Francisella tularensis subsp. *novicida*, "Two-Allele" Transposon Mutant Library, Plate 6 (tnfn1_pw060323p06)

Catalog No. NR-8040

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-8040 represents Plate 6 (tnfn1_pw060323p06) 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-8040 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 6 (tnfn1_pw060323p06), NR-8040."

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:

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.

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Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p06q101	A01	T20	-	pseudogene: hypothetical protein, fragment	pseudogene
tnfn1_pw060323p06q102	B01	T20	pgsA	phosphatidylglycerophosphate synthetase	fatty acids and lipids metabolism
tnfn1_pw060323p06q103	C01	T20	-	predicted metal-dependent hydrolase	putative enzymes
tnfn1_pw060323p06q104	D01	T20	-	acid phosphatase, PAP2 family	putative enzymes
tnfn1_pw060323p06q105	E01	T20	-	ROK family protein	putative enzymes
tnfn1_pw060323p06q106	F01	T20	-	acid phosphatase, PAP2 family	putative enzymes
tnfn1_pw060323p06q107	G01	T20	-	Fe2+/Zn2+ uptake regulator protein	signal transduction and regulation
tnfn1_pw060323p06q108	H01	T20	-	glycosyl hydrolases family 31 protein	carbohydrate metabolism - biosynthesis
tnfn1_pw060323p06q109	A02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p06q110	B02	T20	relA	GDP pyrophosphokinase/GTP pyrophosphokinase	other metabolism - biosynthesis
tnfn1_pw060323p06q111	C02	T20	crcB	CrcB family protein	cell cycle
tnfn1_pw060323p06q112	D02	T20	purL	phosphoribosylformylglycinamide synthase	nucleotides and nucleosides metabolism
tnfn1_pw060323p06q113	E02	T20	-	SAICAR synthetase/phosphoribosylamine-glycine ligase	nucleotides and nucleosides metabolism
tnfn1_pw060323p06q114	F02	T20	-	aldo/keto reductase family protein	putative enzymes
tnfn1_pw060323p06q115	G02	T20	tspO	tryptophan-rich sensory protein	signal transduction and regulation
tnfn1_pw060323p06q116	H02	T20	purH	AICAR transformylase/IMP cyclohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060323p06q117	A03	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p06q118	B03	T20	gcvP2	glycine cleavage system P protein, subunit 2	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q119	C03	T20	wbtH	glutamine amidotransferase/asparagine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060323p06q120	D03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p06q121	E03	T20	-	protein of unknown function, thioesterase superfamily	unknown function - conserved
tnfn1_pw060323p06q122	F03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p06q123	G03	T20	wbtA	dTDP-glucose 4,6-dehydratase	cell wall / LPS / capsule
tnfn1_pw060323p06q124	H03	T20	-	peptidase, M20 family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p06q125	A04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p06q126	B04	T20	-	glutamate:GABA antiporter (APC family) protein	transport - amino-acid
