

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 13 (tnfn1_pw060328p05)**

Catalog No. NR-8047

For research use only. Not for human use.

Contributor:

Colin Manoil, Ph.D., Professor of Genome Sciences,
University of Washington, Seattle, Washington

Product Description:

A comprehensive 16508-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-8047 represents Plate 13 (tnfn1_pw060328p05) of the “two-allele” 3050-member sublibrary. Detailed information for each mutant is shown in Tables 1-3. Information about specific clones may also be accessed through the [Francisella Tularensis Genome Research](#) homepage. **Strain tnfn1_pw060328p05q143 (Well C06) is not available due to quality issues.**

***Francisella tularensis* subsp. *novicida*, strain U112 is excluded from Select Agent status. Please see [CDC Select Agent Program, Notification of Exclusion](#).**

Material Provided:

Each well of the 96-well plate contains approximately 0.25 mL of bacterial culture in 0.7X Tryptic Soy Broth containing 0.1% L-cysteine and 10 µg/mL kanamycin supplemented with 5% glycerol.

Note: Production in the 96-well format has a potential for cross-contamination. Individual mutants should be checked by the recipient prior to use.

Packaging/Storage:

NR-8047 was packaged aseptically in 96-well plates. The product is provided frozen and should be stored at -60°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 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 plate at 37°C for 24–48 hours.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through the NIH Biodefense and Emerging Infections Research Resources Repository, NIAID, NIH: *Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 13 (tnfn1_pw060328p05), NR-8047.”

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, 2007; see www.cdc.gov/od/ohs/biosfty/bmb15/bmb15toc.htm.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government make any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for damages arising from the misidentification or misrepresentation of products.

Use Restrictions:

This material is distributed for internal research, non-commercial purposes only. This material, its product or its derivatives may not be distributed to third parties. Except as performed under a U.S. Government contract, individuals contemplating commercial use of the material, its products or its derivatives must contact the contributor to determine if a license is required. U.S. Government contractors may need a license before first commercial sale.

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.

ATCC® is a trademark of the American Type Culture Collection.



Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p05q101	A01	T20	gdhA	glutamate dehydrogenase (NADP+)	amino acid metabolism - biosynthesis
tnfn1_pw060328p05q102	B01	T20	-	MutT/nudix family protein	putative enzymes
tnfn1_pw060328p05q103	C01	T20	nfnB	dihydropteridine reductase	energy metabolism
tnfn1_pw060328p05q104	D01	T20	udp	uridine phosphorylase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p05q105	E01	T20	-	peptidase, U32 family	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060328p05q106	F01	T20	udp	uridine phosphorylase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p05q107	G01	T20	betT	betaine/carnitine/choline transporter (BCCT) family protein	transport
tnfn1_pw060328p05q108	H01	T20	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p05q109	A02	T20	-	amino acid-polyamine-organocation (APC) superfamily protein	transport - amino-acid
tnfn1_pw060328p05q110	B02	T20	-	4Fe-4S ferredoxin, FAD dependent	energy metabolism
tnfn1_pw060328p05q111	C02	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p05q112	D02	T20	murC	UDP-N-acetylmuramate-alanine ligase	cell wall / LPS / capsule
tnfn1_pw060328p05q113	E02	T20	recO	RecFOR complex, RecO component	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p05q114	F02	T20	-	short-chain dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p05q115	G02	T20	-	acetoacetate decarboxylase	other metabolism - biosynthesis
tnfn1_pw060328p05q116	H02	T20	-	acetyltransferase	putative enzymes
tnfn1_pw060328p05q117	A03	T20	ilvN	acetolactate synthase small subunit	amino acid metabolism - biosynthesis
tnfn1_pw060328p05q118	B03	T20	-	type I restriction-modification system, subunit S	DNA replication, recombination, modification and repair - repair
tnfn1_pw060328p05q119	C03	T20	-	membrane protein of unknown function	unknown function - novel
tnfn1_pw060328p05q120	D03	T20	dnaJ	chaperone, DnaJ family, with C-terminal Zn finger domain	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p05q121	E03	T20	-	restriction endonuclease	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p05q122	F03	T20	-	small conductance mechanosensitive ion channel (MscS) family protein	transport
tnfn1_pw060328p05q123	G03	T20	-	predicted Co/Zn/Cd cation transporter	transport
tnfn1_pw060328p05q124	H03	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q125	A04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q126	B04	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q127	C04	<KAN-2>	-		
tnfn1_pw060328p05q128	D04	<KAN-2>	fbA	fructose bisphosphate aldolase Class II	energy metabolism
tnfn1_pw060328p05q129	E04	<KAN-2>	groEL	chaperonin GroEL (HSP60 family)	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060328p05q130	F04	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060328p05q131	G04	T18	folD	methyleneTHF enzyme/ methenyltetrahydrofolate cyclohydrolase/ methylenetetrahydrofolate dehydrogenase	amino acid metabolism - degradation, utilization, assimilation
tnfn1_pw060328p05q132	H04	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q133	A05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p05q134	B05	T18	-		
tnfn1_pw060328p05q135	C05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p05q136	D05	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p05q137	E05	T18	ftsA	cell division protein FtsA	cell cycle
tnfn1_pw060328p05q138	F05	T18	-	flavodoxin, related to tryptophan repressor binding protein	putative enzymes
tnfn1_pw060328p05q139	G05	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p05q140	H05	T18	mutT	mutator protein	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p05q141	A06	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p05q142	B06	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p05q143	C06	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q144	D06	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p05q145	E06	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q146	F06	T20	pilF	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060328p05q147	G06	T20	-		
tnfn1_pw060328p05q148	H06	T20	nudH	dGTP pyrophosphohydrolase	DNA replication, recombination, modification and repair - restriction/modification

