

***Francisella tularensis* subsp. *novicida*  
“Two-Allele” Transposon Mutant Library,  
Plate 13 (tnfn1\_pw060328p05)**

**Catalog No. NR-51295**

**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-51295 represents plate 13 (tnfn1\_pw060328p05) 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-51295 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 13 (tnfn1\_pw060328p05), NR-51295.”

**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 13 (tnfn1\_pw060328p05) – Transposon Type and Mutated Gene<sup>1</sup>**

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060328p05q101	T20	gdhA	glutamate dehydrogenase (NADP+)	amino acid metabolism - biosynthesis
A02	tnfn1_pw060328p05q109	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
A03	tnfn1_pw060328p05q117	T20	ilvN	acetolactate synthase small subunit	amino acid metabolism - biosynthesis
A04	tnfn1_pw060328p05q125	<KAN-2>	-	protein of unknown function	unknown function - novel
A05	tnfn1_pw060328p05q133	T18	-	hypothetical protein	hypothetical - novel
A06	tnfn1_pw060328p05q141	T18	-	conserved hypothetical protein	hypothetical - conserved
A07	tnfn1_pw060328p05q149	T20	wbtP	galactosyl transferase	cell wall / LPS / capsule
A08	tnfn1_pw060328p05q157	T20	-	pseudogene: hypothetical membrane protein, fragment	pseudogene
A09	tnfn1_pw060328p05q165	T20	-	hypothetical protein	hypothetical - novel
A10	tnfn1_pw060328p05q173	T20	nadE	NAD synthase	cofactors, prosthetic groups, electron carriers metabolism
A11	tnfn1_pw060328p05q181	T20	-	hypothetical membrane protein	hypothetical - novel
A12	tnfn1_pw060328p05q189	<KAN-2>	-	conserved hypothetical protein	hypothetical - conserved
B01	tnfn1_pw060328p05q102	T20	-	MutT/nudix family protein	putative enzymes
B02	tnfn1_pw060328p05q110	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
B03	tnfn1_pw060328p05q118	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - repair
B04	tnfn1_pw060328p05q126	<KAN-2>	-	protein of unknown function	unknown function - novel
B05	tnfn1_pw060328p05q134	T18	-	-	-
B06	tnfn1_pw060328p05q142	T18	-	conserved hypothetical protein	hypothetical - conserved
B07	tnfn1_pw060328p05q150	T20	frgA	siderophore biosynthesis protein	other metabolism - biosynthesis
B08	tnfn1_pw060328p05q158	T20	-	sulfate permease family protein	transport
B09	tnfn1_pw060328p05q166	T20	ribH	riboflavin synthase beta-chain	cofactors, prosthetic groups, electron carriers metabolism
B10	tnfn1_pw060328p05q174	T20	-	4Fe-4S ferredoxin	energy metabolism
B11	tnfn1_pw060328p05q182	T20	nhaD	Na <sup>+</sup> :H <sup>+</sup> antiporter	transport
B12	tnfn1_pw060328p05q190	<KAN-2>	bfr	bacterioferritin	energy metabolism
C01	tnfn1_pw060328p05q103	T20	nfnB	dihydropteridine reductase	energy metabolism
C02	tnfn1_pw060328p05q111	T20	-	hypothetical membrane protein	hypothetical - novel
C03	tnfn1_pw060328p05q119	T20	-	membrane protein of unknown function	unknown function - novel
C04	tnfn1_pw060328p05q127	<KAN-2>	-	-	-
C05	tnfn1_pw060328p05q135	T18	-	hypothetical protein	hypothetical - novel
