

***Francisella tularensis* subsp. *novicida*
“Two-Allele” Transposon Mutant Library,
Plate 8 (tnfn1_pw060323p08)**

Catalog No. NR-51290

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-51290 represents plate 8 (tnfn1_pw060323p08) 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-51290 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 8 (tnfn1_pw060323p08), NR-51290.”

Biosafety Level: 2

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories](#). 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmb15/index.htm.

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References:

- Gallagher, L. A., et al. "A Comprehensive Transposon Mutant Library of *Francisella novicida*, A Bioweapon Surrogate." *Proc. Natl. Acad. Sci. USA* 104 (2007): 1009-1014. PubMed: 17215359.

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Table 1: Plate 8 (tnfn1_pw060323p08) – Transposon Type and Mutated Gene¹

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060323p08q101	T20	-	pilus assembly protein	motility, attachment and secretion structure
A02	tnfn1_pw060323p08q109	<KAN-2>	-	protein of unknown function	unknown function - novel
A03	tnfn1_pw060323p08q117	T18			
A04	tnfn1_pw060323p08q125	T20	tgt	queuine tRNA-ribosyltransferase.	translation, ribosomal structure and biogenesis
A05	tnfn1_pw060323p08q133	T20	-	signal transduction protein with a PAS, a PAC, an EAL and a GGDEF domain	signal transduction and regulation
A06	tnfn1_pw060323p08q141	T20	-	isochorismatase family protein	putative enzymes
A07	tnfn1_pw060323p08q149	T20	-	regulatory factor, Bvg accessory factor family	signal transduction and regulation
A08	tnfn1_pw060323p08q157	T20	-	DNA/RNA helicase	DNA replication, recombination, modification and repair - replication
A09	tnfn1_pw060323p08q165	T20	mfd	transcription-repair coupling factor	transcription
A10	tnfn1_pw060323p08q173	<KAN-2>	-	cytochrome b561 family protein	energy metabolism
A11	tnfn1_pw060323p08q181	T18	rhtB	homoserine/threonine efflux family protein	transport - amino-acid
A12	tnfn1_pw060323p08q189	T20	-	RNA methyltransferase, trmA family	translation, ribosomal structure and biogenesis
B01	tnfn1_pw060323p08q102	T20	-	protein of unknown function	unknown function - novel
B02	tnfn1_pw060323p08q110	T18	-	transposase	mobile and extrachromosomal element functions - transposition
B03	tnfn1_pw060323p08q118	T18	-	DNA uptake protein, SMF family	transport
B04	tnfn1_pw060323p08q126	T20	ilvE	branched-chain amino acid aminotransferase protein (class IV)	amino acid metabolism - biosynthesis
B05	tnfn1_pw060323p08q134	T20	-	conserved membrane protein of unknown function	unknown function - conserved
B06	tnfn1_pw060323p08q142	T20	-	major facilitator superfamily (MFS) transport protein	transport
B07	tnfn1_pw060323p08q150	T20	glpT	glycerol-3-phosphate transporter	transport
B09	tnfn1_pw060323p08q166	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
B10	tnfn1_pw060323p08q174	<KAN-2>	-	hypothetical protein	hypothetical - novel
B11	tnfn1_pw060323p08q182	T18			
B12	tnfn1_pw060323p08q190	T20	rimI	ribosomal-protein-alanine acetyltransferase	translation, ribosomal structure and biogenesis
C01	tnfn1_pw060323p08q103	T20	-	conserved protein of unknown function	unknown function - conserved
C02	tnfn1_pw060323p08q111	T18	-	membrane protein of unknown function	unknown function - novel
C03	tnfn1_pw060323p08q119	T18	-	transcriptional regulator, LysR family	signal transduction and regulation
C04	tnfn1_pw060323p08q127	T20	glpF	glycerol uptake facilitator protein	transport - carbohydrates (sugars, polysaccharides)
C05	tnfn1_pw060323p08q135	T20	-	conserved protein of unknown function	unknown function - conserved
C06	tnfn1_pw060323p08q143	T20	-	protein of unknown function	unknown function - novel
C07	tnfn1_pw060323p08q151	T20	ampG	peptide-acetyl-coenzyme A transporter (PAT) family protein	transport
C08	tnfn1_pw060323p08q159	T20	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	cell wall / LPS / capsule
C09	tnfn1_pw060323p08q167	T20	-	protein of unknown function	unknown function - novel
C10	tnfn1_pw060323p08q175	<KAN-2>	-	protein of unknown function	unknown function - novel
C11	tnfn1_pw060323p08q183	T18	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
C12	tnfn1_pw060323p08q191	T20	rimI	ribosomal-protein-alanine acetyltransferase	translation, ribosomal structure and biogenesis
D01	tnfn1_pw060323p08q104	T20	aroC	chorismate synthase	amino acid metabolism - biosynthesis
D02	tnfn1_pw060323p08q112	T18	-	disulfide bond formation protein, DsbB family	post-translational modification, protein turnover, chaperones - protein modification
D03	tnfn1_pw060323p08q120	T18	carB	carbamoyl-phosphate synthase large chain	nucleotides and nucleosides metabolism
D04	tnfn1_pw060323p08q128	T20	-	protein of unknown function	unknown function - novel
D05	tnfn1_pw060323p08q136	T20	-	hypothetical protein	hypothetical - novel
D06	tnfn1_pw060323p08q144	T20	isfU2	isfU2	IS element
D07	tnfn1_pw060323p08q152	T20	-	conserved protein of unknown function	unknown function - conserved
D08	tnfn1_pw060323p08q160	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
D09	tnfn1_pw060323p08q168	T20	oppD	peptide/opine/nickel uptake transporter (PepT) family protein	transport
D10	tnfn1_pw060323p08q176	<KAN-2>	-	ThiJ/PfpI family protein	putative enzymes
D11	tnfn1_pw060323p08q184	T18			

