

***Francisella tularensis* subsp. *novicida*
“Two-Allele” Transposon Mutant Library,
Plate 23 (tnfn1_pw060419p03)**

Catalog No. NR-51305

For research use only. Not for human use.

Contributor:

Colin Manoil, Ph.D., Professor of Genome Sciences,
University of Washington, Seattle, Washington, USA

Manufacturer:

BEI Resources

Product Description:

Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources does not confirm or validate individual mutants provided by the contributor.

A comprehensive 16,508-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-51305 represents plate 23 (tnfn1_pw060419p03) of the “two-allele” 3,050-member sublibrary. Detailed information for each mutant is shown in Tables 1 to 3.

Francisella tularensis subsp. *novicida*, strain U112 is excluded from Select Agent status. Please see [CDC Select Agent Program, Notification of Exclusion](#).

Material Provided:

Each inoculated well of the 96-well plate contains approximately 50 µL of culture in Tryptic Soy broth containing 0.1% L-cysteine and 10 µg/mL kanamycin supplemented with 5% glycerol.

Packaging/Storage:

NR-51305 was packaged aseptically in a 96-well plate. The product is provided frozen and should be stored at -80°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 broth or 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 plates at 37°C for 1 day.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through BEI Resources, NIAID, NIH: *Francisella tularensis* subsp. *novicida* “Two-Allele” Transposon Mutant Library, Plate 23 (tnfn1_pw060419p03), NR-51305.”

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, 2009; see www.cdc.gov/biosafety/publications/bmb15/index.htm.

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References:

- 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: Plate 23 (tnfn1_pw060419p03) – Transposon Type and Mutated Gene¹

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060419p03q101	T20	-	Transcriptional regulator, LysR family	Signal transduction and regulation
A02	tnfn1_pw060419p03q109	T20	trpA	Tryptophan synthase alpha chain	Amino acid metabolism - biosynthesis
A03	tnfn1_pw060419p03q117	T20	pilC	Type IV pili polytopic inner membrane protein	Motility, attachment and secretion structure
A04	tnfn1_pw060419p03q125	<KAN-2>	-	Pseudogene: hypothetical protein	Pseudogene
A05	tnfn1_pw060419p03q133	T18	-	Glutamine amidotransferase, SNO family	Cofactors, prosthetic groups, electron carriers metabolism
A06	tnfn1_pw060419p03q141	T18	fimT	Type IV pili, pilus assembly protein	Motility, attachment and secretion structure
A07	tnfn1_pw060419p03q149	T20	-	Conserved protein of unknown function	Unknown function - conserved
A08	tnfn1_pw060419p03q157	T20	-	Solute:sodium symporter	Transport
A09	tnfn1_pw060419p03q165	T20	-	Transcriptional regulator, LysR family	Signal transduction and regulation
A10	tnfn1_pw060419p03q173	<KAN-2>	-	Conserved protein of unknown function	Cell wall / LPS / capsule
A11	tnfn1_pw060419p03q181	T18	-	L-lactate dehydrogenase	Other metabolism - degradation, utilization, assimilation
A12	tnfn1_pw060419p03q189	T20	-	Two-component response regulator	Signal transduction and regulation
B01	tnfn1_pw060419p03q102	T20	rnr	Ribonuclease R	Transcription
B02	tnfn1_pw060419p03q110	T20	-	Conserved protein of unknown function	Unknown function - conserved
B03	tnfn1_pw060419p03q118	T20	-	Hypothetical protein	Hypothetical - novel
B04	tnfn1_pw060419p03q126	<KAN-2>	nadE	NAD synthase	Cofactors, prosthetic groups, electron carriers metabolism
B05	tnfn1_pw060419p03q134	T18	-	Hypothetical membrane protein	Hypothetical - novel
B06	tnfn1_pw060419p03q142	T18	-	Hypothetical membrane protein	Hypothetical - novel
B07	tnfn1_pw060419p03q150	T20	-	Membrane protein of unknown function	Unknown function - novel
B08	tnfn1_pw060419p03q158	T20	-	Transcriptional regulator, LysR family	Signal transduction and regulation
B09	tnfn1_pw060419p03q166	T20	wbtA	dTDP-glucose 4,6-dehydratase	Cell wall / LPS / capsule
B10	tnfn1_pw060419p03q174	<KAN-2>	-	Aspartate aminotransferase	Other metabolism - degradation, utilization, assimilation
B11	tnfn1_pw060419p03q182	T18	-	Hypothetical protein	Hypothetical - novel
B12	tnfn1_pw060419p03q190	T20	-	Conserved protein of unknown function	Unknown function - conserved
C01	tnfn1_pw060419p03q103	T20	-	Membrane fusion protein	Transport
C02	tnfn1_pw060419p03q111	T20	tolC	Outer membrane efflux protein, tolC precursor	Transport
C03	tnfn1_pw060419p03q119	T20	-	Conserved protein of unknown function	Unknown function - conserved
C04	tnfn1_pw060419p03q127	<KAN-2>	-	Protein of unknown function	Unknown function - novel
C05	tnfn1_pw060419p03q135	T18	-	Hypothetical protein	Hypothetical - novel
C06	tnfn1_pw060419p03q143	T18	-		
C07	tnfn1_pw060419p03q151	T20	-	ABC-type anion transport system, duplicated permease component	Transport
C08	tnfn1_pw060419p03q159	T20	-	Hydroxy/aromatic amino acid permease (HAAAP) family protein	Transport - amino-acid
C09	tnfn1_pw060419p03q167	T20	-	Conserved hypothetical membrane protein	Hypothetical - conserved
C10	tnfn1_pw060419p03q175	<KAN-2>	-	Hypothetical membrane protein	Hypothetical - novel
C11	tnfn1_pw060419p03q183	T18	-	Conserved hypothetical protein	Hypothetical - conserved
C12	tnfn1_pw060419p03q191	T20	-	Protein of unknown function	Unknown function - novel
D01	tnfn1_pw060419p03q104	T20	-	4Fe-4S ferredoxin, FAD dependent	Energy metabolism
D02	tnfn1_pw060419p03q112	T20	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
D03	tnfn1_pw060419p03q120	T20	-	Conserved outer membrane protein of unknown function	Unknown function - conserved
D04	tnfn1_pw060419p03q128	T20	-	Acyltransferase	Fatty acids and lipids metabolism
D05	tnfn1_pw060419p03q136	T18	clpP	ATP-dependent Clp protease subunit P	Post-translational modification, protein turnover, chaperones - protein degradation
D06	tnfn1_pw060419p03q144	T18	-	Protein of unknown function	Unknown function - novel
D07	tnfn1_pw060419p03q152	T20	-	Protein of unknown function	Unknown function - novel
D08	tnfn1_pw060419p03q160	T20	-	SAM-dependent methyltransferase	Putative enzymes
D09	tnfn1_pw060419p03q168	T20	-	Protein of unknown function	Unknown function - novel
D10	tnfn1_pw060419p03q176	<KAN-2>	-	Protein of unknown function	Unknown function - novel

