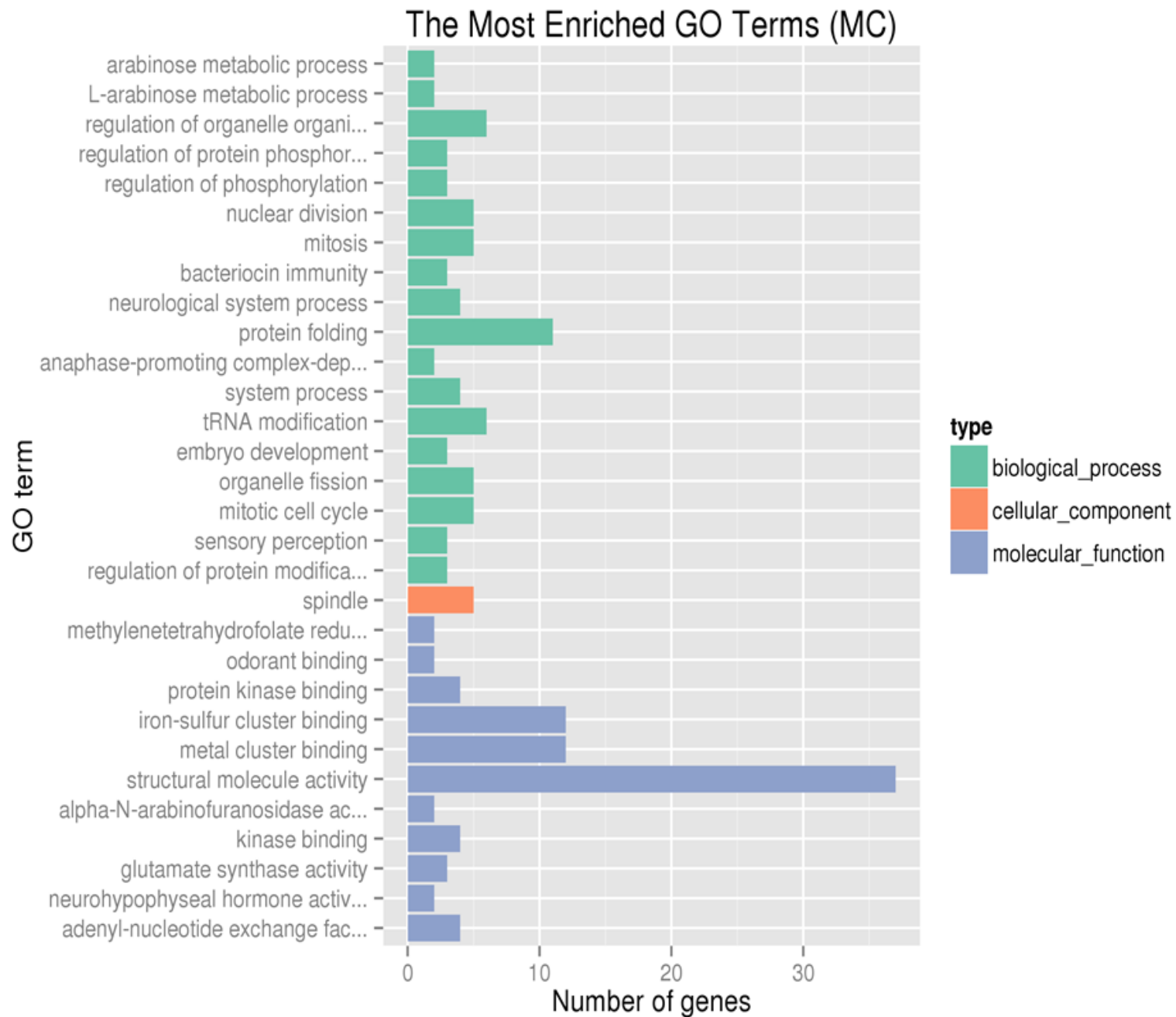
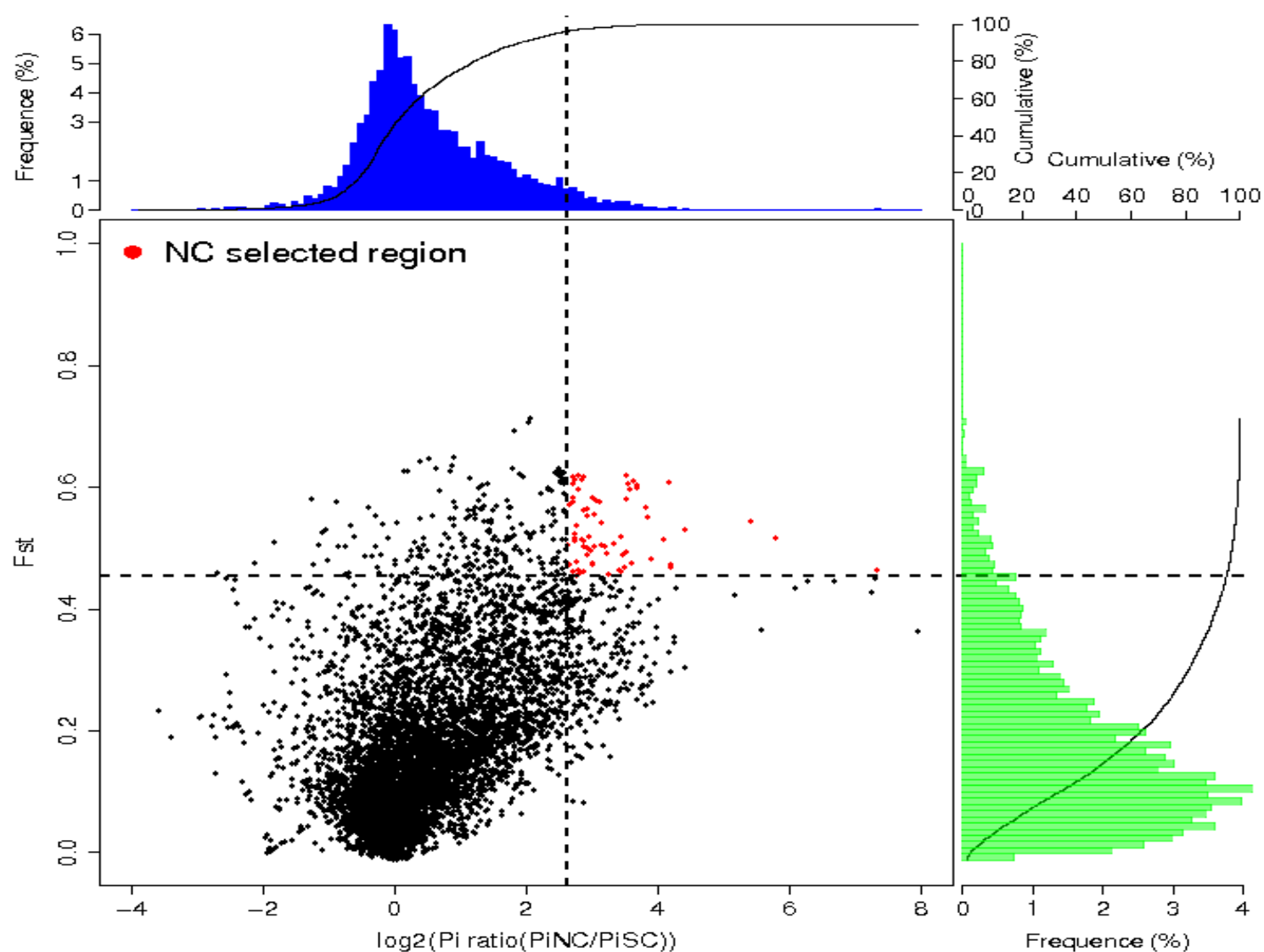


