

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 3 (tnfn1_pw060323p03)**

Catalog No. NR-8037

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-8037 represents Plate 3 (tnfn1_pw060323p03) 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-8037 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 3 (tnfn1_pw060323p03), NR-8037.”

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.

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_pw060323p03q101	A01	T20	hslR	heat shock protein 15 (HSP15)	translation, ribosomal structure and biogenesis
tnfn1_pw060323p03q102	B01	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060323p03q103	C01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q104	D01	T20	prfC	oligopeptidase A	amino acid metabolism
tnfn1_pw060323p03q105	E01	T20	dut	dUTP pyrophosphatase (Deoxyuridine 5'-triphosphate nucleotidohydrolase)	nucleotides and nucleosides metabolism
tnfn1_pw060323p03q106	F01	T20	oppA	ABC-type oligopeptide transport system, periplasmic component	transport
tnfn1_pw060323p03q107	G01	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p03q108	H01	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p03q109	A02	T20	pilQ	type IV pili secretin component	motility, attachment and secretion structure
tnfn1_pw060323p03q110	B02	T20	trpR	trp operon repressor	signal transduction and regulation
tnfn1_pw060323p03q111	C02	T20	-	Sua5/YciO/YrdC family protein	putative enzymes
tnfn1_pw060323p03q112	D02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p03q113	E02	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060323p03q114	F02	T20	tyrA	prephenate dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060323p03q115	G02	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q117	A03	T20	corA	divalent inorganic cation transporter	transport
tnfn1_pw060323p03q118	B03	T20	isftu3	isftu3	IS element
tnfn1_pw060323p03q119	C03	T20	pyrB	aspartate carbamoyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060323p03q120	D03	T20	rnd	ribonuclease D	translation, ribosomal structure and biogenesis
tnfn1_pw060323p03q121	E03	T20	-	aminotransferase	amino acid metabolism
tnfn1_pw060323p03q122	F03	T20	mutL	DNA mismatch repair enzyme with ATPase activity	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p03q123	G03	T20	-	oxidoreductase, short chain dehydrogenase/reductase family	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p03q124	H03	T20	nadC	nicotinate-nucleotide pyrophosphorylase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p03q125	A04	T20	-	ribonuclease II family protein	transcription
tnfn1_pw060323p03q126	B04	<KAN-2>	pilN	Type IV pili associated protein	motility, attachment and secretion structure
tnfn1_pw060323p03q127	C04	T20	-	tRNA synthetase class II (D, K and N)	other metabolism - biosynthesis
tnfn1_pw060323p03q128	D04	<KAN-2>	gcvT	glycine cleavage complex protein T (aminomethyltransferase)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p03q129	E04	<KAN-2>	-	protein of unknown function	hypothetical - novel
tnfn1_pw060323p03q130	F04	<KAN-2>	-	transcriptional regulator	signal transduction and regulation
