

***Francisella tularensis* subsp. *novicida*
“Two-Allele” Transposon Mutant Library,
Plate 27 (tnfn1_pw060420p03)**

Catalog No. NR-51309

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-51309 represents plate 27 (tnfn1_pw060420p03) 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-51309 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 27 (tnfn1_pw060420p03), NR-51309.”

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 27 (tnfn1_pw060420p03) – Transposon Type and Mutated Gene¹

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060420p03q101	T20	-	predicted metal-dependent hydrolase	putative enzymes
A02	tnfn1_pw060420p03q109	T20	-	membrane fusion protein	motility, attachment and secretion structure
A03	tnfn1_pw060420p03q117	T20	-	hypothetical protein	hypothetical - novel
A04	tnfn1_pw060420p03q125	T20	iglA	intracellular growth locus protein A	unknown function - conserved
A05	tnfn1_pw060420p03q133	T18	-	conserved protein of unknown function	unknown function - conserved
A06	tnfn1_pw060420p03q141	T20	-	dehydrogenase related to short-chain alcohol dehydrogenases	putative enzymes
A07	tnfn1_pw060420p03q149	T20	nupC1	nucleoside permease NUP family protein	transport
A08	tnfn1_pw060420p03q157	T20	-	HAM1-like protein, possible xanthosine triphosphate pyrophosphatase	putative enzymes
A09	tnfn1_pw060420p03q165	T20	-	-	-
A10	tnfn1_pw060420p03q173	T20	-	abortive infection bacteriophage resistance protein	mobile and extrachromosomal element functions - phage or plasmid related proteins
A11	tnfn1_pw060420p03q181	T20	-	Na ⁺ /H ⁺ antiporter	transport
A12	tnfn1_pw060420p03q189	T18	-	membrane fusion protein	motility, attachment and secretion structure
B01	tnfn1_pw060420p03q102	T20	ilvB	acetolactate synthase large subunit	amino acid metabolism - biosynthesis
B02	tnfn1_pw060420p03q110	T20	-	drug:H ⁺ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
B03	tnfn1_pw060420p03q118	T20	cphA	cyanophycin synthetase	cell wall / LPS / capsule
B04	tnfn1_pw060420p03q126	T20	fumC	fumarate hydratase, class II	energy metabolism
B05	tnfn1_pw060420p03q134	T18	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
B06	tnfn1_pw060420p03q142	T20	-	conserved hypothetical protein	hypothetical - conserved
B07	tnfn1_pw060420p03q150	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
B08	tnfn1_pw060420p03q158	T20	cydC	ABC-type transport ATP-binding protein CydC	transport
B09	tnfn1_pw060420p03q166	T20	sucD	succinyl-CoA synthetase, alpha subunit	energy metabolism
B10	tnfn1_pw060420p03q174	T20	-	putative rhodanese, sulfurtransferase	putative enzymes
B11	tnfn1_pw060420p03q182	T20	-	hypothetical protein	hypothetical - novel
B12	tnfn1_pw060420p03q190	<KAN-2>	-	-	-
C01	tnfn1_pw060420p03q103	T20	-	protein of unknown function	unknown function - novel
C02	tnfn1_pw060420p03q111	T20	-	conserved protein of unknown function	unknown function - conserved
C03	tnfn1_pw060420p03q119	T20	-	oxidoreductase	putative enzymes
C04	tnfn1_pw060420p03q127	T20	-	protein of unknown function, LamB/YcsF family	unknown function - conserved
