

***Francisella tularensis* subsp. *novicida*, “Two-Allele” Transposon Mutant Library, Plate 20 (tnfn1_pw060418p04)**

Catalog No. NR-8054

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-8054 represents Plate 20 (tnfn1_pw060418p04) 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.

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-8054 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 20 (tnfn1_pw060418p04), NR-8054.”

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:

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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 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060418p04q101	A01	T20	-	two-component regulator, sensor histidine kinase	signal transduction and regulation
tnfn1_pw060418p04q102	B01	T20	-	Mur ligase family protein	cell wall / LPS / capsule
tnfn1_pw060418p04q103	C01	T20	trpC	indole-3-glycerol phosphate synthase (trpC); phosphoribosylanthranilate isomerase (trpF)	amino acid metabolism - biosynthesis
tnfn1_pw060418p04q104	D01	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q105	E01	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p04q106	F01	T20	pdpC	hypothetical protein	hypothetical - novel
tnfn1_pw060418p04q107	G01	T20	-	transcriptional regulator, IclR family	signal transduction and regulation
tnfn1_pw060418p04q108	H01	T20	wzb	low molecular weight (LMW) phosphotyrosine protein phosphatase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p04q109	A02	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q110	B02	T20	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p04q111	C02	T20	-	predicted NAD/FAD-dependent oxidoreductase	putative enzymes
tnfn1_pw060418p04q112	D02	T20	-	predicted NAD/FAD-dependent oxidoreductase	putative enzymes
tnfn1_pw060418p04q113	E02	T20	-	protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q114	F02	T20	-	peptide deformylase	translation, ribosomal structure and biogenesis
tnfn1_pw060418p04q115	G02	T20	-	nitroreductase	energy metabolism
tnfn1_pw060418p04q116	H02	T20	glgX	pullulanase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060418p04q117	A03	T20	-	protein of unknown function containing a von Willebrand factor type A (vWA) domain	unknown function - conserved
tnfn1_pw060418p04q118	B03	T20	-	RND efflux transporter, AcrB/AcrD/AcrF family	transport
tnfn1_pw060418p04q119	C03	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p04q120	D03	T20	-	phosphatidyltransferase	fatty acids and lipids metabolism
tnfn1_pw060418p04q121	E03	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p04q122	F03	T20	-	isochorismatase family protein	putative enzymes
