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Figure S1. Alignment of APETALA2/ethylene-responsive element binding factor (AP2/ERF) domains of 124 ERF family proteins identified from *Vernicia fordii* and *Vernicia montana*. Multiple sequence alignment was conducted with BioEdit and DNAMAN. The GCC box-binding domain of *Arabidopsis* AtERF1 (At4g17500) is indicated at the top. **Blue shadow:** conserved amino acid residues (>50%); **Pink shadow:** conserved amino acid residues (>75%); **Black shadow:** 100% conserved amino acid residues.

VfAP2/ERF063	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VfAP2/ERF064	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VfAP2/ERF065	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VfAP2/ERF066	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VfAP2/ERF067	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VfAP2/ERF068	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VfAP2/ERF069	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VfAP2/ERF070	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VfAP2/ERF071	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VfAP2/ERF072	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VfAP2/ERF073	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VfAP2/ERF074	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF067	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF068	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF069	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VmAP2/ERF070	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VmAP2/ERF071	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VmAP2/ERF072	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VmAP2/ERF073	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
VmAP2/ERF074	RSSCYRGVTRFRWGTGRWESHWDKNCWNESQNKGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF075	RSSCYRGVTRFRWGTGRWESHWDKNCWNESQNKGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF076	RSSCYRGVTRFRWGTGRWESHWDKNCWNESQNKGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF077	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF078	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF079	RTSCYRGVTRFRWGTGRWESHWDNSCKKEGQSRGRQVYLGGYDKEEKAARAYDLAAIKYKGPSTHNNFPLENYKKELEDMK	82
VmAP2/ERF080	RSSCYRGVTFYRRGTGRWESHWD.....CGKQVYLGGFTAHAAARAYDRAAKKFRGVDADNFNVSIDYVEDIKQMS	72
Consensus	rsscyrgvtrfrwgtgrweshwd c e q kgrqvylggyd e aaaraydlaalkywg a infp sdyeel erk	
VfAP2/ERF063	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VfAP2/ERF064	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VfAP2/ERF065	SLTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	135
VfAP2/ERF066	NLNKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	138
VfAP2/ERF067	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	119
VfAP2/ERF068	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VfAP2/ERF069	NMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VfAP2/ERF070	NMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VfAP2/ERF071	YVTKQEFVHILRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VfAP2/ERF072	HMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VfAP2/ERF073	HMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VfAP2/ERF074	HMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF067	HMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF068	YVTKQEFVHILRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF069	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VmAP2/ERF070	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VmAP2/ERF071	SLTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VmAP2/ERF072	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	152
VmAP2/ERF073	NFTKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	119
VmAP2/ERF074	GQSKEEYIGSLRRQSSGFSRGVSYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF075	GQSKEEYIGSLRRQSSGFSRGVSYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	113
VmAP2/ERF076	RMSKEEYIGSLRRQSSGFSRGVSYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF077	NMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF078	NMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF079	HMTRCQEVVAHLRRQSSGFSRGASLYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTQEEAAEAYDIAAIFRGLNAVTFN	163
VmAP2/ERF080	NLNKEEFVHILRRQSTGFSRGSSSYRGVT.LHKCGRWEARMGQFLGKKYIYLGLEDSEIDAAARAYDKAAIKCNGREAVTNF	138
Consensus	n tkeefv hllrrqstgfsrgsssyrgvt l hkcgrwearmgqflgkkyiylglf dseid aaraydkaaikcngreavtnf	

Figure S2. Alignment of AP2/ERF domains of 26 AP2 family proteins identified from *V. fordii* and *V. montana*. Multiple sequence alignment was conducted with BioEdit and DNAMAN. **Blue shadow:** conserved amino acid residues (>50%); **Pink shadow:** conserved amino acid residues (>75%); **Black shadow:** 100% conserved amino acid residues.

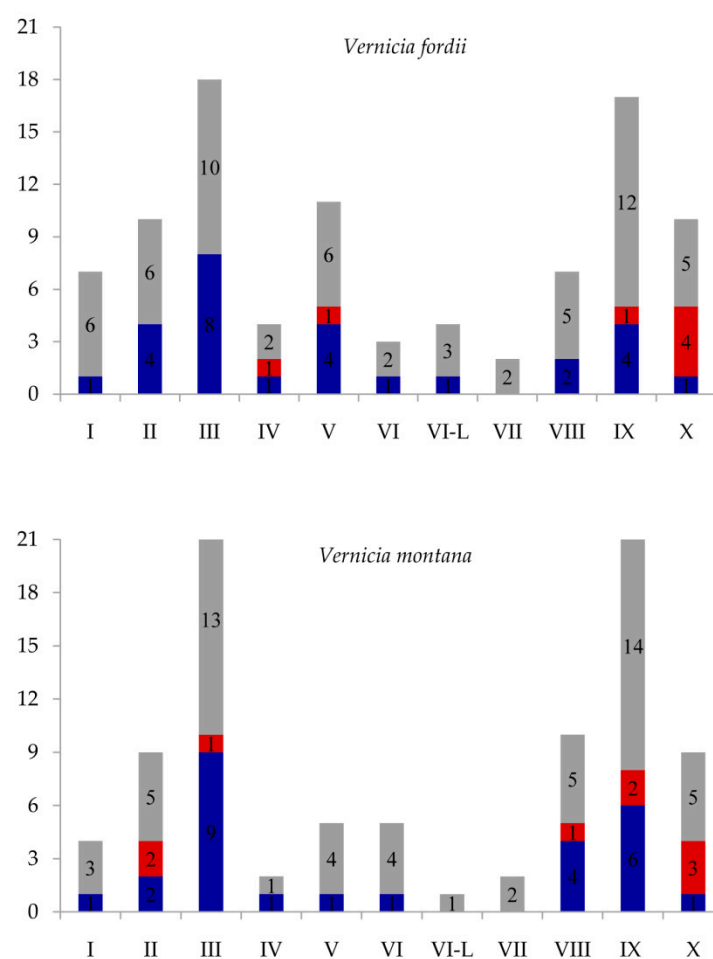


Figure S3. Frequency of ERFs in response to *Fusarium oxysporum* in phylogenetic groups. The full bar indicates the number of ERFs with more than twofold change in at least one infected experiment per group. **Red** indicates members with more than twofold upregulated expression at all the three infected periods. **Blue** indicates members with more than twofold downregulated.

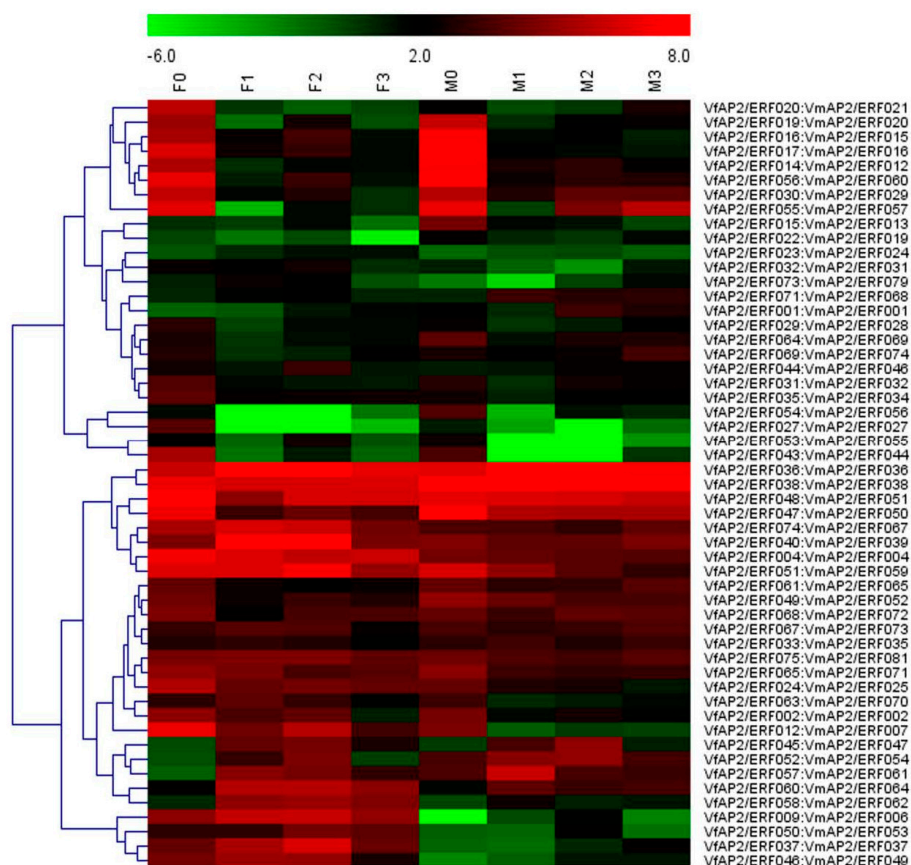


Figure S4. Comparative analysis of the expression trends of 53 pairs of orthologous genes in response to *F. oxysporum*. The heat-map has been generated based on the log₂ transformed reads per kilobase per million mapped reads (RPKM) values and the color scale is shown at the top. **Red** represents high expression and **green** represents low expression.

