Francisella tularensis subsp. *novicida*, "Two-Allele" Transposon Mutant Library, Plate 8 (tnfn1_pw060323p08)

Catalog No. NR-8042

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-8042 represents Plate 8 (tnfn1_pw060323p08) 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_pw060323p08q158 (Well B08) 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-8042 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 8 (tnfn1_pw060323p08), NR-8042."

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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Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p08q101	A01	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p08q102	B01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p08q103	C01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q104	D01	T20	aroC	chorismate synthase	amino acid metabolism - biosynthesis
tnfn1_pw060323p08q105	E01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p08q106	F01	T20	-	transcriptional regulator, ArsR family	signal transduction and regulation
tnfn1_pw060323p08q107	G01	T20	cynT	carbonic anhydrase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p08q108	H01	<KAN-2>	nuoL	NADH dehydrogenase I, L subunit	energy metabolism
tnfn1_pw060323p08q109	A02	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p08q110	B02	T18	-	transposase	mobile and extrachromosomal element functions - transposition
tnfn1_pw060323p08q111	C02	T18	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060323p08q112	D02	T18	-	disulfide bond formation protein, DsbB family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p08q113	E02	T18	-	pseudogene: DNA-3-methyladenine glycosylase	pseudogene
tnfn1_pw060323p08q114	F02	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p08q115	G02	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p08q116	H02	T18			
tnfn1_pw060323p08q117	A03	T18			
tnfn1_pw060323p08q118	B03	T18	-	DNA uptake protein, SMF family	transport
tnfn1_pw060323p08q119	C03	T18	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060323p08q120	D03	T18	carB	carbamoyl-phosphate synthase large chain	nucleotides and nucleosides metabolism
tnfn1_pw060323p08q121	E03	T18			
tnfn1_pw060323p08q122	F03	T18	oxyR	oxidative stress transcriptional regulator	signal transduction and regulation
tnfn1_pw060323p08q123	G03	T20	-	4Fe-4S ferredoxin	energy metabolism
tnfn1_pw060323p08q124	H03	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p08q125	A04	T20	tgt	queuine tRNA-ribosyltransferase.	translation, ribosomal structure and biogenesis
tnfn1_pw060323p08q126	B04	T20	ilvE	branched-chain amino acid aminotransferase protein (class IV)	amino acid metabolism - biosynthesis
tnfn1_pw060323p08q127	C04	T20	glpF	glycerol uptake facilitator protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060323p08q128	D04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p08q129	E04	T20	-	metallopeptidase, M50B family	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060323p08q130	F04	T20	rimK	glutathione synthase/ribosomal protein S6 modification enzyme	translation, ribosomal structure and biogenesis