C07	tnfn1_pw060328p05q151	T20	-	histidine acid phosphatase	putative enzymes
C08	tnfn1_pw060328p05q159	T20	-	serine peptidase, S49 family	post-translational modification, protein turnover, chaperones
C09	tnfn1_pw060328p05q167	T20	htpX	Zn-dependent protease with chaperone function	post-translational modification, protein turnover, chaperones - chaperones
C10	tnfn1_pw060328p05q175	T20	-	dehydrogenase	putative enzymes
C11	tnfn1_pw060328p05q183	<KAN-2>	secG	preprotein translocase, subunit G, membrane protein	motility, attachment and secretion structure
C12	tnfn1_pw060328p05q191	<KAN-2>	feoB	ferrous iron transport protein B	transport
D01	tnfn1_pw060328p05q104	T20	udp	uridine phosphorylase	other metabolism - degradation, utilization, assimilation
D02	tnfn1_pw060328p05q112	T20	murC	UDP-N-acetylmuramate-alanine ligase	cell wall / LPS / capsule
D03	tnfn1_pw060328p05q120	T20	dnaJ	chaperone, DnaJ family, with C-terminal Zn finger domain	post-translational modification, protein turnover, chaperones
D04	tnfn1_pw060328p05q128	<KAN-2>	fbaA	fructose bisphosphate aldolase Class II	energy metabolism
D05	tnfn1_pw060328p05q136	T18	-	conserved hypothetical protein	hypothetical - conserved
D06	tnfn1_pw060328p05q144	T18	-	hypothetical protein	hypothetical - novel
D07	tnfn1_pw060328p05q152	T20	cysC	adenylylsulfate kinase	other metabolism - degradation, utilization, assimilation
D08	tnfn1_pw060328p05q160	T20	dapB	dihydrodipicolinate reductase	amino acid metabolism - biosynthesis
D09	tnfn1_pw060328p05q168	T20	gplX	fructose 1,6-bisphosphatase II	energy metabolism
D10	tnfn1_pw060328p05q176	T20	-	protein of unknown function	unknown function - novel

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D11	tnfn1_pw060328p05q184	<KAN-2>	-	LemA-like protein	putative enzymes
D12	tnfn1_pw060328p05q192	T18	-	conserved protein of unknown function	unknown function - conserved
E01	tnfn1_pw060328p05q105	T20	-	peptidase, U32 family	post-translational modification, protein turnover, chaperones - protein degradation
E02	tnfn1_pw060328p05q113	T20	recO	RecFOR complex, RecO component	DNA replication, recombination, modification and repair - restriction/modification
E03	tnfn1_pw060328p05q121	T20	-	restriction endonuclease	DNA replication, recombination, modification and repair - restriction/modification
E04	tnfn1_pw060328p05q129	<KAN-2>	groEL	chaperonin GroEL (HSP60 family)	post-translational modification, protein turnover, chaperones - chaperones
E05	tnfn1_pw060328p05q137	T18	ftsA	cell division protein FtsA	cell cycle
E06	tnfn1_pw060328p05q145	T18	-	protein of unknown function	unknown function - novel
E07	tnfn1_pw060328p05q153	T20	-	conserved protein of unknown function	unknown function - conserved
E08	tnfn1_pw060328p05q161	T20	rsuA	16S rRNA pseudouridine synthase	translation, ribosomal structure and biogenesis
E09	tnfn1_pw060328p05q169	T20	hitA	histidine triad (HIT) family protein	putative enzymes
E10	tnfn1_pw060328p05q177	T20	-	chitin-binding protein	putative enzymes
