

Supplementary file 1

Sequences of genomic DNA, CDS and proteins

Start-codons are indicated in green, Stop-codons are in red, exons are in yellow.

TaDrAp1-A4 (TraesCS4A02G151500)

TraesCS4A02G151500 REVERSE STRAND

pep chromosome:IWGSC:4A:306315187:306320710:-1 gene:TraesCS4A02G151500

transcript:TraesCS4A02G151500.1 gene_biotype:protein_coding

transcript_biotype:protein_coding description:CCAAT-binding transcription factor C

[Source:UniProtKB/TrEMBL;Acc: A0A0A7LUP0 = <https://www.uniprot.org/uniprot/A0A0A7LUP0>]

>*TaDrAp1-A4*

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TaDrAp1-B4 (TraesCS4B02G161200)

TraesCS4B02G161200 REVERSE STRAND

pep chromosome:IWGSC:4B:316654107:316664575:-1 gene:TraesCS4B02G161200

transcript:TraesCS4B02G161200.1 gene_biotype:protein_coding

transcript_biotype:protein_coding description:CCAAT-binding transcription factor C

[Source:UniProtKB/TrEMBL;Acc:A0A0A7LUF6]

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TraesCS1B02G322000 FORWARD STRAND

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TraesCS1D02G310200 FORWARD STRAND

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Supplementary file 2

Protein sequences of DrAp1, DrAp2, Dr1 and references used in Figure 3

Figure 3A

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Figure 3B

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Figure 3C

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>Sl-101246965

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>Cs-101209714

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>Gh-107927594

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>DmDrAp1-CG10318

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Supplementary file 3

Promotor regions and primer design

TaDrAp1

>*TaDrAp1-A4*

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CGTAGGTCACCTGACCTCCTACTCGTGTGAGGTCCCTCTCCTCCTTCCTTCCTCGCAGGTGCTCGAG
CAAGGAATCGAGCTGGGCAAACGCGACGGCCGGTTCGGATCAATGCCGAATTGACCGGATCCGACGC
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CAACCCTATCTCTTGTTCCTTCCCCACACATACGGACTCTAAAAACAGCCTATACTCTGGTATTTTGAA
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GAAGTGACATCTTGTATATTTTCATCCGAGCCTTGATACGCTCATTGTGGTGGCTTCAAAGTCCTGA
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GACATCCATGTGAGAAGATCCCCTAGTGGATGCAAGAGCCCTATAAGGGAAGATCCATCTAGGGAT
GCAAGACCCCTATATGGGAAGATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTTGAGAAGA
ACCTTTACCTTGTGCTTCCCCCTTTTGAAGTTGTTCTTGCATATTTGTGGATCTCATGTATGCTAT
CTTAGTGATGTGTGATTTGGATTTGTCTGAGTCTTTCTCTCTCTTGTGCTCTTGAGTGTTTCATCCT
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TCTCCTCCTTCCCTTCCCGTAGGTTCGTTGAGCAAGAAATCGAGCTGGGCAAACGTGACGGCTGGCC

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GAGAGGTGGCGGGCAGAGGCGGCGGCACGGTGTCGTTCGGTGGAAGGAGCGGCAATGGAAGCTCCG
CCGACCATGGCGAGGAAAGCGAGATCGGCGGTGAGCTTCGCGGGGTCGGTTGCAGGGCCAAAGGAG
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GTTGGTGGAAAGACAA CAAAACAAGAAATCCAATCGTCAAGAAGAACGAGAAAAGAAAATACACAA
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GAAGCTGGGCACCCGGTTCCCCGCG

1KB Promoter regions:

TaDrAp1-B4	TCACTAGAAATGTTGTACCACATGTCCGGAAGCAAAATGATGGAAGTCTGACGCGCATTG
TaDrAp1-D4	TCACCAGAAATCCTGTACCACATGTCCCGGAAGCAAAATGACGGAAGTCCGACGCGTACGG
TaDrAp1-A4	TCACCAGAAATCCTGTACCACATGTCCGGAAGCAAACTGACGGAAGTCCGATGCGCACTG **** *
TaDrAp1-B4	GACATTTGGACCCTCCCGAGCCACCAGACGTCCGGCAAACACCGGAAATCCCGTACCACC
TaDrAp1-D4	GATGTCTGGACCCTCCCGAGCCACTAGACGTCCGGCAAACACCGGAAATCCCGTACCACC
TaDrAp1-A4	GACATCCGAACACTTCCGAGCCACCAGACGTCCGGCAAACACCGGAAATCAAGTACCACC *
TaDrAp1-B4	TGACCAGAGAAGAAA-TGGCGGAAGTCCGACGCCCCAACAGATGTTCAATCACTCGCGAA
TaDrAp1-D4	TGACCGGAGAAGAAA-TGGCGGAAGTCCGATGCCCAACCGGATGTTCGATCACTCGTGAA
TaDrAp1-A4	TGACCAGAGAAGAAAATGGCGGAAGTCCGGCGCCCCAACCGGACGTTCGGTCACTCGCGAA ***** *
TaDrAp1-B4	CGACCAGACGTCCGGTATTGCGTGTGCGCATCCCGACGGTTTTTCAGCCCATGTACCCCTC
TaDrAp1-D4	CGACCGAACGCCCGGTACTCCCTGTGCGCATCCCGACGGTTTTTCAGCCCATGTACCCCTC
TaDrAp1-A4	CGACTGGGCGTTCCGTACTGCA-TGTGCACATCCCACGGTTTTTCAGCCCATGTACCCCTC ***** *
TaDrAp1-B4	TTTCACACCTAGACTATAAATACCCTTCTCCTACCTCCATCCTAGGGCTGGCAAAGACAT
TaDrAp1-D4	TTTCATCCCTAGACTATAAATACCCTTCTGCTAGCTCCATCCTAGGGCTGGCAAAGACAT
TaDrAp1-A4	TTTCACCCCTAGGCTAT--ATACCCTTCTCCTACATCCATCATAGGGCTGGCAAAGACAT ***** *
TaDrAp1-B4	AATAGAGAATTGCTAGAGCTTTGCTCATATTCATTATTCCTCTTGGAGGTCAAGACCTCC
TaDrAp1-D4	AATAGAGAATTGATAGAGCTTTGCTCATATTCATTATTCCTCTTGGAGGTCAAGACATCC
TaDrAp1-A4	AATAGAGAATTAGTAGAGCTTTGCCATACCTCATTTATTCCTCTTGGAGATCAAGACCTCC ***** *
TaDrAp1-B4	ATGTGAGAAGATCCCCCTAGTGGATGCAAGAGCCCTATAAGGGAATATCAATCTAGGGAT
TaDrAp1-D4	ATGTGAGAAGATCCCC-TAGTGGATGCAAGAGCCCTATAAGGGAAGATCCATCTAGGGAT
TaDrAp1-A4	ATGCGAGAACATCCCC-TAGTGGATGCAAGACCCATATAAGGGAAGATCCATCTAGGGAT *** *
TaDrAp1-B4	GCAAGACCCCTATATGGGAAGATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTG
TaDrAp1-D4	GCAAGACCCCTATATGGGAAGATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTG
TaDrAp1-A4	GCAAGACCCCTATATGGGAAGATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTG ***** *
TaDrAp1-B4	AGAAGAACCTTTACCTTTGTGCTTCCCCCTTTTGACTTGTTAATATATATTTGTGGATCT
TaDrAp1-D4	AGAAGAACCTTTACCTTTGTGCTTCCCCCTTTTGACTTGTTCTTGCATATTTGTGGATCT
TaDrAp1-A4	AGAAGAACCTTTACCTTTGTGCTTCCCCCTTT-GACTTGTTCTTGTATATTTGTGGATCC ***** *
TaDrAp1-B4	CATGTATGCTATCTTAGTGATGTGTGATTGGATTGTTTGAGTCTCTCTCTCTCTCTCT
TaDrAp1-D4	CATGTATGCTATCTTAGTGATGTGTGATTGGATTGTTCTGAGTCTTTCTCTCTCTCT---
TaDrAp1-A4	CAT-----AGTGATGTGTGATTGGTTGTTTGAGTCTCTCTCTCTCTCTCTCTCTCT *** *
TaDrAp1-B4	TGTGTTATTGAGTGTTTCATCCTTTCTCCATCCTCCAAGTGCGAAAAGATCTTGAATCTAG
TaDrAp1-D4	TGTGCTCTTGAGTGTTTCATCCTTTCTCCA-CCTCCAAGTGCGAAAAGATCTCAATCTAG
TaDrAp1-A4	CGTGTTCTTGAATGCTCATCCTTTCCCCA-CCTCCAAGTGCGAAAAGATCTCAAGTCTAG *
TaDrAp1-B4	GGTTTTGCCCTACATCACCATGCCTCCCTAGCCCC-CCTCTCCTCTCCTCCTTCCCTTCC
TaDrAp1-D4	GGTTTTGCCCTACATCACCATGCCTCCCTAGCCCCCTCCTCTCCTCTCCCCCTTCCCTTCC
TaDrAp1-A4	GGTTTTGCCCTACATCACCATGCCTCCCATCCCTCCTCTCCTCTCCTCTTCTCTTCTCT ***** *
TaDrAp1-B4	CGCAGGTCACTGACCTCCTACTTGTGTGCGGTCCCTCTCTTCTTCCCTTCCCGTAGGTC
TaDrAp1-D4	CGCAGGTCACTGACCTCCTACTCATGTGCGGTCCCTCTCCTCTTCCCTTCCCGTAGGTC
TaDrAp1-A4	CGTAGGTCACTGACCTCCTACTCGTGTGCGGTCCCTCTCCTCTTCCCTTCCCTCGCAGGTC *

Primers used for sequencing *TaDrAp1*:

TaDrAp1-A4-seq-F: GACTGGGCGTTCGGTACTGCA 21 bp, 62%GC, T_m=58.3C

TaDrAp1-A4-seq-R: CACGGCACGGGGCACACC 18 bp, 78%GC, T_m=59.4C

TaDrAp1-A4-seq-R (RevCom): GGTGTGCCCCGTGCCGTG

Amplicon size: 1,148 bp

TaDrAp1-B4-seq-F: CAATCACTCGCGAACGACCAGA 22 bp, 55%GC, T_m=56.7C

TaDrAp1-B4-seq-R: TGTCTTTCCACCAACTTGACCAA 24 bp, 46%GC, T_m=55.7C

TaDrAp1-B4-seq-R (RevCom): TTGGTGCAAGTTGGTGGAAAGACA

Amplicon size: 1,162 bp

TaDrAp1-D4-seq-F: GCCCATGTACCCCCTTTTCATC 22 bp, 55%GC, T_m=56.7C

TaDrAp1-D4-seq-R: TTGTCTTTCCACCAACTTACACGG 24 bp, 46%GC, T_m=55.7C

TaDrAp1-D4-seq-R (RevCom): CCGTGTAAGTTGGTGGAAAGACAA

Amplicon size: 1,068 bp

TaDrAp2 - Promotor regions – 2Kb

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AGGAGGTTTCGCCGGTGTTCGCGAGGCCTTCACTCCAGTCTCCGGAGCAGCGGCGGATGCGCGCCTAC
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GCTCTCTCCGGCGCCCGGGCTCCGCGCCATCAGGAAGAAGCTCGACACCCGCTTCCCCGCG

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TGAGACGCGGTGAGGCTACAATGATCTCCACGAGACTGCGGGACTGTAGCCACACCCCTCCCCG
ATCAAGCATGCGTCATTAACATTGCGGCTACAATAACCAGCCAACCAGACCCGCCAGCGGCGGAGG
CGGCCTGTGCGCTTCGTACCAGACCAGTCGACGGGGCTCACCAGGCTGCGGGCCCCAGCAGTCGGC
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GCATTCTCTCCGCGGGGACGCTCCCTCCGGCGCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGA
CACCCGCTTCCCCGCG

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TGCTTGGCTTGGGGGGCAAGTCTCCCTAGGATTTTCCCTAGGGAGATCCAATCTGCTTGGCCGCCG
CCCCCTAGGGGAAACCTAGGGCGCCTCCCCCTCTCCCCTTGCCCATATATATAGTGGAGGGGTAG
GGGGCAGCCGCACCT**CTTCCCTGGCGCAGCCCTCTCCTCCTCCAACCTCCTCCTCCTCCGTAGT**
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CTCCCTCAACTTCTCCTCTCCCCTTGCTGGATCAAGAAGGAGGAGACGTCCCCGGGCTGTAGGTGT
GTTGAACGCGGAGGCGCCGTCCGTTGGCGCTAGATCGGATCTTCCGCGATTTGAATCGCCGCGAG
TACGACTCCATCAACCGCGTTCTTGTAACGCTTCCGCTTAGCGATCTTCAAGGGTATGAAGATGCA
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ATTACTACGTTCCCCAACAGAGGCCCAATGGGATGGGATGGAGCGCGCCCTGGCCTTGTGCGCGGC
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GATGCTTTGGGAGCAGCAGCTGCGGC**TTGAGGAGGAGGAGGAGCGC**GCCCGGCTAGCCGCAATGCC
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CATCCGGGGAACGCGACGCGGACGGCTGACGTGCGGCCGCACGCGCAAACGAGGGAGAGGTCTAAC
TACGCGGGCCCCACATCGCGCTGAGCTTTTACCCACCGCGAAACGTCTCCGTGACCCGGTCCGT
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CAGGAGCTTAGCGTCCACGCGCCGGAGAGTTCGCGCACCGCTGCCCGCTTCGCGCGGCCATTGGCC
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CTCTCCGCCGGGGACGCTCTCTCCGACGCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCC
GCTTCCCCGCG

