

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 11 (tnfn1_pw060328p03)**

Catalog No. NR-8045

For research use only. Not for human use.

Contributor:

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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-8045 represents Plate 11 (tnfn1_pw060328p03) 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_pw060328p03q104 (Well D01) was not available due to quality issues at the time of release of Plate 11, but is now available on Plate 33 (BEI Resources NR-10484).**

Francisella tularensis subsp. *novicida*, strain U112 is excluded from Select Agent status. Please see [CDC Select Agent Program, Notification of Exclusion](#).

Material Provided:

Each well of the 96-well plate contains approximately 0.25 mL of bacterial culture in 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-8045 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 11 (tnfn1_pw060328p03), NR-8045.”

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/bmbl5/bmbl5toc.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_pw060328p03q101	A01	T20	-	ABC-type anion transport system, duplicated permease component	transport
tnfn1_pw060328p03q102	B01	T20	-	NADPH-dependent FMN reductase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q103	C01	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060328p03q104	D01	T20	cydC	ABC-type transport ATP-binding protein CydC	transport
tnfn1_pw060328p03q105	E01	T20	tktA	transketolase I	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q106	F01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q107	G01	T20	kpsF	phosphosugar isomerase	cell wall / LPS / capsule
tnfn1_pw060328p03q108	H01	T20	-	-	-
tnfn1_pw060328p03q109	A02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q110	B02	T20	ansA	L-asparaginase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q111	C02	T20	isftu2	isftu2	IS element
tnfn1_pw060328p03q112	D02	T20	asd	aspartate semialdehyde dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060328p03q113	E02	T20	-	drug/metabolite exporter	transport - drugs / antibacterial compounds
tnfn1_pw060328p03q114	F02	T20	oppF	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060328p03q115	G02	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p03q116	H02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p03q117	A03	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060328p03q118	B03	T20	-	glycosyl transferase	cell wall / LPS / capsule
tnfn1_pw060328p03q119	C03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p03q120	D03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p03q121	E03	T20	gcvT	glycine cleavage complex protein T (aminomethyltransferase)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q122	F03	T20	clpB	chaperone clpB	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060328p03q123	G03	T20	trpB	tryptophan synthase beta chain	amino acid metabolism - biosynthesis