tnfn1_pw060323p03q131	G04	<KAN-2>	-	X-prolyl aminopeptidase 2	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p03q132	H04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q133	A05	<KAN-2>	purA	adenylosuccinate synthetase	nucleotides and nucleosides metabolism
tnfn1_pw060323p03q134	B05	<KAN-2>	lipA	lipic acid synthetase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p03q135	C05	<KAN-2>	-	30S ribosomal protein S21	translation, ribosomal structure and biogenesis
tnfn1_pw060323p03q136	D05	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q137	E05	T18	-		
tnfn1_pw060323p03q138	F05	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p03q139	G05	T18	bioB	biotin synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p03q140	H05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p03q141	A06	T18	-	pseudogene: nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	pseudogene
tnfn1_pw060323p03q142	B06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p03q143	C06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p03q144	D06	T20	pyrD	dihydroorotate oxidase	nucleotides and nucleosides metabolism
tnfn1_pw060323p03q145	E06	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p03q146	F06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p03q147	G06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q148	H06	T20	-	predicted ATPase of the PP-loop superfamily	cell cycle

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tnfn1_pw060323p03q149	A07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q150	B07	T20	-	protein of unknown function with predicted hydrolase and phosphorylase activity	unknown function - conserved
tnfn1_pw060323p03q151	C07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q152	D07	T20	-	glycosyl transferase, family 2	cell wall / LPS / capsule
tnfn1_pw060323p03q153	E07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q154	F07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q155	G07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q156	H07	T20	kdpA	K(+)-ATPase uptake protein	transport
tnfn1_pw060323p03q157	A08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p03q158	B08	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p03q159	C08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q160	D08	T20	cbpA	chitin-binding protein	putative enzymes
tnfn1_pw060323p03q161	E08	T20	mviN	multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) transporter	transport - drugs / antibacterial compounds
tnfn1_pw060323p03q162	F08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q163	G08	T20	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p03q164	H08	T20	-		
tnfn1_pw060323p03q165	A09	T20	-	membrane fusion protein, HlyD family	transport
tnfn1_pw060323p03q166	B09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q167	C09	T20	recR	RecFOR complex, RecR component	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p03q168	D09	T20	isftu2	isftu2	IS element
tnfn1_pw060323p03q169	E09	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060323p03q170	F09	T20	-	protein of unknown function	unknown function - conserved
tnfn1_pw060323p03q171	G09	T20	-	delta 9 acyl-lipid fatty acid desaturase	fatty acids and lipids metabolism
