

***Francisella tularensis* subsp. *novicida*,
“Two-Allele” Transposon Mutant Library,
Plate 16 (tnfn1_pw060328p08)**

Catalog No. NR-8050

For research use only. Not for human use.

Contributor:

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University of Washington, Seattle, Washington, USA

Manufacturer:

BEI Resources

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-8050 represents Plate 16 (tnfn1_pw060328p08) 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_pw060328p08q123 (Well G03) was not available due to quality issues at the time of release of Plate 16, 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 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 increased risk of cross-contamination between adjacent wells. Individual mutants should be purified (e.g. single colony isolation and purification using good microbiological practices) and verified prior to use. BEI Resources cannot confirm or validate any clone not identified on the plate information table.

Packaging/Storage:

NR-8050 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 to 48 hours.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through BEI Resources, NIAID, NIH: *Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 16 (tnfn1_pw060328p08), NR-8050.”

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, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

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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_pw060328p08q101	A01	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q102	B01	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q103	C01	<KAN-2>	mgIB	macrophage growth locus, subunit B	unknown function - conserved
tnfn1_pw060328p08q104	D01	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q105	E01	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q106	F01	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q107	G01	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q108	H01	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q109	A02	<KAN-2>	-	-	-
tnfn1_pw060328p08q110	B02	<KAN-2>	upp	uracil phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060328p08q111	C02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q112	D02	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060328p08q113	E02	T20	-	hypothetical protein	Potentially coding: hypothetical - novel
tnfn1_pw060328p08q114	F02	T20	htpG	chaperone Hsp90, heat shock protein HtpG	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060328p08q115	G02	T20	manB	phosphomannomutase	carbohydrate metabolism - biosynthesis
tnfn1_pw060328p08q116	H02	T20	-	tRNA-dihydrouridine synthase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p08q117	A03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q118	B03	T20	-	acid phosphatase, HAD superfamily protein	putative enzymes
tnfn1_pw060328p08q119	C03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q120	D03	T20	-	tRNA-dihydrouridine synthase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p08q121	E03	T20	-	sugar:cation symporter family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060328p08q122	F03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q123	G03	T20	aceF	pyruvate dehydrogenase complex, E2 component, dihydroipoamide acyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p08q124	H03	T20	radA	DNA repair protein radA	DNA replication, recombination, modification and repair - repair
tnfn1_pw060328p08q125	A04	T20	-	rhodanese-related sulfurtransferase	other metabolism - biosynthesis
tnfn1_pw060328p08q126	B04	T20	-	phage integrase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p08q127	C04	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060328p08q128	D04	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p08q129	E04	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p08q130	F04	T20	-	NAD/FAD-binding protein	putative enzymes
tnfn1_pw060328p08q131	G04	T20	murl	glutamate racemase	cell wall / LPS / capsule
tnfn1_pw060328p08q132	H04	T20	-	regulatory protein, AlpA family	signal transduction and regulation
tnfn1_pw060328p08q133	A05	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060328p08q134	B05	T20	-	sulfate permease family protein	transport
tnfn1_pw060328p08q135	C05	T20	galE	UDP-glucose 4-epimerase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p08q136	D05	T20	-	L-lactate dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p08q137	E05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q138	F05	T20	-	ArsB arsenite/antimonite exporter	transport
tnfn1_pw060328p08q139	G05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q140	H05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q141	A06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q142	B06	T20	isftu1	isftu1	IS element
tnfn1_pw060328p08q143	C06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q144	D06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q145	E06	T20	-	D-alanyl-D-alanine carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060328p08q146	F06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q147	G06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q148	H06	T20	-	conserved hypothetical protein	hypothetical - conserved