tnfn1_pw060418p04q123	G03	T20	pilE	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060418p04q124	H03	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060418p04q125	A04	T20	-	oxidoreductase, short chain dehydrogenase/reductase family	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p04q126	B04	T20	pcm	protein-L-isoaspartate O-methyltransferase	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p04q127	C04	T20	glpF	glycerol uptake facilitator protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p04q128	D04	T20	-	allophanate hydrolase subunit 2	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p04q129	E04	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p04q130	F04	T20	tgt	queuine tRNA-ribosyltransferase.	translation, ribosomal structure and biogenesis
tnfn1_pw060418p04q131	G04	T20	-	D-alanyl-D-alanine carboxypeptidase	cell wall / LPS / capsule
tnfn1_pw060418p04q132	H04	T20	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p04q133	A05	<KAN-2>	-	lipoprotein of unknown function	unknown function - novel
tnfn1_pw060418p04q134	B05	<KAN-2>	hfq	host factor I for bacteriophage Q beta replication	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060418p04q135	C05	<KAN-2>	-	haloacid dehalogenase-like hydrolase	putative enzymes
tnfn1_pw060418p04q136	D05	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q137	E05	T18	-	hypothetical protein	Potentially coding: hypothetical - novel
tnfn1_pw060418p04q138	F05	T18	-	outer membrane efflux protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p04q139	G05	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p04q140	H05	T18	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p04q141	A06	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q142	B06	T18	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060418p04q143	C06	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p04q144	D06	T18	pdxY	pyridoxal kinase	putative enzymes
tnfn1_pw060418p04q145	E06	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p04q146	F06	<KAN-2>	pyk	pyruvate kinase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060418p04q147	G06	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q148	H06	T18	-	protein of unknown function	hypothetical - novel

Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060418p04q149	A07	T18	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q150	B07	T20	-	phage integrase	mobile and extrachromosomal element functions - phage or plasmid related proteins
tnfn1_pw060418p04q151	C07	T20	-	amino acid antiporter	transport - amino-acid
tnfn1_pw060418p04q152	D07	T20	lldD	L-lactate dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p04q153	E07	T20	tyrP	tyrosine permease	transport - amino-acid
tnfn1_pw060418p04q154	F07	T20	tolB	group A colicin translocation; tolB protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p04q155	G07	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060418p04q156	H07	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060418p04q157	A08	T20	-	serine permease	transport - amino-acid
tnfn1_pw060418p04q158	B08	T20	-	5-formyltetrahydrofolate cycloligase	putative enzymes
