

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 24 (tnfn1_pw060419p04)**

Catalog No. NR-8058

For research use only. Not for human use.

Contributor:

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University of Washington, Seattle, Washington

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-8058 represents Plate 24 (tnfn1_pw060419p04) 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-8058 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 24 (tnfn1_pw060419p04), NR-8058.”

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_pw060419p04q101	A01	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p04q102	B01	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060419p04q103	C01	T20	-	manganese/Zinc/Iron chelate uptake transporter family protein	transport
tnfn1_pw060419p04q104	D01	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p04q105	E01	T20	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060419p04q106	F01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q107	G01	T20	-	histidine acid phosphatase	putative enzymes
tnfn1_pw060419p04q108	H01	T20	pdpD	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q109	A02	T20	-	sugar:cation symporter family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060419p04q110	B02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q111	C02	T20	trxB	thioredoxin reductase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q112	D02	T20	pilD	Type IV pili leader peptidase and methylase	motility, attachment and secretion structure
tnfn1_pw060419p04q113	E02	T20	-	arsenate reductase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q114	F02	T20	-	drug/metabolite exporter	transport - drugs / antibacterial compounds
tnfn1_pw060419p04q115	G02	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p04q116	H02	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060419p04q117	A03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p04q118	B03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q119	C03	T20	-	RmuC family protein	putative enzymes
tnfn1_pw060419p04q120	D03	T20	pilV	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060419p04q121	E03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p04q122	F03	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060419p04q123	G03	T20	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	cell wall / LPS / capsule
tnfn1_pw060419p04q124	H03	T20	-	-	-
tnfn1_pw060419p04q125	A04	T20	hflX	protease, GTP-binding subunit	putative enzymes
tnfn1_pw060419p04q126	B04	T20	lysP	lysine:H ⁺ symporter	transport - amino-acid
tnfn1_pw060419p04q127	C04	<KAN-2>	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p04q128	D04	T18	rnd	ribonuclease D	translation, ribosomal structure and biogenesis
tnfn1_pw060419p04q129	E04	<KAN-2>	mgIA	macrophage growth locus, protein A	signal transduction and regulation
tnfn1_pw060419p04q130	F04	<KAN-2>	glpK	glycerol kinase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p04q131	G04	T18	chiB	chitinase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060419p04q132	H04	<KAN-2>	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060419p04q133	A05	T20	lysP	lysine:H ⁺ symporter	transport - amino-acid