E11	tnfn1_pw060328p05q185	<KAN-2>	-	protein of unknown function	unknown function - novel
E12	tnfn1_pw060328p05q193	T18	nupC1	nucleoside permease NUP family protein	transport
F01	tnfn1_pw060328p05q106	T20	udp	uridine phosphorylase	other metabolism - degradation, utilization, assimilation
F02	tnfn1_pw060328p05q114	T20	-	short-chain dehydrogenase	other metabolism - degradation, utilization, assimilation
F03	tnfn1_pw060328p05q122	T20	-	small conductance mechanosensitive ion channel (MscS) family protein	transport
F04	tnfn1_pw060328p05q130	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
F05	tnfn1_pw060328p05q138	T18	-	flavodoxin, related to tryptophan repressor binding protein	putative enzymes
F06	tnfn1_pw060328p05q146	T20	pilF	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
F07	tnfn1_pw060328p05q154	T20	trpG	anthranilate synthase component II	amino acid metabolism - biosynthesis
F08	tnfn1_pw060328p05q162	T20	-	serine-type D-Ala-D-Ala carboxypeptidase	cell wall / LPS / capsule
F09	tnfn1_pw060328p05q170	T20	leuC	isopropylmalate isomerase	amino acid metabolism - biosynthesis
F10	tnfn1_pw060328p05q178	T20	-	hypothetical protein	hypothetical - novel
F11	tnfn1_pw060328p05q186	<KAN-2>	-	protein of unknown function	unknown function - novel
F12	tnfn1_pw060328p05q194	T18	-	pseudogene: O-methyltransferase	pseudogene
G01	tnfn1_pw060328p05q107	T20	betT	betaine/carnitine/choline transporter (BCCT) family protein	transport
G02	tnfn1_pw060328p05q115	T20	-	acetoacetate decarboxylase	other metabolism - biosynthesis
G03	tnfn1_pw060328p05q123	T20	-	predicted Co/Zn/Cd cation transporter	transport
G04	tnfn1_pw060328p05q131	T18	folD	methyleneTHF enzyme/ methenyltetrahydrofolate cyclohydrolase/ methylenetetrahydrofolate dehydrogenase	amino acid metabolism - degradation, utilization, assimilation
G05	tnfn1_pw060328p05q139	T18	-	conserved protein of unknown function	unknown function - conserved
G06	tnfn1_pw060328p05q147	T20	-		
G07	tnfn1_pw060328p05q155	T20	prmA	50S ribosomal protein L11, methyltransferase	translation, ribosomal structure and biogenesis
G08	tnfn1_pw060328p05q163	T20	tdk	thymidine kinase	nucleotides and nucleosides metabolism
G09	tnfn1_pw060328p05q171	T20	-	glucokinase regulatory protein	signal transduction and regulation
G10	tnfn1_pw060328p05q179	T20	polA	DNA polymerase I	DNA replication, recombination, modification and repair - restriction/modification
G11	tnfn1_pw060328p05q187	<KAN-2>	-	hydrolase, HD superfamily	putative enzymes
G12	tnfn1_pw060328p05q195	T18	-		
H01	tnfn1_pw060328p05q108	T20	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	cofactors, prosthetic groups, electron carriers metabolism
H02	tnfn1_pw060328p05q116	T20	-	acetyltransferase	putative enzymes
H03	tnfn1_pw060328p05q124	<KAN-2>	-	protein of unknown function	unknown function - novel
H04	tnfn1_pw060328p05q132	T18	-	protein of unknown function	unknown function - novel
H05	tnfn1_pw060328p05q140	T18	mutT	mutator protein	DNA replication, recombination, modification and repair - restriction/modification