tnfn1_pw060418p04q159	C08	T20	-	transporter-associated protein, HlyC/CorC family	transport
tnfn1_pw060418p04q160	D08	T20	-	glucokinase regulatory protein	signal transduction and regulation
tnfn1_pw060418p04q161	E08	T20	-	dihydroliipoamide dehydrogenase	amino acid metabolism - biosynthesis
tnfn1_pw060418p04q162	F08	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p04q163	G08	T20	metIQ	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	transport - amino-acid
tnfn1_pw060418p04q164	H08	T20	oppC	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060418p04q165	A09	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q166	B09	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q167	C09	T20	asnB	asparagine synthase	amino acid metabolism - biosynthesis
tnfn1_pw060418p04q168	D09	T20	-	ABC transporter, ATP-binding protein	transport
tnfn1_pw060418p04q169	E09	T20	-	short-chain dehydrogenase	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p04q170	F09	T20	-	transcriptional regulator, LysR family	signal transduction and regulation
tnfn1_pw060418p04q171	G09	<KAN-2>	-	rare lipoprotein B family protein	cell wall / LPS / capsule
tnfn1_pw060418p04q172	H09	T20	manC	mannose-1-phosphate guanylyltransferase	cell wall / LPS / capsule
tnfn1_pw060418p04q173	A10	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p04q174	B10	T20	-	methyltransferase	putative enzymes
tnfn1_pw060418p04q175	C10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q176	D10	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q177	E10	T20	-	ThiF family protein	putative enzymes
tnfn1_pw060418p04q178	F10	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p04q179	G10	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q180	H10	T20	wbtE	UDP-glucose/GDP-mannose dehydrogenase family protein	cell wall / LPS / capsule
tnfn1_pw060418p04q181	A11	T20	-	MutT/nudix family protein	putative enzymes
tnfn1_pw060418p04q182	B11	T20	lpxE	lipid A 1-phosphatase	fatty acids and lipids metabolism
tnfn1_pw060418p04q183	C11	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060418p04q184	D11	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p04q185	E11	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p04q186	F11	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q187	G11	T17	bhc	outer membrane lipoprotein	cell wall / LPS / capsule
tnfn1_pw060418p04q188	H11	T20	-	small conductance mechanosensitive ion channel family protein	transport
tnfn1_pw060418p04q189	A12	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060418p04q190	B12	T20	mraW	S-adenosylmethionine-dependent methyltransferase	cell wall / LPS / capsule
tnfn1_pw060418p04q191	C12	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p04q192	D12	T20	-	peptidoglycan hydrolase	cell wall / LPS / capsule
tnfn1_pw060418p04q193	E12	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p04q194	F12	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p04q195	G12	<KAN-2>	-		
