

Table 1 Suppl. Hormone content in different parts of flowering branches in bud stage.

| Hormone | Samples | Flower axis leaf [ng g ⁻¹ (f.m.)] | Flower axis2 [ng g ⁻¹ (f.m.)] | Flower axis1 [ng g ⁻¹ (f.m.)] | Florets [ng g ⁻¹ (f.m.)] |
|---------|---------|---|---|---|--|
| GA | LaF6 | 3.42 | 3.89 | 5.99 | 5.41 |
| | LaF10 | 8.71 | 4.36 | 9.11 | 8.69 |
| | LaF14 | 6.96 | 3.74 | 4.18 | 5.35 |
| ABA | LaF6 | 27.20 | 42.04 | 35.67 | 51.56 |
| | LaF10 | 43.84* | 48.88 | 39.68 | 91.17* |
| | LaF14 | 68.56** | 70.00* | 39.22 | 56.43 |
| IAA | LaF6 | 115.22** | 65.10* | 81.49 | 35.84 |
| | LaF10 | 85.67* | 48.25 | 82.84* | 76.32* |
| | LaF14 | 64.04 | 36.91 | 62.85 | 52.24 |
| ZR | LaF6 | 3.66 | 4.21 | 5.90 | 4.02 |
| | LaF10 | 3.78 | 3.17 | 3.80 | 6.22 |
| | LaF14 | 5.51 | 4.38 | 3.50 | 4.18 |

Table 2 Suppl. Sequence statistics of the lavender transcriptome. LaF6 - 6 florets per flower whorl, LaF10 - 10 florets per flower whorl, LaF14 - 14 florets per flower whorl.

| Sample | Raw reads | Clean reads | Clean bases | Q20 [%] | GC content [%] |
|--------|-----------|-------------|-------------|---------|----------------|
| LaF6 | 45975468 | 44047736 | 6.61G | 96.27 | 48.17 |
| LaF10 | 54285374 | 51139942 | 7.67G | 96.95 | 47.75 |
| LaF14 | 43301158 | 41106448 | 6.17G | 96.21 | 48.09 |

Table 3 Suppl. Annotation of unigene sequences.

| Database | Number of annotated unigenes | [%] |
|-------------------|------------------------------|-------|
| <i>NR</i> | 72820 | 70.32 |
| <i>KO</i> | 30814 | 29.75 |
| <i>Swiss-Prot</i> | 57472 | 55.50 |
| <i>PFAM</i> | 51664 | 49.89 |
| <i>GO</i> | 51985 | 50.20 |
| <i>KOG</i> | 32247 | 31.14 |

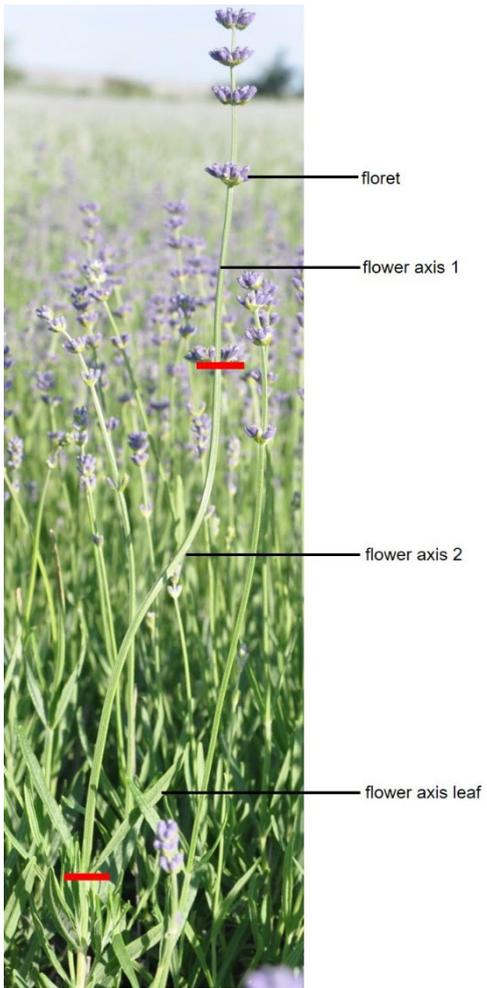


Fig. 1 Suppl. Inflorescence sample classification diagram.

