Francisella tularensis subsp. *novicida* "Two-Allele" Transposon Mutant Library, Plate 10 (tnfn1_pw060328p02)

Catalog No. NR-51292

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-51292 represents plate 10 (tnfn1_pw060328p02) 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-51292 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 10 (tnfn1_pw060328p02), NR-51292."

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.

Disclaimers:
You are authorized to use this product for research use only. It is not intended for human use.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government makes any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for damages arising from the misidentification or misrepresentation of products.

Use Restrictions:
This material is distributed for internal research, non-commercial purposes only. This material, its product or its

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.

Table 1: Plate 10 (tnfn1_pw060328p02) – Transposon Type and Mutated Gene[1]

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060328p02q101	T20	-	Pseudogene: sugar transporter	Pseudogene
A02	tnfn1_pw060328p02q109	T20	metIQ	Methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	Transport - amino-acid
A03	tnfn1_pw060328p02q117	T20	-	C4-dicarboxylate anaerobic carrier	Transport
A04	tnfn1_pw060328p02q125	T20	-	Conserved protein of unknown function	Unknown function - conserved
A05	tnfn1_pw060328p02q133	<KAN-2>	-	Hypothetical membrane protein	Hypothetical - novel
A06	tnfn1_pw060328p02q141	<KAN-2>	sucD	Succinyl-CoA synthetase, alpha subunit	Energy metabolism
A07	tnfn1_pw060328p02q149	<KAN-2>	-	Protein of unknown function	Unknown function - novel
A08	tnfn1_pw060328p02q157	T18	htpG	Chaperone Hsp90, heat shock protein HtpG	Post-translational modification, protein turnover, chaperones - chaperones
A09	tnfn1_pw060328p02q165	T20	-	Amino acid-polyamine-organocation family protein	Transport - amino-acid
A10	tnfn1_pw060328p02q173	T20	-	Hypothetical membrane protein	Hypothetical - novel
A11	tnfn1_pw060328p02q181	T20	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
A12	tnfn1_pw060328p02q189	T20	-	Conserved protein of unknown function	Unknown function - conserved
B01	tnfn1_pw060328p02q102	T20	-	Deoxyribodipyrimidine photolyase	DNA replication, recombination, modification and repair - restriction/modification
B02	tnfn1_pw060328p02q110	T20	-	Protein of unknown function	Unknown function - novel
B03	tnfn1_pw060328p02q118	T20	mltA	Membrane-bound lytic murein transglycosylase	Cell wall / LPS / capsule
B04	tnfn1_pw060328p02q126	T20	-	Conserved hypothetical protein	Hypothetical - conserved
B05	tnfn1_pw060328p02q134	<KAN-2>	-	Acyltransferase	Fatty acids and lipids metabolism
B06	tnfn1_pw060328p02q142	<KAN-2>	-	Pseudogene: hypothetical protein, fragment	Pseudogene
B07	tnfn1_pw060328p02q150	T18	-	Conserved hypothetical protein	Hypothetical - conserved
B08	tnfn1_pw060328p02q158	T18	-	Monovalent cation:proton antiporter family protein	Transport
B09	tnfn1_pw060328p02q166	T20	-	Hypothetical membrane protein	Hypothetical - novel
B10	tnfn1_pw060328p02q174	T20	aroB	3-dehydroquinate synthetase	Amino acid metabolism - biosynthesis
B11	tnfn1_pw060328p02q182	T20	-	Rare lipoprotein B family protein	Cell wall / LPS / capsule
B12	tnfn1_pw060328p02q190	T20	ppdK	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	Energy metabolism
C01	tnfn1_pw060328p02q103	T20	capB	Capsule biosynthesis protein CapB	Cell wall / LPS / capsule
C02	tnfn1_pw060328p02q111	T20	-	Hypothetical protein	Hypothetical - novel
C03	tnfn1_pw060328p02q119	T20	-	Hydroxy/aromatic amino acid permease (HAAAP) family protein	Transport - amino-acid
C04	tnfn1_pw060328p02q127	T20	-	Conserved hypothetical membrane protein	Hypothetical - conserved
C05	tnfn1_pw060328p02q135	<KAN-2>	pyk	Pyruvate kinase	Carbohydrate metabolism - degradation, utilization, assimilation
C06	tnfn1_pw060328p02q143	<KAN-2>	-	Conserved protein of unknown function	Unknown function - conserved
C07	tnfn1_pw060328p02q151	T18	isftu2	Isftu2	IS element
C08	tnfn1_pw060328p02q159	T18	-	Isomerase	Putative enzymes
C09	tnfn1_pw060328p02q167	T20	-	Prophage repressor protein	Signal transduction and regulation
C10	tnfn1_pw060328p02q175	T20	putA	Bifunctional proline dehydrogenase, pyrroline-5-carboxylate dehydrogenase	Amino acid metabolism - degradation, utilization, assimilation
C11	tnfn1_pw060328p02q183	T20	isftu2	Isftu2	IS element
C12	tnfn1_pw060328p02q191	T20			
D01	tnfn1_pw060328p02q104	T20	-	Conserved hypothetical membrane protein	Hypothetical - conserved
D02	tnfn1_pw060328p02q112	T20	dapD	Tetrahydrodipicolinate succinylase subunit	Amino acid metabolism - biosynthesis
D03	tnfn1_pw060328p02q120	T20	glpQ	Glycerophosphoryl diester phosphodiesterase	Other metabolism - degradation, utilization, assimilation
D04	tnfn1_pw060328p02q128	T20	-	Hypothetical membrane protein	Hypothetical - novel
D05	tnfn1_pw060328p02q136	<KAN-2>	atpC	ATP synthase, F1 sector, subunit epsilon	Energy metabolism
D06	tnfn1_pw060328p02q144	<KAN-2>	-	Thioredoxin	Cofactors, prosthetic groups, electron carriers metabolism
D07	tnfn1_pw060328p02q152	T18	-	5-formyltetrahydrofolate cycloligase	Putative enzymes
D08	tnfn1_pw060328p02q160	T18	-	Haloacid dehalogenase-like hydrolase	Putative enzymes
D09	tnfn1_pw060328p02q168	T20	-	Membrane fusion protein	Motility, attachment and secretion structure