tnfn1_pw060418p04q196	H12	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved

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_pw060418p04q101	A01	C	1726589	R	FTN_1617	1726414	1727838	F	475	176(1425)
tnfn1_pw060418p04q102	B01	C	1173420	F	FTN_1111	1172407	1174089	R	561	670(1683)
tnfn1_pw060418p04q103	C01	C	1901321	R	FTN_1770	1900376	1901734	R	453	414(1359)
tnfn1_pw060418p04q104	D01	C	1728137	F	FTN_1618	1727841	1728719	R	293	583(879)
tnfn1_pw060418p04q105	E01	C	1253252	F	FTN_1180	1252995	1253897	R	301	646(903)
tnfn1_pw060418p04q106	F01	C	1392893	R	FTN_1319	1391204	1395178	F	1325	1690(3975)
tnfn1_pw060418p04q107	G01	C	775756	R	FTN_0720	775195	775908	F	238	562(714)
tnfn1_pw060418p04q108	H01	C	1105165	F	FTN_1046	1105060	1105542	R	161	378(483)
tnfn1_pw060418p04q109	A02	U	1233846	R	FTN_1161	1232698	1233897	R	400	52(1200)
tnfn1_pw060418p04q110	B02	C	1431357	R	FTN_1352	1430875	1431669	F	265	483(795)
tnfn1_pw060418p04q111	C02	U	1732067	F	FTN_1621	1731751	1732734	F	328	317(984)
tnfn1_pw060418p04q112	D02	C	1732067	F	FTN_1621	1731751	1732734	F	328	317(984)
tnfn1_pw060418p04q113	E02	C	1091780	F	FTN_1036	1091504	1091932	F	143	277(429)
tnfn1_pw060418p04q114	F02	C	509711	R	FTN_0500	509303	509935	F	211	409(633)
tnfn1_pw060418p04q115	G02	C	106363	R	FTN_0095	106145	106807	R	221	445(663)
tnfn1_pw060418p04q116	H02	U	525922	R	FTN_0512	524688	527897	R	1070	1976(3210)
tnfn1_pw060418p04q117	A03	C	227819	F	FTN_0207	227115	228113	F	333	705(999)
tnfn1_pw060418p04q118	B03	U	1714458	R	FTN_1610	1713789	1716899	F	1037	670(3111)
tnfn1_pw060418p04q119	C03	C	1254163	R	FTN_1181	1253887	1254966	R	360	804(1080)
tnfn1_pw060418p04q120	D03	C	1621786	R	FTN_1525	1621652	1622248	R	199	463(597)
tnfn1_pw060418p04q121	E03	C	1332505	R	FTN_1261	1331640	1333124	F	495	866(1485)
tnfn1_pw060418p04q122	F03	C	1159367	F	FTN_1097	1158946	1159515	R	190	149(570)
tnfn1_pw060418p04q123	G03	C	83318	F	FTN_0070	83199	83603	R	135	286(405)
tnfn1_pw060418p04q124	H03	U	612290	R	FTN_0583	611786	612709	R	308	420(924)
tnfn1_pw060418p04q125	A04	C	669251	R	FTN_0634	668810	669595	R	262	345(786)
tnfn1_pw060418p04q126	B04	U	1826065	F	FTN_1704	1825666	1826283	R	206	219(618)
tnfn1_pw060418p04q127	C04	C	1680164	F	FTN_1583	1679893	1680654	R	254	491(762)
tnfn1_pw060418p04q128	D04	C	100559	R	FTN_0089	100182	100991	F	270	378(810)
tnfn1_pw060418p04q129	E04	C	1163610	F	FTN_1101	1162960	1163790	R	277	181(831)
tnfn1_pw060418p04q130	F04	C	1162024	R	FTN_1100	1161392	1162492	R	367	469(1101)
tnfn1_pw060418p04q131	G04	C	963129	R	FTN_0907	962942	964273	F	444	188(1332)
tnfn1_pw060418p04q132	H04	C	562120	F	FTN_0538	561538	562995	R	486	876(1458)
tnfn1_pw060418p04q133	A05	C	426139	F	FTN_0427	425944	426390	F	149	196(447)
tnfn1_pw060418p04q134	B05	C	1110372	R	FTN_1051	1110274	1110600	R	109	229(327)
tnfn1_pw060418p04q135	C05	U	1028956	F	FTN_0974	1028537	1029115	F	193	420(579)
