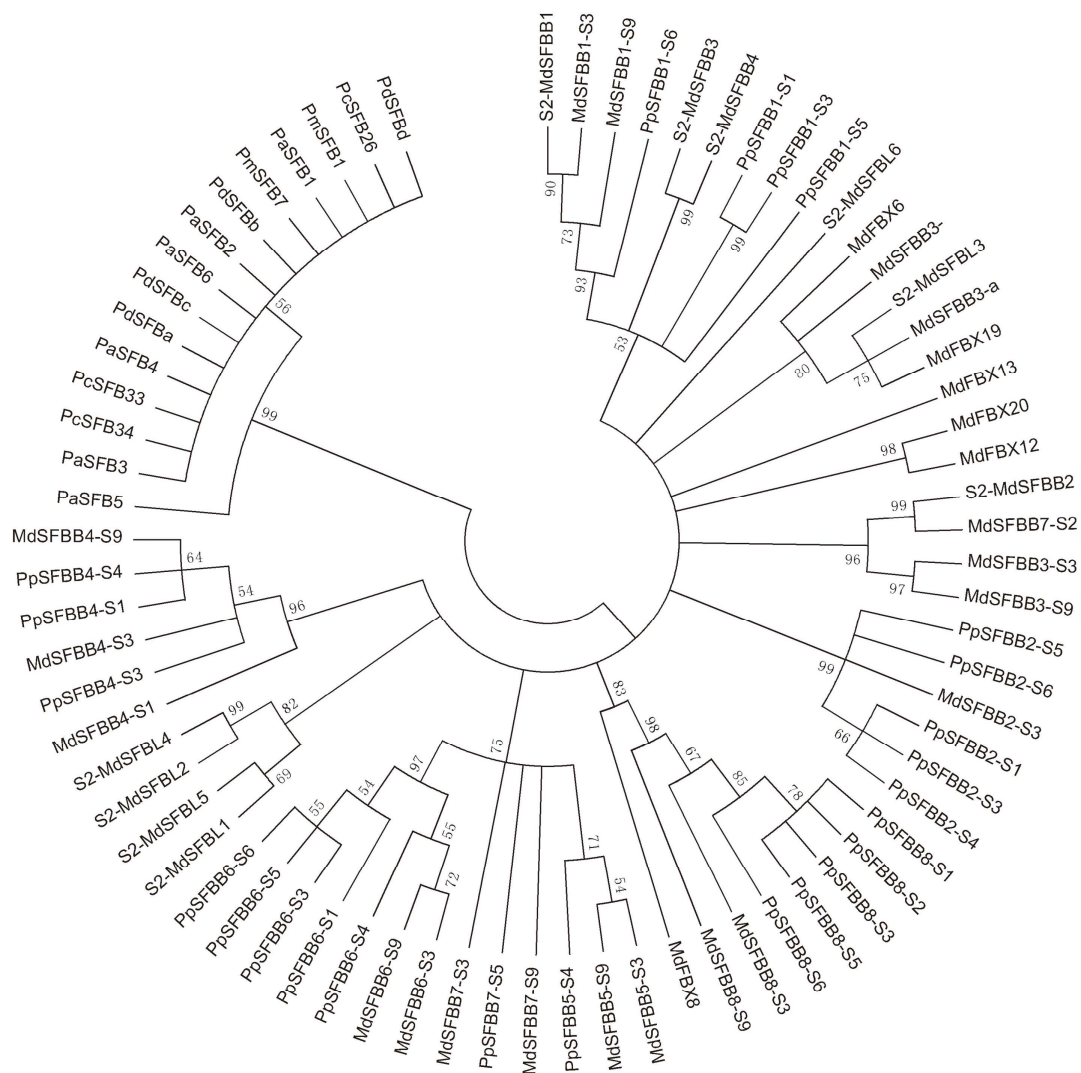


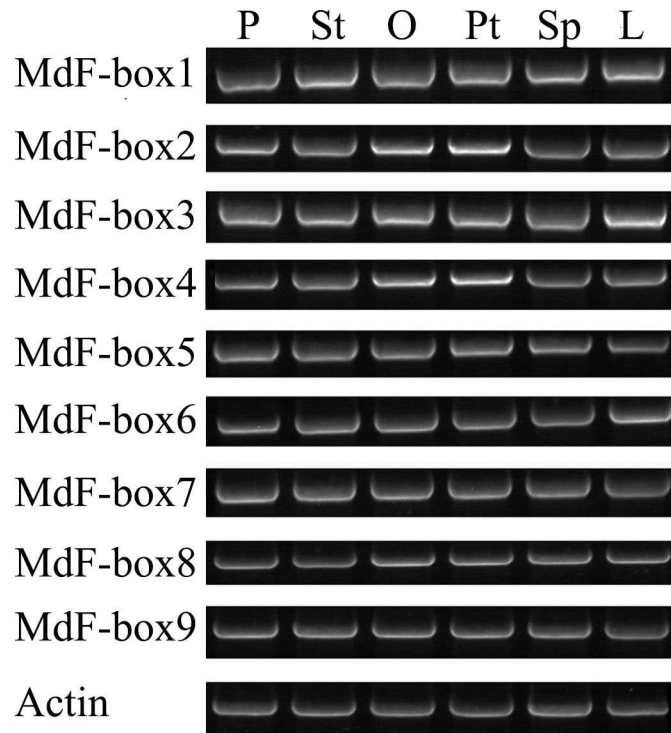
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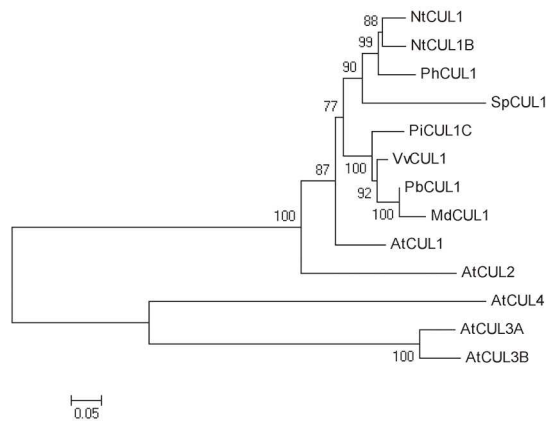
**Supplemental Figure 1** A NJ tree of plant SKP1-like proteins. The deduced amino acid sequences were from Arabidopsis (ASK1-21), Brassica napus (BnSkp1), Zantedeschia hybrid cultivar (ZhSkp1), Humulus lupulus (HISkp1), Capsicum annuum (CaSkp1), Fuji(FujiSkp1-like), Medicago truncatula (MtSkp1), Nicotiana benthamiana (NbSkp1), Pellia endiviifolia (PeSKP1), Triticum aestivum (TaSkp1), Oryza sativa (OsSkp1), Ricinus communis (RcSkp1), human (HsSkp1), Schizosaccharomyces pombe (SpSkp1), Petunia hybrida (PhSSK1), Antirrhinum majus (AhSSK1), Lilium longiflorum (LSK1-3), Vitis vinifera (VvSKP1-like), Hevea brasiliensis (HbSkp1), Pyrus (PbSSK1-2), Prunus (PavSSK1). The NJ tree was generated with 1,000 bootstrap replicates, and bootstrap values of 50% and above are given at branch nodes.



