

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 17 (tnfn1_pw060418p01)**

Catalog No. NR-8051

For research use only. Not for human use.

Contributor:

Colin Manoil, Ph.D., Professor of Genome Sciences,
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-8051 represents Plate 17 (tnfn1_pw060418p01) 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_pw060418p01q108 (Well H01) is not available due to quality issues. The following strains were not available due to quality issues at the time of the release of Plate 17, but are available now on Plate 33 (BEI Resources NR-10484).**

tnfn1_pw060418p01q101 (Well A01)
tnfn1_pw060418p01q102 (Well B01)
tnfn1_pw060418p01q103 (Well C01)
tnfn1_pw060418p01q105 (Well E01)
tnfn1_pw060418p01q106 (Well F01)
tnfn1_pw060418p01q124 (Well H03)
tnfn1_pw060418p01q151 (Well C07)
tnfn1_pw060418p01q152 (Well D07)
tnfn1_pw060418p01q158 (Well B08)
tnfn1_pw060418p01q179 (Well G10)

***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-8051 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 17 (tnfn1_pw060418p01), NR-8051.”

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:

You are authorized to use this product for research use only. It is not intended for human use.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government make any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are

responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for damages arising from the misidentification or misrepresentation of products.

Use Restrictions:

This material is distributed for internal research, non-commercial purposes only. This material, its product or its derivatives may not be distributed to third parties. Except as performed under a U.S. Government contract, individuals contemplating commercial use of the material, its products or its derivatives must contact the contributor to determine if a license is required. U.S. Government contractors may need a license before first commercial sale.

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.

ATCC® is a trademark of the American Type Culture Collection.



Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060418p01q101	A01	T15	atpH	ATP synthase, F1 sector, subunit delta	energy metabolism
tnfn1_pw060418p01q102	B01	T15	-	beta-lactamase class A	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p01q103	C01	T15	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q104	D01	T18	-	-	-
tnfn1_pw060418p01q105	E01	<KAN-2>	-	transcriptional regulator, ArsR family	signal transduction and regulation
tnfn1_pw060418p01q106	F01	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q107	G01	T20	-	-	-
tnfn1_pw060418p01q108	H01	<KAN-2>	sdhA	succinate dehydrogenase flavoprotein	energy metabolism
tnfn1_pw060418p01q109	A02	<KAN-2>	metN	methionine uptake transporter (MUT) family protein	transport - amino-acid
tnfn1_pw060418p01q110	B02	T17	-	UDP-3-O-[3-fatty acid] glucosamine N-acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060418p01q111	C02	T17	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p01q112	D02	T20	-	-	-
tnfn1_pw060418p01q113	E02	T17	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q114	F02	T17	-	peptide methionine sulfoxide reductase-related protein	post-translational modification, protein turnover, chaperones
tnfn1_pw060418p01q115	G02	T17	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q116	H02	T17	-	zinc (Zn ²⁺)-iron (Fe ²⁺) permease (ZIP) family protein	transport
tnfn1_pw060418p01q117	A03	T17	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q118	B03	T17	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060418p01q119	C03	T18	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060418p01q120	D03	T18	cdd	cytidine deaminase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p01q121	E03	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q122	F03	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p01q123	G03	T20	glpQ	glycerophosphoryl diester phosphodiesterase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p01q124	H03	T20	iscS	cysteine desulfurase	amino acid metabolism - biosynthesis
tnfn1_pw060418p01q125	A04	T20	-	-	-
tnfn1_pw060418p01q126	B04	T20	tmpT	thiopurine S-methyltransferase	putative enzymes
tnfn1_pw060418p01q127	C04	T20	adhC	Zn-dependent alcohol dehydrogenase	energy metabolism
tnfn1_pw060418p01q128	D04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q129	E04	T20	-	phage integrase	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060418p01q130	F04	T20	pilT	Type IV pili nucleotide-binding protein	motility, attachment and secretion structure
tnfn1_pw060418p01q131	G04	T20	-	oxidoreductase iron/ascorbate family protein	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p01q132	H04	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p01q133	A05	T20	fbaA	fructose bisphosphate aldolase Class II	energy metabolism
tnfn1_pw060418p01q134	B05	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p01q135	C05	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p01q136	D05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q137	E05	T20	-	-	-
tnfn1_pw060418p01q138	F05	T20	-	transcriptional regulator, ArsR family	signal transduction and regulation
tnfn1_pw060418p01q139	G05	T20	-	MoxR-like ATPase	putative enzymes
tnfn1_pw060418p01q140	H05	T20	-	VacJ like lipoprotein	cell wall / LPS / capsule
tnfn1_pw060418p01q141	A06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q142	B06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q143	C06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q144	D06	T20	kdsA	3-deoxy-D-manno-octulosonic acid 8-phosphate synthase	fatty acids and lipids metabolism
tnfn1_pw060418p01q145	E06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q146	F06	T20	ggT	gamma-glutamyltranspeptidase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p01q147	G06	T20	-	ATP-dependent RNA helicase	nucleotides and nucleosides metabolism
tnfn1_pw060418p01q148	H06	T20	tolA	group A colicin translocation; tolA protein	transport - drugs / antibacterial compounds