tnfn1_pw060328p03q124	H03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q125	A04	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p03q126	B04	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p03q127	C04	T20	-	RmuC family protein	putative enzymes
tnfn1_pw060328p03q128	D04	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p03q129	E04	T20	lon	DNA-binding, ATP-dependent protease La	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p03q130	F04	T20	holC	DNA polymerase III, chi subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p03q131	G04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q132	H04	T20	cphA	cyanophycin synthetase	cell wall / LPS / capsule
tnfn1_pw060328p03q133	A05	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060328p03q134	B05	T20	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060328p03q135	C05	T20	dnaE	DNA polymerase III, alpha subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p03q136	D05	T20	rbn	tRNA processing ribonuclease BN	nucleotides and nucleosides metabolism
tnfn1_pw060328p03q137	E05	T20	tolC	outer membrane efflux protein, tolC precursor	transport
tnfn1_pw060328p03q138	F05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p03q139	G05	<KAN-2>	dcd	deoxycytidine triphosphate deaminase	nucleotides and nucleosides metabolism
tnfn1_pw060328p03q140	H05	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p03q141	A06	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q142	B06	<KAN-2>	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060328p03q143	C06	<KAN-2>	ilvC	ketol-acid reductoisomerase	amino acid metabolism - biosynthesis
tnfn1_pw060328p03q144	D06	<KAN-2>	fumA	fumarate hydratase, class I	energy metabolism
tnfn1_pw060328p03q145	E06	<KAN-2>	nusB	transcription termination factor	transcription
tnfn1_pw060328p03q146	F06	<KAN-2>	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	cell wall / LPS / capsule
tnfn1_pw060328p03q147	G06	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q148	H06	T18	-	Mg-dependent DNase	DNA replication, recombination, modification and repair - degradation

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p03q149	A07	T18	ftsQ	cell division protein FtsQ	cell cycle
tnfn1_pw060328p03q150	B07	T18	trpS	tryptophanyl-tRNA synthetase	other metabolism - biosynthesis
tnfn1_pw060328p03q151	C07	T18	-	signal transduction protein with a PAS, a PAC, an EAL and a GGDEF domain	signal transduction and regulation
tnfn1_pw060328p03q152	D07	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p03q153	E07	T18	miaE	tRNA-(ms(2)io(6)a)-hydroxylase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p03q154	F07	T18	-	two-component regulator, sensor histidine kinase	signal transduction and regulation
tnfn1_pw060328p03q155	G07	T18	ssb	single-strand DNA binding protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p03q156	H07	T18	trpA	tryptophan synthase alpha chain	amino acid metabolism - biosynthesis
