

***Francisella tularensis* subsp. *novicida*
“Two-Allele” Transposon Mutant Library,
Plate 19 (tnfn1_pw060418p03)**

Catalog No. NR-51301

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-51301 represents plate 19 (tnfn1_pw060418p03) 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-51301 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 19 (tnfn1_pw060418p03), NR-51301.”

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.

Disclaimers:

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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 19 (tnfn1_pw060418p03) – Transposon Type and Mutated Gene¹

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060418p03q101	T20	-	ABC-type transport system permease protein	transport
A02	tnfn1_pw060418p03q109	T20	-	fucose: H+ symporter (FHS) family protein	transport - carbohydrates (sugars, polysaccharides)
A03	tnfn1_pw060418p03q117	<KAN-2>	xerD	site-specific recombinase	DNA replication, recombination, modification and repair
A04	tnfn1_pw060418p03q125	T18	-	hypothetical protein	hypothetical - novel
A05	tnfn1_pw060418p03q133	T20	cyoE	heme O synthase	cofactors, prosthetic groups, electron carriers metabolism
A06	tnfn1_pw060418p03q141	T20	-	hypothetical protein	hypothetical - novel
A07	tnfn1_pw060418p03q149	T20	-	predicted Co/Zn/Cd cation transporter	transport
A08	tnfn1_pw060418p03q157	T20	kpsF	phosphosugar isomerase	cell wall / LPS / capsule
A09	tnfn1_pw060418p03q165	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
A10	tnfn1_pw060418p03q173	<KAN-2>	-	thioesterase	putative enzymes
A11	tnfn1_pw060418p03q181	<KAN-2>	-	rhodanese-related sulfurtransferase	other metabolism - biosynthesis
A12	tnfn1_pw060418p03q189	T18	cutC	copper homeostasis protein CutC family protein	cofactors, prosthetic groups, electron carriers metabolism
B01	tnfn1_pw060418p03q102	T20	-	pilus assembly protein	motility, attachment and secretion structure
B02	tnfn1_pw060418p03q110	T20	-	conserved hypothetical protein	hypothetical - conserved
B03	tnfn1_pw060418p03q118	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
B04	tnfn1_pw060418p03q126	T18	-		
B05	tnfn1_pw060418p03q134	T20	-	pirin family protein	putative enzymes
B06	tnfn1_pw060418p03q142	T20	-	short chain dehydrogenase	putative enzymes
B07	tnfn1_pw060418p03q150	T20	-	glycosyl transferase, family 2	cell wall / LPS / capsule
B08	tnfn1_pw060418p03q158	T20	recB	ATP-dependent exoDNAse (exonuclease V) beta subunit	DNA replication, recombination, modification and repair - restriction/modification
B09	tnfn1_pw060418p03q166	T20	-	protein of unknown function with radical SAM domain	unknown function - conserved
B10	tnfn1_pw060418p03q174	<KAN-2>	tig	trigger factor (TF) protein (peptidyl-prolyl cis/trans isomerase)	post-translational modification, protein turnover, chaperones - protein modification
B11	tnfn1_pw060418p03q182	T18	-	conserved protein of unknown function	unknown function - conserved
B12	tnfn1_pw060418p03q190	T18	-	conserved protein of unknown function	unknown function - conserved
