

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 5 (tnfn1_pw060323p05)**

Catalog No. NR-8039

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-8039 represents Plate 5 (tnfn1_pw060323p05) 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-8039 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 5 (tnfn1_pw060323p05), NR-8039.”

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_pw060323p05q101	A01	T18	-	zinc (Zn2+)-iron (Fe2+) permease (ZIP) family protein	transport
tnfn1_pw060323p05q102	B01	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q103	C01	T20	-	aspartate/glutamate transporter	transport - amino-acid
tnfn1_pw060323p05q104	D01	T20	ppx	exopolyphosphatase	other metabolism - biosynthesis
tnfn1_pw060323p05q105	E01	T20	-	thioesterase	putative enzymes
tnfn1_pw060323p05q106	F01	T20	ppx	exopolyphosphatase	other metabolism - biosynthesis
tnfn1_pw060323p05q107	G01	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060323p05q108	H01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q109	A02	T20	-	amino acid-polyamine-organocation (APC) superfamily	transport - amino-acid
tnfn1_pw060323p05q110	B02	T20	kpsC	capsule polysaccharide export protein KpsC	cell wall / LPS / capsule
tnfn1_pw060323p05q111	C02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q112	D02	T20	-	conserved hypothetical protein	Potentially coding: hypothetical - conserved
tnfn1_pw060323p05q113	E02	T20	-	ABC-type transport system permease protein	transport
tnfn1_pw060323p05q114	F02	T20	recC	exodeoxyribonuclease V, gamma subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p05q115	G02	T20	-	o-methyltransferase family protein	putative enzymes
tnfn1_pw060323p05q116	H02	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p05q117	A03	T20	-	ThiF family protein	putative enzymes
tnfn1_pw060323p05q118	B03	T20	cyoB	cytochrome bo terminal oxidase subunit I	energy metabolism
tnfn1_pw060323p05q119	C03	T20	manC	mannose-1-phosphate guanylyltransferase	cell wall / LPS / capsule
tnfn1_pw060323p05q120	D03	T20	pxdY	pyridoxal kinase	putative enzymes
tnfn1_pw060323p05q121	E03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q122	F03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q123	G03	T20	ychF	GTP-binding protein	putative enzymes
tnfn1_pw060323p05q124	H03	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p05q125	A04	T20	galK	galactokinase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p05q126	B04	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060323p05q127	C04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q128	D04	T20	pdpA	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q129	E04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q130	F04	T20	pdpA	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q131	G04	T20	proC	pyrroline-5-carboxylate reductase	amino acid metabolism - biosynthesis
tnfn1_pw060323p05q132	H04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q133	A05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q134	B05	T20	cydA	cytochrome bd-I terminal oxidase subunit I	energy metabolism
tnfn1_pw060323p05q135	C05	T20	-	4Fe-4S ferredoxin	energy metabolism
tnfn1_pw060323p05q136	D05	T20	-	dicarboxylate/amino acid:cation (Na+ or H+) symporter	transport - amino-acid
