

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 10 (tnfn1_pw060328p02)**

Catalog No. NR-8044

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-8044 represents Plate 10 (tnfn1_pw060328p02) 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. **Strain tnfn1_pw060328p02q123 (Well G03) was not available due to quality issues at the time of release of Plate 10, but is now available on Plate 33 (BEI Resources NR-10484).**

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-8044 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 10 (tnfn1_pw060328p02), NR-8044.”

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_pw060328p02q101	A01	T20	-	pseudogene: sugar transporter	pseudogene
tnfn1_pw060328p02q102	B01	T20	-	deoxyribodipyrimidine photolyase	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p02q103	C01	T20	capB	capsule biosynthesis protein CapB	cell wall / LPS / capsule
tnfn1_pw060328p02q104	D01	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p02q105	E01	T20	appB	cytochrome bd-II terminal oxidase subunit II	energy metabolism
tnfn1_pw060328p02q106	F01	T20	-	drug/metabolite transporter superfamily protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p02q107	G01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q108	H01	T20	-	fatty acid hydroxylase	fatty acids and lipids metabolism
tnfn1_pw060328p02q109	A02	T20	metIQ	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	transport - amino-acid
tnfn1_pw060328p02q110	B02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p02q111	C02	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p02q112	D02	T20	dapD	tetrahydronicotinamide succinylase subunit	amino acid metabolism - biosynthesis
tnfn1_pw060328p02q113	E02	T20	clpP	ATP-dependent Clp protease subunit P	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060328p02q114	F02	T20	pip	proline iminopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060328p02q115	G02	T20	iglB	intracellular growth locus protein B	unknown function - conserved
tnfn1_pw060328p02q116	H02	T20	-	conserved protein of unknown function	cell wall / LPS / capsule
tnfn1_pw060328p02q117	A03	T20	-	C4-dicarboxylate anaerobic carrier	transport
tnfn1_pw060328p02q118	B03	T20	mltA	membrane-bound lytic murein transglycosylase	cell wall / LPS / capsule
tnfn1_pw060328p02q119	C03	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
tnfn1_pw060328p02q120	D03	T20	glpQ	glycerophosphoryl diester phosphodiesterase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p02q121	E03	T20	kdpC	potassium-transporting ATPase C chain	transport
tnfn1_pw060328p02q122	F03	T20	-	protein of unknown function	hypothetical - novel