TaDrAp2 – Promotor region

CLUSTAL 2.1 multiple sequence alignment

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TaDrAp2-A1      GACCTTCCTCCTCCGCCACCTGAGGTTCTGCT-GCACGAGCAGGACGAAGAGGCGGCATA
TaDrAp2-D1      GTTCTTGTAACGCTTCCGCTTAGCGATCTTCA-AGGGTATGAAGATGCACTCCCTCTCTC
TaDrAp2-B1      GCAAAGGGTGCCAGGCTGGTTAGAAGTAGACTCATACATAGAGGGAGAAGAGAGCAAGCC
                  *      *      *      *      *      *      *      *      *

TaDrAp2-A1      CCAAGCCGAGCAAGCCCTGCAGCACGCGTTGGAGGCGAGCAGGA-----TCGAGGAG---
TaDrAp2-D1      TCGTTGCTAGCATCTCCTAGATTG-ATCTTGGTGACACGTAGGAAAAATTTGAATAATTA
TaDrAp2-B1      CTGCCTCCTTCTACCTTCAGCATACAGCTCGAGGA---GCACCATGTATTCACTAGTGT
                  *      *      *      *      *      *      *      *

TaDrAp2-A1      -----GAGGCCTAATGGGATGGGATGGAGCGCGCCCTCGCATTTGTCGGTG
TaDrAp2-D1      CTACGTTCCCCAACAGAGGCCCAATGGGATGGGATGGAGCGCGCCCTGGCCTTGTGCGCG
TaDrAp2-B1      CTTAGTGATCATGCGGAGACCCCGCAGAGCAGGACTAAGGGTGTATCTCCTAG--GAGA
                  *** *      *      ***      *      *      *      *

TaDrAp2-A1      GCAGGAGAGTTTCGTCCA--CGCCCCGCTCTTCGACTCGCCTCCACCGCCACCGGCGCTAC
TaDrAp2-D1      GCAGGGGACTCCGTCCA--TGCCCTGCTCTTCGACTCGCCTCCACCGCCGCC-----
TaDrAp2-B1      GCCCAAACCTGGGTAAAGTGCGCCGACTTTTCG---TGTCACGCCTCATCC-----
                  **      *      *      *      ** *      *      ***      *      *      *      *

TaDrAp2-A1      CCATCGTCGAGCCCCAAGCCAGAGCCGGA--GCCGACGCGAAAGTGCTCGCCGCCTCCACC
TaDrAp2-D1      -CATCGTCGAGCCCCAAGCCAGAGTCGGA--GCCGGCGCGGAAGCGCTCGCCGCCTCCACC
TaDrAp2-B1      -CGCTTCCAGGACCCGGCGACGTTCTACTCGTCCCACCATGATAAGCCATCCTTTGGCA
                  *      *      ** *      ** *      *      **      *      *      *      *

TaDrAp2-A1      CACTTGGCCGGAGGAGTCTTACATGTGGACCGACGAGTACCGTGAGTGGATGAGCAC-GC
TaDrAp2-D1      CACTTGGCCGGAGGAGTCTTACACGTGGACCGGCGAGTACCGCGAGTGGGTGAGCGC-GC
TaDrAp2-B1      TATGTGCGACCCAACCCCCAACATGTGCGCATGGATCTGACGCTGGGTGTGTTGTCACTGC
                  *      *      *      **      ** ***      *      *      *      *      *      *

TaDrAp2-A1      CTCCGGTCCACTACGCCGCGAGGCCGGAGGAGGAGGCGGCCACCTTGAGCTCTGGAAGG
TaDrAp2-D1      CTCCGGTCCACTACGCCGCGACGCCGGAGGAGGAGGAGGAGGCGGCCACCTTGAGCGTTGGGAGG
TaDrAp2-B1      CTTTGGGGTGCCAC-CCGTCTGGCATCTGAAGCA--TGGCGCGGCGTGCCTGTTGTACGG
                  **      **      *      *      ***      **      *      *      *      *      *      *

TaDrAp2-A1      CGCATTGGCTCGCCTAGGAGGAGGCCGACGGCG-AGCGGCAGATGCTTTGGGAGCAGCAG
TaDrAp2-D1      CGCACTGGCTCACTCAGGAGGAGGCCGACGGCG-AGCAGCAGATGCTTTGGGAGCAGCAG
TaDrAp2-B1      GGCAACAAGCGCGAGAGGCGGTGGCGACCTCATGGCGGTGGATGTCGGCGCAGTGG-AG
                  ***      ***      *      *      *      *      *      *      *      *

TaDrAp2-A1      CTATGCCGCGATGCGGAGGCGTTGCGGCTTGAGGAGGAGAAAAGAAGAGTGCGCCCAGCTA
TaDrAp2-D1      CT-----GCGGCTTGAGGAGGAG---GAGGAGCGCGCCCCGGCTA
TaDrAp2-B1      TT-----GCATTCTCCGATGCCC--CGTAAGGCACGACAGTCCG
                  *      **      *      *      *      *      *      *      *

TaDrAp2-A1      GCCACAATGTGCGGCGCCCCAGCAGACGCCGGAGGAGGCTGCCCTTGGCAGTGTTACCAAGCG
TaDrAp2-D1      GCCGCAATGCCGCGCCCCAGCAGACGCCGGAGGAGGCTGCCCTTGGCAGAGTACCAAGCG
TaDrAp2-B1      GGCGCCACAATGTGTCTGTTGGTGGATGTCGCTGG--CTCGTCCTGGGATGGATCCAT---
                  *      *      *      *      *      *      *      *      *      *      *

TaDrAp2-A1      GCGTTTGGGTGGGCTGGCCCTGCTCCCGTCTTTATCGACCTCACCGGCGGCGATAGCGAT
TaDrAp2-D1      GCATTTCGGGTGGGCTAGCCCTGCTCCCGCTTCATTCGACCTCACCGGTGGCGATGGCGTC
TaDrAp2-B1      -CGTTGATATGAC---GTCCGAGTTCCGACGAGGAAGAGTAGGACCTAGGAGACGGCGGC
                  *      **      **      *      *      *      ***      *      *      *      *

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TaDrAp2-A1	GTCAAGGGCAAGGGCAAGGCGGAGGACGTCTAGGGCAGCGTGCGGGCGCATATCTTTTTT-
TaDrAp2-D1	GTCAAGGGCAAGGGCAAGGCGGAGGACGTGTAGGGCAGCGTGAGGGCGTAGACTTTTTTTT
TaDrAp2-B1	GCCTTGAGTCCCG-TGAGTCGACTC GTGTTCCATGCCCTACTCTACCT TTTCAGGCGACCG
	* * * * * * * * * * * * *
TaDrAp2-A1	-ATTAATGTTTTTAATTAGGTTTAAGTGGACTTTGGCCGGCGGT-TGACCAACCACTTTA
TaDrAp2-D1	AATTAATGTTT--AATTAGGTTTAAGTGGACTTTGGTCGGCGGT-TGACCAGCCACTTTA
TaDrAp2-B1	AACCAACACTCTGAG--AAGCGCAGCCGACCGCCGGACGTAGGCACGACGGAGGCGGACG
	* ** * * * * * * * * * * *
TaDrAp2-A1	ATGTTTAATTATGTTTATTTCTATGACCTGTTTTT-TTCTACACCGGCAAATTTGGGCCC
TaDrAp2-D1	ATGTTTAATTATGTTTATTTCTACGACCTGTTTTTCTTCTACGCCGACAAATTTGGGTCC
TaDrAp2-B1	AGCTCCGCTTAAAGATCGTTTTACG-----TTGCATGTAATAATATGAATTTGAGGTTT
	* * *** * ** * * * * * * * * * *
TaDrAp2-A1	GTCTTTTCATTGGGCGCACCTGCCGACCAATATGAA AATGCCGACACGCACGTC TGT CTGG
TaDrAp2-D1	GTCTTTTCGTTGGGCGCACCTGCCGACCCATATAAAAAATGCGGACGTGCACGTCCGCCTGA
TaDrAp2-B1	CTACTTTTAGGTATCCGGTTATAAAATCAAACTTTTAAGACGTGATAGGTCATTGTCTG-
	* ** * * * * * * * * * * * * *
TaDrAp2-A1	CCGATCCAAACAGA-TGAAAAGCGAATAAAACGCACGTCCGATTGGGTTCGGCGCG-TTGG
TaDrAp2-D1	CCGATCTAAACGGA-CGAAAAGCGGACAAAACGCGCGTCCGTTTGG-TCGGCGCC-TTGG
TaDrAp2-B1	CGGACACGCCCAGACTTGCTCTGCGGACATTTGAGGGGGCGGGTTTGCGAAGTACGACTGT
	* ** * * * * * * * * * * * * *
TaDrAp2-A1	AGGTGCTCTTACACCCTGAAACATGATTCCCTTTACGTTTACGTTAACACTCCACAAAAC
TaDrAp2-D1	AGGTGCTCTTACACCCTGAAACATGATTCCCTTTACATTTACGTTAACACTCCTCAAAAC
TaDrAp2-B1	ATATCCTCTTACACCCTGAAACATGAT-CCCTTTACGTTTA-GTTAACACTCCTCAAAAC
	* * ***** ***** * * * * *
TaDrAp2-A1	AAA-CATGGCAATGTATTCTTAGCTCACAAAGACAAGTCAAAGCATCTCCCTCCGTTTCC
TaDrAp2-D1	AAA-CACGGCAATCTATTCTGATCTCACAAAGACAAGTCGGAGCAT-----
TaDrAp2-B1	AAAACACGACAAGATATGCCGA-CTCAGTCTTTCAGATGCGCTTATA-----G
	*** ** * *** * * * * * * * * * *
TaDrAp2-A1	TTTTTTACTCTACATATACACTTTGATCAAAGTCAAACATAAACAATGTTTCAACAATTTT
TaDrAp2-D1	-----ACTCTC-----
TaDrAp2-B1	GAATAGAAAATGCGTGTGTGCGTTTATAGGGATAAGCGTATGCG-----
	* *
TaDrAp2-A1	ATATAAAAAAATATTAATATCTACAAATATCAAAGTTATATGGTATATGAAAGTTAATTT
TaDrAp2-D1	-----
TaDrAp2-B1	-----
TaDrAp2-A1	TATGATGCATCTAATAATATTGATTTTCATATTGTGAATATTGCTATTGTTACCAATAAAA
TaDrAp2-D1	-----
TaDrAp2-B1	-----
TaDrAp2-A1	TTAGTCAAACATTATAAAAGTTCGACTTTGACTTTTTTTTTGAGCAAATGAACAATTTTTTT
TaDrAp2-D1	-----
TaDrAp2-B1	-----CGTGTATATGAGCGCTTGCGTCTGTACCGTGTTTAAAAAACACACGGC-----
TaDrAp2-A1	AAGACAAACCAACTTTTATATGCAAACATAAAAAAGAAAACGGAGGAAGTACCCAGATAAAGC
TaDrAp2-D1	-----TACCCAGATAAAGC
TaDrAp2-B1	-----AATCTATTCTGATCTCACAAAGACAAGTCGGAACATGCTATACCCAGATAAAGC