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D12	tnfn1_pw060323p08q192	T20	cysK	cysteine synthase	amino acid metabolism - biosynthesis
E01	tnfn1_pw060323p08q105	T20	-	hypothetical protein	hypothetical - novel
E02	tnfn1_pw060323p08q113	T18	-	pseudogene: DNA-3-methyladenine glycosylase	pseudogene
E03	tnfn1_pw060323p08q121	T18			
E04	tnfn1_pw060323p08q129	T20	-	metallopeptidase, M50B family	post-translational modification, protein turnover, chaperones - protein degradation
E05	tnfn1_pw060323p08q137	T20	-	two-component regulator, sensor histidine kinase	signal transduction and regulation
E06	tnfn1_pw060323p08q145	T20	rpe	D-ribulose-phosphate 3-epimerase	energy metabolism
E07	tnfn1_pw060323p08q153	T20	-	conserved protein of unknown function	unknown function - conserved
E08	tnfn1_pw060323p08q161	T20	hflX	protease, GTP-binding subunit	putative enzymes
E09	tnfn1_pw060323p08q169	T20	recB	ATP-dependent exoDNase (exonuclease V) beta subunit	DNA replication, recombination, modification and repair - restriction/modification
E10	tnfn1_pw060323p08q177	<KAN-2>	hupB	DNA-binding protein HU-beta	DNA replication, recombination, modification and repair - restriction/modification
E11	tnfn1_pw060323p08q185	T18	-	hypothetical membrane protein	hypothetical - novel
E12	tnfn1_pw060323p08q193	T20	purM	phosphoribosylformylglycinamide cyclo-ligase	nucleotides and nucleosides metabolism
F01	tnfn1_pw060323p08q106	T20	-	transcriptional regulator, ArsR family	signal transduction and regulation
F02	tnfn1_pw060323p08q114	T18	-	conserved hypothetical protein	hypothetical - conserved
F03	tnfn1_pw060323p08q122	T18	oxyR	oxidative stress transcriptional regulator	signal transduction and regulation
F04	tnfn1_pw060323p08q130	T20	rimK	glutathione synthase/ribosomal protein S6 modification enzyme	translation, ribosomal structure and biogenesis
F05	tnfn1_pw060323p08q138	T20	-	protein of unknown function with TPR repeat region and von Willebrand factor type A domain	unknown function - conserved
F06	tnfn1_pw060323p08q146	T20	minC	septum formation inhibitor	cell cycle
F07	tnfn1_pw060323p08q154	T20			
F08	tnfn1_pw060323p08q162	T20	-	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	transport
F09	tnfn1_pw060323p08q170	T20	-	conserved protein of unknown function	unknown function - conserved
F10	tnfn1_pw060323p08q178	<KAN-2>	coaE	dephospho-CoA kinase	cofactors, prosthetic groups, electron carriers metabolism
F11	tnfn1_pw060323p08q186	T20	isftu2	isftu2	IS element
F12	tnfn1_pw060323p08q194	T20	purE	N5-carboxyaminoimidazole ribonucleotide mutase	nucleotides and nucleosides metabolism
G01	tnfn1_pw060323p08q107	T20	cynT	carbonic anhydrase	other metabolism - degradation, utilization, assimilation
G02	tnfn1_pw060323p08q115	T18	-	hypothetical protein	hypothetical - novel
G03	tnfn1_pw060323p08q123	T20	-	4Fe-4S ferredoxin	energy metabolism
G04	tnfn1_pw060323p08q131	T20	-	glutathione peroxidase	post-translational modification, protein turnover, chaperones - protein modification
G05	tnfn1_pw060323p08q139	T20			
G06	tnfn1_pw060323p08q147	T20	-	hypothetical membrane protein	hypothetical - novel
G07	tnfn1_pw060323p08q155	T20	-	conserved protein of unknown function	unknown function - conserved
G08	tnfn1_pw060323p08q163	T20	hrpA	HrpA-like helicase	DNA replication, recombination, modification and repair
G09	tnfn1_pw060323p08q171	T20	-	zinc-binding alcohol dehydrogenase	carbohydrate metabolism
G10	tnfn1_pw060323p08q179	T18			
G11	tnfn1_pw060323p08q187	T20	-	DNA and RNA helicases Superfamily I protein	DNA replication, recombination, modification and repair - replication
G12	tnfn1_pw060323p08q195	T20	hemN	coproporphyrinogen III oxidase, anaerobic	cofactors, prosthetic groups, electron carriers metabolism
H01	tnfn1_pw060323p08q108	<KAN-2>	nuoL	NADH dehydrogenase I, L subunit	energy metabolism
H02	tnfn1_pw060323p08q116	T18			
H03	tnfn1_pw060323p08q124	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
H04	tnfn1_pw060323p08q132	T20	oppC	peptide/opine/nickel uptake transporter (PepT) family protein	transport
H05	tnfn1_pw060323p08q140	T20	-	GDSL-like lipolytic enzyme	fatty acids and lipids metabolism
H06	tnfn1_pw060323p08q148	T20	-	conserved protein of unknown function	unknown function - conserved
H07	tnfn1_pw060323p08q156	T20	glpK	glycerol kinase	other metabolism - degradation, utilization, assimilation
H08	tnfn1_pw060323p08q164	T20	-	Dam-replacing family protein	DNA replication, recombination, modification and repair - restriction/modification
H09	tnfn1_pw060323p08q172	<KAN-2>	-	rRNA methylase, SpoU family	translation, ribosomal structure and biogenesis
H10	tnfn1_pw060323p08q180	T18			
H11	tnfn1_pw060323p08q188	T20	-	conserved protein of unknown function	unknown function - conserved
H12	tnfn1_pw060323p08q196	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds