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D10	tnfn1_pw060328p02q176	T20	-	Protein of unknown function	Unknown function - novel
D11	tnfn1_pw060328p02q184	T20	-	Conserved protein of unknown function	Unknown function - conserved
D12	tnfn1_pw060328p02q192	T20	-	Drug:H+ antiporter-1 (DHA1) family protein	Transport - drugs / antibacterial compounds
E01	tnfn1_pw060328p02q105	T20	appB	Cytochrome bd-II terminal oxidase subunit II	Energy metabolism
E02	tnfn1_pw060328p02q113	T20	clpP	ATP-dependent Clp protease subunit P	Post-translational modification, protein turnover, chaperones - protein degradation
E03	tnfn1_pw060328p02q121	T20	kdpC	Potassium-transporting ATPase C chain	Transport
E04	tnfn1_pw060328p02q129	T20	-	Hypothetical protein	Hypothetical - novel
E05	tnfn1_pw060328p02q137	<KAN-2>	-	Protein of unknown function	Unknown function - novel
E06	tnfn1_pw060328p02q145	<KAN-2>	-	Regulatory factor, Bvg accessory factor family	Signal transduction and regulation
E07	tnfn1_pw060328p02q153	T18	era	GTP-binding protein	Putative enzymes
E08	tnfn1_pw060328p02q161	T18	-	GtrA-like protein	Putative enzymes
E09	tnfn1_pw060328p02q169	T20	rdgC	Recombination associated protein	DNA replication, recombination, modification and repair - restriction/modification
E10	tnfn1_pw060328p02q177	T20	-	Protein of unknown function	Unknown function - novel
E11	tnfn1_pw060328p02q185	T20	-	Protein of unknown function, LamB/YcsF family	Unknown function - conserved
E12	tnfn1_pw060328p02q193	T20	-	Dienelactone hydrolase family protein	Putative enzymes
F01	tnfn1_pw060328p02q106	T20	-	Drug/metabolite transporter superfamily protein	Transport - drugs / antibacterial compounds
F02	tnfn1_pw060328p02q114	T20	pip	Proline iminopeptidase	Post-translational modification, protein turnover, chaperones - protein degradation
F03	tnfn1_pw060328p02q122	T20	-	Protein of unknown function	Hypothetical - novel
F04	tnfn1_pw060328p02q130	T20	-	Protein of unknown function with radical SAM domain	Unknown function - conserved
F05	tnfn1_pw060328p02q138	<KAN-2>	-	Conserved hypothetical protein	Hypothetical - conserved
F06	tnfn1_pw060328p02q146	<KAN-2>	nuoH	NADH dehydrogenase I, H subunit	Energy metabolism
F07	tnfn1_pw060328p02q154	T18	-	Predicted hydrolase of the HAD superfamily	Putative enzymes
F08	tnfn1_pw060328p02q162	T18	-	Sugar:cation symporter family protein	Transport - carbohydrates (sugars, polysaccharides)
F09	tnfn1_pw060328p02q170	T20	lpcC	Glycosyl transferase, group 1	Cell wall / LPS / capsule
F10	tnfn1_pw060328p02q178	T20	-	Small conductance mechanosensitive ion channel family protein	Transport
F11	tnfn1_pw060328p02q186	T20	-	Protein of unknown function	Unknown function - novel
F12	tnfn1_pw060328p02q194	T20	-	Pyridoxal-dependent decarboxylase	Amino acid metabolism - biosynthesis
G01	tnfn1_pw060328p02q107	T20	-	Conserved protein of unknown function	Unknown function - conserved
G02	tnfn1_pw060328p02q115	T20	iglB	Intracellular growth locus protein B	Unknown function - conserved
G04	tnfn1_pw060328p02q131	<KAN-2>	sufD	sufS activator complex, sufD subunit	Post-translational modification, protein turnover, chaperones
G05	tnfn1_pw060328p02q139	<KAN-2>	eno	Enolase (2-phosphoglycerate dehydratase)	Carbohydrate metabolism - degradation, utilization, assimilation
G06	tnfn1_pw060328p02q147	<KAN-2>	-	Permease	Transport
G07	tnfn1_pw060328p02q155	T18	-	Nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	Transport
G08	tnfn1_pw060328p02q163	T20	-	Modification methylase, HemK family	Translation, ribosomal structure and biogenesis
G09	tnfn1_pw060328p02q171	T20	-	Major facilitator superfamily (MFS) transport protein	Transport
G10	tnfn1_pw060328p02q179	T20	-	Phage integrase	Mobile and extrachromosomal element functions - phage or plasmid related proteins
G11	tnfn1_pw060328p02q187	T20	-	Heavy metal cation transport ATPase	Transport
G12	tnfn1_pw060328p02q195	T20	-	Conserved protein of unknown function	Unknown function - conserved
H01	tnfn1_pw060328p02q108	T20	-	Fatty acid hydroxylase	Fatty acids and lipids metabolism
H02	tnfn1_pw060328p02q116	T20	-	Conserved protein of unknown function	Cell wall / LPS / capsule
H03	tnfn1_pw060328p02q124	T20	-	Fucose: H+ symporter (FHS) family protein	Transport - carbohydrates (sugars, polysaccharides)
H04	tnfn1_pw060328p02q132	<KAN-2>	wrbA	trp repressor binding protein	Signal transduction and regulation
H05	tnfn1_pw060328p02q140	<KAN-2>	-	Hypothetical membrane protein	Hypothetical - novel
H06	tnfn1_pw060328p02q148	<KAN-2>	-	Transcriptional regulator, ArsR family	Signal transduction and regulation
H07	tnfn1_pw060328p02q156	T18	bcp	Bacterioferritin comigratory protein	Post-translational modification, protein turnover, chaperones - protein modification
H08	tnfn1_pw060328p02q164	T20	-	Transcriptional regulator	Signal transduction and regulation
H09	tnfn1_pw060328p02q172	T20	add	Deoxyadenosine deaminase/adenosine deaminase	Nucleotides and nucleosides metabolism
H10	tnfn1_pw060328p02q180	T20	recF	RecFOR complex, RecF component	DNA replication, recombination, modification and repair - restriction/modification
H11	tnfn1_pw060328p02q188	T20	-	Conserved protein of unknown function	Unknown function - conserved
H12	tnfn1_pw060328p02q196	T20	-	Hypothetical membrane protein	Hypothetical - novel