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p08q149	A07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q150	B07	T20	sun	tRNA and rRNA cytosine-C5-methylases, sun protein	translation, ribosomal structure and biogenesis
tnfn1_pw060328p08q151	C07	<KAN-2>	-	rhodanese-like family protein	putative enzymes
tnfn1_pw060328p08q152	D07	<KAN-2>	cyoC	cytochrome bo terminal oxidase subunit III	energy metabolism
tnfn1_pw060328p08q153	E07	<KAN-2>	potG	ATP-binding cassette putrescine uptake system, ATP-binding protein	transport
tnfn1_pw060328p08q154	F07	<KAN-2>			
tnfn1_pw060328p08q155	G07	T20	pal	peptidoglycan-associated lipoprotein, OmpA family	transport - drugs / antibacterial compounds
tnfn1_pw060328p08q156	H07	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p08q157	A08	<KAN-2>	-	abortive infection bacteriophage resistance protein	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060328p08q158	B08	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q159	C08	<KAN-2>	-	glutamine amidotransferase, class I	other metabolism - biosynthesis
tnfn1_pw060328p08q160	D08	T20	-	tRNA-dihydrouridine synthase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p08q161	E08	T20	isftu1	isftu1	IS element
tnfn1_pw060328p08q162	F08	T20	hdc	pyridoxal-dependent decarboxylase	putative enzymes
tnfn1_pw060328p08q163	G08	T20	-	oxidoreductase	putative enzymes
tnfn1_pw060328p08q164	H08	T20	bioD	dethiobiotin synthetase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p08q165	A09	T20	cls	cardiolipin synthetase	fatty acids and lipids metabolism
tnfn1_pw060328p08q166	B09	T20			
tnfn1_pw060328p08q167	C09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p08q168	D09	T20	-	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	cell wall / LPS / capsule
tnfn1_pw060328p08q169	E09	T20	purT	phosphoribosylglycinamide formyltransferase 2	nucleotides and nucleosides metabolism
tnfn1_pw060328p08q170	F09	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q171	G09	T20	gloA	lactoylglutathione lyase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p08q172	H09	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p08q173	A10	T20	araJ	conserved inner membrane protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q174	B10	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060328p08q175	C10	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p08q176	D10	T20	isftu2	isftu2	IS element
tnfn1_pw060328p08q177	E10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p08q178	F10	T20	-	cardiolipin synthase	fatty acids and lipids metabolism
tnfn1_pw060328p08q179	G10	T20	-	adenine specific DNA methylase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p08q180	H10	T20	ggt	gamma-glutamyltranspeptidase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p08q181	A11	T20	ericC	Cl:-H+ antiporter	transport
tnfn1_pw060328p08q182	B11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p08q183	C11	T20	naoX	uncharacterized NAD(FAD)-dependent dehydrogenase	putative enzymes
tnfn1_pw060328p08q184	D11	T20	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060328p08q185	E11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p08q186	F11	T20	-	protein of unknown function with radical SAM domain	unknown function - conserved
tnfn1_pw060328p08q187	G11	T20	dxs	1-deoxyxylulose-5-phosphate synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p08q188	H11	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p08q189	A12	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p08q190	B12	T20	trmU	tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p08q191	C12	T20	-	ATP binding protein	putative enzymes
tnfn1_pw060328p08q192	D12	T20	-	allophanate hydrolase subunit 1	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p08q193	E12	T20	-	polar amino acid uptake transporter	transport - amino-acid
tnfn1_pw060328p08q194	F12	T20	uspA	universal stress protein	signal transduction and regulation
tnfn1_pw060328p08q195	G12	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p08q196	H12	T20	-	short chain dehydrogenase	putative enzymes

