

***Francisella tularensis* subsp. *novicida*,
“Two-Allele” Transposon Mutant Library,
Plate 31 (tnfn1_pw060510p03)**

Catalog No. NR-8065

For research use only. Not for human use.

Contributor:

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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-8065 represents Plate 31 (tnfn1_pw060510p03) 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_pw060510p03q138 (Well F05) was not available due to quality issues at the time of release of Plate 31, 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 bacterial culture in Tryptic Soy broth containing 0.1% L-cysteine and 10 µg/mL kanamycin supplemented with 5% glycerol. The volume aliquoted per well is incated on the Certificate of Analysis for each lot.

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-8065 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 31 (tnfn1_pw060510p03), NR-8065.”

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/bmb15/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_pw060510p03q101	A01	T20	thrB	homoserine kinase	amino acid metabolism - biosynthesis
tnfn1_pw060510p03q102	B01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p03q103	C01	T20	thrB	homoserine kinase	amino acid metabolism - biosynthesis
tnfn1_pw060510p03q104	D01	T20	glk	glucose kinase (glucokinase)	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q105	E01	T20	trpB	tryptophan synthase beta chain	amino acid metabolism - biosynthesis
tnfn1_pw060510p03q106	F01	T20	recC	exodeoxyribonuclease V, gamma subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q107	G01	T20	wbtD	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060510p03q108	H01	T20	-	DNA/RNA helicase	DNA replication, recombination, modification and repair - replication
tnfn1_pw060510p03q109	A02	T20	ung	uracil DNA glycosylase	DNA replication, recombination, modification and repair - repair
tnfn1_pw060510p03q110	B02	T20	dapD	tetrahydrodipicolinate succinylase subunit	amino acid metabolism - biosynthesis
tnfn1_pw060510p03q111	C02	T20	glgC	glucose-1-phosphate adenylyltransferase	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p03q112	D02	<KAN-2>	-	ThiJ/Pilp family protein	putative enzymes
tnfn1_pw060510p03q113	E02	<KAN-2>	deoD	purine nucleoside phosphorylase	nucleotides and nucleosides metabolism
tnfn1_pw060510p03q114	F02	T18	-	prophage maintenance system killer protein (DOC)	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060510p03q115	G02	T18	tdh	L-threonine 3-dehydrogenase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q116	H02	T18	-		
tnfn1_pw060510p03q117	A03	T18	-	monovalent cation:proton antiporter	transport
tnfn1_pw060510p03q118	B03	<KAN-2>	kdpB	potassium-transporting ATPase B chain	transport
tnfn1_pw060510p03q119	C03	T20	-	glycosyl hydrolase family 3	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p03q120	D03	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060510p03q121	E03	T20	purL	phosphoribosylformylglycinamide synthase	nucleotides and nucleosides metabolism
