Francisella tularensis subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 29 (tnfn1_pw060510p01)

Catalog No. NR-8063

For research use only. Not for human use.

Contributor:
Colin Manoil, Ph.D., Professor of Genome Sciences, University of Washington, Seattle, Washington

Product Description:
A comprehensive 16508-member transposon mutant library[1] 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-8063 represents Plate 29 (tnfn1_pw060510p01) of the “two-allele” 3050-member sublibrary. Detailed information for each mutant is shown in Tables 1-3. Information about specific clones may also be accessed through the Francisella Tularensis Genome Research homepage.

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

Material Provided:
Each well of the 96-well plate contains approximately 0.25 mL of bacterial culture in 0.7X Tryptic Soy Broth containing 0.1% L-cysteine and 10 µg/mL kanamycin supplemented with 5% glycerol.

Note: Production in the 96-well format has a potential for cross-contamination. Individual mutants should be checked by the recipient prior to use.

Packaging/Storage:
NR-8063 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% CO_2
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 29 (tnfn1_pw060510p01), NR-8063.”

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.

Disclaimers:
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References:

1. Gallagher, L. A., et al. "A Comprehensive Transposon Mutant Library of *Francisella novicida*, A Bioweapon Surrogate." Proc. Natl. Acad. Sci. USA 104 (2007): 1009–1014. PubMed: 17215359.

