Table S1. *De novo* assembly statistics of *Castanea sativa* transcriptome before (Contigs) and after redundancy removal (Transcripts).

Transcriptome assembly metrics	
Total number of raw reads	193 896 450
Total number of reads after trimming	134 286 842
Number of contigs in *de novo* transcriptome assembly	164 926
Number of transcripts in *de novo* transcriptome assembly	32 871
Average lenght of the transcripts	906.25
N50	1 230
GC %	44

Table S2 – *Castanea sativa* transcriptome completeness as determined by Benchmarking Universal Single-Copy Orthologous (BUSCO)

BUSCO notation	**BUSCOs**
Complete Single-Copy	86.67%
Complete Duplicated	7.45%
Fragmented	3.53%
Missing	2.35%

Table S3 – List of gene accessions

A-Class	
Given name	**Protein name**
AtAP1	CAA78909.1
OsAP1	XP_015631033
PpAP1	XP_007223821.1
VvAP1	AAT07447.1
PtAP1	AAT39554.1
QsAP1	XP_023910685.1
MdAP1	ABG85297.1
SlAP1	NP_001234665.1
CmAP1	Cm_g17297.t1
BpAP1	CAA67967.1
CuAP1	A0A2H5NVU3_CITUN
CaAP1	Corav.3359
CsAP1	XP_011650331.1
AtrAP1.1	XP_006856356.1
AtrAP1.2	XP_020530401.1
PrAP1	AAB58907.1
FcAP1	BAP28174.1
B-Class	
Given name	**Protein name**
AtAP3	AAD51899.1
CmAP3	Cm_g20682.t1
VvAP3	NP_001267960.1
SlAP3	NP_001234077.2
MtAP3	XP_003603721.1
GmAP3	XP_014629918.1
CsAP3	NP_001295864.1
PpAP3	XP_020415740.1
AcAP3	PSS31295.1
PtAP3	XP_006386194.1
JrAP3	XP_018821033.1
ZmAP3	ACG37775.1
OsAP3	BAH22555.1
QsAP3	QSP122988.0
QrAP3	Qrob_P0454040.2
QruAP3	Quercus_rubra_120313_comp61142_c0_seq1_m.35060
AtrAP3	AAR06678.1
PrPI	AAF28863.1
AtrPI	XP_006847167.2
AtPI	P48007.1
VvPI	AAY79173.1
CsPI	NP_001292651.1
PpPI	XP_020410381.1

MdPI	CAC28022.1
AcPI	ADU15475.1
PtPI	XP_002300964.1
QsPI	XP_023887186.1
SlPI	ABG73411.1
BpPI	CAD32764.1
JrPI	XP_018811340.1
GmPI	XP_003523422.2
MtPI	ACJ36228.1
OsPI	AAC05723.1
ZmPI	ONM35875.1
CmPI	Cm_g4017.t1
QrPI	Qrob_P0600300.2
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PtTM6	XP_024461070.1
MtTM6	XP_003612101.1
CmTM6	maker-scaffold03851-augustus-gene-0.22-mRNA-1
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AtrAG	NP_001292764.1
PrAG	AAD09342.1
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SlAG	NP_001266181.1
CuAG	BAF34911.1
OsAG	XP_015632498.1
PtAG	XP_024455023.1
MdAG	XP_008383546.1
JrAG	XP_018830028.1
VvAG	NP_001268097.1
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QsAG	QSP034737.0
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GmAG	NP_001237504.1
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MtAG	XP_013462626.1
CsAG	NP_001292633.1
ZmAG	XP_008654205.1
AtrAG	NP_001292764.1
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QsSHP1	QS001472.0
CmSHP	Cm_g3306.t1
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CsSTK	NP_001267506.1
CuSTK	GAY61853.1
PpSTK	ABQ85556.1
VvSTK	A0A217EJJ0.1
MdSTK	NP_001280931.1
MtSTK	XP_003598035.1
PtSTK1	XP_024439317.1
PtSTK2	XP_006376118.1
PtSTK3	XP_006371450.1
SlSTK1	XP_004241906.1
SlSTK2	XP_010322781.1
E-Class	
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AtSEP3	NP_564214.2
AtSEP4	NP_178466.1
GmSEP1	AAZ86071.1
MdSEP1	NP_001280893.1
MtSEP1.1	XP_024642411.1
MtSEP1.2	XP_024625956.1
PpSEP1.3	XP_007215876.1
MtSEP1.2	XP_024625956.1
PpSEP1.4	XP_007215877.1
PpSEP1.2	XP_020414319.1
PpSEP1.1	XP_020414318.1
CuSEP1	BAF95941.1
SlSEP1	AAM33104.2
QsSEP1	QSP061360.0

