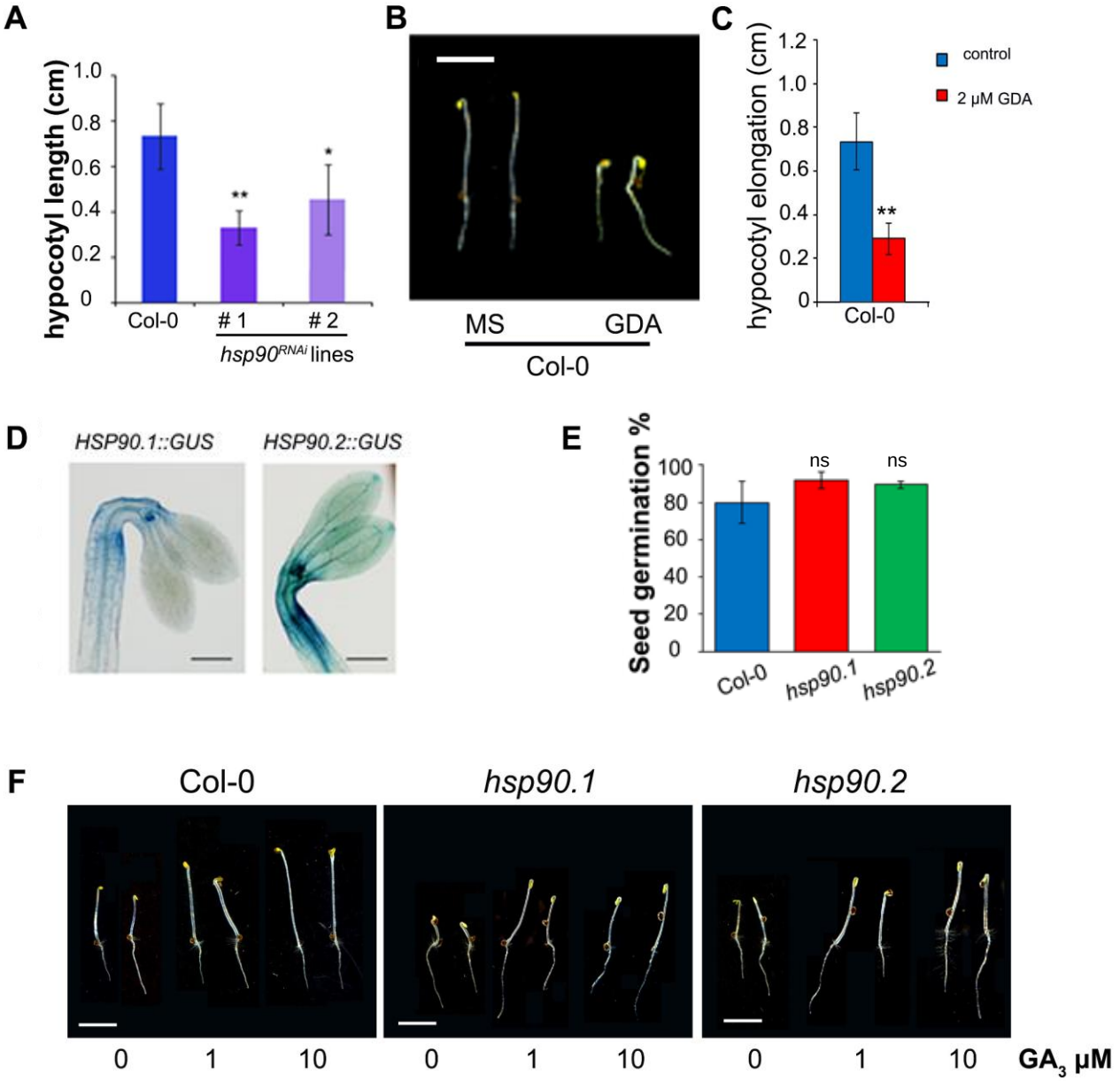



**Figure S1.** *HSP90.1* and *HSP90.2* genes are expressed in etiolated hypocotyls. **(A)** Hypocotyl length of 5-day-old etiolated seedlings of wild type (Col-0) and two independent *hsp90*$^{RNAi}$ lines grown in MS medium. Number of measurements, n > 30. **(B)** The hypocotyl elongation of 5-day-old wild-type (Col-0) etiolated seedlings grown in medium supplemented with 2 µM GDA, was inhibited. Scale bars, 0.5 cm. **(C)** Hypocotyl length measurements of seedlings shown in (C). Number of measurements, n > 30. Data are means and error bars indicate ±SD. (*): p<0.05, (**): p<0.01, ns: non-significant according to two-tailed students' t-test. Black