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Support Provided by NIAID

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060510p01q101	A01	T20	gcvP2	glycine cleavage system P protein, subunit 2	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q102	B01	T20			
tnfn1_pw060510p01q103	C01	T20	ilvE	branched-chain amino acid aminotransferase protein (class IV)	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q104	D01	T18	aroH	chorismate mutase	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q105	E01	T20	-	YGGT family membrane protein	unknown function - conserved
tnfn1_pw060510p01q106	F01	<KAN-2>	pepA	cytosol aminopeptidase	amino acid metabolism
tnfn1_pw060510p01q107	G01	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p01q108	H01	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p01q109	A02	T18	pyrB	aspartate carbamoyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q110	B02	T18	iglD	intracellular growth locus protein D	unknown function - novel
tnfn1_pw060510p01q111	C02	T17	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p01q112	D02	T18			
tnfn1_pw060510p01q113	E02	T18	-	protein of unknown function	hypothetical - novel
tnfn1_pw060510p01q114	F02	T20	-	DNA/RNA endonuclease G	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q115	G02	T18	-	DNA and RNA helicases Superfamily I protein	DNA replication, recombination, modification and repair - replication
tnfn1_pw060510p01q116	H02	T18	-	pseudogene: Membrane Protein. Fucose permease Carbohydrate transport and metabolism	pseudogene
tnfn1_pw060510p01q117	A03	<KAN-2>	udk	uridine kinase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q118	B03	<KAN-2>	nudH	dGTP pyrophosphohydrolase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q119	C03	<KAN-2>	wbtO	transferase	cell wall / LPS / capsule
tnfn1_pw060510p01q120	D03	<KAN-2>	tspO	tryptophan-rich sensory protein	signal transduction and regulation
tnfn1_pw060510p01q121	E03	T20	-	CheB methylesterase/CheR methyltransferase	signal transduction and regulation
tnfn1_pw060510p01q122	F03	T20	dinP	DNA-damage inducible protein P	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q123	G03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p01q124	H03	T20	gcvP1	glycine cleavage system P protein, subunit 1	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q125	A04	T20	-	ThiF family protein	putative enzymes
tnfn1_pw060510p01q126	B04	T20	lysC	aspartate kinase III	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q127	C04	T20	pyrE	orotate phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q128	D04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p01q129	E04	T20	pyrF	orotidine-5'-phosphate decarboxylase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q130	F04	T20	rimK	glutathione synthase/ribosomal protein S6 modification enzyme	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q131	G04	T20	rrmJ	23S rRNA methylase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q132	H04	T20	ruvC	holliday junction endodeoxyribonuclease	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q133	A05	T17	purT	phosphoribosylglycinamide formyltransferase 2	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q134	B05	T20	-	ornithine cyclodeaminase, mu-crystallin homolog	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q135	C05	T20			
tnfn1_pw060510p01q136	D05	T20	-	outer membrane efflux protein	transport - drugs / antibacterial compounds
tnfn1_pw060510p01q137	E05	T20	truA	tRNA pseudouridine synthase A	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q138	F05	T20	rdgC	recombination associated protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q139	G05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p01q140	H05	T20	mutT	mutator protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q141	A06	T20	-	dGTP triphosphohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q142	B06	T20	tktA	transketolase I	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q143	C06	T20	-	glycosyl hydrolases family 31 protein	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p01q144	D06	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060510p01q145	E06	T20	ilvN	acetolactate synthase small subunit	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q146	F06	T20	prfC	peptide chain release factor 3	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q147	G06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060510p01q148	H06	T18	mutL	DNA mismatch repair enzyme with ATPase activity	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_pw060510p01q149	A07	T18	-	carbon-nitrogen hydrolase family protein	putative enzymes