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

Table 2: Plate 8 (tnfn1_pw060323p08) – 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_pw060323p08q101	C	312189	FTN_0303	311969	312892	F	308	221(924)
A02	tnfn1_pw060323p08q109	C	681795	FTN_0643	681664	682170	F	169	132(507)
A03	tnfn1_pw060323p08q117	C	539635	intergenic					
A04	tnfn1_pw060323p08q125	C	1162230	FTN_1100	1161392	1162492	R	367	263(1101)
A05	tnfn1_pw060323p08q133	C	461507	FTN_0456	461255	463570	F	772	253(2316)
A06	tnfn1_pw060323p08q141	C	1074975	FTN_1015	1074646	1075146	R	167	172(501)
A07	tnfn1_pw060323p08q149	C	1432994	FTN_1355	1432777	1433544	F	256	218(768)
A08	tnfn1_pw060323p08q157	C	94857	FTN_0084	93832	96570	F	913	1026(2739)
A09	tnfn1_pw060323p08q165	C	1094674	FTN_1039	1094041	1097463	F	1141	634(3423)
A10	tnfn1_pw060323p08q173	C	104624	FTN_0093	104604	105116	F	171	21(513)
A11	tnfn1_pw060323p08q181	C	1479919	FTN_1401	1479437	1480069	F	211	483(633)
A12	tnfn1_pw060323p08q189	C	647740	FTN_0616	646972	648318	F	449	769(1347)
B01	tnfn1_pw060323p08q102	C	374122	FTN_0371	373472	374326	F	285	651(855)
B02	tnfn1_pw060323p08q110	C	294356	FTN_0286	294223	294783	F	187	134(561)
B03	tnfn1_pw060323p08q118	C	351735	FTN_0345	351044	352147	R	368	413(1104)
B04	tnfn1_pw060323p08q126	C	75004	FTN_0063	74362	75246	R	295	243(885)
B05	tnfn1_pw060323p08q134	C	1341484	FTN_1270	1341158	1341841	R	228	358(684)
B06	tnfn1_pw060323p08q142	C	1192037	FTN_1129	1191487	1192668	R	394	632(1182)
B07	tnfn1_pw060323p08q150	C	671651	FTN_0636	671002	672315	R	438	665(1314)
B09	tnfn1_pw060323p08q166	C	1300607	FTN_1232	1300558	1301340	F	261	50(783)
B10	tnfn1_pw060323p08q174	C	1000085	FTN_0939	1000022	1000177	R	52	93(156)
B11	tnfn1_pw060323p08q182	C	1479429	intergenic					
B12	tnfn1_pw060323p08q190	C	1002105	FTN_0943	1001822	1002259	R	146	155(438)
C01	tnfn1_pw060323p08q103	C	305323	FTN_0297	305086	305721	F	212	238(636)
C02	tnfn1_pw060323p08q111	C	171895	FTN_0157	171471	172004	R	178	110(534)
C03	tnfn1_pw060323p08q119	C	1252429	FTN_1179	1252082	1252978	F	299	348(897)
C04	tnfn1_pw060323p08q127	C	1680335	FTN_1583	1679893	1680654	R	254	320(762)
C05	tnfn1_pw060323p08q135	C	1725004	FTN_1615	1724061	1725338	R	426	335(1278)
C06	tnfn1_pw060323p08q143	C	1303954	FTN_1235	1303554	1304012	R	153	59(459)
C07	tnfn1_pw060323p08q151	C	1753512	FTN_1641	1753261	1754523	F	421	252(1263)
