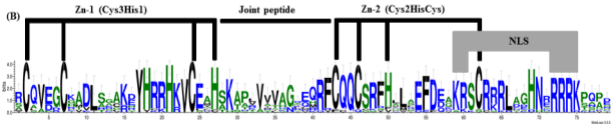
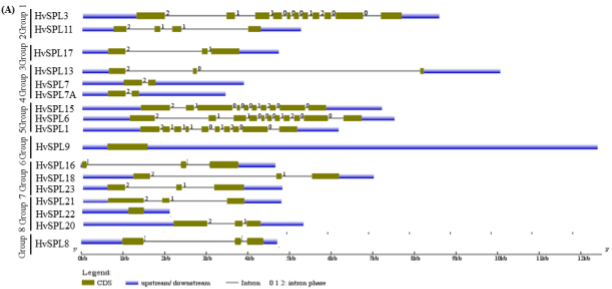


**Genome-wide analysis of the SPL/miR156 module and its interaction with the  
AP2/miR172 unit in barley**

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**Figure S1. Gene structure and sequence logo of barley SBP domain. (A)** The 5' upstream, 3' downstream, exons and introns are represented by boxes and lines, respectively and their sizes can be estimated using the scale bar at bottom. Blue boxes represent 5' and 3' un-translated regions, green boxes represent exons whereas introns are represented with black line. The numbers indicate intron phases. **(B)** Sequence logo of SBP domain was obtained from Weblogo. The overall height of letters represents residue conservation.

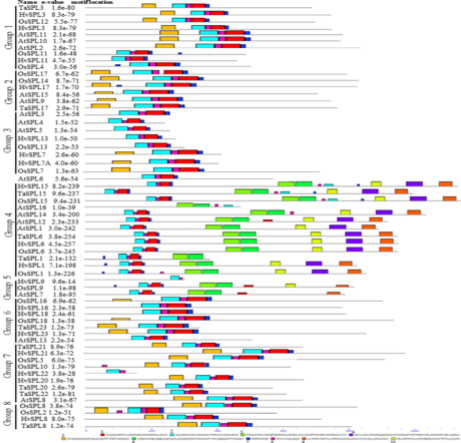
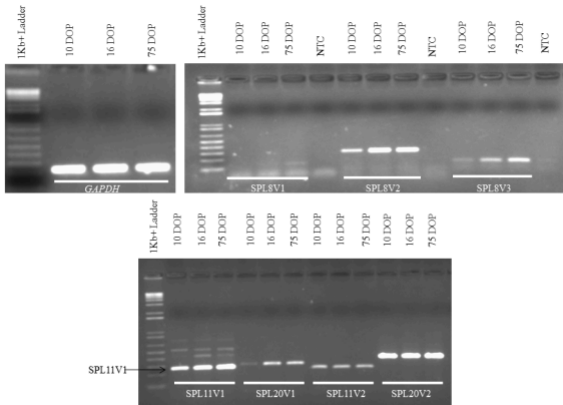
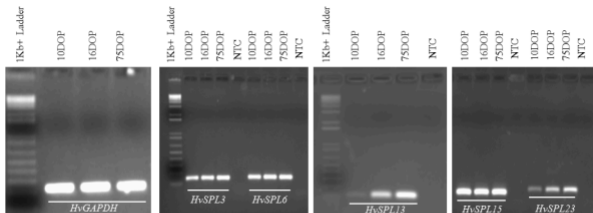


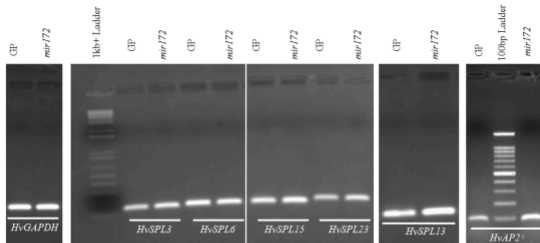
Figure S2. Motif search in SPL proteins. The distribution of 10 conserved motifs is indicated by numbered colored boxes.



**Figure S3.** Full length gel images of semi quantitative RT-PCR of alternative spliced variants of *HvSPL8*, *11* and *20* genes in 10, 16 and 75 DOP of barley growth and development. *HvGAPDH* was used as control.



**Figure S4. Full length gel images of semi-quantitative RT-PCR of *HvSPL* genes in vegetative and reproductive phases of barley. Expression of *HvSPL3*, 6, 13, 15 and 23 in 10, 16, 75 d-old plants. *HvGAPDH* was used as control for semi-quantitative RT-PCR.**



**Figure S5.** Full length gel images of semi-quantitative RT-PCR based expression of *HvSPL3*, *6*, *13*, *15*, *23* and *AP2* in the spike of *mir172* mutant and wild type GP. *HvGAPDH* was used as control for semi-quantitative RT-PCR.

Table S1. Coding sequences of 17 barley SPL genes.

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>HORVU7Hr1G051400.2 cds sequence

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>HORVU5Hr1G076380.9 cds sequence

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>HORVU6Hr1G031450.6 cds sequence



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>HORVU7Hr1G042370.8 cds sequence

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>HORVU2Hr1G097610.1 cds sequence

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>HORVU6Hr1G030490.2 cds sequence

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>HORVU2Hr1G048280.2 cds sequence

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CGGCAGCTGNN  
NN  
GCGAAGCGGTACCACCGCAGGCACAAGGTGTGCGAGGCGCACTCAAAGGCTGCTGTCGTG  
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>HORVU3Hr1G094730.1 cds sequence

GAATTCTCTGGACACAGAGACGTGCGTGCGTGCGCGTGTATTTGGCATGGATTCTTGG  
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GGAGGAGGCGGGCGGGCGGCTGGACCTGAAGCTCGGCGCGCCGACGAGCTGGAGGCCG  
GTCCCGGCGCCGGTGTATCGGTGCAGCAGCAGCAGCAGCAGCAGCAGCCGCCTTCCGCGGCG  
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GCGCCCATGTTGTTGCACACGTCTAACAGATCACAACACGCCGCTGCTACCGCTACCACT  
GCCGTTACTACAAGCACAGCTCCAGCTCCGACGGCGTGCAGATGCAGCAGTACCATGGC  
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>HORVU7Hr1G110980.3 cds sequence

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GACCAGCAGCAGCAGTTCAGGAACGCCATGCAGCTCCACCACCATCAGGAGCACCAGCAC  
TTCATCACCTCCCTCCTGCACGGCAACATCAATAACAGCAACATCCTGTCGTGTTCTCG  
GTGAGCTCCAACACGATGCCATCGGCGGTGGCGGCCAACGGCGAGGACGACAACAACAAC  
ATGCATATGTTTGAGGTGGACTTCATGTAG

