

***Francisella tularensis* subsp. *novicida*  
“Two-Allele” Transposon Mutant Library,  
Plate 12 (tnfn1\_pw060328p04)**

**Catalog No. NR-51294**

**For research use only. Not for human use.**

**Contributor:**

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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<sup>1</sup> 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-51294 represents plate 12 (tnfn1\_pw060328p04) 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-51294 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<sub>2</sub>

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 12 (tnfn1\_pw060328p04), NR-51294.”

**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](http://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 12 (tnfn1\_pw060328p04) – Transposon Type and Mutated Gene<sup>1</sup>**

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060328p04q101	T20	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	Amino acid metabolism - biosynthesis
A02	tnfn1_pw060328p04q102	T20	galP2	Galactose-proton symporter, major facilitator superfamily (MFS) transport protein	Transport - carbohydrates (sugars, polysaccharides)
A03	tnfn1_pw060328p04q103	T20	-	Two-component regulator, sensor histidine kinase	Signal transduction and regulation
A04	tnfn1_pw060328p04q104	T20	lysC	Aspartate kinase III	Amino acid metabolism - biosynthesis
A05	tnfn1_pw060328p04q105	T20	-	ABC-type transport system permease protein	Transport
A06	tnfn1_pw060328p04q106	T20	-	Drug:H+ antiporter-1 (DHA2) family protein	Transport - drugs / antibacterial compounds
A07	tnfn1_pw060328p04q107	T20	-	Protein of unknown function	Unknown function - novel
A08	tnfn1_pw060328p04q108	T20	-	Protein of unknown function	Unknown function - novel
A09	tnfn1_pw060328p04q109	T20	blaA	Beta-lactamase class A	Other metabolism - degradation, utilization, assimilation
A10	tnfn1_pw060328p04q110	T20	-	Protein of unknown function	Unknown function - novel
A11	tnfn1_pw060328p04q111	T20	isftu2	Isftu2	IS element
A12	tnfn1_pw060328p04q112	T20	blaA	Beta-lactamase class A	Other metabolism - degradation, utilization, assimilation
B01	tnfn1_pw060328p04q113	T20	isftu2	Isftu2	IS element
B02	tnfn1_pw060328p04q114	T20	-	Endoribonuclease L-PSP	Translation, ribosomal structure and biogenesis
B03	tnfn1_pw060328p04q115	T20	-	Glycosyl transferase, group 1	Cell wall / LPS / capsule
B04	tnfn1_pw060328p04q116	T20	-	Choloylglycine hydrolase family protein	Cell wall / LPS / capsule
B05	tnfn1_pw060328p04q117	T20	uvrB	Excinuclease ABC, subunit B	DNA replication, recombination, modification and repair - restriction/modification
B06	tnfn1_pw060328p04q118	T20	ispA	Geranyl diphosphate synthase/farnesyl diphosphate synthase	Cofactors, prosthetic groups, electron carriers metabolism
B07	tnfn1_pw060328p04q119	<KAN-2>	-	Membrane protein of unknown function	Unknown function - conserved
B08	tnfn1_pw060328p04q120	<KAN-2>	-	Protein of unknown function	Unknown function - novel
B09	tnfn1_pw060328p04q121	T20	minE	Cell division topological specificity factor protein	Cell cycle
B10	tnfn1_pw060328p04q122	<KAN-2>	-	Protein of unknown function	Unknown function - novel
B11	tnfn1_pw060328p04q123	<KAN-2>	secA	Preprotein translocase, subunit A (ATPase, RNA helicase)	Motility, attachment and secretion structure
B12	tnfn1_pw060328p04q124	<KAN-2>	grxC	Glutaredoxin like protein	Post-translational modification, protein turnover, chaperones
C01	tnfn1_pw060328p04q125	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved
C02	tnfn1_pw060328p04q126	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved
C03	tnfn1_pw060328p04q127	<KAN-2>	-	Glutamine amidotransferases class-II family protein	Putative enzymes
C04	tnfn1_pw060328p04q128	<KAN-2>	pilA	Type IV pili, pilus assembly protein	Motility, attachment and secretion structure
C05	tnfn1_pw060328p04q129	<KAN-2>	-	Protein of unknown function	Unknown function - novel
C06	tnfn1_pw060328p04q130	T18	lpxH	UDP-2,3-diacetylglucosamine hydrolase	Fatty acids and lipids metabolism
C07	tnfn1_pw060328p04q131	T18	-	Amino acid transporter (AAT) family protein	Transport - amino-acid
C08	tnfn1_pw060328p04q132	T18	-	Conserved protein of unknown function	Unknown function - conserved
C09	tnfn1_pw060328p04q133	T18	-	Hypothetical membrane protein	Hypothetical - novel
C10	tnfn1_pw060328p04q134	T18	-	Major facilitator superfamily (MFS) transport protein	Transport
C11	tnfn1_pw060328p04q135	T18	isftu3	Isftu3	IS element
C12	tnfn1_pw060328p04q136	T18	-	Conserved hypothetical membrane protein	Hypothetical - conserved
D01	tnfn1_pw060328p04q137	T18	ung	Uracil DNA glycosylase	DNA replication, recombination, modification and repair - repair
D02	tnfn1_pw060328p04q138	T18	glgC	Glucose-1-phosphate adenyltransferase	Carbohydrate metabolism - biosynthesis
D03	tnfn1_pw060328p04q139	T18	isftu2	Isftu2	IS element
D04	tnfn1_pw060328p04q140	T18	-	Pseudogene: dTDP-D-glucose 4,6-dehydratase	Pseudogene
D05	tnfn1_pw060328p04q141	T18	-	Hypothetical protein	Hypothetical - novel
D06	tnfn1_pw060328p04q142	T18	-	Hypothetical protein	Hypothetical - novel
D07	tnfn1_pw060328p04q143	T18	gidB	Glucose-inhibited cell division protein	Cell wall / LPS / capsule
D08	tnfn1_pw060328p04q144	T18	-	Zn-dependent peptidase, M16 family	Post-translational modification, protein turnover, chaperones - protein modification
D09	tnfn1_pw060328p04q145	T18	-	Choloylglycine hydrolase family protein	Cell wall / LPS / capsule
D10	tnfn1_pw060328p04q146	T18	blc	Outer membrane lipoprotein	Cell wall / LPS / capsule