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D11	tnfn1_pw060419p03q184	T18	-	Conserved protein of unknown function	Unknown function - conserved
D12	tnfn1_pw060419p03q192	T18	treA	Trehalase	Carbohydrate metabolism - degradation, utilization, assimilation
E01	tnfn1_pw060419p03q105	T20	-	Hypothetical membrane protein	Hypothetical - novel
E02	tnfn1_pw060419p03q113	T20	sucC	Succinyl-CoA synthetase, beta chain	Energy metabolism
E03	tnfn1_pw060419p03q121	T20	-	Fatty acid hydroxylase	Fatty acids and lipids metabolism
E04	tnfn1_pw060419p03q129	<KAN-2>	-	ROK family protein	Putative enzymes
E05	tnfn1_pw060419p03q137	T18	-	Amino acid-polyamine-organocation (APC) superfamily protein	Transport - amino-acid
E06	tnfn1_pw060419p03q145	T18	-	Amino acid-polyamine-organocation (APC) superfamily protein	Transport - amino-acid
E07	tnfn1_pw060419p03q153	T18	-	Conserved protein of unknown function	Unknown function - conserved
E08	tnfn1_pw060419p03q161	T20	-	traT-like protein	Mobile and extrachromosomal element functions - phage or plasmid related proteins
E09	tnfn1_pw060419p03q169	T20	nfnB	Dihydropteridine reductase	Energy metabolism
E10	tnfn1_pw060419p03q177	<KAN-2>	-	Protein of unknown function	Unknown function - novel
E11	tnfn1_pw060419p03q185	T18	-	YjeF-related protein of unknown function	Unknown function - conserved
E12	tnfn1_pw060419p03q193	T20	-	Regulatory protein, AlpA family	Signal transduction and regulation
F01	tnfn1_pw060419p03q106	T20	-	Conserved protein of unknown function	Unknown function - conserved
F02	tnfn1_pw060419p03q114	T20	-	Hypothetical protein	Hypothetical - novel
F03	tnfn1_pw060419p03q122	T20	-	Transporter-associated protein, HlyC/CorC family	Transport
F04	tnfn1_pw060419p03q130	<KAN-2>	-	Protein of unknown function	Unknown function - novel
F05	tnfn1_pw060419p03q138	T18	-	Conserved hypothetical protein	Hypothetical - conserved
F06	tnfn1_pw060419p03q146	T18	-	Conserved protein of unknown function	Unknown function - conserved
F07	tnfn1_pw060419p03q154	T20	-	Hypothetical protein	Hypothetical - novel
F08	tnfn1_pw060419p03q162	T20	-	Na ⁺ /H ⁺ antiporter	Transport
F09	tnfn1_pw060419p03q170	T20	-	Hypothetical membrane protein	Hypothetical - novel
F10	tnfn1_pw060419p03q178	T18	-	Protein of unknown function	Unknown function - novel
F11	tnfn1_pw060419p03q186	T18	-	Hypothetical protein	Hypothetical - novel
F12	tnfn1_pw060419p03q194	T20	-	Apolipoprotein N-acyltransferase	Cell wall / LPS / capsule
G01	tnfn1_pw060419p03q107	T20	-	Protein of unknown function	Unknown function - novel
G02	tnfn1_pw060419p03q115	T20	-	Hypothetical protein	Hypothetical - novel
G03	tnfn1_pw060419p03q123	T20	-	Conserved hypothetical protein	Hypothetical - conserved
G04	tnfn1_pw060419p03q131	<KAN-2>	-		
G05	tnfn1_pw060419p03q139	T18	-	Conserved hypothetical protein	Hypothetical - conserved
G06	tnfn1_pw060419p03q147	T18	-	N6-adenine-specific methylase	DNA replication, recombination, modification and repair
G07	tnfn1_pw060419p03q155	T20	-	Ferredoxin	Energy metabolism
G08	tnfn1_pw060419p03q163	T20	-	traT-like protein	Mobile and extrachromosomal element functions - phage or plasmid related proteins
G09	tnfn1_pw060419p03q171	T20	-	Hypothetical protein	Hypothetical - novel
G10	tnfn1_pw060419p03q179	T18	fumC	Fumarate hydratase, class II	Energy metabolism
G11	tnfn1_pw060419p03q187	T18	-	Conserved hypothetical protein	Hypothetical - conserved
G12	tnfn1_pw060419p03q195	T20	-	Sodium bile acid symporter family protein	Transport
H01	tnfn1_pw060419p03q108	T20	-	Hypothetical protein	Hypothetical - novel
H02	tnfn1_pw060419p03q116	T20	sucD	Succinyl-CoA synthetase, alpha subunit	Energy metabolism
H03	tnfn1_pw060419p03q124	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved
H04	tnfn1_pw060419p03q132	T18	-	Conserved hypothetical protein	Hypothetical - conserved
H05	tnfn1_pw060419p03q140	T18	-	Conserved protein of unknown function	Unknown function - conserved
H06	tnfn1_pw060419p03q148	T18	-	Heavy metal cation transport ATPase	Transport
H07	tnfn1_pw060419p03q156	T20	thrA	Aspartate kinase I/homoserine dehydrogenase I	Amino acid metabolism - biosynthesis
H08	tnfn1_pw060419p03q164	T20	pepO	M13 family metallopeptidase	Post-translational modification, protein turnover, chaperones - protein degradation
H09	tnfn1_pw060419p03q172	T18	mutS	MutS, subunit of MutHLS complex, methyl-directed mismatch repair protein	DNA replication, recombination, modification and repair - restriction/modification
H10	tnfn1_pw060419p03q180	T18	-	Peptidase, U61 family	Post-translational modification, protein turnover, chaperones - protein degradation
H11	tnfn1_pw060419p03q188	T18	-	Hypothetical membrane protein	Hypothetical - novel
H12	tnfn1_pw060419p03q196	T20	-	Monovalent cation:proton antiporter-1	Transport