tnfn1_pw060323p08q131	G04	T20	-	glutathione peroxidase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p08q132	H04	T20	oppC	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060323p08q133	A05	T20	-	signal transduction protein with a PAS, a PAC, an EAL and a GGDEF domain	signal transduction and regulation
tnfn1_pw060323p08q134	B05	T20	-	conserved membrane protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q135	C05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q136	D05	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p08q137	E05	T20	-	two-component regulator, sensor histidine kinase	signal transduction and regulation
tnfn1_pw060323p08q138	F05	T20	-	protein of unknown function with TPR repeat region and von Willebrand factor type A domain	unknown function - conserved
tnfn1_pw060323p08q139	G05	T20			
tnfn1_pw060323p08q140	H05	T20	-	GDSL-like lipolytic enzyme	fatty acids and lipids metabolism
tnfn1_pw060323p08q141	A06	T20	-	isochorismatase family protein	putative enzymes
tnfn1_pw060323p08q142	B06	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p08q143	C06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p08q144	D06	T20	isftu2	isftu2	IS element
tnfn1_pw060323p08q145	E06	T20	rpe	D-ribulose-phosphate 3-epimerase	energy metabolism
tnfn1_pw060323p08q146	F06	T20	minC	septum formation inhibitor	cell cycle
tnfn1_pw060323p08q147	G06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p08q148	H06	T20	-	conserved protein of unknown function	unknown function - conserved

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tnfn1_pw060323p08q149	A07	T20	-	regulatory factor, Bvg accessory factor family	signal transduction and regulation
tnfn1_pw060323p08q150	B07	T20	glpT	glycerol-3-phosphate transporter	transport
tnfn1_pw060323p08q151	C07	T20	ampG	peptide-acetyl-coenzyme A transporter (PAT) family protein	transport
tnfn1_pw060323p08q152	D07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q153	E07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q154	F07	T20			
tnfn1_pw060323p08q155	G07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q156	H07	T20	glpK	glycerol kinase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p08q157	A08	T20	-	DNA/RNA helicase	DNA replication, recombination, modification and repair - replication
tnfn1_pw060323p08q158	B08	T20	-	conserved outer membrane protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q159	C08	T20	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	cell wall / LPS / capsule
tnfn1_pw060323p08q160	D08	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p08q161	E08	T20	hflX	protease, GTP-binding subunit	putative enzymes
tnfn1_pw060323p08q162	F08	T20	-	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	transport
tnfn1_pw060323p08q163	G08	T20	hrpA	HrpA-like helicase	DNA replication, recombination, modification and repair
tnfn1_pw060323p08q164	H08	T20	-	Dam-replacing family protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p08q165	A09	T20	mfd	transcription-repair coupling factor	transcription
tnfn1_pw060323p08q166	B09	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p08q167	C09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p08q168	D09	T20	oppD	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060323p08q169	E09	T20	recB	ATP-dependent exoDNAse (exonuclease V) beta subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p08q170	F09	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q171	G09	T20	-	zinc-binding alcohol dehydrogenase	carbohydrate metabolism