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_pw060328p08q101	A01	C	64559	F	FTN_0054	64387	64764	F	126	173(378)
tnfn1_pw060328p08q102	B01	C	1183184	R	FTN_1118	1182986	1183318	R	111	135(333)
tnfn1_pw060328p08q103	C01	C	1362942	F	FTN_1291	1362901	1363305	F	135	42(405)
tnfn1_pw060328p08q104	D01	C	61470	F	FTN_0051	61102	61707	F	202	369(606)
tnfn1_pw060328p08q105	E01	C	1464503	F	FTN_1385	1464367	1464765	F	133	137(399)
tnfn1_pw060328p08q106	F01	C	151818	R	FTN_0139	151697	151867	R	57	50(171)
tnfn1_pw060328p08q107	G01	C	1903663	R	FTN_1774	1903381	1903719	R	113	57(339)
tnfn1_pw060328p08q108	H01	C	1415013	F	FTN_1334	1414639	1415139	F	167	375(501)
tnfn1_pw060328p08q109	A02	C	286842	R	intergenic					
tnfn1_pw060328p08q110	B02	C	662105	F	FTN_0628	661707	662333	F	209	399(627)
tnfn1_pw060328p08q111	C02	C	1340504	F	FTN_1269	1340467	1341162	F	232	38(696)
tnfn1_pw060328p08q112	D02	C	1089004	F	FTN_1032	1087961	1089430	R	490	427(1470)
tnfn1_pw060328p08q113	E02	C	370969	F	-	370947	371300	F	118	23(354)
tnfn1_pw060328p08q114	F02	C	273406	R	FTN_0266	272930	274813	F	628	477(1884)
tnfn1_pw060328p08q115	G02	C	1495267	F	FTN_1417	1494300	1495781	R	494	515(1482)
tnfn1_pw060328p08q116	H02	U	1043037	R	FTN_0987	1042432	1043415	R	328	379(984)
tnfn1_pw060328p08q117	A03	C	1805213	R	FTN_1688	1804888	1805292	R	135	80(405)
tnfn1_pw060328p08q118	B03	C	1654692	F	FTN_1556	1654346	1654927	R	194	236(582)
tnfn1_pw060328p08q119	C03	C	1581466	R	FTN_1489	1581021	1581764	R	248	299(744)
tnfn1_pw060328p08q120	D03	C	1043037	R	FTN_0987	1042432	1043415	R	328	379(984)
tnfn1_pw060328p08q121	E03	C	944112	F	FTN_0886	942996	944261	F	422	1117(1266)
tnfn1_pw060328p08q122	F03	C	1612286	F	FTN_1516	1612172	1612747	F	192	115(576)
tnfn1_pw060328p08q124	H03	C	399064	R	FTN_0399	398092	399459	R	456	396(1368)
tnfn1_pw060328p08q125	A04	C	131361	R	FTN_0120	131219	131638	F	140	143(420)
tnfn1_pw060328p08q126	B04	C	370037	R	FTN_0367	369322	370554	F	411	716(1233)
tnfn1_pw060328p08q127	C04	C	1811028	F	FTN_1693	1809633	1811171	R	513	144(1539)
tnfn1_pw060328p08q128	D04	C	1254708	F	FTN_1181	1253887	1254966	R	360	259(1080)
tnfn1_pw060328p08q129	E04	C	1092787	F	FTN_1037	1091935	1093191	F	419	853(1257)
tnfn1_pw060328p08q130	F04	C	1542782	R	FTN_1454	1542637	1543887	F	417	146(1251)
tnfn1_pw060328p08q131	G04	C	1246397	F	FTN_1174	1246026	1246820	R	265	424(795)
tnfn1_pw060328p08q132	H04	C	374542	R	FTN_0372	374491	374706	F	72	52(216)
tnfn1_pw060328p08q133	A05	C	618759	R	FTN_0589	617747	619189	R	481	431(1443)
tnfn1_pw060328p08q134	B05	C	675474	R	FTN_0638	674546	676087	F	514	929(1542)
tnfn1_pw060328p08q135	C05	C	1290641	F	FTN_1219	1289806	1290822	R	339	182(1017)
tnfn1_pw060328p08q136	D05	C	239460	F	FTN_0217	238429	239583	R	385	124(1155)
tnfn1_pw060328p08q137	E05	C	1641091	R	FTN_1543	1640934	1641398	F	155	158(465)
tnfn1_pw060328p08q138	F05	C	858168	R	FTN_0800	857562	858587	R	342	420(1026)
tnfn1_pw060328p08q139	G05	C	1219898	F	FTN_1153	1219531	1220226	R	232	329(696)
tnfn1_pw060328p08q140	H05	C	1612381	F	FTN_1516	1612172	1612747	F	192	210(576)
tnfn1_pw060328p08q141	A06	C	892841	R	FTN_0835	892311	893027	R	239	187(717)
tnfn1_pw060328p08q142	B06	C	1722249	F	-	1721619	1722539	F	307	631(921)
tnfn1_pw060328p08q143	C06	C	786114	R	FTN_0733	785970	786260	R	97	147(291)
tnfn1_pw060328p08q144	D06	C	395842	F	FTN_0396	395576	396226	F	217	267(651)
tnfn1_pw060328p08q145	E06	C	963616	F	FTN_0907	962942	964273	F	444	675(1332)
tnfn1_pw060328p08q146	F06	C	1022601	R	FTN_0966	1021590	1022996	R	469	396(1407)
tnfn1_pw060328p08q147	G06	C	1199569	F	FTN_1134	1199448	1199690	R	81	122(243)
tnfn1_pw060328p08q148	H06	C	574577	R	FTN_0548	574443	574754	R	104	178(312)