tnfn1_pw060510p03q122	F03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p03q123	G03	T20	sbcB	exodeoxyribonuclease I	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q124	H03	T20	radA	DNA repair protein radA	DNA replication, recombination, modification and repair - repair
tnfn1_pw060510p03q125	A04	T20	gabD	succinate semialdehyde dehydrogenase (NAD(P)+ dependent)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q126	B04	T20	purU	formyltetrahydrofolate deformylase	nucleotides and nucleosides metabolism
tnfn1_pw060510p03q127	C04	T20	-	pseudogene: nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	pseudogene
tnfn1_pw060510p03q128	D04	T20	manC	mannose-1-phosphate guanylyltransferase	cell wall / LPS / capsule
tnfn1_pw060510p03q129	E04	T20	tdk	thymidine kinase	nucleotides and nucleosides metabolism
tnfn1_pw060510p03q130	F04	<KAN-2>	metIQ	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	transport - amino-acid
tnfn1_pw060510p03q131	G04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q132	H04	T18	rnc	ribonuclease III	transcription
tnfn1_pw060510p03q133	A05	T18	-	pyridoxal-dependent decarboxylase	amino acid metabolism - biosynthesis
tnfn1_pw060510p03q134	B05	T20	-	metallopeptidase, M16 family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060510p03q135	C05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q136	D05	T20	-		
tnfn1_pw060510p03q137	E05	T18	pilE	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060510p03q138	F05	T18	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060510p03q139	G05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p03q140	H05	T18	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060510p03q141	A06	T18	aceF	pyruvate dehydrogenase complex, E2 component, dihydroliipoamide acyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q142	B06	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060510p03q143	C06	T20	recD	exodeoxyribonuclease V, alpha subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q144	D06	T20	glxA	glutaminase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q145	E06	T20	pdpA	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q146	F06	T20	-	type I restriction-modification system, subunit M (methyltransferase)	DNA replication, recombination, modification and repair - repair
tnfn1_pw060510p03q147	G06	T20	-	tRNA-methylthiotransferase MiaB protein	translation, ribosomal structure and biogenesis
tnfn1_pw060510p03q148	H06	T20	uvrB	excinuclease ABC, subunit B	DNA replication, recombination, modification and repair - restriction/modification

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060510p03q149	A07	T20	xseA	exodeoxyribonuclease VII large subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q150	B07	T20	rplI	50S ribosomal protein L9	translation, ribosomal structure and biogenesis