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060328p05q149	A07	T20	wbtP	galactosyl transferase	cell wall / LPS / capsule
tnfn1_pw060328p05q150	B07	T20	frgA	siderophore biosynthesis protein	other metabolism - biosynthesis
tnfn1_pw060328p05q151	C07	T20	-	histidine acid phosphatase	putative enzymes
tnfn1_pw060328p05q152	D07	T20	cysC	adenylylsulfate kinase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060328p05q153	E07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p05q154	F07	T20	trpG	anthranilate synthase component II	amino acid metabolism - biosynthesis
tnfn1_pw060328p05q155	G07	T20	prmA	50S ribosomal protein L11, methyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p05q156	H07	T20	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p05q157	A08	T20	-	pseudogene: hypothetical membrane protein, fragment	pseudogene
tnfn1_pw060328p05q158	B08	T20	-	sulfate permease family protein	transport
tnfn1_pw060328p05q159	C08	T20	-	serine peptidase, S49 family	post-translational modification, protein turnover, chaperones
tnfn1_pw060328p05q160	D08	T20	dapB	dihydrodipicolinate reductase	amino acid metabolism - biosynthesis
tnfn1_pw060328p05q161	E08	T20	rsuA	16S rRNA pseudouridine synthase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p05q162	F08	T20	-	serine-type D-Ala-D-Ala carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060328p05q163	G08	T20	tdk	thymidine kinase	nucleotides and nucleosides metabolism
tnfn1_pw060328p05q164	H08	T20	uvrD	DNA helicase II	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p05q165	A09	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p05q166	B09	T20	ribH	riboflavin synthase beta-chain	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p05q167	C09	T20	htpX	Zn-dependent protease with chaperone function	post-translational modification, protein turnover, chaperones - chaperones
tnfn1_pw060328p05q168	D09	T20	gplX	fructose 1,6-bisphosphatase II	energy metabolism
tnfn1_pw060328p05q169	E09	T20	hitA	histidine triad (HIT) family protein	putative enzymes
tnfn1_pw060328p05q170	F09	T20	leuC	isopropylmalate isomerase	amino acid metabolism - biosynthesis
tnfn1_pw060328p05q171	G09	T20	-	glucokinase regulatory protein	signal transduction and regulation
tnfn1_pw060328p05q172	H09	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060328p05q173	A10	T20	nadE	NAD synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060328p05q174	B10	T20	-	4Fe-4S ferredoxin	energy metabolism
tnfn1_pw060328p05q175	C10	T20	-	dehydrogenase	putative enzymes
tnfn1_pw060328p05q176	D10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q177	E10	T20	-	chitin-binding protein	putative enzymes
tnfn1_pw060328p05q178	F10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060328p05q179	G10	T20	polA	DNA polymerase I	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060328p05q180	H10	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p05q181	A11	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060328p05q182	B11	T20	nhaD	Na ⁺ :H ⁺ antiporter	transport
tnfn1_pw060328p05q183	C11	<KAN-2>	secG	preprotein translocase, subunit G, membrane protein	motility, attachment and secretion structure
tnfn1_pw060328p05q184	D11	<KAN-2>	-	LemA-like protein	putative enzymes
tnfn1_pw060328p05q185	E11	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q186	F11	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060328p05q187	G11	<KAN-2>	-	hydrolase, HD superfamily	putative enzymes
tnfn1_pw060328p05q188	H11	<KAN-2>	pnp	polyribonucleotide nucleotidyltransferase	translation, ribosomal structure and biogenesis
tnfn1_pw060328p05q189	A12	<KAN-2>	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060328p05q190	B12	<KAN-2>	bfr	bacterioferritin	energy metabolism
tnfn1_pw060328p05q191	C12	<KAN-2>	feoB	ferrous iron transport protein B	transport
tnfn1_pw060328p05q192	D12	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060328p05q193	E12	T18	nupC1	nucleoside permease NUP family protein	transport
tnfn1_pw060328p05q194	F12	T18	-	pseudogene: O-methyltransferase	pseudogene
tnfn1_pw060328p05q195	G12	T18	-		
tnfn1_pw060328p05q196	H12	T18	isftu2	isftu2	IS element

