# Product Information Sheet for NR-51311

## *Francisella tularensis* subsp. *novicida* "Two-Allele" Transposon Mutant Library, Plate 29 (tnfn1_pw060510p01)

## Catalog No. NR-51311

**For research use only. Not for use in humans.**

### Contributor:
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### 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 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.[1] 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-51311 represents plate 29 (tnfn1_pw060510p01) 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-51311 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 29 (tnfn1_pw060510p01), NR-51311."

### 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 (BMBL). Current Edition. Washington, DC: U.S. Government Printing Office.

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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: Plate 29 (tnfn1_pw060510p01) – Transposon Type and Mutated Gene[1]**

| Well Position | Strain Name | Transposon Type | Gene | Description | Function Class |
|---|---|---|---|---|---|
| A01 | tnfn1_pw060510p01q101 | T20 | gcvP2 | glycine cleavage system P protein, subunit 2 | amino acid metabolism - degradation, utilization, assimilation |
| A02 | tnfn1_pw060510p01q109 | T18 | pyrB | aspartate carbamoyltransferase | nucleotides and nucleosides metabolism |
| A03 | tnfn1_pw060510p01q117 | <KAN-2> | udk | uridine kinase | nucleotides and nucleosides metabolism |
| A04 | tnfn1_pw060510p01q125 | T20 | - | ThiF family protein | putative enzymes |
| A05 | tnfn1_pw060510p01q133 | T17 | purT | phosphoribosylglycinamide formyltransferase 2 | nucleotides and nucleosides metabolism |
| A06 | tnfn1_pw060510p01q141 | T20 | - | dGTP triphosphohydrolase | nucleotides and nucleosides metabolism |
| A07 | tnfn1_pw060510p01q149 | T18 | - | carbon-nitrogen hydrolase family protein | putative enzymes |
| A08 | tnfn1_pw060510p01q157 | T20 | - | peroxiredoxin, AhpC-TSA family protein | other metabolism - degradation, utilization, assimilation |
| A09 | tnfn1_pw060510p01q165 | T18 | - | conserved protein of unknown function | unknown function - conserved |
| A10 | tnfn1_pw060510p01q173 | T20 | priA | primosomal protein N | DNA replication, recombination, modification and repair - restriction/modification |
| A11 | tnfn1_pw060510p01q181 | T18 | - | hypothetical protein | hypothetical - novel |
| A12 | tnfn1_pw060510p01q189 | T17 | rbn | tRNA processing ribonuclease BN | nucleotides and nucleosides metabolism |
| B01 | tnfn1_pw060510p01q102 | T20 | | | |
| B02 | tnfn1_pw060510p01q110 | T18 | iglD | intracellular growth locus protein D | unknown function - novel |
| B03 | tnfn1_pw060510p01q118 | <KAN-2> | nudH | dGTP pyrophosphohydrolase | DNA replication, recombination, modification and repair - restriction/modification |
| B04 | tnfn1_pw060510p01q126 | T20 | lysC | aspartate kinase III | amino acid metabolism - biosynthesis |
| B05 | tnfn1_pw060510p01q134 | T20 | - | ornithine cyclodeaminase, mu-crystallin homolog | amino acid metabolism - degradation, utilization, assimilation |
| B06 | tnfn1_pw060510p01q142 | T20 | tktA | transketolase I | carbohydrate metabolism - degradation, utilization, assimilation |
| B07 | tnfn1_pw060510p01q150 | <KAN-2> | - | bifunctional NMN adenylyltransferase/Nudix hydrolase | cofactors, prosthetic groups, electron carriers metabolism |
| B08 | tnfn1_pw060510p01q158 | T20 | prmA | 50S ribosomal protein L11, methyltransferase | translation, ribosomal structure and biogenesis |
| B09 | tnfn1_pw060510p01q166 | T18 | - | pseudogene: C4-dicarboxylate anaerobic carrier, fragment | pseudogene |
| B10 | tnfn1_pw060510p01q174 | T20 | - | glycosyl transferase, family 2 | cell wall / LPS / capsule |
| B11 | tnfn1_pw060510p01q182 | T18 | dctA | C4-dicarboxylate transport protein | transport |
| B12 | tnfn1_pw060510p01q190 | <KAN-2> | - | RNA methyltransferase, trmA family | translation, ribosomal structure and biogenesis |
| C01 | tnfn1_pw060510p01q103 | T20 | ilvE | branched-chain amino acid aminotransferase protein (class IV) | amino acid metabolism - biosynthesis |
| C02 | tnfn1_pw060510p01q111 | T17 | - | conserved hypothetical protein | hypothetical - conserved |
| C03 | tnfn1_pw060510p01q119 | <KAN-2> | wbtO | transferase | cell wall / LPS / capsule |
| C04 | tnfn1_pw060510p01q127 | T20 | pyrE | orotate phosphoribosyltransferase | nucleotides and nucleosides metabolism |
| C05 | tnfn1_pw060510p01q135 | T20 | | | |
| C06 | tnfn1_pw060510p01q143 | T20 | - | glycosyl hydrolases family 31 protein | carbohydrate metabolism - biosynthesis |
| C07 | tnfn1_pw060510p01q151 | T20 | galM | aldose 1-epimerase | carbohydrate metabolism - degradation, utilization, assimilation |
| C08 | tnfn1_pw060510p01q159 | T20 | add | deoxyadenosine deaminase/adenosine deaminase | nucleotides and nucleosides metabolism |
| C09 | tnfn1_pw060510p01q167 | T18 | - | hypothetical membrane protein | hypothetical - novel |
| C10 | tnfn1_pw060510p01q175 | T20 | - | glutathione peroxidase | post-translational modification, protein turnover, chaperones - protein modification |
| C11 | tnfn1_pw060510p01q183 | T18 | - | protein of unknown function | unknown function - novel |
| C12 | tnfn1_pw060510p01q191 | <KAN-2> | - | membrane fusion protein | motility, attachment and secretion structure |
| D01 | tnfn1_pw060510p01q104 | T18 | aroH | chorismate mutase | amino acid metabolism - biosynthesis |