tnfn1_pw060323p03q172	H09	T20	-	10 TMS drug/metabolite exporter protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p03q173	A10	T20	-	metal-dependent exopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060323p03q174	B10	T20	greA	transcriptional elongation factor	transcription
tnfn1_pw060323p03q175	C10	T20	mreA	FAD binding family protein	energy metabolism
tnfn1_pw060323p03q176	D10	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p03q177	E10	T20	ansB	periplasmic L-asparaginase II precursor	amino acid metabolism - biosynthesis
tnfn1_pw060323p03q178	F10	T20	-	peptide deformylase	translation, ribosomal structure and biogenesis
tnfn1_pw060323p03q179	G10	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p03q180	H10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p03q181	A11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p03q182	B11	T20	wbtO	transferase	cell wall / LPS / capsule
tnfn1_pw060323p03q183	C11	T20	-	phosphatidyltransferase	fatty acids and lipids metabolism
tnfn1_pw060323p03q184	D11	<KAN-2>	cydB	cytochrome bd-I terminal oxidase subunit II	energy metabolism
tnfn1_pw060323p03q185	E11	<KAN-2>	rplQ	50S ribosomal protein L17	translation, ribosomal structure and biogenesis
tnfn1_pw060323p03q186	F11	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p03q187	G11	<KAN-2>	nupC	nucleoside permease NUP family protein	transport
tnfn1_pw060323p03q188	H11	<KAN-2>	-		
tnfn1_pw060323p03q189	A12	<KAN-2>	wbtG	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060323p03q190	B12	<KAN-2>	sdaA	L-serine dehydratase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p03q191	C12	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p03q192	D12	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q193	E12	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q194	F12	<KAN-2>	-	ribonuclease PH	translation, ribosomal structure and biogenesis
tnfn1_pw060323p03q195	G12	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p03q196	H12	<KAN-2>	-	protein of unknown function	unknown function - novel

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_pw060323p03q101	A01	C	757398	F	FTN_0712	757045	757410	R	122	13(366)
tnfn1_pw060323p03q102	B01	C	1327006	R	FTN_1257	1326405	1327673	F	423	602(1269)
tnfn1_pw060323p03q103	C01	C	45847	R	FTN_0041	44369	46582	R	738	736(2214)
tnfn1_pw060323p03q104	D01	C	424883	R	FTN_0425	423396	425399	R	668	517(2004)
tnfn1_pw060323p03q105	E01	C	254770	F	FTN_0233	254764	255207	F	148	7(444)
tnfn1_pw060323p03q106	F01	C	1692418	R	FTN_1593	1691111	1692784	R	558	367(1674)
tnfn1_pw060323p03q107	G01	C	373355	R	FTN_0370	373090	373365	F	92	266(276)
tnfn1_pw060323p03q108	H01	C	402483	R	FTN_0403	402038	402688	R	217	206(651)
tnfn1_pw060323p03q109	A02	C	1202764	F	FTN_1137	1201461	1203242	R	594	479(1782)
tnfn1_pw060323p03q110	B02	C	1907521	R	FTN_1779	1907438	1907722	R	95	202(285)
tnfn1_pw060323p03q111	C02	C	470507	F	FTN_0465	470141	470752	F	204	367(612)
tnfn1_pw060323p03q112	D02	C	1471788	F	FTN_1394	1471522	1471791	R	90	4(270)
tnfn1_pw060323p03q113	E02	C	864914	F	FTN_0807	864451	865230	R	260	317(780)
tnfn1_pw060323p03q114	F02	C	65414	F	FTN_0055	64850	65683	R	278	270(834)
tnfn1_pw060323p03q115	G02	C	1795264	F	intergenic					
tnfn1_pw060323p03q116	H02	C	1296294	F	FTN_1226	1296078	1296404	R	109	111(327)