CmSEP1	Cm_g47769.t1
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PtSEP1	XP_002306051.2
JrSEP1	Juglans_regia_01182017_WALNUT_00001177-RA_mRNA
AcSEP1	PSS35088.1
AcSEP2	PSS33641.1
CmSEP2	Cm_g360.t1
OsSEP3	XP_015648762.1
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CuSEP3	BAF34912.1
PtSEP3	XP_024437662.1
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PpSEP3	XP_007223808.1
VvSEP3	NP_001268114.4
SlSEP3	NP_001234384.1
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AcSEP3.2	PSS28600.1
AcSEP3.3	PSS26973.1
QsSEP4	QSP022774.0
CmSEP4.1	Cm_g17299.t2
CmSEP4.2	Cm_g17299.t1
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PrSEP1	AAD09206.1
PrSEP3	AAD09207.1

Table S4 – List of primers

Amplicon	**Direction**	**Sequence** (5' – 3')
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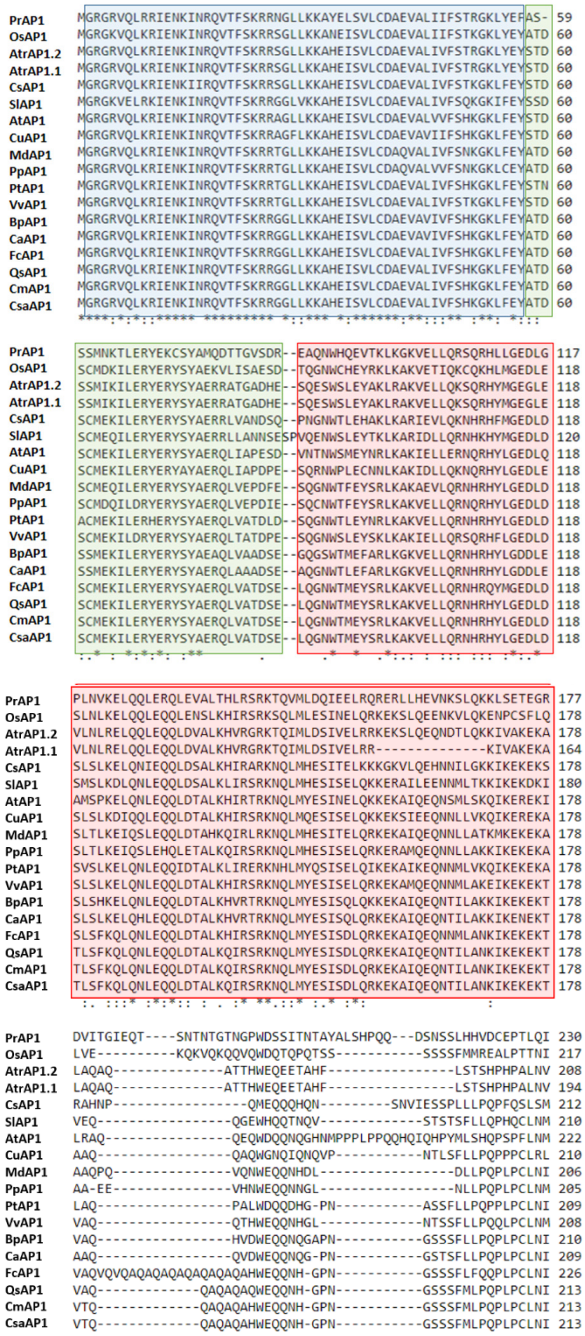
	Reverse	AACTGCAGCTACTCAAGCAAGGTGTAAGTTGTG
CsaPI Y2H	Forward	AGGATCCAAATGGGGAGAGGCAAGATTGAG
	Reverse	AACTGCAGTTACATTCTCTCTTGTAGATTTGGC
CsaTM6 Y2H	Forward	AAAGTCGACAAATGGGTCGTGGAAAGATCGAG
	Reverse	AACTGCAGTCAAGCAAGGCGCAGATCC
CsaAG Y2H	Forward	AGGATCCAAATGGTGTATCCGAACCAATCC
	Reverse	AACTGCAGTTAAACTAATTGAAGAGACATCTG
CsaSHP Y2H	Forward	AGGATCCAAATGGGAAGAGGAAAGGTAGA