tnfn1_pw060419p04q134	B05	<KAN-2>	-	FKBP-type peptidyl-prolyl cis-trans isomerase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p04q135	C05	<KAN-2>	-	thioredoxin	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q136	D05	<KAN-2>	deoC	deoxyribose-phosphate aldolase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p04q137	E05	<KAN-2>	proQ	activator of osmoprotectant transporter ProP	signal transduction and regulation
tnfn1_pw060419p04q138	F05	<KAN-2>	ispA	geranyl diphosphate synthase/farnesyl diphosphate synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q139	G05	<KAN-2>	-	rhodanese-like family protein	putative enzymes
tnfn1_pw060419p04q140	H05	<KAN-2>	-	two-component response regulator	signal transduction and regulation
tnfn1_pw060419p04q141	A06	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p04q142	B06	<KAN-2>	galP1	galactose-proton symporter, major facilitator superfamily (MFS) transport protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060419p04q143	C06	T18	ubiC	chorismate pyruvate lyase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q144	D06	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q145	E06	T18	-	isomerase	putative enzymes
tnfn1_pw060419p04q146	F06	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060419p04q147	G06	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q148	H06	T18	-	-	-

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060419p04q149	A07	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060419p04q150	B07	T18	-	metabolite:H ⁺ symporter (MHS) family protein	transport
tnfn1_pw060419p04q151	C07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q152	D07	T20	-	pseudogene: DNA-3-methyladenine glycosylase	pseudogene
tnfn1_pw060419p04q153	E07	T20	-	protein-disulfide isomerase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p04q154	F07	T20	sohB	peptidase family S49 protein	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p04q155	G07	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060419p04q156	H07	T20	pta	phosphate acetyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060419p04q157	A08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q158	B08	T20	wbtQ	aminotransferase	putative enzymes
tnfn1_pw060419p04q159	C08	T20	-	sulfate permease family protein	transport
tnfn1_pw060419p04q160	D08	T20	paaY	carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	putative enzymes
tnfn1_pw060419p04q161	E08	T20	uspA	universal stress protein	signal transduction and regulation
tnfn1_pw060419p04q162	F08	T20	fadD	long chain fatty acid CoA ligase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060419p04q163	G08	T20	gdhA	glutamate dehydrogenase (NADP ⁺)	amino acid metabolism - biosynthesis
tnfn1_pw060419p04q164	H08	T20	nadA	quinolinate sythetase A	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q165	A09	T20	-		
tnfn1_pw060419p04q166	B09	T20	-	cardiolipin synthase	fatty acids and lipids metabolism
tnfn1_pw060419p04q167	C09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060419p04q168	D09	T20	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	amino acid metabolism - biosynthesis
tnfn1_pw060419p04q169	E09	T20	-	protein of unknown function with radical SAM domain (putative) drug resistance ATPase-1 (Drug RA1) family protein	unknown function - conserved
tnfn1_pw060419p04q170	F09	T20	-		transport - drugs / antibacterial compounds