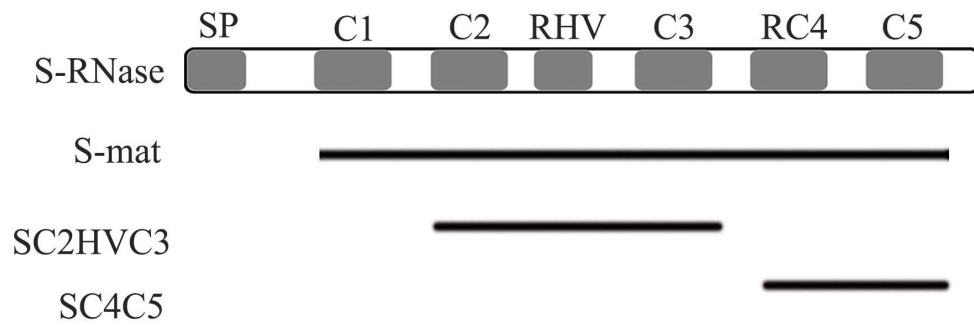
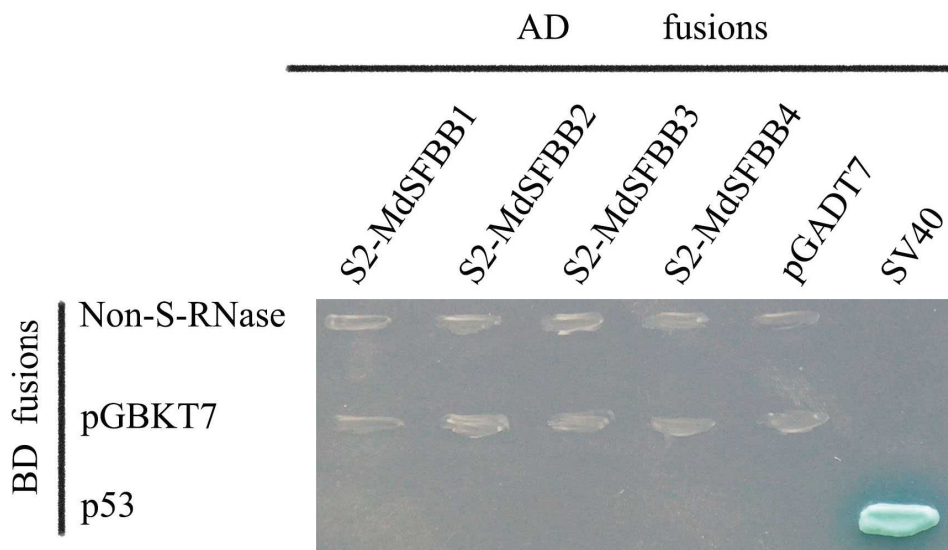
**Supplemental Figure 2** Phylogenetics analysis of the SFBB genes of *Malus*, *Pyrus pyrifolia*, *P. avium*, *P. cerasus*, *P. dulcis*, *P. mume*. The phylogenetic tree was constructed using the Neighbor-Joining method. Numbers on the branches indicate bootstrap values >50%.



**Supplemental Figure 3** The expression patterns of MdF-box1-9. Total RNAs were extracted from different organs. The synthesized cDNA were used as templates in RT-PCR. L, Leaves; Sp, sepals; Pt, petals; O, ovaries; St, styles; p, pollen.



**Supplemental Figure 4** A NJ tree of plant CUL1-like proteins. Arabidopsis(AtCUL1-4), tobacco(NtCUL1A-1B), tomato(SpCUL1), Vitis(VvCUL1), Petunia(PhCUL1,PiCUL1C, PiCUL1G). The NJ tree was generated with 1,000 bootstrap replicates, and bootstrap values of 50% and above are given at branch nodes.