tnfn1_pw060510p03q151	C07	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060510p03q152	D07	T20	glxK	glycerate kinase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q153	E07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q154	F07	T20	glgA	glycogen synthase	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p03q155	G07	T20	sdaA	L-serine dehydratase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q156	H07	T20	rep	UvrD/REP superfamily I DNA and RNA helicases	DNA replication, recombination, modification and repair
tnfn1_pw060510p03q157	A08	T20	-	alanine racemase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q158	B08	<KAN-2>	-	rRNA methylase, SpoU family	translation, ribosomal structure and biogenesis
tnfn1_pw060510p03q159	C08	<KAN-2>	hfq	host factor I for bacteriophage Q beta replication	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060510p03q160	D08	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q161	E08	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p03q162	F08	T18	purH	AICAR transformylase/IMP cyclohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060510p03q163	G08	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p03q164	H08	T18	ipdC	indolepyruvate decarboxylase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q165	A09	T18	galK	galactokinase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q166	B09	T20	fadA	acetyl-CoA acetyltransferase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q167	C09	T20	kbl	2-amino-3-ketobutyrate coenzyme A ligase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q168	D09	T20	-	tRNA-dihydrouridine synthase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p03q169	E09	T20	kbl	2-amino-3-ketobutyrate coenzyme A ligase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q170	F09	T20	galP1	galactose-proton symporter, major facilitator superfamily (MFS) transport protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060510p03q171	G09	T20	-	asparaginase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q172	H09	T20	thrC	threonine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060510p03q173	A10	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p03q174	B10	T20	uvrD	DNA helicase II	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q175	C10	T20	-	Mg-dependent DNase	DNA replication, recombination, modification and repair - degradation
tnfn1_pw060510p03q176	D10	<KAN-2>	yjfH	tRNA/rRNA methyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p03q177	E10	<KAN-2>	cspC	cold shock protein, DNA-binding	signal transduction and regulation
tnfn1_pw060510p03q178	F10	T20	-	amino acid permease	transport - amino-acid
tnfn1_pw060510p03q179	G10	T18	-	sugar porter (SP) family	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060510p03q180	H10	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q181	A11	T18	oppF	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060510p03q182	B11	T20	ackA	propionate kinase 2 / acetate kinase A	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q183	C11	T20	rluD	ribosomal large subunit pseudouridine synthase D	translation, ribosomal structure and biogenesis
tnfn1_pw060510p03q184	D11	T20	kdpD	two component regulator, sensor histidine kinase kdpD	signal transduction and regulation