tnfn1_pw060323p08q172	H09	<KAN-2>	-	rRNA methylase, SpoU family	translation, ribosomal structure and biogenesis
tnfn1_pw060323p08q173	A10	<KAN-2>	-	cytochrome b561 family protein	energy metabolism
tnfn1_pw060323p08q174	B10	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p08q175	C10	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p08q176	D10	<KAN-2>	-	ThiJ/PfpI family protein	putative enzymes
tnfn1_pw060323p08q177	E10	<KAN-2>	hupB	DNA-binding protein HU-beta	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p08q178	F10	<KAN-2>	coaE	dephospho-CoA kinase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p08q179	G10	T18			
tnfn1_pw060323p08q180	H10	T18			
tnfn1_pw060323p08q181	A11	T18	rhtB	homoserine/threonine efflux family protein	transport - amino-acid
tnfn1_pw060323p08q182	B11	T18			
tnfn1_pw060323p08q183	C11	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p08q184	D11	T18			
tnfn1_pw060323p08q185	E11	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p08q186	F11	T20	isftu2	isftu2	IS element
tnfn1_pw060323p08q187	G11	T20	-	DNA and RNA helicases superfamily I protein	DNA replication, recombination, modification and repair - replication
tnfn1_pw060323p08q188	H11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p08q189	A12	T20	-	RNA methyltransferase, trmA family	translation, ribosomal structure and biogenesis
tnfn1_pw060323p08q190	B12	T20	rimI	ribosomal-protein-alanine acetyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060323p08q191	C12	T20	rimI	ribosomal-protein-alanine acetyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060323p08q192	D12	T20	cysK	cysteine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060323p08q193	E12	T20	purM	phosphoribosylformylglycinamide cyclo-ligase	nucleotides and nucleosides metabolism
tnfn1_pw060323p08q194	F12	T20	purE	N5-carboxyaminoimidazole ribonucleotide mutase	nucleotides and nucleosides metabolism
tnfn1_pw060323p08q195	G12	T20	hemN	coproporphyrinogen III oxidase, anaerobic	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p08q196	H12	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds

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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_pw060323p08q101	A01	C	312189	F	FTN_0303	311969	312892	F	308	221(924)
tnfn1_pw060323p08q102	B01	C	374122	F	FTN_0371	373472	374326	F	285	651(855)
tnfn1_pw060323p08q103	C01	C	305323	F	FTN_0297	305086	305721	F	212	238(636)
tnfn1_pw060323p08q104	D01	C	401779	R	FTN_0402	400839	401894	R	352	116(1056)
tnfn1_pw060323p08q105	E01	C	380912	F	FTN_0379	380755	381126	F	124	158(372)
tnfn1_pw060323p08q106	F01	C	858805	R	FTN_0801	858600	858947	R	116	143(348)
tnfn1_pw060323p08q107	G01	C	1149883	R	FTN_1087	1149427	1150110	R	228	228(684)
tnfn1_pw060323p08q108	H01	C	1783813	R	FTN_1669	1783789	1785795	R	669	1983(2007)
tnfn1_pw060323p08q109	A02	C	681795	F	FTN_0643	681664	682170	F	169	132(507)
tnfn1_pw060323p08q110	B02	C	294356	F	FTN_0286	294223	294783	F	187	134(561)
tnfn1_pw060323p08q111	C02	C	171895	F	FTN_0157	171471	172004	R	178	110(534)
tnfn1_pw060323p08q112	D02	C	1454944	F	FTN_1376	1454884	1455417	F	178	61(534)