C08	tnfn1_pw060323p08q159	C	552164	FTN_0530	551516	552883	F	456	649(1368)
C09	tnfn1_pw060323p08q167	C	1862428	FTN_1735	1862274	1862681	F	136	155(408)
C10	tnfn1_pw060323p08q175	C	40916	FTN_0039	40656	41078	R	141	163(423)
C11	tnfn1_pw060323p08q183	C	721973	FTN_0678	721383	722594	R	404	622(1212)
C12	tnfn1_pw060323p08q191	C	1002105	FTN_0943	1001822	1002259	R	146	155(438)
D01	tnfn1_pw060323p08q104	C	401779	FTN_0402	400839	401894	R	352	116(1056)
D02	tnfn1_pw060323p08q112	C	1454944	FTN_1376	1454884	1455417	F	178	61(534)
D03	tnfn1_pw060323p08q120	C	19649	FTN_0020	18120	21401	R	1094	1753(3282)
D04	tnfn1_pw060323p08q128	U	543344	FTN_0523	543248	544063	F	272	97(816)
D05	tnfn1_pw060323p08q136	C	1008535	FTN_0952	1008165	1008644	R	160	110(480)
D06	tnfn1_pw060323p08q144	C	857228	-	856697	857561	R	288.3	334(865)
D07	tnfn1_pw060323p08q152	C	230829	FTN_0210	229966	231588	F	541	864(1623)
D08	tnfn1_pw060323p08q160	C	553908	FTN_0532	553648	554289	R	214	382(642)
D09	tnfn1_pw060323p08q168	C	1688997	FTN_1590	1688316	1689281	R	322	285(966)
D10	tnfn1_pw060323p08q176	C	897397	FTN_0841	897004	897678	F	225	394(675)
D11	tnfn1_pw060323p08q184	C	30800	intergenic					
D12	tnfn1_pw060323p08q192	C	1371422	FTN_1302	1370906	1371826	F	307	517(921)
E01	tnfn1_pw060323p08q105	C	380912	FTN_0379	380755	381126	F	124	158(372)
E02	tnfn1_pw060323p08q113	C	1076324	FTN_1017	1075884	1076462	F	193	441(579)
E03	tnfn1_pw060323p08q121	C	1454241	intergenic					
E04	tnfn1_pw060323p08q129	C	485082	FTN_0479	484555	485208	R	218	127(654)
E05	tnfn1_pw060323p08q137	C	1727089	FTN_1617	1726414	1727838	F	475	676(1425)
E06	tnfn1_pw060323p08q145	C	1292788	FTN_1221	1292193	1292858	R	222	71(666)
E07	tnfn1_pw060323p08q153	C	230829	FTN_0210	229966	231588	F	541	864(1623)
E08	tnfn1_pw060323p08q161	C	1109905	FTN_1050	1108915	1110222	R	436	318(1308)
E09	tnfn1_pw060323p08q169	C	1438451	FTN_1357	1435327	1438974	R	1216	524(3648)
E10	tnfn1_pw060323p08q177	C	1113426	FTN_1054	1113187	1113456	R	90	31(270)
E11	tnfn1_pw060323p08q185	C	1679487	FTN_1582	1679176	1679886	R	237	400(711)
E12	tnfn1_pw060323p08q193	C	417515	FTN_0419	417319	418359	F	347	197(1041)
F01	tnfn1_pw060323p08q106	C	858805	FTN_0801	858600	858947	R	116	143(348)
F02	tnfn1_pw060323p08q114	C	334852	FTN_0326	334524	335054	R	177	203(531)
F03	tnfn1_pw060323p08q122	C	1014196	FTN_0959	1013924	1014790	F	289	273(867)