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060418p01q149	A07	T20	-	GTPase of unknown function	putative enzymes
tnfn1_pw060418p01q150	B07	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p01q151	C07	T20	panD	aspartate 1-decarboxylase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p01q152	D07	T20	fadA	acetyl-CoA acetyltransferase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p01q153	E07	T20	lon	DNA-binding, ATP-dependent protease La	post-translational modification, protein turnover, chaperones
tnfn1_pw060418p01q154	F07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q155	G07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q156	H07	T20	-	dicarboxylate/amino acid:cation (Na+ or H+) symporter	transport - amino-acid
tnfn1_pw060418p01q157	A08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q158	B08	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p01q159	C08	T20	eriC	Cl ⁻ :H ⁺ antiporter	transport
tnfn1_pw060418p01q160	D08	T20	-	serine-type D-Ala-D-Ala carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060418p01q161	E08	T20	glpT	glycerol-3-phosphate transporter	transport
tnfn1_pw060418p01q162	F08	T20	-	10 TMS drug/metabolite exporter protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p01q163	G08	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p01q164	H08	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p01q165	A09	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q166	B09	T20	nadC	nicotinate-nucleotide pyrophosphorylase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p01q167	C09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q168	D09	T20	-	sugar porter (SP) family	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p01q169	E09	T20	cydA	cytochrome bd-I terminal oxidase subunit I	energy metabolism
tnfn1_pw060418p01q170	F09	T20	-	D-isomer specific 2-hydroxyacid dehydrogenase	energy metabolism
tnfn1_pw060418p01q171	G09	T20	nuoN	NADH dehydrogenase I, N subunit	energy metabolism
tnfn1_pw060418p01q172	H09	T20	cfa	cyclopropane fatty acid synthase, methyltransferase	fatty acids and lipids metabolism
tnfn1_pw060418p01q173	A10	T17	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q174	B10	<KAN-2>	deoB	phosphopentomutase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p01q175	C10	T17	bioD	dethiobiotin synthetase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p01q176	D10	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q177	E10	T18	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060418p01q178	F10	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q179	G10	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q180	H10	T18	-	conserved hypothetical protein	Potentially coding: hypothetical - conserved
tnfn1_pw060418p01q181	A11	T18	pilO	Type IV pili glycosylation protein	motility, attachment and secretion structure
tnfn1_pw060418p01q182	B11	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q183	C11	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q184	D11	T18	-	licB-like transmembrane protein	putative enzymes
tnfn1_pw060418p01q185	E11	T20	-	regulatory factor, Bvg accessory factor family	signal transduction and regulation
tnfn1_pw060418p01q186	F11	T20	-	metabolite:H ⁺ symporter (MHS) family protein	transport
tnfn1_pw060418p01q187	G11	T20	-	amino acid-polyamine-organocation family protein	transport - amino-acid
tnfn1_pw060418p01q188	H11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p01q189	A12	T20	-	sterol desaturase	fatty acids and lipids metabolism
