

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 28 (tnfn1_pw060420p04)**

Catalog No. NR-8062

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-8062 represents Plate 28 (tnfn1_pw060420p04) 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_pw060420p04q175 (Well C10) was not available due to quality issues at the time of release of Plate 28, 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-8062 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 28 (tnfn1_pw060420p04), NR-8062.”

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.

Disclaimers:

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References:

1. Gallagher, L. A., et al. "A Comprehensive Transposon Mutant Library of *Francisella novicida*, A Bioweapon Surrogate." Proc. Natl. Acad. Sci. USA 104 (2007): 1009–1014. PubMed: 17215359.

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Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060420p04q101	A01	T20	-	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060420p04q102	B01	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060420p04q103	C01	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060420p04q104	D01	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p04q105	E01	T20	glpD	glycerol-3-phosphate dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060420p04q106	F01	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060420p04q107	G01	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p04q108	H01	T20	-	para-aminobenzoate synthase component I	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060420p04q109	A02	T20	-	nicotinic acid phosphoribosyltransferase	other metabolism - biosynthesis
tnfn1_pw060420p04q110	B02	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p04q111	C02	T20	rhtB	homoserine/threonine efflux family protein	transport - amino-acid
tnfn1_pw060420p04q112	D02	T20	-	small conductance mechanosensitive ion channel (MscS) family protein	transport
tnfn1_pw060420p04q113	E02	T20	-	regulatory factor, Bvg accessory factor family	signal transduction and regulation
tnfn1_pw060420p04q114	F02	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p04q115	G02	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q116	H02	T20	wbtH	glutamine amidotransferase/asparagine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060420p04q117	A03	T20	kdpB	potassium-transporting ATPase B chain	transport
tnfn1_pw060420p04q118	B03	T20	-	ABC-type anion transport system, duplicated permease component	transport
tnfn1_pw060420p04q119	C03	T20	-	lipolytic enzyme	fatty acids and lipids metabolism
tnfn1_pw060420p04q120	D03	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060420p04q121	E03	T20	-	10 TMS drug/metabolite exporter protein	transport - drugs / antibacterial compounds
tnfn1_pw060420p04q122	F03	T20	ilvC	ketol-acid reductoisomerase	amino acid metabolism - biosynthesis
tnfn1_pw060420p04q123	G03	T20	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060420p04q124	H03	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p04q125	A04	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p04q126	B04	<KAN-2>	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p04q127	C04	<KAN-2>	ftnA	ferric iron binding protein, ferritin-like	putative enzymes
tnfn1_pw060420p04q128	D04	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060420p04q129	E04	<KAN-2>	-	acetyltransferase	putative enzymes