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F04	tnfn1_pw060323p08q130	C	167751	FTN_0154	166433	167899	R	489	149(1467)
F05	tnfn1_pw060323p08q138	C	229391	FTN_0209	229107	229973	F	289	285(867)
F06	tnfn1_pw060323p08q146	C	338133	FTN_0331	337781	338464	R	228	332(684)
F07	tnfn1_pw060323p08q154	C	12924	intergenic					
F08	tnfn1_pw060323p08q162	C	163727	FTN_0151	163057	163836	R	260	110(780)
F09	tnfn1_pw060323p08q170	C	620544	FTN_0590	620283	621500	F	406	262(1218)
F10	tnfn1_pw060323p08q178	C	1592919	FTN_1496	1592378	1592989	F	204	542(612)
F11	tnfn1_pw060323p08q186	C	377566	-	377298	378154	F	285.6	269(857)
F12	tnfn1_pw060323p08q194	C	421624	FTN_0422	421370	421858	F	163	255(489)
G01	tnfn1_pw060323p08q107	C	1149883	FTN_1087	1149427	1150110	R	228	228(684)
G02	tnfn1_pw060323p08q115	C	580867	FTN_0556	580679	581239	F	187	189(561)
G03	tnfn1_pw060323p08q123	C	808079	FTN_0755	807847	808089	F	81	233(243)
G04	tnfn1_pw060323p08q131	U	741674	FTN_0698	741553	742020	F	156	122(468)
G05	tnfn1_pw060323p08q139	C	1845767	intergenic					
G06	tnfn1_pw060323p08q147	C	750274	FTN_0706	750173	750673	F	167	102(501)
G07	tnfn1_pw060323p08q155	C	1555019	FTN_1466	1554488	1555576	R	363	558(1089)
G08	tnfn1_pw060323p08q163	C	1515128	FTN_1432	1513195	1517211	R	1339	2084(4017)
G09	tnfn1_pw060323p08q171	C	1889572	FTN_1760	1889010	1889996	F	329	563(987)
G10	tnfn1_pw060323p08q179	C	172721	intergenic					
G11	tnfn1_pw060323p08q187	C	832715	FTN_0776	831494	833557	F	688	1222(2064)
G12	tnfn1_pw060323p08q195	C	1738529	FTN_1626	1738188	1739327	F	380	342(1140)
H01	tnfn1_pw060323p08q108	C	1783813	FTN_1669	1783789	1785795	R	669	1983(2007)
H02	tnfn1_pw060323p08q116	C	1272768	intergenic					
H03	tnfn1_pw060323p08q124	C	901006	FTN_0845	900621	901457	R	279	452(837)
H04	tnfn1_pw060323p08q132	C	1689832	FTN_1591	1689288	1690145	R	286	314(858)
H05	tnfn1_pw060323p08q140	C	1804143	FTN_1687	1803376	1804866	F	497	768(1491)
H06	tnfn1_pw060323p08q148	C	28353	FTN_0027	28044	28592	F	183	310(549)
H07	tnfn1_pw060323p08q156	C	1683684	FTN_1585	1682448	1683947	R	500	264(1500)
H08	tnfn1_pw060323p08q164	C	1816301	FTN_1698	1815852	1816619	R	256	319(768)
H09	tnfn1_pw060323p08q172	C	1365604	FTN_1294	1365139	1365879	R	247	276(741)
H10	tnfn1_pw060323p08q180	C	1216317	intergenic					
H11	tnfn1_pw060323p08q188	C	47203	FTN_0042	46882	47436	F	185	322(555)
H12	tnfn1_pw060323p08q196	U	555185	FTN_0533	554322	555512	R	397	328(1191)

