Francisella tularensis subsp. *novicida* "Two-Allele" Transposon Mutant Library, Plate 22 (tnfn1_pw060419p02)

Catalog No. NR-51304

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 library[1] 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-51304 represents plate 22 (tnfn1_pw060419p02) 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-51304 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% CO_2
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 22 (tnfn1_pw060419p02), NR-51304."

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/bmbl5/index.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.

Support Provided by NIAID

Table 1: Plate 22 (tnfn1_pw060419p02) – Transposon Type and Mutated Gene[1]

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060419p02q101	T20	-	Hypothetical protein	Hypothetical - novel
A02	tnfn1_pw060419p02q109	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved
A03	tnfn1_pw060419p02q117	T18	-	Conserved protein of unknown function	Unknown function - conserved
A04	tnfn1_pw060419p02q125	T18	-	Protein of unknown function	Unknown function - novel
A05	tnfn1_pw060419p02q133	T18			
A06	tnfn1_pw060419p02q141	T20	-	Drug:H+ antiporter-1 (DHA2) family protein	Transport - drugs / antibacterial compounds
A07	tnfn1_pw060419p02q149	T18	-	Conserved protein of unknown function	Unknown function - conserved
A08	tnfn1_pw060419p02q157	T20	-	Aldo/keto reductase family protein	Putative enzymes
A09	tnfn1_pw060419p02q165	T20	-	Protein of unknown function	Unknown function - novel
A10	tnfn1_pw060419p02q173	T20	dnaJ	Chaperone, DnaJ family, with C-terminal Zn finger domain	Post-translational modification, protein turnover, chaperones
A11	tnfn1_pw060419p02q181	T20	-	Thioredoxin	Cofactors, prosthetic groups, electron carriers metabolism
A12	tnfn1_pw060419p02q189	T20	potI	ATP-binding cassette putrescine uptake system, membrane protein, subunit I	Transport
B01	tnfn1_pw060419p02q102	T20	-	Hypothetical protein	Hypothetical - novel
B02	tnfn1_pw060419p02q110	<KAN-2>	-	Protein of unknown function	Unknown function - novel
B03	tnfn1_pw060419p02q118	T18	-	birA-like protein	Post-translational modification, protein turnover, chaperones - protein modification
B04	tnfn1_pw060419p02q126	T18	-	Small conductance mechanosensitive ion channel (MscS) family protein	Transport
B05	tnfn1_pw060419p02q134	T20	emrE	Putative membrane transporter of cations and cationic drugs, multidrug resistance protein	Transport - drugs / antibacterial compounds
B06	tnfn1_pw060419p02q142	T20	-	Conserved protein of unknown function	Unknown function - conserved
B07	tnfn1_pw060419p02q150	T20	-	Acid phosphatase	Fatty acids and lipids metabolism
B08	tnfn1_pw060419p02q158	T20	hslR	Heat shock protein 15 (HSP15)	Translation, ribosomal structure and biogenesis
B09	tnfn1_pw060419p02q166	T20	-	Conserved hypothetical protein	Hypothetical - conserved
B10	tnfn1_pw060419p02q174	T20	bioB	Biotin synthase	Cofactors, prosthetic groups, electron carriers metabolism
B11	tnfn1_pw060419p02q182	T20	-	Protein of unknown function	Unknown function - novel
B12	tnfn1_pw060419p02q190	T20	-	Conserved protein of unknown function	Unknown function - conserved
C01	tnfn1_pw060419p02q103	T18	-	Protein of unknown function with radical SAM domain	Unknown function - conserved
C02	tnfn1_pw060419p02q111	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved
C03	tnfn1_pw060419p02q119	T18	-	Carbon-nitrogen hydrolase	Putative enzymes
C04	tnfn1_pw060419p02q127	T18	-	Hypothetical protein	Hypothetical - novel
C05	tnfn1_pw060419p02q135	T20	ksgA	Dimethyladenosine transferase	Transport - amino-acid
C06	tnfn1_pw060419p02q143	T20	-	Conserved hypothetical protein	Potentially coding: hypothetical - conserved
C07	tnfn1_pw060419p02q151	T20	-	Transcriptional regulator, LysR family	Signal transduction and regulation
C08	tnfn1_pw060419p02q159	T20	ilvD	Dihydroxy-acid dehydratase	Amino acid metabolism - biosynthesis
C09	tnfn1_pw060419p02q167	T20	-	Cation diffusion facilitator (CDF) family protein	Transport
C10	tnfn1_pw060419p02q175	T20	-	Conserved hypothetical membrane protein	Hypothetical - conserved
C11	tnfn1_pw060419p02q183	T20	cyoC	Cytochrome bo terminal oxidase subunit III	Energy metabolism
C12	tnfn1_pw060419p02q191	T20	-	Amino acid-polyamine-organocation family protein	Transport - amino-acid
D01	tnfn1_pw060419p02q104	T20	rpe	D-ribulose-phosphate 3-epimerase	Energy metabolism
D02	tnfn1_pw060419p02q112	<KAN-2>	appC	Cytochrome bd-II terminal oxidase subunit I	Energy metabolism
D03	tnfn1_pw060419p02q120	T18	-	Chitin-binding protein	Putative enzymes
D04	tnfn1_pw060419p02q128	T18	-	Protein of unknown function	Unknown function - novel
D05	tnfn1_pw060419p02q136	T20	-	Metallopeptidase, M50B family	Post-translational modification, protein turnover, chaperones - protein degradation
D06	tnfn1_pw060419p02q144	T20	ribD	Pyrimidine reductase/pyrimidine deaminase	Cofactors, prosthetic groups, electron carriers metabolism