| Well Position | Strain Name | Transposon Type | Gene | Description | Function Class |
|---|---|---|---|---|---|
| D02 | tnfn1_pw060510p01q112 | T18 | | | |
| D03 | tnfn1_pw060510p01q120 | <KAN-2> | tspO | tryptophan-rich sensory protein | signal transduction and regulation |
| D04 | tnfn1_pw060510p01q128 | T20 | - | conserved protein of unknown function | unknown function - conserved |
| D05 | tnfn1_pw060510p01q136 | T20 | - | outer membrane efflux protein | transport - drugs / antibacterial compounds |
| D06 | tnfn1_pw060510p01q144 | T20 | - | conserved hypothetical membrane protein | hypothetical - conserved |
| D07 | tnfn1_pw060510p01q152 | T20 | tyrP | tyrosine permease | transport - amino-acid |
| D08 | tnfn1_pw060510p01q160 | T20 | - | hypothetical protein | hypothetical - novel |
| D09 | tnfn1_pw060510p01q168 | <KAN-2> | ftnA | ferric iron binding protein, ferritin-like | putative enzymes |
| D10 | tnfn1_pw060510p01q176 | T20 | hemK | modification methylase, HemK family | translation, ribosomal structure and biogenesis |
| D11 | tnfn1_pw060510p01q184 | T18 | - | hypothetical protein | hypothetical - novel |
| D12 | tnfn1_pw060510p01q192 | T20 | alr | alanine racemase | amino acid metabolism - degradation, utilization, assimilation |
| E01 | tnfn1_pw060510p01q105 | T20 | - | YGGT family membrane protein | unknown function - conserved |
| E02 | tnfn1_pw060510p01q113 | T18 | - | protein of unknown function | hypothetical - novel |
| E03 | tnfn1_pw060510p01q121 | T20 | - | CheB methylesterase/CheR methyltransferase | signal transduction and regulation |
| E04 | tnfn1_pw060510p01q129 | T20 | pyrF | orotidine-5'-phosphate decarboxylase | nucleotides and nucleosides metabolism |
| E05 | tnfn1_pw060510p01q137 | T20 | truA | tRNA pseudouridine synthase A | translation, ribosomal structure and biogenesis |
| E06 | tnfn1_pw060510p01q145 | T20 | ilvN | acetolactate synthase small subunit | amino acid metabolism - biosynthesis |
| E07 | tnfn1_pw060510p01q153 | T20 | - | type I restriction-modification system, subunit S | DNA replication, recombination, modification and repair - repair |
| E08 | tnfn1_pw060510p01q161 | T20 | - | type I restriction-modification system, subunit S | DNA replication, recombination, modification and repair - restriction/modification |
| E09 | tnfn1_pw060510p01q169 | <KAN-2> | - | protein of unknown function | unknown function - novel |
| E10 | tnfn1_pw060510p01q177 | T20 | hslU | ATP-dependent protease HslVU, ATPase subunit | post-translational modification, protein turnover, chaperones |
| E11 | tnfn1_pw060510p01q185 | T17 | - | hypothetical membrane protein | hypothetical - novel |
| E12 | tnfn1_pw060510p01q193 | <KAN-2> | - | conserved hypothetical membrane protein | hypothetical - conserved |
| F01 | tnfn1_pw060510p01q106 | <KAN-2> | pepA | cytosol aminopeptidase | amino acid metabolism |
| F02 | tnfn1_pw060510p01q114 | T20 | - | DNA/RNA endonuclease G | nucleotides and nucleosides metabolism |
| F03 | tnfn1_pw060510p01q122 | T20 | dinP | DNA-damage inducible protein P | DNA replication, recombination, modification and repair - restriction/modification |
| F04 | tnfn1_pw060510p01q130 | T20 | rimK | glutathione synthase/ribosomal protein S6 modification enzyme | translation, ribosomal structure and biogenesis |
| F05 | tnfn1_pw060510p01q138 | T20 | rdgC | recombination associated protein | DNA replication, recombination, modification and repair - restriction/modification |
| F06 | tnfn1_pw060510p01q146 | T20 | prfC | peptide chain release factor 3 | translation, ribosomal structure and biogenesis |
| F07 | tnfn1_pw060510p01q154 | T20 | - | transposase | mobile and extrachromosomal element functions - transposition |
| F08 | tnfn1_pw060510p01q162 | T20 | - | - | Potentially coding: hypothetical - novel |
| F09 | tnfn1_pw060510p01q170 | T20 | - | aspartate/tyrosine/aromatic aminotransferase | amino acid metabolism - biosynthesis |
| F10 | tnfn1_pw060510p01q178 | T20 | dapB | dihydrodipicolinate reductase | amino acid metabolism - biosynthesis |
| F11 | tnfn1_pw060510p01q186 | T17 | - | conserved hypothetical protein | hypothetical - conserved |
| F12 | tnfn1_pw060510p01q194 | <KAN-2> | | | |
| G01 | tnfn1_pw060510p01q107 | T18 | - | protein of unknown function | unknown function - novel |
| G02 | tnfn1_pw060510p01q115 | T18 | - | DNA and RNA helicases Superfamily I protein | DNA replication, recombination, modification and repair - replication |
| G03 | tnfn1_pw060510p01q123 | T20 | - | protein of unknown function | unknown function - novel |
| G04 | tnfn1_pw060510p01q131 | T20 | rrmJ | 23S rRNA methylase | translation, ribosomal structure and biogenesis |
| G05 | tnfn1_pw060510p01q139 | T20 | - | protein of unknown function | unknown function - novel |
| G06 | tnfn1_pw060510p01q147 | T20 | - | hypothetical membrane protein | hypothetical - novel |
| G07 | tnfn1_pw060510p01q155 | T20 | - | conserved protein of unknown function | unknown function - conserved |
| G08 | tnfn1_pw060510p01q163 | T20 | - | ornithine cyclodeaminase, mu-crystallin homolog | amino acid metabolism - degradation, utilization, assimilation |
| G09 | tnfn1_pw060510p01q171 | T20 | recG | ATP-dependent DNA helicase | DNA replication, recombination, modification and repair - restriction/modification |
| G10 | tnfn1_pw060510p01q179 | T20 | - | pseudogene: C4-dicarboxylate anaerobic carrier, fragment | pseudogene |
| G11 | tnfn1_pw060510p01q187 | T17 | vanY | D-alanyl-D-alanine carboxypeptidase | cell wall / LPS / capsule |
| G12 | tnfn1_pw060510p01q195 | <KAN-2> | fopA | OmpA family protein | cell wall / LPS / capsule |
| H01 | tnfn1_pw060510p01q108 | T18 | - | conserved protein of unknown function | unknown function - conserved |
| H02 | tnfn1_pw060510p01q116 | T18 | - | pseudogene: Membrane Protein. Fucose permease Carbohydrate transport and metabolism | pseudogene |
| H03 | tnfn1_pw060510p01q124 | T20 | gcvP1 | glycine cleavage system P protein, subunit 1 | amino acid metabolism - degradation, utilization, assimilation |
| H04 | tnfn1_pw060510p01q132 | T20 | ruvC | holliday junction endodeoxyribonuclease | DNA replication, recombination, modification and repair - restriction/modification |
| H05 | tnfn1_pw060510p01q140 | T20 | mutT | mutator protein | DNA replication, recombination, modification and repair - restriction/modification |

