Francisella tularensis subsp. *novicida*, "Two-Allele" Transposon Mutant Library, Plate 19 (tnfn1_pw060418p03)

Catalog No. NR-8053

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 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-8053 represents Plate 19 (tnfn1_pw060418p03) 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-8053 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% CO_2
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 19 (tnfn1_pw060418p03), NR-8053."

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/bmbl5/bmbl5toc.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_pw060418p03q101	A01	T20	-	ABC-type transport system permease protein	transport
tnfn1_pw060418p03q102	B01	T20	-	pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060418p03q103	C01	T20	potG	ATP-binding cassette putrescine uptake system, ATP-binding protein	transport
tnfn1_pw060418p03q104	D01	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p03q105	E01	T20	-	metabolite:H+ symporter (MHS) family protein	transport
tnfn1_pw060418p03q106	F01	T20	-	OmpA family protein	cell wall / LPS / capsule
tnfn1_pw060418p03q107	G01	T20	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060418p03q108	H01	T20	-	protein of unknown function with predicted hydrolase and phosphorylase activity	unknown function - conserved
tnfn1_pw060418p03q109	A02	T20	-	fucose: H+ symporter (FHS) family protein	transport - carbohydrates (sugars, polysaccharides)
tnfn1_pw060418p03q110	B02	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p03q111	C02	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p03q112	D02	T20	-	Zn-dependent hydrolase	putative enzymes
tnfn1_pw060418p03q113	E02	T20	-	metal-dependent exopeptidase	post-translational modification, protein turnover, chaperones - protein degradation
tnfn1_pw060418p03q114	F02	T20	-	type I restriction-modification system, subunit R (restriction)	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060418p03q115	G02	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q116	H02	<KAN-2>	-	acyltransferase	fatty acids and lipids metabolism
tnfn1_pw060418p03q117	A03	<KAN-2>	xerD	site-specific recombinase	DNA replication, recombination, modification and repair
tnfn1_pw060418p03q118	B03	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p03q119	C03	<KAN-2>	pilA	Type IV pili, pilus assembly protein	motility, attachment and secretion structure
tnfn1_pw060418p03q120	D03	<KAN-2>	ugpQ	glycerophosphoryl diester phosphodiesterase	cell wall / LPS / capsule
tnfn1_pw060418p03q121	E03	<KAN-2>	capB	capsule biosynthesis protein CapB	cell wall / LPS / capsule
tnfn1_pw060418p03q122	F03	<KAN-2>	-	ATP-binding cassette (ABC) superfamily protein	transport
tnfn1_pw060418p03q123	G03	<KAN-2>	accA	acetyl-CoA carboxylase, carboxytransferase subunit alpha	fatty acids and lipids metabolism
tnfn1_pw060418p03q124	H03	<KAN-2>	ychF	GTP-binding protein	putative enzymes
tnfn1_pw060418p03q125	A04	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p03q126	B04	T18			
tnfn1_pw060418p03q127	C04	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p03q128	D04	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q129	E04	T20	talA	transaldolase	energy metabolism
tnfn1_pw060418p03q130	F04	T18	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p03q131	G04	T20	-	haloacid dehalogenase-like hydrolase	putative enzymes