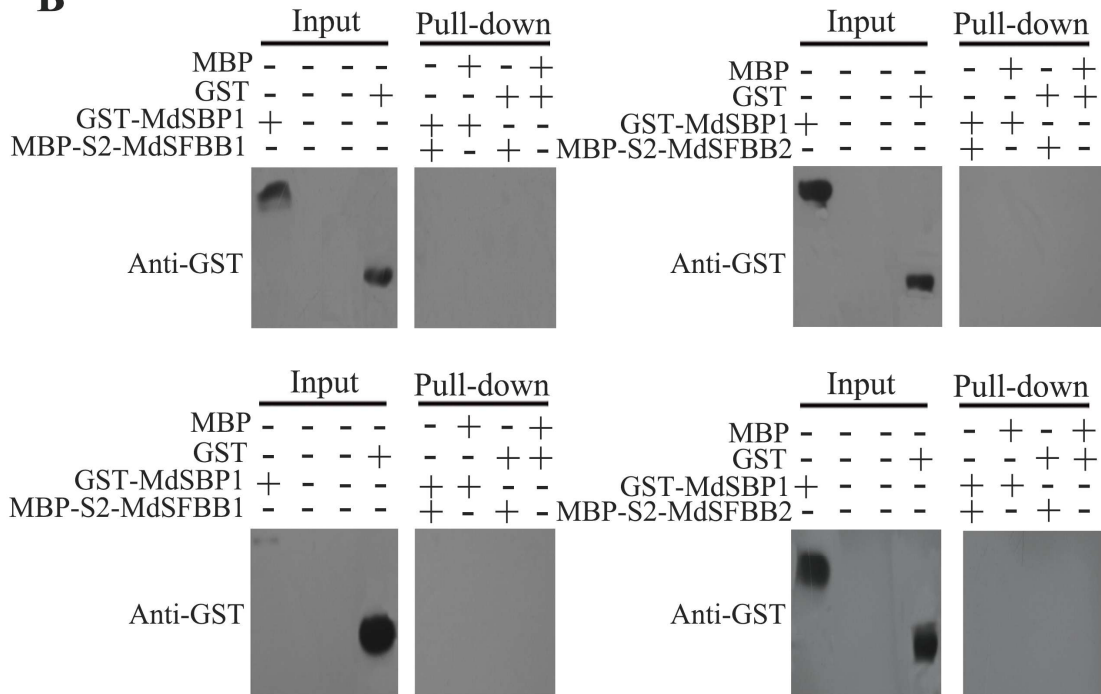
**A****B**

**Supplemental Figure 5** Schematic diagram of S-RNase constructed in Y2H analysis and the interaction between non-S-RNase and *S2-MdSFBB1-4*. (A) C1, C2, C3, RC4 and C5 represent five conserved domains and RHV the hypervariable region, SP meant the signal peptide in Rosaceae S-RNases. (B) Y2H assays between non-S-RNase and *S2-MdSFBB1-4*. The AD fusions and BD fusions were co-transformed into yeast strain AH109. Transformants were grown on selective medium SD/- Ade - His - Leu - Trp for 7 days at 30°C and then were stained by X- $\alpha$ -gal. The p53 and SV40 were used as positive controls, the pGBKT7 and pGADT7 as negative controls.