	Reverse	AACTGCAGTTAAAGGACAACTCCATCTTGAA
CsaSEP2 Y2H	Forward	AGGATCCAAATGGGGAGAGGAAGAGTTGAGC
	Reverse	AACTGCAGCTAAAGCATCCACCCAGGAA
CsaSEP3 Y2H	Forward	AGGATCCAAATGGGTAGAGGAAGAGTGGAG
	Reverse	AACTGCAGTCATGGCATCCACCCTGA
CsaSEP4 Y2H	Forward	AGGATCCAAATGGGAAGGGGGAGAGTG
	Reverse	AACTGCAGTCAAAGCATCCAGCCTGGAAT
CsaAP3	Forward	TGGTGCTGTTATTGGATGCTCA
	Reverse	AGATCTGACCCTGCTCCACT
CsaPI	Forward	CCGAGAAATGCAGATGGAGT
	Reverse	AATAGGCTGCACACGGAAGG
CsaTM6	Forward	CTGCTCGATCTTAGGGCAAG
	Reverse	AGTTGGAGGCACCATTTGTC
CsaAG	Forward	CCAGCTTCTCCGAGCAAAGA
	Reverse	CATCTGGTCTTCACGTGGGT
CsaSHP	Forward	AGGGAAGTTGAGCTGCAAAA
	Reverse	CTGGGAGGTAGTTCCGATCA
CsaSEP2	Forward	CAGGCAGGTGACATTTGCTA
	Reverse	GCTGGCTTCCAATGCACTAT
CsaSEP3	Forward	TCAACACGGACGCAGTACAT
	Reverse	GGCCATATCCCATATCGTTG
CsaSEP4	Forward	GCCCTCATCATCTTCTCCAA
	Reverse	CCTCAACTTTTGCCTTCAGC
CsaPPA2A3	Forward	GGGTTCCCAACATCAAGTTC
	Reverse	TGACCTGATCACTTGACTGC

Figure S1 – GO functional annotation of the *Castanea sativa* de novo transcriptome. The transcripts were uploaded to Blast2GO and a blastx was performed, as well as an InterPro scan. The GO annotated transcripts were categorized according to cellular component **(A)**, biological process **(B)** and molecular function **(C)**.