tnfn1_pw060323p08q113	E02	C	1076324	F	FTN_1017	1075884	1076462	F	193	441(579)
tnfn1_pw060323p08q114	F02	C	334852	F	FTN_0326	334524	335054	R	177	203(531)
tnfn1_pw060323p08q115	G02	C	580867	F	FTN_0556	580679	581239	F	187	189(561)
tnfn1_pw060323p08q116	H02	C	1272768	F	intergenic					
tnfn1_pw060323p08q117	A03	C	539635	R	intergenic					
tnfn1_pw060323p08q118	B03	C	351735	F	FTN_0345	351044	352147	R	368	413(1104)
tnfn1_pw060323p08q119	C03	C	1252429	F	FTN_1179	1252082	1252978	F	299	348(897)
tnfn1_pw060323p08q120	D03	C	19649	F	FTN_0020	18120	21401	R	1094	1753(3282)
tnfn1_pw060323p08q121	E03	C	1454241	R	intergenic					
tnfn1_pw060323p08q122	F03	C	1014196	F	FTN_0959	1013924	1014790	F	289	273(867)
tnfn1_pw060323p08q123	G03	C	808079	F	FTN_0755	807847	808089	F	81	233(243)
tnfn1_pw060323p08q124	H03	C	901006	F	FTN_0845	900621	901457	R	279	452(837)
tnfn1_pw060323p08q125	A04	C	1162230	R	FTN_1100	1161392	1162492	R	367	263(1101)
tnfn1_pw060323p08q126	B04	C	75004	F	FTN_0063	74362	75246	R	295	243(885)
tnfn1_pw060323p08q127	C04	C	1680335	R	FTN_1583	1679893	1680654	R	254	320(762)
tnfn1_pw060323p08q128	D04	U	543344	R	FTN_0523	543248	544063	F	272	97(816)
tnfn1_pw060323p08q129	E04	C	485082	F	FTN_0479	484555	485208	R	218	127(654)
tnfn1_pw060323p08q130	F04	C	167751	R	FTN_0154	166433	167899	R	489	149(1467)
tnfn1_pw060323p08q132	H04	C	1689832	F	FTN_1591	1689288	1690145	R	286	314(858)
tnfn1_pw060323p08q133	A05	C	461507	R	FTN_0456	461255	463570	F	772	253(2316)
tnfn1_pw060323p08q134	B05	C	1341484	R	FTN_1270	1341158	1341841	R	228	358(684)
tnfn1_pw060323p08q135	C05	C	1725004	R	FTN_1615	1724061	1725338	R	426	335(1278)
tnfn1_pw060323p08q136	D05	C	1008535	F	FTN_0952	1008165	1008644	R	160	110(480)
tnfn1_pw060323p08q137	E05	C	1727089	F	FTN_1617	1726414	1727838	F	475	676(1425)
tnfn1_pw060323p08q138	F05	C	229391	R	FTN_0209	229107	229973	F	289	285(867)
tnfn1_pw060323p08q139	G05	C	1845767	F	intergenic					
tnfn1_pw060323p08q140	H05	C	1804143	F	FTN_1687	1803376	1804866	F	497	768(1491)
tnfn1_pw060323p08q141	A06	C	1074975	R	FTN_1015	1074646	1075146	R	167	172(501)
tnfn1_pw060323p08q142	B06	C	1192037	R	FTN_1129	1191487	1192668	R	394	632(1182)
tnfn1_pw060323p08q143	C06	C	1303954	R	FTN_1235	1303554	1304012	R	153	59(459)
tnfn1_pw060323p08q144	D06	C	857228	F	-	856697	857561	R	288.3	334(865)
tnfn1_pw060323p08q145	E06	C	1292788	R	FTN_1221	1292193	1292858	R	222	71(666)
tnfn1_pw060323p08q146	F06	C	338133	F	FTN_0331	337781	338464	R	228	332(684)
tnfn1_pw060323p08q147	G06	C	750274	F	FTN_0706	750173	750673	F	167	102(501)
tnfn1_pw060323p08q148	H06	C	28353	F	FTN_0027	28044	28592	F	183	310(549)

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_pw060323p08q149	A07	C	1432994	R	FTN_1355	1432777	1433544	F	256	218(768)
tnfn1_pw060323p08q150	B07	C	671651	F	FTN_0636	671002	672315	R	438	665(1314)
tnfn1_pw060323p08q151	C07	C	1753512	R	FTN_1641	1753261	1754523	F	421	252(1263)
tnfn1_pw060323p08q152	D07	C	230829	R	FTN_0210	229966	231588	F	541	864(1623)
tnfn1_pw060323p08q153	E07	C	230829	R	FTN_0210	229966	231588	F	541	864(1623)
tnfn1_pw060323p08q154	F07	C	12924	R	intergenic					
tnfn1_pw060323p08q155	G07	C	1555019	R	FTN_1466	1554488	1555576	R	363	558(1089)
tnfn1_pw060323p08q156	H07	C	1683684	F	FTN_1585	1682448	1683947	R	500	264(1500)
