

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 30 (tnfn1_pw060510p02)**

Catalog No. NR-8064

For research use only. Not for human use.

Contributor:

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Product Description:

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

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

NR-8064 represents Plate 30 (tnfn1_pw060510p02) 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_pw060510p02q103 (Well C01) was not available due to quality issues at the time of release of Plate 30, 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-8064 was packaged aseptically in 96-well plates. The product is provided frozen and should be stored at -60°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Media:

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

Incubation:

Temperature: 37°C

Atmosphere: Aerobic with 5% CO₂

Propagation:

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

Citation:

Acknowledgment for publications should read “The following reagent was obtained through the NIH Biodefense and Emerging Infections Research Resources Repository, NIAID, NIH: *Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 30 (tnfn1_pw060510p02), NR-8064.”

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.

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_pw060510p02q101	A01	<KAN-2>	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p02q102	B01	<KAN-2>	gloB	hydroxyacylglutathione hydrolase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q103	C01	T20	prlC	oligopeptidase A	amino acid metabolism
tnfn1_pw060510p02q104	D01	T18	aroH	chorismate mutase	amino acid metabolism - biosynthesis
tnfn1_pw060510p02q105	E01	T18	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060510p02q106	F01	T18	recR	RecFOR complex, RecR component	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q107	G01	T18	apt	adenine phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060510p02q108	H01	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p02q109	A02	T20	-	acid phosphatase, PAP2 family	putative enzymes
tnfn1_pw060510p02q110	B02	T20	mutM	formamidopyrimidine-DNA glycosylase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q111	C02	T20	-	deoxyribodipyrimidine photolyase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q112	D02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p02q113	E02	T20	-	metabolite:H ⁺ symporter (MHS) family protein	transport
tnfn1_pw060510p02q114	F02	T20	-	DNA/RNA endonuclease G	nucleotides and nucleosides metabolism
tnfn1_pw060510p02q115	G02	T20	-	metabolite:H ⁺ symporter (MHS) family protein	transport
tnfn1_pw060510p02q116	H02	T20	-	RNA methyltransferase, trmA family	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q117	A03	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060510p02q118	B03	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060510p02q119	C03	<KAN-2>	-	membrane fusion protein	motility, attachment and secretion structure
tnfn1_pw060510p02q120	D03	T20	ans	asparaginase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q121	E03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p02q122	F03	T20	-	phage integrase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q123	G03	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p02q124	H03	T20	rpiA	ribose 5-phosphate isomerase A	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q125	A04	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060510p02q126	B04	T20	-	galactose mutarotase	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p02q127	C04	T20	-		
tnfn1_pw060510p02q128	D04	T20	purN	phosphoribosylglycinamide formyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060510p02q129	E04	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p02q130	F04	<KAN-2>	clpB	chaperone clpB	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060510p02q131	G04	<KAN-2>	-	UDP-3-O-[3-fatty acid] glucosamine N-acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060510p02q132	H04	T20	pgm	phosphoglucomutase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q133	A05	T20	trpD	anthranilate phosphoribosyltransferase	amino acid metabolism - biosynthesis
tnfn1_pw060510p02q134	B05	T20	cysD	sulfate adenylyltransferase subunit 2	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q135	C05	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p02q136	D05	T20	purM	phosphoribosylformylglycinamide cyclo-ligase	nucleotides and nucleosides metabolism
tnfn1_pw060510p02q137	E05	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p02q138	F05	T20	rng	ribonuclease G	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q139	G05	T20	putP	proline:Na ⁺ symporter	transport - amino-acid
tnfn1_pw060510p02q140	H05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p02q141	A06	T20	-	ribonuclease II family protein	transcription
tnfn1_pw060510p02q142	B06	T20	rng	ribonuclease G	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q143	C06	T20	-	drug/metabolite transporter (DMT) superfamily protein	transport - drugs / antibacterial compounds
tnfn1_pw060510p02q144	D06	T20	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q145	E06	<KAN-2>	rsuA	16S rRNA pseudouridine synthase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q146	F06	<KAN-2>	nusB	transcription termination factor	transcription
tnfn1_pw060510p02q147	G06	<KAN-2>	-	hydrolase, HD superfamily	putative enzymes
tnfn1_pw060510p02q148	H06	T20	uvrB	excinuclease ABC, subunit B	DNA replication, recombination, modification and repair - restriction/modification