D07	tnfn1_pw060419p02q152	T20	-	Hypothetical membrane protein	Hypothetical - novel
D08	tnfn1_pw060419p02q160	T20	-	Hypothetical membrane protein	Hypothetical - novel
D09	tnfn1_pw060419p02q168	T20	gplX	Fructose 1,6-bisphosphatase II	Energy metabolism
D10	tnfn1_pw060419p02q176	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D11	tnfn1_pw060419p02q184	T20	-	Membrane protein of unknown function	Unknown function - novel
D12	tnfn1_pw060419p02q192	T20	blaA	Beta-lactamase class A	Other metabolism - degradation, utilization, assimilation
E01	tnfn1_pw060419p02q105	T20	-	Hypothetical membrane protein	Hypothetical - novel
E02	tnfn1_pw060419p02q113	<KAN-2>	-	Amino acid-polyamine-organocation (APC) superfamily protein	Transport - amino-acid
E03	tnfn1_pw060419p02q121	T18	-	Protein of unknown function	Unknown function - novel
E04	tnfn1_pw060419p02q129	T18	-	Hypothetical protein	Hypothetical - novel
E05	tnfn1_pw060419p02q137	T20	rnfB	Iron-sulfur cluster-binding protein	Putative enzymes
E06	tnfn1_pw060419p02q145	T20	pilQ	Type IV pili secretin component	Motility, attachment and secretion structure
E07	tnfn1_pw060419p02q153	T20	ribD	Pyrimidine reductase/pyrimidine deaminase	Cofactors, prosthetic groups, electron carriers metabolism
E08	tnfn1_pw060419p02q161	T20	-	Hypothetical membrane protein	Hypothetical - novel
E09	tnfn1_pw060419p02q169	T20	parA	Chromosome partition protein A, ATPase	Cell cycle
E10	tnfn1_pw060419p02q177	<KAN-2>	crcB	CrcB family protein	Cell cycle
E11	tnfn1_pw060419p02q185	T20	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
E12	tnfn1_pw060419p02q193	T20	-	Monovalent cation:proton antiporter	Transport
F01	tnfn1_pw060419p02q106	T20	-	Acetoacetate decarboxylase	Other metabolism - biosynthesis
F02	tnfn1_pw060419p02q114	<KAN-2>	-	Hypothetical protein	Hypothetical - novel
F03	tnfn1_pw060419p02q122	T18	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
F04	tnfn1_pw060419p02q130	<KAN-2>	-	Hypothetical protein	Hypothetical - novel
F05	tnfn1_pw060419p02q138	T20	bioF	8-amino-7-oxononanoate synthase	Cofactors, prosthetic groups, electron carriers metabolism
F06	tnfn1_pw060419p02q146	T20	-	Protein of unknown function	Unknown function - novel
F07	tnfn1_pw060419p02q154	T20	-	Hydroxy/aromatic amino acid permease (HAAAP) family protein	Transport - amino-acid
F08	tnfn1_pw060419p02q162	T20	glgX	Pullulanase	Carbohydrate metabolism - degradation, utilization, assimilation
F09	tnfn1_pw060419p02q170	T20	-	Conserved protein of unknown function	Unknown function - conserved
F10	tnfn1_pw060419p02q178	T18	-	Transcriptional regulator	Signal transduction and regulation
F11	tnfn1_pw060419p02q186	T20	-	Conserved protein of unknown function	Unknown function - conserved
F12	tnfn1_pw060419p02q194	T20	-	Amino acid permease	Transport - amino-acid
G01	tnfn1_pw060419p02q107	T20	-	ATP-binding Cassette (ABC) superfamily protein	Transport
G02	tnfn1_pw060419p02q115	<KAN-2>	-	Hypothetical membrane protein	Hypothetical - novel
G03	tnfn1_pw060419p02q123	T18	-	Monovalent cation:proton antiporter family protein	Transport
G04	tnfn1_pw060419p02q131	T18	-	Hypothetical protein	Hypothetical - novel
G05	tnfn1_pw060419p02q139	T20	-	Glycosyl transferase, group 1	Cell wall / LPS / capsule
G06	tnfn1_pw060419p02q147	T20	-	Protein of unknown function	Unknown function - novel
G07	tnfn1_pw060419p02q155	T20	gph	Phosphoglycolate phosphatase	Putative enzymes
G08	tnfn1_pw060419p02q163	T20	-	Conserved hypothetical protein	Hypothetical - conserved
G09	tnfn1_pw060419p02q171	T20	-	Hypothetical protein	Hypothetical - novel
G10	tnfn1_pw060419p02q179	T18	-	ATP-binding Cassette (ABC) superfamily protein	Transport
G11	tnfn1_pw060419p02q187	T20	-	Transcriptional regulator, AraC family	Signal transduction and regulation
G12	tnfn1_pw060419p02q195	T20	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
H01	tnfn1_pw060419p02q108	T20	-	Conserved hypothetical membrane protein	Hypothetical - conserved
H02	tnfn1_pw060419p02q116	T18	-	Conserved protein of unknown function	Unknown function - conserved
H03	tnfn1_pw060419p02q124	T18	pilN	Type IV pili associated protein	Motility, attachment and secretion structure
H04	tnfn1_pw060419p02q132	T18	-	Conserved protein of unknown function	Unknown function - conserved
H05	tnfn1_pw060419p02q140	T20	-	Proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	Transport
H06	tnfn1_pw060419p02q148	T20	-	Protein of unknown function	Unknown function - novel
H07	tnfn1_pw060419p02q156	T20	apaH	Diadenosine tetraphosphatase	Signal transduction and regulation
H08	tnfn1_pw060419p02q164	T20	-	Protein of unknown function	Putative enzymes
H09	tnfn1_pw060419p02q172	T20	pilM	Type IV pili, pilus assembly protein	Motility, attachment and secretion structure
H10	tnfn1_pw060419p02q180	T18	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
H11	tnfn1_pw060419p02q188	T20	-	NAD/FAD-binding protein	Putative enzymes
H12	tnfn1_pw060419p02q196	T20	-	MutT/nudix family protein	Putative enzymes

