

***Francisella tularensis* subsp. *novicida*,
“Two-Allele” Transposon Mutant Library,
Plate 26 (tnfn1_pw060420p02)**

Catalog No. NR-8060

For research use only. Not for human use.

Contributor:

Colin Manoil, Ph.D., Professor of Genome Sciences,
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-8060 represents Plate 26 (tnfn1_pw060420p02) 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_pw060420p02q194 (Well F12) is not available due to quality issues.**

***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-8060 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 26 (tnfn1_pw060420p02), NR-8060.”

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.

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 makes 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_pw060420p02q101	A01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q102	B01	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p02q103	C01	T20	-	acid phosphatase, HAD superfamily protein	putative enzymes
tnfn1_pw060420p02q104	D01	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060420p02q105	E01	T20	kdpA	K(+)-ATPase uptake protein	transport
tnfn1_pw060420p02q106	F01	T20	-	peptidase, M20 family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060420p02q107	G01	T20	pip	proline iminopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060420p02q108	H01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q109	A02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q110	B02	T20	mvnI	multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) transporter	transport - drugs / antibacterial compounds
tnfn1_pw060420p02q111	C02	T20	potF	ATP-binding cassette putrescine uptake system, periplasmic protein	transport
tnfn1_pw060420p02q112	D02	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p02q113	E02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q114	F02	T20	cynT	carbonic anhydrase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060420p02q115	G02	T20	leuB	3-isopropylmalate dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060420p02q116	H02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q117	A03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q118	B03	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q119	C03	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q120	D03	<KAN-2>	sodC	superoxide dismutase (Cu-Zn) precursor	other metabolism - degradation, utilization, assimilation
tnfn1_pw060420p02q121	E03	<KAN-2>	sspA	stringent starvation protein A	signal transduction and regulation
tnfn1_pw060420p02q122	F03	<KAN-2>	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060420p02q123	G03	<KAN-2>	aroC	chorismate synthase	amino acid metabolism - biosynthesis
tnfn1_pw060420p02q124	H03	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q125	A04	<KAN-2>	grxC	glutaredoxin like protein	post-translational modification, protein turnover, chaperones
tnfn1_pw060420p02q126	B04	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q127	C04	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p02q128	D04	T18	-	deoxyribodipyrimidine photolyase-related protein	putative enzymes
tnfn1_pw060420p02q129	E04	T18	-	transcriptional regulator, ArsR family	signal transduction and regulation
tnfn1_pw060420p02q130	F04	T18	-	peptide methionine sulfoxide reductase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060420p02q131	G04	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q132	H04	T18	-	-	-
tnfn1_pw060420p02q133	A05	T18	-	metallo-beta-lactamase superfamily protein	putative enzymes
tnfn1_pw060420p02q134	B05	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q135	C05	T18	-	acid phosphatase/phosphotransferase	putative enzymes
tnfn1_pw060420p02q136	D05	T18	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060420p02q137	E05	T18	-	Fe ²⁺ /Zn ²⁺ uptake regulator protein	signal transduction and regulation
tnfn1_pw060420p02q138	F05	T20	wzx	O antigen flippase	transport
tnfn1_pw060420p02q139	G05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q140	H05	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p02q141	A06	T20	-	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	cell wall / LPS / capsule
tnfn1_pw060420p02q142	B06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q143	C06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q144	D06	T20	-	histidine acid phosphatase	putative enzymes
tnfn1_pw060420p02q145	E06	T20	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060420p02q146	F06	T20	-	glycosyl transferase, group 2	cell wall / LPS / capsule
tnfn1_pw060420p02q147	G06	T20	araJ	conserved inner membrane protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q148	H06	T20	hslU	ATP-dependent protease HslVU, ATPase subunit	post-translational modification, protein turnover, chaperones