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

Table 2: Plate 10 (tnfn1_pw060328p02) – 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_pw060328p02q101	C	1141028	FTN_1078	1140939	1141115	R	59	88(177)
A02	tnfn1_pw060328p02q109	U	1168839	FTN_1107	1168330	1169799	F	490	510(1470)
A03	tnfn1_pw060328p02q117	C	277211	FTN_0269	275914	277422	R	503	212(1509)
A04	tnfn1_pw060328p02q125	C	921996	FTN_0869	921132	923024	F	631	865(1893)
A05	tnfn1_pw060328p02q133	C	1053192	FTN_0994	1052499	1053245	R	249	54(747)
A06	tnfn1_pw060328p02q141	C	624092	FTN_0593	623591	624460	R	290	369(870)
A07	tnfn1_pw060328p02q149	C	372942	FTN_0369	372857	373084	F	76	86(228)
A08	tnfn1_pw060328p02q157	C	273418	FTN_0266	272930	274813	F	628	489(1884)
A09	tnfn1_pw060328p02q165	C	1620635	FTN_1523	1620541	1621251	F	237	95(711)
A10	tnfn1_pw060328p02q173	C	429043	FTN_0431	428206	429645	F	480	838(1440)
A11	tnfn1_pw060328p02q181	C	722287	FTN_0678	721383	722594	R	404	308(1212)
A12	tnfn1_pw060328p02q189	C	890845	FTN_0833	890583	890900	R	106	56(318)
B01	tnfn1_pw060328p02q102	C	363664	FTN_0361	363337	364833	F	499	328(1497)
B02	tnfn1_pw060328p02q110	C	1546232	FTN_1457	1545936	1546451	F	172	297(516)
B03	tnfn1_pw060328p02q118	C	1359557	FTN_1286	1358907	1360070	F	388	651(1164)
B04	tnfn1_pw060328p02q126	C	1535447	FTN_1446	1534991	1536382	R	464	936(1392)
B05	tnfn1_pw060328p02q134	C	1879609	FTN_1750	1879341	1880078	F	246	269(738)
B06	tnfn1_pw060328p02q142	C	1890784	FTN_1761	1889997	1890802	R	268.6	19(806)
B07	tnfn1_pw060328p02q150	C	776756	FTN_0721	776068	777051	R	328	296(984)
B08	tnfn1_pw060328p02q158	C	1073643	FTN_1013	1072741	1073913	R	391	271(1173)
B09	tnfn1_pw060328p02q166	C	1663279	FTN_1566	1663213	1663446	R	78	168(234)
B10	tnfn1_pw060328p02q174	C	1200160	FTN_1135	1199729	1200805	R	359	646(1077)
B11	tnfn1_pw060328p02q182	C	925722	FTN_0871	925584	926156	F	191	139(573)
B12	tnfn1_pw060328p02q190	C	77609	FTN_0064	75648	78278	R	877	670(2631)
C01	tnfn1_pw060328p02q103	C	1275391	FTN_1201	1274526	1275740	R	405	350(1215)
C02	tnfn1_pw060328p02q111	C	155918	FTN_0142	155218	156756	F	513	701(1539)
C03	tnfn1_pw060328p02q119	C	1608947	FTN_1512	1608678	1609847	F	390	270(1170)
C04	tnfn1_pw060328p02q127	C	1294219	FTN_1223	1293973	1294560	R	196	342(588)
C05	tnfn1_pw060328p02q135	C	1408934	FTN_1330	1408823	1410256	R	478	1323(1434)
C06	tnfn1_pw060328p02q143	C	425690	FTN_0426	425491	425859	F	123	200(369)
C07	tnfn1_pw060328p02q151	C	986296	-	986109	986965	R	285.6	670(857)
C08	tnfn1_pw060328p02q159	C	958992	FTN_0901	958727	959317	R	197	326(591)
C09	tnfn1_pw060328p02q167	C	1446271	FTN_1363	1446038	1446688	F	217	234(651)
C10	tnfn1_pw060328p02q175	C	1197349	FTN_1131	1194416	1198477	R	1354	1129(4062)
C11	tnfn1_pw060328p02q183	C	245775	-	245715	246181	R	155.6	407(467)
C12	tnfn1_pw060328p02q191	C	496402	intergenic					
D01	tnfn1_pw060328p02q104	C	785273	FTN_0731	784756	785670	F	305	518(915)
D02	tnfn1_pw060328p02q112	C	1855765	FTN_1727	1855155	1855901	R	249	137(747)
D03	tnfn1_pw060328p02q120	C	1178368	FTN_1114	1177796	1178545	R	250	178(750)
D04	tnfn1_pw060328p02q128	C	400531	FTN_0401	400237	400833	R	199	303(597)
D05	tnfn1_pw060328p02q136	C	1759904	FTN_1645	1759710	1760144	R	145	241(435)
D06	tnfn1_pw060328p02q144	C	911392	FTN_0856	911269	911592	F	108	124(324)
D07	tnfn1_pw060328p02q152	C	1307553	FTN_1239	1307455	1308000	F	182	99(546)
D08	tnfn1_pw060328p02q160	C	1302119	FTN_1233	1301598	1302386	R	263	268(789)
D09	tnfn1_pw060328p02q168	C	1809407	FTN_1692	1808552	1809619	R	356	213(1068)
D10	tnfn1_pw060328p02q176	C	382343	FTN_0381	382197	383180	F	328	147(984)
D11	tnfn1_pw060328p02q184	C	854773	FTN_0798	854146	856299	F	718	628(2154)
D12	tnfn1_pw060328p02q192	C	1798247	FTN_1683	1798000	1799259	F	420	248(1260)
E01	tnfn1_pw060328p02q105	C	1730878	FTN_1620	1730335	1731294	F	320	544(960)
E02	tnfn1_pw060328p02q113	C	1117548	FTN_1057	1117172	1117774	R	201	227(603)
E03	tnfn1_pw060328p02q121	C	1841694	FTN_1716	1841389	1841940	R	184	247(552)
E04	tnfn1_pw060328p02q129	C	1719606	FTN_1612	1719296	1719874	F	193	311(579)
E05	tnfn1_pw060328p02q137	C	298927	FTN_0292	298865	299065	F	67	63(201)
E06	tnfn1_pw060328p02q145	C	1704633	FTN_1603	1704273	1705046	R	258	414(774)
E07	tnfn1_pw060328p02q153	C	1210600	FTN_1145	1210567	1211457	R	297	858(891)
E08	tnfn1_pw060328p02q161	C	1738052	FTN_1625	1737806	1738180	F	125	247(375)
E09	tnfn1_pw060328p02q169	C	849098	FTN_0790	848825	849682	F	286	274(858)
E10	tnfn1_pw060328p02q177	C	1837430	FTN_1713	1837164	1837808	R	215	379(645)
E11	tnfn1_pw060328p02q185	C	99887	FTN_0088	99479	100174	F	232	409(696)
E12	tnfn1_pw060328p02q193	C	198352	FTN_0180	197925	198641	R	239	290(717)
F01	tnfn1_pw060328p02q106	C	941170	FTN_0884	940420	941310	R	297	141(891)
F02	tnfn1_pw060328p02q114	C	1859993	FTN_1731	1859256	1860191	R	312	199(936)

