Table S 1. Relationship across Rosaceae genomes and predicted R2R3MYB based on R2R3MYB gene models collinearity.

Alignment 1: fv5 & pp5. Score=293.0; e-value=2.4e-09

	fv5	pp5	e-value
1- 1:	mrna32268	ppa021568m	1,00E-134
1- 2:	mrna31835	ppa019529m	1,00E-140
1- 3:	mrna25098	ppa018430m	2,00E-81
1- 4:	mrna26007	ppa007562m	2,00E-154
1- 5:	mrna26044	ppa023143m	3,00E-98
1- 6:	mrna09311	ppa021779m	9,00E-79

Alignment 2: fv6 & pp3. Score=332.0; e-value=4e-15

	fv6	pp3	e-value
2- 1:	mrna15383	ppa024533m	5,00E-77
2- 2:	mrna06920	ppa015032m	1,00E-141
2- 3:	mrna04232	ppa016385m	4,00E-61
2- 4:	mrna04423	ppa006769m	4,00E-158
2- 5:	mrna03817	ppa008366m	1,00E-139
2- 6:	mrna28435	ppa011751m	1,00E-108
2- 7:	mrna28021	ppa026877m	1,00E-131

Alignment 3: md12 & pp2. Score = 297.0; e-value=3.4e-08

	md12	pp2	e-value
3- 1:	MDP0000308403	ppa007268m	0
3- 2:	MDP0000157940	ppa009439m	8,00E-141
3- 3:	MDP0000693678	ppa017892m	2,00E-124
3- 4:	MDP0000787808	ppa011549m	1,00E-116
3- 5:	MDP0000152575	ppa019729m	1,00E-152
3- 6:	MDP0000574942	ppa017039m	1,00E-80

Alignment 4: md10 & md5. Score=296.0; e-value=6.5e-10

	md10	md5	e-value
4- 1:	MDP0000291518	MDP0000852158	0
4- 2:	MDP0000897594	MDP0000145050	4,00E-150
4- 3:	MDP0000215675	MDP0000133542	4,00E-176
4- 4:	MDP0000226667	MDP0000289671	4,00E-177
4- 5:	MDP0000492221	MDP0000197283	0
4- 1:	MDP0000143487	MDP0000245462	6,00E-141

Alignment 5: md14 & pp5. Score=294.0; e-value=2.6e-09

	md14	pp5	e-value
5- 1:	MDP0000318376	ppa019529m	1,00E-90
5- 2:	MDP0000852549	ppa018561m	0
5- 3:	MDP0000642761	ppa010908m	5,00E-122
5- 4:	MDP0000298505	ppa023143m	1,00E-126
5- 5:	MDP0000211677	ppa011954m	6,00E-109
5- 6:	MDP0000265114	ppa021779m	7,00E-84

Alignment 6: md15 & pp1. Score=336.0; e-value=5.4e-21

	md15	pp1	e-value
6- 1:	MDP0000261265	ppa026916m	2,00E-113
6- 2:	MDP0000184538	ppa015883m	2,00E-68
6- 3:	MDP0000031172	ppa022205m	2,00E-89
6- 4:	MDP0000262514	ppa024417m	9,00E-142
6- 5:	MDP0000165715	ppa008979m	3,00E-134
6- 5:	MDP0000477900	ppa010735m	6,00E-105
6- 5:	MDP0000175918	ppa008906m	5,00E-134

Alignment 7: md17 & md 9. Score=292.0; e-value=7.4e-14

	md17	md9	e-value
7- 1:	MDP0000144744	MDP0000219359	0
7- 2:	MDP0000742771	MDP0000278681	0
7- 3:	MDP0000468201	MDP0000710259	8,00E-110
7- 4:	MDP0000148689	MDP0000155426	4,00E-61
7- 5:	MDP0000175835	MDP0000176798	1,00E-157
7- 6:	MDP0000823458	MDP0000193056	5,00E-161

Alignment 8: md17 & pp3. Score=396.0; e-value=1.6e17

	md17	pp3	e-value
8- 1:	MDP0000344978	ppa011751m	2,00E-128
8- 2:	MDP0000144744	ppa008366m	3,00E-175
8- 3:	MDP0000742771	ppa006769m	5,00E-168
8- 4:	MDP0000286143	ppa016385m	2,00E-87
8- 5:	MDP0000468201	ppa016708m	0
8- 6:	MDP0000148689	ppa025095m	1,00E-98
8- 7:	MDP0000407613	ppa026553m	2,00E-119
8- 8:	MDP0000175835	ppa017451m	0

Alignment 9: md8 & pp1. Score=297.0; e-value=6.9e-12

	md8	pp1	e-value
9- 1:	MDP0000166645	ppa023812m	1,00E-82
9- 2:	MDP0000266156	ppa019554m	7,00E-108
9- 3:	MDP0000786507	ppa024417m	7,00E-146
9- 4:	MDP0000463846	ppa008979m	1,00E-142
9- 5:	MDP0000894463	ppa010735m	8,00E-107
9- 6:	MDP0000135594	ppa008906m	1,00E-115

Alignment 10: md9 vs pp3. Score=329.0; e-value=1.4e-18

	md9	pp3	e-value
10- 1:	MDP0000303239	ppa026877m	2,00E-121
10- 2:	MDP0000284846	ppa019507m	1,00E-93
10- 3:	MDP0000219359	ppa008366m	2,00E-163
10- 4:	MDP0000278681	ppa006769m	3,00E-166
10- 5:	MDP0000710259	ppa016708m	1,00E-102
10- 6:	MDP0000155426	ppa026553m	6,00E-120
10- 7:	MDP0000176798	ppa017451m	6,00E-122
10- 8:	MDP0000159011	ppa010716m	3,00E-157

pp: Prunus persica , md: Malus domestica and fv: Fragaria vesca , meanwhile the number indicate the analyzed chromosome .