

SUPPLEMENTAL DATA

Supplemental Table 1. Sequences and annotations

AGI accession number	notation	GenBank Accession	consensus with the cDNA sequences obtained from this work (single nucleotide substitutions)
At2g28305	MoBP1	AY086265.1	yes (A154 -> T)
At5g11950	MoBP2	BT011985.1	yes (G732 -> A)
At2g37210	MoBP3	AY102554.1	yes (-)
At4g35190	MoBP4	BT026408.1	yes (-)
At3g53450	MoBP5	*NM_115205.1	yes (-)
At5g03270	MoBP6	AY050382.1	no
At5g06300	MoBP7	AK119117.1	yes (-)
At2g35990	MoBP8	AY924758.1	yes (-)
At5g26140	MoBP9	*NM_122515.1	no

* NCBI Reference Sequence

Supplemental Table 2. Sequences of MoBP cDNAs, being non consistent with the corresponding annotations

AGI accession number	notation	experimental verified sequence from this work
At5g03270	MoBP6	atggagaatg aagagggaaa aagagagatg acgaagaaac aaagttcaag gtttaagagc atttgcgtct tttgtgggag tagcaatggg aacaaagcta gttatcagga tgcagccatt gatttgcca aggaactggt gatgaggaag attgatcttg tttatggtgg aggaagcata ggtttaatgg gtttggtgtc tcaagctgtt catgatggtg gtcgtcatgt tattggagtc atccccaaag tcctcatgtt gcaagagtta actggagaaa cagtaggaga agtgaaggaa gttgcagaca tgcatcagag aaaagctgtg atggctaagc attctgatgc tttcattact ttgcctggtg gctatggtac actagaggag ctacttgaag tgataacttg ggcacaactt ggtgtccatg ataaaccggt cggtttatta aacgttgatg gatattacga tgcattgctg ttattcatcg acaaagccgt cgaagagga tttattcttc caaccgctcg acatattatc gtatctgcac caaccgcaag agagttgttt ataaaattgg aggtatatcg atagatgata cggatttaac cctaaaccga accatacagt atatccaagt catgatcccg ttatgattta ttattttcta gttgaatatg gtatcactag atcgaatata taaacatgca ttatctttgt ttcaagttat gtctaaagct ggtag
At5g26140	MoBP9	atgcatattg agcacatatc tggtgagact gttggagagg taagaattgt ttcagacatg caccgagcga aagctacaat ggctcaagaa gctggggctt tcattgcgct cctaggaggt atgaaactat ggaggaacta ctggagatga

Supplemental Table 3. Oligonucleotide primer sequences used for cloning of *Arabidopsis* MoBP cDNAs