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_pw060328p02q122	C	933930	FTN_0878	933333	934319	F	329	598(987)
F04	tnfn1_pw060328p02q130	C	1005053	FTN_0947	1004368	1005477	R	370	425(1110)
F05	tnfn1_pw060328p02q138	C	919388	FTN_0866	919330	919911	F	194	59(582)
F06	tnfn1_pw060328p02q146	C	1787238	FTN_1673	1787230	1788237	R	336	1000(1008)
F07	tnfn1_pw060328p02q154	C	92443	FTN_0082	92435	92995	F	187	9(561)
F08	tnfn1_pw060328p02q162	C	943169	FTN_0886	942996	944261	F	422	174(1266)
F09	tnfn1_pw060328p02q170	C	1322333	FTN_1253	1321637	1322698	R	354	366(1062)
F10	tnfn1_pw060328p02q178	C	1072371	FTN_1012	1071927	1072757	F	277	445(831)
F11	tnfn1_pw060328p02q186	C	1812997	FTN_1695	1812953	1813585	F	211	45(633)
F12	tnfn1_pw060328p02q194	C	1854440	FTN_1726	1853938	1855098	R	387	659(1161)
G01	tnfn1_pw060328p02q107	C	339121	FTN_0334	339054	339395	R	114	275(342)
G02	tnfn1_pw060328p02q115	C	1398383	FTN_1323	1397638	1399155	R	506	773(1518)
G04	tnfn1_pw060328p02q131	C	909571	FTN_0853	908463	909605	F	381	1109(1143)
G05	tnfn1_pw060328p02q139	C	653832	FTN_0621	652477	653844	F	456	1356(1368)
G06	tnfn1_pw060328p02q147	C	347505	FTN_0342	346275	347585	R	437	81(1311)
G07	tnfn1_pw060328p02q155	C	1074424	FTN_1014	1074014	1074643	R	210	220(630)
G08	tnfn1_pw060328p02q163	C	321922	FTN_0311	321772	322713	F	314	151(942)
G09	tnfn1_pw060328p02q171	C	1770677	FTN_1657	1770083	1771378	R	432	702(1296)
G10	tnfn1_pw060328p02q179	C	375033	FTN_0373	374890	376083	F	398	144(1194)
G11	tnfn1_pw060328p02q187	C	393957	FTN_0394	392909	395071	R	721	1115(2163)
G12	tnfn1_pw060328p02q195	C	161750	FTN_0149	161561	162472	F	304	190(912)
H01	tnfn1_pw060328p02q108	C	853804	FTN_0797	853524	854069	F	182	281(546)
H02	tnfn1_pw060328p02q116	C	1539194	FTN_1449	1538872	1539477	R	202	284(606)
H03	tnfn1_pw060328p02q124	C	866870	FTN_0809	866270	867517	F	416	601(1248)
H04	tnfn1_pw060328p02q132	C	203535	FTN_0186	203016	203609	R	198	75(594)
H05	tnfn1_pw060328p02q140	C	238190	FTN_0216	238094	238426	F	111	97(333)
H06	tnfn1_pw060328p02q148	C	1470559	FTN_1393	1470399	1470698	R	100	140(300)
H07	tnfn1_pw060328p02q156	C	1885448	FTN_1756	1885175	1885651	F	159	274(477)
H08	tnfn1_pw060328p02q164	C	905967	FTN_0850	905800	906207	F	136	168(408)
H09	tnfn1_pw060328p02q172	C	739652	FTN_0695	739415	740452	F	346	238(1038)
H10	tnfn1_pw060328p02q180	C	786932	FTN_0734	786285	787331	R	349	400(1047)
H11	tnfn1_pw060328p02q188	C	830910	FTN_0774	830697	831029	R	111	120(333)
H12	tnfn1_pw060328p02q196	C	1652227	FTN_1554	1651824	1653341	F	506	404(1518)

