

**Figure S2:** Fasta sequences and multiple alignment of 3'ETS variants. **(A)** Fasta sequences of 3'ETS variants. *VAR1* is a consensus sequence of five independent clones from this study and corresponds to *VAR1* type 1 published by Chandrasekhara *et al.* [17]. *VAR2-4* are sequences published by Pontvianne *et al.* [20] while *VAR5* was cloned twice independently in this study. *VAR6* and *VAR7* are new variants identified *in natura* from this study. **(B)** Multiple Sequence Comparison by Log- Expectation (MUSCLE) alignment of *VAR6* and *VAR7* new variants compared to known *VAR1-5* described in Col-0 [17,20,26]. The color codes for R repeats described in Abou-Ellail *et al.* [26] is the following : R1a, b or c in yellow, R2a in a lighter blue than R2b, R3a in a lighter green than R3b, R4a in a lighter red than R4b.

**(A)** Fasta sequences of 3'ETS variants.

>*VAR1*

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GACAGACTTGTCCAAAACGCCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGA
GATAGACTTGTCCAAAAGAAACGGAAGAGAAAGCGTGGGGAGACGCTCACGAAGGT
GCATAGTGAGAAGAGTAAGTCAAGAGACAGACTTGTTTCGAAAAGAAACAGAAGAGAA
TGCTTGGGGTTACACTCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGACAGACT
TGTTTCGAAAAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAGATAGTTCTCA
AGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCATCAAATGATGGATGAAACACAAGGTA
GTTGTTGAAAAGTCAAACACTTGGTGATATGAACACAAACGTTCAATATGACAAACCCA
TGCCAAGTAAAGAGAAAATGAAAACCTGGTGATTGTTGCGGAAATCGTCCAGGATTCTCT
GACCAG
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>*VAR2*

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GACAGACTTGTCCAAAACGCCCACCGCGAAGGTGCATAGTGAGAAGAGTAAGTCAAGA
GACAGACTTGTTCGAAAAGAAACAGAAGAGAATGCTTGGGGTTACACTCACGAAGGTG
CATAGTGAGAAGAGTAAGTCAAGAGACAGACTTGTTTCGAAAAGAAACAAAAGAGAAT
GCTTGGGGGAGATAGAAGTGTGAGATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGA
ACTAGCATCAAATGATGGATGAAACACAAGGTAGTTGTTGAGAAGTCAAACACTTGGTG
ATATGAACACAAACGTTCAATATGACAAACCCATGCCAAGTAAAGAGAAAATGAAAAC
GGTGATTGTTGCGGAAATCGTCCAGGATTCTCTCGACCAG
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>*VAR3*

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GACAGACTTGTCCAAAACGCCCACCACGAAGGTGCATAGTGAGAAGAGTAGGTCAAGA
GATAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGT
GCATAGTGAGAAGAGTAGGTCAAGAGATAGACTTGTTCAAAAAGAAACAGAAGAGAAT
GCTTGGGGTTACACTCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGACAGACTT
GTTCAAAAAGAAACGAAAGAGAATGCTTGGGGGAGATAGAAGTGTGAGATAGTTCTCAA
GCTAAGAAAGTTGTAAAAGCTAAGAACTAGCAAGTAATCGTCCAGGATTCTCTCACCAG
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>*VAR4*

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GACAGACTTGTCCAGAACGCCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGA
GATAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGT
GCATAGTGAGAAGAGTAAGTCAAGAGATAGACTTGTTCAAAAAGAAACAGAAGAGAAT
GCTTGGGGTTACACTCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGATAGACTT
GTTCAAAAAGAAACAAAAGAGAATGCTTGGGGTTACACTCACGAAGGTGCATAGTGAG
AAGAGTAAGTCAAGAGACAGACTTGTTCAAAAAGAAACAAAAGAGAATGCTTGGGGA
GATAGAAGTGTGAGATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCAAG
TAATCGTCCAGGATTCTTCACCAG
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>*VAR5*

