

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 15 (tnfn1_pw060328p07)**

Catalog No. NR-8049

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-8049 represents Plate 15 (tnfn1_pw060328p07) 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. **The following strains are not available due to quality issues:**

tnfn1_pw060328p07q104 (Well D01)
tnfn1_pw060328p07q108 (Well H01)
tnfn1_pw060328p07q116 (Well H02)
tnfn1_pw060328p07q164 (Well H08)
tnfn1_pw060328p07q177 (Well E10)

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-8049 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 15 (tnfn1_pw060328p07), NR-8049.”

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_pw060328p07q101	A01	<KAN-2>	-	disulfide bond formation protein DsbB family	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p07q102	B01	<KAN-2>	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p07q103	C01	<KAN-2>	-	hypothetical protein	Potentially coding: hypothetical - novel
tnfn1_pw060328p07q104	D01	<KAN-2>	rplT	50S ribosomal protein L20	translation, ribosomal structure and biogenesis
tnfn1_pw060328p07q105	E01	<KAN-2>	-	manganese/zinc/iron chelate uptake transporter (MZT) family protein	transport
tnfn1_pw060328p07q106	F01	<KAN-2>	-	haloacid dehalogenase-like hydrolase	putative enzymes
tnfn1_pw060328p07q107	G01	<KAN-2>	gcvH	glycine cleavage system H protein (lipoate-binding)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q108	H01	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p07q109	A02	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p07q110	B02	<KAN-2>	galM	aldose 1-epimerase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q111	C02	T20	potH	ATP-binding cassette putrescine uptake system, membrane protein, subunit H	transport
tnfn1_pw060328p07q112	D02	T18	isftu2	isftu2	IS element
tnfn1_pw060328p07q113	E02	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p07q114	F02	T18	-	HAM1-like protein, possible xanthosine triphosphate pyrophosphatase	putative enzymes
tnfn1_pw060328p07q115	G02	T18	gcp	O-sialoglycoprotein endopeptidase	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p07q116	H02	T18	ans	asparaginase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q117	A03	T18	gcvH	glycine cleavage system H protein (lipoate-binding)	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q118	B03	T18	-	transposase	mobile and extrachromosomal element functions - transposition
tnfn1_pw060328p07q119	C03	T18	serA	D-3-phosphoglycerate dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060328p07q120	D03	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p07q121	E03	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p07q122	F03	T20	hflC	HflK-HflC membrane protein complex, HflC	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060328p07q123	G03	T20	-	putative rhodanese, sulfurtransferase	putative enzymes
