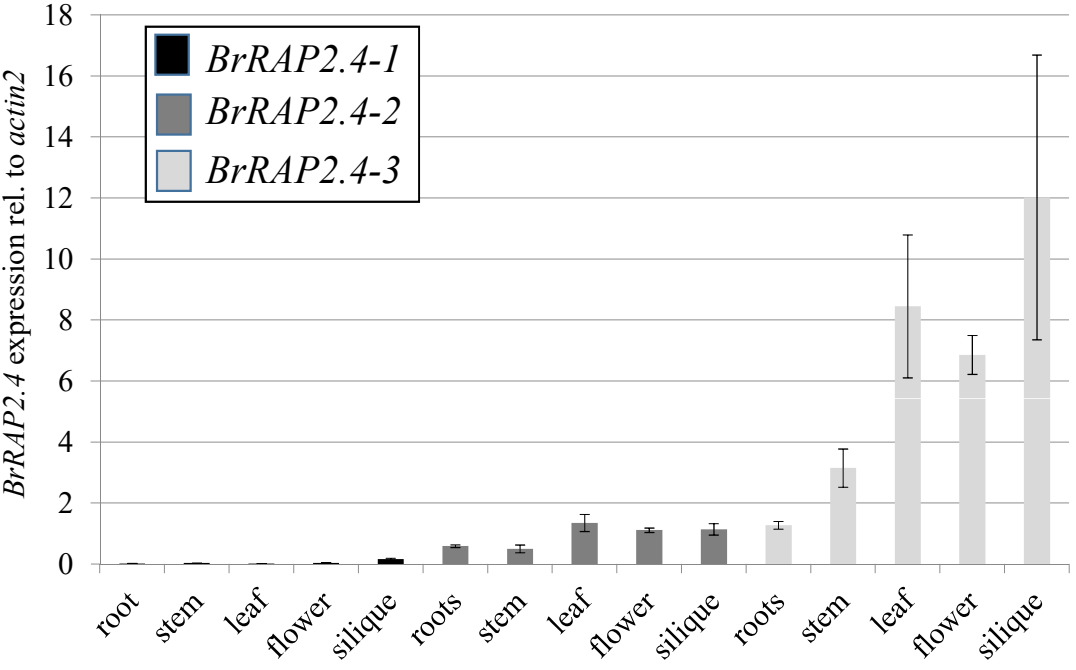

Figure S1. qRT-PCR expression analysis of *BrRAP2.4-1*, *-2*, and *-3* in different tissues of *B. rapa* plants. Shown is a technical replicate. Standard bars represent standard error.

```
atggaagctgctatgaatttgaacagtagcagaacgtttcaacaaccagattcgtttggtggt
 M  E  A  A  M  N  L  N  S  S  R  T  F  Q  Q  P  D  S  F  G  G
ggtggcgaactcatggaagcgcttctacctttatcaaaagcgtttccgactctccttccgcg
 G  G  E  L  M  E  A  L  L  P  F  I  K  S  V  S  D  S  P  S  A
tccgcgtctgcgtttattaatcccgcagcgtctgcgtttcctcttcccaccttccgcgattac
 S  A  S  A  F  I  N  P  A  A  S  A  F  P  L  P  T  F  R  D  Y
aacccggaacactatctgacccaaccgtttccgtacgggtcggatcttcagcaaaccgggtca
 N  P  E  H  Y  L  T  Q  P  F  P  Y  G  S  D  L  Q  Q  T  G  S
ctaatcgggctcaacaacctctcctcttcccaaatccaccagatccaatctcagatccaccac
 L  I  G  L  N  N  L  S  S  S  Q  I  H  Q  I  Q  S  Q  I  H  H
aaccatcctctccctcccaccagatccaacctcaacctcagccccaagccgttactgatgaag
 N  H  P  L  P  P  T  R  S  N  L  N  L  S  P  K  P  L  L  M  K
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 Q  P  G  V  A  G  S  C  F  A  Y  G  A  P  P  K  P  A  K  L  Y
agaggcgtgaggcagcgtcactggggaaaatgggtggcggagatccgtttgccgaggaaccgg
 R  G  V  R  Q  R  H  W  G  K  W  V  A  E  I  R  L  P  R  N  R
actcgtctctggcttgggacgttcgacacggcggaggaagctgcgttggcctacgatacggcg
 T  R  L  W  L  G  T  F  D  T  A  E  E  A  A  L  A  Y  D  T  A
gcgtttaagctgcgcggcgatttcgcccggcttaacttccctaacctgcgtcacgacggatct
 A  F  K  L  R  G  D  F  A  R  L  N  F  P  N  L  R  H  D  G  S
cgcatcggaggcgagttcggcgagtataaacctcttcactccactgtcgacgccaagctcgaa
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 A  I  C  K  S  M  A  E  T  E  K  Q  E  K  T  T  K  A  S  K  K
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 E  E  Q  P  Q  W  N  E  T  F  A  L  E  K  Y  P  S  Y  E  I  D
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 W  D  S  I  L  P  -
```