tnfn1_pw060418p04q136	D05	U	367757	F	FTN_0364	367604	368224	F	207	154(621)
tnfn1_pw060418p04q137	E05	C	371220	F	-	370947	371300	F	118	274(354)
tnfn1_pw060418p04q138	F05	C	1350510	F	FTN_1277	1349725	1351194	F	490	786(1470)
tnfn1_pw060418p04q139	G05	C	10091	F	FTN_0011	10044	10220	R	59	130(177)
tnfn1_pw060418p04q140	H05	C	555861	R	FTN_0534	555784	556824	F	347	78(1041)
tnfn1_pw060418p04q141	A06	C	1386918	F	FTN_1314	1386652	1387170	F	173	267(519)
tnfn1_pw060418p04q142	B06	U	1276319	F	FTN_1202	1275819	1277072	R	418	754(1254)
tnfn1_pw060418p04q143	C06	C	64205	F	FTN_0053	63789	64391	F	201	417(603)
tnfn1_pw060418p04q144	D06	C	223651	F	FTN_0202	223337	224185	R	283	535(849)
tnfn1_pw060418p04q145	E06	U	275027	R	FTN_0267	274900	275400	F	167	128(501)
tnfn1_pw060418p04q146	F06	C	1409294	R	FTN_1330	1408823	1410256	R	478	963(1434)
tnfn1_pw060418p04q147	G06	U	110037	R	FTN_0099	109818	110483	F	222	220(666)
tnfn1_pw060418p04q148	H06	U	933383	R	FTN_0878	933333	934319	F	329	51(987)

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_pw060418p04q149	A07	C	1894901	R	FTN_1765	1894130	1895098	F	323	772(969)
tnfn1_pw060418p04q150	B07	C	14441	R	FTN_0017	13789	15027	R	413	587(1239)
tnfn1_pw060418p04q151	C07	C	903313	R	FTN_0848	902798	904216	R	473	904(1419)
tnfn1_pw060418p04q152	D07	C	1049039	R	FTN_0991	1048716	1049855	R	380	817(1140)
tnfn1_pw060418p04q153	E07	U	1835848	F	FTN_1711	1835372	1836565	R	398	718(1194)
tnfn1_pw060418p04q154	F07	C	359452	F	FTN_0355	358647	359951	F	435	806(1305)
tnfn1_pw060418p04q155	G07	C	1602171	F	FTN_1506	1601515	1602525	R	337	355(1011)
tnfn1_pw060418p04q156	H07	C	992880	F	FTN_0932	992752	994548	F	599	129(1797)
tnfn1_pw060418p04q157	A08	U	655566	F	FTN_0624	654832	656091	R	420	526(1260)
tnfn1_pw060418p04q158	B08	C	1307909	R	FTN_1239	1307455	1308000	F	182	455(546)
tnfn1_pw060418p04q159	C08	U	1065559	F	FTN_1006	1065118	1066374	R	419	816(1257)
tnfn1_pw060418p04q160	D08	C	1599469	R	FTN_1504	1598661	1599542	R	294	74(882)
tnfn1_pw060418p04q161	E08	C	1623653	F	FTN_1526	1622248	1623663	R	472	11(1416)
tnfn1_pw060418p04q162	F08	C	1390885	R	FTN_1318	1390391	1391161	F	257	495(771)
tnfn1_pw060418p04q163	G08	C	1169421	F	FTN_1107	1168330	1169799	F	490	1092(1470)
tnfn1_pw060418p04q164	H08	C	1690070	F	FTN_1591	1689288	1690145	R	286	76(858)
tnfn1_pw060418p04q165	A09	C	815109	R	FTN_0758	814922	815875	F	318	188(954)
tnfn1_pw060418p04q166	B09	C	837069	F	FTN_0779	836764	838143	F	460	306(1380)
tnfn1_pw060418p04q167	C09	C	995751	F	FTN_0935	995336	997186	F	617	416(1851)
tnfn1_pw060418p04q168	D09	C	154676	R	FTN_0141	153815	155128	F	438	862(1314)
tnfn1_pw060418p04q169	E09	C	1251746	R	FTN_1178	1251247	1251966	R	240	221(720)
tnfn1_pw060418p04q170	F09	C	1252712	F	FTN_1179	1252082	1252978	F	299	631(897)
tnfn1_pw060418p04q171	G09	C	925915	F	FTN_0871	925584	926156	F	191	332(573)
tnfn1_pw060418p04q172	H09	C	1496732	R	FTN_1418	1495814	1497217	R	468	486(1404)
