

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 22 (tnfn1_pw060419p02)**

Catalog No. NR-8056

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-8056 represents Plate 22 (tnfn1_pw060419p02) 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-8056 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 22 (tnfn1_pw060419p02), NR-8056.”

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_pw060419p02q101	A01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q102	B01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q103	C01	T18	-	protein of unknown function with radical SAM domain	unknown function - conserved
tnfn1_pw060419p02q104	D01	T20	rpe	D-ribulose-phosphate 3-epimerase	energy metabolism
tnfn1_pw060419p02q105	E01	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p02q106	F01	T20	-	acetoacetate decarboxylase	other metabolism - biosynthesis
tnfn1_pw060419p02q107	G01	T20	-	ATP-binding Cassette (ABC) superfamily protein	transport
tnfn1_pw060419p02q108	H01	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p02q109	A02	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q110	B02	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q111	C02	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q112	D02	<KAN-2>	appC	cytochrome bd-II terminal oxidase subunit I	energy metabolism
tnfn1_pw060419p02q113	E02	<KAN-2>	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060419p02q114	F02	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q115	G02	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p02q116	H02	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q117	A03	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q118	B03	T18	-	birA-like protein	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p02q119	C03	T18	-	carbon-nitrogen hydrolase	putative enzymes
tnfn1_pw060419p02q120	D03	T18	-	chitin-binding protein	putative enzymes
tnfn1_pw060419p02q121	E03	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q122	F03	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p02q123	G03	T18	-	monovalent cation:proton antiporter family protein	transport
tnfn1_pw060419p02q124	H03	T18	pilN	Type IV pili associated protein	motility, attachment and secretion structure
tnfn1_pw060419p02q125	A04	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q126	B04	T18	-	small conductance mechanosensitive ion channel (MscS) family protein	transport
tnfn1_pw060419p02q127	C04	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q128	D04	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q129	E04	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q130	F04	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q131	G04	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q132	H04	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q133	A05	T18	-		
tnfn1_pw060419p02q134	B05	T20	emrE	putative membrane transporter of cations and cationic drugs, multidrug resistance protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p02q135	C05	T20	ksgA	dimethyladenosine transferase	transport - amino-acid
tnfn1_pw060419p02q136	D05	T20	-	metallopeptidase, M50B family	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060419p02q137	E05	T20	rfbB	iron-sulfur cluster-binding protein	putative enzymes