tnfn1_pw060323p06q127	C04	T20	-	magnesium chelatase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p06q128	D04	T20	-	aldo/keto reductase family protein	putative enzymes
tnfn1_pw060323p06q129	E04	T20	gcvP1	glycine cleavage system P protein, subunit 1	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q130	F04	T20	-	Mur ligase family protein	cell wall / LPS / capsule
tnfn1_pw060323p06q131	G04	T20	pepA	cytosol aminopeptidase	amino acid metabolism
tnfn1_pw060323p06q132	H04	T20	-	lipolytic enzyme	fatty acids and lipids metabolism
tnfn1_pw060323p06q133	A05	T20	katG	peroxidase/catalase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q134	B05	T20	priA	primosomal protein N	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p06q135	C05	T20	-	pirin family protein	putative enzymes
tnfn1_pw060323p06q136	D05	T20	wbtN	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060323p06q137	E05	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p06q138	F05	T20	lepA	GTP-binding protein LepA	cell wall / LPS / capsule
tnfn1_pw060323p06q139	G05	T20	-	aldolase/adducin class II family protein	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q140	H05	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p06q141	A06	T20	tig	trigger factor (TF) protein (peptidyl-prolyl cis/trans isomerase)	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p06q142	B06	T20	ilvD	dihydroxy-acid dehydratase	amino acid metabolism - biosynthesis
tnfn1_pw060323p06q143	C06	T20	-	para-aminobenzoate synthase component I	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p06q144	D06	T20	spoU	rRNA methyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060323p06q145	E06	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p06q146	F06	T20	ilvB	acetolactate synthase large subunit	amino acid metabolism - biosynthesis
tnfn1_pw060323p06q147	G06	T20	sucC	succinyl-CoA synthetase, beta chain	energy metabolism
tnfn1_pw060323p06q148	H06	T20	glgP	glycogen phosphorylase	carbohydrate metabolism - degradation, utilization, assimilation

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p06q149	A07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p06q150	B07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p06q151	C07	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p06q152	D07	T20	-	UDP-3-O-[3-fatty acid] glucosamine N-acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060323p06q153	E07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p06q154	F07	T20	glk	glucose kinase (glucokinase)	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q155	G07	T20	-	monovalent cation:proton antiporter	transport
tnfn1_pw060323p06q156	H07	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p06q157	A08	T20	pilO	Type IV pili glycosylation protein	motility, attachment and secretion structure