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 8 (tnfn1_pw060323p08) – 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_pw060323p08q101	EXACT(0)	157	151	129	35	EXACT(0)	200	184	51
A02	tnfn1_pw060323p08q109	EXACT(0)	121	113	97	28	EXACT(0)	200	187	53
A03	tnfn1_pw060323p08q117	EXACT(0)	123	120	93	19	EXACT(0)	200	196	51
A04	tnfn1_pw060323p08q125	EXACT(0)	156	152	128	38	EXACT(0)	200	194	52
A05	tnfn1_pw060323p08q133	EXACT(0)	160	151	129	34	EXACT(0)	176	142	34
A06	tnfn1_pw060323p08q141	EXACT(0)	157	151	129	35	EXACT(0)	200	188	54
A07	tnfn1_pw060323p08q149	EXACT(0)	154	145	126	41	EXACT(0)	200	193	54
A08	tnfn1_pw060323p08q157	EXACT(0)	157	151	132	39	EXACT(0)	200	189	53
A09	tnfn1_pw060323p08q165	EXACT(0)	156	145	128	38	EXACT(0)	200	157	41
A10	tnfn1_pw060323p08q173	EXACT(0)	121	112	78	19	EXACT(0)	200	184	46
A11	tnfn1_pw060323p08q181	EXACT(0)	122	119	89	19	EXACT(0)	200	190	47
A12	tnfn1_pw060323p08q189	EXACT(0)	156	116	98	29	EXACT(0)	200	180	41
B01	tnfn1_pw060323p08q102	EXACT(0)	159	159	133	33	EXACT(0)	200	186	57
B02	tnfn1_pw060323p08q110	EXACT(0)	122	112	78	22	EXACT(0)	200	180	50
B03	tnfn1_pw060323p08q118	EXACT(0)	123	120	93	23	EXACT(0)	200	193	51
B04	tnfn1_pw060323p08q126	EXACT(0)	156	153	123	38	EXACT(0)	200	192	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	tnfn1_pw060323p08q134	EXACT(0)	157	153	131	38	EXACT(0)	200	184	44
B06	tnfn1_pw060323p08q142	EXACT(0)	157	153	131	36	EXACT(0)	200	176	54
B07	tnfn1_pw060323p08q150	EXACT(0)	157	152	133	37	EXACT(0)	200	192	55
B09	tnfn1_pw060323p08q166	EXACT(0)	156	152	112	27	EXACT(0)	200	184	51
B10	tnfn1_pw060323p08q174	EXACT(0)	122	106	86	25	EXACT(0)	200	181	47
B11	tnfn1_pw060323p08q182	EXACT(0)	123	119	92	30	EXACT(0)	200	183	50
B12	tnfn1_pw060323p08q190	EXACT(0)	154	139	107	29	EXACT(0)	200	183	55
C01	tnfn1_pw060323p08q103	EXACT(0)	159	152	137	37	EXACT(0)	200	190	47
C02	tnfn1_pw060323p08q111	EXACT(0)	123	113	81	21	EXACT(0)	200	172	55
C03	tnfn1_pw060323p08q119	EXACT(0)	122	118	94	31	EXACT(0)	200	193	54
C04	tnfn1_pw060323p08q127	EXACT(0)	157	153	131	39	EXACT(0)	200	195	53
C05	tnfn1_pw060323p08q135	EXACT(0)	155	151	130	31	EXACT(0)	200	191	44
C06	tnfn1_pw060323p08q143	EXACT(0)	155	145	123	35	EXACT(0)	200	186	57
C07	tnfn1_pw060323p08q151	EXACT(0)	155	152	131	40	EXACT(0)	200	191	57
C08	tnfn1_pw060323p08q159	EXACT(0)	158	152	144	33	EXACT(0)	200	189	51
C09	tnfn1_pw060323p08q167	EXACT(0)	154	152	68	16	EXACT(0)	200	187	52
C10	tnfn1_pw060323p08q175	EXACT(0)	121	112	96	28	EXACT(0)	133	127	52
C11	tnfn1_pw060323p08q183	EXACT(0)	123	109	63	16	EXACT(0)	201	158	30
C12	tnfn1_pw060323p08q191	EXACT(0)	157	152	120	32	EXACT(0)	200	183	58
D01	tnfn1_pw060323p08q104	EXACT(0)	155	145	129	40	EXACT(0)	200	164	34
D02	tnfn1_pw060323p08q112	EXACT(0)	124	120	85	24	EXACT(0)	200	189	55