C05	tnfn1_pw060420p03q135	T18	gcvH	glycine cleavage system H protein (lipolate-binding)	amino acid metabolism - degradation, utilization, assimilation
C06	tnfn1_pw060420p03q143	T20	kpsC	capsule polysaccharide export protein KpsC	cell wall / LPS / capsule
C07	tnfn1_pw060420p03q151	T20	-	allophanate hydrolase subunit 1	other metabolism - degradation, utilization, assimilation
C08	tnfn1_pw060420p03q159	T20	ribD	pyrimidine reductase/pyrimidine deaminase	cofactors, prosthetic groups, electron carriers metabolism
C09	tnfn1_pw060420p03q167	T20	-	protein of unknown function	unknown function - novel
C10	tnfn1_pw060420p03q175	T20	-	membrane protein of unknown function	unknown function - novel
C11	tnfn1_pw060420p03q183	T20	-	D-isomer specific 2-hydroxyacid dehydrogenase	energy metabolism
C12	tnfn1_pw060420p03q191	<KAN-2>	bfr	bacterioferritin	energy metabolism
D01	tnfn1_pw060420p03q104	T20	oppA	ABC-type oligopeptide transport system, periplasmic component	transport
D02	tnfn1_pw060420p03q112	T20	-	o-methyltransferase family protein	putative enzymes
D03	tnfn1_pw060420p03q120	T20	-	conserved protein of unknown function	unknown function - conserved
D04	tnfn1_pw060420p03q128	T20	-	protein of unknown function	unknown function - novel
D05	tnfn1_pw060420p03q136	T20	-	BNR/Asp-box repeat protein	putative enzymes
D06	tnfn1_pw060420p03q144	T20	pilF	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
D07	tnfn1_pw060420p03q152	T20	-	hypothetical protein	Potentially coding: hypothetical - novel
D08	tnfn1_pw060420p03q160	T20	-	protein of unknown function	unknown function - novel
D09	tnfn1_pw060420p03q168	T20	-	conserved protein of unknown function	unknown function - conserved

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D10	tnfn1_pw060420p03q176	T20	-	GTP binding translational elongation factor Tu and G family protein	putative enzymes
D11	tnfn1_pw060420p03q184	T20	serB	phosphoserine phosphatase	amino acid metabolism - biosynthesis
D12	tnfn1_pw060420p03q192	<KAN-2>	-	prophage repressor protein	signal transduction and regulation
E01	tnfn1_pw060420p03q105	T20	-	hypothetical membrane protein	hypothetical - novel
E02	tnfn1_pw060420p03q113	T20	-	hypothetical membrane protein	hypothetical - novel
E03	tnfn1_pw060420p03q121	T18	-	PhoH family protein, putative ATPase	signal transduction and regulation
E04	tnfn1_pw060420p03q129	T20	bcp	bacterioferritin comigratory protein	post-translational modification, protein turnover, chaperones - protein modification
E05	tnfn1_pw060420p03q137	T20	iglD	intracellular growth locus protein D	unknown function - novel
E06	tnfn1_pw060420p03q145	T20	-	protein of unknown function	unknown function - conserved
E07	tnfn1_pw060420p03q153	T20	mdaB	NADPH-quinone reductase (modulator of drug activity B)	putative enzymes
E08	tnfn1_pw060420p03q161	T20	-	-	-
E09	tnfn1_pw060420p03q169	T20	-	hypothetical protein	hypothetical - novel
E10	tnfn1_pw060420p03q177	T20	-	conserved protein of unknown function	unknown function - conserved
