

Supplementary file 1. Amino acid sequence alignment of plant F3'Hs. Amino acid site is numbered according to HORVU6Hr1G002400.1 without the first 35 amino acids. The positively selected sites were indicated by solid black triangle. Amino acid sites within 5 Å of the substrates were indicated by the blue star symbol. Substrate recognition site (SRS) was boxed in black line rectangle. Two amino acid residues known to reverse the enzyme activity between F3'H and F3'5'H were highlighted in yellow.

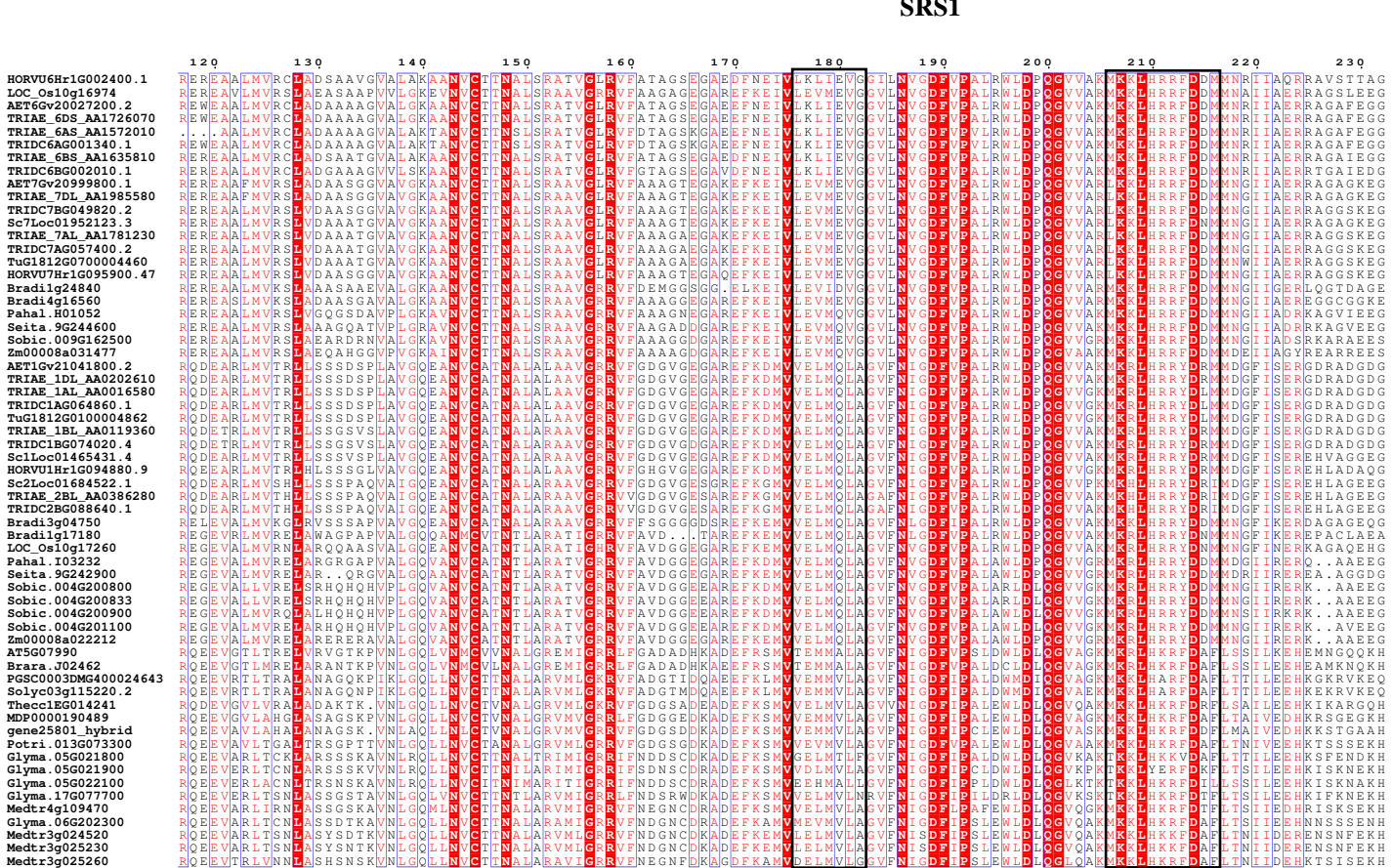
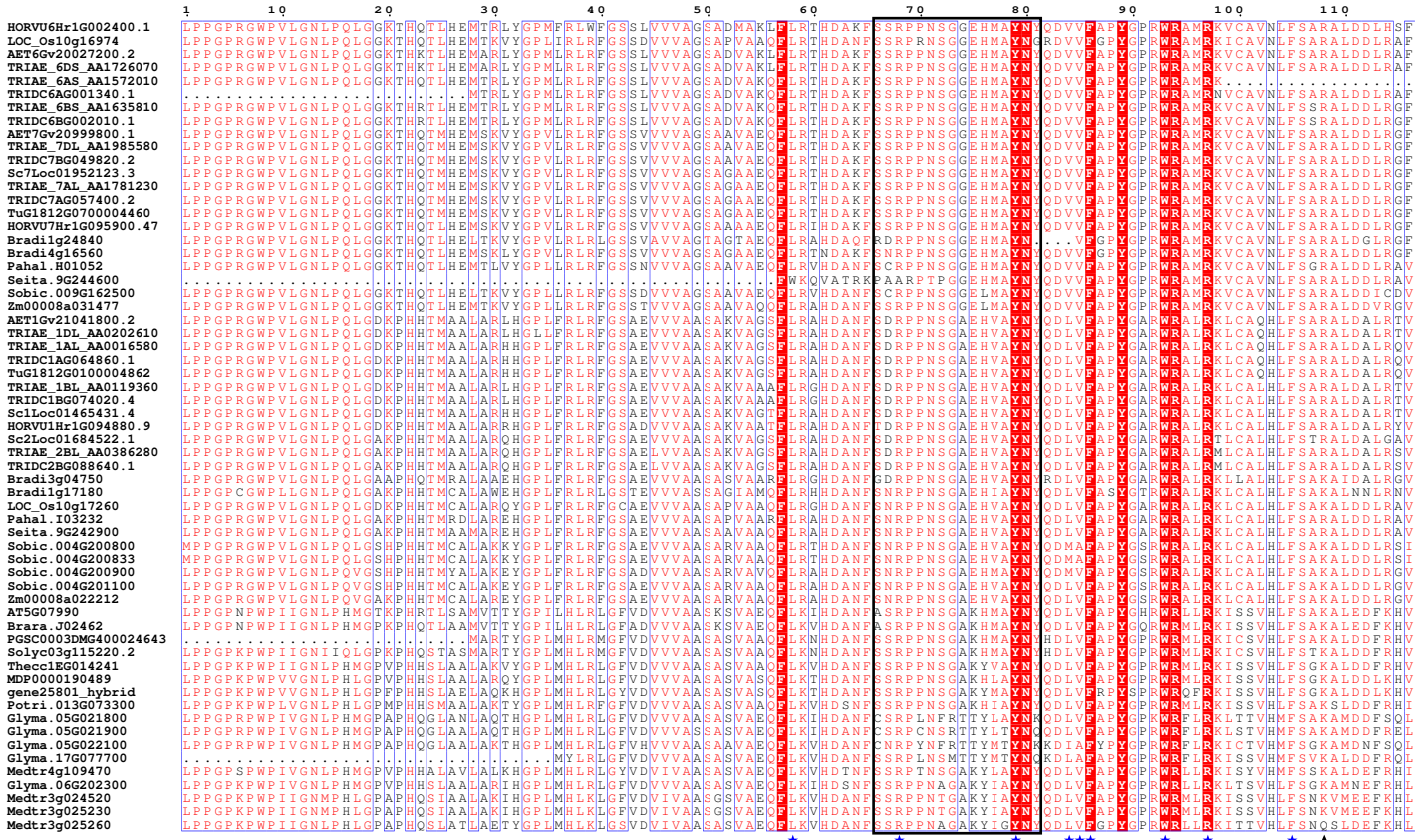


Table with 30 columns (240-340) and 100 rows. Rows are grouped into Class II, Class I, and Eudi. Each row contains a gene ID and a sequence of amino acid residues. A starburst pattern is visible at the bottom of the sequences, with 'SRS4' and 'SRS5' labels.

Table with 30 columns (350-450) and 100 rows. Rows are grouped into Class II, Class I, and Eudi. Each row contains a gene ID and a sequence of amino acid residues. A starburst pattern is visible at the bottom of the sequences, with 'SRS4' and 'SRS5' labels.

Table with 30 columns (450-550) and 100 rows. Rows are grouped into Class II, Class I, and Eudi. Each row contains a gene ID and a sequence of amino acid residues. A starburst pattern is visible at the bottom of the sequences, with 'SRS4' and 'SRS5' labels.