Table 2 - Sequencing and Insertion Location

Strain Name	Well	Sequence confirmation (C, Confirmed; U, unconfirmed)	Effective Genome Position of Insertion	Direction of insertion (F, forward relative to genome; R, reverse)	Locus Tag	ORF left end	ORF right end	Direction of ORF (F, forward relative to genome; R, reverse)	Length of ORF (codons)	Effective position of insertion in ORF [nucleotide of insertion(length of ORF in nucleotides)]
tnfn1_pw060328p05q101	A01	C	1629643	R	FTN_1532	1629170	1630516	F	449	474(1347)
tnfn1_pw060328p05q102	B01	C	241411	F	FTN_0219	241266	241640	F	125	146(375)
tnfn1_pw060328p05q103	C01	C	240898	F	FTN_0218	240476	241126	R	217	229(651)
tnfn1_pw060328p05q104	D01	C	691694	F	FTN_0652	691457	692257	R	267	564(801)
tnfn1_pw060328p05q105	E01	C	1826931	F	FTN_1705	1826603	1827931	F	443	329(1329)
tnfn1_pw060328p05q106	F01	C	691694	F	FTN_0652	691457	692257	R	267	564(801)
tnfn1_pw060328p05q107	G01	C	823955	F	FTN_0767	823200	825149	F	650	756(1950)
tnfn1_pw060328p05q108	H01	C	873189	F	FTN_0816	872849	874177	F	443	341(1329)
tnfn1_pw060328p05q109	A02	C	800562	R	FTN_0747	800413	802020	F	536	150(1608)
tnfn1_pw060328p05q110	B02	C	1208514	F	FTN_1143	1207355	1210072	R	906	1559(2718)
tnfn1_pw060328p05q111	C02	C	1504856	R	FTN_1424	1503994	1505283	R	430	428(1290)
tnfn1_pw060328p05q112	D02	C	89606	F	FTN_0079	89393	90745	F	451	214(1353)
tnfn1_pw060328p05q113	E02	C	1309962	F	FTN_1243	1309687	1310382	R	232	421(696)
tnfn1_pw060328p05q114	F02	C	1251632	R	FTN_1178	1251247	1251966	R	240	335(720)
tnfn1_pw060328p05q115	G02	U	865583	F	FTN_0808	865255	865992	R	246	410(738)
tnfn1_pw060328p05q116	H02	C	324169	F	FTN_0313	323976	324464	F	163	194(489)
tnfn1_pw060328p05q117	A03	C	1098817	R	FTN_1041	1098659	1098973	R	105	157(315)
tnfn1_pw060328p05q118	B03	C	1221884	R	FTN_1154	1220796	1222016	R	407	133(1221)
tnfn1_pw060328p05q119	C03	C	444002	R	FTN_0444	443654	445324	F	557	349(1671)
tnfn1_pw060328p05q120	D03	C	1355796	F	FTN_1283	1354992	1356176	R	395	381(1185)
tnfn1_pw060328p05q121	E03	C	1578358	F	FTN_1487	1577096	1579960	R	955	1603(2865)