tnfn1_pw060328p07q124	H03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p07q125	A04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p07q126	B04	T20	perM	PerM family protein	transport
tnfn1_pw060328p07q127	C04	T20	-	predicted enzyme of enolase superfamily	putative enzymes
tnfn1_pw060328p07q128	D04	T20	minE	cell division topological specificity factor protein	cell cycle
tnfn1_pw060328p07q129	E04	T20	putP	proline:Na ⁺ symporter	transport - amino-acid
tnfn1_pw060328p07q130	F04	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p07q131	G04	T20	sdhC	succinate dehydrogenase, cytochrome b556	energy metabolism
tnfn1_pw060328p07q132	H04	T20	-	outer membrane protein of unknown function	unknown function - novel
tnfn1_pw060328p07q133	A05	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060328p07q134	B05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p07q135	C05	T20	-	peptide methionine sulfoxide reductase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p07q136	D05	T20	recN	DNA repair protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p07q137	E05	T20	iscS	cysteine desulfurase	amino acid metabolism - biosynthesis
tnfn1_pw060328p07q138	F05	T20	-	two-component response regulator	signal transduction and regulation
tnfn1_pw060328p07q139	G05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p07q140	H05	T20	ruvB	holliday junction DNA helicase, subunit B	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p07q141	A06	T20	-	membrane fusion protein	motility, attachment and secretion structure
tnfn1_pw060328p07q142	B06	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p07q143	C06	T20	-	phospholipase D family protein	fatty acids and lipids metabolism
tnfn1_pw060328p07q144	D06	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p07q145	E06	T20	-	oxidoreductase	putative enzymes
tnfn1_pw060328p07q146	F06	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p07q147	G06	T20	metN	methionine uptake transporter (MUT) family protein	transport - amino-acid
tnfn1_pw060328p07q148	H06	T20	-	conserved protein of unknown function	unknown function - conserved

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p07q149	A07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p07q150	B07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p07q151	C07	T20	-	GTP binding translational elongation factor Tu and G family protein	putative enzymes
tnfn1_pw060328p07q152	D07	T20	-	dehydrogenase related to short-chain alcohol dehydrogenases	putative enzymes
tnfn1_pw060328p07q153	E07	T20	-	acetyltransferase	putative enzymes
tnfn1_pw060328p07q154	F07	T20	pilE	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060328p07q155	G07	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p07q156	H07	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p07q157	A08	<KAN-2>	rpsB	30S ribosomal protein S2	translation, ribosomal structure and biogenesis
tnfn1_pw060328p07q158	B08	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p07q159	C08	<KAN-2>	udk	uridine kinase	nucleotides and nucleosides metabolism