cDNA encoding protein	Oligonucleotide	Sequence (5' → 3')
MoBP1	Forward Primer (pQE 80)	ttataggatc catggagata gaatc
	Reverse Primer (pQE 80)	aataggtacc tcactcttgag atttcac
MoBP2	Forward Primer (pQE 80)	cctgagggaa taccttgatt tgtag
	Reverse Primer (pQE 80)	gtttcatatt gcaacaagat ttgag
MoBP3	Forward Primer (pGEM [®] -T Easy)	tcaaagaaac cttaaactgc ttacc
	Forward Primer (pQE 80)	tatatggatc catggaaatc aaaaggtgaa tcgatg
	Reverse Primer (pGEM [®] -T Easy)	caactaatca aaatctatcc cttcc
	Reverse Primer (pQE 80)	ttatatggta cctcactctt cagaggagta acc
MoBP4	Forward Primer (pGEM [®] -T Easy)	tcccaaatcc acaaaagaga g
	Forward Primer (pQE 80)	ttatatggat ccatggaaat agtgaagtcg ag
	Reverse Primer (pGEM [®] -T Easy)	gaaaccccag aaaacaaca ac
	Reverse Primer (pQE 80)	ttatataagc ttctaaaggg caatctcagt ctgc
MoBP5	Forward Primer (pQE 80)	ttatatggat ccatggaggt caacaatgaa ac
	Reverse Primer (pQE 80)	ttatatggta cctcagtctt cagaagagta gtc
MoBP6	Forward Primer (pQE 80)	ttatatggat ccatggaggt caacaatgaa ac
	Reverse Primer (pQE 80)	ttatatggta cctcagtctt cagaagagta gtc
MoBP7	Forward Primer (pQE 80)	ttatatggat ccatggaagag acaaaatcga g
	Reverse Primer (pQE 80)	ttatataagc ttttacgtagc ggtagctac
MoBP8	Forward Primer (pGEM [®] -T Easy)	gtatacttct tcttcacttc cc
	Forward Primer (pQE 80)	ttatatggat ccatggaaga gacaaaatca ag
	Reverse Primer (pGEM [®] -T Easy)	ggcaagttcc attggtatat aagctc
	Reverse Primer (pQE 80)	ttatataagc ttctaaaacg agtcgccttc caaag
MoBP9	Forward Primer (pGEM [®] -T Easy)	gatatcttgg agagtctcat aagg
	Forward Primer (pQE 80)	tatataggat ccatgcatat tgagcacata tctg
	Reverse Primer (pGEM [®] -T Easy)	cagatcactc taattgattc cc
	Reverse Primer (pQE 80)	aaatttaagc tttcattgag gcttgttctc atttag

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At2g28305 1 MMEI-----ESKFKRICVFCGSSAGNKVSYKDAATELGTTELVSRLIDLVIYGGGSLGLMGLISQAVFNGGRHVIG
At5g11950 1 MMEINQ-----RSRFRKICVFCGSSHSCHREVSDDAATELGNELVKRKIDLVIYGGGSLGLMGLISRRVYEGGLEHVLG
At2g37210 1 -MEIKG-----ESMQKSKFRRICVFCGSSQCKKSSYQDAADLDLGNELVSRNIDLVIYGGGSLGLMGLVSQAVHDGGRHVIG
At4g35190 1 -MEIV-----KSRFKRVCVFCGSSSCKKRECYSDAATDLAQELVTRRELNLVIYGGGSLGLMGLVSQAVHEAGGHEVLG
At3g53450 1 -MEVNN-----ETMQKSKFRICVFCGSSQCKKSSYQDAADLDLGNELVLRNIDLVIYGGGSLGLMGLVSQAVHDGGRHVIG
At5g03270 1 -MENEKGKREMTKKQSSRFKSIKICVFCGSSNGKASVQDAADLAKELVMRKIDLVIYGGGSLGLMGLVSQAVHDGGRHVIG
At5g06300 1 -MEET-----KSRFKRICVFCGSSSCKKPSYQEAATQLGNELVRRIDLVIYGGGSLGLMGLVSQAVHHGGRHVIG
At2g35990 1 -MEET-----KSRFRICVFCGSSSCKKTYTHDAALQLAHQLVERNIDLVIYGGGSLGLMGLISQAVHDGGRHVIG
At5g26140 -----

At2g28305 70 VIPKTLMPREITGETVGEVKAIVADMHORKAEMAKHSDAFIALPGGYGTLEELLEVIITWAQLGIHDKPVGLLNVDGYNSL
At5g11950 72 IIPKALMPTEISGETVGDVVRVADMHERKAAQAQAEAFIALPGGYGTMEELLEMITWSQLGIHKKIVGLLNVDGYNNL
At2g37210 75 IIPKTLMPREITGETVGEVRAVADMHORKAEMAKHSDAFIALPGGYGTLEELLEVIITWAQLGIHDKPVGLLNVDGYNSL
At4g35190 70 IIPKTLMDKEITGETYGEVIAVADMHERKAEEMARHSDCFIALPGGYGTLEELLEVIITWAQLGIHDKPVGLLNVDGYNYL
At3g53450 75 VIPKTLMPREITGETVGEVRAVADMHORKAEMARHSDAFIALPGGYGTLEELLEVIITWAQLGIHDKPVGLLNVDGYNSL
At5g03270 80 VIPKLLMLQELTGETVGEVKEVADMHORKAVMAKHSDAFIALPGGYGTLEELLEVIITWAQLGVHDKPVGLLNVDGYNDAL
At5g06300 70 VIPKTLMPREITGETVGEVKAIVADMHORKAEMARQADAFIALPGGYGTLEELLEVIITWAQLGIHRKPVGLLNVDGYNSL
At2g35990 70 IIPKSLAPREITGESIGEVIITVSTMHORKAEMGRQADAFIALPGGYGTLEELLEVIITWSQLGIHKKPVGLLNVDGYNSL
At5g26140 1 -----MHIEHLSGETVGEVRIIVSDMHERKAAQAQAEAFIALLGC-----MKLWRN-----YWR--

