

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 9 (tnfn1_pw060328p01)**

Catalog No. NR-8043

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-8043 represents Plate 9 (tnfn1_pw060328p01) 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-8043 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 9 (tnfn1_pw060328p01), NR-8043.”

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.

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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_pw060328p01q101	A01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q102	B01	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p01q103	C01	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q104	D01	T18	minD	septum formation inhibitor-activating ATPase	cell cycle
tnfn1_pw060328p01q105	E01	T20	-	alanine racemase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q106	F01	T20	prfC	peptide chain release factor 3	translation, ribosomal structure and biogenesis
tnfn1_pw060328p01q107	G01	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060328p01q108	H01	T20	isftu2	isftu2	IS element
tnfn1_pw060328p01q109	A02	T20	-	protein of unknown function containing a von Willebrand factor type A (vWA) domain	unknown function - conserved
tnfn1_pw060328p01q110	B02	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060328p01q111	C02	T20	acnA	aconitate hydratase	energy metabolism
tnfn1_pw060328p01q112	D02	T20	leuA	2-isopropylmalate synthase	amino acid metabolism - biosynthesis
tnfn1_pw060328p01q113	E02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q114	F02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q115	G02	T20	-	peptide methionine sulfoxide reductase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p01q116	H02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q117	A03	T20	trpD	anthranilate phosphoribosyltransferase	amino acid metabolism - biosynthesis
tnfn1_pw060328p01q118	B03	T20	carB	carbamoyl-phosphate synthase large chain	nucleotides and nucleosides metabolism
tnfn1_pw060328p01q119	C03	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q120	D03	T20	-		
tnfn1_pw060328p01q121	E03	T20	ribC	riboflavin synthase alpha chain	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p01q122	F03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q123	G03	T20	oppB	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060328p01q124	H03	T20	kdpD	two component regulator, sensor histidine kinase kdpD	signal transduction and regulation
tnfn1_pw060328p01q125	A04	T20	-	NAD-dependent aldehyde dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q126	B04	T20	mdh	malate dehydrogenase	energy metabolism
tnfn1_pw060328p01q127	C04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q128	D04	T20	mdaB	NADPH-quinone reductase (modulator of drug activity B)	putative enzymes
tnfn1_pw060328p01q129	E04	T20	purU	formyltetrahydrofolate deformylase	nucleotides and nucleosides metabolism
tnfn1_pw060328p01q130	F04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q131	G04	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p01q132	H04	T20	-	glutamine amidotransferase, SNO family	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p01q133	A05	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p01q134	B05	T20	-	amino acid permease	transport - amino-acid