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D11	tnfn1_pw060328p04q147	T18	-	Hypothetical protein	Hypothetical - novel
D12	tnfn1_pw060328p04q148	T18	-	Protein of unknown function	Unknown function - novel
E01	tnfn1_pw060328p04q149	T18	-	Protein of unknown function	Unknown function - novel
E02	tnfn1_pw060328p04q150	T20	pilD	Type IV pili leader peptidase and methylase	Motility, attachment and secretion structure
E03	tnfn1_pw060328p04q151	T18	-	Protein of unknown function	Unknown function - novel
E04	tnfn1_pw060328p04q152	T20	-	VacJ like lipoprotein	Cell wall / LPS / capsule
E05	tnfn1_pw060328p04q153	T20	-	Two-component response regulator	Signal transduction and regulation
E06	tnfn1_pw060328p04q154	T20	-	Hypothetical protein	Hypothetical - novel
E07	tnfn1_pw060328p04q155	T20	isftu2	Isftu2	IS element
E08	tnfn1_pw060328p04q156	T20	ruvC	Holliday junction endodeoxyribonuclease	DNA replication, recombination, modification and repair - restriction/modification
E09	tnfn1_pw060328p04q157	T20	isftu2	Isftu2	IS element
E10	tnfn1_pw060328p04q158	T20	-	Nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	Transport
E11	tnfn1_pw060328p04q159	T20	-	Protein of unknown function	Unknown function - novel
E12	tnfn1_pw060328p04q160	T20	-	Predicted hydrolase of the HAD superfamily	Putative enzymes
F01	tnfn1_pw060328p04q161	T20	tolA	Group A colicin translocation; tolA protein	Transport - drugs / antibacterial compounds
F02	tnfn1_pw060328p04q162	T20	glpD	Glycerol-3-phosphate dehydrogenase	Other metabolism - degradation, utilization, assimilation
F03	tnfn1_pw060328p04q163	T20	-	Metabolite:H+ symporter (MHS) family protein	Transport
F04	tnfn1_pw060328p04q164	T20	-	Conserved hypothetical protein	Hypothetical - conserved
F05	tnfn1_pw060328p04q165	T20	carA	Carbamoyl-phosphate synthase small chain	Nucleotides and nucleosides metabolism
F06	tnfn1_pw060328p04q166	T20	-	Dihydroliipoamide dehydrogenase	Amino acid metabolism - biosynthesis
F07	tnfn1_pw060328p04q167	T20	-	Proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	Transport
F08	tnfn1_pw060328p04q168	T20	cysC	Adenylylsulfate kinase	Other metabolism - degradation, utilization, assimilation
F09	tnfn1_pw060328p04q169	T20	-	(Putative) drug resistance ATPase-1 (Drug RA1) family protein	Transport - drugs / antibacterial compounds
F10	tnfn1_pw060328p04q170	T20	-	Type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
F11	tnfn1_pw060328p04q171	T20	ftsW	Cell division protein FtsW	Cell cycle
F12	tnfn1_pw060328p04q172	T20	-	Lipase/esterase	Fatty acids and lipids metabolism
G01	tnfn1_pw060328p04q173	T20	serB	Phosphoserine phosphatase	Amino acid metabolism - biosynthesis
G02	tnfn1_pw060328p04q174	T20	grxA	Glutaredoxin 1	Post-translational modification, protein turnover, chaperones
G03	tnfn1_pw060328p04q175	T20	-	Lipase/esterase	Fatty acids and lipids metabolism
G04	tnfn1_pw060328p04q176	T20	dinP	DNA-damage inducible protein P	DNA replication, recombination, modification and repair - restriction/modification
G05	tnfn1_pw060328p04q177	T20	-	Amino acid-polyamine-organocation family protein	Transport - amino-acid
G06	tnfn1_pw060328p04q178	T20	-	Proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	Transport
G07	tnfn1_pw060328p04q179	T20	isftu2	Isftu2	IS element
G08	tnfn1_pw060328p04q180	T20	-	Pseudogene: C4-dicarboxylate anaerobic carrier, fragment	Pseudogene
G09	tnfn1_pw060328p04q181	T20	-	Metabolite:H+ symporter (MHS) family protein	Transport
G10	tnfn1_pw060328p04q182	T20	-	Hypothetical membrane protein with von Willebrand factor type A domain	Hypothetical - novel
G11	tnfn1_pw060328p04q183	T20	-	Pseudogene: conserved hypothetical protein	Pseudogene
G12	tnfn1_pw060328p04q184	T20	-	Peptidase, U61 family	Post-translational modification, protein turnover, chaperones - protein degradation
H01	tnfn1_pw060328p04q185	T20	-	Protein of unknown function	Unknown function - novel
H02	tnfn1_pw060328p04q186	T20	galT	Galactose-1-phosphate uridylyltransferase	Carbohydrate metabolism - degradation, utilization, assimilation
H03	tnfn1_pw060328p04q187	T20	-	Conserved protein of unknown function	Unknown function - conserved
H04	tnfn1_pw060328p04q188	T20	-	Metallopeptidase, M16 family	Post-translational modification, protein turnover, chaperones - protein modification
H05	tnfn1_pw060328p04q189	T20	trpC	Indole-3-glycerol phosphate synthase (trpC); phosphoribosylanthranilate isomerase (trpF)	Amino acid metabolism - biosynthesis
H06	tnfn1_pw060328p04q190	T20	-	BolA family protein	Transcription
H07	tnfn1_pw060328p04q191	T20	-	Amino acid-polyamine-organocation (APC) superfamily protein	Transport - amino-acid
H08	tnfn1_pw060328p04q192	T20	purH	AICAR transformylase/IMP cyclohydrolase	Nucleotides and nucleosides metabolism
H09	tnfn1_pw060328p04q193	T20	lysP	Lysine:H+ symporter	Transport - amino-acid
H10	tnfn1_pw060328p04q194	T20	cyoD	Cytochrome bo terminal oxidase subunit IV	Energy metabolism
H11	tnfn1_pw060328p04q195	T20	cca	tRNA nucleotidyl transferase	Translation, ribosomal structure and biogenesis
H12	tnfn1_pw060328p04q196	T20	alr	Alanine racemase	Amino acid metabolism - degradation, utilization, assimilation

