Francisella tularensis subsp. *novicida*, "Two-Allele" Transposon Mutant Library, Plate 7 (tnfn1_pw060323p07)

Catalog No. NR-8041

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-8041 represents Plate 7 (tnfn1_pw060323p07) 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-8041 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 7 (tnfn1_pw060323p07), NR-8041."

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.

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_pw060323p07q101	A01	T20	-	YGGT family membrane protein	unknown function - conserved
tnfn1_pw060323p07q102	B01	T20	rnfB	iron-sulfur cluster-binding protein	putative enzymes
tnfn1_pw060323p07q103	C01	T20	isftu6	isftu6	IS element
tnfn1_pw060323p07q104	D01	T20	-	carbon-nitrogen hydrolase	putative enzymes
tnfn1_pw060323p07q105	E01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q106	F01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q107	G01	T20	-	transcriptional regulator, AraC family	signal transduction and regulation
tnfn1_pw060323p07q108	H01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q109	A02	T20	-	ornithine cyclodeaminase, mu-crystallin homolog	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p07q110	B02	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p07q111	C02	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p07q112	D02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q113	E02	T20	-	deoxyribodipyrimidine photolyase-related protein	putative enzymes
tnfn1_pw060323p07q114	F02	T20	-	drug:H+ antiporter-1 (DHA2) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p07q115	G02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q116	H02	T20	-	two-component response regulator	signal transduction and regulation
tnfn1_pw060323p07q117	A03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q118	B03	T20	ostA1	organic solvent tolerance protein, OstA	cell wall / LPS / capsule
tnfn1_pw060323p07q119	C03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q120	D03	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060323p07q121	E03	T20	hflK	HflK-HflC membrane protein complex, HflK	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060323p07q122	F03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q123	G03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q124	H03	T20	isftu3	isftu3	IS element
tnfn1_pw060323p07q125	A04	T20	aroH	chorismate mutase	amino acid metabolism - biosynthesis
tnfn1_pw060323p07q126	B04	T20	-	protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q127	C04	T20	-	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060323p07q128	D04	T20	trpE	anthranilate synthase component I	amino acid metabolism - biosynthesis
tnfn1_pw060323p07q129	E04	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p07q130	F04	T20	-	amino acid transporter (AAT) family protein	transport - amino-acid
tnfn1_pw060323p07q131	G04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q132	H04	<KAN-2>	ubiB	2-octaprenylphenol hydroxylase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p07q133	A05	<KAN-2>	-	cytochrome b561 family protein	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p07q134	B05	<KAN-2>	secB2	preprotein translocase, subunit B	motility, attachment and secretion structure