tnfn1_pw060510p01q150	B07	<KAN-2>	-	bifunctional NMN adenylyltransferase/Nudix hydrolase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060510p01q151	C07	T20	galM	aldose 1-epimerase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q152	D07	T20	tyrP	tyrosine permease	transport - amino-acid
tnfn1_pw060510p01q153	E07	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - repair
tnfn1_pw060510p01q154	F07	T20	-	transposase	mobile and extrachromosomal element functions - transposition
tnfn1_pw060510p01q155	G07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p01q156	H07	T20	-	dGTP triphosphohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q157	A08	T20	-	peroxiredoxin, AhpC-TSA family protein	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q158	B08	T20	prmA	50S ribosomal protein L11, methyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q159	C08	T20	add	deoxyadenosine deaminase/adenosine deaminase	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q160	D08	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p01q161	E08	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q162	F08	T20	-	-	Potentially coding: hypothetical - novel
tnfn1_pw060510p01q163	G08	T20	-	ornithine cyclodeaminase, mu-crystallin homolog	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q164	H08	T17	purT	phosphoribosylglycinamide formyltransferase 2	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q165	A09	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p01q166	B09	T18	-	pseudogene: C4-dicarboxylate anaerobic carrier, fragment	pseudogene
tnfn1_pw060510p01q167	C09	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060510p01q168	D09	<KAN-2>	ftnA	ferric iron binding protein, ferritin-like	putative enzymes
tnfn1_pw060510p01q169	E09	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p01q170	F09	T20	-	aspartate/tyrosine/aromatic aminotransferase	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q171	G09	T20	recG	ATP-dependent DNA helicase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q172	H09	T20	thrC	threonine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q173	A10	T20	priA	primosomal protein N	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p01q174	B10	T20	-	glycosyl transferase, family 2	cell wall / LPS / capsule
tnfn1_pw060510p01q175	C10	T20	-	glutathione peroxidase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060510p01q176	D10	T20	hemK	modification methylase, HemK family	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q177	E10	T20	hslU	ATP-dependent protease HslVU, ATPase subunit	post-translational modification, protein turnover, chaperones
tnfn1_pw060510p01q178	F10	T20	dapB	dihydrodipicolinate reductase	amino acid metabolism - biosynthesis
tnfn1_pw060510p01q179	G10	T20	-	pseudogene: C4-dicarboxylate anaerobic carrier, fragment	pseudogene
tnfn1_pw060510p01q180	H10	T18	-	birA-like protein	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060510p01q181	A11	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p01q182	B11	T18	dctA	C4-dicarboxylate transport protein	transport
tnfn1_pw060510p01q183	C11	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p01q184	D11	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p01q185	E11	T17	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060510p01q186	F11	T17	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060510p01q187	G11	T17	vanY	D-alanyl-D-alanine carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060510p01q188	H11	T17	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p01q189	A12	T17	rbn	tRNA processing ribonuclease BN	nucleotides and nucleosides metabolism
tnfn1_pw060510p01q190	B12	<KAN-2>	-	RNA methyltransferase, trmA family	translation, ribosomal structure and biogenesis
tnfn1_pw060510p01q191	C12	<KAN-2>	-	membrane fusion protein	motility, attachment and secretion structure
tnfn1_pw060510p01q192	D12	T20	alr	alanine racemase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p01q193	E12	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060510p01q194	F12	<KAN-2>			
tnfn1_pw060510p01q195	G12	<KAN-2>	fopA	OmpA family protein	cell wall / LPS / capsule
tnfn1_pw060510p01q196	H12	T20	gcvP2	glycine cleavage system P protein, subunit 2	amino acid metabolism - degradation, utilization, assimilation