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

Table 2: Plate 22 (tnfn1_pw060419p02) – Sequencing and Insert Location[1]

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_pw060419p02q101	C	503452	FTN_0497	503304	503723	R	140	272(420)
A02	tnfn1_pw060419p02q109	C	1306837	FTN_1238	1306482	1307129	R	216	293(648)
A03	tnfn1_pw060419p02q117	C	494390	FTN_0489	494328	494654	R	109	265(327)
A04	tnfn1_pw060419p02q125	C	771836	FTN_0716	771325	772137	F	271	512(813)
A05	tnfn1_pw060419p02q133	C	1454241	intergenic					
A06	tnfn1_pw060419p02q141	C	708852	FTN_0667	708399	709784	R	462	933(1386)
A07	tnfn1_pw060419p02q149	C	1640370	FTN_1542	1640166	1640927	F	254	205(762)
A08	tnfn1_pw060419p02q157	C	883160	FTN_0825	882250	883320	R	357	161(1071)
A09	tnfn1_pw060419p02q165	C	226963	FTN_0206	226642	227115	F	158	322(474)
A10	tnfn1_pw060419p02q173	C	1355503	FTN_1283	1354992	1356176	R	395	674(1185)
A11	tnfn1_pw060419p02q181	C	911349	FTN_0856	911269	911592	F	108	81(324)
A12	tnfn1_pw060419p02q189	C	791119	FTN_0737	790573	791376	R	268	258(804)
B01	tnfn1_pw060419p02q102	C	850265	FTN_0792	849966	850385	R	140	121(420)
B02	tnfn1_pw060419p02q110	C	1540638	FTN_1451	1540174	1540707	R	178	70(534)
B03	tnfn1_pw060419p02q118	U	594701	FTN_0568	594002	594781	R	260	81(780)
B04	tnfn1_pw060419p02q126	C	1678900	FTN_1581	1678701	1679195	R	165	296(495)
B05	tnfn1_pw060419p02q134	U	856623	FTN_0799	856317	856643	R	109	21(327)
B06	tnfn1_pw060419p02q142	C	855199	FTN_0798	854146	856299	F	718	1054(2154)
B07	tnfn1_pw060419p02q150	C	102034	FTN_0090	101004	102545	R	514	512(1542)
B08	tnfn1_pw060419p02q158	C	757398	FTN_0712	757045	757410	R	122	13(366)
B09	tnfn1_pw060419p02q166	C	776453	FTN_0721	776068	777051	R	328	599(984)
B10	tnfn1_pw060419p02q174	U	872735	FTN_0815	871865	872803	R	313	69(939)
B11	tnfn1_pw060419p02q182	C	150533	FTN_0137	150533	150937	F	135	1(405)
B12	tnfn1_pw060419p02q190	C	1233985	FTN_1162	1233942	1234244	R	101	260(303)
C01	tnfn1_pw060419p02q103	U	819267	FTN_0761	818940	820022	F	361	328(1083)
C02	tnfn1_pw060419p02q111	C	829241	FTN_0772	829228	829515	R	96	275(288)
C03	tnfn1_pw060419p02q119	C	1463140	FTN_1383	1463001	1463768	F	256	140(768)
C04	tnfn1_pw060419p02q127	C	40469	FTN_0038	40369	40650	R	94	182(282)
C05	tnfn1_pw060419p02q135	C	587474	FTN_0560	587181	587966	F	262	294(786)
C06	tnfn1_pw060419p02q143	C	1731709	-	1731290	1731751	F	154	420(462)
C07	tnfn1_pw060419p02q151	C	1740175	FTN_1628	1739841	1740791	R	317	617(951)
C08	tnfn1_pw060419p02q159	C	1101498	FTN_1043	1100825	1102504	R	560	1007(1680)
C09	tnfn1_pw060419p02q167	C	409379	FTN_0411	409260	410144	F	295	120(885)
C10	tnfn1_pw060419p02q175	C	1483970	FTN_1406	1483913	1484686	R	258	717(774)
C11	tnfn1_pw060419p02q183	C	219946	FTN_0197	219561	220160	F	200	386(600)
C12	tnfn1_pw060419p02q191	C	1620586	FTN_1523	1620541	1621251	F	237	46(711)
D01	tnfn1_pw060419p02q104	C	1292461	FTN_1221	1292193	1292858	R	222	398(666)
D02	tnfn1_pw060419p02q112	C	1730310	FTN_1619	1728955	1730328	F	458	1356(1374)
D03	tnfn1_pw060419p02q120	C	1266183	FTN_1192	1265920	1267707	F	596	264(1788)
D04	tnfn1_pw060419p02q128	C	1582413	FTN_1490	1581779	1582627	R	283	215(849)
D05	tnfn1_pw060419p02q136	C	484774	FTN_0479	484555	485208	R	218	435(654)
D06	tnfn1_pw060419p02q144	C	125168	FTN_0114	124591	125655	R	355	488(1065)
D07	tnfn1_pw060419p02q152	C	945707	FTN_0888	945336	945869	F	178	372(534)
D08	tnfn1_pw060419p02q160	C	151535	FTN_0138	151080	151694	F	205	456(615)
D09	tnfn1_pw060419p02q168	C	306092	FTN_0298	305744	306727	F	328	349(984)
D10	tnfn1_pw060419p02q176	C	1242403	FTN_1171	1242057	1243040	R	328	638(984)
D11	tnfn1_pw060419p02q184	C	812591	FTN_0757	810052	814938	F	1629	2540(4887)
D12	tnfn1_pw060419p02q192	C	1062425	FTN_1002	1062223	1063104	F	294	203(882)
E01	tnfn1_pw060419p02q105	C	1330386	FTN_1260	1329874	1331325	F	484	513(1452)
E02	tnfn1_pw060419p02q113	C	598176	FTN_0571	597725	599131	R	469	956(1407)
E03	tnfn1_pw060419p02q121	C	1616872	FTN_1519	1616753	1617106	R	118	235(354)
E04	tnfn1_pw060419p02q129	C	785972	FTN_0733	785970	786260	R	97	289(291)
E05	tnfn1_pw060419p02q137	C	1090680	FTN_1034	1090247	1090873	F	209	434(627)
E06	tnfn1_pw060419p02q145	C	1202168	FTN_1137	1201461	1203242	R	594	1075(1782)
E07	tnfn1_pw060419p02q153	C	125168	FTN_0114	124591	125655	R	355	488(1065)
E08	tnfn1_pw060419p02q161	C	1080661	FTN_1023	1080187	1080771	R	195	111(585)
E09	tnfn1_pw060419p02q169	C	432337	FTN_0433	432195	432833	F	213	143(639)
E10	tnfn1_pw060419p02q177	C	150379	FTN_0136	150192	150533	F	114	188(342)
E11	tnfn1_pw060419p02q185	C	721792	FTN_0678	721383	722594	R	404	803(1212)
E12	tnfn1_pw060419p02q193	U	157391	FTN_0143	156853	158736	F	628	539(1884)
F01	tnfn1_pw060419p02q106	C	865418	FTN_0808	865255	865992	R	246	575(738)
F02	tnfn1_pw060419p02q114	C	151766	FTN_0139	151697	151867	R	57	102(171)