tnfn1_pw060420p04q130	F04	<KAN-2>	atpC	ATP synthase, F1 sector, subunit epsilon	energy metabolism
tnfn1_pw060420p04q131	G04	<KAN-2>	-	peptidase, U32 family	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060420p04q132	H04	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p04q133	A05	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q134	B05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p04q135	C05	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060420p04q136	D05	T20	-	isochorismatase family protein	putative enzymes
tnfn1_pw060420p04q137	E05	T20	-	putative rhodanese, sulfurtransferase	putative enzymes
tnfn1_pw060420p04q138	F05	T20	-	putative rhodanese, sulfurtransferase	putative enzymes
tnfn1_pw060420p04q139	G05	T20	yjjK	(putative) drug resistance ATPase-1 (Drug RA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060420p04q140	H05	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060420p04q141	A06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060420p04q142	B06	T20	wbtN	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060420p04q143	C06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p04q144	D06	T20	glgP	glycogen phosphorylase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060420p04q145	E06	T20	-	glutamine amidotransferases class-II family protein	putative enzymes
tnfn1_pw060420p04q146	F06	T20	-	DJ-1/Pfpl family protein	putative enzymes
tnfn1_pw060420p04q147	G06	T20	galU	UTP--glucose-1-phosphate uridylyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060420p04q148	H06	T20	-	major facilitator superfamily (MFS) transport protein	transport

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060420p04q149	A07	T20	-	10 TMS drug/metabolite exporter protein	transport - drugs / antibacterial compounds
tnfn1_pw060420p04q150	B07	T20	-	competence protein	transport
tnfn1_pw060420p04q151	C07	T20	-	amino acid-polyamine-organocation (APC) superfamily	transport - amino-acid
tnfn1_pw060420p04q152	D07	T20	appB	cytochrome bd-II terminal oxidase subunit II	energy metabolism
tnfn1_pw060420p04q153	E07	T20	-	metallocarboxypeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060420p04q154	F07	T20	-	phospholipase D family protein	fatty acids and lipids metabolism
tnfn1_pw060420p04q155	G07	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q156	H07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060420p04q157	A08	T20	-	AMP-binding enzyme	putative enzymes
tnfn1_pw060420p04q158	B08	T20	-	ArsB arsenite/antimonite exporter	transport
tnfn1_pw060420p04q159	C08	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060420p04q160	D08	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p04q161	E08	T20	-	glycosyl transferase, group 1	cell wall / LPS / capsule
tnfn1_pw060420p04q162	F08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q163	G08	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060420p04q164	H08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q165	A09	T20	-	manganese/zinc/iron chelate uptake transporter (MZT) family protein	transport
tnfn1_pw060420p04q166	B09	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q167	C09	T20	-	hypothetical membrane protein with von Willebrand factor type A domain	hypothetical - novel