tnfn1_pw060323p07q135	C05	<KAN-2>	rpoB	DNA-directed RNA polymerase, beta subunit/140 kD subunit	transcription
tnfn1_pw060323p07q136	D05	T18	tolB	group A colicin translocation; tolB protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p07q137	E05	T18	-	beta-fructofuranosidase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p07q138	F05	T18	-	oligoketide cyclase/lipid transport protein	fatty acids and lipids metabolism
tnfn1_pw060323p07q139	G05	T18	mraW	S-adenosylmethionine-dependent methyltransferase	cell wall / LPS / capsule
tnfn1_pw060323p07q140	H05	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p07q141	A06	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q142	B06	T18	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060323p07q143	C06	T18	gcvT	glycine cleavage complex protein T (aminomethyltransferase)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p07q144	D06	T18			
tnfn1_pw060323p07q145	E06	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q146	F06	T18	-	two-component response regulator	signal transduction and regulation
tnfn1_pw060323p07q147	G06	T18	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060323p07q148	H06	T18	-	hypothetical membrane protein	hypothetical - novel

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tnfn1_pw060323p07q149	A07	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q150	B07	T18	-	pseudogene: hypothetical protein, fragment	pseudogene
tnfn1_pw060323p07q151	C07	T18			
tnfn1_pw060323p07q152	D07	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q153	E07	T18	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060323p07q154	F07	T18	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060323p07q155	G07	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060323p07q156	H07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q157	A08	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060323p07q158	B08	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p07q159	C08	T20	truB	tRNA pseudouridine synthase B	translation, ribosomal structure and biogenesis
tnfn1_pw060323p07q160	D08	T20	kdpB	potassium-transporting ATPase B chain	transport
tnfn1_pw060323p07q161	E08	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q162	F08	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q163	G08	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060323p07q164	H08	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060323p07q165	A09	T20	perM	PerM family protein	transport
tnfn1_pw060323p07q166	B09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p07q167	C09	T20	relA	GDP pyrophosphokinase/GTP pyrophosphokinase	other metabolism - biosynthesis
tnfn1_pw060323p07q168	D09	T20	-	mannose-6-phosphate isomerase	carbohydrate metabolism - biosynthesis
tnfn1_pw060323p07q169	E09	T20	-	bifunctional protein: 3-hydroxacyl-CoA dehydrogenase/acyl-CoA-binding protein	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p07q170	F09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q171	G09	T20	cutC	copper homeostasis protein CutC family protein	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p07q172	H09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p07q173	A10	T20	fadE	Acyl-CoA dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p07q174	B10	T20	-	arsenate reductase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p07q175	C10	T20	-	restriction endonuclease	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p07q176	D10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q177	E10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q178	F10	T20	nusA	transcription elongation factor	transcription