[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 10 (tnfn1_pw060328p02) – 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_pw060328p02q101	EXACT(0)	156	153	124	39	EXACT(0)	200	189	61
A02	tnfn1_pw060328p02q109	EXACT(0)	154	145	132	39	EXACT(0)	200	193	47
A03	tnfn1_pw060328p02q117	EXACT(0)	156	146	124	39	EXACT(0)	181	171	56
A04	tnfn1_pw060328p02q125	EXACT(0)	155	145	114	27	EXACT(0)	200	184	43
A05	tnfn1_pw060328p02q133	EXACT(0)	120	106	101	39	EXACT(0)	200	186	59
A06	tnfn1_pw060328p02q141	EXACT(0)	124	120	97	25	EXACT(0)	200	198	55
A07	tnfn1_pw060328p02q149	EXACT(0)	120	118	77	21	EXACT(0)	138	124	48
A08	tnfn1_pw060328p02q157	NONE	0	0	0	17	ESTIMATE(124)	690	535	28
A09	tnfn1_pw060328p02q165	EXACT(0)	156	151	124	40	EXACT(0)	200	192	58
A10	tnfn1_pw060328p02q173	EXACT(0)	156	153	126	38	EXACT(0)	182	167	52
A11	tnfn1_pw060328p02q181	EXACT(0)	156	152	122	34	EXACT(0)	200	195	57
A12	tnfn1_pw060328p02q189	EXACT(0)	156	152	127	31	EXACT(0)	200	189	55
B01	tnfn1_pw060328p02q102	EXACT(0)	155	145	117	37	EXACT(0)	200	194	53
B02	tnfn1_pw060328p02q110	EXACT(0)	156	148	131	39	EXACT(0)	200	183	54