tnfn1_pw060420p04q168	D09	T20	-	signal transduction protein with a PAS, a PAC, an EAL and a GGDEF domain	signal transduction and regulation
tnfn1_pw060420p04q169	E09	T20	-	predicted NAD/FAD-dependent oxidoreductase	putative enzymes
tnfn1_pw060420p04q170	F09	T20	-	amino acid transporter	transport - amino-acid
tnfn1_pw060420p04q171	G09	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p04q172	H09	T20	hdc	pyridoxal-dependent decarboxylase	putative enzymes
tnfn1_pw060420p04q173	A10	T20	-	predicted ATPase of the PP-loop superfamily	cell cycle
tnfn1_pw060420p04q174	B10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q175	C10	T20	-	transcriptional regulator	signal transduction and regulation
tnfn1_pw060420p04q176	D10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q177	E10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q178	F10	T20	-	drug/metabolite transporter (DMT) superfamily protein	transport - drugs / antibacterial compounds
tnfn1_pw060420p04q179	G10	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p04q180	H10	T20	pepN	aminopeptidase N	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060420p04q181	A11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q182	B11	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H ⁺ symporter	transport
tnfn1_pw060420p04q183	C11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q184	D11	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q185	E11	T20	-	major facilitator superfamily (MFS) transport protein	transport
tnfn1_pw060420p04q186	F11	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060420p04q187	G11	T20	mgIB	macrophage growth locus, subunit B	unknown function - conserved
tnfn1_pw060420p04q188	H11	T20	-	acetyltransferase	putative enzymes
tnfn1_pw060420p04q189	A12	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060420p04q190	B12	T20	birA	biotin-acetyl-CoA-carboxylase ligase	fatty acids and lipids metabolism
tnfn1_pw060420p04q191	C12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q192	D12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060420p04q193	E12	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060420p04q194	F12	T20	gloA	lactoylglutathione lyase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060420p04q195	G12	T20	hslV	ATP-dependent protease HslVU, peptidase subunit	post-translational modification, protein turnover, chaperones
tnfn1_pw060420p04q196	H12	T20	-	membrane protein of unknown function	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_pw060420p04q101	A01	C	1282561	R	FTN_1212	1281922	1282932	R	337	372(1011)
tnfn1_pw060420p04q102	B01	U	1832639	R	FTN_1709	1832414	1834285	R	624	1647(1872)
tnfn1_pw060420p04q103	C01	C	1602955	F	FTN_1507	1602509	1603009	R	167	55(501)
tnfn1_pw060420p04q104	D01	C	4711167	F	FTN_0466	470805	471404	F	200	363(600)
tnfn1_pw060420p04q105	E01	C	1681243	R	FTN_1584	1680667	1682196	R	510	954(1530)
tnfn1_pw060420p04q106	F01	C	200151	R	FTN_0182	199526	200200	R	225	50(675)
tnfn1_pw060420p04q107	G01	C	554167	F	FTN_0532	553648	554289	R	214	123(642)
tnfn1_pw060420p04q108	H01	C	878793	R	FTN_0822	878696	880456	F	587	98(1761)
tnfn1_pw060420p04q109	A02	C	1531656	F	FTN_1443	1531187	1532599	R	471	944(1413)
tnfn1_pw060420p04q110	B02	C	890804	R	FTN_0833	890583	890900	R	106	97(318)
tnfn1_pw060420p04q111	C02	C	1479920	R	FTN_1401	1479437	1480069	F	211	484(633)
tnfn1_pw060420p04q112	D02	U	926534	R	FTN_0872	926220	927407	F	396	315(1188)
