Francisella tularensis subsp. *novicida* "Two-Allele" Transposon Mutant Library, Plate 9 (tnfn1_pw060328p01)

Catalog No. NR-51291

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-51291 represents plate 9 (tnfn1_pw060328p01) 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-51291 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 9 (tnfn1_pw060328p01), NR-51291."

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.

Support Provided by NIAID

Table 1: Plate 9 (tnfn1_pw060328p01) – Transposon Type and Mutated Gene[1]

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
A01	tnfn1_pw060328p01q101	T20	-	conserved protein of unknown function	unknown function - conserved
A02	tnfn1_pw060328p01q109	T20	-	protein of unknown function containing a von Willebrand factor type A (vWA) domain	unknown function - conserved
A03	tnfn1_pw060328p01q117	T20	trpD	anthranilate phosphoribosyltransferase	amino acid metabolism - biosynthesis
A04	tnfn1_pw060328p01q125	T20	-	NAD-dependent aldehyde dehydrogenase	other metabolism - degradation, utilization, assimilation
A05	tnfn1_pw060328p01q133	T20	-	major facilitator superfamily (MFS) transport protein	transport
A06	tnfn1_pw060328p01q141	T20	-	conserved hypothetical protein	hypothetical - conserved
A07	tnfn1_pw060328p01q149	T20	-	conserved protein of unknown function	unknown function - conserved
A08	tnfn1_pw060328p01q157	<KAN-2>	ugpQ	glycerophosphoryl diester phosphodiesterase	cell wall / LPS / capsule
A09	tnfn1_pw060328p01q165	T18	-	conserved protein of unknown function	unknown function - conserved
A10	tnfn1_pw060328p01q173	T18	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
A11	tnfn1_pw060328p01q181	T20	-	protein of unknown function	unknown function - novel
A12	tnfn1_pw060328p01q189	T20	wzx	O antigen flippase	transport
B01	tnfn1_pw060328p01q102	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
B02	tnfn1_pw060328p01q110	T20	-	sugar transporter, MFS superfamily	transport - carbohydrates (sugars, polysaccharides)
B03	tnfn1_pw060328p01q118	T20	carB	carbamoyl-phosphate synthase large chain	nucleotides and nucleosides metabolism
B04	tnfn1_pw060328p01q126	T20	mdh	malate dehydrogenase	energy metabolism
B05	tnfn1_pw060328p01q134	T20	-	amino acid permease	transport - amino-acid
B06	tnfn1_pw060328p01q142	T20	cysD	sulfate adenylyltransferase subunit 2	other metabolism - degradation, utilization, assimilation
B07	tnfn1_pw060328p01q150	<KAN-2>	lysU	lysyl-tRNA synthetase	other metabolism - biosynthesis
B08	tnfn1_pw060328p01q158	T18	-	acid phosphatase/phosphotransferase	putative enzymes
B09	tnfn1_pw060328p01q166	T18	-	hypothetical membrane protein	hypothetical - novel
B10	tnfn1_pw060328p01q174	T18	-	protein of unknown function	unknown function - novel
B11	tnfn1_pw060328p01q182	T20	-	metallo-beta-lactamase superfamily protein	putative enzymes
B12	tnfn1_pw060328p01q190	T20			
C01	tnfn1_pw060328p01q103	T20	-	protein of unknown function	unknown function - novel
C02	tnfn1_pw060328p01q111	T20	acnA	aconitate hydratase	energy metabolism
C03	tnfn1_pw060328p01q119	T20	-	hypothetical protein	hypothetical - novel
C04	tnfn1_pw060328p01q127	T20	-	conserved protein of unknown function	unknown function - conserved
C05	tnfn1_pw060328p01q135	T20	-	pseudogene: Membrane Protein. Fucose permease carbohydrate transport and metabolism	pseudogene
C06	tnfn1_pw060328p01q143	T20	ipdC	indolepyruvate decarboxylase	amino acid metabolism - degradation, utilization, assimilation
C07	tnfn1_pw060328p01q151	<KAN-2>	-	bifunctional protein: glutaredoxin 3 /ribonucleotide reductase beta subunit	nucleotides and nucleosides metabolism
C08	tnfn1_pw060328p01q159	T18	-	outer membrane protein of unknown function	unknown function - novel
C09	tnfn1_pw060328p01q167	T18	minD	septum formation inhibitor-activating ATPase	cell cycle
C10	tnfn1_pw060328p01q175	T18	xerD	site-specific recombinase	DNA replication, recombination, modification and repair
C11	tnfn1_pw060328p01q183	T20	-	metabolite:H+ symporter (MHS) family protein	transport
C12	tnfn1_pw060328p01q191	T20	-	DNA helicase	DNA replication, recombination, modification and repair
D01	tnfn1_pw060328p01q104	T18	minD	septum formation inhibitor-activating ATPase	cell cycle
D02	tnfn1_pw060328p01q112	T20	leuA	2-isopropylmalate synthase	amino acid metabolism - biosynthesis
D03	tnfn1_pw060328p01q120	T20			
D04	tnfn1_pw060328p01q128	T20	mdaB	NADPH-quinone reductase (modulator of drug activity B)	putative enzymes
D05	tnfn1_pw060328p01q136	T20	paaY	carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	putative enzymes
D06	tnfn1_pw060328p01q144	T20	-	hypothetical protein	hypothetical - novel
D07	tnfn1_pw060328p01q152	<KAN-2>	-	Type IV pili, pilus assembly protein	motility, attachment and secretion structure

