

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 23 (tnfn1_pw060419p03)**

Catalog No. NR-8057

For research use only. Not for human use.

Contributor:

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Product Description:

A comprehensive 16508-member transposon mutant library¹ 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-8057 represents Plate 23 (tnfn1_pw060419p03) 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-8057 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% CO₂

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 23 (tnfn1_pw060419p03), NR-8057.”

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/bmb15/bmb15toc.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_pw060419p03q101	A01	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060419p03q102	B01	T20	rnr	ribonuclease R	transcription
tnfn1_pw060419p03q103	C01	T20	-	membrane fusion protein	transport
tnfn1_pw060419p03q104	D01	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060419p03q105	E01	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p03q106	F01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q107	G01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q108	H01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q109	A02	T20	trpA	tryptophan synthase alpha chain	amino acid metabolism - biosynthesis
tnfn1_pw060419p03q110	B02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q111	C02	T20	tolC	outer membrane efflux protein, tolC precursor	transport
tnfn1_pw060419p03q112	D02	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p03q113	E02	T20	sucC	succinyl-CoA synthetase, beta chain	energy metabolism
tnfn1_pw060419p03q114	F02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q115	G02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q116	H02	T20	sucD	succinyl-CoA synthetase, alpha subunit	energy metabolism
tnfn1_pw060419p03q117	A03	T20	pilC	Type IV pili polytopic inner membrane protein	motility, attachment and secretion structure
tnfn1_pw060419p03q118	B03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q119	C03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q120	D03	T20	-	conserved outer membrane protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q121	E03	T20	-	fatty acid hydroxylase	fatty acids and lipids metabolism
tnfn1_pw060419p03q122	F03	T20	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060419p03q123	G03	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p03q124	H03	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q125	A04	<KAN-2>	-	pseudogene: hypothetical protein	pseudogene
tnfn1_pw060419p03q126	B04	<KAN-2>	nadE	NAD synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p03q127	C04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q128	D04	T20	-	acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060419p03q129	E04	<KAN-2>	-	ROK family protein	putative enzymes
tnfn1_pw060419p03q130	F04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q131	G04	<KAN-2>	-		
tnfn1_pw060419p03q132	H04	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p03q133	A05	T18	-	glutamine amidotransferase, SNO family	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p03q134	B05	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p03q135	C05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q136	D05	T18	clpP	ATP-dependent Clp protease subunit P	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060419p03q137	E05	T18	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060419p03q138	F05	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p03q139	G05	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p03q140	H05	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q141	A06	T18	fimT	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060419p03q142	B06	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p03q143	C06	T18	-		
tnfn1_pw060419p03q144	D06	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q145	E06	T18	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060419p03q146	F06	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q147	G06	T18	-	N6-adenine-specific methylase	DNA replication, recombination, modification and repair
tnfn1_pw060419p03q148	H06	T18	-	heavy metal cation transport ATPase	transport

