Product Information Sheet for NR-51284

Francisella tularensis subsp. *novicida* "Two-Allele" Transposon Mutant Library, Plate 2 (tnfn1_pw060323p02)

Catalog No. NR-51284

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-51284 represents Plate 2 (tnfn1_pw060323p02) 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-51284 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 2 (tnfn1_pw060323p02), NR-51284."

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.

Table 1: Plate 2 (tnfn1_pw060323p02) – Transposon Type and Mutated Gene[1]

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060323p02q101	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
A02	tnfn1_pw060323p02q109	T20	-	protein of unknown function	unknown function - novel
A03	tnfn1_pw060323p02q117	T20	-	conserved protein of unknown function	unknown function - conserved
A04	tnfn1_pw060323p02q125	T20	rplI	50S ribosomal protein L9	translation, ribosomal structure and biogenesis
A05	tnfn1_pw060323p02q133	T20	-	sugar porter (SP) family	transport - carbohydrates (sugars, polysaccharides)
A06	tnfn1_pw060323p02q141	T20	clpX	ATP-dependent Clp protease subunit X	post-translational modification, protein turnover, chaperones - protein degradation
A07	tnfn1_pw060323p02q149	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
A08	tnfn1_pw060323p02q157	T20	-	pseudogene: hypothetical membrane protein, fragment	pseudogene
A09	tnfn1_pw060323p02q165	T18	-	DNA uptake protein, SMF family	transport
A10	tnfn1_pw060323p02q173	T18	-	transcriptional regulator, LysR family	signal transduction and regulation
A11	tnfn1_pw060323p02q181	T20	-	hypothetical protein	hypothetical - novel
A12	tnfn1_pw060323p02q189	T20	-	phage integrase	mobile and extrachromosomal element functions - phage or plasmid related proteins
B01	tnfn1_pw060323p02q102	T20	-	ROK family protein	putative enzymes
B02	tnfn1_pw060323p02q110	T20	-	D-isomer specific 2-hydroxyacid dehydrogenase	energy metabolism
B03	tnfn1_pw060323p02q118	T20	-	methyltransferase	putative enzymes
B04	tnfn1_pw060323p02q126	T20	-	protein of unknown function	unknown function - novel
B05	tnfn1_pw060323p02q134	T20	-	conserved protein of unknown function	unknown function - conserved
B06	tnfn1_pw060323p02q142	T20	-	protein of unknown function	unknown function - novel
B07	tnfn1_pw060323p02q150	T20	-	aspartate aminotransferase	other metabolism - degradation, utilization, assimilation
B08	tnfn1_pw060323p02q158	T20	-	conserved hypothetical protein	hypothetical - conserved
B09	tnfn1_pw060323p02q166	T18	-	hypothetical protein	hypothetical - novel
B10	tnfn1_pw060323p02q174	T18	nth	endonuclease III	DNA replication, recombination, modification and repair - restriction/modification
B11	tnfn1_pw060323p02q182	T20	-	hypothetical protein	hypothetical - novel
B12	tnfn1_pw060323p02q190	T20	-	MutT/nudix family protein	putative enzymes
C01	tnfn1_pw060323p02q103	T20	asnB	asparagine synthase	amino acid metabolism - biosynthesis
C02	tnfn1_pw060323p02q111	T20	-	protein of unknown function	unknown function - novel