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]
F03	tnfn1_pw060419p02q122	C	554978	FTN_0533	554322	555512	R	397	535(1191)
F04	tnfn1_pw060419p02q130	C	1000083	FTN_0939	1000022	1000177	R	52	95(156)
F05	tnfn1_pw060419p02q138	C	871127	FTN_0814	870744	871868	R	375	742(1125)
F06	tnfn1_pw060419p02q146	C	1563369	FTN_1475	1563112	1563483	R	124	115(372)
F07	tnfn1_pw060419p02q154	C	1609370	FTN_1512	1608678	1609847	F	390	693(1170)
F08	tnfn1_pw060419p02q162	C	526882	FTN_0512	524688	527897	R	1070	1016(3210)
F09	tnfn1_pw060419p02q170	C	1075375	FTN_1016	1075256	1075756	R	167	382(501)
F10	tnfn1_pw060419p02q178	C	905906	FTN_0850	905800	906207	F	136	107(408)
F11	tnfn1_pw060419p02q186	C	620810	FTN_0590	620283	621500	F	406	528(1218)
F12	tnfn1_pw060419p02q194	U	955149	FTN_0898	954503	956044	R	514	896(1542)
G01	tnfn1_pw060419p02q107	C	1339612	FTN_1267	1338966	1339724	F	253	647(759)
G02	tnfn1_pw060419p02q115	C	1621602	FTN_1524	1621272	1621652	R	127	51(381)
G03	tnfn1_pw060419p02q123	C	1073130	FTN_1013	1072741	1073913	R	391	784(1173)
G04	tnfn1_pw060419p02q131	C	820795	FTN_0764	820728	821078	R	117	284(351)
G05	tnfn1_pw060419p02q139	C	143210	FTN_0130	142461	143402	F	314	750(942)
G06	tnfn1_pw060419p02q147	C	1303689	FTN_1235	1303554	1304012	R	153	324(459)
G07	tnfn1_pw060419p02q155	C	611341	FTN_0582	611071	611742	R	224	402(672)
G08	tnfn1_pw060419p02q163	C	742320	FTN_0699	742065	743228	F	388	256(1164)
G09	tnfn1_pw060419p02q171	C	916635	FTN_0862	916124	917245	F	374	512(1122)
G10	tnfn1_pw060419p02q179	C	1339499	FTN_1267	1338966	1339724	F	253	534(759)
G11	tnfn1_pw060419p02q187	C	1346376	FTN_1274	1346150	1346974	R	275	599(825)
G12	tnfn1_pw060419p02q195	C	323132	FTN_0312	322772	323959	F	396	361(1188)
H01	tnfn1_pw060419p02q108	C	1093585	FTN_1038	1093310	1093993	F	228	276(684)
H02	tnfn1_pw060419p02q116	C	33174	FTN_0033	32974	33519	F	182	201(546)
H03	tnfn1_pw060419p02q124	C	1204642	FTN_1140	1204444	1205004	R	187	363(561)
H04	tnfn1_pw060419p02q132	C	1243659	FTN_1172	1243043	1244494	R	484	836(1452)
H05	tnfn1_pw060419p02q140	C	560996	FTN_0537	560098	561507	F	470	899(1410)
H06	tnfn1_pw060419p02q148	C	1029409	FTN_0975	1029173	1030660	F	496	237(1488)
H07	tnfn1_pw060419p02q156	C	588521	FTN_0561	587981	588805	F	275	541(825)
H08	tnfn1_pw060419p02q164	C	56117	FTN_0047	53754	57527	F	1258	2364(3774)
H09	tnfn1_pw060419p02q172	C	1205829	FTN_1141	1205009	1206010	R	334	182(1002)
H10	tnfn1_pw060419p02q180	U	722093	FTN_0678	721383	722594	R	404	502(1212)
H11	tnfn1_pw060419p02q188	C	1543541	FTN_1454	1542637	1543887	F	417	905(1251)
H12	tnfn1_pw060419p02q196	C	241468	FTN_0219	241266	241640	F	125	203(375)