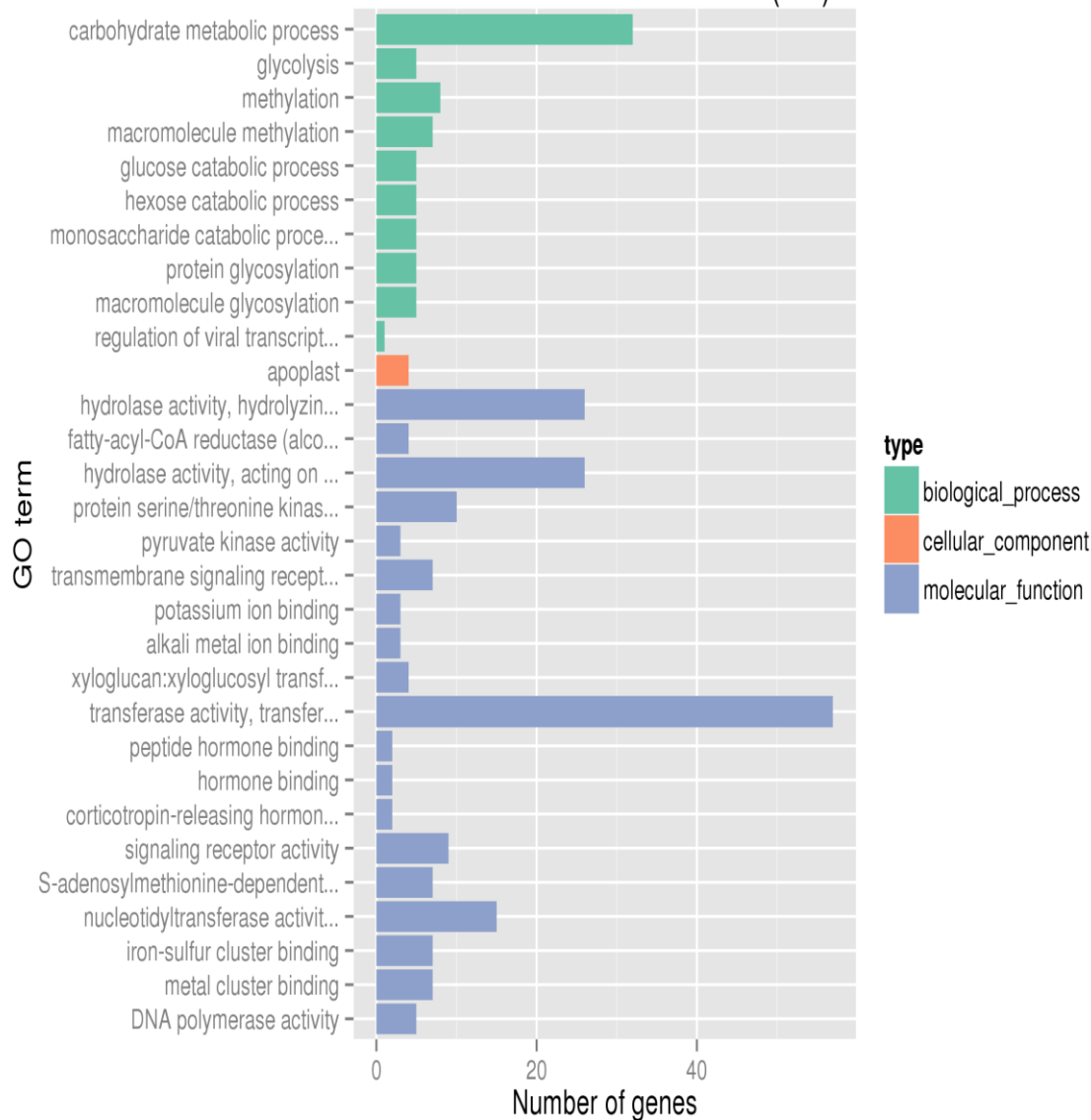
**Figure S1.** Population structure of 410 sesame accessions. (a) – (C) K = 2, 4, and 5, respectively. The y-axis quantifies subgroups membership and the x-axis lists the different accessions. Each color represents one ancestral population. Each accession is represented by a bar, and the length of each colored segment in the bar represents the proportion contributed by that ancestral population.



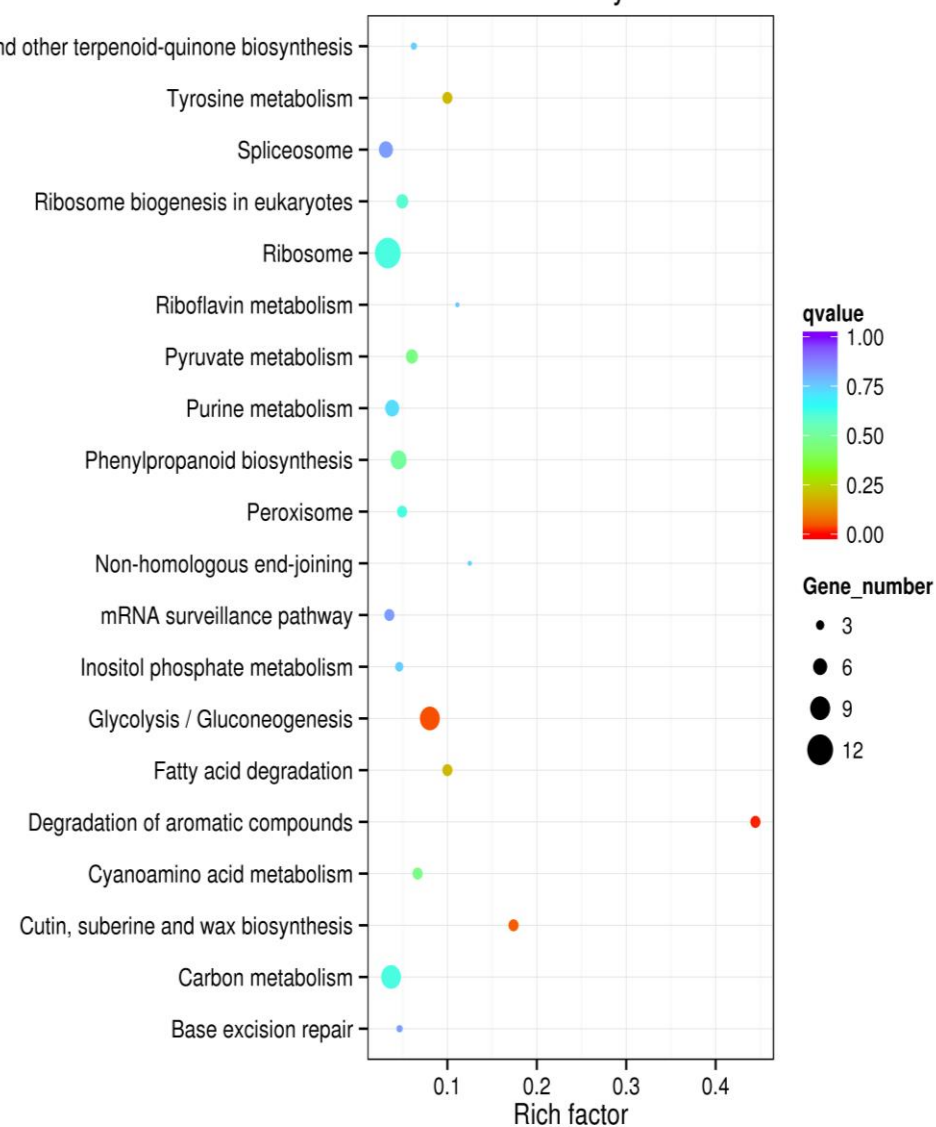
**Figure S2.** GO (Gene Ontology) analysis results of positively selected genes in MC subpopulation.