E11	tnfn1_pw060420p03q185	<KAN-2>	-	protein of unknown function	unknown function - novel
E12	tnfn1_pw060420p03q193	<KAN-2>	tspO	tryptophan-rich sensory protein	signal transduction and regulation
F01	tnfn1_pw060420p03q106	T20	-	conserved protein of unknown function	unknown function - conserved
F02	tnfn1_pw060420p03q114	T20	-	metabolite:H+ symporter (MHS) family	transport
F03	tnfn1_pw060420p03q122	T20	-	conserved protein of unknown function	unknown function - conserved
F04	tnfn1_pw060420p03q130	T20	-	NAD-dependent aldehyde dehydrogenase	other metabolism - degradation, utilization, assimilation
F05	tnfn1_pw060420p03q138	T20	accD	acetyl-CoA carboxylase, carboxytransferase subunit beta	fatty acids and lipids metabolism
F06	tnfn1_pw060420p03q146	T20	-	predicted enzyme of enolase superfamily	putative enzymes
F07	tnfn1_pw060420p03q154	T20	cyoD	cytochrome bo terminal oxidase subunit IV	energy metabolism
F08	tnfn1_pw060420p03q162	T20	-	hypothetical protein	hypothetical - novel
F09	tnfn1_pw060420p03q170	T20	-	protein of unknown function	unknown function - novel
F10	tnfn1_pw060420p03q178	T20	gpsA	glycerol-3-phosphate-dehydrogenase-[NAD+]	fatty acids and lipids metabolism
F11	tnfn1_pw060420p03q186	<KAN-2>	-	hydrolase, HD superfamily	putative enzymes
F12	tnfn1_pw060420p03q194	T20	-	conserved protein of unknown function	unknown function - conserved
G01	tnfn1_pw060420p03q107	T20	-	CheB methyltransferase/CheR methyltransferase	signal transduction and regulation
G02	tnfn1_pw060420p03q115	T20	-	mechanosensitive ion channel protein	transport
G03	tnfn1_pw060420p03q123	T20	-	hypothetical protein	hypothetical - novel
G04	tnfn1_pw060420p03q131	<KAN-2>	-	protein of unknown function with radical SAM domain	unknown function - conserved
G05	tnfn1_pw060420p03q139	T20	-	sugar transferase involved in lipopolysaccharide synthesis	cell wall / LPS / capsule
G06	tnfn1_pw060420p03q147	T20	-	Fe2+/Zn2+ uptake regulator protein	signal transduction and regulation
G07	tnfn1_pw060420p03q155	T20	-	SAICAR synthetase/phosphoribosylamine-glycine ligase	nucleotides and nucleosides metabolism
G08	tnfn1_pw060420p03q163	T20	-	oxidoreductase	putative enzymes
G09	tnfn1_pw060420p03q171	T20	-	membrane fusion protein	motility, attachment and secretion structure
G10	tnfn1_pw060420p03q179	T20	-	phosphosugar binding protein	cell wall / LPS / capsule
G11	tnfn1_pw060420p03q187	<KAN-2>	-	ribonuclease PH	translation, ribosomal structure and biogenesis
G12	tnfn1_pw060420p03q195	T20	potH	ATP-binding cassette putrescine uptake system, membrane protein, subunit H	transport
H01	tnfn1_pw060420p03q108	T20	-	4Fe-4S ferredoxin	energy metabolism
H02	tnfn1_pw060420p03q116	T20	-	major facilitator superfamily (MFS) transport protein	transport
H03	tnfn1_pw060420p03q124	T20	-	hypothetical protein	hypothetical - novel
H04	tnfn1_pw060420p03q132	T18	-	-	Potentially coding; hypothetical - novel
H05	tnfn1_pw060420p03q140	T20	hemN	coproporphyrinogen III oxidase, anaerobic	cofactors, prosthetic groups, electron carriers metabolism
H06	tnfn1_pw060420p03q148	T20	-	-	-