tnfn1_pw060323p08q157	A08	C	94857	F	FTN_0084	93832	96570	F	913	1026(2739)
tnfn1_pw060323p08q158	B08	C	130788	R	FTN_0119	130544	131080	F	179	245(537)
tnfn1_pw060323p08q160	D08	C	553908	R	FTN_0532	553648	554289	R	214	382(642)
tnfn1_pw060323p08q161	E08	C	1109905	R	FTN_1050	1108915	1110222	R	436	318(1308)
tnfn1_pw060323p08q162	F08	C	163727	F	FTN_0151	163057	163836	R	260	110(780)
tnfn1_pw060323p08q163	G08	C	1515128	R	FTN_1432	1513195	1517211	R	1339	2084(4017)
tnfn1_pw060323p08q164	H08	C	1816301	R	FTN_1698	1815852	1816619	R	256	319(768)
tnfn1_pw060323p08q165	A09	C	1094674	F	FTN_1039	1094041	1097463	F	1141	634(3423)
tnfn1_pw060323p08q166	B09	C	1300607	F	FTN_1232	1300558	1301340	F	261	50(783)
tnfn1_pw060323p08q167	C09	C	1862428	R	FTN_1735	1862274	1862681	F	136	155(408)
tnfn1_pw060323p08q168	D09	C	1688997	R	FTN_1590	1688316	1689281	R	322	285(966)
tnfn1_pw060323p08q169	E09	C	1438451	R	FTN_1357	1435327	1438974	R	1216	524(3648)
tnfn1_pw060323p08q170	F09	C	620544	R	FTN_0590	620283	621500	F	406	262(1218)
tnfn1_pw060323p08q171	G09	C	1889572	R	FTN_1760	1889010	1889996	F	329	563(987)
tnfn1_pw060323p08q172	H09	C	1365604	R	FTN_1294	1365139	1365879	R	247	276(741)
tnfn1_pw060323p08q173	A10	C	104624	F	FTN_0093	104604	105116	F	171	21(513)
tnfn1_pw060323p08q174	B10	C	1000085	R	FTN_0939	1000022	1000177	R	52	93(156)
tnfn1_pw060323p08q175	C10	C	40916	R	FTN_0039	40656	41078	R	141	163(423)
tnfn1_pw060323p08q176	D10	C	897397	F	FTN_0841	897004	897678	F	225	394(675)
tnfn1_pw060323p08q177	E10	C	1113426	R	FTN_1054	1113187	1113456	R	90	31(270)
tnfn1_pw060323p08q178	F10	C	1592919	F	FTN_1496	1592378	1592989	F	204	542(612)
tnfn1_pw060323p08q179	G10	C	172721	F	intergenic					
tnfn1_pw060323p08q180	H10	C	1216317	F	intergenic					
tnfn1_pw060323p08q181	A11	C	1479919	R	FTN_1401	1479437	1480069	F	211	483(633)
tnfn1_pw060323p08q182	B11	C	1479429	R	intergenic					
tnfn1_pw060323p08q183	C11	C	721973	R	FTN_0678	721383	722594	R	404	622(1212)
tnfn1_pw060323p08q184	D11	C	30800	F	intergenic					
tnfn1_pw060323p08q185	E11	C	1679487	F	FTN_1582	1679176	1679886	R	237	400(711)
tnfn1_pw060323p08q186	F11	C	377566	R	-	377298	378154	F	285.6	269(857)
tnfn1_pw060323p08q188	H11	C	47203	F	FTN_0042	46882	47436	F	185	322(555)
tnfn1_pw060323p08q189	A12	C	647740	R	FTN_0616	646972	648318	F	449	769(1347)
tnfn1_pw060323p08q190	B12	C	1002105	F	FTN_0943	1001822	1002259	R	146	155(438)
tnfn1_pw060323p08q191	C12	C	1002105	F	FTN_0943	1001822	1002259	R	146	155(438)
tnfn1_pw060323p08q192	D12	C	1371422	R	FTN_1302	1370906	1371826	F	307	517(921)
tnfn1_pw060323p08q193	E12	C	417515	F	FTN_0419	417319	418359	F	347	197(1041)
tnfn1_pw060323p08q194	F12	C	421624	F	FTN_0422	421370	421858	F	163	255(489)
tnfn1_pw060323p08q195	G12	C	1738529	F	FTN_1626	1738188	1739327	F	380	342(1140)
tnfn1_pw060323p08q196	H12	U	555185	R	FTN_0533	554322	555512	R	397	328(1191)

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_pw060323p08q101	A01	EXACT(0)	157	151	129	35	EXACT(0)	200	184	51
tnfn1_pw060323p08q102	B01	EXACT(0)	159	159	133	33	EXACT(0)	200	186	57
tnfn1_pw060323p08q103	C01	EXACT(0)	159	152	137	37	EXACT(0)	200	190	47
tnfn1_pw060323p08q104	D01	EXACT(0)	155	145	129	40	EXACT(0)	200	164	34
tnfn1_pw060323p08q105	E01	EXACT(0)	158	152	138	39	EXACT(0)	172	159	52