tnfn1_pw060328p05q122	F03	C	1679097	F	FTN_1581	1678701	1679195	R	165	99(495)
tnfn1_pw060328p05q123	G03	C	781432	R	FTN_0728	780666	781802	F	379	767(1137)
tnfn1_pw060328p05q124	H03	C	1452894	R	FTN_1372	1451963	1453045	R	361	152(1083)
tnfn1_pw060328p05q125	A04	C	910814	F	FTN_0855	910576	911262	F	229	239(687)
tnfn1_pw060328p05q126	B04	C	885812	R	FTN_0828	885562	885984	R	141	173(423)
tnfn1_pw060328p05q127	C04	C	981935	R	intergenic					
tnfn1_pw060328p05q128	D04	C	1408561	R	FTN_1329	1407743	1408804	R	354	244(1062)
tnfn1_pw060328p05q129	E04	C	1636954	R	FTN_1538	1636884	1638515	R	544	1562(1632)
tnfn1_pw060328p05q130	F04	C	556524	F	FTN_0534	555784	556824	F	347	741(1041)
tnfn1_pw060328p05q131	G04	U	416617	R	FTN_0417	415800	416645	F	282	818(846)
tnfn1_pw060328p05q132	H04	C	1163382	R	FTN_1101	1162960	1163790	R	277	409(831)
tnfn1_pw060328p05q133	A05	C	774809	R	FTN_0719	774796	774996	R	67	188(201)
tnfn1_pw060328p05q134	B05	C	887493	R	intergenic					
tnfn1_pw060328p05q135	C05	C	820958	R	FTN_0764	820728	821078	R	117	121(351)
tnfn1_pw060328p05q136	D05	C	385135	F	FTN_0384	385020	385376	R	119	242(357)
tnfn1_pw060328p05q137	E05	C	177968	F	FTN_0163	176722	177981	F	420	1247(1260)
tnfn1_pw060328p05q138	F05	C	1353043	F	FTN_1280	1352702	1353265	R	188	223(564)
tnfn1_pw060328p05q139	G05	C	807109	R	FTN_0753	806791	807339	F	183	319(549)
tnfn1_pw060328p05q140	H05	C	919105	F	FTN_0865	918875	919291	R	139	187(417)
tnfn1_pw060328p05q141	A06	C	744458	R	FTN_0701	744311	744955	F	215	148(645)
tnfn1_pw060328p05q142	B06	C	1187429	R	FTN_1123	1187288	1187590	F	101	142(303)
tnfn1_pw060328p05q143	C06	U	81868	R	FTN_0067	81421	82032	R	204	165(612)
tnfn1_pw060328p05q144	D06	C	1457595	F	FTN_1378	1457390	1457926	F	179	206(537)
tnfn1_pw060328p05q145	E06	C	713231	F	FTN_0670	712906	713352	R	149	122(447)
tnfn1_pw060328p05q146	F06	C	1003860	R	FTN_0946	1003473	1004375	R	301	516(903)
tnfn1_pw060328p05q147	G06	C	962846	R	intergenic					
tnfn1_pw060328p05q148	H06	C	1651409	F	FTN_1553	1651200	1651661	R	154	253(462)

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.