C01	tnfn1_pw060418p03q103	T20	potG	ATP-binding cassette putrescine uptake system, ATP-binding protein	transport
C02	tnfn1_pw060418p03q111	T20	-	hypothetical membrane protein	hypothetical - novel
C03	tnfn1_pw060418p03q119	<KAN-2>	pilA	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
C04	tnfn1_pw060418p03q127	T18	-	protein of unknown function	unknown function - novel
C05	tnfn1_pw060418p03q135	T20	-	YGGT family membrane protein	unknown function - conserved
C06	tnfn1_pw060418p03q143	T20	-	drug/metabolite transporter (DMT) superfamily protein	transport - drugs / antibacterial compounds
C07	tnfn1_pw060418p03q151	T20	-	hypothetical membrane protein	hypothetical - novel
C08	tnfn1_pw060418p03q159	T20	-	hypothetical protein	hypothetical - novel
C09	tnfn1_pw060418p03q167	T20	sohB	peptidase family S49 protein	post-translational modification, protein turnover, chaperones - protein modification
C10	tnfn1_pw060418p03q175	<KAN-2>	oppB	peptide/opine/nickel uptake transporter (PepT) family protein	transport
C11	tnfn1_pw060418p03q183	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
C12	tnfn1_pw060418p03q191	T18	recX	inhibitor of RecA	signal transduction and regulation
D01	tnfn1_pw060418p03q104	T20	-	conserved hypothetical protein	hypothetical - conserved
D02	tnfn1_pw060418p03q112	T20	-	Zn-dependent hydrolase	putative enzymes
D03	tnfn1_pw060418p03q120	<KAN-2>	ugpQ	glycerophosphoryl diester phosphodiesterase	cell wall / LPS / capsule
D04	tnfn1_pw060418p03q128	T18	-	conserved protein of unknown function	unknown function - conserved
D05	tnfn1_pw060418p03q136	T20	pilP	Type IV pili periplasmic component	motility, attachment and secretion structure
D06	tnfn1_pw060418p03q144	T20	ksgA	dimethyladenosine transferase	transport - amino-acid
D07	tnfn1_pw060418p03q152	T20	-	dehydrogenase	putative enzymes
D08	tnfn1_pw060418p03q160	T20	-		
D09	tnfn1_pw060418p03q168	T20	-	HIT family protein	putative enzymes
D10	tnfn1_pw060418p03q176	<KAN-2>	-	protein of unknown function	unknown function - novel

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D11	tnfn1_pw060418p03q184	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
D12	tnfn1_pw060418p03q192	T18	pheA	prephenate dehydratase	amino acid metabolism - biosynthesis
E01	tnfn1_pw060418p03q105	T20	-	metabolite:H+ symporter (MHS) family protein	transport
E02	tnfn1_pw060418p03q113	T20	-	metal-dependent exopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
E03	tnfn1_pw060418p03q121	<KAN-2>	capB	capsule biosynthesis protein CapB	cell wall / LPS / capsule
E04	tnfn1_pw060418p03q129	T20	talA	transaldolase	energy metabolism
E05	tnfn1_pw060418p03q137	T20	folC	folypoly-gamma-glutamate synthetase/ dihydrofolate synthetase	cofactors, prosthetic groups, electron carriers metabolism
E06	tnfn1_pw060418p03q145	T20	-	polar amino acid uptake transporter	transport - amino-acid
E07	tnfn1_pw060418p03q153	T20	-	hypothetical protein	hypothetical - novel
E08	tnfn1_pw060418p03q161	T20	-	protein of unknown function	unknown function - novel