tnfn1_pw060328p03q157	A08	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q158	B08	T18	-	sodium bile acid symporter family protein	transport
tnfn1_pw060328p03q159	C08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p03q160	D08	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p03q161	E08	T20	-	X-prolyl aminopeptidase 2	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p03q162	F08	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p03q163	G08	T20	-	drug/metabolite transporter superfamily protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p03q164	H08	T20	wbtE	UDP-glucose/GDP-mannose dehydrogenase family protein	cell wall / LPS / capsule
tnfn1_pw060328p03q165	A09	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p03q166	B09	T20	-	pyridoxal-dependent decarboxylase	putative enzymes
tnfn1_pw060328p03q167	C09	T20	tyrP	tyrosine permease	transport - amino-acid
tnfn1_pw060328p03q168	D09	T20	-	metallocarboxypeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060328p03q169	E09	T20	uvrA	excinuclease ABC, subunit A	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p03q170	F09	T20	-	serine-type D-Ala-D-Ala carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060328p03q171	G09	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060328p03q172	H09	T20	appC	cytochrome bd-II terminal oxidase subunit I	energy metabolism
tnfn1_pw060328p03q173	A10	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060328p03q174	B10	T20	pepN	aminopeptidase N	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p03q175	C10	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p03q176	D10	T20	-	Mg-dependent DNase	DNA replication, recombination, modification and repair - degradation
tnfn1_pw060328p03q177	E10	T20	-	monovalent cation:proton antiporter-1	transport
tnfn1_pw060328p03q178	F10	T20	panC	pantoate-beta-alanine ligase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p03q179	G10	T20	-	tRNA-methyltransferase MiaB protein	translation, ribosomal structure and biogenesis
tnfn1_pw060328p03q180	H10	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p03q181	A11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p03q182	B11	T20	-	nicotinic acid phosphoribosyltransferase	other metabolism - biosynthesis
tnfn1_pw060328p03q183	C11	T20	fimT	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060328p03q184	D11	T20	chiB	chitinase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q185	E11	T20	yjfH	tRNA/rRNA methyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p03q186	F11	T20	alaS	alanyl-tRNA synthetase	other metabolism - biosynthesis
tnfn1_pw060328p03q187	G11	T20	-	cation diffusion facilitator (CDF) family protein	transport
tnfn1_pw060328p03q188	H11	T20	parA	chromosome partition protein A, ATPase	cell cycle
tnfn1_pw060328p03q189	A12	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060328p03q190	B12	T20	-	-	-