tnfn1_pw060418p04q173	A10	C	1027183	R	FTN_0972	1026361	1027734	R	458	552(1374)
tnfn1_pw060418p04q174	B10	C	1229520	F	FTN_1158	1229066	1229818	F	251	455(753)
tnfn1_pw060418p04q175	C10	C	520570	F	FTN_0509	519765	523154	F	1130	806(3390)
tnfn1_pw060418p04q176	D10	U	574738	F	FTN_0548	574443	574754	R	104	17(312)
tnfn1_pw060418p04q177	E10	C	1031038	F	FTN_0976	1030667	1031407	F	247	372(741)
tnfn1_pw060418p04q178	F10	U	1758019	R	FTN_1644	1755794	1758634	R	947	616(2841)
tnfn1_pw060418p04q179	G10	C	1273261	F	FTN_1199	1272824	1274032	R	403	772(1209)
tnfn1_pw060418p04q180	H10	C	1507127	R	FTN_1426	1506257	1507564	R	436	438(1308)
tnfn1_pw060418p04q181	A11	U	344734	F	FTN_0338	344391	345035	F	215	344(645)
tnfn1_pw060418p04q182	B11	U	415424	F	FTN_0416	414941	415657	F	239	484(717)
tnfn1_pw060418p04q183	C11	C	313467	F	FTN_0304	312892	314295	F	468	576(1404)
tnfn1_pw060418p04q184	D11	C	113342	R	FTN_0102	112565	113716	F	384	778(1152)
tnfn1_pw060418p04q185	E11	C	1079700	R	FTN_1021	1079294	1079827	F	178	407(534)
tnfn1_pw060418p04q186	F11	U	1138641	F	FTN_1075	1138172	1138876	R	235	236(705)
tnfn1_pw060418p04q187	G11	C	191000	F	FTN_0174	190570	191085	F	172	431(516)
tnfn1_pw060418p04q188	H11	C	1072452	F	FTN_1012	1071927	1072757	F	277	526(831)
tnfn1_pw060418p04q189	A12	C	865216	F	FTN_0807	864451	865230	R	260	15(780)
tnfn1_pw060418p04q190	B12	C	639118	R	FTN_0605	638482	639396	F	305	637(915)
tnfn1_pw060418p04q191	C12	C	110834	F	FTN_0100	110482	111495	R	338	662(1014)
tnfn1_pw060418p04q192	D12	C	1337569	F	FTN_1265	1336964	1337773	F	270	606(810)
tnfn1_pw060418p04q193	E12	C	121161	R	FTN_0109	120740	121717	R	326	557(978)
tnfn1_pw060418p04q194	F12	C	46964	F	FTN_0042	46882	47436	F	185	83(555)
tnfn1_pw060418p04q195	G12	C	847403	F	intergenic					
tnfn1_pw060418p04q196	H12	U	693615	R	FTN_0654	693039	693686	R	216	72(648)

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_pw060418p04q101	A01	EXACT(0)	155	153	135	42	EXACT(0)	199	181	54
tnfn1_pw060418p04q102	B01	EXACT(0)	157	145	141	41	EXACT(0)	199	186	49
tnfn1_pw060418p04q103	C01	EXACT(0)	155	145	126	40	EXACT(0)	200	188	53
tnfn1_pw060418p04q104	D01	EXACT(0)	158	151	140	49	EXACT(0)	200	193	57
tnfn1_pw060418p04q105	E01	EXACT(0)	156	153	132	39	EXACT(0)	200	187	58
tnfn1_pw060418p04q106	F01	EXACT(0)	158	152	138	38	EXACT(0)	199	176	52
tnfn1_pw060418p04q107	G01	EXACT(0)	157	145	133	41	EXACT(0)	200	186	51
tnfn1_pw060418p04q108	H01	EXACT(0)	156	152	109	33	EXACT(0)	200	193	55
tnfn1_pw060418p04q109	A02	EXACT(0)	157	151	132	39	EXACT(0)	200	186	65
tnfn1_pw060418p04q110	B02	EXACT(0)	156	144	133	41	EXACT(0)	200	195	62
tnfn1_pw060418p04q111	C02	EXACT(0)	159	155	129	42	EXACT(0)	200	190	65
tnfn1_pw060418p04q112	D02	EXACT(0)	159	155	129	42	EXACT(0)	200	190	65
tnfn1_pw060418p04q113	E02	EXACT(0)	154	145	119	42	EXACT(0)	200	178	50
tnfn1_pw060418p04q114	F02	EXACT(0)	157	143	128	34	EXACT(0)	200	190	49