tnfn1_pw060328p01q135	C05	T20	-	pseudogene: Membrane Protein. Fucose permease Carbohydrate transport and metabolism	pseudogene
tnfn1_pw060328p01q136	D05	T20	paaY	carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	putative enzymes
tnfn1_pw060328p01q137	E05	T20	-	RimI-like acetyltransferase	putative enzymes
tnfn1_pw060328p01q138	F05	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p01q139	G05	T20	malQ	4-alpha-glucanotransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q140	H05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q141	A06	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p01q142	B06	T20	cysD	sulfate adenyltransferase subunit 2	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q143	C06	T20	ipdC	indolepyruvate decarboxylase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q144	D06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q145	E06	T20	mutS	MutS, subunit of MutHLS complex, methyl-directed mismatch repair protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p01q146	F06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q147	G06	T20	-	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060328p01q148	H06	T20	-	tRNA-methyltransferase MiaB protein	translation, ribosomal structure and biogenesis

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Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p01q149	A07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q150	B07	<KAN-2>	lysU	lysyl-tRNA synthetase	other metabolism - biosynthesis
tnfn1_pw060328p01q151	C07	<KAN-2>	-	bifunctional protein: glutaredoxin 3 /ribonucleotide reductase beta subunit	nucleotides and nucleosides metabolism
tnfn1_pw060328p01q152	D07	<KAN-2>	-	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060328p01q153	E07	<KAN-2>	grpE	chaperone GrpE (heat shock protein). Hsp70/Hsc70 protein regulator activity	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p01q154	F07	<KAN-2>	-	SAICAR synthetase/phosphoribosylamine-glycine ligase	nucleotides and nucleosides metabolism
tnfn1_pw060328p01q155	G07	T20	-	tRNA-methyltransferase MiaB protein	translation, ribosomal structure and biogenesis
tnfn1_pw060328p01q156	H07	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q157	A08	<KAN-2>	ugpQ	glycerophosphoryl diester phosphodiesterase	cell wall / LPS / capsule
tnfn1_pw060328p01q158	B08	T18	-	acid phosphatase/phosphotransferase	putative enzymes
tnfn1_pw060328p01q159	C08	T18	-	outer membrane protein of unknown function	unknown function - novel
tnfn1_pw060328p01q160	D08	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q161	E08	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q162	F08	T18	-	N6-adenine-specific methylase	DNA replication, recombination, modification and repair
tnfn1_pw060328p01q163	G08	T18	-	DedA family protein	putative enzymes
tnfn1_pw060328p01q164	H08	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q165	A09	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q166	B09	T18	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p01q167	C09	T18	minD	septum formation inhibitor-activating ATPase	cell cycle
tnfn1_pw060328p01q168	D09	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p01q169	E09	T18	isftu2	isftu2	IS element