tnfn1_pw060323p06q158	B08	T20	-	amino acid transporter	transport - amino-acid
tnfn1_pw060323p06q159	C08	T20	-	RecB family exonuclease	DNA replication, recombination, modification and repair
tnfn1_pw060323p06q160	D08	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p06q161	E08	T20	wbtF	NAD dependent epimerase	cell wall / LPS / capsule
tnfn1_pw060323p06q162	F08	T20	-	protein of unknown function	unknown function - conserved
tnfn1_pw060323p06q163	G08	T20	glsA	glutaminase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q164	H08	T20	-	serine permease	transport - amino-acid
tnfn1_pw060323p06q165	A09	T20			
tnfn1_pw060323p06q166	B09	T20	-	serine permease	transport - amino-acid
tnfn1_pw060323p06q167	C09	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p06q168	D09	<KAN-2>	-	glycosyl transferase, group 2	cell wall / LPS / capsule
tnfn1_pw060323p06q169	E09	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p06q170	F09	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p06q171	G09	T18	rep	UvrD/REP superfamily I DNA and RNA helicases	DNA replication, recombination, modification and repair
tnfn1_pw060323p06q172	H09	T18	cscK	ROK family protein	putative enzymes
tnfn1_pw060323p06q173	A10	T18	-	ATP-binding Cassette (ABC) superfamily protein	transport
tnfn1_pw060323p06q174	B10	T18	-	conserved membrane protein of unknown function	unknown function - conserved
tnfn1_pw060323p06q175	C10	T18	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060323p06q176	D10	T18	-	tRNA synthetase class II (D, K and N)	other metabolism - biosynthesis
tnfn1_pw060323p06q177	E10	T18	-	tRNA synthetase class II (D, K and N)	other metabolism - biosynthesis
tnfn1_pw060323p06q178	F10	T18	-	conserved hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p06q179	G10	T18	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p06q180	H10	T18	yqhD	Fe-dependent alcohol dehydrogenase	energy metabolism
tnfn1_pw060323p06q181	A11	T18	-	beta-lactamase class A	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p06q182	B11	T18	rng	ribonuclease G	translation, ribosomal structure and biogenesis
tnfn1_pw060323p06q183	C11	T18	leuD	isopropylmalate isomerase small subunit	amino acid metabolism - biosynthesis
tnfn1_pw060323p06q184	D11	T18	pcs	(CDP-alcohol) phosphatidyltransferase	fatty acids and lipids metabolism
tnfn1_pw060323p06q185	E11	T18	-	aminomutase	amino acid metabolism
tnfn1_pw060323p06q186	F11	T18	isftu3	isftu3	IS element
tnfn1_pw060323p06q187	G11	T20	-	kinase-like protein	putative enzymes
tnfn1_pw060323p06q188	H11	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p06q189	A12	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p06q190	B12	T20	dctA	C4-dicarboxylate transport protein	transport
tnfn1_pw060323p06q191	C12	T20	-	sugar transferase involved in lipopolysaccharide synthesis	cell wall / LPS / capsule
tnfn1_pw060323p06q192	D12	T20	-	ferredoxin	energy metabolism