tnfn1_pw060328p02q123	G03	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q124	H03	T20	-	fucose: H+ symporter (FHS) family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060328p02q125	A04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q126	B04	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p02q127	C04	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p02q128	D04	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p02q129	E04	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p02q130	F04	T20	-	protein of unknown function with radical SAM domain	unknown function - conserved
tnfn1_pw060328p02q131	G04	<KAN-2>	sufD	sufS activator complex, sufD subunit	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p02q132	H04	<KAN-2>	wrbA	trp repressor binding protein	signal transduction and regulation
tnfn1_pw060328p02q133	A05	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p02q134	B05	<KAN-2>	-	acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060328p02q135	C05	<KAN-2>	pyk	pyruvate kinase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p02q136	D05	<KAN-2>	atpC	ATP synthase, F1 sector, subunit epsilon	energy metabolism
tnfn1_pw060328p02q137	E05	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p02q138	F05	<KAN-2>	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p02q139	G05	<KAN-2>	eno	enolase (2-phosphoglycerate dehydratase)	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060328p02q140	H05	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p02q141	A06	<KAN-2>	sucD	succinyl-CoA synthetase, alpha subunit	energy metabolism
tnfn1_pw060328p02q142	B06	<KAN-2>	-	pseudogene: hypothetical protein, fragment	pseudogene
tnfn1_pw060328p02q143	C06	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q144	D06	<KAN-2>	-	thioredoxin	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p02q145	E06	<KAN-2>	-	regulatory factor, Bvg accessory factor family	signal transduction and regulation
tnfn1_pw060328p02q146	F06	<KAN-2>	nuoH	NADH dehydrogenase I, H subunit	energy metabolism
tnfn1_pw060328p02q147	G06	<KAN-2>	-	permease	transport
tnfn1_pw060328p02q148	H06	<KAN-2>	-	transcriptional regulator, ArsR family	signal transduction and regulation

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p02q149	A07	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p02q150	B07	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p02q151	C07	T18	isftu2	isftu2	IS element
tnfn1_pw060328p02q152	D07	T18	-	5-formyltetrahydrofolate cycloligase	putative enzymes
tnfn1_pw060328p02q153	E07	T18	era	GTP-binding protein	putative enzymes
tnfn1_pw060328p02q154	F07	T18	-	predicted hydrolase of the HAD superfamily	putative enzymes
tnfn1_pw060328p02q155	G07	T18	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060328p02q156	H07	T18	bcp	bacterioferritin comigratory protein	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060328p02q157	A08	T18	htpG	chaperone Hsp90, heat shock protein HtpG	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060328p02q158	B08	T18	-	monovalent cation:proton antiporter family protein	transport
tnfn1_pw060328p02q159	C08	T18	-	isomerase	putative enzymes