tnfn1_pw060328p01q170	F09	T18	-	Mg-dependent DNase	DNA replication, recombination, modification and repair
tnfn1_pw060328p01q171	G09	T18	-	hypothetical protein	Potentially coding: hypothetical - novel
tnfn1_pw060328p01q172	H09	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p01q173	A10	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p01q174	B10	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q175	C10	T18	xerD	site-specific recombinase	DNA replication, recombination, modification and repair
tnfn1_pw060328p01q176	D10	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q177	E10	T20	-	oxidoreductase iron/ascorbate family protein	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q178	F10	T20	xthA	exodeoxyribonuclease III	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p01q179	G10	T20	-	phage terminase, small subunit	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060328p01q180	H10	T20	sohB	peptidase family S49 protein	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p01q181	A11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q182	B11	T20	-	metallo-beta-lactamase superfamily protein	putative enzymes
tnfn1_pw060328p01q183	C11	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060328p01q184	D11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q185	E11	T20	lpxE	lipid A 1-phosphatase	fatty acids and lipids metabolism
tnfn1_pw060328p01q186	F11	T20	thrA	aspartate kinase I/homoserine dehydrogenase I	amino acid metabolism - biosynthesis
tnfn1_pw060328p01q187	G11	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060328p01q188	H11	T20	-	sugar:cation symporter family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060328p01q189	A12	T20	wzx	O antigen flippase	transport
tnfn1_pw060328p01q190	B12	T20			
tnfn1_pw060328p01q191	C12	T20	-	DNA helicase	DNA replication, recombination, modification and repair
tnfn1_pw060328p01q192	D12	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p01q193	E12	T20	lldD	L-lactate dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p01q194	F12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p01q195	G12	T20	gph	phosphoglycolate phosphatase	putative enzymes
tnfn1_pw060328p01q196	H12	T20	wzx	O antigen flippase	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_pw060328p01q101	A01	C	1646007	R	FTN_1548	1645390	1646757	F	456	618(1368)
tnfn1_pw060328p01q102	B01	C	1015140	F	FTN_0960	1014799	1015527	R	243	388(729)
tnfn1_pw060328p01q103	C01	C	51171	R	FTN_0046	50758	53733	F	992	414(2976)
tnfn1_pw060328p01q104	D01	C	337220	R	FTN_0330	336917	337738	R	274	519(822)
tnfn1_pw060328p01q105	E01	C	326647	F	FTN_0316	325739	326791	R	351	145(1053)
tnfn1_pw060328p01q106	F01	C	1698814	F	FTN_1597	1697609	1699183	R	525	370(1575)
tnfn1_pw060328p01q107	G01	C	1617978	R	FTN_1520	1617143	1618336	R	398	359(1194)
tnfn1_pw060328p01q108	H01	C	851412	R	-	851134	851998	F	288.3	279(865)
tnfn1_pw060328p01q109	A02	C	227527	F	FTN_0207	227115	228113	F	333	413(999)
tnfn1_pw060328p01q110	B02	C	1684902	F	FTN_1586	1684007	1685317	R	437	416(1311)
tnfn1_pw060328p01q111	C02	C	1734015	R	FTN_1623	1733943	1736753	R	937	2739(2811)
tnfn1_pw060328p01q112	D02	C	73413	F	FTN_0062	72771	74348	R	526	936(1578)
tnfn1_pw060328p01q113	E02	C	1813907	R	FTN_1696	1813595	1814374	F	260	313(780)