tnfn1_pw060510p03q185	E11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p03q186	F11	T20	manB	phosphomannomutase	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p03q187	G11	T20	purA	adenylosuccinate synthetase	nucleotides and nucleosides metabolism
tnfn1_pw060510p03q188	H11	T20	chiA	chitinase, glycosyl hydrolase family 18	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p03q189	A12	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q190	B12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p03q191	C12	<KAN-2>	-	peroxiredoxin of the AhpC/TSA family	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060510p03q192	D12	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060510p03q193	E12	T20	xerC	site-specific recombinase	DNA replication, recombination, modification and repair
tnfn1_pw060510p03q194	F12	T18	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060510p03q195	G12	T18	recO	RecFOR complex, RecO component	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p03q196	H12	T18	parB	chromosome partition protein B	cell cycle

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_pw060510p03q101	A01	C	548287	F	FTN_0526	547735	548685	F	317	553(951)
tnfn1_pw060510p03q102	B01	C	1243949	F	FTN_1172	1243043	1244494	R	484	546(1452)
tnfn1_pw060510p03q103	C01	C	548287	F	FTN_0526	547735	548685	F	317	553(951)
tnfn1_pw060510p03q104	D01	C	468669	R	FTN_0462	468195	469208	F	338	475(1014)
tnfn1_pw060510p03q105	E01	C	1867183	F	FTN_1739	1866821	1868008	F	396	363(1188)
tnfn1_pw060510p03q106	F01	C	1440996	R	FTN_1359	1439523	1442759	R	1079	1764(3237)
tnfn1_pw060510p03q107	G01	U	1508315	R	FTN_1427	1507571	1508659	R	363	345(1089)
tnfn1_pw060510p03q108	H01	U	95153	R	FTN_0084	93832	96570	F	913	1322(2739)
tnfn1_pw060510p03q109	A02	C	1576547	F	FTN_1486	1576437	1577096	R	220	550(660)
tnfn1_pw060510p03q110	B02	C	1855386	F	FTN_1727	1855155	1855901	R	249	516(747)
tnfn1_pw060510p03q111	C02	C	531916	R	FTN_0515	531823	533091	F	423	94(1269)
tnfn1_pw060510p03q112	D02	C	897420	F	FTN_0841	897004	897678	F	225	417(675)
tnfn1_pw060510p03q113	E02	C	712527	F	FTN_0669	712184	712903	F	240	344(720)
tnfn1_pw060510p03q114	F02	C	292466	F	FTN_0284	291793	292794	F	334	674(1002)
tnfn1_pw060510p03q115	G02	C	656835	R	FTN_0625	656096	657148	R	351	314(1053)
tnfn1_pw060510p03q116	H02	C	1042360	F	intergenic					
tnfn1_pw060510p03q117	A03	C	158009	R	FTN_0143	156853	158736	F	628	1157(1884)
tnfn1_pw060510p03q118	B03	C	1843398	R	FTN_1717	1841960	1843996	R	679	599(2037)
tnfn1_pw060510p03q119	C03	C	863559	F	FTN_0806	862723	864387	R	555	829(1665)
tnfn1_pw060510p03q120	D03	C	312685	R	FTN_0303	311969	312892	F	308	717(924)
tnfn1_pw060510p03q121	E03	C	1820085	R	FTN_1699	1816650	1820534	R	1295	450(3885)
tnfn1_pw060510p03q122	F03	U	1298905	R	FTN_1229	1298595	1299305	F	237	311(711)
tnfn1_pw060510p03q123	G03	U	1250388	F	FTN_1177	1249665	1251110	R	482	723(1446)
tnfn1_pw060510p03q124	H03	C	398781	F	FTN_0399	398092	399459	R	456	679(1368)
tnfn1_pw060510p03q125	A04	C	138540	R	FTN_0127	137693	139123	F	477	848(1431)
tnfn1_pw060510p03q126	B04	C	662610	F	FTN_0629	662421	663251	F	277	190(831)