H07	tnfn1_pw060420p03q156	T20	hrpA	HrpA-like helicase	DNA replication, recombination, modification and repair
H08	tnfn1_pw060420p03q164	T20	-	cytochrome b561 family protein	cofactors, prosthetic groups, electron carriers metabolism
H09	tnfn1_pw060420p03q172	T20	clpX	ATP-dependent Clp protease subunit X	post-translational modification, protein turnover, chaperones - protein degradation
H10	tnfn1_pw060420p03q180	T20	fopA	OmpA family protein	cell wall / LPS / capsule
H11	tnfn1_pw060420p03q188	<KAN-2>	-	protein of unknown function	unknown function - novel
H12	tnfn1_pw060420p03q196	T20	fumC	fumarate hydratase, class II	energy metabolism

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

Table 2: Plate 27 (tnfn1_pw060420p03) – 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_pw060420p03q101	C	756424	FTN_0711	756324	756980	F	219	101(657)
A02	tnfn1_pw060420p03q109	C	1349015	FTN_1276	1348690	1349712	F	341	326(1023)
A03	tnfn1_pw060420p03q117	C	850808	FTN_0793	850477	851043	F	189	332(567)
A04	tnfn1_pw060420p03q125	C	1399632	FTN_1324	1399172	1399723	R	184	92(552)
A05	tnfn1_pw060420p03q133	C	1555204	FTN_1466	1554488	1555576	R	363	373(1089)
A06	tnfn1_pw060420p03q141	C	362429	FTN_0359	362380	363099	F	240	50(720)
A07	tnfn1_pw060420p03q149	C	1701514	FTN_1600	1701111	1702307	R	399	794(1197)
A08	tnfn1_pw060420p03q157	C	1557013	FTN_1468	1556744	1557319	F	192	270(576)
A09	tnfn1_pw060420p03q165	C	381253	intergenic					
A10	tnfn1_pw060420p03q173	C	749899	FTN_0705	749168	750076	F	303	732(909)
A11	tnfn1_pw060420p03q181	C	126244	FTN_0115	126046	127293	F	416	199(1248)
A12	tnfn1_pw060420p03q189	C	774422	FTN_0718	773937	774791	R	285	370(855)
B01	tnfn1_pw060420p03q102	C	1099582	FTN_1042	1098981	1100675	R	565	1094(1695)
B02	tnfn1_pw060420p03q110	C	827054	FTN_0770	826604	827803	R	400	750(1200)
B03	tnfn1_pw060420p03q118	C	1176368	FTN_1112	1174118	1176937	R	940	570(2820)
B04	tnfn1_pw060420p03q126	C	241870	FTN_0220	241817	243205	F	463	54(1389)
B05	tnfn1_pw060420p03q134	C	755130	FTN_0710	753221	756328	F	1036	1910(3108)
B06	tnfn1_pw060420p03q142	C	1430594	FTN_1351	1430157	1430870	F	238	438(714)
B07	tnfn1_pw060420p03q150	U	1160172	FTN_1098	1159530	1160402	R	291	231(873)
B08	tnfn1_pw060420p03q158	C	679018	FTN_0641	677863	679509	R	549	492(1647)
B09	tnfn1_pw060420p03q166	C	624329	FTN_0593	623591	624460	R	290	132(870)
B10	tnfn1_pw060420p03q174	C	847655	FTN_0789	847645	848631	R	329	977(987)
B11	tnfn1_pw060420p03q182	U	1478182	FTN_1399	1477955	1478668	R	238	487(714)
B12	tnfn1_pw060420p03q190	C	1639711	intergenic					
C01	tnfn1_pw060420p03q103	C	114880	FTN_0103	113788	116088	R	767	1209(2301)
C02	tnfn1_pw060420p03q111	U	992023	FTN_0931	991793	992749	F	319	231(957)
C03	tnfn1_pw060420p03q119	C	1108533	FTN_1049	1107723	1108898	F	392	811(1176)
C04	tnfn1_pw060420p03q127	C	99756	FTN_0088	99479	100174	F	232	278(696)
C05	tnfn1_pw060420p03q135	C	516458	FTN_0506	516080	516460	F	127	379(381)
C06	tnfn1_pw060420p03q143	C	1285990	FTN_1215	1284955	1286112	R	386	123(1158)
C07	tnfn1_pw060420p03q151	C	99222	FTN_0087	98862	99476	F	205	361(615)