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
D08	tnfn1_pw060328p01q160	T18	-	protein of unknown function	unknown function - novel
D09	tnfn1_pw060328p01q168	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
D10	tnfn1_pw060328p01q176	T18	-	hypothetical protein	hypothetical - novel
D11	tnfn1_pw060328p01q184	T20	-	protein of unknown function	unknown function - novel
D12	tnfn1_pw060328p01q192	T20	-	hypothetical protein	hypothetical - novel
E01	tnfn1_pw060328p01q105	T20	-	alanine racemase	amino acid metabolism - degradation, utilization, assimilation
E02	tnfn1_pw060328p01q113	T20	-	protein of unknown function	unknown function - novel
E03	tnfn1_pw060328p01q121	T20	ribC	riboflavin synthase alpha chain	cofactors, prosthetic groups, electron carriers metabolism
E04	tnfn1_pw060328p01q129	T20	purU	formyltetrahydrofolate deformylase	nucleotides and nucleosides metabolism
E05	tnfn1_pw060328p01q137	T20	-	RimI-like acetyltransferase	putative enzymes
E06	tnfn1_pw060328p01q145	T20	mutS	MutS, subunit of MutHLS complex, methyl-directed mismatch repair protein	DNA replication, recombination, modification and repair - restriction/modification
E07	tnfn1_pw060328p01q153	<KAN-2>	grpE	chaperone GrpE (heat shock protein). Hsp70/Hsc70 protein regulator activity	post-translational modification, protein turnover, chaperones
E08	tnfn1_pw060328p01q161	T18	-	hypothetical protein	hypothetical - novel
E09	tnfn1_pw060328p01q169	T18	isftu2	isftu2	IS element
E10	tnfn1_pw060328p01q177	T20	-	oxidoreductase iron/ascorbate family protein	other metabolism - degradation, utilization, assimilation
E11	tnfn1_pw060328p01q185	T20	lpxE	lipid A 1-phosphatase	fatty acids and lipids metabolism
E12	tnfn1_pw060328p01q193	T20	lldD	L-lactate dehydrogenase	other metabolism - degradation, utilization, assimilation
F01	tnfn1_pw060328p01q106	T20	prfC	peptide chain release factor 3	translation, ribosomal structure and biogenesis
F02	tnfn1_pw060328p01q114	T20	-	hypothetical protein	hypothetical - novel
F03	tnfn1_pw060328p01q122	T20	-	protein of unknown function	unknown function - novel
F04	tnfn1_pw060328p01q130	T20	-	hypothetical protein	hypothetical - novel
F05	tnfn1_pw060328p01q138	T20	-	conserved hypothetical protein	hypothetical - conserved
F06	tnfn1_pw060328p01q146	T20	-	conserved protein of unknown function	unknown function - conserved
F07	tnfn1_pw060328p01q154	<KAN-2>	-	SAICAR synthetase/phosphoribosylamine-glycine ligase	nucleotides and nucleosides metabolism
F08	tnfn1_pw060328p01q162	T18	-	N6-adenine-specific methylase	DNA replication, recombination, modification and repair
F09	tnfn1_pw060328p01q170	T18	-	Mg-dependent DNase	DNA replication, recombination, modification and repair
F10	tnfn1_pw060328p01q178	T20	xthA	exodeoxyribonuclease III	DNA replication, recombination, modification and repair - restriction/modification
F11	tnfn1_pw060328p01q186	T20	thrA	aspartate kinase I/homoserine dehydrogenase I	amino acid metabolism - biosynthesis
F12	tnfn1_pw060328p01q194	T20	-	protein of unknown function	unknown function - novel
G01	tnfn1_pw060328p01q107	T20	-	hydroxy/aromatic amino acid permease (HAAAP) family protein	transport - amino-acid
G02	tnfn1_pw060328p01q115	T20	-	peptide methionine sulfoxide reductase	post-translational modification, protein turnover, chaperones - protein modification
G03	tnfn1_pw060328p01q123	T20	oppB	peptide/opine/nickel uptake transporter (PepT) family protein	transport
G04	tnfn1_pw060328p01q131	T20	-	conserved hypothetical protein	hypothetical - conserved
G05	tnfn1_pw060328p01q139	T20	malQ	4-alpha-glucanotransferase	carbohydrate metabolism - degradation, utilization, assimilation
G06	tnfn1_pw060328p01q147	T20	-	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
G07	tnfn1_pw060328p01q155	T20	-	tRNA-methylthiotransferase MiaB protein	translation, ribosomal structure and biogenesis
G08	tnfn1_pw060328p01q163	T18	-	DedA family protein	putative enzymes
G09	tnfn1_pw060328p01q171	T18	-	hypothetical protein	potentially coding: hypothetical - novel
G10	tnfn1_pw060328p01q179	T20	-	phage terminase, small subunit	mobile and extrachromosomal element functions - phage or plasmid related proteins
G11	tnfn1_pw060328p01q187	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
G12	tnfn1_pw060328p01q195	T20	gph	phosphoglycolate phosphatase	putative enzymes
H01	tnfn1_pw060328p01q108	T20	isftu2	isftu2	IS element
H02	tnfn1_pw060328p01q116	T20	-	conserved protein of unknown function	unknown function - conserved
H03	tnfn1_pw060328p01q124	T20	kdpD	two component regulator, sensor histidine kinase kdpD	signal transduction and regulation
H04	tnfn1_pw060328p01q132	T20	-	glutamine amidotransferase, SNO family	cofactors, prosthetic groups, electron carriers metabolism
H05	tnfn1_pw060328p01q140	T20	-	protein of unknown function	unknown function - novel
H06	tnfn1_pw060328p01q148	T20	-	tRNA-methylthiotransferase MiaB protein	translation, ribosomal structure and biogenesis
H07	tnfn1_pw060328p01q156	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
H08	tnfn1_pw060328p01q164	T18	-	protein of unknown function	unknown function - novel
H09	tnfn1_pw060328p01q172	T18	-	conserved protein of unknown function	unknown function - conserved