Figure S2. Alignment of DNA and amino acid sequence of BrRAP2.4-1

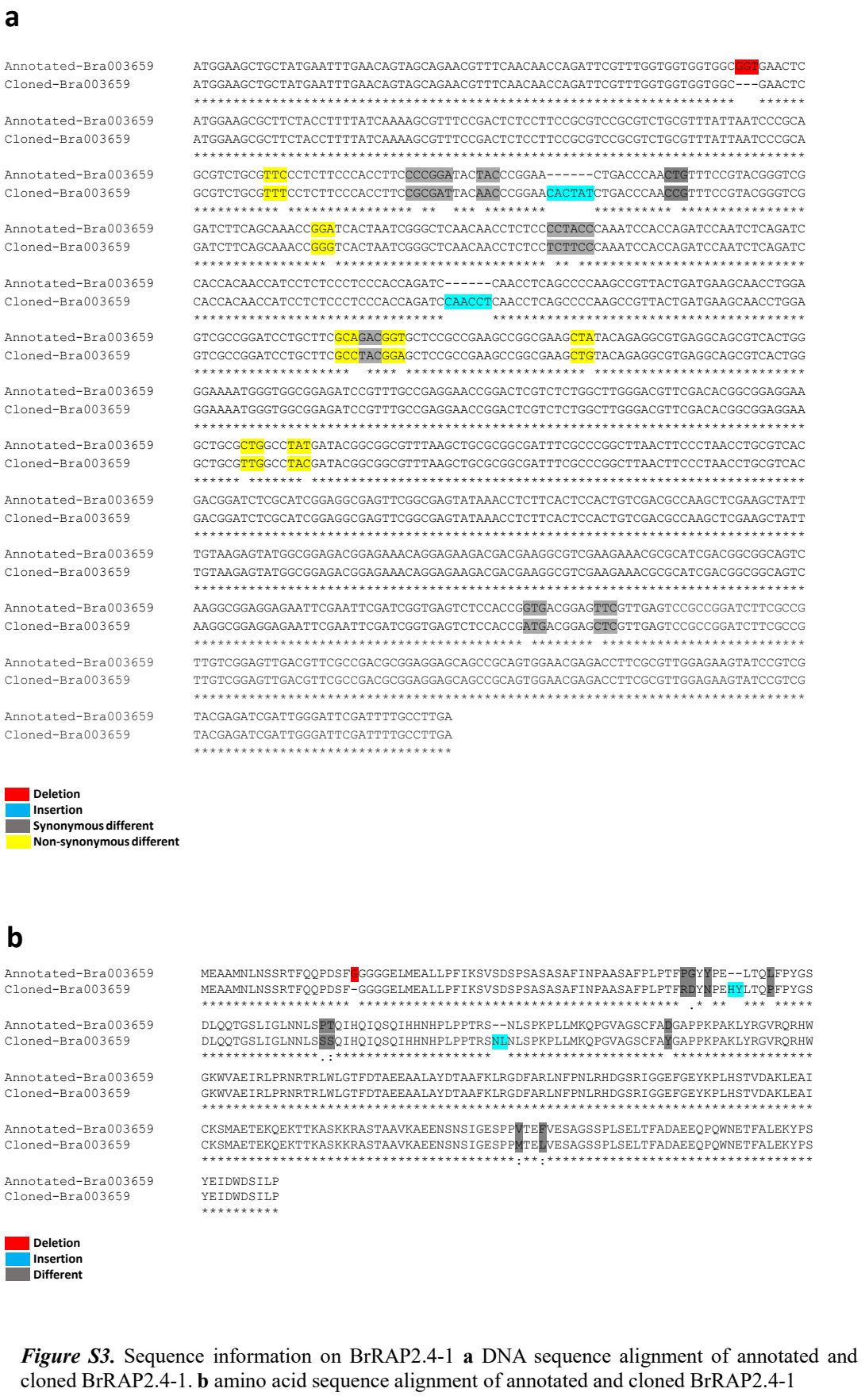

Figure S3. Sequence information on BrRAP2.4-1 **a** DNA sequence alignment of annotated and cloned BrRAP2.4-1. **b** amino acid sequence alignment of annotated and cloned BrRAP2.4-1