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060420p02q149	A07	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p02q150	B07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q151	C07	T20	sdaC	serine permease	transport - amino-acid
tnfn1_pw060420p02q152	D07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q153	E07	T20	ostA2	organic solvent tolerance protein OstA	cell wall / LPS / capsule
tnfn1_pw060420p02q154	F07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q155	G07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p02q156	H07	T20	-		
tnfn1_pw060420p02q157	A08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q158	B08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q159	C08	T20	kdpC	potassium-transporting ATPase C chain	transport
tnfn1_pw060420p02q160	D08	T20	deaD	DEAD-box subfamily ATP-dependent helicase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060420p02q161	E08	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060420p02q162	F08	T20	cbpA	chitin-binding protein	putative enzymes
tnfn1_pw060420p02q163	G08	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p02q164	H08	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p02q165	A09	T20	-	chologylglycine hydrolase family protein	cell wall / LPS / capsule
tnfn1_pw060420p02q166	B09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q167	C09	T20	-	aspartate/glutamate transporter	transport - amino-acid
tnfn1_pw060420p02q168	D09	T20	-	ArsB arsenite/antimonite exporter	transport
tnfn1_pw060420p02q169	E09	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p02q170	F09	<KAN-2>	minC	septum formation inhibitor	cell cycle
tnfn1_pw060420p02q171	G09	<KAN-2>	secB1	preprotein translocase, subunit B	motility, attachment and secretion structure
tnfn1_pw060420p02q172	H09	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q173	A10	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p02q174	B10	T18	-	haloacid dehalogenase-like hydrolase	putative enzymes
tnfn1_pw060420p02q175	C10	T18	cls	cardiolipin synthetase	fatty acids and lipids metabolism
tnfn1_pw060420p02q176	D10	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p02q177	E10	T18	era	GTP-binding protein	putative enzymes
tnfn1_pw060420p02q178	F10	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q179	G10	T18	comL	competence lipoprotein ComL	transport
tnfn1_pw060420p02q180	H10	T18	-	bifunctional NMN adenylyltransferase/Nudix hydrolase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060420p02q181	A11	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q182	B11	T18	-	sugar porter (SP) family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060420p02q183	C11	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q184	D11	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p02q185	E11	T20	-	Rieske (2Fe-2S) domain protein	putative enzymes
tnfn1_pw060420p02q186	F11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p02q187	G11	T20	-	serine peptidase, S49 family	post-translational modification, protein turnover, chaperones
tnfn1_pw060420p02q188	H11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p02q189	A12	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060420p02q190	B12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p02q191	C12	T20	ribC	riboflavin synthase alpha chain	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060420p02q192	D12	T20	betT	betaine/carnitine/choline transporter (BCCT) family protein	transport
tnfn1_pw060420p02q193	E12	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p02q194	F12	T20	mltA	membrane-bound lytic murein transglycosylase	cell wall / LPS / capsule
tnfn1_pw060420p02q195	G12	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p02q196	H12	T20	-	major facilitator superfamily (MFS) transport protein	transport