Well Position	Strain Name	Transposon Type	Gene	Description	Function Class
H10	tnfn1_pw060328p01q180	T20	sohB	peptidase family S49 protein	post-translational modification, protein turnover, chaperones - protein modification
H11	tnfn1_pw060328p01q188	T20	-	sugar:cation symporter family protein	transport - carbohydrates (sugars, polysaccharides)
H12	tnfn1_pw060328p01q196	T20	wzx	O antigen flippase	transport

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

Table 2: Plate 9 (tnfn1_pw060328p01) – 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_pw060328p01q101	C	1646007	FTN_1548	1645390	1646757	F	456	618(1368)
A02	tnfn1_pw060328p01q109	C	227527	FTN_0207	227115	228113	F	333	413(999)
A03	tnfn1_pw060328p01q117	C	1905179	FTN_1776	1904293	1905303	R	337	125(1011)
A04	tnfn1_pw060328p01q125	C	1017681	FTN_0963	1016699	1018192	R	498	512(1494)
A05	tnfn1_pw060328p01q133	C	1069631	FTN_1010	1069039	1070319	F	427	593(1281)
A06	tnfn1_pw060328p01q141	C	12441	FTN_0014	11835	12728	R	298	288(894)
A07	tnfn1_pw060328p01q149	C	1560687	FTN_1472	1560482	1561288	F	269	206(807)
A08	tnfn1_pw060328p01q157	C	674116	FTN_0637	673289	674314	R	342	199(1026)
A09	tnfn1_pw060328p01q165	C	1075695	FTN_1016	1075256	1075756	R	167	62(501)
A10	tnfn1_pw060328p01q173	C	208677	FTN_0190	207626	208801	R	392	125(1176)
A11	tnfn1_pw060328p01q181	C	1601034	FTN_1505	1599542	1601503	R	654	470(1962)
A12	tnfn1_pw060328p01q189	U	1499550	FTN_1420	1498689	1499933	R	415	384(1245)
B01	tnfn1_pw060328p01q102	C	1015140	FTN_0960	1014799	1015527	R	243	388(729)
B02	tnfn1_pw060328p01q110	C	1684902	FTN_1586	1684007	1685317	R	437	416(1311)
B03	tnfn1_pw060328p01q118	C	20482	FTN_0020	18120	21401	R	1094	920(3282)
B04	tnfn1_pw060328p01q126	C	1033588	FTN_0980	1033379	1034335	F	319	210(957)
B05	tnfn1_pw060328p01q134	C	955883	FTN_0898	954503	956044	R	514	162(1542)
B06	tnfn1_pw060328p01q142	C	989383	FTN_0928	988925	989818	R	298	436(894)
B07	tnfn1_pw060328p01q150	C	184814	FTN_0168	183091	184818	F	576	1724(1728)
B08	tnfn1_pw060328p01q158	C	726023	FTN_0681	725743	726366	F	208	281(624)
B09	tnfn1_pw060328p01q166	C	623429	FTN_0592	623054	623476	R	141	48(423)
B10	tnfn1_pw060328p01q174	C	646594	FTN_0615	646311	646880	F	190	284(570)