tnfn1_pw060419p02q138	F05	T20	bioF	8-amino-7-oxononanoate synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p02q139	G05	T20	-	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060419p02q140	H05	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
tnfn1_pw060419p02q141	A06	T20	-	drug:H+ antiporter-1 (DHA2) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p02q142	B06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q143	C06	T20	-	conserved hypothetical protein	Potentially coding: hypothetical - conserved
tnfn1_pw060419p02q144	D06	T20	ribD	pyrimidine reductase/pyrimidine deaminase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p02q145	E06	T20	pilQ	Type IV pili secretin component	motility, attachment and secretion structure
tnfn1_pw060419p02q146	F06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q147	G06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q148	H06	T20	-	protein of unknown function	unknown function - novel

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060419p02q149	A07	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q150	B07	T20	-	acid phosphatase	fatty acids and lipids metabolism
tnfn1_pw060419p02q151	C07	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060419p02q152	D07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p02q153	E07	T20	ribD	pyrimidine reductase/pyrimidine deaminase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p02q154	F07	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060419p02q155	G07	T20	gph	phosphoglycolate phosphatase	putative enzymes
tnfn1_pw060419p02q156	H07	T20	apaH	diadenosine tetraphosphatase	signal transduction and regulation
tnfn1_pw060419p02q157	A08	T20	-	aldo/keto reductase family protein	putative enzymes
tnfn1_pw060419p02q158	B08	T20	hslR	heat shock protein 15 (HSP15)	translation, ribosomal structure and biogenesis
tnfn1_pw060419p02q159	C08	T20	ilvD	dihydroxy-acid dehydratase	amino acid metabolism - biosynthesis
tnfn1_pw060419p02q160	D08	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p02q161	E08	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060419p02q162	F08	T20	glgX	pullulanase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060419p02q163	G08	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p02q164	H08	T20	-	protein of unknown function	putative enzymes
tnfn1_pw060419p02q165	A09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q166	B09	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p02q167	C09	T20	-	cation diffusion facilitator (CDF) family protein	transport
tnfn1_pw060419p02q168	D09	T20	gplX	fructose 1,6-bisphosphatase II	energy metabolism
tnfn1_pw060419p02q169	E09	T20	parA	chromosome partition protein A, ATPase	cell cycle
tnfn1_pw060419p02q170	F09	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q171	G09	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p02q172	H09	T20	pilM	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060419p02q173	A10	T20	dnaJ	chaperone, DnaJ family, with C-terminal Zn finger domain	post-translational modification, protein turnover, chaperones
