

**Table S1 Quantification of lateral root density.**

Table presents the mean number of lateral roots per centimeter of the primary root for each genotype/condition. This analysis includes data from 16 plants per genotype per condition in triplicate. Statistical differences were assessed by a two-way Analysis of Variance (ANOVA). Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

| Genotype         | Growth conditions | Averaged number of lateral root/cm of primary root | Statistical groups |
|------------------|-------------------|--|--------------------|
| Col-0            | nAT               | 2.29   | a                  |
| Col-0            | hAT               | 1.61   | b                  |
| <i>35S::PIF4</i> | nAT               | 1.77   | b                  |
| <i>35S::PIF4</i> | hAT               | 1.59   | b                  |
| <i>phyB</i>      | nAT               | 1.54   | b                  |
| <i>phyB</i>      | hAT               | 1.01   | c                  |
| <i>pif4</i>      | nAT               | 2.12   | a                  |
| <i>pif4</i>      | hAT               | 1.47   | b                  |

**Table S2 Mean of the length of the four longest lateral roots at maturity.**

Table presents the mean of the length of the four longest lateral roots at maturity for each genotype/condition. The analysis encompasses 16 plants for each genotype. Statistical differences were assessed by a two-way Analysis of Variance (ANOVA). Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

| Genotype         | Growth conditions | Averaged lateral root length (cm) | Statistical groups |
|------------------|-------------------|-----------------------------------|--------------------|
| Col-0            | nAT               | 4.28                              | a                  |
| Col-0            | hAT               | 9.20                              | b                  |
| <i>35S::PIF4</i> | nAT               | 5.16                              | a c                |
| <i>35S::PIF4</i> | hAT               | 8.09                              | b                  |
| <i>phyB</i>      | nAT               | 4.48                              | a c                |
| <i>phyB</i>      | hAT               | 6.09                              | c                  |
| <i>pif4</i>      | nAT               | 4.26                              | a                  |
| <i>pif4</i>      | hAT               | 8.53                              | b                  |

**Table S3. Statistical analysis related to Table 2. Anther abortion rate for different genotypes in nAT and hAT**

| <i>Comparing anther phenotype for each genotype at hAT vs nAT</i>            |                           |                         |
|--|---------------------------|-------------------------|
| <b>Genotype</b>  | 7 DAFD - <i>p</i> -values | 9 DAFD <i>p</i> -values |
| Col-0  | 0.18242                   | 0.02465 *               |
| <i>phyB</i>  | 0.00491 *                 | 0.00000 ***             |
| <i>35S::PIF4</i>   | 0.00000 ***               | 0.00000 ***             |
| <i>pif4</i>  | 1.00000                   | 0.45918                 |
| <i>pifq</i>  | 1.00000                   | 0.51969                 |
| * 0.05-0.001; ** < 0.001-0.0001; *** < 0.0001                                |                           |                         |
| <i>Comparing anther phenotype of each genotype with Col-0 at hAT</i>         |                           |                         |
| <b>Genotype</b>  | 7 DAFD - <i>p</i> -values | 9 DAFD <i>p</i> -values |
| <i>phyB</i>  | 0.39965                   | 0.00005 ###             |
| <i>35S::PIF4</i>   | 0.01527 #                 | 0.00576 #               |
| <i>pif4</i>  | 0.10287                   | 0.08243                 |
| <i>pifq</i>  | 0.11841                   | 0.03315 #               |
| # 0.05-0.001; ## <0.001-0.0001; ### < 0.0001                                 |                           |                         |
| <i>Comparing anther phenotype of each genotype at 7 with 9 DAFD under HT</i> |                           |                         |
| <b>Genotype</b>  | <i>p</i> -values          |                         |
| Col-0  | 0.275471698               |                         |
| <i>phyB</i>  | 0.000436936^^             |                         |
| <i>35S::PIF4</i>   | 0.540567636               |                         |
| <i>pif4</i>  | 1                         |                         |
| <i>pifq</i>  | 0.532627646               |                         |
| ^ 0.05-0.001; ^^ <0.001-0.0001; ^^> <0.0001                                  |                           |                         |

The Fisher's exact test was performed for these comparisons. At least 40 anthers for each genotype/condition were examined. The experiments were performed in triplicate.