tnfn1_pw060418p01q190	B12	T20	glpF	glycerol uptake facilitator protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p01q191	C12	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p01q192	D12	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p01q193	E12	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p01q194	F12	T20	wbtG	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060418p01q195	G12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p01q196	H12	T20	-	ROK family protein	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_pw060418p01q101	A01	U	1764488	F	FTN_1649	1764017	1764538	R	174	51(522)
tnfn1_pw060418p01q102	B01	U	1134802	R	FTN_1072	1134341	1135201	F	287	462(861)
tnfn1_pw060418p01q103	C01	U	248954	F	FTN_0225	248455	249375	R	307	422(921)
tnfn1_pw060418p01q104	D01	C	1845785	R	intergenic					
tnfn1_pw060418p01q105	E01	C	858810	R	FTN_0801	858600	858947	R	116	138(348)
tnfn1_pw060418p01q106	F01	C	770015	F	FTN_0715	766940	770707	F	1256	3076(3768)
tnfn1_pw060418p01q107	G01	C	486320	R	intergenic					
tnfn1_pw060418p01q108	H01	C	1750448	R	FTN_1637	1749035	1750825	R	597	378(1791)
tnfn1_pw060418p01q109	A02	C	1167981	F	FTN_1106	1167276	1168349	F	358	706(1074)
tnfn1_pw060418p01q110	B02	C	222304	F	FTN_0200	221524	222564	R	347	261(1041)
tnfn1_pw060418p01q111	C02	C	400833	R	FTN_0401	400237	400833	R	199	1(597)
tnfn1_pw060418p01q112	D02	C	1812676	F	intergenic					
tnfn1_pw060418p01q113	E02	C	830985	R	FTN_0774	830697	831029	R	111	45(333)
tnfn1_pw060418p01q114	F02	U	402851	F	FTN_0404	402710	403219	R	170	369(510)
tnfn1_pw060418p01q115	G02	C	990537	R	FTN_0929	989845	990945	R	367	409(1101)
tnfn1_pw060418p01q116	H02	C	935090	R	FTN_0879	934347	935090	R	248	1(744)
tnfn1_pw060418p01q117	A03	C	7195	F	FTN_0006	6819	7283	R	155	89(465)
tnfn1_pw060418p01q118	B04	C	1089335	F	FTN_1032	1087961	1089430	R	490	96(1470)
tnfn1_pw060418p01q119	C03	C	1831423	R	FTN_1708	1830752	1832410	R	553	988(1659)
tnfn1_pw060418p01q120	D03	C	691209	F	FTN_0651	691035	691433	R	133	225(399)
tnfn1_pw060418p01q121	E03	C	1131312	F	FTN_1070	1130864	1132213	R	450	902(1350)
tnfn1_pw060418p01q122	F03	C	1611750	F	FTN_1515	1611473	1612084	R	204	335(612)
tnfn1_pw060418p01q123	G03	C	1178035	F	FTN_1114	1177796	1178545	R	250	511(750)
tnfn1_pw060418p01q124	H03	C	1311156	R	FTN_1245	1310691	1311863	R	391	708(1173)
tnfn1_pw060418p01q125	A04	C	345787	R	intergenic					
tnfn1_pw060418p01q126	B04	U	24222	F	FTN_0023	24071	24748	R	226	527(678)
tnfn1_pw060418p01q127	C04	C	407200	R	FTN_0409	406706	407815	F	370	495(1110)
tnfn1_pw060418p01q128	D04	U	26761	F	FTN_0025	26213	26797	R	195	37(585)
tnfn1_pw060418p01q129	E04	C	375669	F	FTN_0373	374890	376083	F	398	780(1194)
tnfn1_pw060418p01q130	F04	C	1733076	R	FTN_1622	1732820	1733845	R	342	770(1026)
tnfn1_pw060418p01q131	G04	C	1655698	F	FTN_1557	1654935	1655777	R	281	80(843)
tnfn1_pw060418p01q132	H04	C	901404	R	FTN_0845	900621	901457	R	279	54(837)
tnfn1_pw060418p01q133	A05	C	1408398	R	FTN_1329	1407743	1408804	R	354	407(1062)
tnfn1_pw060418p01q134	B05	C	213720	R	FTN_0194	213220	214584	R	455	865(1365)
tnfn1_pw060418p01q135	C05	U	201808	R	FTN_0184	201197	202417	R	407	610(1221)
tnfn1_pw060418p01q136	D05	C	1561021	F	FTN_1472	1560482	1561288	F	269	540(807)
tnfn1_pw060418p01q137	E05	C	817755	F	intergenic					
tnfn1_pw060418p01q138	F05	C	1470496	R	FTN_1393	1470399	1470698	R	100	203(300)
tnfn1_pw060418p01q139	G05	C	225219	R	FTN_0204	224772	225725	F	318	448(954)
tnfn1_pw060418p01q140	H05	C	332561	R	FTN_0322	331919	333016	F	366	643(1098)
tnfn1_pw060418p01q141	A06	C	874382	F	FTN_0817	874185	874682	R	166	301(498)
tnfn1_pw060418p01q142	B06	C	488291	R	FTN_0482	487800	488777	F	326	492(978)
tnfn1_pw060418p01q143	C06	C	580926	R	FTN_0556	580679	581239	F	187	248(561)
tnfn1_pw060418p01q144	D06	U	644698	R	FTN_0611	644330	645154	F	275	369(825)
tnfn1_pw060418p01q145	E06	U	245316	F	FTN_0222	244745	245710	F	322	572(966)
tnfn1_pw060418p01q146	F06	C	1230760	F	FTN_1159	1229840	1231642	R	601	883(1803)
tnfn1_pw060418p01q147	G06	C	887699	R	FTN_0831	887579	888901	F	441	121(1323)
tnfn1_pw060418p01q148	H06	C	358314	R	FTN_0354	357724	358632	F	303	591(909)

