Francisella tularensis subsp. *novicida*, "Two-Allele" Transposon Mutant Library, Plate 32 (tnfn1_pw060510p04)

Catalog No. NR-8066

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-8066 represents Plate 32 (tnfn1_pw060510p04) 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_pw060510p04q102 (Well B01) is not available due to quality issues.

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

Material Provided:
Each well of the 96-well plate contains approximately 0.25 mL of bacterial culture in 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-8066 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 32 (tnfn1_pw060510p04), NR-8066."

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.

Support Provided by NIAID

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Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060510p04q101	A01	T18			
tnfn1_pw060510p04q102	B01	T18	aceE	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q103	C01	T20	emrE	putative membrane transporter of cations and cationic drugs, multidrug resistance protein	transport - drugs / antibacterial compounds
tnfn1_pw060510p04q104	D01	T20	glgB	1,4-alpha-glucan branching enzyme	carbohydrate metabolism - biosynthesis
tnfn1_pw060510p04q105	E01	T20	leuC	isopropylmalate isomerase	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q106	F01	T20	trpD	anthranilate phosphoribosyltransferase	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q107	G01	T20	ruvA	holliday junction DNA helicase, subunit A	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q108	H01	T18			
tnfn1_pw060510p04q109	A02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p04q110	B02	T20	dapD	tetrahydrodipicolinate succinylase subunit	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q111	C02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q112	D02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p04q113	E02	T20	phrB	deoxyribodipyrimidine photolyase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q114	F02	T20	-	modification methylase, HemK family	translation, ribosomal structure and biogenesis
tnfn1_pw060510p04q115	G02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q116	H02	T20			
tnfn1_pw060510p04q117	A03	<KAN-2>	gltA	citrate synthase	energy metabolism
tnfn1_pw060510p04q118	B03	<KAN-2>	kdpB	potassium-transporting ATPase B chain	transport
tnfn1_pw060510p04q119	C03	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q120	D03	T18	-	glycosyl transferase, family 2	cell wall / LPS / capsule
tnfn1_pw060510p04q121	E03	T18	leuD	isopropylmalate isomerase small subunit	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q122	F03	T18	-	Dam-replacing family protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q123	G03	T18	tag	3-methyladenine DNA glycosylase	DNA replication, recombination, modification and repair - repair
tnfn1_pw060510p04q124	H03	T18			
tnfn1_pw060510p04q125	A04	T20			
tnfn1_pw060510p04q126	B04	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060510p04q127	C04	T20	-	LPS fatty acid acyltransferase	cell wall / LPS / capsule
tnfn1_pw060510p04q128	D04	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060510p04q129	E04	T20	ampD	N-acetylmuramoyl-L-alanine amidase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q130	F04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q131	G04	T20	aroG	phospho-2-dehydro-3-deoxyheptonate aldolase	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q132	H04	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - repair
tnfn1_pw060510p04q133	A05	T20	-	RNA methyltransferase, SpoU family	translation, ribosomal structure and biogenesis
tnfn1_pw060510p04q134	B05	T20	-	metallopeptidase, M16 family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060510p04q135	C05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p04q136	D05	T20	rbsK	ribokinase, pfkB family	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q137	E05	T20	wbtF	NAD dependent epimerase	cell wall / LPS / capsule
tnfn1_pw060510p04q138	F05	T20	-	endoribonuclease L-PSP	translation, ribosomal structure and biogenesis
tnfn1_pw060510p04q139	G05	T20	-	MutT/nudix family protein	putative enzymes
tnfn1_pw060510p04q140	H05	<KAN-2>	cfa	cyclopropane fatty acid synthase, methyltransferase	fatty acids and lipids metabolism
tnfn1_pw060510p04q141	A06	<KAN-2>	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060510p04q142	B06	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060510p04q143	C06	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q144	D06	T18	-	drug:H+ antiporter-1 (DHA2) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060510p04q145	E06	T18			
tnfn1_pw060510p04q146	F06	T20	gloA	lactoylglutathione lyase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q147	G06	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p04q148	H06	T18	-	conserved hypothetical protein	hypothetical - conserved