TaDrAp2-A1	TAGAGCCCAAGAATGGACGATGACTCTCGCAGCCCAAGGCCACGAACGAGACACAGCC--
TaDrAp2-D1	AACAGCCCAAGAATGGACGATGACTCTCGCAGC--AAGGCCACGAACGAGGCACGGC---
TaDrAp2-B1	GAGAGCCCGAGAATGGACGATGACTCTCGCAGCCCAAGGCCACGAACGAGGCACAGCGCC * * * * *
TaDrAp2-A1	-----GCCGGATCCCGCCGACCCCTCGAATCGGACGGCGGACACAGGGAGCGCCACGAA
TaDrAp2-D1	-----GCCACAGCCCGCCGGATCC--CGAATCGGACGGCGGACACAGGGAGCGCCACGAA
TaDrAp2-B1	ACAGCCACCGGATCCCGCCGACCCCGAATCGGACGGCGGACACAGGGAGCGCCACGAA * * * * *
TaDrAp2-A1	CCAGCCAGAAACATGGGGCCACCTCATCCGGGGAACGCGACACGGACGGCTGACCTGCG
TaDrAp2-D1	CCGGCCAGAAACGTGGGGCCACCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCG
TaDrAp2-B1	CCGGCCAGAAACGTGGGGCCACCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCG * * * * *
TaDrAp2-A1	GCCGCACGCGCAAACGGTTCGGGAGAGGTCTAACTACGCGGGCCCCCACATCGCGCTGAG
TaDrAp2-D1	GCCGCACGCGCAAACGA---GGGAGAGGTCTAACTACGCGGGCCCCCACATCGCGCTGAG
TaDrAp2-B1	GCCGCACGCGCAAACGA---GGGAGAGGTCTAACTACGCGGGCCCCCTACATCGCGCCCAG * * * * *
TaDrAp2-A1	CTTTTACCCACCGCGAAACGTCTCCGTGGACCCGGTCCGTTCGCATCCACAGCATGGACCA
TaDrAp2-D1	CTTTTACCCACCGCGAAACGTCTCCGTGGACCCGGTCCGTTCGCATCCGCCACATGGACT-
TaDrAp2-B1	CTTTTACCCACCGCGAAACGTCTCCATAGACCCGGTCCGTTCGCATCC--CCACATGAACCT * * * * *
TaDrAp2-A1	TCTACTACGGTCTTAGCGCCGCACGTGAGGC
TaDrAp2-D1	---CTACGGTCTTAGCGCCGCACGTGAGGCTAAGGCCTATGCGCT
TaDrAp2-B1	T---CTACGGTCTTAGCGCCGCACGTGAGGCTAAGACCTATGCACCGGGTCCAGGAGCTT * * * * *
TaDrAp2-A1	AGCGTCCAT
TaDrAp2-D1	AGCGTCCACGCGCCGGAGAGTTCGCGCACCG
TaDrAp2-B1	AGCCTCCACGCGCCGGAGAGTCGCGCACCTCTGCCCCGCTTCGCGCGGCCATTGGCCGCG * * * * *
TaDrAp2-A1	CTGTTTATGGGGGAAAAAATAGTTTGTTTTATTTT
TaDrAp2-D1	CTGTTTATGGGGGAAAAAATAGTTTGTTTTATTTT
TaDrAp2-B1	CTGTTTATGGGGGAAAAA-----TATATTTTTCCTCGTAAAAAAAGTGAAAAGAT * * * * *
TaDrAp2-A1	AGCGATAACGGAAACCCTAATCCCCAAATCAGAAATCTATCCGAATCGCTATTTATGTTT
TaDrAp2-D1	AGCGATAACGGAAACCCTAATCCCCAAATCAGAAATCTATCCGAATCGCTATTTATGTTT
TaDrAp2-B1	AGCGATAACGGAAACCCTAATCCCCAAATCAGAAATCTATCCGAATCGCTATTTATGTTT * * * * *
TaDrAp2-A1	GTGGCTTTCTCCCCCTCGATCCGATGTCCCCCGCTTCG
TaDrAp2-D1	GTGGCTTTCTCCCCCTCCGATCCGATGTCCCCCGCTTCG
TaDrAp2-B1	GTGGCTTTCTCCCCCTCCGATCCGATGTCCCCCGCTTCGTCGCGCGGCCGATCCGACC * * * * *
TaDrAp2-A1	TCCGCGCGCGTCTCTCTCGCCGGGGACGCTCTCTCCGGCGCCGCCGGCTCCGCGCC
TaDrAp2-D1	TCCAGCCGCGCGTCTCTCTCGCCGGGGACGCTCTCTCCGACGCGCGCGGCTCCGCGCC
TaDrAp2-B1	TCCAGCCGCGCGATTCTCTCTCGCCGGGGACGCTCTCTCCGGCGCCGCCGGCTCCGCGCC * * * * *
TaDrAp2-A1	TGAGGAAGAAGCTCGACACCCGCTTCCCCGCG
TaDrAp2-D1	TGAGGAAGAAGCTCGACACCCGCTTCCCCGCG
TaDrAp2-B1	TGAGGAAGAAGCTCGACACCCGCTTCCCCGCG * * * * *

Primers used for sequencing *TaDrAp2*:

TaDrAp2-A1-seq-F: AATGCCGACACGCACGTC TGTC 22 bp, 59%GC, Tm=58.6C

TaDrAp2-A1-seq-R: AGCGGGCAGAGGTGCGCGG 19 bp, 79%GC, Tm=61.9C

TaDrAp2-A1-seq-R (RevCom): CCGCGCACCTCTGCCCCGCT

Amplicon size: 894 bp

TaDrAp2-A1-seq-F2: TCCGCCACCTGAGGTTCTGC 20 bp, 65%GC, Tm=57.9C

TaDrAp2-A1-seq-R2: GGCAAAAAAAAAATCGCAGGGGCAC 24 bp, 50%GC, Tm=57.4C

TaDrAp2-A1-seq-R2 (RevCom): GTGCCCCCTGCGATTTTTTTTTTGCC

Amplicon size: 1,983+66=2,049 bp

TaDrAp2-B1-seq-F: GTGTTCCATGCCCTACTCTACCT 23 bp, 52%GC, Tm=57.1C

TaDrAp2-B1-seq-R: CGGGCAGAGGTGCGCGAG 18 bp, 78%GC, Tm=59.4C

TaDrAp2-B1-seq-R (RevCom): CTCGCGCACCTCTGCCCCG

Amplicon size: 908 bp

TaDrAp2-B1-seq-F2: GCTACAATAACCAGCCAACCAGA 23 bp, 48%GC, Tm=55.3C

TaDrAp2-B1-seq-R2: CCTGAACCGGCAAAAAATCGCAT 23 bp, 48%GC, Tm=55.3C

TaDrAp2-B1-seq-R2 (RevCom): ATGCGATTTTTTGGCCGGTTCAGG

Amplicon size: 2,003+71=2,074 bp

TaDrAp2-D1-seq-F: TTGAGGAGGAGGAGGAGCGC 20 bp, 65%GC, Tm=57.9C

TaDrAp2-D1-seq-R: ACGCTAAGCTCCTGGACCCA 20 bp, 60%GC, Tm=55.9C

TaDrAp2-D1-seq-R (RevCom): TGGGTCCAGGAGCTTAGCGT

Amplicon size: 912 bp

TaDrAp2-D1-seq-F2: CTTCCCTGGCGCAGCCCT 18 bp, 72%GC, Tm=57.2C

TaDrAp2-D1-seq-R2: CCGGCAAAAAAAAAAACGCAGGGA 23 bp, 49%GC, Tm=55.3C

TaDrAp2-D1-seq-R2 (RevCom): TCCCTGCGTTTTTTTTTTGCCCCG

Amplicon size: 1,943+68=2,011 bp

TaDrAp2 - First intron

>TaDrAp2-A1

GCTCTCTCCGGCGCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCCGCTTCCCCGCGGTAT
GACCCGTGCCCTGCGATTTTTTTTTTGGCGGTTTCAGGCCTCCCCCCCCACGCTGTGCGCGCCGTCG
ATTTTCGCGATTTTTTCTGTGTGCTTCGTCTAGGTTTTGTTTCCGGCGGTTAGGTTTCTGTAAATTG
ACGGCCAATGGACCTGCGATATGCATGTTTGTCTGTTTCTCTCTATTGCTGGGCTTGATAGATGCA
CGTTTGGGGAATTTTTGGGTGCTGTGCTAAATAATATGTAGATTTTCGCAGCACGGTTGGAATTTT
TAGCCTCTCGCGTGTGCTCGTCCTGGGCTTGTTTCATGTACGTTTGTTTTTATGGTGGCTATGGTT
CGCTGTCCCGATGGCAATGAAGCTGCGGTTATAGATGGGCATATGATGTAGGTGGTGGATGCGTGA
AAAATCCTGGATTATGTAGATTCTGCCTACCTGTAAACGTTTCACTAGTATATGGCTTTCCGCGG
ACGAGTGTGCTATTAATCTACTTTATTATTTAATATTTAGGGTCAATTTATTTTATGTTTGACTAAT
TCGTTATGATTAAATCCTTGGGTCATCCTTGTGCTTCAATTGCTAGGCTTGTTCTTTAAGGAACGA
AGTTAACAGAAATTACTTGCATTCACTATTTACTGAAAAAGATGGACATGATTATTAATAACTC
TTTTATAAATATGAGCTTTTTTTTAGGAATGAGAGTTTAACTTAAGCGGATGTGGCTTAATTGTCTC
AAGAGATGATCAACTCCAGGTCTTCTGCGGTGTTCCCTATTTTGATCGGTAGCTTGCTTCAAACCG
GGCCGATTGTACCTAACTAATATTCCACATAATGAACACCAAGTGCTCCTTCCTTTTTTCCCAA
ATTAAGAGAGGAGCGTGATTGTTGGTACAAAGTGCTAACTATAGAATCAAGCATGTGAGTTCCTTT
TATAGTTGTTGATCTGTTGACATTGGTATCATGATTGTTTAGATATAGATTGTGGTGGCAACCTGG
CAGGGAAGCTTCTTAGCCTGATGAGTTAGTACTGTTTCAGATTTTGTAGTATATTTCAAATGGTAAA
TACAGTAGGATTCTACTATTTAACATCTGGCCACACAGGCAATGAGTGTTGGTTAAAGCTGTGT
ACGATCTATAAAAATATATAGTGTAGAGTGTTTATCTTATTCTAAGCATGGTATATTCTCCGATCT
GTTTTTGGTCCATCTTCGGGGGAAGATGCAAGTGTTTTGATGACATATGTTTGCTGTACAATGGAA
TCCTCATGATACTAAAGTTTTTCTACAGTGGATAGAGATACCTTCTTCATTACCTTTTCTTTCACA
AGGGCTAGCAGAATCTCTTTTCTTCATCTGCTAGGACCTGTGCTTATAACCACATGTGAATACTAT
CGCTCTCATGTCCTTTTCCATCGAAGTTGCATCATTGGCCATTTGCACTGTAGTATGCAACAATCA
TAACTATGATTAAATGAGTGTTTTATTATTGACATGTTGTCATAATTTGAAAATGGCAGATTCCCTAC
TACTTTTCAGATGGTATCATGGTACTCTTCTGTTAATGTGATATCAGCTTCCTCTTGTTACTTTGTT
ATACAGCCTCGGATTAAAGAAGATCATGCAAGCAGATGAAGATGTCGGCAAGATTGCTCTAGCTGTA
CCTGTTCTAGTTT

>TaDrAp2-B1

GCATTCTCTCCGCGGGGACGCTCCCTCCGGCGCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGA
CACCCGCTTCCCCGCGGTATGACCCATGCCATGCGATTTTTTGGCGGTTTCAGGCCTCCCCTATGC
TGTGCGCGCCGTCGATTTTCGCGATTTTTTATGTGCCTCGTCTAGGTTTTGTTTCCAGCGGTTAGGT
TTTCGTAAATTGGCGGCCAATGGACCTGCGATGTGCATGTTTACATGTTTCTCTCCATGGCTGGGC
TTGTTAGATGCACGTTTGGGGATTTTTTTGGGTGCTGTGCGTAAATAGCATGTAGATTTTCGCTGCA
CGGTTATGATTTTTAGCCTCTTGCGCGTGCTCATCCTGGGCTTGTTTCATGTACGTTTCTTTTATG
GTGGCTATGGTTCGCTGTCTGATGGCAATGAAGCTGTGGTTATAGATGGGCATATGATGTAGGCA
GGATGCGTGGAAAATCCTGGATTGTGTAGATTCTGCCTACTCTGGTAATGTTTCACTAGTATATGG
CTTTGCCGCCGACGAGAGTGCTCTATTAATCTACTTTGTTATTTAACATCAGGGTCAATTTATTTT
ATGTTTGATTAAATTCGTTATGATTGAATCCTTGGGTCAACCTTGTGCTTCAATTGCTAGGTTTGT
CTCTAAGGAATGAAGGCAACCGAAATTACTTGCATTCACTATTTACTGAAAAAGATGGACATGAT
TATTAATAACTCTTTTATAAATATGAGTTTTTTTAGGAATGAGAGTTCAACTTCAGCGGAGATGG
CTTAATTGTCTCGAGAGAAGATCAACTCCAGGTCTTCTGCGGTGTTTCCTATTTTGGTGGTAGCT
TGCTTCAAACCGGGCCGATTGTACCTAACTAATATTCCACATAATGAACACCAAGTGCTCCTTC
CTTTTTTCTTAAATTAAGAGAGGAGTGCGATTGTTGGTACAAAGTGCTAACTATAGAATCAAGCAT
GTGAGTTCTTTTTATAGTTGTTGATCTGTTGACATTGGTCTCATGATTGTTTAGATATAGATTGTG
GTGGCAGCCTGGCAGGGAAGCATCTTAGCCCGACGAGTTGGTACTGGTCAGATTTTGTAGTATATT
TCAAATGGTAAATAGACAGTAGGATTCTACTATTTAACATCTGGCCACACAGGCAATGAGTGTT