tnfn1_pw060510p03q127	C04	C	650940	F	FTN_0619	650233	651024	F	264	708(792)
tnfn1_pw060510p03q128	D04	C	1497175	R	FTN_1418	1495814	1497217	R	468	43(1404)
tnfn1_pw060510p03q129	E04	C	1120261	F	FTN_1060	1119781	1120371	R	197	111(591)
tnfn1_pw060510p03q130	F04	C	1168893	F	FTN_1107	1168330	1169799	F	490	564(1470)
tnfn1_pw060510p03q131	G04	C	541246	F	FTN_0521	541170	541526	F	119	77(357)
tnfn1_pw060510p03q132	H04	C	1552203	R	FTN_1463	1551794	1552483	R	230	281(690)
tnfn1_pw060510p03q133	A05	C	1854911	R	FTN_1726	1853938	1855098	R	387	188(1161)
tnfn1_pw060510p03q134	B05	C	696196	F	FTN_0657	695532	696782	R	417	587(1251)
tnfn1_pw060510p03q135	C05	C	1323608	F	FTN_1254	1322868	1323953	F	362	741(1086)
tnfn1_pw060510p03q136	D05	C	852339	R	intergenic					
tnfn1_pw060510p03q137	E05	C	83343	F	FTN_0070	83199	83603	R	135	261(405)
tnfn1_pw060510p03q138	F05	C	391600	R	FTN_0392	390793	391710	R	306	111(918)
tnfn1_pw060510p03q139	G05	C	1024803	F	FTN_0969	1024199	1025695	R	499	893(1497)
tnfn1_pw060510p03q140	H05	C	795300	R	FTN_0741	794174	795628	R	485	329(1455)
tnfn1_pw060510p03q141	A06	U	1586479	F	FTN_1493	1586220	1588112	R	631	1634(1893)
tnfn1_pw060510p03q142	B06	C	555156	R	FTN_0533	554322	555512	R	397	357(1191)
tnfn1_pw060510p03q143	C06	C	1435092	R	FTN_1356	1433562	1435358	R	599	267(1797)
tnfn1_pw060510p03q144	D06	C	187877	R	FTN_0171	186730	188268	R	513	392(1539)
tnfn1_pw060510p03q145	E06	U	1378722	F	FTN_1309	1378294	1380753	F	820	429(2460)
tnfn1_pw060510p03q146	F06	C	1219380	F	FTN_1152	1218102	1219547	R	482	168(1446)
tnfn1_pw060510p03q147	G06	C	1123024	R	FTN_1063	1122215	1123540	F	442	810(1326)
tnfn1_pw060510p03q148	H06	C	1248439	F	FTN_1176	1247657	1249660	R	668	1222(2004)

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_pw060510p03q149	A07	C	1238612	R	FTN_1168	1237542	1238924	R	461	313(1383)
tnfn1_pw060510p03q150	B07	C	1007176	R	FTN_0949	1006996	1007448	R	151	273(453)
tnfn1_pw060510p03q151	C07	C	612331	R	FTN_0583	611786	612709	R	308	379(924)
tnfn1_pw060510p03q152	D07	C	718732	F	FTN_0674	717906	719030	R	375	299(1125)
tnfn1_pw060510p03q153	E07	C	1452727	F	FTN_1372	1451963	1453045	R	361	319(1083)
tnfn1_pw060510p03q154	F07	C	534042	F	FTN_0516	533104	534570	F	489	939(1467)
tnfn1_pw060510p03q155	G07	C	804738	F	FTN_0750	803701	805071	F	457	1038(1371)
tnfn1_pw060510p03q156	H07	C	845481	F	FTN_0787	844273	846285	F	671	1209(2013)
tnfn1_pw060510p03q157	A08	C	326469	R	FTN_0316	325739	326791	R	351	323(1053)
tnfn1_pw060510p03q158	B08	C	1365441	R	FTN_1294	1365139	1365879	R	247	439(741)
tnfn1_pw060510p03q159	C08	U	1110468	R	FTN_1051	1110274	1110600	R	109	133(327)
tnfn1_pw060510p03q160	D08	C	1888863	R	FTN_1759	1888512	1888901	R	130	39(390)
tnfn1_pw060510p03q161	E08	C	28448	F	FTN_0027	28044	28592	F	183	405(549)
tnfn1_pw060510p03q162	F08	C	195097	R	FTN_0177	194359	195903	R	515	807(1545)
tnfn1_pw060510p03q163	G08	C	911920	R	FTN_0857	911588	912034	F	149	333(447)
tnfn1_pw060510p03q164	H08	C	128084	R	FTN_0116	127309	129003	R	565	920(1695)
tnfn1_pw060510p03q165	A09	C	728822	R	FTN_0685	728080	729225	R	382	404(1146)
