Francisella tularensis subsp. *novicida* "Two-Allele" Transposon Mutant Library, Plate 7 (tnfn1_pw060323p07)

Catalog No. NR-51289

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-51289 represents plate 7 (tnfn1_pw060323p07) 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-51289 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 7 (tnfn1_pw060323p07), NR-51289."

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:
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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.

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Table 1: Plate 7 (tnfn1_pw060323p07) – Transposon Type and Mutated Gene[1]

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060323p07q101	T20	-	YGGT family membrane protein	unknown function - conserved
A02	tnfn1_pw060323p07q109	T20	-	ornithine cyclodeaminase, mu-crystallin homolog	amino acid metabolism - degradation, utilization, assimilation
A03	tnfn1_pw060323p07q117	T20	-	conserved protein of unknown function	unknown function - conserved
A04	tnfn1_pw060323p07q125	T20	aroH	chorismate mutase	amino acid metabolism - biosynthesis
A05	tnfn1_pw060323p07q133	<KAN-2>	-	cytochrome b561 family protein	cofactors, prosthetic groups, electron carriers metabolism
A06	tnfn1_pw060323p07q141	T18	-	conserved protein of unknown function	unknown function - conserved
A07	tnfn1_pw060323p07q149	T18	-	hypothetical protein	hypothetical - novel
A08	tnfn1_pw060323p07q157	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
A09	tnfn1_pw060323p07q165	T20	perM	PerM family protein	transport
A10	tnfn1_pw060323p07q173	T20	fadE	Acyl-CoA dehydrogenase	other metabolism - degradation, utilization, assimilation
A11	tnfn1_pw060323p07q181	T20	-	protein of unknown function	unknown function - novel
A12	tnfn1_pw060323p07q189	T20	talA	transaldolase	energy metabolism
B01	tnfn1_pw060323p07q102	T20	rnfB	iron-sulfur cluster-binding protein	putative enzymes
B02	tnfn1_pw060323p07q110	T20	-	hypothetical membrane protein	hypothetical - novel
B03	tnfn1_pw060323p07q118	T20	ostA1	organic solvent tolerance protein, OstA	cell wall / LPS / capsule
B04	tnfn1_pw060323p07q126	T20	-	protein of unknown function	unknown function - conserved
B05	tnfn1_pw060323p07q134	<KAN-2>	secB2	preprotein translocase, subunit B	motility, attachment and secretion structure
B06	tnfn1_pw060323p07q142	T18	-	membrane protein of unknown function	unknown function - novel
B07	tnfn1_pw060323p07q150	T18	-	pseudogene: hypothetical protein, fragment	pseudogene
B08	tnfn1_pw060323p07q158	T20	-	major facilitator superfamily (MFS) transport protein	transport
B09	tnfn1_pw060323p07q166	T20	-	major facilitator superfamily (MFS) transport protein	transport
B10	tnfn1_pw060323p07q174	T20	-	arsenate reductase	cofactors, prosthetic groups, electron carriers metabolism
B11	tnfn1_pw060323p07q182	T20	-	solute:sodium symporter	transport
B12	tnfn1_pw060323p07q190	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
C01	tnfn1_pw060323p07q103	T20	isftu6	isftu6	IS element
