Supplemental Method S1. Construction of plasmids for the establishment of transgenic Arabidopsis plants.

Arabidopsis genomic DNA and cDNA were used as templates for PCR to construct the plasmids, as described below. The primers used are shown in Supplemental Table S2.

To construct a plasmid expressing *AtPP2CF1* (*At3G05640*) cDNA under the control of the *PXY/TDR* promoter (*pPXYpro:AtPP2CF1*), a DNA fragment containing the *PXY/TDR* promoter was amplified using PCR with primers P_T21 and P_T22. This PCR fragment was inserted into the HindIII/SalI sites of the *pBI101N2* plasmid (Sugimoto et al., 2014) using the In-Fusion Cloning System (Clontech, Mountain View, CA) according to the manufacturer’s instructions to produce *pPXYpro:GUS*. A DNA fragment containing the *AtPP2CF1* cDNA was obtained using PCR with primers P_T18 and P_T19. This PCR fragment was inserted into the SalI/SacI sites of *pPXYpro:GUS* using the In-Fusion Cloning System.

To construct a plasmid expressing the GFP-RCI2a translational fusion gene under the control of the *SUC2* (*At1G22710*) promoter (*pSUC2pro:GFP-RCI2a*), a DNA fragment containing the *SUC2* promoter was obtained using PCR with primers P_T23 and P_T24. This PCR fragment was inserted into the HindIII/SalI sites of the *pBI101N2* plasmid using the In-Fusion Cloning System to produce *pSUC2pro:GUS*. The modified GFP DNA fragment with an alanine linker was obtained using PCR with primers P_38 and P_1524 to produce the GFP-Ala DNA fragment. The DNA fragment containing the *RCI2a* (*At3G05880*) cDNA was obtained using PCR with primers P_1525 and P_1526, and was inserted into the *pGEM-T Easy* vector (Promega, Madison, WI) to produce *pRCI2a*. The modified *RCI2a* DNA fragment with an alanine linker (10 consecutive alanines) was obtained using PCR with primers P_1527 and P_1528 to produce the Ala-RCI2a DNA fragment. Two sequential PCRs were performed to produce a DNA fragment containing the GFP-RCI2a translational fusion. The first PCR was performed using GFP-Ala and Ala-RCI2a DNA fragments as templates.
without primers. The first PCR product was used as a template for the second PCR using primers P_115 and P_1528. The resulting DNA fragment was inserted into the BamHI/SacI sites of the pBI121 vector (Clontech, Mountain View, CA) using the In-Fusion Cloning System to produce p35Spro:GFP-RCI2a. The modified DNA fragment containing the GFP-RCI2a translational fusion region was obtained using PCR with p35Spro:GFP-RCI2a as a template and primers P_1531 and P_1528. This PCR fragment was inserted into the SalI/SacI sites of pSUC2pro:GUS using the In-Fusion Cloning System.

To construct a plasmid expressing the GUS reporter gene under the control of the NTL9 promoter (pNTL9pro:GUS), a DNA fragment containing the NTL9 promoter was obtained using PCR with primers P_1393 and P_1394. This PCR fragment was inserted into the SalI/BamHI sites of the pAtPP2CF1:GUS plasmid (Sugimoto et al., 2014) using the In-Fusion Cloning System.

To construct a plasmid possessing the NTL9 genomic region containing both the NTL9 promoter and the entire NTL9 gene including introns (pNTL9pro:NTL9g), a DNA fragment containing the NTL9 genomic region was obtained using PCR with primers P_1393 and P_1395. This PCR fragment was inserted into the SalI/EcoRI sites of the pAtPP2CF1:GUS plasmid (Sugimoto et al., 2014) using the In-Fusion Cloning System.

To construct a plasmid expressing the entire NTL9 gene, including introns, under the control of the 35S promoter (p35Spro:NTL9g), two sequential PCRs were performed to produce the modified DNA fragment containing the NTL9 genome. The first PCR was performed using primers P_1407 and P_1408. The first PCR product was used as a template for the second PCR using primers P_115 and P_1408. The resulting DNA fragment containing the NTL9 genome was inserted into the BamHI/SacI sites of the pBI121 vector using the In-Fusion Cloning System.