**a****b**

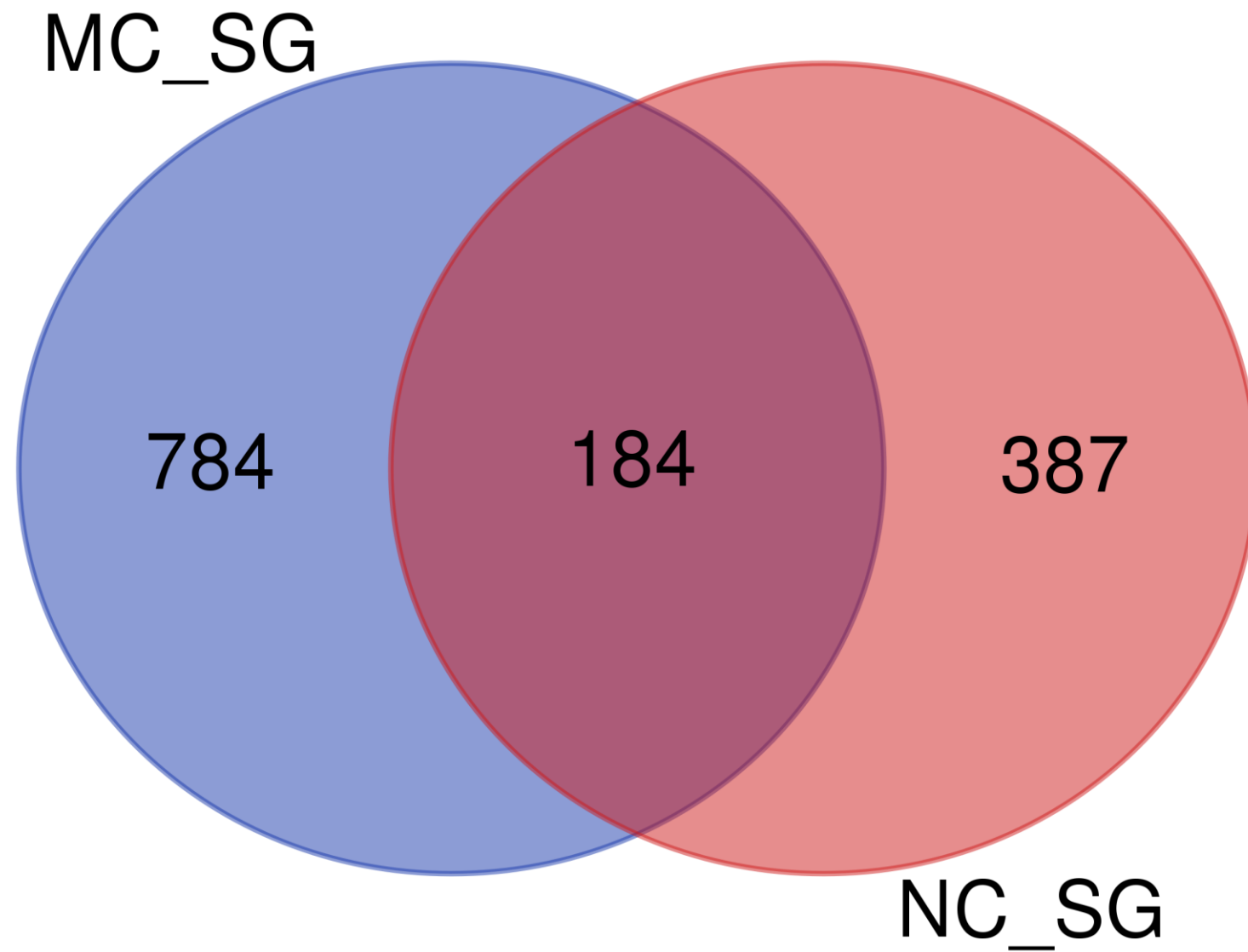
### The Most Enriched GO Terms (NC)