>HORVU5Hr1G117190.5 cds sequence

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AATGAGAAGGATGATGACCCAGTGGGGAACAGTAGCAATGTGCTCAGCTTGAGACTTGGC  
GGCGGCAACTCTGTTGCCGGCGGAGCGGCGGAGGATGGCGGCGTGAACGAGGAGGACAGA  
AATGGTAAGAGGATCAGGGTGCAGGGCGGAAGCTCAAACGGTCCGGCGTGTGAGGTGGAG  
GGCTGCTGCGCTGACCTTAGCGCGGCAAAGGATTACCATCGGCGGCACAAGGTCTGCGAG  
ATGCATGCTAAGGCCAACACTGCGGTGGTTCGGAATAACCGTCCAGCGGTTCTGCCAGCAA  
TGCAGCAGATTTACCTTCTTCAAGAATTTGATGAAGGAAAGCGAAGTTGTGCGCCGGCGT  
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CCTATTGAGGAAAAGTTAGCAGTTATTTATTGTTGAGTCTTCTTGAATATGCGCCAAT  
TTTAACTCTGACAATGCTGAGCGTGTACAAGGTCAGGAGTTGCTATCCAATCTTTGGAGA  
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GTTGAAGATAGTGGATTTAGTAATGGTTTCTTCCCCTTCATAGTTGCTGAGCAGAATGTG  
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AGTGATGCAGAGGATGTATTGGATGCATTGACTGATGACCCTGGACTGGTGGGACTGAAC

GCATGGAGAAATGCGCGAGACGAGACAGGCTTTACCCCTGAAGACTATGCTCGCCAAAGA  
GGCAACGATGCTTACATCAATCTGGTCCAGATGAAGATTGACAGGCATCTTGGCAAAGGT  
CATGTTGTCTTGGTGTTCAGCAGCATGTGCCCTGCAATTACCGATGGGGTGAAGGCA  
GGTGATATCAGCCTGGAGATCTGCAAAGCCATGCCAGTGACAACAACATCCGCCGCAAGG  
TGCAACATTTGCAGTCGTGAGGCTAAGATGTACCCAAGTTCCTTTGCGAGGACCTTCCTG  
TACAGGCCGGCAATGTTACCGTGATGGGCGTCGCCGTGATCTGTGTTTTCGTCGGGATC  
CTCCTCCATACCCTCCCCAAGGTTTATGCCGCACCAAATTCAGATGGGAGCTGTTAGAG  
CGCGGAGCCATGTGA

>HORVU1Hr1G060770.1 cds sequence

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AAAGCCTTTCCTTCTCCTCCCGCGACGAGACGACCAATTCGCCCGCCCTCGTCGCGTCG  
CCGGCCGCTTCTCCCCCTCCCCACCACGCCCGACGCCTCCGCGGAACCGCGAACGAGA  
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CCTGCGCCACCGTCTCCATCTGTTGAGGCCGGGGCAAGCAGACGCGGGCGTCAGAAAGCGC  
GACCCGCGGGTGGTGTGCCCTAACTACCTCGCGGGGATTGTGCCCTGTGCGTGCCCCGAG  
TTGGATGAGATGGCGGCCGCCGCGGAGGTCGAGGAGGTTGCCGCGGAGGTGCTTGCCGGT  
CCGAGGAAGAAGCCCAAGGCCGCCAGCCGGGGTAGCAGCGGGGCGGTAGTCAAACTGGT  
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GTGCCGGGCTGTGAGGCGGATATACGGGAGCTGAAAGGGTACCACAAGCGGCACCGGGTG  
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>HORVU0Hr1G039150.3 CDS sequence

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ACCACCCACCTCGCACCACTACCTCGCCGCCGCCGCGGCAGGAGGCAACGGCAGCCCCTACGGCC  
AATTCGGCGGGGGCGGCGGGCGGGCGGGCGGGCTT  
CCAGTCTTACTACCACAGCAGCCGGGGACGGGCGCGCCCGAGTACTACTTCCCCACCTTGGTCAGC  
TCGGCGGAGGAGAACATGGCGAGCTTCGCGGCC  
ACGCAGCTGGGGTCAACCTCGGTTACCGGACCTACTTCCCGCCAGAGGCGGGCTACACCTACGGC  
CATCACCCGCCCGGTGCCAGGCCGAGGGCTGTA  
AGGCCGACCTCTCGGGTGCCAAGCGCTACCACCGCCGCCACAAGGTCTGCGAGCACCACTCCAAGG  
CGCCCGTTCGTCGTCACCGCCGGCGGCCTCCACCA  
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CAGGAAGCGCCTCGCAGACCACAACCGCCGTCGA  
AGGAAGTCAAAGCCGTCCGACGCCGATGCCGCTGATAAAAGGAGGACACAGGCCAGCAAAGCAGC  
AGCAAGTACCAAAGGCAAAGCAGCCGGAAGCAGCA  
GCAAGAGCACCGGCACCGGAGACGGGATGGACATTCAGGTGCAGCTGGGGAGCGGAGACCTGTCC  
AAAGATCAGGACGAAACCATGGGGCAGGGAGAGGT  
GGTGAAAGAAATGCAGGTGGATCCCAAGGGGAAAGCGTCAATGCAGCTGCAGCAGCAGCAACAGC  
AAGGACACCACGTCCATGGTCTTCACCTGCAGAGC  
CAACATGGCTTCCCTTTCCCTTCGACCTCTGCAGGCTCGTGCTTCCCTCAGAGCCAAGCTGTCTCGAG  
CACTGACAACACATCAAATATCGGCCAAGTGC  
AGCAAGAACAGCTAGGCTTGGGGTTCATCAGCACAGCAACATCCTTCAGCTGGGACAGGCCATGT  
TTGATCTCGACTTCGATCACTAG

>HORVU7Hr1G110950.1 CDS sequence

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TCGGGCTCGGGTTCGGCGGGCGCCACCACCAGCCGCCGCGCTGCCAGGCCGAGGGCTGCAAGGCCG  
ACCTCTCCGGCGCCAAGCACTACCACCGGCGCCA  
CAAGGTGTGCGAGTACCACGCCAAGGCGTCCCTCGTCGCCGCCAACGGCAAGCAGCAGCGCTTCTG  
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TCTCTCTCTCTCTCCCTCCGTAGAAATGGAACAGTAG

Table S2. Amino acid sequences of 17 barley SPL genes.

>HvSPL18

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TVAGREMRFCQQCSR FHLLTEFDEAKRSCRKRLDGHNR RRRRKPQPDPMNSASFMTSQQAF  
LRNPGTRFPSFPTPRPEQNWP GIIKTEENPY YTHQLPLGISNRHHFGGSTSTFAKEGRRF  
PFLQEGEINFATGVALEPAVCQPLLKTVAPPESSSSSSKMFSDGLTPVLDSDCALSLLSA  
PANSSGIDVGMVQQTEHIPIAQPLFSNLQQFSSSSWFSRTQASTGTVSATGFSCPVVEN  
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>HvSPL15