tnfn1_pw060323p06q193	E12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p06q194	F12	T20	thrC	threonine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060323p06q195	G12	T20	-	Zn-dependent hydrolase	putative enzymes
tnfn1_pw060323p06q196	H12	T20	-	hypothetical protein	hypothetical - novel

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_pw060323p06q101	A01	C	1723467	R	FTN_0614	1723371	1723925	R	185	459(555)
tnfn1_pw060323p06q102	B01	C	255776	R	FTN_0234	255214	255807	F	198	563(594)
tnfn1_pw060323p06q103	C01	C	756626	R	FTN_0711	756324	756980	F	219	303(657)
tnfn1_pw060323p06q104	D01	C	1650797	F	FTN_1552	1650561	1651184	F	208	237(624)
tnfn1_pw060323p06q105	E01	C	867952	F	FTN_0810	867532	868413	F	294	421(882)
tnfn1_pw060323p06q106	F01	C	1650797	F	FTN_1552	1650561	1651184	F	208	237(624)
tnfn1_pw060323p06q107	G01	C	936631	R	FTN_0881	936452	936880	F	143	180(429)
tnfn1_pw060323p06q108	H01	C	967514	F	FTN_0911	967156	969192	F	679	359(2037)
tnfn1_pw060323p06q109	A02	C	1225786	R	FTN_1156	1225105	1226655	R	517	870(1551)
tnfn1_pw060323p06q110	B02	C	1615267	F	FTN_1518	1614441	1616447	R	669	1181(2007)
tnfn1_pw060323p06q111	C02	C	150321	R	FTN_0136	150192	150533	F	114	130(342)
tnfn1_pw060323p06q112	D02	C	1818641	F	FTN_1699	1816650	1820534	R	1295	1894(3885)
tnfn1_pw060323p06q113	E02	C	419463	F	FTN_0420	418362	420671	F	770	1102(2310)
tnfn1_pw060323p06q114	F02	C	883047	F	FTN_0825	882250	883320	R	357	274(1071)
tnfn1_pw060323p06q115	G02	U	825439	F	FTN_0768	825148	825621	R	158	183(474)
tnfn1_pw060323p06q116	H02	C	195803	F	FTN_0177	194359	195903	R	515	101(1545)
tnfn1_pw060323p06q117	A03	C	1800879	F	FTN_1685	1800523	1801710	F	396	357(1188)
tnfn1_pw060323p06q118	B03	C	518057	F	FTN_0508	517901	519343	F	481	157(1443)
tnfn1_pw060323p06q119	C03	C	1501392	R	FTN_1421	1499941	1501830	R	630	439(1890)
tnfn1_pw060323p06q120	D03	C	1068202	F	FTN_1009	1068039	1069043	F	335	164(1005)
tnfn1_pw060323p06q121	E03	C	820375	F	FTN_0763	820263	820709	F	149	113(447)
tnfn1_pw060323p06q122	F03	C	88218	F	FTN_0077	87966	88421	R	152	204(456)
tnfn1_pw060323p06q123	G03	C	1512406	R	FTN_1431	1511000	1512733	R	578	328(1734)
tnfn1_pw060323p06q124	H03	C	1239549	F	FTN_1169	1239077	1240234	F	386	473(1158)
tnfn1_pw060323p06q125	A04	C	1187201	R	FTN_1122	1186844	1187230	F	129	358(387)
tnfn1_pw060323p06q126	B04	C	1626568	F	FTN_1529	1625383	1626783	R	467	216(1401)
tnfn1_pw060323p06q127	C04	C	1780155	F	FTN_1665	1778927	1780432	R	502	278(1506)
tnfn1_pw060323p06q128	D04	C	884105	F	FTN_0826	883402	884463	R	354	359(1062)
tnfn1_pw060323p06q129	E04	C	516814	F	FTN_0507	516528	517892	F	455	287(1365)
tnfn1_pw060323p06q130	F04	C	1173717	F	FTN_1111	1172407	1174089	R	561	373(1683)
tnfn1_pw060323p06q131	G04	C	699257	F	FTN_0660	699099	700535	F	479	159(1437)
tnfn1_pw060323p06q132	H04	C	434950	R	FTN_0436	434467	435345	F	293	484(879)
tnfn1_pw060323p06q133	A05	C	668054	F	FTN_0633	666386	668602	R	739	549(2217)
tnfn1_pw060323p06q134	B05	C	205666	R	FTN_0189	205403	207553	F	717	264(2151)