**c**

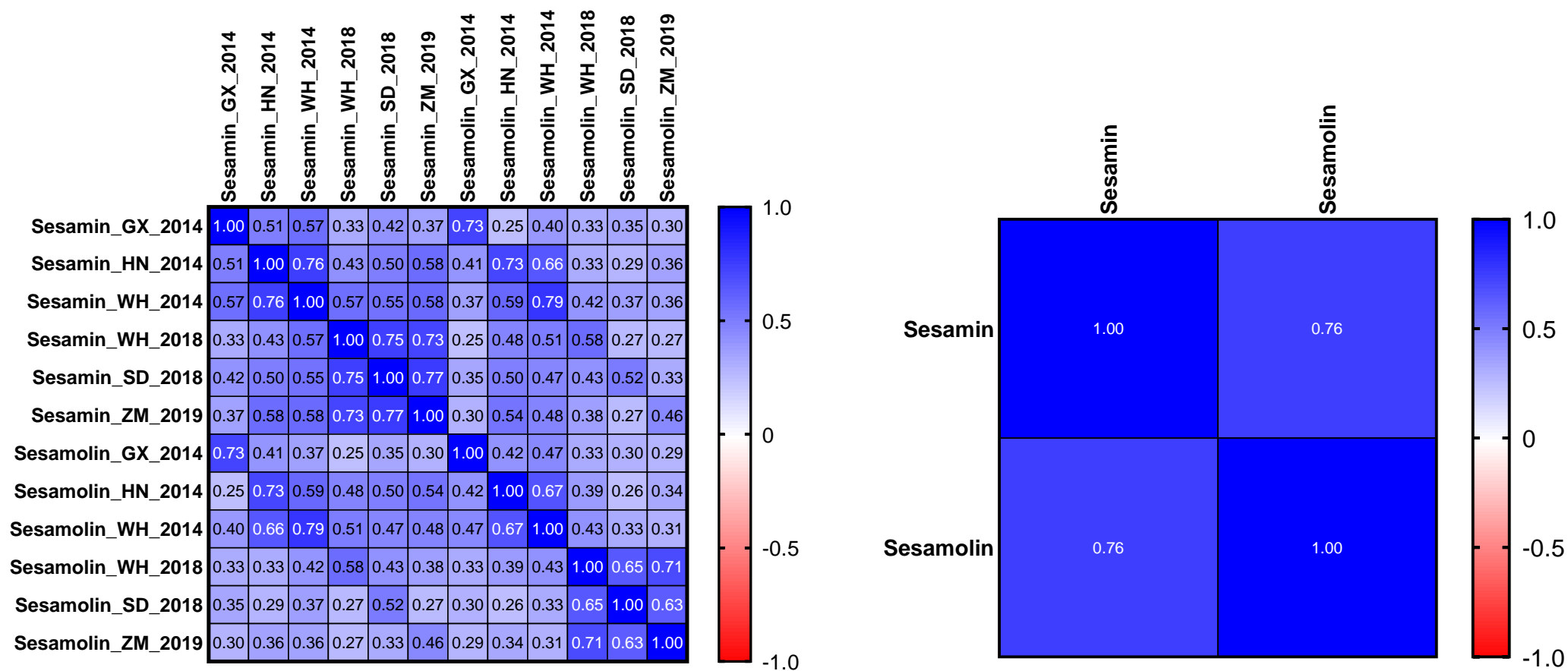
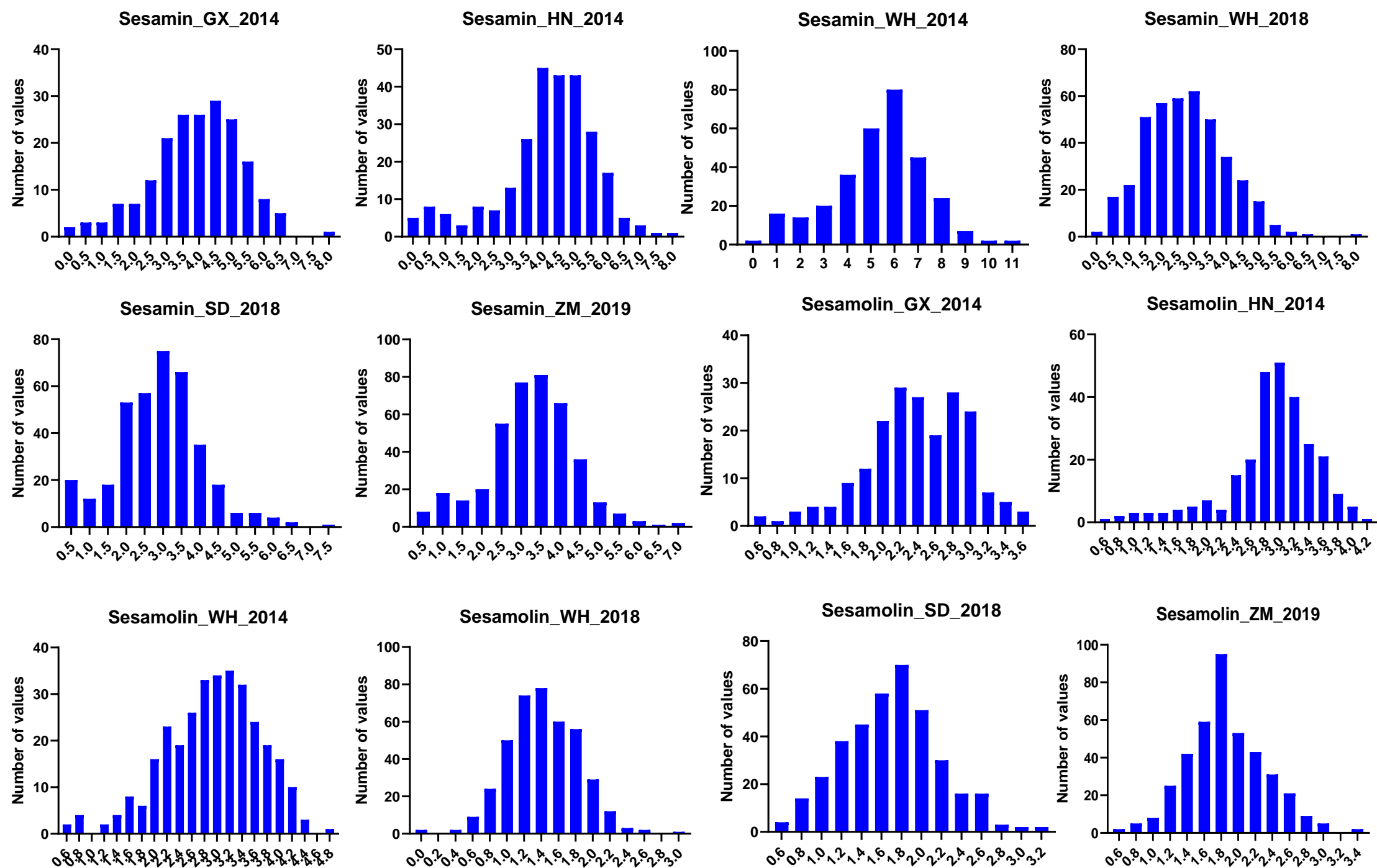
### Statistics of Pathway Enrichment