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LNLREEASMAMDVSP TTTMSSSPSPPARTSQEQ AARPSKRVRSGSPGTASGGGGGGGAGG  
SASGGGSYPMCQVDDCRADLTS AKDYHRRHKVCEIHSKTTKAVVANQMQRFCQQCSR FHP  
LSEFDEGKRSCRRLAGHNRRRRKTQPTDVASQLL LPENQENTANRTQDIVNLITVIARL  
QGGNVGKLP SIPPDPKDNLVQIISKINSINNANSLGKSPPSE AIDLNASHGQQQDSPVQ  
NATKVVDKQTV PSTMDLLTVLSGALGTSTPETNTS QSQGS SDSSGNNKSKSHSTEPACVV  
NSHEKSIRPFPAAGVIRS NSTHGSPPEIYKQPDRDTHPYLSLQLFGNAEVDIPVKMDTAN  
KYLSSSESNPMDERSPSSSPVTRTFFPTRSVNEGIRHPRIADYGEDAATAEISTTRA WC  
APQLELFKDSERPTENGSPNP TYQSCYASTSGSDHSPSTNSSDGQDRTGKIIFKLFGE  
PGSIPGNLRDEVVNWLKHSPTMEGYIRPGCLVLSMYLSMPTIAWDELEENFLQRVNSLV  
QASDLDFWRKGRFLVRSDNQLVSYKDG MTRLKSWRTWNTPELTLVTPIAVVGGRKTSLV  
LKGRNLTIPGTQIHCTSGGKYISKEVLCSA YPGTIYDDSGVETFDLPGEPNLTLGRCFIE  
VENRFRGNSFPVIFASKSICHEL RNLEAELEDSRFPDVSSDDQVHDARRLKPRDQVLHFL  
NELGWLFQAAACTPSIESDVSDSELIQFSTARFRHLLLFSNERDWCSLTKTLLEVLSKR  
SLVSEELSQETLEMLSEIHLLNRAVKRKSSHMVHLLVQFVVICPDNSKLYPFLPNYPGPG  
GLTPLHLAASIDDAEDIVDAL TDDPQQIGLSCWHSVLDDDEGISPEVYAKFRNNGSYNELV  
ARKLVDRKNSQVTIVLNKGEIHMDQ PENAGANNSSGIQALEIRSCSQCAILESGLLRPM  
RSRGLLARPYIHSMLAIAAVCV CVCFMRALLRFNSGRTFKWERLDFGPT

>HvSPL16

IFHVIYVTIHRIFIVSFWV LFAFHFCYFAYXXX CFLWCSSIFIGICSFYVXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXXXXXXX SCAVDGCKADLSKCRDYHRRHKVCEAHSKTPLVVVA  
GREMRFCQQCSR FHMLAEFDEAKRSCRKRLDGHNR RRRRKPQVDSMNSGSMFTTQQGTRFA  
SFSAPRPEPSWSGIKSEDSNPFYSTH QVNF GGATSSYSKEGRRFPFLHEGDQMSFSTGA  
PALEIPVCQPLLKAVAPLPPPESSSSNKMFSDGQLTHVLDSDCALSLLSSPANSSSV DV  
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SNDNEMNCHGIFHV GADGSSEGTSPSLPFSWQ

>HvSPL11

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RLSDHNARRRKPQPD AFSFAPARLPSSLMFDDRRQISFVWDKDPLSHGRPFPCSPWDSPS  
DFKPPQVKEIREVSINGQVHFDKSHLPNAV PALSHDIAELLPMKGP DASATASKLGGAPD  
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>HvSPL1

MSSGLKNKKKKGHEWDLNDWRWDGNLFLA APSSNAEAPSGCGSRELGRAEEGGSFGAADK  
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DGRDYHRRHKVCEVHTKSTLVRIK NIEHRFCQQCSR FHLVQEFDEGKKSCR SRLEKHNGR  
RRKAQAQAVSSSENQSLTNTLLLLL RQLAGQDSAASSSEQINGPNFLVNLLKNLAAVAG  
TQACQDMLKDATSSNAGNYVGNQSGPPVPAE EPPMKRRARNFDLNDTYVEEDEXXXXXX  
XXXXXXXXXXXXTDLRTQVLNWL SHYPSDMESYIRPGCVILTIYLR LPNWMWHKLNVDPA  
PWIENTLISITHGFWETGWLYARVQDRLT LSCNGRLTLVCPWLPVIGDKHQILCVTPIAA



SCKSTANFSVRGFNIAQPTTKLLCIFGGKYLVEATQKLQDDTAVQQGPQCLAFSCSFPS  
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ALKFLHEIGWLLQRSHSRATSSKAPQQHRVVGFLAARFRWLLSFAVDQEWCGVVKMLLDT  
LFQGNIDVPSVFEVFLGESLVFKA VNKRSKPLVDCLLRYTTNSAPVGGGAVATPARFVFT  
PDMTGPSDITPLHSAATISNA AAVLDALTD DPQQ LGIKAWKNARDATGYTPEDYARRRGH  
TSYIQMVQNKINRGLPAAHVS VSM TTTGITEEHADAGRPKSTDQTIFDVEKSLPGCRQCV  
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T

>HvSPL17

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KAPLVVVAGIEQRFCQQCSR FHQLPEFDQGKRSCRRLAGHNERRRKPPP GPMSTRYGR L  
AASFNEDPGRFRSFLDFSYPRAPAGVRDPWPAVQPGDHRMPGTTHWQGGQSHHEQHHAH  
RSAVAGYGDHHA YNGQSSSSGGGAPMIPAGFELPSDECMAGVAADSSCALSLSTQPWD  
SSA HSSSHIRSPAMSTASAFQGSVPVMSMASNYMAAASSSGSWGSPRGARSMQQQH HHH  
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>HvSPL7A

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>HvSPL7

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>HvSPL21

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SNQLQQPFVQSQVTMPTTASSSVLQMPMMTLPGMLMSSSSSLAADACTFGGGGGFLKRED  
GGPFS DIGGGGRIGLNLGRRTYFSPADVLA VDRLLMRSRFGGAGPMGMLGLGLGAAAH H  
QPPRCQAEGCKTDLSAAKH YHRRHKVCEYHAKAATVAASGKQQRFCQQCSR YVVLA EFDE  
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PSASSFSCFQQQHALDNGGQSNNATPTSAPPTLSLAAPPSPQQNDGDFGSLDTMLQM  
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SMQHFFEVD FM

>HvSPL3

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NMEFRFAPVKNPDRNTSENTELGKVDNTRTGTSPSSVVA VSSGEPVIGLKL GKRTYFEDV  
CGGQSVKSSPSGAASVPNKSPALSKKAKAEQQKAHNSYCQVEGCKVDLSSVKEYHRKHRV  
CELH SKAPKVVVAGLERRFCQQCSR FHALSEFDQKKRSCRRLNDHNSRRRKPOPEAISF  
SSSRMSTMFYDARQQPNFLFGQAPYVQMRSCGSSSWDEPGGFKVTHTKAPWLKPTTAAGV  
DGMHLSSQQMSDNVMPHGAHHGFDGFM AFKGTSTKFPNQGVQASAVAPNSSGAPDLQHAL  
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ERLGDH DSELQLPKPSYD HASHFDRMH

>HvSPL13

PSASSPSTHQLAPQFHFC DSSPRRALASFVFIAPHRKAWTARTSLASPPQQRPWQRSP  
RQLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXERC GADLTEAKRYHRRHKVCEAH SKAAVV  
VVAGLRQRFCQQCSR FHELLEFD DQKRSCRRLAGHNERRRKS SAEXNGGDGCRHADQDG  
RSHPGNPPLNHFQIR

>HvSPL23

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>HvSPL20

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>HvSPL6

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RGAM

>HvSPL9

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>HvSPL8

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>HvSPL22

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>AtSPL1

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>AtSPL10

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>AtSPL11

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>AtSPL12

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>AtSPL13

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TFPFHWE

>AtSPL14

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WLFQKNQTSSELREQSDFSLARFKFLLVCSVERDYCALIRTLMLVERNLVNDELNREALDMLAEIQLL  
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>AtSPL15

