

**Additional File 2:**

**A) Comparison of the VvWRKY-20 amino acid sequence with its putative ortholog AtZAP1.**

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AtZAP1      MAEVGKVLASDMELDHSNETKAVDDVVAITDKAEVIEVAVTRTETVVESLESTDCKRELEKLVPHTVASQSEVDVASEVSE 80
VvWRKY-20   -----MVKVPTISDFGTLVQVQDQBEWQSFTYDLNDVDSNKLLQQRQIPD 43

AtZAP1      KAPKVSSESSGALSLEQSGSEGNSPFIREKVMEDGYWRKYEQKIVKGNFVRSYYRCHENCRAKKQLERSAGGQVVDITVY 160
VvWRKY-20   TGVHASQSHQEAIPES-----IIEPKASEDGYWRKYEQKIVKGNFIRSYRCHENCQVKKQLERSHDGQITDITVY 116

AtZAP1      FGEHHDHPKPLAGAVPIINQDKRSDVFTAVSKGEQRIDIVSLIYKLCIVSYDIEFVEKISGSSVQTLRQTEPKIHGGLHVS 240
VvWRKY-20   FGRHHDHEK-LQVDLPIAVGLVVEVQEERPKPS-----SIVVEEKSLDGDGQTSQIIEPVDAP----QP 175

AtZAP1      VIFPADDVKTDISQSSRITGDNTHKDYNSFTAKRRKGGNIELSPVERSTNDSRIVVETQILEDIVNDGYEWRKYEQKISV 320
VvWRKY-20   AIAVSDDCVDRALAVWSRTEDETNDNDDPSKRQKQKINVDATPADKESGEEIRIVVQTVSEVDIVNDGYEWRKYEQKIV 255

AtZAP1      RGSPPMRSYYRCSSEGCFFVKKEVERSSHDAKLLITTYEGKHDEDMPPGRVVTNNMLDSEVDLKEGDANKTEPQSSTLQSI 400
VvWRKY-20   KGNTMRSYYRCSNAGCFVKKEVERASHDEKMMVITTYEGQHDEDMPPARIVTNN---SAGENTTTIDVNDERSRAKSEQSD 332

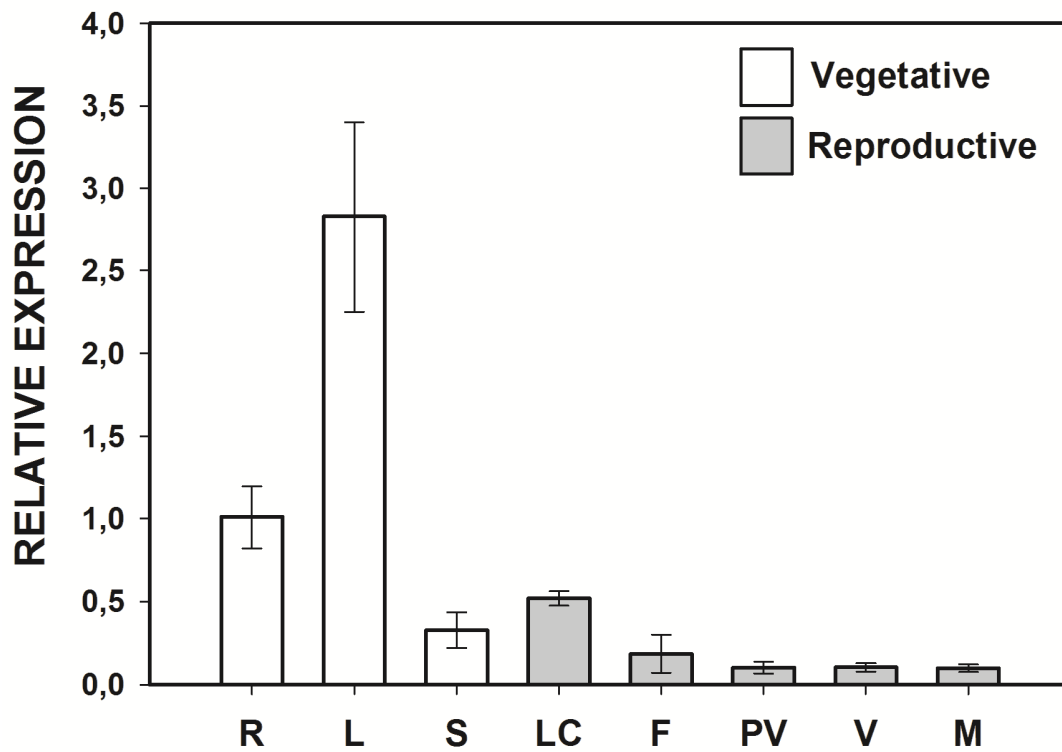
AtZAP1      TKDQVVEDHLEKKTQINGFEKSLDQGPVLDEKLKEEIKERSDANKDHAANHAKPEAKSDDKITVVCQEKAVGTLESEEQKIP 480
VvWRKY-20   NVGLAVVPEYICLGPENN-----KSNL-----QQIP 357

AtZAP1      KTEPAQS- 487
VvWRKY-20   SAEPVQIQ 365

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Alignment was performed with the highest homologous sequence from *Vitis vinifera* L. Genome to AtZAP1 (AT2G04880), named VvWRKY-20 (GSVIVT01030046001, <http://www.genoscope.cns.fr>). Alignments were performed using ClustalW. The WRKY motifs are highlighted in yellow boxes and a blue underline indicates the DNA-binding motifs. Identical residues are blackened and similar residues are highlighted in grey.

**B) Gene expression analysis of *VvWRKY-20* in grapevine tissues.**



Expression profiles of *VvWRKY-20* in R (roots); L (leaves); S (stems); LC (little clusters); F (flowers); PV (pre-veraison fruit); V (whole veraison fruit); M (whole mature fruit). Expression in root samples was adjusted to 1 relative unit. Data represent means  $\pm$  SD (n = 3).