tnfn1_pw060328p07q160	D08	T20	oxyR	oxidative stress transcriptional regulator	signal transduction and regulation
tnfn1_pw060328p07q161	E08	<KAN-2>	gcvH1	glycine cleavage system protein H	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q162	F08	<KAN-2>	-	RNA methyltransferase, SpoU family	translation, ribosomal structure and biogenesis
tnfn1_pw060328p07q163	G08	T20	-	outer membrane efflux protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p07q164	H08	<KAN-2>	sdhB	succinate dehydrogenase iron-sulfur protein	energy metabolism
tnfn1_pw060328p07q165	A09	<KAN-2>	rpsA	30S ribosomal protein S1	translation, ribosomal structure and biogenesis
tnfn1_pw060328p07q166	B09	<KAN-2>	tsf	protein chain elongation factor EF-Ts	translation, ribosomal structure and biogenesis
tnfn1_pw060328p07q167	C09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p07q168	D09	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060328p07q169	E09	T20	rpIA	ribose 5-phosphate isomerase A	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q170	F09	T20	-	OmpA family protein	cell wall / LPS / capsule
tnfn1_pw060328p07q171	G09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p07q172	H09	T20	-	ATP-dependent RNA helicase	nucleotides and nucleosides metabolism
tnfn1_pw060328p07q173	A10	T20	vanY	D-alanyl-D-alanine carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060328p07q174	B10	T20	kdpE	two-component response regulator	signal transduction and regulation
tnfn1_pw060328p07q175	C10	T20	rnpA	ribonuclease P protein component	translation, ribosomal structure and biogenesis
tnfn1_pw060328p07q176	D10	T20	-	arsenate reductase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p07q177	E10	T20	-	BolA family protein	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p07q178	F10	T20	isfU2	isfU2	IS element
tnfn1_pw060328p07q179	G10	T20	capC	capsule biosynthesis protein CapC	cell wall / LPS / capsule
tnfn1_pw060328p07q180	H10	T20	-	peptidoglycan hydrolase	cell wall / LPS / capsule
tnfn1_pw060328p07q181	A11	T20	parB	chromosome partition protein B	cell cycle
tnfn1_pw060328p07q182	B11	T20	tdh	L-threonine 3-dehydrogenase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p07q183	C11	T20	-	FKBP-type peptidyl-prolyl cis-trans isomerase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p07q184	D11	T20	isfU3	isfU3	IS element
tnfn1_pw060328p07q185	E11	T20	dapA	dihydrodipicolinate synthase	amino acid metabolism - biosynthesis
tnfn1_pw060328p07q186	F11	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060328p07q187	G11	T20	-	metabolite:H ⁺ symporter (MHS) family protein	transport
tnfn1_pw060328p07q188	H11	T20	isfU6	isfU6	IS element
tnfn1_pw060328p07q189	A12	T20	-	GTPase of unknown function	putative enzymes
tnfn1_pw060328p07q190	B12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p07q191	C12	T20	trxB	thioredoxin reductase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p07q192	D12	T20	-	nitroreductase	energy metabolism