tnfn1_pw060328p02q160	D08	T18	-	haloacid dehalogenase-like hydrolase	putative enzymes
tnfn1_pw060328p02q161	E08	T18	-	GtrA-like protein	putative enzymes
tnfn1_pw060328p02q162	F08	T18	-	sugar:cation symporter family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060328p02q163	G08	T20	-	modification methylase, HemK family	translation, ribosomal structure and biogenesis
tnfn1_pw060328p02q164	H08	T20	-	transcriptional regulator	signal transduction and regulation
tnfn1_pw060328p02q165	A09	T20	-	amino acid-polyamine-organocation family protein	transport - amino-acid
tnfn1_pw060328p02q166	B09	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p02q167	C09	T20	-	prophage repressor protein	signal transduction and regulation
tnfn1_pw060328p02q168	D09	T20	-	membrane fusion protein	motility, attachment and secretion structure
tnfn1_pw060328p02q169	E09	T20	rdgC	recombination associated protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p02q170	F09	T20	lpcC	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060328p02q171	G09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060328p02q172	H09	T20	add	deoxyadenosine deaminase/adenosine deaminase	nucleotides and nucleosides metabolism
tnfn1_pw060328p02q173	A10	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p02q174	B10	T20	aroB	3-dehydroquinate synthetase	amino acid metabolism - biosynthesis
tnfn1_pw060328p02q175	C10	T20	putA	bifunctional proline dehydrogenase, pyrroline-5-carboxylate dehydrogenase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p02q176	D10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p02q177	E10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p02q178	F10	T20	-	small conductance mechanosensitive ion channel family protein	transport
tnfn1_pw060328p02q179	G10	T20	-	phage integrase	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060328p02q180	H10	T20	recF	RecFOR complex, RecF component	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p02q181	A11	T20	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p02q182	B11	T20	-	rare lipoprotein B family protein	cell wall / LPS / capsule
tnfn1_pw060328p02q183	C11	T20	isftu2	isftu2	IS element
tnfn1_pw060328p02q184	D11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q185	E11	T20	-	protein of unknown function, Lamb/YcsF family	unknown function - conserved
tnfn1_pw060328p02q186	F11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p02q187	G11	T20	-	heavy metal cation transport ATPase	transport
tnfn1_pw060328p02q188	H11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q189	A12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q190	B12	T20	ppdK	phosphoenolpyruvate synthase/pyruvate phosphate dikinase	energy metabolism
tnfn1_pw060328p02q191	C12	T20	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p02q192	D12	T20	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p02q193	E12	T20	-	dienelactone hydrolase family protein	putative enzymes