GGTTAAAGCTGTGTACAATCTATAAAAAATATGTAGTGTAGAGTGTTTATTTTATTCTGAACATGGT
 ATATTCTCTGATCTGTTTTTGGTCCATCTTTGCGGGAAGATGCAAGTGTTTTGATGACATATGTTT
 GCTGTACAATGGAATCCTCATGATACTACAGTTTTTCTACAGTGGATAGAGATACCTTCTTCATTA
 CTCTTTCTTTTACAAGGGCTAGCAGAATCTCTTTACCTCATCTGCTAGGACCTGTGCTTATAACGA
 CATGTGAATACTATCACTGTCTATGTCCTTTTCCATCGAAGTTGCATCGTTGGCCATTTGCACTGAA
 GTATGCAACAATCATAATTATGATTAATGAGTGTTTTATTGATGACATGTTGTCATAATTTCAAAA
 TGGCAGATTCCCCTACTTTTTTCAGATGGTATCATGGTACTCTTCTGTTAATGTGATATCAGCTTCC
 TCTTGTAATTTGTTATACAGCCTCGGATTAAGAAGATCATGCAAGCAGATGAAGATGTCGGCAAGA
 TTGCTCTAGCTGTACCTGTTCTAGTTT

>TaDrAp2-D1

CTCTCCGCGGGGACGCTCTCTCCGACGCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCC
 GCTTCCCCGCGGTATGACCCATGTCCCTGCGTTTTTTTTTTTGGCGGTTTCGGGCCTCCCCCTACGCT
 GTGCGCGCCGTCGATCTCGCGATTTTTTTGTGTGCTTCGTCTAGGTTTTGTTTCCGGCGGTTAGGA
 TTTCGTAAATTGGCGGCCAATGGACCTGCGATATGCATGTTTACCTGTTTCTCTCCATGGCTGGGC
 TTGATAGATGCACGTTTGGCGAATTTTTGGGCGCTGTCGGTAAATAGTATGTAGATTTTCGCAGCAC
 GGTTAGGATTTTTCAGCTCTCGCGTGTGCTCATCTGGGCTTGTTTCATGTACGTTTGTTTTATG
 GTGGCTATGGTTCGCTGTCCCGATGGCAATGAAGCTGCGGTTATAGATGGGCATATATGATGTAGG
 TGGTGGATGCGTGAAAAATCCTGGATTATGTGGATTCTGCCTACCCTGTTAACGTTTCACTAGTAT
 ATTGCTTTCCGCGGACGAGAGTGTGCTATTAATCTACTTTATTATTTAATGTTAGGGTCAATTTAT
 TTTATGTTTGAATAATTCGTTATGATTAAATCCTTGGGTCAACCTTGTTGCTTCAATTGCTAGGCCCT
 TGTTCTTTAAGGAACGAAGTTAACAGAAATTACTTGCATTCACTATTTACTGAAAATAGATGGACA
 TGAATATTAATAACTCTTTTATAAATATGAGCTTTTTTTTAGGAATGAGAGTTTAACTTCAGCGGAG
 GTGGCTTAATTGTCTCAAGAGATGATCAACACCAGGTCTTCTGCGGTGTTTCCTATTTTGATCGGT
 AGCTTGCTTCAAACCGGGCCGATTGTACCTAACTAATATCCACATAATGAACACCAAGTGCTC
 CTTCCTTTTTTTCTTAAATTAAAAGAGGAGCACGATTGTTGGTACAAAGTGCTAACTATAGAATCA
 AGCATGTGAGTTCTTTTTATAGTTGTTGATCTGTTGACATTGGTATCATAGATATAGATTGTGGTG
 GCAACCTGGCAGGGAAGCTTCTTAGCCCGACGAGTTGGTACTGTTTCAATTTTGATAGTATATTTCA
 AATGGTAAATAGACAGTAGGATTCTACTATTTGACATCTGGCCCAACAGGCAATGAGTGTTGGT
 TAAAGCTGTGTACAATCTATAAAAAATATGTAGTGTAGAGTGTTTATCTTATTATGAGCATGGTATA
 TTCTCCAATCTGTTTTTGGTCCATCTTTGGGGGAAGATGCAAGTGTTTTGATGACATACGTTTGCT
 GTACAATGGAATCCTCATGATACTAAAGTTTTTCTACAGTGGATAGAGATACCTTCTTCATTACCC
 TTTCTTTTACAAGGGCTAGTAGAATCTATTTTCTTCATCTGCTAGGACCTGTGCTCATAACCACAT
 GTGAATACTATCGCTGTCTATGTCCTTTTCCATCGAAGTTGCATCGTAGGCCATTTGCACTGTAGTA
 TGCAACAATCATAATTATGATTAATGAGTGTTTTATTGATGACATGTTGTCATAATTTCAAAATGG
 CAGATTCCCTACTACTTTTCAGATGGTATCATGGTACTCTTCTGTTAATGTGACATCAGCTTCCTCT
 TGTATTTTGTTATACAGCCTCGGATTAAGAAGATCATGCAAGCAGATGAAGATGTCGGCAAGATTG
 CTCTAGCAGTACCTGTTCTAGTTT

TaDrAp2 - Fist intron

CLUSTAL 2.1 multiple sequence alignment

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TaDrAp2-A1      -----GCTCTCTCCGGCGCCGCCGGCTCCGCGCCATGAGGAAGAA
TaDrAp2-D1      -----CTCTCCGCGCGGGACGCTCTCTCCGACGCCGCCGGCTCCGCGCCATGAGGAAGAA
TaDrAp2-B1      GCATTCTCTCCGCGCGGGACGCTCCCTCCGCGCGCCGCCGGCTCCGCGCCATGAGGAAGAA
                  ****  *****  *****

TaDrAp2-A1      GCTCGACACCCGCTTCCCCGCGGTATGACCCGTGCCCCCTGCGATTATTTTTTTTGGCGGTTTC
TaDrAp2-D1      GCTCGACACCCGCTTCCCCGCGGTATGACCCATGTCCCTGCGTATTTTTTTTGGCGGTTTC
TaDrAp2-B1      GCTCGACACCCGCTTCCCCGCGGTATGACCCATGCCCCATGCGATTATTTT---TTGCGCGTTTC
                  *****  **  *  ****  ****  *****

TaDrAp2-A1      AGGCCTCCCCCCCACGCTGTGCGCGCCGTCGATTTCGCGATTATTTTCTGTGTGCTTCGT
TaDrAp2-D1      GGGCCTCCCCCT--ACGCTGTGCGCGCCGTCGATCTCGCGATTATTTT-TGTGTGCTTCGT
TaDrAp2-B1      AGGCCTCCCCCT--ATGCTGTGCGCGCCGTCGATTTCGCGATTATTTT--ATGTGCTTCGT
                  *****  *  *****  *****  *****  ****

TaDrAp2-A1      CTAGGTTTTGTTTCCGGCGGTTAGGTTTCTGTAAATTGACGGCCAATGGACCTGCGATAT
TaDrAp2-D1      CTAGGTTTTGTTTCCGGCGGTTAGGAATTCGTAAATTGGCGGCCAATGGACCTGCGATAT
TaDrAp2-B1      CTAGGTTTTGTTTCCAGCGGTTAGGTTTTCGTAAATTGGCGGCCAATGGACCTGCGATGT
                  *****  *****  *  *****  *****  *****

TaDrAp2-A1      GCATGTTTGTCTGTTTCTCTCTATTGCTGGGCTTGATAGATGCACGTTTGGGGAATTTTTT
TaDrAp2-D1      GCATGTTTACCTGTTTCTCTCCATGGCTGGGCTTGATAGATGCACGTTTGGCGAATTTTTT
TaDrAp2-B1      GCATGTTTACATGTTTCTCTCCATGGCTGGGCTTGTTAGATGCACGTTTGGGGATTTTTTT
                  *****  *****  *  *****  *****  *****

TaDrAp2-A1      -GGGTGCTGTCGCTAAATAATATGTAGATTTCGCAGCACGGTTGGAATTTTTTAGCCTCTC
TaDrAp2-D1      -GGGCGCTGTCGGTAAATAGTATGTAGATTTCGCAGCACGGTTAGGATTTTTTAGCCTCTC
TaDrAp2-B1      TGGGTGCTGTCGGTAAATAGCATGTAGATTTCGCTGCACGGTTATGATTTTTTAGCCTCTT
                  ***  *****  *****  *****  *****  *****

TaDrAp2-A1      GCGTGTGCTCGTCCTGGGCTTGTTTCATGTACGTTTGTTTTATGGTGGCTATGGTTCGC
TaDrAp2-D1      GCGTGTGCTCATCTCGGCTTGTTTCATGTACGTTTGTTTTATGGTGGCTATGGTTCGC
TaDrAp2-B1      GCGCGTGTGCTCATCTGGGCTTGTTTCATGTACGTTT-CTTTTATGGTGGCTATGGTTCGC
                  ***  *****  *****  *****  *****

TaDrAp2-A1      TGTCCCGATGGCAATGAAGCTGCGGTTATAGATGGGCATAT--GATGTAGGTGGTGGATG
TaDrAp2-D1      TGTCCCGATGGCAATGAAGCTGCGGTTATAGATGGGCATATATGATGTAGGTGGTGGATG
TaDrAp2-B1      TGTCCGTGATGGCAATGAAGCTGTGTTATAGATGGGCATAT--GATGTAGGCAG--GATG
                  *****  *****  *****  *****  *  ****

TaDrAp2-A1      CGTGAAAAATCCTGGATTATGTAGATTCTGCCTACCCTGTTAACGTTTCACTAGTATATG
TaDrAp2-D1      CGTGAAAAATCCTGGATTATGTGGATTCTGCCTACCCTGTTAACGTTTCACTAGTATATT
TaDrAp2-B1      CGTGAAAAATCCTGGATTGTGTAGATTCTGCCTACTCTGGTAATGTTTCACTAGTATATG
                  *****  *****  ***  *****  ***  ****

TaDrAp2-A1      GCTTT-CCGCGGACGAG--TGTGCTATTAATCTACTTTATTATTTAATATTAGGGTCAAT
TaDrAp2-D1      GCTTT-CCGCGGACGAGAGTGTGCTATTAATCTACTTTATTATTTAATGTTAGGGTCAAT
TaDrAp2-B1      GCTTTGCCGCCGACGAGAGTGTCTATTAATCTACTTTGTTATTTAATCAGGGTCAAT
                  *****  *****  **  *****  *****  *  *****