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_pw060418p01q149	A07	C	1367625	R	FTN_1298	1367030	1368379	F	450	596(1350)
tnfn1_pw060418p01q150	B07	C	1684454	F	FTN_1586	1684007	1685317	R	437	864(1311)
tnfn1_pw060418p01q151	C07	C	1432485	R	FTN_1354	1432438	1432770	F	111	48(333)
tnfn1_pw060418p01q152	D07	C	1528045	F	FTN_1439	1527712	1528896	F	395	334(1185)
tnfn1_pw060418p01q153	E07	C	1115398	R	FTN_1055	1113546	1115867	R	774	470(2322)
tnfn1_pw060418p01q154	F07	C	682058	R	FTN_0643	681664	682170	F	169	395(507)
tnfn1_pw060418p01q155	G07	C	49402	F	FTN_0044	49002	49646	F	215	401(645)
tnfn1_pw060418p01q156	H07	C	1144536	R	FTN_1081	1143901	1145172	F	424	636(1272)
tnfn1_pw060418p01q157	A08	C	921302	F	FTN_0869	921132	923024	F	631	171(1893)
tnfn1_pw060418p01q158	B08	C	1070823	F	FTN_1011	1070332	1071615	R	428	793(1284)
tnfn1_pw060418p01q159	C08	C	1863473	R	FTN_1737	1863156	1864571	F	472	318(1416)
tnfn1_pw060418p01q160	D08	C	670106	F	FTN_0635	669592	670983	R	464	878(1392)
tnfn1_pw060418p01q161	E08	C	672157	F	FTN_0636	671002	672315	R	438	159(1314)
tnfn1_pw060418p01q162	F08	U	1618664	R	FTN_1521	1618541	1619422	F	294	124(882)
tnfn1_pw060418p01q163	G08	C	472369	F	FTN_0467	471407	472627	R	407	259(1221)
tnfn1_pw060418p01q164	H08	C	12271	F	FTN_0014	11835	12728	R	298	458(894)
tnfn1_pw060418p01q165	A09	C	1836933	R	FTN_1712	1836693	1837145	F	151	241(453)
tnfn1_pw060418p01q166	B09	C	737598	F	FTN_0693	737043	737903	F	287	556(861)
tnfn1_pw060418p01q167	C09	C	1862346	R	FTN_1735	1862274	1862681	F	136	73(408)
tnfn1_pw060418p01q168	D09	U	1141761	R	FTN_1079	1141288	1142637	R	450	877(1350)
tnfn1_pw060418p01q169	E09	C	212173	R	FTN_0193	211009	212760	R	584	588(1752)
tnfn1_pw060418p01q170	F09	C	1886536	F	FTN_1757	1885735	1886715	R	327	180(981)
tnfn1_pw060418p01q171	G09	C	1780735	F	FTN_1667	1780707	1782155	R	483	1421(1449)
tnfn1_pw060418p01q172	H09	C	1545579	R	FTN_1456	1544780	1545940	F	387	800(1161)
