

Figure S3: 5'ETS variants identified in Brassicaceae Lineage I, Clade A, Camelinae and Brassicaceae Lineage II, Clade B.

(A) Fasta sequences of 5'ETS variants

Brassicaceae Lineage I, Clade A, Camelinae

AtVARA and AtVARB stands for the two variants known in *Arabidopsis thaliana*.

Ah1 and Ah2 are two independent cloned sequences for *Arabidopsis halleri*.

Al1-3 are two independent cloned sequences for *Arabidopsis lyrata*.

Ap1-4 are four independent cloned sequences for *Arabidopsis pedemontana*.

Ac1 is supported by two independent clones whereas Ac2 sequence was only cloned once for *Arabidopsis cebennensis*.

Brassicaceae Lineage II, Clade B

Bo was only cloned once and shared 100% sequence identity with the published sequence for *Brassica oleracea* [25].

(B) Multiple Sequence Comparison by Log- Expectation (MUSCLE) alignments of 5'ETS variants grouping them in an alignment by length and whether they contain or not an insertion splitting away the conserved U3 snoRNP binding site A¹²³B from the primary processing site P. There is no insertion for *Brassica oleracea* (Bo) and *Arabidopsis cebennensis* (Ac2).

(A) Fasta sequences of 5'ETS variants

Brassicaceae Lineage I, Clade A, Camelinae

>At_VARA

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CTTTTCCGGGCACCTTTTCCGGCGATCGGTTTTGTTGCCTTTTTCCGAGTTTTCTCAGCAGTTCTCGGACAAAACTGCTG
AATCGTCGAGGAGAATGGGCTTGCTTGCCTGGGCTGCCATTAGTTCTTCGAGGCGTTAGGGTGGCGGCGGTATAAAAGTG
TCGGAGTTTTTTCAGCAGTTCTCGGACAAAAATTGCTGAGTGGCCGAGAAGAATGGGCGTGTCATGCGTGGGCTGACATG
GATTCTTCGAGGCCTAGGGGTGGCGGTATATAACTTGTTTCGCATGATATTACCGAGATGTCCCCACGGGCATCTTTTCAC
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CGGCCAAGGGTGATGAACGAAATGTGAACCTTGCTCGCCTAGGTTGGATGGGCGTGCTTCGTTGGAAAGCATGGATCC
GCCTAGGCTGTCCCGAGTGTGAGCGAGGTGTGAGTGTGCGCCATGGGCATCGACACCTTGCGGCTAGGAAGTGAACGAG
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TCCCGAAGTATCTCGCGCTTGACGGCTTTGGCTCGGATTGTCGCTCTTCTTTCTTCTTAGCCGAGTACTTCGGTAGAT
TAGTTGGAACGATTGATGATTTTGAGTTAATTGAACGTTCCGGCGTATGAGTGGTGATCGG
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>At_VARB

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CTTTTCCGGGCACCTTTTCCGGCGATCGGTTTTGTTGCCTTTTTCCGAGTTTTCTCAGCAGTTCTCGGACAAAACTGCTG
AATCGTCGAGGAGAATGGGCTTGCTTGCCTGGGCTGCCATTAGTTCTTCGAGGCGTTAGGGTGGCGGCGGTATAAAAGT
GTCGGAGTTTTTTCAGCAGTTCTCGGACAAAAATTGCTGAGTGGCCGAGAAGAATGGGCGTGTCATGCGTGGGCTGACAT
GGATTCTTCGAGGCCTAGGGGTGGCGGTATATAACTTGTTTCGCATGATATTACCGAGATGTCCCCACGGGCATCTTTTCA
CCTCGTCGCCGAAGAGAATGGGCGTGTCATGGCATGGGCTGACATGGATTCTCCTAGGCCGTTTGGGTGGCGGTATAGTC
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AGCATGGATCCGCCTAGGCTGTCCCGAGTGTGAGCGAGGTGTGAGTGTGCGCCATGGGCATCGACACCTTGCGGCTAGGA
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TCCGCCTAGGCTGACCCGAAGGTATCTCGCGCTTGACGGCTTTGGCTCGGATTGTCGCTCTTCTTTCTTCTTAGCCGA
GTACTTCGGTAGATTAGTTGGAACGATTGATGATTTTGAGTTAATTGAACGTTCCGGCGTATGAGTGGTGATCGG
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>Ah1