tnfn1_pw060328p03q191	C12	T20	pgm	phosphoglucomutase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q192	D12	T20	-	thioredoxin	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p03q193	E12	T20	-	beta-fructofuranosidase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p03q194	F12	T20	-	Rieske (2Fe-2S) domain protein	putative enzymes
tnfn1_pw060328p03q195	G12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p03q196	H12	T20	glfA	citrate synthase	energy metabolism

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_pw060328p03q101	A01	C	164927	F	FTN_0152	163868	165589	R	574	663(1722)
tnfn1_pw060328p03q102	B01	C	475643	F	FTN_0471	475227	475760	R	178	118(534)
tnfn1_pw060328p03q103	C01	C	801232	F	FTN_0747	800413	802020	F	536	820(1608)
tnfn1_pw060328p03q104	D01	C	678748	F	FTN_0641	677863	679509	R	549	762(1647)
tnfn1_pw060328p03q105	E01	C	1413771	R	FTN_1333	1412511	1414499	R	663	729(1989)
tnfn1_pw060328p03q106	F01	C	59953	R	FTN_0050	59569	61089	F	507	385(1521)
tnfn1_pw060328p03q107	G01	C	1293388	R	FTN_1222	1292995	1293963	F	323	394(969)
tnfn1_pw060328p03q108	H01	C	745011	R	intergenic					
tnfn1_pw060328p03q109	A02	C	144401	R	FTN_0131	143590	144894	R	435	494(1305)
tnfn1_pw060328p03q110	B02	C	1150923	F	FTN_1088	1150184	1151218	R	345	296(1035)
tnfn1_pw060328p03q111	C02	U	986622	F	-	986109	986965	R	285.6	344(857)
tnfn1_pw060328p03q112	D02	C	545062	R	FTN_0524	544119	545216	R	366	155(1098)
tnfn1_pw060328p03q113	E02	C	1445274	R	FTN_1361	1444600	1445466	F	289	675(867)
tnfn1_pw060328p03q114	F02	C	1688062	R	FTN_1589	1687341	1688312	R	324	251(972)
tnfn1_pw060328p03q115	G02	C	385135	F	FTN_0384	385020	385376	R	119	242(357)
tnfn1_pw060328p03q116	H02	C	1165890	F	FTN_1104	1165522	1166067	R	182	178(546)
tnfn1_pw060328p03q117	A03	C	316033	R	FTN_0307	315736	316653	F	306	298(918)
tnfn1_pw060328p03q118	B03	C	456503	R	FTN_0453	455936	457249	F	438	568(1314)
tnfn1_pw060328p03q119	C03	C	1534392	R	FTN_1445	1533937	1534848	R	304	457(912)
tnfn1_pw060328p03q120	D03	C	1339936	R	FTN_1268	1339737	1340459	F	241	200(723)
tnfn1_pw060328p03q121	E03	C	515134	F	FTN_0505	514946	516019	F	358	189(1074)
tnfn1_pw060328p03q122	F03	C	1871535	R	FTN_1743	1870244	1872820	F	859	1292(2577)
tnfn1_pw060328p03q123	G03	C	1867465	F	FTN_1739	1866821	1868008	F	396	645(1188)
tnfn1_pw060328p03q124	H03	C	1183536	F	FTN_1119	1183338	1183586	R	83	51(249)
tnfn1_pw060328p03q125	A04	C	294934	R	FTN_0287	294845	295609	F	255	90(765)
tnfn1_pw060328p03q126	B04	C	1686804	F	FTN_1588	1686132	1687331	F	400	673(1200)
tnfn1_pw060328p03q127	C04	C	1081459	R	FTN_1024	1080823	1082235	R	471	777(1413)
tnfn1_pw060328p03q128	D04	C	559011	F	FTN_0536	558170	560008	F	613	842(1839)
tnfn1_pw060328p03q129	E04	C	1114874	F	FTN_1055	1113546	1115867	R	774	994(2322)
tnfn1_pw060328p03q130	F04	C	232809	R	FTN_0213	232787	233224	F	146	23(438)
tnfn1_pw060328p03q131	G04	C	488232	F	FTN_0482	487800	488777	F	326	433(978)
tnfn1_pw060328p03q132	H04	C	1175322	F	FTN_1112	1174118	1176937	R	940	1616(2820)
tnfn1_pw060328p03q133	A05	C	560324	R	FTN_0537	560098	561507	F	470	227(1410)