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

Table 2: Plate 12 (tnfn1\_pw060328p04) – Sequencing and Insert Location<sup>1</sup>

Well Position	Strain Name	Sequencing Confirmation <sup>2</sup>	Effective Genome Position of Insertion <sup>3</sup>	Locus Tag	ORF Left End	ORF Right End	Direction of ORF <sup>4</sup>	Length of ORF (codons)	Effective Position of Insertion in ORF <sup>5</sup>
A01	tnfn1_pw060328p04q101	C	1153149	FTN_1091	1152249	1153523	R	425	375(1275)
A02	tnfn1_pw060328p04q102	C	732132	FTN_0688	731758	733149	F	464	375(1392)
A03	tnfn1_pw060328p04q103	C	1541813	FTN_1453	1541523	1542557	F	345	291(1035)
A04	tnfn1_pw060328p04q104	C	1858228	FTN_1730	1857489	1858841	R	451	614(1353)
A05	tnfn1_pw060328p04q105	C	335605	FTN_0327	335057	335818	R	254	214(762)
A06	tnfn1_pw060328p04q106	C	1347796	FTN_1275	1347139	1348665	F	509	658(1527)
A07	tnfn1_pw060328p04q107	C	762810	FTN_0714	760571	766126	F	1852	2240(5556)
A08	tnfn1_pw060328p04q108	C	288554	FTN_0281	288433	288879	F	149	122(447)
A09	tnfn1_pw060328p04q109	U	1062731	FTN_1002	1062223	1063104	F	294	509(882)
A10	tnfn1_pw060328p04q110	C	601288	FTN_0573	600640	601452	R	271	165(813)
A11	tnfn1_pw060328p04q111	C	1613787	-	1613559	1614423	F	288.3	229(865)
A12	tnfn1_pw060328p04q112	C	1062731	FTN_1002	1062223	1063104	F	294	509(882)
B01	tnfn1_pw060328p04q113	U	619900	-	619309	620173	R	288	274(864)
B02	tnfn1_pw060328p04q114	C	676136	FTN_0639	676090	676467	F	126	47(378)
B03	tnfn1_pw060328p04q115	C	142772	FTN_0130	142461	143402	F	314	312(942)
B04	tnfn1_pw060328p04q116	C	821634	FTN_0765	821246	822211	R	322	578(966)
B05	tnfn1_pw060328p04q117	U	1248802	FTN_1176	1247657	1249660	R	668	859(2004)
B06	tnfn1_pw060328p04q118	C	1558953	FTN_1470	1558719	1559597	F	293	235(879)
B07	tnfn1_pw060328p04q119	C	334216	FTN_0325	333787	334446	R	220	231(660)
B08	tnfn1_pw060328p04q120	C	78697	FTN_0065	78558	78869	R	104	173(312)
B09	tnfn1_pw060328p04q121	U	336719	FTN_0329	336642	336911	R	90	193(270)
B10	tnfn1_pw060328p04q122	C	426624	FTN_0428	426551	427027	F	159	74(477)
B11	tnfn1_pw060328p04q123	C	717110	FTN_0672	714516	717233	F	906	2595(2718)
B12	tnfn1_pw060328p04q124	C	820047	FTN_0762	820018	820263	F	82	30(246)
C01	tnfn1_pw060328p04q125	C	1016482	FTN_0962	1015900	1016691	R	264	210(792)
C02	tnfn1_pw060328p04q126	C	964548	FTN_0908	964309	964590	F	94	240(282)
C03	tnfn1_pw060328p04q127	C	1213464	FTN_1147	1212777	1213580	R	268	117(804)
C04	tnfn1_pw060328p04q128	C	414406	FTN_0415	414152	414556	R	135	151(405)