E09	tnfn1_pw060418p03q169	T20	-	membrane protein of unknown function	unknown function - conserved
E10	tnfn1_pw060418p03q177	<KAN-2>	pcp	pyrrolidone carboxylate peptidase	post-translational modification, protein turnover, chaperones
E11	tnfn1_pw060418p03q185	<KAN-2>	-	S-adenosylmethionine-dependent methyltransferase	putative enzymes
E12	tnfn1_pw060418p03q193	T18	naoX	uncharacterized NAD(FAD)-dependent dehydrogenase	putative enzymes
F01	tnfn1_pw060418p03q106	T20	-	OmpA family protein	cell wall / LPS / capsule
F02	tnfn1_pw060418p03q114	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
F03	tnfn1_pw060418p03q122	<KAN-2>	-	ATP-binding cassette (ABC) superfamily protein	transport
F04	tnfn1_pw060418p03q130	T18	-	protein of unknown function	unknown function - novel
F05	tnfn1_pw060418p03q138	T20	gltB	glutamate synthase domain 2	other metabolism - degradation, utilization, assimilation
F06	tnfn1_pw060418p03q146	T20	-	conserved hypothetical protein	hypothetical - conserved
F07	tnfn1_pw060418p03q154	T20	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
F08	tnfn1_pw060418p03q162	T20	-	MoxR-like ATPase	putative enzymes
F09	tnfn1_pw060418p03q170	T20	-	conserved hypothetical protein, Thioesterase superfamily	hypothetical - conserved
F10	tnfn1_pw060418p03q178	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
F11	tnfn1_pw060418p03q186	<KAN-2>	acnA	aconitate hydratase	energy metabolism
F12	tnfn1_pw060418p03q194	T20	rnr	ribonuclease R	transcription
G01	tnfn1_pw060418p03q107	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
G02	tnfn1_pw060418p03q115	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
G03	tnfn1_pw060418p03q123	<KAN-2>	accA	acetyl-CoA carboxylase, carboxytransferase subunit alpha	fatty acids and lipids metabolism
G04	tnfn1_pw060418p03q131	T20	-	haloacid dehalogenase-like hydrolase	putative enzymes
G05	tnfn1_pw060418p03q139	T20	gapA	glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	energy metabolism
G06	tnfn1_pw060418p03q147	T20	putP	proline:Na+ symporter	transport - amino-acid
G07	tnfn1_pw060418p03q155	T20	-	amino acid transporter (AAT) family protein	transport - amino-acid
G08	tnfn1_pw060418p03q163	T20	udhA	soluble pyridine nucleotide transhydrogenase	cofactors, prosthetic groups, electron carriers metabolism
G09	tnfn1_pw060418p03q171	T20	galU	UTP--glucose-1-phosphate uridylyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
G10	tnfn1_pw060418p03q179	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
G11	tnfn1_pw060418p03q187	T18	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
G12	tnfn1_pw060418p03q195	T18	folE	GTP cyclohydrolase I	cofactors, prosthetic groups, electron carriers metabolism
H01	tnfn1_pw060418p03q108	T20	-	protein of unknown function with predicted hydrolase and phosphorylase activity	unknown function - conserved
H02	tnfn1_pw060418p03q116	<KAN-2>	-	acyltransferase	fatty acids and lipids metabolism
H03	tnfn1_pw060418p03q124	<KAN-2>	ychF	GTP-binding protein	putative enzymes
H04	tnfn1_pw060418p03q132	T20	ansB	periplasmic L-asparaginase II precursor	amino acid metabolism - biosynthesis