tnfn1_pw060419p04q171	G09	T20	-	choloylglycine hydrolase family protein	cell wall / LPS / capsule
tnfn1_pw060419p04q172	H09	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060419p04q173	A10	T20	-	membrane protein of unknown function	unknown function - conserved
tnfn1_pw060419p04q174	B10	T20	accD	acetyl-CoA carboxylase, carboxytransferase subunit beta	fatty acids and lipids metabolism
tnfn1_pw060419p04q175	C10	T20	-	peroxiredoxin of the AhpC/TSA family	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q176	D10	T20	dapA	dihydrodipicolinate synthase	amino acid metabolism - biosynthesis
tnfn1_pw060419p04q177	E10	T20	-	outer membrane protein of unknown function	unknown function - novel
tnfn1_pw060419p04q178	F10	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p04q179	G10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q180	H10	T20	frgA	siderophore biosynthesis protein	other metabolism - biosynthesis
tnfn1_pw060419p04q181	A11	T20	-	thioredoxin	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q182	B11	T20	kdpC	potassium-transporting ATPase C chain	transport
tnfn1_pw060419p04q183	C11	T20	-	BoIa family protein	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060419p04q184	D11	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060419p04q185	E11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q186	F11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q187	G11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q188	H11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q189	A12	<KAN-2>	-		
tnfn1_pw060419p04q190	B12	<KAN-2>	-	LemA-like protein	putative enzymes
tnfn1_pw060419p04q191	C12	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060419p04q192	D12	<KAN-2>	wbtD	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060419p04q193	E12	<KAN-2>	mgIB	macrophage growth locus, subunit B	unknown function - conserved
tnfn1_pw060419p04q194	F12	<KAN-2>	-	protein-disulfide isomerase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060419p04q195	G12	<KAN-2>	secB1	preprotein translocase, subunit B	motility, attachment and secretion structure
tnfn1_pw060419p04q196	H12	T20	ansA	L-asparaginase	amino acid metabolism - degradation, utilization, assimilation

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_pw060419p04q101	A01	C	886669	R	FTN_0829	886126	886842	R	239	174(717)
tnfn1_pw060419p04q102	B01	C	1191850	F	FTN_1129	1191487	1192668	R	394	819(1182)
tnfn1_pw060419p04q103	C01	C	200456	R	FTN_0183	200205	201119	R	305	664(915)
tnfn1_pw060419p04q104	D01	C	64441	F	FTN_0054	64387	64764	F	126	55(378)
tnfn1_pw060419p04q105	E01	C	1798247	F	FTN_1683	1798000	1799259	F	420	248(1260)
tnfn1_pw060419p04q106	F01	C	1739481	R	FTN_1627	1739330	1739779	R	150	299(450)
tnfn1_pw060419p04q107	G01	C	23045	F	FTN_0022	22992	24044	F	351	54(1053)
tnfn1_pw060419p04q108	H01	C	1401137	F	FTN_1325	1399806	1403540	R	1245	2404(3735)
tnfn1_pw060419p04q109	A02	C	966741	R	FTN_0910	965706	967175	F	490	1036(1470)
tnfn1_pw060419p04q110	B02	C	58018	F	FTN_0048	57540	58757	F	406	479(1218)
tnfn1_pw060419p04q111	C02	C	609531	F	FTN_0580	608770	609717	R	316	187(948)
tnfn1_pw060419p04q112	D02	C	1060951	R	FTN_1000	1060511	1061356	F	282	441(846)
tnfn1_pw060419p04q113	E02	C	1520600	R	FTN_1435	1520404	1520820	R	139	221(417)