C05	tnfn1_pw060328p04q129	C	1199171	FTN_1133	1198995	1199375	F	127	177(381)
C06	tnfn1_pw060328p04q130	C	550076	FTN_0528	550021	550740	R	240	665(720)
C07	tnfn1_pw060328p04q131	C	913665	FTN_0860	912967	914316	R	450	652(1350)
C08	tnfn1_pw060328p04q132	C	721044	FTN_0677	721006	721380	F	125	39(375)
C09	tnfn1_pw060328p04q133	C	232544	FTN_0212	232274	232753	F	160	271(480)
C10	tnfn1_pw060328p04q134	C	1033140	FTN_0979	1032719	1033228	R	170	89(510)
C11	tnfn1_pw060328p04q135	C	1717488	-	1716927	1717650	R	241.3	163(724)
C12	tnfn1_pw060328p04q136	C	1484067	FTN_1406	1483913	1484686	R	258	620(774)
D01	tnfn1_pw060328p04q137	C	1576615	FTN_1486	1576437	1577096	R	220	482(660)
D02	tnfn1_pw060328p04q138	C	532466	FTN_0515	531823	533091	F	423	644(1269)
D03	tnfn1_pw060328p04q139	U	619792	-	619309	620173	R	288	382(864)
D04	tnfn1_pw060328p04q140	C	1497575	FTN_1419	1497548	1497892	R	115	318(345)
D05	tnfn1_pw060328p04q141	C	8951	FTN_0009	8784	8963	F	60	168(180)
D06	tnfn1_pw060328p04q142	C	1903276	FTN_1773	1903020	1903385	R	122	110(366)
D07	tnfn1_pw060328p04q143	C	109498	FTN_0098	109204	109818	F	205	295(615)
D08	tnfn1_pw060328p04q144	C	694665	FTN_0656	694302	695522	R	407	858(1221)
D09	tnfn1_pw060328p04q145	C	1369691	FTN_1301	1369632	1370684	F	351	60(1053)
D10	tnfn1_pw060328p04q146	C	190783	FTN_0174	190570	191085	F	172	214(516)
D11	tnfn1_pw060328p04q147	C	1025839	FTN_0970	1025702	1025914	R	71	76(213)
D12	tnfn1_pw060328p04q148	C	224397	FTN_0203	224195	224626	R	144	230(432)
E01	tnfn1_pw060328p04q149	C	49143	FTN_0044	49002	49646	F	215	142(645)
E02	tnfn1_pw060328p04q150	C	1060821	FTN_1000	1060511	1061356	F	282	311(846)
E03	tnfn1_pw060328p04q151	U	224397	FTN_0203	224195	224626	R	144	230(432)
E04	tnfn1_pw060328p04q152	C	332248	FTN_0322	331919	333016	F	366	330(1098)
E05	tnfn1_pw060328p04q153	C	1541014	FTN_1452	1540850	1541536	F	229	165(687)
E06	tnfn1_pw060328p04q154	C	1385689	FTN_1313	1384921	1386648	F	576	769(1728)
E07	tnfn1_pw060328p04q155	U	619948	-	619309	620173	R	288	226(864)
E08	tnfn1_pw060328p04q156	C	1084558	FTN_1027	1084202	1084714	R	171	157(513)
E09	tnfn1_pw060328p04q157	C	619948	-	619309	620173	R	288.3	226(865)
E10	tnfn1_pw060328p04q158	C	205069	FTN_0188	204831	205403	F	191	239(573)
E11	tnfn1_pw060328p04q159	C	115583	FTN_0103	113788	116088	R	767	506(2301)
E12	tnfn1_pw060328p04q160	C	92439	FTN_0082	92435	92995	F	187	5(561)
F01	tnfn1_pw060328p04q161	C	358016	FTN_0354	357724	358632	F	303	293(909)
F02	tnfn1_pw060328p04q162	C	1681884	FTN_1584	1680667	1682196	R	510	313(1530)



