

Regulation of tissue specific expression of *SPATULA*, a bHLH gene involved in carpel development, seedling germination and lateral organ growth in *Arabidopsis*

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Supplementary Fig. S2. Alignment of eight conserved regions of the *SPT* promoter regions of *AtSPT* (*Arabidopsis thaliana*), *BoSPT* (*Brassica oleracea*) and *BrSPTa* and *BrSPTb* (*Brassica rapa*). Residues conserved in 3 or 4 sequences are shaded grey, and gaps are indicated by a hyphen. Putative Auxin Response Elements (AuxREs) (boxed) and adjacent E-boxes (magenta) at locations 1, 2 and 3 are indicated (antisense at location 1). Also highlighted are a CCAAT box (green), a Y patch (cyan), a TCP binding site (red), a TATA box (yellow), the start of transcription (red text), and a GA element (dotted underlined). The likely commencement of translation (underlined) is shown. For *AtSPT*, this may occur at +41 (purple text) or +86 (blue text). For *Brassica SPT* genes, the first methionine codon is equivalent to the second in *Arabidopsis*.

Region 1

								CCAAT box						
AtSPT	-167	ACCGTGAGCTGACACAAGCTCATTGCTAATGCTACAGTAACAGCTACCTTCA	---	CTTTAACTAAATGACAGA	CCAAT	CATTTAACCTCTGTTTTCTT	-71							
BoSPT	-207	ACCGTGCGCTGACACAAGCTCATTGCTTTTGCTAGAGTAACAGCTACAGTCA	---	CTTTAGCGCTATAACAGT	CCAAT	CATTTAACTTCTGTGTCCA	-112							
BrSPTa	-143	-----CTCATGCTTTTGCTACAGTAACAGCTA--GTCTAACTTGAAC	TCGGTGACAGT	CCAAT	CATTATAACCCTTGTGTCTT	-65								
BrSPTb	-168	ACCGTGAGCTGACATAAGCTCATTGCTTATGTTAATGTTACAGCTACCGTCA	---	CGTTTTACTATATGACAGT	CCAAT	CATTTAACCTCTGTCTCCAA	-72							
		E-box AuxRE (location 1)		Y patch		TCP	TATA box							
AtSPT	-70	AGCTGGCGCGTGACAGACA	CTC	-----	TCCCTCTCTCCA	--T	GCCCA	TAAAAATCTCAAAG	-18					
BoSPT	-111	ACCTGGCGCGTGACAAATAA	CTCTCTCT	GCTTTTTTTTTTTTTT	TGGAATCCAATAA	CTCTCTCTCTC	ATTCCCTCTCCAC	-T	GCCCA	TAAAAATAGAAAAA	-16			
BrSPTa	-64	AGCTGGCGCGTGACAGTTACTCTATT	-----	-----	-----	TTCTCTTCTCCATT	T	GCCCA	TAAAAATCAAAAA	-6				
BrSPTb	-71	C-CTGGCGCGTGACAAATAA	CTCTCTCT	-----	-----	CTCTCTCCACTT	C	CCCA	TAAAAATCAAAAA	-18				
		+1 (AtSPT)		+1 (BoSPT, BrSPTa, BrSPTb)				GA element						
AtSPT	-17	A-CTGTTTAAAAA	ATGTTT	TAGCTTTAACTG	CTTTTTTTT	TGTTGTTGGTGTAA	ATGATATCAC	AGAGAGAAGAAAGAGAGAGAA	-----	GAAGC	+77			
BoSPT	-15	CTCTGTTT	TTTTTTT	-----	CTTATATAC	--TTGCC	-----	ATAAAGAGAGAAGAGAGAG	-AGAGAAGC	-----	GAAGA	+47		
BrSPTa	-5	CTCTG	-----	-----	CTTTAATC	-GTT	-----	CACAGAGAGA	-GAGAGAG	-AGAGAGAGCT	GAAGC	+43		
BrSPTb	-17	CTCTGTTT	TTTTTTTTT	-----	CTTA	-----	C	TTGCC	-----	ATAACAAG	-GAGA	-----	GAAGA	+28
			Met											
AtSPT	+78	A	-----	GAGAGT	GATG	-----								
BoSPT	+48	A	-----	GAGAGT	AATG	-----								
BrSPTa	+44	AAC	AAAAAGAA	GAGA	-TAATG	-----								
BrSPTb	+29	-	-----	GAGAGT	AATG	-----								