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_pw060328p08q149	A07	C	437213	F	FTN_0439	436773	437237	F	155	441(465)
tnfn1_pw060328p08q150	B07	C	1426098	F	FTN_1347	1425430	1426707	F	426	669(1278)
tnfn1_pw060328p08q151	C07	C	1171423	F	FTN_1109	1171158	1171904	F	249	266(747)
tnfn1_pw060328p08q152	D07	C	219717	F	FTN_0197	219561	220160	F	200	157(600)
tnfn1_pw060328p08q153	E07	C	792812	R	FTN_0739	792274	793392	R	373	581(1119)
tnfn1_pw060328p08q154	F07	C	417227	F	intergenic					
tnfn1_pw060328p08q155	G07	C	360572	F	FTN_0357	360228	360848	F	207	345(621)
tnfn1_pw060328p08q156	H07	C	345618	R	FTN_0340	345436	345768	R	111	151(333)
tnfn1_pw060328p08q157	A08	C	749254	F	FTN_0705	749168	750076	F	303	87(909)
tnfn1_pw060328p08q158	B08	C	1478537	R	FTN_1399	1477955	1478668	R	238	132(714)
tnfn1_pw060328p08q159	C08	C	434157	F	FTN_0435	433757	434461	F	235	401(705)
tnfn1_pw060328p08q160	D08	C	630439	R	FTN_0598	629508	630488	R	327	50(981)
tnfn1_pw060328p08q161	E08	C	1721876	F	-	1721619	1722539	F	307	258(921)
tnfn1_pw060328p08q162	F08	C	1077775	R	FTN_1019	1077269	1078402	F	378	507(1134)
tnfn1_pw060328p08q163	G08	C	1108384	R	FTN_1049	1107723	1108898	F	392	662(1176)
tnfn1_pw060328p08q164	H08	C	869805	F	FTN_0812	869347	870021	R	225	217(675)
tnfn1_pw060328p08q165	A09	C	932004	R	FTN_0877	931734	933161	F	476	271(1428)
tnfn1_pw060328p08q166	B09	C	1604088	R	intergenic					
tnfn1_pw060328p08q167	C09	C	608440	R	FTN_0579	607388	608659	R	424	220(1272)
tnfn1_pw060328p08q168	D09	C	573410	F	FTN_0546	572304	574064	R	587	655(1761)
tnfn1_pw060328p08q169	E09	C	1876011	R	FTN_1745	1875320	1876477	F	386	692(1158)
tnfn1_pw060328p08q170	F09	C	289364	F	FTN_0282	288913	289806	F	298	452(894)
tnfn1_pw060328p08q171	G09	C	1300313	R	FTN_1231	1300134	1300514	R	127	202(381)
tnfn1_pw060328p08q172	H09	C	1636402	R	FTN_1537	1635781	1636650	R	290	249(870)