¹All information in this table was provided by the depositor at the time of deposition.

Table 2: Plate 23 (tnfn1_pw060419p03) – Sequencing and Insert Location¹

Well Position	Strain Name	Sequencing Confirmation ²	Effective Genome Position of Insertion ³	Locus Tag	ORF Left End	ORF Right End	Direction of ORF ⁴	Length of ORF (codons)	Effective Position of Insertion in ORF ⁵
A01	tnfn1_pw060419p03q101	C	112021	FTN_0101	111569	112462	R	298	442(894)
A02	tnfn1_pw060419p03q109	C	1868534	FTN_1740	1868014	1868817	F	268	521(804)
A03	tnfn1_pw060419p03q117	C	1181028	FTN_1116	1180496	1181722	F	409	533(1227)
A04	tnfn1_pw060419p03q125	U	852049	FTN_0794	851999	852079	R	27	31(81)
A05	tnfn1_pw060419p03q133	C	635239	FTN_0602	634911	635447	F	179	329(537)
A06	tnfn1_pw060419p03q141	C	704668	FTN_0664	704429	705010	F	194	240(582)
A07	tnfn1_pw060419p03q149	C	1777273	FTN_1662	1777161	1777610	R	150	338(450)
A08	tnfn1_pw060419p03q157	C	1364551	FTN_1292	1363308	1364576	R	423	26(1269)
A09	tnfn1_pw060419p03q165	C	1368866	FTN_1300	1368610	1369497	R	296	632(888)
A10	tnfn1_pw060419p03q173	C	1539268	FTN_1449	1538872	1539477	R	202	210(606)
A11	tnfn1_pw060419p03q181	C	239109	FTN_0217	238429	239583	R	385	475(1155)
A12	tnfn1_pw060419p03q189	C	1541444	FTN_1452	1540850	1541536	F	229	595(687)
B01	tnfn1_pw060419p03q102	C	1550360	FTN_1461	1548609	1550903	R	765	544(2295)
B02	tnfn1_pw060419p03q110	C	895456	FTN_0839	895194	896291	F	366	263(1098)
B03	tnfn1_pw060419p03q118	C	380879	FTN_0379	380755	381126	F	124	125(372)
B04	tnfn1_pw060419p03q126	U	1351393	FTN_1278	1351324	1352070	F	249	70(747)
B05	tnfn1_pw060419p03q134	C	1148547	FTN_1086	1148532	1149134	F	201	16(603)
B06	tnfn1_pw060419p03q142	C	499605	FTN_0494	499405	500001	R	199	397(597)
B07	tnfn1_pw060419p03q150	C	1326819	FTN_1257	1326405	1327673	F	423	415(1269)
B08	tnfn1_pw060419p03q158	C	31930	FTN_0031	31335	32201	F	289	596(867)
B09	tnfn1_pw060419p03q166	C	1511577	FTN_1431	1511000	1512733	R	578	1157(1734)
B10	tnfn1_pw060419p03q174	C	1212538	FTN_1146	1211574	1212764	R	397	227(1191)
B11	tnfn1_pw060419p03q182	C	1064968	FTN_1005	1064800	1065075	F	92	169(276)
B12	tnfn1_pw060419p03q190	C	910227	FTN_0854	909700	910479	F	260	528(780)
C01	tnfn1_pw060419p03q103	C	1712729	FTN_1609	1712416	1713786	F	457	314(1371)
C02	tnfn1_pw060419p03q111	C	1824858	FTN_1703	1824128	1825654	R	509	797(1527)
C03	tnfn1_pw060419p03q119	C	846867	FTN_0788	846344	847171	F	276	524(828)
C04	tnfn1_pw060419p03q127	C	299036	FTN_0292	298865	299065	F	67	172(201)
C05	tnfn1_pw060419p03q135	C	58829	FTN_0049	58770	59591	F	274	60(822)
C06	tnfn1_pw060419p03q143	C	285121	intergenic					
C07	tnfn1_pw060419p03q151	C	152366	FTN_0140	151997	153793	F	599	370(1797)
C08	tnfn1_pw060419p03q159	C	1617532	FTN_1520	1617143	1618336	R	398	805(1194)
C09	tnfn1_pw060419p03q167	U	107666	FTN_0096	107210	107899	F	230	457(690)
C10	tnfn1_pw060419p03q175	C	238231	FTN_0216	238094	238426	F	111	138(333)
C11	tnfn1_pw060419p03q183	C	1484730	FTN_1407	1484689	1485012	R	108	283(324)
C12	tnfn1_pw060419p03q191	C	446349	FTN_0445	445344	446786	F	481	1006(1443)
D01	tnfn1_pw060419p03q104	C	689592	FTN_0649	687803	690832	F	1010	1790(3030)
D02	tnfn1_pw060419p03q112	C	1828633	FTN_1706	1827979	1829157	R	393	525(1179)
D03	tnfn1_pw060419p03q120	C	130690	FTN_0119	130544	131080	F	179	147(537)
D04	tnfn1_pw060419p03q128	U	1879379	FTN_1750	1879341	1880078	F	246	39(738)
D05	tnfn1_pw060419p03q136	U	1117652	FTN_1057	1117172	1117774	R	201	123(603)
D06	tnfn1_pw060419p03q144	C	1600255	FTN_1505	1599542	1601503	R	654	1249(1962)
D07	tnfn1_pw060419p03q152	C	995008	FTN_0934	994829	995320	F	164	180(492)
D08	tnfn1_pw060419p03q160	C	90838	FTN_0080	90741	91610	F	290	98(870)
D09	tnfn1_pw060419p03q168	C	81596	FTN_0067	81421	82032	R	204	437(612)
D10	tnfn1_pw060419p03q176	C	144661	FTN_0131	143590	144894	R	435	234(1305)
D11	tnfn1_pw060419p03q184	U	289206	FTN_0282	288913	289806	F	298	294(894)
D12	tnfn1_pw060419p03q192	C	1407004	FTN_1328	1406119	1407570	F	484	886(1452)
E01	tnfn1_pw060419p03q105	C	623295	FTN_0592	623054	623476	R	141	182(423)
E02	tnfn1_pw060419p03q113	C	625472	FTN_0594	624495	625655	R	387	184(1161)
E03	tnfn1_pw060419p03q121	C	854056	FTN_0797	853524	854069	F	182	533(546)
E04	tnfn1_pw060419p03q129	C	648434	FTN_0617	648331	649293	F	321	104(963)
E05	tnfn1_pw060419p03q137	C	247640	FTN_0223	246583	248118	F	512	1058(1536)
E06	tnfn1_pw060419p03q145	C	247640	FTN_0223	246583	248118	F	512	1058(1536)
E07	tnfn1_pw060419p03q153	C	1217566	FTN_1151	1216361	1218106	F	582	1206(1746)
E08	tnfn1_pw060419p03q161	C	325183	FTN_0315	324848	325591	R	248	409(744)
E09	tnfn1_pw060419p03q169	C	241015	FTN_0218	240476	241126	R	217	112(651)
E10	tnfn1_pw060419p03q177	C	144661	FTN_0131	143590	144894	R	435	234(1305)
E11	tnfn1_pw060419p03q185	C	745592	FTN_0702	745266	746765	F	500	327(1500)
E12	tnfn1_pw060419p03q193	C	374634	FTN_0372	374491	374706	F	72	144(216)
F01	tnfn1_pw060419p03q106	C	61104	FTN_0051	61102	61707	F	202	3(606)
F02	tnfn1_pw060419p03q114	C	1386060	FTN_1313	1384921	1386648	F	576	1140(1728)

