

Table S1. The details of RNA-seq data resources of *C. sativus*.

| SRA Accession | BioSample Accession | SRX Accession | Bases | Method | Stage | Tissue |
|---------------|---------------------|---------------|--------|---------------------|-----------|--------|
| SRR8790834 | SAMN11073280 | SRX5580626 | 2.66 G | Illumina HiSeq 2500 | flower | bud |
| SRR8790835 | SAMN11073281 | SRX5580625 | 2.58 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790836 | SAMN11073282 | SRX5580624 | 2.45 G | Illumina HiSeq 2500 | flower | bud |
| SRR8790837 | SAMN11073283 | SRX5580623 | 3.18 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790838 | SAMN11073284 | SRX5580622 | 2.86 G | Illumina HiSeq 2500 | flower | bud |
| SRR8790839 | SAMN11073285 | SRX5580621 | 2.55 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790840 | SAMN11073286 | SRX5580620 | 2.79 G | Illumina HiSeq 2500 | flower | bud |
| SRR8790841 | SAMN11073287 | SRX5580619 | 2.36 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790842 | SAMN11073288 | SRX5580618 | 2.73 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790843 | SAMN11073289 | SRX5580617 | 2.51 G | Illumina HiSeq 2500 | flower | bud |
| SRR8790844 | SAMN11073294 | SRX5580616 | 2.62 G | Illumina HiSeq 2500 | flower | bud |
| SRR8790845 | SAMN11073290 | SRX5580615 | 4.25 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790846 | SAMN11073291 | SRX5580614 | 3.34 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790847 | SAMN11073292 | SRX5580613 | 3.51 G | Illumina HiSeq 2500 | no-flower | bud |
| SRR8790848 | SAMN11073293 | SRX5580612 | 3.21 G | Illumina HiSeq 2500 | flower | bud |

Table S2. list of hub genes related to non-preserved modules.

| Module | Hub gene | GO |
|--------|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Pink | NAC3 | GO:0005634, GO:0005886, GO:0003700, GO:0000976 |
| | ALY3 | GO:0070176, GO:0005654, GO:0006351, GO:0051726, GO:0006357, GO:0000003 |
| | PIA1 | GO:0005737, GO:0005739, GO:0005634, GO:0010313 |
| | Sus3 | GO:0016157, GO:0005985 |
| green | MYB31 | GO:0003700, GO:0009733 |
| | ARF5/MP | GO:0009733, GO:0006355, GO:0048507, GO:0009942, GO:0010305, GO:0010305, GO:0009908, GO:0009793, GO:0009734, GO:0000976, GO:0042802, GO:0003700, GO:0005634 |
| | HD-ZIP | GO:0043565, GO:0000981, GO:0005634 |
| | OR_B | GO:0016020 |
| blue | AGL6a | GO:0045944, GO:0000977, GO:0046983, GO:0003700, GO:0005634 |
| | SEP3d | GO:0045944, GO:0000977, GO:0046983, GO:0003700, GO:0005634 |
| | GRAS | GO:0006355, GO:0000976, GO:0043565, GO:0003700, GO:0005634 |
| | bZIP(TGA1) | GO:0042742, GO:0000976, GO:0043565, GO:0003700, GO:0005634 |

