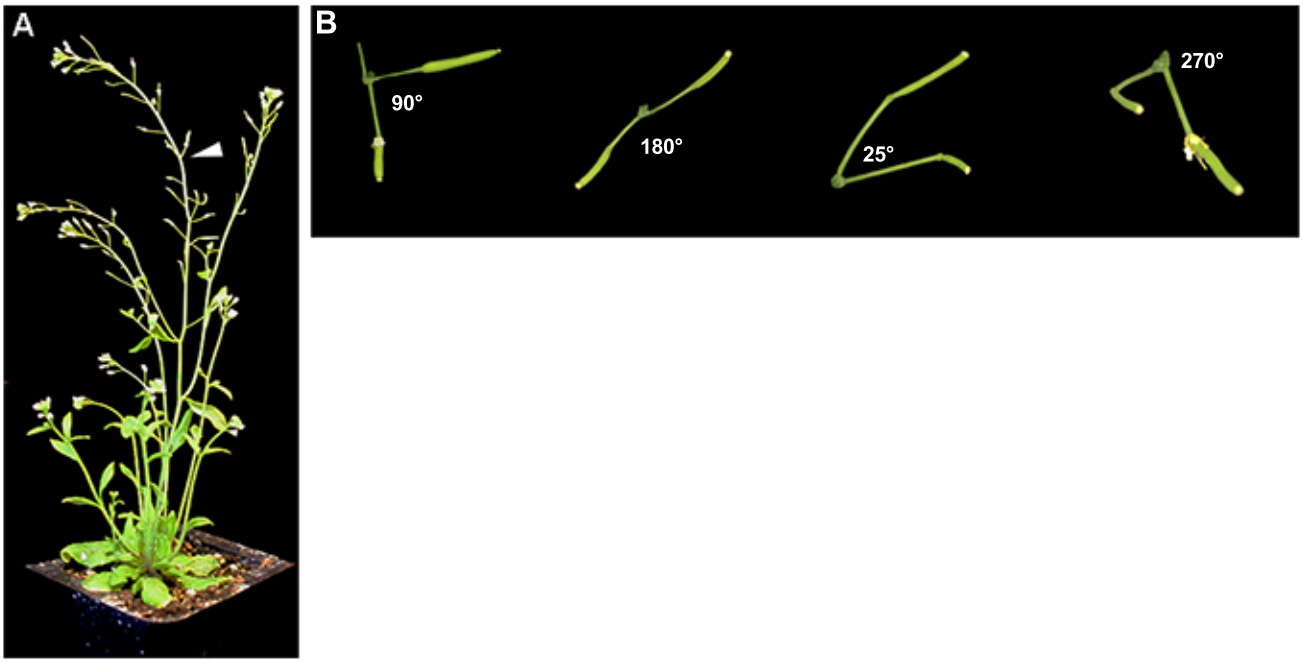
## Supplementary Figure 1

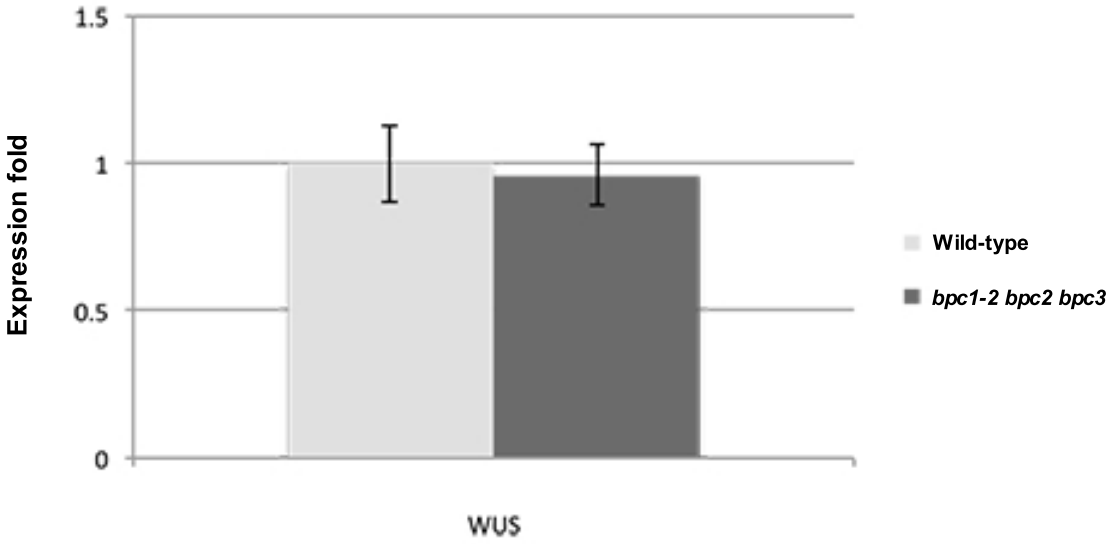



**Supplememtary Figure 1. Angle divergence in *bpc1-2 bpc2 bpc3* mutant**

**(A)** *bpc1-2 bpc2 bpc3* plant. Siliques are randomly positioned along the stem and two siliques arising from the same internode can be frequently observed (arrowhead).

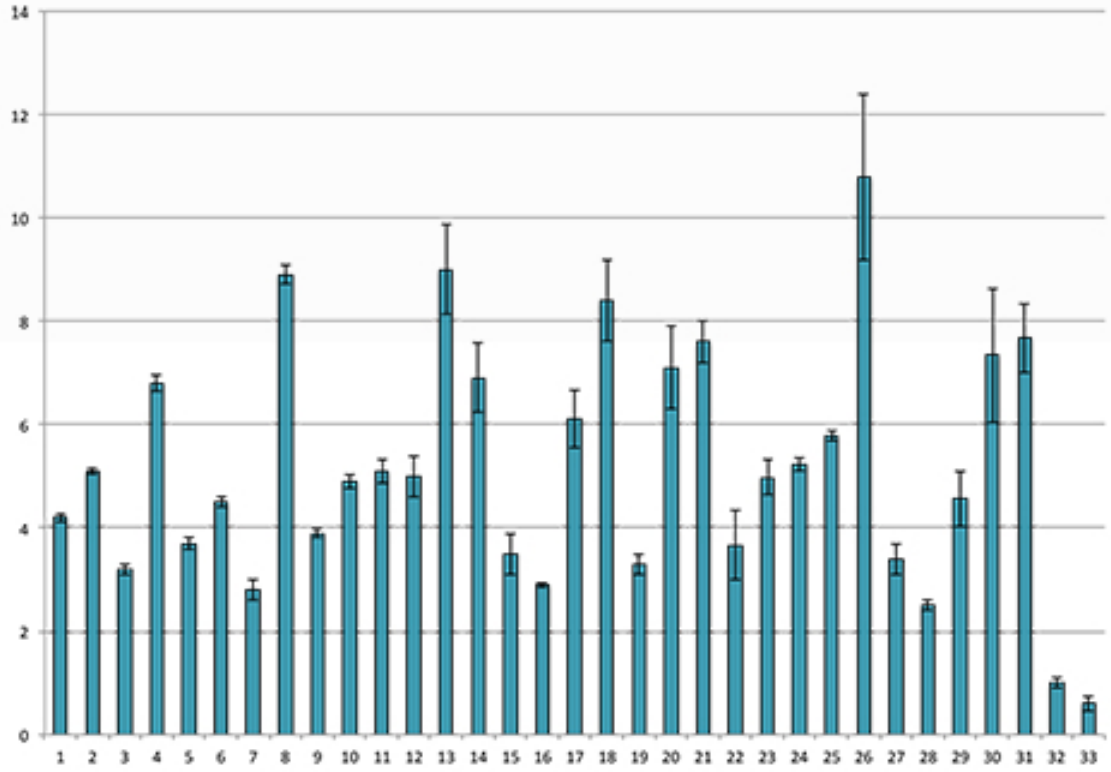
**(B)** Four examples of divergence angles frequently found in the *bpc1-2 bpc2 bpc3* mutant: from left to right 90°, 180°, 25°, 270°.

**Supplementary Figure 2.**




**Supplementary Figure 2. Expression level of *WUS* in *bpc1-2 bpc2 bpc3* mutant.**

**Supplementary Figure 3**




**Supplementary Figure 3. Expression level of BPC1-Ear Motif in plants with strong phenotype.**
From number 1 to number 31: *35S::BPC1 Ear Motif* plants with phenotype.
Numbers 32 and 33: *35S::BPC1 Ear Motif* plants with wild-tpe phenotype.

**Supplementary Figure 4**

***STM promoter***

.....taataatactagtgagagaaagagaagATGGAGAGTGGTTCCAACA....