tnfn1_pw060323p08q106	F01	EXACT(0)	157	153	127	32	EXACT(0)	200	187	50
tnfn1_pw060323p08q107	G01	EXACT(0)	155	146	127	39	EXACT(0)	200	189	54
tnfn1_pw060323p08q108	H01	EXACT(0)	120	106	65	20	EXACT(0)	200	186	50
tnfn1_pw060323p08q109	A02	EXACT(0)	121	113	97	28	EXACT(0)	200	187	53
tnfn1_pw060323p08q110	B02	EXACT(0)	122	112	78	22	EXACT(0)	200	180	50
tnfn1_pw060323p08q111	C02	EXACT(0)	123	113	81	21	EXACT(0)	200	172	55
tnfn1_pw060323p08q112	D02	EXACT(0)	124	120	85	24	EXACT(0)	200	189	55
tnfn1_pw060323p08q113	E02	EXACT(0)	124	120	67	21	EXACT(0)	200	175	51
tnfn1_pw060323p08q114	F02	EXACT(0)	124	115	89	23	EXACT(0)	200	189	51
tnfn1_pw060323p08q115	G02	EXACT(0)	123	118	91	25	EXACT(0)	200	192	52
tnfn1_pw060323p08q116	H02	EXACT(0)	123	120	96	30	EXACT(0)	200	183	55
tnfn1_pw060323p08q117	A03	EXACT(0)	123	120	93	19	EXACT(0)	200	196	51
tnfn1_pw060323p08q118	B03	EXACT(0)	123	120	93	23	EXACT(0)	200	193	51
tnfn1_pw060323p08q119	C03	EXACT(0)	122	118	94	31	EXACT(0)	200	193	54
tnfn1_pw060323p08q120	D03	EXACT(0)	124	119	84	23	EXACT(0)	200	194	51
tnfn1_pw060323p08q121	E03	EXACT(0)	123	120	102	27	EXACT(0)	200	145	36
tnfn1_pw060323p08q122	F03	ADJUSTED(7)	125	113	71	22	ESTIMATE(2)	198	190	52
tnfn1_pw060323p08q123	G03	EXACT(0)	156	151	124	39	EXACT(0)	200	185	42
tnfn1_pw060323p08q124	H03	EXACT(0)	157	151	118	34	EXACT(0)	200	188	46
tnfn1_pw060323p08q125	A04	EXACT(0)	156	152	128	38	EXACT(0)	200	194	52
tnfn1_pw060323p08q126	B04	EXACT(0)	156	153	123	38	EXACT(0)	200	192	58
tnfn1_pw060323p08q127	C04	EXACT(0)	157	153	131	39	EXACT(0)	200	195	53
tnfn1_pw060323p08q128	D04	EXACT(0)	157	145	133	37	EXACT(0)	200	185	61
tnfn1_pw060323p08q129	E04	EXACT(0)	156	152	128	39	EXACT(0)	200	146	40
tnfn1_pw060323p08q130	F04	EXACT(0)	156	153	126	39	EXACT(0)	200	187	50
tnfn1_pw060323p08q131	G04	EXACT(0)	157	153	143	49	EXACT(0)	200	187	67
tnfn1_pw060323p08q132	H04	EXACT(0)	157	148	137	47	EXACT(0)	200	186	46
tnfn1_pw060323p08q133	A05	EXACT(0)	160	151	129	34	EXACT(0)	176	142	34
tnfn1_pw060323p08q134	B05	EXACT(0)	157	153	131	38	EXACT(0)	200	184	44
tnfn1_pw060323p08q135	C05	EXACT(0)	155	151	130	31	EXACT(0)	200	191	44
tnfn1_pw060323p08q136	D05	EXACT(0)	156	153	123	35	EXACT(0)	200	180	56
tnfn1_pw060323p08q137	E05	EXACT(0)	156	153	129	39	EXACT(0)	200	191	55
tnfn1_pw060323p08q138	F05	EXACT(0)	157	152	130	39	EXACT(0)	200	174	44
tnfn1_pw060323p08q139	G05	EXACT(0)	156	153	126	39	EXACT(0)	200	172	54
tnfn1_pw060323p08q140	H05	EXACT(0)	156	152	131	41	EXACT(0)	200	146	36
tnfn1_pw060323p08q141	A06	EXACT(0)	157	151	129	35	EXACT(0)	200	188	54
tnfn1_pw060323p08q142	B06	EXACT(0)	157	153	131	36	EXACT(0)	200	176	54
tnfn1_pw060323p08q143	C06	EXACT(0)	155	145	123	35	EXACT(0)	200	186	57
tnfn1_pw060323p08q144	D06	EXACT(0)	155	152	131	32	EXACT(0)	200	185	52
tnfn1_pw060323p08q145	E06	EXACT(0)	157	145	139	38	EXACT(0)	200	196	52
tnfn1_pw060323p08q146	F06	EXACT(0)	156	152	134	36	EXACT(0)	200	179	48
tnfn1_pw060323p08q147	G06	EXACT(0)	156	139	113	32	EXACT(0)	200	177	53
tnfn1_pw060323p08q148	H06	EXACT(0)	156	146	124	36	EXACT(0)	200	190	55

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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_pw060323p08q149	A07	EXACT(0)	154	145	126	41	EXACT(0)	200	193	54
tnfn1_pw060323p08q150	B07	EXACT(0)	157	152	133	37	EXACT(0)	200	192	55