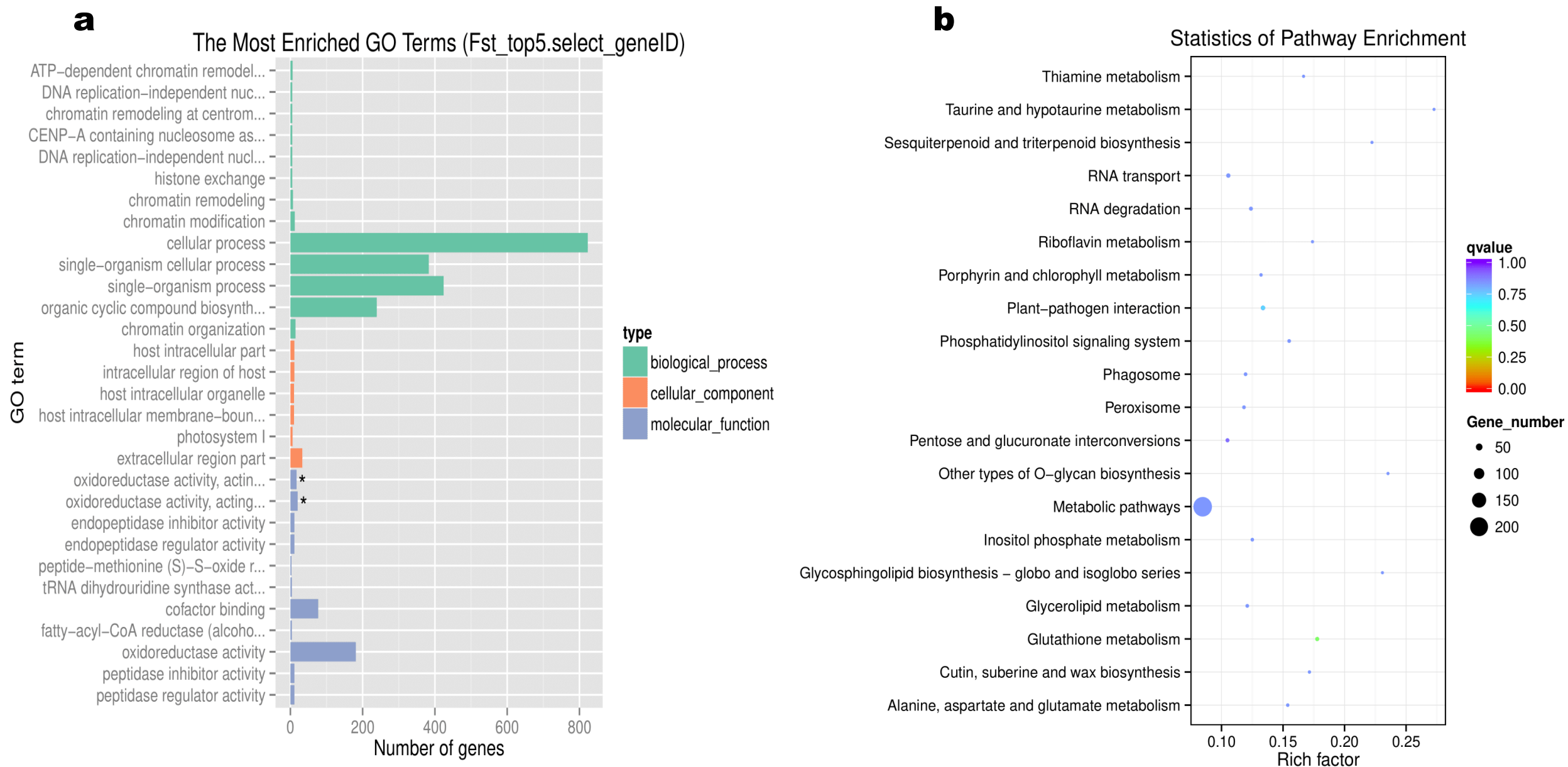
**Figure S3.** Selective sweeps and functional characterization of positively selected genes in NC subpopulation. (a) Selection signatures in NC. Each red dot indicates a positive selective genomic regions. (b) GO enrichment analysis of selected genes. (c) KEGG analysis and enrichment results. The color ruler and p-values are shown on the