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Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060419p03q149	A07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q150	B07	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060419p03q151	C07	T20	-	ABC-type anion transport system, duplicated permease component	transport
tnfn1_pw060419p03q152	D07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q153	E07	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q154	F07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q155	G07	T20	-	ferredoxin	energy metabolism
tnfn1_pw060419p03q156	H07	T20	thrA	aspartate kinase I/homoserine dehydrogenase I	amino acid metabolism - biosynthesis
tnfn1_pw060419p03q157	A08	T20	-	solute:sodium symporter	transport
tnfn1_pw060419p03q158	B08	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060419p03q159	C08	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060419p03q160	D08	T20	-	SAM-dependent methyltransferase	putative enzymes
tnfn1_pw060419p03q161	E08	T20	-	traT-like protein	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060419p03q162	F08	T20	-	Na ⁺ /H ⁺ antiporter	transport
tnfn1_pw060419p03q163	G08	T20	-	traT-like protein	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060419p03q164	H08	T20	pepO	M13 family metalloproteinase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060419p03q165	A09	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060419p03q166	B09	T20	wbtA	dTDP-glucose 4,6-dehydratase	cell wall / LPS / capsule
tnfn1_pw060419p03q167	C09	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p03q168	D09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q169	E09	T20	nfnB	dihydropteridine reductase	energy metabolism
tnfn1_pw060419p03q170	F09	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p03q171	G09	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q172	H09	T18	mutS	MutS, subunit of MutHLS complex, methyl-directed mismatch repair protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060419p03q173	A10	<KAN-2>	-	conserved protein of unknown function	cell wall / LPS / capsule
tnfn1_pw060419p03q174	B10	<KAN-2>	-	aspartate aminotransferase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p03q175	C10	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p03q176	D10	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q177	E10	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q178	F10	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q179	G10	T18	fumC	fumarate hydratase, class II	energy metabolism
tnfn1_pw060419p03q180	H10	T18	-	peptidase, U61 family	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060419p03q181	A11	T18	-	L-lactate dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p03q182	B11	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q183	C11	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p03q184	D11	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q185	E11	T18	-	YjeF-related protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q186	F11	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p03q187	G11	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p03q188	H11	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p03q189	A12	T20	-	two-component response regulator	signal transduction and regulation
tnfn1_pw060419p03q190	B12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p03q191	C12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p03q192	D12	T18	treA	trehalase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060419p03q193	E12	T20	-	regulatory protein, AlpA family	signal transduction and regulation
tnfn1_pw060419p03q194	F12	T20	-	apolipoprotein N-acyltransferase	cell wall / LPS / capsule
tnfn1_pw060419p03q195	G12	T20	-	sodium bile acid symporter family protein	transport
tnfn1_pw060419p03q196	H12	T20	-	monovalent cation:proton antiporter-1	transport