tnfn1_pw060323p03q117	A03	C	6382	R	FTN_0005	5832	6800	F	323	551(969)
tnfn1_pw060323p03q118	B03	C	214925	R	-	214716	215453	R	246	529(738)
tnfn1_pw060323p03q119	C03	C	17633	R	FTN_0019	17052	17975	R	308	343(924)
tnfn1_pw060323p03q120	D03	C	723606	F	FTN_0679	722626	723717	R	364	112(1092)
tnfn1_pw060323p03q121	E03	C	348621	R	FTN_0343	347655	349238	R	528	618(1584)
tnfn1_pw060323p03q122	F03	C	604649	F	FTN_0577	604169	605968	F	600	481(1800)
tnfn1_pw060323p03q123	G03	C	669305	R	FTN_0634	668810	669595	R	262	291(786)
tnfn1_pw060323p03q124	H03	C	737249	F	FTN_0693	737043	737903	F	287	207(861)
tnfn1_pw060323p03q125	A04	C	146678	F	FTN_0133	146389	148242	F	618	290(1854)
tnfn1_pw060323p03q126	B04	C	1204718	R	FTN_1140	1204444	1205004	R	187	287(561)
tnfn1_pw060323p03q127	C04	C	593309	F	FTN_0567	593082	594002	R	307	694(921)
tnfn1_pw060323p03q128	D04	C	515793	F	FTN_0505	514946	516019	F	358	848(1074)
tnfn1_pw060323p03q129	E04	C	844107	F	FTN_0786	843533	844276	F	248	575(744)
tnfn1_pw060323p03q130	F04	C	852235	R	FTN_0795	852101	852310	R	70	76(210)
tnfn1_pw060323p03q131	G04	C	1138050	R	FTN_1074	1136360	1138117	R	586	68(1758)
tnfn1_pw060323p03q132	H04	C	399947	R	FTN_0400	399470	400237	R	256	291(768)
tnfn1_pw060323p03q133	A05	C	196445	F	FTN_0178	196080	197363	F	428	366(1284)
tnfn1_pw060323p03q134	B05	C	1086299	R	FTN_1030	1086265	1087245	R	327	947(981)
tnfn1_pw060323p03q135	C05	C	974804	R	FTN_0916	974783	974977	R	65	174(195)
tnfn1_pw060323p03q136	D05	C	859453	F	FTN_0802	859091	859486	F	132	363(396)
tnfn1_pw060323p03q137	E05	C	1845785	R	intergenic					
tnfn1_pw060323p03q138	F05	C	1611894	R	FTN_1515	1611473	1612084	R	204	191(612)
tnfn1_pw060323p03q139	G05	C	872149	R	FTN_0815	871865	872803	R	313	655(939)
tnfn1_pw060323p03q140	H05	C	1395408	F	FTN_1320	1395199	1395762	F	188	210(564)
tnfn1_pw060323p03q141	A06	C	650407	R	FTN_0619	650233	651024	F	264	175(792)
tnfn1_pw060323p03q142	B06	C	31115	F	FTN_0030	30805	31209	R	135	95(405)
tnfn1_pw060323p03q143	C06	C	1628491	F	FTN_1531	1627995	1628675	R	227	185(681)
tnfn1_pw060323p03q144	D06	C	38143	R	FTN_0036	37864	38601	F	246	280(738)
tnfn1_pw060323p03q145	E06	C	368675	F	FTN_0365	368251	369006	F	252	425(756)
tnfn1_pw060323p03q146	F06	C	1146083	R	FTN_1082	1145210	1146601	R	464	519(1392)
tnfn1_pw060323p03q147	G06	C	991457	R	FTN_0930	990929	991774	R	282	318(846)
tnfn1_pw060323p03q148	H06	C	977905	F	FTN_0920	977672	978472	F	267	234(801)

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_pw060323p03q149	A07	C	1538356	R	FTN_1448	1537385	1538812	R	476	457(1428)
tnfn1_pw060323p03q150	B07	C	958210	F	FTN_0900	956882	958711	R	610	502(1830)
tnfn1_pw060323p03q151	C07	C	387860	F	FTN_0388	387616	387936	R	107	77(321)
tnfn1_pw060323p03q152	D07	C	1283680	F	FTN_1213	1282938	1283942	R	335	263(1005)
tnfn1_pw060323p03q153	E07	C	226874	R	FTN_0206	226642	227115	F	158	233(474)
tnfn1_pw060323p03q154	F07	C	1449735	F	FTN_1369	1449249	1449953	F	235	487(705)
tnfn1_pw060323p03q155	G07	C	1449735	F	FTN_1369	1449249	1449953	F	235	487(705)
tnfn1_pw060323p03q156	H07	C	1845377	R	FTN_1718	1844009	1845727	R	573	351(1719)
tnfn1_pw060323p03q157	A08	C	367669	F	FTN_0264	367604	368224	F	207	66(621)
tnfn1_pw060323p03q158	B08	C	1149024	F	FTN_1086	1148532	1149134	F	201	493(603)