tnfn1_pw060323p06q135	C05	C	1353680	F	FTN_1281	1353283	1353978	R	232	299(696)
tnfn1_pw060323p06q136	D05	C	1502828	R	FTN_1422	1501835	1502944	R	370	117(1110)
tnfn1_pw060323p06q137	E05	C	1894734	R	FTN_1765	1894130	1895098	F	323	605(969)
tnfn1_pw060323p06q138	F05	C	118402	R	FTN_0107	117842	119623	F	594	561(1782)
tnfn1_pw060323p06q139	G05	C	1077057	R	FTN_1018	1076556	1077251	F	232	502(696)
tnfn1_pw060323p06q140	H05	C	562784	R	FTN_0538	561538	562995	R	486	212(1458)
tnfn1_pw060323p06q141	A06	C	1118931	F	FTN_1058	1117803	1119116	R	438	186(1314)
tnfn1_pw060323p06q142	B06	U	1102037	F	FTN_1043	1100825	1102504	R	560	468(1680)
tnfn1_pw060323p06q143	C06	C	879907	F	FTN_0822	878696	880456	F	587	1212(1761)
tnfn1_pw060323p06q144	D06	C	822623	F	FTN_0766	822309	823058	R	250	436(750)
tnfn1_pw060323p06q145	E06	C	323446	F	FTN_0312	322772	323959	F	396	675(1188)
tnfn1_pw060323p06q146	F06	C	1100496	F	FTN_1042	1098981	1100675	R	565	180(1695)
tnfn1_pw060323p06q147	G06	C	624967	F	FTN_0594	624495	625655	R	387	689(1161)
tnfn1_pw060323p06q148	H06	C	535000	F	FTN_0517	534678	536948	F	757	323(2271)

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_pw060323p06q149	A07	C	161053	R	FTN_0148	160862	161488	F	209	192(627)
tnfn1_pw060323p06q150	B07	U	1646007	R	FTN_1548	1645390	1646757	F	456	618(1368)
tnfn1_pw060323p06q151	C07	C	816626	R	FTN_0760	816310	816897	F	196	317(588)
tnfn1_pw060323p06q152	D07	C	222051	F	FTN_0200	221524	222564	R	347	514(1041)
tnfn1_pw060323p06q153	E07	C	111328	R	FTN_0100	110482	111495	R	338	168(1014)
tnfn1_pw060323p06q154	F07	C	468343	R	FTN_0462	468195	469208	F	338	149(1014)
tnfn1_pw060323p06q155	G07	C	157651	R	FTN_0143	156853	158736	F	628	799(1884)
tnfn1_pw060323p06q156	H07	C	315278	R	FTN_0306	315040	315714	F	225	239(675)
tnfn1_pw060323p06q157	A08	C	1204176	R	FTN_1139	1203854	1204447	R	198	272(594)
tnfn1_pw060323p06q158	B08	C	327028	F	FTN_0317	326808	328169	F	454	221(1362)
tnfn1_pw060323p06q159	C08	C	1473080	F	FTN_1396	1472783	1473271	R	163	192(489)
tnfn1_pw060323p06q160	D08	C	214133	F	FTN_0194	213220	214584	R	455	452(1365)
tnfn1_pw060323p06q161	E08	C	1506145	R	FTN_1425	1505283	1506254	R	324	110(972)
tnfn1_pw060323p06q162	F08	C	1388896	R	FTN_1316	1388629	1389249	F	207	268(621)
tnfn1_pw060323p06q163	G08	C	187534	F	FTN_0171	186730	188268	R	513	735(1539)
tnfn1_pw060323p06q164	H08	C	655762	F	FTN_0624	654832	656091	R	420	330(1260)
tnfn1_pw060323p06q165	A09	C	1759111	R	intergenic					
tnfn1_pw060323p06q166	B09	C	193420	R	FTN_0176	193022	194287	F	422	399(1266)
tnfn1_pw060323p06q167	C09	C	1621552	R	FTN_1524	1621272	1621652	R	127	101(381)
tnfn1_pw060323p06q168	D09	C	571412	F	FTN_0545	570952	571905	F	318	461(954)
tnfn1_pw060323p06q169	E09	C	427730	F	FTN_0430	427666	428130	F	155	65(465)
tnfn1_pw060323p06q170	F09	C	874436	F	FTN_0817	874185	874682	R	166	247(498)
tnfn1_pw060323p06q171	G09	C	844737	F	FTN_0787	844273	846285	F	671	465(2013)