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_pw060419p03q101	A01	C	112021	F	FTN_0101	111569	112462	R	298	442(894)
tnfn1_pw060419p03q102	B01	C	1550360	F	FTN_1461	1548609	1550903	R	765	544(2295)
tnfn1_pw060419p03q103	C01	C	1712729	R	FTN_1609	1712416	1713786	F	457	314(1371)
tnfn1_pw060419p03q104	D01	C	689592	F	FTN_0649	687803	690832	F	1010	1790(3030)
tnfn1_pw060419p03q105	E01	C	623295	R	FTN_0592	623054	623476	R	141	182(423)
tnfn1_pw060419p03q106	F01	C	61104	R	FTN_0051	61102	61707	F	202	3(606)
tnfn1_pw060419p03q107	G01	C	849738	R	FTN_0791	849690	849944	F	85	49(255)
tnfn1_pw060419p03q108	H01	C	1164511	R	FTN_1102	1164373	1164600	F	76	139(228)
tnfn1_pw060419p03q109	A02	C	1868534	F	FTN_1740	1868014	1868817	F	268	521(804)
tnfn1_pw060419p03q110	B02	C	895456	R	FTN_0839	895194	896291	F	366	263(1098)
tnfn1_pw060419p03q111	C02	C	1824858	R	FTN_1703	1824128	1825654	R	509	797(1527)
tnfn1_pw060419p03q112	D02	C	1828633	R	FTN_1706	1827979	1829157	R	393	525(1179)
tnfn1_pw060419p03q113	E02	C	625472	R	FTN_0594	624495	625655	R	387	184(1161)
tnfn1_pw060419p03q114	F02	C	1386060	F	FTN_1313	1384921	1386648	F	576	1140(1728)
tnfn1_pw060419p03q115	G02	C	1008265	F	FTN_0952	1008165	1008644	R	160	380(480)
tnfn1_pw060419p03q116	H02	C	624377	R	FTN_0593	623591	624460	R	290	84(870)
tnfn1_pw060419p03q117	A03	C	1181028	F	FTN_1116	1180496	1181722	F	409	533(1227)
tnfn1_pw060419p03q118	B03	C	380879	R	FTN_0379	380755	381126	F	124	125(372)
tnfn1_pw060419p03q119	C03	C	846867	R	FTN_0788	846344	847171	F	276	524(828)
tnfn1_pw060419p03q120	D03	C	130690	R	FTN_0119	130544	131080	F	179	147(537)
tnfn1_pw060419p03q121	E03	C	854056	F	FTN_0797	853524	854069	F	182	533(546)
tnfn1_pw060419p03q122	F03	C	311141	R	FTN_0301	310260	311564	F	435	882(1305)
tnfn1_pw060419p03q123	G03	C	225907	R	FTN_0205	225741	226649	F	303	167(909)
tnfn1_pw060419p03q124	H03	U	282566	F	FTN_0275	282485	283540	F	352	82(1056)
tnfn1_pw060419p03q125	A04	U	852049	R	FTN_0794	851999	852079	R	27	31(81)
tnfn1_pw060419p03q126	B04	U	1351393	F	FTN_1278	1351324	1352070	F	249	70(747)
tnfn1_pw060419p03q127	C04	C	299036	F	FTN_0292	298865	299065	F	67	172(201)
tnfn1_pw060419p03q128	D04	U	1879379	F	FTN_1750	1879341	1880078	F	246	39(738)
tnfn1_pw060419p03q129	E04	C	648434	F	FTN_0617	648331	649293	F	321	104(963)
tnfn1_pw060419p03q130	F04	C	428079	F	FTN_0430	427666	428130	F	155	414(465)
tnfn1_pw060419p03q131	G04	C	1050193	R	intergenic					
tnfn1_pw060419p03q132	H04	C	1384456	R	FTN_1312	1384422	1384913	F	164	35(492)
tnfn1_pw060419p03q133	A05	C	635239	F	FTN_0602	634911	635447	F	179	329(537)
tnfn1_pw060419p03q134	B05	C	1148547	F	FTN_1086	1148532	1149134	F	201	16(603)
tnfn1_pw060419p03q135	C05	C	58829	R	FTN_0049	58770	59591	F	274	60(822)
tnfn1_pw060419p03q136	D05	U	1117652	R	FTN_1057	1117172	1117774	R	201	123(603)
tnfn1_pw060419p03q137	E05	C	247640	F	FTN_0223	246583	248118	F	512	1058(1536)
tnfn1_pw060419p03q138	F05	C	87340	R	FTN_0074	87173	87418	R	82	79(246)
tnfn1_pw060419p03q139	G05	C	222776	F	FTN_0201	222642	223334	R	231	559(693)
tnfn1_pw060419p03q140	H05	C	481906	F	FTN_0477	481348	482232	F	295	559(885)
tnfn1_pw060419p03q141	A06	C	704668	R	FTN_0664	704429	705010	F	194	240(582)
tnfn1_pw060419p03q142	B06	C	499605	R	FTN_0494	499405	500001	R	199	397(597)
tnfn1_pw060419p03q143	C06	C	285121	F	intergenic					
tnfn1_pw060419p03q144	D06	C	1600255	R	FTN_1505	1599542	1601503	R	654	1249(1962)
tnfn1_pw060419p03q145	E06	C	247640	F	FTN_0223	246583	248118	F	512	1058(1536)
tnfn1_pw060419p03q146	F06	C	1086112	F	FTN_1029	1085576	1086232	R	219	121(657)
tnfn1_pw060419p03q147	G06	C	693861	R	FTN_0655	693723	694298	R	192	438(576)
tnfn1_pw060419p03q148	H06	U	394696	F	FTN_0394	392909	395071	R	721	376(2163)