tnfn1_pw060323p07q179	G10	T20	aroG	phospho-2-dehydro-3-deoxyheptonate aldolase	amino acid metabolism - biosynthesis
tnfn1_pw060323p07q180	H10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q181	A11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p07q182	B11	T20	-	solute:sodium symporter	transport
tnfn1_pw060323p07q183	C11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p07q184	D11	T20			
tnfn1_pw060323p07q185	E11	T20	bioF	8-amino-7-oxononanoate synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p07q186	F11	T20	-	GTP binding translational elongation factor Tu and G family protein	putative enzymes
tnfn1_pw060323p07q187	G11	T20	-	CheB methylesterase/CheR methyltransferase	signal transduction and regulation
tnfn1_pw060323p07q188	H11	T20	-	SAM-dependent methyltransferase	putative enzymes
tnfn1_pw060323p07q189	A12	T20	talA	transaldolase	energy metabolism
tnfn1_pw060323p07q190	B12	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060323p07q191	C12	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p07q192	D12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p07q193	E12	T20	isftu2	isftu2	IS element
tnfn1_pw060323p07q194	F12	T20	-	GTPase of unknown function	putative enzymes
tnfn1_pw060323p07q195	G12	T20	deaD	DEAD-box subfamily ATP-dependent helicase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p07q196	H12	T20	-	pilus assembly protein	motility, attachment and secretion structure

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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_pw060323p07q101	A01	C	162560	F	FTN_0150	162491	163057	F	189	70(567)
tnfn1_pw060323p07q102	B01	C	1090395	R	FTN_1034	1090247	1090873	F	209	149(627)
tnfn1_pw060323p07q103	C01	C	720220	R	-	719918	720628	R	237	409(711)
tnfn1_pw060323p07q104	D01	C	1463408	F	FTN_1383	1463001	1463768	F	256	408(768)
tnfn1_pw060323p07q105	E01	C	950655	R	FTN_0895	950585	950917	R	111	263(333)
tnfn1_pw060323p07q106	F01	C	1025449	F	FTN_0969	1024199	1025695	R	499	247(1497)
tnfn1_pw060323p07q107	G01	C	1346755	F	FTN_1274	1346150	1346974	R	275	220(825)
tnfn1_pw060323p07q108	H01	C	1536818	R	FTN_1447	1536391	1537371	R	327	554(981)
tnfn1_pw060323p07q109	A02	C	1533354	R	FTN_1444	1532673	1533686	R	338	333(1014)
tnfn1_pw060323p07q110	B02	C	917591	F	FTN_0863	917341	917775	F	145	251(435)
tnfn1_pw060323p07q111	C02	U	1233110	F	FTN_1161	1232698	1233897	R	400	788(1200)
tnfn1_pw060323p07q112	D02	C	909805	F	FTN_0854	909700	910479	F	260	106(780)
tnfn1_pw060323p07q113	E02	C	365681	R	FTN_0362	364836	366362	F	509	846(1527)
tnfn1_pw060323p07q114	F02	C	709257	R	FTN_0667	708399	709784	R	462	528(1386)
tnfn1_pw060323p07q115	G02	C	296921	R	FTN_0290	296739	297281	F	181	183(543)
tnfn1_pw060323p07q116	H02	C	1541050	R	FTN_1452	1540850	1541536	F	229	201(687)
tnfn1_pw060323p07q117	A03	C	1103619	R	FTN_1044	1102531	1104324	R	598	706(1794)