Figure S4. Amino acid sequence alignment of AtRAP2.4, BnaA07g20720D, and the two annotated and cloned sequences for BrRAP2.4-1

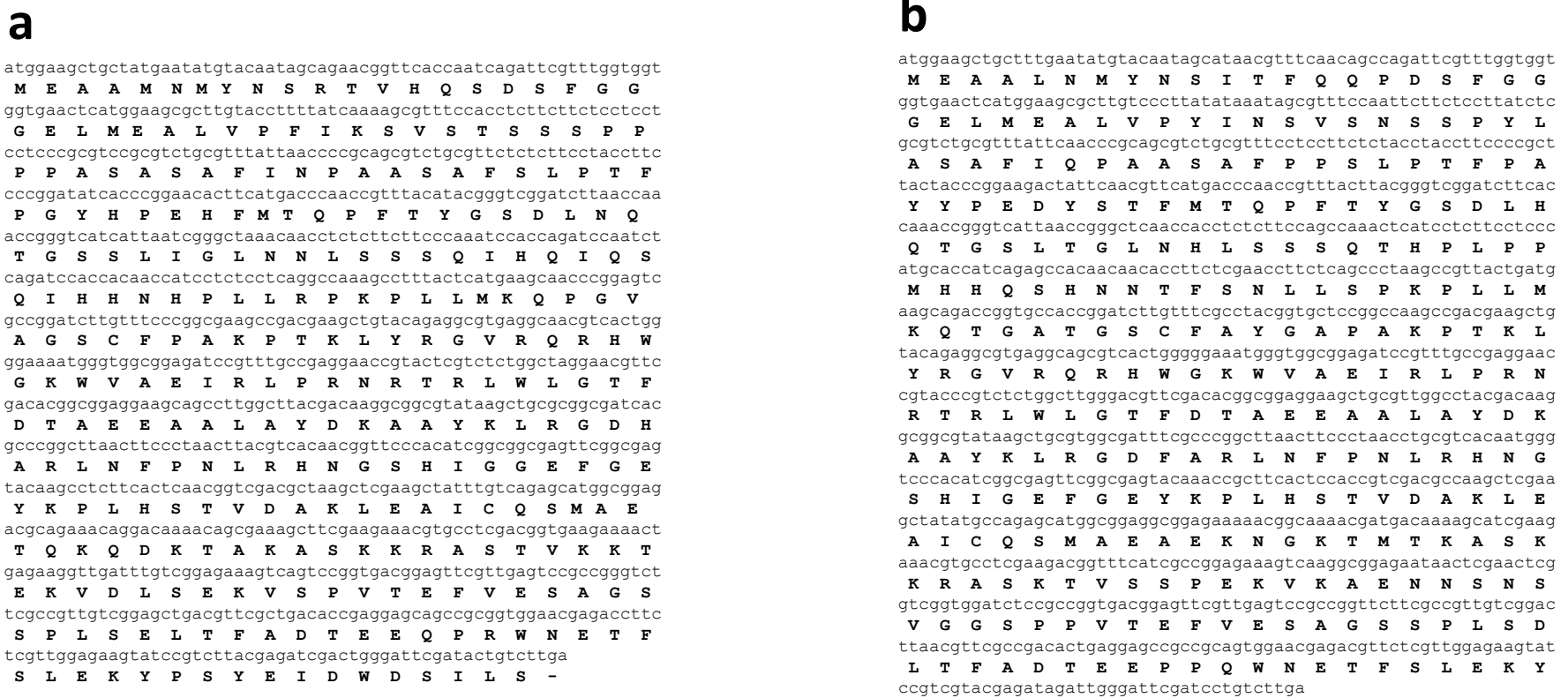

Figure S5. DNA and amino acid sequence of **(a)** BrRAP2.4-2 and **(b)** BrRAP2.4-3