H05	tnfn1_pw060418p03q140	T20	-	conserved protein of unknown function	unknown function - conserved
H06	tnfn1_pw060418p03q148	T20	-	membrane protein of unknown function	unknown function - novel
H07	tnfn1_pw060418p03q156	T20	-	conserved protein of unknown function	unknown function - conserved
H08	tnfn1_pw060418p03q164	T20	emrE	putative membrane transporter of cations and cationic drugs, multidrug resistance protein	transport - drugs / antibacterial compounds
H09	tnfn1_pw060418p03q172	T20	-	glutamine amidotransferase, class I	other metabolism - biosynthesis
H10	tnfn1_pw060418p03q180	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
H11	tnfn1_pw060418p03q188	T18	-	hypothetical protein	hypothetical - novel
H12	tnfn1_pw060418p03q196	T18	-	conserved protein of unknown function	unknown function - conserved

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

Table 2: Plate 19 (tnfn1_pw060418p03) – 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_pw060418p03q101	C	1338589	FTN_1266	1337851	1338948	F	366	739(1098)
A02	tnfn1_pw060418p03q109	C	866540	FTN_0809	866270	867517	F	416	271(1248)
A03	tnfn1_pw060418p03q117	C	1656251	FTN_1558	1655903	1656778	R	292	528(876)
A04	tnfn1_pw060418p03q125	C	714082	FTN_0671	713359	714384	R	342	303(1026)
A05	tnfn1_pw060418p03q133	C	221087	FTN_0199	220528	221373	F	282	560(846)
A06	tnfn1_pw060418p03q141	U	1226367	FTN_1156	1225105	1226655	R	517	289(1551)
A07	tnfn1_pw060418p03q149	C	781150	FTN_0728	780666	781802	F	379	485(1137)
A08	tnfn1_pw060418p03q157	C	1293251	FTN_1222	1292995	1293963	F	323	257(969)
A09	tnfn1_pw060418p03q165	C	557732	FTN_0535	556910	558133	F	408	823(1224)
A10	tnfn1_pw060418p03q173	C	977280	FTN_0919	977263	977676	F	138	18(414)
A11	tnfn1_pw060418p03q181	C	131461	FTN_0120	131219	131638	F	140	243(420)
A12	tnfn1_pw060418p03q189	C	614604	FTN_0585	614004	614723	R	240	120(720)
B01	tnfn1_pw060418p03q102	U	315358	FTN_0306	315040	315714	F	225	319(675)
B02	tnfn1_pw060418p03q110	C	902163	FTN_0847	901867	902790	R	308	628(924)
B03	tnfn1_pw060418p03q118	C	1301336	FTN_1232	1300558	1301340	F	261	779(783)
B04	tnfn1_pw060418p03q126	U	818715	intergenic					
B05	tnfn1_pw060418p03q134	C	1353837	FTN_1281	1353283	1353978	R	232	142(696)
B06	tnfn1_pw060418p03q142	C	1632880	FTN_1535	1632461	1633282	F	274	420(822)
B07	tnfn1_pw060418p03q150	U	1284778	FTN_1214	1283962	1284918	R	319	141(957)
B08	tnfn1_pw060418p03q158	U	1435653	FTN_1357	1435327	1438974	R	1216	3322(3648)
B09	tnfn1_pw060418p03q166	U	819432	FTN_0761	818940	820022	F	361	493(1083)
B10	tnfn1_pw060418p03q174	C	1117990	FTN_1058	1117803	1119116	R	438	1127(1314)
B11	tnfn1_pw060418p03q182	C	395779	FTN_0396	395576	396226	F	217	204(651)
B12	tnfn1_pw060418p03q190	C	1177229	FTN_1113	1177061	1177801	F	247	169(741)
C01	tnfn1_pw060418p03q103	C	792977	FTN_0739	792274	793392	R	373	416(1119)
C02	tnfn1_pw060418p03q111	C	161169	FTN_0148	160862	161488	F	209	308(627)
C03	tnfn1_pw060418p03q119	C	414259	FTN_0415	414152	414556	R	135	298(405)