tnfn1_pw060328p08q173	A10	C	613051	F	FTN_0584	612820	613983	F	388	232(1164)
tnfn1_pw060328p08q174	B10	C	1343431	F	FTN_1272	1342876	1344357	F	494	556(1482)
tnfn1_pw060328p08q175	C10	C	112693	R	FTN_0102	112565	113716	F	384	129(1152)
tnfn1_pw060328p08q176	D10	C	246139	R	-	245715	246181	R	155.6	43(467)
tnfn1_pw060328p08q177	E10	C	1140292	F	FTN_1077	1140193	1140936	F	248	100(744)
tnfn1_pw060328p08q178	F10	C	930501	R	FTN_0876	930215	931639	F	475	287(1425)
tnfn1_pw060328p08q179	G10	C	1584071	R	FTN_1491	1582630	1584609	R	660	539(1980)
tnfn1_pw060328p08q180	H10	C	1231015	R	FTN_1159	1229840	1231642	R	601	628(1803)
tnfn1_pw060328p08q181	A11	C	1863807	R	FTN_1737	1863156	1864571	F	472	652(1416)
tnfn1_pw060328p08q182	B11	C	1769887	F	FTN_1656	1769013	1770077	R	355	191(1065)
tnfn1_pw060328p08q183	C11	C	1469109	F	FTN_1391	1468103	1469791	R	563	683(1689)
tnfn1_pw060328p08q184	D11	C	1861296	R	FTN_1733	1861017	1861637	R	207	342(621)
tnfn1_pw060328p08q185	E11	C	1295055	F	FTN_1224	1294574	1295269	R	232	215(696)
tnfn1_pw060328p08q186	F11	C	819573	R	FTN_0761	818940	820022	F	361	634(1083)
tnfn1_pw060328p08q187	G11	C	950951	R	FTN_0896	950936	952780	R	615	1830(1845)
tnfn1_pw060328p08q188	H11	C	1159894	R	FTN_1098	1159530	1160402	R	291	509(873)
tnfn1_pw060328p08q189	A12	C	1767537	F	FTN_1654	1766782	1768083	F	434	756(1302)
tnfn1_pw060328p08q190	B12	C	119822	R	FTN_0108	119640	120716	F	359	183(1077)
tnfn1_pw060328p08q191	C12	C	1182596	R	FTN_1117	1181802	1182965	R	388	370(1164)
tnfn1_pw060328p08q192	D12	C	99119	F	FTN_0087	98862	99476	F	205	258(615)
tnfn1_pw060328p08q193	E12	C	209239	R	FTN_0191	208872	209609	R	246	371(738)
tnfn1_pw060328p08q194	F12	C	97064	F	FTN_0085	96649	97482	F	278	416(834)
tnfn1_pw060328p08q195	G12	C	1539954	R	FTN_1450	1539655	1540053	R	133	100(399)
tnfn1_pw060328p08q196	H12	C	1547132	F	FTN_1459	1546995	1547735	F	247	138(741)