B11	tnfn1_pw060328p01q182	C	1296993	FTN_1227	1296419	1297378	R	320	386(960)
B12	tnfn1_pw060328p01q190	C	628664	intergenic					
C01	tnfn1_pw060328p01q103	C	51171	FTN_0046	50758	53733	F	992	414(2976)
C02	tnfn1_pw060328p01q111	C	1734015	FTN_1623	1733943	1736753	R	937	2739(2811)
C03	tnfn1_pw060328p01q119	C	850750	FTN_0793	850477	851043	F	189	274(567)
C04	tnfn1_pw060328p01q127	C	1031661	FTN_0977	1031487	1032053	F	189	175(567)
C05	tnfn1_pw060328p01q135	C	1405232	FTN_1327	1404933	1406114	F	394	300(1182)
C06	tnfn1_pw060328p01q143	C	128736	FTN_0116	127309	129003	R	565	268(1695)
C07	tnfn1_pw060328p01q151	C	1037810	FTN_0983	1036585	1037814	F	410	1226(1230)
C08	tnfn1_pw060328p01q159	C	1112797	FTN_1053	1111641	1113071	R	477	275(1431)
C09	tnfn1_pw060328p01q167	C	337220	FTN_0330	336917	337738	R	274	519(822)
C10	tnfn1_pw060328p01q175	C	1656528	FTN_1558	1655903	1656778	R	292	251(876)
C11	tnfn1_pw060328p01q183	C	1884158	FTN_1755	1883615	1884871	F	419	544(1257)
C12	tnfn1_pw060328p01q191	C	1678020	FTN_1580	1677286	1678698	R	471	679(1413)
D01	tnfn1_pw060328p01q104	C	337220	FTN_0330	336917	337738	R	274	519(822)
D02	tnfn1_pw060328p01q112	C	73413	FTN_0062	72771	74348	R	526	936(1578)
D03	tnfn1_pw060328p01q120	C	1454714	intergenic					
D04	tnfn1_pw060328p01q128	C	896542	FTN_0840	896313	896900	F	196	230(588)
D05	tnfn1_pw060328p01q136	C	158807	FTN_0144	158724	159260	F	179	84(537)
D06	tnfn1_pw060328p01q144	C	1386060	FTN_1313	1384921	1386648	F	576	1140(1728)
D07	tnfn1_pw060328p01q152	C	413782	FTN_0414	413585	414019	R	145	238(435)
D08	tnfn1_pw060328p01q160	C	798089	FTN_0744	797981	798376	F	132	109(396)
D09	tnfn1_pw060328p01q168	C	886516	FTN_0829	886126	886842	R	239	327(717)
D10	tnfn1_pw060328p01q176	C	7465	FTN_0007	7364	7678	R	105	214(315)
D11	tnfn1_pw060328p01q184	C	995008	FTN_0934	994829	995320	F	164	180(492)
D12	tnfn1_pw060328p01q192	C	64042	FTN_0053	63789	64391	F	201	254(603)
E01	tnfn1_pw060328p01q105	C	326647	FTN_0316	325739	326791	R	351	145(1053)
E02	tnfn1_pw060328p01q113	C	1813907	FTN_1696	1813595	1814374	F	260	313(780)
E03	tnfn1_pw060328p01q121	C	124293	FTN_0113	123993	124595	R	201	303(603)
E04	tnfn1_pw060328p01q129	C	662796	FTN_0629	662421	663251	F	277	376(831)
E05	tnfn1_pw060328p01q137	C	166298	FTN_0153	166021	166443	R	141	146(423)

