

Additional data:

A

MdMYB124	NPQEESSKKRGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	83
MdMYB88	NPQEESSKKRGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	83
MdFLP	NPQEESSKKRGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	83
AtFLP	MEETKK.....KKKKNI NNQDSKKRGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	95
AtMYB88	MEETTKQNNMKKKKI LLHSDDS KKGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	100
VvMYBa	NQMKKGGNTDAPPKKRGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	90
VvMYBb	NQMKKGGNTDAPPKKRGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	90
FvMYBa	NQEI KKLGNEDS KKGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	91
FvMYBb	NQEI KKLGNEDS KKGRHIVSVSQEDDILRQCI NTGTEWAI IASKFDRTTRQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	91
OsMYBa	MATGPDLTTP AAAASAEAPSASAAKKRHHIVSVSTBEDVLRQIALGTDNTWIIAACFDRTARQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	100
OsMYBb	MATGPDLTTP AAAASAEAPSASAAKKRHHIVSVSTBEDVLRQIALGTDNTWIIAACFDRTARQCRRRVYLYNSDFKGGVSGEDNLLCEAQKIF	100
Consensus	k r h i v w s e d l r q i g t n w i a f d k r q c r r r v y l n s k g g v s e e d l l c e a q	
MdMYB124	GNVTEIAKVVSGRDNVKNRFTLCKRRAKYEALAKENA. ASYI NCNDRVKI RNFNDGTAEATTAPS. KMRRSHPISISE...GERLLEQCG. K	176
MdMYB88	GNVTEIAKVVSGRDNVKNRFTLCKRRAKYEALAKENA. ASYI NCNDRVKI RNFNDGTAEATTAPS. KMRRSHPISISE...GERLLEQCG. K	180
MdFLP	GNVTEIAKVVSGRDNVKNRFTLCKRRAKYEALAKENA. ASYI NCNDRVKI RNFNDGTAEATTAPS. KMRRSHPISISE...GERLLEQCG. K	176
AtFLP	GNVTEIAKVVSGRDNVKNRFTLCKRRAKHEANAKUS.NSNTKRMFLDQI SUPRKS ENETPI AKLKRSHI LDITIE SNYG.RAEC	184
AtMYB88	GNVTEIAKVVSGRDNVKNRFTLCKRRAKHEANAKENRI ACCVNSDNRLLFPDQI SHPLKAESEPLTKMRRSHPINLIEI KSYGDRSHI KVEST	200
VvMYBa	GNVTEIAKVVSGRDNVKNRFTLCKRRAKHEALAKENS. TSYI NSNNRFLFNQFNEDGTIEAAVSL. KMRRTHLPLDTECNCGGETLLSECGTT	188
VvMYBb	GNVTEIAKVVSGRDNVKNRFTLCKRRAKHEALAKENS. TSYI NSNNRFLFNQFNEDGTIEAAVSL. KMRRTHLPLDTECNCGGETLLSECGTT	188
FvMYBa	GNVTEIAKVVSGRDNVKNRFTLCKRRAKYEALAKENA. TSYMNFNGKRVII RNFNDGTENTSPL. KMRRSHPISISEENCYGDRRHQCC. K	187
FvMYBb	GNVTEIAKVVSGRDNVKNRFTLCKRRAKYEALAKENA. TSYMNFNGKRVII RNFNDGTENTSPL. KMRRSHPISISEENCYGDRRHQCC. K	187
OsMYBa	GNVTEIAKVVSGRDNVKNRFTLCKRRARDDELFRENG. SLCSS TSSKRALVQTCLSGAS GSAPPI. KMRPCNS. DFKENMTPNNRLVGQC. K	195
OsMYBb	GNVTEIAKVVSGRDNVKNRFTLCKRRARDDELFRENG. SLCSS TSSKRALVQTCLSGAS GSAPPI. KMRPCNS. DFKENMTPNNRLVGQC. K	195
Consensus	g n w t e i a k v v s g r d n v k n r f t l c k r a k k k r n f n g t i e a a v s l k m r r t h l p l d t e c n c g g e t l l s e c g t t	
MdMYB124	MSQIRAPFAVLIN. VHNVENLPDNNVNGTKEVPVNAVQK. SRFGSFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	273
MdMYB88	INQIRPPFTVLIQN. AHNVENLQCHNGHSI KEVPGNAVON. SKFGSFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	277
MdFLP	MSQIRAPFAVLIN. VHNVENLPDNNVNGTKEVPVNAVQK. SKFGSFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	273
AtFLP	VNGQIRSPFVLARN. ATGI DSIIEBQNTS NVNES DGEQ.NFKLKKDDKVTALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	273
AtMYB88	NQQRPPFVAVLN. ATSSDGTETEQKI GNVKES DGEKSN. G.EVFLKKDDKVTALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	294
VvMYBa	TNGQIRPPFAVLVN. FRSVNSLPYCHHVGS TKEVSNDSQN. NKI CGTFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	285
VvMYBb	TNGQIRPPFAVLVN. FRSVNSLPYCHHVGS TKEVSNDSQN. NKI CGTFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	285
FvMYBa	TNGQIRAPFTVLIQN. I HNVENLQCHTVNI TKDDPSNAQT. NKFGSFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	284
FvMYBb	TNGQIRAPFTVLIQN. I HNVENLQCHTVNI TKDDPSNAQT. NKFGSFLRKDDRI IALNQAELLSSLAIRNAGNTDQCSLENAVKVLCDFLNCSK	284
OsMYBa	STQDSRCPALVYQNNQDNNTDTCNLVAKTAAKQLFAGECNCVKEGFLNKDDRI ATLCRADLLCSLATNTENTSCMDEAVQCLHFLKKDD	295
OsMYBb	STQDSRCPALVYQNNQDNNTDTCNLVAKTAAKQLFAGECNCVKEGFLNKDDRI ATLCRADLLCSLATNTENTSCMDEAVQCLHFLKKDD	295
Consensus	q r p n q f i k d d k l q a l l s i a k n n t q s a w q l	
MdMYB124	DSGI LSYGI NDFDQLEDLKYLLDLRSTTGSRPSVQHC. QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	353
MdMYB88	DSGI LSYGI NDFDQLEDLKYLLDLRSTTGSRPSVQHC. QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSP.....	354
MdFLP	DSGI LSYGI NDFDQLEDLKYLLDLRSTTGSRPSVQHC. QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	350
AtFLP	ENLFRYGI PDI DFKI EEFKELI EOLRSYBENQLSVR...QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	348
AtMYB88	ENLFRYGI PDI DFKI EEFKELI EOLRSYBENQLSVR...QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	374
VvMYBa	ESDMLRFNI SENSDFCLEDFKDVVDELRSSTGSRPSVR...QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	362
VvMYBb	ESDMLRFNI SENSDFCLEDFKDVVDELRSSTGSRPSVR...QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	362
FvMYBa	ESDI LSYGAS EFDQLEDLKYLLDLRSTTGSRPSVR...QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	361
FvMYBb	ESDI LSYGAS EFDQLEDLKYLLDLRSTTGSRPSVR...QPDUEE...SPGSEBYSTGS...TLLSQTEYQVEKNEVEIGSL.....	360
OsMYBa	DNIMSESSNS GNASLLELDLILVDPYENEBEEDQLREQTEQI DVENKQNSQTSNBEVTSQVMPDNKNEDCPNKDS TEDNNMEPCPGEDI PTSNLETA	395
OsMYBb	DNIMSESSNS GNASLLELDLILVDPYENEBEEDQLREQTEQI DVENKQNSQTSNBEVTSQVMPDNKNEDCPNKDS TEDNNMEPCPGEDI PTSNLETA	395
Consensus	d n i m s e s s n s g n a s l l e l d l i l v d p y e n e b e e d q l r e q t e q i d v e n k q n s q t s n b e v t s q v m p d n k n e d c p n k d s t e d n n m e p c p g e d i p t s n l e t a	
MdMYB124	NQEI RPSGCSI PI EGKNGVDCCEKGI FSE...KQ. EI FPS CDEATKDYAVVS ALSSI EFNPSI KVTPIFRS LAAG	424
MdMYB88	NQEI RLGSHSI PI EGQNDVSDCEKGI VSE...KQ. EI FPS CDEGRKDYAVVS ALSNTEFTSPFKVVPFRS LAAG	425
MdFLP	NQEI RPSGCSI PI EGKNGVDCCEKGI FSE...KQ. EI FPS CDEATKDYAVVS ALSSI EFNPSI KVTPIFRS LAAG	421
AtFLP	EHKCVGEELL.....VPKNPEENPI SGEENSSPI QVTPIFRS LADG	391
AtMYB88	SHCCNGGELLQDNGI VSDATVEQVGLLST.....GHEVLKNSNETVPI PGEEFNPSVPCVTPIFRS LAAG	439
VvMYBa	HCEI GVRLQTI PMD. QNGFEECVKVLS GTT. TNQ. EI FPS CDEPKTNDVVAS NLSSTEPSSPLCVTPIFRS LAAG	435
VvMYBb	HCEI GVRLQTI PMD. QNGFEECVKVLS GTT. TNQ. EI FPS CDEPKTNDVVAS NLSSTEPSSPLCVTPIFRS LAAG	436
FvMYBa	NQEI PPESQSI HI GGQNKI GELEKGI VSS GT. RKQ. EI LPS CDEATKEDAVVS ALSSTEPSSPI QVTPIFRS LAAG	435
FvMYBb	NQEI PPESQSI HI GGQNKI GELEKGI VSS GT. RKQ. EI LPS CDEATKEDAVVS ALSSTEPSSPI QVTPIFRS LAAG	434
OsMYBa	AI EDLSLQCVEYSSPVHTVI QAKTAEI AASENLS EVLEHNRLCI QLASPAQTT. PVEANAETPAS EKLEVVCKNNPSCI EFTSPARTVTPFLPYADD	494
OsMYBb	AI EDLSLQCVEYSSPVHTVI QAKTAEI AASENLS EVLEHNRLCI QLASPAQTT. PVEANAETPAS EKLEVVCKNNPSCI EFTSPARTVTPFLPYADD	495
Consensus	f s p p f a	
MdMYB124	IPSPRFSESERNFLLKTLGELSPCPNPSTNPSQPPPCRRSLLCS	468
MdMYB88	IPSPRFSESERNFLLKTLGELSPCPNPSTNPSQPPPCRRSLLCS	469
MdFLP	IPSPRFSESERNFLLKTLGELSPCPNPSTNPSQPPPCRRSLLCS	465
AtFLP	IPSPCFSESERNFLLKTLGIESSPCPNSANPSKPPPCRRVLLHS	435
AtMYB88	IPSPCFSESERNFLLKTLGIESSPCPNSANPSKPPPCRRVLLHS	455
VvMYBa	IPSPRFSESERNFLLRAGMESPTNPSSNPSQPPPCRRALLCS	479
VvMYBb	IPSPRFSESERNFLLRAGMESPTNPSSNPSQPPPCRRALLCS	480
FvMYBa	IPSPRFSESERNFLLKTLGADSPFPNPSTN. SCTPLCKRALLCS	478
FvMYBb	IPSPRFSESERNFLLKTLGADSPFPNPSTN. SCTPLCKRALLCS	477
OsMYBa	NPFPFTASERNFLLSVLELTSPGSRPDT. . GCPSCRRALLNS	536
OsMYBb	NPFPFTASERNFLLSVLELTSPGSRPDT. . GCPSCRRALLNS	537
Consensus	p p f s l	