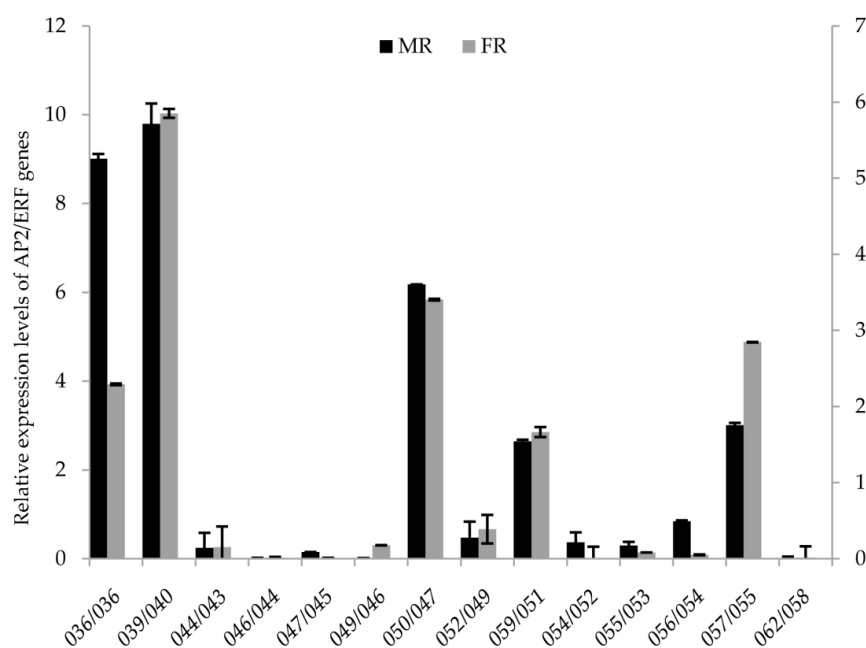


Figure S5. Comparative analysis of the expression levels of the selected AP2/ERF genes in root tissue. MR: root tissue in *V. montana*; FR: root tissue in *V. fordii*.

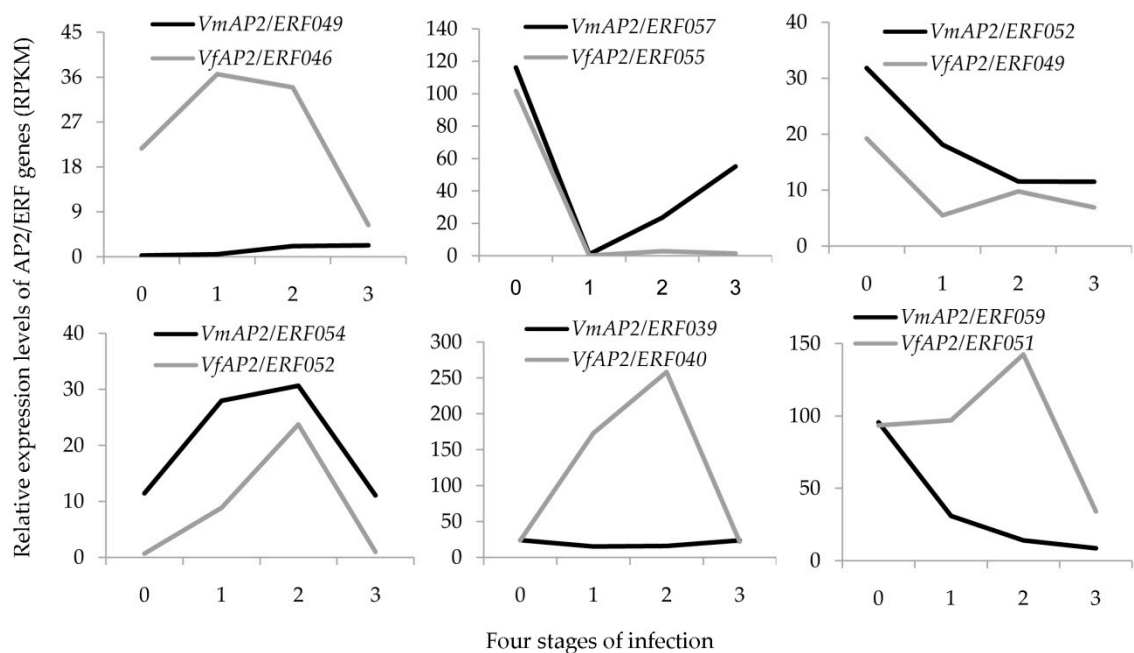


Figure S6. Expression trends of AP2/ERF genes for tissue specific expression analysis in *Vernicia* during the four infection stages. Axis represents averaged RPKM values from three biological experiments. The numbers in the x-axis represent stage of infection, as follows: 0, uninfected stage; 1, early stage of infection; 2, middle stage of infection; 3, late stage of infection.

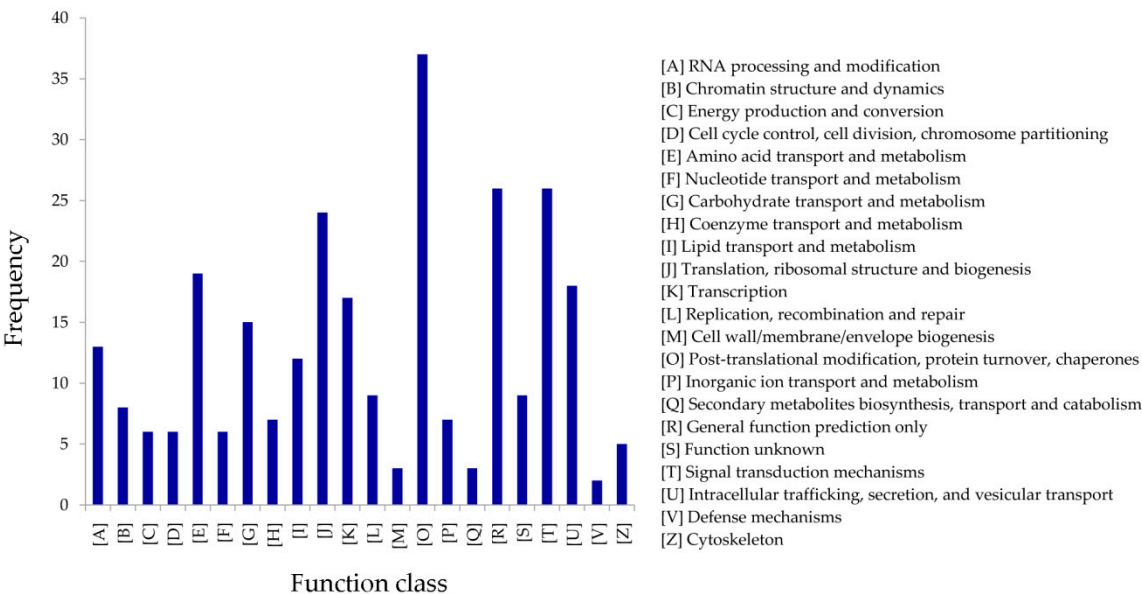


Figure S7. Clusters of orthologous groups (COG) classification. In total, 278 functional genes of whole annotated unigenes were grouped into 22 classifications.