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]
E06	tnfn1_pw060328p01q145	C	1604917	FTN_1509	1604143	1606674	F	844	775(2532)
E07	tnfn1_pw060328p01q153	C	1358647	FTN_1285	1358234	1358818	R	195	172(585)
E08	tnfn1_pw060328p01q161	C	237526	FTN_0215	237281	237943	F	221	246(663)
E09	tnfn1_pw060328p01q169	C	233724	-	233259	234123	R	288.3	400(865)
E10	tnfn1_pw060328p01q177	C	1655432	FTN_1557	1654935	1655777	R	281	346(843)
E11	tnfn1_pw060328p01q185	C	415121	FTN_0416	414941	415657	F	239	181(717)
E12	tnfn1_pw060328p01q193	C	1049568	FTN_0991	1048716	1049855	R	380	288(1140)
F01	tnfn1_pw060328p01q106	C	1698814	FTN_1597	1697609	1699183	R	525	370(1575)
F02	tnfn1_pw060328p01q114	C	11367	FTN_0013	10939	11835	R	299	469(897)
F03	tnfn1_pw060328p01q122	C	1133685	FTN_1071	1132424	1133899	R	492	215(1476)
F04	tnfn1_pw060328p01q130	C	469383	FTN_0463	469216	469476	R	87	94(261)
F05	tnfn1_pw060328p01q138	C	1546655	FTN_1458	1546487	1546990	F	168	169(504)
F06	tnfn1_pw060328p01q146	C	521699	FTN_0509	519765	523154	F	1130	1935(3390)
F07	tnfn1_pw060328p01q154	C	419602	FTN_0420	418362	420671	F	770	1241(2310)
F08	tnfn1_pw060328p01q162	C	693980	FTN_0655	693723	694298	R	192	319(576)
F09	tnfn1_pw060328p01q170	C	1485516	FTN_1408	1485141	1485905	R	255	390(765)
F10	tnfn1_pw060328p01q178	C	894586	FTN_0838	894232	895017	R	262	432(786)
F11	tnfn1_pw060328p01q186	C	546055	FTN_0525	545312	547729	F	806	744(2418)
F12	tnfn1_pw060328p01q194	C	1384110	FTN_1311	1384032	1384406	F	125	79(375)
G01	tnfn1_pw060328p01q107	C	1617978	FTN_1520	1617143	1618336	R	398	359(1194)
G02	tnfn1_pw060328p01q115	C	826240	FTN_0769	825750	826601	F	284	491(852)
G03	tnfn1_pw060328p01q123	C	1690890	FTN_1592	1690148	1691083	R	312	194(936)
G04	tnfn1_pw060328p01q131	C	463982	FTN_0457	463591	464247	F	219	392(657)
G05	tnfn1_pw060328p01q139	C	537227	FTN_0518	536994	538454	F	487	234(1461)
G06	tnfn1_pw060328p01q147	C	388811	FTN_0389	388044	388991	R	316	181(948)
G07	tnfn1_pw060328p01q155	U	1122727	FTN_1063	1122215	1123540	F	442	513(1326)
G08	tnfn1_pw060328p01q163	C	1309165	FTN_1242	1308961	1309605	F	215	205(645)
G09	tnfn1_pw060328p01q171	C	396301	-	396244	396372	R	43	72(129)
G10	tnfn1_pw060328p01q179	C	9590	FTN_0010	9375	9806	R	144	217(432)
G11	tnfn1_pw060328p01q187	C	1833500	FTN_1709	1832414	1834285	R	624	786(1872)
G12	tnfn1_pw060328p01q195	C	611579	FTN_0582	611071	611742	R	224	164(672)
H01	tnfn1_pw060328p01q108	C	851412	-	851134	851998	F	288.3	279(865)
H02	tnfn1_pw060328p01q116	C	35380	FTN_0034	33580	36951	R	1124	1572(3372)
H03	tnfn1_pw060328p01q124	C	1840817	FTN_1715	1838604	1841282	R	893	466(2679)
H04	tnfn1_pw060328p01q132	C	635258	FTN_0602	634911	635447	F	179	348(537)
H05	tnfn1_pw060328p01q140	C	1165178	FTN_1103	1164647	1165492	R	282	315(846)
H06	tnfn1_pw060328p01q148	C	1122727	FTN_1063	1122215	1123540	F	442	513(1326)
H07	tnfn1_pw060328p01q156	C	1531043	FTN_1442	1530875	1531099	R	75	57(225)
H08	tnfn1_pw060328p01q164	C	1286494	FTN_1216	1286108	1286848	R	247	355(741)
H09	tnfn1_pw060328p01q172	C	1640559	FTN_1542	1640166	1640927	F	254	394(762)
H10	tnfn1_pw060328p01q180	C	575922	FTN_0550	575484	576497	F	338	439(1014)
H11	tnfn1_pw060328p01q188	C	966252	FTN_0910	965706	967175	F	490	547(1470)
H12	tnfn1_pw060328p01q196	C	1499550	FTN_1420	1498689	1499933	R	415	384(1245)