tnfn1_pw060419p04q114	F02	C	1445274	R	FTN_1361	1444600	1445466	F	289	675(867)
tnfn1_pw060419p04q115	G02	C	385135	F	FTN_0384	385020	385376	R	119	242(357)
tnfn1_pw060419p04q116	H02	C	294934	R	FTN_0287	294845	295609	F	255	90(765)
tnfn1_pw060419p04q117	A03	U	1226654	F	FTN_1156	1225105	1226655	R	517	2(1551)
tnfn1_pw060419p04q118	B03	U	1244065	F	FTN_1172	1243043	1244494	R	484	430(1452)
tnfn1_pw060419p04q119	C03	C	1081459	R	FTN_1024	1080823	1082235	R	471	777(1413)
tnfn1_pw060419p04q120	D03	C	412510	R	FTN_0413	412120	413349	R	410	840(1230)
tnfn1_pw060419p04q121	E03	C	1165837	F	FTN_1104	1165522	1166067	R	182	231(546)
tnfn1_pw060419p04q122	F03	C	1547449	R	FTN_1459	1546995	1547735	F	247	455(741)
tnfn1_pw060419p04q123	G03	C	551801	F	FTN_0530	551516	552883	F	456	286(1368)
tnfn1_pw060419p04q124	H03	C	843488	R	intergenic					
tnfn1_pw060419p04q125	A04	C	1109382	R	FTN_1050	1108915	1110222	R	436	841(1308)
tnfn1_pw060419p04q126	B04	U	303826	F	FTN_0296	303623	305074	F	484	204(1452)
tnfn1_pw060419p04q127	C04	C	1421246	F	FTN_1342	1421108	1421389	F	94	139(282)
tnfn1_pw060419p04q128	D04	C	723244	R	FTN_0679	722626	723717	R	364	474(1092)
tnfn1_pw060419p04q129	E04	C	1362432	F	FTN_1290	1362282	1362896	F	205	151(615)
tnfn1_pw060419p04q130	F04	C	1682915	R	FTN_1585	1682448	1683947	R	500	1033(1500)
tnfn1_pw060419p04q131	G04	C	1874076	R	FTN_1744	1873074	1875263	F	730	1003(2190)
tnfn1_pw060419p04q132	H04	C	1354933	F	FTN_1282	1354079	1354972	F	298	855(894)
tnfn1_pw060419p04q133	A05	C	304552	F	FTN_0296	303623	305074	F	484	930(1452)
tnfn1_pw060419p04q134	B05	U	978521	F	FTN_0921	978489	979337	F	283	33(849)
tnfn1_pw060419p04q135	C05	C	1492424	F	FTN_1415	1492329	1492649	F	107	96(321)
tnfn1_pw060419p04q136	D05	C	1703014	R	FTN_1601	1702300	1703058	R	253	45(759)
tnfn1_pw060419p04q137	E05	C	296447	F	FTN_0289	296016	296714	F	233	432(699)
tnfn1_pw060419p04q138	F05	C	1559272	F	FTN_1470	1558719	1559597	F	293	554(879)
tnfn1_pw060419p04q139	G05	C	1171603	F	FTN_1109	1171158	1171904	F	249	446(747)
tnfn1_pw060419p04q140	H05	C	1553520	R	FTN_1465	1553361	1554044	R	228	525(684)
tnfn1_pw060419p04q141	A06	C	1183089	R	FTN_1118	1182986	1183318	R	111	230(333)
tnfn1_pw060419p04q142	B06	C	731294	F	FTN_0687	730344	731723	F	460	951(1380)
tnfn1_pw060419p04q143	C06	C	386538	F	FTN_0386	386250	386753	R	168	216(504)
tnfn1_pw060419p04q144	D06	C	425547	R	FTN_0426	425491	425859	F	123	57(369)
tnfn1_pw060419p04q145	E06	C	959043	F	FTN_0901	958727	959317	R	197	275(591)
tnfn1_pw060419p04q146	F06	C	1015700	R	FTN_0961	1015544	1015813	R	90	114(270)
tnfn1_pw060419p04q147	G06	C	339084	F	FTN_0334	339054	339395	R	114	312(342)
tnfn1_pw060419p04q148	H06	C	541619	F	intergenic					

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_pw060419p04q149	A07	C	1596731	R	FTN_1502	1596730	1597764	R	345	1034(1035)
tnfn1_pw060419p04q150	B07	C	3268	R	FTN_0003	2794	4044	R	417	777(1251)
tnfn1_pw060419p04q151	C07	C	1327696	R	FTN_1258	1327694	1328239	R	182	544(546)
tnfn1_pw060419p04q152	D07	C	1076030	R	FTN_1017	1075884	1076462	F	193	147(579)
tnfn1_pw060419p04q153	E07	C	629305	R	FTN_0597	628731	629495	F	255	575(765)
tnfn1_pw060419p04q154	F07	C	575961	R	FTN_0550	575484	576497	F	338	478(1014)
tnfn1_pw060419p04q155	G07	C	1766867	F	FTN_1654	1766782	1768083	F	434	86(1302)
tnfn1_pw060419p04q156	H07	C	137539	R	FTN_0126	135582	137675	F	698	1958(2094)