C03	tnfn1_pw060323p02q119	T20	pilV	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
C04	tnfn1_pw060323p02q127	T20	-	metabolite:H+ symporter (MHS) family protein	transport - carbohydrates (sugars, polysaccharides)
C05	tnfn1_pw060323p02q135	T20	-	membrane protein of unknown function	unknown function - novel
C06	tnfn1_pw060323p02q143	T20	-	pilus assembly protein	motility, attachment and secretion structure
C07	tnfn1_pw060323p02q151	T20	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	translation, ribosomal structure and biogenesis
C08	tnfn1_pw060323p02q159	<KAN-2>	-	lipase/esterase	fatty acids and lipids metabolism
C09	tnfn1_pw060323p02q167	T18	-	conserved protein of unknown function	unknown function - conserved
C10	tnfn1_pw060323p02q175	T20	cspC	cold shock protein, DNA-binding	signal transduction and regulation
C11	tnfn1_pw060323p02q183	T20	-	arsenite-antimonite (ArsB) efflux family protein	transport
C12	tnfn1_pw060323p02q191	T20	-	allophanate hydrolase subunit 2	other metabolism - degradation, utilization, assimilation
D01	tnfn1_pw060323p02q104	T20	proQ	activator of osmoprotectant transporter ProP	signal transduction and regulation
D02	tnfn1_pw060323p02q112	T20	-	hypothetical membrane protein	hypothetical - novel
D03	tnfn1_pw060323p02q120	T20	isftu3	isftu3	IS element
D04	tnfn1_pw060323p02q128	T20	-	ribokinase, pfkB family	carbohydrate metabolism
D05	tnfn1_pw060323p02q136	T20	-	amino acid antiporter	transport - amino-acid
D06	tnfn1_pw060323p02q144	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
D07	tnfn1_pw060323p02q152	T20	-	conserved hypothetical membrane protein	hypothetical - conserved

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D08	tnfn1_pw060323p02q160	<KAN-2>	-	lipase/esterase	fatty acids and lipids metabolism
D09	tnfn1_pw060323p02q168	T18	wzb	low molecular weight (LMW) phosphotyrosine protein phosphatase	post-translational modification, protein turnover, chaperones - protein modification
D10	tnfn1_pw060323p02q176	T20	sdaC	serine permease	transport - amino-acid
D11	tnfn1_pw060323p02q184	T20	pta	phosphate acetyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
D12	tnfn1_pw060323p02q192	T20	-	lipoprotein of unknown function	unknown function - novel
E01	tnfn1_pw060323p02q105	T20	-	hypothetical protein	hypothetical - novel
E02	tnfn1_pw060323p02q113	T20	fur	ferric uptake regulation protein	signal transduction and regulation
E03	tnfn1_pw060323p02q121	T20	-	predicted metal-dependent hydrolase	putative enzymes
E04	tnfn1_pw060323p02q129	T20			
E05	tnfn1_pw060323p02q137	T20	-	AMP-binding enzyme	putative enzymes
E06	tnfn1_pw060323p02q145	T20	-	RmuC family protein	putative enzymes
E07	tnfn1_pw060323p02q153	T20	-	hypothetical protein	hypothetical - novel
E08	tnfn1_pw060323p02q161	<KAN-2>	cyoE	heme O synthase	cofactors, prosthetic groups, electron carriers metabolism
E09	tnfn1_pw060323p02q169	T18	-	protein of unknown function	unknown function - novel
E10	tnfn1_pw060323p02q177	T20	pheA	prephenate dehydratase	amino acid metabolism - biosynthesis