C02	tnfn1_pw060323p07q111	T20	-	conserved hypothetical protein	hypothetical - conserved
C03	tnfn1_pw060323p07q119	T20	-	protein of unknown function	unknown function - novel
C04	tnfn1_pw060323p07q127	T20	-	glycosyl transferase, group 1	cell wall / LPS / capsule
C05	tnfn1_pw060323p07q135	<KAN-2>	rpoB	DNA-directed RNA polymerase, beta subunit/140 kD subunit	transcription
C06	tnfn1_pw060323p07q143	T18	gcvT	glycine cleavage complex protein T (aminomethyltransferase)	amino acid metabolism - degradation, utilization, assimilation
C07	tnfn1_pw060323p07q151	T18			
C08	tnfn1_pw060323p07q159	T20	truB	tRNA pseudouridine synthase B	translation, ribosomal structure and biogenesis
C09	tnfn1_pw060323p07q167	T20	relA	GDP pyrophosphokinase/GTP pyrophosphokinase	other metabolism - biosynthesis
C10	tnfn1_pw060323p07q175	T20	-	restriction endonuclease	DNA replication, recombination, modification and repair - restriction/modification
C11	tnfn1_pw060323p07q183	T20	-	conserved hypothetical protein	hypothetical - conserved
C12	tnfn1_pw060323p07q191	T20	-	hypothetical protein	hypothetical - novel
D01	tnfn1_pw060323p07q104	T20	-	carbon-nitrogen hydrolase	putative enzymes
D02	tnfn1_pw060323p07q112	T20	-	conserved protein of unknown function	unknown function - conserved
D03	tnfn1_pw060323p07q120	T20	-	pilus assembly protein	motility, attachment and secretion structure
D04	tnfn1_pw060323p07q128	T20	trpE	anthranilate synthase component I	amino acid metabolism - biosynthesis
D05	tnfn1_pw060323p07q136	T18	tolB	group A colicin translocation; tolB protein	transport - drugs / antibacterial compounds
D06	tnfn1_pw060323p07q144	T18			
D07	tnfn1_pw060323p07q152	T18	-	protein of unknown function	unknown function - novel
D08	tnfn1_pw060323p07q160	T20	kdpB	potassium-transporting ATPase B chain	transport
D09	tnfn1_pw060323p07q168	T20	-	mannose-6-phosphate isomerase	carbohydrate metabolism - biosynthesis

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D10	tnfn1_pw060323p07q176	T20	-	conserved protein of unknown function	unknown function - conserved
D11	tnfn1_pw060323p07q184	T20			
D12	tnfn1_pw060323p07q192	T20	-	conserved protein of unknown function	unknown function - conserved
E01	tnfn1_pw060323p07q105	T20	-	hypothetical protein	hypothetical - novel
E02	tnfn1_pw060323p07q113	T20	-	deoxyribodipyrimidine photolyase-related protein	putative enzymes
E03	tnfn1_pw060323p07q121	T20	hflK	HflK-HflC membrane protein complex, HflK	post-translational modification, protein turnover, chaperones - protein degradation
E04	tnfn1_pw060323p07q129	T20	-	conserved hypothetical protein	hypothetical - conserved
E05	tnfn1_pw060323p07q137	T18	-	beta-fructofuranosidase	carbohydrate metabolism - degradation, utilization, assimilation
E06	tnfn1_pw060323p07q145	T18	-	conserved protein of unknown function	unknown function - conserved
E07	tnfn1_pw060323p07q153	T18	-	short chain dehydrogenase	putative enzymes
E08	tnfn1_pw060323p07q161	T20	-	hypothetical protein	hypothetical - novel