asterisks, comparison to Col-0. **(D)** *HSP90.1*::GUS and *HSP90.2*::GUS in the hypocotyls of 5-day old etiolated seedlings. Scale bars, 20 µm. **(E)** Percentages (%) of seed germination in the dark of Col-0, *hsp90.1* and *hsp90.2* are means (±SD) from three independent experiments (50 seeds per experiment). **(F)** Phenotypes of 5-day-old etiolated seedlings of *hsp90.1* and *hsp90.2* mutants grown in the presence of different concentrations of $GA_3$. Scale bars, 0.5 cm

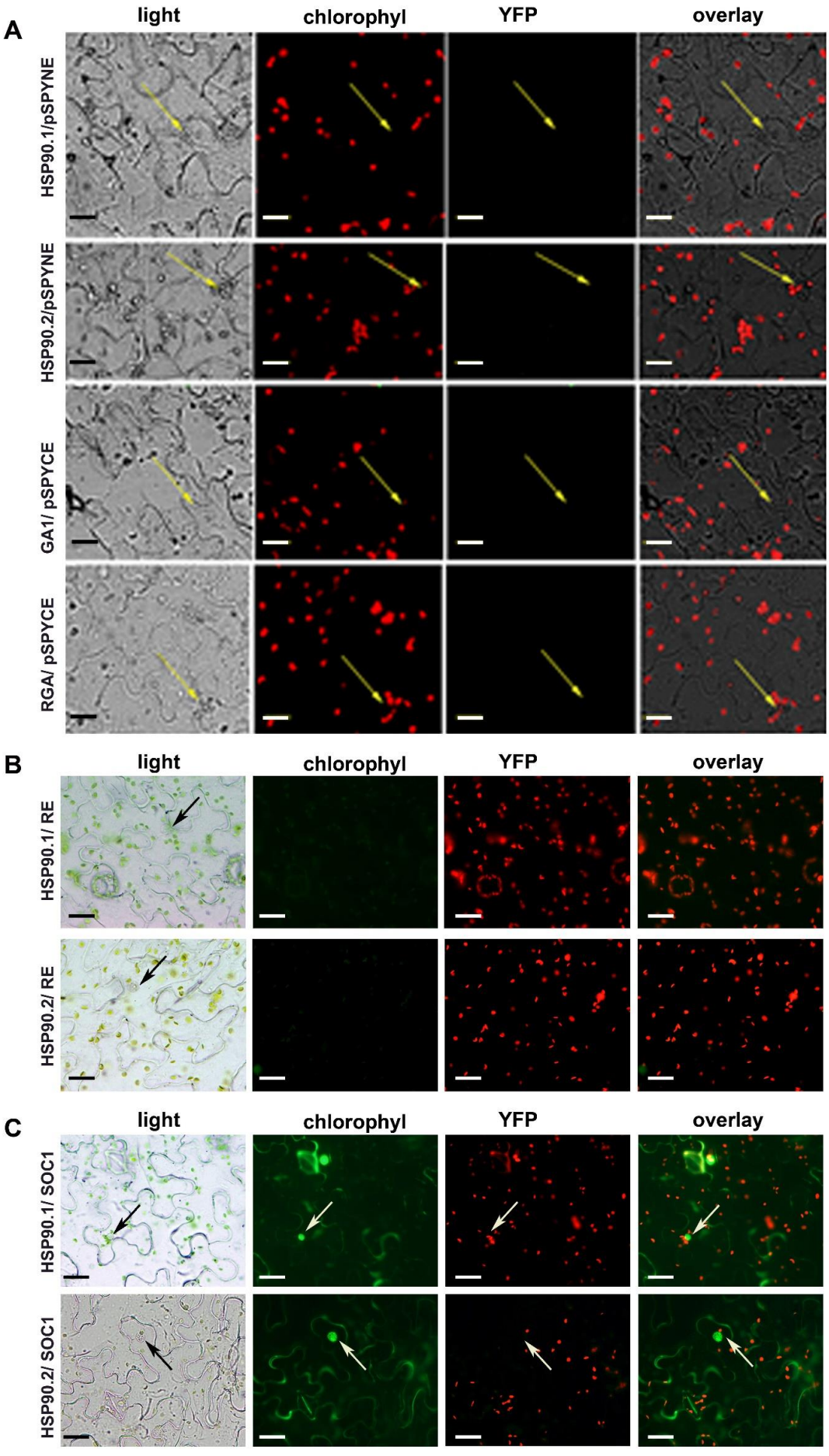

A
light
chlorophyl
YFP
overlay
HSP90.1/pSPYNE
HSP90.2/pSPYNE
GA1/ pSPYCE
RGA/ pSPYCE
B
light
chlorophyl
YFP
overlay
HSP90.1/ RE
HSP90.2/ RE
C
light
chlorophyl
YFP
overlay
HSP90.1/ SOC1
HSP90.2/ SOC1