A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PpAP1 SCMDQILDRYERYSYAERQLVEPDIE--SQCNWTFEYSRLKAKVELLQRNQRHYLGEDLD 118
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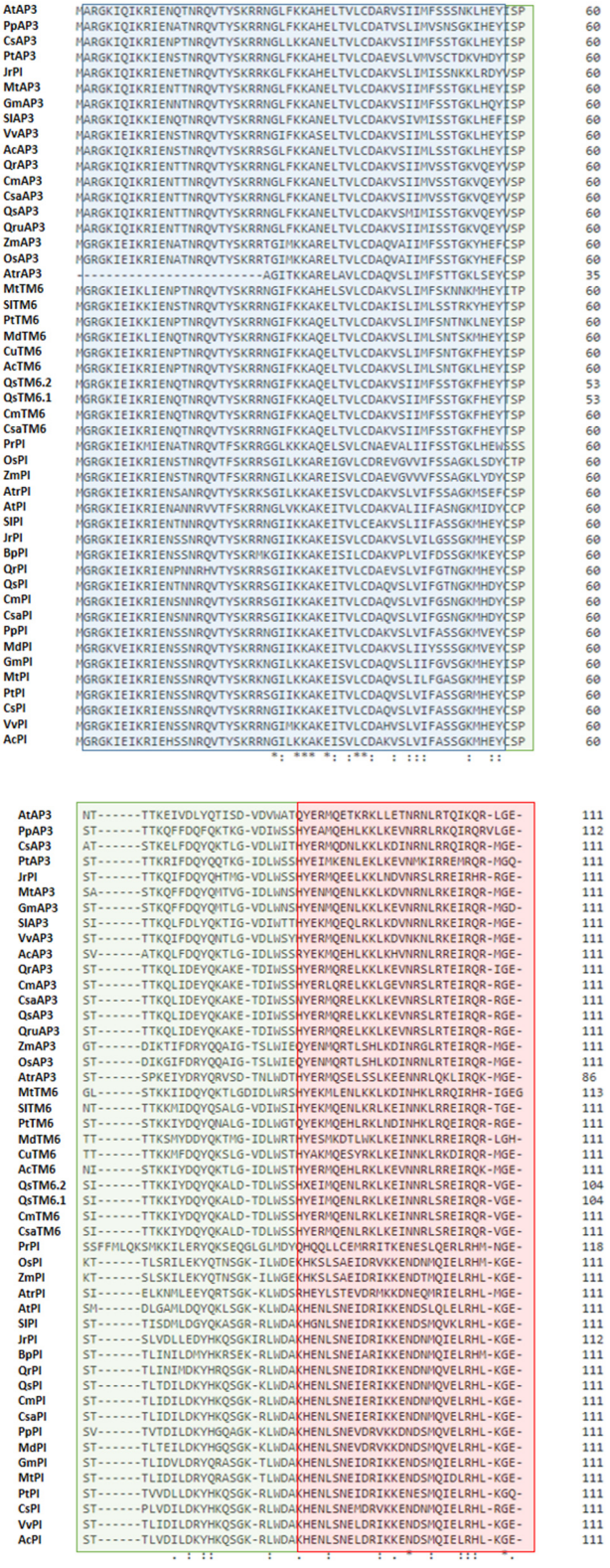
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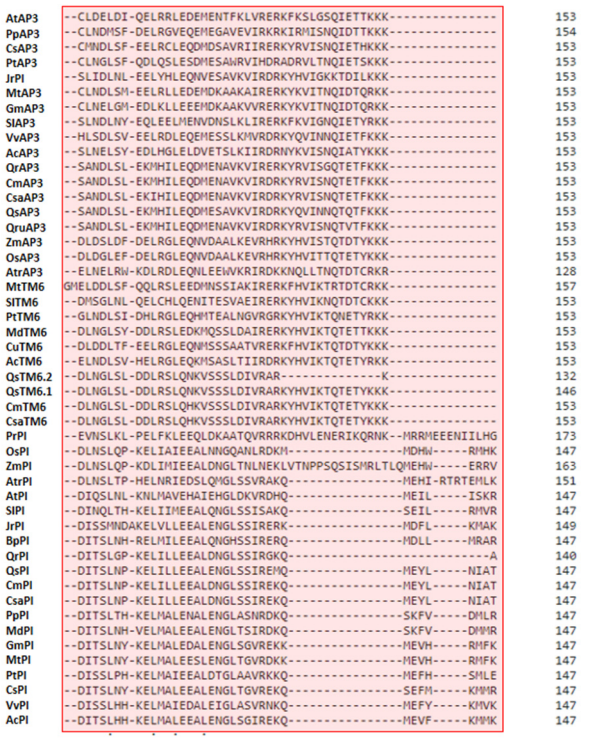