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Table 1 - Transposon Type and Mutated Gene

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tnfn1_pw060510p04q149	A07	T18	-	long chain fatty acid CoA ligase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q150	B07	T18	-	zinc-binding alcohol dehydrogenase	carbohydrate metabolism
tnfn1_pw060510p04q151	C07	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060510p04q152	D07	T20	-	lysine decarboxylase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q153	E07	T20	-	aminotransferase	amino acid metabolism
tnfn1_pw060510p04q154	F07	T20	ndk	nucleoside diphosphate kinase	nucleotides and nucleosides metabolism
tnfn1_pw060510p04q155	G07	T20	polA	DNA polymerase I	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q156	H07	T20	-	ribokinase, pfkB family	carbohydrate metabolism
tnfn1_pw060510p04q157	A08	T20	-	shikimate 5-dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q158	B08	<KAN-2>	galP1	galactose-proton symporter, major facilitator superfamily (MFS) transport protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060510p04q159	C08	T18	oppA	ABC-type oligopeptide transport system, periplasmic component	transport
tnfn1_pw060510p04q160	D08	T20	aroB	3-dehydroquinate synthetase	amino acid metabolism - biosynthesis
tnfn1_pw060510p04q161	E08	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060510p04q162	F08	T18	recJ	single-stranded-DNA-specific exonuclease	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q163	G08	T20	pepA	cytosol aminopeptidase	amino acid metabolism
tnfn1_pw060510p04q164	H08	T18	feoB	ferrous iron transport protein B	transport
tnfn1_pw060510p04q165	A09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p04q166	B09	T20	fadA	acetyl-CoA acetyltransferase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q167	C09	T20	fur	ferric uptake regulation protein	signal transduction and regulation
tnfn1_pw060510p04q168	D09	T20	uvrA	excinuclease ABC, subunit A	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q169	E09	T20	recA	recombinase A protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q170	F09	T20	ftsW	cell division protein FtsW	cell cycle
tnfn1_pw060510p04q171	G09	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060510p04q172	H09	<KAN-2>	purE	N5-carboxyaminoimidazole ribonucleotide mutase	nucleotides and nucleosides metabolism
tnfn1_pw060510p04q173	A10	T18	-	small conductance mechanosensitive ion channel (MscS) family protein	transport
tnfn1_pw060510p04q174	B10	T18	hpt	hypoxanthine-guanine phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060510p04q175	C10	T18	tmpT	thiopurine S-methyltransferase	putative enzymes
tnfn1_pw060510p04q176	D10	T18	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060510p04q177	E10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q178	F10	T20	-	amino acid permease	transport - amino-acid
tnfn1_pw060510p04q179	G10	T20	xthA	exodeoxyribonuclease III	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q180	H10	T20	-	4Fe-4S ferredoxin	energy metabolism
tnfn1_pw060510p04q181	A11	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060510p04q182	B11	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q183	C11	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060510p04q184	D11	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060510p04q185	E11	T18	-	glutamate decarboxylase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q186	F11	T20	recN	DNA repair protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q187	G11	T20	-	C4-dicarboxylate anaerobic carrier	transport
tnfn1_pw060510p04q188	H11	T18			
tnfn1_pw060510p04q189	A12	T18	-	competence protein	transport
tnfn1_pw060510p04q190	B12	T18	upp	uracil phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060510p04q191	C12	T18	-	peroxiredoxin, AhpC-TSA family protein	other metabolism - degradation, utilization, assimilation
tnfn1_pw060510p04q192	D12	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060510p04q193	E12	T20	uvrC	excinuclease ABC, subunit C	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060510p04q194	F12	T20	-	deoxyguanosinetriphosphate triphosphohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060510p04q195	G12	T20	pyrD	dihydroorotate oxidase	nucleotides and nucleosides metabolism
tnfn1_pw060510p04q196	H12	T20	tyrA	prephenate dehydrogenase	amino acid metabolism - biosynthesis