tnfn1_pw060323p05q137	E05	T20	isftu2	isftu2	IS element
tnfn1_pw060323p05q138	F05	T20	isftu2	isftu2	IS element
tnfn1_pw060323p05q139	G05	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060323p05q140	H05	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p05q141	A06	T20	grxB	glutaredoxin 2	post-translational modification, protein turnover, chaperones
tnfn1_pw060323p05q142	B06	T20	-	isochorismatase family protein	putative enzymes
tnfn1_pw060323p05q143	C06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q144	D06	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p05q145	E06	T20	pckA	phosphoenolpyruvate carboxykinase	energy metabolism
tnfn1_pw060323p05q146	F06	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060323p05q147	G06	T20	pilP	Type IV pili periplasmic component	motility, attachment and secretion structure
tnfn1_pw060323p05q148	H06	T20	cydD	ABC-type transport ATP-binding protein CydD	transport

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p05q149	A07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q150	B07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q151	C07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q152	D07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q153	E07	T20	-	glycosyl transferase, group 2	cell wall / LPS / capsule
tnfn1_pw060323p05q154	F07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q155	G07	T20	-	predicted enzyme of enolase superfamily	putative enzymes
tnfn1_pw060323p05q156	H07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q157	A08	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060323p05q158	B08	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p05q159	C08	T20	iglA	intracellular growth locus protein A	unknown function - conserved
tnfn1_pw060323p05q160	D08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q161	E08	T20	-	aspartate:alanine exchanger (AAE) family protein	transport - amino-acid
tnfn1_pw060323p05q162	F08	T20	-	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060323p05q163	G08	<KAN-2>	-	protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q164	H08	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p05q165	A09	T18	nagA	N-acetylglucosamine-6-phosphate deacetylase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p05q166	B09	T18	gtrB	glycosyl transferase	cell wall / LPS / capsule
tnfn1_pw060323p05q167	C09	T18	-	prophage maintenance system killer protein (DOC)	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060323p05q168	D09	T18	-	prophage maintenance system killer protein (DOC)	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060323p05q169	E09	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q170	F09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q171	G09	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p05q172	H09	T18	-	-	-
tnfn1_pw060323p05q173	A10	T18	dsbB	disulfide bond formation protein	putative enzymes
tnfn1_pw060323p05q174	B10	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q175	C10	T20	cysN	sulfate adenylate transferase, subunit 1	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p05q176	D10	T20	-	competence protein	transport
tnfn1_pw060323p05q177	E10	T20	ndh	NADH dehydrogenase	energy metabolism