tnfn1_pw060418p01q173	A10	C	831194	F	FTN_0775	831132	831464	F	111	63(333)
tnfn1_pw060418p01q174	B10	C	1703978	R	FTN_1602	1703024	1704265	R	414	288(1242)
tnfn1_pw060418p01q175	C10	C	869536	F	FTN_0812	869347	870021	R	225	486(675)
tnfn1_pw060418p01q176	D10	U	1452510	R	FTN_1372	1451963	1453045	R	361	536(1083)
tnfn1_pw060418p01q177	E10	C	606819	R	FTN_0578	606155	607375	F	407	665(1221)
tnfn1_pw060418p01q178	F10	C	785760	F	FTN_0732	785679	785882	R	68	123(204)
tnfn1_pw060418p01q179	G10	C	1384035	F	FTN_1311	1384032	1384406	F	125	4(375)
tnfn1_pw060418p01q180	H10	C	1731744	F	-	1731290	1731751	F	154	455(462)
tnfn1_pw060418p01q181	A11	C	1204243	F	FTN_1139	1203854	1204447	R	198	205(594)
tnfn1_pw060418p01q182	B11	C	752268	R	FTN_0708	752105	752347	F	81	164(243)
tnfn1_pw060418p01q183	C11	C	395779	F	FTN_0396	395576	396226	F	217	204(651)
tnfn1_pw060418p01q184	D11	C	1653545	R	FTN_1555	1653462	1654343	F	294	84(882)
tnfn1_pw060418p01q185	E11	C	1433230	F	FTN_1355	1432777	1433544	F	256	454(768)
tnfn1_pw060418p01q186	F11	C	1236869	R	FTN_1166	1235989	1237257	R	423	389(1269)
tnfn1_pw060418p01q187	G11	C	329290	R	FTN_0319	328471	329970	R	500	681(1500)
tnfn1_pw060418p01q188	H11	C	992353	F	FTN_0931	991793	992749	F	319	561(957)
tnfn1_pw060418p01q189	A12	C	404184	R	FTN_0406	403941	404729	F	263	244(789)
tnfn1_pw060418p01q190	B12	C	1680615	F	FTN_1583	1679893	1680654	R	254	40(762)
tnfn1_pw060418p01q191	C12	C	1427464	F	FTN_1349	1427275	1427817	R	181	354(543)
tnfn1_pw060418p01q192	D12	C	744518	F	FTN_0701	744311	744955	F	215	208(645)
tnfn1_pw060418p01q193	E12	C	1536303	R	FTN_1446	1534991	1536382	R	464	80(1392)
tnfn1_pw060418p01q194	F12	C	1503903	F	FTN_1423	1502940	1504025	R	362	123(1086)
tnfn1_pw060418p01q195	G12	C	1183556	F	FTN_1129	1183338	1183586	R	83	31(249)
tnfn1_pw060418p01q196	H12	C	867855	F	FTN_0810	867532	868413	F	294	324(882)