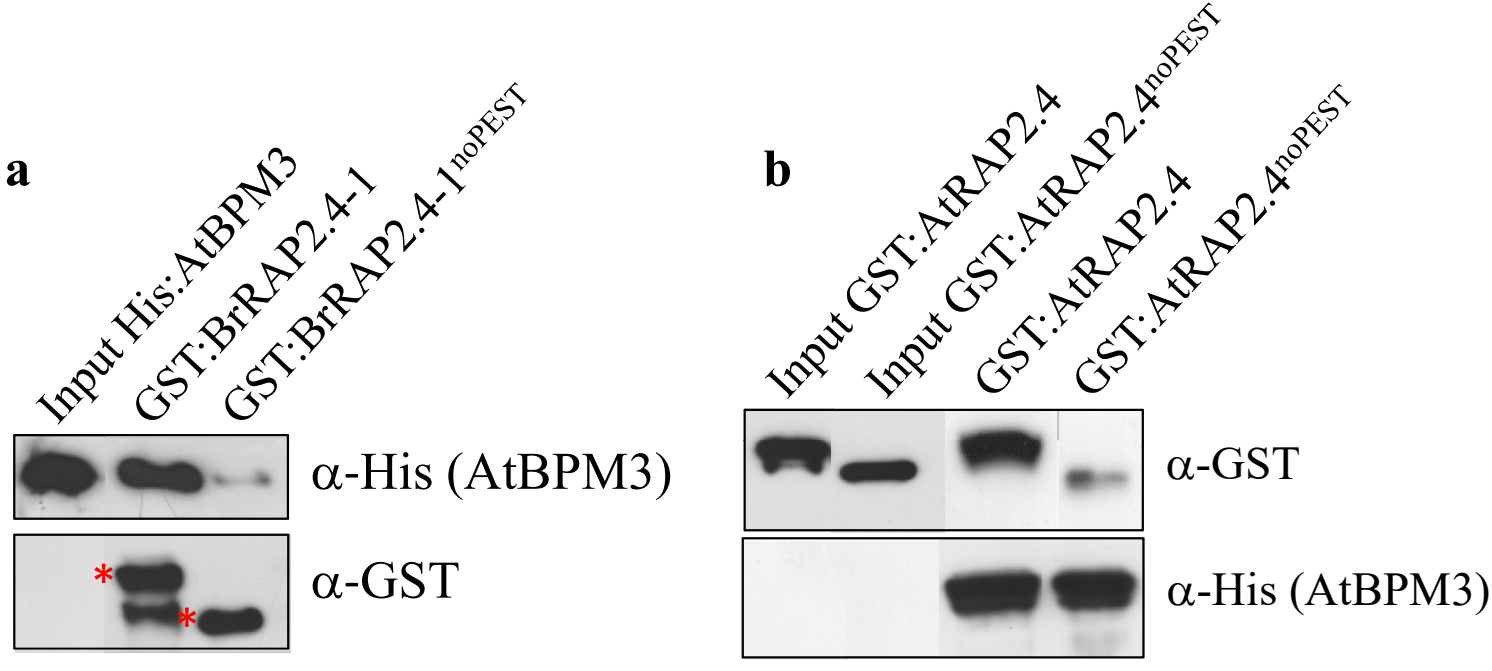

Figure S6. Representative Western blots for Figure 5b-c quantification. **a**) Pulldown analysis with GST:BrRAP2.4 proteins on beads resulted in co-precipitation of eluted His:AtBPM3 protein, shows that the BrRAP2.4-1^{noPEST} does not bind AtBPM3 as efficiently as full-length BrRAP2.4-1. **b**) Pulldown analysis with His:AtBPM3 protein on beads resulted in co-precipitation of eluted GST:AtRAP2.4 proteins shows that the AtRAP2.4^{noPEST} does not bind AtBPM3 as efficiently as full-length AtRAP2.4.