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Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060510p02q149	A07	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060510p02q150	B07	T20	istu6	istu6	IS element
tnfn1_pw060510p02q151	C07	T20	mviN	multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) transporter	transport - drugs / antibacterial compounds
tnfn1_pw060510p02q152	D07	T20	sun	tRNA and rRNA cytosine-C5-methylases, sun protein	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q153	E07	T20	wzx	O antigen flippase	transport
tnfn1_pw060510p02q154	F07	T20	-	shikimate 5-dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060510p02q155	G07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p02q156	H07	T20	-	serine permease	transport - amino-acid
tnfn1_pw060510p02q157	A08	T20	dsbB	disulfide bond formation protein	putative enzymes
tnfn1_pw060510p02q158	B08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p02q159	C08	<KAN-2>	galP2	galactose-proton symporter, major facilitator superfamily (MFS) transport protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060510p02q160	D08	T20	carA	carbamoyl-phosphate synthase small chain	nucleotides and nucleosides metabolism
tnfn1_pw060510p02q161	E08	T20	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	amino acid metabolism - biosynthesis
tnfn1_pw060510p02q162	F08	T20	-	RecB family exonuclease	DNA replication, recombination, modification and repair
tnfn1_pw060510p02q163	G08	T20	rpoZ	DNA-directed RNA polymerase, subunit K/omega	transcription
tnfn1_pw060510p02q164	H08	T20	trpG	anthranilate synthase component II	amino acid metabolism - biosynthesis
tnfn1_pw060510p02q165	A09	T20	rluC	ribosomal large subunit pseudouridine synthase C	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q166	B09	T20	pyrC	dihydroorotase	nucleotides and nucleosides metabolism
tnfn1_pw060510p02q167	C09	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060510p02q168	D09	T20	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	cell wall / LPS / capsule
tnfn1_pw060510p02q169	E09	T20	bglX	glycosyl hydrolase family 3	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q170	F09	T20	-	-	-
tnfn1_pw060510p02q171	G09	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q172	H09	T20	-	ABC-type anion transport system, duplicated permease component	transport
tnfn1_pw060510p02q173	A10	T20	-	acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060510p02q174	B10	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060510p02q175	C10	T20	galE	UDP-glucose 4-epimerase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q176	D10	T20	-	ATPase, AAA family, related to the helicase subunit of the Holliday junction resolvase	DNA replication, recombination, modification and repair
tnfn1_pw060510p02q177	E10	T20	galE	UDP-glucose 4-epimerase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q178	F10	T20	-	L-lactate dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q179	G10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p02q180	H10	T20	-	type I restriction-modification system, subunit M (methyltransferase)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q181	A11	T20	pnp	polyribonucleotide nucleotidyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p02q182	B11	T20	-	DNA helicase	DNA replication, recombination, modification and repair
tnfn1_pw060510p02q183	C11	T20	ftsK	cell division protein FtsK	cell cycle
tnfn1_pw060510p02q184	D11	T20	hdc	pyridoxal-dependent decarboxylase	putative enzymes
tnfn1_pw060510p02q185	E11	T20	ftsK	cell division protein FtsK	cell cycle
tnfn1_pw060510p02q186	F11	T20	recN	DNA repair protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q187	G11	T18	-	aldolase/adducin class II family protein	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q188	H11	T20	rnhB	ribonuclease HII	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q189	A12	T20	-	adenine specific DNA methylase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q190	B12	T20	malQ	4-alpha-glucanotransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p02q191	C12	T20	-	pyridoxal-dependent decarboxylase	putative enzymes
tnfn1_pw060510p02q192	D12	T20	potI	ATP-binding cassette putrescine uptake system, membrane protein, subunit I	transport
tnfn1_pw060510p02q193	E12	T20	-	pyridoxal-dependent decarboxylase	putative enzymes
tnfn1_pw060510p02q194	F12	T20	nth	endonuclease III	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p02q195	G12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p02q196	H12	T20	cydD	ABC-type transport ATP-binding protein CydD	transport

