

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

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Paralogous Pairs	Identity	Similarity (>70%)	Gaps	Score	Segmental duplicates
VmWRKY31–VmWRKY17	254/557 (45.6%)	328/557 (58.9%)	114/557 (20.5%)	1064	N
VmWRKY4–VmWRKY19	347/568 (61.1%)	400/568 (70.4%)	89/568 (15.7%)	1556,5	Y
VmWRKY65–VmWRKY24	378/387 (97.7%)	379/387 (97.9%)	2/387 (0.5%)	1938	Y
VmWRKY11–VmWRKY44	226/344 (65.7%)	259/344 (75.3%)	25/344 (7.3%)	1050	Y
VmWRKY56–VmWRKY30	114/340 (33.5%)	151/340 (44.4%)	115/340 (33.8%)	397	N
VmWRKY14–VmWRKY32	172/288 (59.7%)	202/288 (70.1%)	37/288 (12.8%)	813	Y
VmWRKY61–VmWRKY63	289/321 (90.0%)	298/321 (92.8%)	7/321 (2.2%)	1517,5	Y
VmWRKY36–VmWRKY34	192/350 (54.9%)	244/350 (69.7%)	31/350 (8.9%)	904,5	N
VmWRKY59–VmWRKY28	258/349 (73.9%)	293/349 (84.0%)	16/349 (4.6%)	1326	Y
VmWRKY15–VmWRKY7	204/331 (61.6%)	230/331 (69.5%)	60/331 (18.1%)	950	N
VmWRKY12–VmWRKY8	106/246 (43.1%)	134/246 (54.5%)	38/246 (15.4%)	437,5	N
VmWRKY67–VmWRKY22	94/129 (72.9%)	101/129 (78.3%)	1/129 (0.8%)	489	Y
VmWRKY21–VmWRKY64	104/234 (44.4%)	127/234 (54.3%)	34/234 (14.5%)	421	N
VmWRKY13–VmWRKY25	87/102 (85.3%)	96/102 (94.1%)	0/102 (0.0%)	483	Y
VmWRKY62–VmWRKY55	98/164 (59.8%)	116/164 (70.7%)	14/164 (8.5%)	491	Y
VmWRKY2–VmWRKY16	378/571 (66.2%)	431/571 (75.5%)	20/571 (3.5%)	1865,5	Y
VmWRKY1–VmWRKY3	436/445 (98.0%)	437/445 (98.2%)	4/445 (0.9%)	2310,5	Y
VmWRKY5–VmWRKY35	180/469 (38.4%)	238/469 (50.7%)	85/469 (18.1%)	686,5	N
VmWRKY58–VmWRKY29	158/183 (86.3%)	166/183 (90.7%)	10/183 (5.5%)	803	Y
VmWRKY68–VmWRKY50	96/402 (23.9%)	140/402 (34.8%)	121/402 (30.1%)	115,5	N
VmWRKY53–VmWRKY60	156/391 (39.9%)	206/391 (52.7%)	81/391 (20.7%)	615	N

Figure S4: Pairwise identities between paralogous pairs of *VmWRKY* genes - Y:yes, N: no