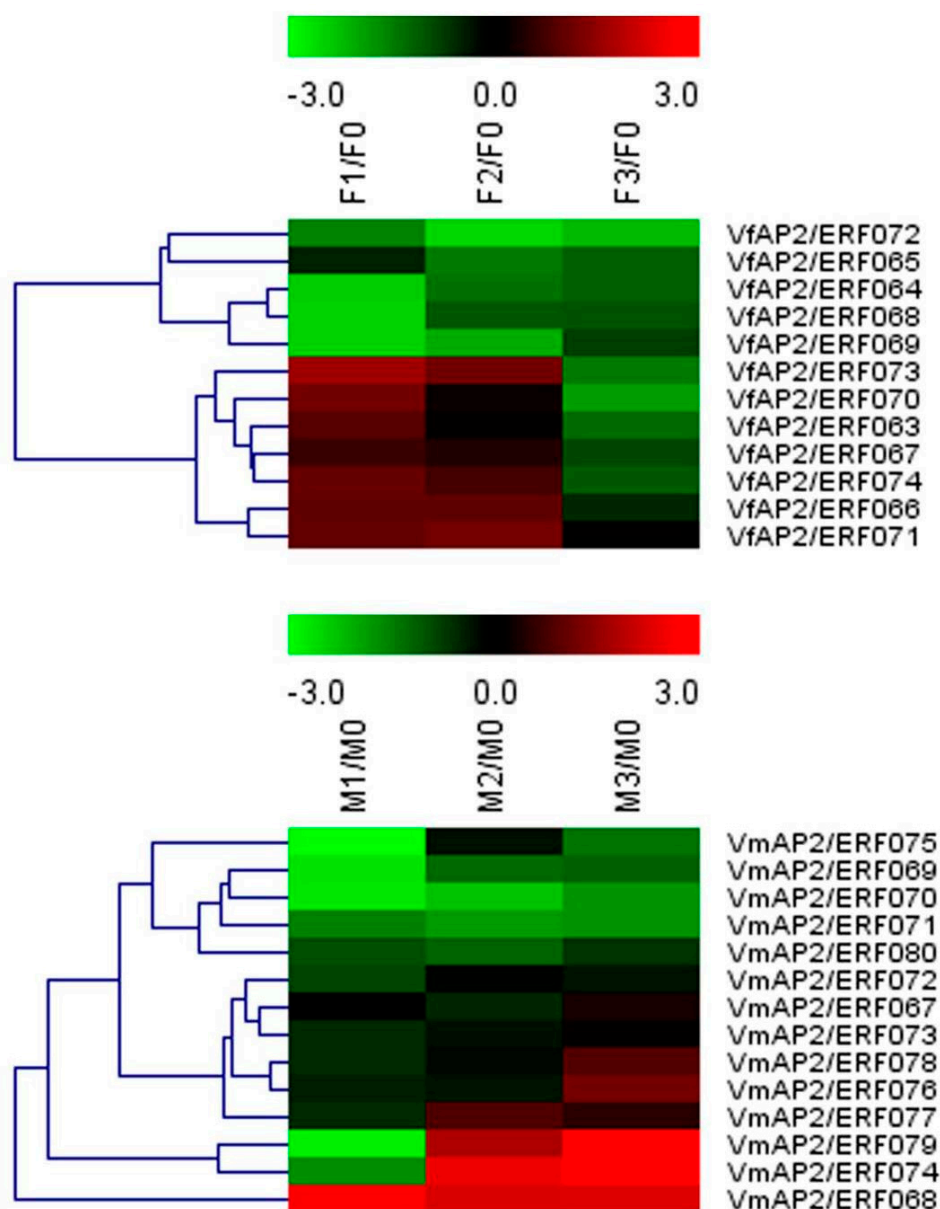


Figure S8. Expression profiles of AP2 genes in response to *F. oxysporum* in the root of *V. fordii* and *V. montana*. The heatmap has been generated based on the log₂-transformed fold-change RPKM values and the color scale is shown at the top. **Red** represents upregulation and **green** represents downregulation.

Table S1. The individual APETALA2/ethylene-responsive element binding factor (AP2/ERF) genes identified in *V. fordii* and *V. montana* transcriptome database.

Group	Transcript_ID	GeneticName	Accession No.	Effective_Length	Annotation
Group1	comp183962_c0_seq1	VfAP2/ERF001	KX868880	1420.00	EREBP-like factor
Group1	comp189672_c0_seq2	VfAP2/ERF002	KX868881	1823.46	EREBP-like factor
Group1	comp185524_c0_seq1	VfAP2/ERF003	KX868882	1915.00	EREBP-like factor
Group1	comp160673_c0_seq2	VfAP2/ERF004	KX868883	1150.82	EREBP-like factor
Group1	comp190709_c2_seq5	VfAP2/ERF005	KX868884	1538.54	EREBP-like factor
Group1	comp192642_c0_seq1	VfAP2/ERF006	KX868885	2520.00	EREBP-like factor
Group2	comp84118_c0_seq1	VfAP2/ERF007	KX868886	462.00	EREBP-like factor
Group2	comp149201_c0_seq1	VfAP2/ERF008	KX868887	459.00	EREBP-like factor
Group2	comp176401_c0_seq4	VfAP2/ERF009	KX868888	1411.21	EREBP-like factor