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_pw060510p02q101	A01	C	1902144	R	FTN_1771	1901829	1902239	R	137	96(411)
tnfn1_pw060510p02q102	B01	C	1450467	R	FTN_1370	1450037	1450792	R	252	326(756)
tnfn1_pw060510p02q103	C01	C	424121	R	FTN_0425	423396	425399	R	668	1279(2004)
tnfn1_pw060510p02q104	D01	C	355183	F	FTN_0349	355001	355360	F	120	183(360)
tnfn1_pw060510p02q105	E01	C	315365	R	FTN_0306	315040	315714	F	225	326(675)
tnfn1_pw060510p02q106	F01	C	1270341	R	FTN_1197	1270028	1270627	F	200	314(600)
tnfn1_pw060510p02q107	G01	C	1743854	R	FTN_1633	1743411	1743935	R	175	82(525)
tnfn1_pw060510p02q108	H01	C	902158	F	FTN_0847	901867	902790	R	308	633(924)
tnfn1_pw060510p02q109	A02	U	1650886	R	FTN_1552	1650561	1651184	F	208	326(624)
tnfn1_pw060510p02q110	B02	C	635872	R	FTN_0603	635462	636283	R	274	412(822)
tnfn1_pw060510p02q111	C02	U	364243	R	FTN_0361	363337	364833	F	499	907(1497)
tnfn1_pw060510p02q112	D02	C	1478371	R	FTN_1399	1477955	1478668	R	238	298(714)
tnfn1_pw060510p02q113	E02	U	1276767	R	FTN_1202	1275819	1277072	R	418	306(1254)
tnfn1_pw060510p02q114	F02	C	1135547	R	FTN_1073	1135198	1136259	R	354	713(1062)
tnfn1_pw060510p02q115	G02	C	664470	F	FTN_0631	663750	664967	F	406	721(1218)
tnfn1_pw060510p02q116	H02	C	647363	F	FTN_0616	646972	648318	F	449	392(1347)
tnfn1_pw060510p02q117	A03	C	688184	F	FTN_0649	687803	690832	F	1010	382(3030)
tnfn1_pw060510p02q118	B03	C	1486060	R	FTN_1409	1485991	1487373	R	461	1314(1383)
tnfn1_pw060510p02q119	C03	U	1349154	F	FTN_1276	1348690	1349712	F	341	465(1023)
tnfn1_pw060510p02q120	D03	C	1278087	R	FTN_1208	1277746	1278606	R	287	520(861)
tnfn1_pw060510p02q121	E03	C	283033	F	FTN_0275	282485	283540	F	352	549(1056)
tnfn1_pw060510p02q122	F03	C	369761	R	FTN_0367	369322	370554	F	411	440(1233)
tnfn1_pw060510p02q123	G03	C	377054	R	FTN_0375	376636	377250	F	205	419(615)
tnfn1_pw060510p02q124	H03	C	1259227	R	FTN_1185	1258782	1259453	F	224	446(672)