[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 9 (tnfn1_pw060328p01) – 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_pw060328p01q101	EXACT(0)	156	142	98	29	EXACT(0)	200	194	53
A02	tnfn1_pw060328p01q109	EXACT(0)	155	152	121	36	EXACT(0)	200	193	52
A03	tnfn1_pw060328p01q117	EXACT(0)	157	153	121	39	EXACT(0)	200	181	58
A04	tnfn1_pw060328p01q125	EXACT(0)	156	152	122	38	EXACT(0)	200	189	58
A05	tnfn1_pw060328p01q133	EXACT(0)	157	152	124	36	EXACT(0)	200	187	57
A06	tnfn1_pw060328p01q141	EXACT(0)	157	152	124	37	EXACT(0)	200	176	56
A07	tnfn1_pw060328p01q149	EXACT(0)	155	146	118	39	EXACT(0)	187	183	47

Product Information Sheet for NR-51291

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
A08	tnfn1_pw060328p01q157	EXACT(0)	123	125	86	22	EXACT(0)	200	188	51
A09	tnfn1_pw060328p01q165	EXACT(0)	124	120	89	26	EXACT(0)	200	183	57
A10	tnfn1_pw060328p01q173	EXACT(0)	124	122	95	27	EXACT(0)	200	187	56
A11	tnfn1_pw060328p01q181	EXACT(0)	156	153	121	34	EXACT(0)	200	191	57
A12	tnfn1_pw060328p01q189	EXACT(0)	159	133	103	25	EXACT(0)	200	184	43
B01	tnfn1_pw060328p01q102	EXACT(0)	157	153	137	46	EXACT(0)	200	185	64
B02	tnfn1_pw060328p01q110	EXACT(0)	158	153	117	32	EXACT(0)	200	194	58
B03	tnfn1_pw060328p01q118	EXACT(0)	154	150	103	24	EXACT(0)	200	198	53
B04	tnfn1_pw060328p01q126	EXACT(0)	155	145	117	39	EXACT(0)	200	191	58
B05	tnfn1_pw060328p01q134	EXACT(0)	156	151	123	34	EXACT(0)	200	190	56
B06	tnfn1_pw060328p01q142	EXACT(0)	156	153	123	40	EXACT(0)	200	191	57
B07	tnfn1_pw060328p01q150	EXACT(0)	122	112	86	25	EXACT(0)	197	173	50
B08	tnfn1_pw060328p01q158	EXACT(0)	122	112	96	31	EXACT(0)	200	178	58
B09	tnfn1_pw060328p01q166	EXACT(0)	123	120	101	27	EXACT(0)	200	174	55
B10	tnfn1_pw060328p01q174	EXACT(0)	122	113	97	29	EXACT(0)	200	191	54
B11	tnfn1_pw060328p01q182	EXACT(0)	155	146	124	39	EXACT(0)	200	196	55
B12	tnfn1_pw060328p01q190	EXACT(0)	156	152	125	32	EXACT(0)	200	183	53
C01	tnfn1_pw060328p01q103	EXACT(0)	157	153	116	32	EXACT(0)	200	189	57
C02	tnfn1_pw060328p01q111	EXACT(0)	156	152	125	39	EXACT(0)	200	181	54
C03	tnfn1_pw060328p01q119	EXACT(0)	156	138	110	33	EXACT(0)	200	173	41
C04	tnfn1_pw060328p01q127	EXACT(0)	157	153	124	36	EXACT(0)	200	173	47
C05	tnfn1_pw060328p01q135	EXACT(0)	156	153	126	41	EXACT(0)	199	184	50
C06	tnfn1_pw060328p01q143	EXACT(0)	155	146	124	43	EXACT(0)	200	195	56
C07	tnfn1_pw060328p01q151	EXACT(0)	121	112	99	31	EXACT(0)	200	188	49
C08	tnfn1_pw060328p01q159	EXACT(0)	121	106	90	28	EXACT(0)	200	186	52
C09	tnfn1_pw060328p01q167	EXACT(0)	123	120	102	34	EXACT(0)	198	79	29
