

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 14 (tnfn1_pw060328p06)**

Catalog No. NR-8048

For research use only. Not for human use.

Contributor:

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University of Washington, Seattle, Washington

Product Description:

A comprehensive 16508-member transposon mutant 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-8048 represents Plate 14 (tnfn1_pw060328p06) 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-8048 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 14 (tnfn1_pw060328p06), NR-8048.”

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_pw060328p06q101	A01	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q102	B01	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q103	C01	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q104	D01	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q105	E01	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p06q106	F01	T20	treA	trehalase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q107	G01	T20	recD	exodeoxyribonuclease V, alpha subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p06q108	H01	T20	recG	ATP-dependent DNA helicase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p06q109	A02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q110	B02	T20	-	transcriptional regulator, MarR family	signal transduction and regulation
tnfn1_pw060328p06q111	C02	T20	pepO	M13 family metalloproteinase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060328p06q112	D02	T20	-	YjeF-related protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q113	E02	T20	pyrC	dihydroorotase	nucleotides and nucleosides metabolism
tnfn1_pw060328p06q114	F02	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060328p06q115	G02	T20	iglC	intracellular growth locus protein C	unknown function - novel
tnfn1_pw060328p06q116	H02	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p06q117	A03	T20	-	membrane fusion protein	transport
tnfn1_pw060328p06q118	B03	T20	nadB	L-aspartate oxidase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p06q119	C03	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p06q120	D03	T20	truA	tRNA pseudouridine synthase A	translation, ribosomal structure and biogenesis
tnfn1_pw060328p06q121	E03	T20	-	tRNA-methyltransferase MiaB protein	translation, ribosomal structure and biogenesis
tnfn1_pw060328p06q122	F03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q123	G03	T20	-	-	-
tnfn1_pw060328p06q124	H03	T20	-	BNR/Asp-box repeat protein	putative enzymes
tnfn1_pw060328p06q125	A04	T20	slt	soluble lytic murein transglycosylase	cell wall / LPS / capsule
tnfn1_pw060328p06q126	B04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p06q127	C04	T20	ostA2	organic solvent tolerance protein OstA	cell wall / LPS / capsule
tnfn1_pw060328p06q128	D04	T20	lysA	diaminopimelate decarboxylase	amino acid metabolism - biosynthesis
tnfn1_pw060328p06q129	E04	T20	-	pseudogene: nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	pseudogene
tnfn1_pw060328p06q130	F04	T20	nadA	quinolinate synthetase A	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p06q131	G04	T20	glxK	glycerate kinase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q132	H04	T20	-	predicted Co/Zn/Cd cation transporter	transport
tnfn1_pw060328p06q133	A05	T20	-	rhodanese-related sulfurtransferase	other metabolism - biosynthesis
tnfn1_pw060328p06q134	B05	T20	maeA	NAD-dependent malic enzyme	energy metabolism
tnfn1_pw060328p06q135	C05	T20	-	ABC-type anion transport system, duplicated permease component	transport
tnfn1_pw060328p06q136	D05	T20	-	-	-
tnfn1_pw060328p06q137	E05	T20	-	Sua5/YciO/YrdC family protein	putative enzymes
tnfn1_pw060328p06q138	F05	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p06q139	G05	T20	gabD	succinate semialdehyde dehydrogenase (NAD(P)+ dependent)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q140	H05	T20	-	type I restriction-modification system, subunit M (methyltransferase)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p06q141	A06	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060328p06q142	B06	T20	-	histidine acid phosphatase	putative enzymes
tnfn1_pw060328p06q143	C06	T20	rpmG	50S ribosomal protein L33	translation, ribosomal structure and biogenesis
tnfn1_pw060328p06q144	D06	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p06q145	E06	T20	-	Mg-dependent DNase	DNA replication, recombination, modification and repair - degradation
tnfn1_pw060328p06q146	F06	T20	isftu2	isftu2	IS element
tnfn1_pw060328p06q147	G06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q148	H06	T20	-	hypothetical protein	hypothetical - novel