C08	tnfn1_pw060420p03q159	C	125430	FTN_0114	124591	125655	R	355	226(1065)
C09	tnfn1_pw060420p03q167	C	765157	FTN_0714	760571	766126	F	1852	4587(5556)
C10	tnfn1_pw060420p03q175	C	444615	FTN_0444	443654	445324	F	557	962(1671)
C11	tnfn1_pw060420p03q183	C	1846535	FTN_1719	1846033	1847178	R	382	644(1146)
C12	tnfn1_pw060420p03q191	C	1487842	FTN_1410	1487622	1488059	F	146	221(438)
D01	tnfn1_pw060420p03q104	U	1691924	FTN_1593	1691111	1692784	R	558	861(1674)
D02	tnfn1_pw060420p03q112	C	1121599	FTN_1062	1121319	1121990	R	224	392(672)
D03	tnfn1_pw060420p03q120	C	1628219	FTN_1531	1627995	1628675	R	227	457(681)
D04	tnfn1_pw060420p03q128	C	1079992	FTN_1022	1079866	1080159	F	98	127(294)
D05	tnfn1_pw060420p03q136	C	500398	FTN_0495	499997	501112	R	372	715(1116)
D06	tnfn1_pw060420p03q144	C	1004124	FTN_0946	1003473	1004375	R	301	252(903)
D07	tnfn1_pw060420p03q152	C	396313	-	396244	396372	R	43	60(129)
D08	tnfn1_pw060420p03q160	C	949575	FTN_0893	949331	949918	F	196	245(588)
D09	tnfn1_pw060420p03q168	C	36576	FTN_0034	33580	36951	R	1124	376(3372)
D10	tnfn1_pw060420p03q176	C	1228628	FTN_1157	1227077	1228891	F	605	1552(1815)
D11	tnfn1_pw060420p03q184	C	796523	FTN_0742	796240	796887	F	216	284(648)
D12	tnfn1_pw060420p03q192	C	1446148	FTN_1363	1446038	1446688	F	217	111(651)
E01	tnfn1_pw060420p03q105	C	1539752	FTN_1450	1539655	1540053	R	133	302(399)
E02	tnfn1_pw060420p03q113	C	504472	FTN_0498	504268	505494	F	409	205(1227)
E03	tnfn1_pw060420p03q121	C	1124139	FTN_1064	1123547	1124527	F	327	593(981)
E04	tnfn1_pw060420p03q129	C	1885515	FTN_1756	1885175	1885651	F	159	341(477)
E05	tnfn1_pw060420p03q137	U	1396792	FTN_1321	1395775	1396968	R	398	177(1194)
E06	tnfn1_pw060420p03q145	C	1262272	FTN_1187	1261659	1262360	R	234	89(702)
E07	tnfn1_pw060420p03q153	C	896585	FTN_0840	896313	896900	F	196	273(588)
E08	tnfn1_pw060420p03q161	C	745052	intergenic					
E09	tnfn1_pw060420p03q169	C	376186	FTN_0374	376108	376314	F	69	79(207)
E10	tnfn1_pw060420p03q177	C	935828	FTN_0880	935096	936310	R	405	483(1215)
E11	tnfn1_pw060420p03q185	C	78840	FTN_0065	78558	78869	R	104	30(312)
E12	tnfn1_pw060420p03q193	C	825449	FTN_0768	825148	825621	R	158	173(474)
F01	tnfn1_pw060420p03q106	C	1068545	FTN_1009	1068039	1069043	F	335	507(1005)
F02	tnfn1_pw060420p03q114	C	929195	FTN_0875	928929	930158	F	410	267(1230)

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_pw060420p03q122	C	1404283	FTN_1326	1403644	1404786	R	381	504(1143)
F04	tnfn1_pw060420p03q130	C	1017386	FTN_0963	1016699	1018192	R	498	807(1494)
F05	tnfn1_pw060420p03q138	C	280802	FTN_0272	279916	280815	F	300	887(900)
F06	tnfn1_pw060420p03q146	C	743455	FTN_0700	743228	744295	F	356	228(1068)
F07	tnfn1_pw060420p03q154	C	220211	FTN_0198	220165	220494	F	110	47(330)
F08	tnfn1_pw060420p03q162	C	13729	FTN_0016	13110	13781	R	224	53(672)
F09	tnfn1_pw060420p03q170	C	1837706	FTN_1713	1837164	1837808	R	215	103(645)
F10	tnfn1_pw060420p03q178	C	396746	FTN_0397	396549	397544	F	332	198(996)
F11	tnfn1_pw060420p03q186	U	435716	FTN_0437	435345	435932	F	196	372(588)