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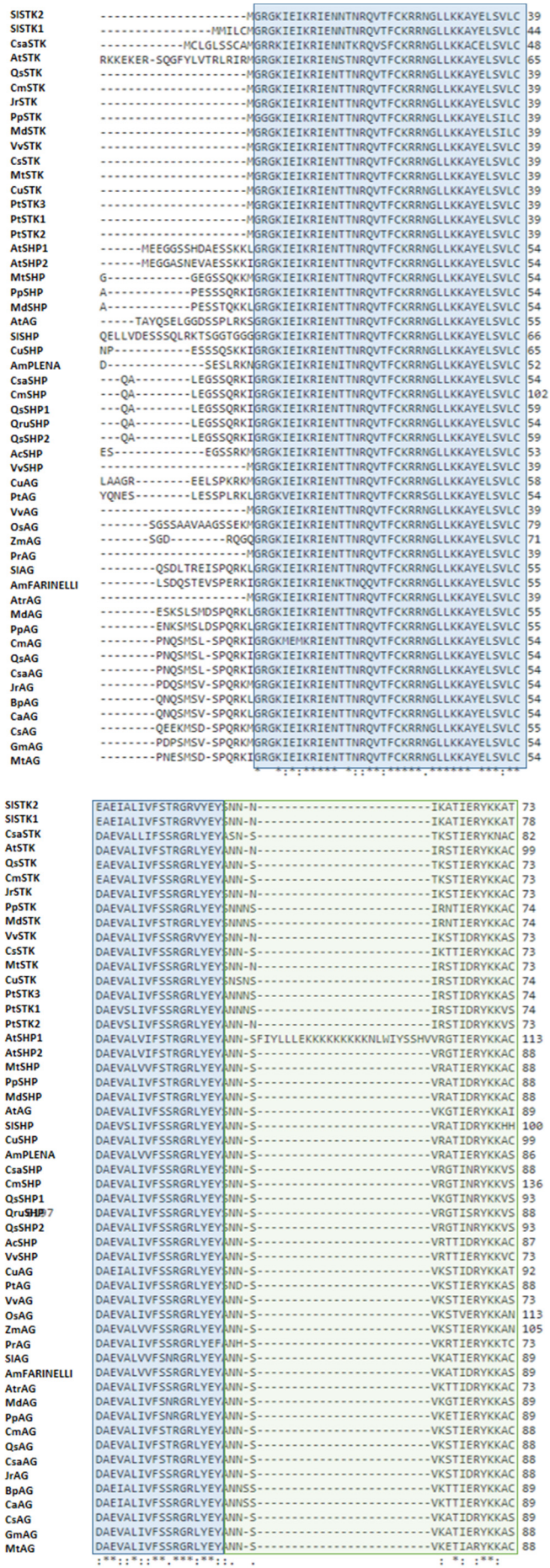
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