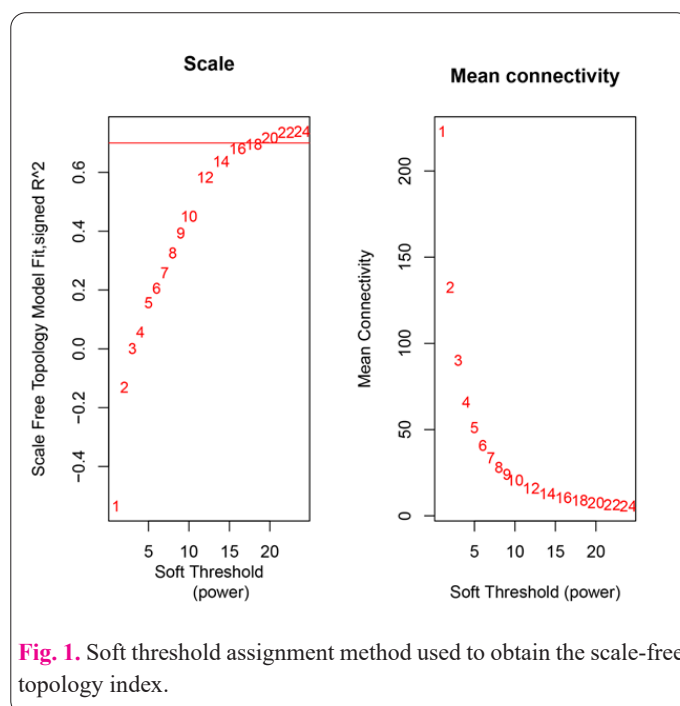


Table S3. Differentially expressed genes assessment in non-preserved module.

| pink module | logFC | logCPM |
|---------------------|--------------|---------------|
| CYP707A1 | -1,90441 | 7,150806 |
| PIA1 | -0,38746 | 6,834097 |
| ALY3 | -0,51592 | 6,274765 |
| NAC90 | -0,7066 | 9,135385 |
| NAC3 | -0,57201 | 4,555735 |
| green module | logFC | logCPM |
| MYB_related | 0,185826 | 8,413457 |
| HB | 0,010408 | 8,870945 |
| Sus3 | -0,23882 | 9,313315 |
| MYB | -0,07167 | 7,508524 |
| MYB31 | -0,12069 | 8,763289 |
| bZIP | -0,2881 | 9,529465 |
| ARF5mp | -0,21189 | 12,35291 |
| HB | -0,06032 | 7,948112 |
| GATA | 0,010281 | 8,158472 |
| SPL | 0,344219 | 10,25071 |
| blue module | logFC | logCPM |
| bZIP | -0,38677 | 10,51778 |
| HD | -0,42778 | 9,132227 |
| C3H | -0,01148 | 8,992042 |
| HD-ZIP | -0,61637 | 9,313907 |
| AGL6a | -0,011 | 8,992041 |
| GRAS | -0,0707 | 9,508756 |
| bZIP | -0,93842 | 9,404795 |
| C3H | -0,20886 | 9,553034 |
| bZIP | -0,85309 | 10,43774 |
| FAR1 | 0,233481 | 7,358004 |
| NAC1 | -0,08253 | 8,439546 |
| bZIP | -0,93318 | 10,74752 |
| bZIP | -1,08584 | 9,44201 |
| TALE | -1,05412 | 9,723713 |
| TALE | -1,02256 | 9,402775 |
| AP2 | -6,19962 | 4,693431 |
| GRAS | -0,15001 | 8,678832 |
| OR-B | -0,38106 | 11,8025 |
| SEP3d | -0,301 | 10,70909 |

Table S4. The list of the functional enrichment analysis for non-preserved modules.