tnfn1_pw060419p04q157	A08	C	915351	R	FTN_0861	914550	915788	F	413	802(1239)
tnfn1_pw060419p04q158	B08	C	1510355	R	FTN_1430	1509879	1510991	R	371	637(1113)
tnfn1_pw060419p04q159	C08	C	675054	R	FTN_0638	674546	676087	F	514	509(1542)
tnfn1_pw060419p04q160	D08	C	158978	R	FTN_0144	158724	159260	F	179	259(537)
tnfn1_pw060419p04q161	E08	C	96774	F	FTN_0085	96649	97482	F	278	126(834)
tnfn1_pw060419p04q162	F08	C	1520966	F	FTN_1436	1520964	1522649	F	562	3(1686)
tnfn1_pw060419p04q163	G08	C	1630099	R	FTN_1532	1629170	1630516	F	449	930(1347)
tnfn1_pw060419p04q164	H08	C	736163	F	FTN_0692	736009	737031	F	341	155(1023)
tnfn1_pw060419p04q165	A09	C	485399	F	intergenic					
tnfn1_pw060419p04q166	B09	C	931420	R	FTN_0876	930215	931639	F	475	1206(1425)
tnfn1_pw060419p04q167	C09	C	651528	F	FTN_0620	651130	652365	F	412	399(1236)
tnfn1_pw060419p04q168	D09	C	1152939	F	FTN_1091	1152249	1153523	R	425	585(1275)
tnfn1_pw060419p04q169	E09	C	818982	F	FTN_0761	818940	820022	F	361	43(1083)
tnfn1_pw060419p04q170	F09	C	1891477	R	FTN_1762	1890747	1892423	R	559	947(1677)
tnfn1_pw060419p04q171	G09	C	1321202	F	FTN_1252	1320488	1321630	F	381	715(1143)
tnfn1_pw060419p04q172	H09	U	811390	R	FTN_0757	810052	814938	F	1629	1339(4887)
tnfn1_pw060419p04q173	A10	C	920830	F	FTN_0868	920419	920994	F	192	412(576)
tnfn1_pw060419p04q174	B10	U	280786	R	FTN_0272	279916	280815	F	300	871(900)
tnfn1_pw060419p04q175	C10	C	1028036	R	FTN_0973	1027802	1028398	R	199	363(597)
tnfn1_pw060419p04q176	D10	C	1856115	F	FTN_1728	1855928	1856812	R	295	698(885)
tnfn1_pw060419p04q177	E10	C	626271	F	FTN_0595	625825	627738	F	638	447(1914)
tnfn1_pw060419p04q178	F10	C	29270	F	FTN_0028	28714	29763	R	350	494(1050)
tnfn1_pw060419p04q179	G10	C	1061815	F	FTN_1001	1061369	1062211	F	281	447(843)
tnfn1_pw060419p04q180	H10	C	1796199	R	FTN_1682	1796074	1797990	F	639	126(1917)
tnfn1_pw060419p04q181	A11	C	1492477	F	FTN_1415	1492329	1492649	F	107	149(321)
tnfn1_pw060419p04q182	B11	C	1841887	F	FTN_1716	1841389	1841940	R	184	54(552)
tnfn1_pw060419p04q183	C11	C	1308016	R	FTN_1240	1308006	1308269	F	88	11(264)
tnfn1_pw060419p04q184	D11	U	1639403	R	FTN_1540	1639091	1639522	F	144	313(432)
tnfn1_pw060419p04q185	E11	C	1726222	F	FTN_1616	1725345	1726298	R	318	77(954)
tnfn1_pw060419p04q186	F11	C	798709	R	FTN_0745	798391	799095	F	235	319(705)
tnfn1_pw060419p04q187	G11	C	833605	R	FTN_0777	833560	834003	R	148	399(444)
tnfn1_pw060419p04q188	H11	U	982571	F	FTN_0925	982223	983200	R	326	630(978)
tnfn1_pw060419p04q189	A12	U	107070	F	intergenic					
tnfn1_pw060419p04q190	B12	C	390641	R	FTN_0391	390170	390742	R	191	102(573)
tnfn1_pw060419p04q191	C12	C	88383	R	FTN_0077	87966	88421	R	152	39(456)
tnfn1_pw060419p04q192	D12	U	1508034	R	FTN_1427	1507571	1508659	R	363	626(1089)
tnfn1_pw060419p04q193	E12	C	1363092	F	FTN_1291	1362901	1363305	F	135	192(405)
tnfn1_pw060419p04q194	F12	C	828239	R	FTN_0771	828086	829204	R	373	966(1119)
tnfn1_pw060419p04q195	G12	C	131881	F	FTN_0121	131668	132114	F	149	214(447)
tnfn1_pw060419p04q196	H12	C	1151137	F	FTN_1088	1150184	1151218	R	345	82(1035)

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_pw060419p04q101	A01	EXACT(0)	156	146	121	41	EXACT(0)	197	192	49
tnfn1_pw060419p04q102	B01	EXACT(0)	158	151	137	37	EXACT(0)	201	116	42
tnfn1_pw060419p04q103	C01	EXACT(0)	158	153	129	31	EXACT(0)	200	190	57