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p06q149	A07	T20	-	glycosyl transferase, family 2	cell wall / LPS / capsule
tnfn1_pw060328p06q150	B07	T20	hslV	ATP-dependent protease HslVU, peptidase subunit	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p06q151	C07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q152	D07	T20	rrmJ	23S rRNA methylase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p06q153	E07	T20	feoA	Fe2+ transport system protein A	transport
tnfn1_pw060328p06q154	F07	<KAN-2>	rpoC	DNA-directed RNA polymerase, beta' subunit/160 kD subunit	transcription
tnfn1_pw060328p06q155	G07	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q156	H07	T18	birA	biotin--acetyl-CoA-carboxylase ligase	fatty acids and lipids metabolism
tnfn1_pw060328p06q157	A08	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p06q158	B08	T18	rnhB	ribonuclease HII	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p06q159	C08	T18	-	-	-
tnfn1_pw060328p06q160	D08	T20	-	hypothetical protein fragment	Potentially coding: hypothetical - novel
tnfn1_pw060328p06q161	E08	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p06q162	F08	T18	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060328p06q163	G08	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q164	H08	T18	-	hypothetical protein	hypothetical - conserved
tnfn1_pw060328p06q165	A09	T18	-	apolipoprotein N-acyltransferase	cell wall / LPS / capsule
tnfn1_pw060328p06q166	B09	T20	-	long chain fatty acid CoA ligase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q167	C09	T20	-	DJ-1/Pfpl family protein	putative enzymes
tnfn1_pw060328p06q168	D09	T20	rbsK	ribokinase, pfkB family	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q169	E09	T20	xerC	site-specific recombinase	DNA replication, recombination, modification and repair
tnfn1_pw060328p06q170	F09	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060328p06q171	G09	T20	comL	competence lipoprotein ComL	transport
tnfn1_pw060328p06q172	H09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q173	A10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p06q174	B10	T20	ackA	propionate kinase 2 / acetate kinase A	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q175	C10	T20	-	metabolite:H+ symporter (MHS) family	transport
tnfn1_pw060328p06q176	D10	T20	hemK	modification methylase, HemK family	translation, ribosomal structure and biogenesis
tnfn1_pw060328p06q177	E10	T20	ampD	N-acetylmuramoyl-L-alanine amidase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p06q178	F10	T20	-	DeaA family protein	putative enzymes
tnfn1_pw060328p06q179	G10	T20	parC	DNA topoisomerase IV subunit A	DNA replication, recombination, modification and repair - replication
tnfn1_pw060328p06q180	H10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p06q181	A11	T20	cyoA	cytochrome bo terminal oxidase subunit II	energy metabolism
tnfn1_pw060328p06q182	B11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p06q183	C11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q184	D11	T20	-	acid phosphatase, HAD superfamily protein	putative enzymes
tnfn1_pw060328p06q185	E11	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p06q186	F11	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060328p06q187	G11	T20	thrB	homoserine kinase	amino acid metabolism - biosynthesis
tnfn1_pw060328p06q188	H11	T20	isfU2	isfU2	IS element
tnfn1_pw060328p06q189	A12	T20	hslV	ATP-dependent protease HslVU, peptidase subunit	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p06q190	B12	T20	-	-	-
tnfn1_pw060328p06q191	C12	T20	-	GDSL-like lipolytic enzyme	fatty acids and lipids metabolism
tnfn1_pw060328p06q192	D12	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060328p06q193	E12	T20	-	bifunctional NMN adenyltransferase/Nudix hydrolase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p06q194	F12	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p06q195	G12	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p06q196	H12	<KAN-2>	yhbY	RNA-binding protein	translation, ribosomal structure and biogenesis