tnfn1_pw060510p03q166	B09	C	1528298	R	FTN_1439	1527712	1528896	F	395	587(1185)
tnfn1_pw060510p03q167	C09	C	657686	R	FTN_0626	657174	658367	R	398	682(1194)
tnfn1_pw060510p03q168	D09	U	629810	F	FTN_0598	629508	630488	R	327	679(981)
tnfn1_pw060510p03q169	E09	C	657686	R	FTN_0626	657174	658367	R	398	682(1194)
tnfn1_pw060510p03q170	F09	C	730851	R	FTN_0687	730344	731723	F	460	508(1380)
tnfn1_pw060510p03q171	G09	U	617214	R	FTN_0588	616823	617740	R	306	527(918)
tnfn1_pw060510p03q172	H09	U	549130	F	FTN_0527	548701	549987	F	429	430(1287)
tnfn1_pw060510p03q173	A10	C	1233110	F	FTN_1161	1232698	1233897	R	400	788(1200)
tnfn1_pw060510p03q174	B10	C	1693676	F	FTN_1594	1692877	1695096	R	740	1421(2220)
tnfn1_pw060510p03q175	C10	U	1860795	F	FTN_1732	1860270	1861013	R	248	219(744)
tnfn1_pw060510p03q176	D10	C	553230	F	FTN_0531	552883	553626	F	248	348(744)
tnfn1_pw060510p03q177	E10	C	493961	R	FTN_0488	493874	494074	R	67	114(201)
tnfn1_pw060510p03q178	F10	C	955383	F	FTN_0898	954503	956044	R	514	662(1542)
tnfn1_pw060510p03q179	G10	C	1142024	F	FTN_1079	1141288	1142637	R	450	614(1350)
tnfn1_pw060510p03q180	H10	C	81773	R	FTN_0067	81421	82032	R	204	260(612)
tnfn1_pw060510p03q181	A11	C	1687784	F	FTN_1589	1687341	1688312	R	324	529(972)
tnfn1_pw060510p03q182	B11	C	134907	F	FTN_0125	134418	135569	F	384	490(1152)
tnfn1_pw060510p03q183	C11	C	1336628	F	FTN_1264	1335988	1336983	F	332	641(996)
tnfn1_pw060510p03q184	D11	C	1840296	R	FTN_1715	1838604	1841282	R	893	987(2679)
tnfn1_pw060510p03q185	E11	U	1641027	R	FTN_1543	1640934	1641398	F	155	94(465)
tnfn1_pw060510p03q186	F11	C	1494680	R	FTN_1417	1494300	1495781	R	494	1102(1482)
tnfn1_pw060510p03q187	G11	U	196997	F	FTN_0178	196080	197363	F	428	918(1284)
tnfn1_pw060510p03q188	H11	C	660124	R	FTN_0627	658901	661510	F	870	1224(2610)
tnfn1_pw060510p03q189	A12	C	293430	R	FTN_0285	292790	294007	F	406	641(1218)
tnfn1_pw060510p03q190	B12	U	374122	F	FTN_0371	373472	374326	F	285	651(855)
tnfn1_pw060510p03q191	C12	C	1028162	R	FTN_0973	1027802	1028398	R	199	237(597)
tnfn1_pw060510p03q192	D12	C	1160195	F	FTN_1098	1159530	1160402	R	291	208(873)
tnfn1_pw060510p03q193	E12	C	1610194	R	FTN_1513	1609860	1610735	F	292	335(876)
tnfn1_pw060510p03q194	F12	C	1740494	R	FTN_1628	1739841	1740791	R	317	298(951)
tnfn1_pw060510p03q195	G12	C	1310123	F	FTN_1243	1309687	1310382	R	232	260(696)
tnfn1_pw060510p03q196	H12	C	433350	R	FTN_0434	432829	433740	F	304	522(912)

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_pw060510p03q101	A01	EXACT(0)	155	145	122	32	EXACT(0)	200	190	57
tnfn1_pw060510p03q102	B01	EXACT(0)	154	152	128	39	EXACT(0)	200	194	56
tnfn1_pw060510p03q103	C01	EXACT(0)	155	140	123	44	EXACT(0)	200	190	55
tnfn1_pw060510p03q104	D01	EXACT(0)	158	153	145	49	EXACT(0)	200	165	47
tnfn1_pw060510p03q105	E01	EXACT(0)	155	145	129	44	EXACT(0)	200	197	58
tnfn1_pw060510p03q106	F01	EXACT(0)	157	153	137	41	EXACT(0)	200	187	56
tnfn1_pw060510p03q107	G01	EXACT(0)	156	153	135	38	EXACT(0)	200	181	56
tnfn1_pw060510p03q108	H01	EXACT(0)	158	152	141	46	EXACT(0)	200	193	64
tnfn1_pw060510p03q109	A02	EXACT(0)	156	153	130	36	EXACT(0)	200	188	41