H06	tnfn1_pw060328p05q148	T20	nudH	dGTP pyrophosphohydrolase	DNA replication, recombination, modification and repair - restriction/modification
H07	tnfn1_pw060328p05q156	T20	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	cofactors, prosthetic groups, electron carriers metabolism
H08	tnfn1_pw060328p05q164	T20	uvrD	DNA helicase II	DNA replication, recombination, modification and repair - restriction/modification
H09	tnfn1_pw060328p05q172	T20	-	drug:H <sup>+</sup> antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
H10	tnfn1_pw060328p05q180	T20	-	conserved hypothetical protein	hypothetical - conserved
H11	tnfn1_pw060328p05q188	<KAN-2>	pnp	polyribonucleotide nucleotidyltransferase	translation, ribosomal structure and biogenesis
H12	tnfn1_pw060328p05q196	T18	isftu2		IS element

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

Table 2: Plate 13 (tnfn1\_pw060328p05) – 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_pw060328p05q101	C	1629643	FTN_1532	1629170	1630516	F	449	474(1347)
A02	tnfn1_pw060328p05q109	C	800562	FTN_0747	800413	802020	F	536	150(1608)
A03	tnfn1_pw060328p05q117	C	1098817	FTN_1041	1098659	1098973	R	105	157(315)
A04	tnfn1_pw060328p05q125	C	910814	FTN_0855	910576	911262	F	229	239(687)
A05	tnfn1_pw060328p05q133	C	774809	FTN_0719	774796	774996	R	67	188(201)
A06	tnfn1_pw060328p05q141	C	744458	FTN_0701	744311	744955	F	215	148(645)
A07	tnfn1_pw060328p05q149	C	1509463	FTN_1429	1509260	1509886	R	209	424(627)
A08	tnfn1_pw060328p05q157	C	1458608	FTN_1379	1457975	1459691	R	572.3	1084(1717)
A09	tnfn1_pw060328p05q165	C	363276	FTN_0360	363126	363353	F	76	151(228)
A10	tnfn1_pw060328p05q173	C	1351746	FTN_1278	1351324	1352070	F	249	423(747)
A11	tnfn1_pw060328p05q181	C	1766671	FTN_1653	1766277	1766705	R	143	35(429)
A12	tnfn1_pw060328p05q189	C	1430491	FTN_1351	1430157	1430870	F	238	335(714)
B01	tnfn1_pw060328p05q102	C	241411	FTN_0219	241266	241640	F	125	146(375)
B02	tnfn1_pw060328p05q110	C	1208514	FTN_1143	1207355	1210072	R	906	1559(2718)
B03	tnfn1_pw060328p05q118	C	1221884	FTN_1154	1220796	1222016	R	407	133(1221)
B04	tnfn1_pw060328p05q126	C	885812	FTN_0828	885562	885984	R	141	173(423)
B05	tnfn1_pw060328p05q134	C	887493	intergenic					
B06	tnfn1_pw060328p05q142	C	1187429	FTN_1123	1187288	1187590	F	101	142(303)
B07	tnfn1_pw060328p05q150	C	1796376	FTN_1682	1796074	1797990	F	639	303(1917)
B08	tnfn1_pw060328p05q158	C	675271	FTN_0638	674546	676087	F	514	726(1542)
B09	tnfn1_pw060328p05q166	C	122517	FTN_0111	122336	122776	R	147	260(441)
B10	tnfn1_pw060328p05q174	C	807962	FTN_0755	807847	808089	F	81	116(243)
B11	tnfn1_pw060328p05q182	C	1829334	FTN_1707	1829332	1830756	F	475	3(1425)
B12	tnfn1_pw060328p05q190	C	1487719	FTN_1410	1487622	1488059	F	146	98(438)
C01	tnfn1_pw060328p05q103	C	240898	FTN_0218	240476	241126	R	217	229(651)
C02	tnfn1_pw060328p05q111	C	1504856	FTN_1424	1503994	1505283	R	430	428(1290)
C03	tnfn1_pw060328p05q119	C	444002	FTN_0444	443654	445324	F	557	349(1671)