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_pw060420p02q101	A01	C	1903156	R	FTN_1773	1903020	1903385	R	122	230(366)
tnfn1_pw060420p02q102	B01	C	1679303	F	FTN_1582	1679176	1679886	R	237	584(711)
tnfn1_pw060420p02q103	C01	C	1121059	R	FTN_1061	1120390	1121136	R	249	78(747)
tnfn1_pw060420p02q104	D01	C	1083382	R	FTN_1026	1082927	1084117	R	397	736(1191)
tnfn1_pw060420p02q105	E01	C	1845169	R	FTN_1718	1844009	1845727	R	573	559(1719)
tnfn1_pw060420p02q106	F01	C	1239287	F	FTN_1169	1239077	1240234	F	386	211(1158)
tnfn1_pw060420p02q107	G01	C	1859602	F	FTN_1731	1859256	1860191	R	312	590(936)
tnfn1_pw060420p02q108	H01	C	10423	R	FTN_0012	10220	10438	R	73	16(219)
tnfn1_pw060420p02q109	A02	C	944297	F	FTN_0887	944252	945208	R	319	912(957)
tnfn1_pw060420p02q110	B02	U	284499	R	FTN_0276	283566	285104	F	513	934(1539)
tnfn1_pw060420p02q111	C02	C	599867	R	FTN_0572	599215	600393	F	393	653(1179)
tnfn1_pw060420p02q112	D02	C	1486060	R	FTN_1409	1485991	1487373	R	461	1314(1383)
tnfn1_pw060420p02q113	E02	C	892933	F	FTN_0835	892311	893027	R	239	95(717)
tnfn1_pw060420p02q114	F02	C	1149775	F	FTN_1087	1149427	1150110	R	228	336(684)
tnfn1_pw060420p02q115	G02	C	70229	F	FTN_0059	69707	70783	R	359	555(1077)
tnfn1_pw060420p02q116	H02	C	1129147	F	FTN_1069	1128158	1130653	R	832	1507(2496)
tnfn1_pw060420p02q117	A03	C	1564107	F	FTN_1476	1563577	1564161	R	195	55(585)
tnfn1_pw060420p02q118	B03	C	1352282	F	FTN_1279	1352177	1352596	F	140	106(420)
tnfn1_pw060420p02q119	C03	C	885672	R	FTN_0828	885562	885984	R	141	313(423)
tnfn1_pw060420p02q120	D03	C	403586	F	FTN_0405	403380	403934	F	185	207(555)
tnfn1_pw060420p02q121	E03	U	575453	F	FTN_0549	574840	575469	F	210	614(630)
tnfn1_pw060420p02q122	F03	C	1483157	R	FTN_1405	1482889	1483809	R	307	653(921)
tnfn1_pw060420p02q123	G03	U	401241	R	FTN_0402	400839	401894	R	352	654(1056)
tnfn1_pw060420p02q124	H03	C	1269902	F	FTN_1196	1269690	1270025	F	112	213(336)