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NWSL

>AtSPL16

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>AtSPL2

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SRFHCLSEFDEKKRSCRRLSDHNARRRKPNGRTYDGKPQVDFVWNRFALIHPRSEEKFIWPSSKHVPS  
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>AtSPL3

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>AtSPL4

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>AtSPL5

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>AtSPL6

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AIYSTEVSIIWDLHETAASRSTRALLSAQSQHLSKFPNTTFSITQPNQNLNHSSTDYHQMEQPLWID  
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>AtSPL7

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>AtSPL8

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>AtSPL9

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>OsSPL1

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>OsSPL2

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>OsSPL3

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>OsSPL4

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>OsSPL5

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>OsSPL6

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>OsSPL7

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>OsSPL8

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>OsSPL9

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RELKGYHRRHRVCLRCAHAAAVMLDGVQKRYCQQCGKFHILLDFEDDKRSCRRKLERHNC  
RRRRKPDSSKILEKDIDDQLDFSADGSGDGELREENIDVTTSETLETVLSNKVLDRETPV  
GSDDVLSSPTCAQPSLQIDQSKSLVTFAASVEACLGTKQENTKLTNSPVHDTKSTYSSSC  
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QHEIFRINITTSKLDTHGPAFVEVENMFGLSNFVPILVGSKHLCSELEQIHDALCGSSDI  
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SS

>OsSPL10

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FEVDFM

>OsSPL11

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>OsSPL12

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QGVDPAACAVVSSNSNGAPDLRRALSLLSSDSWGPADVQAGSQVHPGGVMPPLAVAAATVT  
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>OsSPL13

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>OsSPL14

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>OsSPL15

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>OsSPL16

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>OsSPL17

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>OsSPL18

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VMTSRQPHFVGSPPSATTAAAFSPKEGRRFPFLHEGDQISFGGGGGAAAAATLEISVCQTT



VVAPPPPESSSSNKMFSDDLTTATTTTTTAHHHHHHHHQVLDSDCALSLSSPANSSSVD  
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>TaSPL1

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>TaSPL3

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PNFLFGQAPYVQMRSCGSSSWDDPGGFKVTHTKAPWLKPTTAAGVHGIHLSSQQMSDN  
IMPHGAHHGFDGFMFKGTCTKFPNQGVQASAVASDSSGAPDLQHALSLLSSNPVGAA  
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>TaSPL6

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>TaSPL8

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>TaSPL15

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LNASQGGQQDSSVQNATKVVDKQTVPSTMDLLTVLSGALGTSTPETNTSQQSGSSDSS  
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DSRFPDVPDQVHDARRLKPRDQVLHFLNELGWLFQKAAACTPSTKSDVSHSELIQF  
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>TaSPL17

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GAATGYHGHAYSSHGGGFPPELPPSGCLAGVAADSSCALSLSTQPWDNTPHGASH  
DHRSAFGDHPVGVSPSIMASNYMPPPASPWGGSRGHEGGRNAPHQQLPHDVLHEAH  
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>TaSPL20

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>TaSPL21

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FSPADVLAVDRLLMRSRFGGAGAMGMLGLGLGAAAHQHQTTPRCQAEGCKADLSAAKHY  
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>TaSPL22

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NNNSNHGGGNNNNNNMHLFEVDFM

>TaSPL23

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KVCEAHSKTPVVAVAGQQQRFCQQCSRFHLLGEFDEVKRSCRKRLDGHNRRRRKPPD  
PLNPAGLFANHHGTPS



Table S3. Genomic sequences of 17 barley SPL genes.

>HORVU0Hr1G039170.6 genomic sequence

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ACAAATGTGTGGCTCACGACCTGCCAAACAAGGAAACAACCTGTGGACTGTGGTCGGCTT  
GATTAGCTTTAGTGATGCGTGTGTTATTTTAACCTGTTGAGCCATGCAGAAAGGAAAGTGG  
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AGCCTCCTTGCAAAACAGCCACCCTCGGCAGCTCGGAATGAGAGGGACAGGGGTGAGAGC  
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TGACTACGTGAGCGTGAGCGTGAGCGCGAGCGCGGCATGGACTGGGATCTCAAGATGCCG  
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>HORVU6Hr1G031450.6 genomic sequence

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ATGGTGAGAGGAGGGAGACGATGGCTGATCCGGTG  
CCAGGCTTTTGGCCCTGACCATATCTCTGCGTCGGCCTTTTCTCTTTATCCTCCCATTGACCAATGTTGT  
GGCCGCAGTGCTGCCAGTGGCGACTAGNNNN

Table S4. SBP domain sequences of barley, Arabidopsis, rice and wheat

>HORVU0Hr1G039170  
SCAVDGCRADLSRCRDYHRRHKVCEAHSKTPVVTVAGREMRFCCQCSRFHLLTEFDEAKRSCRKRLDG  
HNRRRRKPQPD

>HORVU7Hr1G051400  
MCQVDDCRADLTSKDYHRRHKVCEIHSKTTKAVVANQMQRFCQCSRFHPLSEFDEGKRSCRRLA  
GHNRRRRKTQPT

>HORVU5Hr1G076380  
SCAVDGCADLSKCRDYHRRHKVCEAHSKTPVVVAGREMRFCCQCSRFHMLAEFDEAKRSCRKRLD  
GHNRRRRKPQVD

>HORVU6Hr1G031450  
RCQVEGCGTELA-AAKEYHRKHRVCEAHTKSPRVVAGQERRFCQCSRFHGLSEFDQKKRSCRRLSD  
HNARRRKPQPD

>HORVU7Hr1G042370  
SCLVDGCHADLRDGRDYHRRHKVCEVHTKSTLVRIKNIEHRFCQCSRFHLVQEFDEGKKSCRSRLEKH  
NGRRRKAQAQ

>HORVU5Hr1G073440  
RCQVEGCGVDLSGGKTYCRHKVCSMHSKAPLVVVAGIEQRFCQCSRFHQLPEFDQGKRSCRRLAG  
HNERRRKP PPG

>HORVU2Hr1G097610  
RCQVEGCHMVLAGAKEYHRRHKVCEAHSKAPRVIVHGAEQRFCQCSRFHAMA-EFDDAKRSCRRLA  
GHNERRRKSAN

>HORVU2Hr1G097580  
RCQVEGCHMVLAGAKEYHRRHKVCEAHSKAPRVIVHGAEQRFCQCSRFHAMA-EFDDAKRSCRRLA  
GHNERRRKSAN

>HORVU6Hr1G030490  
RCQAEGCKTDL-SAAKHYHRRHKVCEYHAKAATVAASGKQQRFCQCSRYVLA-EFDEAKRSCRKRLT  
EHNRRRKPAGA

>HORVU6Hr1G019700  
YQVEGCKVDLSSVKEYHRKHRVCELHSAKPKVVVAGLERRFCQCSRFHALSEFDQKKRSCRRLND  
HNSRRRKPQPE

>HORVU2Hr1G048280  
XXXXERCADL-TEAKRYHRRHKVCEAHSKAAVVVVAGLRQRFCQCSRFHELLEFDDQKRSCRRLA  
GHNERRRKS-SAE

>HORVU3Hr1G094730  
ACSVEGCTADLSRCREYHRRHKVCEAHSKTPVAVAGQQRFCCQCSRFHLLGEFDEVKRSCRKRLDG  
HNRRRRKPQPD

>HORVU7Hr1G110980  
RCQVEDCKADLSGAKHYHRRHKVCEYHAKAALVSTAGKQQRFCQCSRSHVLM-EFDEAKRSCRRLA  
EHNRRRKP-PAAG

>HORVU5Hr1G117190  
ACQVEGCCADLSAAKDYHRRHKVCEMHAKANTAVVGNTVQRFCQCSRFHLLQEFDEGKRSCRRLA  
GHNKRRRKT-RPE

>HORVU1Hr1G060770  
RCQVPGCEADIRELKG-YHKRHRVCLRCAHASAVMLDG-VQKRYCQQCGKXXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX

