

Genome-wide analysis of the MYB gene family in Two *Vernicia* Species

Supplementary Materials

VmMYB001	TRGHRPADEKRELVERYEPH...NWNIAEKLQGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB002	HRGPTPEEDDLKELVYIQRH...WRSPLPKAAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB003	KKGPSTPEEDAKLKAIEQNGTGGN.WIALPQKIGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	105
VmMYB004	KKGPSTPEEDQKLDYIQKHG...N.WRTLPKNAAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB005	VKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB006	RKGLSPPEEDKLNVMYMLNNGC.C.WSDVARNAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB007	VRGPTPEEDAVLQQLVSKF...NWSLIARGIPGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB008	VKGPSTPEEDAVLQQLVSKF...NWSLIARGIPGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB009	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB010	NRGPTPEEDNLRKLVYRNH...K.WGKVVQKTLGRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB011	ARNPTPEEDAKLWELMKKYS...WAMISSAQEGRTGKQVDRYLNKLRPNIKLGDWSVQDELLVVKLKEVGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB012	RGPSTPEEDKLNVIATH...NWSLARCAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB013	ARNPTPEEDAKLWELMKKYS...WAMISSAQEGRTGKQVDRYLNKLRPNIKLGDWSVQDELLVVKLKEVGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB025	NRGPTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB026	NKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB027	NKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB028	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB029	VRGPTPEEDAVLQQLVSKF...NWSLIARGIPGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB030	VRGPTPEEDAVLQQLVSKF...NWSLIARGIPGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB031	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB051	NKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB052	KKGLTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	105
VmMYB053	RGPSTPEEDKLNVIATH...NWSLARCAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB054	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB055	IKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB056	PRGHRPADEKRELVERYEPH...NWNIAEKLQGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB058	PRGHRPADEKRELVERYEPH...NWNIAEKLQGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB059	KKGPSTPEEDDLANVIKKE...N.WRTLPKNAAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB060	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB061	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB062	KKGLTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB063	ARNPTPEEDAKLWELMKKYS...WAMISSAQEGRTGKQVDRYLNKLRPNIKLGDWSVQDELLVVKLKEVGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB064	SPNKTEPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB003	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB004	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB005	NKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB006	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB007	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB008	PRGHRPADEKRELVERYEPH...NWNIAEKLQGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB009	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	105
VmMYB010	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB011	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB013	NKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB014	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB015	RKGLTPEEDKLNVIATH...NWSLARCAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB017	HIVTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB018	TRGHRPADEKRELVERYEPH...NWNIAEKLQGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB025	KKGPSTPEEDDLANVIKKE...N.WRTLPKNAAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB026	KKGPSTPEEDDLANVIKKE...N.WRTLPKNAAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB027	KKGPSTPEEDAKLKAIEQNGTGGN.WIALPQKIGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	105
VmMYB028	VKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB029	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB030	IKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB031	NKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB032	NRGPTPEEDNLRKLVYRNH...K.WGKVVQKTLGRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB033	IKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB034	RGPSTPEEDKLNVIATH...NWSLARCAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB035	KKGPSTPEEDKLRAYVEKYS...N.WRELPKFAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB036	VKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB037	NKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB038	KKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB039	KKGPSTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB040	ERQRRAEDDALRAYVQYQPRENNVLSQRMNTPLNDRDAKSLERWKNYKPGIKKGLSTEEBQLVIRLQAKHGNKWKAAAEVPGRTAKRIGKWWVFKEKQQ	106
VmMYB041	VRGPTPEEDAVLQQLVSKF...NWSLIARGIPGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB042	RGPSTPEEDKLNVIATH...NWSLARCAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB045	ARNPTPEEDAKLWELMKKYS...WAMISSAQEGRTGKQVDRYLNKLRPNIKLGDWSVQDELLVVKLKEVGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
VmMYB050	KKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB051	VKGPSTPEEDQLQKLVQRH...NWSLISQSIPIGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	103
VmMYB052	RKGLTPEEDKLNVIATH...NWSLARCAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB054	KKGLTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB057	KKGLTPEEDKLDYIQKH...K.WRNLPKRAGLRCGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	104
VmMYB058	PRGHRPADEKRELVERYEPH...NWNIAEKLQGRSGKSCRLRWLNQDPRINRSPFTEEBERLLASHRIHGNRWAVIRLPGRTDNVKNHWHVIMARKC	102
Consensus	kgpw peed kl y hg w l aagl rcgkscrlrw nylrp ikrg ft eee il h gnws ia lpgrtdeikn wn lkkl	

Figure S1: Multiple sequence alignments for the sequence with complete MYB domain. Multiple sequence alignment was accomplished by BioEdit and DNAMAN software. The blue shadow, pink shadow and black shadow respectively represent the proportion of conserved amino acid residues > 50%, >75 and 100%.

