

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 1 (tnfn1_pw060323p01)**

Catalog No. NR-8035

For research use only. Not for human use.

Contributor:

Colin Manoil, Ph.D., Professor of Genome Sciences,
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-8035 represents Plate 1 (tnfn1_pw060323p01) 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-8035 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 1 (tnfn1_pw060323p01), NR-8035.”

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/bmbl5/bmbl5toc.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_pw060323p01q101	A01	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q102	B01	<KAN-2>	-	cytochrome b561 family protein	energy metabolism
tnfn1_pw060323p01q103	C01	<KAN-2>	rpmG	50S ribosomal protein L33	translation, ribosomal structure and biogenesis
tnfn1_pw060323p01q104	D01	<KAN-2>	-	inositol monophosphatase family protein	putative enzymes
tnfn1_pw060323p01q105	E01	<KAN-2>	secB2	preprotein translocase, subunit B	motility, attachment and secretion structure
tnfn1_pw060323p01q106	F01	<KAN-2>	frr	ribosome recycling factor	translation, ribosomal structure and biogenesis
tnfn1_pw060323p01q107	G01	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p01q108	H01	T18	-	-	-
tnfn1_pw060323p01q109	A02	<KAN-2>	-	BolA family protein	transcription
tnfn1_pw060323p01q110	B02	<KAN-2>	-	outer membrane protein	cell wall / LPS / capsule
tnfn1_pw060323p01q111	C02	<KAN-2>	-	outer membrane protein	cell wall / LPS / capsule
tnfn1_pw060323p01q112	D02	T18	-	aminomutase	amino acid metabolism
tnfn1_pw060323p01q113	E02	T17	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p01q114	F02	T17	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p01q115	G02	T17	plsC	1-acylglycerol-3-phosphate acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060323p01q116	H02	T17	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p01q117	A03	T17	ruvA	holliday junction DNA helicase, subunit A	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p01q118	B03	T17	ppiC	parvulin-like peptidyl-prolyl isomerase domain	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p01q119	C03	T18	-	amino acid transporter (AAT) family protein	transport - amino-acid
tnfn1_pw060323p01q120	D03	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q121	E03	T18	-	hypothetical protein	potentially coding: hypothetical - novel
tnfn1_pw060323p01q122	F03	T18	ubiC	chorismate pyruvate lyase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p01q123	G03	T18	guaA	GMP synthetase (glutamine-hydrolysing)	nucleotides and nucleosides metabolism
tnfn1_pw060323p01q124	H03	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060323p01q125	A04	T20	-	PhoH family protein, putative ATPase	signal transduction and regulation
tnfn1_pw060323p01q126	B04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q127	C04	T20	-	carbon-nitrogen hydrolase family protein	putative enzymes
tnfn1_pw060323p01q128	D04	T20	-	mechanosensitive ion channel protein	transport
tnfn1_pw060323p01q129	E04	T20	potF	ATP-binding cassette putrescine uptake system, periplasmic protein	transport
tnfn1_pw060323p01q130	F04	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060323p01q131	G04	T20	udhA	soluble pyridine nucleotide transhydrogenase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p01q132	H04	T20	isftu2	isftu2	IS element