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| Well Position | Strain Name | Transposon Type | Gene | Description | Function Class |
|---|---|---|---|---|---|
| H06 | tnfn1_pw060510p01q148 | T18 | mutL | DNA mismatch repair enzyme with ATPase activity | DNA replication, recombination, modification and repair - restriction/modification |
| H07 | tnfn1_pw060510p01q156 | T20 | - | dGTP triphosphohydrolase | nucleotides and nucleosides metabolism |
| H08 | tnfn1_pw060510p01q164 | T17 | purT | phosphoribosylglycinamide formyltransferase 2 | nucleotides and nucleosides metabolism |
| H09 | tnfn1_pw060510p01q172 | T20 | thrC | threonine synthase | amino acid metabolism - biosynthesis |
| H10 | tnfn1_pw060510p01q180 | T18 | - | birA-like protein | post-translational modification, protein turnover, chaperones - protein modification |
| H11 | tnfn1_pw060510p01q188 | T17 | - | hypothetical protein | hypothetical - novel |
| H12 | tnfn1_pw060510p01q196 | T20 | gcvP2 | glycine cleavage system P protein, subunit 2 | amino acid metabolism - degradation, utilization, assimilation |

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

## Table 2: Plate 29 (tnfn1_pw060510p01) – 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_pw060510p01q101 | C | 518602 | FTN_0508 | 517901 | 519343 | F | 481 | 702(1443) |
| A02 | tnfn1_pw060510p01q109 | C | 17434 | FTN_0019 | 17052 | 17975 | R | 308 | 542(924) |
| A03 | tnfn1_pw060510p01q117 | C | 645270 | FTN_0612 | 645168 | 645830 | F | 221 | 103(663) |
| A04 | tnfn1_pw060510p01q125 | C | 1030907 | FTN_0976 | 1030667 | 1031407 | F | 247 | 241(741) |
| A05 | tnfn1_pw060510p01q133 | C | 1875651 | FTN_1745 | 1875320 | 1876477 | F | 386 | 332(1158) |
| A06 | tnfn1_pw060510p01q141 | C | 665758 | FTN_0632 | 664957 | 666279 | R | 441 | 522(1323) |
| A07 | tnfn1_pw060510p01q149 | C | 885311 | FTN_0827 | 884558 | 885481 | R | 308 | 171(924) |
| A08 | tnfn1_pw060510p01q157 | C | 1013424 | FTN_0958 | 1013305 | 1013826 | R | 174 | 403(522) |
| A09 | tnfn1_pw060510p01q165 | C | 591655 | FTN_0565 | 591250 | 591927 | F | 226 | 406(678) |
| A10 | tnfn1_pw060510p01q173 | C | 206400 | FTN_0189 | 205403 | 207553 | F | 717 | 998(2151) |
| A11 | tnfn1_pw060510p01q181 | C | 1147321 | FTN_1083 | 1146713 | 1147327 | F | 205 | 609(615) |
| A12 | tnfn1_pw060510p01q189 | C | 204416 | FTN_0187 | 203616 | 204809 | F | 398 | 801(1194) |
| B01 | tnfn1_pw060510p01q102 | C | 628672 | intergenic | | | | | |
| B02 | tnfn1_pw060510p01q110 | C | 1396072 | FTN_1321 | 1395775 | 1396968 | R | 398 | 897(1194) |
| B03 | tnfn1_pw060510p01q118 | C | 1651548 | FTN_1553 | 1651200 | 1651661 | R | 154 | 114(462) |
| B04 | tnfn1_pw060510p01q126 | C | 1858624 | FTN_1730 | 1857489 | 1858841 | R | 451 | 218(1353) |
| B05 | tnfn1_pw060510p01q134 | C | 1533114 | FTN_1444 | 1532673 | 1533686 | R | 338 | 573(1014) |
| B06 | tnfn1_pw060510p01q142 | C | 1413230 | FTN_1333 | 1412511 | 1414499 | R | 663 | 1270(1989) |