TaDrAp2-A1      TTATTTTATGTTTGACTAATTCGTTATGATTAAATCCTTGGGTCATCCTTGTGCTTCAAT
TaDrAp2-D1      TTATTTTATGTTTGAATAATTCGTTATGATTAAATCCTTGGGTCACCTTGTGCTTCAAT
TaDrAp2-B1      TTATTTTATGTTTGATTAAATTCGTTATGATTGAATCCTTGGGTCACCTTGTGCTTCAAT
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TaDrAp2-A1	TGCTAGGC-TTGTTCTTTAAGGAACGAAGTTAACAGAAATTACTTGCATTCACTATTTAC
TaDrAp2-D1	TGCTAGGCCTTGTTCTTTAAGGAACGAAGTTAACAGAAATTACTTGCATTCACTATTTAC
TaDrAp2-B1	TGCTAGGT-TTGTTCTCTAAGGAATGAAGGCAACCGAAATTACTTGCATTCACTATTTAC *****
TaDrAp2-A1	TGAAAAAAGATGGACATGATTATTAAATAACTCTTTTATAAAATATGAGCTTTTTTTTAGGA
TaDrAp2-D1	TGAAAATAGATGGACATGAATATTAA-TAACTCTTTTATAAAATATGAGCTTTTTTTTAGGA
TaDrAp2-B1	TGAAAAAAGATGGACATGATTATTAAATAACTCTTTTATAAAATATGAG-TTTTTTTTAGGA *****
TaDrAp2-A1	ATGAGAGTTTAACTTAAAGCGGATGTGGCTTAATTGTCTCAAGAGATGATCAACTCCAGGT
TaDrAp2-D1	ATGAGAGTTTAACTTCAGCGGAGGTGGCTTAATTGTCTCAAGAGATGATCAACACCAGGT
TaDrAp2-B1	ATGAGAGTTCAACTTCAGCGGAGATGGCTTAATTGTCTCGAGAGAAGATCAACTCCAGGT *****
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TaDrAp2-D1	CTTCTGCGGTGTTTCCCTATTTTGATCGGTAGCTTGCTTCAAACCGGGCCGATTGTACCTA
TaDrAp2-B1	CTTCTGCGGTGTTTCCCTATTTTGGTCGGTAGCTTGCTTCAAACCGGGCCGATTGTACCTA *****
TaDrAp2-A1	AACTAATATTCCACATAATGAACACCAAGTGCTCCTTCCTTTTTTCCC-AAATTTAAAG
TaDrAp2-D1	AACTAATATTCCACATAATGAACACCAAGTGCTCCTTCCTTTTTTTCCTAAATTTAAAG
TaDrAp2-B1	AACTAATATTCCACATAATGAACACCAAGTGCTCCTTCCTTTTTTTCCT-AAATTAAGAG *****
TaDrAp2-A1	AGGAGCGTGATTGTTGGTACAAAGTGCTAACTATAGAATCAAGCATGTGAGTTCTTTTTA
TaDrAp2-D1	AGGAGCACGATTGTTGGTACAAAGTGCTAACTATAGAATCAAGCATGTGAGTTCTTTTTA
TaDrAp2-B1	AGGAGTCCGATTGTTGGTACAAAGTGCTAACTATAGAATCAAGCATGTGAGTTCTTTTTA *****
TaDrAp2-A1	TAGTTGTTGATCTGTTGACATTGGTATCATGATTGTTTAGATATAGATTGTGGTGGAAC
TaDrAp2-D1	TAGTTGTTGATCTGTTGACATTGGTATCAT-----AGATATAGATTGTGGTGGAAC
TaDrAp2-B1	TAGTTGTTGATCTGTTGACATTGGTCTCATGATTGTTTAGATATAGATTGTGGTGGAAC *****
TaDrAp2-A1	CTGGCAGGGAAGCTTCTTAGCCTGATGAGTTAGTACTGTTTCTAGATTTTGTAGTATATTTCT
TaDrAp2-D1	CTGGCAGGGAAGCTTCTTAGCCCGACGAGTTGGTACTGTTTCTAGATTTTGTAGTATATTTCT
TaDrAp2-B1	CTGGCAGGGAAGCATCTTAGCCCGACGAGTTGGTACTGTTTCTAGATTTTGTAGTATATTTCT *****
TaDrAp2-A1	AAATGGTAAATA--CAGTAGGATTCTACTATTTAACATCTGGCCCACAACAGGCAATGAG
TaDrAp2-D1	AAATGGTAAATAGACAGTAGGATTCTACTATTTGACATCTGGCCCACAACAGGCAATGAG
TaDrAp2-B1	AAATGGTAAATAGACAGTAGGATTCTACTATTTAACATCTGGCCCACAACAGGCAATGAG *****
TaDrAp2-A1	TGTTGGTTAAAGCTGTGTACGATCTATAAAAAATATATAGTGTAGAGTGTATCTTATTTCT
TaDrAp2-D1	TGTTGGTTAAAGCTGTGTACAATCTATAAAAAATATATAGTGTAGAGTGTATCTTATTTCT
TaDrAp2-B1	TGTTGGTTAAAGCTGTGTACAATCTATAAAAAATATATAGTGTAGAGTGTATCTTATTTCT *****
TaDrAp2-A1	TAAGCATGGTATATTCTCCGATCTGTTTTTGGTCCATCTTCGGGGGAAGATGCAAGTGTT
TaDrAp2-D1	TGAGCATGGTATATTCTCCAATCTGTTTTTGGTCCATCTTCGGGGGAAGATGCAAGTGTT
TaDrAp2-B1	TGAACATGGTATATTCTCTGATCTGTTTTTGGTCCATCTTCGCGGGAAGATGCAAGTGTT * * *****
TaDrAp2-A1	TTGATGACATATGTTTGCTGTACAATGGAATCCTCATGATACTAAAGTTTTTCTACAGTG
TaDrAp2-D1	TTGATGACATACGTTTGCTGTACAATGGAATCCTCATGATACTAAAGTTTTTCTACAGTG
TaDrAp2-B1	TTGATGACATATGTTTGCTGTACAATGGAATCCTCATGATACTACAGTTTTTCTACAGTG *****

TaDrAp2-A1	GATAGAGATACCTTCTTCATTACCCTTTCTTTCACAAGGGCTAGCAGAATCTCTTTTCTT
TaDrAp2-D1	GATAGAGATACCTTCTTCATTACCCTTTCTTTCACAAGGGCTAGTAGAATCTATTTTCTT
TaDrAp2-B1	GATAGAGATACCTTCTTCATTACTCTTTCTTTCACAAGGGCTAGCAGAATCTCTTTACCT

TaDrAp2-A1	CATCTGCTAGGACCTGTGCTTATAACCACATGTGAATACTATCGCTCTCATGTCCTTTTC
TaDrAp2-D1	CATCTGCTAGGACCTGTGCTCATAACCACATGTGAATACTATCGCTGTCATGTCCTTTTC
TaDrAp2-B1	CATCTGCTAGGACCTGTGCTTATAACGACATGTGAATACTATCACTGTCATGTCCTTTTC

TaDrAp2-A1	CATCGAAGTTGCATCATTGGCCATTTGCACTGTAGTATGCAACAATCATAACTATGATTA
TaDrAp2-D1	CATCGAAGTTGCATCGTAGGCCATTTGCACTGTAGTATGCAACAATCATAATTATGATTA
TaDrAp2-B1	CATCGAAGTTGCATCGTTGGCCATTTGCACTGAAGTATGCAACAATCATAATTATGATTA

TaDrAp2-A1	ATGAGTGTTTTATTATTGACATGTTGTCATAATTTGAAAAATGGCAGATTCCCTACTACTTT
TaDrAp2-D1	ATGAGTGTTTTATTGATGACATGTTGTCATAATTTCAAAATGGCAGATTCCCTACTACTTT
TaDrAp2-B1	ATGAGTGTTTTATTGATGACATGTTGTCATAATTTCAAAATGGCAGATTCCTACTACTTT

TaDrAp2-A1	TCAGATGGTATCATGGTACTCTTCTGTTAATGTGATATCAGCTTCCTCTTGTACTTTGTT
TaDrAp2-D1	TCAGATGGTATCATGGTACTCTTCTGTTAATGTGACATCAGCTTCCTCTTGTATTTTGTT
TaDrAp2-B1	TCAGATGGTATCATGGTACTCTTCTGTTAATGTGATATCAGCTTCCTCTTGTACTTTGTT

TaDrAp2-A1	ATACAGCCTCGGATTAAGAAGATCATGCAAGCAGATGAAGATGTCGGCAAGATTGCTCTA
TaDrAp2-D1	ATACAGCCTCGGATTAAGAAGATCATGCAAGCAGATGAAGATGTCGGCAAGATTGCTCTA
TaDrAp2-B1	ATACAGCCTCGGATTAAGAAGATCATGCAAGCAGATGAAGATGTCGGCAAGATTGCTCTA

TaDrAp2-A1	GCTGTACCTGTTCTAGTTT
TaDrAp2-D1	GCAGTACCTGTTCTAGTTT
TaDrAp2-B1	GCTGTACCTGTTCTAGTTT
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Supplementary file 4

Sequences, BLAST and primer design, Universal probes and sizes of amplicons generated

TaDrAp1-B4

>cs

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ATAATAGAGAATTGCTAGAGCTTTGCTCATATTCATTATTCCTCTTGGAGGTCAAGACCTCCATGT
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ACTCGAAGCATTTTTTTTAGGTTGCCGATTTTTTCAAGAAAATTTAGAATTTGATAGCTTTTCGT
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>18-4-Female

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>18-5-Male

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GGATCTCACGTTTGCTATTTTAGTGATGTGTGATTTGGATTTGTATGAGTCTCTCTCTCTCTCTCT
TGTGTTACTGAGTGTTTCATCCTTTCTCCACCTCCAAGTGAGAAAAGATCTTGAATCTAGGGTTTTG
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CLUSTAL 2.1 multiple sequence alignment

TaDrAp1-B4

18-4-Female GATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTTGAGAAGAACCTTTACCTTTGT
 18-5-Male GATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTTGAGAAGAACCTTTACCTTTGT
 CS GATCCTCCATGGATGCTAGATCTCATCTCCTTTGGATTTGAGAAGAACCTTTACCTTTGT

18-4-Female GCTTCCCCCTTTTGACTTGTTAATATATATTTGTGGATCTCATGTATGCTATCTTAGTG
 18-5-Male GCTTCCCCCTTTTGACTTGTTAATATATATTTGTGGATCTCATGTATGCTATCTTAGTG
 CS GCTTCCCCCTTTTGACTTGTTAATATATATTTGTGGATCTCATGTATGCTATCTTAGTG

18-4-Female ATGTGTGATTTGGATTTGTTTGAGTCTCTCTCTCTCTCTTGTGTTATTGAGTGTTTCAT
 18-5-Male ATGTGTGATTTGGATTTGTTTGAGTCTCTCTCTCTCTCTTGTGTTATTGAGTGTTTCAT
 CS ATGTGTGATTTGGATTTGTTTGAGTCTCTCTCTCTCTCTTGTGTTATTGAGTGTTTCAT

18-4-Female CCTTTCTCCATCCTCCAAGTGCAGAAAAGATCTTGAATCTAGGGTTTTGCCCTACATCACC
 18-5-Male CCTTTCTCCATCCTCCAAGTGCAGAAAAGATCTTGAATCTAGGGTTTTGCCCTACATCACC
 CS CCTTTCTCCATCCTCCAAGTGCAGAAAAGATCTTGAATCTAGGGTTTTGCCCTACATCACC

18-4-Female ATGCCTCCCTAGCCCCCTCTCCTCTCCTCCTTCCCTTCCCGCAGGTCAGTACCTCCTA
 18-5-Male ATGCCTCCCTAGCCCCCTCTCCTCTCCTCCTTCCCTTCCCGCAGGTCAGTACCTCCTA
 CS ATGCCTCCCTAGCCCCCTCTCCTCTCCTCCTTCCCTTCCCGCAGGTCAGTACCTCCTA

18-4-Female CTTGTGTCGGGTCCCTCTCTTCCTTCCTTCCCCGTAGGTCGTTGAGCAAGGAATCGAACT
 18-5-Male CTTGTGTCGGGTCCCTCTCTTCCTTCCTTCCCCGTAGGTCGTTGAGCAAGGAATCGAACT
 CS CTTGTGTCGGGTCCCTCTCTTCCTTCCTTCCCCGTAGGTCGTTGAGCAAGGAATCGAACT

18-4-Female GGGCAAACGTGACGGCCGGCCGGATCGATGCTGAATTGACCGGATCCGACGTAGGGATCA
 18-5-Male GGGCAAACGTGACGGCCGGCCGGATCGATGCTGAATTGACCGGATCCGACGTAGGGATCA
 CS GGGCAAACGTGACGGCCGGCCGGATCGATGCTGAATTGACCGGATCCGACGTAGGGATCA

18-4-Female CAACAAGGAGGAGGAAGTCGGAGGAAGGAACGGTGGCGGGCAGGGGCGGCGGCTACAATG
 18-5-Male CAACAAGGAGGAGGAAGTCGGAGGAAGGAACGGTGGCGGGCAGGGGCGGCGGCTACAATG
 CS CAACAAGGAGGAGGAAGTCGGAGGAAGGAACGGTGGCGGGCAGGGGCGGCGGCTACAATG

18-4-Female TCGTCGGTGGAAGGAGCGACAATGGAGGCTCCGCCGACCATGGCGAGGAAAGCGAGATCG
 18-5-Male TCGTCGGTGGAAGGAGCGACAATGGAGGCTCCGCCGACCATGGCGAGGAAAGCGAGATCG
 CS TCGTCGGTGGAAGGAGCGACAATGGAGGCTCCGCCGACCATGGCGAGGAAAGCGAGATCG

18-4-Female GCGATGAGCTTCGCGGGGTCCGCTGCGGGGTCAGAGGAGCTGGCCATGGCGACGCGGTGG
 18-5-Male GCGATGAGCTTCGCGGGGTCCGCTGCGGGGTCAGAGGAGCTGGCCATGGCGACGCGGTGG
 CS GCGATGAGCTTCGCGGGGTCCGCTGCGGGGTCAGAGGAGCTGGCCATGGCGACGCGGTGG

TaDrAp1-B4

Primers:

DrAp1-B4-SNP-F1: CTAGGGAGGCATGGTGATGTAG 22 bp, 55%GC, 56.7C
DrAp1-B4-SNP-F1 (RevCom): CTACATCACCATGCCTCCCTAG

DrAp1-B4-SNP-F2: CTAGGGAGGCATGGTGATGTAT 22 bp, 50%GC, 54.8C
DrAp1-B4-SNP-F2 (RevCom): ATACATCACCATGCCTCCCTAG

DrAp1-B4-SNP-R: GTGGATCTCATGTATGCTATCTTAG 25 bp, 40%GC, 54.4C

Amplicon size: 159 bp

Ordered primers:

DrAp1-B4-SNP-F1: GAAGGTGACCAAGTTCATGCTCTAGGGAGGCATGGTGATGTAG
DrAp1-B4-SNP-F2: GAAGGTCGGAGTCAACGGATTCTAGGGAGGCATGGTGATGTAT
DrAp1-B4-SNP-R: GTGGATCTCATGTATGCTATCTTAG

TaDrAp1-D4

>CS

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>18-4-Female

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>18-5-Male

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CLUSTAL 2.1 multiple sequence alignment TaDrAp1-D4