E11	tnfn1_pw060323p02q185	T20	-	dGTP triphosphohydrolase	nucleotides and nucleosides metabolism
E12	tnfn1_pw060323p02q193	T20	-	conserved protein of unknown function	unknown function - conserved
F01	tnfn1_pw060323p02q106	T20	recJ	single-stranded-DNA-specific exonuclease	DNA replication, recombination, modification and repair - restriction/modification
F02	tnfn1_pw060323p02q114	T20	pdpD	protein of unknown function	unknown function - novel
F03	tnfn1_pw060323p02q122	T20	-	sigma54 modulation protein	translation, ribosomal structure and biogenesis
F04	tnfn1_pw060323p02q130	T20	-	protein of unknown function	unknown function - novel
F05	tnfn1_pw060323p02q138	T20	-	hypothetical protein	hypothetical - novel
F06	tnfn1_pw060323p02q146	T20	-	hypothetical membrane protein	hypothetical - novel
F07	tnfn1_pw060323p02q154	T20	-	conserved protein of unknown function	unknown function - conserved
F08	tnfn1_pw060323p02q162	<KAN-2>	sspA	stringent starvation protein A	signal transduction and regulation
F09	tnfn1_pw060323p02q170	T18	-	hypothetical membrane protein	hypothetical - novel
F10	tnfn1_pw060323p02q178	T20	-	protein of unknown function	unknown function - novel
F11	tnfn1_pw060323p02q186	T20	-	protein of unknown function	unknown function - novel
F12	tnfn1_pw060323p02q194	T20	sbcB	exodeoxyribonuclease I	DNA replication, recombination, modification and repair - restriction/modification
G01	tnfn1_pw060323p02q107	T20	-	conserved protein of unknown function	unknown function - conserved
G02	tnfn1_pw060323p02q115	T20	-	10 TMS drug/metabolite exporter protein	transport - drugs / antibacterial compounds
G03	tnfn1_pw060323p02q123	T20	-	disulfide bond formation protein, DsbB family	post-translational modification, protein turnover, chaperones - protein modification
G04	tnfn1_pw060323p02q131	T20	-	RND efflux transporter, AcrB/AcrD/AcrF family	transport
G05	tnfn1_pw060323p02q139	T20	-	protein of unknown function	unknown function - novel
G06	tnfn1_pw060323p02q147	T20	adhC	Zn-dependent alcohol dehydrogenase	energy metabolism
G07	tnfn1_pw060323p02q155	T20	-	protein of unknown function	unknown function - novel
G08	tnfn1_pw060323p02q163	<KAN-2>	smpB	SsrA (tmRNA)-binding protein	translation, ribosomal structure and biogenesis
G09	tnfn1_pw060323p02q171	T18	-	hypothetical protein	hypothetical - novel
G10	tnfn1_pw060323p02q179	T20	-	type I restriction-modification system, subunit M (methyltransferase)	DNA replication, recombination, modification and repair - repair
G11	tnfn1_pw060323p02q187	T20	-	hypothetical membrane protein	hypothetical - novel
G12	tnfn1_pw060323p02q195	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - restriction/modification
H01	tnfn1_pw060323p02q108	T20	-	glycosyl hydrolase family 3	carbohydrate metabolism - biosynthesis
H02	tnfn1_pw060323p02q116	T20	-	hypothetical protein	hypothetical - novel
H03	tnfn1_pw060323p02q124	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - repair