tnfn1_pw060328p07q193	E12	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p07q194	F12	<KAN-2>	-	subunit of DnaJ/DnaK/GrpE: chaperone with DnaK; heat shock protein	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060328p07q195	G12	<KAN-2>	rpoZ	DNA-directed RNA polymerase, subunit K/omega	transcription
tnfn1_pw060328p07q196	H12	<KAN-2>	iglD	intracellular growth locus protein D	unknown function - novel

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_pw060328p07q101	A01	C	1372414	F	FTN_1303	1372091	1372657	F	189	324(567)
tnfn1_pw060328p07q102	B01	C	1015690	R	FTN_0961	1015544	1015813	R	90	124(270)
tnfn1_pw060328p07q103	C01	C	485489	F	-	485416	485517	F	34	74(102)
tnfn1_pw060328p07q104	D01	C	1262426	R	FTN_1188	1262405	1262758	R	118	333(354)
tnfn1_pw060328p07q105	E01	C	199196	R	FTN_0181	198742	199581	R	280	386(840)
tnfn1_pw060328p07q106	F01	C	1028691	F	FTN_0974	1028537	1029115	F	193	155(579)
tnfn1_pw060328p07q107	G01	C	516149	F	FTN_0506	516080	516460	F	127	70(381)
tnfn1_pw060328p07q108	H01	C	1564043	R	FTN_1476	1563577	1564161	R	195	119(585)
tnfn1_pw060328p07q109	A02	C	1462734	R	FTN_1382	1462421	1462831	R	137	98(411)
tnfn1_pw060328p07q110	B02	C	1190065	R	FTN_1127	1189307	1190299	R	331	235(993)
tnfn1_pw060328p07q111	C02	C	791816	R	FTN_0738	791393	792307	R	305	492(915)
tnfn1_pw060328p07q112	D02	C	619489	R	-	619309	620173	R	288.3	685(865)
tnfn1_pw060328p07q113	E02	C	1164461	R	FTN_1102	1164373	1164600	F	76	89(228)
tnfn1_pw060328p07q114	F02	C	1556928	R	FTN_1468	1556744	1557319	F	192	185(576)
tnfn1_pw060328p07q115	G02	C	1662205	R	FTN_1565	1662203	1663210	R	336	1006(1008)
tnfn1_pw060328p07q116	H02	C	1278499	F	FTN_1208	1277746	1278606	R	287	108(861)
tnfn1_pw060328p07q117	A03	C	516458	R	FTN_0506	516080	516460	F	127	379(381)
tnfn1_pw060328p07q118	B03	U	294570	F	FTN_0286	294223	294783	F	187	348(561)
tnfn1_pw060328p07q119	C03	C	1316914	R	FTN_1249	1316412	1317644	F	411	503(1233)
tnfn1_pw060328p07q120	D03	C	1427693	R	FTN_1349	1427275	1427817	R	181	125(543)
tnfn1_pw060328p07q121	E03	C	1802571	F	FTN_1686	1801799	1803325	F	509	773(1527)
tnfn1_pw060328p07q122	F03	C	1105712	F	FTN_1047	1105546	1106469	R	308	758(924)
tnfn1_pw060328p07q123	G03	C	848099	R	FTN_0789	847645	848631	R	329	533(987)
tnfn1_pw060328p07q124	H03	C	1242692	F	FTN_1171	1242057	1243040	R	328	349(984)
tnfn1_pw060328p07q125	A04	C	1342543	R	FTN_1271	1341912	1342637	F	242	632(726)
tnfn1_pw060328p07q126	B04	C	597418	F	FTN_0570	596517	597620	R	368	203(1104)
tnfn1_pw060328p07q127	C04	C	743455	R	FTN_0700	743228	744295	F	356	228(1068)
tnfn1_pw060328p07q128	D04	C	336719	R	FTN_0329	336642	336911	R	90	193(270)
tnfn1_pw060328p07q129	E04	C	307462	R	FTN_0299	306996	308501	F	502	467(1506)
tnfn1_pw060328p07q130	F04	C	1611046	R	FTN_1514	1610738	1611460	F	241	309(723)
tnfn1_pw060328p07q131	G04	U	1751606	R	FTN_1639	1751185	1751655	R	157	50(471)
tnfn1_pw060328p07q132	H04	C	626519	F	FTN_0595	625825	627738	F	638	695(1914)