tnfn1_pw060323p07q118	B03	C	583696	F	FTN_0558	583164	585767	F	868	533(2604)
tnfn1_pw060323p07q119	C03	C	62431	F	FTN_0052	61717	63777	F	687	715(2061)
tnfn1_pw060323p07q120	D03	C	313061	R	FTN_0304	312892	314295	F	468	170(1404)
tnfn1_pw060323p07q121	E03	C	1107198	R	FTN_1048	1106474	1107538	R	355	341(1065)
tnfn1_pw060323p07q122	F03	C	1064857	R	FTN_1005	1064800	1065075	F	92	58(276)
tnfn1_pw060323p07q123	G03	C	1737315	R	FTN_1624	1736861	1737736	R	292	422(876)
tnfn1_pw060323p07q124	H03	C	1721439	F	-	1721384	1721620	R	79	182(237)
tnfn1_pw060323p07q125	A04	C	355104	F	FTN_0349	355001	355360	F	120	104(360)
tnfn1_pw060323p07q126	B04	C	42770	R	FTN_0040	41096	44347	R	1084	1578(3252)
tnfn1_pw060323p07q127	C04	C	1289223	F	FTN_1218	1288573	1289799	R	409	577(1227)
tnfn1_pw060323p07q128	D04	C	1906974	R	FTN_1778	1905885	1907426	R	514	453(1542)
tnfn1_pw060323p07q129	E04	C	816132	F	FTN_0759	816036	816326	F	97	97(291)
tnfn1_pw060323p07q130	F04	C	405739	R	FTN_0407	404710	406101	R	464	363(1392)
tnfn1_pw060323p07q131	G04	C	360070	F	FTN_0356	359964	360206	F	81	107(243)
tnfn1_pw060323p07q132	H04	C	465230	R	FTN_0459	465112	466767	R	552	1538(1656)
tnfn1_pw060323p07q133	A05	C	1883197	F	FTN_1754	1883079	1883585	F	169	119(507)
tnfn1_pw060323p07q134	B05	C	1607053	F	FTN_1510	1606754	1607194	F	147	300(441)
tnfn1_pw060323p07q135	C05	C	1667898	R	FTN_1568	1667867	1671940	R	1358	4043(4074)
tnfn1_pw060323p07q136	D05	C	359369	F	FTN_0355	358647	359951	F	435	723(1305)
tnfn1_pw060323p07q137	E05	C	68787	R	FTN_0058	67916	69628	R	571	842(1713)
tnfn1_pw060323p07q138	F05	C	1234248	F	FTN_1163	1234247	1234675	R	143	428(429)
tnfn1_pw060323p07q139	G05	C	638776	R	FTN_0605	638482	639396	F	305	295(915)
tnfn1_pw060323p07q140	H05	C	1210235	F	FTN_1144	1210136	1210549	R	138	315(414)
tnfn1_pw060323p07q141	A06	C	846546	R	FTN_0788	846344	847171	F	276	203(828)
tnfn1_pw060323p07q142	B06	C	1326041	F	FTN_1256	1324883	1326250	R	456	210(1368)
tnfn1_pw060323p07q143	C06	C	515957	F	FTN_0505	514946	516019	F	358	1012(1074)
tnfn1_pw060323p07q144	D06	C	779086	R	intergenic					
tnfn1_pw060323p07q145	E06	C	467346	F	FTN_0460	466763	467347	R	195	2(585)
tnfn1_pw060323p07q146	F06	C	1541347	F	FTN_1452	1540850	1541536	F	229	498(687)
tnfn1_pw060323p07q147	G06	C	1065666	F	FTN_1006	1065118	1066374	R	419	709(1257)
tnfn1_pw060323p07q148	H06	C	1439459	R	FTN_1358	1439009	1439578	R	190	120(570)

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_pw060323p07q149	A07	C	752176	F	FTN_0708	752105	752347	F	81	72(243)
tnfn1_pw060323p07q150	B07	C	1723869	R	FTN_0614	1723371	1723925	R	185	57(555)
tnfn1_pw060323p07q151	C07	C	1429917	F	intergenic					
tnfn1_pw060323p07q152	D07	C	1131548	F	FTN_1070	1130864	1132213	R	450	666(1350)
tnfn1_pw060323p07q153	E07	C	949191	F	FTN_0892	948491	949213	R	241	23(723)
tnfn1_pw060323p07q154	F07	C	1247256	F	FTN_1175	1246823	1247617	R	265	362(795)
tnfn1_pw060323p07q155	G07	C	794968	R	FTN_0741	794174	795628	R	485	661(1455)
tnfn1_pw060323p07q156	H07	C	481576	F	FTN_0477	481348	482232	F	295	229(885)
tnfn1_pw060323p07q157	A08	C	1832053	R	FTN_1708	1830752	1832410	R	553	358(1659)
tnfn1_pw060323p07q158	B08	C	1486900	F	FTN_1409	1485991	1487373	R	461	474(1383)
tnfn1_pw060323p07q159	C08	C	1551394	F	FTN_1462	1550899	1551804	R	302	411(906)