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_pw060418p01q101	A01	EXACT(0)	196	107	88	33	EXACT(0)	200	188	59
tnfn1_pw060418p01q102	B01	EXACT(0)	179	108	95	18	EXACT(0)	174	151	22
tnfn1_pw060418p01q103	C01	EXACT(0)	107	107	101	45	EXACT(0)	134	131	55
tnfn1_pw060418p01q104	D01	EXACT(0)	122	112	68	19	EXACT(0)	200	185	49
tnfn1_pw060418p01q105	E01	EXACT(0)	122	109	65	22	EXACT(0)	200	187	48
tnfn1_pw060418p01q106	F01	EXACT(0)	121	106	96	31	EXACT(0)	200	194	51
tnfn1_pw060418p01q107	G01	ADJUSTED(1)	157	70	58	28	ESTIMATE(0)	200	174	41
tnfn1_pw060418p01q108	H01	EXACT(0)	114	112	96	34	EXACT(0)	200	195	46
tnfn1_pw060418p01q109	A02	EXACT(0)	120	120	94	27	EXACT(0)	200	192	54
tnfn1_pw060418p01q110	B02	EXACT(0)	124	120	106	27	EXACT(0)	200	189	50
tnfn1_pw060418p01q111	C02	EXACT(0)	123	111	71	23	EXACT(0)	200	192	52
tnfn1_pw060418p01q112	D02	EXACT(0)	164	119	75	19	EXACT(0)	200	142	40
tnfn1_pw060418p01q113	E02	EXACT(0)	123	120	98	36	EXACT(0)	200	187	58
tnfn1_pw060418p01q114	F02	EXACT(0)	123	109	61	17	EXACT(0)	200	196	42
tnfn1_pw060418p01q115	G02	EXACT(0)	123	119	100	30	EXACT(0)	200	175	39
tnfn1_pw060418p01q116	H02	EXACT(0)	121	107	84	19	EXACT(0)	200	188	48
tnfn1_pw060418p01q117	A03	EXACT(0)	123	119	86	24	EXACT(0)	200	177	54
tnfn1_pw060418p01q118	B03	EXACT(0)	122	112	99	26	EXACT(0)	200	180	51
tnfn1_pw060418p01q119	C03	EXACT(0)	123	119	100	32	EXACT(0)	200	190	54
tnfn1_pw060418p01q120	D03	EXACT(0)	123	120	92	27	EXACT(0)	200	190	53
tnfn1_pw060418p01q121	E03	EXACT(0)	124	109	91	28	EXACT(0)	200	186	54
tnfn1_pw060418p01q122	F03	EXACT(0)	157	145	139	41	EXACT(0)	200	176	40
tnfn1_pw060418p01q123	G03	EXACT(0)	155	146	133	38	EXACT(0)	200	178	58
tnfn1_pw060418p01q124	H03	EXACT(0)	154	145	116	32	EXACT(0)	200	191	40