[1]All information in this table was provided by the depositor at the time of deposition.
[2]C: Confirmed; U: Unconfirmed
[3]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.
[4]F, forward relative to genome; R, reverse
[5]Nucleotide of Insertion(Length of ORF in Nucleotides)

Table 3: Plate 22 (tnfn1_pw060419p02) – Sequence Mapping Quality Metrics[1]

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_pw060419p02q101	EXACT(0)	156	142	103	26	EXACT(0)	200	176	47
A02	tnfn1_pw060419p02q109	EXACT(0)	117	119	87	38	EXACT(0)	200	177	48
A03	tnfn1_pw060419p02q117	EXACT(0)	123	120	69	23	EXACT(0)	200	185	54
A04	tnfn1_pw060419p02q125	EXACT(0)	124	119	103	34	EXACT(0)	200	186	51
A05	tnfn1_pw060419p02q133	EXACT(0)	121	120	86	25	EXACT(0)	200	158	37
A06	tnfn1_pw060419p02q141	EXACT(0)	158	153	127	30	EXACT(0)	200	183	53
A07	tnfn1_pw060419p02q149	EXACT(0)	119	111	84	26	EXACT(0)	200	180	52
A08	tnfn1_pw060419p02q157	EXACT(0)	156	152	121	33	EXACT(0)	200	188	58
A09	tnfn1_pw060419p02q165	EXACT(0)	155	116	57	16	EXACT(0)	200	186	51
A10	tnfn1_pw060419p02q173	EXACT(0)	159	151	138	32	EXACT(0)	200	188	50
A11	tnfn1_pw060419p02q181	EXACT(0)	155	114	96	30	EXACT(0)	200	190	43
A12	tnfn1_pw060419p02q189	EXACT(0)	155	145	95	29	EXACT(0)	200	193	55
B01	tnfn1_pw060419p02q102	EXACT(0)	156	145	113	30	EXACT(0)	200	164	42
B02	tnfn1_pw060419p02q110	EXACT(0)	118	107	82	23	EXACT(0)	200	192	52
B03	tnfn1_pw060419p02q118	EXACT(0)	122	112	85	22	EXACT(0)	200	180	54
B04	tnfn1_pw060419p02q126	EXACT(0)	125	120	106	39	EXACT(0)	84	77	51