tnfn1_pw060323p05q178	F10	T20	-	conserved hypothetical protein, Thioesterase superfamily	hypothetical - conserved
tnfn1_pw060323p05q179	G10	T20	pdpB	protein of unknown function	unknown function - novel
tnfn1_pw060323p05q180	H10	T20	-	traT-like protein	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060323p05q181	A11	T20	isftu2	isftu2	IS element
tnfn1_pw060323p05q182	B11	T20	-	lysine decarboxylase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p05q183	C11	T20	-	glycosyl transferase, family 8	cell wall / LPS / capsule
tnfn1_pw060323p05q184	D11	T20	-	potassium channel protein	transport
tnfn1_pw060323p05q185	E11	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060323p05q186	F11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p05q187	G11	T20	-	drug/metabolite exporter	transport - drugs / antibacterial compounds
tnfn1_pw060323p05q188	H11	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060323p05q189	A12	T20	-	glutamate decarboxylase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p05q190	B12	T20	-	small conductance mechanosensitive ion channel (MscS) family protein	transport
tnfn1_pw060323p05q191	C12	T20	apaH	diadenosine tetraphosphatase	signal transduction and regulation
tnfn1_pw060323p05q192	D12	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p05q193	E12	T20	-	methylated DNA-protein cysteine methyltransferase	DNA replication, recombination, modification and repair - repair
tnfn1_pw060323p05q194	F12	T20	glgB	1,4-alpha-glucan branching enzyme	carbohydrate metabolism - biosynthesis
tnfn1_pw060323p05q195	G12	T20	ndk	nucleoside diphosphate kinase	nucleotides and nucleosides metabolism
tnfn1_pw060323p05q196	H12	T20	lepB	signal peptidase I	motility, attachment and secretion structure

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_pw060323p05q101	A01	C	934691	F	FTN_0879	934347	935090	R	248	400(744)
tnfn1_pw060323p05q102	B01	U	331022	F	FTN_0320	330339	331079	R	247	58(741)
tnfn1_pw060323p05q103	C01	C	4689	R	FTN_0004	4244	5764	F	507	446(1521)
tnfn1_pw060323p05q104	D01	C	1491879	F	FTN_1414	1491208	1492131	R	308	253(924)
tnfn1_pw060323p05q105	E01	C	977609	R	FTN_0919	977263	977676	F	138	347(414)
tnfn1_pw060323p05q106	F01	C	1491879	F	FTN_1414	1491208	1492131	R	308	253(924)
tnfn1_pw060323p05q107	G01	C	98019	F	FTN_0086	97601	98827	F	409	419(1227)
tnfn1_pw060323p05q108	H01	C	1327696	R	FTN_1258	1327694	1328239	R	182	544(546)
tnfn1_pw060323p05q109	A02	C	1193397	F	FTN_1130	1192747	1194252	R	502	856(1506)
tnfn1_pw060323p05q110	B02	C	1285449	R	FTN_1215	1284955	1286112	R	386	664(1158)
tnfn1_pw060323p05q111	C02	C	1027427	R	FTN_0972	1026361	1027734	R	458	308(1374)
tnfn1_pw060323p05q112	D02	C	1731332	R	-	1731290	1731751	F	154	43(462)
tnfn1_pw060323p05q113	E02	C	1338318	R	FTN_1266	1337851	1338948	F	366	468(1098)
tnfn1_pw060323p05q114	F02	C	1441903	R	FTN_1359	1439523	1442759	R	1079	857(3237)
tnfn1_pw060323p05q115	G02	C	1121905	R	FTN_1062	1121319	1121990	R	224	86(672)
tnfn1_pw060323p05q116	H02	U	1902144	F	FTN_1771	1901829	1902239	R	137	96(411)
tnfn1_pw060323p05q117	A03	U	1030928	F	FTN_0976	1030667	1031407	F	247	262(741)
tnfn1_pw060323p05q118	B03	C	218032	F	FTN_0196	217534	219561	F	676	499(2028)