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
B03	tnfn1_pw060328p02q118	EXACT(0)	157	151	129	39	EXACT(0)	199	183	45
B04	tnfn1_pw060328p02q126	EXACT(0)	157	151	119	31	EXACT(0)	200	190	56
B05	tnfn1_pw060328p02q134	EXACT(0)	122	119	71	20	EXACT(0)	200	191	44
B06	tnfn1_pw060328p02q142	EXACT(0)	123	126	100	32	EXACT(0)	200	183	40
B07	tnfn1_pw060328p02q150	EXACT(0)	125	86	65	18	EXACT(0)	200	190	43
B08	tnfn1_pw060328p02q158	EXACT(0)	124	119	103	36	EXACT(0)	101	93	48
B09	tnfn1_pw060328p02q166	EXACT(0)	156	153	126	40	EXACT(0)	200	183	52
B10	tnfn1_pw060328p02q174	EXACT(0)	156	151	121	40	EXACT(0)	200	189	56
B11	tnfn1_pw060328p02q182	EXACT(0)	156	153	116	33	EXACT(0)	200	184	57
B12	tnfn1_pw060328p02q190	EXACT(0)	157	153	125	36	EXACT(0)	200	195	55
C01	tnfn1_pw060328p02q103	EXACT(0)	158	153	132	37	EXACT(0)	200	197	56
C02	tnfn1_pw060328p02q111	EXACT(0)	156	151	127	40	EXACT(0)	200	171	43
C03	tnfn1_pw060328p02q119	EXACT(0)	156	146	127	43	EXACT(0)	200	186	55
C04	tnfn1_pw060328p02q127	EXACT(0)	156	153	123	36	EXACT(0)	200	193	57
C05	tnfn1_pw060328p02q135	EXACT(0)	123	125	101	30	EXACT(0)	200	191	52
C06	tnfn1_pw060328p02q143	EXACT(0)	121	120	93	24	EXACT(0)	200	190	53
C07	tnfn1_pw060328p02q151	EXACT(0)	123	112	92	24	EXACT(0)	200	189	54
C08	tnfn1_pw060328p02q159	EXACT(0)	122	113	91	27	EXACT(0)	200	187	57
C09	tnfn1_pw060328p02q167	EXACT(0)	154	138	104	28	EXACT(0)	200	176	45
C10	tnfn1_pw060328p02q175	EXACT(0)	155	145	119	36	EXACT(0)	200	192	57
C11	tnfn1_pw060328p02q183	EXACT(0)	154	144	110	26	EXACT(0)	200	188	52
C12	tnfn1_pw060328p02q191	EXACT(0)	156	152	116	36	EXACT(0)	200	187	56
D01	tnfn1_pw060328p02q104	EXACT(0)	157	150	134	38	EXACT(0)	200	191	58
D02	tnfn1_pw060328p02q112	EXACT(0)	155	145	111	34	EXACT(0)	200	182	57
D03	tnfn1_pw060328p02q120	EXACT(0)	158	151	131	37	EXACT(0)	200	160	44
D04	tnfn1_pw060328p02q128	EXACT(0)	156	145	122	39	EXACT(0)	200	191	54
D05	tnfn1_pw060328p02q136	EXACT(0)	122	119	109	42	EXACT(0)	200	189	59
D06	tnfn1_pw060328p02q144	EXACT(0)	120	112	88	29	EXACT(0)	200	191	64
D07	tnfn1_pw060328p02q152	EXACT(0)	124	120	86	23	EXACT(0)	200	189	53
D08	tnfn1_pw060328p02q160	EXACT(0)	123	120	93	25	EXACT(0)	199	171	37