F12	tnfn1_pw060420p03q194	C	1645750	FTN_1548	1645390	1646757	F	456	361(1368)
G01	tnfn1_pw060420p03q107	U	459175	FTN_0455	458374	461271	F	966	802(2898)
G02	tnfn1_pw060420p03q115	C	591994	FTN_0566	591956	593071	F	372	39(1116)
G03	tnfn1_pw060420p03q123	C	1887955	FTN_1758	1887821	1888438	F	206	135(618)
G04	tnfn1_pw060420p03q131	C	1005147	FTN_0947	1004368	1005477	R	370	331(1110)
G05	tnfn1_pw060420p03q139	C	1292111	FTN_1220	1290818	1292209	R	464	99(1392)
G06	tnfn1_pw060420p03q147	C	936643	FTN_0881	936452	936880	F	143	192(429)
G07	tnfn1_pw060420p03q155	C	419847	FTN_0420	418362	420671	F	770	1486(2310)
G08	tnfn1_pw060420p03q163	C	1466221	FTN_1388	1466005	1466622	F	206	217(618)
G09	tnfn1_pw060420p03q171	C	1809083	FTN_1692	1808552	1809619	R	356	537(1068)
G10	tnfn1_pw060420p03q179	C	1142950	FTN_1080	1142674	1143699	R	342	750(1026)
G11	tnfn1_pw060420p03q187	C	387043	FTN_0387	386852	387556	F	235	192(705)
G12	tnfn1_pw060420p03q195	C	792095	FTN_0738	791393	792307	R	305	213(915)
H01	tnfn1_pw060420p03q108	C	830174	FTN_0773	829606	830691	R	362	518(1086)
H02	tnfn1_pw060420p03q116	C	881855	FTN_0824	881019	882230	R	404	376(1212)
H03	tnfn1_pw060420p03q124	C	1187730	FTN_1124	1187659	1187901	F	81	72(243)
H04	tnfn1_pw060420p03q132	C	9125	-	8981	9148	R	56	24(168)
H05	tnfn1_pw060420p03q140	C	1738786	FTN_1626	1738188	1739327	F	380	599(1140)
H06	tnfn1_pw060420p03q148	U	27031	intergenic					
H07	tnfn1_pw060420p03q156	C	1514173	FTN_1432	1513195	1517211	R	1339	3039(4017)
H08	tnfn1_pw060420p03q164	C	1883113	FTN_1754	1883079	1883585	F	169	35(507)
H09	tnfn1_pw060420p03q172	C	1116377	FTN_1056	1115895	1117145	R	417	769(1251)
H10	tnfn1_pw060420p03q180	U	809021	FTN_0756	808202	809377	F	392	820(1176)
H11	tnfn1_pw060420p03q188	U	1888731	FTN_1759	1888512	1888901	R	130	171(390)
H12	tnfn1_pw060420p03q196	C	242749	FTN_0220	241817	243205	F	463	933(1389)

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 27 (tnfn1_pw060420p03) – 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_pw060420p03q101	EXACT(0)	156	152	120	34	EXACT(0)	200	181	48
A02	tnfn1_pw060420p03q109	EXACT(0)	156	152	120	28	EXACT(0)	200	188	56
A03	tnfn1_pw060420p03q117	EXACT(0)	157	145	98	24	EXACT(0)	200	189	50
A04	tnfn1_pw060420p03q125	EXACT(0)	158	150	126	35	EXACT(0)	200	185	54
A05	tnfn1_pw060420p03q133	EXACT(0)	208	103	74	20	EXACT(0)	200	188	39
A06	tnfn1_pw060420p03q141	EXACT(0)	156	153	129	39	EXACT(0)	199	151	42
A07	tnfn1_pw060420p03q149	EXACT(0)	158	152	122	33	EXACT(0)	200	181	46
A08	tnfn1_pw060420p03q157	EXACT(0)	155	145	122	34	ESTIMATE(65)	135	123	31
A09	tnfn1_pw060420p03q165	EXACT(0)	155	152	121	34	EXACT(0)	200	194	55
A10	tnfn1_pw060420p03q173	EXACT(0)	158	114	90	25	EXACT(0)	200	176	40
A11	tnfn1_pw060420p03q181	EXACT(0)	156	142	99	21	EXACT(0)	200	187	51
A12	tnfn1_pw060420p03q189	EXACT(0)	216	101	81	20	EXACT(0)	200	185	50
B01	tnfn1_pw060420p03q102	EXACT(0)	156	153	111	30	EXACT(0)	200	192	54
B02	tnfn1_pw060420p03q110	EXACT(0)	158	153	118	31	EXACT(0)	200	176	48
B03	tnfn1_pw060420p03q118	EXACT(0)	157	153	131	40	EXACT(0)	200	186	57