tnfn1_pw060323p05q119	C03	C	1496463	F	FTN_1418	1495814	1497217	R	468	755(1404)
tnfn1_pw060323p05q120	D03	C	223912	R	FTN_0202	223337	224185	R	283	274(849)
tnfn1_pw060323p05q121	E03	C	936080	R	FTN_0880	935096	936310	R	405	231(1215)
tnfn1_pw060323p05q122	F03	C	7111	F	FTN_0006	6819	7283	R	155	173(465)
tnfn1_pw060323p05q123	G03	C	1064305	F	FTN_1004	1063694	1064782	F	363	612(1089)
tnfn1_pw060323p05q124	H03	C	1624202	F	FTN_1527	1623669	1624385	R	239	184(717)
tnfn1_pw060323p05q125	A04	C	728596	F	FTN_0685	728080	729225	R	382	630(1146)
tnfn1_pw060323p05q126	B04	C	612304	R	FTN_0583	611786	612709	R	308	406(924)
tnfn1_pw060323p05q127	C04	C	849780	R	FTN_0791	849690	849944	F	85	91(255)
tnfn1_pw060323p05q128	D04	C	1379568	R	FTN_1309	1378294	1380753	F	820	1275(2460)
tnfn1_pw060323p05q129	E04	C	768545	F	FTN_0715	766940	770707	F	1256	1606(3768)
tnfn1_pw060323p05q130	F04	C	1379568	R	FTN_1309	1378294	1380753	F	820	1275(2460)
tnfn1_pw060323p05q131	G04	C	1556183	R	FTN_1467	1555816	1556637	R	274	455(822)
tnfn1_pw060323p05q132	H04	C	714215	F	FTN_0671	713359	714384	R	342	170(1026)
tnfn1_pw060323p05q133	A05	C	1187730	R	FTN_1124	1187659	1187901	F	81	72(243)
tnfn1_pw060323p05q134	B05	C	211771	R	FTN_0193	211009	212760	R	584	990(1752)
tnfn1_pw060323p05q135	C05	C	830274	R	FTN_0773	829606	830691	R	362	418(1086)
tnfn1_pw060323p05q136	D05	C	1144054	F	FTN_1081	1143901	1145172	F	424	154(1272)
tnfn1_pw060323p05q137	E05	C	1887171	F	-	1886855	1887719	F	288.3	317(865)
tnfn1_pw060323p05q138	F05	C	1887171	F	-	1886855	1887719	F	288.3	317(865)
tnfn1_pw060323p05q139	G05	C	1236671	R	FTN_1166	1235989	1237257	R	423	587(1269)
tnfn1_pw060323p05q140	H05	C	483943	R	FTN_0478	483386	484438	R	351	496(1053)
tnfn1_pw060323p05q141	A06	C	1089904	F	FTN_1033	1089601	1090242	F	214	304(642)
tnfn1_pw060323p05q142	B06	C	842640	R	FTN_0785	842442	842945	R	168	306(504)
tnfn1_pw060323p05q143	C06	C	1888169	F	FTN_1758	1887821	1888438	F	206	349(618)
tnfn1_pw060323p05q144	D06	C	202189	F	FTN_0184	201197	202417	R	407	229(1221)
tnfn1_pw060323p05q145	E06	C	565618	F	FTN_0540	564807	566396	F	530	812(1590)
tnfn1_pw060323p05q146	F06	C	1354158	R	FTN_1282	1354079	1354972	F	298	80(894)
tnfn1_pw060323p05q147	G06	C	1203676	F	FTN_1138	1203258	1203845	R	196	170(588)
tnfn1_pw060323p05q148	H06	C	680686	F	FTN_0642	679509	681287	R	593	602(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 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_pw060323p05q149	A07	C	1563419	F	FTN_1475	1563112	1563483	R	124	65(372)
tnfn1_pw060323p05q150	B07	C	991599	R	FTN_0930	990929	991774	R	282	176(846)
tnfn1_pw060323p05q151	C07	C	1836852	F	FTN_1712	1836693	1837145	F	151	160(453)
tnfn1_pw060323p05q152	D07	C	1306918	F	FTN_1238	1306482	1307129	R	216	212(648)
tnfn1_pw060323p05q153	E07	C	309079	F	FTN_0300	308570	310246	F	559	510(1677)
tnfn1_pw060323p05q154	F07	C	1517753	R	FTN_1433	1517238	1518122	R	295	370(885)
tnfn1_pw060323p05q155	G07	C	743453	F	FTN_0700	743228	744295	F	356	226(1068)
tnfn1_pw060323p05q156	H07	C	1582522	R	FTN_1490	1581779	1582627	R	283	106(849)
tnfn1_pw060323p05q157	A08	C	1170076	F	FTN_1108	1169873	1171081	F	403	204(1209)
tnfn1_pw060323p05q158	B08	C	1602042	F	FTN_1506	1601515	1602525	R	337	484(1011)
tnfn1_pw060323p05q159	C08	C	1399546	F	FTN_1324	1399172	1399723	R	184	178(552)