Table 2 - Sequencing and Insertion Location

Strain Name	Well	Sequence confirmation (C, Confirmed; U, unconfirmed)	Effective Genome Position of Insertion	Direction of insertion (F, forward relative to genome; R, reverse)	Locus Tag	ORF left end	ORF right end	Direction of ORF (F, forward relative to genome; R, reverse)	Length of ORF (codons)	Effective position of insertion in ORF [nucleotide of insertion(length of ORF in nucleotides)]
tnfn1_pw060328p05q149	A07	C	1509463	F	FTN_1429	1509260	1509886	R	209	424(627)
tnfn1_pw060328p05q150	B07	C	1796376	R	FTN_1682	1796074	1797990	F	639	303(1917)
tnfn1_pw060328p05q151	C07	C	23623	F	FTN_0022	22992	24044	F	351	632(1053)
tnfn1_pw060328p05q152	D07	C	983754	R	FTN_0926	983655	984254	R	200	501(600)
tnfn1_pw060328p05q153	E07	C	1085116	F	FTN_1028	1084814	1085557	R	248	442(744)
tnfn1_pw060328p05q154	F07	C	1905674	F	FTN_1777	1905303	1905878	R	192	205(576)
tnfn1_pw060328p05q155	G07	C	1043803	R	FTN_0988	1043408	1044250	R	281	448(843)
tnfn1_pw060328p05q156	H07	C	1431011	F	FTN_1352	1430875	1431669	F	265	137(795)
tnfn1_pw060328p05q157	A08	C	1458608	R	FTN_1379	1457975	1459691	R	572.3	1084(1717)
tnfn1_pw060328p05q158	B08	C	675271	R	FTN_0638	674546	676087	F	514	726(1542)
tnfn1_pw060328p05q159	C08	C	130082	R	FTN_0118	129531	130451	F	307	552(921)
tnfn1_pw060328p05q160	D08	C	1857249	F	FTN_1729	1856806	1857474	R	223	226(669)
tnfn1_pw060328p05q161	E08	C	1003357	R	FTN_0945	1002665	1003477	R	271	121(813)
tnfn1_pw060328p05q162	F08	C	670866	R	FTN_0635	669592	670983	R	464	118(1392)
tnfn1_pw060328p05q163	G08	C	1120193	F	FTN_1060	1119781	1120371	R	197	179(591)
tnfn1_pw060328p05q164	H08	C	1694640	R	FTN_1594	1692877	1695096	R	740	457(2220)
tnfn1_pw060328p05q165	A09	C	363276	F	FTN_0360	363126	363353	F	76	151(228)
tnfn1_pw060328p05q166	B09	C	122517	F	FTN_0111	122336	122776	R	147	260(441)
tnfn1_pw060328p05q167	C09	C	389760	R	FTN_0390	389099	390163	R	355	404(1065)
tnfn1_pw060328p05q168	D09	C	306198	F	FTN_0298	305744	306727	F	328	455(984)
tnfn1_pw060328p05q169	E09	C	464838	F	FTN_0458	464768	465103	R	112	266(336)