**Figure S2.** Negative and positive controls of BiFC interaction assays of HSP90.1 and HSP90.2 with RGA or GAI. **(A)** *N. benthamiana* leaf epidermal cells co-transformed with HSP90.1- or HSP90.3-YFPc and pSPYNE-nYFP, or with pSPYCE-YFPc and GAI-nYFP or RGA-nYFP, were used as controls. No fluorescence was detected. **(B)** HSP90.1 and HSP90.2 do not interact with RABBIT EARS (RE) [**37**] , and therefore were introduced in *N. benthamiana* leaf epidermal cells as negative controls. No fluorescence was detected. **(C)** Both HSP90.1 and HSP90.2 interact with SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1 (SOC1) [**37**], and therefore, were introduced in *N. benthamiana* leaf epidermal cells as positive controls. Reconstituted fluorescent signals in the nucleus and cytoplasm demonstrated protein-protein interactions in both cellular compartments. Arrows indicate the nuclei. Scale bars, 20 μm.

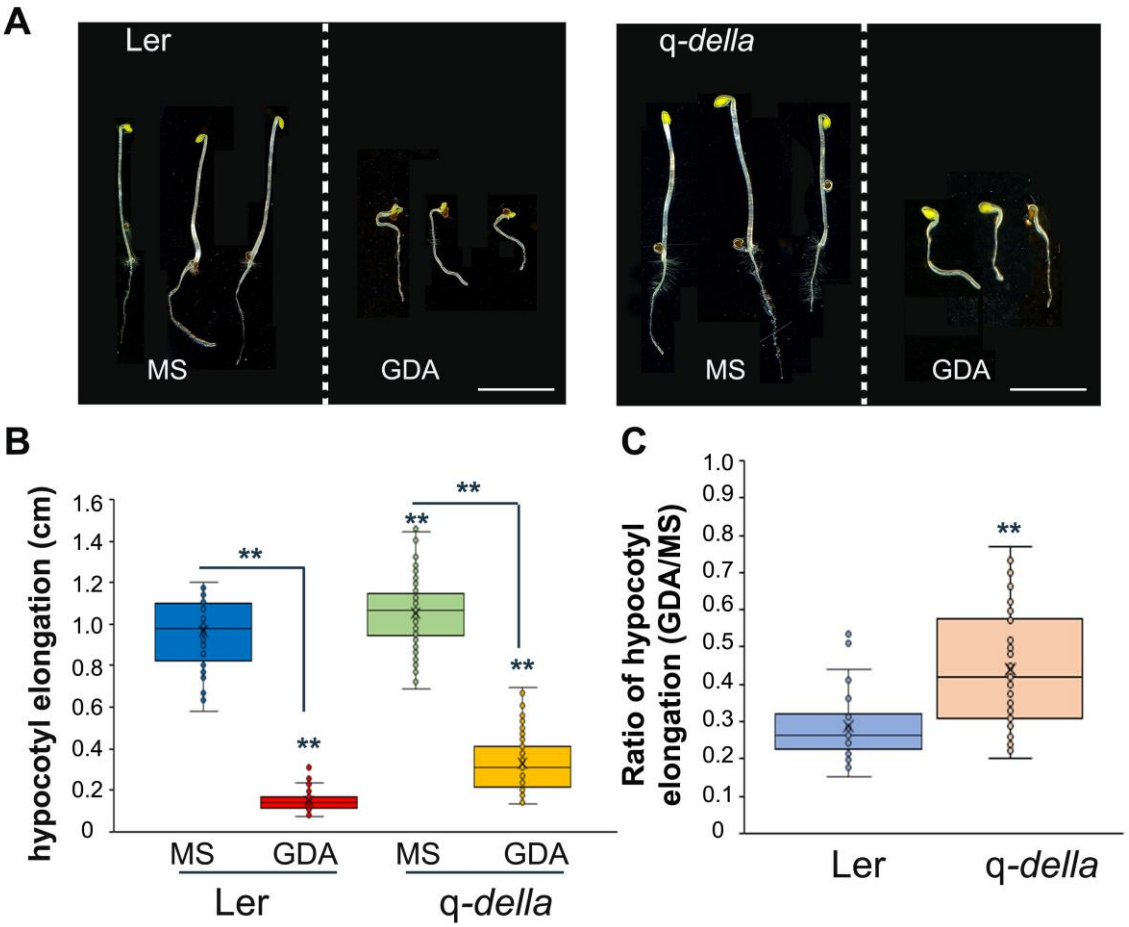



**Figure S3.** The hypocotyl growth of *q-della* mutants is partially insensitive to the inhibition of HSP90 function. **(A)** Hypocotyl images of 5-day-old wild type (Ler) and pentuple *della* etiolated seedlings grown in MS medium in the absence or presence of 2μM GDA. Scale bars, 0.5 cm. **(B)** Hypocotyl lengths of seedlings shown in (**A**). Data are presented as means and error bars indicate ±SD. Number of seedlings, n > 30. Data were analyzed with one-way ANOVA followed by Tukey's test, (**): p<0.01. **(C)** Hypocotyl length ratios (GDA/MS) of the quantified hypocotyl lengths in (B). Data are presented as means and error bars indicate ±SD. Number of measurements ≥ 30. Significant difference was compared to respective wild type. Student's t-test was performed (**): p < 0.01).