***BP promoter***

acagaagagagaagcctttgccttatctcttgtcccttctctcttacctttatttaatttttcaaata
tttctttttgctcccaaagcaaacgacgtcttgtcaatccactcaagccacccaacttcttcatt
attgttaatctctctctctctctctttctctcttcttctctctttctctttttttttttttatttttcttctcttcca
tgtcacttccttgacgaattctatatacctagttcgtttttttcttcctcaaatatatctttttcaatttatt
tggtttttctttgggtgcaacttcacctcacaaaattttctctctttttttatattaatttgagttaggcc
tttttgatttcatagatgagtcgtctagtcgtctggatttgatgtggttatagtcttacagagacctttt
gattgaaataagaacaaaagcaagaatacatacatcctcttcatcttacacccatccttttttta
ttttctagggttttatttttttttaatttatttttttttctttgatttttatattctctctctctctcaaatctttact
catctgggtATGGAAGAATACCAGCATGACA

***ARR7 promoter***

aatcttaaaaaagattcggtgcccaaagattttgacctttgaagacacatttgattatttgtgtttt
ctgacacttcccaaacacataacatcaacacttgacccatttttaagattttgtttcctcttcaaa
gatcttaccccgcaagatccgatcttccaaatctctctctatctactatactagtacttattaaac
cccaccacctctcccttcttatttatgtcacctaacctaacttcttcttctttcattttatcacattca
tttcctttgtcttcaatccaaagctttcctcttcttggaaccaatctgctctctttttttattctgagttt
gacaATGGCGGTTGGTGAGGTCATGAG

**Supplementary Figure 4.**
Localization of GAGA boxes in *STM*, *BP* and *ARR7* promoters.
Red box: transcription start site
Blue box: GAGA box 5’ -3’
Green box: BABA box 3’-5’

**Supplementary table 1. HOMEOBOX genes with GAGA stretch in their promoter sequence (500bp upstreamt the transcription start site).** Green box: at least one GAGA stretch found. Red box: no GAGA sequence found.

| Locus | Gene Name | GAGA |
|---|---|---|
| At4g00730 | ANL2 | |
| At4g32980 | ATH1 | |
| At3g01470 | Athb-1 | |
| At1g79840 | Athb-10 | |
| At3g61890 | Athb-12 | |
| At1g69780 | Athb-13 | |
| At2g34710 | PHB | |
| At1g52150 | CNA | |
| At4g40060 | Athb-16 | |
| At2g01430 | Athb-17 | |
| At4g16780 | Athb-2 | |
| At5g15150 | Athb-3 | |
| At2g44910 | Athb-4 | |
| At5g65310 | Athb-5 | |
| At2g22430 | Athb-6 | |
| At2g46680 | Athb-7 | |
| At4g32880 | Athb-8 | |
| At1g30490 | PHV | |
| At4g21750 | ATML1 | |
| At5g41410 | BEL1 | |
| At4g36870 | BLH2 | |
| At1g75410 | BLH3 | |
| At2g23760 | BLH4 | |
| At1g19700 | BLH5 | |
| At5g02030 | BLR | |
| At4g25530 | FWA | |
| At4g17460 | HAT1 | |
| At5g06710 | HAT14 | |
| At5g47370 | HAT2 | |
| At4g37790 | HAT22 | |
| At3g60390 | HAT3 | |
| At3g19510 | HAT3.1 | |
| At2g22800 | HAT9 | |
| At3g61150 | HD-GL2-1 | |
| At4g08150 | KNAT1 (BP) | |
| At1g70510 | KNAT2 | |
| At5g25220 | KNAT3 | |
| At5g11060 | KNAT4 | |
| At4g32040 | KNAT5 | |
| At1g23380 | KNAT6 | |
| At1g62990 | KNAT7 | |
| At4g02560 | LD | |
| At4g17710 | HDG4 | |
| At1g26960 | ATHB23 | |
| At3g01220 | ATHB20 | |
| At1g17920 | HDG12 | |
| At1g73360 | HDG11 | |
| At1g27050 | ATHB54 | |
| At1g70920 | ATHB18 | |
| At1g05230 | HDG2 | |
| At1g34650 | HDG10 | |
| At2g18550 | ATHB21 | |
| At2g32370 | HDG3 | |
| At2g36610 | ATHB22 | |
| At3g03260 | HDG8 | |
| At4g36740 | ATHB40 | |
| At5g17320 | HDG9 | |
| At5g52170 | HDG7 | |
| At5g03790 | ATHB51 | |
| At5g66700 | ATHB53 | |
| At5g46880 | HDG5 | |
| At1g28420 | HB-1 | |
| At1g75430 | BLH11 | |
| At2g16400 | BLH7 | |
| At2g27220 | BLH5 | |
| At2g35940 | BLH1 | |
| At4g34610 | BLH6 | |
| At5g44180 | | |
| At5g46010 | | |
| At4g03250 | | |
| At5g53980 | ATHB52 | |
| At4g04890 | PDF2 | |
| At2g27990 | POUND-FOOLISH | |
| At4g29940 | PRHA | |
| At5g60690 | REV | |
| At1g62360 | STM | |
| At3g18010 | WOX1 | |
| At1g20710 | WOX10/WOX13B | |
| At3g03660 | WOX11 | |
| At5g17810 | WOX12 | |
| At4g35550 | WOX13 | |
| At1g20700 | WOX14 | |
| At5g59340 | WOX2 | |
| At2g28610 | WOX3 | |
| At1g46480 | WOX4 | |
| At3g11260 | WOX5 | |
| At2g01500 | WOX6 | |
| At5g05770 | WOX7 | |
| At5g45980 | WOX8 | |
| At2g33880 | WOX9 | |