tnfn1_pw060328p03q134	B05	C	1125383	F	FTN_1066	1125001	1125840	F	280	383(840)
tnfn1_pw060328p03q135	C05	C	509205	R	FTN_0499	505748	509224	F	1159	3458(3477)
tnfn1_pw060328p03q136	D05	C	203979	F	FTN_0187	203616	204809	F	398	364(1194)
tnfn1_pw060328p03q137	E05	C	1825092	R	FTN_1703	1824128	1825654	R	509	563(1527)
tnfn1_pw060328p03q138	F05	C	1216654	R	FTN_1151	1216361	1218106	F	582	294(1746)
tnfn1_pw060328p03q139	G05	C	927830	R	FTN_0873	927420	927983	R	188	154(564)
tnfn1_pw060328p03q140	H05	C	356352	R	FTN_0351	356201	356422	R	74	71(222)
tnfn1_pw060328p03q141	A06	C	1540486	R	FTN_1451	1540174	1540707	R	178	222(534)
tnfn1_pw060328p03q142	B06	C	1482684	R	FTN_1404	1482101	1482877	R	259	194(777)
tnfn1_pw060328p03q143	C06	C	1098445	R	FTN_1040	1097588	1098628	R	347	184(1041)
tnfn1_pw060328p03q144	D06	C	342632	F	FTN_0337	342333	343844	F	504	300(1512)
tnfn1_pw060328p03q145	E06	C	1464015	R	FTN_1384	1463758	1464180	R	141	166(423)
tnfn1_pw060328p03q146	F06	C	1172381	F	FTN_1110	1171920	1172396	F	159	462(477)
tnfn1_pw060328p03q147	G06	C	982820	F	FTN_0925	982223	983200	R	326	381(978)
tnfn1_pw060328p03q148	H06	C	787866	F	FTN_0735	787338	788081	R	248	216(744)

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_pw060328p03q149	A07	C	176592	R	FTN_0162	175937	176617	F	227	656(681)
tnfn1_pw060328p03q150	B07	C	1594286	R	FTN_1499	1593289	1594290	F	334	998(1002)
tnfn1_pw060328p03q151	C07	C	454028	F	FTN_0451	452277	454379	R	701	352(2103)
tnfn1_pw060328p03q152	D07	C	912521	F	FTN_0859	912296	912898	R	201	378(603)
tnfn1_pw060328p03q153	E07	C	692620	F	FTN_0653	692373	692981	F	203	248(609)
tnfn1_pw060328p03q154	F07	C	1542346	R	FTN_1453	1541523	1542557	F	345	824(1035)
tnfn1_pw060328p03q155	G07	C	134234	F	FTN_0124	133833	134309	F	159	402(477)
tnfn1_pw060328p03q156	H07	C	1868321	R	FTN_1740	1868014	1868817	F	268	308(804)
tnfn1_pw060328p03q157	A08	C	859455	R	FTN_0802	859091	859486	F	132	365(396)
tnfn1_pw060328p03q158	B08	C	366815	F	FTN_0363	366625	367551	F	309	191(927)
tnfn1_pw060328p03q159	C08	C	451024	R	FTN_0449	450598	451470	F	291	427(873)
tnfn1_pw060328p03q160	D08	C	1368523	R	FTN_1299	1368395	1368586	R	64	64(192)
tnfn1_pw060328p03q161	E08	C	1137538	F	FTN_1074	1136360	1138117	R	586	580(11758)
tnfn1_pw060328p03q162	F08	C	1295806	R	FTN_1225	1295269	1296078	R	270	273(810)
tnfn1_pw060328p03q163	G08	C	940963	F	FTN_0884	940420	941310	R	297	348(891)
tnfn1_pw060328p03q164	H08	C	1506926	F	FTN_1426	1506257	1507564	R	436	639(1308)
tnfn1_pw060328p03q165	A09	C	1728458	F	FTN_1618	1727841	1728719	R	293	262(879)
tnfn1_pw060328p03q166	B09	C	1799847	R	FTN_1684	1799255	1800505	F	417	593(1251)
tnfn1_pw060328p03q167	C09	C	1836417	F	FTN_1711	1835372	1836565	R	398	149(1194)
tnfn1_pw060328p03q168	D09	C	1865297	R	FTN_1738	1864510	1866012	F	501	788(1503)
tnfn1_pw060328p03q169	E09	C	706196	F	FTN_0666	705568	708387	F	940	629(2820)
tnfn1_pw060328p03q170	F09	C	976042	F	FTN_0917	975232	976632	F	467	811(1401)