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_pw060328p06q101	A01	C	1234086	R	FTN_1162	1233942	1234244	R	101	159(303)
tnfn1_pw060328p06q102	B01	C	1154612	R	FTN_1093	1154519	1155004	R	162	393(486)
tnfn1_pw060328p06q103	C01	C	947135	R	FTN_0890	946569	947333	F	255	567(765)
tnfn1_pw060328p06q104	D01	C	591398	R	FTN_0565	591250	591927	F	226	149(678)
tnfn1_pw060328p06q105	E01	C	470965	R	FTN_0466	470805	471404	F	200	161(600)
tnfn1_pw060328p06q106	F01	C	1406527	F	FTN_1328	1406119	1407570	F	484	409(1452)
tnfn1_pw060328p06q107	G01	C	1434609	R	FTN_1356	1433562	1435358	R	599	750(1797)
tnfn1_pw060328p06q108	H01	C	340384	F	FTN_0335	339525	341561	F	679	860(2037)
tnfn1_pw060328p06q109	A02	C	895646	F	FTN_0839	895194	896291	F	366	453(1098)
tnfn1_pw060328p06q110	B02	C	912221	F	FTN_0858	911999	912289	R	97	69(291)
tnfn1_pw060328p06q111	C02	C	1261205	F	FTN_1186	1259507	1261567	R	687	363(2061)
tnfn1_pw060328p06q112	D02	C	746135	F	FTN_0702	745266	746765	F	500	870(1500)
tnfn1_pw060328p06q113	E02	C	25426	F	FTN_0024	24880	26223	F	448	547(1344)
tnfn1_pw060328p06q114	F02	C	664108	R	FTN_0631	663750	664967	F	406	359(1218)
tnfn1_pw060328p06q115	G02	C	1397402	F	FTN_1322	1396992	1397618	R	209	217(627)
tnfn1_pw060328p06q116	H02	U	295348	F	FTN_0287	294845	295609	F	255	504(765)
tnfn1_pw060328p06q117	A03	C	1713110	R	FTN_1609	1712416	1713786	F	457	695(1371)
tnfn1_pw060328p06q118	B03	C	738418	F	FTN_0694	737909	739393	F	495	510(1485)
tnfn1_pw060328p06q119	C03	C	1647212	F	FTN_1549	1646760	1647938	F	393	453(1179)
tnfn1_pw060328p06q120	D03	U	956491	F	FTN_0899	956103	956876	R	258	386(774)
tnfn1_pw060328p06q121	E03	C	361046	R	FTN_0358	360958	362274	F	439	89(1317)
tnfn1_pw060328p06q122	F03	C	1903949	R	FTN_1775	1903791	1904228	R	146	280(438)
tnfn1_pw060328p06q123	G03	C	1412488	R	intergenic					
tnfn1_pw060328p06q124	H03	C	500876	R	FTN_0495	499997	501112	R	372	237(1116)
tnfn1_pw060328p06q125	A04	C	502240	R	FTN_0496	501311	503284	F	658	930(1974)
tnfn1_pw060328p06q126	B04	C	785840	R	FTN_0732	785679	785882	R	68	43(204)
tnfn1_pw060328p06q127	C04	C	758849	F	FTN_0713	757653	760250	R	866	1402(2598)
tnfn1_pw060328p06q128	D04	C	1627193	F	FTN_1530	1626798	1627979	R	394	787(1182)
tnfn1_pw060328p06q129	E04	C	650815	F	FTN_0619	650233	651024	F	264	583(792)
tnfn1_pw060328p06q130	F04	C	736490	R	FTN_0692	736009	737031	F	341	482(1023)
tnfn1_pw060328p06q131	G04	C	718743	R	FTN_0674	717906	719030	R	375	288(1125)
tnfn1_pw060328p06q132	H04	C	781000	F	FTN_0728	780666	781802	F	379	335(1137)
tnfn1_pw060328p06q133	A05	C	1470095	R	FTN_1392	1469819	1470334	R	172	240(516)
tnfn1_pw060328p06q134	B05	C	442297	F	FTN_0443	441678	443489	F	604	620(1812)
tnfn1_pw060328p06q135	C05	C	152904	F	FTN_0140	151997	153793	F	599	908(1797)
tnfn1_pw060328p06q136	D05	C	1520379	R	intergenic					
tnfn1_pw060328p06q137	E05	C	470339	R	FTN_0465	470141	470752	F	204	199(612)
tnfn1_pw060328p06q138	F05	C	1192037	R	FTN_1129	1191487	1192668	R	394	632(1182)
tnfn1_pw060328p06q139	G05	C	138181	R	FTN_0127	137693	139123	F	477	489(1431)
tnfn1_pw060328p06q140	H05	C	748269	F	FTN_0704	747676	749160	F	495	594(1485)
tnfn1_pw060328p06q141	A06	C	316993	R	FTN_0308	316669	318474	F	602	325(1806)
tnfn1_pw060328p06q142	B06	C	1009892	R	FTN_0954	1009684	1010889	F	402	209(1206)
tnfn1_pw060328p06q143	C06	C	338626	F	FTN_0332	338502	338654	R	51	29(153)
tnfn1_pw060328p06q144	D06	C	1384832	F	FTN_1312	1384422	1384913	F	164	411(492)
tnfn1_pw060328p06q145	E06	C	787611	R	FTN_0735	787338	788081	R	248	471(744)
tnfn1_pw060328p06q146	F06	C	672917	R	-	672404	673268	F	288.3	514(865)
tnfn1_pw060328p06q147	G06	C	121584	R	FTN_0109	120740	121717	R	326	134(978)
tnfn1_pw060328p06q148	H06	C	1390557	F	FTN_1318	1390391	1391161	F	257	167(771)