tnfn1_pw060420p02q125	A04	C	820157	F	FTN_0762	820018	820263	F	82	140(246)
tnfn1_pw060420p02q126	B04	C	1220064	R	FTN_1153	1219531	1220226	R	232	163(696)
tnfn1_pw060420p02q127	C04	U	1769263	R	FTN_1656	1769013	1770077	R	355	815(1065)
tnfn1_pw060420p02q128	D04	U	365077	F	FTN_0362	364836	366362	F	509	242(1527)
tnfn1_pw060420p02q129	E04	C	395256	R	FTN_0395	395071	395433	R	121	178(363)
tnfn1_pw060420p02q130	F04	U	825922	R	FTN_0769	825750	826601	F	284	173(852)
tnfn1_pw060420p02q131	G04	C	1471537	F	FTN_1394	1471522	1471791	R	90	255(270)
tnfn1_pw060420p02q132	H04	C	343910	F	intergenic					
tnfn1_pw060420p02q133	A05	C	1297327	R	FTN_1227	1296419	1297378	R	320	52(960)
tnfn1_pw060420p02q134	B05	C	1725055	R	FTN_1615	1724061	1725338	R	426	284(1278)
tnfn1_pw060420p02q135	C05	C	726227	F	FTN_0681	725743	726366	F	208	485(624)
tnfn1_pw060420p02q136	D05	C	1056446	F	FTN_0997	1056320	1057768	F	483	127(1449)
tnfn1_pw060420p02q137	E05	C	936634	F	FTN_0881	936452	936880	F	143	183(429)
tnfn1_pw060420p02q138	F05	U	1499339	R	FTN_1420	1498689	1499933	R	415	595(1245)
tnfn1_pw060420p02q139	G05	C	11493	F	FTN_0013	10939	11835	R	299	343(897)
tnfn1_pw060420p02q140	H05	C	428745	R	FTN_0431	428206	429645	F	480	540(1440)
tnfn1_pw060420p02q141	A06	U	572951	R	FTN_0546	572304	574064	R	587	1114(1761)
tnfn1_pw060420p02q142	B06	C	1517552	F	FTN_1433	1517238	1518122	R	295	571(885)
tnfn1_pw060420p02q143	C06	C	1079105	R	FTN_1020	1078395	1079204	R	270	100(810)
tnfn1_pw060420p02q144	D06	C	1009988	F	FTN_0954	1009684	1010889	F	402	305(1206)
tnfn1_pw060420p02q145	E06	C	873639	F	FTN_0816	872849	874177	F	443	791(1329)
tnfn1_pw060420p02q146	F06	C	309490	R	FTN_0300	308570	310246	F	559	921(1677)
tnfn1_pw060420p02q147	G06	C	613519	F	FTN_0584	612820	613983	F	388	700(1164)
tnfn1_pw060420p02q148	H06	C	1054099	R	FTN_0996	1053996	1055360	F	455	104(1365)