tnfn1_pw060323p06q172	H09	C	684277	F	FTN_0646	683745	684641	R	299	365(897)
tnfn1_pw060323p06q173	A10	C	1339086	F	FTN_1267	1338966	1339724	F	253	121(759)
tnfn1_pw060323p06q174	B10	C	85558	F	FTN_0073	85509	87161	R	551	1604(1653)
tnfn1_pw060323p06q175	C10	C	1047049	R	FTN_0990	1045587	1048394	R	936	1346(2808)
tnfn1_pw060323p06q176	D10	C	593597	R	FTN_0567	593082	594002	R	307	406(921)
tnfn1_pw060323p06q177	E10	C	593597	R	FTN_0567	593082	594002	R	307	406(921)
tnfn1_pw060323p06q178	F10	C	1467109	R	FTN_1389	1466621	1467367	R	249	259(747)
tnfn1_pw060323p06q179	G10	C	314527	F	FTN_0305	314309	314926	F	206	219(618)
tnfn1_pw060323p06q180	H10	C	1045428	R	FTN_0989	1044415	1045569	R	385	142(1155)
tnfn1_pw060323p06q181	A11	C	1134678	F	FTN_1072	1134341	1135201	F	287	338(861)
tnfn1_pw060323p06q182	B11	C	1909331	R	FTN_1782	1908200	1909693	R	498	363(1494)
tnfn1_pw060323p06q183	C11	C	71090	F	FTN_0060	70788	71354	R	189	265(567)
tnfn1_pw060323p06q184	D11	C	1559778	F	FTN_1471	1559648	1560409	F	254	131(762)
tnfn1_pw060323p06q185	E11	C	777405	R	FTN_0722	777263	778246	F	328	143(984)
tnfn1_pw060323p06q186	F11	C	1498375	R	-	1497953	1498693	F	247	423(741)
tnfn1_pw060323p06q187	G11	C	893298	F	FTN_0836	893030	893530	R	167	233(501)
tnfn1_pw060323p06q188	H11	C	562784	R	FTN_0538	561538	562995	R	486	212(1458)
tnfn1_pw060323p06q189	A12	C	562784	R	FTN_0538	561538	562995	R	486	212(1458)
tnfn1_pw060323p06q190	B12	C	677402	R	FTN_0640	676608	677855	F	416	795(1248)
tnfn1_pw060323p06q191	C12	C	1291282	R	FTN_1220	1290818	1292209	R	464	928(1392)
tnfn1_pw060323p06q192	D12	C	129250	F	FTN_0117	129107	129457	R	117	208(351)
tnfn1_pw060323p06q193	E12	C	793892	R	FTN_0740	793798	794055	F	86	95(258)
tnfn1_pw060323p06q194	F12	C	549162	R	FTN_0527	548701	549987	F	429	462(1287)
tnfn1_pw060323p06q195	G12	C	1467679	R	FTN_1390	1467372	1468055	R	228	377(684)
tnfn1_pw060323p06q196	H12	C	893544	R	FTN_0837	893533	894228	R	232	685(696)

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_pw060323p06q101	A01	EXACT(0)	158	159	127	27	EXACT(0)	200	185	57
tnfn1_pw060323p06q102	B01	EXACT(0)	157	152	117	30	EXACT(0)	200	188	57
tnfn1_pw060323p06q103	C01	EXACT(0)	156	153	132	42	EXACT(0)	200	180	54
tnfn1_pw060323p06q104	D01	EXACT(0)	155	152	122	35	EXACT(0)	200	185	55
tnfn1_pw060323p06q105	E01	EXACT(0)	155	145	117	31	EXACT(0)	200	189	50
tnfn1_pw060323p06q106	F01	EXACT(0)	156	153	126	38	EXACT(0)	200	185	55
tnfn1_pw060323p06q107	G01	EXACT(0)	155	139	128	43	EXACT(0)	200	186	53
tnfn1_pw060323p06q108	H01	EXACT(0)	155	145	117	32	EXACT(0)	200	194	51
tnfn1_pw060323p06q109	A02	EXACT(0)	155	145	117	32	EXACT(0)	200	178	50
tnfn1_pw060323p06q110	B02	EXACT(0)	156	151	135	39	EXACT(0)	200	194	57
tnfn1_pw060323p06q111	C02	EXACT(0)	155	139	125	36	EXACT(0)	26	26	37
tnfn1_pw060323p06q112	D02	EXACT(0)	157	146	132	35	EXACT(0)	200	190	55
tnfn1_pw060323p06q113	E02	EXACT(0)	158	146	118	35	EXACT(0)	200	195	56
tnfn1_pw060323p06q114	F02	EXACT(0)	156	152	131	39	EXACT(0)	200	173	44