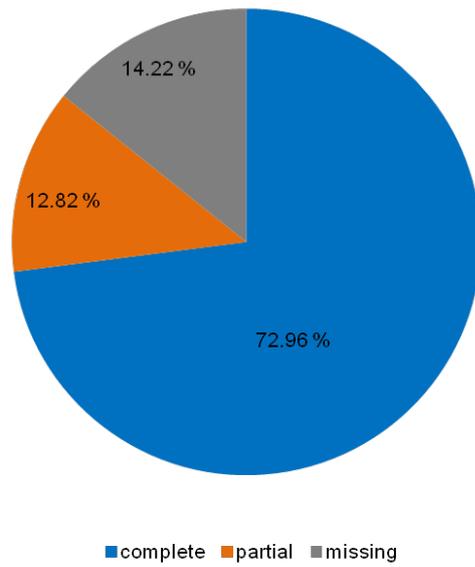


Fig. 2 Suppl. Reference gene-based completeness scores.

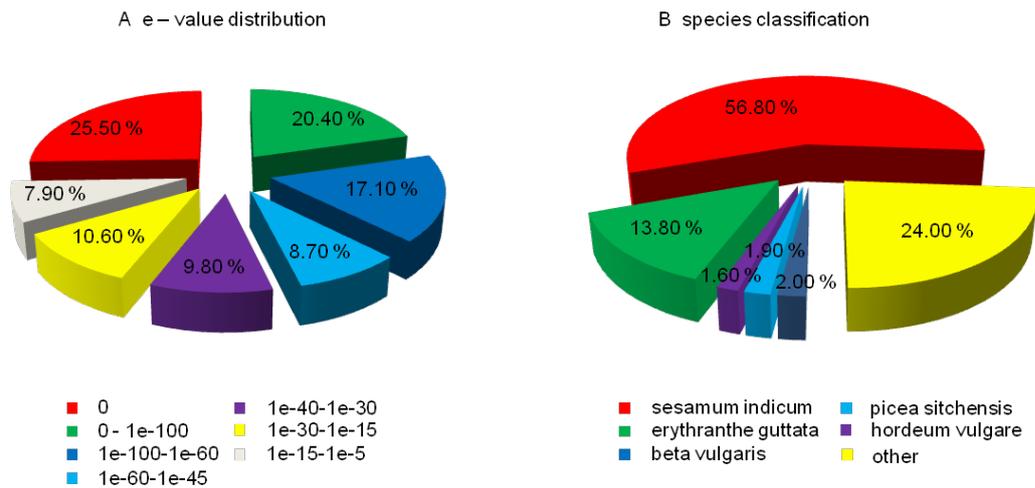


Fig. 3 Suppl. Characteristics of homology search of unigenes aligned by *BLASTx* to the *Nr* database. *A* - E-value distribution of unigenes annotated in the *Nr* database. *B* - Species distribution of the first *BLAST* hits for each sequence with a cut-off E-value $.1.0E^{-5}$.