tnfn1_pw060419p02q174	B10	T20	bioB	biotin synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p02q175	C10	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p02q176	D10	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q177	E10	<KAN-2>	crcB	CrcB family protein	cell cycle
tnfn1_pw060419p02q178	F10	T18	-	transcriptional regulator	signal transduction and regulation
tnfn1_pw060419p02q179	G10	T18	-	ATP-binding Cassette (ABC) superfamily protein	transport
tnfn1_pw060419p02q180	H10	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p02q181	A11	T20	-	thioredoxin	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p02q182	B11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p02q183	C11	T20	cyoC	cytochrome bo terminal oxidase subunit III	energy metabolism
tnfn1_pw060419p02q184	D11	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060419p02q185	E11	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p02q186	F11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q187	G11	T20	-	transcriptional regulator, AraC family	signal transduction and regulation
tnfn1_pw060419p02q188	H11	T20	-	NAD/FAD-binding protein	putative enzymes
tnfn1_pw060419p02q189	A12	T20	potI	ATP-binding cassette putrescine uptake system, membrane protein, subunit I	transport
tnfn1_pw060419p02q190	B12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p02q191	C12	T20	-	amino acid-polyamine-organocation family protein	transport - amino-acid
tnfn1_pw060419p02q192	D12	T20	blaA	beta-lactamase class A	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p02q193	E12	T20	-	monovalent cation:proton antiporter	transport
tnfn1_pw060419p02q194	F12	T20	-	amino acid permease	transport - amino-acid
tnfn1_pw060419p02q195	G12	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p02q196	H12	T20	-	MutT/nudix family protein	putative enzymes

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_pw060419p02q101	A01	C	503452	R	FTN_0497	503304	503723	R	140	272(420)
tnfn1_pw060419p02q102	B01	C	850265	F	FTN_0792	849966	850385	R	140	121(420)
tnfn1_pw060419p02q103	C01	U	819267	R	FTN_0761	818940	820022	F	361	328(1083)
tnfn1_pw060419p02q104	D01	C	1292461	R	FTN_1221	1292193	1292858	R	222	398(666)
tnfn1_pw060419p02q105	E01	C	1330386	F	FTN_1260	1329874	1331325	F	484	513(1452)
tnfn1_pw060419p02q106	F01	C	865418	F	FTN_0808	865255	865992	R	246	575(738)
tnfn1_pw060419p02q107	G01	C	1339612	F	FTN_1267	1338966	1339724	F	253	647(759)
tnfn1_pw060419p02q108	H01	C	1093585	F	FTN_1038	1093310	1093993	F	228	276(684)
tnfn1_pw060419p02q109	A02	C	1306837	R	FTN_1238	1306482	1307129	R	216	293(648)
tnfn1_pw060419p02q110	B02	C	1540638	R	FTN_1451	1540174	1540707	R	178	70(534)
tnfn1_pw060419p02q111	C02	C	829241	R	FTN_0772	829228	829515	R	96	275(288)
tnfn1_pw060419p02q112	D02	C	1730310	F	FTN_1619	1728955	1730328	F	458	1356(1374)
tnfn1_pw060419p02q113	E02	C	598176	R	FTN_0571	597725	599131	R	469	956(1407)
tnfn1_pw060419p02q114	F02	C	151766	R	FTN_0139	151697	151867	R	57	102(171)
tnfn1_pw060419p02q115	G02	C	1621602	R	FTN_1524	1621272	1621652	R	127	51(381)
tnfn1_pw060419p02q116	H02	C	33174	R	FTN_0033	32974	33519	F	182	201(546)
tnfn1_pw060419p02q117	A03	C	494390	F	FTN_0489	494328	494654	R	109	265(327)
tnfn1_pw060419p02q118	B03	U	594701	F	FTN_0568	594002	594781	R	260	81(780)