tnfn1_pw060418p01q125	A04	EXACT(0)	157	145	135	43	EXACT(0)	200	158	43
tnfn1_pw060418p01q126	B04	EXACT(0)	157	153	125	31	EXACT(0)	200	192	65
tnfn1_pw060418p01q127	C04	EXACT(0)	158	153	134	44	EXACT(0)	200	192	49
tnfn1_pw060418p01q128	D04	EXACT(0)	156	145	93	30	EXACT(0)	200	143	50
tnfn1_pw060418p01q129	E04	EXACT(0)	158	153	142	39	EXACT(0)	200	188	54
tnfn1_pw060418p01q130	F04	EXACT(0)	158	153	136	41	EXACT(0)	200	195	52
tnfn1_pw060418p01q131	G04	EXACT(0)	155	145	134	45	EXACT(0)	200	184	63
tnfn1_pw060418p01q132	H04	EXACT(0)	158	152	141	39	EXACT(0)	200	133	38
tnfn1_pw060418p01q133	A05	EXACT(0)	157	152	129	29	EXACT(0)	200	195	44
tnfn1_pw060418p01q134	B05	EXACT(0)	156	153	98	19	EXACT(0)	200	160	33
tnfn1_pw060418p01q135	C05	EXACT(0)	155	144	130	39	EXACT(0)	200	149	51
tnfn1_pw060418p01q136	D05	EXACT(0)	157	152	136	41	EXACT(0)	200	191	57
tnfn1_pw060418p01q137	E05	EXACT(0)	154	145	105	22	EXACT(0)	200	175	39
tnfn1_pw060418p01q138	F05	EXACT(0)	154	152	132	36	EXACT(0)	200	179	49
tnfn1_pw060418p01q139	G05	EXACT(0)	156	153	129	36	EXACT(0)	200	193	51
tnfn1_pw060418p01q140	H05	EXACT(0)	157	145	139	37	EXACT(0)	200	179	51
tnfn1_pw060418p01q141	A06	EXACT(0)	158	153	142	46	EXACT(0)	200	186	54
tnfn1_pw060418p01q142	B06	EXACT(0)	156	145	111	30	EXACT(0)	200	188	50
tnfn1_pw060418p01q143	C06	EXACT(0)	156	150	128	41	EXACT(0)	198	90	41
tnfn1_pw060418p01q144	D06	EXACT(0)	157	151	137	44	EXACT(0)	200	196	64
tnfn1_pw060418p01q145	E06	EXACT(0)	156	145	137	39	EXACT(0)	200	185	53
tnfn1_pw060418p01q146	F06	EXACT(0)	158	153	138	35	EXACT(0)	200	183	52
tnfn1_pw060418p01q147	G06	EXACT(0)	156	150	126	34	EXACT(0)	200	187	54
tnfn1_pw060418p01q148	H06	EXACT(0)	158	153	139	37	EXACT(0)	200	177	56