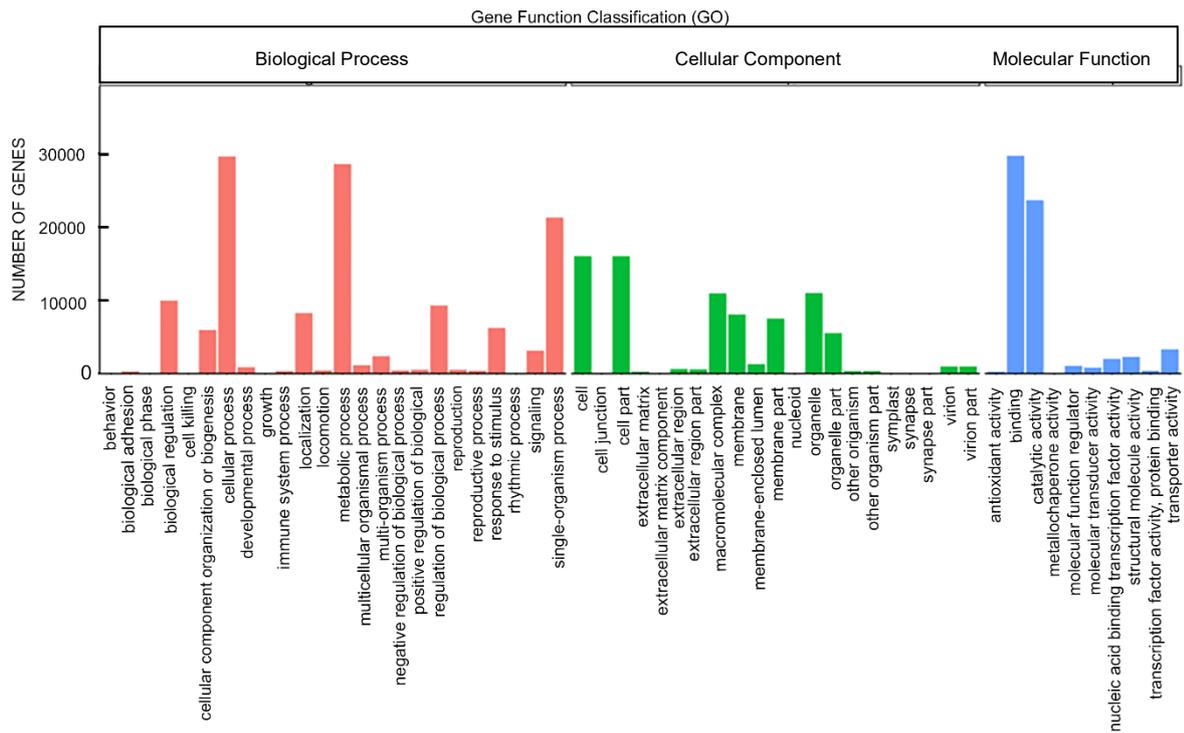


Fig. 4 Suppl. Gene ontology (GO) classification of all unigenes, they are classified into three GO categories: biological process (*red*), cellular component (*green*), and molecular function (*blue*).

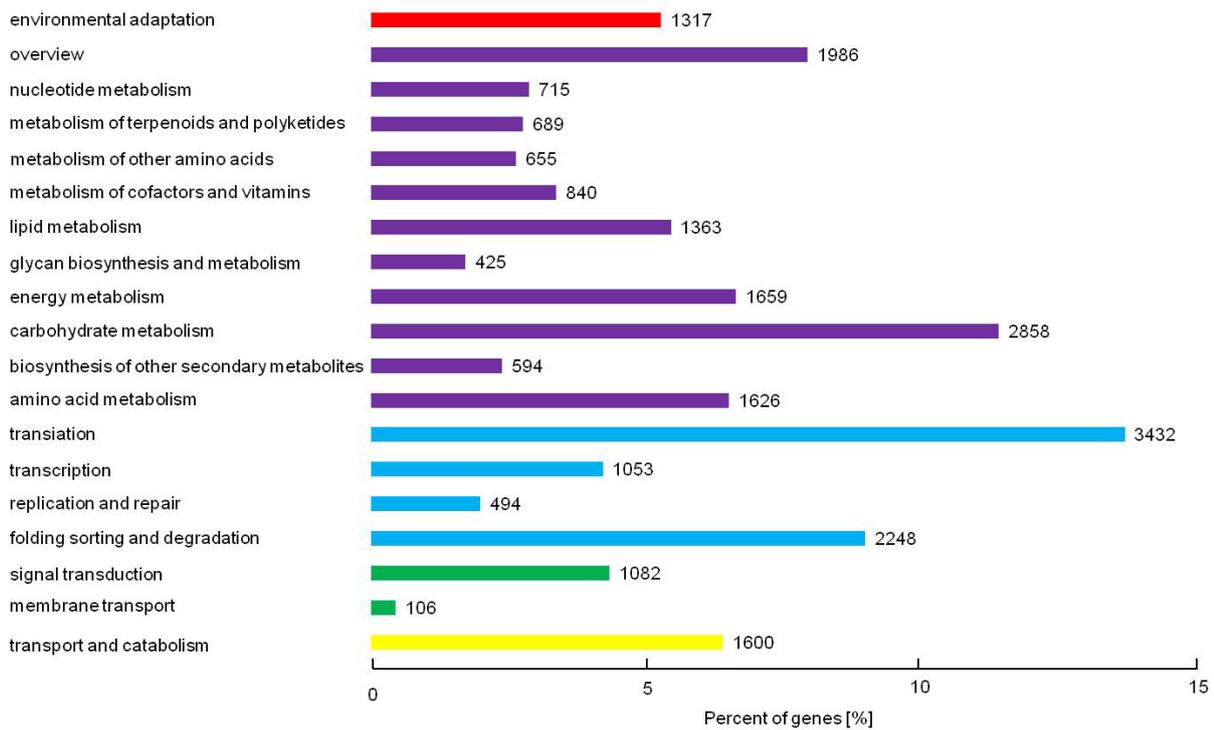


Fig. 5 Suppl. *KEGG* mapping of all unigenes.