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_pw060419p02q134	EXACT(0)	156	138	117	26	EXACT(0)	200	185	32
B06	tnfn1_pw060419p02q142	EXACT(0)	157	153	126	31	EXACT(0)	200	191	59
B07	tnfn1_pw060419p02q150	EXACT(0)	156	153	130	37	EXACT(0)	200	184	45
B08	tnfn1_pw060419p02q158	EXACT(0)	157	152	133	37	EXACT(0)	200	159	39
B09	tnfn1_pw060419p02q166	EXACT(0)	157	152	130	33	EXACT(0)	200	174	47
B10	tnfn1_pw060419p02q174	EXACT(0)	158	153	142	40	EXACT(0)	200	175	35
B11	tnfn1_pw060419p02q182	EXACT(0)	158	145	131	36	EXACT(0)	200	184	49
B12	tnfn1_pw060419p02q190	EXACT(0)	158	145	135	52	EXACT(0)	197	175	52
C01	tnfn1_pw060419p02q103	EXACT(0)	125	119	105	37	EXACT(0)	158	102	33
C02	tnfn1_pw060419p02q111	EXACT(0)	117	111	89	33	EXACT(0)	200	195	46
C03	tnfn1_pw060419p02q119	EXACT(0)	124	117	101	28	EXACT(0)	200	194	57
C04	tnfn1_pw060419p02q127	EXACT(0)	121	112	90	29	EXACT(0)	200	172	53
C05	tnfn1_pw060419p02q135	EXACT(0)	156	145	137	41	EXACT(0)	170	159	51
C06	tnfn1_pw060419p02q143	EXACT(0)	157	145	132	34	EXACT(0)	200	171	60
C07	tnfn1_pw060419p02q151	EXACT(0)	158	152	138	39	EXACT(0)	200	188	58
C08	tnfn1_pw060419p02q159	EXACT(0)	157	153	127	34	EXACT(0)	200	193	54
C09	tnfn1_pw060419p02q167	EXACT(0)	157	145	83	15	EXACT(0)	200	175	50
C10	tnfn1_pw060419p02q175	EXACT(0)	156	144	107	26	EXACT(0)	200	177	56
C11	tnfn1_pw060419p02q183	EXACT(0)	159	145	132	39	EXACT(0)	200	190	53
C12	tnfn1_pw060419p02q191	EXACT(0)	159	153	134	32	EXACT(0)	200	180	56
D01	tnfn1_pw060419p02q104	EXACT(0)	156	151	118	37	EXACT(0)	200	191	56
D02	tnfn1_pw060419p02q112	EXACT(0)	119	112	85	32	EXACT(0)	200	193	48
D03	tnfn1_pw060419p02q120	EXACT(0)	125	119	105	28	EXACT(0)	200	144	30
D04	tnfn1_pw060419p02q128	EXACT(0)	122	120	99	38	EXACT(0)	199	150	45
D05	tnfn1_pw060419p02q136	EXACT(0)	156	145	134	41	EXACT(0)	200	178	65
D06	tnfn1_pw060419p02q144	EXACT(0)	157	153	124	25	EXACT(0)	200	189	48
D07	tnfn1_pw060419p02q152	EXACT(0)	156	151	130	38	EXACT(0)	200	189	55
D08	tnfn1_pw060419p02q160	EXACT(0)	158	153	134	37	ESTIMATE(2)	198	182	60
D09	tnfn1_pw060419p02q168	EXACT(0)	158	153	141	38	EXACT(0)	200	194	53
D10	tnfn1_pw060419p02q176	EXACT(0)	121	120	75	23	EXACT(0)	200	189	49
D11	tnfn1_pw060419p02q184	EXACT(0)	158	144	131	39	EXACT(0)	200	192	56