tnfn1_pw060323p05q160	D08	C	1269717	F	FTN_1196	1269690	1270025	F	112	28(336)
tnfn1_pw060323p05q161	E08	C	350503	F	FTN_0344	349254	350966	R	571	464(1713)
tnfn1_pw060323p05q162	F08	C	1282423	F	FTN_1212	1281922	1282932	R	337	510(1011)
tnfn1_pw060323p05q163	G08	C	574371	R	FTN_0547	574159	574419	R	87	49(261)
tnfn1_pw060323p05q164	H08	C	1484784	R	FTN_1407	1484689	1485012	R	108	229(324)
tnfn1_pw060323p05q165	A09	C	1214518	F	FTN_1149	1214229	1215359	R	377	842(1131)
tnfn1_pw060323p05q166	B09	C	1481418	R	FTN_1403	1481150	1482091	F	314	269(942)
tnfn1_pw060323p05q167	C09	C	292213	R	FTN_0284	291793	292794	F	334	421(1002)
tnfn1_pw060323p05q168	D09	C	292213	R	FTN_0284	291793	292794	F	334	421(1002)
tnfn1_pw060323p05q169	E09	C	1538147	R	FTN_1448	1537385	1538812	R	476	666(1428)
tnfn1_pw060323p05q170	F09	C	10345	R	FTN_0012	10220	10438	R	73	94(219)
tnfn1_pw060323p05q171	G09	C	774800	R	FTN_0719	774796	774996	R	67	197(201)
tnfn1_pw060323p05q172	H09	C	487750	R	intergenic					
tnfn1_pw060323p05q173	A10	C	1712018	R	FTN_1608	1711912	1712400	F	163	107(489)
tnfn1_pw060323p05q174	B10	C	1177219	R	FTN_1113	1177061	1177801	F	247	159(741)
tnfn1_pw060323p05q175	C10	C	985025	F	FTN_0927	984277	985686	R	470	662(1410)
tnfn1_pw060323p05q176	D10	C	168693	R	FTN_0155	168063	170075	F	671	631(2013)
tnfn1_pw060323p05q177	E10	C	969866	F	FTN_0912	969311	970570	R	420	705(1260)
tnfn1_pw060323p05q178	F10	C	1529127	F	FTN_1440	1528961	1529446	F	162	167(486)
tnfn1_pw060323p05q179	G10	C	1382049	R	FTN_1310	1380761	1384039	F	1093	1289(3279)
tnfn1_pw060323p05q180	H10	C	325506	R	FTN_0315	324848	325591	R	248	86(744)
tnfn1_pw060323p05q181	A11	C	39487	R	-	38962	39826	F	288.3	526(865)
tnfn1_pw060323p05q182	B11	C	513305	F	FTN_0504	512714	514852	F	713	592(2139)
tnfn1_pw060323p05q183	C11	C	1324328	F	FTN_1255	1323964	1324851	F	296	365(888)
tnfn1_pw060323p05q184	D11	C	1058001	F	FTN_0998	1057851	1059008	F	386	151(1158)
tnfn1_pw060323p05q185	E11	C	1368886	R	FTN_1300	1368610	1369497	R	296	612(888)
tnfn1_pw060323p05q186	F11	C	1298988	F	FTN_1229	1298595	1299305	F	237	394(711)
tnfn1_pw060323p05q187	G11	C	1444824	F	FTN_1361	1444600	1445466	F	289	225(867)
tnfn1_pw060323p05q188	H11	C	1083742	F	FTN_1026	1082927	1084117	R	397	376(1191)
tnfn1_pw060323p05q189	A12	C	1822784	F	FTN_1701	1822121	1823464	R	448	681(1344)
tnfn1_pw060323p05q190	B12	C	926801	R	FTN_0872	926220	927407	F	396	582(1188)
tnfn1_pw060323p05q191	C12	C	588147	F	FTN_0561	587981	588805	F	275	167(825)
tnfn1_pw060323p05q192	D12	C	293226	R	FTN_0285	292790	294007	F	406	437(1218)
tnfn1_pw060323p05q193	E12	C	1624794	R	FTN_1528	1624415	1624975	F	187	380(561)
tnfn1_pw060323p05q194	F12	C	528981	F	FTN_0513	527934	529853	R	640	873(1920)
tnfn1_pw060323p05q195	G12	C	279686	F	FTN_0271	279453	279872	F	140	234(420)
tnfn1_pw060323p05q196	H12	C	1552542	R	FTN_1464	1552493	1553353	R	287	812(861)

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_pw060323p05q101	A01	EXACT(0)	120	71	67	26	EXACT(0)	200	193	55
tnfn1_pw060323p05q102	B01	EXACT(0)	127	83	58	24	EXACT(0)	200	187	45
tnfn1_pw060323p05q103	C01	EXACT(0)	158	145	120	39	EXACT(0)	200	189	57
tnfn1_pw060323p05q104	D01	EXACT(0)	156	146	121	35	EXACT(0)	200	123	35
tnfn1_pw060323p05q105	E01	EXACT(0)	157	145	135	39	EXACT(0)	200	190	53