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_pw060328p08q101	A01	EXACT(0)	120	106	92	25	EXACT(0)	200	198	52
tnfn1_pw060328p08q102	B01	EXACT(0)	121	119	109	47	EXACT(0)	199	154	48
tnfn1_pw060328p08q103	C01	EXACT(0)	120	112	96	30	EXACT(0)	194	184	51
tnfn1_pw060328p08q104	D01	EXACT(0)	122	109	91	23	EXACT(0)	200	168	46
tnfn1_pw060328p08q105	E01	EXACT(0)	123	125	95	21	EXACT(0)	200	193	55
tnfn1_pw060328p08q106	F01	EXACT(0)	121	118	91	22	EXACT(0)	200	187	53
tnfn1_pw060328p08q107	G01	EXACT(0)	120	112	102	42	EXACT(0)	200	191	52
tnfn1_pw060328p08q108	H01	EXACT(0)	124	118	102	27	EXACT(0)	200	177	42
tnfn1_pw060328p08q109	A02	EXACT(0)	121	120	64	26	EXACT(0)	200	185	46
tnfn1_pw060328p08q110	B02	EXACT(0)	120	120	99	27	EXACT(0)	200	194	50
tnfn1_pw060328p08q111	C02	EXACT(0)	155	138	100	23	EXACT(0)	199	173	40
tnfn1_pw060328p08q112	D02	EXACT(0)	155	151	124	38	EXACT(0)	200	187	55
tnfn1_pw060328p08q113	E02	EXACT(0)	156	153	126	41	EXACT(0)	200	188	52
tnfn1_pw060328p08q114	F02	EXACT(0)	157	151	126	29	EXACT(0)	200	193	56
tnfn1_pw060328p08q115	G02	EXACT(0)	156	152	124	32	EXACT(0)	200	190	58
tnfn1_pw060328p08q116	H02	EXACT(0)	154	146	130	30	EXACT(0)	200	194	41
tnfn1_pw060328p08q117	A03	EXACT(0)	156	146	127	42	EXACT(0)	200	191	54
tnfn1_pw060328p08q118	B03	EXACT(0)	156	153	122	35	EXACT(0)	200	191	54
tnfn1_pw060328p08q119	C03	EXACT(0)	156	151	118	30	EXACT(0)	200	183	51
tnfn1_pw060328p08q120	D03	EXACT(0)	156	153	132	40	EXACT(0)	200	194	56
tnfn1_pw060328p08q121	E03	EXACT(0)	156	118	112	35	EXACT(0)	200	184	56
tnfn1_pw060328p08q122	F03	EXACT(0)	156	153	123	39	EXACT(0)	200	185	57
tnfn1_pw060328p08q124	H03	EXACT(0)	157	152	126	34	EXACT(0)	200	194	46
tnfn1_pw060328p08q125	A04	EXACT(0)	154	145	109	31	EXACT(0)	200	181	58
tnfn1_pw060328p08q126	B04	EXACT(0)	157	151	119	32	EXACT(0)	200	190	56
tnfn1_pw060328p08q127	C04	EXACT(0)	153	145	90	19	EXACT(0)	200	180	52
tnfn1_pw060328p08q128	D04	EXACT(0)	157	152	133	37	EXACT(0)	194	156	42
tnfn1_pw060328p08q129	E04	EXACT(0)	155	146	121	38	EXACT(0)	200	173	47
tnfn1_pw060328p08q130	F04	EXACT(0)	156	139	124	45	EXACT(0)	198	127	39
tnfn1_pw060328p08q131	G04	EXACT(0)	155	153	129	41	EXACT(0)	200	189	53
tnfn1_pw060328p08q132	H04	EXACT(0)	159	142	101	20	EXACT(0)	200	181	49
tnfn1_pw060328p08q133	A05	EXACT(0)	158	146	122	37	EXACT(0)	200	192	52
tnfn1_pw060328p08q134	B05	EXACT(0)	158	152	128	38	EXACT(0)	200	192	59
tnfn1_pw060328p08q135	C05	EXACT(0)	156	152	128	42	EXACT(0)	149	140	51
tnfn1_pw060328p08q136	D05	EXACT(0)	157	151	126	38	EXACT(0)	200	190	51
tnfn1_pw060328p08q137	E05	EXACT(0)	157	32	23	16	EXACT(0)	200	192	42
tnfn1_pw060328p08q138	F05	EXACT(0)	155	145	123	40	EXACT(0)	200	183	54
tnfn1_pw060328p08q139	G05	EXACT(0)	158	151	137	29	EXACT(0)	200	177	42
tnfn1_pw060328p08q140	H05	EXACT(0)	156	151	124	37	EXACT(0)	198	180	51
tnfn1_pw060328p08q141	A06	EXACT(0)	159	151	120	27	EXACT(0)	200	184	58
tnfn1_pw060328p08q142	B06	EXACT(0)	157	153	131	30	EXACT(0)	156	145	54
tnfn1_pw060328p08q143	C06	EXACT(0)	155	151	127	38	EXACT(0)	200	178	59
tnfn1_pw060328p08q144	D06	EXACT(0)	156	152	136	41	EXACT(0)	199	173	45
tnfn1_pw060328p08q145	E06	EXACT(0)	158	151	127	32	EXACT(0)	200	191	58
tnfn1_pw060328p08q146	F06	EXACT(0)	155	145	120	39	EXACT(0)	200	189	59
tnfn1_pw060328p08q147	G06	EXACT(0)	155	152	121	29	EXACT(0)	200	179	56
tnfn1_pw060328p08q148	H06	EXACT(0)	156	153	135	42	EXACT(0)	200	187	48