D12	tnfn1_pw060419p02q192	EXACT(0)	157	145	82	18	EXACT(0)	200	186	53
E01	tnfn1_pw060419p02q105	EXACT(0)	155	153	123	37	EXACT(0)	200	192	55
E02	tnfn1_pw060419p02q113	EXACT(0)	121	119	104	38	EXACT(0)	200	190	62
E03	tnfn1_pw060419p02q121	EXACT(0)	123	120	104	35	EXACT(0)	200	175	50
E04	tnfn1_pw060419p02q129	EXACT(0)	122	119	92	29	EXACT(0)	200	170	58
E05	tnfn1_pw060419p02q137	EXACT(0)	158	153	139	40	EXACT(0)	200	165	43
E06	tnfn1_pw060419p02q145	EXACT(0)	156	153	135	40	EXACT(0)	200	198	53
E07	tnfn1_pw060419p02q153	EXACT(0)	158	153	123	32	EXACT(0)	200	189	54
E08	tnfn1_pw060419p02q161	EXACT(0)	157	145	129	49	EXACT(0)	200	160	27
E09	tnfn1_pw060419p02q169	EXACT(0)	156	145	112	28	EXACT(0)	200	186	49
E10	tnfn1_pw060419p02q177	EXACT(0)	116	112	92	31	EXACT(0)	196	161	24
E11	tnfn1_pw060419p02q185	EXACT(0)	157	152	123	31	EXACT(0)	200	187	57
E12	tnfn1_pw060419p02q193	EXACT(0)	156	145	131	44	EXACT(0)	200	180	51
F01	tnfn1_pw060419p02q106	EXACT(0)	156	145	140	44	EXACT(0)	200	182	57
F02	tnfn1_pw060419p02q114	EXACT(0)	116	112	97	37	EXACT(0)	200	182	59
F03	tnfn1_pw060419p02q122	EXACT(0)	125	120	115	37	EXACT(0)	200	186	54
F04	tnfn1_pw060419p02q130	ADJUSTED(1)	122	111	58	21	ESTIMATE(56)	143	72	24
F05	tnfn1_pw060419p02q138	EXACT(0)	158	152	128	36	EXACT(0)	200	184	55
F06	tnfn1_pw060419p02q146	EXACT(0)	157	145	139	44	ESTIMATE(48)	152	122	25
F07	tnfn1_pw060419p02q154	EXACT(0)	155	152	131	40	EXACT(0)	201	99	23
F08	tnfn1_pw060419p02q162	EXACT(0)	158	153	132	32	EXACT(0)	197	184	52
F09	tnfn1_pw060419p02q170	EXACT(0)	155	150	126	38	EXACT(0)	99	97	36
F10	tnfn1_pw060419p02q178	EXACT(0)	121	106	88	31	EXACT(0)	199	143	35
F11	tnfn1_pw060419p02q186	EXACT(0)	156	145	134	49	EXACT(0)	200	161	51
F12	tnfn1_pw060419p02q194	EXACT(0)	157	145	133	44	EXACT(0)	200	186	65
G01	tnfn1_pw060419p02q107	EXACT(0)	161	150	136	34	EXACT(0)	200	184	56
G02	tnfn1_pw060419p02q115	EXACT(0)	117	107	90	36	EXACT(0)	200	187	36
G03	tnfn1_pw060419p02q123	EXACT(0)	125	115	109	31	EXACT(0)	200	172	48
G04	tnfn1_pw060419p02q131	EXACT(0)	125	120	94	23	EXACT(0)	200	180	43
G05	tnfn1_pw060419p02q139	EXACT(0)	159	153	119	30	EXACT(0)	200	187	55
G06	tnfn1_pw060419p02q147	EXACT(0)	156	152	128	34	EXACT(0)	200	174	58