tnfn1_pw060510p03q110	B02	EXACT(0)	157	145	127	45	EXACT(0)	156	149	52
tnfn1_pw060510p03q111	C02	EXACT(0)	155	152	128	44	EXACT(0)	200	191	50
tnfn1_pw060510p03q112	D02	EXACT(0)	120	111	67	24	EXACT(0)	199	118	30
tnfn1_pw060510p03q113	E02	EXACT(0)	123	118	99	32	EXACT(0)	201	117	51
tnfn1_pw060510p03q114	F02	EXACT(0)	123	119	100	40	EXACT(0)	200	192	47
tnfn1_pw060510p03q115	G02	EXACT(0)	124	120	74	28	EXACT(0)	200	196	57
tnfn1_pw060510p03q116	H02	EXACT(0)	124	120	104	36	EXACT(0)	200	188	52
tnfn1_pw060510p03q117	A03	EXACT(0)	119	120	93	39	EXACT(0)	200	190	59
tnfn1_pw060510p03q118	B03	EXACT(0)	121	119	96	30	EXACT(0)	200	194	52
tnfn1_pw060510p03q119	C03	EXACT(0)	156	152	127	43	EXACT(0)	200	191	61
tnfn1_pw060510p03q120	D03	EXACT(0)	156	148	122	39	EXACT(0)	200	188	58
tnfn1_pw060510p03q121	E03	EXACT(0)	153	139	128	46	EXACT(0)	200	191	57
tnfn1_pw060510p03q122	F03	EXACT(0)	155	145	129	47	EXACT(0)	200	188	45
tnfn1_pw060510p03q123	G03	EXACT(0)	156	144	138	44	EXACT(0)	199	183	58
tnfn1_pw060510p03q124	H03	EXACT(0)	156	145	109	38	EXACT(0)	200	151	42
tnfn1_pw060510p03q125	A04	EXACT(0)	155	153	132	43	EXACT(0)	200	196	56
tnfn1_pw060510p03q126	B04	EXACT(0)	155	152	128	40	EXACT(0)	200	189	58
tnfn1_pw060510p03q127	C04	EXACT(0)	155	145	129	45	EXACT(0)	199	175	54
tnfn1_pw060510p03q128	D04	EXACT(0)	153	145	123	38	EXACT(0)	200	196	53
tnfn1_pw060510p03q129	E04	EXACT(0)	156	145	125	31	EXACT(0)	200	189	58
tnfn1_pw060510p03q130	F04	EXACT(0)	120	112	93	42	EXACT(0)	200	192	57
tnfn1_pw060510p03q131	G04	EXACT(0)	122	120	104	39	EXACT(0)	56	55	41
tnfn1_pw060510p03q132	H04	EXACT(0)	133	103	81	26	EXACT(0)	200	124	24
tnfn1_pw060510p03q133	A05	EXACT(0)	121	110	90	34	EXACT(0)	200	187	49
tnfn1_pw060510p03q134	B05	EXACT(0)	154	145	129	39	EXACT(0)	200	192	48
tnfn1_pw060510p03q135	C05	EXACT(0)	155	152	128	44	EXACT(0)	200	189	40
tnfn1_pw060510p03q136	D05	EXACT(0)	156	145	122	34	EXACT(0)	200	187	48
tnfn1_pw060510p03q137	E05	EXACT(0)	120	119	95	35	EXACT(0)	200	195	58
tnfn1_pw060510p03q138	F05	EXACT(0)	119	119	98	39	EXACT(0)	200	189	56
tnfn1_pw060510p03q139	G05	EXACT(0)	120	112	94	38	EXACT(0)	200	191	59
tnfn1_pw060510p03q140	H05	EXACT(0)	123	117	80	32	EXACT(0)	200	164	28
tnfn1_pw060510p03q141	A06	EXACT(0)	124	120	106	34	EXACT(0)	200	168	36
tnfn1_pw060510p03q142	B06	EXACT(0)	121	112	96	39	EXACT(0)	200	190	58
tnfn1_pw060510p03q143	C06	EXACT(0)	133	117	102	39	EXACT(0)	200	185	51
tnfn1_pw060510p03q144	D06	EXACT(0)	133	116	107	39	EXACT(0)	200	194	52
tnfn1_pw060510p03q145	E06	EXACT(0)	157	145	133	36	EXACT(0)	200	180	58
tnfn1_pw060510p03q146	F06	EXACT(0)	155	152	125	36	EXACT(0)	200	182	42
tnfn1_pw060510p03q147	G06	EXACT(0)	155	139	125	34	EXACT(0)	117	113	42
tnfn1_pw060510p03q148	H06	EXACT(0)	157	152	100	28	EXACT(0)	200	195	49

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_pw060510p03q149	A07	EXACT(0)	148	145	125	39	EXACT(0)	200	189	53
tnfn1_pw060510p03q150	B07	EXACT(0)	154	145	126	42	EXACT(0)	200	193	58
tnfn1_pw060510p03q151	C07	EXACT(0)	154	145	129	44	EXACT(0)	200	187	57
tnfn1_pw060510p03q152	D07	EXACT(0)	156	153	129	39	EXACT(0)	200	177	54