tnfn1_pw060418p03q132	H04	T20	ansB	periplasmic L-asparaginase II precursor	amino acid metabolism - biosynthesis
tnfn1_pw060418p03q133	A05	T20	cyoE	heme O synthase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p03q134	B05	T20	-	pirin family protein	putative enzymes
tnfn1_pw060418p03q135	C05	T20	-	YGGT family membrane protein	unknown function - conserved
tnfn1_pw060418p03q136	D05	T20	pilP	Type IV pili periplasmic component	motility, attachment and secretion structure
tnfn1_pw060418p03q137	E05	T20	folC	folylpoly-gamma-glutamate synthetase/ dihydrofolate synthetase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p03q138	F05	T20	gltB	glutamate synthase domain 2	other metabolism - degradation, utilization, assimilation
tnfn1_pw060418p03q139	G05	T20	gapA	glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	energy metabolism
tnfn1_pw060418p03q140	H05	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q141	A06	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p03q142	B06	T20	-	short chain dehydrogenase	putative enzymes
tnfn1_pw060418p03q143	C06	T20	-	drug/metabolite transporter (DMT) superfamily protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p03q144	D06	T20	ksgA	dimethyladenosine transferase	transport - amino-acid
tnfn1_pw060418p03q145	E06	T20	-	polar amino acid uptake transporter	transport - amino-acid
tnfn1_pw060418p03q146	F06	T20	-	conserved hypothetical protein	hypothetical - conserved
tnfn1_pw060418p03q147	G06	T20	putP	proline:Na+ symporter	transport - amino-acid
tnfn1_pw060418p03q148	H06	T20	-	membrane protein of unknown function	unknown function - novel

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Table 1 - Transposon Type and Mutated Gene

Strain Name	Well	Transposon type	Gene	Description	Function Class
tnfn1_pw060418p03q149	A07	T20	-	predicted Co/Zn/Cd cation transporter	transport
tnfn1_pw060418p03q150	B07	T20	-	glycosyl transferase, family 2	cell wall / LPS / capsule
tnfn1_pw060418p03q151	C07	T20	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p03q152	D07	T20	-	dehydrogenase	putative enzymes
tnfn1_pw060418p03q153	E07	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p03q154	F07	T20	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060418p03q155	G07	T20	-	amino acid transporter (AAT) family protein	transport - amino-acid
tnfn1_pw060418p03q156	H07	T20	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q157	A08	T20	kpsF	phosphosugar isomerase	cell wall / LPS / capsule
tnfn1_pw060418p03q158	B08	T20	recB	ATP-dependent exoDNAse (exonuclease V) beta subunit	DNA replication, recombination, modification and repair - restriction/modification
tnfn1_pw060418p03q159	C08	T20	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p03q160	D08	T20			
tnfn1_pw060418p03q161	E08	T20	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p03q162	F08	T20	-	MoxR-like ATPase	putative enzymes
tnfn1_pw060418p03q163	G08	T20	udhA	soluble pyridine nucleotide transhydrogenase	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p03q164	H08	T20	emrE	putative membrane transporter of cations and cationic drugs, multidrug resistance protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p03q165	A09	T20	-	drug:H+ antiporter-1 (DHA1) family protein	transport - drugs / antibacterial compounds
tnfn1_pw060418p03q166	B09	T20	-	protein of unknown function with radical SAM domain	unknown function - conserved