| B07 | tnfn1_pw060510p01q150 | C | 489456 | FTN_0483 | 488789 | 489829 | F | 347 | 668(1041) |
| B08 | tnfn1_pw060510p01q158 | C | 1043723 | FTN_0988 | 1043408 | 1044250 | R | 281 | 528(843) |
| B09 | tnfn1_pw060510p01q166 | U | 275709 | FTN_0268 | 275553 | 275780 | R | 76 | 72(228) |
| B10 | tnfn1_pw060510p01q174 | C | 1284675 | FTN_1214 | 1283962 | 1284918 | R | 319 | 244(957) |
| B11 | tnfn1_pw060510p01q182 | C | 677470 | FTN_0640 | 676608 | 677855 | F | 416 | 863(1248) |
| B12 | tnfn1_pw060510p01q190 | C | 647589 | FTN_0616 | 646972 | 648318 | F | 449 | 618(1347) |
| C01 | tnfn1_pw060510p01q103 | C | 74800 | FTN_0063 | 74362 | 75246 | R | 295 | 447(885) |
| C02 | tnfn1_pw060510p01q111 | C | 1546543 | FTN_1458 | 1546487 | 1546990 | F | 168 | 57(504) |
| C03 | tnfn1_pw060510p01q119 | C | 1509106 | FTN_1428 | 1508659 | 1509267 | R | 203 | 162(609) |
| C04 | tnfn1_pw060510p01q127 | C | 551044 | FTN_0529 | 550733 | 551356 | R | 208 | 313(624) |
| C05 | tnfn1_pw060510p01q135 | U | 1280992 | intergenic | | | | | |
| C06 | tnfn1_pw060510p01q143 | C | 968181 | FTN_0911 | 967156 | 969192 | F | 679 | 1026(2037) |
| C07 | tnfn1_pw060510p01q151 | C | 1189563 | FTN_1127 | 1189307 | 1190299 | R | 331 | 737(993) |
| C08 | tnfn1_pw060510p01q159 | U | 739566 | FTN_0695 | 739415 | 740452 | F | 346 | 152(1038) |
| C09 | tnfn1_pw060510p01q167 | U | 499514 | FTN_0494 | 499405 | 500001 | R | 199 | 488(597) |
| C10 | tnfn1_pw060510p01q175 | C | 741674 | FTN_0698 | 741553 | 742020 | F | 156 | 122(468) |
| C11 | tnfn1_pw060510p01q183 | C | 840749 | FTN_0782 | 840650 | 841222 | F | 191 | 100(573) |
| C12 | tnfn1_pw060510p01q191 | C | 1808834 | FTN_1692 | 1808552 | 1809619 | R | 356 | 786(1068) |
| D01 | tnfn1_pw060510p01q104 | C | 355183 | FTN_0349 | 355001 | 355360 | F | 120 | 183(360) |
| D02 | tnfn1_pw060510p01q112 | C | 853068 | intergenic | | | | | |
| D03 | tnfn1_pw060510p01q120 | C | 825439 | FTN_0768 | 825148 | 825621 | R | 158 | 183(474) |
| D04 | tnfn1_pw060510p01q128 | C | 1241144 | FTN_1170 | 1240289 | 1242037 | R | 583 | 894(1749) |
| D05 | tnfn1_pw060510p01q136 | C | 1350839 | FTN_1277 | 1349725 | 1351194 | F | 490 | 1115(1470) |
| D06 | tnfn1_pw060510p01q144 | C | 693534 | FTN_0654 | 693039 | 693686 | R | 216 | 153(648) |
| D07 | tnfn1_pw060510p01q152 | C | 1836066 | FTN_1711 | 1835372 | 1836565 | R | 398 | 500(1194) |
| D08 | tnfn1_pw060510p01q160 | C | 1461244 | FTN_1381 | 1460964 | 1462379 | F | 472 | 281(1416) |
| D09 | tnfn1_pw060510p01q168 | C | 1087575 | FTN_1031 | 1087455 | 1087952 | F | 166 | 121(498) |
| D10 | tnfn1_pw060510p01q176 | U | 1641787 | FTN_1544 | 1641395 | 1642246 | R | 284 | 460(852) |
| D11 | tnfn1_pw060510p01q184 | C | 1368545 | FTN_1299 | 1368395 | 1368586 | R | 64 | 42(192) |
| D12 | tnfn1_pw060510p01q192 | C | 799985 | FTN_0746 | 799235 | 800329 | F | 365 | 751(1095) |
| E01 | tnfn1_pw060510p01q105 | C | 162956 | FTN_0150 | 162491 | 163057 | F | 189 | 466(567) |