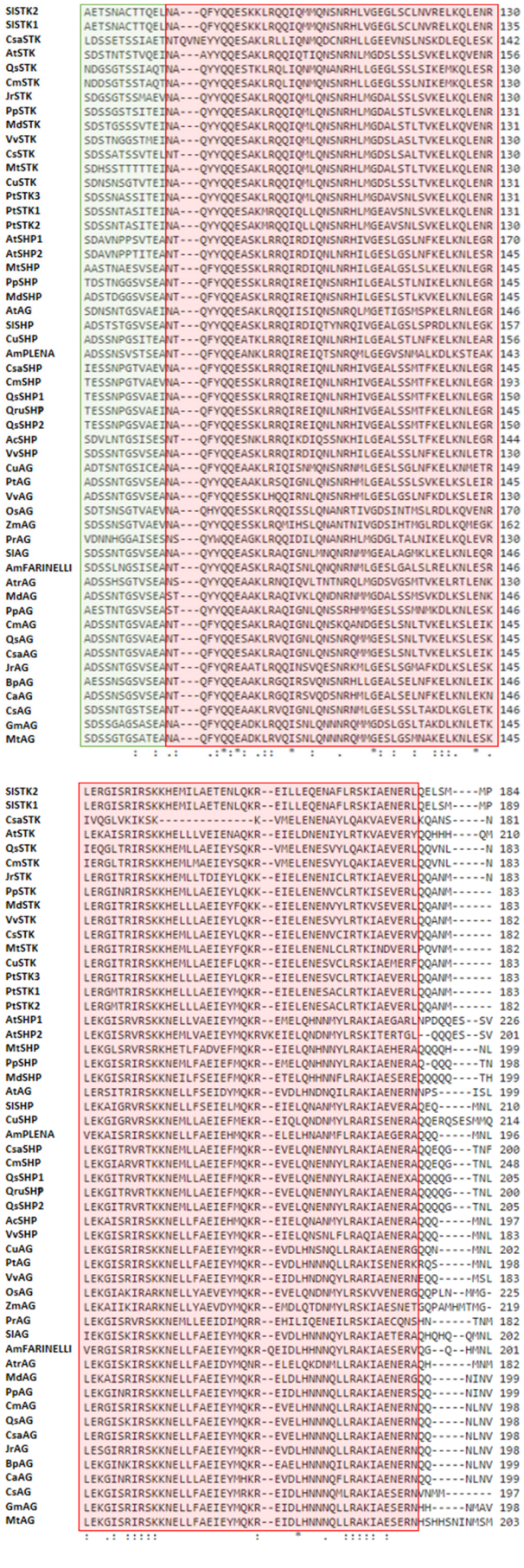
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