tnfn1_pw060510p02q125	A04	C	994211	F	FTN_0932	992752	994548	F	599	1460(1797)
tnfn1_pw060510p02q126	B04	C	1814704	R	FTN_1697	1814406	1815263	R	286	560(858)
tnfn1_pw060510p02q127	C04	U	477487	F	intergenic					
tnfn1_pw060510p02q128	D04	U	420707	F	FTN_0421	420678	421250	F	191	30(573)
tnfn1_pw060510p02q129	E04	C	283033	F	FTN_0275	282485	283540	F	352	549(1056)
tnfn1_pw060510p02q130	F04	C	1870794	F	FTN_1743	1870244	1872820	F	859	551(2577)
tnfn1_pw060510p02q131	G04	C	221776	R	FTN_0200	221524	222564	R	347	789(1041)
tnfn1_pw060510p02q132	H04	C	531166	R	FTN_0514	530155	531786	F	544	1012(1632)
tnfn1_pw060510p02q133	A05	C	1904808	R	FTN_1776	1904293	1905303	R	337	496(1011)
tnfn1_pw060510p02q134	B05	C	989608	R	FTN_0928	988925	989818	R	298	211(894)
tnfn1_pw060510p02q135	C05	U	1594754	R	FTN_1500	1594295	1595017	F	241	460(723)
tnfn1_pw060510p02q136	D05	C	417741	R	FTN_0419	417319	418359	F	347	423(1041)
tnfn1_pw060510p02q137	E05	C	1232804	F	FTN_1161	1232698	1233897	R	400	1094(1200)
tnfn1_pw060510p02q138	F05	C	1908668	R	FTN_1782	1908200	1909693	R	498	1026(1494)
tnfn1_pw060510p02q139	G05	C	308243	R	FTN_0299	306996	308501	F	502	1248(1506)
tnfn1_pw060510p02q140	H05	C	1138501	F	FTN_1075	1138172	1138876	R	235	376(705)
tnfn1_pw060510p02q141	A06	C	147638	F	FTN_0133	146389	148242	F	618	1250(1854)
tnfn1_pw060510p02q142	B06	C	1908668	R	FTN_1782	1908200	1909693	R	498	1026(1494)
tnfn1_pw060510p02q143	C06	U	1895717	R	FTN_1766	1895114	1896115	R	334	399(1002)
tnfn1_pw060510p02q144	D06	C	1302862	R	FTN_1234	1302512	1303525	R	338	664(1014)
tnfn1_pw060510p02q145	E06	C	1003108	R	FTN_0945	1002665	1003477	R	271	370(813)
tnfn1_pw060510p02q146	F06	C	1463921	R	FTN_1384	1463758	1464180	R	141	260(423)
tnfn1_pw060510p02q147	G06	C	435716	F	FTN_0437	435345	435932	F	196	372(588)
tnfn1_pw060510p02q148	H06	C	1248439	F	FTN_1176	1247657	1249660	R	668	1222(2004)