tnfn1_pw060418p03q167	C09	T20	sohB	peptidase family S49 protein	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p03q168	D09	T20	-	HIT family protein	putative enzymes
tnfn1_pw060418p03q169	E09	T20	-	membrane protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q170	F09	T20	-	conserved hypothetical protein, Thioesterase superfamily	hypothetical - conserved
tnfn1_pw060418p03q171	G09	T20	galU	UTP--glucose-1-phosphate uridylyltransferase	carbohydrate metabolism - degradation, utilization, assimilation
tnfn1_pw060418p03q172	H09	T20	-	glutamine amidotransferase, class I	other metabolism - biosynthesis
tnfn1_pw060418p03q173	A10	<KAN-2>	-	thioesterase	putative enzymes
tnfn1_pw060418p03q174	B10	<KAN-2>	tig	trigger factor (TF) protein (peptidyl-prolyl cis/trans isomerase)	post-translational modification, protein turnover, chaperones - protein modification
tnfn1_pw060418p03q175	C10	<KAN-2>	oppB	peptide/opine/nickel uptake transporter (PepT) family protein	transport
tnfn1_pw060418p03q176	D10	<KAN-2>	-	protein of unknown function	unknown function - novel
tnfn1_pw060418p03q177	E10	<KAN-2>	pcp	pyrrolidone carboxylylate peptidase	post-translational modification, protein turnover, chaperones
tnfn1_pw060418p03q178	F10	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q179	G10	<KAN-2>	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q180	H10	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p03q181	A11	<KAN-2>	-	rhodanese-related sulfurtransferase	other metabolism - biosynthesis
tnfn1_pw060418p03q182	B11	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q183	C11	<KAN-2>	-	conserved hypothetical membrane protein	hypothetical - conserved
tnfn1_pw060418p03q184	D11	<KAN-2>	-	hypothetical membrane protein	hypothetical - novel
tnfn1_pw060418p03q185	E11	<KAN-2>	-	S-adenosylmethionine-dependent methyltransferase	putative enzymes
tnfn1_pw060418p03q186	F11	<KAN-2>	acnA	aconitate hydratase	energy metabolism
tnfn1_pw060418p03q187	G11	T18	-	nicotinamide ribonucleoside (NR) uptake permease (PnuC) family protein	transport
tnfn1_pw060418p03q188	H11	T18	-	hypothetical protein	hypothetical - novel
tnfn1_pw060418p03q189	A12	T18	cutC	copper homeostasis protein CutC family protein	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p03q190	B12	T18	-	conserved protein of unknown function	unknown function - conserved
tnfn1_pw060418p03q191	C12	T18	recX	inhibitor of RecA	signal transduction and regulation
tnfn1_pw060418p03q192	D12	T18	pheA	prephenate dehydratase	amino acid metabolism - biosynthesis
tnfn1_pw060418p03q193	E12	T18	naoX	uncharacterized NAD(FAD)-dependent dehydrogenase	putative enzymes
tnfn1_pw060418p03q194	F12	T20	rnr	ribonuclease R	transcription
tnfn1_pw060418p03q195	G12	T18	folE	GTP cyclohydrolase I	cofactors, prosthetic groups, electron carriers metabolism
tnfn1_pw060418p03q196	H12	T18	-	conserved protein of unknown function	unknown function - conserved

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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_pw060418p03q101	A01	C	1338589	R	FTN_1266	1337851	1338948	F	366	739(1098)
tnfn1_pw060418p03q102	B01	U	315358	R	FTN_0306	315040	315714	F	225	319(675)
tnfn1_pw060418p03q103	C01	C	792977	R	FTN_0739	792274	793392	R	373	416(1119)
tnfn1_pw060418p03q104	D01	C	334704	R	FTN_0326	334524	335054	R	177	351(531)
tnfn1_pw060418p03q105	E01	C	98155	R	FTN_0086	97601	98827	F	409	555(1227)