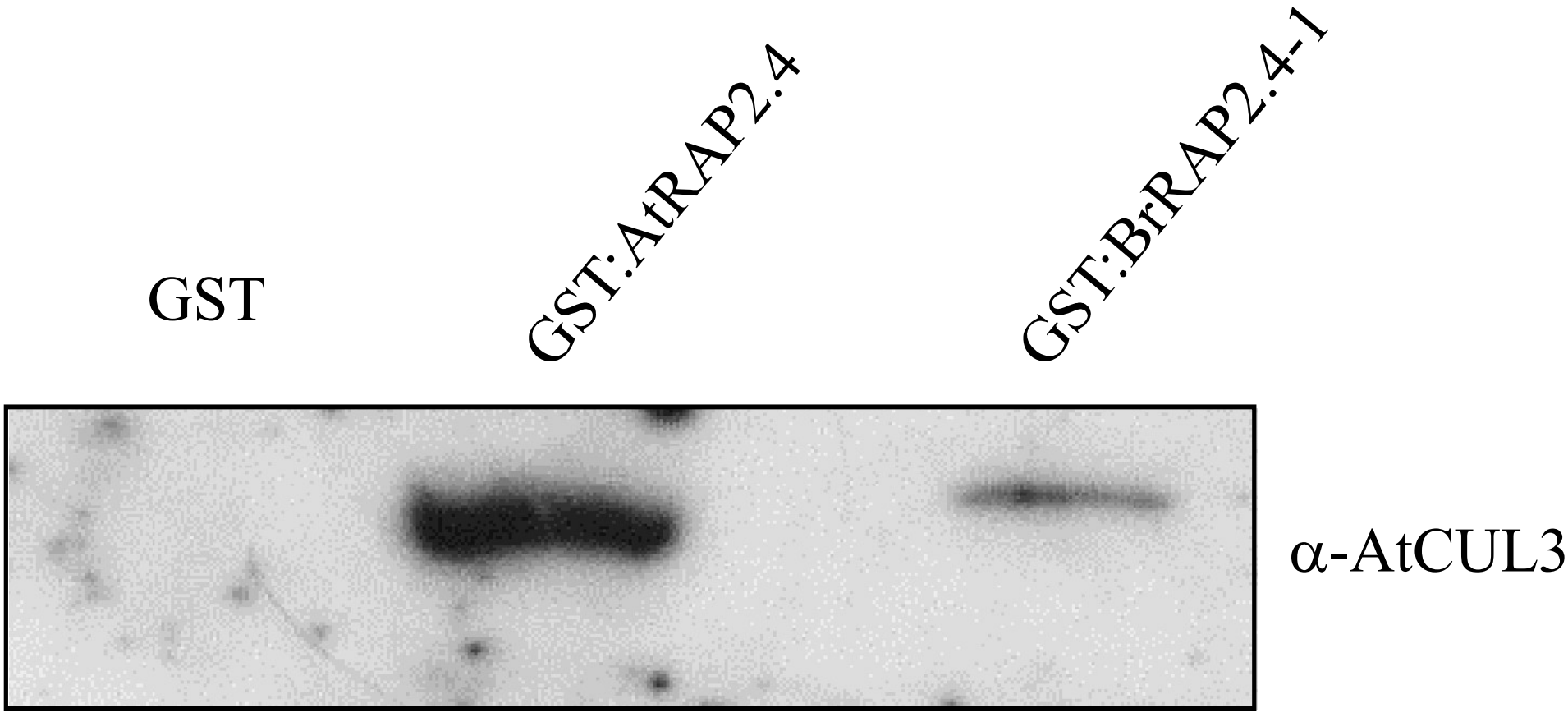

Figure S7. Pulldown analysis showing that GST:AtRAP2.4 and GST:BrRAP2.4-1 can pulldown AtCUL3 from plants extracts, while GST alone can not.