At2g28305 150 LSFIDKAVEEGFISPTARHIIVSAPSAKELVKKLEDYVPRHEKVASKKSWEMEQIGLSPTCEISR-----
At5g11950 152 LALFDITGVEEGFIKPGARNIIVSAPTAKELMEKMEBYTPSHMHVASHESMKVEELGDYPGQENKQP-----
At2g37210 155 LSFIDKAVEEGFISPTAREIIVSAPTAKELVKKLEBYAPCHERVATKLCWEMERIGYSSEE-----
At4g35190 150 LTFIDKAVDDGFIKPSQRHIFVSAPNAKELVQKLEAYKPVNDGVIASRWEVEKKVQQPQQQQVFCNSNTSMQTEIAL
At3g53450 155 LSFIDKAVEEGFISTNARQIIVSAPTAKELVKKLEBYSPCHESVATKLCWEIERIDYSSD-----
At5g03270 160 LLFIDKAVEEGFILPTARHIIVSAPTARELFIKLEVYR-----
At5g06300 150 LTFIDKAVEEGFISPMARRIIVSAPNAKELVRQLEBYEPEFDEITSKLVWDEVDRISYVPGSEVATAT-----
At2g35990 150 LTFIDKAVEEGFVSSSTARRIIVSAPNAPOLLQLEBYVPEKHDDFVSMVWNTTDAFTLEGDSF-----
At5g26140 -----

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Supplemental Figure 1. Sequence-alignment of *Arabidopsis* MoBP proteins. The alignment was generated with ClustalW. Identical residues are shaded in black and similar residues are shaded in grey. The lysine decarboxylase associated motif is boxed in red.

	Exon1	Exon2	
At2g28305	MMEI-----ESKFKRICVFCGSSAGNKVSYKDAAI	ELGTELVSRNIDL	VYGGGS 49
At5g11950	MMEDNQ-----RSRFRKICVFCGSHSGHREVFSDAAI	ELGNELVKRKID	LVDYGGGS 51
At2g37210	-MEIKG-----ESMQKSKFRRICVFCGSSQKKSSYQDAAVD	LGNELVSRNIDL	VYGGGS 54
At4g35190	-MEIV-----KSRFRKVCVFCGSSSGKRECYSDAATDLAQEL	VTRRLNL	VYGGGS 49
At3g53450	-MEVNN-----ETMQKSKFGRICVFCGSSQKKSSYQDAAVD	LGNELVLRNIDL	VYGGGS 54
At5g03270	-MENEKGKREMTKKQSSRFKICVFCGSSNGNKASYQDAADLAKEL	VMRKIDL	VYGGGS 59
At5g06300	-MEET-----KSRFRKICVFCGSSSGKKPSYQEAAL	QLGNELVERRIDL	VYGGGS 49
At2g35990	-MEET-----KSRFRKICVFCGSSSGNKTTYHDAALQLAHQL	VERNIDL	VYGGGS 49