B

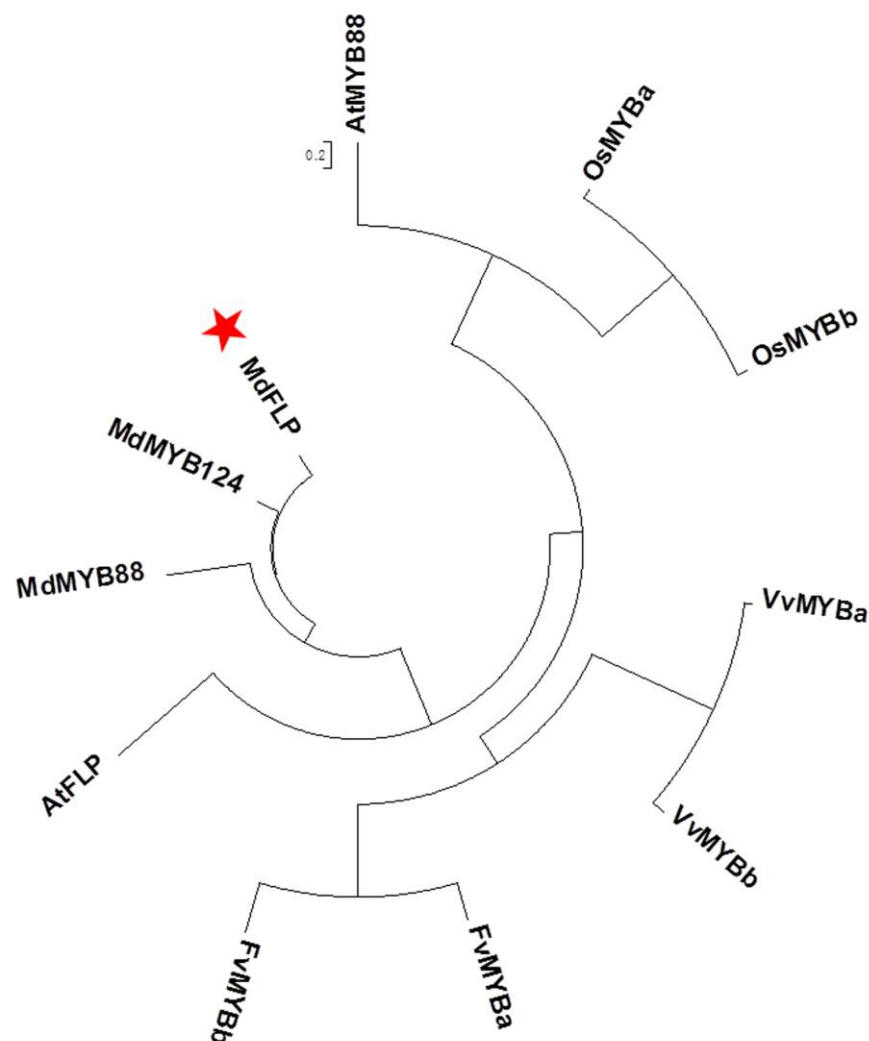


Fig. S1 Comparison of MdFLP with their close homologs in plant species. (A) Comparison of amino acid sequences of MdFLP with their close homologs. The accession numbers for the aligned proteins are: *AtMYB88*, Arabidopsis thaliana NP_001030957.1; *AtMYB124* (*MdFLP*), Arabidopsis thaliana NP_563948.1; *MdFLP*, Malus domestica XP_017192102.1; *MdMYB88*, Malus domestica ASW25823.1; *MdMYB124*, Malus domestica ASW25824.1; *VvMYB a*, Vitis vinifera XP_010652303.1; *VvMYB b*, Vitis vinifera XP_010652298.1; *FvMYB a*, Fragaria vesca XP_004297324.1; *FvMYB b*, Fragaria vesca XP_011463081.1; *OsMYB a*, Oryza sativa EEC82494.1; *OsMYB b*, Oryza sativa NP_001060344.1. (B) Phylogenetic tree of MdFLP and their close homologs in plant species. The protein identities are the same as in A, red star represents MdFLP.