E09	tnfn1_pw060323p07q169	T20	-	bifunctional protein: 3-hydroxacyl-CoA dehydrogenase/acyl-CoA-binding protein	other metabolism - degradation, utilization, assimilation
E10	tnfn1_pw060323p07q177	T20	-	conserved protein of unknown function	unknown function - conserved
E11	tnfn1_pw060323p07q185	T20	bioF	8-amino-7-oxononanoate synthase	cofactors, prosthetic groups, electron carriers metabolism
E12	tnfn1_pw060323p07q193	T20	isftu2	isftu2	IS element
F01	tnfn1_pw060323p07q106	T20	-	hypothetical protein	hypothetical - novel
F02	tnfn1_pw060323p07q114	T20	-	drug:H+ antiporter-1 (DHA2) family protein	transport - drugs / antibacterial compounds
F03	tnfn1_pw060323p07q122	T20	-	hypothetical protein	hypothetical - novel
F04	tnfn1_pw060323p07q130	T20	-	amino acid transporter (AAT) family protein	transport - amino-acid
F05	tnfn1_pw060323p07q138	T18	-	oligoketide cyclase/lipid transport protein	fatty acids and lipids metabolism
F06	tnfn1_pw060323p07q146	T18	-	two-component response regulator	signal transduction and regulation
F07	tnfn1_pw060323p07q154	T18	-	membrane protein of unknown function	unknown function - novel
F08	tnfn1_pw060323p07q162	T20	-	hypothetical protein	hypothetical - novel
F09	tnfn1_pw060323p07q170	T20	-	protein of unknown function	unknown function - novel
F10	tnfn1_pw060323p07q178	T20	nusA	transcription elongation factor	transcription
F11	tnfn1_pw060323p07q186	T20	-	GTP binding translational elongation factor Tu and G family protein	putative enzymes
F12	tnfn1_pw060323p07q194	T20	-	GTPase of unknown function	putative enzymes
G01	tnfn1_pw060323p07q107	T20	-	transcriptional regulator, AraC family	signal transduction and regulation
G02	tnfn1_pw060323p07q115	T20	-	protein of unknown function	unknown function - novel
G03	tnfn1_pw060323p07q123	T20	-	conserved protein of unknown function	unknown function - conserved
G04	tnfn1_pw060323p07q131	<KAN-2>	-	protein of unknown function	unknown function - novel
G05	tnfn1_pw060323p07q139	T18	mraW	S-adenosylmethionine-dependent methyltransferase	cell wall / LPS / capsule
G06	tnfn1_pw060323p07q147	T18	-	transporter-associated protein, HlyC/CorC family	transport
G07	tnfn1_pw060323p07q155	T20	-	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	transport
G08	tnfn1_pw060323p07q163	T20	-	ABC transporter, ATP-binding protein	transport
G09	tnfn1_pw060323p07q171	T20	cutC	copper homeostasis protein CutC family protein	cofactors, prosthetic groups, electron carriers metabolism
G10	tnfn1_pw060323p07q179	T20	aroG	phospho-2-dehydro-3-deoxyheptonate aldolase	amino acid metabolism - biosynthesis
G11	tnfn1_pw060323p07q187	T20	-	CheB methylesterase/CheR methyltransferase	signal transduction and regulation
G12	tnfn1_pw060323p07q195	T20	deaD	DEAD-box subfamily ATP-dependent helicase	DNA replication, recombination, modification and repair - restriction/modification
H01	tnfn1_pw060323p07q108	T20	-	conserved protein of unknown function	unknown function - conserved
H02	tnfn1_pw060323p07q116	T20	-	two-component response regulator	signal transduction and regulation
H03	tnfn1_pw060323p07q124	T20	isftu3	isftu3	IS element