D09	tnfn1_pw060328p02q168	EXACT(0)	156	152	131	39	EXACT(0)	200	194	54
D10	tnfn1_pw060328p02q176	EXACT(0)	156	152	125	38	EXACT(0)	197	193	53
D11	tnfn1_pw060328p02q184	EXACT(0)	156	151	129	38	EXACT(0)	200	194	51
D12	tnfn1_pw060328p02q192	EXACT(0)	155	145	123	38	EXACT(0)	200	155	39
E01	tnfn1_pw060328p02q105	EXACT(0)	156	152	129	31	EXACT(0)	200	193	57
E02	tnfn1_pw060328p02q113	EXACT(0)	156	142	125	36	EXACT(0)	79	60	30
E03	tnfn1_pw060328p02q121	EXACT(0)	156	151	124	39	EXACT(0)	200	193	48
E04	tnfn1_pw060328p02q129	EXACT(0)	157	151	131	40	EXACT(0)	200	151	40
E05	tnfn1_pw060328p02q137	EXACT(0)	121	118	97	33	EXACT(0)	200	185	57
E06	tnfn1_pw060328p02q145	EXACT(0)	121	118	108	38	EXACT(0)	200	185	50
E07	tnfn1_pw060328p02q153	EXACT(0)	121	112	94	29	EXACT(0)	200	187	57
E08	tnfn1_pw060328p02q161	ADJUSTED(1)	120	104	54	18	ESTIMATE(1)	199	182	45
E09	tnfn1_pw060328p02q169	EXACT(0)	155	151	104	26	EXACT(0)	200	182	52
E10	tnfn1_pw060328p02q177	EXACT(0)	155	145	126	44	EXACT(0)	134	128	53
E11	tnfn1_pw060328p02q185	EXACT(0)	156	152	125	40	EXACT(0)	200	189	59
E12	tnfn1_pw060328p02q193	EXACT(0)	155	145	126	40	EXACT(0)	200	182	50
F01	tnfn1_pw060328p02q106	EXACT(0)	155	138	112	27	EXACT(0)	200	190	51
F02	tnfn1_pw060328p02q114	EXACT(0)	156	153	129	42	EXACT(0)	200	194	53
F03	tnfn1_pw060328p02q122	EXACT(0)	156	151	130	37	EXACT(0)	200	180	47
F04	tnfn1_pw060328p02q130	EXACT(0)	156	151	127	42	EXACT(0)	200	195	59
F05	tnfn1_pw060328p02q138	EXACT(0)	122	119	101	34	EXACT(0)	188	152	40
F06	tnfn1_pw060328p02q146	EXACT(0)	121	112	96	37	EXACT(0)	200	191	49
F07	tnfn1_pw060328p02q154	EXACT(0)	120	112	91	33	EXACT(0)	200	186	59
F08	tnfn1_pw060328p02q162	NONE	0	0	0	21	ESTIMATE(121)	601	498	35
F09	tnfn1_pw060328p02q170	EXACT(0)	157	152	111	29	EXACT(0)	200	190	52
F10	tnfn1_pw060328p02q178	EXACT(0)	155	145	126	39	EXACT(0)	200	120	39
F11	tnfn1_pw060328p02q186	EXACT(0)	156	152	125	35	EXACT(0)	200	172	53
F12	tnfn1_pw060328p02q194	EXACT(0)	156	152	116	38	EXACT(0)	200	189	54
G01	tnfn1_pw060328p02q107	EXACT(0)	157	153	131	40	EXACT(0)	116	111	48
G02	tnfn1_pw060328p02q115	EXACT(0)	157	146	126	39	EXACT(0)	200	186	57
G04	tnfn1_pw060328p02q131	EXACT(0)	120	118	103	46	EXACT(0)	200	181	66