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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_pw060510p04q101	A01	C	1183335	R	intergenic					
tnfn1_pw060510p04q102	B01	U	1589916	R	FTN_1494	1588133	1590811	R	893	896(2679)
tnfn1_pw060510p04q103	C01	C	856623	R	FTN_0799	856317	856643	R	109	21(327)
tnfn1_pw060510p04q104	D01	C	529270	F	FTN_0513	527934	529853	R	640	584(1920)
tnfn1_pw060510p04q105	E01	U	72364	F	FTN_0061	71360	72766	R	469	403(1407)
tnfn1_pw060510p04q106	F01	C	1904831	R	FTN_1776	1904293	1905303	R	337	473(1011)
tnfn1_pw060510p04q107	G01	C	1082868	R	FTN_1025	1082264	1082911	R	216	44(648)
tnfn1_pw060510p04q108	H01	C	1042360	F	intergenic					
tnfn1_pw060510p04q109	A02	U	426816	R	FTN_0428	426551	427027	F	159	266(477)
tnfn1_pw060510p04q110	B02	C	1855386	F	FTN_1727	1855155	1855901	R	249	516(747)
tnfn1_pw060510p04q111	C02	U	915114	R	FTN_0861	914550	915788	F	413	565(1239)
tnfn1_pw060510p04q112	D02	C	345526	R	FTN_0340	345436	345768	R	111	243(333)
tnfn1_pw060510p04q113	E02	U	1185386	F	FTN_1121	1184715	1186106	F	464	672(1392)
tnfn1_pw060510p04q114	F02	C	322166	R	FTN_0311	321772	322713	F	314	395(942)
tnfn1_pw060510p04q115	G02	C	248634	F	FTN_0225	248455	249375	R	307	742(921)
tnfn1_pw060510p04q116	H02	U	1042254	F	intergenic					
tnfn1_pw060510p04q117	A03	C	1752348	F	FTN_1640	1751913	1753169	F	419	436(1257)
tnfn1_pw060510p04q118	B03	C	1843398	R	FTN_1717	1841960	1843996	R	679	599(2037)
tnfn1_pw060510p04q119	C03	C	289409	R	FTN_0282	288913	289806	F	298	497(894)
tnfn1_pw060510p04q120	D03	C	1283591	R	FTN_1213	1282938	1283942	R	335	352(1005)
tnfn1_pw060510p04q121	E03	C	71013	F	FTN_0060	70788	71354	R	189	342(567)
tnfn1_pw060510p04q122	F03	C	1816608	F	FTN_1698	1815852	1816619	R	256	12(768)
tnfn1_pw060510p04q123	G03	C	717558	R	FTN_0673	717345	717908	F	188	214(564)
tnfn1_pw060510p04q124	H03	C	1042360	F	intergenic					
tnfn1_pw060510p04q125	A04	U	1034372	R	intergenic					
tnfn1_pw060510p04q126	B04	U	693165	R	FTN_0654	693039	693686	R	216	522(648)
tnfn1_pw060510p04q127	C04	C	83932	R	FTN_0071	83619	84539	R	307	608(921)
tnfn1_pw060510p04q128	D04	C	1015140	F	FTN_0960	1014799	1015527	R	243	388(729)
tnfn1_pw060510p04q129	E04	U	1650142	R	FTN_1551	1649966	1650487	R	174	346(522)
tnfn1_pw060510p04q130	F04	C	1243666	R	FTN_1172	1243043	1244494	R	484	829(1452)
tnfn1_pw060510p04q131	G04	C	898664	F	FTN_0842	897754	898863	R	370	200(1110)
tnfn1_pw060510p04q132	H04	U	1224416	F	FTN_1155	1222624	1224969	R	782	554(2346)
tnfn1_pw060510p04q133	A05	U	578984	F	FTN_0554	578694	579158	F	155	291(465)
tnfn1_pw060510p04q134	B05	C	696196	F	FTN_0657	695532	696782	R	417	587(1251)
tnfn1_pw060510p04q135	C05	C	1323608	F	FTN_1254	1322868	1323953	F	362	741(1086)
tnfn1_pw060510p04q136	D05	C	1896816	F	FTN_1767	1896135	1897052	R	306	237(918)
tnfn1_pw060510p04q137	E05	C	1505648	F	FTN_1425	1505283	1506254	R	324	607(972)
tnfn1_pw060510p04q138	F05	C	676278	F	FTN_0639	676090	676467	F	126	189(378)
tnfn1_pw060510p04q139	G05	C	344640	R	FTN_0338	344391	345035	F	215	250(645)
tnfn1_pw060510p04q140	H05	C	1545335	F	FTN_1456	1544780	1545940	F	387	556(1161)
tnfn1_pw060510p04q141	A06	C	336497	R	FTN_0328	335825	336625	R	267	129(801)
tnfn1_pw060510p04q142	B06	C	555156	R	FTN_0533	554322	555512	R	397	357(1191)
tnfn1_pw060510p04q143	C06	U	110082	F	FTN_0099	109818	110483	F	222	265(666)
tnfn1_pw060510p04q144	D06	C	1347327	F	FTN_1275	1347139	1348665	F	509	189(1527)
tnfn1_pw060510p04q145	E06	C	1471500	F	intergenic					
tnfn1_pw060510p04q146	F06	C	1300401	R	FTN_1231	1300134	1300514	R	127	114(381)
tnfn1_pw060510p04q147	G06	C	630917	R	FTN_0599	630525	631322	R	266	406(798)
tnfn1_pw060510p04q148	H06	U	998621	F	FTN_0937	998435	999334	F	300	187(900)