C04	tnfn1_pw060418p03q127	C	994993	FTN_0934	994829	995320	F	164	165(492)
C05	tnfn1_pw060418p03q135	U	162956	FTN_0150	162491	163057	F	189	466(567)
C06	tnfn1_pw060418p03q143	C	1895365	FTN_1766	1895114	1896115	R	334	751(1002)
C07	tnfn1_pw060418p03q151	C	232582	FTN_0212	232274	232753	F	160	309(480)
C08	tnfn1_pw060418p03q159	C	1863002	FTN_1736	1862687	1863082	F	132	316(396)
C09	tnfn1_pw060418p03q167	C	575857	FTN_0550	575484	576497	F	338	374(1014)
C10	tnfn1_pw060418p03q175	C	1690943	FTN_1592	1690148	1691083	R	312	141(936)
C11	tnfn1_pw060418p03q183	C	1301169	FTN_1232	1300558	1301340	F	261	612(783)
C12	tnfn1_pw060418p03q191	C	133444	FTN_0123	133207	133656	F	150	238(450)
D01	tnfn1_pw060418p03q104	C	334704	FTN_0326	334524	335054	R	177	351(531)
D02	tnfn1_pw060418p03q112	C	1467898	FTN_1390	1467372	1468055	R	228	158(684)
D03	tnfn1_pw060418p03q120	C	673790	FTN_0637	673289	674314	R	342	525(1026)
D04	tnfn1_pw060418p03q128	U	1031832	FTN_0977	1031487	1032053	F	189	346(567)
D05	tnfn1_pw060418p03q136	C	1203457	FTN_1138	1203258	1203845	R	196	389(588)
D06	tnfn1_pw060418p03q144	C	587694	FTN_0560	587181	587966	F	262	514(786)
D07	tnfn1_pw060418p03q152	C	1018842	FTN_0964	1018209	1019321	R	371	480(1113)
D08	tnfn1_pw060418p03q160	C	981936	intergenic					
D09	tnfn1_pw060418p03q168	C	727817	FTN_0684	727685	728077	F	131	133(393)
D10	tnfn1_pw060418p03q176	C	224592	FTN_0203	224195	224626	R	144	35(432)
D11	tnfn1_pw060418p03q184	C	917688	FTN_0863	917341	917775	F	145	348(435)
D12	tnfn1_pw060418p03q192	C	802350	FTN_0748	802109	802948	F	280	242(840)
E01	tnfn1_pw060418p03q105	C	98155	FTN_0086	97601	98827	F	409	555(1227)
E02	tnfn1_pw060418p03q113	C	1020909	FTN_0965	1019741	1021147	F	469	1169(1407)
E03	tnfn1_pw060418p03q121	C	1274872	FTN_1201	1274526	1275740	R	405	869(1215)
E04	tnfn1_pw060418p03q129	C	839693	FTN_0781	839608	840624	F	339	86(1017)
E05	tnfn1_pw060418p03q137	C	281637	FTN_0273	280833	282011	F	393	805(1179)
E06	tnfn1_pw060418p03q145	U	209385	FTN_0191	208872	209609	R	246	225(738)
E07	tnfn1_pw060418p03q153	C	1119551	FTN_1059	1119271	1119732	F	154	281(462)
E08	tnfn1_pw060418p03q161	C	288635	FTN_0281	288433	288879	F	149	203(447)
E09	tnfn1_pw060418p03q169	C	333884	FTN_0325	333787	334446	R	220	563(660)
E10	tnfn1_pw060418p03q177	C	231870	FTN_0211	231598	232263	F	222	273(666)
E11	tnfn1_pw060418p03q185	C	1478819	FTN_1400	1478681	1479367	R	229	549(687)
E12	tnfn1_pw060418p03q193	C	1469548	FTN_1391	1468103	1469791	R	563	244(1689)
F01	tnfn1_pw060418p03q106	C	352570	FTN_0346	352150	353400	R	417	831(1251)
F02	tnfn1_pw060418p03q114	C	295406	FTN_0287	294845	295609	F	255	562(765)

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F03	tnfn1_pw060418p03q122	U	1482458	FTN_1404	1482101	1482877	R	259	420(777)
F04	tnfn1_pw060418p03q130	C	1296212	FTN_1226	1296078	1296404	R	109	193(327)
F05	tnfn1_pw060418p03q138	C	1444051	FTN_1360	1442839	1444422	R	528	372(1584)
F06	tnfn1_pw060418p03q146	C	998832	FTN_0937	998435	999334	F	300	398(900)
F07	tnfn1_pw060418p03q154	C	204937	FTN_0188	204831	205403	F	191	107(573)
F08	tnfn1_pw060418p03q162	C	224917	FTN_0204	224772	225725	F	318	146(954)