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_pw060419p02q155	EXACT(0)	156	142	70	16	EXACT(0)	200	187	50
G08	tnfn1_pw060419p02q163	EXACT(0)	156	153	132	44	EXACT(0)	201	169	39
G09	tnfn1_pw060419p02q171	EXACT(0)	157	145	136	40	EXACT(0)	200	182	55
G10	tnfn1_pw060419p02q179	EXACT(0)	123	106	92	27	EXACT(0)	200	190	48
G11	tnfn1_pw060419p02q187	EXACT(0)	157	152	144	50	EXACT(0)	200	198	58
G12	tnfn1_pw060419p02q195	EXACT(0)	155	114	85	22	EXACT(0)	200	193	48
H01	tnfn1_pw060419p02q108	EXACT(0)	156	145	128	47	EXACT(0)	200	146	48
H02	tnfn1_pw060419p02q116	EXACT(0)	123	112	94	27	EXACT(0)	200	176	48
H03	tnfn1_pw060419p02q124	EXACT(0)	122	112	90	26	EXACT(0)	200	182	55
H04	tnfn1_pw060419p02q132	EXACT(0)	124	112	81	22	EXACT(0)	200	194	54
H05	tnfn1_pw060419p02q140	EXACT(0)	155	145	126	38	EXACT(0)	200	180	57
H06	tnfn1_pw060419p02q148	EXACT(0)	158	145	133	48	EXACT(0)	200	179	56
H07	tnfn1_pw060419p02q156	EXACT(0)	158	152	125	33	EXACT(0)	200	189	53
H08	tnfn1_pw060419p02q164	EXACT(0)	159	152	146	38	EXACT(0)	193	176	55
H09	tnfn1_pw060419p02q172	EXACT(0)	162	152	125	38	EXACT(0)	200	187	47
H10	tnfn1_pw060419p02q180	NONE	0	0	0	18	ESTIMATE(146)	216	135	21
H11	tnfn1_pw060419p02q188	EXACT(0)	156	153	121	35	EXACT(0)	200	189	60
H12	tnfn1_pw060419p02q196	EXACT(0)	157	145	136	43	EXACT(0)	200	187	39

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

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