tnfn1_pw060323p03q159	C08	C	771720	F	FTN_0716	771325	772137	F	271	396(813)
tnfn1_pw060323p03q160	D08	C	1575625	R	FTN_1485	1574733	1576397	F	555	893(1665)
tnfn1_pw060323p03q161	E08	C	284114	R	FTN_0276	283566	285104	F	513	549(1539)
tnfn1_pw060323p03q162	F08	C	1739636	F	FTN_1627	1739330	1739779	R	150	144(450)
tnfn1_pw060323p03q163	G08	C	1798453	F	FTN_1683	1798000	1799259	F	420	454(1260)
tnfn1_pw060323p03q164	H08	C	1051552	F	intergenic					
tnfn1_pw060323p03q165	A09	C	29870	R	FTN_0029	29753	30715	R	321	846(963)
tnfn1_pw060323p03q166	B09	C	1869085	R	FTN_1741	1868878	1869228	R	117	144(351)
tnfn1_pw060323p03q167	C09	C	1270290	R	FTN_1197	1270028	1270627	F	200	263(600)
tnfn1_pw060323p03q168	D09	C	1055711	F	-	1055368	1056224	F	285.6	344(857)
tnfn1_pw060323p03q169	E09	C	336175	R	FTN_0328	335825	336625	R	267	451(801)
tnfn1_pw060323p03q170	F09	C	1262219	F	FTN_1187	1261659	1262360	R	234	142(702)
tnfn1_pw060323p03q171	G09	C	1547944	F	FTN_1460	1547752	1548579	F	276	193(828)
tnfn1_pw060323p03q172	H09	C	8505	R	FTN_0008	7771	8640	R	290	136(870)
tnfn1_pw060323p03q173	A10	C	1020909	F	FTN_0965	1019741	1021147	F	469	1169(1407)
tnfn1_pw060323p03q174	B10	C	705109	R	FTN_0665	705047	705526	F	160	63(480)
tnfn1_pw060323p03q175	C10	C	1334723	F	FTN_1262	1333174	1334967	R	598	245(1794)
tnfn1_pw060323p03q176	D10	C	1295893	R	FTN_1225	1295269	1296078	R	270	186(810)
tnfn1_pw060323p03q177	E10	C	579522	F	FTN_0555	579267	580328	F	354	256(1062)
tnfn1_pw060323p03q178	F10	C	509413	F	FTN_0500	509303	509935	F	211	111(633)
tnfn1_pw060323p03q179	G10	C	1386753	F	FTN_1314	1386652	1387170	F	173	102(519)
tnfn1_pw060323p03q180	H10	C	288179	R	FTN_0280	288029	288421	F	131	151(393)
tnfn1_pw060323p03q181	A11	C	1544120	R	FTN_1455	1543884	1544657	F	258	237(774)
tnfn1_pw060323p03q182	B11	C	1509149	R	FTN_1428	1508659	1509267	R	203	119(609)
tnfn1_pw060323p03q183	C11	C	1621994	F	FTN_1525	1621652	1622248	R	199	255(597)
tnfn1_pw060323p03q184	D11	C	210760	R	FTN_0192	209805	210995	R	397	236(1191)
tnfn1_pw060323p03q185	E11	C	272739	F	FTN_0265	272307	272741	F	145	433(435)
tnfn1_pw060323p03q186	F11	C	785235	F	FTN_0731	784756	785670	F	305	480(915)
tnfn1_pw060323p03q187	G11	C	1700551	R	FTN_1599	1699890	1701089	R	400	539(1200)
tnfn1_pw060323p03q188	H11	C	485626	F	intergenic					
tnfn1_pw060323p03q189	A12	C	1503808	R	FTN_1423	1502940	1504025	R	362	218(1086)
tnfn1_pw060323p03q190	B12	C	804378	F	FTN_0750	803701	805071	F	457	678(1371)
tnfn1_pw060323p03q191	C12	C	603604	F	FTN_0576	603499	604158	F	220	106(660)
tnfn1_pw060323p03q192	D12	C	833751	R	FTN_0777	833560	834003	R	148	253(444)
tnfn1_pw060323p03q193	E12	C	949447	F	FTN_0893	949331	949918	F	196	117(588)
tnfn1_pw060323p03q194	F12	C	387168	F	FTN_0387	386852	387556	F	235	317(705)
tnfn1_pw060323p03q195	G12	C	1300015	R	FTN_1230	1299559	1300131	R	191	117(573)
tnfn1_pw060323p03q196	H12	C	150832	F	FTN_0137	150533	150937	F	135	300(405)

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_pw060323p03q101	A01	EXACT(0)	156	80	68	14	EXACT(0)	200	160	29
tnfn1_pw060323p03q102	B01	EXACT(0)	156	152	109	26	EXACT(0)	200	182	57
tnfn1_pw060323p03q103	C01	EXACT(0)	155	138	105	30	EXACT(0)	200	184	52
tnfn1_pw060323p03q104	D01	EXACT(0)	156	153	129	40	EXACT(0)	200	180	49
tnfn1_pw060323p03q105	E01	EXACT(0)	155	145	126	40	EXACT(0)	200	191	54