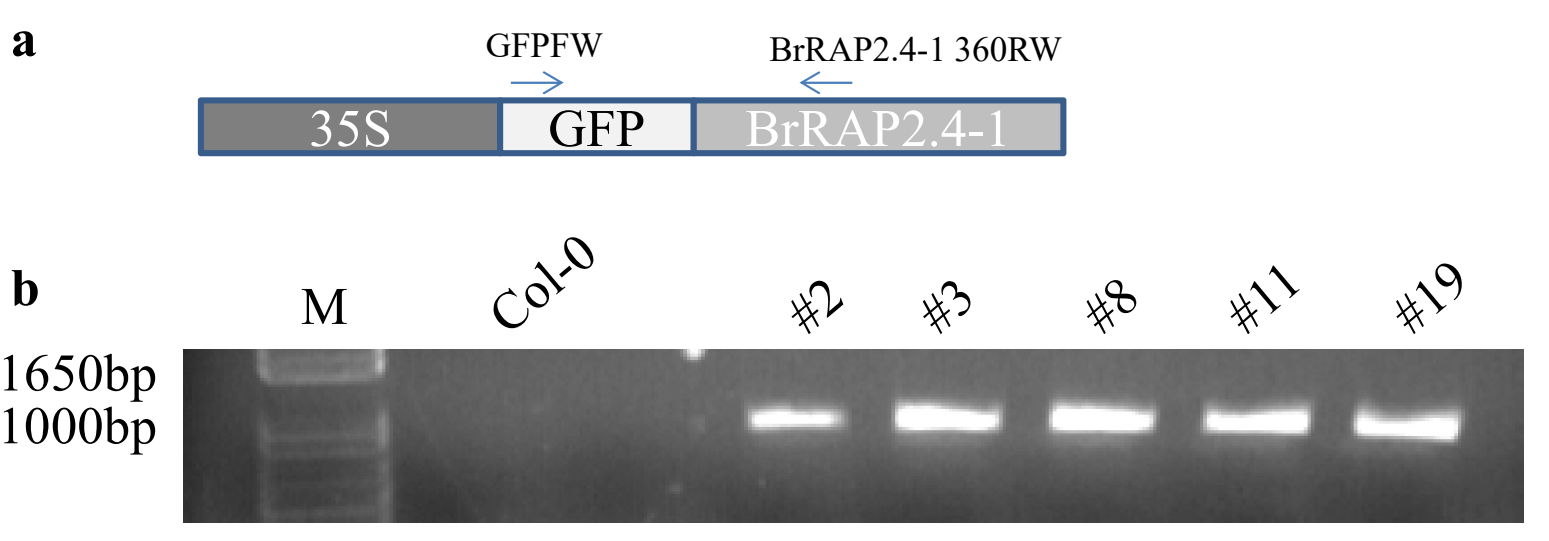

Figure S8. Basic expression analysis of GFP:BrRAP2.4-1 in Arabidopsis. **a**) schematic drawing of the introduced construct. Arrows indicate primers used in (b). **b**) Total RNA was isolated from 10-day old seedlings, converted to cDNA, and used for a standard PCR. Product was detected in five transgenic lines (indicated by numbers), but not in Col-0 wild type. M, 100-bp DNA marker.

