

Genome-Wide Expression of WRKY Transcription Factors in Blueberry: Go Wild and Duplicate

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Paralogous Pairs	Identity	Similarity (>70%)	Gaps	Score	Distance (in Chromosome < 100kb)	Tandem duplicates
VmWRKY2–VmWRKY3	134/399 (33.6%)	178/399 (44.6%)	114/399 (28.6%)	458	4,421	N
VmWRKY26–VmWRKY27	58/190 (30.5%)	95/190 (50.0%)	13/190 (6.8%)	228,5	102,076	N
VmWRKY37–VmWRKY38	349/417 (83.7%)	368/417 (88.2%)	4/417 (1.0%)	1770	23,629	Y
VmWRKY40–VmWRKY41	240/241 (99.6%)	240/241 (99.6%)	0/241 (0.0%)	1276	37,603	Y
VmWRKY40–VmWRKY42	43/86 (50.0%)	58/86 (67.4%)	5/86 (5.8%)	235,5	64,764	N
VmWRKY40–VmWRKY43	34/100 (34.0%)	46/100 (46.0%)	22/100 (22.0%)	152	68,637	N
VmWRKY41–VmWRKY42	43/86 (50.0%)	58/86 (67.4%)	5/86 (5.8%)	235,5	23,667	N
VmWRKY41–VmWRKY43	34/100 (34.0%)	46/100 (46.0%)	22/100 (22.0%)	152	27,54	N
VmWRKY42–VmWRKY43	44/87 (50.6%)	56/87 (64.4%)	12/87 (13.8%)	230,5	3,357	N
VmWRKY46–VmWRKY47	209/335 (62.4%)	247/335 (73.7%)	15/335 (4.5%)	1007	7,765	Y
VmWRKY48–VmWRKY49	129/184 (70.1%)	146/184 (79.3%)	11/184 (6.0%)	692	51,301	Y
VmWRKY62–VmWRKY63	52/193 (26.9%)	69/193 (35.8%)	72/193 (37.3%)	188	57,14	N
VmWRKY55–VmWRKY56	47/141 (33.3%)	65/141 (46.1%)	27/141 (19.1%)	178,5	19,538	N
VmWRKY58–VmWRKY59	36/98 (36.7%)	51/98 (52.0%)	18/98 (18.4%)	156	4,016	N

Figure S3: Pairwise identities between paralogous pairs of *VmWRKY* genes - Y:yes, N: no.