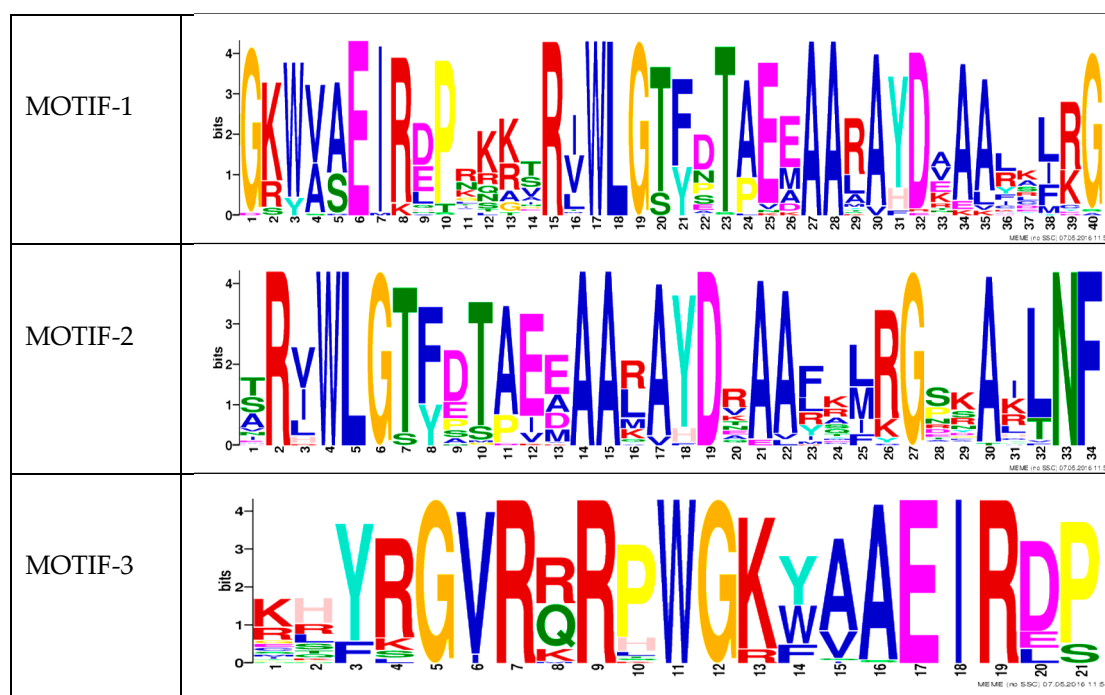
Group2	comp160987_c0_seq1	VfAP2/ERF010	KX868889	602.00	EREBP-like factor
Group2	comp160830_c0_seq2	VfAP2/ERF011	KX868890	563.42	EREBP-like factor
Group2	comp184966_c0_seq2	VfAP2/ERF012	KX868891	1048.51	EREBP-like factor
Group3	comp159254_c1_seq1	VfAP2/ERF013	KX868892	405.00	EREBP-like factor
Group3	comp180080_c0_seq3	VfAP2/ERF014	KX868893	1570.07	EREBP-like factor
Group3	comp169343_c0_seq2	VfAP2/ERF015	KX868894	1213.62	EREBP-like factor
Group3	comp181674_c0_seq1	VfAP2/ERF016	KX868895	972.04	EREBP-like factor
Group3	comp181389_c0_seq1	VfAP2/ERF017	KX868896	1182.00	EREBP-like factor
Group3	comp173409_c0_seq1	VfAP2/ERF018	KX868897	824.84	EREBP-like factor
Group3	comp183897_c0_seq3	VfAP2/ERF019	KX868898	1046.09	EREBP-like factor
Group3	comp176265_c0_seq1	VfAP2/ERF020	KX868899	879.01	EREBP-like factor
Group3	comp164645_c0_seq1	VfAP2/ERF021	KX868900	661.00	EREBP-like factor
Group3	comp173281_c0_seq1	VfAP2/ERF022	KX868901	804.00	EREBP-like factor
Group4	comp171489_c1_seq1	VfAP2/ERF023	KX868902	714.00	EREBP-like factor
Group4	comp189934_c0_seq4	VfAP2/ERF024	KX868903	850.79	EREBP-like factor
Group5	comp148732_c0_seq1	VfAP2/ERF025	KX868904	432.00	EREBP-like factor
Group5	comp166681_c0_seq2	VfAP2/ERF026	KX868905	726.43	EREBP-like factor
Group5	comp158438_c0_seq3	VfAP2/ERF027	KX868906	1528.82	EREBP-like factor
Group5	comp149900_c0_seq1	VfAP2/ERF028	KX868907	1294.00	EREBP-like factor
Group5	comp181196_c0_seq1	VfAP2/ERF029	KX868908	1095.15	EREBP-like factor
Group5	comp188688_c0_seq1	VfAP2/ERF030	KX868909	1229.26	EREBP-like factor
Group6	comp189868_c0_seq1	VfAP2/ERF031	KX868910	1820.54	EREBP-like factor
Group6	comp186790_c1_seq1	VfAP2/ERF032	KX868911	1526.84	EREBP-like factor
Group6-l	comp192264_c0_seq1	VfAP2/ERF033	KX868912	1971.00	EREBP-like factor
Group6-l	comp116494_c0_seq1	VfAP2/ERF034	KX868913	864.00	EREBP-like factor
Group6-l	comp183367_c0_seq5	VfAP2/ERF035	KX868914	1480.92	EREBP-like factor
Group7	comp178925_c0_seq2	VfAP2/ERF036	KX868915	747.64	EREBP-like factor
Group7	comp180742_c0_seq2	VfAP2/ERF037	KX868916	1335.90	EREBP-like factor
Group7	comp187442_c0_seq1	VfAP2/ERF038	KX868917	1701.00	EREBP-like factor
Group8	comp101758_c0_seq1	VfAP2/ERF039	KX868918	336.00	EREBP-like factor
Group8	comp179927_c0_seq1	VfAP2/ERF040	KX868919	1018.00	EREBP-like factor
Group8	comp177967_c0_seq1	VfAP2/ERF041	KX868920	742.00	EREBP-like factor
Group8	comp157807_c0_seq2	VfAP2/ERF042	KX868921	956.08	EREBP-like factor
Group8	comp160872_c0_seq1	VfAP2/ERF043	KX868922	806.00	EREBP-like factor
Group9	comp172871_c0_seq1	VfAP2/ERF044	KX868923	612.00	EREBP-like factor
Group9	comp174782_c0_seq3	VfAP2/ERF045	KX868924	864.06	EREBP-like factor
Group9	comp175038_c0_seq1	VfAP2/ERF046	KX868925	667.00	EREBP-like factor
Group9	comp189715_c1_seq1	VfAP2/ERF047	KX868926	964.00	EREBP-like factor
Group9	comp192585_c1_seq1	VfAP2/ERF048	KX868927	1237.00	EREBP-like factor
Group9	comp179276_c0_seq1	VfAP2/ERF049	KX868928	1501.09	EREBP-like factor
Group9	comp186047_c0_seq1	VfAP2/ERF050	KX868929	531.42	EREBP-like factor
Group9	comp181356_c0_seq5	VfAP2/ERF051	KX868930	792.80	EREBP-like factor
Group9	comp171620_c0_seq1	VfAP2/ERF052	KX868931	825.00	EREBP-like factor
Group9	comp181105_c0_seq2	VfAP2/ERF053	KX868932	843.07	EREBP-like factor
Group9	comp136851_c0_seq1	VfAP2/ERF054	KX868933	768.00	EREBP-like factor
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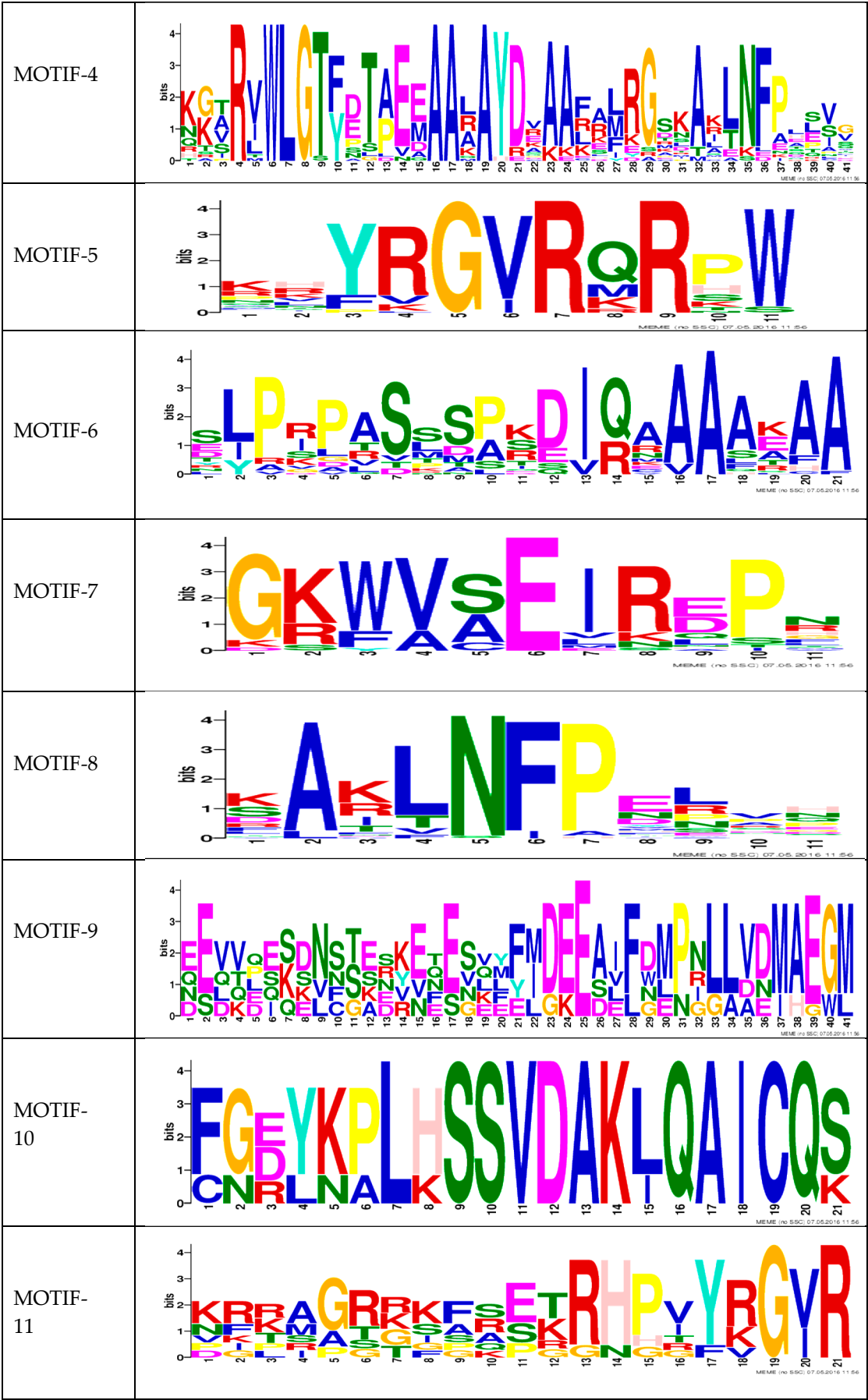
Group10	comp174721_c0_seq1	VfAP2/ERF056	KX868935	1173.00	EREBP-like factor
Group10	comp184569_c0_seq5	VfAP2/ERF057	KX868936	1684.12	EREBP-like factor
Group10	comp181627_c0_seq2	VfAP2/ERF058	KX868937	1352.93	EREBP-like factor
Group10	comp181660_c0_seq2	VfAP2/ERF059	KX868938	1323.16	EREBP-like factor
Group10	comp194219_c2_seq5	VfAP2/ERF060	KX868939	1147.02	EREBP-like factor
RAV	comp189189_c0_seq2	VfAP2/ERF061	KX868940	1061.98	RAV-like factor
RAV	comp176028_c0_seq1	VfAP2/ERF062	KX868941	1300.00	RAV-like factor
AP2	comp192732_c0_seq6	VfAP2/ERF063	KX868942	796.07	AP2-like factor, euAP2 lineage
AP2	comp191512_c0_seq2	VfAP2/ERF064	KX868943	1193.76	AP2-like factor, euAP2 lineage
AP2	comp195632_c1_seq20	VfAP2/ERF065	KX868944	1373.64	AP2-like factor, euAP2 lineage
AP2	comp191268_c0_seq4	VfAP2/ERF066	KX868945	1482.02	AP2-like factor, euAP2 lineage
AP2	comp184116_c0_seq1	VfAP2/ERF067	KX868946	1035.46	AP2-like factor, euAP2 lineage
AP2	comp186054_c0_seq1	VfAP2/ERF068	KX868947	1949.28	AP2-like factor, euAP2 lineage
AP2	comp179411_c0_seq1	VfAP2/ERF069	KX868948	1795.38	AP2-like factor, ANT lineage
AP2	comp178775_c0_seq3	VfAP2/ERF070	KX868949	1188.85	AP2-like factor, ANT lineage
AP2	comp191827_c0_seq1	VfAP2/ERF071	KX868950	2271.00	AP2-like factor, ANT lineage
AP2	comp184446_c1_seq1	VfAP2/ERF072	KX868951	1584.00	AP2-like factor, ANT lineage
AP2	comp184446_c0_seq1	VfAP2/ERF073	KX868952	732.00	AP2-like factor, ANT lineage
AP2	comp184881_c0_seq5	VfAP2/ERF074	KX868953	1055.28	AP2-like factor, ANT lineage
solosist	comp191237_c1_seq13	VfAP2/ERF075	KX868954	1272.47	-
Group1	comp138429_c0_seq4	VmAP2/ERF001	KX868799	1510.61	EREBP-like factor
Group1	comp164853_c0_seq3	VmAP2/ERF002	KX868800	2120.15	EREBP-like factor
Group1	comp137524_c0_seq1	VmAP2/ERF003	KX868801	2219.00	EREBP-like factor
Group1	comp64502_c0_seq1	VmAP2/ERF004	KX868802	1676.00	EREBP-like factor
Group1	comp164758_c0_seq1	VmAP2/ERF005	KX868803	1245	EREBP-like factor
Group2	comp116109_c0_seq1	VmAP2/ERF006	KX868804	1132.00	EREBP-like factor
Group2	comp157844_c0_seq1	VmAP2/ERF007	KX868805	1068.00	EREBP-like factor
Group2	comp128472_c0_seq1	VmAP2/ERF008	KX868806	580.33	EREBP-like factor
Group2	comp129700_c0_seq1	VmAP2/ERF009	KX868807	418.00	EREBP-like factor
Group2	comp186932_c0_seq1	VmAP2/ERF010	KX868808	466.00	EREBP-like factor
Group3	comp251319_c0_seq1	VmAP2/ERF011	KX868809	431.00	EREBP-like factor
Group3	comp124868_c0_seq1	VmAP2/ERF012	KX868810	1177.00	EREBP-like factor
Group3	comp128319_c0_seq1	VmAP2/ERF013	KX868811	774.65	EREBP-like factor
Group3	comp143146_c0_seq1	VmAP2/ERF014	KX868812	1004	EREBP-like factor
Group3	comp138574_c0_seq4	VmAP2/ERF015	KX868813	1122.79	EREBP-like factor
Group3	comp129405_c0_seq1	VmAP2/ERF016	KX868814	1216.00	EREBP-like factor
Group3	comp85604_c0_seq1	VmAP2/ERF017	KX868815	548.00	EREBP-like factor
Group3	comp107282_c0_seq1	VmAP2/ERF018	KX868816	728.14	EREBP-like factor
Group3	comp143204_c0_seq1	VmAP2/ERF019	KX868817	917.00	EREBP-like factor
Group3	comp127938_c0_seq1	VmAP2/ERF020	KX868818	1056.00	EREBP-like factor
Group3	comp145334_c1_seq1	VmAP2/ERF021	KX868819	928.31	EREBP-like factor