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_pw060419p03q149	A07	C	1777273	R	FTN_1662	1777161	1777610	R	150	338(450)
tnfn1_pw060419p03q150	B07	C	1326819	F	FTN_1257	1326405	1327673	F	423	415(1269)
tnfn1_pw060419p03q151	C07	C	152366	F	FTN_0140	151997	153793	F	599	370(1797)
tnfn1_pw060419p03q152	D07	C	995008	R	FTN_0934	994829	995320	F	164	180(492)
tnfn1_pw060419p03q153	E07	C	1217566	R	FTN_1151	1216361	1218106	F	582	1206(1746)
tnfn1_pw060419p03q154	F07	C	944990	F	FTN_0887	944252	945208	R	319	219(957)
tnfn1_pw060419p03q155	G07	C	129413	F	FTN_0117	129107	129457	R	117	45(351)
tnfn1_pw060419p03q156	H07	C	546779	R	FTN_0525	545312	547729	F	806	1468(2418)
tnfn1_pw060419p03q157	A08	C	1364551	F	FTN_1292	1363308	1364576	R	423	26(1269)
tnfn1_pw060419p03q158	B08	C	31930	R	FTN_0031	31335	32201	F	289	596(867)
tnfn1_pw060419p03q159	C08	C	1617532	R	FTN_1520	1617143	1618336	R	398	805(1194)
tnfn1_pw060419p03q160	D08	C	90838	R	FTN_0080	90741	91610	F	290	98(870)
tnfn1_pw060419p03q161	E08	C	325183	R	FTN_0315	324848	325591	R	248	409(744)
tnfn1_pw060419p03q162	F08	C	126823	R	FTN_0115	126046	127293	F	416	778(1248)
tnfn1_pw060419p03q163	G08	C	325183	R	FTN_0315	324848	325591	R	248	409(744)
tnfn1_pw060419p03q164	H08	C	1260135	R	FTN_1186	1259507	1261567	R	687	1433(2061)
tnfn1_pw060419p03q165	A09	C	1368866	R	FTN_1300	1368610	1369497	R	296	632(888)
tnfn1_pw060419p03q166	B09	C	1511577	F	FTN_1431	1511000	1512733	R	578	1157(1734)
tnfn1_pw060419p03q167	C09	U	107666	R	FTN_0096	107210	107899	F	230	457(690)
tnfn1_pw060419p03q168	D09	C	81596	R	FTN_0067	81421	82032	R	204	437(612)
tnfn1_pw060419p03q169	E09	C	241015	F	FTN_0218	240476	241126	R	217	112(651)
tnfn1_pw060419p03q170	F09	C	780061	R	FTN_0727	780006	780572	F	189	56(567)
tnfn1_pw060419p03q171	G09	C	155822	R	FTN_0142	155218	156756	F	513	605(1539)
tnfn1_pw060419p03q172	H09	C	1605543	F	FTN_1509	1604143	1606674	F	844	1401(2532)