To construct a plasmid expressing NTL9.1 cDNA under the control of the 35S promoter (p35Spro:NTL9.1c), a DNA fragment containing the NTL9.1 cDNA was obtained using PCR with primers P_1400 and P_1401. This PCR fragment was inserted into the pGEM-T Easy vector to produce pNTL9.1c. Two sequential PCRs were performed to produce the modified DNA fragment containing the NTL9.1 cDNA. The first PCR was performed using pNTL9.1c as a template with primers P_1407 and P_1408. The first PCR product was used as a template for the second PCR using primers P_115 and P_1408. The resulting DNA fragment containing the NTL9.1 cDNA was inserted into the BamHI/SacI sites of the pBI121 vector using the In-Fusion Cloning System.
**Supplemental Method S2.** Map-based cloning of the PCT gene.

F₂ populations derived from crosses between the pct mutant and wild-type Landsberg erecta (Ler)-0 were used for genetic linkage mapping of the PCT locus. The PCT gene was mapped using sets of cleaved amplified polymorphic sequence (CAPS) and simple sequence length polymorphic (SSLP) markers listed in Supplemental Table S4. To identify the pct mutation, the genomic region around the PCT locus was compared between wild-type and pct mutants using whole-genome sequencing with next-generation sequencing, and one base insertion (a nucleotide A) in the coding region of NTL9 (At4G35580) was identified.
Supplemental Figure S1 Isolation of an original pct.o mutant. Transverse primary inflorescence stem sections from wild-type (A) and pct.o mutant (B) plants. Basal regions (20 mm from the rosette base) of primary inflorescence stems from 9-week-old plants were used for observations. Cross-sections were 100-μm-thick and stained with toluidine blue. Ca, cambium; Ph, phloem; Xy, xylem. Scale bars, 100 μm.
Supplemental Figure S2 Transcript levels of cambium-, phloem-, and xylem-marker genes. Total RNA was isolated from three different regions (top, middle, and base) of 9-week-old inflorescence stems and subjected to RT-qPCR. The expression ratio of each gene to the UBC9 gene was calculated for each sample. The values of samples for the top regions of the wild-type were set at 1 and used to determine the relative abundance for the other samples. A, Transcript levels of cambium-marker genes. B, Transcript levels of phloem-marker genes. C, Transcript levels of xylem-marker genes. Values represent the mean ± S.D. of three biological and technical replicates (*, $P < 0.05$; **, $P < 0.01$; Welch’s t-test).
Supplemental Figure S3 High resolution of genetic and physical maps of the PCT locus. The genetic and physical linkage map representing the relative position of PCT to the CAPS and SSLP markers on the long arm of chromosome 4. The left parts show CAPS and SSLP markers (Supplemental Table S3). The nucleotide position on chromosome 4 is indicated in parenthesis. To identify the PCT gene, we mapped PCT to chromosome 4, delimited to a locus within a 500-kb region between the markers Chr.4_16.7 Mb and Chr.4_17.2 Mb using 72 F2 chromosomes. The values on the right are the numbers of recombinants in the intervals between the PCT locus and each marker.
Supplemental Figure S4 Overexpression of the wild-type NTL9 gene in the pct mutant background restored stem vascular growth to wild-type levels. A and B, The 25-d-old (A) and 9-week-old (B) pct/35Spro:NTL9g line plants. Two independent pct/35Spro:NTL9g line plants (T2009 and T2085) were examined. Scale bars, 10 mm (A); 50 mm (B). C, Height of 8-week-old plants. Two independent
pct/35Spro:NTL9g line plants (T2009 and T2085) were examined. Values represent the mean ± S.D. *, P < 0.05; **, P < 0.01; ***, P < 0.001; one-way ANOVA followed by the Tukey–Kramer test; n = 4 for Col-0, n = 6 for pct, n = 5 for T2009, n = 5 for T2085. D, Transverse primary inflorescence stem sections from pct/35Spro:NTL9g line plants. Basal parts (20 mm from the rosette base) of primary inflorescence stems in 8-week-old plants were used for observations. Two independent pct/35Spro:NTL9g line plants (T2009 and T2085) were examined. Enlarged images of vascular bundles are shown. Cross-sections were 100-μm-thick and stained with toluidine blue. Ca, cambium; Ph, phloem; Xy, xylem. Scale bars, 100 μm. E, Differentiation levels of the basal regions of inflorescence stems. Differentiation levels were determined as a percentage of the number of differentiated interfascicular regions, based on whether the interfascicular cambium-derived (ICD) tissues interconnected two adjacent primary vascular bundles, to total interfascicular regions analyzed. Two independent pct/35Spro:NTL9g line plants (T2009 and T2085) were examined. F, Quantitative analysis of cambial activity. The cambial activity was determined as a lateral extension of ICD tissues at basal regions (20 mm from the rosette base) of primary inflorescence stems of 8-week-old plants. See Figure 1, F and G for the definition of ICD tissues. Two independent pct/35Spro:NTL9g line plants (T2009 and T2085) were examined. See also Materials and methods for boxplot definition. **, P < 0.01; Kruskal–Wallis test followed by the Steel–Dwass test; n = 35 for Col-0, n = 27 for pct, n = 25 for T2009, n = 23 for T2085.