tnfn1_pw060323p01q133	A05	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060323p01q134	B05	T20	wbtD	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060323p01q135	C05	T20	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060323p01q136	D05	T20	-	prophage maintenance system killer protein (DOC)	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060323p01q137	E05	T20	pcm	protein-L-isoaspartate O-methyltransferase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060323p01q138	F05	T20	-	aspartate/tyrosine/aromatic aminotransferase	amino acid metabolism - biosynthesis
tnfn1_pw060323p01q139	G05	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060323p01q140	H05	T20	kbl	2-amino-3-ketobutyrate coenzyme A ligase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q141	A06	T20	-	pseudogene: type I restriction-modification system, subunit M (methyltransferase)	pseudogene
tnfn1_pw060323p01q142	B06	T20	-	aspartate/tyrosine/aromatic aminotransferase	amino acid metabolism - biosynthesis
tnfn1_pw060323p01q143	C06	T20	-	GTPase of unknown function	putative enzymes
tnfn1_pw060323p01q144	D06	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p01q145	E06	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060323p01q146	F06	T20	chiA	chitinase, glycosyl hydrolase family 18	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q147	G06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q148	H06	T20	pabA	para-aminobenzoate synthase component II	cofactors, prosthetic groups, electron carriers metabolism

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060323p01q149	A07	T20	fadD	long chain fatty acid CoA ligase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q150	B07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q151	C07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q152	D07	T20	recA	recombinase A protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p01q153	E07	T20	-	protein of unknown function	putative enzymes
tnfn1_pw060323p01q154	F07	T20	phnA	phosphonoacetate hydrolase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q155	G07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p01q156	H07	T20	sodC	superoxide dismutase (Cu-Zn) precursor	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q157	A08	T20	-	-	-
tnfn1_pw060323p01q158	B08	T20	-	peptide methionine sulfoxide reductase-related protein	post-translational modification, protein turnover, chaperones
tnfn1_pw060323p01q159	C08	T20	pepB	cytosol aminopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060323p01q160	D08	T20	pepB	cytosol aminopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060323p01q161	E08	T20	-	VacJ like lipoprotein	cell wall / LPS / capsule
tnfn1_pw060323p01q162	F08	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060323p01q163	G08	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060323p01q164	H08	T20	pilC	Type IV pili polytopic inner membrane protein	motility, attachment and secretion structure
tnfn1_pw060323p01q165	A09	T20	-	deoxyguanosinetriphosphate triphosphohydrolase	nucleotides and nucleosides metabolism
tnfn1_pw060323p01q166	B09	T20	apt	adenine phosphoribosyltransferase	nucleotides and nucleosides metabolism