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
G05	tnfn1_pw060328p02q139	EXACT(0)	120	119	104	39	EXACT(0)	200	182	58
G06	tnfn1_pw060328p02q147	EXACT(0)	122	125	99	28	EXACT(0)	200	196	51
G07	tnfn1_pw060328p02q155	EXACT(0)	123	119	101	29	EXACT(0)	199	124	36
G08	tnfn1_pw060328p02q163	EXACT(0)	156	153	126	37	EXACT(0)	200	189	55
G09	tnfn1_pw060328p02q171	EXACT(0)	156	145	115	33	EXACT(0)	200	192	50
G10	tnfn1_pw060328p02q179	EXACT(0)	155	145	120	41	EXACT(0)	200	191	54
G11	tnfn1_pw060328p02q187	EXACT(0)	155	145	119	34	EXACT(0)	200	196	55
G12	tnfn1_pw060328p02q195	EXACT(0)	157	152	126	37	EXACT(0)	200	188	51
H01	tnfn1_pw060328p02q108	EXACT(0)	156	145	124	34	EXACT(0)	200	182	54
H02	tnfn1_pw060328p02q116	EXACT(0)	159	153	138	40	EXACT(0)	200	196	56
H03	tnfn1_pw060328p02q124	EXACT(0)	157	153	128	41	EXACT(0)	200	180	56
H04	tnfn1_pw060328p02q132	EXACT(0)	123	119	103	37	EXACT(0)	200	196	52
H05	tnfn1_pw060328p02q140	EXACT(0)	121	112	99	28	EXACT(0)	200	188	58
H06	tnfn1_pw060328p02q148	EXACT(0)	121	117	87	27	EXACT(0)	199	164	40
H07	tnfn1_pw060328p02q156	EXACT(0)	123	118	99	28	EXACT(0)	200	192	55
H08	tnfn1_pw060328p02q164	EXACT(0)	164	133	109	28	EXACT(0)	200	190	38
H09	tnfn1_pw060328p02q172	EXACT(0)	155	146	127	38	EXACT(0)	200	194	57
H10	tnfn1_pw060328p02q180	EXACT(0)	154	145	110	34	EXACT(0)	200	188	56
H11	tnfn1_pw060328p02q188	EXACT(0)	155	139	125	40	EXACT(0)	199	139	43
H12	tnfn1_pw060328p02q196	EXACT(0)	150	92	80	31	EXACT(0)	200	183	46

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