| 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] |
|---|---|---|---|---|---|---|---|---|---|
| E02 | tnfn1_pw060510p01q113 | C | 933728 | FTN_0878 | 933333 | 934319 | F | 329 | 396(987) |
| E03 | tnfn1_pw060510p01q121 | U | 459394 | FTN_0455 | 458374 | 461271 | F | 966 | 1021(2898) |
| E04 | tnfn1_pw060510p01q129 | C | 37341 | FTN_0035 | 37218 | 37859 | F | 214 | 124(642) |
| E05 | tnfn1_pw060510p01q137 | C | 956554 | FTN_0899 | 956103 | 956876 | R | 258 | 323(774) |
| E06 | tnfn1_pw060510p01q145 | U | 1098871 | FTN_1041 | 1098659 | 1098973 | R | 105 | 103(315) |
| E07 | tnfn1_pw060510p01q153 | C | 1221278 | FTN_1154 | 1220796 | 1222016 | R | 407 | 739(1221) |
| E08 | tnfn1_pw060510p01q161 | C | 751632 | FTN_0707 | 750859 | 752076 | F | 406 | 774(1218) |
| E09 | tnfn1_pw060510p01q169 | U | 1452470 | FTN_1372 | 1451963 | 1453045 | R | 361 | 576(1083) |
| E10 | tnfn1_pw060510p01q177 | C | 1054618 | FTN_0996 | 1053996 | 1055360 | F | 455 | 623(1365) |
| E11 | tnfn1_pw060510p01q185 | C | 1802328 | FTN_1686 | 1801799 | 1803325 | F | 509 | 530(1527) |
| E12 | tnfn1_pw060510p01q193 | C | 185579 | FTN_0169 | 185208 | 185747 | R | 180 | 169(540) |
| F01 | tnfn1_pw060510p01q106 | C | 699634 | FTN_0660 | 699099 | 700535 | F | 479 | 536(1437) |
| F02 | tnfn1_pw060510p01q114 | C | 1135547 | FTN_1073 | 1135198 | 1136259 | R | 354 | 713(1062) |
| F03 | tnfn1_pw060510p01q122 | C | 1041093 | FTN_0986 | 1040426 | 1041472 | F | 349 | 668(1047) |
| F04 | tnfn1_pw060510p01q130 | C | 166882 | FTN_0154 | 166433 | 167899 | R | 489 | 1018(1467) |
| F05 | tnfn1_pw060510p01q138 | C | 849348 | FTN_0790 | 848825 | 849682 | F | 286 | 524(858) |
| F06 | tnfn1_pw060510p01q146 | C | 1698290 | FTN_1597 | 1697609 | 1699183 | R | 525 | 894(1575) |
| F07 | tnfn1_pw060510p01q154 | C | 294564 | FTN_0286 | 294223 | 294783 | F | 187 | 342(561) |
| F08 | tnfn1_pw060510p01q162 | C | 9096 | - | 8981 | 9148 | R | 56 | 53(168) |
| F09 | tnfn1_pw060510p01q170 | C | 1459936 | FTN_1380 | 1459763 | 1460893 | F | 377 | 174(1131) |
| F10 | tnfn1_pw060510p01q178 | C | 1857038 | FTN_1729 | 1856806 | 1857474 | R | 223 | 437(669) |
| F11 | tnfn1_pw060510p01q186 | C | 1546543 | FTN_1458 | 1546487 | 1546990 | F | 168 | 57(504) |
| F12 | tnfn1_pw060510p01q194 | C | 1593152 | intergenic | | | | | |
| G01 | tnfn1_pw060510p01q107 | C | 331022 | FTN_0320 | 330339 | 331079 | R | 247 | 58(741) |
| G02 | tnfn1_pw060510p01q115 | U | 831830 | FTN_0776 | 831494 | 833557 | F | 688 | 337(2064) |
| G03 | tnfn1_pw060510p01q123 | C | 145707 | FTN_0132 | 145235 | 146200 | R | 322 | 494(966) |
| G04 | tnfn1_pw060510p01q131 | C | 436115 | FTN_0438 | 435998 | 436615 | R | 206 | 501(618) |
| G05 | tnfn1_pw060510p01q139 | C | 1757702 | FTN_1644 | 1755794 | 1758634 | R | 947 | 933(2841) |
| G06 | tnfn1_pw060510p01q147 | C | 402245 | FTN_0403 | 402038 | 402688 | R | 217 | 444(651) |
| G07 | tnfn1_pw060510p01q155 | C | 230436 | FTN_0210 | 229966 | 231588 | F | 541 | 471(1623) |
| G08 | tnfn1_pw060510p01q163 | C | 1533114 | FTN_1444 | 1532673 | 1533686 | R | 338 | 573(1014) |
| G09 | tnfn1_pw060510p01q171 | C | 340874 | FTN_0335 | 339525 | 341561 | F | 679 | 1350(2037) |
| G10 | tnfn1_pw060510p01q179 | C | 275609 | FTN_0268 | 275553 | 275780 | R | 76 | 172(228) |
| G11 | tnfn1_pw060510p01q187 | C | 1023128 | FTN_0967 | 1022986 | 1023456 | R | 157 | 329(471) |
| G12 | tnfn1_pw060510p01q195 | C | 808955 | FTN_0756 | 808202 | 809377 | F | 392 | 754(1176) |
| H01 | tnfn1_pw060510p01q108 | C | 1031947 | FTN_0977 | 1031487 | 1032053 | F | 189 | 461(567) |
| H02 | tnfn1_pw060510p01q116 | C | 1405540 | FTN_1327 | 1404933 | 1406114 | F | 394 | 608(1182) |
| H03 | tnfn1_pw060510p01q124 | C | 517336 | FTN_0507 | 516528 | 517892 | F | 455 | 809(1365) |
| H04 | tnfn1_pw060510p01q132 | C | 1084461 | FTN_1027 | 1084202 | 1084714 | R | 171 | 254(513) |
| H05 | tnfn1_pw060510p01q140 | U | 919004 | FTN_0865 | 918875 | 919291 | R | 139 | 288(417) |
| H06 | tnfn1_pw060510p01q148 | C | 605062 | FTN_0577 | 604169 | 605968 | F | 600 | 894(1800) |
| H07 | tnfn1_pw060510p01q156 | C | 665758 | FTN_0632 | 664957 | 666279 | R | 441 | 522(1323) |
| H08 | tnfn1_pw060510p01q164 | C | 1875651 | FTN_1745 | 1875320 | 1876477 | F | 386 | 332(1158) |
| H09 | tnfn1_pw060510p01q172 | C | 549289 | FTN_0527 | 548701 | 549987 | F | 429 | 589(1287) |
| H10 | tnfn1_pw060510p01q180 | C | 594701 | FTN_0568 | 594002 | 594781 | R | 260 | 81(780) |
| H11 | tnfn1_pw060510p01q188 | C | 1225932 | FTN_1156 | 1225105 | 1226655 | R | 517 | 724(1551) |
| H12 | tnfn1_pw060510p01q196 | C | 518602 | FTN_0508 | 517901 | 519343 | F | 481 | 702(1443) |