F09	tnfn1_pw060418p03q170	C	1529162	FTN_1440	1528961	1529446	F	162	202(486)
F10	tnfn1_pw060418p03q178	U	427309	FTN_0429	427130	427630	F	167	180(501)
F11	tnfn1_pw060418p03q186	C	1734010	FTN_1623	1733943	1736753	R	937	2744(2811)
F12	tnfn1_pw060418p03q194	C	1549393	FTN_1461	1548609	1550903	R	765	1511(2295)
G01	tnfn1_pw060418p03q107	C	1287409	FTN_1217	1286888	1288573	R	562	1165(1686)
G02	tnfn1_pw060418p03q115	C	1085285	FTN_1028	1084814	1085557	R	248	273(744)
G03	tnfn1_pw060418p03q123	C	1603036	FTN_1508	1603032	1603976	R	315	941(945)
G04	tnfn1_pw060418p03q131	C	1281470	FTN_1211	1281241	1281900	R	220	431(660)
G05	tnfn1_pw060418p03q139	U	1411484	FTN_1332	1411472	1412470	R	333	987(999)
G06	tnfn1_pw060418p03q147	C	308041	FTN_0299	306996	308501	F	502	1046(1506)
G07	tnfn1_pw060418p03q155	C	405515	FTN_0407	404710	406101	R	464	587(1392)
G08	tnfn1_pw060418p03q163	C	1060015	FTN_0999	1059107	1060504	F	466	909(1398)
G09	tnfn1_pw060418p03q171	C	781950	FTN_0729	781822	782682	F	287	129(861)
G10	tnfn1_pw060418p03q179	C	1537201	FTN_1447	1536391	1537371	R	327	171(981)
G11	tnfn1_pw060418p03q187	C	1861426	FTN_1733	1861017	1861637	R	207	212(621)
G12	tnfn1_pw060418p03q195	C	887427	FTN_0830	886835	887452	R	206	26(618)
H01	tnfn1_pw060418p03q108	C	957475	FTN_0900	956882	958711	R	610	1237(1830)
H02	tnfn1_pw060418p03q116	C	1879783	FTN_1750	1879341	1880078	F	246	443(738)
H03	tnfn1_pw060418p03q124	C	1063954	FTN_1004	1063694	1064782	F	363	261(1089)
H04	tnfn1_pw060418p03q132	C	579930	FTN_0555	579267	580328	F	354	664(1062)
H05	tnfn1_pw060418p03q140	C	93175	FTN_0083	93070	93825	F	252	106(756)
H06	tnfn1_pw060418p03q148	C	317488	FTN_0308	316669	318474	F	602	820(1806)
H07	tnfn1_pw060418p03q156	C	450789	FTN_0449	450598	451470	F	291	192(873)
H08	tnfn1_pw060418p03q164	U	856319	FTN_0799	856317	856643	R	109	325(327)
H09	tnfn1_pw060418p03q172	C	434094	FTN_0435	433757	434461	F	235	338(705)
H10	tnfn1_pw060418p03q180	U	185541	FTN_0169	185208	185747	R	180	207(540)
H11	tnfn1_pw060418p03q188	U	1127938	FTN_1068	1127581	1128000	F	140	358(420)
H12	tnfn1_pw060418p03q196	C	1342588	FTN_1271	1341912	1342637	F	242	677(726)

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 19 (tnfn1_pw060418p03) – 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_pw060418p03q101	EXACT(0)	156	150	137	41	EXACT(0)	85	83	55
A02	tnfn1_pw060418p03q109	EXACT(0)	156	142	105	28	EXACT(0)	200	175	43
A03	tnfn1_pw060418p03q117	EXACT(0)	121	120	84	23	EXACT(0)	200	195	48
A04	tnfn1_pw060418p03q125	EXACT(0)	121	112	89	27	EXACT(0)	200	192	51
A05	tnfn1_pw060418p03q133	EXACT(0)	155	145	79	16	EXACT(0)	200	163	34
A06	tnfn1_pw060418p03q141	EXACT(0)	155	145	119	38	EXACT(0)	200	156	38
A07	tnfn1_pw060418p03q149	EXACT(0)	158	153	136	41	EXACT(0)	200	190	43
A08	tnfn1_pw060418p03q157	EXACT(0)	155	144	124	44	EXACT(0)	199	116	31
A09	tnfn1_pw060418p03q165	EXACT(0)	155	145	123	42	EXACT(0)	200	169	46
A10	tnfn1_pw060418p03q173	EXACT(0)	122	112	94	25	EXACT(0)	200	186	52
A11	tnfn1_pw060418p03q181	EXACT(0)	121	119	109	37	EXACT(0)	200	136	45