D03	tnfn1_pw060323p08q120	EXACT(0)	124	119	84	23	EXACT(0)	200	194	51
D04	tnfn1_pw060323p08q128	EXACT(0)	157	145	133	37	EXACT(0)	200	185	61
D05	tnfn1_pw060323p08q136	EXACT(0)	156	153	123	35	EXACT(0)	200	180	56
D06	tnfn1_pw060323p08q144	EXACT(0)	155	152	131	32	EXACT(0)	200	185	52
D07	tnfn1_pw060323p08q152	EXACT(0)	155	151	121	25	EXACT(0)	200	194	50
D08	tnfn1_pw060323p08q160	EXACT(0)	156	152	129	29	EXACT(0)	200	178	55
D09	tnfn1_pw060323p08q168	EXACT(0)	156	152	128	37	EXACT(0)	200	194	55
D10	tnfn1_pw060323p08q176	EXACT(0)	122	125	99	28	EXACT(0)	200	176	37
D11	tnfn1_pw060323p08q184	EXACT(0)	121	83	59	24	EXACT(0)	200	161	43
D12	tnfn1_pw060323p08q192	EXACT(0)	157	152	129	33	EXACT(0)	200	181	56
E01	tnfn1_pw060323p08q105	EXACT(0)	158	152	138	39	EXACT(0)	172	159	52
E02	tnfn1_pw060323p08q113	EXACT(0)	124	120	67	21	EXACT(0)	200	175	51
E03	tnfn1_pw060323p08q121	EXACT(0)	123	120	102	27	EXACT(0)	200	145	36
E04	tnfn1_pw060323p08q129	EXACT(0)	156	152	128	39	EXACT(0)	200	146	40
E05	tnfn1_pw060323p08q137	EXACT(0)	156	153	129	39	EXACT(0)	200	191	55
E06	tnfn1_pw060323p08q145	EXACT(0)	157	145	139	38	EXACT(0)	200	196	52
E07	tnfn1_pw060323p08q153	EXACT(0)	155	151	127	37	EXACT(0)	200	194	52
E08	tnfn1_pw060323p08q161	EXACT(0)	153	139	120	42	EXACT(0)	139	136	53
E09	tnfn1_pw060323p08q169	EXACT(0)	156	153	132	42	EXACT(0)	156	145	54
E10	tnfn1_pw060323p08q177	EXACT(0)	112	111	65	21	EXACT(0)	192	154	21
E11	tnfn1_pw060323p08q185	EXACT(0)	123	119	95	35	EXACT(0)	200	181	56
E12	tnfn1_pw060323p08q193	EXACT(0)	156	152	133	38	EXACT(0)	187	178	49
F01	tnfn1_pw060323p08q106	EXACT(0)	157	153	127	32	EXACT(0)	200	187	50
F02	tnfn1_pw060323p08q114	EXACT(0)	124	115	89	23	EXACT(0)	200	189	51
F03	tnfn1_pw060323p08q122	ADJUSTED(7)	125	113	71	22	ESTIMATE(2)	198	190	52
F04	tnfn1_pw060323p08q130	EXACT(0)	156	153	126	39	EXACT(0)	200	187	50
F05	tnfn1_pw060323p08q138	EXACT(0)	157	152	130	39	EXACT(0)	200	174	44
F06	tnfn1_pw060323p08q146	EXACT(0)	156	152	134	36	EXACT(0)	200	179	48
F07	tnfn1_pw060323p08q154	EXACT(0)	156	152	125	34	EXACT(0)	200	188	57
F08	tnfn1_pw060323p08q162	EXACT(0)	156	152	125	37	EXACT(0)	200	179	54
F09	tnfn1_pw060323p08q170	EXACT(0)	155	145	118	33	EXACT(0)	200	181	49
F10	tnfn1_pw060323p08q178	EXACT(0)	124	113	94	28	EXACT(0)	200	194	52
F11	tnfn1_pw060323p08q186	EXACT(0)	157	145	131	34	EXACT(0)	199	164	38
F12	tnfn1_pw060323p08q194	EXACT(0)	157	153	127	38	EXACT(0)	200	197	55
G01	tnfn1_pw060323p08q107	EXACT(0)	155	146	127	39	EXACT(0)	200	189	54
G02	tnfn1_pw060323p08q115	EXACT(0)	123	118	91	25	EXACT(0)	200	192	52
G03	tnfn1_pw060323p08q123	EXACT(0)	156	151	124	39	EXACT(0)	200	185	42
G04	tnfn1_pw060323p08q131	EXACT(0)	157	153	143	49	EXACT(0)	200	187	67
G05	tnfn1_pw060323p08q139	EXACT(0)	156	153	126	39	EXACT(0)	200	172	54
G06	tnfn1_pw060323p08q147	EXACT(0)	156	139	113	32	EXACT(0)	200	177	53