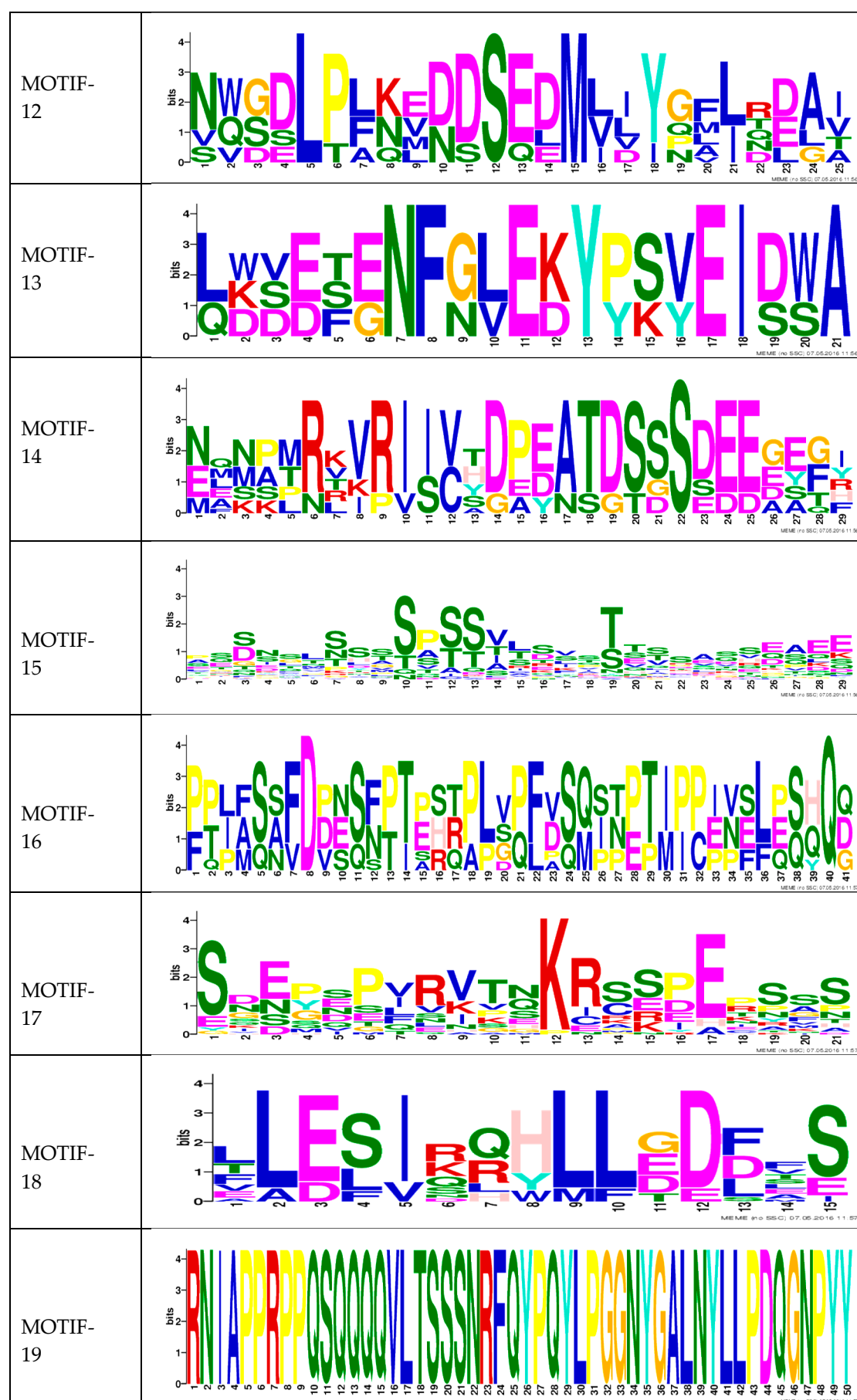
Group3	comp151923_c1_seq1	VmAP2/ERF022	KX868820	545.50	EREBP-like factor
Group3	comp208000_c0_seq1	VmAP2/ERF023	KX868821	882.00	EREBP-like factor
Group4	comp397454_c0_seq1	VmAP2/ERF024	KX868822	706.00	EREBP-like factor
Group4	comp144341_c0_seq1	VmAP2/ERF025	KX868823	1078.00	EREBP-like factor
Group5	comp63102_c0_seq1	VmAP2/ERF026	KX868824	506.00	EREBP-like factor
Group5	comp110005_c0_seq1	VmAP2/ERF027	KX868825	1074.00	EREBP-like factor
Group5	comp150298_c0_seq3	VmAP2/ERF028	KX868826	795.88	EREBP-like factor
Group5	comp157176_c0_seq1	VmAP2/ERF029	KX868827	1026.69	EREBP-like factor
Group6	comp129421_c0_seq1	VmAP2/ERF030	KX868828	1099.00	EREBP-like factor
Group6	comp137242_c0_seq2	VmAP2/ERF031	KX868829	1513.65	EREBP-like factor
Group6	comp137462_c0_seq3	VmAP2/ERF032	KX868830	1707.28	EREBP-like factor
Group6	comp161719_c1_seq4	VmAP2/ERF033	KX868831	867.29	EREBP-like factor
Group6-1	comp160313_c0_seq1	VmAP2/ERF034	KX868832	1412.00	EREBP-like factor
Group6-1	comp162707_c0_seq1	VmAP2/ERF035	KX868833	2013.00	EREBP-like factor
Group7	comp139704_c0_seq1	VmAP2/ERF036	KX868834	2079.00	EREBP-like factor
Group7	comp151256_c0_seq3	VmAP2/ERF037	KX868835	997.94	EREBP-like factor
Group7	comp162529_c0_seq1	VmAP2/ERF038	KX868836	1536.01	EREBP-like factor
Group8	comp146876_c0_seq1	VmAP2/ERF039	KX868837	1089.00	EREBP-like factor
Group8	comp149810_c0_seq1	VmAP2/ERF040	KX868838	1518.34	EREBP-like factor
Group8	comp128719_c0_seq1	VmAP2/ERF041	KX868839	1098.00	EREBP-like factor
Group8	comp140154_c0_seq1	VmAP2/ERF042	KX868840	1365.00	EREBP-like factor
Group8	comp141925_c0_seq1	VmAP2/ERF043	KX868841	341.75	EREBP-like factor
Group8	comp173049_c0_seq1	VmAP2/ERF044	KX868842	795.00	EREBP-like factor
Group9	comp227613_c0_seq1	VmAP2/ERF045	KX868843	420.00	EREBP-like factor
Group9	comp139267_c0_seq1	VmAP2/ERF046	KX868844	870.00	EREBP-like factor
Group9	comp144276_c0_seq3	VmAP2/ERF047	KX868845	1155.52	EREBP-like factor
Group9	comp109538_c0_seq1	VmAP2/ERF048	KX868846	650.00	EREBP-like factor
Group9	comp163543_c0_seq2	VmAP2/ERF049	KX868847	1056.75	EREBP-like factor
Group9	comp141156_c0_seq3	VmAP2/ERF050	KX868848	1144.45	EREBP-like factor
Group9	comp155356_c1_seq1	VmAP2/ERF051	KX868849	1230.00	EREBP-like factor
Group9	comp145295_c0_seq1	VmAP2/ERF052	KX868850	1078.00	EREBP-like factor
Group9	comp149797_c0_seq1	VmAP2/ERF053	KX868851	1037.00	EREBP-like factor
Group9	comp129078_c0_seq3	VmAP2/ERF054	KX868852	1034.51	EREBP-like factor
Group9	comp137888_c0_seq1	VmAP2/ERF055	KX868853	919.00	EREBP-like factor
Group9	comp79448_c0_seq1	VmAP2/ERF056	KX868854	766.00	EREBP-like factor
Group9	comp149261_c0_seq1	VmAP2/ERF057	KX868855	845.31	EREBP-like factor
Group9	comp156406_c1_seq2	VmAP2/ERF058	KX868856	379.16	EREBP-like factor
Group9	comp128686_c0_seq1	VmAP2/ERF059	KX868857	1229.00	EREBP-like factor
Group10	comp122372_c0_seq1	VmAP2/ERF060	KX868858	1976.49	EREBP-like factor
Group10	comp154312_c0_seq2	VmAP2/ERF061	KX868859	1766.91	EREBP-like factor
Group10	comp154195_c0_seq1	VmAP2/ERF062	KX868860	1201.03	EREBP-like factor
Group10	comp143779_c0_seq1	VmAP2/ERF063	KX868861	795.00	EREBP-like factor
Group10	comp162260_c0_seq3	VmAP2/ERF064	KX868862	720.48	EREBP-like factor
RAV	comp159597_c0_seq2	VmAP2/ERF065	KX868863	1253.54	RAV-like factor
RAV	comp169832_c0_seq1	VmAP2/ERF066	KX868864	1305.00	RAV-like factor