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_pw060510p02q149	A07	U	1170156	F	FTN_1108	1169873	1171081	F	403	284(1209)
tnfn1_pw060510p02q150	B07	C	720289	R	-	719918	720628	R	237	340(711)
tnfn1_pw060510p02q151	C07	U	284365	R	FTN_0276	283566	285104	F	513	800(1539)
tnfn1_pw060510p02q152	D07	C	1425706	F	FTN_1347	1425430	1426707	F	426	277(1278)
tnfn1_pw060510p02q153	E07	C	1499212	R	FTN_1420	1498689	1499933	R	415	722(1245)
tnfn1_pw060510p02q154	F07	C	524542	F	FTN_0511	523817	524659	R	281	118(843)
tnfn1_pw060510p02q155	G07	U	92006	F	FTN_0081	91627	92358	R	244	353(732)
tnfn1_pw060510p02q156	H07	C	655495	R	FTN_0624	654832	656091	R	420	597(1260)
tnfn1_pw060510p02q157	A08	C	1712018	F	FTN_1608	1711912	1712400	F	163	107(489)
tnfn1_pw060510p02q158	B08	C	543616	F	FTN_0523	543248	544063	F	272	369(816)
tnfn1_pw060510p02q159	C08	U	732412	F	FTN_0688	731758	733149	F	464	655(1392)
tnfn1_pw060510p02q160	D08	C	21897	R	FTN_0021	21409	22572	R	388	676(1164)
tnfn1_pw060510p02q161	E08	C	1152856	R	FTN_1091	1152249	1153523	R	425	668(1275)
tnfn1_pw060510p02q162	F08	C	1473225	F	FTN_1396	1472783	1473271	R	163	47(489)
tnfn1_pw060510p02q163	G08	C	645849	R	FTN_0613	645826	646041	F	72	24(216)
tnfn1_pw060510p02q164	H08	C	1905478	R	FTN_1777	1905303	1905878	R	192	401(576)
tnfn1_pw060510p02q165	A09	C	1768579	F	FTN_1655	1768091	1769017	R	309	439(927)
tnfn1_pw060510p02q166	B09	C	25155	R	FTN_0024	24880	26223	F	448	276(1344)
tnfn1_pw060510p02q167	C09	U	664232	R	FTN_0631	663750	664967	F	406	483(1218)
tnfn1_pw060510p02q168	D09	U	541016	F	FTN_0520	539650	541086	F	479	1367(1437)
tnfn1_pw060510p02q169	E09	C	1562050	F	FTN_1474	1561674	1562807	R	378	758(1134)
tnfn1_pw060510p02q170	F09	C	1164133	F	intergenic					
tnfn1_pw060510p02q171	G09	C	747143	R	FTN_0703	746848	747417	F	190	296(570)
tnfn1_pw060510p02q172	H09	C	164661	F	FTN_0152	163868	165589	R	574	929(1722)