H04	tnfn1_pw060323p07q132	<KAN-2>	ubiB	2-octaprenylphenol hydroxylase	cofactors, prosthetic groups, electron carriers metabolism
H05	tnfn1_pw060323p07q140	T18	-	hypothetical membrane protein	hypothetical - novel
H06	tnfn1_pw060323p07q148	T18	-	hypothetical membrane protein	hypothetical - novel
H07	tnfn1_pw060323p07q156	T20	-	conserved protein of unknown function	unknown function - conserved
H08	tnfn1_pw060323p07q164	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
H09	tnfn1_pw060323p07q172	T20	-	major facilitator superfamily (MFS) transport protein	transport
H10	tnfn1_pw060323p07q180	T20	-	protein of unknown function	unknown function - novel
H11	tnfn1_pw060323p07q188	T20	-	SAM-dependent methyltransferase	putative enzymes
H12	tnfn1_pw060323p07q196	T20	-	pilus assembly protein	motility, attachment and secretion structure

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

Table 2: Plate 7 (tnfn1_pw060323p07) – 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_pw060323p07q101	C	162560	FTN_0150	162491	163057	F	189	70(567)
A02	tnfn1_pw060323p07q109	C	1533354	FTN_1444	1532673	1533686	R	338	333(1014)
A03	tnfn1_pw060323p07q117	C	1103619	FTN_1044	1102531	1104324	R	598	706(1794)
A04	tnfn1_pw060323p07q125	C	355104	FTN_0349	355001	355360	F	120	104(360)
A05	tnfn1_pw060323p07q133	C	1883197	FTN_1754	1883079	1883585	F	169	119(507)
A06	tnfn1_pw060323p07q141	C	846546	FTN_0788	846344	847171	F	276	203(828)
A07	tnfn1_pw060323p07q149	C	752176	FTN_0708	752105	752347	F	81	72(243)
A08	tnfn1_pw060323p07q157	C	1832053	FTN_1708	1830752	1832410	R	553	358(1659)
A09	tnfn1_pw060323p07q165	C	596889	FTN_0570	596517	597620	R	368	732(1104)
A10	tnfn1_pw060323p07q173	C	1523216	FTN_1437	1522690	1524927	F	746	527(2238)
A11	tnfn1_pw060323p07q181	C	1061519	FTN_1001	1061369	1062211	F	281	151(843)
A12	tnfn1_pw060323p07q189	C	840038	FTN_0781	839608	840624	F	339	431(1017)
B01	tnfn1_pw060323p07q102	C	1090395	FTN_1034	1090247	1090873	F	209	149(627)
B02	tnfn1_pw060323p07q110	C	917591	FTN_0863	917341	917775	F	145	251(435)
B03	tnfn1_pw060323p07q118	C	583696	FTN_0558	583164	585767	F	868	533(2604)
B04	tnfn1_pw060323p07q126	C	42770	FTN_0040	41096	44347	R	1084	1578(3252)
B05	tnfn1_pw060323p07q134	C	1607053	FTN_1510	1606754	1607194	F	147	300(441)
B06	tnfn1_pw060323p07q142	C	1326041	FTN_1256	1324883	1326250	R	456	210(1368)
B07	tnfn1_pw060323p07q150	C	1723869	FTN_0614	1723371	1723925	R	185	57(555)
B08	tnfn1_pw060323p07q158	C	1486900	FTN_1409	1485991	1487373	R	461	474(1383)
B09	tnfn1_pw060323p07q166	C	881794	FTN_0824	881019	882230	R	404	437(1212)
B10	tnfn1_pw060323p07q174	C	345305	FTN_0339	345056	345406	F	117	250(351)
B11	tnfn1_pw060323p07q182	C	1363845	FTN_1292	1363308	1364576	R	423	732(1269)
B12	tnfn1_pw060323p07q190	C	472055	FTN_0467	471407	472627	R	407	573(1221)
C01	tnfn1_pw060323p07q103	C	720220	-	719918	720628	R	237	409(711)
C02	tnfn1_pw060323p07q111	U	1233110	FTN_1161	1232698	1233897	R	400	788(1200)
C03	tnfn1_pw060323p07q119	C	62431	FTN_0052	61717	63777	F	687	715(2061)