tnfn1_pw060323p07q160	D08	C	1843007	R	FTN_1717	1841960	1843996	R	679	990(2037)
tnfn1_pw060323p07q161	E08	C	997590	F	FTN_0936	997186	998415	F	410	405(1230)
tnfn1_pw060323p07q162	F08	C	990791	F	FTN_0929	989845	990945	R	367	155(1101)
tnfn1_pw060323p07q163	G08	C	1038449	R	FTN_0984	1037817	1039706	R	630	1258(1890)
tnfn1_pw060323p07q164	H08	C	1483532	R	FTN_1405	1482889	1483809	R	307	278(921)
tnfn1_pw060323p07q165	A09	C	596889	F	FTN_0570	596517	597620	R	368	732(1104)
tnfn1_pw060323p07q166	B09	C	881794	R	FTN_0824	881019	882230	R	404	437(1212)
tnfn1_pw060323p07q167	C09	C	1615535	F	FTN_1518	1614441	1616447	R	669	913(2007)
tnfn1_pw060323p07q168	D09	C	406287	R	FTN_0408	406141	406611	F	157	147(471)
tnfn1_pw060323p07q169	E09	C	1526074	F	FTN_1438	1525003	1527696	F	898	1072(2694)
tnfn1_pw060323p07q170	F09	C	1332119	R	FTN_1261	1331640	1333124	F	495	480(1485)
tnfn1_pw060323p07q171	G09	C	614612	R	FTN_0585	614004	614723	R	240	112(720)
tnfn1_pw060323p07q172	H09	C	1422709	R	FTN_1344	1422190	1423386	F	399	520(1197)
tnfn1_pw060323p07q173	A10	C	1523216	R	FTN_1437	1522690	1524927	F	746	527(2238)
tnfn1_pw060323p07q174	B10	C	345305	F	FTN_0339	345056	345406	F	117	250(351)
tnfn1_pw060323p07q175	C10	C	1579957	R	FTN_1487	1577096	1579960	R	955	4(2865)
tnfn1_pw060323p07q176	D10	C	1631994	R	FTN_1534	1631854	1632321	F	156	141(468)
tnfn1_pw060323p07q177	E10	C	1451719	R	FTN_1371	1450809	1451963	R	385	245(1155)
tnfn1_pw060323p07q178	F10	C	1775905	R	FTN_1661	1775674	1777140	R	489	1236(1467)
tnfn1_pw060323p07q179	G10	C	898376	R	FTN_0842	897754	898863	R	370	488(1110)
tnfn1_pw060323p07q180	H10	C	275096	R	FTN_0267	274900	275400	F	167	197(501)
tnfn1_pw060323p07q181	A11	C	1061519	F	FTN_1001	1061369	1062211	F	281	151(843)
tnfn1_pw060323p07q182	B11	C	1363845	R	FTN_1292	1363308	1364576	R	423	732(1269)
tnfn1_pw060323p07q183	C11	C	381533	F	FTN_0380	381374	381616	F	81	160(243)
tnfn1_pw060323p07q184	D11	C	988456	R	intergenic					
tnfn1_pw060323p07q185	E11	C	871531	F	FTN_0814	870744	871868	R	375	338(1125)
tnfn1_pw060323p07q186	F11	C	1227916	F	FTN_1157	1227077	1228891	F	605	840(1815)
tnfn1_pw060323p07q187	G11	C	459584	R	FTN_0455	458374	461271	F	966	1211(2898)
tnfn1_pw060323p07q188	H11	C	91102	F	FTN_0080	90741	91610	F	290	362(870)
tnfn1_pw060323p07q189	A12	C	840038	F	FTN_0781	839608	840624	F	339	431(1017)
tnfn1_pw060323p07q190	B12	C	472055	F	FTN_0467	471407	472627	R	407	573(1221)
tnfn1_pw060323p07q191	C12	C	639659	F	FTN_0606	639396	639743	F	116	264(348)
tnfn1_pw060323p07q192	D12	U	1138561	F	FTN_1075	1138172	1138876	R	235	316(705)
tnfn1_pw060323p07q193	E12	C	1635345	F	-	1634886	1635750	F	288.3	460(865)
tnfn1_pw060323p07q194	F12	C	1367258	F	FTN_1298	1367030	1368379	F	450	229(1350)
tnfn1_pw060323p07q195	G12	C	734136	F	FTN_0690	733590	735296	F	569	547(1707)
tnfn1_pw060323p07q196	H12	C	312189	F	FTN_0303	311969	312892	F	308	221(924)

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_pw060323p07q101	A01	EXACT(0)	157	152	116	27	EXACT(0)	200	189	51
tnfn1_pw060323p07q102	B01	EXACT(0)	156	153	120	29	EXACT(0)	200	181	56
tnfn1_pw060323p07q103	C01	EXACT(0)	156	153	123	34	EXACT(0)	200	187	56
tnfn1_pw060323p07q104	D01	EXACT(0)	156	152	133	35	EXACT(0)	200	181	43
tnfn1_pw060323p07q105	E01	EXACT(0)	157	152	117	25	EXACT(0)	200	184	52
tnfn1_pw060323p07q106	F01	EXACT(0)	157	153	131	41	EXACT(0)	190	156	37