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_pw060510p01q101	A01	C	518602	R	FTN_0508	517901	519343	F	481	702(1443)
tnfn1_pw060510p01q102	B01	C	628672	R	intergenic					
tnfn1_pw060510p01q103	C01	C	74800	F	FTN_0063	74362	75246	R	295	447(885)
tnfn1_pw060510p01q104	D01	C	355183	F	FTN_0349	355001	355360	F	120	183(360)
tnfn1_pw060510p01q105	E01	C	162956	F	FTN_0150	162491	163057	F	189	466(567)
tnfn1_pw060510p01q106	F01	C	699634	F	FTN_0660	699099	700535	F	479	536(1437)
tnfn1_pw060510p01q107	G01	C	331022	F	FTN_0320	330339	331079	R	247	58(741)
tnfn1_pw060510p01q108	H01	C	1031947	R	FTN_0977	1031487	1032053	F	189	461(567)
tnfn1_pw060510p01q109	A02	C	17434	R	FTN_0019	17052	17975	R	308	542(924)
tnfn1_pw060510p01q110	B02	C	1396072	R	FTN_1321	1395775	1396968	R	398	897(1194)
tnfn1_pw060510p01q111	C02	C	1546543	F	FTN_1458	1546487	1546990	F	168	57(504)
tnfn1_pw060510p01q112	D02	C	853068	R	intergenic					
tnfn1_pw060510p01q113	E02	C	933728	F	FTN_0878	933333	934319	F	329	396(987)
tnfn1_pw060510p01q114	F02	C	1135547	R	FTN_1073	1135198	1136259	R	354	713(1062)
tnfn1_pw060510p01q115	G02	U	831830	R	FTN_0776	831494	833557	F	688	337(2064)
tnfn1_pw060510p01q116	H02	C	1405540	R	FTN_1327	1404933	1406114	F	394	608(1182)
tnfn1_pw060510p01q117	A03	C	645270	F	FTN_0612	645168	645830	F	221	103(663)
tnfn1_pw060510p01q118	B03	C	1651548	R	FTN_1553	1651200	1651661	R	154	114(462)
tnfn1_pw060510p01q119	C03	C	1509106	R	FTN_1428	1508659	1509267	R	203	162(609)
tnfn1_pw060510p01q120	D03	C	825439	R	FTN_0768	825148	825621	R	158	183(474)
tnfn1_pw060510p01q121	E03	U	459394	R	FTN_0455	458374	461271	F	966	1021(2898)
tnfn1_pw060510p01q122	F03	C	1041093	R	FTN_0986	1040426	1041472	F	349	668(1047)
tnfn1_pw060510p01q123	G03	C	145707	F	FTN_0132	145235	146200	R	322	494(966)
tnfn1_pw060510p01q124	H03	C	517336	F	FTN_0507	516528	517892	F	455	809(1365)
tnfn1_pw060510p01q125	A04	C	1030907	F	FTN_0976	1030667	1031407	F	247	241(741)
tnfn1_pw060510p01q126	B04	C	1858624	R	FTN_1730	1857489	1858841	R	451	218(1353)
tnfn1_pw060510p01q127	C04	C	551044	F	FTN_0529	550733	551356	R	208	313(624)
tnfn1_pw060510p01q128	D04	C	1241144	R	FTN_1170	1240289	1242037	R	583	894(1749)
tnfn1_pw060510p01q129	E04	C	37341	R	FTN_0035	37218	37859	F	214	124(642)
tnfn1_pw060510p01q130	F04	C	166882	F	FTN_0154	166433	167899	R	489	1018(1467)
tnfn1_pw060510p01q131	G04	C	436115	R	FTN_0438	435998	436615	R	206	501(618)
tnfn1_pw060510p01q132	H04	C	1084461	R	FTN_1027	1084202	1084714	R	171	254(513)
tnfn1_pw060510p01q133	A05	C	1875651	R	FTN_1745	1875320	1876477	F	386	332(1158)
tnfn1_pw060510p01q134	B05	C	1533114	F	FTN_1444	1532673	1533686	R	338	573(1014)
tnfn1_pw060510p01q135	C05	U	1280992	F	intergenic					
tnfn1_pw060510p01q136	D05	C	1350839	F	FTN_1277	1349725	1351194	F	490	1115(1470)
tnfn1_pw060510p01q137	E05	C	956554	R	FTN_0899	956103	956876	R	258	323(774)
tnfn1_pw060510p01q138	F05	C	849348	R	FTN_0790	848825	849682	F	286	524(858)
tnfn1_pw060510p01q139	G05	C	1757702	R	FTN_1644	1755794	1758634	R	947	933(2841)
tnfn1_pw060510p01q140	H05	U	919004	R	FTN_0865	918875	919291	R	139	288(417)
tnfn1_pw060510p01q141	A06	C	665758	F	FTN_0632	664957	666279	R	441	522(1323)
tnfn1_pw060510p01q142	B06	C	1413230	F	FTN_1333	1412511	1414499	R	663	1270(1989)
tnfn1_pw060510p01q143	C06	C	968181	F	FTN_0911	967156	969192	F	679	1026(2037)
tnfn1_pw060510p01q144	D06	C	693534	R	FTN_0654	693039	693686	R	216	153(648)
tnfn1_pw060510p01q145	E06	U	1098871	F	FTN_1041	1098659	1098973	R	105	103(315)
tnfn1_pw060510p01q146	F06	C	1698290	R	FTN_1597	1697609	1699183	R	525	894(1575)
tnfn1_pw060510p01q147	G06	C	402245	F	FTN_0403	402038	402688	R	217	444(651)
tnfn1_pw060510p01q148	H06	C	605062	F	FTN_0577	604169	605968	F	600	894(1800)