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.

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tnfn1_pw060510p04q149	A07	C	1344703	R	FTN_1273	1344468	1346156	F	563	236(1689)
tnfn1_pw060510p04q150	B07	C	1889296	R	FTN_1760	1889010	1889996	F	329	287(987)
tnfn1_pw060510p04q151	C07	C	612331	R	FTN_0583	611786	612709	R	308	379(924)
tnfn1_pw060510p04q152	D07	C	513989	F	FTN_0504	512714	514852	F	713	1276(2139)
tnfn1_pw060510p04q153	E07	C	348193	F	FTN_0343	347655	349238	R	528	1046(1584)
tnfn1_pw060510p04q154	F07	C	279742	F	FTN_0271	279453	279872	F	140	290(420)
tnfn1_pw060510p04q155	G07	C	1706004	F	FTN_1604	1705069	1707759	R	897	1756(2691)
tnfn1_pw060510p04q156	H07	C	1280468	R	FTN_1210	1279841	1280944	F	368	628(1104)
tnfn1_pw060510p04q157	A08	C	524542	F	FTN_0511	523817	524659	R	281	118(843)
tnfn1_pw060510p04q158	B08	C	730718	F	FTN_0687	730344	731723	F	460	375(1380)
tnfn1_pw060510p04q159	C08	U	1691765	R	FTN_1593	1691111	1692784	R	558	1020(1674)
tnfn1_pw060510p04q160	D08	C	1200464	F	FTN_1135	1199729	1200805	R	359	342(1077)
tnfn1_pw060510p04q161	E08	C	945481	F	FTN_0888	945336	945869	F	178	146(534)
tnfn1_pw060510p04q162	F08	C	596272	R	FTN_0569	594781	596520	R	580	249(1740)
tnfn1_pw060510p04q163	G08	C	700029	R	FTN_0660	699099	700535	F	479	931(1437)
tnfn1_pw060510p04q164	H08	C	79846	F	FTN_0066	79071	81317	R	749	1472(2247)
tnfn1_pw060510p04q165	A09	C	275243	F	FTN_0267	274900	275400	F	167	344(501)
tnfn1_pw060510p04q166	B09	C	1528298	R	FTN_1439	1527712	1528896	F	395	587(1185)
tnfn1_pw060510p04q167	C09	C	1795565	R	FTN_1681	1795398	1795817	F	140	168(420)
tnfn1_pw060510p04q168	D09	C	707281	F	FTN_0666	705568	708387	F	940	1714(2820)
tnfn1_pw060510p04q169	E09	C	132457	F	FTN_0122	132141	133217	F	359	317(1077)
tnfn1_pw060510p04q170	F09	U	569803	F	FTN_0543	568834	570036	F	401	970(1203)
tnfn1_pw060510p04q171	G09	C	1000083	R	FTN_0939	1000022	1000177	R	52	95(156)