tnfn1_pw060420p04q113	E02	C	1704729	R	FTN_1603	1704273	1705046	R	258	318(774)
tnfn1_pw060420p04q114	F02	C	622533	F	FTN_0591	621630	622667	R	346	135(1038)
tnfn1_pw060420p04q115	G02	C	646675	R	FTN_0615	646311	646880	F	190	365(570)
tnfn1_pw060420p04q116	H02	C	1500896	F	FTN_1421	1499941	1501830	R	630	935(1890)
tnfn1_pw060420p04q117	A03	U	1843713	R	FTN_1717	1841960	1843996	R	679	284(2037)
tnfn1_pw060420p04q118	B03	U	164583	R	FTN_0152	163868	165589	R	574	1007(1722)
tnfn1_pw060420p04q119	C03	C	434590	R	FTN_0436	434467	435345	F	293	124(879)
tnfn1_pw060420p04q120	D03	C	314835	R	FTN_0305	314309	314926	F	206	527(618)
tnfn1_pw060420p04q121	E03	C	1619369	F	FTN_1521	1618541	1619422	F	294	829(882)
tnfn1_pw060420p04q122	F03	C	1097801	R	FTN_1040	1097588	1098628	R	347	828(1041)
tnfn1_pw060420p04q123	G03	C	1125166	R	FTN_1066	1125001	1125840	F	280	166(840)
tnfn1_pw060420p04q124	H03	C	384683	R	FTN_0383	384611	384997	R	129	315(387)
tnfn1_pw060420p04q125	A04	U	303436	F	intergenic					
tnfn1_pw060420p04q126	B04	C	469326	R	FTN_0463	469216	469476	R	87	151(261)
tnfn1_pw060420p04q127	C04	U	1087538	F	FTN_1031	1087455	1087952	F	166	84(498)
tnfn1_pw060420p04q128	D04	U	900583	R	FTN_0844	900355	900618	R	88	36(264)
tnfn1_pw060420p04q129	E04	U	1427009	R	FTN_1348	1426691	1427179	R	163	171(489)
tnfn1_pw060420p04q130	F04	C	1759888	R	FTN_1645	1759710	1760144	R	145	257(435)
tnfn1_pw060420p04q131	G04	C	1827502	F	FTN_1705	1826603	1827931	F	443	900(1329)
tnfn1_pw060420p04q132	H04	C	457588	R	FTN_0454	457266	458279	F	338	323(1014)
tnfn1_pw060420p04q133	A05	U	1388301	R	FTN_1315	1387186	1388613	F	476	1116(1428)
tnfn1_pw060420p04q134	B05	C	305452	F	FTN_0297	305086	305721	F	212	367(636)
tnfn1_pw060420p04q135	C05	U	391032	R	FTN_0392	390793	391710	R	306	679(918)
tnfn1_pw060420p04q136	D05	C	842541	F	FTN_0785	842442	842945	R	168	405(504)
tnfn1_pw060420p04q137	E05	C	1531143	R	intergenic					
tnfn1_pw060420p04q138	F05	C	848340	R	FTN_0789	847645	848631	R	329	292(987)
tnfn1_pw060420p04q139	G05	C	558525	F	FTN_0536	558170	560008	F	613	356(1839)
tnfn1_pw060420p04q140	H05	C	1012889	R	FTN_0957	1012691	1013299	R	203	411(609)
tnfn1_pw060420p04q141	A06	C	288341	F	FTN_0280	288029	288421	F	131	313(393)
tnfn1_pw060420p04q142	B06	C	1502256	F	FTN_1422	1501835	1502944	R	370	689(1110)
tnfn1_pw060420p04q143	C06	C	162108	R	FTN_0149	161561	162472	F	304	548(912)
tnfn1_pw060420p04q144	D06	C	536030	F	FTN_0517	534678	536948	F	757	1353(2271)
tnfn1_pw060420p04q145	E06	C	1213289	R	FTN_1147	1212777	1213580	R	268	292(804)
tnfn1_pw060420p04q146	F06	C	1040194	R	FTN_0985	1039817	1040416	F	200	378(600)
tnfn1_pw060420p04q147	G06	U	782290	R	FTN_0729	781822	782682	F	287	469(861)
tnfn1_pw060420p04q148	H06	C	1422579	F	FTN_1344	1422190	1423386	F	399	390(1197)

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_pw060420p04q149	A07	C	7957	F	FTN_0008	7771	8640	R	290	684(870)
tnfn1_pw060420p04q150	B07	U	168986	F	FTN_0155	168063	170075	F	671	924(2013)
tnfn1_pw060420p04q151	C07	C	1194038	F	FTN_1130	1192747	1194252	R	502	215(1506)
tnfn1_pw060420p04q152	D07	C	1730462	R	FTN_1620	1730335	1731294	F	320	128(960)
tnfn1_pw060420p04q153	E07	C	1865010	F	FTN_1738	1864510	1866012	F	501	501(1503)
tnfn1_pw060420p04q154	F07	C	610063	F	FTN_0581	609811	611025	R	405	963(1215)
tnfn1_pw060420p04q155	G07	C	40779	F	FTN_0039	40656	41078	R	141	300(423)