Region 2

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                                AuxRE   E-box (location 2)
pAtSPT -252 GAGTAGTAGTTT-----AGTGFGT-----CTCACGTCCGACGAGGAAAAGTTTT -209
pBoSPT -485 GAGTACTAGTTTAGGAGTAGTGTGCTTAACTCTCACGCGGGACGAGGAAACTTTTT -429
pBrSPTa -265 TAGTACTAGTTTAGTA--AGTGFAT-----CTCACGTCCGACGAGGAATAGTTTT -218
pBrSPTb -226 TAGTACTAGTTTAGT--AGTGFGT-----CTCACGTCCGACGAGGAAACCCTTT -180
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Region 3

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pAtSPT -518 CAAATTACTAGAAATGGA-AATACTTTTGTCAAAACAAC-AAGACGTATAACTTTGTTTTCTATAGATTAATGGAC-TTCTTAAAAATCTCTCCATCAG -422
pBoSPT -1344 CAAATTACTAAAAGTAGATAATGTTTTGTCAAAACAACCGAAGACGCATAACTTC-GTTTTCTATAAACTAATGGCA-TTGTTCAAATCTCTCCAACAA -1247
pBrSPTa -530 CAAATTACTTAAAAAAGG-AATTTTTTTGTCAACA-CAAAAGACGTATTACTTC-ATTTCTATAAACTTATGGAAGTTTTCAAATTTATCCGTCAA -446
pBrSPTb -845 CAAATTACTAAAAGTGGATAATGTTTTGTCAAAACAACGGAAAACGTATAACTTC-GTTTTCTATAAACTAACGAAA-TTGTTCAAAGTGTCTCCAATAA -761

pAtSPT -421 A-TTAAAC-----TTTTGAGAT-ATACAAATACAGTTTTTGTCTTCTAAATGATATGAATATTAACCTTTATCGATT-TCATCCG -344
pBoSPT -1246 AAATAATTGGGCTCGTTTTTTTTCTTTCCCTAAACTAAATAAATATTCATTTCTATTGTGTTTCATCCAT---ATCAAGAAGAATATACATATGCATGTT -1150
pBrSPTa -445 AATTAAAC-----TCTGAAAT---ATAAA-ATTCATTTTATCAGAGTTTCATCCGTGGTAGCAGATAGAACATGCTTG-ACATTTT -364
pBrSPTb -760 AA-TA-----TAATTCATTTGTTTTTAATAAACTAAATTAATCTTCATTTCTATTGTGTTCCATCCATATCAAGAAGAAGAATATACATATGCATCTT -656

pAtSPT -343 TAGCAGATTTCCATTTTAAATAATAAACTATGAGAAAACAGATAAAAGTTGTATATTATTTGTTACCCAAAAAAAAAAAAAAAAA -297
pBoSPT -1149 A-ACAGATTTCTATTTTAAATAATGGACTATGAGAAACCATATAAAAGGT-TGTATCATTGTTACCGAGAAAAAAAAAACATA -1069
pBrSPTa -363 ATACAGACTTCTATTTTAAACAATGGGTTACAAGAAAGCATATAAAAGCT-TGTATCATTGTTACCCAAAAAATAAAATAAA -276
pBrSPTb -655 A-ACAGATTTCTATTTTAAATAATGGACTATGATAAAACCATATAAAAGGT-TGTATAATTTGTTACCAAAGAAAAAAAAAACATA -575
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Region 4

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pAtSPT -743 GAGGTATATAGTTGAAAAACACACA---CCGTAAAGTTAATAATTTTC-----ACAACACAAGAACAAATC--AAAGTCGCAAGT-AATTTAAC -662
pBoSPT -1919 GAAATGTATAGTTGAAAAGAAAAGACACCGTAAATTCAGTA--TTACTGGGTCCTGCCTGCAATACAAGAACTGATTTTAAAGTCTCACGTTAATTTAAC -1822
pBrSPTa -799 GAATTGTATAATTGAGAAGAACAG-----TAAATTCATAATTTTCAGTATTCATCGTCAATACAAGAACTGATTT-AAAGTCGCACGTTAATTTAAC -707

pAtSPT -661 GCAT--GTCAGTAGCATGGGCT -642
pBoSPT -1821 GCATATGTCAGTGGCATGGGCT -1800
pBrSPTa -706 GCATATGTCAGTAGCATGGGCT -685
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Region 5

E-box AuxRE E-box (location 3)