tnfn1_pw060323p05q106	F01	EXACT(0)	157	151	132	38	EXACT(0)	200	193	49
tnfn1_pw060323p05q107	G01	EXACT(0)	155	145	129	37	EXACT(0)	200	192	55
tnfn1_pw060323p05q108	H01	EXACT(0)	156	117	87	28	EXACT(0)	200	154	40
tnfn1_pw060323p05q109	A02	EXACT(0)	157	153	140	39	EXACT(0)	200	161	48
tnfn1_pw060323p05q110	B02	EXACT(0)	157	151	123	35	EXACT(0)	200	172	55
tnfn1_pw060323p05q111	C02	EXACT(0)	157	153	137	38	EXACT(0)	200	193	54
tnfn1_pw060323p05q112	D02	EXACT(0)	157	145	123	33	EXACT(0)	200	180	55
tnfn1_pw060323p05q113	E02	EXACT(0)	156	153	120	31	EXACT(0)	200	185	51
tnfn1_pw060323p05q114	F02	EXACT(0)	156	153	132	41	EXACT(0)	200	190	55
tnfn1_pw060323p05q115	G02	EXACT(0)	156	153	126	37	EXACT(0)	200	195	55
tnfn1_pw060323p05q116	H02	EXACT(0)	155	145	120	37	EXACT(0)	198	183	60
tnfn1_pw060323p05q117	A03	EXACT(0)	158	150	136	49	EXACT(0)	200	174	56
tnfn1_pw060323p05q118	B03	EXACT(0)	157	153	130	35	EXACT(0)	200	147	39
tnfn1_pw060323p05q119	C03	EXACT(0)	157	153	134	41	EXACT(0)	200	189	57
tnfn1_pw060323p05q120	D03	EXACT(0)	156	153	129	37	EXACT(0)	200	194	51
tnfn1_pw060323p05q121	E03	EXACT(0)	156	146	133	44	EXACT(0)	199	122	35
tnfn1_pw060323p05q122	F03	EXACT(0)	158	153	123	35	EXACT(0)	200	187	55
tnfn1_pw060323p05q123	G03	EXACT(0)	153	153	116	38	EXACT(0)	198	182	46
tnfn1_pw060323p05q124	H03	EXACT(0)	154	139	72	18	EXACT(0)	200	177	52
tnfn1_pw060323p05q125	A04	EXACT(0)	156	153	123	39	EXACT(0)	200	192	56
tnfn1_pw060323p05q126	B04	EXACT(0)	158	151	116	32	EXACT(0)	200	185	56
tnfn1_pw060323p05q127	C04	EXACT(0)	157	153	134	39	EXACT(0)	196	168	40
tnfn1_pw060323p05q128	D04	EXACT(0)	156	152	122	43	EXACT(0)	200	181	66
tnfn1_pw060323p05q129	E04	EXACT(0)	154	145	111	30	EXACT(0)	200	192	52
tnfn1_pw060323p05q130	F04	EXACT(0)	157	152	121	36	EXACT(0)	200	181	53
tnfn1_pw060323p05q131	G04	EXACT(0)	156	153	132	42	EXACT(0)	180	174	51
tnfn1_pw060323p05q132	H04	EXACT(0)	156	139	125	37	EXACT(0)	110	104	52
tnfn1_pw060323p05q133	A05	EXACT(0)	158	153	115	30	EXACT(0)	200	189	51
tnfn1_pw060323p05q134	B05	EXACT(0)	157	153	133	37	EXACT(0)	200	198	55
tnfn1_pw060323p05q135	C05	EXACT(0)	157	153	134	40	EXACT(0)	200	197	46
tnfn1_pw060323p05q136	D05	EXACT(0)	156	152	134	37	EXACT(0)	200	158	42
tnfn1_pw060323p05q137	E05	EXACT(0)	156	153	129	43	EXACT(0)	200	193	58
tnfn1_pw060323p05q138	F05	EXACT(0)	156	146	132	42	EXACT(0)	200	193	57
tnfn1_pw060323p05q139	G05	EXACT(0)	156	145	131	41	EXACT(0)	200	191	56
tnfn1_pw060323p05q140	H05	EXACT(0)	155	142	117	32	ESTIMATE(72)	66	49	24
tnfn1_pw060323p05q141	A06	EXACT(0)	157	151	132	38	EXACT(0)	200	185	57
tnfn1_pw060323p05q142	B06	EXACT(0)	158	142	103	26	EXACT(0)	200	187	53
tnfn1_pw060323p05q143	C06	EXACT(0)	157	146	126	36	EXACT(0)	200	191	54
tnfn1_pw060323p05q144	D06	EXACT(0)	156	145	131	32	EXACT(0)	200	190	55
tnfn1_pw060323p05q145	E06	EXACT(0)	155	153	124	40	EXACT(0)	200	190	58
tnfn1_pw060323p05q146	F06	EXACT(0)	156	153	132	37	EXACT(0)	200	177	55
tnfn1_pw060323p05q147	G06	EXACT(0)	155	152	128	41	EXACT(0)	200	182	50
tnfn1_pw060323p05q148	H06	EXACT(0)	156	153	126	34	EXACT(0)	200	193	52

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_pw060323p05q149	A07	EXACT(0)	157	150	125	33	EXACT(0)	200	185	57
tnfn1_pw060323p05q150	B07	EXACT(0)	154	145	119	36	EXACT(0)	200	194	52