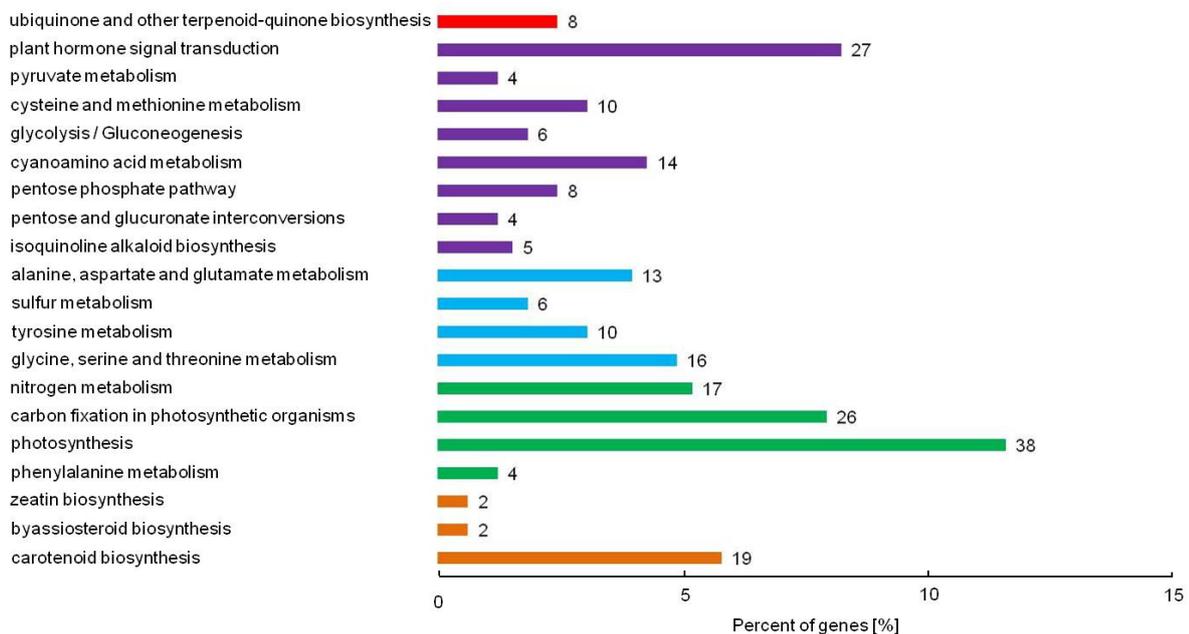


Fig. 6 Suppl. TOP 20 *KEGG* pathway DEGs enrichment analysis.