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_pw060510p01q149	A07	C	885311	F	FTN_0827	884558	885481	R	308	171(924)
tnfn1_pw060510p01q150	B07	C	489456	F	FTN_0483	488789	489829	F	347	668(1041)
tnfn1_pw060510p01q151	C07	C	1189563	F	FTN_1127	1189307	1190299	R	331	737(993)
tnfn1_pw060510p01q152	D07	C	1836066	R	FTN_1711	1835372	1836565	R	398	500(1194)
tnfn1_pw060510p01q153	E07	C	1221278	R	FTN_1154	1220796	1222016	R	407	739(1221)
tnfn1_pw060510p01q154	F07	C	294564	R	FTN_0286	294223	294783	F	187	342(561)
tnfn1_pw060510p01q155	G07	C	230436	F	FTN_0210	229966	231588	F	541	471(1623)
tnfn1_pw060510p01q156	H07	C	665758	F	FTN_0632	664957	666279	R	441	522(1323)
tnfn1_pw060510p01q157	A08	C	1013424	F	FTN_0958	1013305	1013826	R	174	403(522)
tnfn1_pw060510p01q158	B08	C	1043723	F	FTN_0988	1043408	1044250	R	281	528(843)
tnfn1_pw060510p01q159	C08	U	739566	F	FTN_0695	739415	740452	F	346	152(1038)
tnfn1_pw060510p01q160	D08	C	1461244	F	FTN_1381	1460964	1462379	F	472	281(1416)
tnfn1_pw060510p01q161	E08	C	751632	F	FTN_0707	750859	752076	F	406	774(1218)
tnfn1_pw060510p01q162	F08	C	9096	R	-	8981	9148	R	56	53(168)
tnfn1_pw060510p01q163	G08	C	1533114	F	FTN_1444	1532673	1533686	R	338	573(1014)
tnfn1_pw060510p01q164	H08	C	1875651	R	FTN_1745	1875320	1876477	F	386	332(1158)
tnfn1_pw060510p01q165	A09	C	591655	R	FTN_0565	591250	591927	F	226	406(678)
tnfn1_pw060510p01q166	B09	U	275709	F	FTN_0268	275553	275780	R	76	72(228)
tnfn1_pw060510p01q167	C09	U	499514	R	FTN_0494	499405	500001	R	199	488(597)
tnfn1_pw060510p01q168	D09	C	1087575	F	FTN_1031	1087455	1087952	F	166	121(498)
tnfn1_pw060510p01q169	E09	U	1452470	R	FTN_1372	1451963	1453045	R	361	576(1083)
tnfn1_pw060510p01q170	F09	C	1459936	F	FTN_1380	1459763	1460893	F	377	174(1131)
tnfn1_pw060510p01q171	G09	C	340874	R	FTN_0335	339525	341561	F	679	1350(2037)
tnfn1_pw060510p01q172	H09	C	549289	F	FTN_0527	548701	549987	F	429	589(1287)