tnfn1_pw060328p01q114	F02	C	11367	F	FTN_0013	10939	11835	R	299	469(897)
tnfn1_pw060328p01q115	G02	C	826240	F	FTN_0769	825750	826601	F	284	491(852)
tnfn1_pw060328p01q116	H02	C	35380	R	FTN_0034	33580	36951	R	1124	1572(3372)
tnfn1_pw060328p01q117	A03	C	1905179	F	FTN_1776	1904293	1905303	R	337	125(1011)
tnfn1_pw060328p01q118	B03	C	20482	F	FTN_0020	18120	21401	R	1094	920(3282)
tnfn1_pw060328p01q119	C03	C	850750	R	FTN_0793	850477	851043	F	189	274(567)
tnfn1_pw060328p01q121	E03	C	124293	R	FTN_0113	123993	124595	R	201	303(603)
tnfn1_pw060328p01q122	F03	C	1133685	F	FTN_1071	1132424	1133899	R	492	215(1476)
tnfn1_pw060328p01q123	G03	C	1690890	F	FTN_1592	1690148	1691083	R	312	194(936)
tnfn1_pw060328p01q124	H03	C	1840817	R	FTN_1715	1838604	1841282	R	893	466(2679)
tnfn1_pw060328p01q125	A04	C	1017681	R	FTN_0963	1016699	1018192	R	498	512(1494)
tnfn1_pw060328p01q126	B04	C	1033588	F	FTN_0980	1033379	1034335	F	319	210(957)
tnfn1_pw060328p01q127	C04	C	1031661	R	FTN_0977	1031487	1032053	F	189	175(567)
tnfn1_pw060328p01q128	D04	C	896542	R	FTN_0840	896313	896900	F	196	230(588)
tnfn1_pw060328p01q129	E04	C	662796	F	FTN_0629	662421	663251	F	277	376(831)
tnfn1_pw060328p01q130	F04	C	469383	R	FTN_0463	469216	469476	R	87	94(261)
tnfn1_pw060328p01q131	G04	C	463982	F	FTN_0457	463591	464247	F	219	392(657)
tnfn1_pw060328p01q132	H04	C	635258	R	FTN_0602	634911	635447	F	179	348(537)
tnfn1_pw060328p01q133	A05	C	1069631	F	FTN_1010	1069039	1070319	F	427	593(1281)
tnfn1_pw060328p01q134	B05	C	955883	F	FTN_0898	954503	956044	R	514	162(1542)
tnfn1_pw060328p01q135	C05	C	1405232	R	FTN_1327	1404933	1406114	F	394	300(1182)
tnfn1_pw060328p01q136	D05	C	158807	F	FTN_0144	158724	159260	F	179	84(537)
tnfn1_pw060328p01q137	E05	C	166298	F	FTN_0153	166021	166443	R	141	146(423)
tnfn1_pw060328p01q138	F05	C	1546655	F	FTN_1458	1546487	1546990	F	168	169(504)
tnfn1_pw060328p01q139	G05	C	537227	R	FTN_0518	536994	538454	F	487	234(1461)
tnfn1_pw060328p01q140	H05	C	1165178	R	FTN_1103	1164647	1165492	R	282	315(846)
tnfn1_pw060328p01q141	A06	C	12441	F	FTN_0014	11835	12728	R	298	288(894)
tnfn1_pw060328p01q142	B06	C	989383	R	FTN_0928	988925	989818	R	298	436(894)
tnfn1_pw060328p01q143	C06	C	128736	R	FTN_0116	127309	129003	R	565	268(1695)
tnfn1_pw060328p01q144	D06	C	1386060	F	FTN_1313	1384921	1386648	F	576	1140(1728)
tnfn1_pw060328p01q145	E06	C	1604917	F	FTN_1509	1604143	1606674	F	844	775(2532)
tnfn1_pw060328p01q146	F06	C	521699	R	FTN_0509	519765	523154	F	1130	1935(3390)
tnfn1_pw060328p01q147	G06	C	388811	R	FTN_0389	388044	388991	R	316	181(948)
tnfn1_pw060328p01q148	H06	C	1122727	R	FTN_1063	1122215	1123540	F	442	513(1326)

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_pw060328p01q149	A07	C	1560687	F	FTN_1472	1560482	1561288	F	269	206(807)
tnfn1_pw060328p01q150	B07	C	184814	F	FTN_0168	183091	184818	F	576	1724(1728)
tnfn1_pw060328p01q151	C07	C	1037810	F	FTN_0983	1036585	1037814	F	410	1226(1230)
tnfn1_pw060328p01q152	D07	C	413782	R	FTN_0414	413585	414019	R	145	238(435)
tnfn1_pw060328p01q153	E07	C	1358647	R	FTN_1285	1358234	1358818	R	195	172(585)
tnfn1_pw060328p01q154	F07	C	419602	F	FTN_0420	418362	420671	F	770	1241(2310)
tnfn1_pw060328p01q155	G07	U	1122727	R	FTN_1063	1122215	1123540	F	442	513(1326)
tnfn1_pw060328p01q156	H07	C	1531043	R	FTN_1442	1530875	1531099	R	75	57(225)