**Table S4. Ovule defective phenotypes for the different genotypes at nAT and hAT**

| Genotype         | Growth conditions | Normal | n   | % of total defects | % collapsed embryo sac | % collapsed synergids | % unfused CC nuclei | % other defects |
|------------------|-------------------|--------|-----|--------------------|------------------------|-----------------------|---------------------|-----------------|
| Col-0            | nAT               | 122    | 129 | 5.4                | 0                      | 5.4                   | 0.0                 | 0.0             |
| Col-0            | hAT               | 102    | 147 | 30.6               | 17.5                   | 8.5                   | 2.0                 | 2.6             |
| <i>35S::PIF4</i> | nAT               | 115    | 137 | 16.1               | 7.1                    | 4.8                   | 2.1                 | 2.1             |
| <i>35S::PIF4</i> | hAT               | 16     | 102 | 84.3               | 67.8                   | 6.4                   | 0.9                 | 9.2             |
| <i>phyB</i>      | nAT               | 78     | 95  | 17.9               | 2.1                    | 6.3                   | 8.4                 | 1.1             |
| <i>phyB</i>      | hAT               | 31     | 83  | 62.6               | 24.8                   | 14.9                  | 3.1                 | 19.8            |
| <i>pif4</i>      | nAT               | 90     | 98  | 8.2                | 4.9                    | 0.0                   | 0.0                 | 3.5             |
| <i>pif4</i>      | hAT               | 55     | 76  | 27.6               | 18.4                   | 5.6                   | 0.0                 | 3.6             |
| <i>pifq</i>      | nAT               | 77     | 85  | 9.4                | 7.0                    | 2.4                   | 0.0                 | 0.0             |
| <i>pifq</i>      | hAT               | 37     | 68  | 45.6               | 33.8                   | 7.4                   | 0.0                 | 4.4             |

The experiments were performed in triplicate. Relates to Table 4. Ovule defective phenotypes for the different genotypes at nAT and hAT

**Table S5. Transcriptomic data summary**

| <b>Sample</b>        | <b>replicate</b> | <b>clean reads</b> | <b>GC %</b> | <b>quality scores<br/>Q20</b> | <b>quality scores<br/>Q30</b> |
|----------------------|------------------|--------------------|-------------|-------------------------------|-------------------------------|
| Col-0 nAT            | 1                | 42 060 406         | 46.01       | 98.07                         | 94.13                         |
| Col-0 nAT            | 2                | 40 429 238         | 45.73       | 97.85                         | 93.58                         |
| Col-0 nAT            | 3                | 40 740 204         | 45.72       | 97.96                         | 93.84                         |
| Col-0 nAT            | 4                | 52 496 928         | 45.76       | 97.79                         | 93.5                          |
| Col-0 hAT            | 1                | 52 031 214         | 44.63       | 98.05                         | 94.04                         |
| Col-0 hAT            | 2                | 43 336 384         | 44.67       | 97.70                         | 93.15                         |
| Col-0 hAT            | 3                | 47 869 856         | 44.70       | 98.04                         | 94.14                         |
| <i>phyB</i> nAT      | 1                | 52 254 686         | 44.70       | 97.91                         | 93.68                         |
| <i>phyB</i> nAT      | 2                | 48 593 332         | 45.14       | 97.97                         | 93.80                         |
| <i>phyB</i> nAT      | 3                | 46 759 364         | 44.77       | 97.97                         | 93.81                         |
| <i>phyB</i> nAT      | 4                | 52 854 984         | 44.69       | 98.00                         | 93.96                         |
| <i>phyB</i> hAT      | 1                | 45 987 996         | 44.72       | 97.93                         | 93.74                         |
| <i>phyB</i> hAT      | 2                | 45 703 752         | 44.83       | 97.93                         | 93.95                         |
| <i>phyB</i> hAT      | 3                | 47 669 986         | 45.11       | 97.81                         | 93.58                         |
| <i>phyB</i> hAT      | 4                | 65 471 960         | 45.03       | 97.81                         | 93.58                         |
| <i>35S::PIF4</i> nAT | 1                | 43 886 772         | 45.13       | 98.34                         | 94.99                         |
| <i>35S::PIF4</i> nAT | 2                | 50 746 592         | 44.72       | 98.02                         | 93.95                         |
| <i>35S::PIF4</i> nAT | 3                | 65 893 110         | 44.99       | 98.06                         | 94.21                         |
| <i>35S::PIF4</i> nAT | 4                | 55 254 998         | 44.83       | 98.15                         | 94.29                         |
| <i>35S::PIF4</i> hAT | 1                | 46 380 078         | 44.91       | 97.97                         | 93.85                         |
| <i>35S::PIF4</i> hAT | 2                | 43 825 406         | 44.64       | 98.03                         | 93.98                         |
| <i>35S::PIF4</i> hAT | 3                | 48 510 456         | 44.67       | 97.88                         | 93.60                         |
| <i>35S::PIF4</i> hAT | 4                | 42 629 628         | 44.57       | 98.01                         | 93.91                         |

**Table S6. Mean of suspensor length for each genotype/condition.**

| Genotype         | Growth conditions | Suspensor length ( $\mu\text{m}$ ) | n  | Statistical groups |
|------------------|-------------------|------------------------------------|----|--------------------|
| Col-0            | nAT               | 97.18                              | 26 | a                  |
| Col-0            | hAT               | 86.14                              | 23 | c                  |
| <i>35S::PIF4</i> | nAT               | 110.96                             | 29 | b                  |
| <i>35S::PIF4</i> | hAT               | 74.86                              | 5  | c d                |
| <i>phyB</i>      | nAT               | 98.22                              | 30 | a                  |
| <i>phyB</i>      | hAT               | 84.20                              | 17 | c                  |
| <i>pif4</i>      | nAT               | 104.00                             | 24 | a b                |
| <i>pif4</i>      | hAT               | 75.66                              | 8  | c d                |
| <i>pifq</i>      | nAT               | 101.31                             | 16 | a b                |
| <i>pifq</i>      | hAT               | 66.90                              | 27 | d                  |