tnfn1_pw060419p02q119	C03	C	1463140	F	FTN_1383	1463001	1463768	F	256	140(768)
tnfn1_pw060419p02q120	D03	C	1266183	R	FTN_1192	1265920	1267707	F	596	264(1788)
tnfn1_pw060419p02q121	E03	C	1616872	F	FTN_1519	1616753	1617106	R	118	235(354)
tnfn1_pw060419p02q122	F03	C	554978	F	FTN_0533	554322	555512	R	397	535(1191)
tnfn1_pw060419p02q123	G03	C	1073130	F	FTN_1013	1072741	1073913	R	391	784(1173)
tnfn1_pw060419p02q124	H03	C	1204642	R	FTN_1140	1204444	1205004	R	187	363(561)
tnfn1_pw060419p02q125	A04	C	771836	F	FTN_0716	771325	772137	F	271	512(813)
tnfn1_pw060419p02q126	B04	C	1678900	F	FTN_1581	1678701	1679195	R	165	296(495)
tnfn1_pw060419p02q127	C04	C	40469	F	FTN_0038	40369	40650	R	94	182(282)
tnfn1_pw060419p02q128	D04	C	1582413	F	FTN_1490	1581779	1582627	R	283	215(849)
tnfn1_pw060419p02q129	E04	C	785972	R	FTN_0733	785970	786260	R	97	289(291)
tnfn1_pw060419p02q130	F04	C	1000083	R	FTN_0939	1000022	1000177	R	52	95(156)
tnfn1_pw060419p02q131	G04	C	820795	F	FTN_0764	820728	821078	R	117	284(351)
tnfn1_pw060419p02q132	H04	C	1243659	F	FTN_1172	1243043	1244494	R	484	836(1452)
tnfn1_pw060419p02q133	A05	C	1454241	R	intergenic					
tnfn1_pw060419p02q134	B05	U	856623	R	FTN_0799	856317	856643	R	109	21(327)
tnfn1_pw060419p02q135	C05	C	587474	R	FTN_0560	587181	587966	F	262	294(786)
tnfn1_pw060419p02q136	D05	C	484774	R	FTN_0479	484555	485208	R	218	435(654)
tnfn1_pw060419p02q137	E05	C	1090680	F	FTN_1034	1090247	1090873	F	209	434(627)
tnfn1_pw060419p02q138	F05	C	871127	R	FTN_0814	870744	871868	R	375	742(1125)
tnfn1_pw060419p02q139	G05	C	143210	F	FTN_0130	142461	143402	F	314	750(942)
tnfn1_pw060419p02q140	H05	C	560996	R	FTN_0537	560098	561507	F	470	899(1410)
tnfn1_pw060419p02q141	A06	C	708852	R	FTN_0667	708399	709784	R	462	933(1386)
tnfn1_pw060419p02q142	B06	C	855199	R	FTN_0798	854146	856299	F	718	1054(2154)
tnfn1_pw060419p02q143	C06	C	1731709	R	-	1731290	1731751	F	154	420(462)
tnfn1_pw060419p02q144	D06	C	125168	R	FTN_0114	124591	125655	R	355	488(1065)
tnfn1_pw060419p02q145	E06	C	1202168	R	FTN_1137	1201461	1203242	R	594	1075(1782)
tnfn1_pw060419p02q146	F06	C	1563369	R	FTN_1475	1563112	1563483	R	124	115(372)
tnfn1_pw060419p02q147	G06	C	1303689	R	FTN_1235	1303554	1304012	R	153	324(459)
tnfn1_pw060419p02q148	H06	C	1029409	R	FTN_0975	1029173	1030660	F	496	237(1488)

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_pw060419p02q149	A07	C	1640370	R	FTN_1542	1640166	1640927	F	254	205(762)
tnfn1_pw060419p02q150	B07	C	102034	R	FTN_0090	101004	102545	R	514	512(1542)
tnfn1_pw060419p02q151	C07	C	1740175	R	FTN_1628	1739841	1740791	R	317	617(951)
tnfn1_pw060419p02q152	D07	C	945707	F	FTN_0888	945336	945869	F	178	372(534)
tnfn1_pw060419p02q153	E07	C	125168	R	FTN_0114	124591	125655	R	355	488(1065)
tnfn1_pw060419p02q154	F07	C	1609370	F	FTN_1512	1608678	1609847	F	390	693(1170)
tnfn1_pw060419p02q155	G07	C	611341	F	FTN_0582	611071	611742	R	224	402(672)
tnfn1_pw060419p02q156	H07	C	588521	R	FTN_0561	587981	588805	F	275	541(825)
tnfn1_pw060419p02q157	A08	C	883160	F	FTN_0825	882250	883320	R	357	161(1071)
tnfn1_pw060419p02q158	B08	C	757398	R	FTN_0712	757045	757410	R	122	13(366)
tnfn1_pw060419p02q159	C08	C	1101498	R	FTN_1043	1100825	1102504	R	560	1007(1680)
tnfn1_pw060419p02q160	D08	C	151535	F	FTN_0138	151080	151694	F	205	456(615)