tnfn1_pw060328p03q171	G09	C	941563	R	FTN_0885	941338	942810	R	491	1248(1473)
tnfn1_pw060328p03q172	H09	C	1729032	R	FTN_1619	1728955	1730328	F	458	78(1374)
tnfn1_pw060328p03q173	A10	C	688580	R	FTN_0649	687803	690832	F	1010	778(3030)
tnfn1_pw060328p03q174	B10	C	1898414	R	FTN_1768	1897173	1899746	R	858	1333(2574)
tnfn1_pw060328p03q175	C10	C	622163	F	FTN_0591	621630	622667	R	346	505(1038)
tnfn1_pw060328p03q176	D10	C	1860672	R	FTN_1732	1860270	1861013	R	248	342(744)
tnfn1_pw060328p03q177	E10	C	1595854	F	FTN_1501	1595030	1596325	F	432	825(1296)
tnfn1_pw060328p03q178	F10	C	1431933	F	FTN_1353	1431659	1432441	F	261	275(783)
tnfn1_pw060328p03q179	G10	C	361664	F	FTN_0358	360958	362274	F	439	707(1317)
tnfn1_pw060328p03q180	H10	C	1330499	F	FTN_1260	1329874	1331325	F	484	626(1452)
tnfn1_pw060328p03q181	A11	C	1129586	F	FTN_1069	1128158	1130653	R	832	1068(2496)
tnfn1_pw060328p03q182	B11	C	1532213	R	FTN_1443	1531187	1532599	R	471	387(1413)
tnfn1_pw060328p03q183	C11	C	704731	R	FTN_0664	704429	705010	F	194	303(582)
tnfn1_pw060328p03q184	D11	C	1873423	R	FTN_1744	1873074	1875263	F	730	350(2190)
tnfn1_pw060328p03q185	E11	C	552992	R	FTN_0531	552883	553626	F	248	110(744)
tnfn1_pw060328p03q186	F11	C	836751	F	FTN_0778	834159	836753	F	865	2593(2595)
tnfn1_pw060328p03q187	G11	C	409640	R	FTN_0411	409260	410144	F	295	381(885)
tnfn1_pw060328p03q188	H11	U	432520	F	FTN_0433	432195	432833	F	213	326(639)
tnfn1_pw060328p03q189	A12	C	154151	F	FTN_0141	153815	155128	F	438	337(1314)
tnfn1_pw060328p03q190	B12	C	1658981	R	intergenic					
tnfn1_pw060328p03q191	C12	C	530500	F	FTN_0514	530155	531786	F	544	346(1632)
tnfn1_pw060328p03q192	D12	C	1492477	F	FTN_1415	1492329	1492649	F	107	149(321)
tnfn1_pw060328p03q193	E12	C	68748	F	FTN_0058	67916	69628	R	571	881(1713)
tnfn1_pw060328p03q194	F12	C	1882388	F	FTN_1753	1882116	1883009	F	298	273(894)
tnfn1_pw060328p03q195	G12	U	110037	R	FTN_0099	109818	110483	F	222	220(666)
tnfn1_pw060328p03q196	H12	C	1752106	F	FTN_1640	1751913	1753169	F	419	194(1257)

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_pw060328p03q101	A01	EXACT(0)	156	151	124	38	EXACT(0)	200	197	59
tnfn1_pw060328p03q102	B01	EXACT(0)	156	145	134	48	EXACT(0)	200	167	60
tnfn1_pw060328p03q103	C01	EXACT(0)	156	151	118	41	EXACT(0)	200	192	57
tnfn1_pw060328p03q104	D01	EXACT(0)	155	145	129	51	EXACT(0)	200	188	67
tnfn1_pw060328p03q105	E01	EXACT(0)	157	151	129	39	EXACT(0)	99	99	55
tnfn1_pw060328p03q106	F01	EXACT(0)	157	139	111	36	EXACT(0)	200	192	56
tnfn1_pw060328p03q107	G01	EXACT(0)	154	145	108	28	EXACT(0)	178	170	53
tnfn1_pw060328p03q108	H01	EXACT(0)	159	142	99	21	EXACT(0)	200	184	49
tnfn1_pw060328p03q109	A02	EXACT(0)	155	152	122	39	EXACT(0)	200	181	59
tnfn1_pw060328p03q110	B02	EXACT(0)	157	151	126	32	EXACT(0)	200	188	55
tnfn1_pw060328p03q111	C02	EXACT(0)	156	145	131	49	EXACT(0)	200	183	60
tnfn1_pw060328p03q112	D02	EXACT(0)	156	146	132	42	EXACT(0)	200	196	58
tnfn1_pw060328p03q113	E02	EXACT(0)	156	152	130	40	EXACT(0)	200	183	59