tnfn1_pw060323p01q167	C09	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q168	D09	T20	glgA	glycogen synthase	carbohydrate metabolism - biosynthesis
tnfn1_pw060323p01q169	E09	T20	-	hypothetical protein	Potentially coding: hypothetical - novel
tnfn1_pw060323p01q170	F09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q171	G09	T20	pdpC	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q172	H09	T20	acs	acyl-coenzyme A synthetase/AMP-(fatty) acid ligases	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q173	A10	T20	deoC	deoxyribose-phosphate aldolase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q174	B10	T20	uvrC	excinuclease ABC, subunit C	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p01q175	C10	T20	-	sugar porter (SP) family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060323p01q176	D10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q177	E10	T20	emrE	putative membrane transporter of cations and cationic drugs, multidrug resistance protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p01q178	F10	T20	rnhA	ribonuclease H	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060323p01q179	G10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q180	H10	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060323p01q181	A11	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q182	B11	T20	-	ROK family protein	putative enzymes
tnfn1_pw060323p01q183	C11	T20	aroE	shikimate 5-dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060323p01q184	D11	T20	-	pseudogene: O-methyltransferase	pseudogene
tnfn1_pw060323p01q185	E11	T20	-	haloacid dehalogenase-like hydrolase	putative enzymes
tnfn1_pw060323p01q186	F11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q187	G11	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060323p01q188	H11	<KAN-2>	-	glutaredoxin-related protein	putative enzymes
tnfn1_pw060323p01q189	A12	T17	bioD	dethiobiotin synthetase	metabolism
tnfn1_pw060323p01q190	B12	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q191	C12	T18	-	-	-
tnfn1_pw060323p01q192	D12	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060323p01q193	E12	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p01q194	F12	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060323p01q195	G12	T18	bglX	glycosyl hydrolase family 3	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060323p01q196	H12	T20	-	-	potentially coding: hypothetical - 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_pw060323p01q101	A01	C	1805213	R	FTN_1688	1804888	1805292	R	135	80(405)
tnfn1_pw060323p01q102	B01	C	104653	F	FTN_0093	104604	105116	F	171	50(513)
tnfn1_pw060323p01q103	C01	C	338602	R	FTN_0332	338502	338654	R	51	53(153)
tnfn1_pw060323p01q104	D01	C	1424722	F	FTN_1346	1424642	1425427	F	262	81(786)
tnfn1_pw060323p01q105	E01	C	1606934	F	FTN_1510	1606754	1607194	F	147	181(441)
tnfn1_pw060323p01q106	F01	C	253133	F	FTN_0230	252583	253137	F	185	551(555)
tnfn1_pw060323p01q107	G01	U	1777557	R	FTN_1662	1777161	1777610	R	150	54(450)
tnfn1_pw060323p01q108	H01	C	900352	F	intergenic					
tnfn1_pw060323p01q109	A02	C	333247	R	FTN_0323	333241	333474	R	78	228(234)
tnfn1_pw060323p01q110	B02	C	202854	R	FTN_0185	202541	203002	R	154	149(462)
tnfn1_pw060323p01q111	C02	U	202790	R	FTN_0185	202541	203002	R	154	213(462)
tnfn1_pw060323p01q112	D02	C	777502	R	FTN_0722	777263	778246	F	328	240(984)