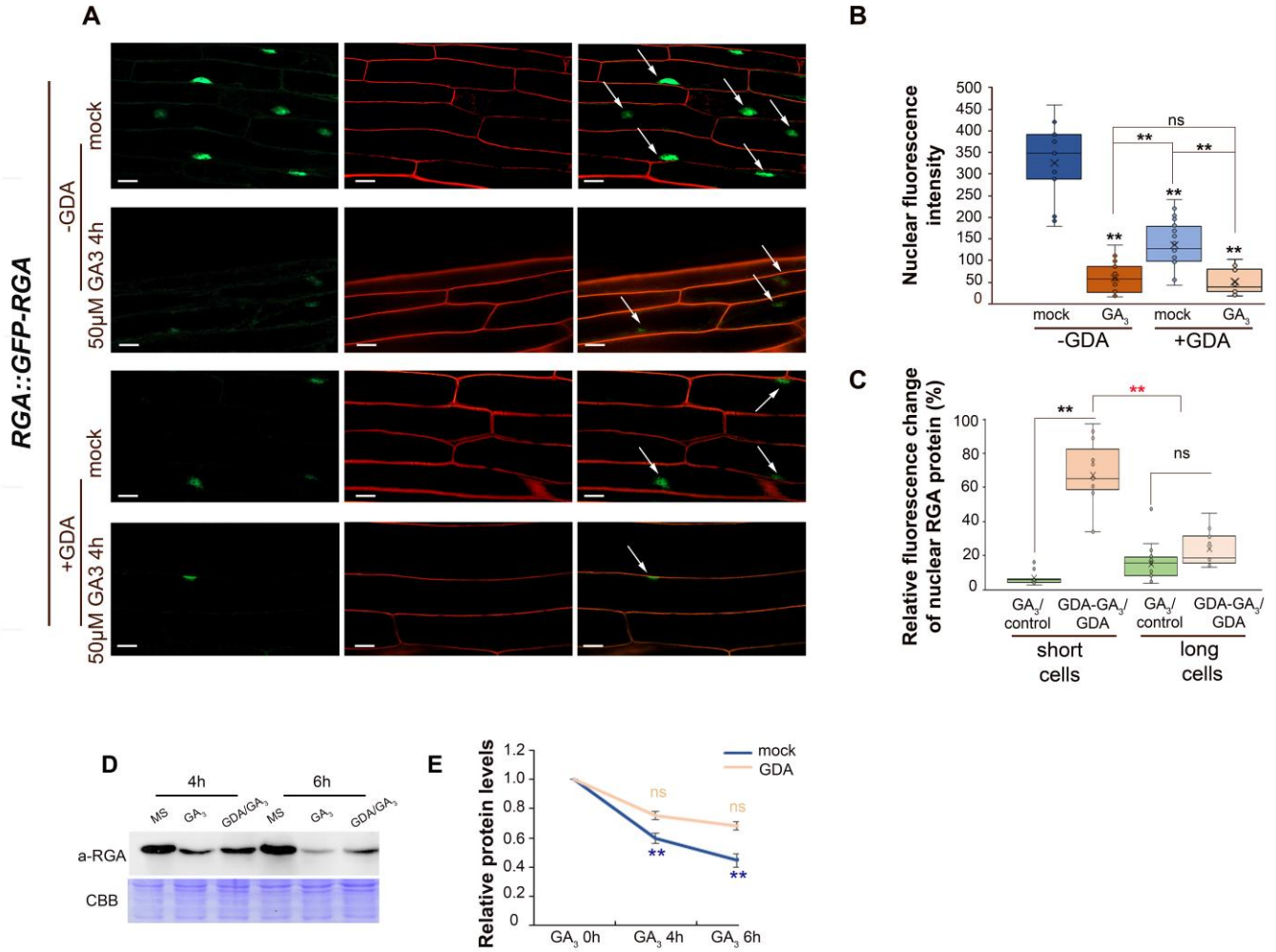



**Figure S4.** The effect of HSP90 pharmacological inhibition on RGA protein levels in the elongated hypocotyl cells of dark grown seedlings. **(A)** Fluorescent images of fully elongated hypocotyl cells showing GFP- RGA levels. 5-day-old etiolated *RGA*::RGA-GFP seedlings with or without 50μM $GA_3$ treatment for 4h, in the absence or presence of 2μM GDA for 12h. The cell patterns were visualized by using PI. Scale bars, 50 μm. **(B)** Quantification of the nuclear fluorescence intensity in fully elongated hypocotyl cells of 5-day-old etiolated seedlings treated as indicated in (A). Box plots display the first and third quartiles, split by the median; whiskers extend to include the max/min values. Statistical analysis was performed using one-way analysis of variance (ANOVA) followed by Tukey test for multiple comparisons, **p<0.01. (**C**) Nuclear GFP-RGA fluorescence change (%) was assessed by the fluorescence ratios of short (**Figure 3B**) and long hypocotyl cells (**B**) under the indicated treatments, respectively. Statistical analysis was performed using two-way analysis (ANOVA) followed by Tukey test **(D)** Time course analysis of RGA protein levels in 5-day-old etiolated seedlings grown in control conditions and then treated with 25 μM $GA_3$ or 2 μM GDA and 25 μM $GA_3$ for the indicated time. Coomassie brilliant blue (CBB) was used for the evaluation of total protein levels. **(E)** Quantification of RGA relative protein levels after $GA_3$ application in the presence or absence of 2 μM GDA. Data are means and error bars indicate ±SD. **(**):** P<0.01, ns**:** non-significant according to one-way analysis ANOVA followed by Tukey for multiple comparison.