tnfn1_pw060418p03q106	F01	C	352570	R	FTN_0346	352150	353400	R	417	831(1251)
tnfn1_pw060418p03q107	G01	C	1287409	R	FTN_1217	1286888	1288573	R	562	1165(1686)
tnfn1_pw060418p03q108	H01	C	957475	R	FTN_0900	956882	958711	R	610	1237(1830)
tnfn1_pw060418p03q109	A02	C	866540	R	FTN_0809	866270	867517	F	416	271(1248)
tnfn1_pw060418p03q110	B02	C	902163	R	FTN_0847	901867	902790	R	308	628(924)
tnfn1_pw060418p03q111	C02	C	161169	R	FTN_0148	160862	161488	F	209	308(627)
tnfn1_pw060418p03q112	D02	C	1467898	F	FTN_1390	1467372	1468055	R	228	158(684)
tnfn1_pw060418p03q113	E02	C	1020909	F	FTN_0965	1019741	1021147	F	469	1169(1407)
tnfn1_pw060418p03q114	F02	C	295406	F	FTN_0287	294845	295609	F	255	562(765)
tnfn1_pw060418p03q115	G02	C	1085285	R	FTN_1028	1084814	1085557	R	248	273(744)
tnfn1_pw060418p03q116	H02	C	1879783	F	FTN_1750	1879341	1880078	F	246	443(738)
tnfn1_pw060418p03q117	A03	C	1656251	R	FTN_1558	1655903	1656778	R	292	528(876)
tnfn1_pw060418p03q118	B03	C	1301336	F	FTN_1232	1300558	1301340	F	261	779(783)
tnfn1_pw060418p03q119	C03	C	414259	R	FTN_0415	414152	414556	R	135	298(405)
tnfn1_pw060418p03q120	D03	C	673790	R	FTN_0637	673289	674314	R	342	525(1026)
tnfn1_pw060418p03q121	E03	C	1274872	R	FTN_1201	1274526	1275740	R	405	869(1215)
tnfn1_pw060418p03q122	F03	U	1482458	R	FTN_1404	1482101	1482877	R	259	420(777)
tnfn1_pw060418p03q123	G03	C	1603036	R	FTN_1508	1603032	1603976	R	315	941(945)
tnfn1_pw060418p03q124	H03	C	1063954	F	FTN_1004	1063694	1064782	F	363	261(1089)
tnfn1_pw060418p03q125	A04	C	714082	F	FTN_0671	713359	714384	R	342	303(1026)
tnfn1_pw060418p03q126	B04	U	818715	F	intergenic					
tnfn1_pw060418p03q127	C04	C	994993	R	FTN_0934	994829	995320	F	164	165(492)
tnfn1_pw060418p03q128	D04	U	1031832	R	FTN_0977	1031487	1032053	F	189	346(567)
tnfn1_pw060418p03q129	E04	C	839693	F	FTN_0781	839608	840624	F	339	86(1017)
tnfn1_pw060418p03q130	F04	C	1296212	F	FTN_1226	1296078	1296404	R	109	193(327)
tnfn1_pw060418p03q131	G04	C	1281470	F	FTN_1211	1281241	1281900	R	220	431(660)
tnfn1_pw060418p03q132	H04	C	579930	R	FTN_0555	579267	580328	F	354	664(1062)
tnfn1_pw060418p03q133	A05	C	221087	R	FTN_0199	220528	221373	F	282	560(846)
tnfn1_pw060418p03q134	B05	C	1353837	R	FTN_1281	1353283	1353978	R	232	142(696)
tnfn1_pw060418p03q135	C05	U	162956	F	FTN_0150	162491	163057	F	189	466(567)
tnfn1_pw060418p03q136	D05	C	1203457	F	FTN_1138	1203258	1203845	R	196	389(588)
tnfn1_pw060418p03q137	E05	C	281637	F	FTN_0273	280833	282011	F	393	805(1179)
tnfn1_pw060418p03q138	F05	C	1444051	R	FTN_1360	1442839	1444422	R	528	372(1584)
tnfn1_pw060418p03q139	G05	U	1411484	F	FTN_1332	1411472	1412470	R	333	987(999)
tnfn1_pw060418p03q140	H05	C	93175	R	FTN_0083	93070	93825	F	252	106(756)
tnfn1_pw060418p03q141	A06	U	1226367	R	FTN_1156	1225105	1226655	R	517	289(1551)
tnfn1_pw060418p03q142	B06	C	1632880	R	FTN_1535	1632461	1633282	F	274	420(822)
tnfn1_pw060418p03q143	C06	C	1895365	R	FTN_1766	1895114	1896115	R	334	751(1002)
tnfn1_pw060418p03q144	D06	C	587694	F	FTN_0560	587181	587966	F	262	514(786)
tnfn1_pw060418p03q145	E06	U	209385	R	FTN_0191	208872	209609	R	246	225(738)
tnfn1_pw060418p03q146	F06	C	998832	F	FTN_0937	998435	999334	F	300	398(900)
tnfn1_pw060418p03q147	G06	C	308041	F	FTN_0299	306996	308501	F	502	1046(1506)
tnfn1_pw060418p03q148	H06	C	317488	R	FTN_0308	316669	318474	F	602	820(1806)

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.