tnfn1_pw060328p05q170	F09	C	72065	R	FTN_0061	71360	72766	R	469	702(1407)
tnfn1_pw060328p05q171	G09	C	1599207	R	FTN_1504	1598661	1599542	R	294	336(882)
tnfn1_pw060328p05q172	H09	C	1828848	F	FTN_1706	1827979	1829157	R	393	310(1179)
tnfn1_pw060328p05q173	A10	C	1351746	F	FTN_1278	1351324	1352070	F	249	423(747)
tnfn1_pw060328p05q174	B10	C	807962	F	FTN_0755	807847	808089	F	81	116(243)
tnfn1_pw060328p05q175	C10	C	1018733	F	FTN_0964	1018209	1019321	R	371	589(1113)
tnfn1_pw060328p05q176	D10	C	1448079	R	FTN_1367	1447268	1448899	R	544	821(1632)
tnfn1_pw060328p05q177	E10	C	1266701	R	FTN_1192	1265920	1267707	F	596	782(1788)
tnfn1_pw060328p05q178	F10	C	1127663	R	FTN_1068	1127581	1128000	F	140	83(420)
tnfn1_pw060328p05q179	G10	C	1706947	R	FTN_1604	1705069	1707759	R	897	813(2691)
tnfn1_pw060328p05q180	H10	C	223280	F	FTN_0201	222642	223334	R	231	55(693)
tnfn1_pw060328p05q181	A11	C	1766671	F	FTN_1653	1766277	1766705	R	143	35(429)
tnfn1_pw060328p05q182	B11	C	1829334	R	FTN_1707	1829332	1830756	F	475	3(1425)
tnfn1_pw060328p05q183	C11	C	1741052	R	FTN_1630	1740964	1741314	R	117	263(351)
tnfn1_pw060328p05q184	D11	C	390681	R	FTN_0391	390170	390742	R	191	62(573)
tnfn1_pw060328p05q185	E11	C	1862049	F	FTN_1734	1861861	1862250	F	130	189(390)
tnfn1_pw060328p05q186	F11	C	1340685	F	FTN_1269	1340467	1341162	F	232	219(696)
tnfn1_pw060328p05q187	G11	C	435580	F	FTN_0437	435345	435932	F	196	236(588)
tnfn1_pw060328p05q188	H11	C	643601	F	FTN_0609	641862	643940	F	693	1740(2079)
tnfn1_pw060328p05q189	A12	C	1430491	F	FTN_1351	1430157	1430870	F	238	335(714)
tnfn1_pw060328p05q190	B12	C	1487719	F	FTN_1410	1487622	1488059	F	146	98(438)
tnfn1_pw060328p05q191	C12	C	80179	R	FTN_0066	79071	81317	R	749	1139(2247)
tnfn1_pw060328p05q192	D12	C	249049	F	FTN_0225	248455	249375	R	307	327(921)
tnfn1_pw060328p05q193	E12	C	1701856	F	FTN_1600	1701111	1702307	R	399	452(1197)
tnfn1_pw060328p05q194	F12	C	1877068	R	FTN_1746	1876485	1877140	R	218.6	73(656)
tnfn1_pw060328p05q195	G12	C	133794	F	intergenic					
tnfn1_pw060328p05q196	H12	C	378090	F	-	377298	378154	F	285.6	793(857)