AP2	comp159240_c0_seq11	<i>VmAP2/ERF067</i>	KX868865	1080.48	AP2-like factor, ANT lineage
AP2	comp165608_c0_seq13	<i>VmAP2/ERF068</i>	KX868866	2246.56	AP2-like factor, ANT lineage
AP2	comp166307_c0_seq9	<i>VmAP2/ERF069</i>	KX868867	1326.76	AP2-like factor, euAP2 lineage
AP2	comp166849_c0_seq3	<i>VmAP2/ERF070</i>	KX868868	1041.65	AP2-like factor, euAP2 lineage
AP2	comp165181_c0_seq84	<i>VmAP2/ERF071</i>	KX868869	2623.48	AP2-like factor, euAP2 lineage
AP2	comp156517_c1_seq1	<i>VmAP2/ERF072</i>	KX868870	1899.00	AP2-like factor, euAP2 lineage
AP2	comp165500_c1_seq5	<i>VmAP2/ERF073</i>	KX868871	1306.33	AP2-like factor, euAP2 lineage
AP2	comp105036_c0_seq1	<i>VmAP2/ERF074</i>	KX868872	942.00	AP2-like factor, ANT lineage
AP2	comp86450_c0_seq1	<i>VmAP2/ERF075</i>	KX868873	561.00	AP2-like factor, ANT lineage
AP2	comp293964_c0_seq1	<i>VmAP2/ERF076</i>	KX868874	1269.00	AP2-like factor, ANT lineage
AP2	comp111892_c0_seq2	<i>VmAP2/ERF077</i>	KX868875	1085.13	AP2-like factor, ANT lineage
AP2	comp149426_c0_seq2	<i>VmAP2/ERF078</i>	KX868876	1275.65	AP2-like factor, ANT lineage
AP2	comp104878_c0_seq1	<i>VmAP2/ERF079</i>	KX868877	1493.00	AP2-like factor, ANT lineage
AP2	comp155189_c0_seq1	<i>VmAP2/ERF080</i>	KX868878	1066.98	AP2-like factor, euAP2 lineage
solosist	comp167675_c0_seq10	<i>VmAP2/ERF081</i>	KX868879	1694.73	-

Table S2. Conserved motifs identified from the ERF family in *V. fordii* and *V. montana*.