tnfn1_pw060328p07q133	A05	C	246788	F	FTN_0223	246583	248118	F	512	206(1536)
tnfn1_pw060328p07q134	B05	C	1645026	R	FTN_1547	1644749	1645384	F	212	278(636)
tnfn1_pw060328p07q135	C05	C	1902677	R	FTN_1772	1902247	1902933	R	229	257(687)
tnfn1_pw060328p07q136	D05	C	410573	F	FTN_0412	410233	411879	F	549	341(1647)
tnfn1_pw060328p07q137	E05	C	1311485	F	FTN_1245	1310691	1311863	R	391	379(1173)
tnfn1_pw060328p07q138	F05	U	1553776	R	FTN_1465	1553361	1554044	R	228	269(684)
tnfn1_pw060328p07q139	G05	U	1598599	R	FTN_1503	1598264	1598656	R	131	58(393)
tnfn1_pw060328p07q140	H05	C	947928	F	FTN_0891	947381	948424	R	348	497(1044)
tnfn1_pw060328p07q141	A06	C	774343	R	FTN_0718	773937	774791	R	285	449(855)
tnfn1_pw060328p07q142	B06	C	1080552	F	FTN_1023	1080187	1080771	R	195	220(585)
tnfn1_pw060328p07q143	C06	C	610530	R	FTN_0581	609811	611025	R	405	496(1215)
tnfn1_pw060328p07q144	D06	U	765157	R	FTN_0714	760571	766126	F	1852	4587(5556)
tnfn1_pw060328p07q145	E06	C	1466221	F	FTN_1388	1466005	1466622	F	206	217(618)
tnfn1_pw060328p07q146	F06	C	384875	F	FTN_0383	384611	384997	R	129	123(387)
tnfn1_pw060328p07q147	G06	C	1167456	F	FTN_1106	1167276	1168349	F	358	181(1074)
tnfn1_pw060328p07q148	H06	C	1630798	R	FTN_1533	1630614	1631801	F	396	185(1188)

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_pw060328p07q149	A07	C	1253724	F	FTN_1180	1252995	1253897	R	301	174(903)
tnfn1_pw060328p07q150	B07	U	1241349	F	FTN_1170	1240289	1242037	R	583	689(1749)
tnfn1_pw060328p07q151	C07	C	1228628	R	FTN_1157	1227077	1228891	F	605	1552(1815)
tnfn1_pw060328p07q152	D07	C	362495	R	FTN_0359	362380	363099	F	240	116(720)
tnfn1_pw060328p07q153	E07	C	1477779	F	FTN_1398	1477435	1477947	R	171	169(513)
tnfn1_pw060328p07q154	F07	C	83458	R	FTN_0070	83199	83603	R	135	146(405)
tnfn1_pw060328p07q155	G07	C	916630	F	FTN_0862	916124	917245	F	374	507(1122)
tnfn1_pw060328p07q156	H07	C	829403	R	FTN_0772	829228	829515	R	96	113(288)
tnfn1_pw060328p07q157	A08	C	250873	F	FTN_0227	250191	250907	F	239	683(717)
tnfn1_pw060328p07q158	B08	C	328341	R	FTN_0318	328177	328455	R	93	115(279)
tnfn1_pw060328p07q159	C08	C	645460	F	FTN_0612	645168	645830	F	221	293(663)
tnfn1_pw060328p07q160	D08	U	1014520	R	FTN_0959	1013924	1014790	F	289	597(867)
tnfn1_pw060328p07q161	E08	C	1268187	R	FTN_1194	1268084	1268461	R	126	275(378)
tnfn1_pw060328p07q162	F08	C	578843	F	FTN_0554	578694	579158	F	155	150(465)
tnfn1_pw060328p07q163	G08	C	1349931	R	FTN_1277	1349725	1351194	F	490	207(1470)
tnfn1_pw060328p07q164	H08	C	1748608	R	FTN_1636	1748316	1749014	R	233	407(699)
tnfn1_pw060328p07q165	A09	C	173089	R	FTN_0159	172770	174437	R	556	1349(1668)
tnfn1_pw060328p07q166	B09	C	251778	F	FTN_0228	250932	251798	F	289	847(867)
tnfn1_pw060328p07q167	C09	C	49983	R	FTN_0045	49665	50741	F	359	319(1077)
tnfn1_pw060328p07q168	D09	C	1071185	F	FTN_1011	1070332	1071615	R	428	431(1284)
tnfn1_pw060328p07q169	E09	C	1258998	R	FTN_1185	1258782	1259453	F	224	217(672)