tnfn1_pw060420p04q156	H07	C	1451359	F	FTN_1371	1450809	1451963	R	385	605(1155)
tnfn1_pw060420p04q157	A08	C	877626	F	FTN_0821	877333	878700	F	456	294(1368)
tnfn1_pw060420p04q158	B08	C	858168	R	FTN_0800	857562	858587	R	342	420(1026)
tnfn1_pw060420p04q159	C08	C	1294476	F	FTN_1223	1293973	1294560	R	196	85(588)
tnfn1_pw060420p04q160	D08	U	570332	R	FTN_0544	570050	570853	R	268	522(804)
tnfn1_pw060420p04q161	E08	C	1289732	R	FTN_1218	1288573	1289799	R	409	68(1227)
tnfn1_pw060420p04q162	F08	C	49730	R	FTN_0045	49665	50741	F	359	66(1077)
tnfn1_pw060420p04q163	G08	C	618242	R	FTN_0589	617747	619189	R	481	948(1443)
tnfn1_pw060420p04q164	H08	C	1868931	R	FTN_1741	1868878	1869228	R	117	298(351)
tnfn1_pw060420p04q165	A09	C	199369	R	FTN_0181	198742	199581	R	280	213(840)
tnfn1_pw060420p04q166	B09	C	980593	F	FTN_0923	980427	980855	R	143	263(429)
tnfn1_pw060420p04q167	C09	C	228476	R	FTN_0208	228118	229113	F	332	359(996)
tnfn1_pw060420p04q168	D09	C	453096	F	FTN_0451	452277	454379	R	701	1284(2103)
tnfn1_pw060420p04q169	E09	C	1732426	R	FTN_1621	1731751	1732734	F	328	676(984)
tnfn1_pw060420p04q170	F09	C	327377	R	FTN_0317	326808	328169	F	454	570(1362)
tnfn1_pw060420p04q171	G09	C	67584	R	FTN_0057	66665	67894	R	410	311(1230)
tnfn1_pw060420p04q172	H09	C	1078115	R	FTN_1019	1077269	1078402	F	378	847(1134)
tnfn1_pw060420p04q173	A10	C	1235415	R	FTN_1165	1235224	1235982	F	253	192(759)
tnfn1_pw060420p04q174	B10	C	833884	F	FTN_0777	833560	834003	R	148	120(444)
tnfn1_pw060420p04q175	C10	C	905906	R	FTN_0850	905800	906207	F	136	107(408)
tnfn1_pw060420p04q176	D10	C	910721	R	FTN_0855	910576	911262	F	229	146(687)
tnfn1_pw060420p04q177	E10	C	1390132	F	FTN_1317	1389274	1390422	F	383	859(1149)
tnfn1_pw060420p04q178	F10	C	1895719	R	FTN_1766	1895114	1896115	R	334	397(1002)
tnfn1_pw060420p04q179	G10	C	1486770	R	FTN_1409	1485991	1487373	R	461	604(1383)
tnfn1_pw060420p04q180	H10	C	1899365	R	FTN_1768	1897173	1899746	R	858	382(2574)
tnfn1_pw060420p04q181	A11	C	1685477	R	FTN_1587	1685390	1685998	R	203	522(609)
tnfn1_pw060420p04q182	B11	C	1319777	F	FTN_1251	1318855	1320288	R	478	512(1434)
tnfn1_pw060420p04q183	C11	C	1464672	R	FTN_1385	1464367	1464765	F	133	306(399)
tnfn1_pw060420p04q184	D11	C	1286226	F	FTN_1216	1286108	1286848	R	247	623(741)
tnfn1_pw060420p04q185	E11	C	1422463	F	FTN_1344	1422190	1423386	F	399	274(1197)
tnfn1_pw060420p04q186	F11	C	1482188	R	FTN_1404	1482101	1482877	R	259	690(777)
tnfn1_pw060420p04q187	G11	C	1362967	R	FTN_1291	1362901	1363305	F	135	67(405)
tnfn1_pw060420p04q188	H11	U	1477713	R	FTN_1398	1477435	1477947	R	171	235(513)
tnfn1_pw060420p04q189	A12	C	1543992	R	FTN_1455	1543884	1544657	F	258	109(774)
tnfn1_pw060420p04q190	B12	C	868567	F	FTN_0811	868439	869398	F	320	129(960)
tnfn1_pw060420p04q191	C12	C	1903480	R	FTN_1774	1903381	1903719	R	113	240(339)
tnfn1_pw060420p04q192	D12	C	1861898	R	FTN_1734	1861861	1862250	F	130	38(390)
tnfn1_pw060420p04q193	E12	C	316416	R	FTN_0307	315736	316653	F	306	681(918)
tnfn1_pw060420p04q194	F12	C	1300401	R	FTN_1231	1300134	1300514	R	127	114(381)
tnfn1_pw060420p04q195	G12	C	1053739	F	FTN_0995	1053437	1053985	F	183	303(549)
tnfn1_pw060420p04q196	H12	U	1325449	F	FTN_1256	1324883	1326250	R	456	802(1368)

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_pw060420p04q101	A01	EXACT(0)	155	116	113	40	EXACT(0)	200	185	54
tnfn1_pw060420p04q102	B01	EXACT(0)	156	152	128	43	EXACT(0)	70	66	52