tnfn1_pw060328p02q194	F12	T20	-	pyridoxal-dependent decarboxylase	amino acid metabolism - biosynthesis
tnfn1_pw060328p02q195	G12	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p02q196	H12	T20	-	hypothetical membrane protein	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_pw060328p02q101	A01	C	1141028	R	FTN_1078	1140939	1141115	R	59	88(177)
tnfn1_pw060328p02q102	B01	C	363664	R	FTN_0361	363337	364833	F	499	328(1497)
tnfn1_pw060328p02q103	C01	C	1275391	R	FTN_1201	1274526	1275740	R	405	350(1215)
tnfn1_pw060328p02q104	D01	C	785273	F	FTN_0731	784756	785670	F	305	518(915)
tnfn1_pw060328p02q105	E01	C	1730878	F	FTN_1620	1730335	1731294	F	320	544(960)
tnfn1_pw060328p02q106	F01	C	941170	R	FTN_0884	940420	941310	R	297	141(891)
tnfn1_pw060328p02q107	G01	C	339121	F	FTN_0334	339054	339395	R	114	275(342)
tnfn1_pw060328p02q108	H01	C	853804	F	FTN_0797	853524	854069	F	182	281(546)
tnfn1_pw060328p02q109	A02	U	1168839	F	FTN_1107	1168330	1169799	F	490	510(1470)
tnfn1_pw060328p02q111	C02	C	155918	F	FTN_0142	155218	156756	F	513	701(1539)
tnfn1_pw060328p02q112	D02	C	1855765	F	FTN_1727	1855155	1855901	R	249	137(747)
tnfn1_pw060328p02q113	E02	C	1117548	F	FTN_1057	1117172	1117774	R	201	227(603)
tnfn1_pw060328p02q114	F02	C	1859993	R	FTN_1731	1859256	1860191	R	312	199(936)
tnfn1_pw060328p02q115	G02	C	1398383	R	FTN_1323	1397638	1399155	R	506	773(1518)
tnfn1_pw060328p02q116	H02	C	1539194	R	FTN_1449	1538872	1539477	R	202	284(606)
tnfn1_pw060328p02q117	A03	C	277211	F	FTN_0269	275914	277422	R	503	212(1509)
tnfn1_pw060328p02q118	B03	C	1359557	R	FTN_1286	1358907	1360070	F	388	651(1164)
tnfn1_pw060328p02q119	C03	C	1608947	F	FTN_1512	1608678	1609847	F	390	270(1170)
tnfn1_pw060328p02q120	D03	C	1178368	R	FTN_1114	1177796	1178545	R	250	178(750)
tnfn1_pw060328p02q121	E03	C	1841694	R	FTN_1716	1841389	1841940	R	184	247(552)
tnfn1_pw060328p02q122	F03	C	933930	R	FTN_0878	933333	934319	F	329	598(987)
tnfn1_pw060328p02q123	G03	C	741261	F	FTN_0697	741230	741517	F	96	32(288)
tnfn1_pw060328p02q124	H03	C	866870	R	FTN_0809	866270	867517	F	416	601(1248)
tnfn1_pw060328p02q125	A04	C	921996	F	FTN_0869	921132	923024	F	631	865(1893)
tnfn1_pw060328p02q126	B04	C	1535447	F	FTN_1446	1534991	1536382	R	464	936(1392)
tnfn1_pw060328p02q127	C04	C	1294219	R	FTN_1223	1293973	1294560	R	196	342(588)
tnfn1_pw060328p02q128	D04	C	400531	F	FTN_0401	400237	400833	R	199	303(597)
tnfn1_pw060328p02q129	E04	C	1719606	R	FTN_1612	1719296	1719874	F	193	311(579)
tnfn1_pw060328p02q130	F04	C	1005053	F	FTN_0947	1004368	1005477	R	370	425(1110)
tnfn1_pw060328p02q131	G04	C	909571	F	FTN_0853	908463	909605	F	381	1109(1143)
tnfn1_pw060328p02q132	H04	C	203535	R	FTN_0186	203016	203609	R	198	75(594)
tnfn1_pw060328p02q133	A05	C	1053192	R	FTN_0994	1052499	1053245	R	249	54(747)
tnfn1_pw060328p02q134	B05	C	1879609	F	FTN_1750	1879341	1880078	F	246	269(738)