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TACCGAGATGTCCCCACGGGCATCGTTTCACTCCGTCGCCGAAGAGAATGGGCGTGTCATGACATGGGCTGACATGGATT
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GATCGG

>Ah2

CTTTTCCGGGCACCTTTTCCGGCGATCGGTTTTGTGCGAGTTTTCCGGCATTCTCGGACAAAAATCGCTGAGTGGTCGCG
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GATCGG

>Al1

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>Al2

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>Al3

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G

>Ap1

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ATGAGTGGTGATCGG

>Ap2

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ATGAGTGGTGATCGG

>Ap3

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ATGAGTGGTGATCGG

>Ap4

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TCGGAGTTGTCTAGTTTACCTTTTGCGGATGTTTTTGGCAACCATCTTTTCGATGGGAAGTGGATATCGGAAGTCAGTCTT
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CGTCTTCTCTCTTCTCAGCCGAATATTTTCGGAGGAGTCGGGGAACGATTGATGTTTTTGGGTCAATTGAACGTTTCGGCGT
ATGAGTGGTGATCGG

>Ac1

CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGGTTCGAGTTTTTCCGAGTTTTTTTCAGCAGTTCTCGGACAAAAATTGCTG
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GACATGGATTCTCCTAGGCCGTGGGTGGCTGTATATTCGGGAATGCGCACGAAATACCGAGATGTCCCATGGGCATCG
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CGTATGAGTGGTGATCGG

>Ac2

CTTTTCCGGGCACTTTTCCGGTGGACATTTTGGCCCTAAATCAAATTTTCGCGCTTGTGTGGTCTTGGCCTGGTTTCA
TCCGTCTTCCAGTGCTCTTTTGATTACATCTCGAGAGTGTTGGAAAGATTGATGTTAGCGGGCAATGAACGTTTCGGC
GTATGAGTGGTGATCGA

Brassicaceae Lineage II, Clade B

>Bo

CTTTTCCGGGCACTTTTCCGGCGACTTTTCCGGTGGACATTTTGGCCCTAAATCAAATTTTCGCGCTTGTGTGGTCTTGGCCTGGTTTCA
GCCCTGGTTTTCATCCGTCTTCCAGTGCTCTTTTGATTACATCTCGAGAGTGTTGGAAAGATTGATGTTAGCGGGCAATGAACGTTTCGGC
TTGAACGTGCGGCGTATGAGTGGTGATCGG

(B) MUSCLE alignment of 5'ETS variants

Arabidopsis genus variants with the exception of the *A. cebennensis* insertion free Ac2 variant

	A2	A3	B
At_VARA	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTTGCCTTTTCCGAGTTTTCTCAGCAG		
At_VARB	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTTGCCTTTTCCGAGTTTTCTCAGCAG		
Ac1	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTGGTCGC-----AGTTT-----		
Ah1	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTCGC-----AGTTT-----		
Ah2	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTCGC-----AGTTT-----		
Al1	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTTGC-----AGTTT-----		
Al2	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTTGC-----AGTTT-----		
Al3	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTTGC-----AGTTT-----		
Ap1	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTCGC-----AGTTT-----		
Ap2	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTGTC-----AGTTT-----		
Ap3	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTCGC-----AGTTT-----		
Ap4	CTTTTCCGGGCACTTTTCCGGCGATCGGTTTTGTGTC-----AGTTT-----		
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D1a Gruendler