H04	tnfn1_pw060323p02q132	T20	-	ABC transporter, ATP-binding protein	transport
H05	tnfn1_pw060323p02q140	T20	-	hypothetical protein	hypothetical - novel
H06	tnfn1_pw060323p02q148	T20	-	protein of unknown function	unknown function - novel
H07	tnfn1_pw060323p02q156	T20	-	protein of unknown function	unknown function - novel
H08	tnfn1_pw060323p02q164	<KAN-2>	rplY	50S ribosomal protein L25	translation, ribosomal structure and biogenesis
H09	tnfn1_pw060323p02q172	T18	-	licB-like transmembrane protein	putative enzymes
H10	tnfn1_pw060323p02q180	T20	-	hypothetical protein	hypothetical - novel
H11	tnfn1_pw060323p02q188	T20	pilM	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
H12	tnfn1_pw060323p02q196	T20	-	conserved hypothetical membrane protein	hypothetical - conserved

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

Table 2: Plate 2 (tnfn1_pw060323p02) – 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_pw060323p02q101	C	753902	FTN_0710	753221	756328	F	1036	682(3108)
A02	tnfn1_pw060323p02q109	C	146043	FTN_0132	145235	146200	R	322	158(966)
A03	tnfn1_pw060323p02q117	C	93417	FTN_0083	93070	93825	F	252	348(756)
A04	tnfn1_pw060323p02q125	C	1007312	FTN_0949	1006996	1007448	R	151	137(453)
A05	tnfn1_pw060323p02q133	C	1142263	FTN_1079	1141288	1142637	R	450	375(1350)
A06	tnfn1_pw060323p02q141	C	1117073	FTN_1056	1115895	1117145	R	417	73(1251)
A07	tnfn1_pw060323p02q149	C	1634011	FTN_1536	1633310	1634656	R	449	646(1347)
A08	tnfn1_pw060323p02q157	C	1459603	FTN_1379	1457975	1459691	R	572.3	89(1717)
A09	tnfn1_pw060323p02q165	C	351083	FTN_0345	351044	352147	R	368	1065(1104)
A10	tnfn1_pw060323p02q173	C	112145	FTN_0101	111569	112462	R	298	318(894)
A11	tnfn1_pw060323p02q181	C	191659	FTN_0175	191251	192873	F	541	409(1623)
A12	tnfn1_pw060323p02q189	C	14837	FTN_0017	13789	15027	R	413	191(1239)
B01	tnfn1_pw060323p02q102	C	648705	FTN_0617	648331	649293	F	321	375(963)
B02	tnfn1_pw060323p02q110	C	1846779	FTN_1719	1846033	1847178	R	382	400(1146)
B03	tnfn1_pw060323p02q118	C	1229294	FTN_1158	1229066	1229818	F	251	229(753)
B04	tnfn1_pw060323p02q126	C	1352230	FTN_1279	1352177	1352596	F	140	54(420)
B05	tnfn1_pw060323p02q134	C	48037	FTN_0043	47436	48965	F	510	602(1530)
B06	tnfn1_pw060323p02q142	C	1390127	FTN_1317	1389274	1390422	F	383	854(1149)
B07	tnfn1_pw060323p02q150	C	1212220	FTN_1146	1211574	1212764	R	397	545(1191)
B08	tnfn1_pw060323p02q158	C	87349	FTN_0074	87173	87418	R	82	70(246)
B09	tnfn1_pw060323p02q166	C	40337	FTN_0037	40006	40347	R	114	11(342)
B10	tnfn1_pw060323p02q174	C	1091038	FTN_1035	1090869	1091504	F	212	170(636)
B11	tnfn1_pw060323p02q182	C	376195	FTN_0374	376108	376314	F	69	88(207)
B12	tnfn1_pw060323p02q190	C	344628	FTN_0338	344391	345035	F	215	238(645)
C01	tnfn1_pw060323p02q103	C	996119	FTN_0935	995336	997186	F	617	784(1851)
C02	tnfn1_pw060323p02q111	C	146043	FTN_0132	145235	146200	R	322	158(966)
C03	tnfn1_pw060323p02q119	C	412980	FTN_0413	412120	413349	R	410	370(1230)
C04	tnfn1_pw060323p02q127	C	139640	FTN_0128	139163	140368	F	402	478(1206)
C05	tnfn1_pw060323p02q135	C	1151997	FTN_1090	1151656	1152243	R	196	247(588)