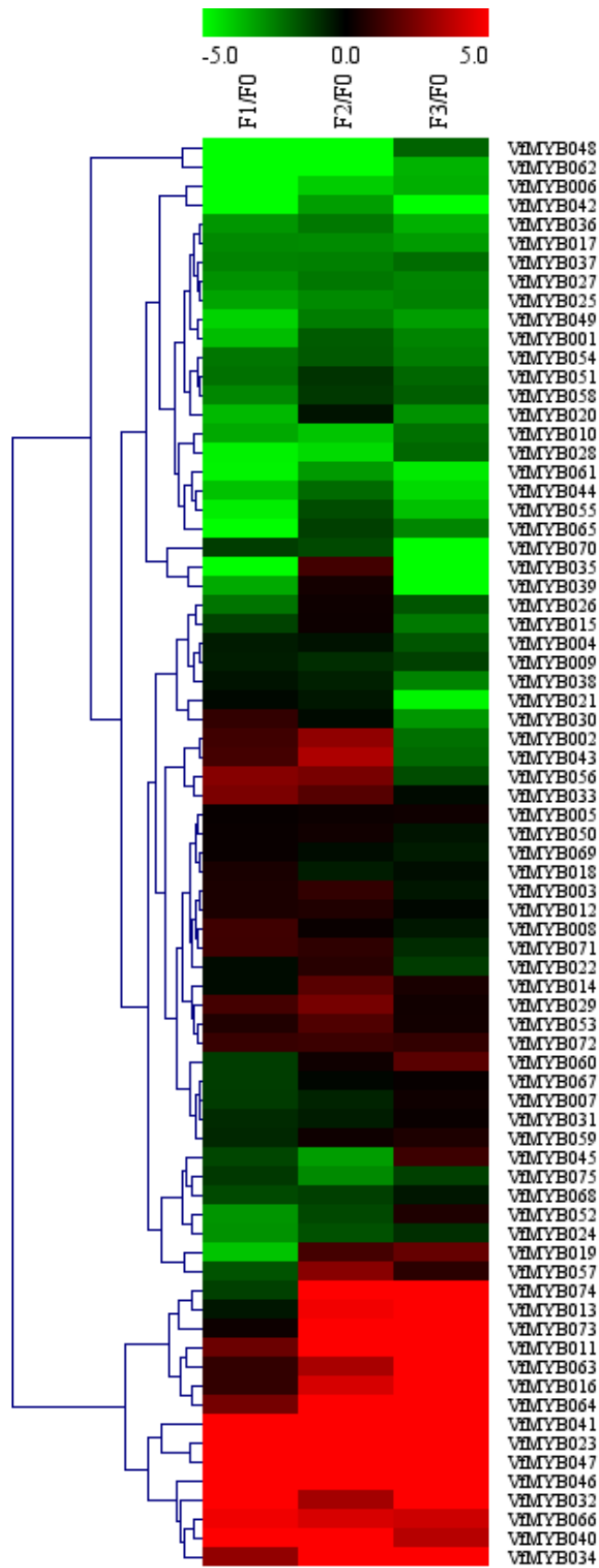


Figure S2: Expression profiles under infection by *F. oxysporum* in *V. fordii*.