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F03	tnfn1_pw060419p03q122	C	311141	FTN_0301	310260	311564	F	435	882(1305)
F04	tnfn1_pw060419p03q130	C	428079	FTN_0430	427666	428130	F	155	414(465)
F05	tnfn1_pw060419p03q138	C	87340	FTN_0074	87173	87418	R	82	79(246)
F06	tnfn1_pw060419p03q146	C	1086112	FTN_1029	1085576	1086232	R	219	121(657)
F07	tnfn1_pw060419p03q154	C	944990	FTN_0887	944252	945208	R	319	219(957)
F08	tnfn1_pw060419p03q162	C	126823	FTN_0115	126046	127293	F	416	778(1248)
F09	tnfn1_pw060419p03q170	C	780061	FTN_0727	780006	780572	F	189	56(567)
F10	tnfn1_pw060419p03q178	C	1299739	FTN_1230	1299559	1300131	R	191	393(573)
F11	tnfn1_pw060419p03q186	U	376862	FTN_0375	376636	377250	F	205	227(615)
F12	tnfn1_pw060419p03q194	C	1125999	FTN_1067	1125843	1127330	F	496	157(1488)
G01	tnfn1_pw060419p03q107	C	849738	FTN_0791	849690	849944	F	85	49(255)
G02	tnfn1_pw060419p03q115	C	1008265	FTN_0952	1008165	1008644	R	160	380(480)
G03	tnfn1_pw060419p03q123	C	225907	FTN_0205	225741	226649	F	303	167(909)
G04	tnfn1_pw060419p03q131	C	1050193	intergenic					
G05	tnfn1_pw060419p03q139	C	222776	FTN_0201	222642	223334	R	231	559(693)
G06	tnfn1_pw060419p03q147	C	693861	FTN_0655	693723	694298	R	192	438(576)
G07	tnfn1_pw060419p03q155	C	129413	FTN_0117	129107	129457	R	117	45(351)
G08	tnfn1_pw060419p03q163	C	325183	FTN_0315	324848	325591	R	248	409(744)
G09	tnfn1_pw060419p03q171	C	155822	FTN_0142	155218	156756	F	513	605(1539)
G10	tnfn1_pw060419p03q179	C	241891	FTN_0220	241817	243205	F	463	75(1389)
G11	tnfn1_pw060419p03q187	C	1187304	FTN_1123	1187288	1187590	F	101	17(303)
G12	tnfn1_pw060419p03q195	C	366716	FTN_0363	366625	367551	F	309	92(927)
H01	tnfn1_pw060419p03q108	C	1164511	FTN_1102	1164373	1164600	F	76	139(228)
H02	tnfn1_pw060419p03q116	C	624377	FTN_0593	623591	624460	R	290	84(870)
H03	tnfn1_pw060419p03q124	U	282566	FTN_0275	282485	283540	F	352	82(1056)
H04	tnfn1_pw060419p03q132	C	1384456	FTN_1312	1384422	1384913	F	164	35(492)
H05	tnfn1_pw060419p03q140	C	481906	FTN_0477	481348	482232	F	295	559(885)
H06	tnfn1_pw060419p03q148	U	394696	FTN_0394	392909	395071	R	721	376(2163)
H07	tnfn1_pw060419p03q156	C	546779	FTN_0525	545312	547729	F	806	1468(2418)
H08	tnfn1_pw060419p03q164	C	1260135	FTN_1186	1259507	1261567	R	687	1433(2061)
H09	tnfn1_pw060419p03q172	C	1605543	FTN_1509	1604143	1606674	F	844	1401(2532)
H10	tnfn1_pw060419p03q180	C	1720626	FTN_1613	1720110	1721120	R	337	495(1011)
H11	tnfn1_pw060419p03q188	U	740568	FTN_0696	740453	741076	R	208	509(624)
H12	tnfn1_pw060419p03q196	C	1595125	FTN_1501	1595030	1596325	F	432	96(1296)

