

APPENDIX S6. Multiple sequence alignment of *CYP76AD1*-like gene sequences. The dendrogram is obtained from a maximum likelihood method using nucleotide sequences of *Amaranthus tricolor* transcript sequences (contig74588, contig83066, contig14699, contig17428, contig17897, and contig15583). The dark arrows point at the gene sequences that were used in RT-qPCR for their transcript quantification. * indicates the VIGS target, *AtriCYP76AD1*. Contig74588 and contig14699 are potential homologs of *BvCYP76AD5* and *BvCYP76AD6*, respectively. The betalainic species included in the phylogeny are as follows: KR376385.1 *Froelichia latifolia*; KR376382.1 *Alternanthera caracasana*; KR376378.1 *Alternanthera ficoidea*; KT962274.1 *Beta vulgaris*; KR376381.1 *Beta vulgaris* subsp. *maritima*; HQ656026.1 *Mirabilis jalapa*; HQ656025.1 *Amaranthus cruentus* cv. Kerala; HQ656023.1 *Beta vulgaris* cv. W357B; KC857455.1 *Celosia cristata*; and KM592961.1 *Beta vulgaris*.