tnfn1_pw060328p07q170	F09	C	353283	R	FTN_0346	352150	353400	R	417	118(1251)
tnfn1_pw060328p07q171	G09	C	67384	F	FTN_0057	66665	67894	R	410	511(1230)
tnfn1_pw060328p07q172	H09	C	888002	R	FTN_0831	887579	888901	F	441	424(1323)
tnfn1_pw060328p07q173	A10	C	1023327	R	FTN_0967	1022986	1023456	R	157	130(471)
tnfn1_pw060328p07q174	B10	C	1838306	R	FTN_1714	1837876	1838559	R	228	254(684)
tnfn1_pw060328p07q175	C10	C	87428	F	FTN_0075	87397	87747	R	117	320(351)
tnfn1_pw060328p07q176	D10	C	1520700	R	FTN_1435	1520404	1520820	R	139	121(417)
tnfn1_pw060328p07q177	E10	C	1308021	R	FTN_1240	1308006	1308269	F	88	16(264)
tnfn1_pw060328p07q178	F10	C	1056005	F	-	1055368	1056224	F	285.6	638(857)
tnfn1_pw060328p07q179	G10	C	1274382	F	FTN_1200	1274037	1274498	R	154	117(462)
tnfn1_pw060328p07q180	H10	C	1337482	F	FTN_1265	1336964	1337773	F	270	519(810)
tnfn1_pw060328p07q181	A11	C	432983	F	FTN_0434	432829	433740	F	304	155(912)
tnfn1_pw060328p07q182	B11	C	656586	R	FTN_0625	656096	657148	R	351	563(1053)
tnfn1_pw060328p07q183	C11	C	978967	R	FTN_0921	978489	979337	F	283	479(849)
tnfn1_pw060328p07q184	D11	C	215190	R	-	214716	215453	R	246	264(738)
tnfn1_pw060328p07q185	E11	C	1856435	F	FTN_1728	1855928	1856812	R	295	378(885)
tnfn1_pw060328p07q186	F11	C	31645	F	FTN_0031	31335	32201	F	289	311(867)
tnfn1_pw060328p07q187	G11	C	1276601	R	FTN_1202	1275819	1277072	R	418	472(1254)
tnfn1_pw060328p07q188	H11	C	1866355	R	-	1866016	1866726	F	237	340(711)
tnfn1_pw060328p07q189	A12	C	602167	R	FTN_0574	601674	602558	R	295	392(885)
tnfn1_pw060328p07q190	B12	C	1617006	F	FTN_1519	1616753	1617106	R	118	101(354)
tnfn1_pw060328p07q191	C12	C	609268	F	FTN_0580	608770	609717	R	316	450(948)
tnfn1_pw060328p07q192	D12	C	106765	R	FTN_0095	106145	106807	R	221	43(663)
tnfn1_pw060328p07q193	E12	C	773174	F	FTN_0717	772243	773937	R	565	764(1695)
tnfn1_pw060328p07q194	F12	C	1620237	R	FTN_1522	1619418	1620341	R	308	105(924)
tnfn1_pw060328p07q195	G12	C	645847	F	FTN_0613	645826	646041	F	72	22(216)
tnfn1_pw060328p07q196	H12	C	1396727	R	FTN_1321	1395775	1396968	R	398	242(1194)

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_pw060328p07q101	A01	EXACT(0)	122	112	71	19	EXACT(0)	200	189	46
tnfn1_pw060328p07q102	B01	EXACT(0)	121	106	95	23	EXACT(0)	200	181	49
tnfn1_pw060328p07q103	C01	EXACT(0)	121	120	93	25	EXACT(0)	193	185	50
tnfn1_pw060328p07q104	D01	EXACT(0)	122	118	70	22	EXACT(0)	200	167	42
tnfn1_pw060328p07q105	E01	EXACT(0)	118	112	93	32	EXACT(0)	200	186	61
tnfn1_pw060328p07q106	F01	EXACT(0)	123	126	103	32	EXACT(0)	186	174	50
tnfn1_pw060328p07q107	G01	EXACT(0)	122	106	75	20	EXACT(0)	200	194	44
tnfn1_pw060328p07q108	H01	EXACT(0)	111	112	102	48	EXACT(0)	200	189	65
tnfn1_pw060328p07q109	A02	EXACT(0)	122	117	95	21	EXACT(0)	200	181	44
tnfn1_pw060328p07q110	B02	EXACT(0)	121	112	87	25	EXACT(0)	200	188	56
tnfn1_pw060328p07q111	C02	EXACT(0)	157	153	134	42	EXACT(0)	200	188	61
tnfn1_pw060328p07q112	D02	EXACT(0)	122	113	94	26	EXACT(0)	200	186	51
tnfn1_pw060328p07q113	E02	EXACT(0)	123	109	80	21	EXACT(0)	30	27	46