At_VARA	TTCTCGGACAAAACTGCTGAATCGTCGAGGAGAATGGGCTTG-CTTGCCTGGGCTGCCA
At_VARB	TTCTCGGACAAAACTGCTGAATCGTCGAGGAGAATGGGCTTGCTTGCCTGGGCTGCCA
Ac1	-----
Ah1	-----
Ah2	-----
Al1	-----
Al2	-----
Al3	-----
Ap1	-----
Ap2	-----
Ap3	-----
Ap4	-----

At_VARA	TTAGTTCTTCGAGGCGTTAGGGTGGCGGCGGTATAAAAGTGTCGGAGTTTTTTTCAGCAGT
At_VARB	TTAGTTCTTCGAGGCGTTAGGGTGGCGGCGGTATAAAAGTGTCGGAGTTTTTTTCAGCAGT
Ac1	-----TCCGAGTTTTTTTCAGCAGT
Ah1	-----TCGG-----GCATT
Ah2	-----TCGG-----GCATT
Al1	-----TCCGAGTTTTTTTCAGCAGT
Al2	-----TT-GAGTTTTTTTCAGCAGT
Al3	-----TCCGAGTTTTTTTCAGCAGT
Ap1	-----TCCGAGTTTTTTTCAGCAGT
Ap2	-----TCCGAGTTTTTTTCAGCAGT
Ap3	-----TCCGAGTTTTTTTCAGCAGT
Ap4	-----TCCGAGTTTTTTTCAGCAGT
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D1b Gruendler

At_VARA	TCTCGGACAAAAATTGCTGAGTGGCCGAGAAGAATGGGCGTGTCATGCGTGGGCTGACAT
At_VARB	TCTCGGACAAAAATTGCTGAGTGGCCGAGAAGAATGGGCGTGTCATGCGTGGGCTGACAT
Ac1	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Ah1	TCTCGGACAAAAATCGCTGAGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Ah2	TCTCGGACAAAAATCGCTGAGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Al1	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Al2	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Al3	TCTCGGACAAAAATTGCTGAGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Ap1	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Ap2	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Ap3	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT
Ap4	TCTCGGACAAAAATTGCTGTGTGGTTCGCGGAGAATGGGCGTGTCATGCGTGGGATGACAT

At_VARA	GGATTCTTCGAGGCCTAGGGGTGGCGGTATATAACT-TGTTTCGCATGATAT	TACCGAGAT
At_VARB	GGATTCTTCGAGGCCTAGGGGTGGCGGTATATAACT-TGTTTCGCATGATAT	TACCGAGAT
Ac1	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGAGCGCATGGTA-	TACCGAGAT
Ah1	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGATCGCACAAATA-	TACCGAGAT
Ah2	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGATCGCACAAATA-	TACCGAGAT
Al1	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATTGGG-AAAGCGCATTGTA-	TACCGAGAT
Al2	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATTGGG-AAAGCGCATTGTA-	TACCGAGAT
Al3	GGATTCTTCGAGACCTTGGGGTGGCGGTATATAACTCTCCACGCATGGTA-	TACCGAGAT
Ap1	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGAGCGCATGGTA-	TACCGAGAT
Ap2	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGAGCGCATGGTA-	TACCGAGAT
Ap3	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGAGCGCATGGTA-	TACCGAGAT
Ap4	GGATTCTTCGAGGCCTTGGGGTGGCGGTATATAAGG-AGAGCGCATGGTA-	TACCGAGAT