tnfn1_pw060420p04q103	C01	EXACT(0)	155	145	129	42	EXACT(0)	200	192	54
tnfn1_pw060420p04q104	D01	EXACT(0)	157	151	122	30	EXACT(0)	200	186	56
tnfn1_pw060420p04q105	E01	EXACT(0)	159	153	128	34	EXACT(0)	200	190	48
tnfn1_pw060420p04q106	F01	EXACT(0)	158	153	129	33	EXACT(0)	200	191	50
tnfn1_pw060420p04q107	G01	EXACT(0)	154	145	116	35	EXACT(0)	200	181	53
tnfn1_pw060420p04q108	H01	EXACT(0)	155	139	119	37	EXACT(0)	200	178	50
tnfn1_pw060420p04q109	A02	EXACT(0)	156	150	121	32	EXACT(0)	200	188	54
tnfn1_pw060420p04q110	B02	EXACT(0)	156	145	134	39	EXACT(0)	192	180	50
tnfn1_pw060420p04q111	C02	EXACT(0)	156	138	123	36	EXACT(0)	200	191	53
tnfn1_pw060420p04q112	D02	EXACT(0)	155	152	128	39	EXACT(0)	200	182	59
tnfn1_pw060420p04q113	E02	EXACT(0)	157	142	113	31	EXACT(0)	200	193	45
tnfn1_pw060420p04q114	F02	EXACT(0)	156	145	120	34	EXACT(0)	200	182	55
tnfn1_pw060420p04q115	G02	EXACT(0)	159	153	119	22	EXACT(0)	200	191	50
tnfn1_pw060420p04q116	H02	EXACT(0)	157	153	139	28	EXACT(0)	200	175	26
tnfn1_pw060420p04q117	A03	EXACT(0)	157	145	126	35	EXACT(0)	200	194	49
tnfn1_pw060420p04q118	B03	EXACT(0)	155	145	121	39	EXACT(0)	200	195	52
tnfn1_pw060420p04q119	C03	EXACT(0)	157	145	100	22	EXACT(0)	200	189	52
tnfn1_pw060420p04q120	D03	EXACT(0)	156	152	136	41	EXACT(0)	200	180	51
tnfn1_pw060420p04q121	E03	EXACT(0)	157	152	126	37	EXACT(0)	200	190	55
tnfn1_pw060420p04q122	F03	EXACT(0)	156	145	118	31	EXACT(0)	200	181	42
tnfn1_pw060420p04q123	G03	EXACT(0)	156	150	125	33	EXACT(0)	200	188	52
tnfn1_pw060420p04q124	H03	EXACT(0)	156	145	107	27	EXACT(0)	200	183	51
tnfn1_pw060420p04q125	A04	EXACT(0)	119	119	109	39	EXACT(0)	200	179	54
tnfn1_pw060420p04q126	B04	EXACT(0)	123	125	98	30	EXACT(0)	138	121	51
tnfn1_pw060420p04q127	C04	EXACT(0)	122	120	110	37	EXACT(0)	200	194	53
tnfn1_pw060420p04q128	D04	EXACT(0)	115	117	102	26	EXACT(0)	176	70	15
tnfn1_pw060420p04q129	E04	EXACT(0)	117	119	104	38	EXACT(0)	200	186	55
tnfn1_pw060420p04q130	F04	EXACT(0)	120	105	100	36	EXACT(0)	200	154	31
tnfn1_pw060420p04q131	G04	EXACT(0)	122	112	42	16	EXACT(0)	200	197	42
tnfn1_pw060420p04q132	H04	EXACT(0)	156	152	139	41	EXACT(0)	200	186	58
tnfn1_pw060420p04q133	A05	EXACT(0)	158	145	135	35	EXACT(0)	200	183	52
tnfn1_pw060420p04q134	B05	EXACT(0)	155	145	126	40	EXACT(0)	200	191	56
tnfn1_pw060420p04q135	C05	EXACT(0)	155	151	98	27	EXACT(0)	200	187	53
tnfn1_pw060420p04q136	D05	EXACT(0)	157	145	132	30	EXACT(0)	200	176	42
tnfn1_pw060420p04q137	E05	EXACT(0)	154	119	107	37	EXACT(0)	200	168	45
tnfn1_pw060420p04q138	F05	EXACT(0)	157	145	136	40	EXACT(0)	200	191	50
tnfn1_pw060420p04q139	G05	EXACT(0)	157	153	131	36	EXACT(0)	183	177	51
tnfn1_pw060420p04q140	H05	EXACT(0)	157	152	139	33	EXACT(0)	200	190	53
tnfn1_pw060420p04q141	A06	EXACT(0)	157	153	133	35	EXACT(0)	200	189	56
tnfn1_pw060420p04q142	B06	EXACT(0)	157	149	128	34	EXACT(0)	200	172	47
tnfn1_pw060420p04q143	C06	EXACT(0)	157	145	126	33	EXACT(0)	200	195	52
tnfn1_pw060420p04q144	D06	EXACT(0)	156	152	136	36	EXACT(0)	200	182	60
tnfn1_pw060420p04q145	E06	EXACT(0)	156	152	121	33	EXACT(0)	200	195	54
tnfn1_pw060420p04q146	F06	EXACT(0)	158	152	125	28	EXACT(0)	200	187	49
tnfn1_pw060420p04q147	G06	EXACT(0)	155	153	123	39	EXACT(0)	200	186	47
tnfn1_pw060420p04q148	H06	EXACT(0)	160	153	134	39	EXACT(0)	200	187	55

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_pw060420p04q149	A07	EXACT(0)	157	152	127	39	EXACT(0)	200	180	57