tnfn1_pw060328p03q114	F02	EXACT(0)	156	145	128	39	EXACT(0)	200	155	42
tnfn1_pw060328p03q115	G02	EXACT(0)	156	151	123	33	EXACT(0)	173	160	52
tnfn1_pw060328p03q116	H02	EXACT(0)	155	145	99	28	EXACT(0)	200	149	30
tnfn1_pw060328p03q117	A03	EXACT(0)	156	145	118	36	EXACT(0)	200	186	55
tnfn1_pw060328p03q118	B03	EXACT(0)	155	152	125	36	EXACT(0)	200	194	58
tnfn1_pw060328p03q119	C03	EXACT(0)	156	153	129	39	EXACT(0)	200	171	50
tnfn1_pw060328p03q120	D03	EXACT(0)	157	152	136	40	EXACT(0)	199	147	40
tnfn1_pw060328p03q121	E03	EXACT(0)	155	145	126	42	EXACT(0)	200	189	55
tnfn1_pw060328p03q122	F03	EXACT(0)	155	146	124	39	EXACT(0)	200	192	55
tnfn1_pw060328p03q123	G03	EXACT(0)	155	145	126	42	EXACT(0)	200	193	52
tnfn1_pw060328p03q124	H03	EXACT(0)	167	128	105	26	EXACT(0)	200	168	37
tnfn1_pw060328p03q125	A04	EXACT(0)	156	153	126	37	EXACT(0)	200	141	39
tnfn1_pw060328p03q126	B04	EXACT(0)	157	152	114	35	EXACT(0)	200	186	55
tnfn1_pw060328p03q127	C04	EXACT(0)	155	146	124	40	EXACT(0)	200	164	49
tnfn1_pw060328p03q128	D04	EXACT(0)	156	152	125	41	EXACT(0)	200	185	53
tnfn1_pw060328p03q129	E04	EXACT(0)	156	151	121	37	EXACT(0)	200	190	55
tnfn1_pw060328p03q130	F04	EXACT(0)	147	81	72	30	EXACT(0)	166	128	24
tnfn1_pw060328p03q131	G04	EXACT(0)	158	152	132	37	EXACT(0)	200	182	58
tnfn1_pw060328p03q132	H04	EXACT(0)	156	151	123	35	EXACT(0)	200	195	59
tnfn1_pw060328p03q133	A05	EXACT(0)	155	145	114	33	EXACT(0)	200	186	57
tnfn1_pw060328p03q134	B05	EXACT(0)	157	152	127	38	EXACT(0)	200	190	56
tnfn1_pw060328p03q135	C05	EXACT(0)	155	145	123	41	EXACT(0)	200	187	59
tnfn1_pw060328p03q136	D05	EXACT(0)	156	153	132	41	EXACT(0)	199	149	42
tnfn1_pw060328p03q137	E05	EXACT(0)	156	151	133	39	EXACT(0)	200	163	34
tnfn1_pw060328p03q138	F05	EXACT(0)	155	152	131	42	EXACT(0)	200	193	56
tnfn1_pw060328p03q139	G05	EXACT(0)	122	113	99	34	EXACT(0)	200	186	57
tnfn1_pw060328p03q140	H05	EXACT(0)	121	120	99	33	EXACT(0)	200	198	53
tnfn1_pw060328p03q141	A06	EXACT(0)	121	113	97	23	EXACT(0)	200	186	46
tnfn1_pw060328p03q142	B06	EXACT(0)	120	112	63	22	EXACT(0)	200	186	52
tnfn1_pw060328p03q143	C06	EXACT(0)	121	118	85	24	EXACT(0)	200	192	45
tnfn1_pw060328p03q144	D06	EXACT(0)	121	118	97	23	EXACT(0)	200	193	52
tnfn1_pw060328p03q145	E06	EXACT(0)	121	118	91	22	EXACT(0)	200	190	53
tnfn1_pw060328p03q146	F06	EXACT(0)	121	118	76	21	EXACT(0)	200	187	49
tnfn1_pw060328p03q147	G06	EXACT(0)	123	112	54	21	EXACT(0)	200	184	55
tnfn1_pw060328p03q148	H06	EXACT(0)	123	116	70	18	EXACT(0)	200	182	54

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_pw060328p03q149	A07	EXACT(0)	122	105	69	20	EXACT(0)	200	162	28
tnfn1_pw060328p03q150	B07	EXACT(0)	123	112	86	34	EXACT(0)	200	189	57
tnfn1_pw060328p03q151	C07	EXACT(0)	123	119	103	30	EXACT(0)	200	189	44
tnfn1_pw060328p03q152	D07	EXACT(0)	124	119	103	33	EXACT(0)	200	169	41
tnfn1_pw060328p03q153	E07	EXACT(0)	123	105	78	21	EXACT(0)	200	192	45
tnfn1_pw060328p03q154	F07	EXACT(0)	121	112	93	29	EXACT(0)	200	169	58