tnfn1_pw060323p03q106	F01	EXACT(0)	156	151	125	34	EXACT(0)	200	194	55
tnfn1_pw060323p03q107	G01	EXACT(0)	156	153	119	32	EXACT(0)	200	186	58
tnfn1_pw060323p03q108	H01	EXACT(0)	158	145	113	36	EXACT(0)	200	185	43
tnfn1_pw060323p03q109	A02	EXACT(0)	157	145	142	46	EXACT(0)	200	188	64
tnfn1_pw060323p03q110	B02	EXACT(0)	157	153	122	29	EXACT(0)	200	177	53
tnfn1_pw060323p03q111	C02	EXACT(0)	156	146	130	42	EXACT(0)	200	195	49
tnfn1_pw060323p03q112	D02	EXACT(0)	155	139	116	32	EXACT(0)	198	177	47
tnfn1_pw060323p03q113	E02	EXACT(0)	156	152	130	38	EXACT(0)	200	188	58
tnfn1_pw060323p03q114	F02	EXACT(0)	157	152	133	37	EXACT(0)	200	187	49
tnfn1_pw060323p03q115	G02	EXACT(0)	133	18	16	26	EXACT(0)	200	176	47
tnfn1_pw060323p03q116	H02	EXACT(0)	155	138	106	29	EXACT(0)	200	191	55
tnfn1_pw060323p03q117	A03	EXACT(0)	156	153	111	33	EXACT(0)	200	183	47
tnfn1_pw060323p03q118	B03	EXACT(0)	156	152	121	33	EXACT(0)	200	181	54
tnfn1_pw060323p03q119	C03	EXACT(0)	157	153	131	36	EXACT(0)	200	195	54
tnfn1_pw060323p03q120	D03	EXACT(0)	155	145	93	25	EXACT(0)	200	176	52
tnfn1_pw060323p03q121	E03	EXACT(0)	156	153	132	41	EXACT(0)	85	82	53
tnfn1_pw060323p03q122	F03	EXACT(0)	157	153	129	39	EXACT(0)	200	185	54
tnfn1_pw060323p03q123	G03	EXACT(0)	156	153	126	37	EXACT(0)	200	191	55
tnfn1_pw060323p03q124	H03	EXACT(0)	155	153	119	33	EXACT(0)	200	191	56
tnfn1_pw060323p03q125	A04	EXACT(0)	156	153	128	34	EXACT(0)	200	184	55
tnfn1_pw060323p03q126	B04	EXACT(0)	121	118	94	33	EXACT(0)	200	184	56
tnfn1_pw060323p03q127	C04	EXACT(0)	157	114	92	29	EXACT(0)	200	187	51
tnfn1_pw060323p03q128	D04	EXACT(0)	121	112	99	29	EXACT(0)	200	139	35
tnfn1_pw060323p03q129	E04	EXACT(0)	122	125	96	26	EXACT(0)	200	186	54
tnfn1_pw060323p03q130	F04	EXACT(0)	120	112	62	21	EXACT(0)	200	189	49
tnfn1_pw060323p03q131	G04	EXACT(0)	122	119	98	32	EXACT(0)	200	196	56
tnfn1_pw060323p03q132	H04	EXACT(0)	123	125	99	23	EXACT(0)	200	187	53
tnfn1_pw060323p03q133	A05	EXACT(0)	122	112	93	25	EXACT(0)	200	188	51
tnfn1_pw060323p03q134	B05	EXACT(0)	123	125	104	29	EXACT(0)	197	163	40
tnfn1_pw060323p03q135	C05	EXACT(0)	124	119	102	26	EXACT(0)	200	185	55
tnfn1_pw060323p03q136	D05	EXACT(0)	124	120	104	36	EXACT(0)	200	192	56
tnfn1_pw060323p03q137	E05	EXACT(0)	123	120	87	22	EXACT(0)	200	185	51
tnfn1_pw060323p03q138	F05	EXACT(0)	123	120	72	23	EXACT(0)	200	184	56
tnfn1_pw060323p03q139	G05	EXACT(0)	122	119	74	22	EXACT(0)	200	189	55
tnfn1_pw060323p03q140	H05	EXACT(0)	126	122	81	24	EXACT(0)	200	181	56
tnfn1_pw060323p03q141	A06	EXACT(0)	123	119	95	25	EXACT(0)	200	181	56
tnfn1_pw060323p03q142	B06	EXACT(0)	155	139	109	30	EXACT(0)	200	180	50
tnfn1_pw060323p03q143	C06	EXACT(0)	156	152	125	37	EXACT(0)	200	189	52
tnfn1_pw060323p03q144	D06	EXACT(0)	154	145	123	35	EXACT(0)	200	196	56
tnfn1_pw060323p03q145	E06	EXACT(0)	155	145	129	37	EXACT(0)	200	192	53
tnfn1_pw060323p03q146	F06	EXACT(0)	156	152	138	41	EXACT(0)	193	143	35
tnfn1_pw060323p03q147	G06	EXACT(0)	159	159	130	33	EXACT(0)	200	191	49
tnfn1_pw060323p03q148	H06	EXACT(0)	155	146	127	38	EXACT(0)	200	195	53

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_pw060323p03q149	A07	EXACT(0)	155	145	123	37	EXACT(0)	200	189	56
tnfn1_pw060323p03q150	B07	EXACT(0)	155	145	111	32	EXACT(0)	200	191	56