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.

Table 3 - Sequence Mapping Quality Metrics

Strain Name	Well	Junction information	Position in sequence read of last vector nucleotide	Length of match to transposon	Transposon match score	Average phred score for transposon match	Genome position information	Length of match to genome	Genome match score	Average phred score for genome match
tnfn1_pw060328p05q101	A01	EXACT(0)	157	146	138	40	EXACT(0)	200	197	59
tnfn1_pw060328p05q102	B01	EXACT(0)	155	153	132	38	EXACT(0)	200	194	57
tnfn1_pw060328p05q103	C01	EXACT(0)	157	153	124	33	EXACT(0)	200	183	55
tnfn1_pw060328p05q104	D01	EXACT(0)	158	151	140	43	EXACT(0)	200	195	53
tnfn1_pw060328p05q105	E01	EXACT(0)	156	153	132	39	EXACT(0)	200	194	57
tnfn1_pw060328p05q106	F01	EXACT(0)	157	152	136	42	EXACT(0)	200	183	41
tnfn1_pw060328p05q107	G01	EXACT(0)	156	150	126	39	EXACT(0)	200	187	57
tnfn1_pw060328p05q108	H01	EXACT(0)	156	152	131	39	EXACT(0)	200	192	58
tnfn1_pw060328p05q109	A02	EXACT(0)	157	151	126	36	EXACT(0)	200	172	40
tnfn1_pw060328p05q110	B02	EXACT(0)	155	153	129	40	EXACT(0)	200	194	57
tnfn1_pw060328p05q111	C02	EXACT(0)	156	138	99	27	EXACT(0)	200	175	52
tnfn1_pw060328p05q112	D02	EXACT(0)	155	145	117	33	EXACT(0)	200	196	57
tnfn1_pw060328p05q113	E02	EXACT(0)	155	146	124	37	EXACT(0)	200	181	58
tnfn1_pw060328p05q114	F02	EXACT(0)	156	146	127	36	EXACT(0)	200	194	54
tnfn1_pw060328p05q115	G02	EXACT(0)	154	145	126	41	EXACT(0)	200	195	60
tnfn1_pw060328p05q116	H02	EXACT(0)	156	151	105	29	EXACT(0)	200	185	52
tnfn1_pw060328p05q117	A03	EXACT(0)	156	153	122	36	EXACT(0)	200	183	59
tnfn1_pw060328p05q118	B03	EXACT(0)	157	153	130	41	EXACT(0)	200	186	54
tnfn1_pw060328p05q119	C03	EXACT(0)	156	153	131	40	EXACT(0)	200	196	52
tnfn1_pw060328p05q120	D03	EXACT(0)	155	145	120	34	EXACT(0)	200	192	53
tnfn1_pw060328p05q121	E03	EXACT(0)	155	145	123	38	EXACT(0)	200	190	56
tnfn1_pw060328p05q122	F03	EXACT(0)	156	146	127	44	EXACT(0)	200	187	60
tnfn1_pw060328p05q123	G03	EXACT(0)	154	145	117	33	EXACT(0)	202	137	25
tnfn1_pw060328p05q124	H03	EXACT(0)	121	117	96	38	EXACT(0)	200	186	57
tnfn1_pw060328p05q125	A04	EXACT(0)	122	120	102	35	EXACT(0)	196	177	48
tnfn1_pw060328p05q126	B04	EXACT(0)	109	112	74	28	EXACT(0)	200	189	58
tnfn1_pw060328p05q127	C04	EXACT(0)	124	109	84	22	EXACT(0)	200	184	46
tnfn1_pw060328p05q128	D04	EXACT(0)	120	112	99	31	EXACT(0)	199	155	40
tnfn1_pw060328p05q129	E04	EXACT(0)	123	120	83	22	EXACT(0)	200	193	54
tnfn1_pw060328p05q130	F04	EXACT(0)	123	118	99	29	EXACT(0)	198	91	27
tnfn1_pw060328p05q131	G04	EXACT(0)	126	120	96	23	EXACT(0)	200	195	37
tnfn1_pw060328p05q132	H04	EXACT(0)	123	113	97	31	EXACT(0)	200	193	54
tnfn1_pw060328p05q133	A05	EXACT(0)	123	106	82	23	EXACT(0)	200	188	56
tnfn1_pw060328p05q134	B05	EXACT(0)	123	120	93	25	EXACT(0)	200	184	54
tnfn1_pw060328p05q135	C05	EXACT(0)	124	120	98	27	EXACT(0)	200	198	52
tnfn1_pw060328p05q136	D05	EXACT(0)	123	109	69	17	EXACT(0)	183	168	46
tnfn1_pw060328p05q137	E05	EXACT(0)	122	119	92	29	EXACT(0)	200	186	57
tnfn1_pw060328p05q138	F05	EXACT(0)	123	112	101	37	EXACT(0)	200	191	58
tnfn1_pw060328p05q139	G05	EXACT(0)	123	113	99	22	EXACT(0)	200	194	50
tnfn1_pw060328p05q140	H05	EXACT(0)	123	120	93	22	EXACT(0)	200	185	56
tnfn1_pw060328p05q141	A06	EXACT(0)	122	112	91	25	EXACT(0)	200	181	53
tnfn1_pw060328p05q142	B06	EXACT(0)	123	119	103	30	EXACT(0)	101	96	49
tnfn1_pw060328p05q143	C06	EXACT(0)	122	112	87	27	EXACT(0)	200	187	50
tnfn1_pw060328p05q144	D06	EXACT(0)	121	112	78	23	EXACT(0)	200	189	49
tnfn1_pw060328p05q145	E06	EXACT(0)	124	112	97	24	EXACT(0)	200	180	47
tnfn1_pw060328p05q146	F06	EXACT(0)	155	146	118	34	EXACT(0)	200	185	57
tnfn1_pw060328p05q147	G06	EXACT(0)	156	153	138	39	EXACT(0)	200	184	64
tnfn1_pw060328p05q148	H06	EXACT(0)	156	152	124	39	EXACT(0)	200	198	53