tnfn1_pw060323p06q115	G02	EXACT(0)	159	152	127	38	EXACT(0)	200	190	61
tnfn1_pw060323p06q116	H02	EXACT(0)	157	153	134	38	EXACT(0)	200	176	56
tnfn1_pw060323p06q117	A03	EXACT(0)	156	146	124	42	EXACT(0)	200	189	59
tnfn1_pw060323p06q118	B03	EXACT(0)	157	151	132	42	EXACT(0)	200	171	44
tnfn1_pw060323p06q119	C03	EXACT(0)	155	152	128	40	EXACT(0)	200	191	56
tnfn1_pw060323p06q120	D03	EXACT(0)	156	153	120	27	EXACT(0)	200	193	53
tnfn1_pw060323p06q121	E03	EXACT(0)	157	153	133	36	EXACT(0)	200	195	53
tnfn1_pw060323p06q122	F03	EXACT(0)	157	143	125	35	EXACT(0)	200	195	44
tnfn1_pw060323p06q123	G03	EXACT(0)	156	153	129	35	EXACT(0)	200	191	54
tnfn1_pw060323p06q124	H03	EXACT(0)	157	146	126	40	EXACT(0)	200	174	42
tnfn1_pw060323p06q125	A04	EXACT(0)	157	151	132	36	EXACT(0)	125	119	47
tnfn1_pw060323p06q126	B04	EXACT(0)	156	151	121	37	EXACT(0)	200	192	54
tnfn1_pw060323p06q127	C04	EXACT(0)	156	153	132	42	EXACT(0)	200	195	59
tnfn1_pw060323p06q128	D04	EXACT(0)	154	145	126	41	EXACT(0)	200	192	55
tnfn1_pw060323p06q129	E04	EXACT(0)	157	153	129	40	EXACT(0)	200	198	54
tnfn1_pw060323p06q130	F04	EXACT(0)	157	151	135	41	EXACT(0)	182	165	48
tnfn1_pw060323p06q131	G04	EXACT(0)	158	153	129	35	EXACT(0)	200	187	53
tnfn1_pw060323p06q132	H04	EXACT(0)	156	153	117	34	EXACT(0)	200	185	58
tnfn1_pw060323p06q133	A05	EXACT(0)	156	153	117	28	EXACT(0)	200	195	56
tnfn1_pw060323p06q134	B05	EXACT(0)	152	145	116	39	EXACT(0)	200	189	54
tnfn1_pw060323p06q135	C05	EXACT(0)	153	146	114	39	EXACT(0)	200	193	48
tnfn1_pw060323p06q136	D05	EXACT(0)	156	153	129	35	EXACT(0)	200	170	45
tnfn1_pw060323p06q137	E05	EXACT(0)	155	152	107	32	EXACT(0)	200	181	54
tnfn1_pw060323p06q138	F05	EXACT(0)	156	153	135	41	EXACT(0)	200	194	54
tnfn1_pw060323p06q139	G05	EXACT(0)	156	153	126	37	EXACT(0)	200	190	47
tnfn1_pw060323p06q140	H05	EXACT(0)	155	152	104	23	EXACT(0)	200	183	51
tnfn1_pw060323p06q141	A06	EXACT(0)	156	145	118	37	EXACT(0)	200	178	48
tnfn1_pw060323p06q142	B06	EXACT(0)	155	145	134	51	EXACT(0)	200	193	61
tnfn1_pw060323p06q143	C06	EXACT(0)	154	145	120	36	EXACT(0)	200	180	47
tnfn1_pw060323p06q144	D06	EXACT(0)	155	151	130	38	EXACT(0)	200	193	55
tnfn1_pw060323p06q145	E06	EXACT(0)	157	146	132	39	EXACT(0)	200	181	50
tnfn1_pw060323p06q146	F06	EXACT(0)	155	152	128	42	EXACT(0)	200	192	58
tnfn1_pw060323p06q147	G06	EXACT(0)	156	151	138	39	EXACT(0)	200	196	56
tnfn1_pw060323p06q148	H06	EXACT(0)	156	153	123	33	EXACT(0)	200	190	55

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_pw060323p06q149	A07	EXACT(0)	157	153	112	32	EXACT(0)	200	189	56
tnfn1_pw060323p06q150	B07	EXACT(0)	166	136	86	24	EXACT(0)	200	182	25
tnfn1_pw060323p06q151	C07	EXACT(0)	155	151	133	39	EXACT(0)	199	186	48
tnfn1_pw060323p06q152	D07	EXACT(0)	155	151	133	39	EXACT(0)	200	150	45
tnfn1_pw060323p06q153	E07	EXACT(0)	157	153	140	43	EXACT(0)	97	90	54
tnfn1_pw060323p06q154	F07	EXACT(0)	157	152	131	33	EXACT(0)	200	185	53