Well Position	Strain Name	Sequencing Confirmation <sup>2</sup>	Effective Genome Position of Insertion <sup>3</sup>	Locus Tag	ORF Left End	ORF Right End	Direction of ORF <sup>4</sup>	Length of ORF (codons)	Effective Position of Insertion in ORF <sup>5</sup>
F03	tnfn1_pw060328p04q163	C	3679	FTN_0003	2794	4044	R	417	366(1251)
F04	tnfn1_pw060328p04q164	C	815327	FTN_0758	814922	815875	F	318	406(954)
F05	tnfn1_pw060328p04q165	C	22412	FTN_0021	21409	22572	R	388	161(1164)
F06	tnfn1_pw060328p04q166	C	1623451	FTN_1526	1622248	1623663	R	472	213(1416)
F07	tnfn1_pw060328p04q167	C	1057126	FTN_0997	1056320	1057768	F	483	807(1449)
F08	tnfn1_pw060328p04q168	C	984151	FTN_0926	983655	984254	R	200	104(600)
F09	tnfn1_pw060328p04q169	C	1891937	FTN_1762	1890747	1892423	R	559	487(1677)
F10	tnfn1_pw060328p04q170	C	751508	FTN_0707	750859	752076	F	406	650(1218)
F11	tnfn1_pw060328p04q171	C	568836	FTN_0543	568834	570036	F	401	3(1203)
F12	tnfn1_pw060328p04q172	C	875139	FTN_0818	874701	875618	R	306	480(918)
G01	tnfn1_pw060328p04q173	C	796386	FTN_0742	796240	796887	F	216	147(648)
G02	tnfn1_pw060328p04q174	C	1036547	FTN_0982	1036318	1036575	F	86	230(258)
G03	tnfn1_pw060328p04q175	C	875139	FTN_0818	874701	875618	R	306	480(918)
G04	tnfn1_pw060328p04q176	C	1040768	FTN_0986	1040426	1041472	F	349	343(1047)
G05	tnfn1_pw060328p04q177	C	329589	FTN_0319	328471	329970	R	500	382(1500)
G06	tnfn1_pw060328p04q178	C	1319441	FTN_1251	1318855	1320288	R	478	848(1434)
G07	tnfn1_pw060328p04q179	C	239894	-	239611	240475	F	288.3	284(865)
G08	tnfn1_pw060328p04q180	C	275728	FTN_0268	275553	275780	R	76	53(228)
G09	tnfn1_pw060328p04q181	C	1892909	FTN_1763	1892635	1893852	F	406	275(1218)
G10	tnfn1_pw060328p04q182	C	228347	FTN_0208	228118	229113	F	332	230(996)
G11	tnfn1_pw060328p04q183	C	378424	FTN_0377	378265	379017	F	251	160(753)
G12	tnfn1_pw060328p04q184	C	1720973	FTN_1613	1720110	1721120	R	337	148(1011)
H01	tnfn1_pw060328p04q185	C	1725728	FTN_1616	1725345	1726298	R	318	571(954)
H02	tnfn1_pw060328p04q186	C	729765	FTN_0686	729231	730253	R	341	489(1023)
H03	tnfn1_pw060328p04q187	C	57821	FTN_0048	57540	58757	F	406	282(1218)
H04	tnfn1_pw060328p04q188	C	696014	FTN_0657	695532	696782	R	417	769(1251)
H05	tnfn1_pw060328p04q189	C	1901147	FTN_1770	1900376	1901734	R	453	588(1359)
H06	tnfn1_pw060328p04q190	C	333393	FTN_0323	333241	333474	R	78	82(234)
H07	tnfn1_pw060328p04q191	C	598775	FTN_0571	597725	599131	R	469	357(1407)
H08	tnfn1_pw060328p04q192	C	195595	FTN_0177	194359	195903	R	515	309(1545)
H09	tnfn1_pw060328p04q193	C	304303	FTN_0296	303623	305074	F	484	681(1452)
H10	tnfn1_pw060328p04q194	C	220309	FTN_0198	220165	220494	F	110	145(330)
H11	tnfn1_pw060328p04q195	C	1711331	FTN_1607	1710763	1711869	F	369	569(1107)
H12	tnfn1_pw060328p04q196	C	799655	FTN_0746	799235	800329	F	365	421(1095)

