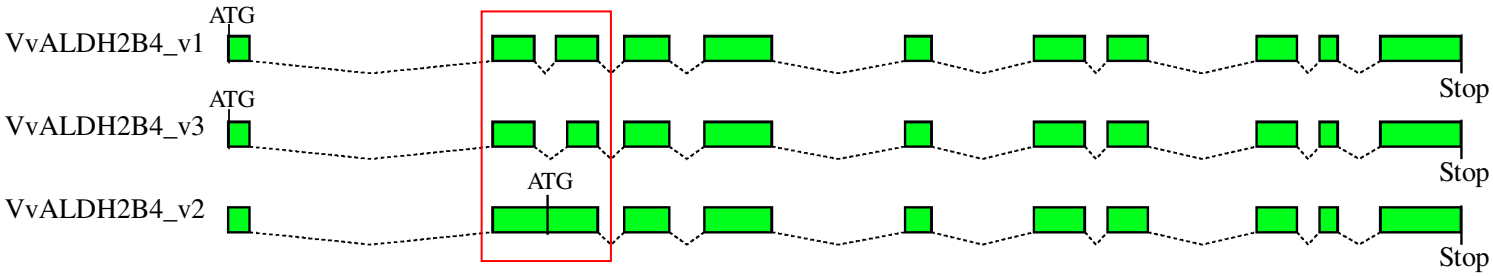
A



B

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VvALDH2B4_v1   ATGGCGGCTAGGAGGATCTCCTCGTTGCTCTCTCGTTCTCTCTCTGTCTCTTCTGCTTTTTCTCTTTCTCTAGGCAAAAA   80
VvALDH2B4_v3   ATGGCGGCTAGGAGGATCTCCTCGTTGCTCTCTCGTTCTCTCTCTGTCTCTTCTGCTTTTTCTCTTTCTCTAGGCAAAAA   80
VvALDH2B4_v2   ATGGCGGCTAGGAGGATCTCCTCGTTGCTCTCTCGTTCTCTCTCTGTCTCTTCTGCTTTTTCTCTTTCTCTAGGCAAAAA   80

VvALDH2B4_v1   TTTCAACAGAGGGAAAAGCATCCATCGCTTTAGCACTGCAGCAGCAGCAGCAGTTGAAGAACTCATCACTCCAACTGTTC   160
VvALDH2B4_v3   TTTCAACAGAGGGAAAAGCATCCATCGCTTTAGCACTGCAGCAGCAGCAGCAGTTGAAGAACTCATCACTCCAACTGTTC   160
VvALDH2B4_v2   TTTCAACAGAGGGAAAAGCATCCATCGCTTTAGCACTGCAGCAGCAGCAGCAGTTGAAGAACTCATCACTCCAACTGTTC   160

VvALDH2B4_v1   AGATAAATTACACTCAACTTCTAATTAATGGGCAATTTGTAGATGCAGCATCGG------------------------   214
VvALDH2B4_v3   AGATAAATTACACTCAACTTCTAATTAATGGGCAATTTGTAGATGCAGCATCGG------------------------   214
VvALDH2B4_v2   AGATAAATTACACTCAACTTCTAATTAATGGGCAATTTGTAGATGCAGCATCGGGTAATCATTTTTGTGTGGGCAATGTT   240

VvALDH2B4_v1   ------------------------------------------------GAAAAACATTCCCCACCTTTGACCCTCGCACG   246
VvALDH2B4_v3   ------------------------------------------------------------------------------   214
VvALDH2B4_v2   TCCATCATTAATGAATCATGTATGAAACCGATGTCGGTATCATTACAGGAAAAACATTCCCCACCTTTGACCCTCGCACG   320

VvALDH2B4_v1   GGAGAAGTGATTGCTAATGTTGCAGAAGGTGATGCAGAAGATATCAATCGGGCAGTGTCCGCTGCTCGAAAGGCGTTTGA   326
VvALDH2B4_v3   -------TGATTGCTAATGTTGCAGAAGGTGATGCAGAAGATATCAATCGGGCAGTGTCCGCTGCTCGAAAGGCGTTTGA   287
VvALDH2B4_v2   GGAGAAGTGATTGCTAATGTTGCAGAAGGTGATGCAGAAGATATCAATCGGGCAGTGTCCGCTGCTCGAAAGGCGTTTGA   400

VvALDH2B4_v1   TGAAGGACCATGGCCAAGGATGAGCCCCTATGAAAGGTCGCGGATATTGTTGCGGTTTGCTGATTTAGCCGAGAAACACA   406
VvALDH2B4_v3   TGAAGGACCATGGCCAAGGATGAGCCCCTATGAAAGGTCGCGGATATTGTTGCGGTTTGCTGATTTAGCCGAGAAACACA   367
VvALDH2B4_v2   TGAAGGACCATGGCCAAGGATGAGCCCCTATGAAAGGTCGCGGATATTGTTGCGGTTTGCTGATTTAGCCGAGAAACACA   480

VvALDH2B4_v1   ATGATGAGCTTGCAGCTCTA                                                              426
VvALDH2B4_v3   ATGATGAGCTTGCAGCTCTA                                                              387
VvALDH2B4_v2   ATGATGAGCTTGCAGCTCTA                                                              500
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Figure S1 Alternatively spliced transcripts of *VvALDH2B4*. (A) Exon-intron structure of alternatively spliced transcripts of *VvALDH2B4*; (B) Alignment of the 5'-open reading frame (ORF) sequences of the three alternative splice variants of *VvALDH2B4*. Translational initiation sites are marked with blue boxes. The 113 bp retained intron of *VvALDH2B4_v2* causes a frame shift in translation and a different translational initiation site.