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tnfn1_pw060418p03q149	A07	C	781150	F	FTN_0728	780666	781802	F	379	485(1137)
tnfn1_pw060418p03q150	B07	U	1284778	F	FTN_1214	1283962	1284918	R	319	141(957)
tnfn1_pw060418p03q151	C07	C	232582	F	FTN_0212	232274	232753	F	160	309(480)
tnfn1_pw060418p03q152	D07	C	1018842	R	FTN_0964	1018209	1019321	R	371	480(1113)
tnfn1_pw060418p03q153	E07	C	1119551	F	FTN_1059	1119271	1119732	F	154	281(462)
tnfn1_pw060418p03q154	F07	C	204937	F	FTN_0188	204831	205403	F	191	107(573)
tnfn1_pw060418p03q155	G07	C	405515	F	FTN_0407	404710	406101	R	464	587(1392)
tnfn1_pw060418p03q156	H07	C	450789	R	FTN_0449	450598	451470	F	291	192(873)
tnfn1_pw060418p03q157	A08	C	1293251	R	FTN_1222	1292995	1293963	F	323	257(969)
tnfn1_pw060418p03q158	B08	U	1435653	F	FTN_1357	1435327	1438974	R	1216	3322(3648)
tnfn1_pw060418p03q159	C08	C	1863002	F	FTN_1736	1862687	1863082	F	132	316(396)
tnfn1_pw060418p03q160	D08	C	981936	R	intergenic					
tnfn1_pw060418p03q161	E08	C	288635	R	FTN_0281	288433	288879	F	149	203(447)
tnfn1_pw060418p03q162	F08	C	224917	F	FTN_0204	224772	225725	F	318	146(954)
tnfn1_pw060418p03q163	G08	C	1060015	R	FTN_0999	1059107	1060504	F	466	909(1398)
tnfn1_pw060418p03q164	H08	U	856319	R	FTN_0799	856317	856643	R	109	325(327)
tnfn1_pw060418p03q165	A09	C	557732	F	FTN_0535	556910	558133	F	408	823(1224)
tnfn1_pw060418p03q166	B09	U	819432	F	FTN_0761	818940	820022	F	361	493(1083)
tnfn1_pw060418p03q167	C09	C	575857	F	FTN_0550	575484	576497	F	338	374(1014)
tnfn1_pw060418p03q168	D09	C	727817	R	FTN_0684	727685	728077	F	131	133(393)
tnfn1_pw060418p03q169	E09	C	333884	F	FTN_0325	333787	334446	R	220	563(660)
tnfn1_pw060418p03q170	F09	C	1529162	R	FTN_1440	1528961	1529446	F	162	202(486)
tnfn1_pw060418p03q171	G09	C	781950	F	FTN_0729	781822	782682	F	287	129(861)
tnfn1_pw060418p03q172	H09	C	434094	F	FTN_0435	433757	434461	F	235	338(705)
tnfn1_pw060418p03q173	A10	C	977280	F	FTN_0919	977263	977676	F	138	18(414)
tnfn1_pw060418p03q174	B10	C	1117990	R	FTN_1058	1117803	1119116	R	438	1127(1314)
tnfn1_pw060418p03q175	C10	C	1690943	R	FTN_1592	1690148	1691083	R	312	141(936)
tnfn1_pw060418p03q176	D10	C	224592	R	FTN_0203	224195	224626	R	144	35(432)
tnfn1_pw060418p03q177	E10	C	231870	F	FTN_0211	231598	232263	F	222	273(666)
tnfn1_pw060418p03q178	F10	U	427309	F	FTN_0429	427130	427630	F	167	180(501)
tnfn1_pw060418p03q179	G10	C	1537201	R	FTN_1447	1536391	1537371	R	327	171(981)
tnfn1_pw060418p03q180	H10	U	185541	R	FTN_0169	185208	185747	R	180	207(540)
tnfn1_pw060418p03q181	A11	C	131461	F	FTN_0120	131219	131638	F	140	243(420)
tnfn1_pw060418p03q182	B11	C	395779	F	FTN_0396	395576	396226	F	217	204(651)
tnfn1_pw060418p03q183	C11	C	1301169	F	FTN_1232	1300558	1301340	F	261	612(783)
tnfn1_pw060418p03q184	D11	C	917688	F	FTN_0863	917341	917775	F	145	348(435)
tnfn1_pw060418p03q185	E11	C	1478819	R	FTN_1400	1478681	1479367	R	229	549(687)
tnfn1_pw060418p03q186	F11	C	1734010	R	FTN_1623	1733943	1736753	R	937	2744(2811)
tnfn1_pw060418p03q187	G11	C	1861426	F	FTN_1733	1861017	1861637	R	207	212(621)
tnfn1_pw060418p03q188	H11	U	1127938	R	FTN_1068	1127581	1128000	F	140	358(420)
tnfn1_pw060418p03q189	A12	C	614604	R	FTN_0585	614004	614723	R	240	120(720)
tnfn1_pw060418p03q190	B12	C	1177229	F	FTN_1113	1177061	1177801	F	247	169(741)
tnfn1_pw060418p03q191	C12	C	133444	F	FTN_0123	133207	133656	F	150	238(450)
tnfn1_pw060418p03q192	D12	C	802350	R	FTN_0748	802109	802948	F	280	242(840)
tnfn1_pw060418p03q193	E12	C	1469548	F	FTN_1391	1468103	1469791	R	563	244(1689)
tnfn1_pw060418p03q194	F12	C	1549393	F	FTN_1461	1548609	1550903	R	765	1511(2295)
tnfn1_pw060418p03q195	G12	C	887427	F	FTN_0830	886835	887452	R	206	26(618)
tnfn1_pw060418p03q196	H12	C	1342588	F	FTN_1271	1341912	1342637	F	242	677(726)

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.