¹All information in this table was provided by the depositor at the time of deposition.

²C: Confirmed; U: Unconfirmed

³The 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.

⁴F, forward relative to genome; R, reverse

⁵Nucleotide of Insertion(Length of ORF in Nucleotides)

Table 3: Plate 23 (tnfn1_pw060419p03) – Sequence Mapping Quality Metrics¹

Well Position	Strain Name	Junction Info	Position in Sequence Read of Last Vector (Nucleotide)	Length of Match to Transposon	Transposon Match Score	Average Phred Score for Transposon Match	Genome Position Info	Length of Match to Genome	Genome Match Score	Average Phred Score for Genome Match
A01	tnfn1_pw060419p03q101	EXACT(0)	172	137	95	25	EXACT(0)	200	170	45
A02	tnfn1_pw060419p03q109	EXACT(0)	158	151	140	39	EXACT(0)	143	141	45
A03	tnfn1_pw060419p03q117	EXACT(0)	155	145	129	41	EXACT(0)	200	193	56
A04	tnfn1_pw060419p03q125	EXACT(0)	121	119	109	44	EXACT(0)	200	183	67
A05	tnfn1_pw060419p03q133	EXACT(0)	122	112	101	29	EXACT(0)	200	176	52
A06	tnfn1_pw060419p03q141	EXACT(0)	124	120	86	24	EXACT(0)	200	192	56
A07	tnfn1_pw060419p03q149	EXACT(0)	157	153	142	38	EXACT(0)	200	181	54
A08	tnfn1_pw060419p03q157	EXACT(0)	157	153	124	31	EXACT(0)	200	185	56
A09	tnfn1_pw060419p03q165	EXACT(0)	154	145	121	41	EXACT(0)	200	148	35
A10	tnfn1_pw060419p03q173	EXACT(0)	120	119	104	45	EXACT(0)	200	196	59
A11	tnfn1_pw060419p03q181	EXACT(0)	123	120	101	31	EXACT(0)	200	197	56
A12	tnfn1_pw060419p03q189	EXACT(0)	155	139	128	44	EXACT(0)	200	193	36
B01	tnfn1_pw060419p03q102	EXACT(0)	157	151	135	40	EXACT(0)	200	144	43
B02	tnfn1_pw060419p03q110	EXACT(0)	159	152	143	43	EXACT(0)	200	195	58
B03	tnfn1_pw060419p03q118	EXACT(0)	156	152	120	37	EXACT(0)	200	180	54
B04	tnfn1_pw060419p03q126	EXACT(0)	119	113	103	39	EXACT(0)	200	194	60