tnfn1_pw060510p01q173	A10	C	206400	F	FTN_0189	205403	207553	F	717	998(2151)
tnfn1_pw060510p01q174	B10	C	1284675	F	FTN_1214	1283962	1284918	R	319	244(957)
tnfn1_pw060510p01q175	C10	C	741674	F	FTN_0698	741553	742020	F	156	122(468)
tnfn1_pw060510p01q176	D10	U	1641787	R	FTN_1544	1641395	1642246	R	284	460(852)
tnfn1_pw060510p01q177	E10	C	1054618	F	FTN_0996	1053996	1055360	F	455	623(1365)
tnfn1_pw060510p01q178	F10	C	1857038	R	FTN_1729	1856806	1857474	R	223	437(669)
tnfn1_pw060510p01q179	G10	C	275609	R	FTN_0268	275553	275780	R	76	172(228)
tnfn1_pw060510p01q180	H10	C	594701	R	FTN_0568	594002	594781	R	260	81(780)
tnfn1_pw060510p01q181	A11	C	1147321	F	FTN_1083	1146713	1147327	F	205	609(615)
tnfn1_pw060510p01q182	B11	C	677470	R	FTN_0640	676608	677855	F	416	863(1248)
tnfn1_pw060510p01q183	C11	C	840749	F	FTN_0782	840650	841222	F	191	100(573)
tnfn1_pw060510p01q184	D11	C	1368545	F	FTN_1299	1368395	1368586	R	64	42(192)
tnfn1_pw060510p01q185	E11	C	1802328	R	FTN_1686	1801799	1803325	F	509	530(1527)
tnfn1_pw060510p01q186	F11	C	1546543	F	FTN_1458	1546487	1546990	F	168	57(504)
tnfn1_pw060510p01q187	G11	C	1023128	R	FTN_0967	1022986	1023456	R	157	329(471)
tnfn1_pw060510p01q188	H11	C	1225932	R	FTN_1156	1225105	1226655	R	517	724(1551)
tnfn1_pw060510p01q189	A12	C	204416	R	FTN_0187	203616	204809	F	398	801(1194)
tnfn1_pw060510p01q190	B12	C	647589	F	FTN_0616	646972	648318	F	449	618(1347)
tnfn1_pw060510p01q191	C12	C	1808834	R	FTN_1692	1808552	1809619	R	356	786(1068)
tnfn1_pw060510p01q192	D12	C	799985	R	FTN_0746	799235	800329	F	365	751(1095)
tnfn1_pw060510p01q193	E12	C	185579	R	FTN_0169	185208	185747	R	180	169(540)
tnfn1_pw060510p01q194	F12	C	1593152	F	intergenic					
tnfn1_pw060510p01q195	G12	C	808955	F	FTN_0756	808202	809377	F	392	754(1176)
tnfn1_pw060510p01q196	H12	C	518602	R	FTN_0508	517901	519343	F	481	702(1443)