B04	tnfn1_pw060420p03q126	EXACT(0)	158	152	133	34	EXACT(0)	200	195	55

Well Position	Strain Name	Junction Info	Position in Sequence Read of Last Vector (Nucleotide)	Length of Match to Transposon	Transposon Match Score	Average Phred Score for Transposon Match	Genome Position Info	Length of Match to Genome	Genome Match Score	Average Phred Score for Genome Match
B05	tfnf1_pw060420p03q134	EXACT(0)	123	112	98	26	EXACT(0)	200	191	51
B06	tfnf1_pw060420p03q142	EXACT(0)	160	159	132	31	EXACT(0)	200	191	52
B07	tfnf1_pw060420p03q150	EXACT(0)	156	145	136	39	EXACT(0)	200	182	51
B08	tfnf1_pw060420p03q158	EXACT(0)	156	152	133	45	EXACT(0)	200	191	59
B09	tfnf1_pw060420p03q166	EXACT(0)	157	145	126	29	EXACT(0)	200	193	48
B10	tfnf1_pw060420p03q174	EXACT(0)	156	152	126	33	EXACT(0)	200	181	56
B11	tfnf1_pw060420p03q182	EXACT(0)	157	152	136	39	EXACT(0)	200	185	51
B12	tfnf1_pw060420p03q190	EXACT(0)	120	120	105	38	EXACT(0)	200	199	52
C01	tfnf1_pw060420p03q103	EXACT(0)	158	153	129	34	EXACT(0)	200	190	55
C02	tfnf1_pw060420p03q111	EXACT(0)	156	152	118	28	EXACT(0)	200	186	51
C03	tfnf1_pw060420p03q119	EXACT(0)	157	145	118	23	EXACT(0)	200	171	40
C04	tfnf1_pw060420p03q127	EXACT(0)	156	152	129	35	EXACT(0)	200	177	44
C05	tfnf1_pw060420p03q135	EXACT(0)	125	120	97	23	EXACT(0)	200	196	53
C06	tfnf1_pw060420p03q143	EXACT(0)	158	153	110	20	EXACT(0)	200	184	46
C07	tfnf1_pw060420p03q151	EXACT(0)	155	145	76	19	EXACT(0)	200	191	54
C08	tfnf1_pw060420p03q159	EXACT(0)	156	145	117	34	EXACT(0)	200	194	49
C09	tfnf1_pw060420p03q167	EXACT(0)	156	152	130	38	EXACT(0)	200	191	56
C10	tfnf1_pw060420p03q175	EXACT(0)	154	139	122	38	EXACT(0)	200	189	57
C11	tfnf1_pw060420p03q183	EXACT(0)	160	153	127	32	EXACT(0)	200	181	57
C12	tfnf1_pw060420p03q191	EXACT(0)	120	112	96	34	EXACT(0)	200	184	50
D01	tfnf1_pw060420p03q104	EXACT(0)	156	153	116	33	EXACT(0)	200	191	54
D02	tfnf1_pw060420p03q112	EXACT(0)	155	145	128	35	EXACT(0)	200	195	41
D03	tfnf1_pw060420p03q120	EXACT(0)	157	152	126	35	EXACT(0)	200	184	56
D04	tfnf1_pw060420p03q128	EXACT(0)	156	145	118	39	EXACT(0)	200	151	35
D05	tfnf1_pw060420p03q136	EXACT(0)	155	142	108	30	EXACT(0)	200	189	50
D06	tfnf1_pw060420p03q144	EXACT(0)	158	154	136	32	EXACT(0)	200	183	46
D07	tfnf1_pw060420p03q152	EXACT(0)	159	159	142	37	EXACT(0)	200	192	46
D08	tfnf1_pw060420p03q160	EXACT(0)	154	139	125	36	EXACT(0)	200	188	45
D09	tfnf1_pw060420p03q168	EXACT(0)	154	145	113	29	EXACT(0)	200	186	53
D10	tfnf1_pw060420p03q176	EXACT(0)	157	150	121	33	EXACT(0)	200	195	50
D11	tfnf1_pw060420p03q184	EXACT(0)	154	145	107	28	EXACT(0)	200	181	50
D12	tfnf1_pw060420p03q192	EXACT(0)	120	112	102	32	EXACT(0)	200	195	45
E01	tfnf1_pw060420p03q105	EXACT(0)	156	139	86	21	EXACT(0)	200	185	47
E02	tfnf1_pw060420p03q113	EXACT(0)	155	152	122	35	EXACT(0)	200	184	28
E03	tfnf1_pw060420p03q121	EXACT(0)	122	81	60	21	ESTIMATE(5)	192	157	24
E04	tfnf1_pw060420p03q129	EXACT(0)	158	152	134	37	EXACT(0)	200	193	50
E05	tfnf1_pw060420p03q137	EXACT(0)	155	150	97	25	EXACT(0)	200	179	44
E06	tfnf1_pw060420p03q145	EXACT(0)	154	144	119	37	EXACT(0)	200	167	37
