	153	137	42	EXACT(0)	199	188	41
tnfn1_pw060418p02q145	E06	EXACT(0)	156	145	115	36	EXACT(0)	200	187	59
tnfn1_pw060418p02q146	F06	EXACT(0)	155	144	109	26	EXACT(0)	147	138	40
tnfn1_pw060418p02q147	G06	EXACT(0)	156	151	118	39	EXACT(0)	200	187	63
tnfn1_pw060418p02q148	H06	EXACT(0)	156	153	137	40	EXACT(0)	200	186	57

**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_pw060418p02q149	A07	EXACT(0)	154	145	126	35	EXACT(0)	197	171	30
tnfn1_pw060418p02q150	B07	EXACT(0)	153	145	129	39	EXACT(0)	199	182	45
tnfn1_pw060418p02q151	C07	EXACT(0)	156	153	119	24	EXACT(0)	200	186	52
tnfn1_pw060418p02q152	D07	EXACT(0)	156	139	133	42	EXACT(0)	200	179	57
tnfn1_pw060418p02q153	E07	EXACT(0)	157	151	137	47	EXACT(0)	201	130	42
tnfn1_pw060418p02q154	F07	EXACT(0)	154	144	130	35	EXACT(0)	52	49	36
tnfn1_pw060418p02q155	G07	EXACT(0)	156	144	130	45	EXACT(0)	200	172	46
tnfn1_pw060418p02q156	H07	EXACT(0)	155	152	131	43	EXACT(0)	200	187	61
tnfn1_pw060418p02q157	A08	EXACT(0)	157	149	135	38	EXACT(0)	200	190	56
tnfn1_pw060418p02q158	B08	EXACT(0)	155	145	126	47	EXACT(0)	200	172	49
tnfn1_pw060418p02q159	C08	EXACT(0)	155	153	129	41	EXACT(0)	200	194	60
tnfn1_pw060418p02q160	D08	EXACT(0)	157	145	126	31	EXACT(0)	200	191	54
tnfn1_pw060418p02q161	E08	EXACT(0)	156	153	122	34	EXACT(0)	200	191	57
tnfn1_pw060418p02q162	F08	EXACT(0)	140	139	117	29	EXACT(0)	200	195	41
tnfn1_pw060418p02q163	G08	EXACT(0)	155	116	104	36	EXACT(0)	200	174	62
tnfn1_pw060418p02q164	H08	EXACT(0)	155	145	119	38	EXACT(0)	200	183	63
tnfn1_pw060418p02q165	A09	EXACT(0)	154	138	126	40	EXACT(0)	200	93	37
tnfn1_pw060418p02q166	B09	EXACT(0)	156	142	125	39	EXACT(0)	200	192	60
tnfn1_pw060418p02q167	C09	EXACT(0)	121	120	99	28	EXACT(0)	200	176	42
tnfn1_pw060418p02q168	D09	EXACT(0)	122	119	89	23	EXACT(0)	182	172	52
tnfn1_pw060418p02q169	E09	EXACT(0)	121	112	68	21	EXACT(0)	200	192	53
tnfn1_pw060418p02q170	F09	EXACT(0)	122	117	86	26	EXACT(0)	201	131	37
tnfn1_pw060418p02q171	G09	EXACT(0)	158	153	139	38	EXACT(0)	200	166	42
tnfn1_pw060418p02q172	H09	EXACT(0)	157	153	135	35	EXACT(0)	200	186	48
tnfn1_pw060418p02q173	A10	EXACT(0)	122	118	100	34	EXACT(0)	200	182	41
tnfn1_pw060418p02q174	B10	EXACT(0)	154	138	124	34	EXACT(0)	200	192	54
tnfn1_pw060418p02q175	C10	EXACT(0)	123	109	97	30	EXACT(0)	193	177	49
tnfn1_pw060418p02q176	D10	EXACT(0)	121	111	85	27	EXACT(0)	200	181	52
tnfn1_pw060418p02q177	E10	EXACT(0)	124	118	110	37	EXACT(0)	200	141	40
tnfn1_pw060418p02q178	F10	EXACT(0)	156	145	126	36	EXACT(0)	200	194	46
tnfn1_pw060418p02q179	G10	EXACT(0)	122	112	101	34	EXACT(0)	125	116	54
tnfn1_pw060418p02q180	H10	EXACT(0)	155	153	126	39	EXACT(0)	199	183	50
tnfn1_pw060418p02q181	A11	EXACT(0)	157	152	129	35	EXACT(0)	200	196	38
tnfn1_pw060418p02q182	B11	EXACT(0)	116	111	88	41	EXACT(0)	200	187	45
tnfn1_pw060418p02q183	C11	EXACT(0)	155	145	128	42	EXACT(0)	200	197	52
tnfn1_pw060418p02q184	D11	EXACT(0)	156	145	127	39	EXACT(0)	200	190	54
tnfn1_pw060418p02q185	E11	EXACT(0)	155	145	129	36	EXACT(0)	200	180	56
tnfn1_pw060418p02q186	F11	EXACT(0)	155	145	134	43	EXACT(0)	200	189	59
tnfn1_pw060418p02q187	G11	EXACT(0)	156	152	110	35	EXACT(0)	200	191	57
tnfn1_pw060418p02q188	H11	EXACT(0)	157	152	128	31	EXACT(0)	200	196	54
tnfn1_pw060418p02q189	A12	EXACT(0)	154	145	129	43	EXACT(0)	200	181	57
tnfn1_pw060418p02q190	B12	EXACT(0)	155	145	126	40	EXACT(0)	186	179	52
tnfn1_pw060418p02q191	C12	EXACT(0)	156	153	131	40	EXACT(0)	198	150	39
tnfn1_pw060418p02q192	D12	EXACT(0)	154	145	120	36	EXACT(0)	200	169	55
tnfn1_pw060418p02q193	E12	EXACT(0)	154	145	119	36	EXACT(0)	200	190	57
tnfn1_pw060418p02q194	F12	EXACT(0)	159	153	113	31	EXACT(0)	200	190	56
tnfn1_pw060418p02q195	G12	EXACT(0)	156	145	128	40	EXACT(0)	200	195	57
tnfn1_pw060418p02q196	H12	EXACT(0)	159	153	125	36	EXACT(0)	200	193	51