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18-4-Female	CTCAAATCTAGGGTTTTGCCCTACATCACCGTGCCTCCCTAGCCCCCTCCTCTCCTCTCCC
18-5-Male	CTCAAATCTAGGGTTTTGCCCTACATCACCGTGCCTCCCTAGCCCCCTCCTCTCCTCTCCC
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18-5-Male	CCTTCCTTCCCCGCAGGTCACTGACCTCCTACTCATGTGCGGGTCCCTCTCCTCCTTCCTT
CS	CCCCGTAGGTCGTTGAGCAAGAAATCGAGCTGGGCAAACGTGACGGCTGGCCGGATCAAT
18-4-Female	CCCCGTAGGTCGTTGAGCAAGAAATCGAGCTGGGCAAACGTGACGGCTGGCCGGATCAAT
18-5-Male	CCCCGTAGGTCGTTGAGCAAGAAATCGAGCTGGGCAAACGTGACGGCTGGCCGGATCAAT
CS	GCCGAGTTGTCCGGATCCGACGCAGGGATCACAACAAGGAGGAGGAAGTCGGAGGAAAGA
18-4-Female	GCCGAGTTGTCCGGATCCGACGCAGGGATCACAACAAGGAGGAGGAAGTCGGAGGAAAGA
18-5-Male	GCCGAGTTGTCCGGATCCGACGCAGGGATCACAACAAGGAGGAGGAAGTCGGAGGAAAGA
CS	GAGGTGGCGGGCAGAGGCGGCGGCGACGGTGTCTGTCGGTGGAAGGAGCGGCAATGGAAGC
18-4-Female	GAGGTGGCGGGCAGAGGCGGCGGCGACGGTGTCTGTCGGTGGAAGGAGCGGCAATGGAAGC
18-5-Male	GAGGTGGCGGGCAGAGGCGGCGGCGACGGTGTCTGTCGGTGGAAGGAGCGGCAATGGAAGC
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18-4-Female	TCCGCCGACCATGGCGAGGAAAAGCGAGATCGGCGGTGAGCTTCGCGGGGTTCGGTTGCAGG
18-5-Male	TCCGCCGACCATGGCGAGGAAAAGCGAGATCGGCGGTGAGCTTCGCGGGGTTCGGTTGCAGG
CS	GCCAAAGGAGCTGGCCATGGCGACGTGATGGCCGGCGGGAGAGCGGAGGCAGCGTTCCGG
18-4-Female	GCCAAAGGAGCTGGCCATGGCGACGTGATGGCCGGCGGGAGAGCGGAGGCAGCGTTCCGG
18-5-Male	GCCAAAGGAGCTGGCCATGGCGACGTGATGGCCGGCGGGAGAGCGGAGGCAGCGTTCCGG
CS	TTGCGCGCGGGTAGAAAAAGGTAGCTATTGGGTTTCATGATGCAACCACTCTTTTGTGAC
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18-5-Male	TTGCGCGCGGGTAGAAAAAGGTAGCTATTGGGTTTCATGATGCAACCACTCTTTTGTGAC
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18-4-Female	GTAGCCTTTCTGTGCTTAAAAACAATTCGTGTGTGAAAATAATAGGGCTGGGAGAT
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CS	GCGGTAATTATCTTTTGGCACGAGTCCGCGTGCCGTGTAAGTTGGTGAAAGACAA
18-4-Female	GCGGT-----
18-5-Male	GCGGCT-----

TaDrAp1-D4

Primers:

DrAp1-D4-SNP-F1: CACGAAAGGCTACCGAATTCTAA 23 bp, 43%GC, 53.5C
DrAp1D4-SNP-F1 (RevCom): TTAGAATTCGGTAGCCTTTCGTG

DrAp1-D4-SNP-F2: CACGAAAGGCTACCGAATTCTAT 23 bp, 43%GC, 53.5C
DrAp1D4-SNP-F2 (RevCom): ATAGAATTCGGTAGCCTTTCGTG

DrAp1-D4-SNP-R: GGTTCAGGGCCAAAGGA 18 bp, 61%GC, 52.6C

Amplicon size: 202 bp

Ordered primers:

DrAp1-D4-SNP-F1: GAAGGTGACCAAGTTCATGCTCACGAAAGGCTACCGAATTCTAA
DrAp1-D4-SNP-F2: GAAGGTCGGAGTCAACGGATTACGAAAGGCTACCGAATTCTAT
DrAp1-D4-SNP-R: GGTTCAGGGCCAAAGGA

TaDrAp2-B1

>cs

GTGTTCCATGCCCTACTCTACCTTTTCAGGCGACCGAACCAACACTCTGAGAAGCGCAGCCGACCGC
CGGACGTAGGCACGACGGAGGCGGACGAGCTCCGCTTAAAGATCGTTTTACGTTGCATGTAATAAT
ATGAATTTGAGGTTTCTACTTTTAGGTATCCGGTTATAAAATCAAACCTTTAAGACGTGATAGGTC
ATTGTCTGCGGACACGCCCAGACTTGTCTGCGGACATTTGAGGGGGCGGGTTTGCGAAGTACGACT
GTATATCCTCTTACACCCTGAAACATGATCCCTTTACGTTTAGTTAACACTCCTCAAAACAAAACA
CGACAAGATATGCCGACTCAGTCTTTTACAGATGCGCTTATAGGAATAGAAAATGCGTGTGTGCGTTT
ATAGGGATAAGCGTATGCGCGTGTATATGAGCGCTTGCCTGTACCGTGTGTTAAAAAACACACG
GCAATCTATTCTGATCTCACAAAGACAAGTCGGAACATGCTATATACCCAGATAAAGCGAGAGCCCGA
GAATGGACGATGACTCTCGCAGCCCAAGGCCACGAACGAGGCACAGCGCCACAGCCACCGGATCCC
GCCGACCCCCGAATCGGACGGCGGACACAGGGAGCGCCACGAACCGGCCAGAAACGTGGGGCCCA
CCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCGGCCGCACGCGCAAACGAGGGAGAGGTCT
AACTACGCGGGCCCCCTACATCGCGCCAGCTTTTACCCACCGCGAAACGTCTCCATAGACCCGGTC
CGTCGCATCCCCACATGAACCTTCTACGGTCTTAGCGCCGCACGTGAGGCTAAGACCTATGCACCG
GGTCCAGGAGCTTAGCCTCCACGCGCCGGAGAGCTCGCGCACCTCTGCCCGCTTCGCGCGGCCATT
GGCCGCGCTGTTTATGGGGGAAAAATATATATTTTCCCGTAAAAAAGTGAAAAGATAGCGATAAC
GGAAACCCTAATCCCCAAATCAGAAATCTATCCGAATCGCTATTTATGTTTGTGGCTTTCTCCCC
CTCCGATCCGATGTCCCCGCTTCGTCCGCGCGCCGATCCGACCTCCAGCCGCGCAATTCTCTCC
GCCGGGACGCTCCCTCCGGCGCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCCGCTTCC
CCGCGGTATGACCCATGCCCATGCGATTTTTTGCCGGTTCAGG

>TaDrAp2-B1-18-4-Female

TTTTTCCTCNCNCNTCCNAACCTTTAAGGGGCCCCGAACCAACCCCTTTGGAAAGGGGGACCGACC
CCCCGNACCTAGGCCCGACGGAGGCGGGCGAGCTTCGCTTAAAGATCCGTTTTACATTGCACGTAA
TAATATGAAATTGAAGTTTGTACTCTTAGGTATCCGGTTATAAATCAAACCTTTAAGATGTGAT
AGGTCAATTGTNTGCGGACACGCCCAGAATTTTCTGTGGACATTTGAGGGGGCGGGTTTGCGAAGT
ACGACTGTATATCCTCTTACACCCTGAAACATGATTCCTTTACGCTTAGTTAACACTCCTCAAAAC
AAAACACGACAAGATATGCCGACTCAGTCTTTTACAGATGCGCTTATAGGAATAGAAAATGCGTGTGT
GCGTTTATAGGGATAAGCGTATGCGCGTATATATGAGCGCTTGCCTGTACCGTGTGTTAAACAA
CACACGGCAATCTATTCTGATCTCACAAAGACAAGTCGGAACATGCTATACCCAGATAAAGCGAGA
GCCCCGAGAATGGACGATGACTCTCGCAGCCCAAGGCCACGAACGAGGCACAGCGCCACAGCCACCG
GATCCCGCCGACCCCCCGAATCGGACGGCGGACACAGGGAGCGCCACGAACCGGCCAGAAACGTGG
GGCCACCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCGGCCGCACGCGCAAACGAGGGAG
AGGTCTAACTACGCGGGCCCCCTACATCGCGCCAGCTTTTACCCACCGCGAAACGTCTCCATAGAC
CCGGTCCGTGCGATCCCCACATGAACCTTCTACGGTCTTAGCGCCGCACGTGAGGCTAAGACCTAT
GCACCGGGTCCAGGAGCTTAGCCTCCACGCGCCGGAGAGCTCGCGCACCTCTGCCCGCTTCGCGCG
GCCATTGGCCGCGCTGTTTATGGGGGAAAAATATGTTTGTGTTTATTTTTTCCCGTAAAAAAGTGA
AAAGATAGCGATAACGGAAACCCTAATCCCCAAATCAGAAATCTATCCGAATCGCTATTTATGTTT
GTGGCTTTCTCCCCCTCCGATCCGATGTCCCCGCTTCGTCCGCGCGCCGATCCGACCTCCAGC
CGCCGCTTCTCTCCGCGGGGACGCTCCCTCCGGCGCCGCGGCTCCGCGCCATGAGGAAGAAGC
TCGACACCCGCTTCCCCGCGGTTGACCCCCCCCC

>TaDrAp2-B1-18-5-Male

TTTTACTTTTCAGGCGACCGAACCAACATTTGAGAAGCGCAGCCGACCGCCGGACGTAGGCACGACG
GAGGCGGACGAGNTCCGCTTAAAGATCGTTTTACGTTGCATGTAATAATATGAATTTGAGGTTTCT
ACTTTTAGGTATCCGGTTATAAAATCAAACCTTTAAGACGTGATAGGTCATTGTCTGCGGACACGC
CCAGACTTGTCTGCGGACATTTGAGGGGGCGGGTTTGCGAAGTACGACTGTATATCCTCTTACACC
CTGAAACATGATCCCTTTACGTTTAGTTAACACTCCTCAAAACAAAACACGACAAGATATGCCGAC

TCAGTCTTTCAGATGCGCTTATAGGAATAGAAAATGCGTGTGTGCGTTTATAGGGATAAGCGTATG
CGCGTGTATATGAGCGCTTGCCTGTACCGTGTTTAAAAAACACACGGCAATCTATTCTGATCT
CACAAAGACAAGTCGGAACATGCTATACCCAGATAAAGCGAGAGCCCGAGAATGGACGATGACTCT
CGCAGCCCAAGGCCACGAACGAGGCACAGCGCCACAGCCACCGGATCCCGCCGACCCCCGAATCG
GACGGCGGACACAGGGAGCGCCACGAACCGGCCAGAAACGTGGGGCCACCTCATCCGGGGAACGC
GACGCGGACGGCTGACGTGCGGCCGCACGCGCAAACGAGGGAGAGGTCTAACTACGCGGGCCCCTA
CATCGCGCCCAGCTTTTACCCACCGCGAAACGTCTCCATAGACCCGGTCCGTGCGATCCCCACATG
AACCTTCTACGGTCTTAGCGCCGCACGTGAGGCTAAGACCTATGCACCGGGTCCAGGAGCTTAGCC
TCCACGCGCCGAGAGCTCGCGCACCTCTGCCGCTTCGCGCGGCCATTGGCCGCGCTGTTTATGG
GGGAAAAATATAATTTTTTCCCGTAAAAAAGTGAAAAGATAGCGATAACGGAAACCCTAATCCCCA
AATCAGAAATCTATCCGAATCGCTATTTATGTTTGTGGCTTCTCCCCCTCCGATCCGATGTCCC
CCGCTTCGTCCGCCGCGCCGATCCGACCTCCAGCCGCCGCAATTCTCTCCGCCGGGGACGCTCCCTC
CGGCGCCCGCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCCGCTTCCCCGCGGTTACCCCCNNN
N