C06	tnfn1_pw060323p02q143	C	1602828	FTN_1507	1602509	1603009	R	167	182(501)
C07	tnfn1_pw060323p02q151	C	1303193	FTN_1234	1302512	1303525	R	338	333(1014)
C08	tnfn1_pw060323p02q159	C	875581	FTN_0818	874701	875618	R	306	38(918)
C09	tnfn1_pw060323p02q167	C	391999	FTN_0393	391849	392901	F	351	151(1053)
C10	tnfn1_pw060323p02q175	C	494000	FTN_0488	493874	494074	R	67	75(201)
C11	tnfn1_pw060323p02q183	C	384242	FTN_0382	383357	384592	F	412	886(1236)
C12	tnfn1_pw060323p02q191	C	100405	FTN_0089	100182	100991	F	270	224(810)
D01	tnfn1_pw060323p02q104	C	296191	FTN_0289	296016	296714	F	233	176(699)
D02	tnfn1_pw060323p02q112	U	499961	FTN_0494	499405	500001	R	199	41(597)
D03	tnfn1_pw060323p02q120	C	1717230	-	1716927	1717650	R	241.3	421(724)
D04	tnfn1_pw060323p02q128	C	1280057	FTN_1210	1279841	1280944	F	368	217(1104)
D05	tnfn1_pw060323p02q136	C	903767	FTN_0848	902798	904216	R	473	450(1419)
D06	tnfn1_pw060323p02q144	C	1046843	FTN_0990	1045587	1048394	R	936	1552(2808)
D07	tnfn1_pw060323p02q152	C	1093416	FTN_1038	1093310	1093993	F	228	107(684)
D08	tnfn1_pw060323p02q160	C	875581	FTN_0818	874701	875618	R	306	38(918)
D09	tnfn1_pw060323p02q168	C	1105371	FTN_1046	1105060	1105542	R	161	172(483)
D10	tnfn1_pw060323p02q176	C	16741	FTN_0018	15688	16908	R	407	168(1221)
D11	tnfn1_pw060323p02q184	C	136284	FTN_0126	135582	137675	F	698	703(2094)
D12	tnfn1_pw060323p02q192	C	426168	FTN_0427	425944	426390	F	149	225(447)
E01	tnfn1_pw060323p02q105	C	1862806	FTN_1736	1862687	1863082	F	132	120(396)
E02	tnfn1_pw060323p02q113	U	1795568	FTN_1681	1795398	1795817	F	140	171(420)
E03	tnfn1_pw060323p02q121	C	803611	FTN_0749	802977	803642	F	222	635(666)
E04	tnfn1_pw060323p02q129	C	1639766	intergenic					
E05	tnfn1_pw060323p02q137	C	878005	FTN_0821	877333	878700	F	456	673(1368)
E06	tnfn1_pw060323p02q145	C	1081661	FTN_1024	1080823	1082235	R	471	575(1413)
E07	tnfn1_pw060323p02q153	C	371861	FTN_0368	371729	372250	F	174	133(522)
E08	tnfn1_pw060323p02q161	C	221025	FTN_0199	220528	221373	F	282	498(846)
E09	tnfn1_pw060323p02q169	C	1685652	FTN_1587	1685390	1685998	R	203	347(609)
E10	tnfn1_pw060323p02q177	C	802429	FTN_0748	802109	802948	F	280	321(840)
E11	tnfn1_pw060323p02q185	C	666145	FTN_0632	664957	666279	R	441	135(1323)
E12	tnfn1_pw060323p02q193	C	283186	FTN_0275	282485	283540	F	352	702(1056)
F01	tnfn1_pw060323p02q106	C	595540	FTN_0569	594781	596520	R	580	981(1740)
F02	tnfn1_pw060323p02q114	C	1402305	FTN_1325	1399806	1403540	R	1245	1236(3735)

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_pw060323p02q122	C	1366369	FTN_1296	1366367	1366660	R	98	292(294)
F04	tnfn1_pw060323p02q130	C	91934	FTN_0081	91627	92358	R	244	425(732)
F05	tnfn1_pw060323p02q138	C	950655	FTN_0895	950585	950917	R	111	263(333)
F06	tnfn1_pw060323p02q146	C	505003	FTN_0498	504268	505494	F	409	736(1227)
F07	tnfn1_pw060323p02q154	C	494555	FTN_0489	494328	494654	R	109	100(327)
F08	tnfn1_pw060323p02q162	C	575437	FTN_0549	574840	575469	F	210	598(630)
F09	tnfn1_pw060323p02q170	C	397793	FTN_0398	397551	398084	R	178	292(534)