>HORVU0Hr1G039150  
RCQAEGCKADLSGAKRYHRRHKVCEHHSKAPVVVTAGGLHQRFCQCSRFHLLDEFDDAKKSCRKRL  
ADHNRRRKR-SKP

>HORVU7Hr1G110950  
RCQAEGCKADLSGAKHYHRRHKVCEYHAKASLVAANGKQQRFCQCSRSEPXXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXX



>AtSPL1

VCQVENCEADLSKVVDYHRRHKVCEMHSKATSATVGGILQRFCQQCSRFLHLLQEFDEGKRSCRRLAG  
HNKRRRKTNP

>AtSPL2

HCQVEGCNLDLSSAKDYHRKHRICENHSKFPKVVVSGVERRFCQQCSRFLHCLSEFDEKKRSCRRLSDH  
NARRRKPNG

>AtSPL3

VCQVESCTADMSKAKQYHKRHKVCQFHAKAPHVRISGLHQRFCQQCSRFLHALSEFDEAKRSCRRLAG  
HNERRRKTSTTD

>AtSPL4

LCQVDRCTADMKEAKLYHRRHKVCEVHAKASSVFLSGLNQRFCQQCSRFLHDLQEFDEAKRSCRRLA  
GHNERRRKSSE

>AtSPL5

LCQVDRCTVNLTEAKQYYRRHRVCEVHAKASAATVAGVRQRFCQQCSRFLHELPEFDEAKRSCRRLAG  
HNERRRKISGD

>AtSPL6

LCQVYGCSKDLSSSKDYHKRHRVCEAHSKTSVVIVNGLEQRFCQQCSRFLHFLSEFDDGKRSCRRLAGH  
NERRRKP

>AtSPL7

RCQVPDCEADISELKGYHKRHRVCLRCATASFVLDGENKRYCQQCGKFHLLPDFDEGKRSCRRLER  
HNNRRRKRK

>AtSPL8

RCQAEGCNADLSHAKHYHRRHKVCEFHSKASTVVAAGLSQRFCQQCSRFLHLLSEFDNGKRSCRRLAD  
HNNRRRKRCHQS

>AtSPL9

RCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFLHQLPEFDLEKRSCRRLAG  
HNERRRKP

>AtSPL10

RCQIDGCELDLSSSKDYHRKHRVCETHSKCPKVVVSGLERRFCQQCSRFLHAVSEFDEKKRSCRRLSHH  
NARRRKP

>AtSPL11

RCQIDGCELDLSSAKGYHRKHKVCEKHSKCPKVSVSGLERRFCQQCSRFLHAVSEFDEKKRSCRRLSHH  
NARRRKP

>AtSPL12

CCQVDNCGADLSKVVDYHRRHKVCEIHSKATTALVGGIMQRFCQQCSRFLHVLEEFDEGKRSCRRLAG  
HNKRRRKAN

>AtSPL13A

ICLVDGCDSDFSNCREYHKRHKVCDVHSKTPVVTINGHKQRFCQQCSRFLHLEEFDEGKRSCRRLDGH  
NRRRKP

>AtSPL14

MCQVDNCTEDLSHAKDYHRRHKVCEVHSKATKALVGKQMQRFCQQCSRFLHLLSEFDEGKRSCRRLA  
GHNRRRKR

>AtSPL15

RCQVEGCRMDLSNVKAYYSRHKVCCIHSKSSKVVVSGLHQRFCQQCSRFLHQLSEFDLEKRSCRRLACH  
NERRRKP

>AtSPL16

KCQVDNCKEDLSIAKDYHRRHKVCEVHSKATKALVGKQMQRFCQQCSRFLHLLSEFDEGKRSCRRLDG  
HNNRRRKT

>OsSPL1

CCQVDGCTVNLSSARDYNKRHKVCEVHTKSGVVRIKNVEHRFCQQCSRFLHLLQEFDEGKKSCSRSLAQ  
HNNRRRKR

>OsSPL2

ACSVEGCAADLSKCVRDYHRRHKVCEAHSKTAVVTVAGQQQRFCCQCSRFFHLLGEFDEEKRSCRKRL  
DGHNKRRRKPPD  
>OsSPL3  
HCQVEGCNVDLSSAKPYHRKHRVCEPHSKTLKVIVAGLERRFCQQCSRFFHGLAEFDQKKRSCRRLHD  
HNARRRKPPQPE  
>OsSPL4  
RCQVEGCGVELVGVKDYHRKHRVCEAHSKFPRVVVAGQERRFCQQCSRFFHALSEFDQKKRSCRRLY  
DHNARRRKPPQTD  
>OsSPL5  
RCQAEGCKADLSAAKHYYHRRHKVCFDFAKAAAVLAAGKQQRFCQQCSRFFHVLAEFDEAKRSCRKRLT  
EHNRRRKPTAG  
>OsSPL6  
ACQVEGCTADLTGVRDYHRRHKVCEMHAKATTA VVGNTVQRFCQQCSRFFHPLQEFDEGKRSCRRLA  
GHNRRRKTRPE  
>OsSPL7  
RCQVEGCDITLQGVKEYHRRHKVCEVHAKAPRVVHVGTEQRFCQQCSRFFHVLAEFDDAKKSCRRLA  
GHNERRRSNAS  
>OsSPL8  
RCQAEGCKADLSSAKRYHRRHKVCEHHSKAPVVVTAGGLHQRFCQQCSRFFHLLDEFDDAKKSCRKRL  
ADHNRRRKSKPS  
>OsSPL9  
KCQVPGCEADIRELKGYYHRRHRVCLRCAHAAAVMLDGVQKRYCQQCGKFHILLDFDEDKRSCRKLE  
RHNKRRRKPPDS  
>OsSPL10  
RCQAEGCKADLSGAKHYHRRHKVCEYHAKASVVAASGKQQRFCQQCSRFFHVLTEFDEAKRSCRKRLA  
EHNRRRKPAAA  
>OsSPL11  
RCQVEGCGLELGGYKEYYRKHRVCEPHTKCLR VVVAGQDRRFCQQCSRFFHAPSEFDQEKRSCRRLSD  
HNARRRKPPQTD  
>OsSPL12  
YCQVEGCKVDLSSAREYHRKHKVCEAHSKAPKVIVSGLERRFCQQCSRFFHGLAEFDQKKKSCRRLSD  
HNARRRKPPQE  
>OsSPL13  
RCQVERCGVDLSEAGRYNRRHKVCQTHSKEPVVLVAGLRQRFCQQCSRFFHELTEFDDAKRSCRRLAG  
HNERRRKSAAAD  
>OsSPL14  
RCQVEGCGADLSGIKNYYCRHKVCFMHSKAPRVV VAGLEQRFCQQCSRFFHLLPEFDQGKRSCRRLAG  
HNERRRPQTP  
>OsSPL15  
MCQVDDCRADLTNAKDYHRRHKVCEIHGKTTKALVGNQMQRFCQQCSRFFHPLSEFDEGKRSCRRLA  
GHNRRRKTPQPT  
>OsSPL16  
SCAVDGCKEDLSKCRDYHRRHKVCEAHSKTPLVVVSGREMRFCCQCSRFFHLLQEFDEAKRSCRKRLDG  
HNRRRRKPPD  
>OsSPL17  
RCQVEGCGVDLSGVKPYCRHKVCYMHAKAPIVVVAGLEQRFCQQCSRCSVHMVRFHQLPEFDQEKK  
SCRRLAGHNERRRKPTPG  
>OsSPL18  
SCAVDGCKADLSKHRDYHRRHKVCEPHSKTPVVVSGREMRFCCQCSRFFHLLGEFDEAKRSCRKRLDG  
HNRRRRKPPAD  
>TaSPL1  
SCQVDGCHADLSDDRKYHRRHKVCEPHTKSTLVRIKNIHRFCQQCSRFFHLVQEFDEGKKSCRSLATH