tnfn1_pw060323p07q107	G01	EXACT(0)	157	146	132	38	EXACT(0)	145	143	53
tnfn1_pw060323p07q108	H01	EXACT(0)	157	151	132	40	EXACT(0)	200	187	49
tnfn1_pw060323p07q109	A02	EXACT(0)	157	159	126	35	EXACT(0)	200	190	57
tnfn1_pw060323p07q110	B02	EXACT(0)	157	151	132	37	EXACT(0)	200	188	49
tnfn1_pw060323p07q111	C02	EXACT(0)	156	87	75	29	EXACT(0)	200	189	53
tnfn1_pw060323p07q112	D02	EXACT(0)	157	152	130	37	EXACT(0)	200	190	53
tnfn1_pw060323p07q113	E02	EXACT(0)	155	152	131	41	EXACT(0)	150	143	51
tnfn1_pw060323p07q114	F02	EXACT(0)	155	145	117	35	EXACT(0)	200	179	45
tnfn1_pw060323p07q115	G02	EXACT(0)	156	151	132	41	EXACT(0)	200	165	43
tnfn1_pw060323p07q116	H02	NONE	0	0	0	31	ESTIMATE(154)	731	626	36
tnfn1_pw060323p07q117	A03	EXACT(0)	156	153	125	37	EXACT(0)	200	192	53
tnfn1_pw060323p07q118	B03	EXACT(0)	156	152	121	36	EXACT(0)	198	184	51
tnfn1_pw060323p07q119	C03	EXACT(0)	155	142	99	20	EXACT(0)	200	188	53
tnfn1_pw060323p07q120	D03	EXACT(0)	156	145	131	37	EXACT(0)	200	182	55
tnfn1_pw060323p07q121	E03	EXACT(0)	153	153	116	41	EXACT(0)	200	189	56
tnfn1_pw060323p07q122	F03	EXACT(0)	157	153	137	41	EXACT(0)	200	170	39
tnfn1_pw060323p07q123	G03	EXACT(0)	156	153	129	31	EXACT(0)	200	188	50
tnfn1_pw060323p07q124	H03	EXACT(0)	158	152	132	37	EXACT(0)	200	192	52
tnfn1_pw060323p07q125	A04	EXACT(0)	157	153	134	37	EXACT(0)	200	195	56
tnfn1_pw060323p07q126	B04	EXACT(0)	155	153	122	32	EXACT(0)	200	180	47
tnfn1_pw060323p07q127	C04	EXACT(0)	152	145	100	34	EXACT(0)	200	184	56
tnfn1_pw060323p07q128	D04	EXACT(0)	155	145	125	42	EXACT(0)	200	185	57
tnfn1_pw060323p07q129	E04	EXACT(0)	155	151	124	30	EXACT(0)	200	191	54
tnfn1_pw060323p07q130	F04	EXACT(0)	157	152	127	36	EXACT(0)	200	186	53
tnfn1_pw060323p07q131	G04	EXACT(0)	125	120	96	25	EXACT(0)	200	188	55
tnfn1_pw060323p07q132	H04	EXACT(0)	122	125	99	28	EXACT(0)	200	180	51
tnfn1_pw060323p07q133	A05	EXACT(0)	122	125	99	27	EXACT(0)	200	189	50
tnfn1_pw060323p07q134	B05	EXACT(0)	120	112	62	21	EXACT(0)	200	187	51
tnfn1_pw060323p07q135	C05	EXACT(0)	123	120	97	26	EXACT(0)	200	185	55
tnfn1_pw060323p07q136	D05	EXACT(0)	125	118	107	31	EXACT(0)	200	193	53
tnfn1_pw060323p07q137	E05	EXACT(0)	123	120	90	24	EXACT(0)	200	187	51
tnfn1_pw060323p07q138	F05	EXACT(0)	123	120	99	33	EXACT(0)	200	190	50
tnfn1_pw060323p07q139	G05	EXACT(0)	122	113	94	26	EXACT(0)	200	187	49
tnfn1_pw060323p07q140	H05	EXACT(0)	123	118	102	27	EXACT(0)	199	178	45
tnfn1_pw060323p07q141	A06	EXACT(0)	121	116	91	30	EXACT(0)	200	185	56
tnfn1_pw060323p07q142	B06	EXACT(0)	122	109	72	22	EXACT(0)	172	149	44
tnfn1_pw060323p07q143	C06	EXACT(0)	123	112	101	27	EXACT(0)	200	183	47
tnfn1_pw060323p07q144	D06	EXACT(0)	122	113	97	26	EXACT(0)	200	174	48
tnfn1_pw060323p07q145	E06	EXACT(0)	123	117	96	29	EXACT(0)	200	179	43
tnfn1_pw060323p07q146	F06	EXACT(0)	122	119	101	34	EXACT(0)	200	186	43
tnfn1_pw060323p07q147	G06	EXACT(0)	122	120	96	32	EXACT(0)	200	180	55
tnfn1_pw060323p07q148	H06	EXACT(0)	124	120	104	35	EXACT(0)	200	185	47

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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_pw060323p07q149	A07	EXACT(0)	123	109	70	20	EXACT(0)	200	171	36
tnfn1_pw060323p07q150	B07	EXACT(0)	124	119	94	24	EXACT(0)	200	187	48
tnfn1_pw060323p07q151	C07	EXACT(0)	122	118	57	19	EXACT(0)	200	174	48