C04	tnfn1_pw060323p07q127	C	1289223	FTN_1218	1288573	1289799	R	409	577(1227)
C05	tnfn1_pw060323p07q135	C	1667898	FTN_1568	1667867	1671940	R	1358	4043(4074)
C06	tnfn1_pw060323p07q143	C	515957	FTN_0505	514946	516019	F	358	1012(1074)
C07	tnfn1_pw060323p07q151	C	1429917	intergenic					
C08	tnfn1_pw060323p07q159	C	1551394	FTN_1462	1550899	1551804	R	302	411(906)
C09	tnfn1_pw060323p07q167	C	1615535	FTN_1518	1614441	1616447	R	669	913(2007)
C10	tnfn1_pw060323p07q175	C	1579957	FTN_1487	1577096	1579960	R	955	4(2865)
C11	tnfn1_pw060323p07q183	C	381533	FTN_0380	381374	381616	F	81	160(243)
C12	tnfn1_pw060323p07q191	C	639659	FTN_0606	639396	639743	F	116	264(348)
D01	tnfn1_pw060323p07q104	C	1463408	FTN_1383	1463001	1463768	F	256	408(768)
D02	tnfn1_pw060323p07q112	C	909805	FTN_0854	909700	910479	F	260	106(780)
D03	tnfn1_pw060323p07q120	C	313061	FTN_0304	312892	314295	F	468	170(1404)
D04	tnfn1_pw060323p07q128	C	1906974	FTN_1778	1905885	1907426	R	514	453(1542)
D05	tnfn1_pw060323p07q136	C	359369	FTN_0355	358647	359951	F	435	723(1305)
D06	tnfn1_pw060323p07q144	C	779086	intergenic					
D07	tnfn1_pw060323p07q152	C	1131548	FTN_1070	1130864	1132213	R	450	666(1350)
D08	tnfn1_pw060323p07q160	C	1843007	FTN_1717	1841960	1843996	R	679	990(2037)
D09	tnfn1_pw060323p07q168	C	406287	FTN_0408	406141	406611	F	157	147(471)
D10	tnfn1_pw060323p07q176	C	1631994	FTN_1534	1631854	1632321	F	156	141(468)
D11	tnfn1_pw060323p07q184	C	988456	intergenic					
D12	tnfn1_pw060323p07q192	U	1138561	FTN_1075	1138172	1138876	R	235	316(705)
E01	tnfn1_pw060323p07q105	C	950655	FTN_0895	950585	950917	R	111	263(333)
E02	tnfn1_pw060323p07q113	C	365681	FTN_0362	364836	366362	F	509	846(1527)
E03	tnfn1_pw060323p07q121	C	1107198	FTN_1048	1106474	1107538	R	355	341(1065)
E04	tnfn1_pw060323p07q129	C	816132	FTN_0759	816036	816326	F	97	97(291)
E05	tnfn1_pw060323p07q137	C	68787	FTN_0058	67916	69628	R	571	842(1713)
E06	tnfn1_pw060323p07q145	C	467346	FTN_0460	466763	467347	R	195	2(585)
E07	tnfn1_pw060323p07q153	C	949191	FTN_0892	948491	949213	R	241	23(723)
E08	tnfn1_pw060323p07q161	C	997590	FTN_0936	997186	998415	F	410	405(1230)
E09	tnfn1_pw060323p07q169	C	1526074	FTN_1438	1525003	1527696	F	898	1072(2694)
E10	tnfn1_pw060323p07q177	C	1451719	FTN_1371	1450809	1451963	R	385	245(1155)
E11	tnfn1_pw060323p07q185	C	871531	FTN_0814	870744	871868	R	375	338(1125)
E12	tnfn1_pw060323p07q193	C	1635345	-	1634886	1635750	F	288.3	460(865)
F01	tnfn1_pw060323p07q106	C	1025449	FTN_0969	1024199	1025695	R	499	247(1497)
F02	tnfn1_pw060323p07q114	C	709257	FTN_0667	708399	709784	R	462	528(1386)

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_pw060323p07q122	C	1064857	FTN_1005	1064800	1065075	F	92	58(276)
F04	tnfn1_pw060323p07q130	C	405739	FTN_0407	404710	406101	R	464	363(1392)
F05	tnfn1_pw060323p07q138	C	1234248	FTN_1163	1234247	1234675	R	143	428(429)
F06	tnfn1_pw060323p07q146	C	1541347	FTN_1452	1540850	1541536	F	229	498(687)
F07	tnfn1_pw060323p07q154	C	1247256	FTN_1175	1246823	1247617	R	265	362(795)
F08	tnfn1_pw060323p07q162	C	990791	FTN_0929	989845	990945	R	367	155(1101)