Well Position	Strain Name	Junction Info	Position in Sequence Read of Last Vector (Nucleotide)	Length of Match to Transposon	Transposon Match Score	Average Phred Score for Transposon Match	Genome Position Info	Length of Match to Genome	Genome Match Score	Average Phred Score for Genome Match
B05	tnfn1_pw060419p03q134	EXACT(0)	123	112	86	24	EXACT(0)	200	181	51
B06	tnfn1_pw060419p03q142	EXACT(0)	121	112	87	24	EXACT(0)	200	183	57
B07	tnfn1_pw060419p03q150	EXACT(0)	156	145	118	32	EXACT(0)	200	182	52
B08	tnfn1_pw060419p03q158	EXACT(0)	155	144	129	40	EXACT(0)	200	190	62
B09	tnfn1_pw060419p03q166	EXACT(0)	154	146	116	38	EXACT(0)	200	193	58
B10	tnfn1_pw060419p03q174	EXACT(0)	121	119	104	43	EXACT(0)	200	197	63
B11	tnfn1_pw060419p03q182	EXACT(0)	124	120	104	31	EXACT(0)	200	184	56
B12	tnfn1_pw060419p03q190	EXACT(0)	157	145	139	51	EXACT(0)	200	190	56
C01	tnfn1_pw060419p03q103	EXACT(0)	157	153	137	39	EXACT(0)	200	186	45
C02	tnfn1_pw060419p03q111	EXACT(0)	158	153	135	36	EXACT(0)	200	190	56
C03	tnfn1_pw060419p03q119	EXACT(0)	156	145	127	38	EXACT(0)	200	183	58
C04	tnfn1_pw060419p03q127	EXACT(0)	122	120	90	29	EXACT(0)	200	174	54
C05	tnfn1_pw060419p03q135	EXACT(0)	124	116	102	32	EXACT(0)	200	181	61
C06	tnfn1_pw060419p03q143	EXACT(0)	125	120	100	31	EXACT(0)	200	187	53
C07	tnfn1_pw060419p03q151	EXACT(0)	153	152	126	42	EXACT(0)	200	153	41
C08	tnfn1_pw060419p03q159	EXACT(0)	156	139	133	45	EXACT(0)	200	185	65
C09	tnfn1_pw060419p03q167	EXACT(0)	155	153	135	49	EXACT(0)	200	190	63
C10	tnfn1_pw060419p03q175	EXACT(0)	121	119	77	24	EXACT(0)	200	187	52
C11	tnfn1_pw060419p03q183	EXACT(0)	124	119	70	18	EXACT(0)	200	176	42
C12	tnfn1_pw060419p03q191	EXACT(0)	158	152	141	47	EXACT(0)	200	173	54
D01	tnfn1_pw060419p03q104	EXACT(0)	157	153	130	36	EXACT(0)	200	196	58
D02	tnfn1_pw060419p03q112	EXACT(0)	156	153	134	39	EXACT(0)	200	118	35
D03	tnfn1_pw060419p03q120	EXACT(0)	157	153	136	40	EXACT(0)	200	192	57
D04	tnfn1_pw060419p03q128	NONE	0	0	0	24	ESTIMATE(122)	802	679	32
D05	tnfn1_pw060419p03q136	EXACT(0)	121	112	99	37	EXACT(0)	200	195	58
D06	tnfn1_pw060419p03q144	EXACT(0)	122	112	101	34	EXACT(0)	200	190	57
D07	tnfn1_pw060419p03q152	EXACT(0)	154	145	123	39	EXACT(0)	200	179	47
D08	tnfn1_pw060419p03q160	EXACT(0)	157	153	130	27	EXACT(0)	200	189	53
D09	tnfn1_pw060419p03q168	EXACT(0)	156	145	131	35	EXACT(0)	200	184	53