[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 29 (tnfn1_pw060510p01) – 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_pw060510p01q101 | EXACT(0) | 157 | 153 | 137 | 45 | EXACT(0) | 200 | 196 | 56 |
| A02 | tnfn1_pw060510p01q109 | EXACT(0) | 122 | 107 | 90 | 40 | EXACT(0) | 200 | 188 | 58 |
| A03 | tnfn1_pw060510p01q117 | EXACT(0) | 125 | 73 | 64 | 34 | EXACT(0) | 200 | 186 | 55 |

# Product Information Sheet for NR-51311

| 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 |
|---|---|---|---|---|---|---|---|---|---|---|
| A04 | tnfn1_pw060510p01q125 | EXACT(0) | 162 | 152 | 114 | 34 | EXACT(0) | 200 | 186 | 49 |
| A05 | tnfn1_pw060510p01q133 | EXACT(0) | 121 | 119 | 98 | 39 | EXACT(0) | 200 | 193 | 57 |
| A06 | tnfn1_pw060510p01q141 | EXACT(0) | 154 | 139 | 128 | 46 | EXACT(0) | 200 | 192 | 57 |
| A07 | tnfn1_pw060510p01q149 | EXACT(0) | 123 | 120 | 101 | 31 | EXACT(0) | 200 | 189 | 37 |
| A08 | tnfn1_pw060510p01q157 | EXACT(0) | 154 | 145 | 129 | 42 | EXACT(0) | 200 | 190 | 58 |
| A09 | tnfn1_pw060510p01q165 | EXACT(0) | 123 | 116 | 97 | 36 | EXACT(0) | 200 | 178 | 59 |
| A10 | tnfn1_pw060510p01q173 | EXACT(0) | 155 | 153 | 132 | 44 | EXACT(0) | 200 | 187 | 56 |
| A11 | tnfn1_pw060510p01q181 | EXACT(0) | 123 | 113 | 102 | 41 | EXACT(0) | 200 | 184 | 51 |
| A12 | tnfn1_pw060510p01q189 | EXACT(0) | 121 | 112 | 96 | 41 | EXACT(0) | 200 | 188 | 59 |
| B01 | tnfn1_pw060510p01q102 | EXACT(0) | 154 | 145 | 126 | 41 | EXACT(0) | 185 | 160 | 45 |
| B02 | tnfn1_pw060510p01q110 | EXACT(0) | 126 | 75 | 72 | 36 | EXACT(0) | 200 | 188 | 48 |
| B03 | tnfn1_pw060510p01q118 | EXACT(0) | 121 | 113 | 100 | 38 | EXACT(0) | 200 | 195 | 54 |
| B04 | tnfn1_pw060510p01q126 | EXACT(0) | 155 | 145 | 126 | 39 | EXACT(0) | 200 | 189 | 56 |
| B05 | tnfn1_pw060510p01q134 | EXACT(0) | 154 | 145 | 129 | 46 | EXACT(0) | 200 | 190 | 58 |
| B06 | tnfn1_pw060510p01q142 | EXACT(0) | 152 | 145 | 132 | 45 | EXACT(0) | 200 | 195 | 53 |
| B07 | tnfn1_pw060510p01q150 | EXACT(0) | 120 | 106 | 95 | 46 | EXACT(0) | 200 | 195 | 58 |
| B08 | tnfn1_pw060510p01q158 | EXACT(0) | 156 | 151 | 138 | 33 | EXACT(0) | 200 | 191 | 48 |
| B09 | tnfn1_pw060510p01q166 | EXACT(0) | 120 | 105 | 94 | 33 | EXACT(0) | 200 | 176 | 30 |
| B10 | tnfn1_pw060510p01q174 | EXACT(0) | 155 | 150 | 116 | 35 | EXACT(0) | 200 | 148 | 47 |
| B11 | tnfn1_pw060510p01q182 | EXACT(0) | 124 | 120 | 101 | 27 | EXACT(0) | 200 | 179 | 49 |
| B12 | tnfn1_pw060510p01q190 | EXACT(0) | 122 | 125 | 72 | 34 | EXACT(0) | 122 | 115 | 46 |
| C01 | tnfn1_pw060510p01q103 | EXACT(0) | 156 | 151 | 120 | 37 | EXACT(0) | 200 | 192 | 58 |
| C02 | tnfn1_pw060510p01q111 | EXACT(0) | 124 | 120 | 101 | 32 | EXACT(0) | 200 | 195 | 49 |
| C03 | tnfn1_pw060510p01q119 | EXACT(0) | 121 | 119 | 104 | 51 | EXACT(0) | 200 | 181 | 67 |
| C04 | tnfn1_pw060510p01q127 | EXACT(0) | 157 | 145 | 141 | 47 | EXACT(0) | 200 | 197 | 58 |
| C05 | tnfn1_pw060510p01q135 | EXACT(0) | 155 | 145 | 128 | 42 | EXACT(0) | 200 | 184 | 56 |
| C06 | tnfn1_pw060510p01q143 | EXACT(0) | 158 | 152 | 141 | 44 | EXACT(0) | 200 | 192 | 64 |
| C07 | tnfn1_pw060510p01q151 | EXACT(0) | 155 | 139 | 134 | 45 | EXACT(0) | 200 | 168 | 46 |