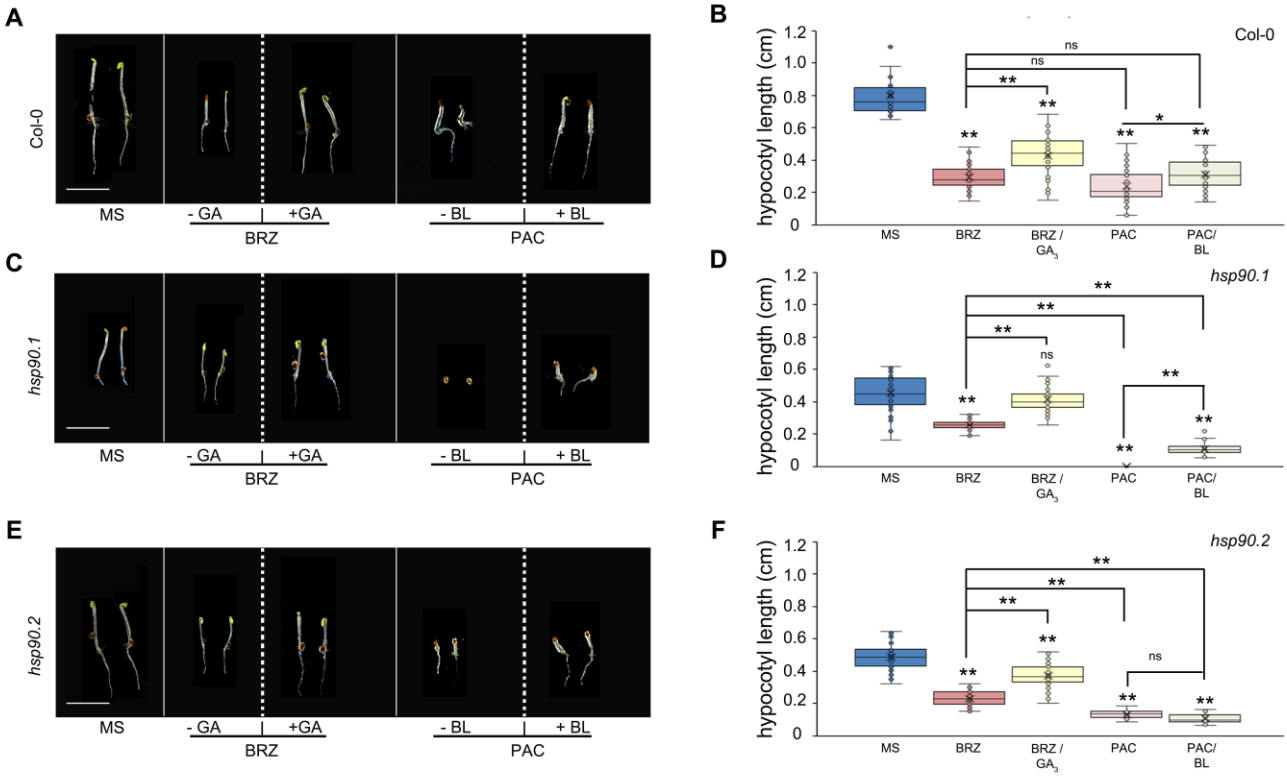



**Figure S5.** Hypocotyl elongation assays of wild type *hsp90* etiolated seedlings under deficiency of BRs or GAs. **(A, C, E)** Images of 5-day-old etiolated seedlings Col-0 (**A**), *hsp90.1* (**C**) and *hsp90.2* (**E**) growing in the indicated conditions. (**B, D, F**) Hypocotyl elongation of 5-day-old Col-0 (**B**), *hsp90.1* (**D**) and *hsp90.2* (**F**) growing on control MS medium, or in the presence of 0.5 μM BRZ, or in combination of 0.5 μM BRZ with 10 μM GA3 or in the presence of 0.1 μM PAC or in combination of 0.1 μM PAC with 60 nM BL. Box plots display the first and third