tnfn1_pw060328p07q114	F02	EXACT(0)	225	106	70	18	EXACT(0)	200	187	53
tnfn1_pw060328p07q115	G02	EXACT(0)	123	116	91	22	EXACT(0)	200	188	50
tnfn1_pw060328p07q116	H02	EXACT(0)	124	118	99	27	EXACT(0)	200	185	57
tnfn1_pw060328p07q117	A03	EXACT(0)	126	119	89	24	EXACT(0)	200	196	51
tnfn1_pw060328p07q118	B03	ADJUSTED(5)	133	90	58	22	ESTIMATE(3)	174	33	14
tnfn1_pw060328p07q119	C03	EXACT(0)	209	110	41	14	EXACT(0)	200	196	39
tnfn1_pw060328p07q120	D03	EXACT(0)	122	113	94	42	EXACT(0)	200	186	57
tnfn1_pw060328p07q121	E03	EXACT(0)	168	137	118	24	EXACT(0)	200	197	40
tnfn1_pw060328p07q122	F03	EXACT(0)	156	152	121	37	EXACT(0)	200	193	58
tnfn1_pw060328p07q123	G03	EXACT(0)	155	145	129	42	EXACT(0)	200	191	57
tnfn1_pw060328p07q124	H03	EXACT(0)	157	146	131	40	EXACT(0)	200	145	42
tnfn1_pw060328p07q125	A04	EXACT(0)	156	145	122	29	EXACT(0)	200	185	57
tnfn1_pw060328p07q126	B04	EXACT(0)	156	151	117	31	EXACT(0)	200	182	58
tnfn1_pw060328p07q127	C04	EXACT(0)	156	145	127	35	EXACT(0)	128	119	45
tnfn1_pw060328p07q128	D04	EXACT(0)	156	145	119	36	EXACT(0)	159	121	29
tnfn1_pw060328p07q129	E04	EXACT(0)	155	145	126	42	EXACT(0)	200	192	55
tnfn1_pw060328p07q130	F04	EXACT(0)	156	146	130	43	EXACT(0)	77	77	55
tnfn1_pw060328p07q131	G04	EXACT(0)	156	152	128	38	EXACT(0)	200	196	58
tnfn1_pw060328p07q132	H04	EXACT(0)	157	153	137	45	EXACT(0)	200	156	38
tnfn1_pw060328p07q133	A05	EXACT(0)	156	152	122	31	EXACT(0)	200	191	58
tnfn1_pw060328p07q134	B05	EXACT(0)	155	151	124	39	EXACT(0)	200	190	58
tnfn1_pw060328p07q135	C05	EXACT(0)	156	153	125	40	EXACT(0)	200	187	57
tnfn1_pw060328p07q136	D05	EXACT(0)	156	153	132	42	EXACT(0)	200	188	56
tnfn1_pw060328p07q137	E05	EXACT(0)	157	145	136	43	EXACT(0)	200	193	62
tnfn1_pw060328p07q138	F05	EXACT(0)	169	122	109	23	EXACT(0)	200	190	40
tnfn1_pw060328p07q139	G05	EXACT(0)	165	138	93	23	EXACT(0)	200	196	38
tnfn1_pw060328p07q140	H05	EXACT(0)	156	142	112	35	EXACT(0)	200	195	52
tnfn1_pw060328p07q141	A06	EXACT(0)	156	146	103	25	EXACT(0)	200	192	55
tnfn1_pw060328p07q142	B06	EXACT(0)	155	146	124	37	EXACT(0)	200	144	42
tnfn1_pw060328p07q143	C06	EXACT(0)	156	144	119	38	EXACT(0)	124	112	41
tnfn1_pw060328p07q144	D06	EXACT(0)	154	152	114	24	EXACT(0)	200	191	48
tnfn1_pw060328p07q145	E06	EXACT(0)	153	145	124	42	EXACT(0)	200	184	53
tnfn1_pw060328p07q146	F06	EXACT(0)	155	152	115	36	EXACT(0)	200	190	52
tnfn1_pw060328p07q147	G06	EXACT(0)	155	145	123	41	EXACT(0)	200	190	55
tnfn1_pw060328p07q148	H06	EXACT(0)	157	152	135	40	EXACT(0)	200	125	26

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_pw060328p07q149	A07	EXACT(0)	157	153	124	35	EXACT(0)	200	184	56
tnfn1_pw060328p07q150	B07	EXACT(0)	157	152	130	43	EXACT(0)	201	132	36
tnfn1_pw060328p07q151	C07	EXACT(0)	155	151	121	38	EXACT(0)	200	195	56
tnfn1_pw060328p07q152	D07	EXACT(0)	156	152	134	42	EXACT(0)	196	156	44
tnfn1_pw060328p07q153	E07	EXACT(0)	156	153	126	38	EXACT(0)	200	189	56
tnfn1_pw060328p07q154	F07	EXACT(0)	156	114	95	33	EXACT(0)	200	198	45