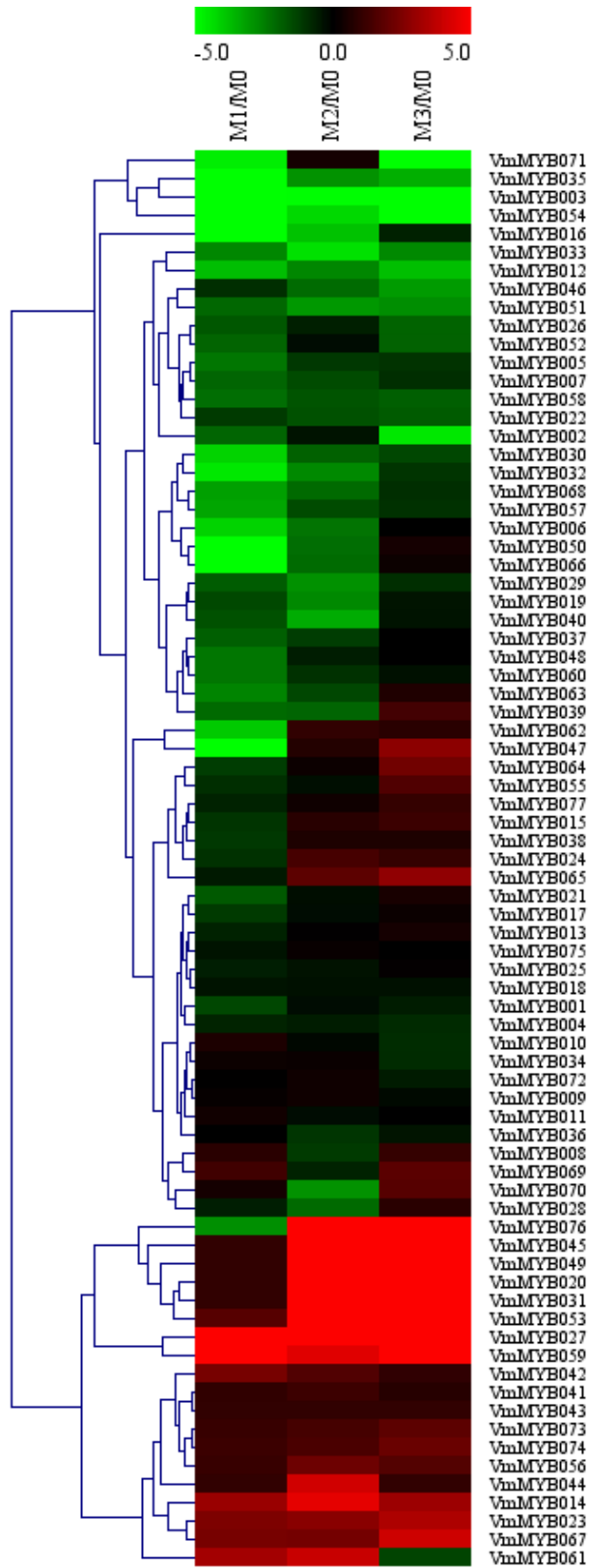


Figure S3: Expression profiles under infection by *F. oxysporum* in *V. Montana*.

Table S1.

The nonsynonymous and synonymous substitution ratio (ka and ks) of the duplicated genes.

		Method	Ka	Ks	Ka/Ks	P-Value(Fisher)
VfMYB010	VmMYB032	NG	0	0.00973968	0	0
VfMYB019	VmMYB022	NG	0	0.0163624	0	0
VfMYB058	VmMYB008	NG	0	0.0167041	0	0
VfMYB003	VmMYB027	NG	0.00175822	0.039334	0.0446996	0.000516185
VfMYB072	VmMYB074	NG	0.00176724	0.019051	0.0927637	0.0327365
VfMYB012	VmMYB034	NG	0.00406656	0.0432242	0.0940807	0.002188
VfMYB052	VmMYB031	NG	0.00215487	0.0164029	0.131371	0.10389
VfMYB031	VmMYB007	NG	0.01221	0.0795659	0.153458	0.00302661
VfMYB030	VmMYB040	NG	0.00364069	0.0231698	0.157131	0.0324978
VfMYB051	VmMYB005	NG	0.0037521	0.0226209	0.165869	0.0578724
VfMYB029	VmMYB041	NG	0.005734	0.0283449	0.202293	0.0417717
VfMYB053	VmMYB042	NG	0.0117464	0.0565472	0.207728	0.0232356
VfMYB013	VmMYB045	NG	0.0203269	0.0937741	0.216764	0.000305005
VfMYB060	VmMYB038	NG	0.00707194	0.0258012	0.274094	0.0723635
VfMYB066	VmMYB073	NG	0.00949058	0.0220953	0.42953	0.44069
VfMYB075	VmMYB077	NG	0.0479113	0.0919707	0.520941	0.119258
VfMYB035	VmMYB035	NG	0.00466866	0.00888032	0.525731	0.496194
VfMYB006	VmMYB052	NG	2.30671	3.73095	0.618264	0.530365
VfMYB008	VmMYB036	NG	1.692	2.43366	0.695249	0.260495
VfMYB015	VmMYB023	NG	0.0247142	0.0350926	0.704257	0.481764
VfMYB022	VmMYB046	NG	2.10217	2.38699	0.880678	0.884878
VfMYB056	VmMYB026	NG	0.176845	0.190784	0.926937	0.708047
VfMYB005	VmMYB051	NG	0.242176	0.227676	1.06368	0.886933
VfMYB001	VmMYB018	NG	0.0847576	0.0367226	2.30805	0.0823034
VfMYB009	VmMYB013	NG	0	0	NA	0
VfMYB017	VmMYB016	NG	0	0	NA	0
VfMYB023	VmMYB059	NG	0	0	NA	0
VfMYB025	VmMYB001	NG	0	0	NA	0
VfMYB026	VmMYB037	NG	0	0	NA	0
VfMYB027	VmMYB030	NG	0	0	NA	0
VfMYB028	VmMYB004	NG	0	0	NA	0
VfMYB036	VmMYB053	NG	0	0	NA	0
VfMYB037	VmMYB068	NG	0	0	NA	0
VfMYB038	VmMYB063	NG	0	0	NA	0
VfMYB039	VmMYB066	NG	0	0	NA	0
VfMYB044	VmMYB043	NG	0	0	NA	0
VfMYB047	VmMYB039	NG	0	0	NA	0
VfMYB048	VmMYB057	NG	0	0	NA	0
VfMYB049	VmMYB048	NG	0	0	NA	0
VfMYB054	VmMYB029	NG	0	0	NA	0

VfMYB059	VmMYB025	NG	0	0	NA	0
VfMYB062	VmMYB054	NG	0	0	NA	0
VfMYB065	VmMYB071	NG	0	0	NA	0
VfMYB068	VmMYB072	NG	0	0	NA	0
VfMYB070	VmMYB070	NG	0	0	NA	0
VfMYB071	VmMYB075	NG	0	0	NA	0
VfMYB020	VmMYB006	NG	0.00847181	0	NA	0
VfMYB050	VmMYB058	NG	2.31306	NA	NA	0.0368432
VfMYB055	VmMYB033	NG	0.00198389	0	NA	0