MdFLP.seq	CNNATNNNTNNNN . ANNNNTNNNNANATGCCCGAGGAGGATCAAGAAGAAGGACGCCACATCGTTAGTTGGTCTCAAGAGCAAGATGATATACTGA	98
MdoMYB148.seq	CNNATNNNNNNNNNNNNNNNNNNANATGCCCGAGGAGGATCAAGAAGAAGGACGCCACATCGTTAGTTGGTCTCAAGAGCAAGATGATATACTGA	100
Consensus	cnnatnn nnn annnnnnnnnnanattgccgcaggaggagtc aaagaagaaggagcgccacatcgttagttggctctcaaggaggaagatgatatactga	
MdFLP.seq	CGAATCAAAATTAACACCCATGGAACAGAAAATTTGGGCTATCATTGCATCTAAATTCAGGATAAAACAACAGACAGTGCAGGACAAGATGGTACACATA	198
MdoMYB148.seq	CGAATCAAAATTAACACCCATGGAACAGAAAATTTGGGCTATCATTGCATCTAAATTCAGGATAAAACAACAGACAGTGCAGGACAAGATGGTACACATA	200
Consensus	ggaatcaaattaacacccatggaacagaaaattgggctatcattgcattcaaatcaaggataaaacaaccagacagtcaggaggaagatggtacacata	
MdFLP.seq	CTTGAATTCCTGACTTCAAGAAAGGAGGGTGTCTACAGAGGAAGACATGCTCTTGTCCGAGGCTCAAAAGATATTTCGGAACAGATGCAGACAAAATAGCC	298
MdoMYB148.seq	CTTGAATTCCTGACTTCAAGAAAGGAGGGTGTCTACAGAGGAAGACATGCTCTTGTCCGAGGCTCAAAAGATATTTCGGAACAGATGCAGACAAAATAGCC	300
Consensus	cttgaattctgacttcaagaaaggagggtgttcaccagaggaagacatgctcttgtgcgaggctcaaaagatatcggaaacagatggacagaaatagcg	
MdFLP.seq	AAGGTGTTTCGGGAAGAACTGACATGCTGTGAAAAACCGGTTTTCCACCTTGTGCAAGAAGAGAGCAAAATATGAAGCCTTACCTAAAGAGAATGCCG	398
MdoMYB148.seq	AAGGTGTTTCGGGAAGAACTGACATGCTGTGAAAAACCGGTTTTCCACCTTGTGCAAGAAGAGAGCAAAATATGAAGCCTTACCTAAAGAGAATGCCG	400
Consensus	aagggtgtttcgggaagaactgacaatgctgtgaaaaacccgggtttccaccttgtgcaagaagagagcaaaatatgaagccttagctaaagagaatgccg	
MdFLP.seq	CTTCATATATCAATCAGAATGACAAAAGGCTCAAAATCCGAAATGGATTCAATACAGATGGAACAGCAGAACTACAGCACCTTCTAAGAAGATGAGGAG	498
MdoMYB148.seq	CTTCATATATCAATCAGAATGACAAAAGGCTCAAAATCCGAAATGGATTCAATACAGATGGAACAGCAGAACTACAGCACCTTCTAAGAAGATGAGGAG	500
Consensus	cttcataatcaatcagaatgacaaaagggtcaaaatccgaaatggattcaatcacagatggaacagcagaactacagcaccttcaagaagatgaggag	
MdFLP.seq	AAGCCACATCCCTAGTCTCTCCGAGGGGACAGACTACTCGAGCAGTGTGGAAGATGAGTCAGCAGCTAAGAGCTCCATTTCGAGTGTGATTGAGAAT	598
MdoMYB148.seq	AAGCCACATCCCTAGTCTCTCCGAGGGGACAGACTACTCGAGCAGTGTGGAAGATGAGTCAGCAGCTAAGAGCTCCATTTCGAGTGTGATTGAGAAT	600
Consensus	aagccaatccctagtctctccgaggggacagactactcgagcagtggtgaaagatgagtcagcagctaaagctccatttcgagtggtgattcagaat	
MdFLP.seq	CTCCACAATGTAGAGAATCTGCCAGACCAGAAATATGTGAATGGCACCAAGGAAGTCCCGTGAATGCAGTACAAAAGACCAAGTTTACGGATCATTTC	698
MdoMYB148.seq	CTCCACAATGTAGAGAATCTGCCAGACCAGAAATATGTGAATGGCACCAAGGAAGTCCCGTGAATGCAGTACAAAAGACCAAGTTTACGGATCATTTC	700
Consensus	gtccacaatgtagagaatctgccagaccagaataatgtaagtggcaccaagggaagtcctcgatgaatgcagtaaaaaagacaagtttcacggatcatttc	
MdFLP.seq	TCAGAAGGATGATCCGAAGATAATCGCTTTCATGCAACAAGCAGAATTCCTCAGCTCGCTGGCATTAAAGTTAATGCAGAGAACACAGACCAGAGTCT	798
MdoMYB148.seq	TCAGAAGGATGATCCGAAGATAATCGCTTTCATGCAACAAGCAGAATTCCTCAGCTCGCTGGCATTAAAGTTAATGCAGAGAACACAGACCAGAGTCT	800
Consensus	tcaagaaggatgatccgaagataatcgcttgcacacaagcagaatgctcagctcgctggcattaaaaagttaatgcagagaacacagaccagagtcct	
MdFLP.seq	TGAAAAATGCATGGAAGGTGCTCCAAGATTCTTGAATCAAGCAAGATAGTGACATCCTCAGTTATGGAATTAAAGATTTTGATTTTCAACTCGAAGAT	898
MdoMYB148.seq	TGAAAAATGCATGGAAGGTGCTCCAAGATTCTTGAATCAAGCAAGATAGTGACATCCTCAGTTATGGAATTAAAGATTTTGATTTTCAACTCGAAGAT	900
Consensus	tgaaaatgcattggaaggtgctccaagatttcttgaatcaagcagaagatgacatcctcagttatggaattaacgattttgattttcaactcgaagat	
MdFLP.seq	CTTAATATCTGTTAGAGGACTTAAGGACCACTGAAGGAAGCCGACCATCTTGCAGCAGCCTGATTATACGAGGAGTCTCCAGGAAGTTCGGAAT	998
MdoMYB148.seq	CTTAATATCTGTTAGAGGACTTAAGGACCACTGAAGGAAGCCGACCATCTTGCAGCAGCCTGATTATACGAGGAGTCTCCAGGAAGTTCGGAAT	1000
Consensus	cttaaatatctgttagaggacttaaggagaccactgaagggaagccgaccatcttggcagcagcctgatttatacgaggagtcctccaggaaagttccgaat	
MdFLP.seq	ACAGTACAGGGTCAACTCTTCTGTCCCAACAGAACTACTATCAAGTGGAAAAAATCAAGTTGAAATAGGTTCACTGAATCAGGAGATTTCGACCAGGGTC	1098
MdoMYB148.seq	ACAGTACAGGGTCAACTCTTCTGTCCCAACAGAACTACTATCAAGTGGAAAAAATCAAGTTGAAATAGGTTCACTGAATCAGGAGATTTCGACCAGGGTC	1100
Consensus	acagtacagggccaactcttctgtcccaacagaatactatcaagtggaaaaaaatcaagttgaaataggttcactgaatcaggagatttcgaccagggtc	
MdFLP.seq	ACAGTCAATTCCTATTGAAGGGAATAATCGTGTGGTGAATGTGAGAAAGGGATTTTTCGAAAAGCAAGAGATATTTCATCATGTGATGAAGCAACA	1198
MdoMYB148.seq	ACAGTCAATTCCTATTGAAGGGAATAATCGTGTGGTGAATGTGAGAAAGGGATTTTTCGAAAAGCAAGAGATATTTCATCATGTGATGAAGCAACA	1200
Consensus	acagtcatttcctattgaagggaataatcggtgtggatgttgagaagggtttttccgaaaagcaagagatatccatcatgtgatgaagcaaca	
MdFLP.seq	AAAGACTACGCAGTTGTTTCTGCATTGTCAAGTATAGAGTTCAATTTCTCTATTAAGTTACCCCATTTGTTAGATCTTGGCAGCAGGAATTCCTAGCC	1298
MdoMYB148.seq	AAAGACTACGCAGTTGTTTCTGCATTGTCAAGTATAGAGTTCAATTTCTCTATTAAGTTACCCCATTTGTTAGATCTTGGCAGCAGGAATTCCTAGCC	1300
Consensus	aaagactacgcagttgtttctgcattgtcaagtatagagttcaatttctcctattaaagttaccccatgttcagatcctggcagcaggaatcctagcc	
MdFLP.seq	CAAAATTTTCTGAAAGTGAAGGAATTTCTTGCTCAAAACGCTTGGAGAGGACTCCCTTGCCTCCCAACCCAGCACCACCTTTCACACCCGCCACCTTG	1398
MdoMYB148.seq	CAAAATTTTCTGAAAGTGAAGGAATTTCTTGCTCAAAACGCTTGGAGAGGACTCCCTTGCCTCCCAACCCAGCACCACCTTTCACACCCGCCACCTTG	1400
Consensus	caaaattttctgaaagtgaagggaatttcttgcctcaaaacgcttggagaggactcccttgcctcccaacccaagcacaatccttcacaaccgccaccttg	
MdFLP.seq	CAAACGATCCCTTCTCCAAAGTCTATTA	1426
MdoMYB148.seq	CAAACGATCCCTTCTCCAAAGTCTATTA	1500
Consensus	caaacgatcccttctccaaa t a	
MdFLP.seq	CTTGATTTTACAGTTGTACAGAATCTGCTATATCCCTAGTTCAGAGTGTGAGACTAATGTAAGCATACATAGGCAGCTCGCCGATATTTCCGCTA	1426
MdoMYB148.seq	CTTGATTTTACAGTTGTACAGAATCTGCTATATCCCTAGTTCAGAGTGTGAGACTAATGTAAGCATACATAGGCAGCTCGCCGATATTTCCGCTA	1598
Consensus		

Fig. S2 Nucleotides alignment of MdFLP with MdoMYB148 from GDR. Comparison of nucleotide sequences of MdFLP we cloned and MdoMYB148 (MDP000210970) downloaded from GDR. The similarity is 88.68%. GDR, Genome Database for Rosaceae.