F10	tnfn1_pw060323p02q178	C	244971	FTN_0222	244745	245710	F	322	227(966)
F11	tnfn1_pw060323p02q186	C	1757039	FTN_1644	1755794	1758634	R	947	1596(2841)
F12	tnfn1_pw060323p02q194	C	1250675	FTN_1177	1249665	1251110	R	482	436(1446)
G01	tnfn1_pw060323p02q107	U	992353	FTN_0931	991793	992749	F	319	561(957)
G02	tnfn1_pw060323p02q115	C	1619008	FTN_1521	1618541	1619422	F	294	468(882)
G03	tnfn1_pw060323p02q123	C	1455051	FTN_1376	1454884	1455417	F	178	168(534)
G04	tnfn1_pw060323p02q131	C	1715466	FTN_1610	1713789	1716899	F	1037	1678(3111)
G05	tnfn1_pw060323p02q139	C	1079926	FTN_1022	1079866	1080159	F	98	61(294)
G06	tnfn1_pw060323p02q147	C	406949	FTN_0409	406706	407815	F	370	244(1110)
G07	tnfn1_pw060323p02q155	C	1322976	FTN_1254	1322868	1323953	F	362	109(1086)
G08	tnfn1_pw060323p02q163	C	1235178	FTN_1164	1234750	1235220	F	157	429(471)
G09	tnfn1_pw060323p02q171	C	27140	FTN_0026	27076	27327	F	84	65(252)
G10	tnfn1_pw060323p02q179	C	1219012	FTN_1152	1218102	1219547	R	482	536(1446)
G11	tnfn1_pw060323p02q187	C	151085	FTN_0138	151080	151694	F	205	6(615)
G12	tnfn1_pw060323p02q195	C	747055	FTN_0703	746848	747417	F	190	208(570)
H01	tnfn1_pw060323p02q108	C	863831	FTN_0806	862723	864387	R	555	557(1665)
H02	tnfn1_pw060323p02q116	C	26439	FTN_0025	26213	26797	R	195	359(585)
H03	tnfn1_pw060323p02q124	C	1223789	FTN_1155	1222624	1224969	R	782	1181(2346)
H04	tnfn1_pw060323p02q132	C	993455	FTN_0932	992752	994548	F	599	704(1797)
H05	tnfn1_pw060323p02q140	C	950655	FTN_0895	950585	950917	R	111	263(333)
H06	tnfn1_pw060323p02q148	C	798642	FTN_0745	798391	799095	F	235	252(705)
H07	tnfn1_pw060323p02q156	C	1322976	FTN_1254	1322868	1323953	F	362	109(1086)
H08	tnfn1_pw060323p02q164	C	1066479	FTN_1007	1066473	1066760	R	96	282(288)
H09	tnfn1_pw060323p02q172	C	1653776	FTN_1555	1653462	1654343	F	294	315(882)
H10	tnfn1_pw060323p02q180	C	311758	FTN_0302	311638	311982	F	115	121(345)
H11	tnfn1_pw060323p02q188	C	1205553	FTN_1141	1205009	1206010	R	334	458(1002)
H12	tnfn1_pw060323p02q196	U	693534	FTN_0654	693039	693686	R	216	153(648)

[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 2 (tnfn1_pw060323p02) – 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_pw060323p02q101	EXACT(0)	155	153	131	39	EXACT(0)	175	126	28
A02	tnfn1_pw060323p02q109	EXACT(0)	157	151	129	35	EXACT(0)	200	185	57
A03	tnfn1_pw060323p02q117	EXACT(0)	156	153	129	39	EXACT(0)	118	104	53
A04	tnfn1_pw060323p02q125	EXACT(0)	155	144	124	34	EXACT(0)	200	169	45
A05	tnfn1_pw060323p02q133	EXACT(0)	156	142	100	31	EXACT(0)	166	70	27
A06	tnfn1_pw060323p02q141	EXACT(0)	156	152	125	40	EXACT(0)	200	186	53
A07	tnfn1_pw060323p02q149	EXACT(0)	156	146	125	34	EXACT(0)	200	187	52
A08	tnfn1_pw060323p02q157	EXACT(0)	157	151	135	42	EXACT(0)	200	177	56
A09	tnfn1_pw060323p02q165	EXACT(0)	123	120	66	21	ESTIMATE(2)	198	176	53
A10	tnfn1_pw060323p02q173	EXACT(0)	122	113	97	30	EXACT(0)	200	187	57
A11	tnfn1_pw060323p02q181	EXACT(0)	155	145	120	36	EXACT(0)	200	194	45
A12	tnfn1_pw060323p02q189	EXACT(0)	155	142	108	31	EXACT(0)	200	172	48