Supplemental Figure S5 NTL9 splice variants. The upper part shows NTL9 splice variant (NTL9.1–3) structures, with boxes representing exons and thin lines representing introns. The open reading frame of each NTL9 splice variant is depicted as blue boxes. The position of a single adenine nucleotide insertion in the pct mutant is indicated. Two primer set positions are indicated by arrows. Primers (F1 and R1) spanning exons 3 to 4 were synthesized and used; these were the DNA fragments identical in length across all splice variants of NTL9 gene. Primers (F2 and R2) spanning exons 5 to 6 were used to distinguish between each splice variant of NTL9 gene. The central part shows the protein structure encoded by each NTL9 splice variant. The NAC transcriptional domain and transmembrane domain are depicted as green and purple boxes, respectively. The start position of the frameshifted sequence caused by pct mutation is indicated. Functional domains were identified using the programmes PROSITE (Falquet et al., 2002) and TMHMM (Krogh et al., 2001). The bottom part shows alignments of C-terminal sequences of wild-type and mutant NTL9 variants. The corresponding residues in transmembrane domain of NTL9.1 are boxed in purple. In mutated NTL9.1, resulting from the pct mutation (mNTL9.1), a single adenine nucleotide insertion would be expected to result in mistranslated sequence of C-terminus of NTL9.1, which is the dominant form of NTL9 variants, but might be instead replaced with newly translated amino acids. Multiple sequence alignment was obtained with ClustalW (Thompson et al., 1994). The residues in black boxes are identical in at least three of the four NTL9 variants. Amino acid numbers for each NTL9 variant are shown on the left. The asterisks represent stop codons.
Supplemental Figure S6 Expression profiles of the *NTL9* gene in different vascular cell types. Average normalized read count values were obtained from the Arabidopsis fluorescence-activated nucleus sorting (FANS)– and laser capture microdissection (LCM)–derived transcriptome data website (https://arabidopsis-stem.cos.uni-heidelberg.de/; Shi et al., 2021) using *At4G35580* as the query. A, *NTL9* gene-expression profile based on the FANS-derived RNA-seq datasets. B, *NTL9* gene-expression profile based on the LCM-derived RNA-seq datasets.
Supplemental Figure S7 Expression of the NTL9 transcripts in the aerial parts of 3-week-old plants. Total RNA was isolated from the aerial parts of wild-type and pct mutant plants and subjected to RT-qPCR. Primers (F1 and R1), which span exons 3 to 4 of the NTL9 gene (shown in Supplemental Figure S5), were used. The expression ratio of NTL9 gene to the UBC9 gene was calculated for each sample. The values for wild-type samples were set at 1 and used to determine the relative abundance for the pct mutant samples. Values represent the mean ± S.D. of four biological and three technical replicates (**, P < 0.01; Welch’s t-test).
**Supplemental Figure S8** Expression profiles of phytohormone-regulated and stem secondary growth-associated genes. Total RNA was isolated from three different regions (top, middle, and base) of 9-week-old inflorescence stems and subjected to RT-qPCR. The expression ratio of each gene to the UBC9 gene was calculated for each sample. The values of samples for the top regions of the wild-type were set at 1 and used to determine the relative abundance for the other samples. A, Transcript levels of phytohormone (auxin, ethylene, and jasmonate)-regulated genes. B, Transcript levels of stem secondary growth-associated genes. Values represent the mean ± S.D. of three biological and technical replicates (*, *P* < 0.05; Welch’s *t*-test).
### Supplemental Table S1
Segregation of *pct* mutant vascular phenotype in primary inflorescence stems with or without the original transgene (*PXYpro:AtPP2CF1*) in F₂ progenies derived from backcrossing wild-type and *pct.o*.