A12	tnfn1_pw060418p03q189	EXACT(0)	124	120	101	29	EXACT(0)	142	141	53
B01	tnfn1_pw060418p03q102	EXACT(0)	157	152	96	37	EXACT(0)	201	155	41
B02	tnfn1_pw060418p03q110	EXACT(0)	155	150	129	42	EXACT(0)	198	111	31
B03	tnfn1_pw060418p03q118	EXACT(0)	122	125	98	28	EXACT(0)	200	182	55
B04	tnfn1_pw060418p03q126	EXACT(0)	122	119	101	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
B05	tfnf1_pw060418p03q134	EXACT(0)	155	152	131	39	EXACT(0)	200	188	48
B06	tfnf1_pw060418p03q142	EXACT(0)	156	152	136	40	EXACT(0)	192	182	52
B07	tfnf1_pw060418p03q150	EXACT(0)	157	150	131	34	EXACT(0)	200	157	45
B08	tfnf1_pw060418p03q158	NONE	0	0	0	14	ESTIMATE(153)	435	353	24
B09	tfnf1_pw060418p03q166	EXACT(0)	156	145	136	44	EXACT(0)	200	198	46
B10	tfnf1_pw060418p03q174	EXACT(0)	121	120	99	30	EXACT(0)	199	159	40
B11	tfnf1_pw060418p03q182	EXACT(0)	121	112	88	39	EXACT(0)	200	191	53
B12	tfnf1_pw060418p03q190	EXACT(0)	129	103	82	26	EXACT(0)	200	188	45
C01	tfnf1_pw060418p03q103	EXACT(0)	157	148	134	39	EXACT(0)	200	172	50
C02	tfnf1_pw060418p03q111	EXACT(0)	157	145	132	38	EXACT(0)	200	194	50
C03	tfnf1_pw060418p03q119	EXACT(0)	120	112	76	22	EXACT(0)	200	191	46
C04	tfnf1_pw060418p03q127	EXACT(0)	121	112	90	25	EXACT(0)	200	181	47
C05	tfnf1_pw060418p03q135	EXACT(0)	160	153	125	25	EXACT(0)	200	188	59
C06	tfnf1_pw060418p03q143	EXACT(0)	159	143	92	25	EXACT(0)	200	194	47
C07	tfnf1_pw060418p03q151	EXACT(0)	157	145	129	27	EXACT(0)	200	179	46
C08	tfnf1_pw060418p03q159	EXACT(0)	155	152	131	38	EXACT(0)	200	187	52
C09	tfnf1_pw060418p03q167	EXACT(0)	157	145	129	32	EXACT(0)	200	193	53
C10	tfnf1_pw060418p03q175	EXACT(0)	123	120	103	34	EXACT(0)	200	146	36
C11	tfnf1_pw060418p03q183	EXACT(0)	120	112	78	22	EXACT(0)	200	186	47
C12	tfnf1_pw060418p03q191	EXACT(0)	133	109	54	16	EXACT(0)	200	177	36
D01	tfnf1_pw060418p03q104	EXACT(0)	154	145	120	40	EXACT(0)	199	186	47
D02	tfnf1_pw060418p03q112	EXACT(0)	157	152	141	39	EXACT(0)	200	188	60
D03	tfnf1_pw060418p03q120	EXACT(0)	123	120	112	31	EXACT(0)	200	178	41
D04	tfnf1_pw060418p03q128	EXACT(0)	126	120	105	30	EXACT(0)	200	176	46
D05	tfnf1_pw060418p03q136	EXACT(0)	156	145	134	44	EXACT(0)	200	190	65
D06	tfnf1_pw060418p03q144	EXACT(0)	158	153	142	39	EXACT(0)	200	184	49
D07	tfnf1_pw060418p03q152	EXACT(0)	155	152	131	37	EXACT(0)	199	191	54
D08	tfnf1_pw060418p03q160	EXACT(0)	158	148	145	38	EXACT(0)	200	184	54
D09	tfnf1_pw060418p03q168	EXACT(0)	156	152	132	33	EXACT(0)	200	188	57
D10	tfnf1_pw060418p03q176	EXACT(0)	122	125	105	43	EXACT(0)	200	188	65
D11	tfnf1_pw060418p03q184	EXACT(0)	121	120	96	23	EXACT(0)	200	175	51
D12	tfnf1_pw060418p03q192	EXACT(0)	121	112	81	23	EXACT(0)	200	190	54
E01	tfnf1_pw060418p03q105	EXACT(0)	158	153	142	40	EXACT(0)	200	192	54
E02	tfnf1_pw060418p03q113	EXACT(0)	155	152	125	38	EXACT(0)	200	113	28
E03	tfnf1_pw060418p03q121	EXACT(0)	121	81	60	22	EXACT(0)	200	189	51
E04	tfnf1_pw060418p03q129	EXACT(0)	157	145	126	31	EXACT(0)	200	189	52
E05	tfnf1_pw060418p03q137	EXACT(0)	155	145	129	33	EXACT(0)	200	193	51
E06	tfnf1_pw060418p03q145	EXACT(0)	156	145	78	21	EXACT(0)	200	181	49