tnfn1_pw060419p04q104	D01	EXACT(0)	154	152	134	41	EXACT(0)	200	133	25
tnfn1_pw060419p04q105	E01	EXACT(0)	156	101	100	34	EXACT(0)	200	145	25
tnfn1_pw060419p04q106	F01	EXACT(0)	157	151	135	36	EXACT(0)	200	182	48
tnfn1_pw060419p04q107	G01	EXACT(0)	154	146	127	45	EXACT(0)	200	194	50
tnfn1_pw060419p04q108	H01	EXACT(0)	156	145	130	48	EXACT(0)	200	190	67
tnfn1_pw060419p04q109	A02	EXACT(0)	158	150	139	44	EXACT(0)	196	187	59
tnfn1_pw060419p04q110	B02	EXACT(0)	156	152	136	41	EXACT(0)	126	117	50
tnfn1_pw060419p04q111	C02	EXACT(0)	155	145	125	45	EXACT(0)	200	162	39
tnfn1_pw060419p04q112	D02	EXACT(0)	157	145	139	39	EXACT(0)	201	98	43
tnfn1_pw060419p04q113	E02	EXACT(0)	158	153	142	48	EXACT(0)	200	129	47
tnfn1_pw060419p04q114	F02	EXACT(0)	158	153	132	29	EXACT(0)	200	183	57
tnfn1_pw060419p04q115	G02	EXACT(0)	156	153	123	33	EXACT(0)	173	160	54
tnfn1_pw060419p04q116	H02	EXACT(0)	154	145	112	34	ESTIMATE(80)	120	63	21
tnfn1_pw060419p04q117	A03	EXACT(0)	158	157	144	40	ESTIMATE(95)	105	85	24
tnfn1_pw060419p04q118	B03	EXACT(0)	156	145	134	48	EXACT(0)	200	191	66
tnfn1_pw060419p04q119	C03	EXACT(0)	156	145	131	37	EXACT(0)	200	171	48
tnfn1_pw060419p04q120	D03	EXACT(0)	157	145	139	46	EXACT(0)	200	194	58
tnfn1_pw060419p04q121	E03	EXACT(0)	153	145	127	47	EXACT(0)	165	146	38
tnfn1_pw060419p04q122	F03	EXACT(0)	157	153	134	41	EXACT(0)	200	186	49
tnfn1_pw060419p04q123	G03	EXACT(0)	157	153	134	40	EXACT(0)	108	101	53
tnfn1_pw060419p04q124	H03	EXACT(0)	155	152	131	40	EXACT(0)	158	132	57
tnfn1_pw060419p04q125	A04	EXACT(0)	155	145	123	41	EXACT(0)	200	126	34
tnfn1_pw060419p04q126	B04	EXACT(0)	158	153	134	44	EXACT(0)	200	187	59
tnfn1_pw060419p04q127	C04	EXACT(0)	122	120	92	24	EXACT(0)	200	192	54
tnfn1_pw060419p04q128	D04	EXACT(0)	123	112	95	29	EXACT(0)	201	119	38
tnfn1_pw060419p04q129	E04	NONE	0	0	0	15	ESTIMATE(119)	218	69	11
tnfn1_pw060419p04q130	F04	EXACT(0)	117	112	97	42	EXACT(0)	200	195	62
tnfn1_pw060419p04q131	G04	EXACT(0)	124	115	101	26	EXACT(0)	200	188	41
tnfn1_pw060419p04q132	H04	EXACT(0)	116	112	97	37	EXACT(0)	200	185	47
tnfn1_pw060419p04q133	A05	EXACT(0)	157	153	125	38	EXACT(0)	183	178	54
tnfn1_pw060419p04q134	B05	EXACT(0)	116	112	92	36	EXACT(0)	200	190	45
tnfn1_pw060419p04q135	C05	EXACT(0)	122	122	95	23	EXACT(0)	201	123	33
tnfn1_pw060419p04q136	D05	EXACT(0)	121	112	70	23	EXACT(0)	200	192	46
tnfn1_pw060419p04q137	E05	EXACT(0)	116	103	98	46	EXACT(0)	200	196	67
tnfn1_pw060419p04q138	F05	EXACT(0)	118	85	85	39	EXACT(0)	200	180	23
tnfn1_pw060419p04q139	G05	EXACT(0)	118	112	102	38	EXACT(0)	200	158	49
tnfn1_pw060419p04q140	H05	EXACT(0)	121	120	96	30	EXACT(0)	200	184	57
tnfn1_pw060419p04q141	A06	EXACT(0)	119	112	107	41	EXACT(0)	199	163	57
tnfn1_pw060419p04q142	B06	EXACT(0)	123	125	67	20	EXACT(0)	200	186	45
tnfn1_pw060419p04q143	C06	EXACT(0)	122	120	83	25	EXACT(0)	200	186	50
tnfn1_pw060419p04q144	D06	EXACT(0)	123	105	91	25	EXACT(0)	200	180	45
tnfn1_pw060419p04q145	E06	EXACT(0)	123	112	68	21	EXACT(0)	200	184	52
tnfn1_pw060419p04q146	F06	EXACT(0)	123	105	93	27	EXACT(0)	200	183	50
tnfn1_pw060419p04q147	G06	EXACT(0)	125	117	103	30	EXACT(0)	200	187	52
tnfn1_pw060419p04q148	H06	EXACT(0)	126	124	107	22	EXACT(0)	200	172	31

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_pw060419p04q149	A07	EXACT(0)	122	105	75	23	EXACT(0)	200	149	35