C04	tnfn1_pw060328p05q127	C	981935	intergenic					
C05	tnfn1_pw060328p05q135	C	820958	FTN_0764	820728	821078	R	117	121(351)
C07	tnfn1_pw060328p05q151	C	23623	FTN_0022	22992	24044	F	351	632(1053)
C08	tnfn1_pw060328p05q159	C	130082	FTN_0118	129531	130451	F	307	552(921)
C09	tnfn1_pw060328p05q167	C	389760	FTN_0390	389099	390163	R	355	404(1065)
C10	tnfn1_pw060328p05q175	C	1018733	FTN_0964	1018209	1019321	R	371	589(1113)
C11	tnfn1_pw060328p05q183	C	1741052	FTN_1630	1740964	1741314	R	117	263(351)
C12	tnfn1_pw060328p05q191	C	80179	FTN_0066	79071	81317	R	749	1139(2247)
D01	tnfn1_pw060328p05q104	C	691694	FTN_0652	691457	692257	R	267	564(801)
D02	tnfn1_pw060328p05q112	C	89606	FTN_0079	89393	90745	F	451	214(1353)
D03	tnfn1_pw060328p05q120	C	1355796	FTN_1283	1354992	1356176	R	395	381(1185)
D04	tnfn1_pw060328p05q128	C	1408561	FTN_1329	1407743	1408804	R	354	244(1062)
D05	tnfn1_pw060328p05q136	C	385135	FTN_0384	385020	385376	R	119	242(357)
D06	tnfn1_pw060328p05q144	C	1457595	FTN_1378	1457390	1457926	F	179	206(537)
D07	tnfn1_pw060328p05q152	C	983754	FTN_0926	983655	984254	R	200	501(600)
D08	tnfn1_pw060328p05q160	C	1857249	FTN_1729	1856806	1857474	R	223	226(669)
D09	tnfn1_pw060328p05q168	C	306198	FTN_0298	305744	306727	F	328	455(984)
D10	tnfn1_pw060328p05q176	C	1448079	FTN_1367	1447268	1448899	R	544	821(1632)
D11	tnfn1_pw060328p05q184	C	390681	FTN_0391	390170	390742	R	191	62(573)
D12	tnfn1_pw060328p05q192	C	249049	FTN_0225	248455	249375	R	307	327(921)
E01	tnfn1_pw060328p05q105	C	1826931	FTN_1705	1826603	1827931	F	443	329(1329)
E02	tnfn1_pw060328p05q113	C	1309962	FTN_1243	1309687	1310382	R	232	421(696)
E03	tnfn1_pw060328p05q121	C	1578358	FTN_1487	1577096	1579960	R	955	1603(2865)
E04	tnfn1_pw060328p05q129	C	1636954	FTN_1538	1636884	1638515	R	544	1562(1632)
E05	tnfn1_pw060328p05q137	C	177968	FTN_0163	176722	177981	F	420	1247(1260)
E06	tnfn1_pw060328p05q145	C	713231	FTN_0670	712906	713352	R	149	122(447)
E07	tnfn1_pw060328p05q153	C	1085116	FTN_1028	1084814	1085557	R	248	442(744)
E08	tnfn1_pw060328p05q161	C	1003357	FTN_0945	1002665	1003477	R	271	121(813)
E09	tnfn1_pw060328p05q169	C	464838	FTN_0458	464768	465103	R	112	266(336)
E10	tnfn1_pw060328p05q177	C	1266701	FTN_1192	1265920	1267707	F	596	782(1788)
E11	tnfn1_pw060328p05q185	C	1862049	FTN_1734	1861861	1862250	F	130	189(390)
E12	tnfn1_pw060328p05q193	C	1701856	FTN_1600	1701111	1702307	R	399	452(1197)
F01	tnfn1_pw060328p05q106	C	691694	FTN_0652	691457	692257	R	267	564(801)
F02	tnfn1_pw060328p05q114	C	1251632	FTN_1178	1251247	1251966	R	240	335(720)
F03	tnfn1_pw060328p05q122	C	1679097	FTN_1581	1678701	1679195	R	165	99(495)



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>
F04	tnfn1_pw060328p05q130	C	556524	FTN_0534	555784	556824	F	347	741(1041)
F05	tnfn1_pw060328p05q138	C	1353043	FTN_1280	1352702	1353265	R	188	223(564)
F06	tnfn1_pw060328p05q146	C	1003860	FTN_0946	1003473	1004375	R	301	516(903)
F07	tnfn1_pw060328p05q154	C	1905674	FTN_1777	1905303	1905878	R	192	205(576)
F08	tnfn1_pw060328p05q162	C	670866	FTN_0635	669592	670983	R	464	118(1392)