tnfn1_pw060328p07q155	G07	EXACT(0)	120	119	104	49	EXACT(0)	200	182	60
tnfn1_pw060328p07q156	H07	EXACT(0)	121	106	74	21	EXACT(0)	200	184	50
tnfn1_pw060328p07q157	A08	EXACT(0)	121	112	93	34	EXACT(0)	200	189	55
tnfn1_pw060328p07q158	B08	EXACT(0)	122	117	80	21	EXACT(0)	200	186	52
tnfn1_pw060328p07q159	C08	EXACT(0)	114	112	107	40	EXACT(0)	200	189	61
tnfn1_pw060328p07q160	D08	EXACT(0)	156	146	120	28	EXACT(0)	200	184	52
tnfn1_pw060328p07q161	E08	EXACT(0)	122	113	88	26	EXACT(0)	200	187	50
tnfn1_pw060328p07q162	F08	EXACT(0)	113	113	103	34	EXACT(0)	200	188	36
tnfn1_pw060328p07q163	G08	EXACT(0)	157	153	109	35	EXACT(0)	200	192	61
tnfn1_pw060328p07q164	H08	EXACT(0)	106	106	96	50	EXACT(0)	200	168	55
tnfn1_pw060328p07q165	A09	EXACT(0)	120	119	104	42	EXACT(0)	200	193	64
tnfn1_pw060328p07q166	B09	EXACT(0)	121	112	96	37	EXACT(0)	200	190	54
tnfn1_pw060328p07q167	C09	EXACT(0)	156	151	124	37	EXACT(0)	200	184	54
tnfn1_pw060328p07q168	D09	EXACT(0)	157	152	127	37	EXACT(0)	200	193	53
tnfn1_pw060328p07q169	E09	EXACT(0)	156	152	113	33	EXACT(0)	200	193	56
tnfn1_pw060328p07q170	F09	EXACT(0)	156	151	124	35	EXACT(0)	199	157	38
tnfn1_pw060328p07q171	G09	EXACT(0)	157	152	133	38	EXACT(0)	38	36	53
tnfn1_pw060328p07q172	H09	EXACT(0)	158	153	131	36	EXACT(0)	200	189	55
tnfn1_pw060328p07q173	A10	EXACT(0)	155	145	120	39	EXACT(0)	200	191	56
tnfn1_pw060328p07q174	B10	EXACT(0)	156	152	125	40	EXACT(0)	200	187	56
tnfn1_pw060328p07q175	C10	EXACT(0)	156	151	127	39	EXACT(0)	200	185	48
tnfn1_pw060328p07q176	D10	EXACT(0)	155	152	128	38	EXACT(0)	200	184	54
tnfn1_pw060328p07q177	E10	EXACT(0)	155	139	116	26	EXACT(0)	200	158	46
tnfn1_pw060328p07q178	F10	EXACT(0)	155	145	117	36	EXACT(0)	200	182	55
tnfn1_pw060328p07q179	G10	EXACT(0)	154	152	123	41	EXACT(0)	200	188	59
tnfn1_pw060328p07q180	H10	EXACT(0)	155	152	104	26	EXACT(0)	200	191	56
tnfn1_pw060328p07q181	A11	EXACT(0)	157	152	120	37	EXACT(0)	200	194	57
tnfn1_pw060328p07q182	B11	EXACT(0)	156	152	119	36	EXACT(0)	200	193	49
tnfn1_pw060328p07q183	C11	EXACT(0)	156	146	118	35	EXACT(0)	200	185	53
tnfn1_pw060328p07q184	D11	EXACT(0)	157	153	128	40	EXACT(0)	200	142	38
tnfn1_pw060328p07q185	E11	EXACT(0)	156	153	123	38	EXACT(0)	200	190	52
tnfn1_pw060328p07q186	F11	EXACT(0)	155	152	113	35	EXACT(0)	200	179	53
tnfn1_pw060328p07q187	G11	EXACT(0)	156	151	121	37	EXACT(0)	200	189	55
tnfn1_pw060328p07q188	H11	EXACT(0)	152	90	90	31	EXACT(0)	201	127	35
tnfn1_pw060328p07q189	A12	EXACT(0)	154	138	123	37	EXACT(0)	200	184	57
tnfn1_pw060328p07q190	B12	EXACT(0)	155	145	123	40	EXACT(0)	200	186	57
tnfn1_pw060328p07q191	C12	EXACT(0)	156	152	119	38	EXACT(0)	185	170	48
tnfn1_pw060328p07q192	D12	EXACT(0)	157	152	127	33	EXACT(0)	200	194	56
tnfn1_pw060328p07q193	E12	EXACT(0)	156	148	129	38	EXACT(0)	200	178	56
tnfn1_pw060328p07q194	F12	EXACT(0)	122	119	109	43	EXACT(0)	200	173	48
tnfn1_pw060328p07q195	G12	EXACT(0)	122	119	106	40	EXACT(0)	200	185	57
tnfn1_pw060328p07q196	H12	EXACT(0)	121	112	107	44	EXACT(0)	200	187	58