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pAtSPT -1296 ATAATTGAATCAAAGCAGATGCTGAACAAATAGCTGCAG-CTTTTAGCAATTGCTCTCCATATGCTTTTCTTTGTTTCAAAAATGTATATACGAGG- -1199
pBoSPT -2568 ATAAT-AATTGAAAAGCGGACGATGAAAAATT-GCTGCAGGCTTTCAGTAATTGCTCTCCATTGCTTTTCTTTGGTCCAGAAAATGAAAATACGAGGA -2471
pBrSPTa -1928 ATAAT---ATGAAGGCAGCTGCTGAAAAAAT-GCTGCAGGCTTTTAGCAACTGCTCTCCATATGCTTTTCTTTGTTTTCAGAAAATGTAAATACGAGGA -1834
pBrSPTb -1835 AAAAT-AATTGAAAAGCGGACGATGAAAAATT-GCTGCAGGCTTTCAGTAATTGCTCTCCCGTTTGCTTTTCTGTGTTCCAGAAAATGTAAATACGAGGA -1738

pAtSPT -1198 ---TTAAGT-----GAATGTT--GCAATGAAATAAATGATGCAGTTG--TGCATTCATCAAGCGAACCAAGTACGATTGATGTTTTCAGTGCAA -1117
pBoSPT -2470 ---TAAATGTA CTGGTTGAATGTT--GCAGTGAACAAATGATGCAGTTAGAGCGCATTTCATCAATGGAACAAGTACGAGTATGTTTTCAGCGCAA -2377
pBrSPTa -1833 TAATTAAGTACTTATGTTTGAATGTTTTCAGTGAACAAATAATGCAGTTAGGGCGCATTTCATTAAGAGAAAAGTGCAGTATGATGTTTCTGTGCAA -1734
pBrSPTb -1737 ---TAAATGTA CTGGTTGAATGTT--GCAGTGAACAAATGATGAAGTTAGCGCGCTTCATCAATGGAACAAGTACGAGTATGTTTTCAGCGCAG -1644

pAtSPT -1116 ---AACTAAAATAAAATA -1101
pBoSPT -2376 A--AAAATATATAGAGTA -2360
pBrSPTa -1733 GTTAAAATAAAAGAAAATA -1715
pBrSPTb -1643 AGAAAACTATATAGAGGA -1625
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Region 6

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pAtSPT -2593 TTCCAAGTGGGGAGTTGCTTGGGGATCTCATTGACGTGTGATCTTGAATTTTGTATAGAGATCCTAATGATCTCGTGGTCCCTCTCGCAG -2502
pBoSPT -xxxx TTCCAAGTGGGGAGTTGCTCGGGG-TC TCATTGACGTGTGATGATGAATTTATGTAAGAGACCCTAATAATCTCGTGGTCCCTCTCGCAG -xxxx
pBrSPTa-2802 TTCCAAGTGGGGAGTTATCTCGGGGCTCATTGACGTGTGATGTTGAATTTATGAAAGATATTCTAATGATCTCGTGGTCCCTTTACAG -2711
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Region 7

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pAtSPT -4924 CTGATTAGGCAATAAAATAAAA-CGATTTTGCTTTCCGACTTCACCAACAAAGTCTT-----AAAGGTGTTTTACATCCCAACATGTTAT CAAA -4837
pBoSPT -xxxx CTGATAAGTCAATAAAAAATC-CGATTTTGCTTTCCGAATGCACCACAAAGTCTTGACTCTAAACGAATGAAAGGTGTTTTACATCCTGATATGTTTT AAA- -xxxx
pBrSPTa-7175 CTGTTAAGTCAATAAAAAAAACGATTTTGCTTTCCGAATGCACCACAAAGTCTTGACTCTAAACGAATGAAAGGTGTTTTACATCCTGATATGTTTT AAAA -7072
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Region 8

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pAtSPT -5288 GTGGAAGTGGTGAAGAATCAATTA AACGCACACAGCTTCATCATATATTGTGCTCCTTCGCCGACAATCTTCTTACCTTATGCTTTGTTTGTCCCA -5189
pBoSPT -xxxx GTGGAAGTGGGAGAAGAATCAATTA AAC-CACACACAACTTCGT-ATAT-TTGTGTCTTTCACCAGACAATTTCTTACCTTATGCTTTGTTTGTCCCA -xxxx
pBrSPTa-7713 GTGGAAGTGGGAGAAGAATCAATTA AAC-CACACACAACTTCGT-ATAT-T-GTGTCTTTCACCAGACAATTTCTTACCTTATGCTTTGTTTGTCCCA -7618

pAtSPT -5188 TCGCTTTCAACACAAATTTCCATTATAGTAAACTCTCA -5151
pBoSPT -xxxx TCACTTTCA-CATATTTTCCATTATAGTAAACTTCA -xxxx
pBrSPTa-7617 TCACTTTCA-CATATTTTCCATTATAGTAAACTTCA -7581
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