tnfn1_pw060328p02q135	C05	C	1408934	R	FTN_1330	1408823	1410256	R	478	1323(1434)
tnfn1_pw060328p02q136	D05	C	1759904	R	FTN_1645	1759710	1760144	R	145	241(435)
tnfn1_pw060328p02q137	E05	C	298927	F	FTN_0292	298865	299065	F	67	63(201)
tnfn1_pw060328p02q138	F05	C	919388	F	FTN_0866	919330	919911	F	194	59(582)
tnfn1_pw060328p02q139	G05	C	653832	F	FTN_0621	652477	653844	F	456	1356(1368)
tnfn1_pw060328p02q140	H05	C	238190	F	FTN_0216	238094	238426	F	111	97(333)
tnfn1_pw060328p02q141	A06	C	624092	R	FTN_0593	623591	624460	R	290	369(870)
tnfn1_pw060328p02q142	B06	C	1890784	R	FTN_1761	1889997	1890802	R	268.6	19(806)
tnfn1_pw060328p02q143	C06	C	425690	F	FTN_0426	425491	425859	F	123	200(369)
tnfn1_pw060328p02q144	D06	C	911392	F	FTN_0856	911269	911592	F	108	124(324)
tnfn1_pw060328p02q145	E06	C	1704633	R	FTN_1603	1704273	1705046	R	258	414(774)
tnfn1_pw060328p02q146	F06	C	1787238	R	FTN_1673	1787230	1788237	R	336	1000(1008)
tnfn1_pw060328p02q147	G06	C	347505	R	FTN_0342	346275	347585	R	437	81(1311)
tnfn1_pw060328p02q148	H06	C	1470559	R	FTN_1393	1470399	1470698	R	100	140(300)

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_pw060328p02q149	A07	C	372942	F	FTN_0369	372857	373084	F	76	86(228)
tnfn1_pw060328p02q150	B07	C	776756	R	FTN_0721	776068	777051	R	328	296(984)
tnfn1_pw060328p02q151	C07	C	986296	F	-	986109	986965	R	285.6	670(857)
tnfn1_pw060328p02q152	D07	C	1307553	R	FTN_1239	1307455	1308000	F	182	99(546)
tnfn1_pw060328p02q153	E07	C	1210600	R	FTN_1145	1210567	1211457	R	297	858(891)
tnfn1_pw060328p02q154	F07	C	92443	R	FTN_0082	92435	92995	F	187	9(561)
tnfn1_pw060328p02q155	G07	C	1074424	F	FTN_1014	1074014	1074643	R	210	220(630)
tnfn1_pw060328p02q156	H07	C	1885448	F	FTN_1756	1885175	1885651	F	159	274(477)
tnfn1_pw060328p02q157	A08	C	273418	F	FTN_0266	272930	274813	F	628	489(1884)
tnfn1_pw060328p02q158	B08	C	1073643	R	FTN_1013	1072741	1073913	R	391	271(1173)
tnfn1_pw060328p02q159	C08	C	958992	F	FTN_0901	958727	959317	R	197	326(591)
tnfn1_pw060328p02q160	D08	C	1302119	F	FTN_1233	1301598	1302386	R	263	268(789)
tnfn1_pw060328p02q161	E08	C	1738052	R	FTN_1625	1737806	1738180	F	125	247(375)
tnfn1_pw060328p02q162	F08	C	943169	R	FTN_0886	942996	944261	F	422	174(1266)
tnfn1_pw060328p02q163	G08	C	321922	F	FTN_0311	321772	322713	F	314	151(942)
tnfn1_pw060328p02q164	H08	C	905967	R	FTN_0850	905800	906207	F	136	168(408)
tnfn1_pw060328p02q165	A09	C	1620635	F	FTN_1523	1620541	1621251	F	237	95(711)
tnfn1_pw060328p02q166	B09	C	1663279	R	FTN_1566	1663213	1663446	R	78	168(234)
tnfn1_pw060328p02q167	C09	C	1446271	F	FTN_1363	1446038	1446688	F	217	234(651)
tnfn1_pw060328p02q168	D09	C	1809407	F	FTN_1692	1808552	1809619	R	356	213(1068)
tnfn1_pw060328p02q169	E09	C	849098	F	FTN_0790	848825	849682	F	286	274(858)
tnfn1_pw060328p02q170	F09	C	1322333	R	FTN_1253	1321637	1322698	R	354	366(1062)
tnfn1_pw060328p02q171	G09	C	1770677	R	FTN_1657	1770083	1771378	R	432	702(1296)