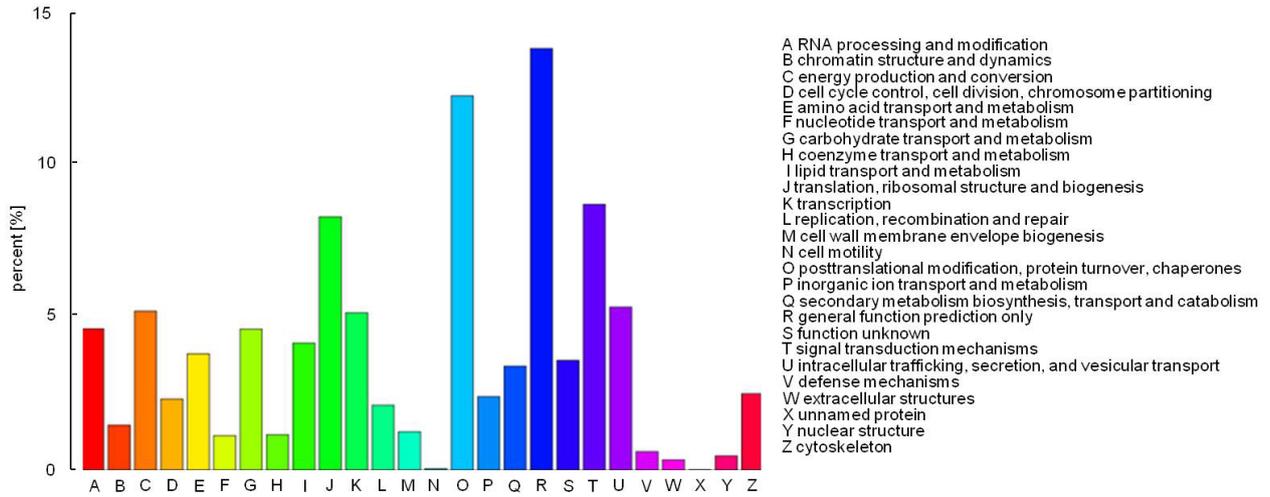


Fig. 7 Suppl. KOG function classification of all unigenes.

Plant hormone signal transduction

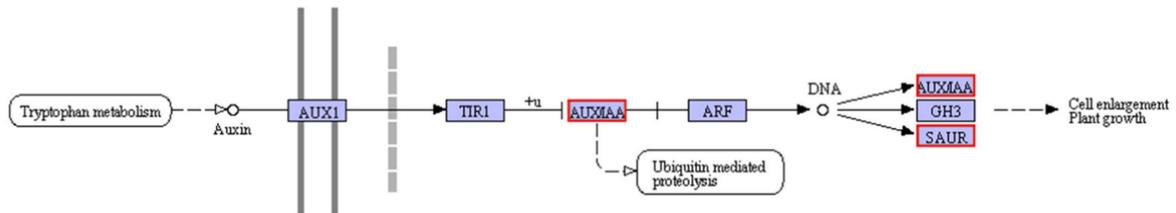


Fig. 8 Suppl. Plant hormone IAA (auxin) signal transduction.

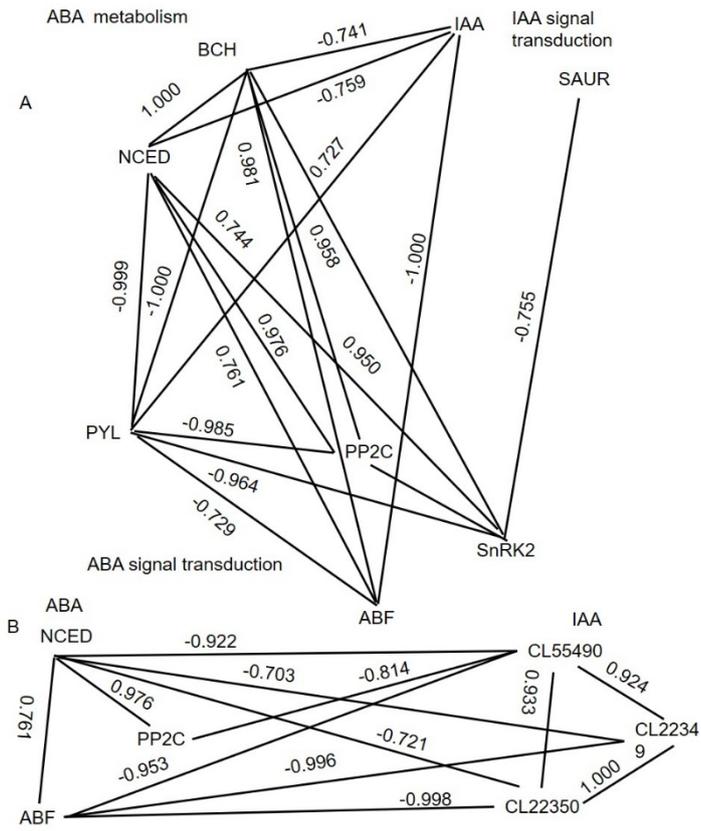


Fig. 9 Suppl. Common regulatory network of hormone signaling pathway. *A* - Common regulatory network of IAA signal transduction and ABA metabolism and transduction. *B* - Common regulatory network of IAA DEGs and key factors of ABA metabolism and transduction.