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_pw060328p06q149	A07	C	1284618	F	FTN_1214	1283962	1284918	R	319	301(957)
tnfn1_pw060328p06q150	B07	U	1053350	F	FTN_0995	1053437	1053985	F	183	-87
tnfn1_pw060328p06q151	C07	C	1594642	R	FTN_1500	1594295	1595017	F	241	348(723)
tnfn1_pw060328p06q152	D07	C	436311	F	FTN_0438	435998	436615	R	206	305(618)
tnfn1_pw060328p06q153	E07	C	1448993	F	FTN_1368	1448919	1449140	R	74	148(222)
tnfn1_pw060328p06q154	F07	C	1663699	R	FTN_1567	1663552	1667802	R	1417	4104(4251)
tnfn1_pw060328p06q155	G07	C	1893992	R	FTN_1764	1893875	1894084	R	70	93(210)
tnfn1_pw060328p06q156	H07	C	868840	R	FTN_0811	868439	869398	F	320	402(960)
tnfn1_pw060328p06q157	A08	C	186585	F	FTN_0170	185849	186718	R	290	134(870)
tnfn1_pw060328p06q158	B08	C	1364956	F	FTN_1293	1364580	1365134	R	185	179(555)
tnfn1_pw060328p06q159	C08	C	470118	F	intergenic					
tnfn1_pw060328p06q160	D08	C	464689	R	-	464617	464745	F	43	73(129)
tnfn1_pw060328p06q161	E08	C	107283	F	FTN_0096	107210	107899	F	230	74(690)
tnfn1_pw060328p06q162	F08	C	108637	F	FTN_0097	107902	109104	R	401	468(1203)
tnfn1_pw060328p06q163	G08	C	1387483	F	FTN_1315	1387186	1388613	F	476	298(1428)
tnfn1_pw060328p06q164	H08	C	663512	F	FTN_0630	663345	663686	F	114	168(342)
tnfn1_pw060328p06q165	A09	C	1126431	F	FTN_1067	1125843	1127330	F	496	589(1488)
tnfn1_pw060328p06q166	B09	C	1345152	R	FTN_1273	1344468	1346156	F	563	685(1689)
tnfn1_pw060328p06q167	C09	C	1040278	F	FTN_0985	1039817	1040416	F	200	462(600)
tnfn1_pw060328p06q168	D09	C	1896816	F	FTN_1767	1896135	1897052	R	306	237(918)
tnfn1_pw060328p06q169	E09	C	1610292	R	FTN_1513	1609860	1610735	F	292	433(876)
tnfn1_pw060328p06q170	F09	C	1160948	R	FTN_1099	1160507	1161379	F	291	442(873)
tnfn1_pw060328p06q171	G09	C	1335891	F	FTN_1263	1335078	1335899	R	274	9(822)
tnfn1_pw060328p06q172	H09	C	1888674	R	FTN_1759	1888512	1888901	R	130	228(390)
tnfn1_pw060328p06q173	A10	C	630936	R	FTN_0599	630525	631322	R	266	387(798)
tnfn1_pw060328p06q174	B10	C	134843	F	FTN_0125	134418	135569	F	384	426(1152)
tnfn1_pw060328p06q175	C10	C	929108	F	FTN_0875	928929	930158	F	410	180(1230)
tnfn1_pw060328p06q176	D10	C	1642058	R	FTN_1544	1641395	1642246	R	284	189(852)
tnfn1_pw060328p06q177	E10	C	1650379	R	FTN_1551	1649966	1650487	R	174	109(522)
tnfn1_pw060328p06q178	F10	U	1308442	F	FTN_1241	1308279	1308902	F	208	164(624)
tnfn1_pw060328p06q179	G10	C	498589	F	FTN_0492	496504	498729	F	742	2086(2226)
tnfn1_pw060328p06q180	H10	C	40614	R	FTN_0038	40369	40650	R	94	37(282)
tnfn1_pw060328p06q181	A11	C	216917	R	FTN_0195	216593	217492	F	300	325(900)
tnfn1_pw060328p06q182	B11	C	1472466	R	FTN_1395	1471775	1472776	R	334	311(1002)
tnfn1_pw060328p06q183	C11	C	1404375	F	FTN_1326	1403644	1404786	R	381	412(1143)
tnfn1_pw060328p06q184	D11	C	1120917	R	FTN_1061	1120390	1121136	R	249	220(747)
tnfn1_pw060328p06q185	E11	C	752557	R	FTN_0709	752359	753102	F	248	199(744)
tnfn1_pw060328p06q186	F11	C	1245203	F	FTN_1173	1244658	1245932	R	425	730(1275)
tnfn1_pw060328p06q187	G11	C	548185	F	FTN_0526	547735	548685	F	317	451(951)
tnfn1_pw060328p06q188	H11	C	482679	F	-	482310	483174	R	288.3	496(865)
tnfn1_pw060328p06q189	A12	C	1053524	F	FTN_0995	1053437	1053985	F	183	88(549)
tnfn1_pw060328p06q190	B12	C	946307	R	intergenic					
tnfn1_pw060328p06q191	C12	C	950339	F	FTN_0894	949934	950560	R	209	222(627)
tnfn1_pw060328p06q192	D12	C	105652	R	FTN_0094	105129	106073	R	315	422(945)
tnfn1_pw060328p06q193	E12	C	489353	R	FTN_0483	488789	489829	F	347	565(1041)
tnfn1_pw060328p06q194	F12	C	998725	R	FTN_0937	998435	999334	F	300	291(900)
tnfn1_pw060328p06q195	G12	C	427380	F	FTN_0429	427130	427630	F	167	251(501)
tnfn1_pw060328p06q196	H12	C	577492	F	FTN_0552	577430	577705	F	92	63(276)