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

<sup>2</sup>C: Confirmed; U: Unconfirmed

<sup>3</sup>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.

<sup>4</sup>F, forward relative to genome; R, reverse

<sup>5</sup>Nucleotide of Insertion(Length of ORF in Nucleotides)

Table 3: Plate 12 (tnfn1\_pw060328p04) – Sequence Mapping Quality Metrics<sup>1</sup>

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_pw060328p04q101	EXACT(0)	157	151	126	33	EXACT(0)	200	193	55
A02	tnfn1_pw060328p04q102	EXACT(0)	156	142	113	26	EXACT(0)	200	185	55
A03	tnfn1_pw060328p04q103	EXACT(0)	158	153	125	33	EXACT(0)	193	184	53
A04	tnfn1_pw060328p04q104	EXACT(0)	157	152	130	39	EXACT(0)	200	196	52
A05	tnfn1_pw060328p04q105	EXACT(0)	157	146	129	36	EXACT(0)	200	197	55
A06	tnfn1_pw060328p04q106	EXACT(0)	156	150	120	29	EXACT(0)	200	180	58
A07	tnfn1_pw060328p04q107	EXACT(0)	156	153	114	33	EXACT(0)	200	192	56
A08	tnfn1_pw060328p04q108	EXACT(0)	157	146	123	41	EXACT(0)	160	150	55
A09	tnfn1_pw060328p04q109	EXACT(0)	167	138	116	23	EXACT(0)	200	189	38
A10	tnfn1_pw060328p04q110	EXACT(0)	157	151	128	37	EXACT(0)	200	189	56
A11	tnfn1_pw060328p04q111	EXACT(0)	156	152	128	40	EXACT(0)	200	191	58
A12	tnfn1_pw060328p04q112	EXACT(0)	156	142	110	25	EXACT(0)	200	190	49
B01	tnfn1_pw060328p04q113	EXACT(0)	167	143	99	25	EXACT(0)	200	182	38
B02	tnfn1_pw060328p04q114	EXACT(0)	156	146	133	41	EXACT(0)	200	140	34
B03	tnfn1_pw060328p04q115	EXACT(0)	157	153	130	35	EXACT(0)	200	178	59
B04	tnfn1_pw060328p04q116	EXACT(0)	157	152	133	37	EXACT(0)	199	184	48