F09	tnfn1_pw060323p07q170	C	1332119	FTN_1261	1331640	1333124	F	495	480(1485)
F10	tnfn1_pw060323p07q178	C	1775905	FTN_1661	1775674	1777140	R	489	1236(1467)
F11	tnfn1_pw060323p07q186	C	1227916	FTN_1157	1227077	1228891	F	605	840(1815)
F12	tnfn1_pw060323p07q194	C	1367258	FTN_1298	1367030	1368379	F	450	229(1350)
G01	tnfn1_pw060323p07q107	C	1346755	FTN_1274	1346150	1346974	R	275	220(825)
G02	tnfn1_pw060323p07q115	C	296921	FTN_0290	296739	297281	F	181	183(543)
G03	tnfn1_pw060323p07q123	C	1737315	FTN_1624	1736861	1737736	R	292	422(876)
G04	tnfn1_pw060323p07q131	C	360070	FTN_0356	359964	360206	F	81	107(243)
G05	tnfn1_pw060323p07q139	C	638776	FTN_0605	638482	639396	F	305	295(915)
G06	tnfn1_pw060323p07q147	C	1065666	FTN_1006	1065118	1066374	R	419	709(1257)
G07	tnfn1_pw060323p07q155	C	794968	FTN_0741	794174	795628	R	485	661(1455)
G08	tnfn1_pw060323p07q163	C	1038449	FTN_0984	1037817	1039706	R	630	1258(1890)
G09	tnfn1_pw060323p07q171	C	614612	FTN_0585	614004	614723	R	240	112(720)
G10	tnfn1_pw060323p07q179	C	898376	FTN_0842	897754	898863	R	370	488(1110)
G11	tnfn1_pw060323p07q187	C	459584	FTN_0455	458374	461271	F	966	1211(2898)
G12	tnfn1_pw060323p07q195	C	734136	FTN_0690	733590	735296	F	569	547(1707)
H01	tnfn1_pw060323p07q108	C	1536818	FTN_1447	1536391	1537371	R	327	554(981)
H02	tnfn1_pw060323p07q116	C	1541050	FTN_1452	1540850	1541536	F	229	201(687)
H03	tnfn1_pw060323p07q124	C	1721439	-	1721384	1721620	R	79	182(237)
H04	tnfn1_pw060323p07q132	C	465230	FTN_0459	465112	466767	R	552	1538(1656)
H05	tnfn1_pw060323p07q140	C	1210235	FTN_1144	1210136	1210549	R	138	315(414)
H06	tnfn1_pw060323p07q148	C	1439459	FTN_1358	1439009	1439578	R	190	120(570)
H07	tnfn1_pw060323p07q156	C	481576	FTN_0477	481348	482232	F	295	229(885)
H08	tnfn1_pw060323p07q164	C	1483532	FTN_1405	1482889	1483809	R	307	278(921)
H09	tnfn1_pw060323p07q172	C	1422709	FTN_1344	1422190	1423386	F	399	520(1197)
H10	tnfn1_pw060323p07q180	C	275096	FTN_0267	274900	275400	F	167	197(501)
H11	tnfn1_pw060323p07q188	C	91102	FTN_0080	90741	91610	F	290	362(870)
H12	tnfn1_pw060323p07q196	C	312189	FTN_0303	311969	312892	F	308	221(924)

[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 7 (tnfn1_pw060323p07) – 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_pw060323p07q101	EXACT(0)	157	152	116	27	EXACT(0)	200	189	51
A02	tnfn1_pw060323p07q109	EXACT(0)	157	159	126	35	EXACT(0)	200	190	57
A03	tnfn1_pw060323p07q117	EXACT(0)	156	153	125	37	EXACT(0)	200	192	53
A04	tnfn1_pw060323p07q125	EXACT(0)	157	153	134	37	EXACT(0)	200	195	56
A05	tnfn1_pw060323p07q133	EXACT(0)	122	125	99	27	EXACT(0)	200	189	50
A06	tnfn1_pw060323p07q141	EXACT(0)	121	116	91	30	EXACT(0)	200	185	56
A07	tnfn1_pw060323p07q149	EXACT(0)	123	109	70	20	EXACT(0)	200	171	36
A08	tnfn1_pw060323p07q157	EXACT(0)	156	145	110	31	EXACT(0)	200	184	50
A09	tnfn1_pw060323p07q165	EXACT(0)	154	145	120	37	EXACT(0)	200	187	57
A10	tnfn1_pw060323p07q173	EXACT(0)	155	152	125	39	EXACT(0)	200	199	56
A11	tnfn1_pw060323p07q181	EXACT(0)	156	152	125	37	EXACT(0)	200	186	54
A12	tnfn1_pw060323p07q189	EXACT(0)	156	145	128	34	EXACT(0)	200	192	56