tnfn1_pw060323p01q113	E02	C	1421704	R	FTN_1343	1421385	1422068	R	228	365(684)
tnfn1_pw060323p01q114	F02	C	225960	R	FTN_0205	225741	226649	F	303	220(909)
tnfn1_pw060323p01q115	G02	C	170340	F	FTN_0156	170179	171063	F	295	162(885)
tnfn1_pw060323p01q116	H02	C	1147839	F	FTN_1085	1147596	1148465	F	290	244(870)
tnfn1_pw060323p01q117	A03	C	1082612	F	FTN_1025	1082264	1082911	R	216	300(648)
tnfn1_pw060323p01q118	B03	C	733434	R	FTN_0689	733247	733522	F	92	188(276)
tnfn1_pw060323p01q119	C03	C	913223	F	FTN_0860	912967	914316	R	450	1094(1350)
tnfn1_pw060323p01q120	D03	C	682351	R	FTN_0644	682201	682398	F	66	151(198)
tnfn1_pw060323p01q121	E03	C	1158772	F	-	1158655	1158855	R	68	87(204)
tnfn1_pw060323p01q122	F03	C	386464	F	FTN_0386	386250	386753	R	168	290(504)
tnfn1_pw060323p01q123	G03	C	953203	R	FTN_0897	952865	954412	R	516	1210(1548)
tnfn1_pw060323p01q124	H03	C	1639378	F	FTN_1540	1639091	1639522	F	144	288(432)
tnfn1_pw060323p01q125	A04	C	1123758	F	FTN_1064	1123547	1124527	F	327	212(981)
tnfn1_pw060323p01q126	B04	C	59107	F	FTN_0049	58770	59591	F	274	338(822)
tnfn1_pw060323p01q127	C04	C	885213	R	FTN_0827	884558	885481	R	308	269(924)
tnfn1_pw060323p01q128	D04	C	592544	F	FTN_0566	591956	593071	F	372	589(1116)
tnfn1_pw060323p01q129	E04	C	599639	F	FTN_0572	599215	600393	F	393	425(1179)
tnfn1_pw060323p01q130	F04	C	890057	R	FTN_0832	888904	890442	R	513	386(1539)
tnfn1_pw060323p01q131	G04	C	1059330	F	FTN_0999	1059107	1060504	F	466	224(1398)
tnfn1_pw060323p01q132	H04	C	1723174	F	-	1722538	1723402	R	288.3	229(865)
tnfn1_pw060323p01q133	A05	C	391566	F	FTN_0392	390793	391710	R	306	145(918)
tnfn1_pw060323p01q134	B05	C	1508540	F	FTN_1427	1507571	1508659	R	363	120(1089)
tnfn1_pw060323p01q135	C05	C	1305263	R	FTN_1236	1304037	1305269	R	411	7(1233)
tnfn1_pw060323p01q136	D05	C	1580557	F	FTN_1488	1579953	1580906	R	318	350(954)
tnfn1_pw060323p01q137	E05	C	1825977	F	FTN_1704	1825666	1826283	R	206	307(618)
tnfn1_pw060323p01q138	F05	C	1460396	R	FTN_1380	1459763	1460893	F	377	634(1131)
tnfn1_pw060323p01q139	G05	U	1039260	R	FTN_0984	1037817	1039706	R	630	447(1890)
tnfn1_pw060323p01q140	H05	C	658042	F	FTN_0626	657174	658367	R	398	326(1194)
tnfn1_pw060323p01q141	A06	C	290511	R	FTN_0283	289901	291434	F	511.3	611(1534)
tnfn1_pw060323p01q142	B06	C	408393	R	FTN_0410	407870	409057	R	396	665(1188)
tnfn1_pw060323p01q143	C06	C	602393	R	FTN_0574	601674	602558	R	295	166(885)
tnfn1_pw060323p01q144	D06	C	1421179	F	FTN_1342	1421108	1421389	F	94	72(282)
tnfn1_pw060323p01q145	E06	C	651787	F	FTN_0620	651130	652365	F	412	658(1236)
tnfn1_pw060323p01q146	F06	C	659770	F	FTN_0627	658901	661510	F	870	870(2610)
tnfn1_pw060323p01q147	G06	C	1461320	F	FTN_1381	1460964	1462379	F	472	357(1416)
tnfn1_pw060323p01q148	H06	C	880608	F	FTN_0823	880461	881012	F	184	148(552)

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_pw060323p01q149	A07	C	1521579	R	FTN_1436	1520964	1522649	F	562	616(1686)
tnfn1_pw060323p01q150	B07	C	346106	R	FTN_0341	345948	346190	R	81	85(243)
tnfn1_pw060323p01q151	C07	C	346106	R	FTN_0341	345948	346190	R	81	85(243)
tnfn1_pw060323p01q152	D07	C	132763	R	FTN_0122	132141	133217	F	359	623(1077)
tnfn1_pw060323p01q153	E07	C	54175	F	FTN_0047	53754	57527	F	1258	422(3774)
tnfn1_pw060323p01q154	F07	C	1026208	R	FTN_0971	1025923	1026252	R	110	45(330)
tnfn1_pw060323p01q155	G07	C	740530	F	FTN_0696	740453	741076	R	208	547(624)