tnfn1_pw060323p03q151	C07	EXACT(0)	156	153	119	28	EXACT(0)	200	177	52
tnfn1_pw060323p03q152	D07	EXACT(0)	155	139	115	33	EXACT(0)	200	187	54
tnfn1_pw060323p03q153	E07	EXACT(0)	155	139	95	26	EXACT(0)	200	188	53
tnfn1_pw060323p03q154	F07	EXACT(0)	156	151	130	38	EXACT(0)	49	49	50
tnfn1_pw060323p03q155	G07	EXACT(0)	156	153	135	40	ESTIMATE(119)	81	64	18
tnfn1_pw060323p03q156	H07	EXACT(0)	156	153	123	37	EXACT(0)	200	194	56
tnfn1_pw060323p03q157	A08	EXACT(0)	157	145	130	39	ESTIMATE(73)	127	115	41
tnfn1_pw060323p03q158	B08	EXACT(0)	156	153	129	35	EXACT(0)	200	175	58
tnfn1_pw060323p03q159	C08	EXACT(0)	155	152	131	43	EXACT(0)	200	195	55
tnfn1_pw060323p03q160	D08	EXACT(0)	154	145	111	32	EXACT(0)	200	186	56
tnfn1_pw060323p03q161	E08	EXACT(0)	155	139	131	43	EXACT(0)	121	112	55
tnfn1_pw060323p03q162	F08	EXACT(0)	156	149	135	41	EXACT(0)	198	159	40
tnfn1_pw060323p03q163	G08	EXACT(0)	155	145	117	34	EXACT(0)	200	178	57
tnfn1_pw060323p03q164	H08	EXACT(0)	157	152	130	38	EXACT(0)	178	166	53
tnfn1_pw060323p03q165	A09	EXACT(0)	156	152	123	35	EXACT(0)	200	183	53
tnfn1_pw060323p03q166	B09	EXACT(0)	156	153	123	37	EXACT(0)	200	180	55
tnfn1_pw060323p03q167	C09	EXACT(0)	155	145	132	38	EXACT(0)	200	190	48
tnfn1_pw060323p03q168	D09	EXACT(0)	155	146	130	41	EXACT(0)	200	193	55
tnfn1_pw060323p03q169	E09	EXACT(0)	157	150	128	37	EXACT(0)	200	192	55
tnfn1_pw060323p03q170	F09	EXACT(0)	156	146	121	36	EXACT(0)	200	173	52
tnfn1_pw060323p03q171	G09	EXACT(0)	157	153	127	33	EXACT(0)	200	197	53
tnfn1_pw060323p03q172	H09	EXACT(0)	154	145	114	35	EXACT(0)	200	189	57
tnfn1_pw060323p03q173	A10	EXACT(0)	155	145	126	39	EXACT(0)	200	97	29
tnfn1_pw060323p03q174	B10	EXACT(0)	156	152	122	32	EXACT(0)	200	193	54
tnfn1_pw060323p03q175	C10	EXACT(0)	155	145	113	33	EXACT(0)	200	190	56
tnfn1_pw060323p03q176	D10	EXACT(0)	155	153	132	39	EXACT(0)	200	188	54
tnfn1_pw060323p03q177	E10	EXACT(0)	156	150	126	37	EXACT(0)	200	190	54
tnfn1_pw060323p03q178	F10	EXACT(0)	155	145	129	35	EXACT(0)	200	186	49
tnfn1_pw060323p03q179	G10	EXACT(0)	151	145	106	36	EXACT(0)	200	185	55
tnfn1_pw060323p03q180	H10	EXACT(0)	154	145	104	28	EXACT(0)	200	186	51
tnfn1_pw060323p03q181	A11	EXACT(0)	155	144	127	35	EXACT(0)	200	113	33
tnfn1_pw060323p03q182	B11	EXACT(0)	156	152	119	37	EXACT(0)	200	179	58
tnfn1_pw060323p03q183	C11	EXACT(0)	155	138	111	34	EXACT(0)	201	148	39
tnfn1_pw060323p03q184	D11	EXACT(0)	120	106	59	21	EXACT(0)	200	192	41
tnfn1_pw060323p03q185	E11	EXACT(0)	123	119	63	20	EXACT(0)	200	169	48
tnfn1_pw060323p03q186	F11	EXACT(0)	121	96	49	20	EXACT(0)	200	187	44
tnfn1_pw060323p03q187	G11	EXACT(0)	121	112	81	24	EXACT(0)	200	189	53
tnfn1_pw060323p03q188	H11	EXACT(0)	118	76	51	23	EXACT(0)	48	47	42
tnfn1_pw060323p03q189	A12	EXACT(0)	119	112	97	37	EXACT(0)	200	177	67
tnfn1_pw060323p03q190	B12	EXACT(0)	122	109	83	23	EXACT(0)	200	182	41
tnfn1_pw060323p03q191	C12	EXACT(0)	121	119	89	25	EXACT(0)	200	190	55
tnfn1_pw060323p03q192	D12	EXACT(0)	119	106	72	24	EXACT(0)	200	195	54
tnfn1_pw060323p03q193	E12	EXACT(0)	121	119	109	42	EXACT(0)	200	166	58
tnfn1_pw060323p03q194	F12	EXACT(0)	123	120	101	32	EXACT(0)	149	147	53
tnfn1_pw060323p03q195	G12	EXACT(0)	121	112	99	30	EXACT(0)	200	190	52
tnfn1_pw060323p03q196	H12	EXACT(0)	121	112	99	31	EXACT(0)	200	181	50