tnfn1_pw060510p02q173	A10	C	1879702	F	FTN_1750	1879341	1880078	F	246	362(738)
tnfn1_pw060510p02q174	B10	C	201977	F	FTN_0184	201197	202417	R	407	441(1221)
tnfn1_pw060510p02q175	C10	C	1290409	R	FTN_1219	1289806	1290822	R	339	414(1017)
tnfn1_pw060510p02q176	D10	C	1490231	R	FTN_1413	1489726	1490961	R	412	731(1236)
tnfn1_pw060510p02q177	E10	C	1290409	R	FTN_1219	1289806	1290822	R	339	414(1017)
tnfn1_pw060510p02q178	F10	C	239460	F	FTN_0217	238429	239583	R	385	124(1155)
tnfn1_pw060510p02q179	G10	C	1219898	F	FTN_1153	1219531	1220226	R	232	329(696)
tnfn1_pw060510p02q180	H10	C	747986	F	FTN_0704	747676	749160	F	495	311(1485)
tnfn1_pw060510p02q181	A11	U	643877	R	FTN_0609	641862	643940	F	693	2016(2079)
tnfn1_pw060510p02q182	B11	C	1678424	R	FTN_1580	1677286	1678698	R	471	275(1413)
tnfn1_pw060510p02q183	C11	C	300411	F	FTN_0294	300088	302586	R	833	2176(2499)
tnfn1_pw060510p02q184	D11	C	1078115	R	FTN_1019	1077269	1078402	F	378	847(1134)
tnfn1_pw060510p02q185	E11	C	300411	F	FTN_0294	300088	302586	R	833	2176(2499)
tnfn1_pw060510p02q186	F11	C	411419	F	FTN_0412	410233	411879	F	549	1187(1647)
tnfn1_pw060510p02q187	G11	C	1077091	R	FTN_1018	1076556	1077251	F	232	536(696)
tnfn1_pw060510p02q188	H11	C	1364734	R	FTN_1293	1364580	1365134	R	185	401(555)
tnfn1_pw060510p02q189	A12	U	1583567	R	FTN_1491	1582630	1584609	R	660	1043(1980)
tnfn1_pw060510p02q190	B12	C	537507	R	FTN_0518	536994	538454	F	487	514(1461)
tnfn1_pw060510p02q191	C12	C	1799993	R	FTN_1684	1799255	1800505	F	417	739(1251)
tnfn1_pw060510p02q192	D12	U	790968	F	FTN_0737	790573	791376	R	268	409(804)
tnfn1_pw060510p02q193	E12	C	1799993	R	FTN_1684	1799255	1800505	F	417	739(1251)
tnfn1_pw060510p02q194	F12	C	1091152	F	FTN_1035	1090869	1091504	F	212	284(636)
tnfn1_pw060510p02q195	G12	U	346041	F	FTN_0341	345948	346190	R	81	150(243)
tnfn1_pw060510p02q196	H12	U	680341	F	FTN_0642	679509	681287	R	593	947(1779)