**Supplementary table 2. Primer used in this manuscript.**

| Gene | Primer sequences |
|---|---|
| ***BPC1-EAR motif*** **construct** | **Fw-** CACCATGGACGATGATGGATTTCGC<br>**Rev-** CTAAGCAAATCCAAGTCTAAGTTCAAGATC<br>AAGATCAAGTCTGATCGTGACAAACTTATTGG |
| ***BPC1-EAR motif*** **expression** | **Fw-** GCTCTTGTTTTTCTTCATTGATCG<br>**Rev-** CAAGATCAAGATCAAGTCTGATCGTGACAAACTTATTGG |
| ***KNAT4*** **promoter** | **Fw-** CGTCAAACACACATACACATCG<br>**Rev-** GATGTTGTTGTTGGTCGGTG |
| ***KNAT5*** **promoter** | **Fw-** ACTCTCCCGTCACATTCTGG<br>**Rev-** GTCTTGGATTAGTTGAGCGG |
| ***KNAT6*** **promoter** | **Fw-** CGACCTATGAAGCCTGAAGC<br>**Rev-** CTCCTCCGTCTTCTAAATCGC |
| ***KNAT7*** **promoter** | **Fw-** GGACCAGACCCGTGTATAAC<br>**Rev-** TACCTAGTGCCGCTTCTTGC |
| ***BP*** **promoter** | **Fw-** TCAATCCACTCAAGCCACCC<br>**Rev-** TCGTCAAGGAAGTGACATGG |
| ***BP*** **expression** | **Fw-** CACCGTCTGTCTCTGCCTCC<br>**Rev-** TCCCCTCCGCTGTTATTCTC |
| ***STM*** **promoter** | **Fw-** CTTACTCTTTTAGGGTTTCC<br>**Rev-** ATCATAGGACACATCGGACC |
| ***STM*** **expression** | **Fw-** CCTCACCTTCCTCTTTCTCC<br>**Rev-** TGTTGACGAGCTTCTTTAGG |
| ***WUS*** **promoter** | **Fw-** AAGCACATTTTTCAATAGGG<br>**Rev-** CGGCTTGATGATGATGATGC |
| ***WUS*** **expression** | ***Gregis et al., 2013*** |
| ***WOX3*** **promoter** | **Fw-** TGGGAGCATATGAGATTGGG<br>**Rev-** CGGCTTGATGATGATGATGC |
| ***WOX9*** **promoter** | **Fw-** ATGAAAACAGGTTGGGTAGG<br>**Rev-** AGAGACAGGGAACAGAATGG |
| ***RPL*** **promoter** | **Fw-** TGCTCATACTAAATTCCTCC<br>**Rev-** GGATGATGTCGATGAGATGC |
| ***BLH1*** **promoter** | **Fw-** GGCGTACTAAGGACTGTGGG<br>**Rev-** ATCATCTCAAGCTGCAAAAGG |
| ***CRN*** **promoter** | **Fw-** CTTTTACAGGCATTATTGGG<br>**Rev-** GGAATGGGGAAGGTCAGAGG |
| ***ARR7*** **promoter** | **Fw-** AAAGTTCCAGGTCACGAGGG<br>**Rev-** AGGTGGTGGGGTTTAATAAG |
| ***IPT7*** **expression** | ***Takano et al., 2010*** |