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D2a Gruendler

At_VARA	GTCCCCACGGGCATCTTTTCACTCGTCGCCGAAGAGAATGGGCGTGTCATGGCATGGGC
At_VARB	GTCCCCACGGGCATCTTTTCACTCGTCGCCGAAGAGAATGGGCGTGTCATGGCATGGGC
Ac1	GTCCCCACGGGCATCGTTTCACTCCCTTGGCGAAGAGAATGGGCGTGTCATGACATGGGC
Ah1	GTCCCCACGGGCATCGTTTCACTCCCTCGTCGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Ah2	GTCCCCACGGGCATCGTTTCACTCCCTCGTCGCCGAAGAGAATGGTCTGTCATGACATGGGC
Al1	GTCCCCACGGGCATCGTTTCACTCCCTCGTCGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Al2	GTCCCCACGGGCATCGTTTCACTCCCTCGTCGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Al3	GTCCCCACGGGCATCGTTTCACTCCCTCGTCGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Ap1	GTCTCCACGGGCATCGTTTCACTCCGTTGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Ap2	GTCTCCACGGGCATCGTTTCACTCCGTTGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Ap3	GTCTCCACGGGCATCGTTTCACTCCGTTGCCGAAGAGAATGGGCGTGTCATGACATGGGC
Ap4	GTCTCCACGGGCATCGTTTCACTCCGTTGCCGAAGATTAATGGGCGTGTCATGACATGGGC

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D12 Gruendler

At_VARA	TGACATGGATTCTCCTAGGCCGTTTGGGTGGCGGTATAGTC--GTCTTGCGCACGAAATA
At_VARB	TGACATGGATTCTCCTAGGCCGTTTGGGTGGCGGTATAGTC--GTCTTGCGCACGAAATA
Ac1	TGACATGGATTCTCCTAGGCCG--TGGGTGGCTGTATATTCGGGGAATGCGCACGAAATA
Ah1	TGACATGGATTCTCCAAGGCCG--TGGGTGGCGGTACATTC--GGAATGCACACGAAATA
Ah2	TGACATGGATTCTCCAAGGCCG--TGGGTGGTGGTATATTC--GGAATGCACACGAAATA
Al1	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCCCGAAATA
Al2	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCCCGAAATA
Al3	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCCCGAAATA
Ap1	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCACGATATA
Ap2	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCACGATATA
Ap3	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCACGATATA
Ap4	TGACATGGATTCTCCTAGGCCG--TGGGTGGCGGTATATTC--GGAATGCGCACGATATA

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D2b Gruendler **C3 repeat** 28

At_VARA	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	CG
At_VARB	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ac1	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ah1	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ah2	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Al1	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Al2	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Al3	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ap1	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ap2	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ap3	CCGAGTTGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG
Ap4	CCGAGATGTCCCCATGGGCATCGATTCCACC	CGCCTAGGTTGGATGGGCGTGCTTCGTT	TG