tnfn1_pw060510p04q172	H09	C	421534	F	FTN_0422	421370	421858	F	163	165(489)
tnfn1_pw060510p04q173	A10	C	926696	F	FTN_0872	926220	927407	F	396	477(1188)
tnfn1_pw060510p04q174	B10	C	197567	F	FTN_0179	197370	197900	F	177	198(531)
tnfn1_pw060510p04q175	C10	C	24478	R	FTN_0023	24071	24748	R	226	271(678)
tnfn1_pw060510p04q176	D10	C	199808	F	FTN_0182	199526	200200	R	225	393(675)
tnfn1_pw060510p04q177	E10	C	896093	F	FTN_0839	895194	896291	F	366	900(1098)
tnfn1_pw060510p04q178	F10	C	955383	F	FTN_0898	954503	956044	R	514	662(1542)
tnfn1_pw060510p04q179	G10	C	894870	R	FTN_0838	894232	895017	R	262	148(786)
tnfn1_pw060510p04q180	H10	C	830167	R	FTN_0773	829606	830691	R	362	525(1086)
tnfn1_pw060510p04q181	A11	U	245043	F	FTN_0222	244745	245710	F	322	299(966)
tnfn1_pw060510p04q182	B11	C	992106	F	FTN_0931	991793	992749	F	319	314(957)
tnfn1_pw060510p04q183	C11	C	367668	F	FTN_0364	367604	368224	F	207	65(621)
tnfn1_pw060510p04q184	D11	C	1504548	R	FTN_1424	1503994	1505283	R	430	736(1290)
tnfn1_pw060510p04q185	E11	C	1823099	F	FTN_1701	1822121	1823464	R	448	366(1344)
tnfn1_pw060510p04q186	F11	C	411419	F	FTN_0412	410233	411879	F	549	1187(1647)
tnfn1_pw060510p04q187	G11	C	276523	R	FTN_0269	275914	277422	R	503	900(1509)
tnfn1_pw060510p04q188	H11	C	987983	R	intergenic					
tnfn1_pw060510p04q189	A12	U	169495	R	FTN_0155	168063	170075	F	671	1433(2013)
tnfn1_pw060510p04q190	B12	C	661755	R	FTN_0628	661707	662333	F	209	49(627)
tnfn1_pw060510p04q191	C12	U	1013660	R	FTN_0958	1013305	1013826	R	174	167(522)
tnfn1_pw060510p04q192	D12	C	1160195	F	FTN_1098	1159530	1160402	R	291	208(873)
tnfn1_pw060510p04q193	E12	C	724612	F	FTN_0680	723838	725673	F	612	775(1836)
tnfn1_pw060510p04q194	F12	C	615825	R	FTN_0587	615588	616814	F	409	238(1227)
tnfn1_pw060510p04q195	G12	C	38354	F	FTN_0036	37864	38601	F	246	491(738)
tnfn1_pw060510p04q196	H12	U	65214	R	FTN_0055	64850	65683	R	278	470(834)

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.