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_pw060510p02q101	A01	EXACT(0)	120	120	96	37	EXACT(0)	200	193	55
tnfn1_pw060510p02q102	B01	EXACT(0)	110	112	97	42	EXACT(0)	200	194	44
tnfn1_pw060510p02q103	C01	EXACT(0)	155	145	129	46	EXACT(0)	200	197	66
tnfn1_pw060510p02q104	D01	EXACT(0)	123	118	105	41	EXACT(0)	200	191	57
tnfn1_pw060510p02q105	E01	EXACT(0)	124	119	108	37	EXACT(0)	201	147	41
tnfn1_pw060510p02q106	F01	EXACT(0)	125	120	94	30	EXACT(0)	200	194	49
tnfn1_pw060510p02q107	G01	EXACT(0)	122	119	98	39	EXACT(0)	200	195	51
tnfn1_pw060510p02q108	H01	ADJUSTED(7)	124	45	41	21	ESTIMATE(0)	200	177	39
tnfn1_pw060510p02q109	A02	EXACT(0)	154	116	107	31	EXACT(0)	200	186	56
tnfn1_pw060510p02q110	B02	EXACT(0)	156	153	123	37	EXACT(0)	200	190	56
tnfn1_pw060510p02q111	C02	EXACT(0)	156	153	125	42	EXACT(0)	200	192	61
tnfn1_pw060510p02q112	D02	EXACT(0)	155	139	105	29	EXACT(0)	200	180	49
tnfn1_pw060510p02q113	E02	EXACT(0)	156	145	114	31	EXACT(0)	200	190	43
tnfn1_pw060510p02q114	F02	EXACT(0)	156	152	139	44	EXACT(0)	200	188	46
tnfn1_pw060510p02q115	G02	EXACT(0)	147	78	70	32	EXACT(0)	200	190	49
tnfn1_pw060510p02q116	H02	EXACT(0)	155	151	99	35	EXACT(0)	200	155	45
tnfn1_pw060510p02q117	A03	EXACT(0)	151	145	123	39	EXACT(0)	200	196	58
tnfn1_pw060510p02q118	B03	EXACT(0)	153	139	125	46	EXACT(0)	200	184	56
tnfn1_pw060510p02q119	C03	EXACT(0)	113	112	97	39	EXACT(0)	200	192	63
tnfn1_pw060510p02q120	D03	EXACT(0)	160	133	94	21	EXACT(0)	200	177	34
tnfn1_pw060510p02q121	E03	EXACT(0)	122	124	100	29	EXACT(0)	200	172	29
tnfn1_pw060510p02q122	F03	EXACT(0)	152	144	133	46	EXACT(0)	200	179	56
tnfn1_pw060510p02q123	G03	EXACT(0)	122	119	95	37	EXACT(0)	200	184	48
tnfn1_pw060510p02q124	H03	EXACT(0)	157	152	138	46	EXACT(0)	135	131	66
tnfn1_pw060510p02q125	A04	EXACT(0)	153	153	96	27	EXACT(0)	200	187	43
tnfn1_pw060510p02q126	B04	EXACT(0)	155	152	131	43	EXACT(0)	200	193	50
tnfn1_pw060510p02q127	C04	EXACT(0)	159	145	130	37	EXACT(0)	200	200	55
tnfn1_pw060510p02q128	D04	EXACT(0)	159	152	136	43	EXACT(0)	200	186	41
tnfn1_pw060510p02q129	E04	EXACT(0)	123	73	66	29	EXACT(0)	200	192	41
tnfn1_pw060510p02q130	F04	EXACT(0)	132	111	73	35	EXACT(0)	200	195	51
tnfn1_pw060510p02q131	G04	EXACT(0)	120	111	95	41	EXACT(0)	200	197	58
tnfn1_pw060510p02q132	H04	EXACT(0)	155	139	124	36	EXACT(0)	200	197	58
tnfn1_pw060510p02q133	A05	EXACT(0)	155	144	133	46	EXACT(0)	168	162	61
tnfn1_pw060510p02q134	B05	EXACT(0)	154	145	132	49	EXACT(0)	200	195	57
tnfn1_pw060510p02q135	C05	EXACT(0)	124	119	106	32	EXACT(0)	100	96	52
tnfn1_pw060510p02q136	D05	EXACT(0)	156	145	127	40	EXACT(0)	200	168	42
tnfn1_pw060510p02q137	E05	EXACT(0)	154	139	128	46	EXACT(0)	200	192	60
tnfn1_pw060510p02q138	F05	EXACT(0)	157	152	125	35	EXACT(0)	200	186	59
tnfn1_pw060510p02q139	G05	EXACT(0)	155	151	127	43	EXACT(0)	200	195	59
tnfn1_pw060510p02q140	H05	EXACT(0)	158	152	103	31	EXACT(0)	200	180	33
tnfn1_pw060510p02q141	A06	EXACT(0)	218	154	121	29	EXACT(0)	200	195	46
tnfn1_pw060510p02q142	B06	EXACT(0)	154	153	125	45	EXACT(0)	200	186	60
tnfn1_pw060510p02q143	C06	EXACT(0)	156	145	115	35	EXACT(0)	199	148	36
tnfn1_pw060510p02q144	D06	EXACT(0)	157	153	121	37	EXACT(0)	200	160	47
tnfn1_pw060510p02q145	E06	EXACT(0)	120	120	105	38	EXACT(0)	200	193	57
tnfn1_pw060510p02q146	F06	EXACT(0)	120	120	105	37	EXACT(0)	200	189	54
tnfn1_pw060510p02q147	G06	EXACT(0)	121	112	95	37	EXACT(0)	200	140	40
tnfn1_pw060510p02q148	H06	EXACT(0)	151	139	128	46	EXACT(0)	200	195	55