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	C3 repeat	C1 repeat
At_VARA	GAAAGCATGGATCCGCCTAGGCTGTCCCAGTGTGAGC	GAGGTGTGAGTGTGCGCCATGG
At_VARB	GAAAGCATGGATCCGCCTAGGCTGTCCCAGTGTGAGC	GAGGTGTGAGTGTGCGCCATGG
Ac1	GAAAGCATGGATCTGCCTAGGCTGTCCCAGGG	TGAGCAAGGTGTGAGTGTGCGCCATGG
Ah1	GAAAGCATGGATCCGCCTAGGCTGTCCCAGGGATGAGCAAGGTGTGAGTGTGCGCCATGG	
Ah2	GAAAGCATGGATCCGCCTAGGCTGTCCCAGGGATGAGCAAGGTGTGAGTGTGCGCCATGG	
Al1	GAAAGCATGGATCCGCCTAGGCTGTCCCAGT	TGAGCAAGGTGTGAGTGTGCGCCATGG
Al2	GAAAGCATGGATCCGCCTAGGCTGTCCCAGT	TGAGCAAGGTGTGAGTGTGCGCCATGG
Al3	GAAAGCATGGATCCGCCTAGGCTGTCCCAGT	TGAGCAAGGTGTGAGTGTGCGCCATGG
Ap1	GAAAGCATGGATCTGCCTAGGCTGTCCCAGGG	TGAGCAAGGTGTGAGTGTGCGT
Ap2	GAAAGCATGGATCTGCCTAGGCTGTCCCAGGG	TGAGCAAGGTGTGAGTGTGCGT
Ap3	GAAAGCATGGATCTGCCTAGGCTGTCCCAGGG	TGAGCAAGGTGTGAGTGTGCGT
Ap4	GAAAGCATGGATCTGCCTAGGCTGTCCCAGGG	TGAGCAAGGTGTGAGTGTGCGT
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	130
At_VARA	GCATCGACACCTTGCGGCTAGGAACCTGGAACGAGACGGGTGGCAAAGATTTTCGAGTAGCA
At_VARB	GCATCGACACCTTGCGGCTAGGAACCTGGAACGAGACGGGTAGCAAAGATTTTCGAGTAGCA
Ac1	GCATCGACACCTTGCGTCTTTGAACGGAACGAA--GGTAAGCAGAGGATT-----G-A
Ah1	GCATCGACACCTTGCGGCTTGAACGGAACGGA--GGTAAGCACAGGATT-----GTA
Ah2	GCATCGACACCTTGCGGCTTGAACGGAACGGA--GGTAAGCACAGGATT-----GTA
Al1	GCATCGACACCTTGCGGCTTTGAACGAAACGGA--GGTACGCGCAGCTGT-----TA
Al2	GCATCGACACCTTGCGGCTTTGAACGAAACGGA--GGTACGCGCAGCTGT-----TA
Al3	GCATCGACACCTTGCGGCTTTGAACGAAACGGA--GGTACGCGCAGCTGT-----TA
Ap1	GCATCGACACCTTGCGTCTTTGAACGGAAGCGAA--GGTAAGCGGATGATT-----G-A
Ap2	GCATCGACACCTTGCGTCTTTGAACGGAAGCGAA--GGTAAGCGGATGATT-----G-A
Ap3	GCATCGACACCTTGCGTCTTTGAACGGAAGCGAA--GGTAAGCGGATGATT-----G-A
Ap4	GCATCGACACCTTGCGTCTTTGAACGGAAGCGAA--GGTAAGCGGATGATT-----G-A