C10	tnfn1_pw060328p01q175	EXACT(0)	122	119	95	34	EXACT(0)	200	185	56
C11	tnfn1_pw060328p01q183	EXACT(0)	156	153	126	39	EXACT(0)	191	185	55
C12	tnfn1_pw060328p01q191	EXACT(0)	157	153	115	29	EXACT(0)	200	197	54
D01	tnfn1_pw060328p01q104	EXACT(0)	123	120	102	34	EXACT(0)	199	87	29
D02	tnfn1_pw060328p01q112	EXACT(0)	156	152	122	40	EXACT(0)	200	189	55
D03	tnfn1_pw060328p01q120	EXACT(0)	154	145	103	26	EXACT(0)	200	181	55
D04	tnfn1_pw060328p01q128	EXACT(0)	159	153	130	37	EXACT(0)	200	191	55
D05	tnfn1_pw060328p01q136	EXACT(0)	155	145	126	40	EXACT(0)	200	196	57
D06	tnfn1_pw060328p01q144	EXACT(0)	156	144	117	25	EXACT(0)	200	175	58
D07	tnfn1_pw060328p01q152	EXACT(0)	123	118	99	26	EXACT(0)	200	195	53
D08	tnfn1_pw060328p01q160	EXACT(0)	121	112	93	29	EXACT(0)	200	188	63
D09	tnfn1_pw060328p01q168	EXACT(0)	123	120	66	20	EXACT(0)	200	194	51
D10	tnfn1_pw060328p01q176	EXACT(0)	123	119	103	33	EXACT(0)	200	184	61
D11	tnfn1_pw060328p01q184	EXACT(0)	156	153	126	37	EXACT(0)	200	182	52
D12	tnfn1_pw060328p01q192	EXACT(0)	156	153	123	39	EXACT(0)	199	179	52
E01	tnfn1_pw060328p01q105	EXACT(0)	157	146	135	39	EXACT(0)	200	179	59
E02	tnfn1_pw060328p01q113	EXACT(0)	156	146	127	41	EXACT(0)	200	184	49
E03	tnfn1_pw060328p01q121	EXACT(0)	156	153	125	35	EXACT(0)	200	190	57
E04	tnfn1_pw060328p01q129	EXACT(0)	156	146	127	37	EXACT(0)	200	187	52
E05	tnfn1_pw060328p01q137	EXACT(0)	155	145	126	42	EXACT(0)	200	182	51
E06	tnfn1_pw060328p01q145	EXACT(0)	155	146	130	44	EXACT(0)	200	188	59
E07	tnfn1_pw060328p01q153	EXACT(0)	115	111	88	40	EXACT(0)	200	182	28
E08	tnfn1_pw060328p01q161	EXACT(0)	122	118	73	24	EXACT(0)	200	184	55
E09	tnfn1_pw060328p01q169	EXACT(0)	122	112	89	37	EXACT(0)	200	187	55
E10	tnfn1_pw060328p01q177	EXACT(0)	156	152	134	43	EXACT(0)	200	147	42
E11	tnfn1_pw060328p01q185	EXACT(0)	156	152	120	33	EXACT(0)	200	180	54
E12	tnfn1_pw060328p01q193	EXACT(0)	154	152	120	41	EXACT(0)	183	155	37
F01	tnfn1_pw060328p01q106	EXACT(0)	155	139	128	40	EXACT(0)	200	195	53
F02	tnfn1_pw060328p01q114	EXACT(0)	157	152	127	38	EXACT(0)	200	189	55
F03	tnfn1_pw060328p01q122	EXACT(0)	154	118	80	28	EXACT(0)	200	176	46
F04	tnfn1_pw060328p01q130	EXACT(0)	155	145	126	43	EXACT(0)	196	177	53
F05	tnfn1_pw060328p01q138	EXACT(0)	154	145	129	42	EXACT(0)	196	189	52
F06	tnfn1_pw060328p01q146	EXACT(0)	155	145	129	44	EXACT(0)	188	173	55
F07	tnfn1_pw060328p01q154	EXACT(0)	121	112	90	26	EXACT(0)	200	194	54
F08	tnfn1_pw060328p01q162	EXACT(0)	122	112	78	26	EXACT(0)	200	182	39
F09	tnfn1_pw060328p01q170	EXACT(0)	121	120	85	25	EXACT(0)	200	191	57