**Figure S4.** Venn diagram showing the common genes that were positively selected in MC and NC subpopulations.

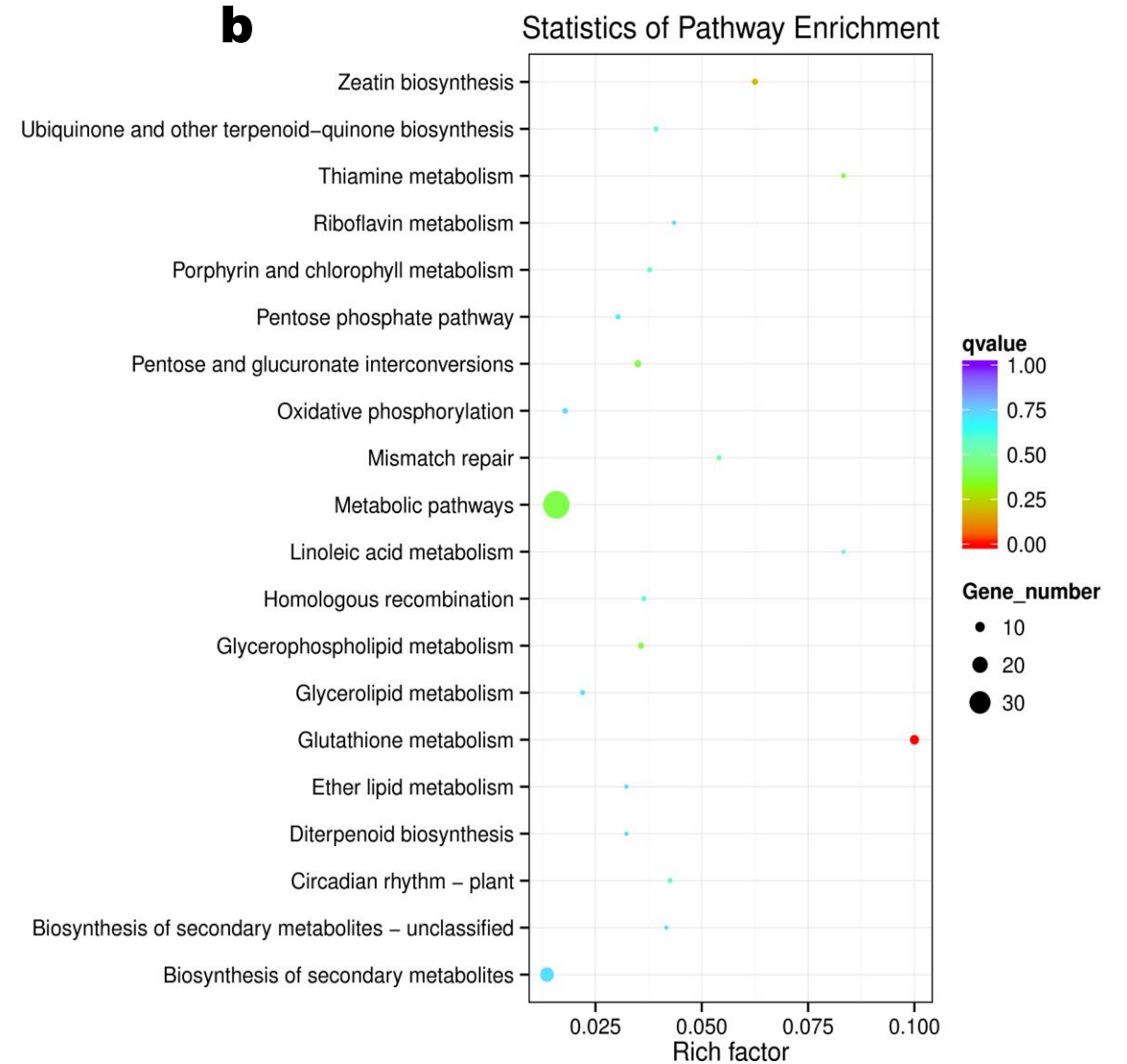
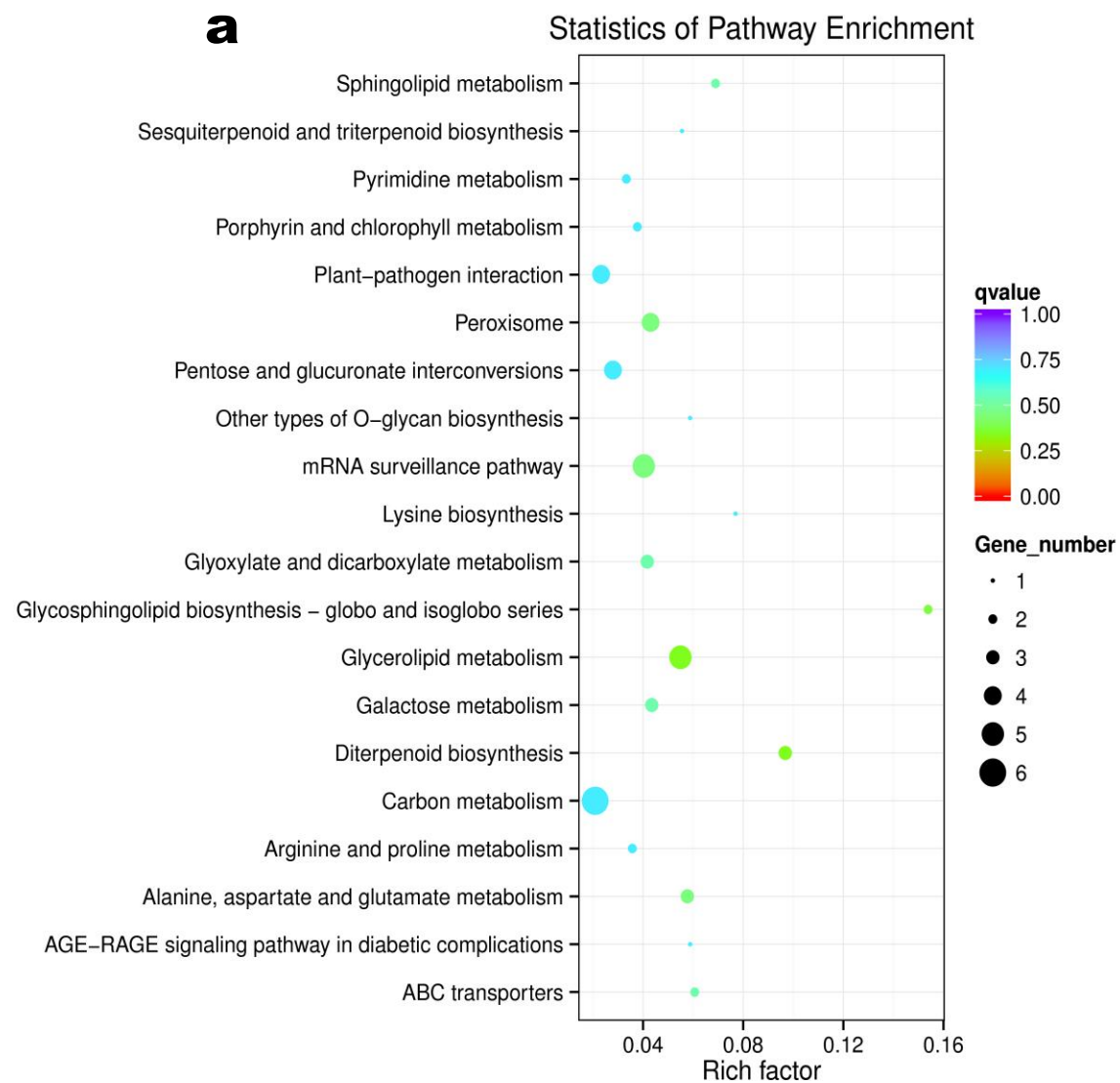