MdFLP.seq	CNNATNNTNNNNNNNNNNNNANATCCCGCAGGAGGACTCAAGAAGAACGAGCGCCATCGTTACTTGGTCTCAAGAGGAGATGATATACTGAGC	100
MdMYB124.seq	CNNATNNTNNNNNNNNNNNNANATCCCGCAGGAGGACTCAAGAAGAACGAGCGCCATCGTTACTTGGTCTCAAGAGGAGATGATATACTGAGC	100
MdMYB88.seq	CNNATNNTNNNNNNNNNNNNANATCCCGCAGGAGGACTCAAGAAGAACGAGCGCCATCGTTACTTGGTCTCAAGAGGAGATGATATACTGAGC	100
Consensus	cnnatnntnnnnnnnnnnnnanattcccgaggaggagtc aaagaagaaggagcgcca atcggtta ttggctctcaaggaga gatga atactgagg	
MdFLP.seq	AATCAAAATTAACCCATGGAACAGAAAATTGGGCTATCATTCGATCTAAATTCAGGATAAAACAACACAGACACTGCAGGAGAAGATGTTACACATACT	200
MdMYB124.seq	AATCAAAATTAACCCATGGAACAGAAAATTGGGCTATCATTCGATCTAAATTCAGGATAAAACAACACAGACACTGCAGGAGAAGATGTTACACATACT	200
MdMYB88.seq	AATCAAAATTAACCCATGGAACAGAAAATTGGGCTATCATTCGATCTAAATTCAGGATAAAACAACACAGACACTGCAGGAGAAGATGTTACACATACT	200
Consensus	aatcaaat a c ccatggaacagaaaattgggct tcatctgcatctaaattcaaggataaaacaaccagacagtgcaggagaagatggatcacatact	
MdFLP.seq	TGAATTCCTGACTTCAAGAAAGGAGGCTGGTCACCAGAGGAAGACATGCTCTTGTCGAGGCTCAAGATATTCCGAACAGATGGACAGAAATAGCGAA	300
MdMYB124.seq	TGAATTCCTGACTTCAAGAAAGGAGGCTGGTCACCAGAGGAAGACATGCTCTTGTCGAGGCTCAAGATATTCCGAACAGATGGACAGAAATAGCGAA	300
MdMYB88.seq	TGAATTCCTGACTTCAAGAAAGGAGGCTGGTCACCAGAGGAAGACATGCTCTTGTCGAGGCTCAAGATATTCCGAACAGATGGACAGAAATAGCGAA	300
Consensus	tgaattctgacttcaagaa ggagg tggtcaccagaggaagacatgctcttgtcgaggctca aagatattcgg aacagatggacagaaatagc aa	
MdFLP.seq	GGTGTTCCTGGGAAGAACTGACAATGCTGTGAAAACCGGTTTTTCACCTTCTGCAAGAAGACAGCAAAATATGAGCCTTAGCTAAAGCAATGCCGT	400
MdMYB124.seq	GGTGTTCCTGGGAAGAACTGACAATGCTGTGAAAACCGGTTTTTCACCTTCTGCAAGAAGACAGCAAAATATGAGCCTTAGCTAAAGCAATGCCGT	400
MdMYB88.seq	GGTGTTCCTGGGAAGAACTGACAATGCTGTGAAAACCGGTTTTTCACCTTCTGCAAGAAGACAGCAAAATATGAGCCTTAGCTAAAGCAATGCCGT	400
Consensus	ggt gtttc ggaagaactgacaatgc gtgaaaaccgggttttc ac ttgtgcaagaagagagcaaaatata gccttagctaaaga aatgc t	
MdFLP.seq	TCATATATCAATCAGATGACAAAAGGCTCAAAATCGAAATGGATTCAATACAGATGGAACAACAGAAATACAGCACCTTCTAAGAAGATGAGGAGAA	500
MdMYB124.seq	TCATATATCAATCAGATGACAAAAGGCTCAAAATCGAAATGGATTCAATACAGATGGAACAACAGAAATACAGCACCTTCTAAGAAGATGAGGAGAA	500
MdMYB88.seq	TCATATATCAATCAGATGACAAAAGGCTCAAAATCGAAATGGATTCAATACAGATGGAACAACAGAAATACAGCACCTTCTAAGAAGATGAGGAGAA	500
Consensus	tc ta at aatca aatgacaaaagggtca aat cgaattggattc aaatcacagatggaaca cagaac acagacc ctaagaagatgaggagaa	
MdFLP.seq	GCCACATCCCTAGTCTCTCCAG.....GGGGACAGACTACTCGACAGTGTGGAAGATGATCAGCAGCTAAGAGCTCGATTTCAGTGT	588
MdMYB124.seq	GCCACATCCCTAGTCTCTCCAG.....GGGGACAGACTACTCGACAGTGTGGAAGATGATCAGCAGCTAAGAGCTCGATTTCAGTGT	588
MdMYB88.seq	GCCACATCCCTAGTCTCTCCAG.....GGGGACAGACTACTCGACAGTGTGGAAGATGATCAGCAGCTAAGAGCTCGATTTCAGTGT	600
Consensus	gccacatcccta tctctcc a ggggacagactac ga cagtggtggaagat a ttagcagctaaaga ctcc ttt c ggtgt	
MdFLP.seq	GATTCAGAATCTCCACAATGTAGAGAATCTGCGAGACCAATAAATCTGAATGCAACAAGGAAGTCCCCGTAATGCAAGTACAAAACAGCAAGTTTCA	688
MdMYB124.seq	GATTCAGAATCTCCACAATGTAGAGAATCTGCGAGACCAATAAATCTGAATGCAACAAGGAAGTCCCCGTAATGCAAGTACAAAACAGCAAGTTTCA	688
MdMYB88.seq	GATTCAGAATCTCCACAATGTAGAGAATCTGCGAGACCAATAAATCTGAATGCAACAAGGAAGTCCCCGTAATGCAAGTACAAAACAGCAAGTTTCA	700
Consensus	gattcagaatg cacaatgtagagaatctgc agaccag ataa g g at gca caaggaggtccccg gaatgcagttacaaa agcaagtttca	
MdFLP.seq	GGATCATTTCTCAGAAGGATGACCGAAGATAATCGCTTTGATGCAACAACCGAATTGCTCAGCTCGCTGGCATTAAAGTTAACTCAGAGAACACAG	788