NRRRRKAPAE

>TaSPL3

YCQVEGCKVDLSSVKDYHRKHRVCELHSAKPKVVVAGLERRFCQQCSRFBALAEFDQKKRSCRRRLN  
DHNSRRRKQPPE

>TaSPL6

ACQVEGCCADLSAAKDYHRRHKVCEMHAKANTAVVGNTVQRFCCQCSRFBLLQEFDEGKRSCRRRLA  
GHNKRRRKTRPE

>TaSPL8

RCQAEGCKADLSGAKRYHRRHKVCEHHSKAPVVVVTAGGLHQRFCQQCSRFBLLDEFDDAKKSCRKRL  
ADHNRRRRKSKPS

>TaSPL15

MCQVDDCRADLTSADYHRRHKVCEIHSKTTKAVVGNQMQRFCQQCSRFBPLSEFDEGKRSCRRRLA  
GHNRRRRKTQPT

>TaSPL17

RCQVEGCGVDLSGAKQYHSRHKVCSMHTKEPRVVVAGLEQRFCQQCSRFBQLPEFDQGKRSCRRRLA  
GHNERRRKAPPG

>TaSPL20

RCQVXDCXADLSGAKHYHRRHKVCEYHAKAXLVSAAGKQQRFCQQCSRFBVLTEFDEAKRSCRRRLA  
EHNRRRRKPAAG

>TaSPL21

RCQAEGCKADLSAAKHYHRRHKVCEYHAKAATVAASGKQQRFCQQCSRFBVLAEFDEAKRSCRKRLT  
EHNRRRRKPAGA

>TaSPL22

RCQAEGCKADLSGAKHYHRRHKVCEYHAKASLVAAAGKQQRFCQQCSRFBVLTEFDEAKRSCRKRLA  
EHNRRRRKPASS

>TaSPL23

PCSVEGCTADLSRCREYHRRHKVCEAHSKTPVVAVAGQQRFCCQCSRFBLLGEFDEVKRSCRKRLDG  
HNRRRRKPQPD

**Table S5.** Details of miR156 complementary site in *HvSPL* genes.

miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_fragment	Target_aligned_fragment	Inhibition	Multiplicity
hvu-miR156a	HORVU5Hr1G076380	1	-1	1	21	4216	4236	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156a	HORVU3Hr1G094730	1	-1	1	21	3542	3562	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156a	HORVU0Hr1G039170	1	-1	1	21	5953	5973	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156a	HORVU5Hr1G073440	1	-1	1	21	3463	3483	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156a	HORVU6Hr1G031450	1	-1	1	21	4119	4139	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156a	HORVU6Hr1G019700	1	-1	1	21	6811	6831	UGACAGAAGAGAGUGAGCACA	CAUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156a	HORVU2Hr1G048280	1	-1	1	21	8382	8402	UGACAGAAGAGAGUGAGCACA	CAUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU5Hr1G076380	1	-1	1	21	4216	4236	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU5Hr1G073440	1	-1	1	21	3463	3483	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU0Hr1G039170	1	-1	1	21	5953	5973	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU3Hr1G094730	1	-1	1	21	3542	3562	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU6Hr1G031450	1	-1	1	21	4119	4139	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU6Hr1G019700	1	-1	1	21	6811	6831	UGACAGAAGAGAGUGAGCACA	CAUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR156b	HORVU2Hr1G048280	1	-1	1	21	8382	8402	UGACAGAAGAGAGUGAGCACA	CAUGCUCUCUCUCUUCUGUCA	Cleavage	1
hvu-miR5049c	HORVU6Hr1G019700	2.5	-1	1	23	6478	6500	AGACAAUUUUUUUGGGACGGAGG	CCUCCGUCUCAAUUUUUGGGACGGAGG	Cleavage	1
hvu-miR5049c	HORVU1Hr1G060770	2.5	-1	1	23	9210	9232	AGACAAUUUUUUUGGGACGGAGG	CCUCCAUCCCAUUUUUGGGACGGAGG	Cleavage	1

**Table S6.** Details of splice variants produced from *HvSPL* genes.

<b>HORVU0Hr1G039170</b>	Chromosome chrUn: 248,141,188-248,147,114 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU0Hr1G039170.1	2625	290aa	Protein coding
Novel	HORVU0Hr1G039170.3	2507	227aa	Protein coding
Novel	HORVU0Hr1G039170.5	1845	394aa	Protein coding
Novel	HORVU0Hr1G039170.7	1631	52aa	Protein coding
Novel	HORVU0Hr1G039170.8	1456	58aa	Protein coding
Novel	HORVU0Hr1G039170.4	1369	212aa	Protein coding
Novel	HORVU0Hr1G039170.6	1249	400aa	Protein coding
Novel	HORVU0Hr1G039170.2	985	272aa	Protein coding
Novel	HORVU0Hr1G039170.9	365	120aa	Protein coding
<b>HORVU7Hr1G051400</b>	Chromosome chr7H: 192,879,289-192,885,430 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU7Hr1G051400.1	4960	732aa	Protein coding
Novel	HORVU7Hr1G051400.3	4884	1130aa	Protein coding
Novel	HORVU7Hr1G051400.2	4874	1130aa	Protein coding
Novel	HORVU7Hr1G051400.5	4723	612aa	Protein coding
Novel	HORVU7Hr1G051400.4	4624	612aa	Protein coding
Novel	HORVU7Hr1G051400.6	4444	613aa	Protein coding
Novel	HORVU7Hr1G051400.7	3837	508aa	Protein coding
Novel	HORVU7Hr1G051400.9	3372	609aa	Protein coding
Novel	HORVU7Hr1G051400.8	3321	1106aa	Protein coding
Novel	HORVU7Hr1G051400.10	1131	237aa	Protein coding
<b>HORVU5Hr1G076380</b>	Chromosome chr5H: 551,053,196-551,057,389 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU5Hr1G076380.2	3828	159aa	Protein coding
Novel	HORVU5Hr1G076380.1	1727	159aa	Protein coding
Novel	HORVU5Hr1G076380.3	1652	159aa	Protein coding
Novel	HORVU5Hr1G076380.6	1636	159aa	Protein coding
Novel	HORVU5Hr1G076380.9	1179	392aa	Protein coding
Novel	HORVU5Hr1G076380.8	1137	264aa	Protein coding
Novel	HORVU5Hr1G076380.4	1124	306aa	Protein coding
Novel	HORVU5Hr1G076380.7	1084	279aa	Protein coding
Novel	HORVU5Hr1G076380.11	1002	333aa	Protein coding
Novel	HORVU5Hr1G076380.10	996	331aa	Protein coding
Novel	HORVU5Hr1G076380.5	917	159aa	Protein coding
<b>HORVU6Hr1G031450</b>	Chromosome chr6H: 133,169,150-133,173,306 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype