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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_pw060510p04q101	A01	EXACT(0)	123	112	86	20	EXACT(0)	200	176	56
tnfn1_pw060510p04q102	B01	EXACT(0)	122	120	102	37	EXACT(0)	200	191	60
tnfn1_pw060510p04q103	C01	EXACT(0)	147	145	129	41	EXACT(0)	186	172	53
tnfn1_pw060510p04q104	D01	EXACT(0)	151	107	77	34	EXACT(0)	200	192	51
tnfn1_pw060510p04q105	E01	EXACT(0)	157	152	139	48	EXACT(0)	200	195	58
tnfn1_pw060510p04q106	F01	EXACT(0)	155	139	122	39	EXACT(0)	200	189	40
tnfn1_pw060510p04q107	G01	EXACT(0)	134	109	91	37	EXACT(0)	139	120	28
tnfn1_pw060510p04q108	H01	EXACT(0)	120	112	88	23	EXACT(0)	200	185	38
tnfn1_pw060510p04q109	A02	EXACT(0)	157	151	138	43	EXACT(0)	200	187	44
tnfn1_pw060510p04q110	B02	EXACT(0)	156	153	131	43	EXACT(0)	200	183	45
tnfn1_pw060510p04q111	C02	EXACT(0)	159	145	129	34	EXACT(0)	200	188	60
tnfn1_pw060510p04q112	D02	EXACT(0)	156	153	125	35	EXACT(0)	200	194	51
tnfn1_pw060510p04q113	E02	EXACT(0)	157	153	128	24	EXACT(0)	200	182	29
tnfn1_pw060510p04q114	F02	EXACT(0)	154	145	126	39	EXACT(0)	200	182	34
tnfn1_pw060510p04q115	G02	EXACT(0)	155	153	129	44	EXACT(0)	200	189	55
tnfn1_pw060510p04q116	H02	NONE	0	0	0	22	ESTIMATE(106)	514	347	24
tnfn1_pw060510p04q117	A03	EXACT(0)	120	112	99	36	EXACT(0)	200	186	39
tnfn1_pw060510p04q118	B03	EXACT(0)	120	112	96	41	EXACT(0)	200	192	47
tnfn1_pw060510p04q119	C03	EXACT(0)	123	120	107	43	EXACT(0)	200	189	56
tnfn1_pw060510p04q120	D03	EXACT(0)	119	112	93	42	EXACT(0)	200	190	54
tnfn1_pw060510p04q121	E03	EXACT(0)	121	112	96	38	EXACT(0)	200	190	55
tnfn1_pw060510p04q122	F03	EXACT(0)	122	112	99	38	EXACT(0)	200	195	44
tnfn1_pw060510p04q123	G03	EXACT(0)	124	118	102	35	EXACT(0)	200	192	49
tnfn1_pw060510p04q124	H03	EXACT(0)	126	118	112	30	EXACT(0)	200	188	59
tnfn1_pw060510p04q125	A04	EXACT(0)	215	112	93	26	EXACT(0)	64	41	15
tnfn1_pw060510p04q126	B04	EXACT(0)	157	152	139	43	EXACT(0)	200	172	49
tnfn1_pw060510p04q127	C04	EXACT(0)	157	153	137	49	EXACT(0)	180	176	64
tnfn1_pw060510p04q128	D04	EXACT(0)	154	145	123	43	EXACT(0)	200	185	50
tnfn1_pw060510p04q129	E04	EXACT(0)	160	152	132	41	EXACT(0)	200	187	56
tnfn1_pw060510p04q130	F04	EXACT(0)	156	145	116	37	EXACT(0)	200	191	52
tnfn1_pw060510p04q131	G04	EXACT(0)	156	153	134	40	EXACT(0)	200	187	40
tnfn1_pw060510p04q132	H04	EXACT(0)	157	153	143	42	EXACT(0)	200	190	57
tnfn1_pw060510p04q133	A05	EXACT(0)	156	152	131	39	EXACT(0)	200	188	62
tnfn1_pw060510p04q134	B05	EXACT(0)	154	145	126	37	EXACT(0)	200	192	56
tnfn1_pw060510p04q135	C05	EXACT(0)	150	150	127	36	EXACT(0)	200	191	56
tnfn1_pw060510p04q136	D05	EXACT(0)	152	139	120	43	EXACT(0)	200	187	54
tnfn1_pw060510p04q137	E05	EXACT(0)	157	145	125	49	EXACT(0)	200	187	56
tnfn1_pw060510p04q138	F05	EXACT(0)	154	145	126	42	EXACT(0)	200	194	58
tnfn1_pw060510p04q139	G05	EXACT(0)	154	139	131	41	EXACT(0)	200	171	31
tnfn1_pw060510p04q140	H05	EXACT(0)	120	119	104	39	EXACT(0)	200	198	60
tnfn1_pw060510p04q141	A06	EXACT(0)	116	115	105	37	EXACT(0)	200	196	55
tnfn1_pw060510p04q142	B06	EXACT(0)	120	112	91	40	EXACT(0)	200	190	59
tnfn1_pw060510p04q143	C06	EXACT(0)	122	119	92	31	EXACT(0)	200	185	39
tnfn1_pw060510p04q144	D06	EXACT(0)	120	106	90	41	EXACT(0)	200	124	37
tnfn1_pw060510p04q145	E06	EXACT(0)	122	112	87	28	EXACT(0)	200	187	48
tnfn1_pw060510p04q146	F06	EXACT(0)	154	139	109	21	ESTIMATE(5)	194	181	23
tnfn1_pw060510p04q147	G06	EXACT(0)	123	109	91	28	EXACT(0)	200	177	38
tnfn1_pw060510p04q148	H06	EXACT(0)	122	105	80	25	EXACT(0)	200	188	44