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_pw060420p02q149	A07	C	606968	F	FTN_0578	606155	607375	F	407	814(1221)
tnfn1_pw060420p02q150	B07	U	1079105	R	FTN_1020	1078395	1079204	R	270	100(810)
tnfn1_pw060420p02q151	C07	C	16134	F	FTN_0018	15688	16908	R	407	775(1221)
tnfn1_pw060420p02q152	D07	C	1581719	F	FTN_1489	1581021	1581764	R	248	46(744)
tnfn1_pw060420p02q153	E07	C	758849	F	FTN_0713	757653	760250	R	866	1402(2598)
tnfn1_pw060420p02q154	F07	C	379944	F	FTN_0378	379010	380461	F	484	935(1452)
tnfn1_pw060420p02q155	G07	C	30808	R	FTN_0030	30805	31209	R	135	402(405)
tnfn1_pw060420p02q156	H07	U	709944	R	intergenic					
tnfn1_pw060420p02q157	A08	C	1598383	R	FTN_1503	1598264	1598656	R	131	274(393)
tnfn1_pw060420p02q158	B08	C	1132828	R	FTN_1071	1132424	1133899	R	492	1072(1476)
tnfn1_pw060420p02q159	C08	C	1841738	R	FTN_1716	1841389	1841940	R	184	203(552)
tnfn1_pw060420p02q160	D08	C	734348	F	FTN_0690	733590	735296	F	569	759(1707)
tnfn1_pw060420p02q161	E08	C	1161191	F	FTN_1099	1160507	1161379	F	291	685(873)
tnfn1_pw060420p02q162	F08	C	1575384	F	FTN_1485	1574733	1576397	F	555	652(1665)
tnfn1_pw060420p02q163	G08	C	397586	F	FTN_0398	397551	398084	R	178	499(534)
tnfn1_pw060420p02q164	H08	C	1052652	R	FTN_0994	1052499	1053245	R	249	594(747)
tnfn1_pw060420p02q165	A09	C	821950	R	FTN_0765	821246	822211	R	322	262(966)
tnfn1_pw060420p02q166	B09	C	840685	R	FTN_0782	840650	841222	F	191	36(573)
tnfn1_pw060420p02q167	C09	C	4924	R	FTN_0004	4244	5764	F	507	681(1521)
tnfn1_pw060420p02q168	D09	C	857888	F	FTN_0800	857562	858587	R	342	700(1026)
tnfn1_pw060420p02q169	E09	C	7443	R	FTN_0007	7364	7678	R	105	236(315)
tnfn1_pw060420p02q170	F09	C	338163	R	FTN_0331	337781	338464	R	228	302(684)
tnfn1_pw060420p02q171	G09	C	131836	F	FTN_0121	131668	132114	F	149	169(447)
tnfn1_pw060420p02q172	H09	C	769418	F	FTN_0715	766940	770707	F	1256	2479(3768)
tnfn1_pw060420p02q173	A10	C	185443	R	FTN_0169	185208	185747	R	180	305(540)
tnfn1_pw060420p02q174	B10	C	1301821	F	FTN_1233	1301598	1302386	R	263	566(789)
tnfn1_pw060420p02q175	C10	C	932181	F	FTN_0877	931734	933161	F	476	448(1428)
tnfn1_pw060420p02q176	D10	U	1802379	R	FTN_1686	1801799	1803325	F	509	581(1527)
tnfn1_pw060420p02q177	E10	C	1210600	R	FTN_1145	1210567	1211457	R	297	858(891)
tnfn1_pw060420p02q178	F10	C	974402	R	FTN_0915	974276	974719	R	148	318(444)
tnfn1_pw060420p02q179	G10	C	1335113	R	FTN_1263	1335078	1335899	R	274	787(822)
tnfn1_pw060420p02q180	H10	U	489451	R	FTN_0483	488789	489829	F	347	663(1041)
tnfn1_pw060420p02q181	A11	C	994761	R	FTN_0933	994548	994829	F	94	214(282)
tnfn1_pw060420p02q182	B11	C	1529900	F	FTN_1441	1529445	1530722	R	426	823(1278)
tnfn1_pw060420p02q183	C11	C	1546004	F	FTN_1457	1545936	1546451	F	172	69(516)
tnfn1_pw060420p02q184	D11	C	1814146	F	FTN_1696	1813595	1814374	F	260	552(780)
tnfn1_pw060420p02q185	E11	U	1882607	F	FTN_1753	1882116	1883009	F	298	492(894)
tnfn1_pw060420p02q186	F11	C	1608181	F	FTN_1511	1607392	1608612	F	407	790(1221)
tnfn1_pw060420p02q187	G11	C	129706	F	FTN_0118	129531	130451	F	307	176(921)
tnfn1_pw060420p02q188	H11	C	1148123	R	FTN_1085	1147596	1148465	F	290	528(870)
tnfn1_pw060420p02q189	A12	U	795376	R	FTN_0741	794174	795628	R	485	253(1455)
tnfn1_pw060420p02q190	B12	C	1339892	F	FTN_1268	1339737	1340459	F	241	156(723)
tnfn1_pw060420p02q191	C12	C	124364	F	FTN_0113	123993	124595	R	201	232(603)
tnfn1_pw060420p02q192	D12	C	824521	R	FTN_0767	823200	825149	F	650	1322(1950)
tnfn1_pw060420p02q193	E12	C	1686347	F	FTN_1588	1686132	1687331	F	400	216(1200)
tnfn1_pw060420p02q194	F12	C	1358991	R	FTN_1286	1358907	1360070	F	388	85(1164)
tnfn1_pw060420p02q195	G12	C	1423920	F	FTN_1345	1423503	1424552	F	350	418(1050)
tnfn1_pw060420p02q196	H12	C	607810	R	FTN_0579	607388	608659	R	424	850(1272)