MdMYB124.seq	GGATCATTTCTCAGAAGGATGACCGAAGATAATCGCTTTGATGCAACAACCGAATTGCTCAGCTCGCTGGCATTAAAGTTAACTCAGAGAACACAG	788
MdMYB88.seq	GGATCATTTCTCAGAAGGATGACCGAAGATAATCGCTTTGATGCAACAACCGAATTGCTCAGCTCGCTGGCATTAAAGTTAACTCAGAGAACACAG	800
Consensus	ggatcatttctc agaaggatga cagaagataat cgtttgtgcaaacagc ga ttgctcagctcgctggcattaaagttaa cagaagaacag	
MdFLP.seq	ACCAGAGTCTTGAAATGCGTGAAGGGTGCTCCAAGATTCTTGAATCAAAGCAAAAGATAGTACATCCTCAGTIATGGAATTACGATTTTGATTTC	888
MdMYB124.seq	ACCAGAGTCTTGAAATGCGTGAAGGGTGCTCCAAGATTCTTGAATCAAAGCAAAAGATAGTACATCCTCAGTIATGGAATTACGATTTTGATTTC	888
MdMYB88.seq	ACCAGAGTCTTGAAATGCGTGAAGGGTGCTCCAAGATTCTTGAATCAAAGCAAAAGATAGTACATCCTCAGTIATGGAATTACGATTTTGATTTC	900
Consensus	accagagtcttgaaatgc tgaagggtgtccaagatttcttgaatcaaagcaaaagatagtgacatcctcagttatggaatt acgattttgattttca	
MdFLP.seq	ACTCGAAGATCTTAAATATCTGTTAGAGGACTTAAGGAGACACTGAAAGGAAGCCGACCATCTTGGCA.....GCAGCGATGATATACGAGG	979
MdMYB124.seq	ACTCGAAGATCTTAAATATCTGTTAGAGGACTTAAGGAGACACTGAAAGGAAGCCGACCATCTTGGCA.....GCAGCGATGATATACGAGG	988
MdMYB88.seq	ACTCGAAGATCTTAAATATCTGTTAGAGGACTTAAGGAGACACTGAAAGGAAGCCGACCATCTTGGCA.....GCAGCGATGATATACGAGG	991
Consensus	actcgaagatctttaaattctgttagaggacttaaggag ac actga ggaagccgaccatcttggca gcagcc gat tat cga ga	
MdFLP.seq	TCTCCAGGAAGTTCCGAATACAGTACAGGTCACACTCTTCTGTCCCAAAACAGAACTATCAAGTGGAAATAAATGAAGTTGAAATAGGTTCACTCAATC	1079
MdMYB124.seq	TCTCCAGGAAGTTCCGAATACAGTACAGGTCACACTCTTCTGTCCCAAAACAGAACTATCAAGTGGAAATAAATGAAGTTGAAATAGGTTCACTCAATC	1088
MdMYB88.seq	TCTCCAGGAAGTTCCGAATACAGTACAGGTCACACTCTTCTGTCCCAAAACAGAACTATCAAGTGGAAATAAATGAAGTTGAAATAGGTTCACTCAATC	1091
Consensus	tctccaggaagtcc gaatcacagtacagggtcaactcttctgtcccaaacagaat ctatcaagtggaa aaaaatgaagttgaaataggttcac gaatc	
MdFLP.seq	AGGAGATTTCGACAGGGTCACACTCAATTCCTATTGAAGGCCAAAATGCTGTGCTGATTGTGAGAAAGGGATTTTTCCGAAAAGCAAGAGATATTTC	1179
MdMYB124.seq	AGGAGATTTCGACAGGGTCACACTCAATTCCTATTGAAGGCCAAAATGCTGTGCTGATTGTGAGAAAGGGATTTTTCCGAAAAGCAAGAGATATTTC	1188
MdMYB88.seq	AGGAGATTTCGACAGGGTCACACTCAATTCCTATTGAAGGCCAAAATGCTGTGCTGATTGTGAGAAAGGGATTTTTCCGAAAAGCAAGAGATATTTC	1191
Consensus	aggagatttcgac agggtcaca tcaattcctattgaaggg aaaaatg tgtt gtgattgtgagaaaggatt tttccgaaaagcaagagatatttcc	
MdFLP.seq	ATCATGTGATGAAGCAAAAAGACTACCGAGTTGTTTCGGATTGTCAACTATAGAGTTCAATTTCTCTATTAAAGTTACCCCATTTGTCAGATCCTTG	1279
MdMYB124.seq	ATCATGTGATGAAGCAAAAAGACTACCGAGTTGTTTCGGATTGTCAACTATAGAGTTCAATTTCTCTATTAAAGTTACCCCATTTGTCAGATCCTTG	1288
MdMYB88.seq	ATCATGTGATGAAGCAAAAAGACTACCGAGTTGTTTCGGATTGTCAACTATAGAGTTCAATTTCTCTATTAAAGTTACCCCATTTGTCAGATCCTTG	1291
Consensus	atcatgtgatgaag aa aaaaagactacgcagttgtttctgc ttgtcaa ta gatttca ttctct ttaaagtt cccattgttcagatccttg	
MdFLP.seq	GCAGCAGGAATTCCTAGCCCAAAATTTTCTGAAAGTGAAGGAATTTCTTGCTCAAAACGCTTGGAGAGGACTCCCCCTGCCCAACCAAGCACAATC	1379
MdMYB124.seq	GCAGCAGGAATTCCTAGCCCAAAATTTTCTGAAAGTGAAGGAATTTCTTGCTCAAAACGCTTGGAGAGGACTCCCCCTGCCCAACCAAGCACAATC	1388
MdMYB88.seq	GCAGCAGGAATTCCTAGCCCAAAATTTTCTGAAAGTGAAGGAATTTCTTGCTCAAAACGCTTGGAGAGGACTCCCCCTGCCCAACCAAGCACAATC	1391
Consensus	gcagcaggaattcctagcccaaaattttctgaaagtga aggaatttctgtctcaaaacgcttggagaggactccccctgccca cccaagcacaatc	
MdFLP.seq	CTTCACAACCGCCACCTGCAACGATCCCTCTCCAAACTCTATA	1425
MdMYB124.seq	CTTCACAACCGCCACCTGCAACGATCCCTCTCCAAACTCTATA	1434
MdMYB88.seq	CTTCACAACCGCCACCTGCAACGATCCCTCTCCAAACTCTATA	1437
Consensus	cttcacaacgcccacctgcaaacgatccct ctccaaagtctata	