quartiles, split by the median; whiskers extend to include the max/min values. Statistical analysis was performed using one-way analysis of variance (ANOVA) followed by Tukey test for multiple comparisons, ns: non-significant, * $p<0.05$, ** $p<0.01$.

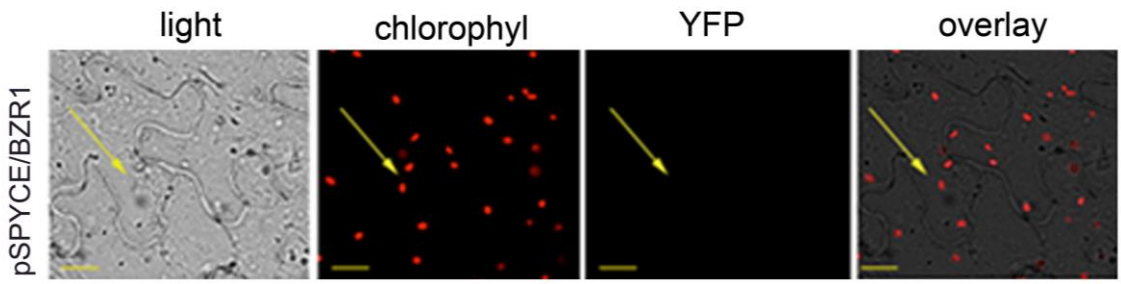
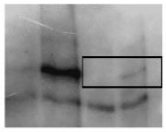
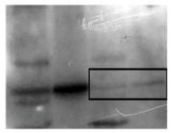



**Figure S6.** Negative control of HSP90.1 or HSP90.2 BiFC interaction assays with BZR1. *N. benthamiana* leaf epidermal cells co-transformed with pSPYCE-YFPc and BZR1-nYFP were used as controls. No fluorescence was detected. Arrows indicate the nucleus. Scale bars, 20 μm.