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GACAGACTTGTCCAAAACGCCCACCGCGAAGGTGCATAGTGAGAAGAGTAAGTCAAGA
GATAGACTTGTTCAAAAGAAACAGAAGAGAATGCTTGGGGTTACACTCACGAAGGTG
CATAGTGAGAAGAGTAAGTCAAGAGACAGACTTGTTCAAAAAGAAACAAAAGAGAAT
GCTTGGGGGAGATAGAAGTGTGAGATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGA
ACTAGCAAGTAATCGTCCAGGATTCTCTCGACCAG
```

>VAR6

GACAGACTTGTCCAAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGA  
GATAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGT  
GCATAGTGAGAAGAGTAAGTCAAGAGATAGACTTGTTCAAAAAGAAACAGAAGAGAAT  
GCTTGGGGTTACACTCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGACAGACTT  
GTTTCGAAAAGAAACAAAAGAGAATGCTTGGGGTTACACTCACGAAGGTGCATAGTGAG  
AAGAGTAAGTCAAGAGACAGACTTGTTCGAAAAGAAACAAAAGAGAATGCTTGGGGA  
GATAGAAGTGTGAGATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCATC  
AAATGATGGATGAAACACAAGGTAGTTGTTGAAAAGTCAAACACTTGGTGATATGAACA  
CAAACGTTCAATATGACAAACCCATGCCAAGTAAAGAGAAAAATGAAAAGTGGTGATTGT  
TGCGGAAATCGTCCAGGATTCCTCGACCAG

>VAR7

GACAGACTTGTCCAAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGA  
GATAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGT  
GCATAGTGAGAAGAGTAAGTCAAGAGATAGACTTGTAGAGAATGCTTGGGGTTACACTC  
ACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGACAGACTTGTTCAAAAAGAAACA  
AAAGAGAATGCTTGGGGAGATAGAAGTGTGAGATAGTTCTCAAGCTAAGAAAGTTGTA  
AAAGCTAAGAACTAGCAAGTAATCGTCCAGGATTCCTCGACCAG

**(B)** MULTiple Sequence Comparison by Log- Expectation (MUSCLE) alignment of VAR6 and VAR7 new variants compared to known VAR1-5 described in Col-0

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VAR1      GACAGACTTGTCCAAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGA
VAR2      GACAGACTTGTCCAAAACGCCAC-----
VAR3      GACAGACTTGTCCAAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAGTCAAGAGA
VAR4      GACAGACTTGTCCAGAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGA
VAR5      GACAGACTTGTCCAAAACGCCAC-----
VAR6      GACAGACTTGTCCAAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGA
VAR7      GACAGACTTGTCCAAAACGCCACCACGAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGA
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VAR1      TAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGTGCATA
VAR2      -----CGCGAAGGTGCATA
VAR3      TAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGTGCATA
VAR4      TAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGTGCATA
VAR5      -----CGCGAAGGTGCATA
VAR6      TAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGTGCATA
VAR7      TAGACTTGTCCAAAAGAAACGGAAGAGAAAGCTTGGGGAGACGCTCACGAAGGTGCATA
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VAR1      GTGAGAAGAGTAAGTCAAGAGACAGACTTGTTCGAAAAGAAACAGA-----
VAR2      GTGAGAAGAGTAAGTCAAGAGACAGACTTGTTCGAAAAGAAACAGA-----
VAR3      GTGAGAAGAGTAGGTCAAGAGATAGACTTGTTCAAAAGAAACAGA-----
VAR4      GTGAGAAGAGTAAGTCAAGAGATAGACTTGTTCAAAAGAAACAGAAGAGAATGCTTGGG
VAR5      GTGAGAAGAGTAAGTCAAGAGATAGACTTGTTCAAAAGAAACAGA-----
VAR6      GTGAGAAGAGTAAGTCAAGAGATAGACTTGTTCAAAAGAAACAGAAGAGAATGCTTGGG
VAR7      GTGAGAAGAGTAAGTCAAGAGATAGACTTGT-----
**      ***      **      *****      *****
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VAR1      -----
VAR2      -----
VAR3      -----
VAR4      GTTACACTCAGAAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGATAGACTTGTTCAAA
VAR5      -----
VAR6      GTTACACTCAGAAAGGTGCATAGTGAGAAGAGTAAGTCAAGAGACAGACTTGTTCGAAA
VAR7      -----
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VAR1 -----AGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
VAR2 -----AGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
VAR3 -----AGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
VAR4 GAAACAAAAGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
VAR5 -----AGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
VAR6 GAAACAAAAGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
VAR7 -----AGAGAATGCTTGGGGTTACACTCACG AAGGTGCATAGTGAGAAGAGTAAGTC  
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VAR1 AAGAGACAGACTTGTTCGAA AAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
VAR2 AAGAGACAGACTTGTTCGAA AAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
VAR3 AAGAGACAGACTTGTTCAAAA AAGAAACGAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
VAR4 AAGAGACAGACTTGTTCAAAA AAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
VAR5 AAGAGACAGACTTGTTCAAAA AAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
VAR6 AAGAGACAGACTTGTTCGAA AAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
VAR7 AAGAGACAGACTTGTTCAAAA AAGAAACAAAAGAGAATGCTTGGGGAGATAGAAGTGTGAG  
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VAR1 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCATCAAATGATGGATGAAA  
VAR2 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCATCAAATGATGGATGAAA  
VAR3 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCA-----  
VAR4 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCA-----  
VAR5 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCA-----  
VAR6 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCATCAAATGATGGATGAAA  
VAR7 ATAGTTCTCAAGCTAAGAAAGTTGTAAAAGCTAAGAACTAGCA-----  
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VAR1 CACAAGGTAGTTGTTGAAAAGTCAAACACTTGGTGATATGAACACAAACGTTCAATATGA  
VAR2 CACAAGGTAGTTGTTGAGAAGTCAAACACTTGGTGATATGAACACAAACGTTCAATATGA  
VAR3 -----  
VAR4 -----  
VAR5 -----  
VAR6 CACAAGGTAGTTGTTGAAAAGTCAAACACTTGGTGATATGAACACAAACGTTCAATATGA  
VAR7 -----

VAR1 CAAACCCATGCCAAGTAAAGAGAAAATGAAAACCTGGTGATTGTTGCGGAAATCGTCCAGG  
VAR2 CAAACCCATGCCAAGTAAAGAGAAAATGAAAACCTGGTGATTGTTGCGGAAATCGTCCAGG  
VAR3 -----AGTAATCGTCCAGG  
VAR4 -----AGTAATCGTCCAGG  
VAR5 -----AGTAATCGTCCAGG  
VAR6 CAAACCCATGCCAAGTAAAGAGAAAATGAAAACCTGGTGATTGTTGCGGAAATCGTCCAGG  
VAR7 -----AGTAATCGTCCAGG  
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VAR1 ATTCCTCGACCAG  
VAR2 ATTCCTCGACCAG  
VAR3 ATTCCTCCACCAG  
VAR4 ATTCCTTCACCAG  
VAR5 ATTCCTCGACCAG  
VAR6 ATTCCTCGACCAG  
VAR7 ATTCCTCGACCAG  
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