tnfn1_pw060328p01q157	A08	C	674116	R	FTN_0637	673289	674314	R	342	199(1026)
tnfn1_pw060328p01q158	B08	C	726023	R	FTN_0681	725743	726366	F	208	281(624)
tnfn1_pw060328p01q159	C08	C	1112797	F	FTN_1053	1111641	1113071	R	477	275(1431)
tnfn1_pw060328p01q160	D08	C	798089	R	FTN_0744	797981	798376	F	132	109(396)
tnfn1_pw060328p01q161	E08	C	237526	R	FTN_0215	237281	237943	F	221	246(663)
tnfn1_pw060328p01q162	F08	C	693980	R	FTN_0655	693723	694298	R	192	319(576)
tnfn1_pw060328p01q163	G08	C	1309165	F	FTN_1242	1308961	1309605	F	215	205(645)
tnfn1_pw060328p01q164	H08	C	1286494	R	FTN_1216	1286108	1286848	R	247	355(741)
tnfn1_pw060328p01q165	A09	C	1075695	F	FTN_1016	1075256	1075756	R	167	62(501)
tnfn1_pw060328p01q166	B09	C	623429	F	FTN_0592	623054	623476	R	141	48(423)
tnfn1_pw060328p01q167	C09	C	337220	R	FTN_0330	336917	337738	R	274	519(822)
tnfn1_pw060328p01q168	D09	C	886516	F	FTN_0829	886126	886842	R	239	327(717)
tnfn1_pw060328p01q169	E09	C	233724	R	-	233259	234123	R	288.3	400(865)
tnfn1_pw060328p01q170	F09	C	1485516	F	FTN_1408	1485141	1485905	R	255	390(765)
tnfn1_pw060328p01q171	G09	C	396301	R	-	396244	396372	R	43	72(129)
tnfn1_pw060328p01q172	H09	C	1640559	R	FTN_1542	1640166	1640927	F	254	394(762)
tnfn1_pw060328p01q173	A10	C	208677	R	FTN_0190	207626	208801	R	392	125(1176)
tnfn1_pw060328p01q174	B10	C	646594	F	FTN_0615	646311	646880	F	190	284(570)
tnfn1_pw060328p01q175	C10	C	1656528	F	FTN_1558	1655903	1656778	R	292	251(876)
tnfn1_pw060328p01q176	D10	C	7465	R	FTN_0007	7364	7678	R	105	214(315)
tnfn1_pw060328p01q177	E10	C	1655432	F	FTN_1557	1654935	1655777	R	281	346(843)
tnfn1_pw060328p01q178	F10	C	894586	R	FTN_0838	894232	895017	R	262	432(786)
tnfn1_pw060328p01q179	G10	C	9590	R	FTN_0010	9375	9806	R	144	217(432)
tnfn1_pw060328p01q180	H10	C	575922	F	FTN_0550	575484	576497	F	338	439(1014)
tnfn1_pw060328p01q181	A11	C	1601034	R	FTN_1505	1599542	1601503	R	654	470(1962)
tnfn1_pw060328p01q182	B11	C	1296993	F	FTN_1227	1296419	1297378	R	320	386(960)
tnfn1_pw060328p01q183	C11	C	1884158	R	FTN_1755	1883615	1884871	F	419	544(1257)
tnfn1_pw060328p01q184	D11	C	995008	R	FTN_0934	994829	995320	F	164	180(492)
tnfn1_pw060328p01q185	E11	C	415121	R	FTN_0416	414941	415657	F	239	181(717)
tnfn1_pw060328p01q186	F11	C	546055	R	FTN_0525	545312	547729	F	806	744(2418)
tnfn1_pw060328p01q187	G11	C	1833500	R	FTN_1709	1832414	1834285	R	624	786(1872)
tnfn1_pw060328p01q188	H11	C	966252	R	FTN_0910	965706	967175	F	490	547(1470)
tnfn1_pw060328p01q189	A12	U	1499550	F	FTN_1420	1498689	1499933	R	415	384(1245)
tnfn1_pw060328p01q190	B12	C	628664	F	intergenic					
tnfn1_pw060328p01q191	C12	C	1678020	F	FTN_1580	1677286	1678698	R	471	679(1413)
tnfn1_pw060328p01q192	D12	C	64042	R	FTN_0053	63789	64391	F	201	254(603)
tnfn1_pw060328p01q193	E12	C	1049568	R	FTN_0991	1048716	1049855	R	380	288(1140)
tnfn1_pw060328p01q194	F12	C	1384110	R	FTN_1311	1384032	1384406	F	125	79(375)
tnfn1_pw060328p01q195	G12	C	611579	F	FTN_0582	611071	611742	R	224	164(672)
tnfn1_pw060328p01q196	H12	C	1499550	F	FTN_1420	1498689	1499933	R	415	384(1245)

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_pw060328p01q101	A01	EXACT(0)	156	142	98	29	EXACT(0)	200	194	53
tnfn1_pw060328p01q102	B01	EXACT(0)	157	153	137	46	EXACT(0)	200	185	64
tnfn1_pw060328p01q103	C01	EXACT(0)	157	153	116	32	EXACT(0)	200	189	57