Fig. S3 Comparison of nucleotide sequences of MdFLP, MdMYB88 and MdMYB124.

AAAAAAGGATTAAATAAAAACAGAGTTCATTTTATAAAGGACCCACTTTATTAGACTGACATAAAAAACAGAGGAGCAGATTTT
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 CGACATTCATTCCCGCGCGCATGACATCCGCGCATTTCTCCGAAACCGCGACGCTTTGTCCCGRCAGGCATTCAAAACGTC
 CGTCGTAGTCCAACCTCAGCTTCAGCCCGGGCTCTTCTCCGCGGGGGGCTTGGGAATCGGACTCGCTCCTTCGCGCAT
 TCCGCTGTGATTTCGATTCT(b)CAAGACCGACAGTTTCTCCACCTCTCTCTCTCTCTCTCTGCTGTGGCCGCTCGCGGA
 CGCCGGGCGCGAAGATGACAGATTTGTGTAATCTGGCGAGATTTCAAGAACATCTACGGTGGGAAAACTCCACCGATTC
 CCTCGTCGACGTGCCTCAACGGCCTCACTCCTCCTCTCTCGACCCGACCTCGAATTTCCCGCCAAATCCGAGCCCTATTG
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 GATTCGAGAGAGTTGAGGAGGAGAGAGGTTGAGGTGAGGTTGATGTGGACGCGATTAACTATGCAAGCTCGAA
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 GAAACAAAAAATTCAGATTTCTTCAGCTGAAGAACACACAAAAACAGAGGAGATGAAGTCATGGAATTTGTTGAATTCAGTTGTT
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TCCACAATAGAATTATTGGGAAGAAATATCTTCGTAGTCTCAAGAGTGCATGGAGTGATATATAAATGTTGTCCATGGACACAA
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 CTATTACTTATTGCAATTTTTTAATATTTTTAGCCACAGAAAAATAGATAACAAATAAAGTAATGAAACGAACATATGGAGGTATTCC
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 CTA(**e**)CATATATGTAATCAAAATACCATCCCTCCTTCGACCAAAAAAATAATAAAAAATACCTTCCCTCCTTAACCCAAAAACCTTA
 ACCCTAGAGCCCAATACAGACTCTTTTCTAAAAAATAAAAAAGGAAACCAACTGAAATATAAAAAACCAAAATCACTTTC
 TGAGAGCCGGAAG**AGCGC**AGTGTGTTGGGAGCTGAAGTGCATGCTTGCTC(**f**)GCAACTCTCAAGCTCTATTCTTTCTGCTTA
TACCCACCCACACACACTCCCCGTAACCTAAACACACATGCTCTCCCTCCTCTTCCCCCTTTCATCATCAGCCCCACCA
 CCACATCCAGCGCTTACTCTCTCTTCTTCCCACTACTTCTCTCCACAAATCCTCACCTCCCCAGAAACAGAGCAACAAGAA
 TAACTTTCTGATTGGGTTTTTACCCTGTCACCAAG