tnfn1_pw060323p01q156	H07	C	403619	F	FTN_0405	403380	403934	F	185	240(555)
tnfn1_pw060323p01q157	A08	C	190536	F	intergenic					
tnfn1_pw060323p01q158	B08	C	403110	R	FTN_0404	402710	403219	R	170	110(510)
tnfn1_pw060323p01q159	C08	C	838908	R	FTN_0780	838149	839525	F	459	760(1377)
tnfn1_pw060323p01q160	D08	C	838908	R	FTN_0780	838149	839525	F	459	760(1377)
tnfn1_pw060323p01q161	E08	C	1232171	R	FTN_1160	1231701	1232618	R	306	448(918)
tnfn1_pw060323p01q162	F08	C	1145886	F	FTN_1082	1145210	1146601	R	464	716(1392)
tnfn1_pw060323p01q163	G08	C	780229	F	FTN_0727	780006	780572	F	189	224(567)
tnfn1_pw060323p01q164	H08	C	1180955	F	FTN_1116	1180496	1181722	F	409	460(1227)
tnfn1_pw060323p01q165	A09	C	616323	F	FTN_0587	615588	616814	F	409	736(1227)
tnfn1_pw060323p01q166	B09	C	1743702	R	FTN_1633	1743411	1743935	R	175	234(525)
tnfn1_pw060323p01q167	C09	C	503662	R	FTN_0497	503304	503723	R	140	62(420)
tnfn1_pw060323p01q168	D09	C	533618	R	FTN_0516	533104	534570	F	489	515(1467)
tnfn1_pw060323p01q169	E09	C	372599	F	-	372500	372739	F	80	100(240)
tnfn1_pw060323p01q170	F09	C	1612915	F	FTN_1517	1612827	1613456	F	210	89(630)
tnfn1_pw060323p01q171	G09	C	1392081	R	FTN_1319	1391204	1395178	F	1325	878(3975)
tnfn1_pw060323p01q172	H09	C	783861	R	FTN_0730	782807	784741	F	645	1055(1935)
tnfn1_pw060323p01q173	A10	C	1702502	R	FTN_1601	1702300	1703058	R	253	557(759)
tnfn1_pw060323p01q174	B10	C	724063	F	FTN_0680	723838	725673	F	612	226(1836)
tnfn1_pw060323p01q175	C10	C	1530420	R	FTN_1441	1529445	1530722	R	426	303(1278)
tnfn1_pw060323p01q176	D10	C	1119398	F	FTN_1059	1119271	1119732	F	154	128(462)
tnfn1_pw060323p01q177	E10	C	856596	F	FTN_0799	856317	856643	R	109	48(327)
tnfn1_pw060323p01q178	F10	C	1151588	F	FTN_1089	1151223	1151678	R	152	91(456)
tnfn1_pw060323p01q179	G10	C	628141	R	FTN_0596	627752	628633	R	294	493(882)
tnfn1_pw060323p01q180	H10	C	827378	R	FTN_0770	826604	827803	R	400	426(1200)
tnfn1_pw060323p01q181	A11	C	341622	F	FTN_0336	341568	341762	F	65	55(195)
tnfn1_pw060323p01q182	B11	C	649732	R	FTN_0618	649296	650240	F	315	437(945)
tnfn1_pw060323p01q183	C11	C	88941	F	FTN_0078	88548	89318	F	257	394(771)
tnfn1_pw060323p01q184	D11	C	1876616	R	FTN_1746	1876485	1877140	R	218.6	525(656)
tnfn1_pw060323p01q185	E11	C	1281869	R	FTN_1211	1281241	1281900	R	220	32(660)
tnfn1_pw060323p01q186	F11	C	980609	F	FTN_0923	980427	980855	R	143	247(429)
tnfn1_pw060323p01q187	G11	C	994600	F	FTN_0933	994548	994829	F	94	53(282)
tnfn1_pw060323p01q188	H11	C	1755527	F	FTN_1643	1755445	1755771	F	109	83(327)
tnfn1_pw060323p01q189	A12	C	869536	F	FTN_0812	869347	870021	R	225	486(675)
tnfn1_pw060323p01q190	B12	C	1147024	R	FTN_1083	1146713	1147327	F	205	312(615)
tnfn1_pw060323p01q191	C12	C	1662197	F	intergenic					
tnfn1_pw060323p01q192	D12	C	455232	F	FTN_0452	454529	455929	F	467	704(1401)
tnfn1_pw060323p01q193	E12	C	373352	R	FTN_0370	373090	373365	F	92	263(276)
tnfn1_pw060323p01q194	F12	C	615225	R	FTN_0586	615044	615559	F	172	182(516)
tnfn1_pw060323p01q195	G12	C	1562582	R	FTN_1474	1561674	1562807	R	378	226(1134)
tnfn1_pw060323p01q196	H12	U	9096	R	-	8981	9148	R	56	53(168)

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_pw060323p01q101	A01	EXACT(0)	120	106	62	21	EXACT(0)	200	188	42
tnfn1_pw060323p01q102	B01	EXACT(0)	123	109	67	18	EXACT(0)	205	155	29