tnfn1_pw060418p04q115	G02	EXACT(0)	155	145	117	33	EXACT(0)	200	193	52
tnfn1_pw060418p04q116	H02	EXACT(0)	158	153	139	39	EXACT(0)	200	187	61
tnfn1_pw060418p04q117	A03	EXACT(0)	157	153	144	43	EXACT(0)	200	189	47
tnfn1_pw060418p04q118	B03	EXACT(0)	158	151	136	45	EXACT(0)	200	197	62
tnfn1_pw060418p04q119	C03	EXACT(0)	157	145	119	35	EXACT(0)	199	174	46
tnfn1_pw060418p04q120	D03	EXACT(0)	156	145	131	39	EXACT(0)	200	175	54
tnfn1_pw060418p04q121	E03	EXACT(0)	156	139	124	36	EXACT(0)	200	181	55
tnfn1_pw060418p04q122	F03	EXACT(0)	157	153	131	42	EXACT(0)	200	182	50
tnfn1_pw060418p04q123	G03	EXACT(0)	156	145	136	45	EXACT(0)	200	196	59
tnfn1_pw060418p04q124	H03	EXACT(0)	159	159	130	40	EXACT(0)	200	184	62
tnfn1_pw060418p04q125	A04	EXACT(0)	158	145	129	39	EXACT(0)	200	187	44
tnfn1_pw060418p04q126	B04	EXACT(0)	162	144	111	31	EXACT(0)	199	176	44
tnfn1_pw060418p04q127	C04	EXACT(0)	156	152	133	40	EXACT(0)	200	194	57
tnfn1_pw060418p04q128	D04	EXACT(0)	157	153	130	29	EXACT(0)	200	191	51
tnfn1_pw060418p04q129	E04	EXACT(0)	156	150	125	41	EXACT(0)	200	174	33
tnfn1_pw060418p04q130	F04	EXACT(0)	155	140	132	44	EXACT(0)	200	174	44
tnfn1_pw060418p04q131	G04	EXACT(0)	156	152	136	41	EXACT(0)	110	110	50
tnfn1_pw060418p04q132	H04	EXACT(0)	157	155	120	42	EXACT(0)	200	187	59
tnfn1_pw060418p04q133	A05	EXACT(0)	121	112	80	26	EXACT(0)	200	192	58
tnfn1_pw060418p04q134	B05	EXACT(0)	121	120	105	36	EXACT(0)	200	188	56
tnfn1_pw060418p04q135	C05	EXACT(0)	115	111	63	19	EXACT(0)	200	190	55
tnfn1_pw060418p04q136	D05	EXACT(0)	120	111	88	23	EXACT(0)	200	176	50
tnfn1_pw060418p04q137	E05	EXACT(0)	122	106	97	26	EXACT(0)	199	171	47
tnfn1_pw060418p04q138	F05	EXACT(0)	124	112	86	23	EXACT(0)	200	191	45
tnfn1_pw060418p04q139	G05	EXACT(0)	123	125	56	20	EXACT(0)	200	176	45
tnfn1_pw060418p04q140	H05	EXACT(0)	124	118	96	27	EXACT(0)	200	177	56
tnfn1_pw060418p04q141	A06	EXACT(0)	122	83	77	25	EXACT(0)	200	182	43
tnfn1_pw060418p04q142	B06	EXACT(0)	122	119	95	37	EXACT(0)	199	163	45
tnfn1_pw060418p04q143	C06	EXACT(0)	121	112	99	31	EXACT(0)	199	181	53
tnfn1_pw060418p04q144	D06	EXACT(0)	126	120	110	27	EXACT(0)	96	92	44
tnfn1_pw060418p04q145	E06	EXACT(0)	125	120	106	29	EXACT(0)	200	181	54
tnfn1_pw060418p04q146	F06	EXACT(0)	118	112	99	31	EXACT(0)	182	166	42
tnfn1_pw060418p04q147	G06	EXACT(0)	158	153	142	46	EXACT(0)	200	194	66
tnfn1_pw060418p04q148	H06	EXACT(0)	122	112	93	35	EXACT(0)	200	171	59

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_pw060418p04q149	A07	EXACT(0)	122	105	69	32	EXACT(0)	200	186	47
tnfn1_pw060418p04q150	B07	EXACT(0)	156	116	104	40	EXACT(0)	200	188	46
tnfn1_pw060418p04q151	C07	EXACT(0)	157	153	123	32	EXACT(0)	199	165	34
tnfn1_pw060418p04q152	D07	EXACT(0)	154	145	129	42	EXACT(0)	200	191	51
tnfn1_pw060418p04q153	E07	EXACT(0)	155	145	132	47	EXACT(0)	200	187	65
tnfn1_pw060418p04q154	F07	EXACT(0)	154	144	128	39	EXACT(0)	200	186	47
tnfn1_pw060418p04q155	G07	EXACT(0)	156	145	134	40	EXACT(0)	200	193	58