tnfn1_pw060323p05q151	C07	EXACT(0)	155	145	123	42	EXACT(0)	200	194	55
tnfn1_pw060323p05q152	D07	EXACT(0)	154	145	129	38	EXACT(0)	200	163	46
tnfn1_pw060323p05q153	E07	EXACT(0)	155	145	132	41	EXACT(0)	200	191	59
tnfn1_pw060323p05q154	F07	EXACT(0)	155	153	135	37	EXACT(0)	200	189	58
tnfn1_pw060323p05q155	G07	EXACT(0)	155	145	123	36	EXACT(0)	200	187	53
tnfn1_pw060323p05q156	H07	EXACT(0)	155	151	133	39	EXACT(0)	32	30	43
tnfn1_pw060323p05q157	A08	EXACT(0)	156	145	118	32	EXACT(0)	200	181	49
tnfn1_pw060323p05q158	B08	EXACT(0)	155	142	82	23	EXACT(0)	184	173	51
tnfn1_pw060323p05q159	C08	EXACT(0)	155	145	129	41	EXACT(0)	200	184	56
tnfn1_pw060323p05q160	D08	EXACT(0)	156	151	127	39	EXACT(0)	200	191	50
tnfn1_pw060323p05q161	E08	EXACT(0)	157	152	139	39	EXACT(0)	200	199	54
tnfn1_pw060323p05q162	F08	EXACT(0)	156	146	126	39	EXACT(0)	200	182	57
tnfn1_pw060323p05q163	G08	EXACT(0)	121	96	58	18	EXACT(0)	136	131	39
tnfn1_pw060323p05q164	H08	EXACT(0)	121	105	69	19	EXACT(0)	200	190	47
tnfn1_pw060323p05q165	A09	EXACT(0)	122	106	98	34	EXACT(0)	200	196	53
tnfn1_pw060323p05q166	B09	EXACT(0)	120	83	63	23	EXACT(0)	200	193	47
tnfn1_pw060323p05q167	C09	EXACT(0)	121	106	92	27	EXACT(0)	200	178	47
tnfn1_pw060323p05q168	D09	EXACT(0)	122	112	87	23	EXACT(0)	200	176	49
tnfn1_pw060323p05q169	E09	EXACT(0)	123	118	97	34	EXACT(0)	141	136	51
tnfn1_pw060323p05q170	F09	EXACT(0)	119	112	88	30	EXACT(0)	200	181	58
tnfn1_pw060323p05q171	G09	EXACT(0)	114	50	41	28	ESTIMATE(51)	87	29	15
tnfn1_pw060323p05q172	H09	EXACT(0)	120	109	65	20	EXACT(0)	200	174	35
tnfn1_pw060323p05q173	A10	EXACT(0)	122	105	60	22	ESTIMATE(2)	198	180	48
tnfn1_pw060323p05q174	B10	EXACT(0)	123	113	90	31	EXACT(0)	200	189	53
tnfn1_pw060323p05q175	C10	EXACT(0)	156	153	128	37	EXACT(0)	200	190	44
tnfn1_pw060323p05q176	D10	EXACT(0)	154	139	110	33	EXACT(0)	200	192	51
tnfn1_pw060323p05q177	E10	EXACT(0)	156	145	118	33	EXACT(0)	200	189	55
tnfn1_pw060323p05q178	F10	EXACT(0)	156	153	123	37	EXACT(0)	200	190	57
tnfn1_pw060323p05q179	G10	EXACT(0)	157	153	121	32	EXACT(0)	200	186	55
tnfn1_pw060323p05q180	H10	EXACT(0)	156	153	132	37	EXACT(0)	200	187	54
tnfn1_pw060323p05q181	A11	EXACT(0)	155	145	126	41	EXACT(0)	200	193	57
tnfn1_pw060323p05q182	B11	EXACT(0)	158	153	118	30	EXACT(0)	200	191	56
tnfn1_pw060323p05q183	C11	EXACT(0)	155	145	120	37	EXACT(0)	200	186	55
tnfn1_pw060323p05q184	D11	EXACT(0)	153	139	105	30	EXACT(0)	200	185	54
tnfn1_pw060323p05q185	E11	EXACT(0)	157	152	139	41	EXACT(0)	200	174	38
tnfn1_pw060323p05q186	F11	EXACT(0)	157	152	133	38	EXACT(0)	200	175	38
tnfn1_pw060323p05q187	G11	EXACT(0)	157	151	132	42	EXACT(0)	196	142	37
tnfn1_pw060323p05q188	H11	EXACT(0)	157	153	137	37	EXACT(0)	200	188	56
tnfn1_pw060323p05q189	A12	EXACT(0)	157	152	135	40	EXACT(0)	200	193	52
tnfn1_pw060323p05q190	B12	EXACT(0)	160	145	131	41	EXACT(0)	200	187	60
tnfn1_pw060323p05q191	C12	EXACT(0)	154	142	96	25	EXACT(0)	200	186	51
tnfn1_pw060323p05q192	D12	EXACT(0)	158	153	147	45	EXACT(0)	200	188	55
tnfn1_pw060323p05q193	E12	EXACT(0)	156	142	119	34	EXACT(0)	200	174	48
tnfn1_pw060323p05q194	F12	EXACT(0)	157	153	125	38	EXACT(0)	200	194	57
tnfn1_pw060323p05q195	G12	EXACT(0)	155	145	117	32	EXACT(0)	200	194	49
tnfn1_pw060323p05q196	H12	EXACT(0)	157	152	133	41	EXACT(0)	200	188	55