tnfn1_pw060323p01q103	C01	EXACT(0)	121	120	72	22	EXACT(0)	200	187	48
tnfn1_pw060323p01q104	D01	EXACT(0)	123	120	92	23	EXACT(0)	200	186	51
tnfn1_pw060323p01q105	E01	NONE	0	0	0	31	ESTIMATE(122)	594	410	27
tnfn1_pw060323p01q106	F01	EXACT(0)	123	109	94	23	EXACT(0)	200	186	50
tnfn1_pw060323p01q107	G01	EXACT(0)	114	113	102	37	EXACT(0)	200	190	54
tnfn1_pw060323p01q108	H01	EXACT(0)	125	20	15	22	EXACT(0)	200	176	46
tnfn1_pw060323p01q109	A02	EXACT(0)	122	120	93	24	EXACT(0)	200	170	53
tnfn1_pw060323p01q110	B02	EXACT(0)	124	112	93	33	EXACT(0)	200	127	26
tnfn1_pw060323p01q111	C02	NONE	0	0	0	30	ESTIMATE(114)	439	328	27
tnfn1_pw060323p01q112	D02	EXACT(0)	124	110	87	22	EXACT(0)	200	190	51
tnfn1_pw060323p01q113	E02	EXACT(0)	125	120	79	23	EXACT(0)	200	182	57
tnfn1_pw060323p01q114	F02	EXACT(0)	122	112	96	33	EXACT(0)	200	196	48
tnfn1_pw060323p01q115	G02	EXACT(0)	121	105	90	26	EXACT(0)	200	186	54
tnfn1_pw060323p01q116	H02	EXACT(0)	121	109	87	22	EXACT(0)	200	189	49
tnfn1_pw060323p01q117	A03	EXACT(0)	122	118	100	32	EXACT(0)	200	190	51
tnfn1_pw060323p01q118	B03	EXACT(0)	125	118	95	27	EXACT(0)	200	194	56
tnfn1_pw060323p01q119	C03	EXACT(0)	123	119	88	23	EXACT(0)	200	187	54
tnfn1_pw060323p01q120	D03	EXACT(0)	116	105	84	23	EXACT(0)	200	187	55
tnfn1_pw060323p01q121	E03	EXACT(0)	123	113	100	36	EXACT(0)	200	174	45
tnfn1_pw060323p01q122	F03	EXACT(0)	123	117	90	25	EXACT(0)	200	191	52
tnfn1_pw060323p01q123	G03	NONE	0	0	0	16	ESTIMATE(121)	408	362	42
tnfn1_pw060323p01q124	H03	EXACT(0)	122	112	93	37	EXACT(0)	192	180	55
tnfn1_pw060323p01q125	A04	EXACT(0)	156	150	123	36	EXACT(0)	200	189	57
tnfn1_pw060323p01q126	B04	EXACT(0)	158	144	106	22	EXACT(0)	200	179	45
tnfn1_pw060323p01q127	C04	EXACT(0)	157	142	103	30	EXACT(0)	200	186	54
tnfn1_pw060323p01q128	D04	EXACT(0)	156	153	132	38	EXACT(0)	200	188	53
tnfn1_pw060323p01q129	E04	EXACT(0)	155	145	119	34	EXACT(0)	200	188	53
tnfn1_pw060323p01q130	F04	EXACT(0)	157	151	111	33	EXACT(0)	200	190	56
tnfn1_pw060323p01q131	G04	EXACT(0)	155	142	86	21	EXACT(0)	200	189	54
tnfn1_pw060323p01q132	H04	EXACT(0)	155	145	123	36	EXACT(0)	200	181	59
tnfn1_pw060323p01q133	A05	EXACT(0)	156	152	122	35	EXACT(0)	200	184	48
tnfn1_pw060323p01q134	B05	EXACT(0)	155	145	126	39	EXACT(0)	200	184	55
tnfn1_pw060323p01q135	C05	EXACT(0)	159	153	136	37	EXACT(0)	200	186	49
tnfn1_pw060323p01q136	D05	EXACT(0)	156	142	83	22	EXACT(0)	200	186	51
tnfn1_pw060323p01q137	E05	EXACT(0)	158	153	139	36	EXACT(0)	155	128	25
tnfn1_pw060323p01q138	F05	EXACT(0)	156	153	129	40	EXACT(0)	200	187	59
tnfn1_pw060323p01q139	G05	EXACT(0)	159	153	140	46	EXACT(0)	200	160	51
tnfn1_pw060323p01q140	H05	EXACT(0)	157	159	124	36	EXACT(0)	200	194	54
tnfn1_pw060323p01q141	A06	EXACT(0)	156	153	132	41	EXACT(0)	200	196	52
tnfn1_pw060323p01q142	B06	EXACT(0)	155	145	123	41	EXACT(0)	200	196	58
tnfn1_pw060323p01q143	C06	EXACT(0)	156	152	131	42	EXACT(0)	171	121	24
tnfn1_pw060323p01q144	D06	EXACT(0)	155	151	130	35	EXACT(0)	200	193	53
tnfn1_pw060323p01q145	E06	EXACT(0)	155	151	133	41	EXACT(0)	200	188	54
tnfn1_pw060323p01q146	F06	EXACT(0)	157	152	124	35	EXACT(0)	200	194	54
tnfn1_pw060323p01q147	G06	EXACT(0)	155	153	129	40	EXACT(0)	200	182	52
tnfn1_pw060323p01q148	H06	EXACT(0)	154	145	126	38	EXACT(0)	200	191	50

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_pw060323p01q149	A07	EXACT(0)	155	145	126	39	EXACT(0)	200	189	52