**Figure S5.** Frequency distribution and correlation between sesamin and sesamolin in six different environments

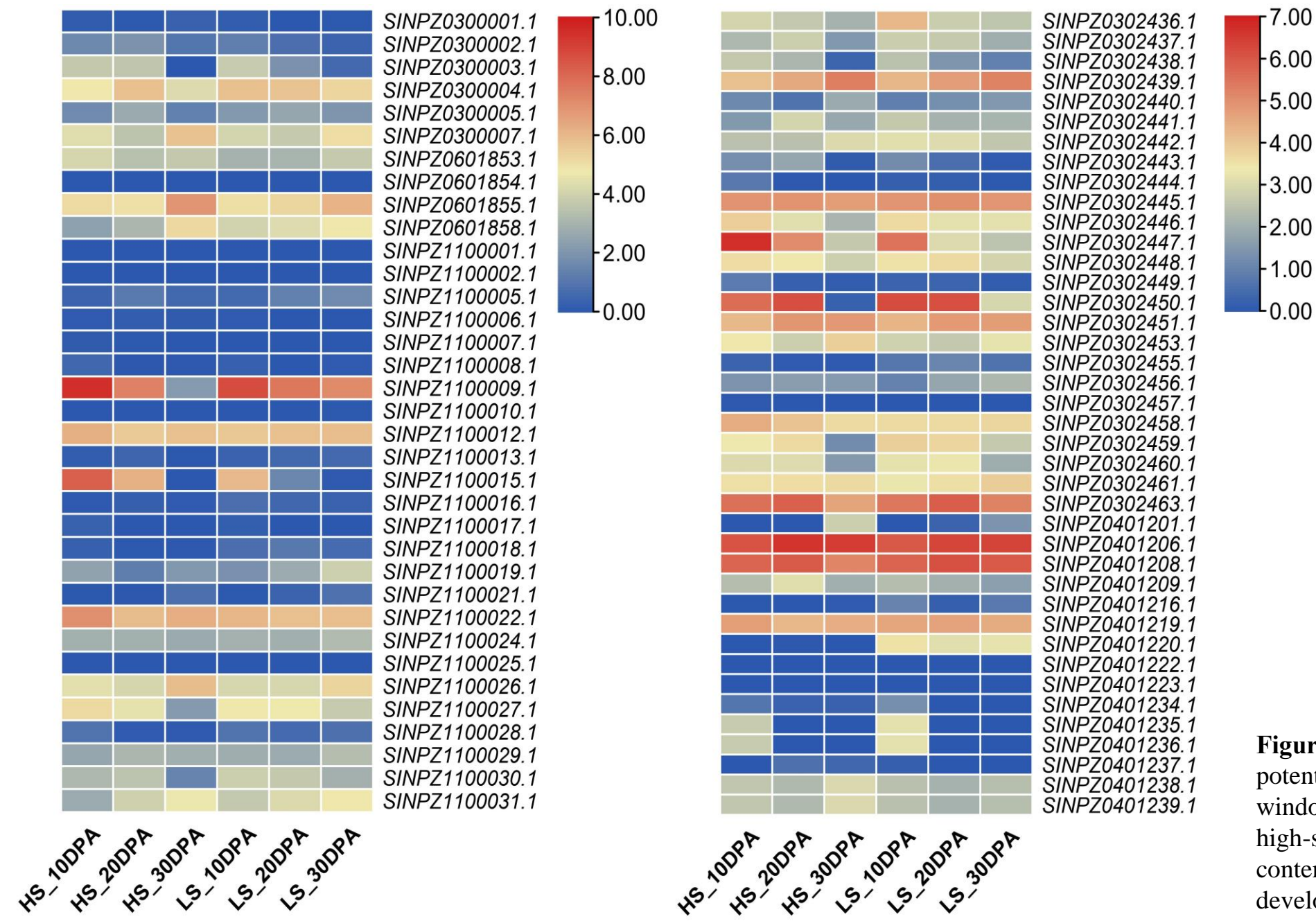


**Figure S6.** GO terms enrichment (a) and KEGG enrichments results (b) of genes identified at the significant divergent genomic regions between in high-sesamin and low-sesamin content sesame accessions.



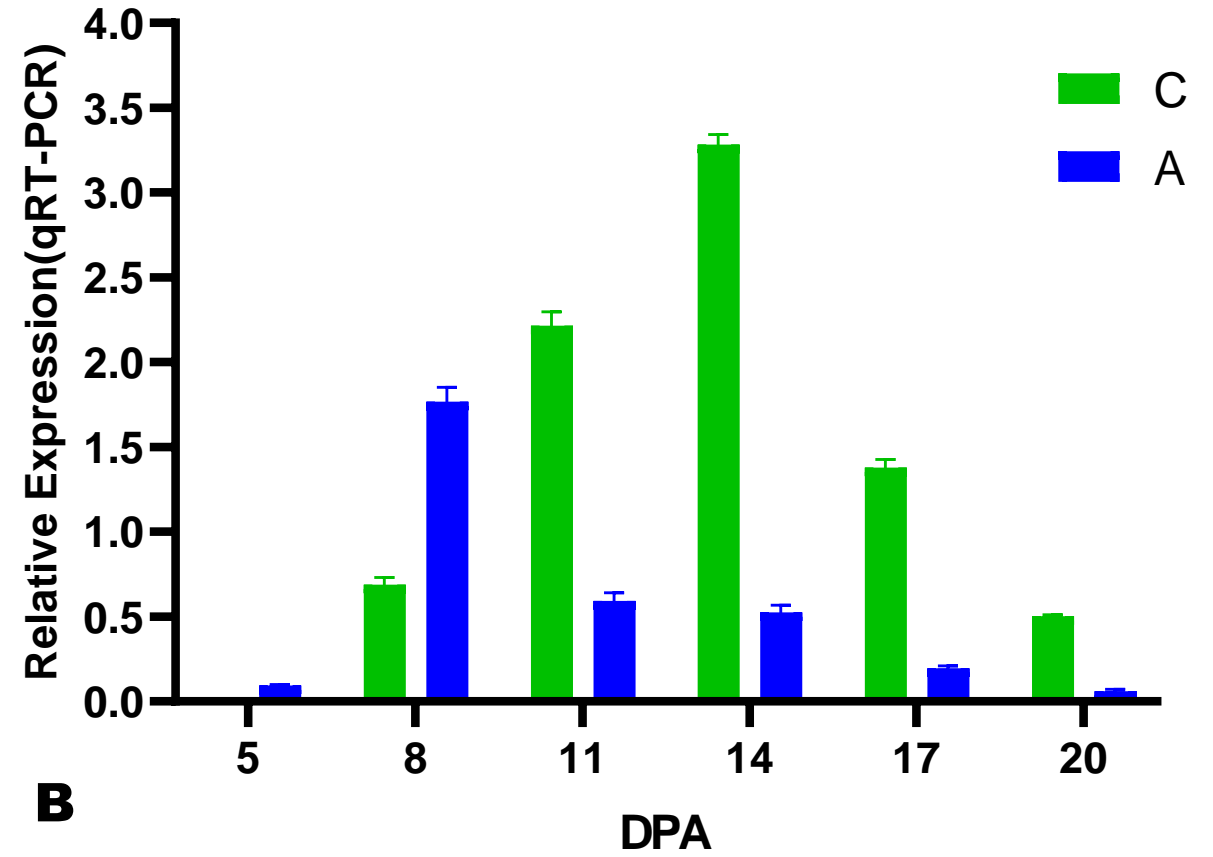
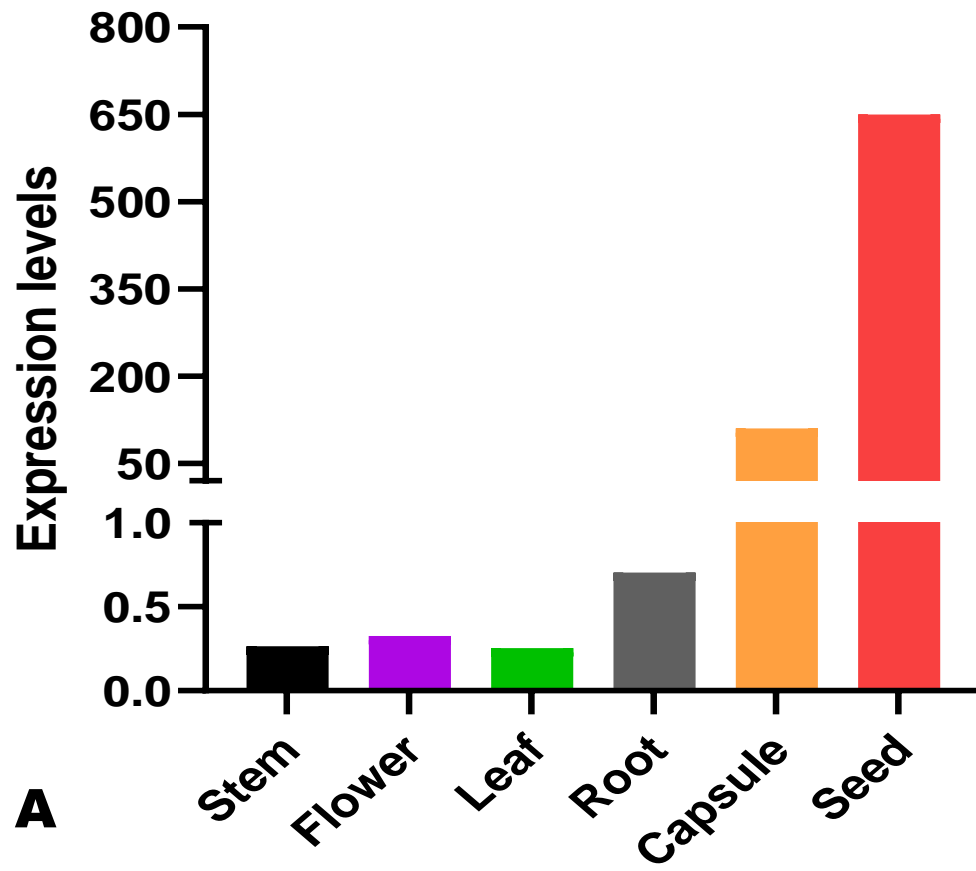


**Figure S7.** KEGG enrichments results of the candidate selected genes in: (a) high-sesamin content sesame accessions and (b) ) low-sesamin content sesame accessions.