tnfn1_pw060419p03q173	A10	C	1539268	R	FTN_1449	1538872	1539477	R	202	210(606)
tnfn1_pw060419p03q174	B10	C	1212538	R	FTN_1146	1211574	1212764	R	397	227(1191)
tnfn1_pw060419p03q175	C10	C	238231	F	FTN_0216	238094	238426	F	111	138(333)
tnfn1_pw060419p03q176	D10	C	144661	R	FTN_0131	143590	144894	R	435	234(1305)
tnfn1_pw060419p03q177	E10	C	144661	R	FTN_0131	143590	144894	R	435	234(1305)
tnfn1_pw060419p03q178	F10	C	1299739	F	FTN_1230	1299559	1300131	R	191	393(573)
tnfn1_pw060419p03q179	G10	C	241891	R	FTN_0220	241817	243205	F	463	75(1389)
tnfn1_pw060419p03q180	H10	C	1720626	R	FTN_1613	1720110	1721120	R	337	495(1011)
tnfn1_pw060419p03q181	A11	C	239109	F	FTN_0217	238429	239583	R	385	475(1155)
tnfn1_pw060419p03q182	B11	C	1064968	F	FTN_1005	1064800	1065075	F	92	169(276)
tnfn1_pw060419p03q183	C11	C	1484730	R	FTN_1407	1484689	1485012	R	108	283(324)
tnfn1_pw060419p03q184	D11	U	289206	F	FTN_0282	288913	289806	F	298	294(894)
tnfn1_pw060419p03q185	E11	C	745592	F	FTN_0702	745266	746765	F	500	327(1500)
tnfn1_pw060419p03q186	F11	U	376862	F	FTN_0375	376636	377250	F	205	227(615)
tnfn1_pw060419p03q187	G11	C	1187304	F	FTN_1123	1187288	1187590	F	101	17(303)
tnfn1_pw060419p03q188	H11	U	740568	F	FTN_0696	740453	741076	R	208	509(624)
tnfn1_pw060419p03q189	A12	C	1541444	F	FTN_1452	1540850	1541536	F	229	595(687)
tnfn1_pw060419p03q190	B12	C	910227	R	FTN_0854	909700	910479	F	260	528(780)
tnfn1_pw060419p03q191	C12	C	446349	F	FTN_0445	445344	446786	F	481	1006(1443)
tnfn1_pw060419p03q192	D12	C	1407004	R	FTN_1328	1406119	1407570	F	484	886(1452)
tnfn1_pw060419p03q193	E12	C	374634	F	FTN_0372	374491	374706	F	72	144(216)
tnfn1_pw060419p03q194	F12	C	1125999	F	FTN_1067	1125843	1127330	F	496	157(1488)
tnfn1_pw060419p03q195	G12	C	366716	R	FTN_0363	366625	367551	F	309	92(927)
tnfn1_pw060419p03q196	H12	C	1595125	R	FTN_1501	1595030	1596325	F	432	96(1296)