B01	tnfn1_pw060323p07q102	EXACT(0)	156	153	120	29	EXACT(0)	200	181	56
B02	tnfn1_pw060323p07q110	EXACT(0)	157	151	132	37	EXACT(0)	200	188	49
B03	tnfn1_pw060323p07q118	EXACT(0)	156	152	121	36	EXACT(0)	198	184	51
B04	tnfn1_pw060323p07q126	EXACT(0)	155	153	122	32	EXACT(0)	200	180	47

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_pw060323p07q134	EXACT(0)	120	112	62	21	EXACT(0)	200	187	51
B06	tnfn1_pw060323p07q142	EXACT(0)	122	109	72	22	EXACT(0)	172	149	44
B07	tnfn1_pw060323p07q150	EXACT(0)	124	119	94	24	EXACT(0)	200	187	48
B08	tnfn1_pw060323p07q158	EXACT(0)	156	146	130	42	EXACT(0)	133	119	50
B09	tnfn1_pw060323p07q166	EXACT(0)	156	152	134	39	ESTIMATE(58)	142	110	26
B10	tnfn1_pw060323p07q174	EXACT(0)	156	152	125	39	EXACT(0)	200	193	53
B11	tnfn1_pw060323p07q182	EXACT(0)	156	145	124	34	EXACT(0)	200	191	53
B12	tnfn1_pw060323p07q190	EXACT(0)	156	152	128	42	EXACT(0)	200	193	59
C01	tnfn1_pw060323p07q103	EXACT(0)	156	153	123	34	EXACT(0)	200	187	56
C02	tnfn1_pw060323p07q111	EXACT(0)	156	87	75	29	EXACT(0)	200	189	53
C03	tnfn1_pw060323p07q119	EXACT(0)	155	142	99	20	EXACT(0)	200	188	53
C04	tnfn1_pw060323p07q127	EXACT(0)	152	145	100	34	EXACT(0)	200	184	56
C05	tnfn1_pw060323p07q135	EXACT(0)	123	120	97	26	EXACT(0)	200	185	55
C06	tnfn1_pw060323p07q143	EXACT(0)	123	112	101	27	EXACT(0)	200	183	47
C07	tnfn1_pw060323p07q151	EXACT(0)	122	118	57	19	EXACT(0)	200	174	48
C08	tnfn1_pw060323p07q159	EXACT(0)	156	151	130	40	EXACT(0)	200	192	41
C09	tnfn1_pw060323p07q167	EXACT(0)	155	145	126	40	EXACT(0)	200	191	55
C10	tnfn1_pw060323p07q175	EXACT(0)	155	146	120	36	EXACT(0)	200	180	55
C11	tnfn1_pw060323p07q183	EXACT(0)	155	145	135	43	EXACT(0)	200	160	43
C12	tnfn1_pw060323p07q191	EXACT(0)	157	142	112	33	EXACT(0)	163	135	42
D01	tnfn1_pw060323p07q104	EXACT(0)	156	152	133	35	EXACT(0)	200	181	43
D02	tnfn1_pw060323p07q112	EXACT(0)	157	152	130	37	EXACT(0)	200	190	53
D03	tnfn1_pw060323p07q120	EXACT(0)	156	145	131	37	EXACT(0)	200	182	55
D04	tnfn1_pw060323p07q128	EXACT(0)	155	145	125	42	EXACT(0)	200	185	57
D05	tnfn1_pw060323p07q136	EXACT(0)	125	118	107	31	EXACT(0)	200	193	53
D06	tnfn1_pw060323p07q144	EXACT(0)	122	113	97	26	EXACT(0)	200	174	48
D07	tnfn1_pw060323p07q152	EXACT(0)	122	113	94	28	EXACT(0)	200	185	50
D08	tnfn1_pw060323p07q160	EXACT(0)	155	145	129	42	EXACT(0)	200	191	56
D09	tnfn1_pw060323p07q168	EXACT(0)	155	152	128	36	EXACT(0)	200	186	56
D10	tnfn1_pw060323p07q176	EXACT(0)	156	146	130	42	EXACT(0)	200	189	54
D11	tnfn1_pw060323p07q184	EXACT(0)	156	151	117	29	EXACT(0)	200	184	53
D12	tnfn1_pw060323p07q192	EXACT(0)	158	152	147	46	EXACT(0)	149	140	62
E01	tnfn1_pw060323p07q105	EXACT(0)	157	152	117	25	EXACT(0)	200	184	52
E02	tnfn1_pw060323p07q113	EXACT(0)	155	152	131	41	EXACT(0)	150	143	51
E03	tnfn1_pw060323p07q121	EXACT(0)	153	153	116	41	EXACT(0)	200	189	56
E04	tnfn1_pw060323p07q129	EXACT(0)	155	151	124	30	EXACT(0)	200	191	54
E05	tnfn1_pw060323p07q137	EXACT(0)	123	120	90	24	EXACT(0)	200	187	51
E06	tnfn1_pw060323p07q145	EXACT(0)	123	117	96	29	EXACT(0)	200	179	43