F09	tnfn1_pw060328p05q170	C	72065	FTN_0061	71360	72766	R	469	702(1407)
F10	tnfn1_pw060328p05q178	C	1127663	FTN_1068	1127581	1128000	F	140	83(420)
F11	tnfn1_pw060328p05q186	C	1340685	FTN_1269	1340467	1341162	F	232	219(696)
F12	tnfn1_pw060328p05q194	C	1877068	FTN_1746	1876485	1877140	R	218.6	73(656)
G01	tnfn1_pw060328p05q107	C	823955	FTN_0767	823200	825149	F	650	756(1950)
G02	tnfn1_pw060328p05q115	U	865583	FTN_0808	865255	865992	R	246	410(738)
G03	tnfn1_pw060328p05q123	C	781432	FTN_0728	780666	781802	F	379	767(1137)
G04	tnfn1_pw060328p05q131	U	416617	FTN_0417	415800	416645	F	282	818(846)
G05	tnfn1_pw060328p05q139	C	807109	FTN_0753	806791	807339	F	183	319(549)
G06	tnfn1_pw060328p05q147	C	962846	intergenic					
G07	tnfn1_pw060328p05q155	C	1043803	FTN_0988	1043408	1044250	R	281	448(843)
G08	tnfn1_pw060328p05q163	C	1120193	FTN_1060	1119781	1120371	R	197	179(591)
G09	tnfn1_pw060328p05q171	C	1599207	FTN_1504	1598661	1599542	R	294	336(882)
G10	tnfn1_pw060328p05q179	C	1706947	FTN_1604	1705069	1707759	R	897	813(2691)
G11	tnfn1_pw060328p05q187	C	435580	FTN_0437	435345	435932	F	196	236(588)
G12	tnfn1_pw060328p05q195	C	133794	intergenic					
H01	tnfn1_pw060328p05q108	C	873189	FTN_0816	872849	874177	F	443	341(1329)
H02	tnfn1_pw060328p05q116	C	324169	FTN_0313	323976	324464	F	163	194(489)
H03	tnfn1_pw060328p05q124	C	1452894	FTN_1372	1451963	1453045	R	361	152(1083)
H04	tnfn1_pw060328p05q132	C	1163382	FTN_1101	1162960	1163790	R	277	409(831)
H05	tnfn1_pw060328p05q140	C	919105	FTN_0865	918875	919291	R	139	187(417)
H06	tnfn1_pw060328p05q148	C	1651409	FTN_1553	1651200	1651661	R	154	253(462)
H07	tnfn1_pw060328p05q156	C	1431011	FTN_1352	1430875	1431669	F	265	137(795)
H08	tnfn1_pw060328p05q164	C	1694640	FTN_1594	1692877	1695096	R	740	457(2220)
H09	tnfn1_pw060328p05q172	C	1828848	FTN_1706	1827979	1829157	R	393	310(1179)
H10	tnfn1_pw060328p05q180	C	223280	FTN_0201	222642	223334	R	231	55(693)
H11	tnfn1_pw060328p05q188	C	643601	FTN_0609	641862	643940	F	693	1740(2079)
H12	tnfn1_pw060328p05q196	C	378090	-	377298	378154	F	285.6	793(857)

<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 13 (tnfn1\_pw060328p05) – 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_pw060328p05q101	EXACT(0)	157	146	138	40	EXACT(0)	200	197	59
A02	tnfn1_pw060328p05q109	EXACT(0)	157	151	126	36	EXACT(0)	200	172	40
A03	tnfn1_pw060328p05q117	EXACT(0)	156	153	122	36	EXACT(0)	200	183	59
A04	tnfn1_pw060328p05q125	EXACT(0)	122	120	102	35	EXACT(0)	196	177	48
A05	tnfn1_pw060328p05q133	EXACT(0)	123	106	82	23	EXACT(0)	200	188	56
A06	tnfn1_pw060328p05q141	EXACT(0)	122	112	91	25	EXACT(0)	200	181	53
A07	tnfn1_pw060328p05q149	EXACT(0)	155	138	118	35	EXACT(0)	200	194	51
A08	tnfn1_pw060328p05q157	EXACT(0)	157	153	118	32	EXACT(0)	200	182	57
A09	tnfn1_pw060328p05q165	EXACT(0)	155	153	129	41	EXACT(0)	200	192	59
A10	tnfn1_pw060328p05q173	EXACT(0)	156	153	126	38	EXACT(0)	200	193	48
A11	tnfn1_pw060328p05q181	EXACT(0)	156	145	118	37	EXACT(0)	200	185	58