tnfn1_pw060328p01q104	D01	EXACT(0)	123	120	102	34	EXACT(0)	199	87	29
tnfn1_pw060328p01q105	E01	EXACT(0)	157	146	135	39	EXACT(0)	200	179	59
tnfn1_pw060328p01q106	F01	EXACT(0)	155	139	128	40	EXACT(0)	200	195	53
tnfn1_pw060328p01q107	G01	EXACT(0)	156	153	123	30	EXACT(0)	200	179	55
tnfn1_pw060328p01q108	H01	EXACT(0)	155	145	115	42	EXACT(0)	200	184	56
tnfn1_pw060328p01q109	A02	EXACT(0)	155	152	121	36	EXACT(0)	200	193	52
tnfn1_pw060328p01q110	B02	EXACT(0)	158	153	117	32	EXACT(0)	200	194	58
tnfn1_pw060328p01q111	C02	EXACT(0)	156	152	125	39	EXACT(0)	200	181	54
tnfn1_pw060328p01q112	D02	EXACT(0)	156	152	122	40	EXACT(0)	200	189	55
tnfn1_pw060328p01q113	E02	EXACT(0)	156	146	127	41	EXACT(0)	200	184	49
tnfn1_pw060328p01q114	F02	EXACT(0)	157	152	127	38	EXACT(0)	200	189	55
tnfn1_pw060328p01q115	G02	EXACT(0)	157	151	117	36	EXACT(0)	200	187	56
tnfn1_pw060328p01q116	H02	EXACT(0)	157	148	134	40	EXACT(0)	200	194	59
tnfn1_pw060328p01q117	A03	EXACT(0)	157	153	121	39	EXACT(0)	200	181	58
tnfn1_pw060328p01q118	B03	EXACT(0)	154	150	103	24	EXACT(0)	200	198	53
tnfn1_pw060328p01q119	C03	EXACT(0)	156	138	110	33	EXACT(0)	200	173	41
tnfn1_pw060328p01q120	D03	EXACT(0)	154	145	103	26	EXACT(0)	200	181	55
tnfn1_pw060328p01q121	E03	EXACT(0)	156	153	125	35	EXACT(0)	200	190	57
tnfn1_pw060328p01q122	F03	EXACT(0)	154	118	80	28	EXACT(0)	200	176	46
tnfn1_pw060328p01q123	G03	EXACT(0)	158	159	140	37	EXACT(0)	200	190	57
tnfn1_pw060328p01q124	H03	EXACT(0)	155	145	120	41	EXACT(0)	200	188	57
tnfn1_pw060328p01q125	A04	EXACT(0)	156	152	122	38	EXACT(0)	200	189	58
tnfn1_pw060328p01q126	B04	EXACT(0)	155	145	117	39	EXACT(0)	200	191	58
tnfn1_pw060328p01q127	C04	EXACT(0)	157	153	124	36	EXACT(0)	200	173	47
tnfn1_pw060328p01q128	D04	EXACT(0)	159	153	130	37	EXACT(0)	200	191	55
tnfn1_pw060328p01q129	E04	EXACT(0)	156	146	127	37	EXACT(0)	200	187	52
tnfn1_pw060328p01q130	F04	EXACT(0)	155	145	126	43	EXACT(0)	196	177	53
tnfn1_pw060328p01q131	G04	EXACT(0)	155	146	118	38	EXACT(0)	200	192	57
tnfn1_pw060328p01q132	H04	EXACT(0)	154	139	122	43	EXACT(0)	200	188	53
tnfn1_pw060328p01q133	A05	EXACT(0)	157	152	124	36	EXACT(0)	200	187	57
tnfn1_pw060328p01q134	B05	EXACT(0)	156	151	123	34	EXACT(0)	200	190	56
tnfn1_pw060328p01q135	C05	EXACT(0)	156	153	126	41	EXACT(0)	199	184	50
tnfn1_pw060328p01q136	D05	EXACT(0)	155	145	126	40	EXACT(0)	200	196	57
tnfn1_pw060328p01q137	E05	EXACT(0)	155	145	126	42	EXACT(0)	200	182	51
tnfn1_pw060328p01q138	F05	EXACT(0)	154	145	129	42	EXACT(0)	196	189	52
tnfn1_pw060328p01q139	G05	EXACT(0)	155	145	126	41	EXACT(0)	200	193	53
tnfn1_pw060328p01q140	H05	EXACT(0)	155	145	123	42	EXACT(0)	197	189	51
tnfn1_pw060328p01q141	A06	EXACT(0)	157	152	124	37	EXACT(0)	200	176	56
tnfn1_pw060328p01q142	B06	EXACT(0)	156	153	123	40	EXACT(0)	200	191	57
tnfn1_pw060328p01q143	C06	EXACT(0)	155	146	124	43	EXACT(0)	200	195	56
tnfn1_pw060328p01q144	D06	EXACT(0)	156	144	117	25	EXACT(0)	200	175	58
tnfn1_pw060328p01q145	E06	EXACT(0)	155	146	130	44	EXACT(0)	200	188	59
tnfn1_pw060328p01q146	F06	EXACT(0)	155	145	129	44	EXACT(0)	188	173	55
tnfn1_pw060328p01q147	G06	EXACT(0)	155	146	133	39	EXACT(0)	200	192	56
tnfn1_pw060328p01q148	H06	EXACT(0)	154	145	120	37	EXACT(0)	200	194	51

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_pw060328p01q149	A07	EXACT(0)	155	146	118	39	EXACT(0)	187	183	47