| C08 | tnfn1_pw060510p01q159 | EXACT(0) | 157 | 145 | 136 | 48 | EXACT(0) | 199 | 173 | 54 |
| C09 | tnfn1_pw060510p01q167 | EXACT(0) | 123 | 119 | 106 | 34 | EXACT(0) | 200 | 188 | 52 |
| C10 | tnfn1_pw060510p01q175 | EXACT(0) | 155 | 145 | 129 | 35 | EXACT(0) | 200 | 185 | 34 |
| C11 | tnfn1_pw060510p01q183 | EXACT(0) | 119 | 106 | 93 | 44 | EXACT(0) | 200 | 190 | 59 |
| C12 | tnfn1_pw060510p01q191 | EXACT(0) | 120 | 119 | 98 | 36 | EXACT(0) | 200 | 192 | 57 |
| D01 | tnfn1_pw060510p01q104 | EXACT(0) | 123 | 118 | 90 | 27 | EXACT(0) | 200 | 191 | 48 |
| D02 | tnfn1_pw060510p01q112 | EXACT(0) | 122 | 119 | 98 | 39 | EXACT(0) | 200 | 196 | 54 |
| D03 | tnfn1_pw060510p01q120 | EXACT(0) | 120 | 112 | 96 | 35 | EXACT(0) | 200 | 188 | 55 |
| D04 | tnfn1_pw060510p01q128 | EXACT(0) | 156 | 153 | 100 | 30 | EXACT(0) | 200 | 184 | 54 |
| D05 | tnfn1_pw060510p01q136 | EXACT(0) | 153 | 114 | 110 | 38 | EXACT(0) | 200 | 187 | 59 |
| D06 | tnfn1_pw060510p01q144 | EXACT(0) | 156 | 153 | 134 | 34 | EXACT(0) | 200 | 184 | 52 |
| D07 | tnfn1_pw060510p01q152 | EXACT(0) | 147 | 144 | 128 | 47 | EXACT(0) | 200 | 185 | 56 |
| D08 | tnfn1_pw060510p01q160 | EXACT(0) | 156 | 152 | 127 | 38 | EXACT(0) | 200 | 158 | 27 |
| D09 | tnfn1_pw060510p01q168 | ADJUSTED(5) | 120 | 115 | 83 | 26 | ESTIMATE(3) | 197 | 186 | 64 |
| D10 | tnfn1_pw060510p01q176 | EXACT(0) | 155 | 148 | 89 | 23 | EXACT(0) | 200 | 191 | 49 |
| D11 | tnfn1_pw060510p01q184 | EXACT(0) | 123 | 120 | 90 | 30 | EXACT(0) | 200 | 181 | 52 |
| D12 | tnfn1_pw060510p01q192 | EXACT(0) | 155 | 145 | 114 | 30 | EXACT(0) | 200 | 186 | 62 |
| E01 | tnfn1_pw060510p01q105 | EXACT(0) | 159 | 153 | 135 | 38 | EXACT(0) | 200 | 188 | 59 |
| E02 | tnfn1_pw060510p01q113 | EXACT(0) | 123 | 120 | 93 | 28 | EXACT(0) | 200 | 190 | 54 |
| E03 | tnfn1_pw060510p01q121 | EXACT(0) | 155 | 152 | 99 | 26 | EXACT(0) | 200 | 190 | 44 |
| E04 | tnfn1_pw060510p01q129 | EXACT(0) | 159 | 152 | 116 | 28 | EXACT(0) | 200 | 187 | 49 |
| E05 | tnfn1_pw060510p01q137 | EXACT(0) | 156 | 145 | 131 | 43 | EXACT(0) | 200 | 188 | 50 |
| E06 | tnfn1_pw060510p01q145 | EXACT(0) | 155 | 145 | 126 | 51 | EXACT(0) | 199 | 168 | 51 |
| E07 | tnfn1_pw060510p01q153 | EXACT(0) | 157 | 90 | 81 | 26 | EXACT(0) | 200 | 182 | 30 |
| E08 | tnfn1_pw060510p01q161 | EXACT(0) | 156 | 153 | 126 | 39 | EXACT(0) | 199 | 182 | 66 |
| E09 | tnfn1_pw060510p01q169 | EXACT(0) | 119 | 112 | 87 | 29 | EXACT(0) | 201 | 129 | 54 |
| E10 | tnfn1_pw060510p01q177 | EXACT(0) | 157 | 153 | 124 | 34 | EXACT(0) | 200 | 190 | 45 |
| E11 | tnfn1_pw060510p01q185 | EXACT(0) | 122 | 119 | 74 | 28 | EXACT(0) | 200 | 195 | 52 |
| E12 | tnfn1_pw060510p01q193 | EXACT(0) | 120 | 119 | 98 | 42 | EXACT(0) | 200 | 193 | 58 |
| F01 | tnfn1_pw060510p01q106 | EXACT(0) | 124 | 118 | 98 | 38 | EXACT(0) | 200 | 192 | 56 |
| F02 | tnfn1_pw060510p01q114 | EXACT(0) | 155 | 145 | 110 | 33 | EXACT(0) | 200 | 180 | 24 |
| F03 | tnfn1_pw060510p01q122 | EXACT(0) | 156 | 145 | 115 | 32 | EXACT(0) | 200 | 191 | 55 |
| F04 | tnfn1_pw060510p01q130 | EXACT(0) | 154 | 145 | 129 | 47 | EXACT(0) | 200 | 191 | 57 |
| F05 | tnfn1_pw060510p01q138 | EXACT(0) | 156 | 145 | 128 | 36 | EXACT(0) | 200 | 187 | 58 |