	Exon2	Exon3	Exon4		
At2g28305	IGLMGLISQAVFNGGRHVI	GVIPKTLMPREIT	TGETVGEVKAVADMHQKAE	MAKHSDAFI 109	
At5g11950	VGLMGLISRRVYEGGLHVL	GIIPKALMPIEIS	GETVGDVRRVADMHERKAAMAQ	EAEAFI 111	
At2g37210	IGLMGLVSQAVHDGGRHVI	GIIPKTLMPRELT	TGETVGEVRAVADMHQKAE	MAKHSDAFI 114	
At4g35190	IGLMGLVSQAVHEAGGHVLC	GIIPRTLMDKEIT	GETYGEVIAVADMHERKAEMARHSDCFI	109	
At3g53450	IGLMGLVSQAVHDGGRHVI	GVIPKTLMPRELT	TGETVGEVRAVADMHQKAE	MARHSDAFI 114	
At5g03270	IGLMGLVSQAVHDGGRHVI	GVIPKLLMLQELT	TGETVGEVKEVADMHQKAV	MAKHSDAFI 119	
At5g06300	VGLMGLVSQAVHHGGRHVL	GVIPKTLMPREIT	GETIGEVEKAVADMHQKAE	MARQADAFI 109	
At2g35990	VGLMGLISQAVHDGGRHVL	GIIPKSLAPREIT	GESIGEVI	TVSTMHQKAE	MGRQADAFI 109

	Exon5	Exon6	
At2g28305	ALPGGYGTLEELLELEVITWAQLGIHDKP	VGLLNVDGYNSLLSFIDKAVEEGFISPTARHI	169
At5g11950	ALPGGYGTMEELLEMITWSQLGIHKKTV	GLLNVDGYNNLLALFDTGVEEGFIKPGARNI	171
At2g37210	ALPGGYGTLEELLELEVITWAQLGIHDKP	VGLLNVDGYNSLLSFIDKAVEEGFISPTAREI	174
At4g35190	ALPGGYGTLEELLEVIWAQQLGIHDKP	VGLLNVDGYNYLLTFIDKAVDDGF	IKPSQRHI 169
At3g53450	ALPGGYGTLEELLELEVITWAQLGIHDKP	VGLLNVDGYNSLLSFIDKAVEEGFISTNARQI	174
At5g03270	TLPGGYGTLEELLELEVITWAQLGVHDKP	VGLLNVDGYDALLLIDKAVEEGFILPTARHI	179
At5g06300	ALPGGYGTLEELLELEVITWAQLGIHRKP	VGLLNVDGYNSLLTFIDKAVDEGFISPMARRI	169
At2g35990	ALPGGYGTFEELLELEVITWSQLGIHTKP	VGLLNVDGFYDSLTFIDKAVDEGFVSSTARRI	169

	Exon6	Exon7	
At2g28305	IVSAPSAKELVKKLE	DYVPRHEKVASKKSWEMEQIGLSPTCEISR	----- 214
At5g11950	VVSAPTAKELMEKME	EYTPSHMHVASHESWKVEELGDYPGQENKPO	----- 217
At2g37210	IVSAPTAKELVKKLE	EYAPCHERVATKLCWEMERIGYSSEE	----- 215
At4g35190	FVSAPNAKELVQKLE	AYKPVNDGVIAKSRWEVEKKVQQPQQQQVVFCSNTSMQTEIAL	----- 228
At3g53450	IISAPTAKELVKKLE	EYSPCHESVATKLCWEIERIDYSSD	----- 215
At5g03270	IVSAPTARELF	IKLEVYR	----- 197
At5g06300	IVSAPNAKELVRQLE	EYEPFDEITSKLVWDEVDRISYVPGSEVATAT	----- 217
At2g35990	IVSAPNAPQLLQLE	EYVPKHDDFVSKMVDNNTTDAFTLEGDSF	----- 213

Supplemental Figure 2. Exons attributing to the primary sequence of *Arabidopsis* MoBP proteins. Sequence sections encoded by single exons are variously colored black and grey. Non colored residues are encoded by two exons. The alignment was generated with ClustalW.