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_pw060323p08q155	EXACT(0)	156	153	132	38	EXACT(0)	200	183	56
G08	tnfn1_pw060323p08q163	EXACT(0)	158	152	135	40	EXACT(0)	200	197	50
G09	tnfn1_pw060323p08q171	EXACT(0)	158	152	125	33	EXACT(0)	200	192	46
G10	tnfn1_pw060323p08q179	EXACT(0)	124	120	104	26	EXACT(0)	200	192	51
G11	tnfn1_pw060323p08q187	EXACT(0)	154	145	126	47	EXACT(0)	199	175	53
G12	tnfn1_pw060323p08q195	EXACT(0)	156	145	119	34	EXACT(0)	201	121	33
H01	tnfn1_pw060323p08q108	EXACT(0)	120	106	65	20	EXACT(0)	200	186	50
H02	tnfn1_pw060323p08q116	EXACT(0)	123	120	96	30	EXACT(0)	200	183	55
H03	tnfn1_pw060323p08q124	EXACT(0)	157	151	118	34	EXACT(0)	200	188	46
H04	tnfn1_pw060323p08q132	EXACT(0)	157	148	137	47	EXACT(0)	200	186	46
H05	tnfn1_pw060323p08q140	EXACT(0)	156	152	131	41	EXACT(0)	200	146	36
H06	tnfn1_pw060323p08q148	EXACT(0)	156	146	124	36	EXACT(0)	200	190	55
H07	tnfn1_pw060323p08q156	EXACT(0)	156	152	128	34	EXACT(0)	200	192	55
H08	tnfn1_pw060323p08q164	EXACT(0)	155	145	120	37	EXACT(0)	200	187	54
H09	tnfn1_pw060323p08q172	EXACT(0)	122	124	102	29	EXACT(0)	200	190	50
H10	tnfn1_pw060323p08q180	EXACT(0)	124	119	103	31	EXACT(0)	200	186	52
H11	tnfn1_pw060323p08q188	EXACT(0)	156	145	101	23	EXACT(0)	200	167	43
H12	tnfn1_pw060323p08q196	EXACT(0)	159	145	134	42	EXACT(0)	200	193	50

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