B01	tnfn1_pw060323p02q102	EXACT(0)	157	152	136	41	EXACT(0)	200	176	41
B02	tnfn1_pw060323p02q110	EXACT(0)	156	153	129	40	EXACT(0)	200	191	59
B03	tnfn1_pw060323p02q118	EXACT(0)	156	150	120	33	EXACT(0)	200	191	55
B04	tnfn1_pw060323p02q126	EXACT(0)	155	145	123	39	EXACT(0)	200	183	44

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_pw060323p02q134	EXACT(0)	154	150	121	39	EXACT(0)	55	46	23
B06	tnfn1_pw060323p02q142	EXACT(0)	156	153	129	38	EXACT(0)	200	185	54
B07	tnfn1_pw060323p02q150	EXACT(0)	156	153	129	38	EXACT(0)	200	190	56
B08	tnfn1_pw060323p02q158	EXACT(0)	156	151	127	41	EXACT(0)	200	192	54
B09	tnfn1_pw060323p02q166	EXACT(0)	124	119	106	35	EXACT(0)	200	183	54
B10	tnfn1_pw060323p02q174	EXACT(0)	122	119	101	29	EXACT(0)	200	184	51
B11	tnfn1_pw060323p02q182	EXACT(0)	157	152	136	41	EXACT(0)	200	190	55
B12	tnfn1_pw060323p02q190	EXACT(0)	157	145	108	33	EXACT(0)	200	186	54
C01	tnfn1_pw060323p02q103	EXACT(0)	157	146	120	38	EXACT(0)	200	189	56
C02	tnfn1_pw060323p02q111	EXACT(0)	156	146	123	35	EXACT(0)	200	185	58
C03	tnfn1_pw060323p02q119	EXACT(0)	157	146	129	40	EXACT(0)	200	195	55
C04	tnfn1_pw060323p02q127	EXACT(0)	157	153	130	37	EXACT(0)	143	127	33
C05	tnfn1_pw060323p02q135	EXACT(0)	156	146	121	39	EXACT(0)	201	123	40
C06	tnfn1_pw060323p02q143	EXACT(0)	155	145	117	32	EXACT(0)	200	187	52
C07	tnfn1_pw060323p02q151	EXACT(0)	155	146	130	40	EXACT(0)	200	194	55
C08	tnfn1_pw060323p02q159	EXACT(0)	122	119	98	26	EXACT(0)	200	190	55
C09	tnfn1_pw060323p02q167	EXACT(0)	123	117	87	24	EXACT(0)	200	192	56
C10	tnfn1_pw060323p02q175	EXACT(0)	155	146	130	39	EXACT(0)	162	154	53
C11	tnfn1_pw060323p02q183	EXACT(0)	158	151	140	39	EXACT(0)	200	192	54
C12	tnfn1_pw060323p02q191	EXACT(0)	157	152	129	36	EXACT(0)	150	148	54
D01	tnfn1_pw060323p02q104	EXACT(0)	156	153	129	39	EXACT(0)	200	189	55
D02	tnfn1_pw060323p02q112	EXACT(0)	156	152	128	43	EXACT(0)	200	184	67
D03	tnfn1_pw060323p02q120	EXACT(0)	155	145	123	39	EXACT(0)	200	192	54
D04	tnfn1_pw060323p02q128	EXACT(0)	155	145	126	39	EXACT(0)	200	193	49
D05	tnfn1_pw060323p02q136	EXACT(0)	156	150	123	38	EXACT(0)	200	189	55
D06	tnfn1_pw060323p02q144	EXACT(0)	156	152	133	38	EXACT(0)	200	190	54
D07	tnfn1_pw060323p02q152	EXACT(0)	154	136	125	45	EXACT(0)	200	191	53
D08	tnfn1_pw060323p02q160	EXACT(0)	122	118	97	26	EXACT(0)	200	190	54
D09	tnfn1_pw060323p02q168	EXACT(0)	122	112	99	36	EXACT(0)	200	162	43
D10	tnfn1_pw060323p02q176	EXACT(0)	156	150	123	34	EXACT(0)	200	187	53
D11	tnfn1_pw060323p02q184	EXACT(0)	154	145	126	37	EXACT(0)	200	190	56
D12	tnfn1_pw060323p02q192	EXACT(0)	155	153	122	34	EXACT(0)	200	193	57
E01	tnfn1_pw060323p02q105	EXACT(0)	156	153	122	36	EXACT(0)	200	194	57
E02	tnfn1_pw060323p02q113	EXACT(0)	154	145	126	50	EXACT(0)	199	187	57
E03	tnfn1_pw060323p02q121	EXACT(0)	156	146	127	40	EXACT(0)	198	186	52
E04	tnfn1_pw060323p02q129	EXACT(0)	156	152	131	42	EXACT(0)	199	187	54
E05	tnfn1_pw060323p02q137	EXACT(0)	156	152	128	38	EXACT(0)	200	192	43
E06	tnfn1_pw060323p02q145	EXACT(0)	155	145	129	40	EXACT(0)	200	193	51
