Table S1. Sequencing and Assembly Statistics for the fifteen Transcriptome Data of *L. gibbosa* at Five Times of AR Treatment.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| TimeGroup | sample ID | No. of clean reads (×106)a |  No. of clean bases (×10 9) | GC Content(%) | Q30(%) | No. of mappedreads (×106) | Mappedpercentage (%) |
| 0 h | CK-1 | 22.37 | 6.69 | 59.98% | 92.74% | 39.67 | 88.65% |
| CK-2 | 20.65 | 6.16 | 60.22% | 93.16% | 36.90 | 89.33% |
| CK-3 | 21.78 | 6.51 | 60.29% | 93.12% | 38.97 | 89.48% |
| 3 h | QSH1-0 | 23.03 | 6.89 | 60.12% | 92.70% | 40.55 | 88.02% |
| QSH1-1 | 25.99 | 7.78 | 60.34% | 91.56% | 45.91 | 88.30% |
| QSH1-2 | 23.41 | 7.00 | 60.18% | 92.42% | 41.94 | 89.57% |
| 7 h | QSH2-0 | 22.49 | 6.73 | 60.29% | 92.58% | 39.24 | 87.22% |
| QSH2-1 | 26.44 | 7.91 | 60.27% | 91.32% | 46.75 | 88.40% |
| QSH2-2 | 25.97 | 7.77 | 60.30% | 91.96% | 46.38 | 89.31% |
| 10 h | QSH3-0 | 21.38 | 6.40 | 60.26% | 92.47% | 37.34 | 87.30% |
| QSH3-1 | 25.53 | 7.64 | 60.38% | 92.12% | 45.64 | 89.39% |
| QSH3-2 | 27.96 | 8.37 | 60.34% | 92.58% | 50.48 | 90.28% |
| 14 h | QSH4-0 | 24.40 | 7.30 | 60.22% | 92.35% | 43.77 | 89.68% |
| QSH4-1 | 23.58 | 7.05 | 60.35% | 92.70% | 42.44 | 90.01% |
| QSH4-2 | 30.37 | 9.09 | 60.13% | 93.25% | 55.47 | 91.32% |
|  | Total |  | 109.29 |  |  |  |  |
| a Here, no. is short for number. |

Table S2. The number summarizes all annotated expressed genes and new genes.

|  |  |  |  |
| --- | --- | --- | --- |
| The annotated genes | Total | Database | Over all |
| GO | COG | KEGG | KOG | Pfam | Swiss Prot | eggNOG | NR |
| All genes | Number | 12921 | 5346 | 3648 | 3616 | 4947 | 7074 | 5602 | 8736 | 10551 | 10560 |
| Percentage (%) | 100 | 41.37 | 28.23 | 27.99 | 38.27 | 54.75 | 43.36 | 67.61 | 81.66 | 81.72 |

Table S3. The number of DEGs and the number summary of the annotated DEGs.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Group | DEGs total | DEGs up | DEGs down | Annotation number | Annotation percentage(%) |
| CK vs QSH1 | 620 | 288 | 332 | 578 | 93.23 |
| CK vs QSH2 | 663 | 232 | 431 | 595 | 89.74 |
| CK vs QSH3 | 543 | 182 | 361 | 511 | 94.11 |
| CK vs QSH4 | 792 | 313 | 479 | 749 | 94.57 |
| QSH1vs QSH2 | 120 | 69 | 51 | 103 | 85.83 |
| QSH1vs QSH3 | 107 | 58 | 49 | 94 | 87.85 |
| QSH1vs QSH4 | 278 | 127 | 151 | 262 | 94.24 |
| QSH2vs QSH3 | 62 | 31 | 31 | 57 | 91.94 |
| QSH2vs QSH4 | 109 | 46 | 63 | 97 | 88.99 |
| QSH3vs QSH4 | 44 | 27 | 17 | 38 | 86.36 |
| Total | 1480 | -- | -- | 1370 | 92.57 |