tnfn1_pw060418p04q156	H07	EXACT(0)	158	152	132	31	EXACT(0)	200	186	63
tnfn1_pw060418p04q157	A08	EXACT(0)	156	153	137	37	EXACT(0)	200	173	64
tnfn1_pw060418p04q158	B08	EXACT(0)	157	153	137	42	EXACT(0)	200	173	39
tnfn1_pw060418p04q159	C08	EXACT(0)	158	153	133	44	EXACT(0)	200	182	66
tnfn1_pw060418p04q160	D08	EXACT(0)	156	145	128	48	EXACT(0)	200	192	59
tnfn1_pw060418p04q161	E08	EXACT(0)	157	145	139	49	EXACT(0)	200	188	66
tnfn1_pw060418p04q162	F08	EXACT(0)	156	152	133	37	EXACT(0)	200	79	33
tnfn1_pw060418p04q163	G08	EXACT(0)	158	153	141	47	EXACT(0)	200	191	60
tnfn1_pw060418p04q164	H08	EXACT(0)	153	145	99	20	EXACT(0)	200	183	50
tnfn1_pw060418p04q165	A09	EXACT(0)	157	153	137	43	EXACT(0)	200	189	63
tnfn1_pw060418p04q166	B09	EXACT(0)	156	145	114	36	EXACT(0)	200	190	56
tnfn1_pw060418p04q167	C09	EXACT(0)	157	153	134	36	EXACT(0)	200	153	41
tnfn1_pw060418p04q168	D09	EXACT(0)	157	153	137	49	EXACT(0)	200	197	62
tnfn1_pw060418p04q169	E09	EXACT(0)	155	145	126	40	EXACT(0)	200	193	42
tnfn1_pw060418p04q170	F09	EXACT(0)	155	153	132	46	EXACT(0)	200	173	52
tnfn1_pw060418p04q171	G09	EXACT(0)	124	105	46	13	EXACT(0)	200	156	36
tnfn1_pw060418p04q172	H09	EXACT(0)	155	140	113	24	EXACT(0)	199	185	38
tnfn1_pw060418p04q173	A10	EXACT(0)	158	152	141	40	EXACT(0)	200	194	58
tnfn1_pw060418p04q174	B10	EXACT(0)	157	145	139	45	EXACT(0)	200	188	59
tnfn1_pw060418p04q175	C10	EXACT(0)	155	153	132	40	EXACT(0)	200	197	50
tnfn1_pw060418p04q176	D10	EXACT(0)	156	152	133	45	EXACT(0)	200	180	67
tnfn1_pw060418p04q177	E10	EXACT(0)	157	153	134	37	EXACT(0)	200	189	40
tnfn1_pw060418p04q178	F10	EXACT(0)	158	152	131	35	EXACT(0)	200	182	56
tnfn1_pw060418p04q179	G10	EXACT(0)	157	152	133	45	EXACT(0)	200	189	65
tnfn1_pw060418p04q180	H10	EXACT(0)	156	152	130	44	EXACT(0)	200	191	61
tnfn1_pw060418p04q181	A11	EXACT(0)	155	145	107	34	EXACT(0)	200	183	60
tnfn1_pw060418p04q182	B11	EXACT(0)	152	145	94	25	EXACT(0)	200	189	54
tnfn1_pw060418p04q183	C11	EXACT(0)	155	151	133	49	EXACT(0)	201	98	35
tnfn1_pw060418p04q184	D11	EXACT(0)	156	153	137	45	EXACT(0)	200	183	65
tnfn1_pw060418p04q185	E11	EXACT(0)	157	151	128	42	EXACT(0)	200	193	60
tnfn1_pw060418p04q186	F11	EXACT(0)	157	145	133	47	EXACT(0)	200	183	58
tnfn1_pw060418p04q187	G11	EXACT(0)	122	81	69	27	EXACT(0)	200	185	50
tnfn1_pw060418p04q188	H11	EXACT(0)	157	152	141	43	EXACT(0)	200	181	66
tnfn1_pw060418p04q189	A12	EXACT(0)	158	150	145	45	EXACT(0)	199	172	46
tnfn1_pw060418p04q190	B12	EXACT(0)	154	114	105	40	EXACT(0)	200	190	53
tnfn1_pw060418p04q191	C12	EXACT(0)	155	150	123	34	EXACT(0)	199	185	43
tnfn1_pw060418p04q192	D12	EXACT(0)	155	145	100	25	EXACT(0)	200	186	53
tnfn1_pw060418p04q193	E12	EXACT(0)	158	153	139	44	EXACT(0)	200	192	66
tnfn1_pw060418p04q194	F12	EXACT(0)	120	112	93	30	EXACT(0)	200	190	53
tnfn1_pw060418p04q195	G12	EXACT(0)	122	112	64	23	EXACT(0)	200	182	51
tnfn1_pw060418p04q196	H12	EXACT(0)	121	111	98	28	EXACT(0)	200	184	57