E07	tfnf1_pw060420p03q153	EXACT(0)	158	152	131	30	EXACT(0)	200	194	52
E08	tfnf1_pw060420p03q161	EXACT(0)	157	142	81	20	EXACT(0)	200	170	48
E09	tfnf1_pw060420p03q169	EXACT(0)	158	152	131	36	EXACT(0)	200	191	55
E10	tfnf1_pw060420p03q177	EXACT(0)	158	153	128	31	EXACT(0)	200	181	55
E11	tfnf1_pw060420p03q185	EXACT(0)	122	119	106	35	EXACT(0)	200	185	56
E12	tfnf1_pw060420p03q193	EXACT(0)	121	120	105	37	EXACT(0)	200	177	43
F01	tfnf1_pw060420p03q106	EXACT(0)	156	145	129	36	EXACT(0)	200	191	49
F02	tfnf1_pw060420p03q114	EXACT(0)	155	145	128	36	EXACT(0)	201	153	43
F03	tfnf1_pw060420p03q122	EXACT(0)	161	155	132	34	EXACT(0)	197	189	52
F04	tfnf1_pw060420p03q130	EXACT(0)	158	153	139	35	EXACT(0)	200	195	55
F05	tfnf1_pw060420p03q138	EXACT(0)	155	145	94	17	EXACT(0)	200	183	39
F06	tfnf1_pw060420p03q146	EXACT(0)	157	153	131	33	EXACT(0)	200	195	55
F07	tfnf1_pw060420p03q154	EXACT(0)	155	145	131	41	EXACT(0)	200	193	45
F08	tfnf1_pw060420p03q162	EXACT(0)	158	152	135	36	EXACT(0)	200	169	57
F09	tfnf1_pw060420p03q170	EXACT(0)	156	145	136	37	EXACT(0)	200	185	52
F10	tfnf1_pw060420p03q178	EXACT(0)	155	139	121	34	EXACT(0)	200	188	54
F11	tfnf1_pw060420p03q186	EXACT(0)	120	120	105	38	EXACT(0)	200	184	50
F12	tfnf1_pw060420p03q194	EXACT(0)	156	145	134	36	EXACT(0)	200	189	48
G01	tfnf1_pw060420p03q107	EXACT(0)	157	152	138	40	EXACT(0)	200	195	51
G02	tfnf1_pw060420p03q115	EXACT(0)	156	152	133	37	EXACT(0)	200	180	56
G03	tfnf1_pw060420p03q123	EXACT(0)	155	145	113	26	EXACT(0)	200	178	45
G04	tfnf1_pw060420p03q131	EXACT(0)	122	119	86	21	EXACT(0)	200	195	50
G05	tfnf1_pw060420p03q139	EXACT(0)	157	153	124	34	EXACT(0)	200	182	55
G06	tfnf1_pw060420p03q147	EXACT(0)	159	153	140	36	EXACT(0)	200	190	51

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_pw060420p03q155	EXACT(0)	157	152	127	36	EXACT(0)	200	199	51
G08	tnfn1_pw060420p03q163	EXACT(0)	158	153	138	38	EXACT(0)	200	184	57
G09	tnfn1_pw060420p03q171	EXACT(0)	156	152	122	32	EXACT(0)	200	193	54
G10	tnfn1_pw060420p03q179	EXACT(0)	157	148	118	35	EXACT(0)	200	189	57
G11	tnfn1_pw060420p03q187	EXACT(0)	123	120	104	32	EXACT(0)	200	198	54
G12	tnfn1_pw060420p03q195	EXACT(0)	157	138	106	22	EXACT(0)	200	177	49
H01	tnfn1_pw060420p03q108	EXACT(0)	157	145	119	37	EXACT(0)	199	121	25
H02	tnfn1_pw060420p03q116	EXACT(0)	156	145	111	20	EXACT(0)	200	192	46
H03	tnfn1_pw060420p03q124	EXACT(0)	157	145	124	35	EXACT(0)	179	165	46
H04	tnfn1_pw060420p03q132	EXACT(0)	122	107	66	17	EXACT(0)	200	170	32
H05	tnfn1_pw060420p03q140	EXACT(0)	157	154	133	34	EXACT(0)	200	183	58
H06	tnfn1_pw060420p03q148	EXACT(0)	155	144	107	36	EXACT(0)	200	186	56
H07	tnfn1_pw060420p03q156	EXACT(0)	158	153	139	40	EXACT(0)	200	178	52
H08	tnfn1_pw060420p03q164	EXACT(0)	157	153	134	36	EXACT(0)	200	189	43
H09	tnfn1_pw060420p03q172	EXACT(0)	156	139	114	39	EXACT(0)	200	195	58
H10	tnfn1_pw060420p03q180	EXACT(0)	157	151	120	37	EXACT(0)	200	190	47
H11	tnfn1_pw060420p03q188	EXACT(0)	120	120	101	27	EXACT(0)	200	193	40
H12	tnfn1_pw060420p03q196	EXACT(0)	155	116	113	38	EXACT(0)	200	194	56

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