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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_pw060510p04q149	A07	EXACT(0)	124	109	97	29	EXACT(0)	201	145	27
tnfn1_pw060510p04q150	B07	EXACT(0)	122	119	98	38	EXACT(0)	181	173	49
tnfn1_pw060510p04q151	C07	EXACT(0)	133	116	116	44	EXACT(0)	200	187	53
tnfn1_pw060510p04q152	D07	EXACT(0)	156	145	133	29	EXACT(0)	200	191	59
tnfn1_pw060510p04q153	E07	EXACT(0)	151	139	128	44	EXACT(0)	200	191	56
tnfn1_pw060510p04q154	F07	EXACT(0)	154	145	117	34	EXACT(0)	200	193	48
tnfn1_pw060510p04q155	G07	EXACT(0)	152	152	134	44	EXACT(0)	200	195	58
tnfn1_pw060510p04q156	H07	EXACT(0)	153	145	124	40	EXACT(0)	200	196	42
tnfn1_pw060510p04q157	A08	EXACT(0)	153	153	132	44	EXACT(0)	200	187	58
tnfn1_pw060510p04q158	B08	EXACT(0)	118	111	96	33	EXACT(0)	200	192	55
tnfn1_pw060510p04q159	C08	EXACT(0)	121	106	83	29	EXACT(0)	200	193	54
tnfn1_pw060510p04q160	D08	EXACT(0)	156	153	135	38	EXACT(0)	200	190	55
tnfn1_pw060510p04q161	E08	EXACT(0)	120	84	79	42	EXACT(0)	200	185	51
tnfn1_pw060510p04q162	F08	EXACT(0)	120	112	94	41	EXACT(0)	136	134	52
tnfn1_pw060510p04q163	G08	EXACT(0)	153	144	128	43	EXACT(0)	200	192	60
tnfn1_pw060510p04q164	H08	ADJUSTED(2)	113	110	100	37	ESTIMATE(0)	200	190	48
tnfn1_pw060510p04q165	A09	EXACT(0)	156	145	118	36	EXACT(0)	200	173	48
tnfn1_pw060510p04q166	B09	EXACT(0)	155	145	129	48	EXACT(0)	200	194	60
tnfn1_pw060510p04q167	C09	EXACT(0)	153	153	117	37	EXACT(0)	200	188	40
tnfn1_pw060510p04q168	D09	EXACT(0)	155	152	128	41	EXACT(0)	200	192	52
tnfn1_pw060510p04q169	E09	EXACT(0)	154	145	126	41	EXACT(0)	200	196	51
tnfn1_pw060510p04q170	F09	EXACT(0)	158	77	59	19	EXACT(0)	200	184	34
tnfn1_pw060510p04q171	G09	ADJUSTED(5)	120	107	82	31	ESTIMATE(3)	197	185	48
tnfn1_pw060510p04q172	H09	EXACT(0)	120	112	96	38	EXACT(0)	200	198	57