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_pw060328p06q101	A01	EXACT(0)	122	112	96	35	EXACT(0)	200	188	52
tnfn1_pw060328p06q102	B01	EXACT(0)	123	119	95	34	EXACT(0)	200	191	53
tnfn1_pw060328p06q103	C01	EXACT(0)	122	119	68	18	EXACT(0)	200	192	37
tnfn1_pw060328p06q104	D01	EXACT(0)	121	119	84	24	EXACT(0)	200	182	52
tnfn1_pw060328p06q105	E01	EXACT(0)	157	146	129	41	EXACT(0)	200	179	55
tnfn1_pw060328p06q106	F01	EXACT(0)	156	146	127	33	EXACT(0)	200	187	56
tnfn1_pw060328p06q107	G01	EXACT(0)	158	143	72	19	EXACT(0)	200	192	55
tnfn1_pw060328p06q108	H01	EXACT(0)	156	151	129	40	EXACT(0)	200	194	57
tnfn1_pw060328p06q109	A02	EXACT(0)	157	153	124	24	EXACT(0)	191	86	14
tnfn1_pw060328p06q110	B02	EXACT(0)	155	145	114	31	EXACT(0)	200	182	59
tnfn1_pw060328p06q111	C02	EXACT(0)	155	138	99	27	EXACT(0)	200	180	50
tnfn1_pw060328p06q112	D02	EXACT(0)	155	152	121	32	EXACT(0)	199	183	41
tnfn1_pw060328p06q113	E02	EXACT(0)	156	146	127	41	EXACT(0)	200	193	52
tnfn1_pw060328p06q114	F02	EXACT(0)	156	152	131	40	EXACT(0)	192	175	50
tnfn1_pw060328p06q115	G02	EXACT(0)	160	153	137	37	EXACT(0)	200	196	53
tnfn1_pw060328p06q116	H02	EXACT(0)	156	145	140	49	EXACT(0)	200	194	57
tnfn1_pw060328p06q117	A03	EXACT(0)	157	151	129	41	EXACT(0)	200	155	47
tnfn1_pw060328p06q118	B03	EXACT(0)	155	145	129	39	EXACT(0)	200	193	55
tnfn1_pw060328p06q119	C03	EXACT(0)	155	145	123	40	EXACT(0)	183	108	35
tnfn1_pw060328p06q120	D03	EXACT(0)	153	145	121	43	EXACT(0)	200	192	59
tnfn1_pw060328p06q121	E03	EXACT(0)	156	150	114	24	EXACT(0)	200	183	52
tnfn1_pw060328p06q122	F03	EXACT(0)	155	145	117	36	EXACT(0)	200	178	58
tnfn1_pw060328p06q123	G03	EXACT(0)	154	145	126	42	EXACT(0)	200	190	58
tnfn1_pw060328p06q124	H03	EXACT(0)	156	146	124	39	EXACT(0)	200	191	55