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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_pw060418p03q101	A01	EXACT(0)	156	150	137	41	EXACT(0)	85	83	55
tnfn1_pw060418p03q102	B01	EXACT(0)	157	152	96	37	EXACT(0)	201	155	41
tnfn1_pw060418p03q103	C01	EXACT(0)	157	148	134	39	EXACT(0)	200	172	50
tnfn1_pw060418p03q104	D01	EXACT(0)	154	145	120	40	EXACT(0)	199	186	47
tnfn1_pw060418p03q105	E01	EXACT(0)	158	153	142	40	EXACT(0)	200	192	54
tnfn1_pw060418p03q106	F01	EXACT(0)	154	153	122	35	EXACT(0)	200	187	52
tnfn1_pw060418p03q107	G01	EXACT(0)	157	152	126	33	EXACT(0)	200	191	54
tnfn1_pw060418p03q108	H01	EXACT(0)	156	139	103	35	EXACT(0)	200	197	55
tnfn1_pw060418p03q109	A02	EXACT(0)	156	142	105	28	EXACT(0)	200	175	43
tnfn1_pw060418p03q110	B02	EXACT(0)	155	150	129	42	EXACT(0)	198	111	31
tnfn1_pw060418p03q111	C02	EXACT(0)	157	145	132	38	EXACT(0)	200	194	50
tnfn1_pw060418p03q112	D02	EXACT(0)	157	152	141	39	EXACT(0)	200	188	60
tnfn1_pw060418p03q113	E02	EXACT(0)	155	152	125	38	EXACT(0)	200	113	28
tnfn1_pw060418p03q114	F02	EXACT(0)	154	138	121	38	EXACT(0)	200	193	49
tnfn1_pw060418p03q115	G02	EXACT(0)	121	107	75	21	EXACT(0)	200	194	47
tnfn1_pw060418p03q116	H02	EXACT(0)	122	120	107	33	EXACT(0)	200	193	66
tnfn1_pw060418p03q117	A03	EXACT(0)	121	120	84	23	EXACT(0)	200	195	48
tnfn1_pw060418p03q118	B03	EXACT(0)	122	125	98	28	EXACT(0)	200	182	55
tnfn1_pw060418p03q119	C03	EXACT(0)	120	112	76	22	EXACT(0)	200	191	46
tnfn1_pw060418p03q120	D03	EXACT(0)	123	120	112	31	EXACT(0)	200	178	41
tnfn1_pw060418p03q121	E03	EXACT(0)	121	81	60	22	EXACT(0)	200	189	51
tnfn1_pw060418p03q122	F03	EXACT(0)	127	89	72	33	EXACT(0)	200	186	67
tnfn1_pw060418p03q123	G03	EXACT(0)	121	112	102	30	EXACT(0)	200	178	30
tnfn1_pw060418p03q124	H03	EXACT(0)	122	120	101	47	EXACT(0)	199	185	57
tnfn1_pw060418p03q125	A04	EXACT(0)	121	112	89	27	EXACT(0)	200	192	51
tnfn1_pw060418p03q126	B04	EXACT(0)	122	119	101	34	EXACT(0)	200	174	58
tnfn1_pw060418p03q127	C04	EXACT(0)	121	112	90	25	EXACT(0)	200	181	47
tnfn1_pw060418p03q128	D04	EXACT(0)	126	120	105	30	EXACT(0)	200	176	46
tnfn1_pw060418p03q129	E04	EXACT(0)	157	145	126	31	EXACT(0)	200	189	52
tnfn1_pw060418p03q130	F04	EXACT(0)	121	103	77	24	EXACT(0)	199	155	31
tnfn1_pw060418p03q131	G04	EXACT(0)	158	152	131	35	EXACT(0)	200	185	57
tnfn1_pw060418p03q132	H04	EXACT(0)	155	145	122	39	EXACT(0)	200	188	61