Fig. S4 MdFLP may be able to bind to the *cis*-element of AGCCG in the promoter region of *MdPIN3* and *MdPIN10*. (A-B) Promoter sequence of *MdPIN3* and *MdPIN10*, respectively. MdFLP recognition sites and core binding sites in promoter regions of *MdPIN3* and *MdPIN10* are highlighted in bold with red color. Sequences underlined indicate PCR products of a-f fragments. d is a negative control.

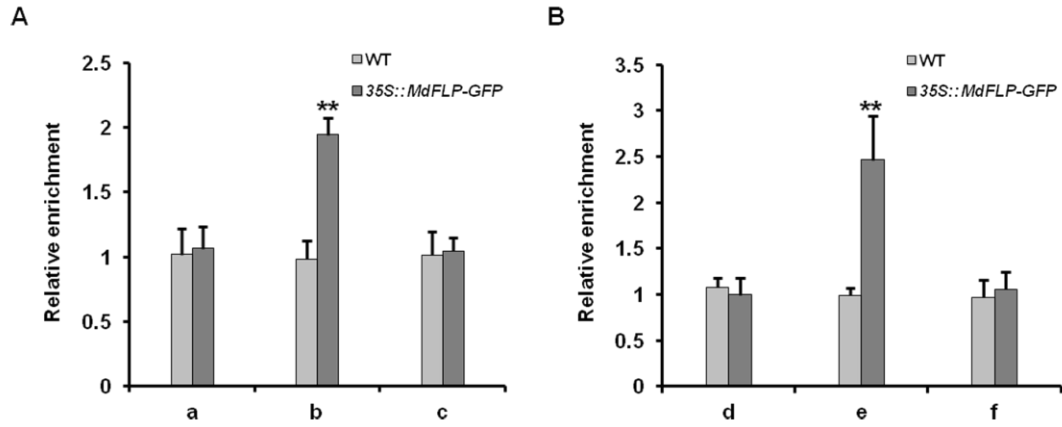


Fig. S5 MdFLP directly bind to the promoters of *MdPIN3* and *MdPIN10*. (A-B) Chromatin immunoprecipitation - quantitative PCR (ChIP-qPCR) assays were performed using apple transgenic roots harbouring *35S::MdFLP-GFP* and probed using anti-GFP antibodies. PCR products that are generated by primer pairs at position ‘b’, ‘e’ shown in Fig.S5, which, include element AGCCG, are enriched in *35S::MdFLP-GFP* transgenic plants. Error bars represent $\pm$ SE. Significant differences were determined by Student’s *t*-test (**P < 0.01).

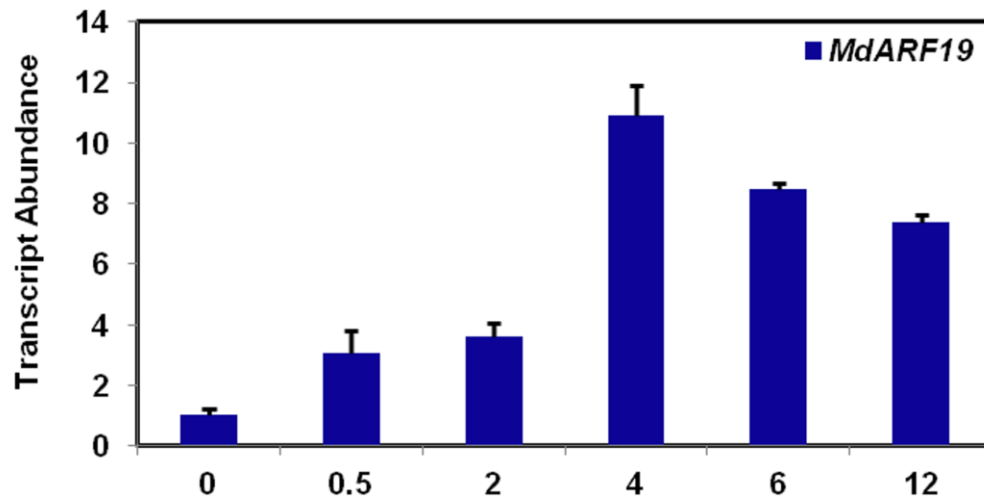


Fig. S6 *MdARF19* expression in response to auxin in apple self-rooted stock. qRT-PCR analysis of *MdARF19* expression during 0h, 0.5h, 2h, 4h, 6h, 12h auxin (10mM NAA) time course from roots of 13-22. Error bars indicate $\pm$ SD (n=3, from three technical replicates). Values in Fig.S6 were derived from experiments that were performed at least three times with similar results, and representative data from one repetition were shown.