| Stem phenotype | Wild-type | *pct* mutant | Total | χ²<sup>b</sup> |
|----------------|-----------|--------------|-------|----------------|
| Transgene<sup>a</sup> | + | - | + | - | + | - | Total | χ²<sup>b</sup> |
| F₂ progenies | 16 | 9 | 14 | 1 | 40 | 3.33 |

<sup>a</sup> +/- indicate plants with or without the transgene, respectively.

<sup>b</sup> χ² value for wild-type : mutant stem phenotype segregation of 3 : 1 was calculated using two phenotypic classes (one degree of freedom). The 95% confidence limit for rejecting the expected 3 : 1 segregation is ≥3.84 and the 99% limit is ≥6.63.

### Supplemental Table S2
Primers for the construction of plasmids.

| Primer Names | Primer Sequences (5' to 3') |
|--------------|------------------------------|
| P_38         | AGGATCCGGGATGTCAGCTCCTTATGAGCAAGGGCCGAGGA |
| P_115        | TGGGAGAAACACCGGGGGACTCTAGAGGATCCCCGGGTGGTCAGTC |
| P_1393       | GGCCTTTAATTAAACTAGTGAGCTCGAGGTCAGGTAGTTATGAT |
| P_1394       | GTAACATATAGGGACTCCACCCGGGGATCTGCAATTCCTCTTCTTTAGGTT TTC |
| P_1395       | ACGAGTTGTTAAAACGCAGCGCCAGTTACTGACGAGTTTCAAAA |
| P_1400       | AGGATCCGGGATGTCAGCTCCTTATGAGCAAGGGCCGAGGA |
| P_1401       | TAAATGATGTTGGTACATTTATATTTG |
| P_1407       | CCCCGGTTGGTACAGCTCCTCCTATGAGGTTGCTGATCGATGGA |
| P_1408       | TGGGAGAGAACACGGGGGACTCTAGAGGATCCCCGGGTGGTCAGTC |
| P_1524       | TTGGGAGAGAACACGGGGGACTCTAGAGGATCCCCGGGTGGTCAGTC |
| P_1525       | ATGAGTACAGCTACTTTCGT |
| P_1526       | AATGGTTAATGTTGGTTCCT |
| P_1527       | CAGCTGCAGCTGACGTCACCAATGACAGCTACTTTCAG |
| P_1528       | TTGGGAGAGAACACGGGGGACTCTAGAGGATCCCCGGGTGGTCAGTC |
| P_1531       | ACTTTCTTTGGGTTTTGCAATATGTCAGACATGGTAGCGACGAGCAAGGGGCGAAG |
| P_T18        | TTCTTTCTAAAGCTAGCGTCAGCTCGAGGACATTTGTCAGTC |
| P_T19        | GAACGATCGGGGAAATCAGCTGCTCTTACTAGAGATGCGACG |
| P_T21        | TGGGAGAGAACACGGGGGACTCTAGAGGATCCCCGGGTGGTCAGTC |
| P_T22        | ACGAGTTGTTAAAACGCAGCGCCAGTTACTGACGAGTTTCAAAA |
| P_T23        | TTGGGAGAGAACACGGGGGACTCTAGAGGATCCCCGGGTGGTCAGTC |
| P_T24        | ACGAGTTGTTAAAACGCAGCGCCAGTTACTGACGAGTTTCAAAA |
**Supplemental Table S3** Primers for genotyping.

| Primer Sequences (5’ to 3’) | Restriction Enzymes Used | Expected Sizes of DNA Fragments |
|-----------------------------|--------------------------|---------------------------------|
| pPXYpro:AtPP2CF1            | —                        | 497 bp                          |

For the identification of T-DNA (pPXYpro:AtPP2CF1) insertion

AAGCCAGACCATGTAGACGCA
AGGGACCATGTCCATCGAAT

For derived cleaved amplified polymorphic sequence (dCAPS) for the identification of pct mutation

CTCAAAATAAAGCTCAAGGGCGCGGGGAACTATAGGGCCCCTGT
TGGGGAGAGACGACGATTGA

**Supplemental Table S4** Cleaved amplified polymorphic sequence (CAPS) and simple sequence length polymorphic (SSLP) markers.