CLUSTAL 2.1 multiple sequence alignment TaDrAp2-B1

18-5-Male	TTGAGGGGGCGGGTTTGCGAAGTACGACTGTATATCCTCTTACACCCTGAAACATGATC
CS	TTGAGGGGGCGGGTTTGCGAAGTACGACTGTATATCCTCTTACACCCTGAAACATGATC
18-4-Female	TTGAGGGGGCGGGTTTGCGAAGTACGACTGTATATCCTCTTACACCCTGAAACATGATC *****
18-5-Male	CCTTTACGTTTAGTTAACAACCTCCTCAAAACAAAAACACGACAAGATATGCCGACTCAGTCT
CS	CCTTTACGTTTAGTTAACAACCTCCTCAAAACAAAAACACGACAAGATATGCCGACTCAGTCT
18-4-Female	CCTTTACGTTTAGTTAACAACCTCCTCAAAACAAAAACACGACAAGATATGCCGACTCAGTCT *****
18-5-Male	TTCAGATGCGCTTATAGGAATAGAAAATGCGTGTGTGCGTTTATAGGGATAAGCGTATGC
CS	TTCAGATGCGCTTATAGGAATAGAAAATGCGTGTGTGCGTTTATAGGGATAAGCGTATGC
18-4-Female	TTCAGATGCGCTTATAGGAATAGAAAATGCGTGTGTGCGTTTATAGGGATAAGCGTATGC *****
18-5-Male	GCGTGTATATGAGCGCTTGCCTGTGTACCGTGTTTAAAAAACACACGGCAATCTATTCT
CS	GCGTGTATATGAGCGCTTGCCTGTGTACCGTGTTTAAAAAACACACGGCAATCTATTCT
18-4-Female	GCGTGTATATGAGCGCTTGCCTGTGTACCGTGTTTAAAAAACACACGGCAATCTATTCT **** *****
18-5-Male	GATCTCACAAAGACAAGTCGGAACATGCTATACCCAGATAAAGCGAGAGCCCGAGAATGG
CS	GATCTCACAAAGACAAGTCGGAACATGCTATACCCAGATAAAGCGAGAGCCCGAGAATGG
18-4-Female	GATCTCACAAAGACAAGTCGGAACATGCTATACCCAGATAAAGCGAGAGCCCGAGAATGG *****
18-5-Male	ACGATGACTCTCGCAGCCCAAGGCCACGAACGAGGCACAGCGCCACAGCCACCGGATCCC
CS	ACGATGACTCTCGCAGCCCAAGGCCACGAACGAGGCACAGCGCCACAGCCACCGGATCCC
18-4-Female	ACGATGACTCTCGCAGCCCAAGGCCACGAACGAGGCACAGCGCCACAGCCACCGGATCCC *****
18-5-Male	GCCGACCCCCGAATCGGACGGCGGACACAGGGAGCGCCACGAACCGGCCAGAAACGTGG
CS	GCCGACCCCCGAATCGGACGGCGGACACAGGGAGCGCCACGAACCGGCCAGAAACGTGG
18-4-Female	GCCGACCCCCGAATCGGACGGCGGACACAGGGAGCGCCACGAACCGGCCAGAAACGTGG *****
18-5-Male	GGCCACCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCGGGCCGCACGCGCAAACG
CS	GGCCACCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCGGGCCGCACGCGCAAACG
18-4-Female	GGCCACCTCATCCGGGGAACGCGACGCGGACGGCTGACGTGCGGGCCGCACGCGCAAACG *****

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18-5-Male      AGGGAGAGGTCTAACTACGCGGGCCCCCTACATCGCGCCCAGCTTTTACCCACCGCGAAAC
CS             AGGGAGAGGTCTAACTACGCGGGCCCCCTACATCGCGCCCAGCTTTTACCCACCGCGAAAC
18-4-Female    AGGGAGAGGTCTAACTACGCGGGCCCCCTACATCGCGCCCAGCTTTTACCCACCGCGAAAC
                *****

18-5-Male      GTCTCCATAGACCCGGTCCGTTCGCATCCCCACATGAACCTTCTACGGTCTTAGCGCCGCA
CS             GTCTCCATAGACCCGGTCCGTTCGCATCCCCACATGAACCTTCTACGGTCTTAGCGCCGCA
18-4-Female    GTCTCCATAGACCCGGTCCGTTCGCATCCCCACATGAACCTTCTACGGTCTTAGCGCCGCA
                *****

18-5-Male      CGTGAGGCTAAGACCTATGCACCGGGTCCAGGAGCTTAGCCTCCACGCGCCGGAGAGCTC
CS             CGTGAGGCTAAGACCTATGCACCGGGTCCAGGAGCTTAGCCTCCACGCGCCGGAGAGCTC
18-4-Female    CGTGAGGCTAAGACCTATGCACCGGGTCCAGGAGCTTAGCCTCCACGCGCCGGAGAGCTC
                *****

18-5-Male      GCGCACCTCTGCCCCTTCGCGCGGCCATTGGCCGCGCTGTTTATGGGGGAAAAA-----
CS             GCGCACCTCTGCCCCTTCGCGCGGCCATTGGCCGCGCTGTTTATGGGGGAAAAA-----
18-4-Female    GCGCACCTCTGCCCCTTCGCGCGGCCATTGGCCGCGCTGTTTATGGGGGAAAAAATAGT
                *****

18-5-Male      ----TATATTTTTTCCCGTAAAAAAAGTGAAAAGATAGCGATAACGGAACCCCTAATCCC
CS             ----TATATTTTTTCCCGTAAAAAAAGTGAAAAGATAGCGATAACGGAACCCCTAATCCC
18-4-Female    TTGTATTTTTTTCCCGTAAAAAAAGTGAAAAGATAGCGATAACGGAACCCCTAATCCC
                * *****

18-5-Male      CAAATCAGAAATCTATCCGAATCGCTATTTATGTTTGTGGCTTTCTCCCCCTCCGATCC
CS             CAAATCAGAAATCTATCCGAATCGCTATTTATGTTTGTGGCTTTCTCCCCCTCCGATCC
18-4-Female    CAAATCAGAAATCTATCCGAATCGCTATTTATGTTTGTGGCTTTCTCCCCCTCCGATCC
                *****

18-5-Male      GATGTCCCCCGCTTCGTCCGCCGCGCCGATCCGACCTCCAGCCGCCGCATTCTCTCCGCC
CS             GATGTCCCCCGCTTCGTCCGCCGCGCCGATCCGACCTCCAGCCGCCGCATTCTCTCCGCC
18-4-Female    GATGTCCCCCGCTTCGTCCGCCGCGCCGATCCGACCTCCAGCCGCCGCATTCTCTCCGCC
                *****

18-5-Male      GGGGACGCTCCCTCCGGCGCCGCCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCCGCT
CS             GGGGACGCTCCCTCCGGCGCCGCCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCCGCT
18-4-Female    GGGGACGCTCCCTCCGGCGCCGCCGGCTCCGCGCCATGAGGAAGAAGCTCGACACCCGCT
                *****

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TaDrAp2-B1

Primers:

DrAp2-B1-SNP-F1: ACAGACGCAAGCGCTCATATAT 22 bp, 45%GC, 53C

DrAp2-B1-SNP-F1 (Rev-Com): ATATATGAGCGCTTGCGTCTGT

DrAp2-B1-SNP-F2: ACAGACGCAAGCGCTCATATAC 22 bp, 50%GC, 54.8C

DrAp2-B1-SNP-F2 (Rev-Com): GTATATGAGCGCTTGCGTCTGT

DrAp2-B1-SNP-R: CACGACAAGATATGCCGACTCA 22 bp, 50%GC, 54.8C

Amplicon size: 112 bp

Ordered primers:

DrAp2-B1-SNP-F1: GAAGGTGACCAAGTTCATGCTACAGACGCAAGCGCTCATATAT

DrAp2-B1-SNP-F2: GAAGGTCGGAGTCAACGGATTACAGACGCAAGCGCTCATATAC

DrAp2-B1-SNP-R: CACGACAAGATATGCCGACTCA

Supplementary file 5

Primer design and sequences for RT-qPCR

TaDrAp1

TaDrAp1-Total-Fq: GACGCCAGCTGTGATTTCAAAG 22bp; 50% GC; 54.8C

TaDrAp1-Total-Rq: GTACAACACCAGGAGAACTGTC 22bp; 50% GC; 54.8C

TaDrAp1-Total-Rq (RevCom): GACAGTTCTCCTGGTGTGTAC

Amplicon size = 219 bp

TaDrAp1-A4-Fq: AGTGGAGGCTCCATCAGCCA 20bp; 60% GC; 55.9C

TaDrAp1-A4-Rq: ATGACTATGCCTAATCCTCATTTG 23bp; 39% GC; 51.7C

TaDrAp1-A4-Rq (RevCom): CAATGAGGATTAGGCATAGTCAT

Amplicon size = 191 bp

TaDrAp1-B4-Fq: CTAGTGGAGGCTCCATCGGT 20bp; 60% GC; 55.9C

TaDrAp1-B4-Rq: GCATATGATGAATGAGAGGATGG 23bp; 43% GC; 53.5C

TaDrAp1-B4-Rq (RevCom): CATCCTCTCATTCATCATATGC

Amplicon size = 209 bp

TaDrAp1-D4-Fq: TGAGGATGTTGGCAAAATTGCG 22bp; 45% GC; 53C

TaDrAp1-D4-Rq: ATTCACCGCCACCAAGATCC 20bp; 55% GC; 53.8C

TaDrAp1-D4-Rq (RevCom): GATCTTGGTGGCGGTGAAT

Amplicon size = 221 bp

CLUSTAL 2.1 multiple sequence alignment

```
B4      ATGAGGAAGAAGCTGGGCACCCGGTTCCCCGCGGCACGGATCAAAAAGATAATGCAAGCA
D4      ATGAGGAAGAAGCTGGGCACCCGGTTCCCCGCGGCACGGATCAAAAAGATAATGCAAGCA
A4      ATGAGGAAGAAGCTGGGCACCCGGTTCCCCGCGGCACGGATCAAAAAGATAATGCAAGCA
*****

B4      GATGAGGATGTTGGCAAAATTGCACTGGCTGTGCCTGTTTTAGTTTCGAGAGCCCTTGAA
D4      GATGAGGATGTTGGCAAAATTGCGCTGGCTGTGCCTGTTTTAGTTTCGAGAGCCCTTGAA
A4      GATGAGGATGTTGGCAAAATTGCACTGGCTGTGCCTGTTTTAGTTTCGAGAGCCCTTGAA
*****

B4      TTGTTTCTGCAAGATTTGATTGACCGCTCATACAAAATTACTCTTCAAAGTGGTGCAAAG
D4      TTGTTTCTGCAAGATTTGATTGACCGCTCATACAAAATTACTCTTCAAAGTGGTGCAAAG
A4      TTGTTTCTGCAAGATTTGATGACCTCATACAAAATTACTCTTCAAAGTGGTGCAAAG
*****

B4      ACACTGAATTCCTTCCACCTAAAGCAATGTGTGAAGAGGTACAGCTCTTTTGACTTCCTA
D4      ACACTGAATTCCTTCCACCTAAAGCAATGTGTGAAGAGGTACAGCTCTTTTGACTTCCTA
A4      ACACTGAATTCCTTCCACCTAAAGCAATGTGTGAAGAGGTACAGCTCTTTTGACTTCCTA
*****

B4      ACTGAGATTGTCAACAAGGTGCCAGATCTCGGTGGCGGTGAATCTTGTGGAGATGAAAGA
D4      ACTGAGATTGTCAACAAGGTGCCGATCTCGGTGGCGGTGAATCTTGTGGAGATGAAAGA
A4      ACTGAGATTGTCAACAAGGTGCCAGATCTCGGTGGCGGTGAATCTTGTGGAGATGAAAGA
*****

B4      GGATTACCCAGAAGAAGGAAATTTTCAAATGGAAGCGACCCAGAGAATGAGGAGCCCCGA
D4      GGATTACCCAGAAGAAGGAAATTTTCAAATGGAAGCGACCCAGAGAATGAGGAGCCCCGA
A4      GGATTACCCAGAAGAAGGAAATTTTCAAATGGAAGCGACCCAGAGAATGAGGAGCCCCGA
*****
```

B4 TCTAGCAAAATGCCCATAGAAGCTTGAACACTAGTCCCAGAGGACGAGGCAGAGGTCGA
 D4 TCTAGCAAAATGCCCATAGAAGCTTGAACACTAGTCCCAGAGGACGAGGCAGAGGTCGA
 A4 TCTAGCAAAATGCCCATAGAAGCTTGAACACAGTCCCAGAGGACGAGGCAGAGGTCGA

B4 GGAAGAGGGCGAGGGCGGCCTCCAACCAAGAGAAAGGAAATTGGTTATGTACAGTTTGAG
 D4 GGAAGAGGGCGAGGGCGGCCTCCAACCAAGAGAAAGGAAATTGGTTATGTACAGTTTGAG
 A4 GGAAGAGGGCGAGGGCGGCCTCCAACCAAGAGAAAGGAAATTGGTTATGTACAGTTTGAG

B4 GATGAGAGCAGCATGTTTGTCTGAACAAAGTGAACCCCTGCCAGGAGATGAGATAGTTCCA
 D4 GATGAGAGCAGCATGTTTGTCTGAACAAAGTGAACCCCTGCCAGGAGATGAGATAGTTCCA
 A4 GATGAGAGCAGCATGTTTGTCTGAACAAAGTGAACCCCTGCCAGGAGATGAGATAGTTCC

B4 GAGACCAACCGTGGCAATGAGATATTCCCCAAAGCTCACATCCTCTAGTGGAGGCTCCA
 D4 GAGACCAACCGTGGCAATGAGAGTATTCCCCAAAGCTCACATCCTCTAGTGGAGGCTCCA
 A4 GAGACCAACCGTGGCAATGAGAGTATTCCCCAAAGCTCACATCCTCTAGTGGAGGCTCCA