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_pw060418p01q149	A07	EXACT(0)	156	148	124	26	EXACT(0)	200	184	49
tnfn1_pw060418p01q150	B07	EXACT(0)	158	153	142	39	EXACT(0)	200	187	54
tnfn1_pw060418p01q151	C07	EXACT(0)	155	152	130	42	EXACT(0)	200	144	37
tnfn1_pw060418p01q152	D07	EXACT(0)	155	152	128	36	EXACT(0)	200	192	54
tnfn1_pw060418p01q153	E07	EXACT(0)	155	116	89	23	EXACT(0)	200	186	47
tnfn1_pw060418p01q154	F07	EXACT(0)	156	153	132	34	EXACT(0)	200	178	39
tnfn1_pw060418p01q155	G07	EXACT(0)	155	112	94	26	EXACT(0)	200	192	46
tnfn1_pw060418p01q156	H07	EXACT(0)	151	145	119	41	EXACT(0)	200	139	36
tnfn1_pw060418p01q157	A08	EXACT(0)	156	145	113	35	EXACT(0)	200	182	61
tnfn1_pw060418p01q158	B08	EXACT(0)	157	145	129	32	EXACT(0)	200	180	65
tnfn1_pw060418p01q159	C08	EXACT(0)	156	142	102	29	EXACT(0)	200	187	50
tnfn1_pw060418p01q160	D08	EXACT(0)	155	145	126	37	EXACT(0)	200	186	55
tnfn1_pw060418p01q161	E08	EXACT(0)	158	152	137	32	EXACT(0)	200	191	61
tnfn1_pw060418p01q162	F08	EXACT(0)	153	116	79	33	EXACT(0)	200	184	55
tnfn1_pw060418p01q163	G08	EXACT(0)	159	153	134	48	EXACT(0)	200	169	54
tnfn1_pw060418p01q164	H08	EXACT(0)	156	153	125	34	EXACT(0)	200	157	47
tnfn1_pw060418p01q165	A09	EXACT(0)	157	152	137	43	EXACT(0)	200	192	59
tnfn1_pw060418p01q166	B09	EXACT(0)	155	153	126	34	EXACT(0)	200	190	52
tnfn1_pw060418p01q167	C09	EXACT(0)	155	145	113	31	EXACT(0)	200	185	61
tnfn1_pw060418p01q168	D09	EXACT(0)	158	152	129	41	EXACT(0)	200	192	56
tnfn1_pw060418p01q169	E09	EXACT(0)	158	153	142	40	EXACT(0)	200	191	45
tnfn1_pw060418p01q170	F09	EXACT(0)	157	152	128	36	EXACT(0)	200	181	49
tnfn1_pw060418p01q171	G09	EXACT(0)	157	153	138	41	EXACT(0)	200	193	53
tnfn1_pw060418p01q172	H09	EXACT(0)	155	145	125	36	EXACT(0)	200	194	52
tnfn1_pw060418p01q173	A10	EXACT(0)	117	111	70	17	EXACT(0)	88	48	15
tnfn1_pw060418p01q174	B10	EXACT(0)	127	119	79	23	EXACT(0)	199	131	47
tnfn1_pw060418p01q175	C10	EXACT(0)	125	120	91	23	EXACT(0)	200	190	53
tnfn1_pw060418p01q176	D10	EXACT(0)	121	83	80	29	ESTIMATE(27)	66	56	22
tnfn1_pw060418p01q177	E10	EXACT(0)	125	117	79	23	EXACT(0)	200	186	56
tnfn1_pw060418p01q178	F10	EXACT(0)	126	120	105	29	EXACT(0)	87	69	21
tnfn1_pw060418p01q179	G10	EXACT(0)	121	81	66	23	EXACT(0)	200	170	37
tnfn1_pw060418p01q180	H10	EXACT(0)	123	117	92	22	EXACT(0)	200	196	52
tnfn1_pw060418p01q181	A11	EXACT(0)	121	112	81	24	EXACT(0)	200	191	50
tnfn1_pw060418p01q182	B11	EXACT(0)	121	112	96	32	EXACT(0)	200	179	52
tnfn1_pw060418p01q183	C11	EXACT(0)	123	120	104	35	EXACT(0)	200	191	55
tnfn1_pw060418p01q184	D11	EXACT(0)	122	112	98	25	EXACT(0)	200	179	51
tnfn1_pw060418p01q185	E11	EXACT(0)	156	152	133	36	EXACT(0)	200	192	49
tnfn1_pw060418p01q186	F11	EXACT(0)	155	145	126	42	EXACT(0)	199	138	36
tnfn1_pw060418p01q187	G11	EXACT(0)	157	152	138	37	EXACT(0)	200	195	59
tnfn1_pw060418p01q188	H11	EXACT(0)	157	152	124	42	EXACT(0)	200	185	61
tnfn1_pw060418p01q189	A12	EXACT(0)	155	114	84	32	EXACT(0)	200	193	47
tnfn1_pw060418p01q190	B12	EXACT(0)	154	152	123	39	EXACT(0)	197	188	57
tnfn1_pw060418p01q191	C12	EXACT(0)	157	145	139	41	EXACT(0)	200	186	57
tnfn1_pw060418p01q192	D12	EXACT(0)	156	152	125	40	EXACT(0)	200	188	28
tnfn1_pw060418p01q193	E12	EXACT(0)	155	78	70	21	EXACT(0)	200	188	48
tnfn1_pw060418p01q194	F12	EXACT(0)	157	153	124	39	EXACT(0)	199	175	52
tnfn1_pw060418p01q195	G12	EXACT(0)	156	145	134	34	EXACT(0)	200	171	54
tnfn1_pw060418p01q196	H12	EXACT(0)	155	145	119	37	EXACT(0)	200	193	58