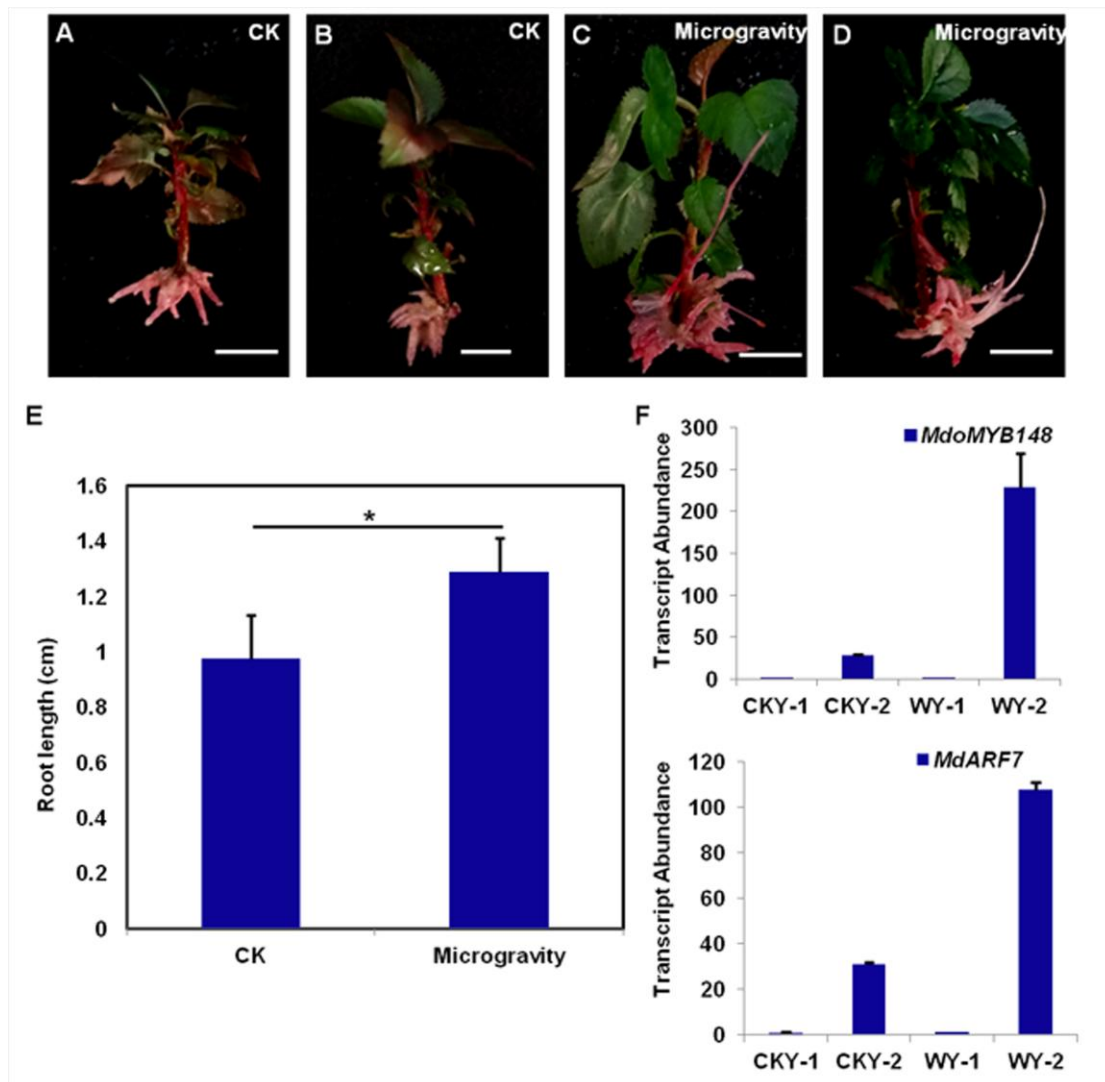


Figure S7. The microgravity promote plant root growth. (A-D) The external morphological observations of the whole roots at 14(d) of apple stock 12-2. Scale bars = 1cm. (E) Quantification of root length shown in (A-D). Error bars represent standard deviation [n=3 in (E), technical replicates;36 in (F), thirty-six roots were used to measure root length. Error bars represent $\pm$ SE. Significant differences were determined by Student's *t*-test (* $P < 0.05$). (F) Transcript levels of endogenous gravity-responsive gene of *MdoMYB148*, AUXIN RESPONSE FACTOR7 (*MdARF7*) in apple stock in vitro(12-2). Values in Fig.S7 were derived from experiments that were performed at least three times with similar results, and representative data from one repetition were shown.

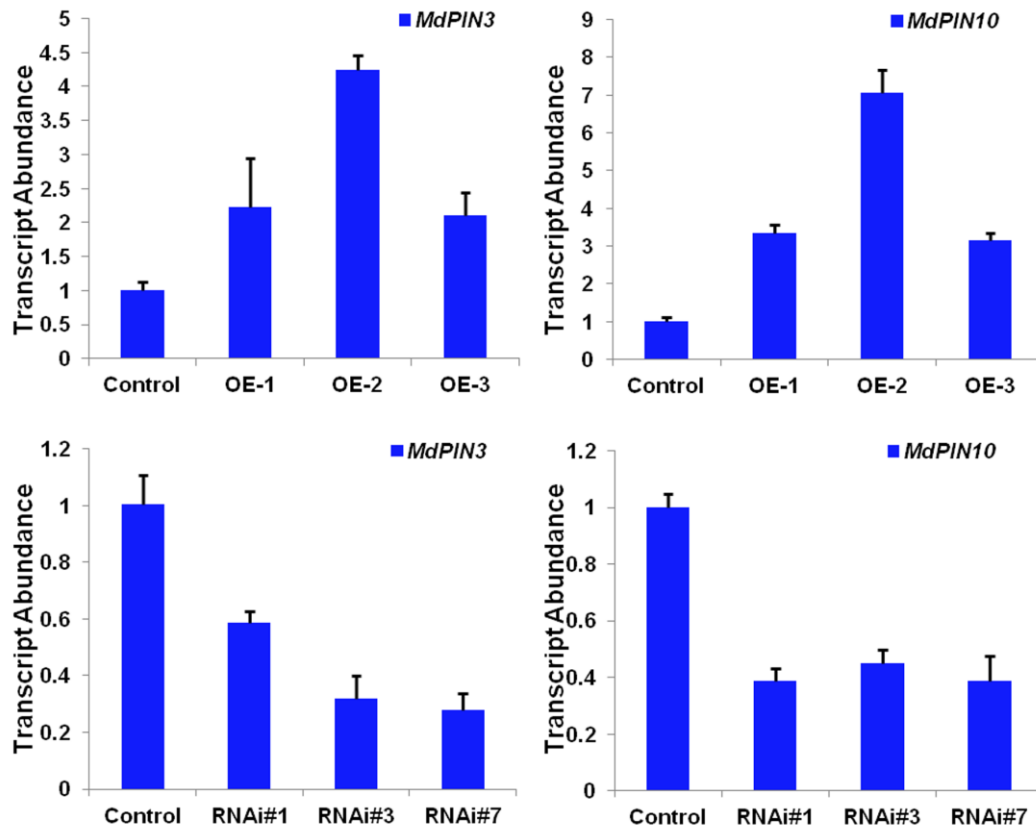


Fig. S8 Transcript levels of *MdPIN3* and *MdPIN10* genes in transgenic apple roots. Transcript levels of endogenous angle-responsive genes of auxin transporters of the PIN-former (PIN) family genes (*MdPIN3* and *MdPIN10*) in transgenic plant roots. Error bars indicate $\pm$ SD (n=3, from three technical replicates). Values in Fig.S8 were derived from experiments that were performed at least three times with similar results, and representative data from one repetition were shown.