tnfn1_pw060328p02q172	H09	C	739652	R	FTN_0695	739415	740452	F	346	238(1038)
tnfn1_pw060328p02q173	A10	C	429043	F	FTN_0431	428206	429645	F	480	838(1440)
tnfn1_pw060328p02q174	B10	C	1200160	F	FTN_1135	1199729	1200805	R	359	646(1077)
tnfn1_pw060328p02q175	C10	C	1197349	F	FTN_1131	1194416	1198477	R	1354	1129(4062)
tnfn1_pw060328p02q176	D10	C	382343	F	FTN_0381	382197	383180	F	328	147(984)
tnfn1_pw060328p02q177	E10	C	1837430	F	FTN_1713	1837164	1837808	R	215	379(645)
tnfn1_pw060328p02q178	F10	C	1072371	R	FTN_1012	1071927	1072757	F	277	445(831)
tnfn1_pw060328p02q179	G10	C	375033	R	FTN_0373	374890	376083	F	398	144(1194)
tnfn1_pw060328p02q180	H10	C	786932	R	FTN_0734	786285	787331	R	349	400(1047)
tnfn1_pw060328p02q181	A11	C	722287	R	FTN_0678	721383	722594	R	404	308(1212)
tnfn1_pw060328p02q182	B11	C	925722	F	FTN_0871	925584	926156	F	191	139(573)
tnfn1_pw060328p02q183	C11	C	245775	F	-	245715	246181	R	155.6	407(467)
tnfn1_pw060328p02q184	D11	C	854773	R	FTN_0798	854146	856299	F	718	628(2154)
tnfn1_pw060328p02q185	E11	C	99887	R	FTN_0088	99479	100174	F	232	409(696)
tnfn1_pw060328p02q186	F11	C	1812997	R	FTN_1695	1812953	1813585	F	211	45(633)
tnfn1_pw060328p02q187	G11	C	393957	R	FTN_0394	392909	395071	R	721	1115(2163)
tnfn1_pw060328p02q188	H11	C	830910	F	FTN_0774	830697	831029	R	111	120(333)
tnfn1_pw060328p02q189	A12	C	890845	R	FTN_0833	890583	890900	R	106	56(318)
tnfn1_pw060328p02q190	B12	C	77609	R	FTN_0064	75648	78278	R	877	670(2631)
tnfn1_pw060328p02q191	C12	C	496402	F	intergenic					
tnfn1_pw060328p02q192	D12	C	1798247	F	FTN_1683	1798000	1799259	F	420	248(1260)
tnfn1_pw060328p02q193	E12	C	198352	R	FTN_0180	197925	198641	R	239	290(717)
tnfn1_pw060328p02q194	F12	C	1854440	F	FTN_1726	1853938	1855098	R	387	659(1161)
tnfn1_pw060328p02q195	G12	C	161750	R	FTN_0149	161561	162472	F	304	190(912)
tnfn1_pw060328p02q196	H12	C	1652227	F	FTN_1554	1651824	1653341	F	506	404(1518)

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_pw060328p02q101	A01	EXACT(0)	156	153	124	39	EXACT(0)	200	189	61
tnfn1_pw060328p02q102	B01	EXACT(0)	155	145	117	37	EXACT(0)	200	194	53
tnfn1_pw060328p02q103	C01	EXACT(0)	158	153	132	37	EXACT(0)	200	197	56
tnfn1_pw060328p02q104	D01	EXACT(0)	157	150	134	38	EXACT(0)	200	191	58
tnfn1_pw060328p02q105	E01	EXACT(0)	156	152	129	31	EXACT(0)	200	193	57
tnfn1_pw060328p02q106	F01	EXACT(0)	155	138	112	27	EXACT(0)	200	190	51
tnfn1_pw060328p02q107	G01	EXACT(0)	157	153	131	40	EXACT(0)	116	111	48
tnfn1_pw060328p02q108	H01	EXACT(0)	156	145	124	34	EXACT(0)	200	182	54
tnfn1_pw060328p02q109	A02	EXACT(0)	154	145	132	39	EXACT(0)	200	193	47
tnfn1_pw060328p02q110	B02	EXACT(0)	156	148	131	39	EXACT(0)	200	183	54
tnfn1_pw060328p02q111	C02	EXACT(0)	156	151	127	40	EXACT(0)	200	171	43
tnfn1_pw060328p02q112	D02	EXACT(0)	155	145	111	34	EXACT(0)	200	182	57
tnfn1_pw060328p02q113	E02	EXACT(0)	156	142	125	36	EXACT(0)	79	60	30
tnfn1_pw060328p02q114	F02	EXACT(0)	156	153	129	42	EXACT(0)	200	194	53