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_pw060328p04q117	EXACT(0)	165	136	99	24	ESTIMATE(2)	176	76	18
B06	tnfn1_pw060328p04q118	EXACT(0)	156	138	84	22	EXACT(0)	157	138	29
B07	tnfn1_pw060328p04q119	EXACT(0)	118	107	78	27	EXACT(0)	200	190	41
B08	tnfn1_pw060328p04q120	EXACT(0)	117	111	81	32	EXACT(0)	200	183	58
B09	tnfn1_pw060328p04q121	EXACT(0)	157	146	90	23	EXACT(0)	200	183	40
B10	tnfn1_pw060328p04q122	EXACT(0)	123	109	98	32	EXACT(0)	200	152	41
B11	tnfn1_pw060328p04q123	EXACT(0)	122	125	96	22	EXACT(0)	200	189	51
B12	tnfn1_pw060328p04q124	EXACT(0)	121	119	71	21	EXACT(0)	200	191	54
C01	tnfn1_pw060328p04q125	EXACT(0)	120	121	111	37	EXACT(0)	200	188	63
C02	tnfn1_pw060328p04q126	EXACT(0)	121	112	90	37	EXACT(0)	200	189	56
C03	tnfn1_pw060328p04q127	EXACT(0)	121	112	93	23	EXACT(0)	200	198	53
C04	tnfn1_pw060328p04q128	EXACT(0)	121	119	83	22	EXACT(0)	200	195	48
C05	tnfn1_pw060328p04q129	EXACT(0)	122	119	98	25	EXACT(0)	200	190	49
C06	tnfn1_pw060328p04q130	EXACT(0)	123	109	91	24	EXACT(0)	200	186	40
C07	tnfn1_pw060328p04q131	EXACT(0)	123	112	71	20	EXACT(0)	200	183	46
C08	tnfn1_pw060328p04q132	EXACT(0)	123	120	96	24	EXACT(0)	200	193	54
C09	tnfn1_pw060328p04q133	EXACT(0)	124	117	89	24	EXACT(0)	200	191	50
C10	tnfn1_pw060328p04q134	EXACT(0)	123	106	97	29	EXACT(0)	200	178	45
C11	tnfn1_pw060328p04q135	EXACT(0)	123	120	96	29	EXACT(0)	127	120	50
C12	tnfn1_pw060328p04q136	EXACT(0)	123	109	95	29	EXACT(0)	200	188	48
D01	tnfn1_pw060328p04q137	EXACT(0)	123	113	90	34	EXACT(0)	200	190	51
D02	tnfn1_pw060328p04q138	EXACT(0)	123	120	102	32	EXACT(0)	180	165	52
D03	tnfn1_pw060328p04q139	NONE	0	0	0	15	ESTIMATE(488)	375	66	10
D04	tnfn1_pw060328p04q140	EXACT(0)	122	112	96	26	EXACT(0)	200	183	53
D05	tnfn1_pw060328p04q141	EXACT(0)	123	119	95	29	EXACT(0)	200	176	50
D06	tnfn1_pw060328p04q142	EXACT(0)	122	106	88	28	EXACT(0)	200	147	37
D07	tnfn1_pw060328p04q143	EXACT(0)	122	119	74	20	EXACT(0)	200	193	48
D08	tnfn1_pw060328p04q144	EXACT(0)	123	117	93	25	EXACT(0)	200	89	31
D09	tnfn1_pw060328p04q145	EXACT(0)	123	119	94	25	EXACT(0)	200	184	54
D10	tnfn1_pw060328p04q146	EXACT(0)	122	112	81	23	EXACT(0)	200	188	55
D11	tnfn1_pw060328p04q147	EXACT(0)	120	119	84	22	EXACT(0)	200	183	54
D12	tnfn1_pw060328p04q148	EXACT(0)	122	119	101	36	EXACT(0)	200	184	53
E01	tnfn1_pw060328p04q149	EXACT(0)	122	105	87	29	EXACT(0)	200	102	28
E02	tnfn1_pw060328p04q150	EXACT(0)	156	153	123	37	EXACT(0)	200	184	56
E03	tnfn1_pw060328p04q151	EXACT(0)	124	111	91	24	EXACT(0)	200	172	37
E04	tnfn1_pw060328p04q152	EXACT(0)	156	152	130	40	EXACT(0)	200	193	58
E05	tnfn1_pw060328p04q153	NONE	0	0	0	43	ESTIMATE(149)	184	159	51
E06	tnfn1_pw060328p04q154	EXACT(0)	156	138	95	28	EXACT(0)	200	177	45
E07	tnfn1_pw060328p04q155	EXACT(0)	159	132	85	22	EXACT(0)	200	180	40
E08	tnfn1_pw060328p04q156	EXACT(0)	156	153	132	42	EXACT(0)	200	193	58
E09	tnfn1_pw060328p04q157	EXACT(0)	156	152	108	26	EXACT(0)	200	180	58
E10	tnfn1_pw060328p04q158	EXACT(0)	156	152	117	32	EXACT(0)	200	187	59
E11	tnfn1_pw060328p04q159	EXACT(0)	157	152	120	29	EXACT(0)	200	187	58
E12	tnfn1_pw060328p04q160	EXACT(0)	156	152	117	30	EXACT(0)	200	194	53
F01	tnfn1_pw060328p04q161	EXACT(0)	155	151	115	33	EXACT(0)	200	180	54
F02	tnfn1_pw060328p04q162	EXACT(0)	155	152	119	36	EXACT(0)	200	187	59
F03	tnfn1_pw060328p04q163	EXACT(0)	157	152	121	31	EXACT(0)	38	35	46
F04	tnfn1_pw060328p04q164	EXACT(0)	156	153	126	36	EXACT(0)	193	182	55
F05	tnfn1_pw060328p04q165	EXACT(0)	154	138	105	29	EXACT(0)	200	150	41
F06	tnfn1_pw060328p04q166	EXACT(0)	157	153	131	37	EXACT(0)	200	190	57
F07	tnfn1_pw060328p04q167	EXACT(0)	156	152	131	38	EXACT(0)	200	167	44
F08	tnfn1_pw060328p04q168	EXACT(0)	155	150	100	27	EXACT(0)	200	187	52
F09	tnfn1_pw060328p04q169	EXACT(0)	155	152	134	40	EXACT(0)	200	183	42
F10	tnfn1_pw060328p04q170	EXACT(0)	155	150	123	36	EXACT(0)	200	190	48
F11	tnfn1_pw060328p04q171	EXACT(0)	157	142	101	23	EXACT(0)	200	192	55
F12	tnfn1_pw060328p04q172	EXACT(0)	157	145	119	32	EXACT(0)	200	189	55
G01	tnfn1_pw060328p04q173	EXACT(0)	156	152	131	41	EXACT(0)	200	188	55
G02	tnfn1_pw060328p04q174	EXACT(0)	156	152	128	37	EXACT(0)	200	188	54
G03	tnfn1_pw060328p04q175	EXACT(0)	157	152	129	37	EXACT(0)	200	189	55
G04	tnfn1_pw060328p04q176	EXACT(0)	156	116	89	31	EXACT(0)	200	196	51
G05	tnfn1_pw060328p04q177	EXACT(0)	156	153	126	40	EXACT(0)	200	197	57
G06	tnfn1_pw060328p04q178	EXACT(0)	155	142	88	22	EXACT(0)	200	181	39