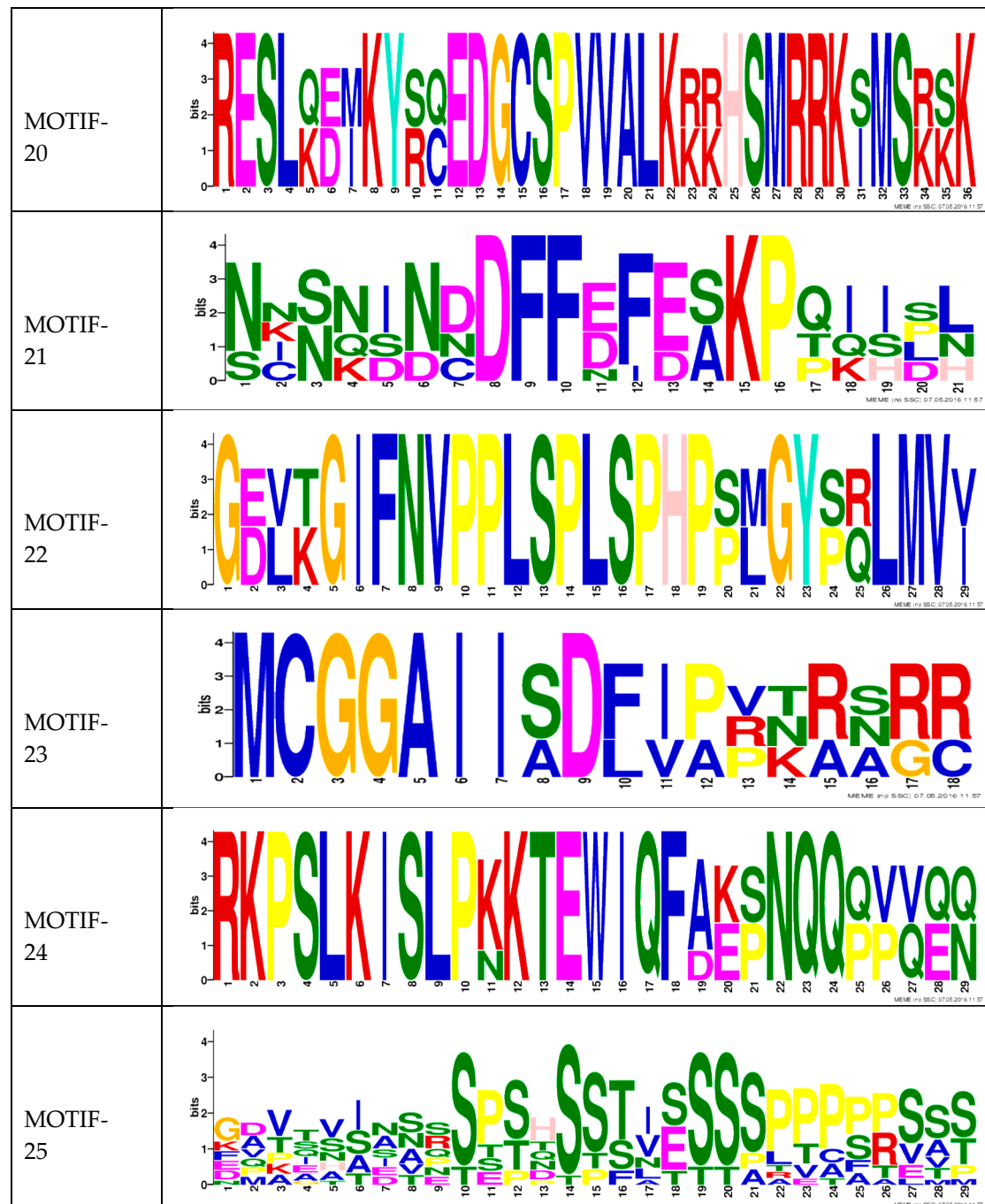


Table S3. The one to one orthologous gene pairs and their corresponding Ka/Ks ratios.

Vf-Transcript-ID	Vm-Transcript-ID	Ka	Ks	Ka/Ks	pValue
comp181389_c0_seq1	comp129405_c0	0	0.00612149	0	0
comp189934_c0_seq4	comp144341_c0	0	0.0125965	0	0
comp189868_c0_seq1	comp137462_c0	0	0.00433721	0	0
comp187442_c0_seq1	comp162529_c0	0	0.0169105	0	0
comp186047_c0_seq1	comp149797_c0	0	0.00631718	0	0
comp189189_c0_seq2	comp159597_c0	0	0.00514015	0	0
comp192732_c0_seq6	comp166849_c0	0	0.00535543	0	0
comp191512_c0_seq2	comp166307_c0	0	0.0192735	0	0
comp179411_c0_seq1	comp149426_c0	0.00169139	0.101434	0.0166748	5.50004×10^{-19}
comp191827_c0_seq1	comp165608_c0	0.0017379	0.0323087	0.0537903	4.51682×10^{-6}
comp184446_c0_seq1	comp104878_c0	0.00208492	0.0364062	0.0572683	0.00264178
comp174782_c0_seq3	comp144276_c0	0.00201057	0.0215903	0.0931237	0.0330677

comp192264_c0_seq1	comp162707_c0	0.0059197	0.0300008	0.197318	0.00640571
comp194219_c2_seq5	comp162260_c0	0.0142319	0.0661226	0.215235	0.0504604
comp176401_c0_seq4	comp116109_c0	0.00276959	0.00946959	0.292472	0.351771
comp191237_c1_seq13	comp167675_c0	0.00186162	0.00634927	0.293202	0.35172
comp178204_c0_seq1	comp149261_c0	0.0046603	0.0158211	0.294562325	0.0888517
comp180742_c0_seq2	comp151256_c0	0.00668351	0.0188792	0.354015	0.116641
comp195632_c1_seq20	comp165181_c0	0.00339996	0.0087504	0.388549	0.195599
comp184881_c0_seq5	comp159240_c0	0.006005	0.013469	0.445838592	0
comp169343_c0_seq2	comp128319_c0	0.00601339	0.0129221	0.465355	0.340267
comp175038_c0_seq1	comp163543_c0	0.0251589	0.0467847	0.53776	0.30829
comp179927_c0_seq1	comp146876_c0	1.66988	2.90621	0.574591	0.127146
comp184116_c0_seq1	comp165500_c1	0.00186881	0.00315658	0.592036	0.529337
comp173281_c0_seq1	comp143204_c0	0.0490596	0.0818801	0.599164	0.292438
comp181356_c0_seq5	comp128686_c0	0.00421772	0.0059239	0.711983	0.582043
comp181196_c0_seq1	comp150298_c0	0.0176049	0.0244858	0.718984064	0.0337182
comp171489_c1_seq1	comp397454_c0	0.0111181	0.0132456	0.839379	0.391042
comp186790_c1_seq1	comp137242_c0	0.116244	0.121525	0.956542	0.818689
comp171620_c0_seq1	comp129078_c0	0.0103302	0.0103997	0.993317115	0.564387
comp181674_c0_seq1	comp138574_c0	2.21627	2.20093	1.00697	1
comp181660_c0_seq2	comp154195_c0	1.34183	1.2143	1.10502	0.536572
comp184569_c0_seq5	comp154312_c0	0.746161	0.624663	1.1945	0.12609
comp160673_c0_seq2	comp64502_c0	2.02707	1.67002	1.2138	0.485206
comp183962_c0_seq1	comp138429_c0	1.27227	0.949497	1.33994	0.29544
comp181105_c0_seq2	comp137888_c0	0.0880494	0.0573395	1.53558	0.32824
comp178925_c0_seq2	comp139704_c0	2.52379	1.60025	1.57713	0.10624
comp184966_c0_seq2	comp157844_c0	0	0	NA	0
comp180080_c0_seq3	comp124868_c0	0	0	NA	0
comp183897_c0_seq3	comp127938_c0	0	0	NA	0
comp176265_c0_seq1	comp145334_c1	0	0	NA	0
comp158438_c0_seq3	comp110005_c0	0	0	NA	0
comp188688_c0_seq1	comp157176_c0	0	0	NA	0
comp183367_c0_seq5	comp160313_c0	0	0	NA	0
comp160872_c0_seq1	comp173049_c0	0	0	NA	0
comp172871_c0_seq1	comp139267_c0	0	0	NA	0
comp189715_c1_seq1	comp141156_c0	0	0	NA	0
comp192585_c1_seq1	comp155356_c1	0	0	NA	0
comp179276_c0_seq1	comp145295_c0	0	0	NA	0
comp129744_c0_seq1	comp79448_c0	0	0	NA	0
comp174721_c0_seq1	comp122372_c0	0	0	NA	0
comp186054_c0_seq1	comp156517_c1	0	0	NA	0

Table S4. List of specific primer sequences used for real-time PCR analysis.