tnfn1_pw060328p06q125	A04	EXACT(0)	157	153	130	37	EXACT(0)	200	188	60
tnfn1_pw060328p06q126	B04	EXACT(0)	155	150	105	32	EXACT(0)	200	191	57
tnfn1_pw060328p06q127	C04	EXACT(0)	155	152	125	39	EXACT(0)	200	192	58
tnfn1_pw060328p06q128	D04	EXACT(0)	156	146	127	44	EXACT(0)	200	191	58
tnfn1_pw060328p06q129	E04	EXACT(0)	156	153	126	33	EXACT(0)	200	188	55
tnfn1_pw060328p06q130	F04	EXACT(0)	156	153	116	31	EXACT(0)	200	194	57
tnfn1_pw060328p06q131	G04	EXACT(0)	157	153	137	41	EXACT(0)	128	83	30
tnfn1_pw060328p06q132	H04	EXACT(0)	155	145	129	45	EXACT(0)	200	140	36
tnfn1_pw060328p06q133	A05	EXACT(0)	155	145	120	39	EXACT(0)	200	194	54
tnfn1_pw060328p06q134	B05	EXACT(0)	156	145	122	31	EXACT(0)	200	194	57
tnfn1_pw060328p06q135	C05	EXACT(0)	155	152	125	40	EXACT(0)	200	182	55
tnfn1_pw060328p06q136	D05	EXACT(0)	156	153	117	34	EXACT(0)	200	192	58
tnfn1_pw060328p06q137	E05	EXACT(0)	152	145	110	40	EXACT(0)	200	184	58
tnfn1_pw060328p06q138	F05	EXACT(0)	155	145	123	39	EXACT(0)	200	176	38
tnfn1_pw060328p06q139	G05	EXACT(0)	156	153	132	41	EXACT(0)	200	198	55
tnfn1_pw060328p06q140	H05	EXACT(0)	156	151	132	40	EXACT(0)	200	194	54
tnfn1_pw060328p06q141	A06	EXACT(0)	156	152	121	31	EXACT(0)	200	192	58
tnfn1_pw060328p06q142	B06	EXACT(0)	158	146	125	33	EXACT(0)	199	92	33
tnfn1_pw060328p06q143	C06	EXACT(0)	156	153	122	31	EXACT(0)	200	188	51
tnfn1_pw060328p06q144	D06	EXACT(0)	155	145	112	24	EXACT(0)	200	179	56
tnfn1_pw060328p06q145	E06	EXACT(0)	157	152	54	15	EXACT(0)	200	187	46
tnfn1_pw060328p06q146	F06	EXACT(0)	157	151	122	36	EXACT(0)	200	193	55
tnfn1_pw060328p06q147	G06	EXACT(0)	154	145	126	42	EXACT(0)	200	192	58
tnfn1_pw060328p06q148	H06	EXACT(0)	156	144	112	37	EXACT(0)	200	116	30