Novel	HORVU6Hr1G031450.3	2870	209aa	Protein coding
Novel	HORVU6Hr1G031450.7	2659	113aa	Protein coding
Novel	HORVU6Hr1G031450.10	2571	182aa	Protein coding
Novel	HORVU6Hr1G031450.4	2196	191aa	Protein coding
Novel	HORVU6Hr1G031450.1	1740	104aa	Protein coding
Novel	HORVU6Hr1G031450.9	1640	184aa	Protein coding
Novel	HORVU6Hr1G031450.2	1523	184aa	Protein coding
Novel	HORVU6Hr1G031450.6	1429	326aa	Protein coding
Novel	HORVU6Hr1G031450.5	1030	104aa	Protein coding
Novel	HORVU6Hr1G031450.8	1020	104aa	Protein coding
<b>HORVU7Hr1G042370</b>	Chromosome chr7H: 122,553,615-122,558,679 forward strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU7Hr1G042370.5	3086	328aa	Protein coding
Novel	HORVU7Hr1G042370.10	2775	245aa	Protein coding
Novel	HORVU7Hr1G042370.7	2685	541aa	Protein coding
Novel	HORVU7Hr1G042370.8	2526	841aa	Protein coding
Novel	HORVU7Hr1G042370.14	2251	328aa	Protein coding
Novel	HORVU7Hr1G042370.6	2247	389aa	Protein coding
Novel	HORVU7Hr1G042370.13	2104	328aa	Protein coding
Novel	HORVU7Hr1G042370.9	2008	512aa	Protein coding
Novel	HORVU7Hr1G042370.20	1988	328aa	Protein coding
Novel	HORVU7Hr1G042370.18	1957	328aa	Protein coding
Novel	HORVU7Hr1G042370.12	1929	328aa	Protein coding
Novel	HORVU7Hr1G042370.15	1915	328aa	Protein coding
Novel	HORVU7Hr1G042370.19	1825	328aa	Protein coding
Novel	HORVU7Hr1G042370.16	1781	500aa	Protein coding
Novel	HORVU7Hr1G042370.11	1747	328aa	Protein coding
Novel	HORVU7Hr1G042370.1	1701	221aa	Protein coding
Novel	HORVU7Hr1G042370.3	1443	306aa	Protein coding
Novel	HORVU7Hr1G042370.4	1417	221aa	Protein coding
Novel	HORVU7Hr1G042370.2	1302	221aa	Protein coding
Novel	HORVU7Hr1G042370.17	1081	189aa	Protein coding
<b>HORVU5Hr1G073440</b>	Chromosome chr5H: 539,014,598-539,018,210 forward strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU5Hr1G073440.12	3082	196aa	Protein coding
Novel	HORVU5Hr1G073440.13	2977	301aa	Protein coding
Novel	HORVU5Hr1G073440.4	2513	198aa	Protein coding
Novel	HORVU5Hr1G073440.7	1616	416aa	Protein coding
Novel	HORVU5Hr1G073440.6	1613	415aa	Protein coding
Novel	HORVU5Hr1G073440.14	1483	82aa	Protein coding
Novel	HORVU5Hr1G073440.10	1413	363aa	Protein coding

Novel	HORVU5Hr1G073440.9	1413	363aa	Protein coding
Novel	HORVU5Hr1G073440.11	1261	196aa	Protein coding
Novel	HORVU5Hr1G073440.8	1185	394aa	Protein coding
Novel	HORVU5Hr1G073440.5	1153	384aa	Protein coding
Novel	HORVU5Hr1G073440.1	647	215aa	Protein coding
Novel	HORVU5Hr1G073440.2	644	214aa	Protein coding
Novel	HORVU5Hr1G073440.3	636	212aa	Protein coding
<b>HORVU2Hr1G097610</b>	Chromosome chr2H: 679,689,970-679,692,277 forward strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU2Hr1G097610.1	2156	203aa	Protein coding
Novel	HORVU2Hr1G097610.2	559	125aa	Protein coding
<b>HORVU2Hr1G097580</b>	Chromosome chr2H: 679,640,052-679,642,809 forward strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU2Hr1G097580.1	2606	209aa	Protein coding
Novel	HORVU2Hr1G097580.2	552	122aa	Protein coding
<b>HORVU6Hr1G030490</b>	Chromosome chr6H: 127,986,525-127,990,179 forward strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU6Hr1G030490.3	1727	473aa	Protein coding
Novel	HORVU6Hr1G030490.2	1711	491aa	Protein coding
Novel	HORVU6Hr1G030490.1	884	294aa	Protein coding
Novel	HORVU6Hr1G030490.4	797	142aa	Protein coding
<b>HORVU6Hr1G019700</b>	Chromosome chr6H: 53,909,817-53,916,886 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU6Hr1G019700.1	7070	232aa	Protein coding
Novel	HORVU6Hr1G019700.2	4686	474aa	Protein coding
Novel	HORVU6Hr1G019700.17	4575	384aa	Protein coding
Novel	HORVU6Hr1G019700.10	4312	232aa	Protein coding
Novel	HORVU6Hr1G019700.4	3625	474aa	Protein coding
Novel	HORVU6Hr1G019700.16	3273	384aa	Protein coding
Novel	HORVU6Hr1G019700.11	3240	232aa	Protein coding
Novel	HORVU6Hr1G019700.3	3212	507aa	Protein coding
Novel	HORVU6Hr1G019700.9	3133	232aa	Protein coding
Novel	HORVU6Hr1G019700.6	3118	474aa	Protein coding
Novel	HORVU6Hr1G019700.13	2933	474aa	Protein coding
Novel	HORVU6Hr1G019700.18	2912	366aa	Protein coding
Novel	HORVU6Hr1G019700.12	2788	474aa	Protein coding
Novel	HORVU6Hr1G019700.5	2553	474aa	Protein coding
Novel	HORVU6Hr1G019700.15	2203	474aa	Protein coding
Novel	HORVU6Hr1G019700.7	2158	474aa	Protein coding
Novel	HORVU6Hr1G019700.14	1868	474aa	Protein coding
Novel	HORVU6Hr1G019700.8	1063	180aa	Protein coding