tnfn1_pw060323p07q152	D07	EXACT(0)	122	113	94	28	EXACT(0)	200	185	50
tnfn1_pw060323p07q153	E07	EXACT(0)	123	119	80	22	EXACT(0)	200	181	52
tnfn1_pw060323p07q154	F07	EXACT(0)	123	112	92	26	EXACT(0)	200	187	54
tnfn1_pw060323p07q155	G07	EXACT(0)	156	152	134	40	EXACT(0)	200	187	57
tnfn1_pw060323p07q156	H07	EXACT(0)	156	151	121	36	EXACT(0)	200	192	54
tnfn1_pw060323p07q157	A08	EXACT(0)	156	145	110	31	EXACT(0)	200	184	50
tnfn1_pw060323p07q158	B08	EXACT(0)	156	146	130	42	EXACT(0)	133	119	50
tnfn1_pw060323p07q159	C08	EXACT(0)	156	151	130	40	EXACT(0)	200	192	41
tnfn1_pw060323p07q160	D08	EXACT(0)	155	145	129	42	EXACT(0)	200	191	56
tnfn1_pw060323p07q161	E08	EXACT(0)	155	145	120	36	EXACT(0)	200	174	51
tnfn1_pw060323p07q162	F08	EXACT(0)	155	153	108	25	EXACT(0)	200	180	43
tnfn1_pw060323p07q163	G08	EXACT(0)	156	152	128	39	EXACT(0)	200	194	57
tnfn1_pw060323p07q164	H08	EXACT(0)	156	145	137	39	EXACT(0)	200	188	46
tnfn1_pw060323p07q165	A09	EXACT(0)	154	145	120	37	EXACT(0)	200	187	57
tnfn1_pw060323p07q166	B09	EXACT(0)	156	152	134	39	ESTIMATE(58)	142	110	26
tnfn1_pw060323p07q167	C09	EXACT(0)	155	145	126	40	EXACT(0)	200	191	55
tnfn1_pw060323p07q168	D09	EXACT(0)	155	152	128	36	EXACT(0)	200	186	56
tnfn1_pw060323p07q169	E09	EXACT(0)	156	146	127	40	EXACT(0)	200	192	50
tnfn1_pw060323p07q170	F09	EXACT(0)	157	152	127	35	EXACT(0)	200	177	54
tnfn1_pw060323p07q171	G09	EXACT(0)	156	152	134	39	EXACT(0)	150	149	54
tnfn1_pw060323p07q172	H09	EXACT(0)	156	145	128	39	EXACT(0)	200	192	57
tnfn1_pw060323p07q173	A10	EXACT(0)	155	152	125	39	EXACT(0)	200	199	56
tnfn1_pw060323p07q174	B10	EXACT(0)	156	152	125	39	EXACT(0)	200	193	53
tnfn1_pw060323p07q175	C10	EXACT(0)	155	146	120	36	EXACT(0)	200	180	55
tnfn1_pw060323p07q176	D10	EXACT(0)	156	146	130	42	EXACT(0)	200	189	54
tnfn1_pw060323p07q177	E10	EXACT(0)	157	153	116	33	EXACT(0)	200	188	57
tnfn1_pw060323p07q178	F10	EXACT(0)	156	146	121	40	EXACT(0)	200	193	49
tnfn1_pw060323p07q179	G10	EXACT(0)	158	153	134	37	EXACT(0)	200	180	45
tnfn1_pw060323p07q180	H10	EXACT(0)	155	153	132	39	EXACT(0)	200	181	49
tnfn1_pw060323p07q181	A11	EXACT(0)	156	152	125	37	EXACT(0)	200	186	54
tnfn1_pw060323p07q182	B11	EXACT(0)	156	145	124	34	EXACT(0)	200	191	53
tnfn1_pw060323p07q183	C11	EXACT(0)	155	145	135	43	EXACT(0)	200	160	43
tnfn1_pw060323p07q184	D11	EXACT(0)	156	151	117	29	EXACT(0)	200	184	53
tnfn1_pw060323p07q185	E11	EXACT(0)	156	153	126	37	EXACT(0)	200	187	57
tnfn1_pw060323p07q186	F11	EXACT(0)	155	145	123	41	EXACT(0)	200	196	49
tnfn1_pw060323p07q187	G11	EXACT(0)	155	145	126	41	EXACT(0)	200	190	57
tnfn1_pw060323p07q188	H11	EXACT(0)	153	108	99	41	EXACT(0)	200	195	52
tnfn1_pw060323p07q189	A12	EXACT(0)	156	145	128	34	EXACT(0)	200	192	56
tnfn1_pw060323p07q190	B12	EXACT(0)	156	152	128	42	EXACT(0)	200	193	59
tnfn1_pw060323p07q191	C12	EXACT(0)	157	142	112	33	EXACT(0)	163	135	42
tnfn1_pw060323p07q192	D12	EXACT(0)	158	152	147	46	EXACT(0)	149	140	62
tnfn1_pw060323p07q193	E12	EXACT(0)	151	139	119	41	EXACT(0)	79	51	21
tnfn1_pw060323p07q194	F12	EXACT(0)	156	152	118	33	EXACT(0)	200	194	53
tnfn1_pw060323p07q195	G12	EXACT(0)	157	153	137	40	EXACT(0)	200	190	64
tnfn1_pw060323p07q196	H12	EXACT(0)	156	152	117	29	EXACT(0)	200	184	48

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