tnfn1_pw060418p03q133	A05	EXACT(0)	155	145	79	16	EXACT(0)	200	163	34
tnfn1_pw060418p03q134	B05	EXACT(0)	155	152	131	39	EXACT(0)	200	188	48
tnfn1_pw060418p03q135	C05	EXACT(0)	160	153	125	25	EXACT(0)	200	188	59
tnfn1_pw060418p03q136	D05	EXACT(0)	156	145	134	44	EXACT(0)	200	190	65
tnfn1_pw060418p03q137	E05	EXACT(0)	155	145	129	33	EXACT(0)	200	193	51
tnfn1_pw060418p03q138	F05	EXACT(0)	156	153	134	32	EXACT(0)	200	195	47
tnfn1_pw060418p03q139	G05	EXACT(0)	155	152	131	42	EXACT(0)	200	192	63
tnfn1_pw060418p03q140	H05	EXACT(0)	154	145	75	17	EXACT(0)	200	175	54
tnfn1_pw060418p03q141	A06	EXACT(0)	155	145	119	38	EXACT(0)	200	156	38
tnfn1_pw060418p03q142	B06	EXACT(0)	156	152	136	40	EXACT(0)	192	182	52
tnfn1_pw060418p03q143	C06	EXACT(0)	159	143	92	25	EXACT(0)	200	194	47
tnfn1_pw060418p03q144	D06	EXACT(0)	158	153	142	39	EXACT(0)	200	184	49
tnfn1_pw060418p03q145	E06	EXACT(0)	156	145	78	21	EXACT(0)	200	181	49
tnfn1_pw060418p03q146	F06	EXACT(0)	155	152	134	36	EXACT(0)	200	192	55
tnfn1_pw060418p03q147	G06	EXACT(0)	158	145	138	51	EXACT(0)	200	156	45
tnfn1_pw060418p03q148	H06	EXACT(0)	159	153	136	43	EXACT(0)	200	171	52

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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_pw060418p03q149	A07	EXACT(0)	158	153	136	41	EXACT(0)	200	190	43
tnfn1_pw060418p03q150	B07	EXACT(0)	157	150	131	34	EXACT(0)	200	157	45
tnfn1_pw060418p03q151	C07	EXACT(0)	157	145	129	27	EXACT(0)	200	179	46
tnfn1_pw060418p03q152	D07	EXACT(0)	155	152	131	37	EXACT(0)	199	191	54
tnfn1_pw060418p03q153	E07	EXACT(0)	153	139	120	39	EXACT(0)	200	183	58
tnfn1_pw060418p03q154	F07	EXACT(0)	155	152	128	40	EXACT(0)	200	178	45
tnfn1_pw060418p03q155	G07	EXACT(0)	157	145	136	48	EXACT(0)	200	186	50
tnfn1_pw060418p03q156	H07	EXACT(0)	155	144	119	34	EXACT(0)	200	190	49
tnfn1_pw060418p03q157	A08	EXACT(0)	155	144	124	44	EXACT(0)	199	116	31
tnfn1_pw060418p03q158	B08	NONE	0	0	0	14	ESTIMATE(153)	435	353	24
tnfn1_pw060418p03q159	C08	EXACT(0)	155	152	131	38	EXACT(0)	200	187	52
tnfn1_pw060418p03q160	D08	EXACT(0)	158	148	145	38	EXACT(0)	200	184	54
tnfn1_pw060418p03q161	E08	EXACT(0)	156	117	117	46	EXACT(0)	200	189	56
tnfn1_pw060418p03q162	F08	EXACT(0)	155	145	132	41	EXACT(0)	200	195	53
tnfn1_pw060418p03q163	G08	EXACT(0)	155	144	124	36	EXACT(0)	200	193	53
tnfn1_pw060418p03q164	H08	EXACT(0)	155	145	126	38	EXACT(0)	200	178	62