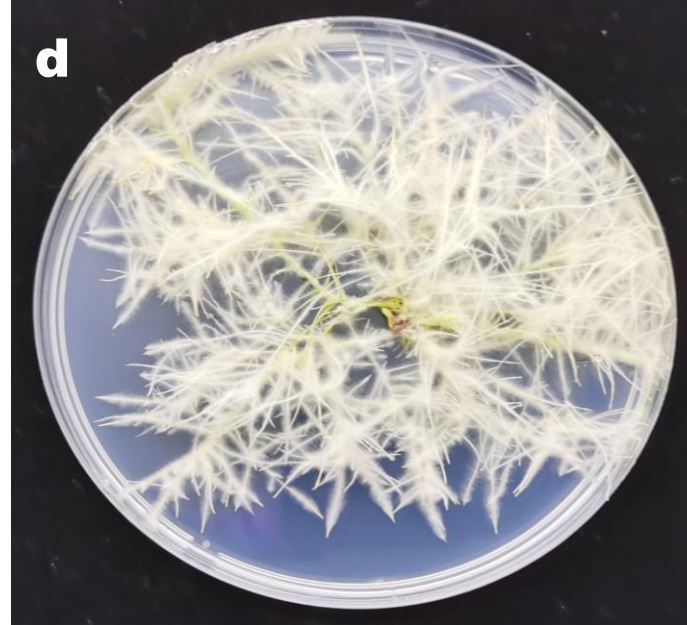
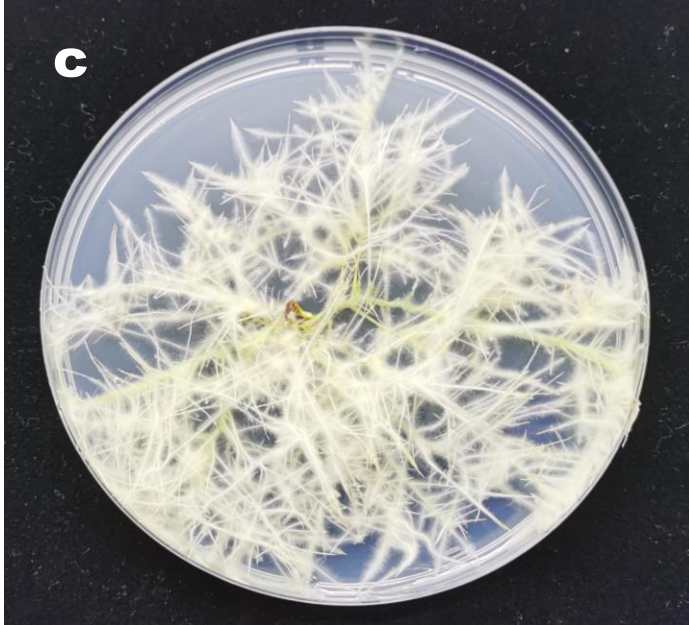
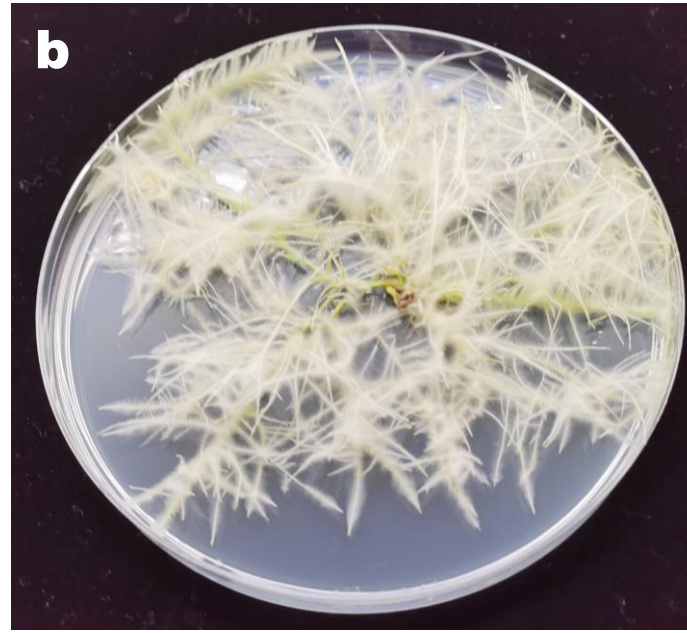
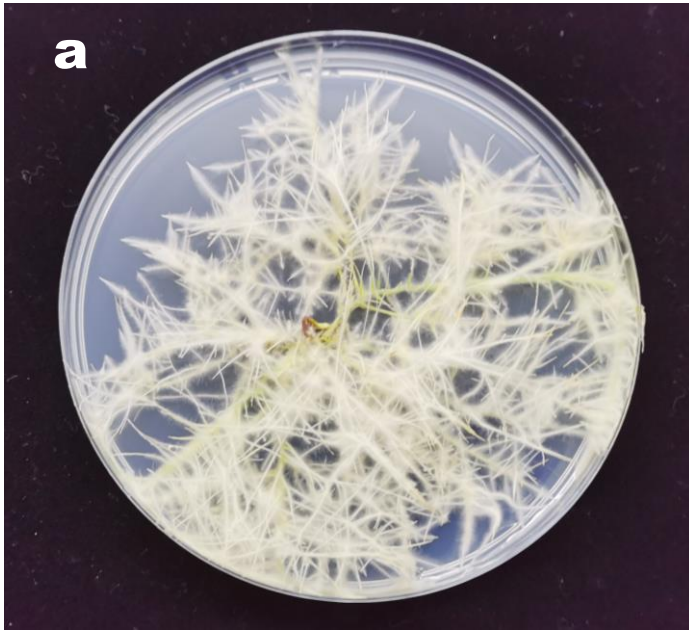


**Figure S8.** Relative expression of the potential candidate genes detected in the LD windows of non-synonymous SNP loci in a high-sesamin (HS) and low-sesamin (LS) content sesame accession at different seed developmental stages.





**Figure S9.** Expression level of *SiNST1* in different organs of sesame (A). Relative expression of *SiNST1* in sesame accessions with “A” and “C” alleles, respectively, at different seed developmental stages (B).



**Figure S10:** Representative photos of sesame hairy roots. (a) and (b), Control; (c) and (d) SiNST1-overexpressing lines (OE).