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_pw060419p03q101	A01	EXACT(0)	172	137	95	25	EXACT(0)	200	170	45
tnfn1_pw060419p03q102	B01	EXACT(0)	157	151	135	40	EXACT(0)	200	144	43
tnfn1_pw060419p03q103	C01	EXACT(0)	157	153	137	39	EXACT(0)	200	186	45
tnfn1_pw060419p03q104	D01	EXACT(0)	157	153	130	36	EXACT(0)	200	196	58
tnfn1_pw060419p03q105	E01	EXACT(0)	156	142	122	38	EXACT(0)	200	197	52
tnfn1_pw060419p03q106	F01	EXACT(0)	154	145	129	38	EXACT(0)	200	167	45
tnfn1_pw060419p03q107	G01	EXACT(0)	156	152	130	38	EXACT(0)	200	181	52
tnfn1_pw060419p03q108	H01	EXACT(0)	156	144	133	41	EXACT(0)	80	71	52
tnfn1_pw060419p03q109	A02	EXACT(0)	158	151	140	39	EXACT(0)	143	141	45
tnfn1_pw060419p03q110	B02	EXACT(0)	159	152	143	43	EXACT(0)	200	195	58
tnfn1_pw060419p03q111	C02	EXACT(0)	158	153	135	36	EXACT(0)	200	190	56
tnfn1_pw060419p03q112	D02	EXACT(0)	156	153	134	39	EXACT(0)	200	118	35
tnfn1_pw060419p03q113	E02	EXACT(0)	160	144	90	22	EXACT(0)	200	195	52
tnfn1_pw060419p03q114	F02	EXACT(0)	156	144	117	25	EXACT(0)	200	175	58
tnfn1_pw060419p03q115	G02	EXACT(0)	156	142	112	29	EXACT(0)	200	182	56
tnfn1_pw060419p03q116	H02	EXACT(0)	156	139	133	49	EXACT(0)	200	199	61
tnfn1_pw060419p03q117	A03	EXACT(0)	155	145	129	41	EXACT(0)	200	193	56
tnfn1_pw060419p03q118	B03	EXACT(0)	156	152	120	37	EXACT(0)	200	180	54
tnfn1_pw060419p03q119	C03	EXACT(0)	156	145	127	38	EXACT(0)	200	183	58
tnfn1_pw060419p03q120	D03	EXACT(0)	157	153	136	40	EXACT(0)	200	192	57
tnfn1_pw060419p03q121	E03	EXACT(0)	156	152	139	48	EXACT(0)	200	176	55
tnfn1_pw060419p03q122	F03	EXACT(0)	158	145	123	30	EXACT(0)	200	186	57
tnfn1_pw060419p03q123	G03	EXACT(0)	152	153	116	40	EXACT(0)	142	137	51
tnfn1_pw060419p03q124	H03	EXACT(0)	120	119	104	43	EXACT(0)	200	193	64
tnfn1_pw060419p03q125	A04	EXACT(0)	121	119	109	44	EXACT(0)	200	183	67
tnfn1_pw060419p03q126	B04	EXACT(0)	119	113	103	39	EXACT(0)	200	194	60
tnfn1_pw060419p03q127	C04	EXACT(0)	122	120	90	29	EXACT(0)	200	174	54
tnfn1_pw060419p03q128	D04	NONE	0	0	0	24	ESTIMATE(122)	802	679	32
tnfn1_pw060419p03q129	E04	EXACT(0)	124	120	103	27	EXACT(0)	200	187	53
tnfn1_pw060419p03q130	F04	EXACT(0)	126	118	78	22	EXACT(0)	200	181	48
tnfn1_pw060419p03q131	G04	EXACT(0)	120	109	62	25	EXACT(0)	200	173	61
tnfn1_pw060419p03q132	H04	EXACT(0)	121	105	82	21	ESTIMATE(112)	88	76	28
tnfn1_pw060419p03q133	A05	EXACT(0)	122	112	101	29	EXACT(0)	200	176	52
tnfn1_pw060419p03q134	B05	EXACT(0)	123	112	86	24	EXACT(0)	200	181	51
tnfn1_pw060419p03q135	C05	EXACT(0)	124	116	102	32	EXACT(0)	200	181	61
tnfn1_pw060419p03q136	D05	EXACT(0)	121	112	99	37	EXACT(0)	200	195	58
tnfn1_pw060419p03q137	E05	EXACT(0)	124	120	101	35	EXACT(0)	200	186	56
tnfn1_pw060419p03q138	F05	EXACT(0)	125	120	67	23	EXACT(0)	200	192	50
tnfn1_pw060419p03q139	G05	EXACT(0)	126	121	97	25	EXACT(0)	200	188	56
tnfn1_pw060419p03q140	H05	EXACT(0)	124	112	51	21	EXACT(0)	200	195	48
tnfn1_pw060419p03q141	A06	EXACT(0)	124	120	86	24	EXACT(0)	200	192	56
tnfn1_pw060419p03q142	B06	EXACT(0)	121	112	87	24	EXACT(0)	200	183	57
tnfn1_pw060419p03q143	C06	EXACT(0)	125	120	100	31	EXACT(0)	200	187	53
tnfn1_pw060419p03q144	D06	EXACT(0)	122	112	101	34	EXACT(0)	200	190	57
tnfn1_pw060419p03q145	E06	EXACT(0)	125	120	112	32	EXACT(0)	200	186	58
tnfn1_pw060419p03q146	F06	EXACT(0)	123	116	105	32	EXACT(0)	200	186	65
tnfn1_pw060419p03q147	G06	EXACT(0)	121	112	88	24	EXACT(0)	200	181	60
tnfn1_pw060419p03q148	H06	EXACT(0)	121	120	97	33	EXACT(0)	200	189	61