Novel	HORVU6Hr1G019700.19	949	289aa	Protein coding
Novel	HORVU6Hr1G019700.20	897	283aa	Protein coding
<b>HORVU2Hr1G048280</b>	Chromosome chr2H: 269,391,017-269,400,061 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU2Hr1G048280.1	1375	105aa	Protein coding
Novel	HORVU2Hr1G048280.2	588	195aa	Protein coding
Novel	HORVU2Hr1G048280.3	571	190aa	Protein coding
Novel	HORVU2Hr1G048280.4	235	78aa	Protein coding
<b>HORVU3Hr1G094730</b>	Chromosome chr3H: 647,368,957-647,372,642 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU3Hr1G094730.5	2272	227aa	Protein coding
Novel	HORVU3Hr1G094730.9	1733	328aa	Protein coding
Novel	HORVU3Hr1G094730.8	1663	256aa	Protein coding
Novel	HORVU3Hr1G094730.1	1630	429aa	Protein coding
Novel	HORVU3Hr1G094730.2	1630	429aa	Protein coding
Novel	HORVU3Hr1G094730.3	1610	426aa	Protein coding
Novel	HORVU3Hr1G094730.7	1582	357aa	Protein coding
Novel	HORVU3Hr1G094730.6	1477	227aa	Protein coding
Novel	HORVU3Hr1G094730.4	1344	295aa	Protein coding
Novel	HORVU3Hr1G094730.10	1307	345aa	Protein coding
Novel	HORVU3Hr1G094730.11	610	199aa	Protein coding
Novel	HORVU3Hr1G094730.12	356	118aa	Protein coding
<b>HORVU7Hr1G110980</b>	Chromosome chr7H: 631,945,657-631,949,862 forward strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU7Hr1G110980.2	1749	365aa	Protein coding
Novel	HORVU7Hr1G110980.5	1726	424aa	Protein coding
Novel	HORVU7Hr1G110980.4	1724	423aa	Protein coding
Novel	HORVU7Hr1G110980.3	1710	449aa	Protein coding
Novel	HORVU7Hr1G110980.7	1431	171aa	Protein coding
Novel	HORVU7Hr1G110980.6	1214	292aa	Protein coding
Novel	HORVU7Hr1G110980.1	904	237aa	Protein coding
<b>HORVU5Hr1G117190</b>				
	Chromosome chr5H: 650,559,269-650,565,702 reverse strand.			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU5Hr1G117190.3	3817	473aa	Protein coding
Novel	HORVU5Hr1G117190.4	3774	473aa	Protein coding
Novel	HORVU5Hr1G117190.2	3723	498aa	Protein coding
Novel	HORVU5Hr1G117190.1	3661	473aa	Protein coding
Novel	HORVU5Hr1G117190.5	3584	964aa	Protein coding
Novel	HORVU5Hr1G117190.6	2333	442aa	Protein coding
<b>HORVU1Hr1G060770</b>	Chromosome chr1H: 441,051,831-441,063,137 forward strand.			



Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU1Hr1G060770.2	2940	573aa	Protein coding
Novel	HORVU1Hr1G060770.3	2631	235aa	Protein coding
Novel	HORVU1Hr1G060770.4	2544	641aa	Protein coding
Novel	HORVU1Hr1G060770.6	2535	643aa	Protein coding
Novel	HORVU1Hr1G060770.5	2531	567aa	Protein coding
Novel	HORVU1Hr1G060770.10	2366	486aa	Protein coding
Novel	HORVU1Hr1G060770.8	2283	598aa	Protein coding
Novel	HORVU1Hr1G060770.9	1906	468aa	Protein coding
Novel	HORVU1Hr1G060770.1	1287	325aa	Protein coding
Novel	HORVU1Hr1G060770.7	880	83aa	Protein coding
Novel	HORVU1Hr1G060770.11	832	277aa	Protein coding
<b>HORVU0Hr1G039150</b>	chrUn:248118980..248122768 forward			
Name	Transcript ID	bp	Protein	Biotype
Novel	HORVU0Hr1G039150.3	1423	362	Protein coding
Novel	HORVU0Hr1G039150.2	1420	361	Protein coding
Novel	HORVU0Hr1G039150.4	1162	349	Protein coding
Novel	HORVU0Hr1G039150.5	994	120	Protein coding
Novel	HORVU0Hr1G039150.1	1152	383	Protein coding





## HORVU2Hr1G048280

miRNA_Acc.	Target_Acc.	Expectatic	UPES	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_fragment	Target_aligned_fragment	Inhibition	Target_Desc.	Multiplicity
hvu-miR156a	HORVU2Hr1G048280.1	1	-1	1	21	112	132	UGACAGAAGAGAGUGAGCACA	CAUGCUCUCCUCUCUCUGUCA	Cleavage	cdna:protein_coding	1
hvu-miR156b	HORVU2Hr1G048280.1	1	-1	1	21	112	132	UGACAGAAGAGAGUGAGCACA	CAUGCUCUCCUCUCUCUGUCA	Cleavage	cdna:protein_coding	1

**Table S8.** Primer sequences used in this study.

<b>Primer Names</b>	<b>Primer sequences</b>
<i>HvSPL3_qFP</i>	GATGTCTGTGGAGGGCAGAG
<i>HvSPL3_qRP</i>	CTTGCAGCCTTCAACCTGAC
<i>HvSPL6_qFP</i>	GAAGGAAAGCGAAGTTGTGC
<i>HvSPL6_qRP</i>	AAATTGGCGCATATTCCAAG
<i>HvSPL13_qFP</i>	GTGACCCGGGAAGTAGTCAG
<i>HvSPL13_qRP</i>	GCCACAAATTATCCCAGCAG
<i>HvSPL15_qFP</i>	CGGTAGCAGGGGTATAAATGG
<i>HvSPL15_qRP</i>	TCAAAACGGGAAGTAGGAGAG
<i>HvSPL23_qFP</i>	AGTGCAGCAGGTTCCATTTG
<i>HvSPL23_qRP</i>	CTCCGTGGTGATTAGCGAAC
<i>HvSPL11.1V_FP</i>	CGCTTCGAAATTAGGTGGAG
<i>HvSPL11.1V_RP</i>	TGGATTCATAGCCACTGCTG
<i>HvSPL11.2V_FP</i>	TGCAAACCTGTGGTTATACAGC
<i>HvSPL11.2V_RP</i>	ATTGCCACCTTTCTCATC
<i>HvSPL20.1V_FP</i>	AGGAGCACCAGCACTTCATC
<i>HvSPL20.1V_RP</i>	TGCTAAAGCCCAATACACC
<i>HvSPL20.2V_FP</i>	GCAAGAAAGAGGGTCTGTGC
<i>HvSPL20.2V_RP</i>	GCATGTGAATCCAGTGATGC
<i>HvSPL8.1V_FP</i>	CAGCCGGAATGTTCTTTCCGGTC
<i>HvSPL8.1V_RP</i>	GGTGTATCATCAATCTATCCATAGC
<i>HvSPL8.2V_FP</i>	TACTTCCCCACCTTGGTCAG
<i>HvSPL8.2V_RP</i>	ACTGCTGGCAGAACCTCTGG
<i>HvSPL8.3V_FP</i>	CCGTCCATGTTTCTCTACC
<i>HvSPL8.3V_RP</i>	CCGGCTGCTTCTGTTTAC
<i>HvActinF</i>	GCCGTGCTTTCCCTCTATG
<i>HvActinR</i>	GCTTCTCCTTGATGTCCCTTA
<i>HvGAPDHF</i>	GTGAGGCTGGTGCTGATTA
<i>HvGAPDHR</i>	CGTGGTGCAGCTAGCATTTGAGAC
<i>HvAP2_FP</i>	AGGCCAAGTTCGACCAGAA
<i>HvAP2_RP</i>	CTGGGACTGAACTGCATGTG