tnfn1_pw060419p02q161	E08	C	1080661	F	FTN_1023	1080187	1080771	R	195	111(585)
tnfn1_pw060419p02q162	F08	C	526882	F	FTN_0512	524688	527897	R	1070	1016(3210)
tnfn1_pw060419p02q163	G08	C	742320	R	FTN_0699	742065	743228	F	388	256(1164)
tnfn1_pw060419p02q164	H08	C	56117	R	FTN_0047	53754	57527	F	1258	2364(3774)
tnfn1_pw060419p02q165	A09	C	226963	R	FTN_0206	226642	227115	F	158	322(474)
tnfn1_pw060419p02q166	B09	C	776453	F	FTN_0721	776068	777051	R	328	599(984)
tnfn1_pw060419p02q167	C09	C	409379	R	FTN_0411	409260	410144	F	295	120(885)
tnfn1_pw060419p02q168	D09	C	306092	F	FTN_0298	305744	306727	F	328	349(984)
tnfn1_pw060419p02q169	E09	C	432337	R	FTN_0433	432195	432833	F	213	143(639)
tnfn1_pw060419p02q170	F09	C	1075375	R	FTN_1016	1075256	1075756	R	167	382(501)
tnfn1_pw060419p02q171	G09	C	916635	F	FTN_0862	916124	917245	F	374	512(1122)
tnfn1_pw060419p02q172	H09	C	1205829	R	FTN_1141	1205009	1206010	R	334	182(1002)
tnfn1_pw060419p02q173	A10	C	1355503	R	FTN_1283	1354992	1356176	R	395	674(1185)
tnfn1_pw060419p02q174	B10	U	872735	F	FTN_0815	871865	872803	R	313	69(939)
tnfn1_pw060419p02q175	C10	C	1483970	R	FTN_1406	1483913	1484686	R	258	717(774)
tnfn1_pw060419p02q176	D10	C	1242403	R	FTN_1171	1242057	1243040	R	328	638(984)
tnfn1_pw060419p02q177	E10	C	150379	F	FTN_0136	150192	150533	F	114	188(342)
tnfn1_pw060419p02q178	F10	C	905906	F	FTN_0850	905800	906207	F	136	107(408)
tnfn1_pw060419p02q179	G10	C	1339499	F	FTN_1267	1338966	1339724	F	253	534(759)
tnfn1_pw060419p02q180	H10	U	722093	R	FTN_0678	721383	722594	R	404	502(1212)
tnfn1_pw060419p02q181	A11	C	911349	F	FTN_0856	911269	911592	F	108	81(324)
tnfn1_pw060419p02q182	B11	C	150533	R	FTN_0137	150533	150937	F	135	1(405)
tnfn1_pw060419p02q183	C11	C	219946	F	FTN_0197	219561	220160	F	200	386(600)
tnfn1_pw060419p02q184	D11	C	812591	F	FTN_0757	810052	814938	F	1629	2540(4887)
tnfn1_pw060419p02q185	E11	C	721792	R	FTN_0678	721383	722594	R	404	803(1212)
tnfn1_pw060419p02q186	F11	C	620810	R	FTN_0590	620283	621500	F	406	528(1218)
tnfn1_pw060419p02q187	G11	C	1346376	F	FTN_1274	1346150	1346974	R	275	599(825)
tnfn1_pw060419p02q188	H11	C	1543541	R	FTN_1454	1542637	1543887	F	417	905(1251)
tnfn1_pw060419p02q189	A12	C	791119	R	FTN_0737	790573	791376	R	268	258(804)
tnfn1_pw060419p02q190	B12	C	1233985	F	FTN_1162	1233942	1234244	R	101	260(303)
tnfn1_pw060419p02q191	C12	C	1620586	R	FTN_1523	1620541	1621251	F	237	46(711)
tnfn1_pw060419p02q192	D12	C	1062425	F	FTN_1002	1062223	1063104	F	294	203(882)
tnfn1_pw060419p02q193	E12	U	157391	F	FTN_0143	156853	158736	F	628	539(1884)
tnfn1_pw060419p02q194	F12	U	955149	R	FTN_0898	954503	956044	R	514	896(1542)
tnfn1_pw060419p02q195	G12	C	323132	F	FTN_0312	322772	323959	F	396	361(1188)
tnfn1_pw060419p02q196	H12	C	241468	R	FTN_0219	241266	241640	F	125	203(375)

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_pw060419p02q101	A01	EXACT(0)	156	142	103	26	EXACT(0)	200	176	47
tnfn1_pw060419p02q102	B01	EXACT(0)	156	145	113	30	EXACT(0)	200	164	42
tnfn1_pw060419p02q103	C01	EXACT(0)	125	119	105	37	EXACT(0)	158	102	33
tnfn1_pw060419p02q104	D01	EXACT(0)	156	151	118	37	EXACT(0)	200	191	56
tnfn1_pw060419p02q105	E01	EXACT(0)	155	153	123	37	EXACT(0)	200	192	55