tnfn1_pw060328p03q155	G07	NONE	0	0	0	22	ESTIMATE(116)	626	548	36
tnfn1_pw060328p03q156	H07	EXACT(0)	121	112	96	38	EXACT(0)	200	197	55
tnfn1_pw060328p03q157	A08	EXACT(0)	121	105	94	32	EXACT(0)	200	72	29
tnfn1_pw060328p03q158	B08	EXACT(0)	123	113	99	38	EXACT(0)	127	122	55
tnfn1_pw060328p03q159	C08	EXACT(0)	156	151	130	40	EXACT(0)	200	189	54
tnfn1_pw060328p03q160	D08	EXACT(0)	122	111	66	18	EXACT(0)	199	182	32
tnfn1_pw060328p03q161	E08	EXACT(0)	156	152	133	39	EXACT(0)	155	148	53
tnfn1_pw060328p03q162	F08	EXACT(0)	156	153	123	38	EXACT(0)	200	187	46
tnfn1_pw060328p03q163	G08	EXACT(0)	155	150	114	32	EXACT(0)	200	190	49
tnfn1_pw060328p03q164	H08	EXACT(0)	156	145	128	34	EXACT(0)	200	190	55
tnfn1_pw060328p03q165	A09	EXACT(0)	153	145	108	39	EXACT(0)	200	190	56
tnfn1_pw060328p03q166	B09	EXACT(0)	155	153	120	33	EXACT(0)	200	185	58
tnfn1_pw060328p03q167	C09	EXACT(0)	156	152	125	35	EXACT(0)	200	185	58
tnfn1_pw060328p03q168	D09	EXACT(0)	156	145	119	43	EXACT(0)	200	186	59
tnfn1_pw060328p03q169	E09	EXACT(0)	155	145	123	40	EXACT(0)	200	191	58
tnfn1_pw060328p03q170	F09	EXACT(0)	154	145	120	41	EXACT(0)	200	194	57
tnfn1_pw060328p03q171	G09	EXACT(0)	154	145	118	33	EXACT(0)	200	180	39
tnfn1_pw060328p03q172	H09	EXACT(0)	156	145	131	39	EXACT(0)	200	187	53
tnfn1_pw060328p03q173	A10	EXACT(0)	155	145	117	39	EXACT(0)	200	179	56
tnfn1_pw060328p03q174	B10	EXACT(0)	156	153	117	29	EXACT(0)	200	173	41
tnfn1_pw060328p03q175	C10	EXACT(0)	157	152	114	27	EXACT(0)	200	187	54
tnfn1_pw060328p03q176	D10	EXACT(0)	155	145	117	35	EXACT(0)	200	195	55
tnfn1_pw060328p03q177	E10	EXACT(0)	155	145	120	36	EXACT(0)	200	188	48
tnfn1_pw060328p03q178	F10	EXACT(0)	157	153	130	34	EXACT(0)	200	137	37
tnfn1_pw060328p03q179	G10	EXACT(0)	155	151	124	38	EXACT(0)	200	195	57
tnfn1_pw060328p03q180	H10	EXACT(0)	156	144	98	25	EXACT(0)	200	195	51
tnfn1_pw060328p03q181	A11	EXACT(0)	155	145	126	44	EXACT(0)	198	192	55
tnfn1_pw060328p03q182	B11	EXACT(0)	155	145	123	43	EXACT(0)	200	181	53
tnfn1_pw060328p03q183	C11	EXACT(0)	155	152	116	37	EXACT(0)	200	194	58
tnfn1_pw060328p03q184	D11	EXACT(0)	156	152	128	40	EXACT(0)	200	199	55
tnfn1_pw060328p03q185	E11	EXACT(0)	154	146	113	39	EXACT(0)	167	149	53
tnfn1_pw060328p03q186	F11	EXACT(0)	157	145	121	38	EXACT(0)	191	184	53
tnfn1_pw060328p03q187	G11	EXACT(0)	155	145	120	42	EXACT(0)	200	187	55
tnfn1_pw060328p03q188	H11	EXACT(0)	159	152	143	45	EXACT(0)	200	194	63
tnfn1_pw060328p03q189	A12	EXACT(0)	154	145	123	43	EXACT(0)	200	191	48
tnfn1_pw060328p03q190	B12	EXACT(0)	157	153	103	22	EXACT(0)	200	192	46
tnfn1_pw060328p03q191	C12	EXACT(0)	157	152	123	33	EXACT(0)	200	189	50
tnfn1_pw060328p03q192	D12	EXACT(0)	156	152	125	40	EXACT(0)	200	190	59
tnfn1_pw060328p03q193	E12	EXACT(0)	156	153	116	36	EXACT(0)	200	189	56
tnfn1_pw060328p03q194	F12	EXACT(0)	157	153	125	36	EXACT(0)	184	176	54
tnfn1_pw060328p03q195	G12	EXACT(0)	158	153	142	46	EXACT(0)	200	194	66
tnfn1_pw060328p03q196	H12	EXACT(0)	155	151	124	30	EXACT(0)	200	194	46