tnfn1_pw060419p04q150	B07	EXACT(0)	124	112	94	22	EXACT(0)	200	179	45
tnfn1_pw060419p04q151	C07	EXACT(0)	157	153	124	35	EXACT(0)	200	183	56
tnfn1_pw060419p04q152	D07	EXACT(0)	157	152	131	33	EXACT(0)	200	180	53
tnfn1_pw060419p04q153	E07	EXACT(0)	156	152	136	42	EXACT(0)	185	179	51
tnfn1_pw060419p04q154	F07	EXACT(0)	152	153	119	42	EXACT(0)	176	108	29
tnfn1_pw060419p04q155	G07	EXACT(0)	155	152	130	37	EXACT(0)	200	191	55
tnfn1_pw060419p04q156	H07	EXACT(0)	158	145	136	42	EXACT(0)	200	197	54
tnfn1_pw060419p04q157	A08	EXACT(0)	156	152	133	42	EXACT(0)	200	185	54
tnfn1_pw060419p04q158	B08	EXACT(0)	157	145	132	38	EXACT(0)	200	190	57
tnfn1_pw060419p04q159	C08	EXACT(0)	155	145	126	43	EXACT(0)	90	84	51
tnfn1_pw060419p04q160	D08	EXACT(0)	158	145	135	39	EXACT(0)	200	181	50
tnfn1_pw060419p04q161	E08	EXACT(0)	158	151	131	37	EXACT(0)	200	185	43
tnfn1_pw060419p04q162	F08	EXACT(0)	157	152	141	39	EXACT(0)	200	188	58
tnfn1_pw060419p04q163	G08	EXACT(0)	155	153	131	37	EXACT(0)	200	193	51
tnfn1_pw060419p04q164	H08	EXACT(0)	155	145	132	41	EXACT(0)	161	156	54
tnfn1_pw060419p04q165	A09	EXACT(0)	158	152	138	40	EXACT(0)	201	121	37
tnfn1_pw060419p04q166	B09	EXACT(0)	154	145	126	42	EXACT(0)	200	185	55
tnfn1_pw060419p04q167	C09	EXACT(0)	156	152	128	34	EXACT(0)	170	157	51
tnfn1_pw060419p04q168	D09	EXACT(0)	156	145	125	31	EXACT(0)	200	197	48
tnfn1_pw060419p04q169	E09	EXACT(0)	157	145	139	50	EXACT(0)	166	162	61
tnfn1_pw060419p04q170	F09	EXACT(0)	156	145	132	33	EXACT(0)	200	193	49
tnfn1_pw060419p04q171	G09	EXACT(0)	156	145	108	22	EXACT(0)	200	192	46
tnfn1_pw060419p04q172	H09	EXACT(0)	158	145	138	41	EXACT(0)	200	187	66
tnfn1_pw060419p04q173	A10	EXACT(0)	156	145	109	29	EXACT(0)	112	106	51
tnfn1_pw060419p04q174	B10	EXACT(0)	155	145	137	51	EXACT(0)	200	191	62
tnfn1_pw060419p04q175	C10	EXACT(0)	156	142	128	34	EXACT(0)	200	171	33
tnfn1_pw060419p04q176	D10	EXACT(0)	157	151	138	46	EXACT(0)	198	188	43
tnfn1_pw060419p04q177	E10	EXACT(0)	157	145	133	37	EXACT(0)	200	192	53
tnfn1_pw060419p04q178	F10	EXACT(0)	158	152	131	38	EXACT(0)	200	186	59
tnfn1_pw060419p04q179	G10	EXACT(0)	157	145	117	38	EXACT(0)	200	195	51
tnfn1_pw060419p04q180	H10	EXACT(0)	157	116	85	20	EXACT(0)	200	162	40
tnfn1_pw060419p04q181	A11	EXACT(0)	156	145	112	32	EXACT(0)	200	190	54
tnfn1_pw060419p04q182	B11	EXACT(0)	156	145	134	39	EXACT(0)	200	194	57
tnfn1_pw060419p04q183	C11	EXACT(0)	156	116	77	23	EXACT(0)	200	189	44
tnfn1_pw060419p04q184	D11	EXACT(0)	155	145	134	48	EXACT(0)	200	162	51
tnfn1_pw060419p04q185	E11	EXACT(0)	156	145	125	32	EXACT(0)	200	166	64
tnfn1_pw060419p04q186	F11	EXACT(0)	158	144	125	38	EXACT(0)	199	181	54
tnfn1_pw060419p04q187	G11	EXACT(0)	156	152	128	40	ESTIMATE(35)	165	138	42
tnfn1_pw060419p04q188	H11	EXACT(0)	154	88	65	23	EXACT(0)	200	181	57
tnfn1_pw060419p04q189	A12	EXACT(0)	108	106	93	35	EXACT(0)	140	77	17
tnfn1_pw060419p04q190	B12	EXACT(0)	115	112	89	34	EXACT(0)	200	137	31
tnfn1_pw060419p04q191	C12	EXACT(0)	123	119	73	21	EXACT(0)	200	195	50
tnfn1_pw060419p04q192	D12	EXACT(0)	111	112	102	34	EXACT(0)	200	184	59
tnfn1_pw060419p04q193	E12	EXACT(0)	110	102	92	44	EXACT(0)	199	169	46
tnfn1_pw060419p04q194	F12	EXACT(0)	116	112	97	37	EXACT(0)	200	193	54
tnfn1_pw060419p04q195	G12	EXACT(0)	117	112	102	31	EXACT(0)	200	195	64
tnfn1_pw060419p04q196	H12	EXACT(0)	157	145	136	44	EXACT(0)	200	190	65