| Markers | Marker Type | Nucleotide Positions on Chromosome 4 | Primer Sequences (5’ to 3’) | Restriction Enzymes Used | Expected Sizes of DNA Fragments |
|---------|-------------|-------------------------------------|-----------------------------|--------------------------|---------------------------------|
| Chr.4_9.6 Mb | CAPS        | 9,631,247                           | GGACGTAGAAATCTGAGGAGCTC   | HindIII                  | Col-0: 565 bp                   |
|         |             |                                     | GGTCAATCCGGTCCAGGTGTAAG    |                          | Ler-0: 474 bp                   |
| Chr.4_11.2 Mb | SSLP       | 11,223,633                          | TTGGACCGTCCAGAAAGAGG       | —                        | Col-0: 218 bp                   |
|         |             |                                     | TGGGTCCTGAAACGGTCCTTG      |                          | Ler-0: 292 bp                   |
| Chr.4_12.4 Mb | CAPS        | 12,403,900                          | GAAGGTCGGCTAGAAGAGATCT    | MseI                     | Col-0: 202 bp                   |
|         |             |                                     | TATCTTGAAGCCTGGGCTGCA      |                          | Ler-0: 303 bp                   |
| Chr.4_13.3 Mb | SSLP       | 13,318,421                          | AACCAGGTCTTTGATTTTAGAG     | —                        | Col-0: 150 bp                   |
|         |             |                                     | AAGTACCTACCTGGATTTG        |                          | Ler-0: 198 bp                   |
| Chr.4_14.3 Mb | SSLP       | 14,258,363                          | CCGCATGATAAAGCTAAAGTGA    | —                        | Col-0: 124 bp                   |
|         |             |                                     | ACTTGAAACACTTACCCTGGTAAAGT|                          | Ler-0: 164 bp                   |
| Chr.4_15.3 Mb | CAPS        | 15,282,518                          | GGCGGCACCTGGGTGGTAGAG     | MnII                     | Col-0: 188 bp                   |
|         |             |                                     | GTGTGCCCCGTGTAAAAGAGACC   |                          | Ler-0: 328 bp                   |
| Chr.4_16.2 Mb | SSLP       | 16,203,894                          | CATGGGGGCAATGTATTTACAC    | —                        | Col-0: 161 bp                   |
|         |             |                                     | TAGAGTTCATCCTTCACGCAC      |                          | Ler-0: 120 bp                   |
| Chr.4_16.5 Mb | CAPS        | 16,533,271                          | CCAGTTGGTCTGACCTAAAAACCC  | RsaI                     | Col-0: 161 bp                   |
|         |             |                                     | AAATTCACAGGACACTAAACTCGAC |                          | Ler-0: 300 bp                   |
| Chr.4_16.7 Mb | SSLP       | 16,720,709                          | GTTAGCATTGAGGCTCCACAT     | —                        | Col-0: 157 bp                   |
|         |             |                                     | CACCAGGCAATTTTCTACCCAG    |                          | Ler-0: 122 bp                   |
| Chr.4_17.0 Mb | SSLP       | 17,000,896                          | TGAAGAAGAAGAATCTGAGCTCCTTT | —                       | Col-0: 155 bp                   |
|         |             |                                     | AACCACAAGAGCTCCGTT      |                          | Ler-0: 193 bp                   |
| Chr.4_17.2 Mb | SSLP       | 17,212,441                          | GCTTAAATCCTCACTAATCTAAAGC | —                       | Col-0: 162 bp                   |
|         |             |                                     | CTATGGAGGTTCTAAAACCTTTAAC |                          | Ler-0: 211 bp                   |
| Chr.4_17.7 Mb | SSLP       | 17,663,620                          | AGTTACTGTGATCAAAACTCTTTTAC | —                       | Col-0: 215 bp                   |
|         |             |                                     | TCGACATGTTTTAAGTCAAG       |                          | Ler-0: 128 bp                   |
| Chr.4_18.5 Mb | CAPS        | 18,537,948                          | AGAGAGAATGAGAATGGAGG      | MboII                    | Col-0: 1,082 bp                 |
|         |             |                                     | CAAGTGACCTGAGAGAATCG      |                          | Ler-0: 553 bp                   |
### Supplemental Table S5 Gene-specific primers for RT-qPCR and RT-PCR analyses.