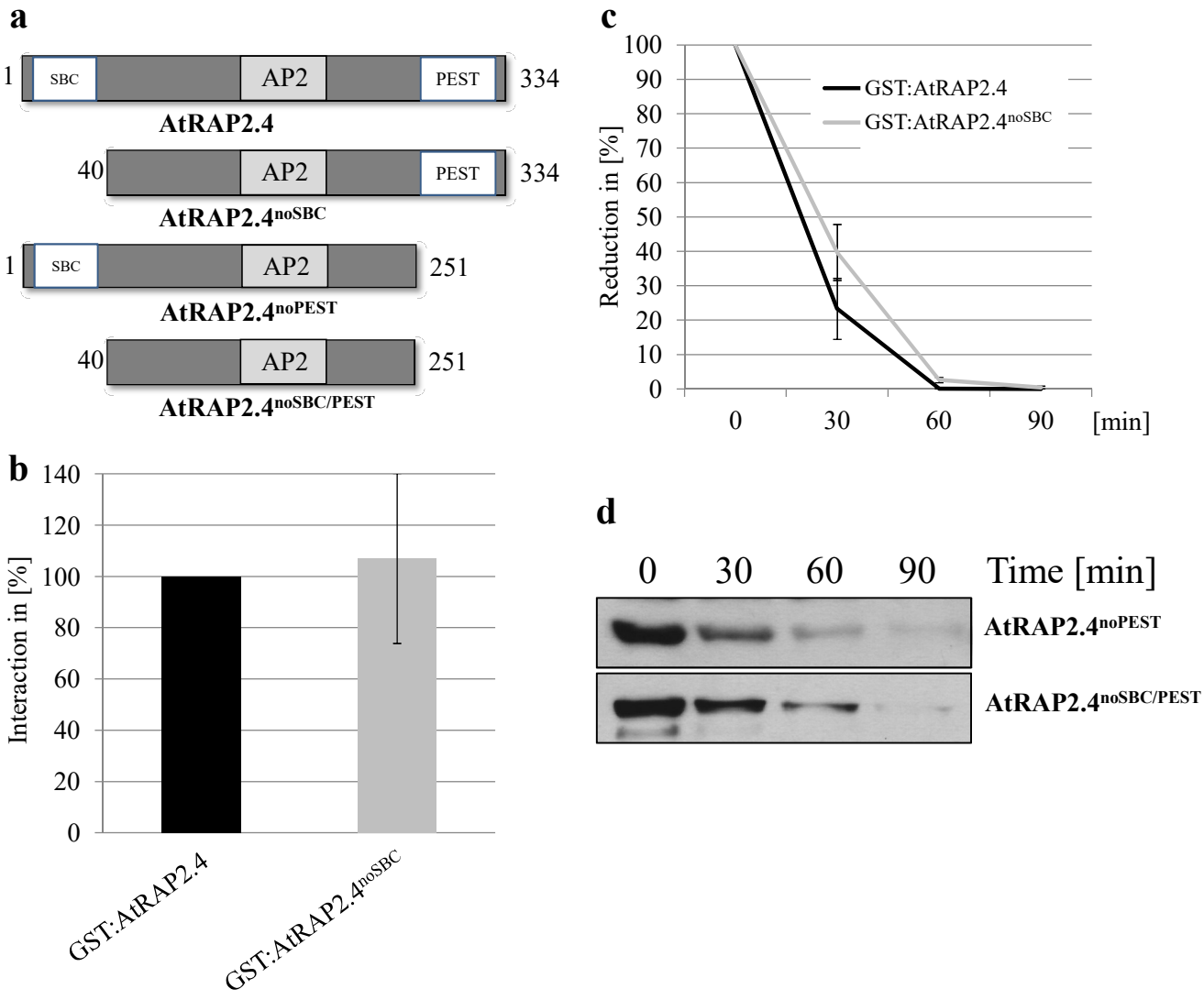

Figure S9. Deletion of the SBC motif in AtRAP2.4 does not significantly alter stability or interaction with AtBPM3. **a)** Schematic drawing of AtRAP2.4 and AtRAP2.4^{noSBC}. **b**) Quantification of GST:AtRAP2.4 and GST:AtRAP2.4^{noSBC} did not show any significant differences. **c**) AtRAP2.4^{noSBC} degradation is only mildly but not significantly delayed in a cell free system. **d**) Cell-free degradation assays comparing stability of AtRAP2.4^{noPEST} with AtRAP2.4$^{noSBC/PEST}$. Deletion of both, the SBC and the PEST motif, does not dramatically increase stability of the mutated AtRAP2.4$^{noSBC/PEST}$ protein when compared to AtRAP2.4^{noPEST}.

Table S1: List of Primers used in this work	
Primers used for BrRAP2.4 cloning	
Bra003659FW	ATGGAAGCTGCTATGAATTTG
Bra003659RW	TCAAGGCAAAATCGAATCCC
Bra003659noPEST-RW	CTACTCCTGTTTCTCCGTCTC
Bra003659PEST-FW	CAGGAGAAGACGACGAAGGCG
Bra008343FW	ATGGAAGCTGCTATGAATATG
Bra008343RW	TCAAGACAGTATCGAATCCC
Bra015634FW	ATGGAAGCTGCTTTGAATATG
Bra015634RW	TCAAGACAGGATCGAATCCC
Primer used for qRT-PCR Analysis	
qRTAktinBra034778FW1	GCTATGTATGTCGCTATC
qRTAktinBra034778RW1	CATCTCCAGAGTCCAATA
Bra003659RT-FW	ACCTCTTCACTCCACTGT
Bra003659RT-RW	TCGTCGTCTTCTCCTGTT
Bra008343RT-FW	AACGGTTCACCAATCAGA
Bra008343RT-RW	GGAGAAGAAGAGGTGGAA
Bra015634RT-FW	GTTTCAACAGCCAGATTC
Bra015634RT-RW	GCGAGATAAGGAGAAGAA
Primers used for checking Arabidopsis GFP:BrRAP2.4 transgenic lines	
GFP-FW	ATGAGTAAAGGAGAAGAACTTTTC
Bra003659-360RW	GGGGCTGAGGTTGAGGTTGG
Primers used for AtRAP2.4 cloning	
AtRAP2.4 FW	ATGGCAGCTGCTATGAATTTG
AtRAP2.4 RW	CTAAGCTAGAATCGAATCCC
AtRAP2.4 noSBC-FW	ATGTCTGCAGCGTCTGCGTCT
AtRAP2.4 noPEST-RW	CTACGATTTGTCCTGTTTCTG