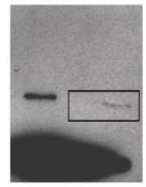
Unprocessed Western Blot Fig.2B
coIP anti-c-myc



Unprocessed Western Blot Fig.2B
input anti-c-myc



Unprocessed Western Blot Fig.2B
coIP anti-HSP90



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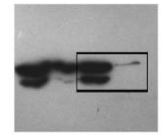
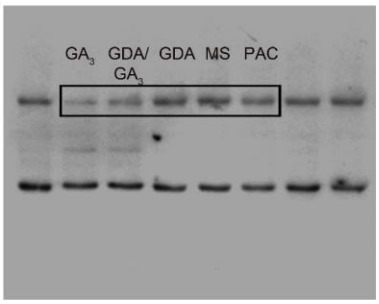
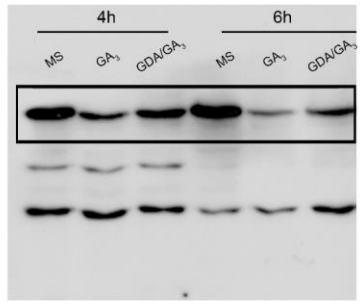
input anti-HSP90



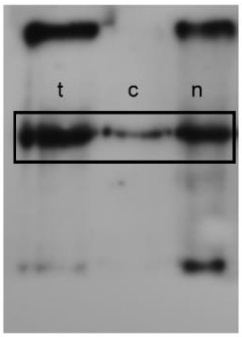
Unprocessed Western Blot Fig.3C



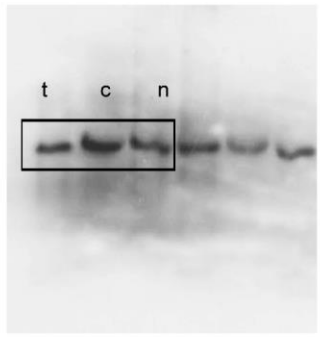

Unprocessed Western Blot Fig.3E



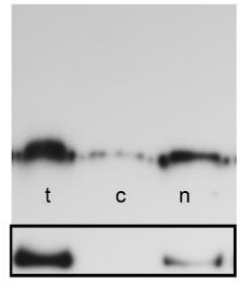

Unprocessed Western Blot Fig.5B
HSP90.1/BZR1 anti-c-myc CoIP



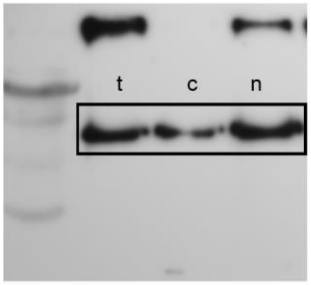

Unprocessed Western Blot Fig.5B
HSP90.1/BZR1 anti- c-myc input



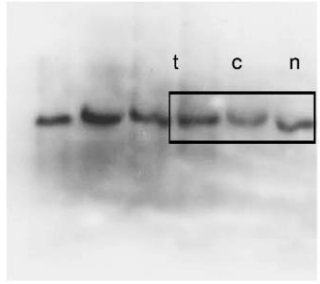

Unprocessed Western Blot Fig.5B
HSP90.1/BZR1 anti-acH3




Unprocessed Western Blot Fig.5B
HSP90.2/BZR1 anti-c-myc CoIP




Unprocessed Western Blot Fig.5B
HSP90.2/BZR1 anti- c-myc input




Unprocessed Western Blot Fig.5B
HSP90.2/BZR1 anti-acH3

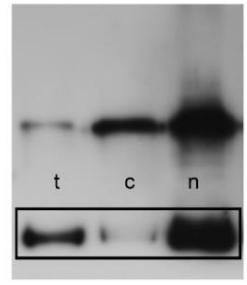



**Figure S7.** Unprocessed Western blot images used in this study.

Table S1. List of primers used in this study

| ***Primers for yeast two hybrid interacrions*** | | |
|---|---|---|
| Gene | Primer | Sequence |
| At5g52640 | Hsp90.1yeastFor | 5’-AAAGGATCCCGATGGCGGATGTTCAG-3’ |
| | Hsp90.1yeastRev | 5’–TTTCTCGAGGTCGACTTCCTCCATCTTGC-3’, |
| At5g56030 | Hsp90.2yeastFor | 5’-ATACATATGATGGCGGACGCTGAAACC-3’ |
| | Hsp90.2yeastRev | 5’-ATAATCGATTTAGTCGACTTTTGTGTG-3’ |
| At1g75080 | Bzr1yeastFor | 5’-TTTTCATATGATGACTTCGGATGGAGCTACGTCG-3’ |
| | Bzr1yeastRev | 5’-AAAACCCGGGACCACGAGCCTTCCCA-3’ |
| At2g01570 | RGA1yeast For | 5’-CCTCGGATCCGAATGAAGAGAGATCATCATCATCATC-3’ |
| | RGA1yeast Rev | 5’-ATTTGTCGACATTGGTGGAGAGTTTCCACGC-3’ |
| At1g14920 | GAI1yeast For | 5’-ATATGGATCCGAATGAAGAGAGATCATCACCAATTCC-3’ |
| | GAI1yeast Rev | 5’-TTTTGTCGACGTACGCCGCCGTCGA-3’ |
| | | |
| | | |