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_pw060510p01q101	A01	EXACT(0)	157	153	137	45	EXACT(0)	200	196	56
tnfn1_pw060510p01q102	B01	EXACT(0)	154	145	126	41	EXACT(0)	185	160	45
tnfn1_pw060510p01q103	C01	EXACT(0)	156	151	120	37	EXACT(0)	200	192	58
tnfn1_pw060510p01q104	D01	EXACT(0)	123	118	90	27	EXACT(0)	200	191	48
tnfn1_pw060510p01q105	E01	EXACT(0)	159	153	135	38	EXACT(0)	200	188	59
tnfn1_pw060510p01q106	F01	EXACT(0)	124	118	98	38	EXACT(0)	200	192	56
tnfn1_pw060510p01q107	G01	EXACT(0)	120	83	78	39	EXACT(0)	200	184	44
tnfn1_pw060510p01q108	H01	EXACT(0)	121	120	91	40	EXACT(0)	200	191	59
tnfn1_pw060510p01q109	A02	EXACT(0)	122	107	90	40	EXACT(0)	200	188	58
tnfn1_pw060510p01q110	B02	EXACT(0)	126	75	72	36	EXACT(0)	200	188	48
tnfn1_pw060510p01q111	C02	EXACT(0)	124	120	101	32	EXACT(0)	200	195	49
tnfn1_pw060510p01q112	D02	EXACT(0)	122	119	98	39	EXACT(0)	200	196	54
tnfn1_pw060510p01q113	E02	EXACT(0)	123	120	93	28	EXACT(0)	200	190	54
tnfn1_pw060510p01q114	F02	EXACT(0)	155	145	110	33	EXACT(0)	200	180	24
tnfn1_pw060510p01q115	G02	EXACT(0)	124	120	105	28	EXACT(0)	168	122	20
tnfn1_pw060510p01q116	H02	EXACT(0)	121	74	64	40	EXACT(0)	200	183	53
tnfn1_pw060510p01q117	A03	EXACT(0)	125	73	64	34	EXACT(0)	200	186	55
tnfn1_pw060510p01q118	B03	EXACT(0)	121	113	100	38	EXACT(0)	200	195	54
tnfn1_pw060510p01q119	C03	EXACT(0)	121	119	104	51	EXACT(0)	200	181	67
tnfn1_pw060510p01q120	D03	EXACT(0)	120	112	96	35	EXACT(0)	200	188	55
tnfn1_pw060510p01q121	E03	EXACT(0)	155	152	99	26	EXACT(0)	200	190	44
tnfn1_pw060510p01q122	F03	EXACT(0)	156	145	115	32	EXACT(0)	200	191	55
tnfn1_pw060510p01q123	G03	EXACT(0)	156	153	119	35	EXACT(0)	200	187	57
tnfn1_pw060510p01q124	H03	EXACT(0)	156	152	136	36	EXACT(0)	200	198	53
tnfn1_pw060510p01q125	A04	EXACT(0)	162	152	114	34	EXACT(0)	200	186	49
tnfn1_pw060510p01q126	B04	EXACT(0)	155	145	126	39	EXACT(0)	200	189	56
tnfn1_pw060510p01q127	C04	EXACT(0)	157	145	141	47	EXACT(0)	200	197	58
tnfn1_pw060510p01q128	D04	EXACT(0)	156	153	100	30	EXACT(0)	200	184	54
tnfn1_pw060510p01q129	E04	EXACT(0)	159	152	116	28	EXACT(0)	200	187	49
tnfn1_pw060510p01q130	F04	EXACT(0)	154	145	129	47	EXACT(0)	200	191	57
tnfn1_pw060510p01q131	G04	EXACT(0)	155	145	132	46	EXACT(0)	200	182	59
tnfn1_pw060510p01q132	H04	EXACT(0)	154	145	132	47	EXACT(0)	129	126	52
tnfn1_pw060510p01q133	A05	EXACT(0)	121	119	98	39	EXACT(0)	200	193	57
tnfn1_pw060510p01q134	B05	EXACT(0)	154	145	129	46	EXACT(0)	200	190	58
tnfn1_pw060510p01q135	C05	EXACT(0)	155	145	128	42	EXACT(0)	200	184	56
tnfn1_pw060510p01q136	D05	EXACT(0)	153	114	110	38	EXACT(0)	200	187	59
tnfn1_pw060510p01q137	E05	EXACT(0)	156	145	131	43	EXACT(0)	200	188	50
tnfn1_pw060510p01q138	F05	EXACT(0)	156	145	128	36	EXACT(0)	200	187	58
tnfn1_pw060510p01q139	G05	EXACT(0)	156	145	136	35	EXACT(0)	200	192	36
tnfn1_pw060510p01q140	H05	ADJUSTED(2)	156	112	87	30	ESTIMATE(28)	172	150	52
tnfn1_pw060510p01q141	A06	EXACT(0)	154	139	128	46	EXACT(0)	200	192	57
tnfn1_pw060510p01q142	B06	EXACT(0)	152	145	132	45	EXACT(0)	200	195	53
tnfn1_pw060510p01q143	C06	EXACT(0)	158	152	141	44	EXACT(0)	200	192	64
tnfn1_pw060510p01q144	D06	EXACT(0)	156	153	134	34	EXACT(0)	200	184	52
tnfn1_pw060510p01q145	E06	EXACT(0)	155	145	126	51	EXACT(0)	199	168	51
tnfn1_pw060510p01q146	F06	EXACT(0)	155	139	122	33	EXACT(0)	200	140	32
tnfn1_pw060510p01q147	G06	EXACT(0)	155	138	117	38	EXACT(0)	200	185	60
tnfn1_pw060510p01q148	H06	EXACT(0)	122	112	107	37	EXACT(0)	200	182	47