| Genes | Primer Sequences (5' to 3') | References |
|-------|-----------------------------|------------|
| **NTL9 (At4G35580)** | | this study |
| F1: | AGTCTGCAGCACCAGAGGATG | this study |
| R1: | CACTTGGCAACCAGAAGCTC | |
| For RT-qPCR analysis | | |
| F2: | TCAAATAAAGCTCAGGCGGC | |
| R2: | CCCTGTCTCCTTGTGTCG | |
| **APL (At4G79430)** | ACCAAGTCCTCGACCATCACA | Guo et al., 2009 |
| **RTM (At1G05760)** | TCTGTTAAGCCTGGCCGATGAGT | Guo et al., 2009 |
| **Ah13 (At1G57350)** | GTGCTTATGAGTTCTGTCG | Guo et al., 2009 |
| **SEOR1 (At3G01680)** | TCTCAAATAAAGCTCAGGCGGC | Cho et al., 2018 |
| **ANT (At4G37750)** | GATGTAGCAGCAATTAAGTTCCG | |
| **EXP9 (At5G02260)** | TCTGTTAAGCCTGGCCGATGAGT | Guo et al., 2009 |
| **PXY/TDR (At5G61480)** | ACCGCTTACCCTGCTTGG | Agusti et al., 2011 |
| **WOX4 (At1G46480)** | TGGTGGAAGGGAGAGGG | Agusti et al., 2011 |
| **IRX2 (At4G18780)** | CATCCCAACGCTATCAAACCTA | Guo et al., 2009 |
| **IRX3 (At5G17420)** | CAAAAGGTCCTCAAACGCTCA | Cho et al., 2018 |
| **IRX5 (At5G44030)** | TCTGTTAAGCCTGGCCGATGAGT | Guo et al., 2009 |
| **HCa2 (At5G62940)** | CAATTTGGTGAGGATGATGGA | Miyashima et al., 2019 |
| **COV1 (At2G02120)** | CCGAGGAGGAACCTTTGAGTC | Guo et al., 2009 |
| **MOL1 (At5G51350)** | GACCGTCTAGCTGTCATTCA | Agusti et al., 2011 |
| **RUL1 (At5G05160)** | CCATGGTGCTCAAACGCTCAA | Agusti et al., 2011 |
| **JUL1 (At2G15680)** | CACCTGCTCACAATGGCCAGTA | this study |
| **JUL2 (At5G25490)** | TGGTTTCAAGTGTGGCCGCTTGA | this study |
| **ARF3 (At2G33860)** | ATCTGGTGGAGTGGGATGAGTTG | Liu et al., 2018 |
| **ARF4 (At5G60450)** | ACCATGACCTTGGCTGCCC | this study |
| **ARF5 (At1G19850)** | GGTGCCCTTGGCCTGCTCTGA | Liu et al., 2018 |
| **JAZ7 (At2G34600)** | ACCATGCTCAGCTGTCCTGGA | this study |
| **JAZ10 (At5G3220)** | ATCTGCGTCTTGAATCTGCTGCT | this study |
| **MYC2 (At1G32640)** | AACGTCCTGCGAGAGGAGAGA | this study |
| **Ah10 (At4G17500)** | CCGTCTGCTTCTCCTGCTGCTG | Etchells et al., 2012 |
| **ERF018 (At1G74930)** | TCTGCCTCTTCCGCTGACG | Etchells et al., 2012 |
| **ERF109 (At4Gg34410)** | CATTCTCGATATCTGCACTCAT | Etchells et al., 2012 |
| **UBC9 (At4Gg27960)** | TCACTACGTTTGTTGATGCTGCTG | Sugimoto et al., 2014 |
### Supplemental Table S6 Gene-specific primers for 3'-RACE.

| Primer Names | Positions in *NTL9.1* Splice Variant | Primer Sequences (5' to 3')                      |
|--------------|--------------------------------------|--------------------------------------------------|
| P_F19        | Exons 4/5                            | CGAGGCCAAAGAAGCTGCAG                              |
| P_F20        | Exon 5                               | CCTCAAAATAAGCTCAGGTC                             |
| P_F21        | Exon 6                               | GGACACTGGTGAGTTCATGA                              |