**A**

MdSBP1	MALPQHFFQQHYPQQQQQQQ...QQQSKSFRNLYTI.DGQLSPAVAYYDPGNLQDHPQQHPPYVPPFHVGEFAGPVAAT	77
ScSBP1	MALPHHHLQLHI...QQQPHQQQSKSYRDLYNMMDGQITTPVVYFNGSNLPEQS.QHPPYIPPFQVVGLAPGTAD..	72
NaSBP1	MALPHHHLQLHS...IQQQ...QQQSNFRDIYNMMDGQISTPVAYFNGSNLPEQS.QHPPYIPAFQVVGLAPGPAD..	70
PiSBP1	MALPHHHLQLHI...QQQP...QQQSKSYRDIYNMMDGQISTPVAYFNGSNLPEQS.QHPPYIPPFQVVGLAPGLVD..	70
PhSBP1	...GTSHLQLHI...QQQP...QQQSKSYRDIYNMMDGQISTPVAYFNGSNLPEQS.QHPPYIPPFQVVGLAPGLVD..	67
MdSBP1	DGSDNGADLQWHYGFESKRKRLKEQDFLENNNSQISSIDFLQPRSVSTGLGLSLDNT.RMVSTGDSSLLSVIGDDVDHELQ	156
ScSBP1	...DGGLDLQWNYGLEPKKRRPKEQDFMENNSQISSVDLQRRSVSTGLGLSLDNGRLASSCDSAFGLVGDIERELQ	149
NaSBP1	...EGGLDLQWNYGLEPKKRRPKEQDFLENNNSQISSVDLQRRSVSTGLGLSLDNGRLGSCGDSAFGLVGDIERELQ	147
PiSBP1	...DGGLDLQWNYGLEPKKRRPKEQDFLENNNSQISSIDFLQPRSVSTGLGLSLDNGRLASSGDSAFGLVGDIERELQ	147
PhSBP1	...DGGLDLQWNYGLEPKKRRPKEQDFLENNNSQISSIDFLQPRSVSTGLGLSLDNGRLASSGDSAFGLVGDIERELQ	144
MdSBP1	RQDAEIDRFLKAQGDRLRQTILDKVQATQLQTLSEVDEKVLRLKREKEAEVESISKKNMELEEQMEQLAVEAGAWQQIAR	236
ScSBP1	RQDAEIDRYIKVQGDRLRQAVLEKQANQIQAITVVEEKVLQKLRERDTEVDDINKKNMELELRMEQLDLEANAWQORAK	229
NaSBP1	RQDADIDRYIKVQGDRLRQAILEKQANQLQITTCVVEEKVIQKLRKEAEVEDINKKNMELELRMEQLALEANAWQORAK	227
PiSBP1	RQDAEIDRYIKVQGDRLRQAILEKQANQLQTVTYVEEKVIQKLRKEETEVEDINKKNMELELRTEQLALEANAWQORAK	227
PhSBP1	RQDAEIDRYIKVQGDRLRQAILEKQANQLQTVTYVEEKVIQKLRKEETEVEDINKKNMELELRTEQLALEANAWQORAK	224
MdSBP1	RNENMISSLRFNLQHVYAQSRDSKEGCGDSEVDDTASCNGRINLDMFRKENNDGKEMMTCKACRVNEVCMLLLPCKHL	316
ScSBP1	YNENLINTLKVNLQHVYAQSRDSKEGCGDSEVDDTASCNGRATDLHLLCRDSKEMKELMTCVCRVNEVCMLLLPCKHL	309
NaSBP1	YNENLINTLKVNLQHVYAQSRDSKEGCGDSEVDDTASCNGRATDFHLLCRDSNEMKELMTCVCRVNEVCMLLLPCKHL	307
PiSBP1	YNENLINTLKVNLQHVYAQSRDSKEGCGDSEVDDTASCNGRATDLHLLCRDSNEMKELMTCVCRVNEVCMLLLPCKHL	307
PhSBP1	YNENLINTLKVNLQHVYAQSRDSKEGCGDSEVDDTASCNGRATDLHLLCRDSNEMKELMTCVCRVNEVCMLLLPCKHL	304
MdSBP1	CLCKDCESKLSVCPLCQSSKFIGMEVFY	344
ScSBP1	CLCKECESKLSLCLCQSTKYIGMEVYM	337
NaSBP1	CLCKECESKLSLCLCQSTKYIGMEVYV	335
PiSBP1	CLCKECESKLSLCLCQSTKYIGMEIYM	335
PhSBP1	CLCKECESKLSLCLCQSTKYIGMEIYM	332