At_VARA	CTTCATAC	TACCGTGGGTTTTTTAAACCTTCC--GAGTTTTGTTGATGTTATTCCGAGAA
At_VARB	CTTCATAC	TACCGTGGGTTTTTTAAACCTTCCCTAGTTTTGTTGATGTTATTCCGAGAA
Ac1	CGACGAGC-----	GGGTCTCTCGGTGTTT--TCTAGTTTACCTTTAGC-----
Ah1	CGCCGAGC-----	GGGTGTCTTGGAGTCA--TCCAGTTTACCTTTTGC-----
Ah2	CGCCGAGC-----	GGGTGTCTTGGAGTCA--TCCAGTTTACCTTTTGC-----
Al1	CGTCGTGCA----	GGGTTTTCTCGGCGTCACTTCTAG--CGGCTTTTGC-----
Al2	CGTCGTGCA----	GGGTTTTCTCGGCGTCACTTCTAG--CGGCTTTTGC-----
Al3	CGTCGTGCA----	GGGTTTTCTCGGCGTCACTTCTAG--CGGCTTTTGC-----
Ap1	CGACGAGC-----	GGGTCTCTCGGAGTTG--TCTAGTTTACCTTTTGC-----
Ap2	CGACGAGC-----	GGGTCTCTCGGAGTTG--TCTAGTTTACCTTTTGC-----
Ap3	CGACGAGC-----	GGGTCTCTCGGAGTTG--TCTAGTTTACCTTTTGC-----
Ap4	CGACGAGC-----	GGGTCTCTCGGAGTTG--TCTAGTTTACCTTTTGC-----
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At_VARA	TTAGCAAACCGTAACGAAGATGTTT	TTGGCAACCATCTTTTGATGGGAGTCCGGCTGTT
At_VARB	TTAGCAAACCGTAACGAAGATGTTT	TTGGCAACCATCTTTTGATGGGAGTCCGGCTGTT
Ac1	-----	GGATGTTCTTTGGCAACCATCTTTTCGATGGGAA--GTGGATA--T
Ah1	-----	GGATGTTT--ATGGCAACCATCTTTTGATGGGAA--GTGGATA--T
Ah2	-----	GGATGTTT--ATGGCAACCATCTTTTGATGGGAA--GTGGATA--T
Al1	-----	GGATGTTT--TTGGCAACCATCTTTTGATGGGGAAGTGGATA--T
Al2	-----	GGATGTTT--TTGGCAACCATCTTTTGATGGGGAAGTGGATA--T
Al3	-----	GGATGTTT--TTGGCAACCATCTTTTGATGGGGAAGTGGATA--T
Ap1	-----	GGATGTTT--TTGGCAACCATCTTTTCGATGGGAA--GTGGATA--T
Ap2	-----	GGATGTTT--TTGGGAACCATCTTTTCGATGGGAA--GTGGATA--T
Ap3	-----	GGATGTTT--TTGGCAACCATCTTTTCGATGGGAA--GTGGATA--T
Ap4	-----	GGATGTTT--TTGGCAACCATCTTTTCGATGGGAA--GTGGATA--T
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At_VARA	CGATAGCCGGCC-----AAGG	GTGATGAACGAAATGTGAACCCTTGTCTCGCCTAG
At_VARB	CGAAAGCCGGCC-----AAGG	GTGATGAACGAAATGTGAACCCTTGTCTC-----
Ac1	CGGAAGTCAGTCTTTGGACCG	AGAAGTGAC--ACGAAGT-----ACCCAG
Ah1	CGGAAGTCAGTCTTT-GACCGT	GAAGTGCC--ATGAAGT-----TCCCAG
Ah2	CGGAAGTCAGTCTTT-GACCGT	GAAGTGCC--ATGAAGT-----TCCCAG
Al1	CGG-----CT-GGT-----	AGTGAC--ACGAGGC-----TCCC-G
Al2	CGG-----CT-GGT-----	AGTGAC--ACGAGGC-----TCCC-G
Al3	CGG-----CT-GGT-----	AGTGAC--ACGAGGC-----TCCC-G
Ap1	CGGAAGTCAGTCTTTGGACCG	AGAAGTTAC--ACGAAGT-----ACCCAG
Ap2	CGGAAGTCAGTCTTTGGACCG	AGAAGTTAC--ACGAAGT-----ACCCAG
Ap3	CGGAAGTCAGTCTTTGGACCG	AGAAGTTAC--ACGAAGT-----ACCCAG
Ap4	CGGAAGTCAGTCTTTGGACCG	AGAAGTTAC--ACGAAGT-----ACCCAG
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		C3 repeat
At_VARA	GTTGGATGGGCGTGCTT	CGTTGGAAAGCATGGATCCGCCTAGGCTGTCCCAGTGTGAGC
At_VARB	-----	-----
Ac1	GCTTTGTGTGTAACCTCCG	-----
Ah1	GCTTTGTGTATAACTTCCG	-----
Ah2	GCTTTGTGTATAACTTCCG	-----
Al1	GTCTTGTGTGTATCCTTCG	-----
Al2	GTCTTGTGTGTATCCTTCG	-----
Al3	GTCTTGTGTGTATCCTTCG	-----
Ap1	GCTTTGTGCGTAACCTCCG	-----
Ap2	GCTTTGTGCGTAACCTCCG	-----
Ap3	GCTTTGTGCGTAACCTCCG	-----
Ap4	GCTTTGTGCGTAACCTCCG	-----
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		C2 repeat
At_VARA	GAGGTGTGAGTGTGCGCCCATGGGCATCGACACCTTGCGGCTAGGAACTGGAACGAGACGG	
At_VARB	-----	
Ac1	-----	CAC--TGCGGCTACGA-----
Ah1	-----	GAC--TGCGGCTTCGA-----
Ah2	-----	GAC--TGCGGCTTCGA-----
Al1	-----	CAC--TGCGGCTCCGA-----
Al2	-----	CAC--TGCGGCTCCGA-----
Al3	-----	CAC--TGCGGCTCCGA-----
Ap1	-----	CAC--TGCGGCTACGA-----
Ap2	-----	CAC--TGCGGCTACGA-----
Ap3	-----	CAC--TGCGGCTACGA-----
Ap4	-----	CAC--TGCGGCTACGA-----