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_pw060510p02q149	A07	EXACT(0)	156	145	106	30	EXACT(0)	200	172	43
tnfn1_pw060510p02q150	B07	EXACT(0)	155	152	131	44	EXACT(0)	200	186	60
tnfn1_pw060510p02q151	C07	EXACT(0)	155	152	134	44	EXACT(0)	200	192	61
tnfn1_pw060510p02q152	D07	EXACT(0)	164	138	124	38	EXACT(0)	200	183	45
tnfn1_pw060510p02q153	E07	EXACT(0)	214	152	113	22	EXACT(0)	200	188	35
tnfn1_pw060510p02q154	F07	EXACT(0)	151	145	129	46	EXACT(0)	200	187	57
tnfn1_pw060510p02q155	G07	EXACT(0)	156	144	132	44	EXACT(0)	200	189	55
tnfn1_pw060510p02q156	H07	EXACT(0)	153	105	93	28	EXACT(0)	200	174	28
tnfn1_pw060510p02q157	A08	EXACT(0)	154	148	121	48	EXACT(0)	200	191	66
tnfn1_pw060510p02q158	B08	EXACT(0)	156	139	118	35	EXACT(0)	200	190	53
tnfn1_pw060510p02q159	C08	EXACT(0)	116	112	107	41	EXACT(0)	200	191	52
tnfn1_pw060510p02q160	D08	EXACT(0)	155	145	134	46	EXACT(0)	200	93	39
tnfn1_pw060510p02q161	E08	EXACT(0)	154	139	125	41	EXACT(0)	200	193	53
tnfn1_pw060510p02q162	F08	EXACT(0)	157	144	126	35	EXACT(0)	200	184	52
tnfn1_pw060510p02q163	G08	EXACT(0)	156	144	127	38	EXACT(0)	200	176	43
tnfn1_pw060510p02q164	H08	EXACT(0)	154	153	127	45	EXACT(0)	199	175	53
tnfn1_pw060510p02q165	A09	EXACT(0)	154	152	134	42	EXACT(0)	200	196	55
tnfn1_pw060510p02q166	B09	EXACT(0)	154	152	113	34	EXACT(0)	200	193	53
tnfn1_pw060510p02q167	C09	EXACT(0)	155	145	129	40	EXACT(0)	200	193	55
tnfn1_pw060510p02q168	D09	EXACT(0)	154	61	49	14	EXACT(0)	200	162	21
tnfn1_pw060510p02q169	E09	EXACT(0)	154	145	120	39	EXACT(0)	125	121	50
tnfn1_pw060510p02q170	F09	EXACT(0)	154	145	129	50	EXACT(0)	200	185	64
tnfn1_pw060510p02q171	G09	EXACT(0)	153	145	118	38	EXACT(0)	200	174	44
tnfn1_pw060510p02q172	H09	EXACT(0)	154	145	129	44	EXACT(0)	200	190	52
tnfn1_pw060510p02q173	A10	EXACT(0)	152	145	113	34	EXACT(0)	200	193	48
tnfn1_pw060510p02q174	B10	EXACT(0)	155	145	125	35	EXACT(0)	200	192	41
tnfn1_pw060510p02q175	C10	EXACT(0)	156	153	135	42	EXACT(0)	199	184	43
tnfn1_pw060510p02q176	D10	EXACT(0)	157	153	134	37	EXACT(0)	200	195	51
tnfn1_pw060510p02q177	E10	EXACT(0)	153	139	131	48	EXACT(0)	200	195	56
tnfn1_pw060510p02q178	F10	EXACT(0)	155	145	131	45	EXACT(0)	200	190	60
tnfn1_pw060510p02q179	G10	EXACT(0)	154	152	111	35	EXACT(0)	199	151	39
tnfn1_pw060510p02q180	H10	EXACT(0)	157	152	133	40	EXACT(0)	200	186	58
tnfn1_pw060510p02q181	A11	EXACT(0)	157	153	137	40	EXACT(0)	200	192	52
tnfn1_pw060510p02q182	B11	EXACT(0)	154	145	123	43	EXACT(0)	200	186	59
tnfn1_pw060510p02q183	C11	EXACT(0)	157	152	136	44	EXACT(0)	200	143	40
tnfn1_pw060510p02q184	D11	EXACT(0)	155	138	108	31	EXACT(0)	200	184	37
tnfn1_pw060510p02q185	E11	EXACT(0)	155	152	131	45	EXACT(0)	67	66	53
tnfn1_pw060510p02q186	F11	EXACT(0)	154	145	123	41	EXACT(0)	200	197	52
tnfn1_pw060510p02q187	G11	EXACT(0)	121	112	93	36	EXACT(0)	200	176	41
tnfn1_pw060510p02q188	H11	EXACT(0)	157	152	120	38	EXACT(0)	200	185	57
tnfn1_pw060510p02q189	A12	EXACT(0)	158	142	103	31	EXACT(0)	200	179	38
tnfn1_pw060510p02q190	B12	EXACT(0)	152	87	64	31	EXACT(0)	200	188	51
tnfn1_pw060510p02q191	C12	EXACT(0)	154	145	113	37	EXACT(0)	200	193	53
tnfn1_pw060510p02q192	D12	EXACT(0)	155	142	125	35	EXACT(0)	200	192	53
tnfn1_pw060510p02q193	E12	EXACT(0)	154	145	129	47	EXACT(0)	200	193	60
tnfn1_pw060510p02q194	F12	EXACT(0)	155	146	130	48	EXACT(0)	200	193	53
tnfn1_pw060510p02q195	G12	EXACT(0)	156	145	137	44	EXACT(0)	200	187	49
tnfn1_pw060510p02q196	H12	EXACT(0)	155	153	132	41	EXACT(0)	110	106	51