tnfn1_pw060510p04q173	A10	EXACT(0)	124	119	100	34	EXACT(0)	200	192	54
tnfn1_pw060510p04q174	B10	EXACT(0)	119	106	84	34	EXACT(0)	200	187	53
tnfn1_pw060510p04q175	C10	EXACT(0)	120	112	91	41	EXACT(0)	200	190	57
tnfn1_pw060510p04q176	D10	EXACT(0)	122	118	97	35	EXACT(0)	200	175	43
tnfn1_pw060510p04q177	E10	EXACT(0)	154	145	132	44	EXACT(0)	171	167	53
tnfn1_pw060510p04q178	F10	EXACT(0)	156	153	134	37	EXACT(0)	200	189	56
tnfn1_pw060510p04q179	G10	EXACT(0)	154	145	126	40	EXACT(0)	105	99	55
tnfn1_pw060510p04q180	H10	EXACT(0)	152	104	79	21	EXACT(0)	200	152	23
tnfn1_pw060510p04q181	A11	EXACT(0)	117	112	102	38	EXACT(0)	200	195	52
tnfn1_pw060510p04q182	B11	EXACT(0)	116	112	92	33	EXACT(0)	200	193	36
tnfn1_pw060510p04q183	C11	EXACT(0)	117	112	102	38	EXACT(0)	200	182	40
tnfn1_pw060510p04q184	D11	EXACT(0)	122	124	103	34	EXACT(0)	200	84	32
tnfn1_pw060510p04q185	E11	EXACT(0)	119	120	99	40	EXACT(0)	200	198	55
tnfn1_pw060510p04q186	F11	EXACT(0)	155	152	119	35	EXACT(0)	199	189	47
tnfn1_pw060510p04q187	G11	EXACT(0)	156	152	133	37	EXACT(0)	200	192	56
tnfn1_pw060510p04q188	H11	EXACT(0)	124	119	79	30	EXACT(0)	200	188	45
tnfn1_pw060510p04q189	A12	EXACT(0)	123	119	89	26	EXACT(0)	200	186	51
tnfn1_pw060510p04q190	B12	EXACT(0)	124	118	99	31	EXACT(0)	200	176	54
tnfn1_pw060510p04q191	C12	EXACT(0)	124	106	97	36	EXACT(0)	200	192	52
tnfn1_pw060510p04q192	D12	EXACT(0)	121	112	93	32	EXACT(0)	200	181	55
tnfn1_pw060510p04q193	E12	EXACT(0)	155	145	134	48	EXACT(0)	200	191	60
tnfn1_pw060510p04q194	F12	EXACT(0)	151	145	113	43	EXACT(0)	200	174	49
tnfn1_pw060510p04q195	G12	EXACT(0)	158	145	138	48	EXACT(0)	200	195	59
tnfn1_pw060510p04q196	H12	EXACT(0)	157	145	133	40	EXACT(0)	200	190	59

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