At_VARA	GTAGCAAAGATTTTCGAGTAGCACTTCATACTACCGTGGGTTTTTTAAACCTTCCTAGTTT
At_VARB	-----
Ac1	-----
Ah1	-----
Ah2	-----
Al1	-----
Al2	-----
Al3	-----
Ap1	-----
Ap2	-----
Ap3	-----
Ap4	-----

At_VARA	TGTTGATGTTATTCCGAGAATTAGCAAACCGTAACGAAGATGTTCTTGGAACCATCTTT
At_VARB	-----
Ac1	-----
Ah1	-----
Ah2	-----
Al1	-----
Al2	-----
Al3	-----
Ap1	-----
Ap2	-----
Ap3	-----
Ap4	-----

At_VARA	TGATGGGAGTCCGGCTGTTTCGAAAGCCGGCCAAGGGTGATGAACGAAATGTGAACCCTTG
At_VARB	-----
Ac1	-----TATTCGCA-----
Ah1	-----TATTCGCA-----
Ah2	-----TATTCGCA-----
Al1	-----TATTCGCA-----
Al2	-----TATTCGCA-----
Al3	-----TATTCGCA-----
Ap1	-----TATTCGCA-----
Ap2	-----TATTCGCA-----
Ap3	-----TATTCGCA-----
Ap4	-----TATTCGCA-----

		C3 repeat	
At_VARA	TCTC	GCCTAGGTTGGATGGGCGTGCTTCGTTGGAAAGCATGGATCCGCCTAGGCTGTCC	CC
At_VARB	----	GCCTAGGTTGGATGGGCGTGCTTCGTTGGAAAGCATGGATCCGCCTAGGCTGTACCC	
Ac1	----	GCCTAGGTTGGATGGGCGTGC-----GAAAGCATGGATCCGCCTAGGCTGTCTT	
Ah1	----	GCCTAGGTTGGATGGGCGTGC-----GAAAGCATAGATCCGCCTAGGCTGTCC	
Ah2	----	GCCTAGGTTGGATGGGCGTGC-----GAAAGCATAGATCCGCCTAGGCTGTCC	
Al1	----	GCCTAGGTTGGATGGGCGTGC-----GAAAGCATGGATCTGCCTAGGCTGTCTC	
Al2	----	GCCTAGGTTGGATGGGCGTGC-----GAAAGCATGGATCTGCCTAGGCTGTCTC	
Al3	----	GCCTAGGTTGGATGGGCGTGC-----GAAAGCATGGATCTGCCTAGGCTGTCTC	
Ap1	----	GCCTAGGTTGGATGGGCGTGC-----TAAAGCATGGATCCGCCTAGGCTGTCTT	
Ap2	----	GCCTAGGTTGGATGGGCGTGC-----TAAAGCATGGATCCGCCTAGGCTGTCTC	
Ap3	----	GCCTAGGTTGGATGGGCGTGC-----TAAAGCATGGATCCGCCTTGGCTGTCTT	
Ap4	----	GCCTAGGTTGGATGGGCGTGC-----TAAAGCATGGATCCGCCTAGGCTGTCTT	
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		P-site	
At_VARA	GA-AGT	ATCTCGCGCTTGACGGCTTTGGCTCGGATTCGTCCGTCTTCTTTCTTCTTAGC	
At_VARB	GAAGGT	ATCTCGCGCTTGACGGCTTTGGCTCGGATTCGTCCGTCTTCTTTCTTCTTAGC	
Ac1	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Ah1	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Ah2	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Al1	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Al2	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Al3	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Ap1	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Ap2	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Ap3	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
Ap4	GACGGTTTTT	TCGCGCTTGTCGGCTTTGGCTTGGATTCGTCCGTCTTCTCTCTTCTCAGC	
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