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_pw060420p02q101	A01	EXACT(0)	156	142	107	25	EXACT(0)	200	146	26
tnfn1_pw060420p02q102	B01	EXACT(0)	156	145	130	40	EXACT(0)	199	176	50
tnfn1_pw060420p02q103	C01	EXACT(0)	154	139	125	37	EXACT(0)	199	148	32
tnfn1_pw060420p02q104	D01	EXACT(0)	156	142	94	23	EXACT(0)	200	175	53
tnfn1_pw060420p02q105	E01	EXACT(0)	159	151	142	43	EXACT(0)	200	186	50
tnfn1_pw060420p02q106	F01	EXACT(0)	155	145	110	29	EXACT(0)	199	190	55
tnfn1_pw060420p02q107	G01	EXACT(0)	159	152	142	37	EXACT(0)	199	188	49
tnfn1_pw060420p02q108	H01	EXACT(0)	157	136	91	23	EXACT(0)	193	157	20
tnfn1_pw060420p02q109	A02	EXACT(0)	157	145	121	36	EXACT(0)	200	189	50
tnfn1_pw060420p02q110	B02	EXACT(0)	156	152	125	41	EXACT(0)	200	191	66
tnfn1_pw060420p02q111	C02	EXACT(0)	157	116	98	28	EXACT(0)	200	191	58
tnfn1_pw060420p02q112	D02	EXACT(0)	158	152	125	29	EXACT(0)	199	179	47
tnfn1_pw060420p02q113	E02	EXACT(0)	156	145	108	30	EXACT(0)	200	185	51
tnfn1_pw060420p02q114	F02	EXACT(0)	155	148	120	40	EXACT(0)	200	191	61
tnfn1_pw060420p02q115	G02	EXACT(0)	160	152	141	38	EXACT(0)	173	159	51
tnfn1_pw060420p02q116	H02	EXACT(0)	157	143	134	26	EXACT(0)	199	188	31
tnfn1_pw060420p02q117	A03	EXACT(0)	158	145	107	23	EXACT(0)	200	171	62
tnfn1_pw060420p02q118	B03	EXACT(0)	120	120	105	38	EXACT(0)	200	184	48
tnfn1_pw060420p02q119	C03	EXACT(0)	114	112	97	44	EXACT(0)	200	178	65
tnfn1_pw060420p02q120	D03	EXACT(0)	121	112	89	22	EXACT(0)	200	198	45
tnfn1_pw060420p02q121	E03	EXACT(0)	116	112	107	47	EXACT(0)	200	189	61
tnfn1_pw060420p02q122	F03	EXACT(0)	112	106	96	45	EXACT(0)	200	187	61
tnfn1_pw060420p02q123	G03	EXACT(0)	112	106	96	40	EXACT(0)	200	196	63
tnfn1_pw060420p02q124	H03	EXACT(0)	107	106	96	50	EXACT(0)	200	181	51
tnfn1_pw060420p02q125	A04	EXACT(0)	116	118	97	31	EXACT(0)	200	189	65
tnfn1_pw060420p02q126	B04	EXACT(0)	124	120	95	24	EXACT(0)	199	182	50
tnfn1_pw060420p02q127	C04	EXACT(0)	123	112	101	32	EXACT(0)	200	179	54
tnfn1_pw060420p02q128	D04	EXACT(0)	121	112	94	32	EXACT(0)	200	161	40
tnfn1_pw060420p02q129	E04	EXACT(0)	122	109	93	35	EXACT(0)	186	165	43
tnfn1_pw060420p02q130	F04	EXACT(0)	123	112	101	30	EXACT(0)	200	189	44
tnfn1_pw060420p02q131	G04	EXACT(0)	123	112	86	20	EXACT(0)	200	173	43
tnfn1_pw060420p02q132	H04	EXACT(0)	123	109	81	23	EXACT(0)	200	183	41
tnfn1_pw060420p02q133	A05	EXACT(0)	123	112	45	17	EXACT(0)	199	178	30
tnfn1_pw060420p02q134	B05	EXACT(0)	125	120	109	28	EXACT(0)	200	193	49
tnfn1_pw060420p02q135	C05	EXACT(0)	123	112	89	26	EXACT(0)	200	189	54
tnfn1_pw060420p02q136	D05	EXACT(0)	122	112	90	20	EXACT(0)	199	179	44
tnfn1_pw060420p02q137	E05	EXACT(0)	125	120	100	30	EXACT(0)	200	184	48
tnfn1_pw060420p02q138	F05	EXACT(0)	162	150	118	33	EXACT(0)	200	185	48
tnfn1_pw060420p02q139	G05	EXACT(0)	156	145	134	39	EXACT(0)	200	183	44
tnfn1_pw060420p02q140	H05	EXACT(0)	155	145	124	40	EXACT(0)	195	171	43
tnfn1_pw060420p02q141	A06	EXACT(0)	156	153	94	34	EXACT(0)	200	189	62
tnfn1_pw060420p02q142	B06	EXACT(0)	158	153	135	34	EXACT(0)	199	183	45
tnfn1_pw060420p02q143	C06	EXACT(0)	155	145	106	31	EXACT(0)	200	174	45
tnfn1_pw060420p02q144	D06	EXACT(0)	157	145	132	34	EXACT(0)	163	150	43
tnfn1_pw060420p02q145	E06	EXACT(0)	157	153	137	39	EXACT(0)	200	188	57
tnfn1_pw060420p02q146	F06	EXACT(0)	158	157	131	31	EXACT(0)	199	184	49
tnfn1_pw060420p02q147	G06	EXACT(0)	157	150	126	28	EXACT(0)	199	184	52
tnfn1_pw060420p02q148	H06	EXACT(0)	156	153	132	46	EXACT(0)	200	183	67