E07	tnfn1_pw060323p02q153	EXACT(0)	156	153	129	48	EXACT(0)	59	55	54
E08	tnfn1_pw060323p02q161	EXACT(0)	121	118	97	30	EXACT(0)	200	187	52
E09	tnfn1_pw060323p02q169	EXACT(0)	122	118	100	34	EXACT(0)	200	194	51
E10	tnfn1_pw060323p02q177	EXACT(0)	156	152	131	43	EXACT(0)	201	143	45
E11	tnfn1_pw060323p02q185	EXACT(0)	156	152	124	39	EXACT(0)	200	184	57
E12	tnfn1_pw060323p02q193	EXACT(0)	157	152	144	37	EXACT(0)	200	195	51
F01	tnfn1_pw060323p02q106	EXACT(0)	157	153	131	35	EXACT(0)	170	162	55
F02	tnfn1_pw060323p02q114	EXACT(0)	156	153	126	38	EXACT(0)	200	185	58
F03	tnfn1_pw060323p02q122	EXACT(0)	155	145	123	38	EXACT(0)	200	182	52
F04	tnfn1_pw060323p02q130	EXACT(0)	156	151	118	35	EXACT(0)	200	191	59
F05	tnfn1_pw060323p02q138	EXACT(0)	155	151	118	30	EXACT(0)	200	184	54
F06	tnfn1_pw060323p02q146	EXACT(0)	155	152	116	33	EXACT(0)	200	188	56
F07	tnfn1_pw060323p02q154	EXACT(0)	155	153	132	39	EXACT(0)	200	182	58
F08	tnfn1_pw060323p02q162	EXACT(0)	122	120	93	26	EXACT(0)	200	191	49
F09	tnfn1_pw060323p02q170	EXACT(0)	124	120	104	32	EXACT(0)	115	109	50
F10	tnfn1_pw060323p02q178	EXACT(0)	157	152	126	36	EXACT(0)	200	196	53
F11	tnfn1_pw060323p02q186	EXACT(0)	156	152	125	40	EXACT(0)	200	190	57
F12	tnfn1_pw060323p02q194	EXACT(0)	157	153	134	39	EXACT(0)	200	186	56
G01	tnfn1_pw060323p02q107	EXACT(0)	157	152	124	42	EXACT(0)	200	185	61
G02	tnfn1_pw060323p02q115	EXACT(0)	155	153	124	38	EXACT(0)	200	192	51
G03	tnfn1_pw060323p02q123	EXACT(0)	157	151	128	32	EXACT(0)	200	188	56
G04	tnfn1_pw060323p02q131	EXACT(0)	156	152	121	35	EXACT(0)	200	194	54
G05	tnfn1_pw060323p02q139	EXACT(0)	156	153	132	41	EXACT(0)	76	75	56
G06	tnfn1_pw060323p02q147	EXACT(0)	155	146	127	41	EXACT(0)	200	196	57

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_pw060323p02q155	EXACT(0)	155	153	135	41	EXACT(0)	200	186	56
G08	tnfn1_pw060323p02q163	EXACT(0)	123	106	49	31	EXACT(0)	200	192	59
G09	tnfn1_pw060323p02q171	EXACT(0)	123	112	47	14	ESTIMATE(8)	192	173	37
G10	tnfn1_pw060323p02q179	EXACT(0)	155	152	125	39	EXACT(0)	200	197	52
G11	tnfn1_pw060323p02q187	EXACT(0)	156	152	118	33	EXACT(0)	200	172	57
G12	tnfn1_pw060323p02q195	EXACT(0)	156	152	128	40	EXACT(0)	200	184	56
H01	tnfn1_pw060323p02q108	EXACT(0)	157	153	121	33	EXACT(0)	200	190	53
H02	tnfn1_pw060323p02q116	EXACT(0)	156	145	128	37	EXACT(0)	200	173	48
H03	tnfn1_pw060323p02q124	EXACT(0)	156	153	126	39	EXACT(0)	200	195	58
H04	tnfn1_pw060323p02q132	EXACT(0)	155	152	126	38	EXACT(0)	200	182	55
H05	tnfn1_pw060323p02q140	EXACT(0)	155	153	122	33	EXACT(0)	200	181	56
H06	tnfn1_pw060323p02q148	EXACT(0)	156	150	126	36	EXACT(0)	200	186	58
H07	tnfn1_pw060323p02q156	EXACT(0)	154	150	115	35	EXACT(0)	200	186	54
H08	tnfn1_pw060323p02q164	EXACT(0)	121	112	87	25	EXACT(0)	173	146	50
H09	tnfn1_pw060323p02q172	EXACT(0)	123	119	96	27	EXACT(0)	200	187	51
H10	tnfn1_pw060323p02q180	EXACT(0)	155	78	64	18	EXACT(0)	200	187	47
H11	tnfn1_pw060323p02q188	EXACT(0)	155	142	88	25	EXACT(0)	139	132	44
H12	tnfn1_pw060323p02q196	EXACT(0)	156	151	135	46	EXACT(0)	200	184	65

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