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_pw060328p08q149	A07	EXACT(0)	155	146	124	38	EXACT(0)	200	189	50
tnfn1_pw060328p08q150	B07	EXACT(0)	156	151	121	36	EXACT(0)	200	189	46
tnfn1_pw060328p08q151	C07	EXACT(0)	122	125	96	27	EXACT(0)	200	194	53
tnfn1_pw060328p08q152	D07	EXACT(0)	121	118	94	31	EXACT(0)	200	191	51
tnfn1_pw060328p08q153	E07	EXACT(0)	122	118	90	24	EXACT(0)	200	192	51
tnfn1_pw060328p08q154	F07	EXACT(0)	121	112	93	29	EXACT(0)	200	187	51
tnfn1_pw060328p08q155	G07	EXACT(0)	155	152	125	35	EXACT(0)	199	156	48
tnfn1_pw060328p08q156	H07	EXACT(0)	121	112	81	24	EXACT(0)	200	190	57
tnfn1_pw060328p08q157	A08	EXACT(0)	121	112	101	33	EXACT(0)	200	185	48
tnfn1_pw060328p08q158	B08	EXACT(0)	124	112	94	26	EXACT(0)	200	185	51
tnfn1_pw060328p08q159	C08	EXACT(0)	121	118	97	36	EXACT(0)	200	193	51
tnfn1_pw060328p08q160	D08	EXACT(0)	155	145	129	39	EXACT(0)	200	194	55
tnfn1_pw060328p08q161	E08	EXACT(0)	153	152	112	36	EXACT(0)	200	184	57
tnfn1_pw060328p08q162	F08	EXACT(0)	155	145	123	38	EXACT(0)	200	179	54
tnfn1_pw060328p08q163	G08	EXACT(0)	156	153	132	41	EXACT(0)	200	184	59
tnfn1_pw060328p08q164	H08	EXACT(0)	156	152	134	38	EXACT(0)	200	150	38
tnfn1_pw060328p08q165	A09	EXACT(0)	154	145	114	35	EXACT(0)	200	183	57
tnfn1_pw060328p08q166	B09	EXACT(0)	156	152	122	37	EXACT(0)	200	180	57
tnfn1_pw060328p08q167	C09	EXACT(0)	156	145	125	36	EXACT(0)	200	185	52
tnfn1_pw060328p08q168	D09	EXACT(0)	156	152	131	41	EXACT(0)	200	193	50
tnfn1_pw060328p08q169	E09	EXACT(0)	155	145	123	40	EXACT(0)	200	194	55
tnfn1_pw060328p08q170	F09	EXACT(0)	155	145	123	38	EXACT(0)	200	188	56
tnfn1_pw060328p08q171	G09	EXACT(0)	156	150	120	37	EXACT(0)	200	189	49
tnfn1_pw060328p08q172	H09	EXACT(0)	153	152	118	40	EXACT(0)	200	125	39
tnfn1_pw060328p08q173	A10	EXACT(0)	154	145	93	22	EXACT(0)	200	184	47
tnfn1_pw060328p08q174	B10	EXACT(0)	156	153	129	38	EXACT(0)	200	145	49
tnfn1_pw060328p08q175	C10	EXACT(0)	155	145	120	38	EXACT(0)	200	184	54
tnfn1_pw060328p08q176	D10	EXACT(0)	154	153	127	40	EXACT(0)	200	189	59
tnfn1_pw060328p08q177	E10	EXACT(0)	155	145	120	40	EXACT(0)	200	192	57
tnfn1_pw060328p08q178	F10	EXACT(0)	157	153	124	33	EXACT(0)	144	136	53
tnfn1_pw060328p08q179	G10	EXACT(0)	156	153	129	39	EXACT(0)	200	190	56
tnfn1_pw060328p08q180	H10	EXACT(0)	157	153	127	35	EXACT(0)	200	192	53
tnfn1_pw060328p08q181	A11	EXACT(0)	156	150	120	32	EXACT(0)	200	193	56
tnfn1_pw060328p08q182	B11	EXACT(0)	155	145	117	37	EXACT(0)	198	177	34
tnfn1_pw060328p08q183	C11	EXACT(0)	156	122	103	28	EXACT(0)	200	192	43
tnfn1_pw060328p08q184	D11	EXACT(0)	156	150	120	32	EXACT(0)	200	156	38
tnfn1_pw060328p08q185	E11	EXACT(0)	154	145	123	40	EXACT(0)	200	181	49
tnfn1_pw060328p08q186	F11	EXACT(0)	157	152	129	29	EXACT(0)	200	196	53
tnfn1_pw060328p08q187	G11	EXACT(0)	154	139	107	30	EXACT(0)	200	186	46
tnfn1_pw060328p08q188	H11	EXACT(0)	155	145	100	24	EXACT(0)	200	182	49
tnfn1_pw060328p08q189	A12	EXACT(0)	156	148	128	35	EXACT(0)	200	194	56
tnfn1_pw060328p08q190	B12	EXACT(0)	155	152	122	39	EXACT(0)	200	184	50
tnfn1_pw060328p08q191	C12	EXACT(0)	155	145	114	32	EXACT(0)	200	194	56
tnfn1_pw060328p08q192	D12	EXACT(0)	157	153	126	39	EXACT(0)	200	192	56
tnfn1_pw060328p08q193	E12	EXACT(0)	153	145	109	38	EXACT(0)	200	177	56
tnfn1_pw060328p08q194	F12	EXACT(0)	155	152	118	35	EXACT(0)	200	187	55
tnfn1_pw060328p08q195	G12	EXACT(0)	154	139	116	35	EXACT(0)	200	180	44
tnfn1_pw060328p08q196	H12	EXACT(0)	157	141	83	23	EXACT(0)	200	189	39