tnfn1_pw060420p04q150	B07	EXACT(0)	158	151	140	38	EXACT(0)	154	143	55
tnfn1_pw060420p04q151	C07	EXACT(0)	158	153	136	38	EXACT(0)	143	138	53
tnfn1_pw060420p04q152	D07	EXACT(0)	157	145	133	35	EXACT(0)	199	153	39
tnfn1_pw060420p04q153	E07	EXACT(0)	155	145	103	23	EXACT(0)	200	187	54
tnfn1_pw060420p04q154	F07	EXACT(0)	156	144	110	28	EXACT(0)	200	163	39
tnfn1_pw060420p04q155	G07	EXACT(0)	156	145	127	37	EXACT(0)	200	189	47
tnfn1_pw060420p04q156	H07	EXACT(0)	158	152	138	39	EXACT(0)	200	190	57
tnfn1_pw060420p04q157	A08	EXACT(0)	157	146	135	43	EXACT(0)	200	126	34
tnfn1_pw060420p04q158	B08	EXACT(0)	156	145	90	23	EXACT(0)	200	183	51
tnfn1_pw060420p04q159	C08	EXACT(0)	158	151	124	25	EXACT(0)	200	180	57
tnfn1_pw060420p04q160	D08	EXACT(0)	154	145	132	47	EXACT(0)	199	185	59
tnfn1_pw060420p04q161	E08	EXACT(0)	157	145	127	37	EXACT(0)	200	187	51
tnfn1_pw060420p04q162	F08	EXACT(0)	156	153	114	33	EXACT(0)	200	183	58
tnfn1_pw060420p04q163	G08	EXACT(0)	155	153	109	31	EXACT(0)	200	191	56
tnfn1_pw060420p04q164	H08	EXACT(0)	155	152	115	35	EXACT(0)	200	179	56
tnfn1_pw060420p04q165	A09	EXACT(0)	157	145	113	20	EXACT(0)	200	190	48
tnfn1_pw060420p04q166	B09	EXACT(0)	155	152	109	26	EXACT(0)	200	192	52
tnfn1_pw060420p04q167	C09	EXACT(0)	158	152	131	32	EXACT(0)	200	193	49
tnfn1_pw060420p04q168	D09	EXACT(0)	156	144	128	30	EXACT(0)	200	197	47
tnfn1_pw060420p04q169	E09	EXACT(0)	158	152	135	31	EXACT(0)	200	185	53
tnfn1_pw060420p04q170	F09	EXACT(0)	157	152	125	35	EXACT(0)	200	182	48
tnfn1_pw060420p04q171	G09	EXACT(0)	154	139	122	39	EXACT(0)	200	146	38
tnfn1_pw060420p04q172	H09	EXACT(0)	156	153	128	43	EXACT(0)	200	181	45
tnfn1_pw060420p04q173	A10	EXACT(0)	156	142	80	18	EXACT(0)	200	191	46
tnfn1_pw060420p04q174	B10	EXACT(0)	157	153	137	42	EXACT(0)	200	137	28
tnfn1_pw060420p04q175	C10	EXACT(0)	156	152	127	35	EXACT(0)	200	183	56
tnfn1_pw060420p04q176	D10	EXACT(0)	159	152	127	33	EXACT(0)	200	184	55
tnfn1_pw060420p04q177	E10	EXACT(0)	156	152	112	28	EXACT(0)	200	185	53
tnfn1_pw060420p04q178	F10	EXACT(0)	156	145	124	35	EXACT(0)	201	96	33
tnfn1_pw060420p04q179	G10	EXACT(0)	156	151	130	41	EXACT(0)	200	179	53
tnfn1_pw060420p04q180	H10	EXACT(0)	155	145	123	42	EXACT(0)	200	191	58
tnfn1_pw060420p04q181	A11	EXACT(0)	156	152	123	33	EXACT(0)	200	180	62
tnfn1_pw060420p04q182	B11	EXACT(0)	157	153	140	43	EXACT(0)	199	174	45
tnfn1_pw060420p04q183	C11	EXACT(0)	155	114	60	19	EXACT(0)	200	194	49
tnfn1_pw060420p04q184	D11	EXACT(0)	158	152	128	35	EXACT(0)	200	181	59
tnfn1_pw060420p04q185	E11	EXACT(0)	157	145	126	28	EXACT(0)	200	191	48
tnfn1_pw060420p04q186	F11	EXACT(0)	156	145	124	35	EXACT(0)	200	189	53
tnfn1_pw060420p04q187	G11	EXACT(0)	159	151	148	42	EXACT(0)	200	187	57
tnfn1_pw060420p04q188	H11	EXACT(0)	156	145	128	37	EXACT(0)	193	181	46
tnfn1_pw060420p04q189	A12	EXACT(0)	155	145	100	23	EXACT(0)	200	190	54
tnfn1_pw060420p04q190	B12	EXACT(0)	156	152	133	34	EXACT(0)	200	162	30
tnfn1_pw060420p04q191	C12	EXACT(0)	155	152	121	34	EXACT(0)	200	178	51
tnfn1_pw060420p04q192	D12	EXACT(0)	156	153	125	37	EXACT(0)	200	174	43
tnfn1_pw060420p04q193	E12	EXACT(0)	156	154	132	38	EXACT(0)	200	189	53
tnfn1_pw060420p04q194	F12	EXACT(0)	156	152	124	40	EXACT(0)	200	193	54
tnfn1_pw060420p04q195	G12	EXACT(0)	156	145	111	30	EXACT(0)	200	142	31
tnfn1_pw060420p04q196	H12	EXACT(0)	157	152	114	32	EXACT(0)	199	117	23