**Table S1.** DEGs with conserved domains in overlapping sets of P_S_U and SAH_D.

| Transcript/ Gene Name | Conserved Domains |
|---|---|
| MSTRG.1324.1 | TRX_family/ Thioredoxin_like super family/ RPA_2b-aaRSs_OBF_like super family |
| g5534 | Aldo-keto reductase (AKR) superfamily |
| g11932 | Major Facilitator Superfamily |
| g6062 | fungal_TF_MHR/ PHA02682 super family/ fungal_TF_MHR |
| g1172 | RT_like super family/ EEP super family |
| g10415 | Epoxide hydrolase N-terminus |
| g13879 | Methyltransferase/ AdoMet_MTases super family |
| g14240 | Ctr copper transporter family |
| g17528 | Aldo-keto reductase (AKR) superfamily |
| g18490 | Alpha-crystallin domain (ACD) of alpha-crystallin-type small(s) heat shock proteins |
| g6371 | CTH/ methionine gamma-lyase/ Cys/Met metabolism PLP-dependent enzyme |

**Table S2.** DEGs with conserved domains in overlapping sets of P_S_D and SAH_U.

| Transcript/ Gene Name | Conserved Domains | Transcript/ Gene Name | Conserved Domains |
|---|---|---|---|
| g6994 | Rossmann-fold NAD(P)(+)-binding proteins | g2292 | Thioredoxin-like domai/Glucosyltransferase |
| g18588 | Rossmann-fold NAD(P)(+)-binding proteins/ choline dehydrogenase | g10210 | maltase-glucoamylase |
| g18589 | Putative thiazole synthesis | g10234 | Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB |
| g1624 | Ankyrin repeat [Signal transduction mechanisms] | g10647 | FAD dependent oxidoreductase |
| g7989 | glutamyl-tRNA synthetase | g2774 | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
| g19472 | DUF4470 super family | g11689 | YEATS domain family, chromatin reader proteins |
| g8168 | N-terminal domain of mixed lineage kinase domain-like protein (MLKL) and similar proteins | g13386 | P-loop containing Nucleoside Triphosphate Hydrolases |
| g278 | Glyco_18 domain | g3789 | DNA mismatch repair ATPase MutS |
| g8878 | Putative threonine/serine exporter | g13987 | Protein Kinases, catalytic domain |
| g8818 | Catalase-like heme-binding proteins and protein domains | g5642 | alpha/beta hydrolases |
| g8821 | ALG3 protein | g14566 | GTP cyclohydrolase II (RibA) |
| g8836 | NADPH-dependent FMN reductase | g4685 | Heterokaryon incompatibility protein Het-C |
| g8860 | Tetraspanin family | g15519 | Rossmann-fold NAD(P)(+)-binding proteins |
| g9534 | cyclin box found in Saccharomyces cerevisiae G1/S-specific cyclin PCL1, PCL2 and similar proteins | g4827 | G-protein alpha subuni |
| g16617 | Cytochrome b5-like Heme/Steroid binding domain | g17824 | FAD binding domain |

**Table S3.** The primers of DEGs for qRT-PCR.

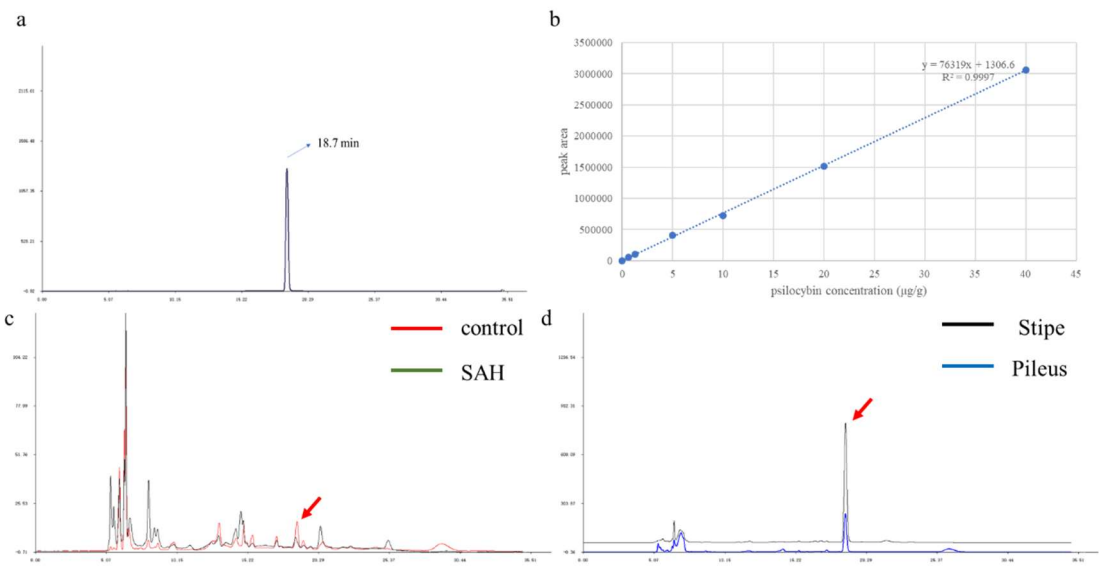| Name | Forward Primer (5' to 3') | Reverse Primer (5' to 3') |
|---|---|---|
| *gapdh* | GGCGGAGATAATGACCTTCTT | CCACTGGTGCTGAGTACATT |
| *ras* | GTATCCAGGACATCGAGAAGAG | GGGAAGTCTGCTCTGACTATT |
| *gdcth1* | GAAACTGGAGCTGTGATTCCT | TACTCAAAGCCCTTGTGGATG |
| *gdcth2* | AGAACTTCAAGCCGTGGTAG | GTGTCATCGTTGACTCTGGAA |
| *gdcth3* | GACGTACAAGCAGTCAGGAAT | CGCCTCAAGATAGGCAAGAG |
| *gdmet17* | GGGTGTTTCTCGAGGTATTGAG | GCTTCTGCAAGGACTTGAAAC |
| *gdsds* | CCAATCTACGCTGGACGTTT | GATCTTGGGCAACCAACTCT |