E07	tfnf1_pw060418p03q153	EXACT(0)	153	139	120	39	EXACT(0)	200	183	58
E08	tfnf1_pw060418p03q161	EXACT(0)	156	117	117	46	EXACT(0)	200	189	56
E09	tfnf1_pw060418p03q169	EXACT(0)	155	152	121	30	EXACT(0)	200	187	56
E10	tfnf1_pw060418p03q177	EXACT(0)	122	119	114	40	EXACT(0)	200	194	62
E11	tfnf1_pw060418p03q185	EXACT(0)	121	106	101	57	EXACT(0)	199	144	45
E12	tfnf1_pw060418p03q193	EXACT(0)	121	106	98	40	EXACT(0)	200	196	57
F01	tfnf1_pw060418p03q106	EXACT(0)	154	153	122	35	EXACT(0)	200	187	52
F02	tfnf1_pw060418p03q114	EXACT(0)	154	138	121	38	EXACT(0)	200	193	49
F03	tfnf1_pw060418p03q122	EXACT(0)	127	89	72	33	EXACT(0)	200	186	67
F04	tfnf1_pw060418p03q130	EXACT(0)	121	103	77	24	EXACT(0)	199	155	31
F05	tfnf1_pw060418p03q138	EXACT(0)	156	153	134	32	EXACT(0)	200	195	47
F06	tfnf1_pw060418p03q146	EXACT(0)	155	152	134	36	EXACT(0)	200	192	55
F07	tfnf1_pw060418p03q154	EXACT(0)	155	152	128	40	EXACT(0)	200	178	45
F08	tfnf1_pw060418p03q162	EXACT(0)	155	145	132	41	EXACT(0)	200	195	53
F09	tfnf1_pw060418p03q170	EXACT(0)	158	151	126	30	EXACT(0)	200	191	52
F10	tfnf1_pw060418p03q178	EXACT(0)	123	125	109	37	EXACT(0)	200	186	63
F11	tfnf1_pw060418p03q186	EXACT(0)	121	120	96	30	EXACT(0)	200	179	53
F12	tfnf1_pw060418p03q194	EXACT(0)	157	153	131	39	EXACT(0)	200	193	55
G01	tfnf1_pw060418p03q107	EXACT(0)	157	152	126	33	EXACT(0)	200	191	54
G02	tfnf1_pw060418p03q115	EXACT(0)	121	107	75	21	EXACT(0)	200	194	47
G03	tfnf1_pw060418p03q123	EXACT(0)	121	112	102	30	EXACT(0)	200	178	30
G04	tfnf1_pw060418p03q131	EXACT(0)	158	152	131	35	EXACT(0)	200	185	57
G05	tfnf1_pw060418p03q139	EXACT(0)	155	152	131	42	EXACT(0)	200	192	63
G06	tfnf1_pw060418p03q147	EXACT(0)	158	145	138	51	EXACT(0)	200	156	45

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_pw060418p03q155	EXACT(0)	157	145	136	48	EXACT(0)	200	186	50
G08	tnfn1_pw060418p03q163	EXACT(0)	155	144	124	36	EXACT(0)	200	193	53
G09	tnfn1_pw060418p03q171	EXACT(0)	157	152	136	45	EXACT(0)	200	186	58
G10	tnfn1_pw060418p03q179	EXACT(0)	122	118	99	27	EXACT(0)	200	191	47
G11	tnfn1_pw060418p03q187	EXACT(0)	121	105	73	20	EXACT(0)	200	184	50
G12	tnfn1_pw060418p03q195	EXACT(0)	124	119	84	24	EXACT(0)	200	175	56
H01	tnfn1_pw060418p03q108	EXACT(0)	156	139	103	35	EXACT(0)	200	197	55
H02	tnfn1_pw060418p03q116	EXACT(0)	122	120	107	33	EXACT(0)	200	193	66
H03	tnfn1_pw060418p03q124	EXACT(0)	122	120	101	47	EXACT(0)	199	185	57
H04	tnfn1_pw060418p03q132	EXACT(0)	155	145	122	39	EXACT(0)	200	188	61
H05	tnfn1_pw060418p03q140	EXACT(0)	154	145	75	17	EXACT(0)	200	175	54
H06	tnfn1_pw060418p03q148	EXACT(0)	159	153	136	43	EXACT(0)	200	171	52
H07	tnfn1_pw060418p03q156	EXACT(0)	155	144	119	34	EXACT(0)	200	190	49
H08	tnfn1_pw060418p03q164	EXACT(0)	155	145	126	38	EXACT(0)	200	178	62
H09	tnfn1_pw060418p03q172	EXACT(0)	155	140	125	26	EXACT(0)	200	186	33
H10	tnfn1_pw060418p03q180	EXACT(0)	121	120	105	43	EXACT(0)	200	185	54
H11	tnfn1_pw060418p03q188	EXACT(0)	121	103	89	28	EXACT(0)	200	182	54
H12	tnfn1_pw060418p03q196	EXACT(0)	121	105	84	25	EXACT(0)	200	186	52

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