A12	tnfn1_pw060328p05q189	EXACT(0)	122	121	100	34	EXACT(0)	200	192	57
B01	tnfn1_pw060328p05q102	EXACT(0)	155	153	132	38	EXACT(0)	200	194	57
B02	tnfn1_pw060328p05q110	EXACT(0)	155	153	129	40	EXACT(0)	200	194	57
B03	tnfn1_pw060328p05q118	EXACT(0)	157	153	130	41	EXACT(0)	200	186	54
B04	tnfn1_pw060328p05q126	EXACT(0)	109	112	74	28	EXACT(0)	200	189	58
B05	tnfn1_pw060328p05q134	EXACT(0)	123	120	93	25	EXACT(0)	200	184	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
B06	tnfn1_pw060328p05q142	EXACT(0)	123	119	103	30	EXACT(0)	101	96	49
B07	tnfn1_pw060328p05q150	EXACT(0)	155	142	100	28	EXACT(0)	200	140	40
B08	tnfn1_pw060328p05q158	EXACT(0)	155	145	126	41	EXACT(0)	200	187	57
B09	tnfn1_pw060328p05q166	EXACT(0)	156	153	123	40	EXACT(0)	200	193	57
B10	tnfn1_pw060328p05q174	EXACT(0)	158	146	134	43	EXACT(0)	200	189	58
B11	tnfn1_pw060328p05q182	EXACT(0)	155	152	110	28	EXACT(0)	200	175	57
B12	tnfn1_pw060328p05q190	EXACT(0)	121	106	64	21	EXACT(0)	200	190	46
C01	tnfn1_pw060328p05q103	EXACT(0)	157	153	124	33	EXACT(0)	200	183	55
C02	tnfn1_pw060328p05q111	EXACT(0)	156	138	99	27	EXACT(0)	200	175	52
C03	tnfn1_pw060328p05q119	EXACT(0)	156	153	131	40	EXACT(0)	200	196	52
C04	tnfn1_pw060328p05q127	EXACT(0)	124	109	84	22	EXACT(0)	200	184	46
C05	tnfn1_pw060328p05q135	EXACT(0)	124	120	98	27	EXACT(0)	200	198	52
C07	tnfn1_pw060328p05q151	EXACT(0)	154	139	128	34	EXACT(0)	200	193	52
C08	tnfn1_pw060328p05q159	EXACT(0)	155	145	126	42	EXACT(0)	200	194	55
C09	tnfn1_pw060328p05q167	EXACT(0)	156	153	123	37	EXACT(0)	200	195	56
C10	tnfn1_pw060328p05q175	EXACT(0)	155	138	113	30	EXACT(0)	200	194	52
C11	tnfn1_pw060328p05q183	EXACT(0)	123	121	84	21	EXACT(0)	200	199	52
C12	tnfn1_pw060328p05q191	EXACT(0)	115	112	102	34	EXACT(0)	200	192	52
D01	tnfn1_pw060328p05q104	EXACT(0)	158	151	140	43	EXACT(0)	200	195	53
D02	tnfn1_pw060328p05q112	EXACT(0)	155	145	117	33	EXACT(0)	200	196	57
D03	tnfn1_pw060328p05q120	EXACT(0)	155	145	120	34	EXACT(0)	200	192	53
D04	tnfn1_pw060328p05q128	EXACT(0)	120	112	99	31	EXACT(0)	199	155	40
D05	tnfn1_pw060328p05q136	EXACT(0)	123	109	69	17	EXACT(0)	183	168	46
D06	tnfn1_pw060328p05q144	EXACT(0)	121	112	78	23	EXACT(0)	200	189	49
D07	tnfn1_pw060328p05q152	EXACT(0)	156	142	84	16	ESTIMATE(145)	54	42	28
D08	tnfn1_pw060328p05q160	EXACT(0)	154	151	122	40	EXACT(0)	200	191	55
D09	tnfn1_pw060328p05q168	EXACT(0)	155	139	128	43	EXACT(0)	200	194	51
D10	tnfn1_pw060328p05q176	EXACT(0)	156	153	132	40	EXACT(0)	199	172	46
D11	tnfn1_pw060328p05q184	EXACT(0)	121	112	96	27	EXACT(0)	200	153	36
D12	tnfn1_pw060328p05q192	EXACT(0)	123	119	98	28	EXACT(0)	200	192	54
E01	tnfn1_pw060328p05q105	EXACT(0)	156	153	132	39	EXACT(0)	200	194	57
E02	tnfn1_pw060328p05q113	EXACT(0)	155	146	124	37	EXACT(0)	200	181	58
E03	tnfn1_pw060328p05q121	EXACT(0)	155	145	123	38	EXACT(0)	200	190	56
E04	tnfn1_pw060328p05q129	EXACT(0)	123	120	83	22	EXACT(0)	200	193	54
E05	tnfn1_pw060328p05q137	EXACT(0)	122	119	92	29	EXACT(0)	200	186	57
E06	tnfn1_pw060328p05q145	EXACT(0)	124	112	97	24	EXACT(0)	200	180	47
E07	tnfn1_pw060328p05q153	EXACT(0)	156	153	135	42	EXACT(0)	200	188	48