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_pw060420p02q149	A07	EXACT(0)	156	153	128	37	EXACT(0)	200	186	57
tnfn1_pw060420p02q150	B07	EXACT(0)	155	145	106	31	EXACT(0)	200	174	45
tnfn1_pw060420p02q151	C07	EXACT(0)	155	152	131	41	EXACT(0)	200	187	66
tnfn1_pw060420p02q152	D07	EXACT(0)	155	151	133	46	EXACT(0)	200	169	61
tnfn1_pw060420p02q153	E07	EXACT(0)	155	152	131	45	EXACT(0)	200	192	66
tnfn1_pw060420p02q154	F07	EXACT(0)	156	145	136	37	EXACT(0)	200	155	39
tnfn1_pw060420p02q155	G07	EXACT(0)	155	145	116	34	EXACT(0)	200	188	53
tnfn1_pw060420p02q156	H07	EXACT(0)	155	145	53	15	ESTIMATE(37)	160	58	17
tnfn1_pw060420p02q157	A08	EXACT(0)	160	153	141	36	EXACT(0)	200	187	55
tnfn1_pw060420p02q158	B08	EXACT(0)	155	145	122	42	EXACT(0)	200	181	51
tnfn1_pw060420p02q159	C08	EXACT(0)	156	153	137	48	EXACT(0)	200	197	60
tnfn1_pw060420p02q160	D08	EXACT(0)	158	153	136	37	EXACT(0)	199	186	42
tnfn1_pw060420p02q161	E08	EXACT(0)	156	152	130	42	EXACT(0)	200	185	66
tnfn1_pw060420p02q162	F08	EXACT(0)	158	153	138	37	EXACT(0)	199	184	53
tnfn1_pw060420p02q163	G08	EXACT(0)	156	154	130	37	EXACT(0)	199	185	44
tnfn1_pw060420p02q164	H08	EXACT(0)	157	153	125	41	EXACT(0)	200	182	64
tnfn1_pw060420p02q165	A09	EXACT(0)	155	145	97	26	EXACT(0)	200	193	51
tnfn1_pw060420p02q166	B09	EXACT(0)	157	151	138	42	EXACT(0)	200	180	65
tnfn1_pw060420p02q167	C09	EXACT(0)	159	145	131	31	EXACT(0)	200	190	54
tnfn1_pw060420p02q168	D09	EXACT(0)	156	145	124	38	EXACT(0)	201	136	41
tnfn1_pw060420p02q169	E09	EXACT(0)	118	112	77	22	EXACT(0)	200	137	17
tnfn1_pw060420p02q170	F09	EXACT(0)	120	112	102	46	EXACT(0)	200	195	60
tnfn1_pw060420p02q171	G09	EXACT(0)	121	112	101	27	EXACT(0)	200	193	60
tnfn1_pw060420p02q172	H09	EXACT(0)	110	111	96	43	EXACT(0)	200	191	63
tnfn1_pw060420p02q173	A10	EXACT(0)	108	106	106	39	EXACT(0)	200	181	42
tnfn1_pw060420p02q174	B10	EXACT(0)	125	110	100	26	EXACT(0)	200	189	44
tnfn1_pw060420p02q175	C10	EXACT(0)	124	120	89	22	EXACT(0)	200	186	39
tnfn1_pw060420p02q176	D10	EXACT(0)	122	105	79	23	EXACT(0)	108	100	32
tnfn1_pw060420p02q177	E10	EXACT(0)	124	109	51	13	EXACT(0)	199	176	35
tnfn1_pw060420p02q178	F10	EXACT(0)	121	112	93	27	EXACT(0)	200	187	36
tnfn1_pw060420p02q179	G10	EXACT(0)	125	120	104	33	EXACT(0)	199	179	45
tnfn1_pw060420p02q180	H10	EXACT(0)	122	112	96	30	EXACT(0)	200	177	47
tnfn1_pw060420p02q181	A11	EXACT(0)	122	120	94	29	EXACT(0)	200	184	51
tnfn1_pw060420p02q182	B11	EXACT(0)	123	119	98	31	EXACT(0)	200	188	57
tnfn1_pw060420p02q183	C11	EXACT(0)	121	105	76	21	EXACT(0)	200	188	50
tnfn1_pw060420p02q184	D11	EXACT(0)	126	119	110	26	EXACT(0)	200	188	51
tnfn1_pw060420p02q185	E11	EXACT(0)	157	145	126	31	EXACT(0)	198	181	47
tnfn1_pw060420p02q186	F11	EXACT(0)	159	155	129	36	EXACT(0)	199	185	43
tnfn1_pw060420p02q187	G11	EXACT(0)	155	145	132	44	EXACT(0)	200	160	48
tnfn1_pw060420p02q188	H11	EXACT(0)	156	146	107	31	EXACT(0)	200	189	46
tnfn1_pw060420p02q189	A12	EXACT(0)	155	144	109	33	EXACT(0)	200	192	58
tnfn1_pw060420p02q190	B12	EXACT(0)	157	114	90	24	EXACT(0)	200	187	50
tnfn1_pw060420p02q191	C12	EXACT(0)	155	142	79	20	EXACT(0)	200	186	47
tnfn1_pw060420p02q192	D12	EXACT(0)	156	154	107	32	EXACT(0)	200	193	57
tnfn1_pw060420p02q193	E12	EXACT(0)	157	145	132	40	EXACT(0)	200	192	60
tnfn1_pw060420p02q194	F12	EXACT(0)	157	153	131	38	EXACT(0)	200	171	51
tnfn1_pw060420p02q195	G12	EXACT(0)	156	153	137	41	EXACT(0)	200	197	48
tnfn1_pw060420p02q196	H12	EXACT(0)	156	153	129	37	EXACT(0)	200	185	56