B4 TCGGTCGTGACGCCAGCTGTGATTTCAAAGGTTGAAAAAGCCACCAACCATCAGCCA
 D4 TCAGCCGCGACGCCAGCTGTGATTTCAAAGGTTGAAAAAGCTAGCACCAACCATCAGCCA
 A4 TCAGCCGTCGTGACGCCAGCTGTGATTTCAAAGGTTGAAAGCTAGCACCAACCATCAGCCA
 ** * * *****

B4 GATTTGCCTATGCCAGATGCCATTGGAGGCATTGGTGTGGACCTCCAGTTTTGGACAT
 D4 GATTTGCCTATGCCAGATGCCATTGGAGGCATTGGTGTGGACCATCCAGTTTTGGACAT
 A4 GATTGCCTATGCCAGATGCCATTGGAGGCATTGGTGTGGACCATCCAGTTTTGGACAT
 **** *****

B4 CTGACAGTGCAGGTTGATGAGGAAGAGGACTACGATAATGAGGATAGGCATAGCATCC
 D4 CTGACGGTGCAGGTTGATGAGGAAGAGGACTACGATAATGAGGATAGGCATAGTCATCC
 A4 CTGACAGTGCAGGTTGATGAGGTAGAGGACTACGAAATGAGGATAGGCATAGTCATCC

B4 TCTCATTTCATCATATGCTCTAACAGGACAGTTCTCCTGGTGTGTACATTGTAAATATTG
 D4 TCTCATTTCATCATATGCTCTAACAGGACAGTTCTCCTGGTGTGTACATTGTAAATATTG
 A4 TCTCATTTCATCATATGCTCTAACAGGACAGTTCTCCTGGTGTGTACATTGTAAATATTG

B4 TTTCAAGTAGTTACCGCAGCTATGATGTGTAACCTATTTCTTTTTCCCAATAATTGGTTT
 D4 TTTCAAGTAGTTACCGCAGCTATGATGTGTAACCTATTTCTTTTTCCCAATAATTGGTTT
 A4 TTTCAAGTAGTTACCGCAGCTATGATGTGTAACCTATTTCTTTTTCCCAATAATTGGTTT

B4 CGAGTTGCCTCGCATTGTTGACTTAACTGACTAGGATGTGCTAAATTAACCTGTATTT
 D4 CGAGTTGCCTCGCACTGTTGACTTAACTGACTAGGATGTGCTAAATTAACCTGTATTT
 A4 TGAGTTGCCGCAATTGTTGACTTAACTGACTAGGATGTGCTAAATTAACCTGTATTT

B4 GACGGTTGAAGCAGTGATATTCTGTCGTCTGTTACATTGTACATGTTTAACACAGCAGT
 D4 GACGGTTGAAGCAGTGATATTCTGTCGTCTGTTACATTGTACATGTTTAACACAGCAGT
 A4 GACGGTTGAAGCAGTGATATTCTGTCGTCTGTTACATTGTACATGTTTAACACAGCAGT

B4 AACTTTTT---CTAGTATATCATGTCGTGACCATCATGCCACGAAATCACGTCATTTCAG
 D4 AATTATTT---CTAGTATATCATGTCGTGACCATCATGCCACGAAATCACGTCATTTCAG
 A4 AATTTTGTGTTA---CTAGTATATCATGTCGTGACCATCATGCCACGAAATCA---TTCAG
 ** * * *****

TaDrAp2

TaDrAp2-Total-Fq: TCACAGTTGAAAGAAGAAGTGG 22bp; 41% GC; 51.1C

TaDrAp2-Total-Rq: CGTCCTCCTCTAATCTATGGT 21bp; 48% GC; 52.4C

TaDrAp2-Total-Rq (RevCom): ACCATAGATTAGAGGAGGACG

Amplicon size = 124 bp

TaDrAp2-A1-Fq: SCAAAAGAAGGAAACATGGTGAG 23bp; 43% GC; 53.5C

TaDrAp2-A1-Rq: TGGCATTGCTCAAAGGGGTG 20bp; 55% GC; 55.8C

TaDrAp2-A1-Rq (RevCom): CACCCCTTTGAGCAATGCCA

Amplicon size = 267 bp

TaDrAp2-B1-Fq: GAAGAATGATGTGACTCTAGTTTG 24bp; 38% GC; 52.3C

TaDrAp2-B1-Rq: AGCAACCATGATTTACAACCGGA 23bp; 43% GC; 53.5C

TaDrAp2-B1-Rq (RevCom): TCCGGTTGTAAATCATGGTTGCT

Amplicon size = 253 bp

TaDrAp2-D1-Fq: AGTCCAGCCTTCGGCTCCT 19bp; 63% GC; 55.4C

TaDrAp2-D1-Rq: CTAAATCCACGCTAGAGTCACG 22bp; 50% GC; 54.8C

TaDrAp2-D1-Rq (RevCom): CGTGA CTAGCGTGGATTTAG

Amplicon size = 242 bp

CLUSTAL 2.1 multiple sequence alignment

```
A1      ATGAGGAAGAAGCTCGACACCCGCTTCCCCGCGCCTCGGATTAAGAAGATCATGCAAGCA
D1      ATGAGGAAGAAGCTCGACACCCGCTTCCCCGCGCCTCGGATTAAGAAGATCATGCAAGCA
B1      ATGAGGAAGAAGCTCGACACCCGCTTCCCCGCGCCTCGGATTAAGAAGATCATGCAAGCA
*****

A1      GATGAAGATGTCTGGCAAGATTGCTCTAGCTGTACCTGTTCTAGTTTCCAAAGCGTTGGAG
D1      GATGAAGATGTCTGGCAAGATTGCTCTAGCA GTACCTGTTCTAGTTTCCAAAGCGTTGGAG
B1      GATGAAGATGTCTGGCAAGATTGCTCTAGCTGTACCTGTTCTAGTTTCCAAAGCGTTGGAG
*****

A1      CTATTTTGTCAAGACTTATGTGATAGGACATATAATATCACTGTTGAAAAAGGGGTCAAA
D1      CTATTTTGTCAAGACTTATGTGATAGGACATATAATATCACTGTTGAAAAAGGGGTCAAA
B1      CTATTTTGTCAAGACTTATGCGATAGGACATATAACATCACTGTTGAAAAAGGGGTCAAA
*****

A1      ACAGTGAGTTCATCACATCTGAAACAGTGCATTCATAGTTACGATGTGTATGATTTTTTG
D1      ACAGTGAGTTCATCACATCTGAAACAGTGCATTCATAGTTACGATGTGTATGATTTTTTG
B1      ACAGTGAGTTCATCACATCTGAAACAGTGCATTCATAGTTACGATGTGTATGATTTTTTG
*****

A1      AAGAACGTTGCCAGCAAAGTTCCAGATTTGGGTGCACCTGATTCTAGTGTTGATGATAAG
D1      AAGAACGTAGCCAGCAAAGTTCCAGATTTGGGTGCACCTGATTCTAGTGTTGATGATAAA
B1      AAGAACGTTTCTAGCAAAGTTCCAGATTTGGGTCCACCTGATTCTAGTGTTGATGATAAG
*****

A1      CTTGSCAAAAGAAGGAAACATGGTGAGGATGAAAGCGAGGAGGAATCGAAGCGGACAAGA
D1      CTTGGCAAAAGAAGGAAACATGGTGAAAGATGAAAGCGAGGAGGAATCGAAGCGGACAAGA
B1      CTTGGCAAAAGAAGGAAACATGGTGAAAGATGAAAGCGAGGAGGAATCGAAGCGGACAAGA
*****

A1      AATGAGGCAGCATGCCACACAAGCAACGGCAGAGGGCGTGGGAGGGGACGTGGGAGAGGT
D1      AATGAGGCAGCATGCCACACAAGCAACGGCAGAGGGCGGGGAGGGGACGTGGGAGAGGT
B1      AATGAGGCAGCATGCCACACAAGCAACGGCAGAGGGCGTGGGAGGGGACGTGGGAGAGGT
*****
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A1 CGCGGTGCTGGGCGTGGAGCTGAGAGGGAGATTGAACACCATGAATTAGGTTGTGCCCAA
D1 CGCCGTGCTGGGCGTGGAGCTGAGAGGGAGATTGAACACCATGAATTAGGTTGTGCCCAA
B1 CGCCGTGCTGGGCGTGGAGCTGAGAGGGAGATTGAACACCATGAATTAGGTTGTGCCCAA

A1 TTTAGCAAACCAGGCCACCTGAAGGTAGAGATTGGAGACGGGGTTTGTGGACACAAGTGAA
D1 TTTAGCAAACCAGGCCACCTGAAGGTAGAGATTGGAGACGTTGTTCTGGACACAAGTGAA
B1 TTTAGCAAACCAGGCCACCTGAAGGTAGAGATTGGAGACGTTGTTCTGGACACAAGTGAA
***** *** *****

A1 ACCAAAGAGCACAACCCCTTTGAGCAATGCCA GGCCTCCTTAAGGAACATTGACTTGAAC
D1 ACCAAAGAGCATACCCCTTTGAGCAATGCCAGGGCCTCCTTAAGGAACATTGACTTGAAC
B1 ACCAAAGAGCATACCCCTTTGAGCAATGCCAGGGCCTCCTTAAGGAACATTGACTTGAAC

A1 TTAGATCTTGCTGACTACGAGGAGGATA CAGTGGCGCCGCAAGTCCAGCCTTC-----
D1 TTAGATCTTGCTGACTACGAGGAGGATAC ----- GCCGCA AGTCCAGCCTTG GCTCCT
B1 TTAGATCTTGCTGACTACGAGGAGGATA CAGTGGCGCCGCAAGTCCAGCCTTC-----
***** *

A1 --AGCTCCTGTGGTGACCGTGGCGCCGCAAGTCCAGACTTCAGGACCATCGGTTTCACAG
D1 TCAGCTCCTGTGGTGACCGTGGCACCGCAAGTCCAGACTTCAGGACCGTCGGTTTCACAG
B1 --AGCTCCTGTGGTGACCGTGGCACCGCAAGTCCAGACTTCAGGACCATCGGTTTCACAG
***** *****

A1 TTGAAAGAAGAAGTGGCGACCAAGGATTTCTGGGCTGGCAAATGCCTGAGATGAACAAG
D1 TTGAAAGAAGAAGTGGAGACCAAGGATTTCTGGGCTGGCAAATGCCTGAGATGAACAAG
B1 TTGAAAGAAGAAGTGGAGACCAAGGATTTCTGGGCTGGCAAATGCCTGAGATGAACAAG

A1 ATGGCCATGGACCCGGTGCAGTTTTGCGCTGTCGTCAAAACCATAGATTAGAGGAGGACGAA
D1 ATGGCCATGGACCCGGTGCAGTTTTGCGCTGTCGTCAAAACCATAGATTAGAGGAGGACGAA
B1 ATGGCCATGGACCCGGTGCAGTTTTGCGTTGTCGTCAAAACCATAGATTAGAGGAGGACGAA

A1 GACTATGACAATGAAGAA TGATGTGACTCTAGCGTGGATTTAGTTTGAGAAGCTGATAGG
D1 GACTATGACAATGAAGAA TGACTGTGACTCTAGCGTGGATTTAGTTTGAGAAGCTGATAGG
B1 GACTATGACAAT GAAGAA TGATGTGACTC ----- TAGTTTTGAGAAGCTGATAGG
***** *

A1 TAGACATGACATGATGTACATCCTAGCAGGCCCAGCTTGACAATGTAGTAGCAATTCTCT
D1 TAGACATGACATGATGTACATCCTAGCAGGCCCAGCTTGACAATGTAGTAGCAATTCTCT
B1 TAGACATGACATGATGTACATCCTAGCAGGCCAAGCTTGACAATGTAGTAGCAATTCTCT

A1 TGTAGTATGTGTACCCGCAGATGCTGCAGAAGTAATTTAGGATGTGACATATGTTGATTG
D1 TGTAGTATGTGTACCCGCAGATGCTGCAGAAGTGATTTAGGATGTGACATATGTTGATTG
B1 TGTAGTATGTGTACTGGCAGATGCTGCAGAAGTAATTTAGGATGTGACATATGTTGATTG

A1 CTCAATAGCCAGTAGTAGCTAGTATCTTGTTGTAGCAACTATATAGTGTAGCGACTATATA
D1 CTCAATAGCCAGTAGTAGCTAGTATTTTGTGTAGCAACTATATAGTGTAGCAACTATATA
B1 CTCAATAGCCAGTAGTAGCTAGTATTTTGTGTAGCAACTATATAGTGTAGCAACTATATA

A1 ACTAGACA GTTTCGCCGGTTGTAAATCATGGTTGCTTTTAGATCAAATGCTATGTCATAA
D1 ACTAGACAGTTTCGCCGGTTGTAAATCATGGTTGCTTTTAGATCAAATGCTATGTCATAA
B1 ACTAGACAGGTTCTDCGGTTGTAAATCATGGTTGCTTTTAGATCAAATGCTATGTCATAA