Table 3 - Sequence Mapping Quality Metrics

Strain Name	Well	Junction information	Position in sequence read of last vector nucleotide	Length of match to transposon	Transposon match score	Average phred score for transposon match	Genome position information	Length of match to genome	Genome match score	Average phred score for genome match
tnfn1_pw060328p05q149	A07	EXACT(0)	155	138	118	35	EXACT(0)	200	194	51
tnfn1_pw060328p05q150	B07	EXACT(0)	155	142	100	28	EXACT(0)	200	140	40
tnfn1_pw060328p05q151	C07	EXACT(0)	154	139	128	34	EXACT(0)	200	193	52
tnfn1_pw060328p05q152	D07	EXACT(0)	156	142	84	16	ESTIMATE(145)	54	42	28
tnfn1_pw060328p05q153	E07	EXACT(0)	156	153	135	42	EXACT(0)	200	188	48
tnfn1_pw060328p05q154	F07	EXACT(0)	155	145	129	44	EXACT(0)	200	181	58
tnfn1_pw060328p05q155	G07	EXACT(0)	155	146	127	41	EXACT(0)	200	193	59
tnfn1_pw060328p05q156	H07	EXACT(0)	155	145	126	39	EXACT(0)	194	190	49
tnfn1_pw060328p05q157	A08	EXACT(0)	157	153	118	32	EXACT(0)	200	182	57
tnfn1_pw060328p05q158	B08	EXACT(0)	155	145	126	41	EXACT(0)	200	187	57
tnfn1_pw060328p05q159	C08	EXACT(0)	155	145	126	42	EXACT(0)	200	194	55
tnfn1_pw060328p05q160	D08	EXACT(0)	154	151	122	40	EXACT(0)	200	191	55
tnfn1_pw060328p05q161	E08	EXACT(0)	155	145	123	40	EXACT(0)	200	194	57
tnfn1_pw060328p05q162	F08	EXACT(0)	154	152	120	36	EXACT(0)	200	188	53
tnfn1_pw060328p05q163	G08	EXACT(0)	156	152	131	41	EXACT(0)	200	191	56
tnfn1_pw060328p05q164	H08	EXACT(0)	155	145	129	43	EXACT(0)	197	180	54
tnfn1_pw060328p05q165	A09	EXACT(0)	155	153	129	41	EXACT(0)	200	192	59
tnfn1_pw060328p05q166	B09	EXACT(0)	156	153	123	40	EXACT(0)	200	193	57
tnfn1_pw060328p05q167	C09	EXACT(0)	156	153	123	37	EXACT(0)	200	195	56
tnfn1_pw060328p05q168	D09	EXACT(0)	155	139	128	43	EXACT(0)	200	194	51
tnfn1_pw060328p05q169	E09	EXACT(0)	154	145	121	39	EXACT(0)	161	152	53
tnfn1_pw060328p05q170	F09	EXACT(0)	157	146	126	40	EXACT(0)	200	193	56
tnfn1_pw060328p05q171	G09	EXACT(0)	157	153	128	37	EXACT(0)	200	193	58
tnfn1_pw060328p05q172	H09	EXACT(0)	155	145	114	37	EXACT(0)	200	190	54
tnfn1_pw060328p05q173	A10	EXACT(0)	156	153	126	38	EXACT(0)	200	193	48
tnfn1_pw060328p05q174	B10	EXACT(0)	158	146	134	43	EXACT(0)	200	189	58
tnfn1_pw060328p05q175	C10	EXACT(0)	155	138	113	30	EXACT(0)	200	194	52
tnfn1_pw060328p05q176	D10	EXACT(0)	156	153	132	40	EXACT(0)	199	172	46
tnfn1_pw060328p05q177	E10	EXACT(0)	156	153	126	38	EXACT(0)	200	195	58
tnfn1_pw060328p05q178	F10	EXACT(0)	155	145	120	39	EXACT(0)	200	172	58
tnfn1_pw060328p05q179	G10	EXACT(0)	155	152	119	33	EXACT(0)	200	190	56
tnfn1_pw060328p05q180	H10	EXACT(0)	155	152	128	42	EXACT(0)	200	189	55
tnfn1_pw060328p05q181	A11	EXACT(0)	156	145	118	37	EXACT(0)	200	185	58
tnfn1_pw060328p05q182	B11	EXACT(0)	155	152	110	28	EXACT(0)	200	175	57
tnfn1_pw060328p05q183	C11	EXACT(0)	123	121	84	21	EXACT(0)	200	199	52
tnfn1_pw060328p05q184	D11	EXACT(0)	121	112	96	27	EXACT(0)	200	153	36
tnfn1_pw060328p05q185	E11	EXACT(0)	117	112	102	40	EXACT(0)	200	188	56
tnfn1_pw060328p05q186	F11	EXACT(0)	122	113	70	22	EXACT(0)	200	188	56
tnfn1_pw060328p05q187	G11	EXACT(0)	121	112	96	26	EXACT(0)	200	159	34
tnfn1_pw060328p05q188	H11	EXACT(0)	122	121	100	29	EXACT(0)	200	188	51
tnfn1_pw060328p05q189	A12	EXACT(0)	122	121	100	34	EXACT(0)	200	192	57
tnfn1_pw060328p05q190	B12	EXACT(0)	121	106	64	21	EXACT(0)	200	190	46
tnfn1_pw060328p05q191	C12	EXACT(0)	115	112	102	34	EXACT(0)	200	192	52
tnfn1_pw060328p05q192	D12	EXACT(0)	123	119	98	28	EXACT(0)	200	192	54
tnfn1_pw060328p05q193	E12	EXACT(0)	123	112	98	27	EXACT(0)	200	169	42
tnfn1_pw060328p05q194	F12	EXACT(0)	123	120	87	26	EXACT(0)	200	191	51
tnfn1_pw060328p05q195	G12	EXACT(0)	123	112	83	21	EXACT(0)	200	187	49
tnfn1_pw060328p05q196	H12	EXACT(0)	123	120	95	26	EXACT(0)	200	186	54