Table S4 GO enrichment DEGs differential grouping

|  |
| --- |
| CK vs QSH1 Up-expression DEGs |
|  | GO Term | -log10(KS) | Gene |
| Biological Process | GO:0000041 transition metal ion transport | 2.66 | gene\_1787,gene\_356 |
| GO:0046274 lignin catabolic process | 2.52 | gene\_3889,gene\_3902 |
| GO:0006605 protein targeting | 2.43 | gene\_1001,gene\_5208,gene\_5690 |
| GO:0006511 ubiquitin-dependent protein catabolic process | 2.40 | gene\_1966,gene\_3334,gene\_3672,gene\_7006,gene\_963 |
| GO:0072594 establishment of protein localization to organelle | 2.28 | gene\_1001,gene\_5208,gene\_5690 |
| GO:0000001 mitochondrion inheritance | 2.14 | gene\_7356 |
| GO:0006696 ergosterol biosynthetic process | 2.14 | gene\_10067 |
| Cellular Component | GO:0005741 mitochondrial outer membrane | 2.60 | gene\_5690 |
| Molecular Function | GO:0020037 heme binding | 3.82 | gene\_11537,gene\_11851,gene\_4,gene\_4488,gene\_5216,gene\_7628,gene\_8611,gene\_9113 |
| GO:0004601 peroxidase activity | 2.51 | gene\_11537,gene\_11851,gene\_4178,gene\_8611 |
| GO:0003723 RNA binding | 2.42 | gene\_1305,gene\_4029,gene\_8065,gene\_8816,gene\_9056,gene\_963 |
| GO:0004298 threonine-type endopeptidase activity | 2.06 | gene\_1966,gene\_3334,gene\_3672,gene\_7006,gene\_963,gene\_965 |
| CK vs QSH1 Down-expression DEGs |
| Biological Process | GO:0006536 glutamate metabolic process | 2.74 | gene\_1202,gene\_7547,gene\_7548,gene\_796 |
| GO:0035966 response to topologically incorrect protein | 2.29 | gene\_2464,gene\_6466 |
| GO:0006605 protein targeting | 2.23 | gene\_5601,gene\_688 |
| GO:0072594 establishment of protein localization to organelle | 2.09 | gene\_5601,gene\_688 |
| GO:0000001 mitochondrion inheritance | 2.05 | gene\_3864 |
| Cellular Component | GO:0005741 mitochondrial outer membrane | 2.06 | gene\_1180 |
| Molecular Function | GO:0020037 heme binding | 3.23 | gene\_22,gene\_4787,gene\_713,gene\_7522,gene\_8119 |
| GO:0004521 endoribonuclease activity | 2.78 | gene\_3969,gene\_3993 |
| GO:0050660 flavin adenine dinucleotide binding | 2.19 | gene\_1807,gene\_22,gene\_2875,gene\_3556,gene\_9842 |
| GO:0016620 oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | 2.17 | gene\_1202,gene\_7919 |
| QSH1 vs QSH4 Up-expression DEGs |
| Biological Process | GO:0006605 protein targeting | 2.38 | gene\_5601 |
| GO:0072594 establishment of protein localization to organelle | 2.24 | gene\_5601 |
| Molecular Function | GO:0016620 oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | 2.49 | gene\_3674,gene\_7919 |
| GO:0020037 heme binding | 2.42 | gene\_5139 |
| GO:0003723 RNA binding | 2.2 | gene\_1305,gene\_802 |
| GO:0004540 ribonuclease activity | 2.05 | gene\_802 |
| QSH1 vs QSH4 Down-expression DEGs |
| Biological Process | GO:0046274 lignin catabolic process | 2.64 | gene\_3889,gene\_3902 |
| GO:0072593 reactive oxygen species metabolic process | 2.40 | gene\_7517 |
| GO:0006696 ergosterol biosynthetic process | 2.18 | gene\_10067,gene\_10936 |
| GO:0010035 response to inorganic substance | 2.12 | gene\_4178,gene\_7517 |
| GO:1901701 cellular response to oxygen-containing compound | 2.02 | gene\_7517 |
| Cellular Component | GO:0005741 mitochondrial outer membrane | 2.70 | gene\_10936,gene\_5809 |
| Molecular Function | GO:0020037 heme binding | 3.37 | gene\_4,gene\_4487,gene\_5216,gene\_5570 |
| GO:0004601 peroxidase activity | 2.21 | gene\_274,gene\_4178 |
| Note: KS: the significant statistics of the enrichment of the GO category, the smaller the KS value is the larger the log10(KS) is, indicating the more significant the enrichment. |

Table S5 DEGs from four important GO terms.

|  |  |  |
| --- | --- | --- |
| GO term | Gene function | Gene No. |
| Heme binding (GO:0020037) | 4-hydroxysphinganine ceramide fatty acyl 2-hydroxylase | gene\_5570 |
| Versatile peroxidase | gene\_11851, \_11537, \_713 |
| MnP | gene\_8611 |
| Acyl-CoA dehydrogenase | gene\_22, \_4 |
| Cytochrome P450 | gene\_7628,\_9113,\_4488,\_5216,\_11472,\_4487, gene\_5139,\_7522,\_10935,\_6568 |
| Fumarate reductase | gene\_8119 |
| L-lactate dehydrogenase (cytochrome) | gene\_4787 |
| nitric oxide dioxygenase | gene\_10651 |
| Lignin catabolic (GO:0046274) | Laccase | gene\_3889,\_3902,\_1741 |
| oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as the acceptor (GO:0046274) | 1-pyrroline-5-carboxylate dehydrogenase | gene\_1202 |
| aldehyde dehydrogenase (NAD+) | gene\_3674 |
| Peroxidase activity (GO:0004601) | Versatile peroxidase | gene\_11851,\_11537, \_713 |
| MnP | gene\_8611 |