E07	tnfn1_pw060323p07q153	EXACT(0)	123	119	80	22	EXACT(0)	200	181	52
E08	tnfn1_pw060323p07q161	EXACT(0)	155	145	120	36	EXACT(0)	200	174	51
E09	tnfn1_pw060323p07q169	EXACT(0)	156	146	127	40	EXACT(0)	200	192	50
E10	tnfn1_pw060323p07q177	EXACT(0)	157	153	116	33	EXACT(0)	200	188	57
E11	tnfn1_pw060323p07q185	EXACT(0)	156	153	126	37	EXACT(0)	200	187	57
E12	tnfn1_pw060323p07q193	EXACT(0)	151	139	119	41	EXACT(0)	79	51	21
F01	tnfn1_pw060323p07q106	EXACT(0)	157	153	131	41	EXACT(0)	190	156	37
F02	tnfn1_pw060323p07q114	EXACT(0)	155	145	117	35	EXACT(0)	200	179	45
F03	tnfn1_pw060323p07q122	EXACT(0)	157	153	137	41	EXACT(0)	200	170	39
F04	tnfn1_pw060323p07q130	EXACT(0)	157	152	127	36	EXACT(0)	200	186	53
F05	tnfn1_pw060323p07q138	EXACT(0)	123	120	99	33	EXACT(0)	200	190	50
F06	tnfn1_pw060323p07q146	EXACT(0)	122	119	101	34	EXACT(0)	200	186	43
F07	tnfn1_pw060323p07q154	EXACT(0)	123	112	92	26	EXACT(0)	200	187	54
F08	tnfn1_pw060323p07q162	EXACT(0)	155	153	108	25	EXACT(0)	200	180	43
F09	tnfn1_pw060323p07q170	EXACT(0)	157	152	127	35	EXACT(0)	200	177	54
F10	tnfn1_pw060323p07q178	EXACT(0)	156	146	121	40	EXACT(0)	200	193	49
F11	tnfn1_pw060323p07q186	EXACT(0)	155	145	123	41	EXACT(0)	200	196	49
F12	tnfn1_pw060323p07q194	EXACT(0)	156	152	118	33	EXACT(0)	200	194	53
G01	tnfn1_pw060323p07q107	EXACT(0)	157	146	132	38	EXACT(0)	145	143	53
G02	tnfn1_pw060323p07q115	EXACT(0)	156	151	132	41	EXACT(0)	200	165	43
G03	tnfn1_pw060323p07q123	EXACT(0)	156	153	129	31	EXACT(0)	200	188	50
G04	tnfn1_pw060323p07q131	EXACT(0)	125	120	96	25	EXACT(0)	200	188	55
G05	tnfn1_pw060323p07q139	EXACT(0)	122	113	94	26	EXACT(0)	200	187	49
G06	tnfn1_pw060323p07q147	EXACT(0)	122	120	96	32	EXACT(0)	200	180	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
G07	tnfn1_pw060323p07q155	EXACT(0)	156	152	134	40	EXACT(0)	200	187	57
G08	tnfn1_pw060323p07q163	EXACT(0)	156	152	128	39	EXACT(0)	200	194	57
G09	tnfn1_pw060323p07q171	EXACT(0)	156	152	134	39	EXACT(0)	150	149	54
G10	tnfn1_pw060323p07q179	EXACT(0)	158	153	134	37	EXACT(0)	200	180	45
G11	tnfn1_pw060323p07q187	EXACT(0)	155	145	126	41	EXACT(0)	200	190	57
G12	tnfn1_pw060323p07q195	EXACT(0)	157	153	137	40	EXACT(0)	200	190	64
H01	tnfn1_pw060323p07q108	EXACT(0)	157	151	132	40	EXACT(0)	200	187	49
H02	tnfn1_pw060323p07q116	NONE	0	0	0	31	ESTIMATE(154)	731	626	36
H03	tnfn1_pw060323p07q124	EXACT(0)	158	152	132	37	EXACT(0)	200	192	52
H04	tnfn1_pw060323p07q132	EXACT(0)	122	125	99	28	EXACT(0)	200	180	51
H05	tnfn1_pw060323p07q140	EXACT(0)	123	118	102	27	EXACT(0)	199	178	45
H06	tnfn1_pw060323p07q148	EXACT(0)	124	120	104	35	EXACT(0)	200	185	47
H07	tnfn1_pw060323p07q156	EXACT(0)	156	151	121	36	EXACT(0)	200	192	54
H08	tnfn1_pw060323p07q164	EXACT(0)	156	145	137	39	EXACT(0)	200	188	46
H09	tnfn1_pw060323p07q172	EXACT(0)	156	145	128	39	EXACT(0)	200	192	57
H10	tnfn1_pw060323p07q180	EXACT(0)	155	153	132	39	EXACT(0)	200	181	49
H11	tnfn1_pw060323p07q188	EXACT(0)	153	108	99	41	EXACT(0)	200	195	52
H12	tnfn1_pw060323p07q196	EXACT(0)	156	152	117	29	EXACT(0)	200	184	48

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