D10	tnfn1_pw060419p03q176	EXACT(0)	123	118	70	22	EXACT(0)	200	182	51
D11	tnfn1_pw060419p03q184	EXACT(0)	124	119	96	34	ESTIMATE(3)	197	185	52
D12	tnfn1_pw060419p03q192	EXACT(0)	123	120	99	32	EXACT(0)	200	192	52
E01	tnfn1_pw060419p03q105	EXACT(0)	156	142	122	38	EXACT(0)	200	197	52
E02	tnfn1_pw060419p03q113	EXACT(0)	160	144	90	22	EXACT(0)	200	195	52
E03	tnfn1_pw060419p03q121	EXACT(0)	156	152	139	48	EXACT(0)	200	176	55
E04	tnfn1_pw060419p03q129	EXACT(0)	124	120	103	27	EXACT(0)	200	187	53
E05	tnfn1_pw060419p03q137	EXACT(0)	124	120	101	35	EXACT(0)	200	186	56
E06	tnfn1_pw060419p03q145	EXACT(0)	125	120	112	32	EXACT(0)	200	186	58
E07	tnfn1_pw060419p03q153	EXACT(0)	123	73	66	24	EXACT(0)	200	181	50
E08	tnfn1_pw060419p03q161	EXACT(0)	156	142	111	30	EXACT(0)	200	131	31
E09	tnfn1_pw060419p03q169	EXACT(0)	157	145	142	43	EXACT(0)	200	174	50
E10	tnfn1_pw060419p03q177	EXACT(0)	121	119	109	36	EXACT(0)	200	182	59
E11	tnfn1_pw060419p03q185	EXACT(0)	125	118	107	35	EXACT(0)	200	189	61
E12	tnfn1_pw060419p03q193	EXACT(0)	157	145	111	25	EXACT(0)	200	192	54
F01	tnfn1_pw060419p03q106	EXACT(0)	154	145	129	38	EXACT(0)	200	167	45
F02	tnfn1_pw060419p03q114	EXACT(0)	156	144	117	25	EXACT(0)	200	175	58
F03	tnfn1_pw060419p03q122	EXACT(0)	158	145	123	30	EXACT(0)	200	186	57
F04	tnfn1_pw060419p03q130	EXACT(0)	126	118	78	22	EXACT(0)	200	181	48
F05	tnfn1_pw060419p03q138	EXACT(0)	125	120	67	23	EXACT(0)	200	192	50
F06	tnfn1_pw060419p03q146	EXACT(0)	123	116	105	32	EXACT(0)	200	186	65
F07	tnfn1_pw060419p03q154	ADJUSTED(2)	160	142	98	23	ESTIMATE(0)	200	183	59
F08	tnfn1_pw060419p03q162	EXACT(0)	155	152	136	42	EXACT(0)	200	190	54
F09	tnfn1_pw060419p03q170	EXACT(0)	159	153	122	27	EXACT(0)	200	181	52
F10	tnfn1_pw060419p03q178	EXACT(0)	122	113	94	32	EXACT(0)	200	189	65
F11	tnfn1_pw060419p03q186	EXACT(0)	122	112	75	23	ESTIMATE(3)	197	174	49
F12	tnfn1_pw060419p03q194	EXACT(0)	158	151	140	50	EXACT(0)	197	163	41
G01	tnfn1_pw060419p03q107	EXACT(0)	156	152	130	38	EXACT(0)	200	181	52
G02	tnfn1_pw060419p03q115	EXACT(0)	156	142	112	29	EXACT(0)	200	182	56
G03	tnfn1_pw060419p03q123	EXACT(0)	152	153	116	40	EXACT(0)	142	137	51
G04	tnfn1_pw060419p03q131	EXACT(0)	120	109	62	25	EXACT(0)	200	173	61
G05	tnfn1_pw060419p03q139	EXACT(0)	126	121	97	25	EXACT(0)	200	188	56
G06	tnfn1_pw060419p03q147	EXACT(0)	121	112	88	24	EXACT(0)	200	181	60