**B**



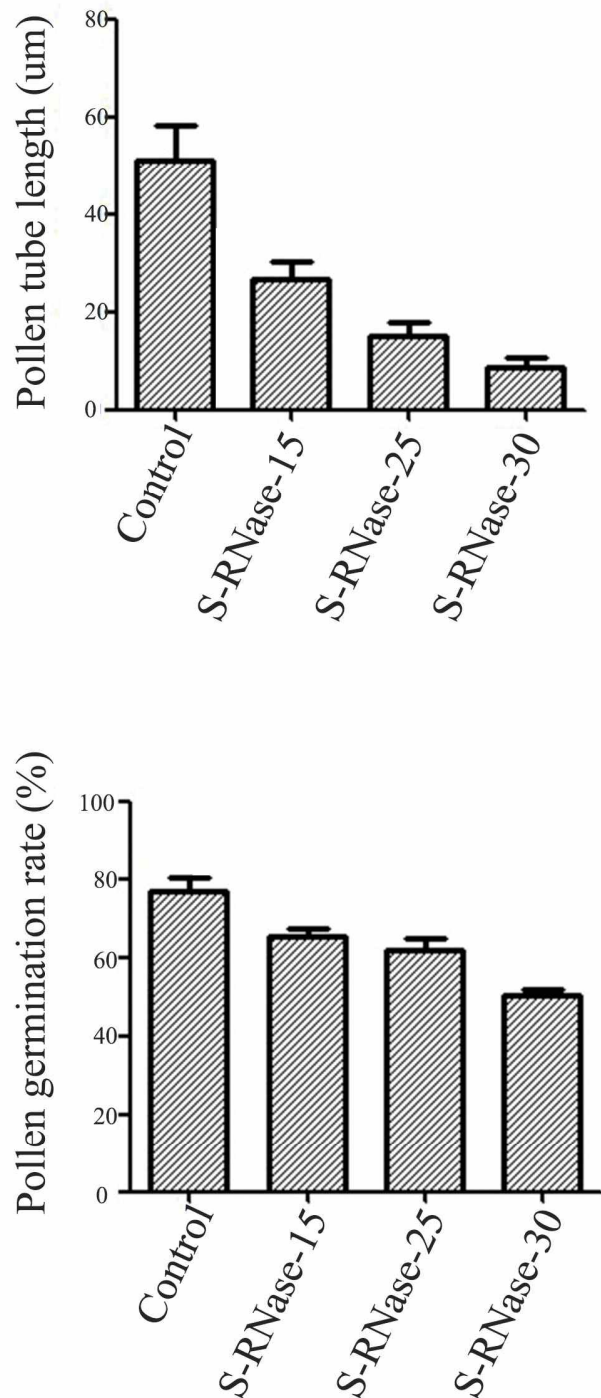
**Supplemental Figure 6** The structure of MdSBP1 and pull-down analysis between MdSBP1 and S2-MdSFBB1-4. (A) Sequence alignment and structural elements of MdSBP1 and other SBP1 proteins. The pentagrams indicate the conserved cysteines. NaSBP1, PiSBP1, PhSBP1, ScSBP1, MdSBP1(from this study). (B) pull-down analysis between MdSBP1 and S2-MdSFBB1-4. Purified S2-MdSFBB1-4 were used as bait against purified GST-MdSBP1. Bound proteins were examined with anti-GST

antibody. GST and MBP were used as negative controls.

**A**



**B**



**Supplemental Figure 7** The pollen germination and pollen tube length after treated with *S*-RNase. (A) Pollen growth status with different concentration *S*-RNase treated. (B) The pollen germination rate (3 replicated with 100-pollen grains,  $p < 0.01$ ) and

pollen tube length (3 replicated with 100-pollen grains,  $p < 0.01$ ) under different treatment by S-RNase.

**The Primers used for analysis of expression pattern**

<b>Primer</b>	<b>Sequence</b>
S2-MdSFBB1-F	ATAGCAGGGACAAGTCTTATTGATAA
S2-MdSFBB1-R	AAAATCTCTA ACTTCATTG GAATA
S2-MdSFBB2-F	AATCTTCCATTGATAGTGATGTACAT
S2-MdSFBB2-R	GAAAAGCCCCAAAATAAGCCAACT
S2-MdSFBB3-F	CTTCATTGATAAATGTTCTT
S2-MdSFBB3-R	GGATTCACCC TTCGAAATGTTG
S2-MdSFBB4-F	CAGTCGCAAGATCAAGAAGT
S2-MdSFBB4-R	CTAAATCAAATGAAAGTATGTATT
S2-MdSFBL1-F	ATGGAATACCATCATCCTGTATTGATTC
S2-MdSFBL1-R	TGACTGATT CATTATACAGA AAAAGA
S2-MdSFBL2-F	GTTCTTGAATTGTTTCGGAATTAAC
S2-MdSFBL2-R	ATTCCTCCAA GATCCACTTCTTT
S2-MdSFBL3-F	TGTGTGTCAAAGTGAATCTCTA
S2-MdSFBL3-R	TATGAACAATACTTTTTACATAA
S2-MdSFBL4-F	TGGAAGACCATCATCCTGTAGT
S2-MdSFBL4-R	TGAGAAAAGGAGGTGGAGAACG
S2-MdSFBL5-F	ACCCCTGCAGATAAGGCGGTCGAA
S2-MdSFBL5-R	TTACTTGATAGGAACAATAGTTTCC
S2-MdSFBL6-F	GGTGCATGAAAATGAAACTCTT
S2-MdSFBL6-R	ATGAAACAATACTTTTCACATAC

Supplemental Table 1