tnfn1_pw060323p08q151	C07	EXACT(0)	155	152	131	40	EXACT(0)	200	191	57
tnfn1_pw060323p08q152	D07	EXACT(0)	155	151	121	25	EXACT(0)	200	194	50
tnfn1_pw060323p08q153	E07	EXACT(0)	155	151	127	37	EXACT(0)	200	194	52
tnfn1_pw060323p08q154	F07	EXACT(0)	156	152	125	34	EXACT(0)	200	188	57
tnfn1_pw060323p08q155	G07	EXACT(0)	156	153	132	38	EXACT(0)	200	183	56
tnfn1_pw060323p08q156	H07	EXACT(0)	156	152	128	34	EXACT(0)	200	192	55
tnfn1_pw060323p08q157	A08	EXACT(0)	157	151	132	39	EXACT(0)	200	189	53
tnfn1_pw060323p08q158	B08	EXACT(0)	157	153	137	48	EXACT(0)	200	194	67
tnfn1_pw060323p08q159	C08	EXACT(0)	158	152	144	33	EXACT(0)	200	189	51
tnfn1_pw060323p08q160	D08	EXACT(0)	156	152	129	29	EXACT(0)	200	178	55
tnfn1_pw060323p08q161	E08	EXACT(0)	153	139	120	42	EXACT(0)	139	136	53
tnfn1_pw060323p08q162	F08	EXACT(0)	156	152	125	37	EXACT(0)	200	179	54
tnfn1_pw060323p08q163	G08	EXACT(0)	158	152	135	40	EXACT(0)	200	197	50
tnfn1_pw060323p08q164	H08	EXACT(0)	155	145	120	37	EXACT(0)	200	187	54
tnfn1_pw060323p08q165	A09	EXACT(0)	156	145	128	38	EXACT(0)	200	157	41
tnfn1_pw060323p08q166	B09	EXACT(0)	156	152	112	27	EXACT(0)	200	184	51
tnfn1_pw060323p08q167	C09	EXACT(0)	154	152	68	16	EXACT(0)	200	187	52
tnfn1_pw060323p08q168	D09	EXACT(0)	156	152	128	37	EXACT(0)	200	194	55
tnfn1_pw060323p08q169	E09	EXACT(0)	156	153	132	42	EXACT(0)	156	145	54
tnfn1_pw060323p08q170	F09	EXACT(0)	155	145	118	33	EXACT(0)	200	181	49
tnfn1_pw060323p08q171	G09	EXACT(0)	158	152	125	33	EXACT(0)	200	192	46
tnfn1_pw060323p08q172	H09	EXACT(0)	122	124	102	29	EXACT(0)	200	190	50
tnfn1_pw060323p08q173	A10	EXACT(0)	121	112	78	19	EXACT(0)	200	184	46
tnfn1_pw060323p08q174	B10	EXACT(0)	122	106	86	25	EXACT(0)	200	181	47
tnfn1_pw060323p08q175	C10	EXACT(0)	121	112	96	28	EXACT(0)	133	127	52
tnfn1_pw060323p08q176	D10	EXACT(0)	122	125	99	28	EXACT(0)	200	176	37
tnfn1_pw060323p08q177	E10	EXACT(0)	112	111	65	21	EXACT(0)	192	154	21
tnfn1_pw060323p08q178	F10	EXACT(0)	124	113	94	28	EXACT(0)	200	194	52
tnfn1_pw060323p08q179	G10	EXACT(0)	124	120	104	26	EXACT(0)	200	192	51
tnfn1_pw060323p08q180	H10	EXACT(0)	124	119	103	31	EXACT(0)	200	186	52
tnfn1_pw060323p08q181	A11	EXACT(0)	122	119	89	19	EXACT(0)	200	190	47
tnfn1_pw060323p08q182	B11	EXACT(0)	123	119	92	30	EXACT(0)	200	183	50
tnfn1_pw060323p08q183	C11	EXACT(0)	123	109	63	16	EXACT(0)	201	158	30
tnfn1_pw060323p08q184	D11	EXACT(0)	121	83	59	24	EXACT(0)	200	161	43
tnfn1_pw060323p08q185	E11	EXACT(0)	123	119	95	35	EXACT(0)	200	181	56
tnfn1_pw060323p08q186	F11	EXACT(0)	157	145	131	34	EXACT(0)	199	164	38
tnfn1_pw060323p08q187	G11	EXACT(0)	154	145	126	47	EXACT(0)	199	175	53
tnfn1_pw060323p08q188	H11	EXACT(0)	156	145	101	23	EXACT(0)	200	167	43
tnfn1_pw060323p08q189	A12	EXACT(0)	156	116	98	29	EXACT(0)	200	180	41
tnfn1_pw060323p08q190	B12	EXACT(0)	154	139	107	29	EXACT(0)	200	183	55
tnfn1_pw060323p08q191	C12	EXACT(0)	157	152	120	32	EXACT(0)	200	183	58
tnfn1_pw060323p08q192	D12	EXACT(0)	157	152	129	33	EXACT(0)	200	181	56
tnfn1_pw060323p08q193	E12	EXACT(0)	156	152	133	38	EXACT(0)	187	178	49
tnfn1_pw060323p08q194	F12	EXACT(0)	157	153	127	38	EXACT(0)	200	197	55
tnfn1_pw060323p08q195	G12	EXACT(0)	156	145	119	34	EXACT(0)	201	121	33
tnfn1_pw060323p08q196	H12	EXACT(0)	159	145	134	42	EXACT(0)	200	193	50

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