tnfn1_pw060328p02q115	G02	EXACT(0)	157	146	126	39	EXACT(0)	200	186	57
tnfn1_pw060328p02q116	H02	EXACT(0)	159	153	138	40	EXACT(0)	200	196	56
tnfn1_pw060328p02q117	A03	EXACT(0)	156	146	124	39	EXACT(0)	181	171	56
tnfn1_pw060328p02q118	B03	EXACT(0)	157	151	129	39	EXACT(0)	199	183	45
tnfn1_pw060328p02q119	C03	EXACT(0)	156	146	127	43	EXACT(0)	200	186	55
tnfn1_pw060328p02q120	D03	EXACT(0)	158	151	131	37	EXACT(0)	200	160	44
tnfn1_pw060328p02q121	E03	EXACT(0)	156	151	124	39	EXACT(0)	200	193	48
tnfn1_pw060328p02q122	F03	EXACT(0)	156	151	130	37	EXACT(0)	200	180	47
tnfn1_pw060328p02q123	G03	EXACT(0)	156	146	130	38	EXACT(0)	200	180	49
tnfn1_pw060328p02q124	H03	EXACT(0)	157	153	128	41	EXACT(0)	200	180	56
tnfn1_pw060328p02q125	A04	EXACT(0)	155	145	114	27	EXACT(0)	200	184	43
tnfn1_pw060328p02q126	B04	EXACT(0)	157	151	119	31	EXACT(0)	200	190	56
tnfn1_pw060328p02q127	C04	EXACT(0)	156	153	123	36	EXACT(0)	200	193	57
tnfn1_pw060328p02q128	D04	EXACT(0)	156	145	122	39	EXACT(0)	200	191	54
tnfn1_pw060328p02q129	E04	EXACT(0)	157	151	131	40	EXACT(0)	200	151	40
tnfn1_pw060328p02q130	F04	EXACT(0)	156	151	127	42	EXACT(0)	200	195	59
tnfn1_pw060328p02q131	G04	EXACT(0)	120	118	103	46	EXACT(0)	200	181	66
tnfn1_pw060328p02q132	H04	EXACT(0)	123	119	103	37	EXACT(0)	200	196	52
tnfn1_pw060328p02q133	A05	EXACT(0)	120	106	101	39	EXACT(0)	200	186	59
tnfn1_pw060328p02q134	B05	EXACT(0)	122	119	71	20	EXACT(0)	200	191	44
tnfn1_pw060328p02q135	C05	EXACT(0)	123	125	101	30	EXACT(0)	200	191	52
tnfn1_pw060328p02q136	D05	EXACT(0)	122	119	109	42	EXACT(0)	200	189	59
tnfn1_pw060328p02q137	E05	EXACT(0)	121	118	97	33	EXACT(0)	200	185	57
tnfn1_pw060328p02q138	F05	EXACT(0)	122	119	101	34	EXACT(0)	188	152	40
tnfn1_pw060328p02q139	G05	EXACT(0)	120	119	104	39	EXACT(0)	200	182	58
tnfn1_pw060328p02q140	H05	EXACT(0)	121	112	99	28	EXACT(0)	200	188	58
tnfn1_pw060328p02q141	A06	EXACT(0)	124	120	97	25	EXACT(0)	200	198	55
tnfn1_pw060328p02q142	B06	EXACT(0)	123	126	100	32	EXACT(0)	200	183	40
tnfn1_pw060328p02q143	C06	EXACT(0)	121	120	93	24	EXACT(0)	200	190	53
tnfn1_pw060328p02q144	D06	EXACT(0)	120	112	88	29	EXACT(0)	200	191	64
tnfn1_pw060328p02q145	E06	EXACT(0)	121	118	108	38	EXACT(0)	200	185	50
tnfn1_pw060328p02q146	F06	EXACT(0)	121	112	96	37	EXACT(0)	200	191	49
tnfn1_pw060328p02q147	G06	EXACT(0)	122	125	99	28	EXACT(0)	200	196	51
tnfn1_pw060328p02q148	H06	EXACT(0)	121	117	87	27	EXACT(0)	199	164	40

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_pw060328p02q149	A07	EXACT(0)	120	118	77	21	EXACT(0)	138	124	48
tnfn1_pw060328p02q150	B07	EXACT(0)	125	86	65	18	EXACT(0)	200	190	43
tnfn1_pw060328p02q151	C07	EXACT(0)	123	112	92	24	EXACT(0)	200	189	54
tnfn1_pw060328p02q152	D07	EXACT(0)	124	120	86	23	EXACT(0)	200	189	53
tnfn1_pw060328p02q153	E07	EXACT(0)	121	112	94	29	EXACT(0)	200	187	57
tnfn1_pw060328p02q154	F07	EXACT(0)	120	112	91	33	EXACT(0)	200	186	59
tnfn1_pw060328p02q155	G07	EXACT(0)	123	119	101	29	EXACT(0)	199	124	36