tnfn1_pw060419p02q106	F01	EXACT(0)	156	145	140	44	EXACT(0)	200	182	57
tnfn1_pw060419p02q107	G01	EXACT(0)	161	150	136	34	EXACT(0)	200	184	56
tnfn1_pw060419p02q108	H01	EXACT(0)	156	145	128	47	EXACT(0)	200	146	48
tnfn1_pw060419p02q109	A02	EXACT(0)	117	119	87	38	EXACT(0)	200	177	48
tnfn1_pw060419p02q110	B02	EXACT(0)	118	107	82	23	EXACT(0)	200	192	52
tnfn1_pw060419p02q111	C02	EXACT(0)	117	111	89	33	EXACT(0)	200	195	46
tnfn1_pw060419p02q112	D02	EXACT(0)	119	112	85	32	EXACT(0)	200	193	48
tnfn1_pw060419p02q113	E02	EXACT(0)	121	119	104	38	EXACT(0)	200	190	62
tnfn1_pw060419p02q114	F02	EXACT(0)	116	112	97	37	EXACT(0)	200	182	59
tnfn1_pw060419p02q115	G02	EXACT(0)	117	107	90	36	EXACT(0)	200	187	36
tnfn1_pw060419p02q116	H02	EXACT(0)	123	112	94	27	EXACT(0)	200	176	48
tnfn1_pw060419p02q117	A03	EXACT(0)	123	120	69	23	EXACT(0)	200	185	54
tnfn1_pw060419p02q118	B03	EXACT(0)	122	112	85	22	EXACT(0)	200	180	54
tnfn1_pw060419p02q119	C03	EXACT(0)	124	117	101	28	EXACT(0)	200	194	57
tnfn1_pw060419p02q120	D03	EXACT(0)	125	119	105	28	EXACT(0)	200	144	30
tnfn1_pw060419p02q121	E03	EXACT(0)	123	120	104	35	EXACT(0)	200	175	50
tnfn1_pw060419p02q122	F03	EXACT(0)	125	120	115	37	EXACT(0)	200	186	54
tnfn1_pw060419p02q123	G03	EXACT(0)	125	115	109	31	EXACT(0)	200	172	48
tnfn1_pw060419p02q124	H03	EXACT(0)	122	112	90	26	EXACT(0)	200	182	55
tnfn1_pw060419p02q125	A04	EXACT(0)	124	119	103	34	EXACT(0)	200	186	51
tnfn1_pw060419p02q126	B04	EXACT(0)	125	120	106	39	EXACT(0)	84	77	51
tnfn1_pw060419p02q127	C04	EXACT(0)	121	112	90	29	EXACT(0)	200	172	53
tnfn1_pw060419p02q128	D04	EXACT(0)	122	120	99	38	EXACT(0)	199	150	45
tnfn1_pw060419p02q129	E04	EXACT(0)	122	119	92	29	EXACT(0)	200	170	58
tnfn1_pw060419p02q130	F04	ADJUSTED(1)	122	111	58	21	ESTIMATE(56)	143	72	24
tnfn1_pw060419p02q131	G04	EXACT(0)	125	120	94	23	EXACT(0)	200	180	43
tnfn1_pw060419p02q132	H04	EXACT(0)	124	112	81	22	EXACT(0)	200	194	54
tnfn1_pw060419p02q133	A05	EXACT(0)	121	120	86	25	EXACT(0)	200	158	37
tnfn1_pw060419p02q134	B05	EXACT(0)	156	138	117	26	EXACT(0)	200	185	32
tnfn1_pw060419p02q135	C05	EXACT(0)	156	145	137	41	EXACT(0)	170	159	51
tnfn1_pw060419p02q136	D05	EXACT(0)	156	145	134	41	EXACT(0)	200	178	65
tnfn1_pw060419p02q137	E05	EXACT(0)	158	153	139	40	EXACT(0)	200	165	43
tnfn1_pw060419p02q138	F05	EXACT(0)	158	152	128	36	EXACT(0)	200	184	55
tnfn1_pw060419p02q139	G05	EXACT(0)	159	153	119	30	EXACT(0)	200	187	55
tnfn1_pw060419p02q140	H05	EXACT(0)	155	145	126	38	EXACT(0)	200	180	57
tnfn1_pw060419p02q141	A06	EXACT(0)	158	153	127	30	EXACT(0)	200	183	53
tnfn1_pw060419p02q142	B06	EXACT(0)	157	153	126	31	EXACT(0)	200	191	59
tnfn1_pw060419p02q143	C06	EXACT(0)	157	145	132	34	EXACT(0)	200	171	60
tnfn1_pw060419p02q144	D06	EXACT(0)	157	153	124	25	EXACT(0)	200	189	48
tnfn1_pw060419p02q145	E06	EXACT(0)	156	153	135	40	EXACT(0)	200	198	53
tnfn1_pw060419p02q146	F06	EXACT(0)	157	145	139	44	ESTIMATE(48)	152	122	25
tnfn1_pw060419p02q147	G06	EXACT(0)	156	152	128	34	EXACT(0)	200	174	58
tnfn1_pw060419p02q148	H06	EXACT(0)	158	145	133	48	EXACT(0)	200	179	56

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_pw060419p02q149	A07	EXACT(0)	119	111	84	26	EXACT(0)	200	180	52
tnfn1_pw060419p02q150	B07	EXACT(0)	156	153	130	37	EXACT(0)	200	184	45