Well Position	Strain Name	Junction Info	Position in Sequence Read of Last Vector (Nucleotide)	Length of Match to Transposon	Transposon Match Score	Average Phred Score for Transposon Match	Genome Position Info	Length of Match to Genome	Genome Match Score	Average Phred Score for Genome Match
G07	tnfn1_pw060419p03q155	EXACT(0)	159	152	130	35	EXACT(0)	200	188	57
G08	tnfn1_pw060419p03q163	EXACT(0)	156	114	105	33	EXACT(0)	200	196	53
G09	tnfn1_pw060419p03q171	EXACT(0)	157	145	133	37	EXACT(0)	200	193	55
G10	tnfn1_pw060419p03q179	EXACT(0)	121	112	90	27	EXACT(0)	200	186	58
G11	tnfn1_pw060419p03q187	EXACT(0)	123	112	71	23	ESTIMATE(4)	196	189	50
G12	tnfn1_pw060419p03q195	EXACT(0)	155	145	110	31	EXACT(0)	200	178	57
H01	tnfn1_pw060419p03q108	EXACT(0)	156	144	133	41	EXACT(0)	80	71	52
H02	tnfn1_pw060419p03q116	EXACT(0)	156	139	133	49	EXACT(0)	200	199	61
H03	tnfn1_pw060419p03q124	EXACT(0)	120	119	104	43	EXACT(0)	200	193	64
H04	tnfn1_pw060419p03q132	EXACT(0)	121	105	82	21	ESTIMATE(112)	88	76	28
H05	tnfn1_pw060419p03q140	EXACT(0)	124	112	51	21	EXACT(0)	200	195	48
H06	tnfn1_pw060419p03q148	EXACT(0)	121	120	97	33	EXACT(0)	200	189	61
H07	tnfn1_pw060419p03q156	EXACT(0)	156	152	128	35	EXACT(0)	200	192	54
H08	tnfn1_pw060419p03q164	EXACT(0)	158	152	134	36	EXACT(0)	200	193	52
H09	tnfn1_pw060419p03q172	EXACT(0)	121	112	99	44	EXACT(0)	200	190	63
H10	tnfn1_pw060419p03q180	EXACT(0)	122	112	80	25	EXACT(0)	200	184	59
H11	tnfn1_pw060419p03q188	ADJUSTED(1)	122	111	62	20	ESTIMATE(2)	198	185	55
H12	tnfn1_pw060419p03q196	EXACT(0)	156	145	109	29	EXACT(0)	200	186	58

¹All information in this table was provided by the depositor at the time of deposition.