tnfn1_pw060510p03q153	E07	EXACT(0)	154	145	129	43	EXACT(0)	200	190	50
tnfn1_pw060510p03q154	F07	EXACT(0)	156	144	130	40	EXACT(0)	200	191	52
tnfn1_pw060510p03q155	G07	EXACT(0)	155	153	132	46	EXACT(0)	200	197	58
tnfn1_pw060510p03q156	H07	EXACT(0)	154	139	125	29	EXACT(0)	200	185	26
tnfn1_pw060510p03q157	A08	EXACT(0)	155	153	132	42	EXACT(0)	200	178	56
tnfn1_pw060510p03q158	B08	EXACT(0)	117	113	55	9	EXACT(0)	199	131	12
tnfn1_pw060510p03q159	C08	EXACT(0)	116	111	77	11	EXACT(0)	198	160	17
tnfn1_pw060510p03q160	D08	EXACT(0)	123	118	98	18	EXACT(0)	200	181	25
tnfn1_pw060510p03q161	E08	EXACT(0)	114	112	96	32	EXACT(0)	200	186	50
tnfn1_pw060510p03q162	F08	EXACT(0)	100	84	78	23	EXACT(0)	200	192	27
tnfn1_pw060510p03q163	G08	EXACT(0)	123	109	75	20	EXACT(0)	200	182	48
tnfn1_pw060510p03q164	H08	EXACT(0)	121	119	90	35	EXACT(0)	200	188	52
tnfn1_pw060510p03q165	A09	EXACT(0)	118	119	93	39	EXACT(0)	200	192	56
tnfn1_pw060510p03q166	B09	EXACT(0)	154	145	129	46	EXACT(0)	200	194	60
tnfn1_pw060510p03q167	C09	EXACT(0)	155	144	112	36	EXACT(0)	200	189	57
tnfn1_pw060510p03q168	D09	EXACT(0)	125	116	104	32	ESTIMATE(5)	194	42	12
tnfn1_pw060510p03q169	E09	EXACT(0)	152	145	135	45	EXACT(0)	200	192	56
tnfn1_pw060510p03q170	F09	EXACT(0)	134	115	102	30	EXACT(0)	200	184	33
tnfn1_pw060510p03q171	G09	EXACT(0)	155	145	128	43	EXACT(0)	200	194	51
tnfn1_pw060510p03q172	H09	NONE	0	0	0	16	ESTIMATE(272)	331	219	15
tnfn1_pw060510p03q173	A10	EXACT(0)	154	145	129	45	EXACT(0)	200	189	58
tnfn1_pw060510p03q174	B10	EXACT(0)	153	145	126	40	EXACT(0)	200	190	51
tnfn1_pw060510p03q175	C10	EXACT(0)	157	145	113	30	EXACT(0)	200	148	43
tnfn1_pw060510p03q176	D10	EXACT(0)	120	119	98	36	EXACT(0)	200	196	55
tnfn1_pw060510p03q177	E10	EXACT(0)	120	112	96	40	EXACT(0)	200	191	41
tnfn1_pw060510p03q178	F10	EXACT(0)	216	152	116	27	EXACT(0)	173	154	28
tnfn1_pw060510p03q179	G10	EXACT(0)	118	112	93	32	EXACT(0)	200	195	52
tnfn1_pw060510p03q180	H10	EXACT(0)	123	109	64	17	ESTIMATE(2)	198	183	58
tnfn1_pw060510p03q181	A11	EXACT(0)	123	106	91	36	EXACT(0)	200	191	58
tnfn1_pw060510p03q182	B11	EXACT(0)	158	153	141	40	EXACT(0)	200	196	48
tnfn1_pw060510p03q183	C11	EXACT(0)	151	139	131	47	EXACT(0)	200	190	60
tnfn1_pw060510p03q184	D11	EXACT(0)	155	136	119	40	EXACT(0)	188	174	51
tnfn1_pw060510p03q185	E11	EXACT(0)	133	134	94	20	ESTIMATE(2)	155	67	12
tnfn1_pw060510p03q186	F11	EXACT(0)	154	145	117	39	EXACT(0)	200	191	47
tnfn1_pw060510p03q187	G11	EXACT(0)	155	145	135	46	EXACT(0)	200	191	66
tnfn1_pw060510p03q188	H11	EXACT(0)	155	145	135	47	EXACT(0)	200	199	56
tnfn1_pw060510p03q189	A12	EXACT(0)	158	157	146	50	EXACT(0)	200	165	44
tnfn1_pw060510p03q190	B12	EXACT(0)	155	145	126	41	EXACT(0)	200	186	63
tnfn1_pw060510p03q191	C12	EXACT(0)	120	120	99	39	EXACT(0)	121	113	36
tnfn1_pw060510p03q192	D12	EXACT(0)	122	112	96	32	EXACT(0)	200	181	58
tnfn1_pw060510p03q193	E12	EXACT(0)	155	133	85	25	EXACT(0)	200	190	45
tnfn1_pw060510p03q194	F12	EXACT(0)	122	119	98	39	EXACT(0)	200	179	43
tnfn1_pw060510p03q195	G12	EXACT(0)	118	112	87	37	EXACT(0)	200	187	57
tnfn1_pw060510p03q196	H12	EXACT(0)	121	112	96	40	EXACT(0)	200	191	58