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_pw060419p03q149	A07	EXACT(0)	157	153	142	38	EXACT(0)	200	181	54
tnfn1_pw060419p03q150	B07	EXACT(0)	156	145	118	32	EXACT(0)	200	182	52
tnfn1_pw060419p03q151	C07	EXACT(0)	153	152	126	42	EXACT(0)	200	153	41
tnfn1_pw060419p03q152	D07	EXACT(0)	154	145	123	39	EXACT(0)	200	179	47
tnfn1_pw060419p03q153	E07	EXACT(0)	123	73	66	24	EXACT(0)	200	181	50
tnfn1_pw060419p03q154	F07	ADJUSTED(2)	160	142	98	23	ESTIMATE(0)	200	183	59
tnfn1_pw060419p03q155	G07	EXACT(0)	159	152	130	35	EXACT(0)	200	188	57
tnfn1_pw060419p03q156	H07	EXACT(0)	156	152	128	35	EXACT(0)	200	192	54
tnfn1_pw060419p03q157	A08	EXACT(0)	157	153	124	31	EXACT(0)	200	185	56
tnfn1_pw060419p03q158	B08	EXACT(0)	155	144	129	40	EXACT(0)	200	190	62
tnfn1_pw060419p03q159	C08	EXACT(0)	156	139	133	45	EXACT(0)	200	185	65
tnfn1_pw060419p03q160	D08	EXACT(0)	157	153	130	27	EXACT(0)	200	189	53
tnfn1_pw060419p03q161	E08	EXACT(0)	156	142	111	30	EXACT(0)	200	131	31
tnfn1_pw060419p03q162	F08	EXACT(0)	155	152	136	42	EXACT(0)	200	190	54
tnfn1_pw060419p03q163	G08	EXACT(0)	156	114	105	33	EXACT(0)	200	196	53
tnfn1_pw060419p03q164	H08	EXACT(0)	158	152	134	36	EXACT(0)	200	193	52
tnfn1_pw060419p03q165	A09	EXACT(0)	154	145	121	41	EXACT(0)	200	148	35
tnfn1_pw060419p03q166	B09	EXACT(0)	154	146	116	38	EXACT(0)	200	193	58
tnfn1_pw060419p03q167	C09	EXACT(0)	155	153	135	49	EXACT(0)	200	190	63
tnfn1_pw060419p03q168	D09	EXACT(0)	156	145	131	35	EXACT(0)	200	184	53
tnfn1_pw060419p03q169	E09	EXACT(0)	157	145	142	43	EXACT(0)	200	174	50
tnfn1_pw060419p03q170	F09	EXACT(0)	159	153	122	27	EXACT(0)	200	181	52
tnfn1_pw060419p03q171	G09	EXACT(0)	157	145	133	37	EXACT(0)	200	193	55
tnfn1_pw060419p03q172	H09	EXACT(0)	121	112	99	44	EXACT(0)	200	190	63
tnfn1_pw060419p03q173	A10	EXACT(0)	120	119	104	45	EXACT(0)	200	196	59
tnfn1_pw060419p03q174	B10	EXACT(0)	121	119	104	43	EXACT(0)	200	197	63
tnfn1_pw060419p03q175	C10	EXACT(0)	121	119	77	24	EXACT(0)	200	187	52
tnfn1_pw060419p03q176	D10	EXACT(0)	123	118	70	22	EXACT(0)	200	182	51
tnfn1_pw060419p03q177	E10	EXACT(0)	121	119	109	36	EXACT(0)	200	182	59
tnfn1_pw060419p03q178	F10	EXACT(0)	122	113	94	32	EXACT(0)	200	189	65
tnfn1_pw060419p03q179	G10	EXACT(0)	121	112	90	27	EXACT(0)	200	186	58
tnfn1_pw060419p03q180	H10	EXACT(0)	122	112	80	25	EXACT(0)	200	184	59
tnfn1_pw060419p03q181	A11	EXACT(0)	123	120	101	31	EXACT(0)	200	197	56
tnfn1_pw060419p03q182	B11	EXACT(0)	124	120	104	31	EXACT(0)	200	184	56
tnfn1_pw060419p03q183	C11	EXACT(0)	124	119	70	18	EXACT(0)	200	176	42
tnfn1_pw060419p03q184	D11	EXACT(0)	124	119	96	34	ESTIMATE(3)	197	185	52
tnfn1_pw060419p03q185	E11	EXACT(0)	125	118	107	35	EXACT(0)	200	189	61
tnfn1_pw060419p03q186	F11	EXACT(0)	122	112	75	23	ESTIMATE(3)	197	174	49
tnfn1_pw060419p03q187	G11	EXACT(0)	123	112	71	23	ESTIMATE(4)	196	189	50
tnfn1_pw060419p03q188	H11	ADJUSTED(1)	122	111	62	20	ESTIMATE(2)	198	185	55
tnfn1_pw060419p03q189	A12	EXACT(0)	155	139	128	44	EXACT(0)	200	193	36
tnfn1_pw060419p03q190	B12	EXACT(0)	157	145	139	51	EXACT(0)	200	190	56
tnfn1_pw060419p03q191	C12	EXACT(0)	158	152	141	47	EXACT(0)	200	173	54
tnfn1_pw060419p03q192	D12	EXACT(0)	123	120	99	32	EXACT(0)	200	192	52
tnfn1_pw060419p03q193	E12	EXACT(0)	157	145	111	25	EXACT(0)	200	192	54
tnfn1_pw060419p03q194	F12	EXACT(0)	158	151	140	50	EXACT(0)	197	163	41
tnfn1_pw060419p03q195	G12	EXACT(0)	155	145	110	31	EXACT(0)	200	178	57
tnfn1_pw060419p03q196	H12	EXACT(0)	156	145	109	29	EXACT(0)	200	186	58