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_pw060510p01q149	A07	EXACT(0)	123	120	101	31	EXACT(0)	200	189	37
tnfn1_pw060510p01q150	B07	EXACT(0)	120	106	95	46	EXACT(0)	200	195	58
tnfn1_pw060510p01q151	C07	EXACT(0)	155	139	134	45	EXACT(0)	200	168	46
tnfn1_pw060510p01q152	D07	EXACT(0)	147	144	128	47	EXACT(0)	200	185	56
tnfn1_pw060510p01q153	E07	EXACT(0)	157	90	81	26	EXACT(0)	200	182	30
tnfn1_pw060510p01q154	F07	EXACT(0)	155	145	132	46	EXACT(0)	200	187	67
tnfn1_pw060510p01q155	G07	EXACT(0)	154	145	129	45	EXACT(0)	200	189	58
tnfn1_pw060510p01q156	H07	EXACT(0)	155	136	116	40	EXACT(0)	200	192	52
tnfn1_pw060510p01q157	A08	EXACT(0)	154	145	129	42	EXACT(0)	200	190	58
tnfn1_pw060510p01q158	B08	EXACT(0)	156	151	138	33	EXACT(0)	200	191	48
tnfn1_pw060510p01q159	C08	EXACT(0)	157	145	136	48	EXACT(0)	199	173	54
tnfn1_pw060510p01q160	D08	EXACT(0)	156	152	127	38	EXACT(0)	200	158	27
tnfn1_pw060510p01q161	E08	EXACT(0)	156	153	126	39	EXACT(0)	199	182	66
tnfn1_pw060510p01q162	F08	EXACT(0)	151	145	129	47	EXACT(0)	200	180	59
tnfn1_pw060510p01q163	G08	EXACT(0)	155	151	130	43	EXACT(0)	200	190	58
tnfn1_pw060510p01q164	H08	EXACT(0)	124	117	100	21	EXACT(0)	200	193	42
tnfn1_pw060510p01q165	A09	EXACT(0)	123	116	97	36	EXACT(0)	200	178	59
tnfn1_pw060510p01q166	B09	EXACT(0)	120	105	94	33	EXACT(0)	200	176	30
tnfn1_pw060510p01q167	C09	EXACT(0)	123	119	106	34	EXACT(0)	200	188	52
tnfn1_pw060510p01q168	D09	ADJUSTED(5)	120	115	83	26	ESTIMATE(3)	197	186	64
tnfn1_pw060510p01q169	E09	EXACT(0)	119	112	87	29	EXACT(0)	201	129	54
tnfn1_pw060510p01q170	F09	EXACT(0)	156	151	127	38	EXACT(0)	200	193	64
tnfn1_pw060510p01q171	G09	EXACT(0)	155	152	136	41	EXACT(0)	200	193	56
tnfn1_pw060510p01q172	H09	EXACT(0)	154	139	128	44	EXACT(0)	200	186	55
tnfn1_pw060510p01q173	A10	EXACT(0)	155	153	132	44	EXACT(0)	200	187	56
tnfn1_pw060510p01q174	B10	EXACT(0)	155	150	116	35	EXACT(0)	200	148	47
tnfn1_pw060510p01q175	C10	EXACT(0)	155	145	129	35	EXACT(0)	200	185	34
tnfn1_pw060510p01q176	D10	EXACT(0)	155	148	89	23	EXACT(0)	200	191	49
tnfn1_pw060510p01q177	E10	EXACT(0)	157	153	124	34	EXACT(0)	200	190	45
tnfn1_pw060510p01q178	F10	EXACT(0)	154	145	120	33	EXACT(0)	200	191	54
tnfn1_pw060510p01q179	G10	EXACT(0)	155	144	112	34	EXACT(0)	200	187	64
tnfn1_pw060510p01q180	H10	EXACT(0)	121	112	87	29	EXACT(0)	94	89	48
tnfn1_pw060510p01q181	A11	EXACT(0)	123	113	102	41	EXACT(0)	200	184	51
tnfn1_pw060510p01q182	B11	EXACT(0)	124	120	101	27	EXACT(0)	200	179	49
tnfn1_pw060510p01q183	C11	EXACT(0)	119	106	93	44	EXACT(0)	200	190	59
tnfn1_pw060510p01q184	D11	EXACT(0)	123	120	90	30	EXACT(0)	200	181	52
tnfn1_pw060510p01q185	E11	EXACT(0)	122	119	74	28	EXACT(0)	200	195	52
tnfn1_pw060510p01q186	F11	EXACT(0)	112	112	85	28	EXACT(0)	200	195	50
tnfn1_pw060510p01q187	G11	EXACT(0)	120	112	91	42	EXACT(0)	200	186	54
tnfn1_pw060510p01q188	H11	EXACT(0)	121	112	90	33	EXACT(0)	200	185	57
tnfn1_pw060510p01q189	A12	EXACT(0)	121	112	96	41	EXACT(0)	200	188	59
tnfn1_pw060510p01q190	B12	EXACT(0)	122	125	72	34	EXACT(0)	122	115	46
tnfn1_pw060510p01q191	C12	EXACT(0)	120	119	98	36	EXACT(0)	200	192	57
tnfn1_pw060510p01q192	D12	EXACT(0)	155	145	114	30	EXACT(0)	200	186	62
tnfn1_pw060510p01q193	E12	EXACT(0)	120	119	98	42	EXACT(0)	200	193	58
tnfn1_pw060510p01q194	F12	EXACT(0)	120	120	99	30	EXACT(0)	200	163	35
tnfn1_pw060510p01q195	G12	EXACT(0)	121	119	101	39	EXACT(0)	199	66	30
tnfn1_pw060510p01q196	H12	EXACT(0)	155	145	129	44	EXACT(0)	200	196	54