The experiments were performed in triplicate. Relates to Figure 5. Statistical differences were assessed by a two-way Analysis of Variance (ANOVA). Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

**Table S7. Seed size**

The surface area of 1 000 seeds for each genotype were analyzed in triplicate at nAT and hAT. Relates to Fig. 9b. Statistical differences were assessed by a two-way Analysis of Variance (ANOVA). Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

| Genotype         | Growth conditions | Mean seed surface (mm <sup>2</sup> ) | Statistical groups |
|------------------|-------------------|--------------------------------------|--------------------|
| Col-0            | nAT               | 0.0804                               | a                  |
| Col-0            | hAT               | 0.1084                               | c                  |
| <i>35S::PIF4</i> | nAT               | 0.0814                               | a                  |
| <i>35S::PIF4</i> | hAT               | 0.1072                               | c                  |
| <i>phyB</i>      | nAT               | 0.0847                               | b                  |
| <i>phyB</i>      | hAT               | 0.1252                               | d                  |
| <i>pif4</i>      | nAT               | 0.0837                               | b                  |
| <i>pif4</i>      | hAT               | 0.1047                               | e                  |
| <i>pifq</i>      | nAT               | 0.0790                               | a                  |
| <i>pifq</i>      | hAT               | 0.1167                               | f                  |

**Table S8. Seed shape**

Ratio of seed length over seed area of about 1 000 seeds for each genotype were analyzed in triplicate from plants grown at nAT and hAT. Relates to Fig. 9c. Statistical differences were assessed by a two-way Analysis of Variance (ANOVA). Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

| Genotype         | Growth conditions | seed length / area | Statistical groups |
|------------------|-------------------|--------------------|--------------------|
| Col-0            | nAT               | 5.1517             | a c                |
| Col-0            | hAT               | 4.4843             | d g                |
| <i>35S::PIF4</i> | nAT               | 5.1986             | a                  |
| <i>35S::PIF4</i> | hAT               | 4.3479             | f                  |
| <i>phyB</i>      | nAT               | 4.7850             | b                  |
| <i>phyB</i>      | hAT               | 4.1510             | e                  |
| <i>pif4</i>      | nAT               | 4.7850             | b                  |
| <i>pif4</i>      | hAT               | 4.5037             | g                  |
| <i>pifq</i>      | nAT               | 5.1286             | c                  |
| <i>pifq</i>      | hAT               | 4.3639             | d f                |



**Table S9. Number of seeds produced per silique.**

The number of seeds per silique was calculated from at least 12 siliques per genotype from plants grown at nAT and hAT. Relates to Fig. 9d. Statistical differences were assessed by a two-way Analysis of Variance (ANOVA). Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

| Genotype         | Growth conditions | Averaged number of seeds per silique | Statistical groups |
|------------------|-------------------|--------------------------------------|--------------------|
| Col-0            | nAT               | 62.16                                | a                  |
| Col-0            | hAT               | 42.14                                | b                  |
| <i>35S::PIF4</i> | nAT               | 52.09                                | a                  |
| <i>35S::PIF4</i> | hAT               | 25.50                                | b                  |
| <i>phyB</i>      | nAT               | 47.75                                | a                  |
| <i>phyB</i>      | hAT               | 36.48                                | b                  |
| <i>pif4</i>      | nAT               | 62.96                                | a                  |
| <i>pif4</i>      | hAT               | 43.33                                | b                  |
| <i>pifq</i>      | nAT               | 60.36                                | a                  |
| <i>pifq</i>      | hAT               | 44.35                                | b                  |

**Table S10. The 100-seed weight.**

The weight of 100 seeds from each genotype is measured in triplicate from plants grown at nAT and hAT. Relates to Fig. 9e. To assess differences per genotypes and between the two different conditions, a two-way Analysis of Variance (ANOVA) was performed. Subsequently, *post-hoc* analysis using Tukey's test was conducted to identify specific group differences. Genotypes that share the same letter are not statistically different.

| Genotype         | Growth conditions | 100-seed mass (mg) | Statistical group |
|------------------|-------------------|--------------------|-------------------|
| Col-0            | nAT               | 1.80               | a                 |
| Col-0            | hAT               | 2.33               | b d               |
| <i>35S::PIF4</i> | nAT               | 1.93               | a                 |
| <i>35S::PIF4</i> | hAT               | 2.30               | b d               |
| <i>phyB</i>      | nAT               | 2.26               | b d               |
| <i>phyB</i>      | hAT               | 3.25               | c                 |
| <i>pif4</i>      | nAT               | 1.93               | a                 |
| <i>pif4</i>      | hAT               | 2.26               | b d               |
| <i>pifq</i>      | nAT               | 2.00               | a b               |
| <i>pifq</i>      | hAT               | 2.56               | d                 |