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_pw060328p04q179	EXACT(0)	156	145	104	28	EXACT(0)	204	100	28
G08	tnfn1_pw060328p04q180	EXACT(0)	154	116	92	29	EXACT(0)	200	197	45
G09	tnfn1_pw060328p04q181	EXACT(0)	154	145	109	34	EXACT(0)	163	154	56
G10	tnfn1_pw060328p04q182	EXACT(0)	156	152	125	40	EXACT(0)	200	191	53
G11	tnfn1_pw060328p04q183	EXACT(0)	156	152	115	36	EXACT(0)	200	197	58
G12	tnfn1_pw060328p04q184	EXACT(0)	156	152	115	33	EXACT(0)	200	184	54
H01	tnfn1_pw060328p04q185	EXACT(0)	156	152	122	39	EXACT(0)	189	182	53
H02	tnfn1_pw060328p04q186	EXACT(0)	156	153	120	35	EXACT(0)	200	190	59
H03	tnfn1_pw060328p04q187	EXACT(0)	155	145	123	39	EXACT(0)	195	177	50
H04	tnfn1_pw060328p04q188	EXACT(0)	154	143	109	33	EXACT(0)	200	189	52
H05	tnfn1_pw060328p04q189	EXACT(0)	158	150	103	27	EXACT(0)	200	163	44
H06	tnfn1_pw060328p04q190	EXACT(0)	155	144	112	34	EXACT(0)	201	104	38
H07	tnfn1_pw060328p04q191	EXACT(0)	156	139	102	36	EXACT(0)	80	78	46
H08	tnfn1_pw060328p04q192	EXACT(0)	157	152	108	29	EXACT(0)	200	193	56
H09	tnfn1_pw060328p04q193	EXACT(0)	156	152	118	36	EXACT(0)	200	189	57
H10	tnfn1_pw060328p04q194	EXACT(0)	156	152	131	38	EXACT(0)	200	168	49
H11	tnfn1_pw060328p04q195	EXACT(0)	165	129	89	25	EXACT(0)	148	141	39
H12	tnfn1_pw060328p04q196	EXACT(0)	155	139	90	27	EXACT(0)	200	187	58

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