GeneticName	Primer (5'-3')	Length
<i>VfAP2/ERF012-F1</i>	ACCGTGTCTTCAGTAGTTTCG	22
<i>VfAP2/ERF012-R1</i>	GGTCCTGTTAATGGTGCAAAAA	22
<i>VfAP2/ERF022-F1</i>	GTTTCAACTCCTCTTCATCTC	21
<i>VfAP2/ERF022-R1</i>	GATGTTTTTTCTAATGGGTCT	21
<i>VfAP2/ERF043-F1</i>	CTGTTTGTTTCTTTCATGGCGT	22
<i>VfAP2/ERF043-R1</i>	AGCTTCTTCTGGTGTGTCGAATG	23
<i>VfAP2/ERF054-F1</i>	TTCACCAGTAACTGGTTGCCAA	22
<i>VfAP2/ERF054-R1</i>	CCGATGATTATGTGCCGATTAG	22
<i>VfAP2/ERF031-F1</i>	TGATACCGATGCTATTTGG	19
<i>VfAP2/ERF031-R1</i>	CTGCTGCTGTTGTACGTTT	19
<i>VfAP2/ERF027-F1</i>	GTCTAATAATGAACCAGCGGCA	22
<i>VfAP2/ERF027-R1</i>	CAACTCTACTACTGAGCACGGAT	23
<i>VfAP2/ERF047-F1</i>	GGACCTTCGACACAGCTATCGA	22

VfAP2/ERF047-R1	GGTGCGTGTATTCAACTTCCCA	22
VfAP2/ERF058-F1	CTCAGCCCTAGCTCAAGTCATT	22
VfAP2/ERF058-R1	GTGCGTTTGATTGTGGTGGTAT	22
VfAP2/ERF044-F1	CTGCTGCTTTTTTCTTGCTC	21
VfAP2/ERF044-R1	TTCCGGTGGAAATTGTTAG	19
VfAP2/ERF036-F1	TCTCTCTTGCAAACATGTGTGGT	23
VfAP2/ERF036-R1	GGTAGGGATTGATCTTTATTGCC	23
VfAP2/ERF040-F1	GCCGCCGAAATAAGAGATCC	20
VfAP2/ERF040-R1	GCTTTAGCGCCACGAAAGTC	20
VfAP2/ERF045-F1	GTCAAGAAGATGGTTGCTCAC	21
VfAP2/ERF045-R1	GTTGTTCCAAATAATCAGGG	20
VfAP2/ERF046-F1	AGGTAGTGAAATCTTCAAGGATGG	24
VfAP2/ERF046-R1	TGAAGCTAAACCTCCAAAATCACTC	25
VfAP2/ERF049-F1	TGGAGGCTGGACTGGCTGAT	20
VfAP2/ERF049-R1	AGGGTTTCCTGATAACGGTG	20
VfAP2/ERF051-F1	TTCTTCTTCATCTTTGTCGG	20
VfAP2/ERF051-R1	CATTTTCGCATTTCTAACCC	19
VfAP2/ERF052-F1	CATTTTCCTCTCACTTTCCTTC	22
VfAP2/ERF052-R1	CCATGTCTTGAGTCATTCTCAT	24
VfAP2/ERF053-F1	ATGATCGTGTACGGTGCTCTTC	22
VfAP2/ERF053-R1	GCGTTACTCTCACTTGCTGCTG	22
VfAP2/ERF055-F1	AACGGTATCTTCTTGAAGACG	21
VfAP2/ERF055-R1	TCAAACCTGAACCTAACGGAGTC	21
VmAP2/ERF007-F1	ACCCGATATTAACATTTTCGG	21
VmAP2/ERF007-R1	AGTCTTGATTTTGGGGAGGA	20
VmAP2/ERF019-F1	ACCATCTTTGCCTACAACCGCC	22
VmAP2/ERF019-R1	CATTTGCCCCAACTTCTCATCC	22
VmAP2/ERF044-F1	CTGTTTGTTTCTTTCATGGCGT	22
VmAP2/ERF044-R1	AGCTTCTTCTGGTGTGTGCAATG	23
VmAP2/ERF056-F1	TTCACCAGTAACCTGGTTGCCAA	22
VmAP2/ERF056-R1	CCGATGATTATGTGCCGATTAG	22
VmAP2/ERF032-F1	CAATACCAGAGGCAAAACCACT	22
VmAP2/ERF032-R1	GATGACCTGCTTCTCCAAATAG	22
VmAP2/ERF027-F1	GACTTCCTTCTTCCTCGCAAACC	23
VmAP2/ERF027-R1	AAACAACCACACCCTTGACGCT	22
VmAP2/ERF050-F1	GATTGTAGAGGAGCAAGCGAA	21
VmAP2/ERF050-R1	TGGATGAGGAGATAACGGAGAC	22
VmAP2/ERF062-F1	CACACAAAGACAGATCGACGTAA	23
VmAP2/ERF062-R1	GGCTGAAAAAAGAGGGGAGAAT	22
VmAP2/ERF046-F1	CTGCTGCTTTTTTCTTGCTC	21
VmAP2/ERF046-R1	TTCCGGTGGAAATTGTTAG	19
VmAP2/ERF036-F1	GGGAAATGGGCTGCTGAGAT	20
VmAP2/ERF036-R1	ACTGCTGGTGGTTGTTGTGA	20
VmAP2/ERF039-F1	AAACCATCACCACACAACCACC	22
VmAP2/ERF039-R1	CTTTCGGAGCCATTTTCGCA	19
VmAP2/ERF047-F1	CAACAAGGCATGGAATTAGA	20
VmAP2/ERF047-R1	TTAGAGCAACAACAGGTGAGC	21
VmAP2/ERF049-F1	CTTCCTTGCTCTTCCTATTTC	22
VmAP2/ERF049-R1	GATGATGAACAAGCTACAGGTGA	23
VmAP2/ERF052-F1	TGGAGGCTGGACTGGCTGAT	20
VmAP2/ERF052-R1	AGGGTTTCCTGATAACGGTG	20
VmAP2/ERF059-F1	CCCGAAGTACAGCTGCCAGAGA	22

<i>VmAP2/ERF059-R1</i>	CTAACCAAACCCGAGCCCCAT	21
<i>VmAP2/ERF054-F1</i>	GCAACATCAACAACATCATCCTC	22
<i>VmAP2/ERF054-R1</i>	CTTCCGTTATCGTGCTACTCTC	22
<i>VmAP2/ERF055-F1</i>	TAGAGCAGCCTAATAAAAAGA	21
<i>VmAP2/ERF055-R1</i>	CCATTATCCAAAGTGAATCAAACA	24
<i>VmAP2/ERF057-F1</i>	TCAAACCTGAACCTAACGGAGTCG	22
<i>VmAP2/ERF057-R1</i>	GCGGTATCTTCTCGAAGACGA	21

Table S5. Pearson correlation (r) between transcriptome data and qRT-PCR result of selected orthologous genes in *V. fordii* and *V. montana*.

#	GeneticName	r
1	<i>VfAP2/ERF012</i>	0.875
2	<i>VfAP2/ERF022</i>	0.574
3	<i>VfAP2/ERF043</i>	0.997
4	<i>VfAP2/ERF054</i>	0.996
5	<i>VfAP2/ERF031</i>	0.986
6	<i>VfAP2/ERF027</i>	0.997
7	<i>VfAP2/ERF047</i>	0.718
8	<i>VfAP2/ERF058</i>	0.685
9	<i>VfAP2/ERF044</i>	0.825
10	<i>VfAP2/ERF045</i>	0.048
11	<i>VfAP2/ERF053</i>	0.732
12	<i>VmAP2/ERF007</i>	0.999
13	<i>VmAP2/ERF019</i>	0.978
14	<i>VmAP2/ERF044</i>	0.994
15	<i>VmAP2/ERF056</i>	0.993
16	<i>VmAP2/ERF032</i>	0.96
17	<i>VmAP2/ERF027</i>	0.361
18	<i>VmAP2/ERF050</i>	0.994
19	<i>VmAP2/ERF062</i>	0.947
20	<i>VmAP2/ERF046</i>	0.337
21	<i>VmAP2/ERF047</i>	0.978
22	<i>VmAP2/ERF055</i>	0.968