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_pw060328p06q149	A07	EXACT(0)	156	142	96	25	EXACT(0)	184	169	48
tnfn1_pw060328p06q150	B07	NONE	0	0	0	22	ESTIMATE(166)	160	149	39
tnfn1_pw060328p06q151	C07	EXACT(0)	155	145	123	36	EXACT(0)	200	194	59
tnfn1_pw060328p06q152	D07	EXACT(0)	155	145	129	41	EXACT(0)	134	131	55
tnfn1_pw060328p06q153	E07	EXACT(0)	155	146	130	42	EXACT(0)	200	185	59
tnfn1_pw060328p06q154	F07	EXACT(0)	122	112	98	26	EXACT(0)	200	186	57
tnfn1_pw060328p06q155	G07	EXACT(0)	122	119	98	27	EXACT(0)	200	175	50
tnfn1_pw060328p06q156	H07	EXACT(0)	122	119	95	32	EXACT(0)	200	182	55
tnfn1_pw060328p06q157	A08	EXACT(0)	125	119	102	31	EXACT(0)	200	184	58
tnfn1_pw060328p06q158	B08	EXACT(0)	122	120	102	33	EXACT(0)	200	190	48
tnfn1_pw060328p06q159	C08	EXACT(0)	123	118	99	33	EXACT(0)	200	183	58
tnfn1_pw060328p06q160	D08	EXACT(0)	155	145	117	31	EXACT(0)	200	172	55
tnfn1_pw060328p06q161	E08	EXACT(0)	123	120	99	35	EXACT(0)	200	191	55
tnfn1_pw060328p06q162	F08	EXACT(0)	122	119	95	38	EXACT(0)	159	149	54
tnfn1_pw060328p06q163	G08	EXACT(0)	122	112	93	30	EXACT(0)	200	185	41
tnfn1_pw060328p06q164	H08	EXACT(0)	124	120	107	29	EXACT(0)	163	156	53
tnfn1_pw060328p06q165	A09	EXACT(0)	123	120	92	24	EXACT(0)	200	190	57
tnfn1_pw060328p06q166	B09	EXACT(0)	157	152	123	28	EXACT(0)	200	182	58
tnfn1_pw060328p06q167	C09	EXACT(0)	155	152	125	37	EXACT(0)	200	183	48
tnfn1_pw060328p06q168	D09	EXACT(0)	155	145	123	37	EXACT(0)	200	187	56
tnfn1_pw060328p06q169	E09	EXACT(0)	155	146	127	41	EXACT(0)	200	194	52
tnfn1_pw060328p06q170	F09	EXACT(0)	157	153	125	37	EXACT(0)	200	185	52
tnfn1_pw060328p06q171	G09	EXACT(0)	156	152	131	40	EXACT(0)	200	177	58
tnfn1_pw060328p06q172	H09	EXACT(0)	156	146	133	42	EXACT(0)	200	190	45
tnfn1_pw060328p06q173	A10	EXACT(0)	154	153	121	37	EXACT(0)	199	146	45
tnfn1_pw060328p06q174	B10	EXACT(0)	156	145	131	35	EXACT(0)	200	196	47
tnfn1_pw060328p06q175	C10	EXACT(0)	156	151	121	33	EXACT(0)	200	190	58
tnfn1_pw060328p06q176	D10	EXACT(0)	156	145	128	38	EXACT(0)	197	190	49
tnfn1_pw060328p06q177	E10	EXACT(0)	156	151	126	39	EXACT(0)	200	187	48
tnfn1_pw060328p06q178	F10	EXACT(0)	155	139	115	40	EXACT(0)	200	189	49
tnfn1_pw060328p06q179	G10	EXACT(0)	156	152	125	41	EXACT(0)	200	189	58
tnfn1_pw060328p06q180	H10	EXACT(0)	157	139	96	24	EXACT(0)	200	174	52
tnfn1_pw060328p06q181	A11	EXACT(0)	156	153	126	37	EXACT(0)	200	193	59
tnfn1_pw060328p06q182	B11	EXACT(0)	157	152	130	38	EXACT(0)	200	156	43
tnfn1_pw060328p06q183	C11	EXACT(0)	157	152	127	35	EXACT(0)	200	189	52
tnfn1_pw060328p06q184	D11	EXACT(0)	156	152	118	34	EXACT(0)	200	193	55
tnfn1_pw060328p06q185	E11	EXACT(0)	152	145	101	31	EXACT(0)	200	182	58
tnfn1_pw060328p06q186	F11	EXACT(0)	155	145	126	37	EXACT(0)	200	192	53
tnfn1_pw060328p06q187	G11	EXACT(0)	156	139	118	33	EXACT(0)	200	195	45
tnfn1_pw060328p06q188	H11	EXACT(0)	155	146	105	32	EXACT(0)	200	193	54
tnfn1_pw060328p06q189	A12	EXACT(0)	158	152	129	39	EXACT(0)	160	149	53
tnfn1_pw060328p06q190	B12	EXACT(0)	156	145	106	30	EXACT(0)	200	184	56
tnfn1_pw060328p06q191	C12	EXACT(0)	156	151	135	36	EXACT(0)	200	189	55
tnfn1_pw060328p06q192	D12	EXACT(0)	155	144	116	33	EXACT(0)	200	191	54
tnfn1_pw060328p06q193	E12	EXACT(0)	155	152	121	37	EXACT(0)	200	183	57
tnfn1_pw060328p06q194	F12	EXACT(0)	155	145	88	28	EXACT(0)	200	180	53
tnfn1_pw060328p06q195	G12	EXACT(0)	124	125	104	24	EXACT(0)	192	176	49
tnfn1_pw060328p06q196	H12	EXACT(0)	118	76	53	23	EXACT(0)	200	191	47