| ***Primers for BiFC contructs*** | | |
| Gene | Primer | Sequence |
| At5g52640 | Hsp90.1splitFor | 5’-TTAATGGATCCAAGTTCGTTGCGATGGCGGATG-3’ |
| | Hsp90.1splitRev | 5’- TTTCTCGAGGTCGACTTCCTCCATCTTGC-3’ |
| At5g56030 | Hsp90.2splitFor | 5’-ATATCTAGAACGACAATGGCGGACGCTGAAACC-3’ |
| | Hsp90.2splitRev | 5’-ATAGGTACCGTCGACTTCCTCCATCTT-3’ |
| At1g75080 | Bzr1splitFor | 5’-ACTAGTATGACTTCGGATGGAGCTACG-3’ |
| | Bzr1splitRev | 5’-TTTTGGTACCACCACGAGCCTTCCCATTTCC-3’ |
| At2g01570 | RGA1split For | 5’-CCTCGGATCCATGAAGAGAGATCATCATCATCATC-3’ |
| | RGA1split Rev | 5’-ATTTGTCGACATTGGTGGAGAGTTTCCACGC-3’ |
| At1g14920 | GAI1split For | 5’-ATATGGATCCATGAAGAGAGATCATCACCAATTCC-3’ |
| | GAI1split Rev | 5’-TTTTGTCGACGTACGCCGCCGTCGA-3’ |
| | | |
| | | |
| ***Primers for Quantitative RT PCR (qPCR)*** | | |
| Gene | Primer | Sequence |
| | oligo -dT | 5’-GTCGACCTCGAGTTTTTTTTTTTTTTTT-3’ |
| At1g02400 | qGA2ox6 - F | 5' -ATCCAACGACGTAGATGGACTTG-3’ |
| | qGA2ox6 - R | 5' -CCTATGCCTCACGCTAGTGAAT-3’ |
| At1g05160 | qKAO1 fwd | 5' -TGAGGTTCTACAAAGAGCAAAGGC-3’ |
| | qKAO1 rev | 5' -ACTCGAAGTGTCTCATCGACAACC-3’ |
| At4g25420 | qGa20_ox1 fwd | 5' -AGATTACTTCTGCGATGCGTTGG-3’ |
| | qGa20_ox1 rev | 5' -CGAATGGAGCGCCATTGATTTTC-3’ |
| At1g30040 | qGa2_ox2 fwd | 5' -AGATGGAAGTTGGGTCGCTGTC-3’ |
| | qGa2_ox2 rev | 5' -TGTATCGGCTAAGACCCTGTG-3’ |
| At1g15550 | qGA3ox1 - F | 5' -GTCTAGCAGCTCATACCGACTC-3’ |
| | qGA3ox1 - R | 5' -CCATTGGATAGGATGTGGAAGAGG-3’ |
| At1g13440 | qGAPDH - F | GCCAAGAAGGTTGTTATCTCTGCCC-3’ |
| | qGAPDH - R | 5' -GCTCGACCTGTTGTCGCCAACG-3’ |
| At2g37640 | qEXP3-F | 5' -TCCATCTATTCTTGTGACGGCGAC-3’ |

| | | |
|---|---|---|
| | qEXP3-R | 5' -TCCCTCCTATCTTCCGACAAGGTA-3′ |
| At2g40610 | qEXP8 F | 5' -TCCTCCTCTTCAGCATTTCGACCT-3' |
| | qEXP8 R | 5' -CTTGCCACGACTGTGTTTTTGAGC-3′ |
| At4g30290 | qXTH19-F | 5' -GACCCAACCGCTAACTTTCACAC-3′ |
| | qXTH19-R | 5' -AGGAGCTTTTGACCAATCTGTTTTCTC-3′ |
| At1g10550 | qXTH33-F | 5' -ATACCCTCATTTGGAACTCCCACC-3′ |
| | qXTH33-R | 5' -CACTTAACTCCACGTCAGCAACG-3′ |