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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
F10	tnfn1_pw060328p01q178	EXACT(0)	159	153	139	40	EXACT(0)	200	191	56
F11	tnfn1_pw060328p01q186	EXACT(0)	156	153	129	40	EXACT(0)	200	192	51
F12	tnfn1_pw060328p01q194	EXACT(0)	158	153	123	36	EXACT(0)	200	186	49
G01	tnfn1_pw060328p01q107	EXACT(0)	156	153	123	30	EXACT(0)	200	179	55
G02	tnfn1_pw060328p01q115	EXACT(0)	157	151	117	36	EXACT(0)	200	187	56
G03	tnfn1_pw060328p01q123	EXACT(0)	158	159	140	37	EXACT(0)	200	190	57
G04	tnfn1_pw060328p01q131	EXACT(0)	155	146	118	38	EXACT(0)	200	192	57
G05	tnfn1_pw060328p01q139	EXACT(0)	155	145	126	41	EXACT(0)	200	193	53
G06	tnfn1_pw060328p01q147	EXACT(0)	155	146	133	39	EXACT(0)	200	192	56
G07	tnfn1_pw060328p01q155	EXACT(0)	158	141	112	22	EXACT(0)	200	191	39
G08	tnfn1_pw060328p01q163	EXACT(0)	122	119	83	21	EXACT(0)	197	186	48
G09	tnfn1_pw060328p01q171	EXACT(0)	124	120	101	35	EXACT(0)	200	181	52
G10	tnfn1_pw060328p01q179	EXACT(0)	155	146	127	41	EXACT(0)	192	177	54
G11	tnfn1_pw060328p01q187	EXACT(0)	157	153	118	33	EXACT(0)	200	190	56
G12	tnfn1_pw060328p01q195	EXACT(0)	156	145	131	39	EXACT(0)	160	124	39
H01	tnfn1_pw060328p01q108	EXACT(0)	155	145	115	42	EXACT(0)	200	184	56
H02	tnfn1_pw060328p01q116	EXACT(0)	157	148	134	40	EXACT(0)	200	194	59
H03	tnfn1_pw060328p01q124	EXACT(0)	155	145	120	41	EXACT(0)	200	188	57
H04	tnfn1_pw060328p01q132	EXACT(0)	154	139	122	43	EXACT(0)	200	188	53
H05	tnfn1_pw060328p01q140	EXACT(0)	155	145	123	42	EXACT(0)	197	189	51
H06	tnfn1_pw060328p01q148	EXACT(0)	154	145	120	37	EXACT(0)	200	194	51
H07	tnfn1_pw060328p01q156	EXACT(0)	121	112	72	23	EXACT(0)	200	175	49
H08	tnfn1_pw060328p01q164	EXACT(0)	122	105	79	23	EXACT(0)	200	180	46
H09	tnfn1_pw060328p01q172	EXACT(0)	122	113	94	33	EXACT(0)	136	129	55
H10	tnfn1_pw060328p01q180	EXACT(0)	154	145	120	38	EXACT(0)	200	185	46
H11	tnfn1_pw060328p01q188	EXACT(0)	156	145	122	35	EXACT(0)	200	190	52
H12	tnfn1_pw060328p01q196	EXACT(0)	157	152	117	35	EXACT(0)	200	172	47

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

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