tnfn1_pw060323p06q155	G07	EXACT(0)	157	153	133	36	EXACT(0)	200	185	51
tnfn1_pw060323p06q156	H07	EXACT(0)	156	152	131	41	EXACT(0)	201	165	35
tnfn1_pw060323p06q157	A08	EXACT(0)	155	152	129	42	EXACT(0)	35	35	51
tnfn1_pw060323p06q158	B08	EXACT(0)	157	151	128	35	EXACT(0)	200	188	53
tnfn1_pw060323p06q159	C08	EXACT(0)	157	145	136	40	EXACT(0)	200	137	40
tnfn1_pw060323p06q160	D08	EXACT(0)	155	151	127	38	EXACT(0)	199	197	43
tnfn1_pw060323p06q161	E08	EXACT(0)	157	149	138	39	EXACT(0)	168	158	50
tnfn1_pw060323p06q162	F08	EXACT(0)	155	153	127	36	EXACT(0)	200	152	41
tnfn1_pw060323p06q163	G08	EXACT(0)	156	151	124	38	EXACT(0)	200	141	44
tnfn1_pw060323p06q164	H08	EXACT(0)	155	145	129	40	EXACT(0)	200	187	55
tnfn1_pw060323p06q165	A09	EXACT(0)	156	138	108	34	EXACT(0)	104	92	52
tnfn1_pw060323p06q166	B09	EXACT(0)	156	139	127	41	EXACT(0)	200	192	57
tnfn1_pw060323p06q167	C09	EXACT(0)	121	118	91	24	EXACT(0)	200	190	49
tnfn1_pw060323p06q168	D09	EXACT(0)	121	109	78	22	EXACT(0)	200	174	38
tnfn1_pw060323p06q169	E09	EXACT(0)	121	112	84	24	EXACT(0)	200	192	49
tnfn1_pw060323p06q170	F09	EXACT(0)	123	113	91	27	EXACT(0)	200	189	50
tnfn1_pw060323p06q171	G09	EXACT(0)	122	112	99	37	EXACT(0)	201	151	37
tnfn1_pw060323p06q172	H09	EXACT(0)	123	118	94	25	EXACT(0)	200	194	55
tnfn1_pw060323p06q173	A10	EXACT(0)	123	120	96	26	EXACT(0)	200	192	52
tnfn1_pw060323p06q174	B10	EXACT(0)	123	112	101	32	EXACT(0)	200	190	52
tnfn1_pw060323p06q175	C10	EXACT(0)	123	119	101	35	EXACT(0)	200	160	41
tnfn1_pw060323p06q176	D10	EXACT(0)	120	106	81	24	EXACT(0)	201	177	47
tnfn1_pw060323p06q177	E10	EXACT(0)	122	105	50	20	EXACT(0)	200	179	41
tnfn1_pw060323p06q178	F10	EXACT(0)	124	119	105	33	EXACT(0)	200	183	50
tnfn1_pw060323p06q179	G10	EXACT(0)	123	112	86	24	EXACT(0)	200	188	55
tnfn1_pw060323p06q180	H10	EXACT(0)	122	119	95	31	EXACT(0)	199	178	40
tnfn1_pw060323p06q181	A11	EXACT(0)	122	112	78	22	EXACT(0)	200	173	44
tnfn1_pw060323p06q182	B11	EXACT(0)	122	120	99	31	EXACT(0)	200	189	51
tnfn1_pw060323p06q183	C11	EXACT(0)	122	112	90	26	EXACT(0)	200	192	57
tnfn1_pw060323p06q184	D11	EXACT(0)	122	112	96	30	EXACT(0)	200	188	50
tnfn1_pw060323p06q185	E11	EXACT(0)	121	112	99	26	EXACT(0)	200	184	50
tnfn1_pw060323p06q186	F11	EXACT(0)	123	120	102	28	EXACT(0)	200	166	38
tnfn1_pw060323p06q187	G11	EXACT(0)	157	146	128	37	EXACT(0)	200	170	38
tnfn1_pw060323p06q188	H11	EXACT(0)	155	145	110	34	EXACT(0)	200	183	54
tnfn1_pw060323p06q189	A12	EXACT(0)	157	144	114	32	EXACT(0)	200	183	63
tnfn1_pw060323p06q190	B12	EXACT(0)	157	152	127	39	EXACT(0)	200	182	52
tnfn1_pw060323p06q191	C12	EXACT(0)	156	145	121	36	EXACT(0)	180	170	49
tnfn1_pw060323p06q192	D12	EXACT(0)	156	152	121	33	EXACT(0)	200	191	53
tnfn1_pw060323p06q193	E12	EXACT(0)	156	152	136	38	EXACT(0)	200	180	50
tnfn1_pw060323p06q194	F12	EXACT(0)	156	145	109	31	EXACT(0)	200	194	51
tnfn1_pw060323p06q195	G12	EXACT(0)	156	152	133	37	EXACT(0)	200	193	56
tnfn1_pw060323p06q196	H12	EXACT(0)	151	108	96	42	EXACT(0)	168	158	54