tnfn1_pw060328p01q150	B07	EXACT(0)	122	112	86	25	EXACT(0)	197	173	50
tnfn1_pw060328p01q151	C07	EXACT(0)	121	112	99	31	EXACT(0)	200	188	49
tnfn1_pw060328p01q152	D07	EXACT(0)	123	118	99	26	EXACT(0)	200	195	53
tnfn1_pw060328p01q153	E07	EXACT(0)	115	111	88	40	EXACT(0)	200	182	28
tnfn1_pw060328p01q154	F07	EXACT(0)	121	112	90	26	EXACT(0)	200	194	54
tnfn1_pw060328p01q155	G07	EXACT(0)	158	141	112	22	EXACT(0)	200	191	39
tnfn1_pw060328p01q156	H07	EXACT(0)	121	112	72	23	EXACT(0)	200	175	49
tnfn1_pw060328p01q157	A08	EXACT(0)	123	125	86	22	EXACT(0)	200	188	51
tnfn1_pw060328p01q158	B08	EXACT(0)	122	112	96	31	EXACT(0)	200	178	58
tnfn1_pw060328p01q159	C08	EXACT(0)	121	106	90	28	EXACT(0)	200	186	52
tnfn1_pw060328p01q160	D08	EXACT(0)	121	112	93	29	EXACT(0)	200	188	63
tnfn1_pw060328p01q161	E08	EXACT(0)	122	118	73	24	EXACT(0)	200	184	55
tnfn1_pw060328p01q162	F08	EXACT(0)	122	112	78	26	EXACT(0)	200	182	39
tnfn1_pw060328p01q163	G08	EXACT(0)	122	119	83	21	EXACT(0)	197	186	48
tnfn1_pw060328p01q164	H08	EXACT(0)	122	105	79	23	EXACT(0)	200	180	46
tnfn1_pw060328p01q165	A09	EXACT(0)	124	120	89	26	EXACT(0)	200	183	57
tnfn1_pw060328p01q166	B09	EXACT(0)	123	120	101	27	EXACT(0)	200	174	55
tnfn1_pw060328p01q167	C09	EXACT(0)	123	120	102	34	EXACT(0)	198	79	29
tnfn1_pw060328p01q168	D09	EXACT(0)	123	120	66	20	EXACT(0)	200	194	51
tnfn1_pw060328p01q169	E09	EXACT(0)	122	112	89	37	EXACT(0)	200	187	55
tnfn1_pw060328p01q170	F09	EXACT(0)	121	120	85	25	EXACT(0)	200	191	57
tnfn1_pw060328p01q171	G09	EXACT(0)	124	120	101	35	EXACT(0)	200	181	52
tnfn1_pw060328p01q172	H09	EXACT(0)	122	113	94	33	EXACT(0)	136	129	55
tnfn1_pw060328p01q173	A10	EXACT(0)	124	122	95	27	EXACT(0)	200	187	56
tnfn1_pw060328p01q174	B10	EXACT(0)	122	113	97	29	EXACT(0)	200	191	54
tnfn1_pw060328p01q175	C10	EXACT(0)	122	119	95	34	EXACT(0)	200	185	56
tnfn1_pw060328p01q176	D10	EXACT(0)	123	119	103	33	EXACT(0)	200	184	61
tnfn1_pw060328p01q177	E10	EXACT(0)	156	152	134	43	EXACT(0)	200	147	42
tnfn1_pw060328p01q178	F10	EXACT(0)	159	153	139	40	EXACT(0)	200	191	56
tnfn1_pw060328p01q179	G10	EXACT(0)	155	146	127	41	EXACT(0)	192	177	54
tnfn1_pw060328p01q180	H10	EXACT(0)	154	145	120	38	EXACT(0)	200	185	46
tnfn1_pw060328p01q181	A11	EXACT(0)	156	153	121	34	EXACT(0)	200	191	57
tnfn1_pw060328p01q182	B11	EXACT(0)	155	146	124	39	EXACT(0)	200	196	55
tnfn1_pw060328p01q183	C11	EXACT(0)	156	153	126	39	EXACT(0)	191	185	55
tnfn1_pw060328p01q184	D11	EXACT(0)	156	153	126	37	EXACT(0)	200	182	52
tnfn1_pw060328p01q185	E11	EXACT(0)	156	152	120	33	EXACT(0)	200	180	54
tnfn1_pw060328p01q186	F11	EXACT(0)	156	153	129	40	EXACT(0)	200	192	51
tnfn1_pw060328p01q187	G11	EXACT(0)	157	153	118	33	EXACT(0)	200	190	56
tnfn1_pw060328p01q188	H11	EXACT(0)	156	145	122	35	EXACT(0)	200	190	52
tnfn1_pw060328p01q189	A12	EXACT(0)	159	133	103	25	EXACT(0)	200	184	43
tnfn1_pw060328p01q190	B12	EXACT(0)	156	152	125	32	EXACT(0)	200	183	53
tnfn1_pw060328p01q191	C12	EXACT(0)	157	153	115	29	EXACT(0)	200	197	54
tnfn1_pw060328p01q192	D12	EXACT(0)	156	153	123	39	EXACT(0)	199	179	52
tnfn1_pw060328p01q193	E12	EXACT(0)	154	152	120	41	EXACT(0)	183	155	37
tnfn1_pw060328p01q194	F12	EXACT(0)	158	153	123	36	EXACT(0)	200	186	49
tnfn1_pw060328p01q195	G12	EXACT(0)	156	145	131	39	EXACT(0)	160	124	39
tnfn1_pw060328p01q196	H12	EXACT(0)	157	152	117	35	EXACT(0)	200	172	47