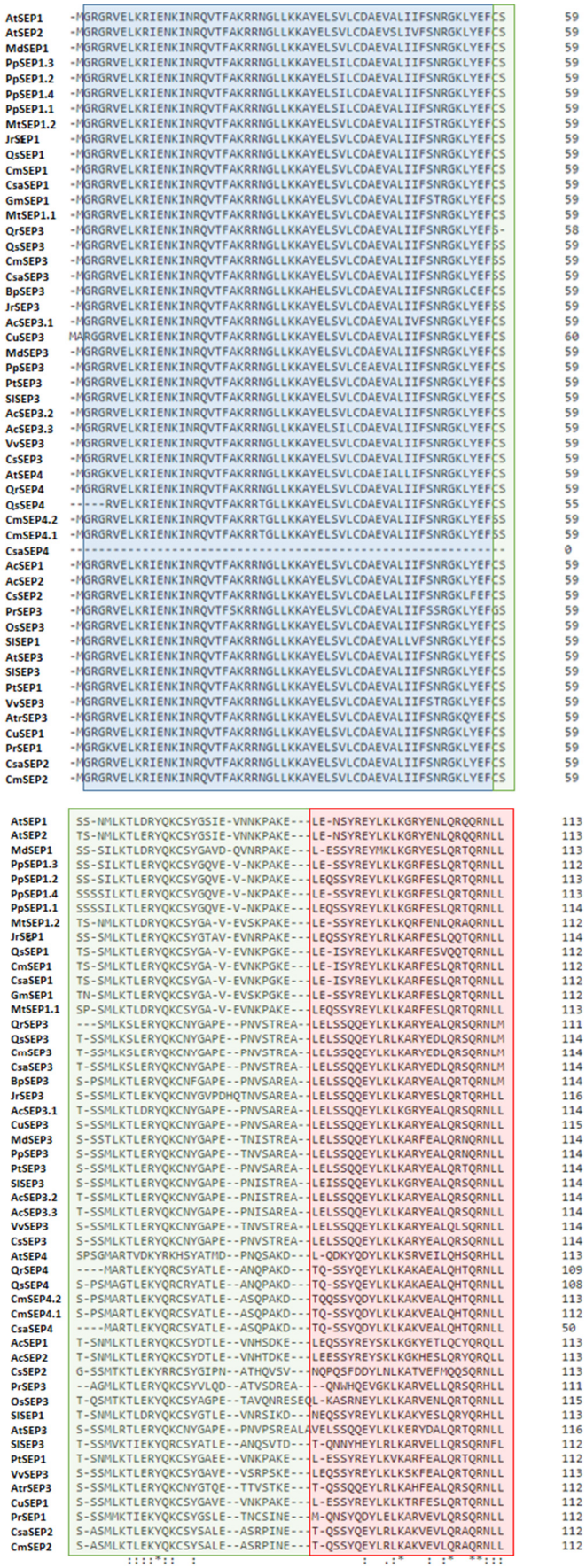
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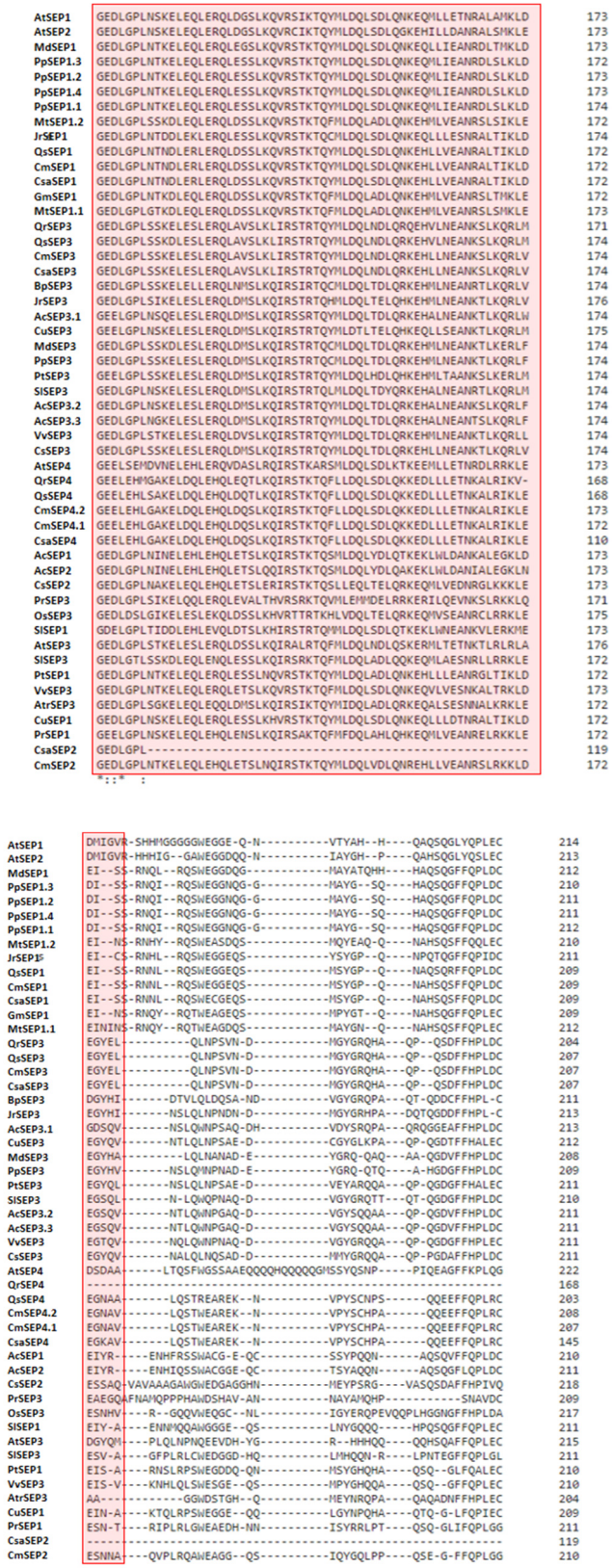