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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 |
|---|---|---|---|---|---|---|---|---|---|---|
| F06 | tnfn1_pw060510p01q146 | EXACT(0) | 155 | 139 | 122 | 33 | EXACT(0) | 200 | 140 | 32 |
| F07 | tnfn1_pw060510p01q154 | EXACT(0) | 155 | 145 | 132 | 46 | EXACT(0) | 200 | 187 | 67 |
| F08 | tnfn1_pw060510p01q162 | EXACT(0) | 151 | 145 | 129 | 47 | EXACT(0) | 200 | 180 | 59 |
| F09 | tnfn1_pw060510p01q170 | EXACT(0) | 156 | 151 | 127 | 38 | EXACT(0) | 200 | 193 | 64 |
| F10 | tnfn1_pw060510p01q178 | EXACT(0) | 154 | 145 | 120 | 33 | EXACT(0) | 200 | 191 | 54 |
| F11 | tnfn1_pw060510p01q186 | EXACT(0) | 112 | 112 | 85 | 28 | EXACT(0) | 200 | 195 | 50 |
| F12 | tnfn1_pw060510p01q194 | EXACT(0) | 120 | 120 | 99 | 30 | EXACT(0) | 200 | 163 | 35 |
| G01 | tnfn1_pw060510p01q107 | EXACT(0) | 120 | 83 | 78 | 39 | EXACT(0) | 200 | 184 | 44 |
| G02 | tnfn1_pw060510p01q115 | EXACT(0) | 124 | 120 | 105 | 28 | EXACT(0) | 168 | 122 | 20 |
| G03 | tnfn1_pw060510p01q123 | EXACT(0) | 156 | 153 | 119 | 35 | EXACT(0) | 200 | 187 | 57 |
| G04 | tnfn1_pw060510p01q131 | EXACT(0) | 155 | 145 | 132 | 46 | EXACT(0) | 200 | 182 | 59 |
| G05 | tnfn1_pw060510p01q139 | EXACT(0) | 156 | 145 | 136 | 35 | EXACT(0) | 200 | 192 | 36 |
| G06 | tnfn1_pw060510p01q147 | EXACT(0) | 155 | 138 | 117 | 38 | EXACT(0) | 200 | 185 | 60 |
| G07 | tnfn1_pw060510p01q155 | EXACT(0) | 154 | 145 | 129 | 45 | EXACT(0) | 200 | 189 | 58 |
| G08 | tnfn1_pw060510p01q163 | EXACT(0) | 155 | 151 | 130 | 43 | EXACT(0) | 200 | 190 | 58 |
| G09 | tnfn1_pw060510p01q171 | EXACT(0) | 155 | 152 | 136 | 41 | EXACT(0) | 200 | 193 | 56 |
| G10 | tnfn1_pw060510p01q179 | EXACT(0) | 155 | 144 | 112 | 34 | EXACT(0) | 200 | 187 | 64 |
| G11 | tnfn1_pw060510p01q187 | EXACT(0) | 120 | 112 | 91 | 42 | EXACT(0) | 200 | 186 | 54 |
| G12 | tnfn1_pw060510p01q195 | EXACT(0) | 121 | 119 | 101 | 39 | EXACT(0) | 199 | 66 | 30 |
| H01 | tnfn1_pw060510p01q108 | EXACT(0) | 121 | 120 | 91 | 40 | EXACT(0) | 200 | 191 | 59 |
| H02 | tnfn1_pw060510p01q116 | EXACT(0) | 121 | 74 | 64 | 40 | EXACT(0) | 200 | 183 | 53 |
| H03 | tnfn1_pw060510p01q124 | EXACT(0) | 156 | 152 | 136 | 36 | EXACT(0) | 200 | 198 | 53 |
| H04 | tnfn1_pw060510p01q132 | EXACT(0) | 154 | 145 | 132 | 47 | EXACT(0) | 129 | 126 | 52 |
| H05 | tnfn1_pw060510p01q140 | ADJUSTED(2) | 156 | 112 | 87 | 30 | ESTIMATE(28) | 172 | 150 | 52 |
| H06 | tnfn1_pw060510p01q148 | EXACT(0) | 122 | 112 | 107 | 37 | EXACT(0) | 200 | 182 | 47 |
| H07 | tnfn1_pw060510p01q156 | EXACT(0) | 155 | 136 | 116 | 40 | EXACT(0) | 200 | 192 | 52 |
| H08 | tnfn1_pw060510p01q164 | EXACT(0) | 124 | 117 | 100 | 21 | EXACT(0) | 200 | 193 | 42 |
| H09 | tnfn1_pw060510p01q172 | EXACT(0) | 154 | 139 | 128 | 44 | EXACT(0) | 200 | 186 | 55 |
| H10 | tnfn1_pw060510p01q180 | EXACT(0) | 121 | 112 | 87 | 29 | EXACT(0) | 94 | 89 | 48 |
| H11 | tnfn1_pw060510p01q188 | EXACT(0) | 121 | 112 | 90 | 33 | EXACT(0) | 200 | 185 | 57 |
| H12 | tnfn1_pw060510p01q196 | EXACT(0) | 155 | 145 | 129 | 44 | EXACT(0) | 200 | 196 | 54 |

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

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