**Figure S1.** UPLC profiles of reference substances (**a**), linear equation of psilocybin standard substances (**b**), UPLC profiles of samples treated by SAH (**c**), UPLC profiles of samples of stipe and pileus (**d**).
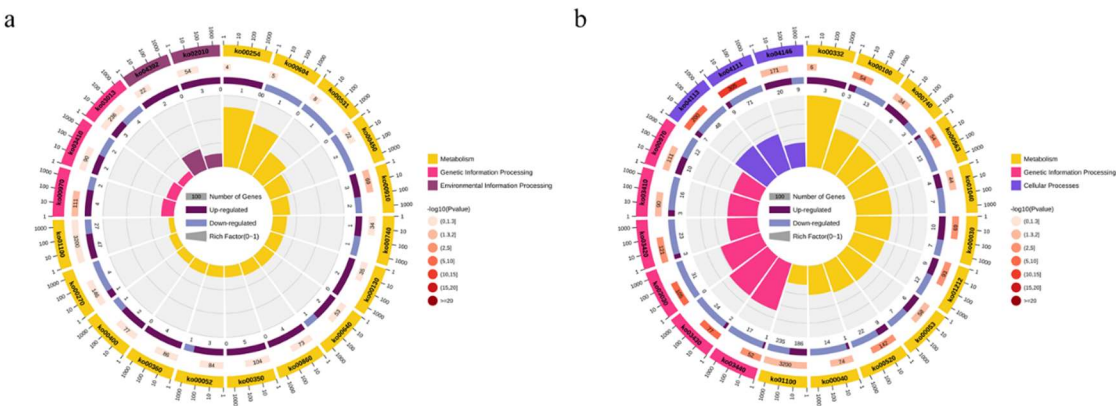


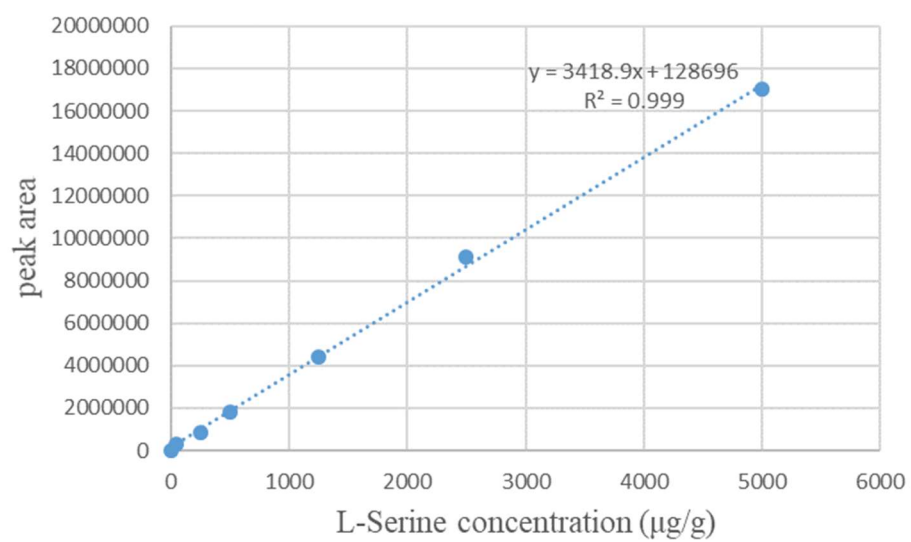**Figure S2.** KEGG enrichment analysis of DEGs under different treatments (**a**) and parts (**b**) of *G. dilepis*.

**Figure S3.** The linear equation of L-serine standard substances.