tnfn1_pw060418p03q165	A09	EXACT(0)	155	145	123	42	EXACT(0)	200	169	46
tnfn1_pw060418p03q166	B09	EXACT(0)	156	145	136	44	EXACT(0)	200	198	46
tnfn1_pw060418p03q167	C09	EXACT(0)	157	145	129	32	EXACT(0)	200	193	53
tnfn1_pw060418p03q168	D09	EXACT(0)	156	152	132	33	EXACT(0)	200	188	57
tnfn1_pw060418p03q169	E09	EXACT(0)	155	152	121	30	EXACT(0)	200	187	56
tnfn1_pw060418p03q170	F09	EXACT(0)	158	151	126	30	EXACT(0)	200	191	52
tnfn1_pw060418p03q171	G09	EXACT(0)	157	152	136	45	EXACT(0)	200	186	58
tnfn1_pw060418p03q172	H09	EXACT(0)	155	140	125	26	EXACT(0)	200	186	33
tnfn1_pw060418p03q173	A10	EXACT(0)	122	112	94	25	EXACT(0)	200	186	52
tnfn1_pw060418p03q174	B10	EXACT(0)	121	120	99	30	EXACT(0)	199	159	40
tnfn1_pw060418p03q175	C10	EXACT(0)	123	120	103	34	EXACT(0)	200	146	36
tnfn1_pw060418p03q176	D10	EXACT(0)	122	125	105	43	EXACT(0)	200	188	65
tnfn1_pw060418p03q177	E10	EXACT(0)	122	119	114	40	EXACT(0)	200	194	62
tnfn1_pw060418p03q178	F10	EXACT(0)	123	125	109	37	EXACT(0)	200	186	63
tnfn1_pw060418p03q179	G10	EXACT(0)	122	118	99	27	EXACT(0)	200	191	47
tnfn1_pw060418p03q180	H10	EXACT(0)	121	120	105	43	EXACT(0)	200	185	54
tnfn1_pw060418p03q181	A11	EXACT(0)	121	119	109	37	EXACT(0)	200	136	45
tnfn1_pw060418p03q182	B11	EXACT(0)	121	112	88	39	EXACT(0)	200	191	53
tnfn1_pw060418p03q183	C11	EXACT(0)	120	112	78	22	EXACT(0)	200	186	47
tnfn1_pw060418p03q184	D11	EXACT(0)	121	120	96	23	EXACT(0)	200	175	51
tnfn1_pw060418p03q185	E11	EXACT(0)	121	106	101	57	EXACT(0)	199	144	45
tnfn1_pw060418p03q186	F11	EXACT(0)	121	120	96	30	EXACT(0)	200	179	53
tnfn1_pw060418p03q187	G11	EXACT(0)	121	105	73	20	EXACT(0)	200	184	50
tnfn1_pw060418p03q188	H11	EXACT(0)	121	103	89	28	EXACT(0)	200	182	54
tnfn1_pw060418p03q189	A12	EXACT(0)	124	120	101	29	EXACT(0)	142	141	53
tnfn1_pw060418p03q190	B12	EXACT(0)	129	103	82	26	EXACT(0)	200	188	45
tnfn1_pw060418p03q191	C12	EXACT(0)	133	109	54	16	EXACT(0)	200	177	36
tnfn1_pw060418p03q192	D12	EXACT(0)	121	112	81	23	EXACT(0)	200	190	54
tnfn1_pw060418p03q193	E12	EXACT(0)	121	106	98	40	EXACT(0)	200	196	57
tnfn1_pw060418p03q194	F12	EXACT(0)	157	153	131	39	EXACT(0)	200	193	55
tnfn1_pw060418p03q195	G12	EXACT(0)	124	119	84	24	EXACT(0)	200	175	56
tnfn1_pw060418p03q196	H12	EXACT(0)	121	105	84	25	EXACT(0)	200	186	52

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