Figure S2 – Alignment of ABCDE-like amino acid sequences. Boxes indicate the conserved domains: MADS-domain (blue), I domain (green), and K domain (red). **A)** A-class proteins; **B)** B-class proteins; **C)** C and D-class proteins **D)** E-class proteins

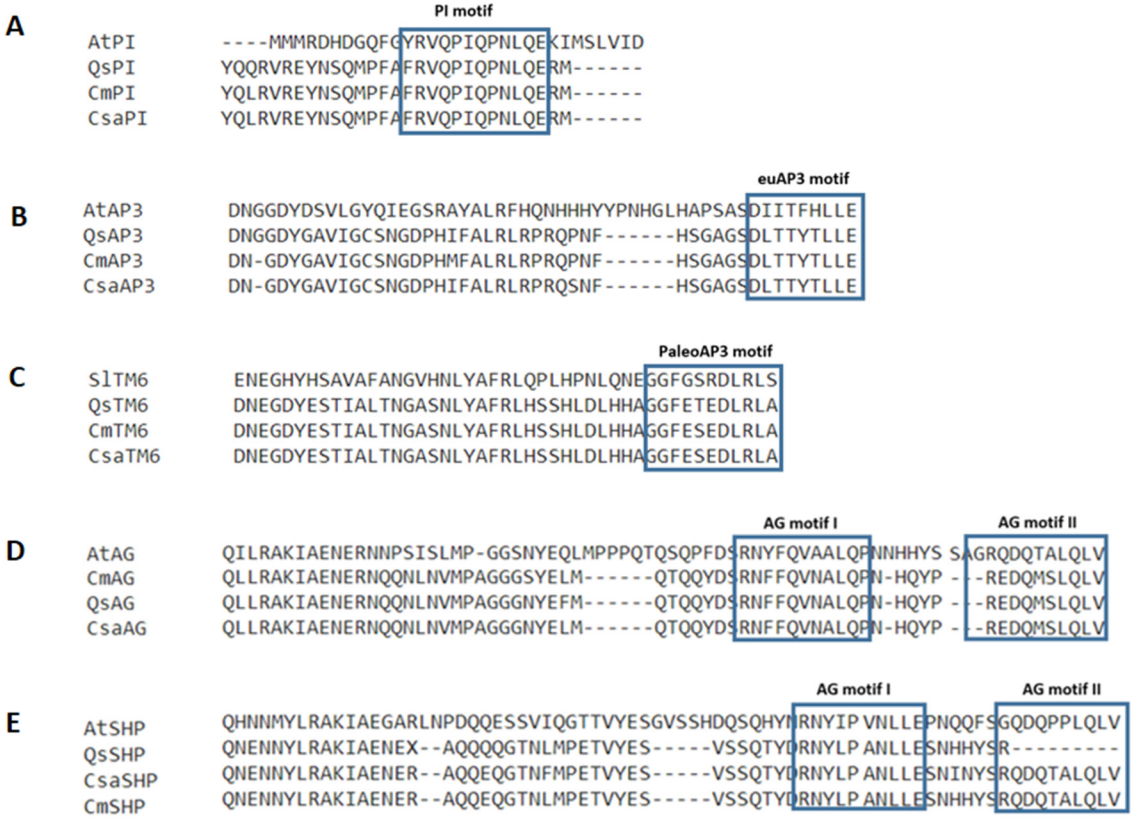

Figure S3 – Motif similarity in B and C MADS-box proteins between *C. sativa* and *A.thaliana*, *Q. suber* and *C. mollissima* (or *S. lycopersicum* in the case of TM6). **A)** PI-like proteins; **B)** AP3-like proteins; **C)** TM6-like proteins; **D)** AG-like proteins; **E)** SHP-like proteins