tnfn1_pw060323p01q150	B07	EXACT(0)	156	153	129	40	EXACT(0)	200	160	35
tnfn1_pw060323p01q151	C07	EXACT(0)	156	153	132	40	EXACT(0)	201	103	37
tnfn1_pw060323p01q152	D07	EXACT(0)	157	152	136	42	EXACT(0)	200	198	50
tnfn1_pw060323p01q153	E07	EXACT(0)	157	155	134	38	EXACT(0)	200	185	54
tnfn1_pw060323p01q154	F07	EXACT(0)	156	138	105	30	EXACT(0)	200	189	54
tnfn1_pw060323p01q155	G07	EXACT(0)	156	153	125	35	EXACT(0)	200	191	50
tnfn1_pw060323p01q156	H07	EXACT(0)	155	145	132	42	EXACT(0)	200	199	50
tnfn1_pw060323p01q157	A08	EXACT(0)	156	153	119	33	EXACT(0)	200	185	56
tnfn1_pw060323p01q158	B08	EXACT(0)	154	152	126	41	EXACT(0)	200	143	30
tnfn1_pw060323p01q159	C08	EXACT(0)	155	145	126	41	EXACT(0)	200	196	57
tnfn1_pw060323p01q160	D08	EXACT(0)	155	151	133	41	EXACT(0)	200	196	57
tnfn1_pw060323p01q161	E08	EXACT(0)	154	139	104	36	EXACT(0)	200	193	57
tnfn1_pw060323p01q162	F08	EXACT(0)	156	142	120	37	EXACT(0)	192	186	52
tnfn1_pw060323p01q163	G08	EXACT(0)	155	136	121	39	EXACT(0)	200	187	51
tnfn1_pw060323p01q164	H08	EXACT(0)	155	145	123	41	EXACT(0)	200	193	58
tnfn1_pw060323p01q165	A09	EXACT(0)	156	153	123	41	EXACT(0)	200	185	59
tnfn1_pw060323p01q166	B09	EXACT(0)	157	153	131	41	EXACT(0)	200	195	54
tnfn1_pw060323p01q167	C09	EXACT(0)	157	151	117	30	EXACT(0)	200	173	45
tnfn1_pw060323p01q168	D09	EXACT(0)	155	151	124	36	EXACT(0)	200	196	56
tnfn1_pw060323p01q169	E09	EXACT(0)	154	145	129	39	EXACT(0)	200	152	45
tnfn1_pw060323p01q170	F09	EXACT(0)	155	145	129	41	EXACT(0)	200	193	56
tnfn1_pw060323p01q171	G09	EXACT(0)	155	152	126	40	EXACT(0)	170	157	52
tnfn1_pw060323p01q172	H09	EXACT(0)	156	153	129	42	EXACT(0)	200	194	55
tnfn1_pw060323p01q173	A10	EXACT(0)	154	138	114	36	EXACT(0)	200	191	54
tnfn1_pw060323p01q174	B10	EXACT(0)	154	145	124	44	EXACT(0)	98	91	55
tnfn1_pw060323p01q175	C10	EXACT(0)	154	145	129	36	EXACT(0)	200	179	48
tnfn1_pw060323p01q176	D10	EXACT(0)	156	150	98	32	EXACT(0)	200	185	52
tnfn1_pw060323p01q177	E10	EXACT(0)	155	116	101	36	ESTIMATE(32)	168	126	25
tnfn1_pw060323p01q178	F10	EXACT(0)	158	146	130	39	EXACT(0)	200	190	47
tnfn1_pw060323p01q179	G10	EXACT(0)	155	145	124	35	EXACT(0)	173	165	53
tnfn1_pw060323p01q180	H10	EXACT(0)	156	138	116	34	EXACT(0)	200	191	54
tnfn1_pw060323p01q181	A11	EXACT(0)	155	145	126	40	EXACT(0)	200	178	57
tnfn1_pw060323p01q182	B11	EXACT(0)	160	153	135	40	EXACT(0)	200	150	45
tnfn1_pw060323p01q183	C11	EXACT(0)	156	152	119	35	EXACT(0)	200	191	57
tnfn1_pw060323p01q184	D11	EXACT(0)	156	152	131	37	EXACT(0)	200	181	53
tnfn1_pw060323p01q185	E11	EXACT(0)	156	145	128	39	EXACT(0)	183	175	54
tnfn1_pw060323p01q186	F11	EXACT(0)	154	26	21	10	EXACT(0)	201	162	32
tnfn1_pw060323p01q187	G11	EXACT(0)	121	106	61	20	EXACT(0)	200	188	50
tnfn1_pw060323p01q188	H11	EXACT(0)	120	106	94	30	EXACT(0)	162	160	49
tnfn1_pw060323p01q189	A12	EXACT(0)	123	112	86	23	EXACT(0)	200	190	52
tnfn1_pw060323p01q190	B12	EXACT(0)	122	112	93	28	EXACT(0)	200	190	55
tnfn1_pw060323p01q191	C12	EXACT(0)	122	113	97	41	EXACT(0)	200	191	58
tnfn1_pw060323p01q192	D12	EXACT(0)	123	120	96	27	EXACT(0)	200	186	48
tnfn1_pw060323p01q193	E12	EXACT(0)	125	112	69	23	EXACT(0)	200	185	55
tnfn1_pw060323p01q194	F12	EXACT(0)	122	103	73	25	EXACT(0)	200	189	50
tnfn1_pw060323p01q195	G12	EXACT(0)	122	105	84	23	EXACT(0)	201	98	27
tnfn1_pw060323p01q196	H12	EXACT(0)	154	144	122	42	EXACT(0)	200	172	52