E08	tnfn1_pw060328p05q161	EXACT(0)	155	145	123	40	EXACT(0)	200	194	57
E09	tnfn1_pw060328p05q169	EXACT(0)	154	145	121	39	EXACT(0)	161	152	53
E10	tnfn1_pw060328p05q177	EXACT(0)	156	153	126	38	EXACT(0)	200	195	58
E11	tnfn1_pw060328p05q185	EXACT(0)	117	112	102	40	EXACT(0)	200	188	56
E12	tnfn1_pw060328p05q193	EXACT(0)	123	112	98	27	EXACT(0)	200	169	42
F01	tnfn1_pw060328p05q106	EXACT(0)	157	152	136	42	EXACT(0)	200	183	41
F02	tnfn1_pw060328p05q114	EXACT(0)	156	146	127	36	EXACT(0)	200	194	54
F03	tnfn1_pw060328p05q122	EXACT(0)	156	146	127	44	EXACT(0)	200	187	60
F04	tnfn1_pw060328p05q130	EXACT(0)	123	118	99	29	EXACT(0)	198	91	27
F05	tnfn1_pw060328p05q138	EXACT(0)	123	112	101	37	EXACT(0)	200	191	58
F06	tnfn1_pw060328p05q146	EXACT(0)	155	146	118	34	EXACT(0)	200	185	57
F07	tnfn1_pw060328p05q154	EXACT(0)	155	145	129	44	EXACT(0)	200	181	58
F08	tnfn1_pw060328p05q162	EXACT(0)	154	152	120	36	EXACT(0)	200	188	53
F09	tnfn1_pw060328p05q170	EXACT(0)	157	146	126	40	EXACT(0)	200	193	56
F10	tnfn1_pw060328p05q178	EXACT(0)	155	145	120	39	EXACT(0)	200	172	58
F11	tnfn1_pw060328p05q186	EXACT(0)	122	113	70	22	EXACT(0)	200	188	56
F12	tnfn1_pw060328p05q194	EXACT(0)	123	120	87	26	EXACT(0)	200	191	51
G01	tnfn1_pw060328p05q107	EXACT(0)	156	150	126	39	EXACT(0)	200	187	57
G02	tnfn1_pw060328p05q115	EXACT(0)	154	145	126	41	EXACT(0)	200	195	60
G03	tnfn1_pw060328p05q123	EXACT(0)	154	145	117	33	EXACT(0)	202	137	25
G04	tnfn1_pw060328p05q131	EXACT(0)	126	120	96	23	EXACT(0)	200	195	37
G05	tnfn1_pw060328p05q139	EXACT(0)	123	113	99	22	EXACT(0)	200	194	50
G06	tnfn1_pw060328p05q147	EXACT(0)	156	153	138	39	EXACT(0)	200	184	64
G07	tnfn1_pw060328p05q155	EXACT(0)	155	146	127	41	EXACT(0)	200	193	59
G08	tnfn1_pw060328p05q163	EXACT(0)	156	152	131	41	EXACT(0)	200	191	56

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
G09	tnfn1_pw060328p05q171	EXACT(0)	157	153	128	37	EXACT(0)	200	193	58
G10	tnfn1_pw060328p05q179	EXACT(0)	155	152	119	33	EXACT(0)	200	190	56
G11	tnfn1_pw060328p05q187	EXACT(0)	121	112	96	26	EXACT(0)	200	159	34
G12	tnfn1_pw060328p05q195	EXACT(0)	123	112	83	21	EXACT(0)	200	187	49
H01	tnfn1_pw060328p05q108	EXACT(0)	156	152	131	39	EXACT(0)	200	192	58
H02	tnfn1_pw060328p05q116	EXACT(0)	156	151	105	29	EXACT(0)	200	185	52
H03	tnfn1_pw060328p05q124	EXACT(0)	121	117	96	38	EXACT(0)	200	186	57
H04	tnfn1_pw060328p05q132	EXACT(0)	123	113	97	31	EXACT(0)	200	193	54
H05	tnfn1_pw060328p05q140	EXACT(0)	123	120	93	22	EXACT(0)	200	185	56
H06	tnfn1_pw060328p05q148	EXACT(0)	156	152	124	39	EXACT(0)	200	198	53
H07	tnfn1_pw060328p05q156	EXACT(0)	155	145	126	39	EXACT(0)	194	190	49
H08	tnfn1_pw060328p05q164	EXACT(0)	155	145	129	43	EXACT(0)	197	180	54
H09	tnfn1_pw060328p05q172	EXACT(0)	155	145	114	37	EXACT(0)	200	190	54
H10	tnfn1_pw060328p05q180	EXACT(0)	155	152	128	42	EXACT(0)	200	189	55
H11	tnfn1_pw060328p05q188	EXACT(0)	122	121	100	29	EXACT(0)	200	188	51
H12	tnfn1_pw060328p05q196	EXACT(0)	123	120	95	26	EXACT(0)	200	186	54

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