tnfn1_pw060419p02q151	C07	EXACT(0)	158	152	138	39	EXACT(0)	200	188	58
tnfn1_pw060419p02q152	D07	EXACT(0)	156	151	130	38	EXACT(0)	200	189	55
tnfn1_pw060419p02q153	E07	EXACT(0)	158	153	123	32	EXACT(0)	200	189	54
tnfn1_pw060419p02q154	F07	EXACT(0)	155	152	131	40	EXACT(0)	201	99	23
tnfn1_pw060419p02q155	G07	EXACT(0)	156	142	70	16	EXACT(0)	200	187	50
tnfn1_pw060419p02q156	H07	EXACT(0)	158	152	125	33	EXACT(0)	200	189	53
tnfn1_pw060419p02q157	A08	EXACT(0)	156	152	121	33	EXACT(0)	200	188	58
tnfn1_pw060419p02q158	B08	EXACT(0)	157	152	133	37	EXACT(0)	200	159	39
tnfn1_pw060419p02q159	C08	EXACT(0)	157	153	127	34	EXACT(0)	200	193	54
tnfn1_pw060419p02q160	D08	EXACT(0)	158	153	134	37	ESTIMATE(2)	198	182	60
tnfn1_pw060419p02q161	E08	EXACT(0)	157	145	129	49	EXACT(0)	200	160	27
tnfn1_pw060419p02q162	F08	EXACT(0)	158	153	132	32	EXACT(0)	197	184	52
tnfn1_pw060419p02q163	G08	EXACT(0)	156	153	132	44	EXACT(0)	201	169	39
tnfn1_pw060419p02q164	H08	EXACT(0)	159	152	146	38	EXACT(0)	193	176	55
tnfn1_pw060419p02q165	A09	EXACT(0)	155	116	57	16	EXACT(0)	200	186	51
tnfn1_pw060419p02q166	B09	EXACT(0)	157	152	130	33	EXACT(0)	200	174	47
tnfn1_pw060419p02q167	C09	EXACT(0)	157	145	83	15	EXACT(0)	200	175	50
tnfn1_pw060419p02q168	D09	EXACT(0)	158	153	141	38	EXACT(0)	200	194	53
tnfn1_pw060419p02q169	E09	EXACT(0)	156	145	112	28	EXACT(0)	200	186	49
tnfn1_pw060419p02q170	F09	EXACT(0)	155	150	126	38	EXACT(0)	99	97	36
tnfn1_pw060419p02q171	G09	EXACT(0)	157	145	136	40	EXACT(0)	200	182	55
tnfn1_pw060419p02q172	H09	EXACT(0)	162	152	125	38	EXACT(0)	200	187	47
tnfn1_pw060419p02q173	A10	EXACT(0)	159	151	138	32	EXACT(0)	200	188	50
tnfn1_pw060419p02q174	B10	EXACT(0)	158	153	142	40	EXACT(0)	200	175	35
tnfn1_pw060419p02q175	C10	EXACT(0)	156	144	107	26	EXACT(0)	200	177	56
tnfn1_pw060419p02q176	D10	EXACT(0)	121	120	75	23	EXACT(0)	200	189	49
tnfn1_pw060419p02q177	E10	EXACT(0)	116	112	92	31	EXACT(0)	196	161	24
tnfn1_pw060419p02q178	F10	EXACT(0)	121	106	88	31	EXACT(0)	199	143	35
tnfn1_pw060419p02q179	G10	EXACT(0)	123	106	92	27	EXACT(0)	200	190	48
tnfn1_pw060419p02q180	H10	NONE	0	0	0	18	ESTIMATE(146)	216	135	21
tnfn1_pw060419p02q181	A11	EXACT(0)	155	114	96	30	EXACT(0)	200	190	43
tnfn1_pw060419p02q182	B11	EXACT(0)	158	145	131	36	EXACT(0)	200	184	49
tnfn1_pw060419p02q183	C11	EXACT(0)	159	145	132	39	EXACT(0)	200	190	53
tnfn1_pw060419p02q184	D11	EXACT(0)	158	144	131	39	EXACT(0)	200	192	56
tnfn1_pw060419p02q185	E11	EXACT(0)	157	152	123	31	EXACT(0)	200	187	57
tnfn1_pw060419p02q186	F11	EXACT(0)	156	145	134	49	EXACT(0)	200	161	51
tnfn1_pw060419p02q187	G11	EXACT(0)	157	152	144	50	EXACT(0)	200	198	58
tnfn1_pw060419p02q188	H11	EXACT(0)	156	153	121	35	EXACT(0)	200	189	60
tnfn1_pw060419p02q189	A12	EXACT(0)	155	145	95	29	EXACT(0)	200	193	55
tnfn1_pw060419p02q190	B12	EXACT(0)	158	145	135	52	EXACT(0)	197	175	52
tnfn1_pw060419p02q191	C12	EXACT(0)	159	153	134	32	EXACT(0)	200	180	56
tnfn1_pw060419p02q192	D12	EXACT(0)	157	145	82	18	EXACT(0)	200	186	53
tnfn1_pw060419p02q193	E12	EXACT(0)	156	145	131	44	EXACT(0)	200	180	51
tnfn1_pw060419p02q194	F12	EXACT(0)	157	145	133	44	EXACT(0)	200	186	65
tnfn1_pw060419p02q195	G12	EXACT(0)	155	114	85	22	EXACT(0)	200	193	48
tnfn1_pw060419p02q196	H12	EXACT(0)	157	145	136	43	EXACT(0)	200	187	39