| gene | target_name | evalue | GO_accessions |
|-----------------------------------------------------|------------------|--------|-------------------------------------------------------------------|
| EF535581.1 | LOC_Os03g21030.1 | 5E-75 | GO:0045449 GO:0034645 GO:0003677 |
| MZ855833.1 | LOC_Os01g59660.1 | 2E-53 | GO:0045449 GO:0034645 GO:0003677 |
| OM936973.1 | LOC_Os02g33149.1 | 8E-105 | GO:0031072 GO:0006457 GO:0044260 GO:0051082 |
| TRINITY_DN11674_c0_g1_i2 | LOC_Os05g03740.1 | 5E-33 | GO:0003677 |
| TRINITY_DN13123_c0_g1_i4 | LOC_Os03g57040.2 | 2E-82 | GO:0006468 GO:0016192 GO:0044260 GO:0006886 GO:0006461 GO:0005515 |
| TRINITY_DN15096_c0_g1_i1abscisic | LOC_Os02g47470.1 | 1E-126 | GO:0004672 GO:0030131 GO:0030130 GO:0005524 |
| TRINITY_DN15096_c0_g1_i3abscisic | LOC_Os02g47470.1 | 2E-122 | GO:0004497 GO:0020037 GO:0006118 |
| TRINITY_DN16112_c2_g1_i1 | LOC_Os07g43580.1 | 2E-41 | GO:0045449 GO:0034645 GO:0003677 |
| TRINITY_DN17143_c0_g2_i11 | LOC_Os11g05740.1 | 6E-42 | GO:0006355 GO:0034645 GO:0003677 |
| TRINITY_DN1735_c0_g1_i12 | LOC_Os11g05640.1 | 5E-19 | GO:0043565 GO:0003700 GO:0005634 GO:0006355 GO:0034645 GO:0046983 |
| TRINITY_DN18479_c1_g2_i1 | LOC_Os08g38990.2 | 7E-34 | GO:0003700 GO:0043565 GO:0005634 GO:0045449 GO:0034645 |
| TRINITY_DN18895_c0_g1_i2 | LOC_Os03g01890.2 | 1E-57 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 GO:0043565 |
| TRINITY_DN18895_c1_g1_i2 | LOC_Os03g01890.2 | 5E-29 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 GO:0043565 |
| TRINITY_DN21554_c0_g1_i1 | LOC_Os11g35390.1 | 4E-36 | GO:0045449 GO:0034645 GO:0003677 |
| TRINITY_DN21703_c0_g1_i9 | LOC_Os07g25710.1 | 1E-19 | GO:0045449 GO:0034645 GO:0003677 |
| TRINITY_DN2277_c1_g1_i1 | LOC_Os03g16700.1 | 5E-24 | GO:0045449 GO:0006464 GO:0034645 GO:0003677 |
| TRINITY_DN23227_c1_g2_i11 | LOC_Os04g55560.3 | 2E-37 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 |
| TRINITY_DN23227_c1_g2_i15 | LOC_Os04g55560.3 | 5E-38 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 |
| TRINITY_DN23227_c1_g2_i2 | LOC_Os04g55560.3 | 2E-35 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 |
| TRINITY_DN2824_c1_g1_i1cyclin-dependent-kinase-B2-1 | LOC_Os08g40170.1 | 1E-27 | GO:0004674 GO:0006468 GO:0004713 GO:0005524 GO:0044260 |
| TRINITY_DN3268_c0_g1_i1cyclin-B1-2-like | LOC_Os02g55720.1 | 2E-27 | GO:0003824 GO:0005488 GO:0008152 |
| TRINITY_DN3434_c0_g1_i6PIB | LOC_Os01g66030.1 | 3E-73 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 GO:0043565 |
| TRINITY_DN37471_c0_g1_i1 | LOC_Os09g30400.1 | 2E-14 | GO:0003700 GO:0043565 GO:0005634 GO:0045449 GO:0034645 |
| TRINITY_DN3754_c1_g1_i4 | LOC_Os07g03770.1 | 3E-87 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 GO:0043565 |
| TRINITY_DN3754_c1_g1_i4TSA | LOC_Os07g03770.1 | 3E-87 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 GO:0043565 |
| TRINITY_DN40455_c0_g1_i2 | LOC_Os01g09850.2 | 4E-30 | GO:0008270 GO:0003676 GO:0005622 |
| TRINITY_DN4620_c0_g1_i1 | LOC_Os02g08544.1 | 5E-103 | GO:0003700 GO:0006355 GO:0005634 GO:0034645 GO:0043565 |
| TRINITY_DN6351_c0_g1_i1 | LOC_Os11g05640.1 | 1E-19 | GO:0043565 GO:0003700 GO:0005634 GO:0006355 GO:0034645 GO:0046983 |
| TRINITY_DN7294_c0_g1_i17 | LOC_Os07g09600.1 | 9E-55 | GO:0016021 GO:0016192 |
| TRINITY_DN7514_c0_g1_i1 | LOC_Os08g33150.1 | 1E-28 | GO:0045449 GO:0034645 GO:0003677 |
| TRINITY_DN7419_c0_g2_i1 | LOC_Os06g43800.1 | 2E-137 | GO:0008168 GO:0008152 |
| TRINITY_DN7546_c1_g2_i2 | LOC_Os06g47150.2 | 0 | GO:0009725 GO:0005634 GO:0006355 GO:0034645 GO:0003677 GO:0046983 |
| TRINITY_DN7847_c0_g1_i3 | LOC_Os02g34680.1 | 3E-74 | GO:0008270 GO:0003676 GO:0005622 |
| TRINITY_DN8283_c0_g1_i5 | LOC_Os05g04820.1 | 3E-28 | GO:0045449 GO:0034645 GO:0003677 |