tnfn1_pw060328p02q156	H07	EXACT(0)	123	118	99	28	EXACT(0)	200	192	55
tnfn1_pw060328p02q157	A08	NONE	0	0	0	17	ESTIMATE(124)	690	535	28
tnfn1_pw060328p02q158	B08	EXACT(0)	124	119	103	36	EXACT(0)	101	93	48
tnfn1_pw060328p02q159	C08	EXACT(0)	122	113	91	27	EXACT(0)	200	187	57
tnfn1_pw060328p02q160	D08	EXACT(0)	123	120	93	25	EXACT(0)	199	171	37
tnfn1_pw060328p02q161	E08	ADJUSTED(1)	120	104	54	18	ESTIMATE(1)	199	182	45
tnfn1_pw060328p02q162	F08	NONE	0	0	0	21	ESTIMATE(121)	601	498	35
tnfn1_pw060328p02q163	G08	EXACT(0)	156	153	126	37	EXACT(0)	200	189	55
tnfn1_pw060328p02q164	H08	EXACT(0)	164	133	109	28	EXACT(0)	200	190	38
tnfn1_pw060328p02q165	A09	EXACT(0)	156	151	124	40	EXACT(0)	200	192	58
tnfn1_pw060328p02q166	B09	EXACT(0)	156	153	126	40	EXACT(0)	200	183	52
tnfn1_pw060328p02q167	C09	EXACT(0)	154	138	104	28	EXACT(0)	200	176	45
tnfn1_pw060328p02q168	D09	EXACT(0)	156	152	131	39	EXACT(0)	200	194	54
tnfn1_pw060328p02q169	E09	EXACT(0)	155	151	104	26	EXACT(0)	200	182	52
tnfn1_pw060328p02q170	F09	EXACT(0)	157	152	111	29	EXACT(0)	200	190	52
tnfn1_pw060328p02q171	G09	EXACT(0)	156	145	115	33	EXACT(0)	200	192	50
tnfn1_pw060328p02q172	H09	EXACT(0)	155	146	127	38	EXACT(0)	200	194	57
tnfn1_pw060328p02q173	A10	EXACT(0)	156	153	126	38	EXACT(0)	182	167	52
tnfn1_pw060328p02q174	B10	EXACT(0)	156	151	121	40	EXACT(0)	200	189	56
tnfn1_pw060328p02q175	C10	EXACT(0)	155	145	119	36	EXACT(0)	200	192	57
tnfn1_pw060328p02q176	D10	EXACT(0)	156	152	125	38	EXACT(0)	197	193	53
tnfn1_pw060328p02q177	E10	EXACT(0)	155	145	126	44	EXACT(0)	134	128	53
tnfn1_pw060328p02q178	F10	EXACT(0)	155	145	126	39	EXACT(0)	200	120	39
tnfn1_pw060328p02q179	G10	EXACT(0)	155	145	120	41	EXACT(0)	200	191	54
tnfn1_pw060328p02q180	H10	EXACT(0)	154	145	110	34	EXACT(0)	200	188	56
tnfn1_pw060328p02q181	A11	EXACT(0)	156	152	122	34	EXACT(0)	200	195	57
tnfn1_pw060328p02q182	B11	EXACT(0)	156	153	116	33	EXACT(0)	200	184	57
tnfn1_pw060328p02q183	C11	EXACT(0)	154	144	110	26	EXACT(0)	200	188	52
tnfn1_pw060328p02q184	D11	EXACT(0)	156	151	129	38	EXACT(0)	200	194	51
tnfn1_pw060328p02q185	E11	EXACT(0)	156	152	125	40	EXACT(0)	200	189	59
tnfn1_pw060328p02q186	F11	EXACT(0)	156	152	125	35	EXACT(0)	200	172	53
tnfn1_pw060328p02q187	G11	EXACT(0)	155	145	119	34	EXACT(0)	200	196	55
tnfn1_pw060328p02q188	H11	EXACT(0)	155	139	125	40	EXACT(0)	199	139	43
tnfn1_pw060328p02q189	A12	EXACT(0)	156	152	127	31	EXACT(0)	200	189	55
tnfn1_pw060328p02q190	B12	EXACT(0)	157	153	125	36	EXACT(0)	200	195	55
tnfn1_pw060328p02q191	C12	EXACT(0)	156	152	116	36	EXACT(0)	200	187	56
tnfn1_pw060328p02q192	D12	EXACT(0)	155	145	123	38	EXACT(0)	200	155	39
tnfn1_pw060328p02q193	E12	EXACT(0)	155	145	126	40	EXACT(0)	200	182	50
tnfn1_pw060328p02q194	F12	EXACT(0)	156	152	116	38	EXACT(0)	200	189	54
tnfn1_pw060328p02q195	G12	EXACT(0)	157	152	126	37	EXACT(0)	200	188	51
tnfn1_pw060328p02q196	H12	EXACT(0)	150	92	80	31	EXACT(0)	200	183	46