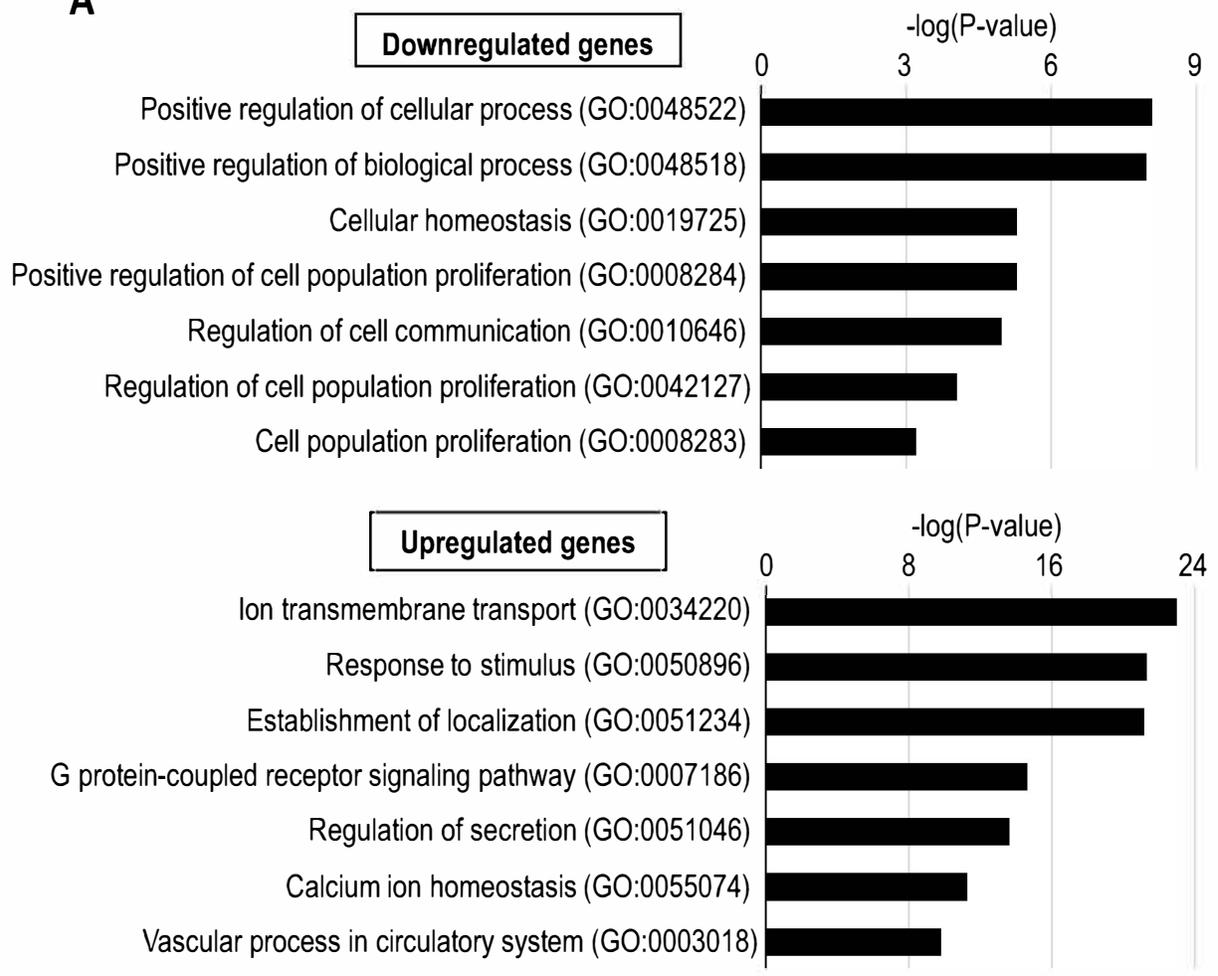
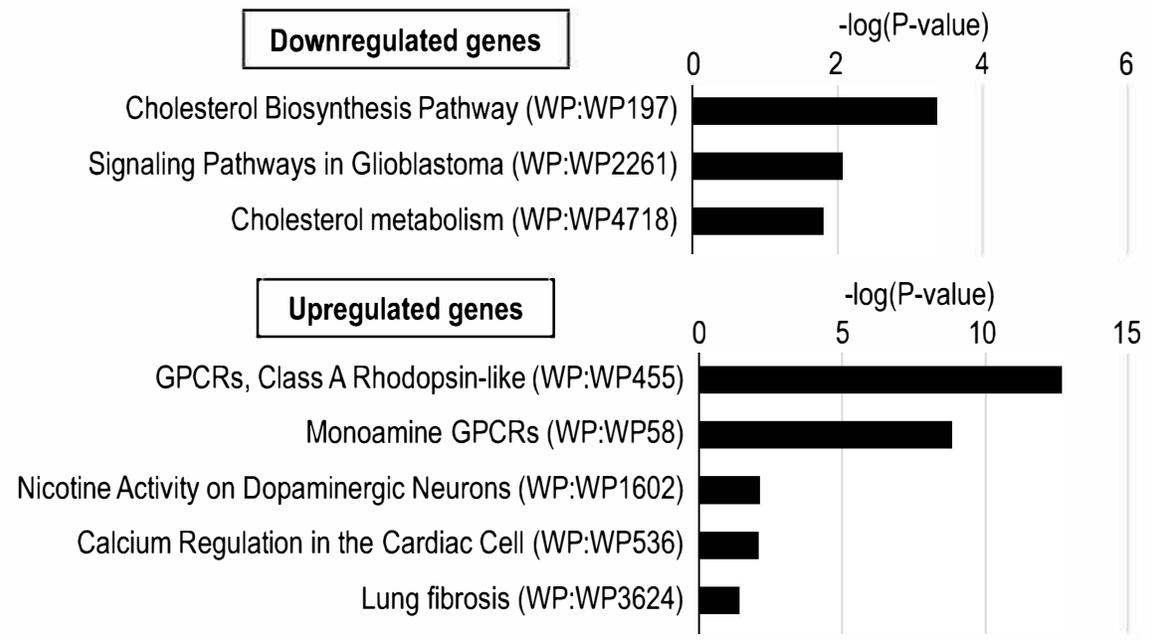


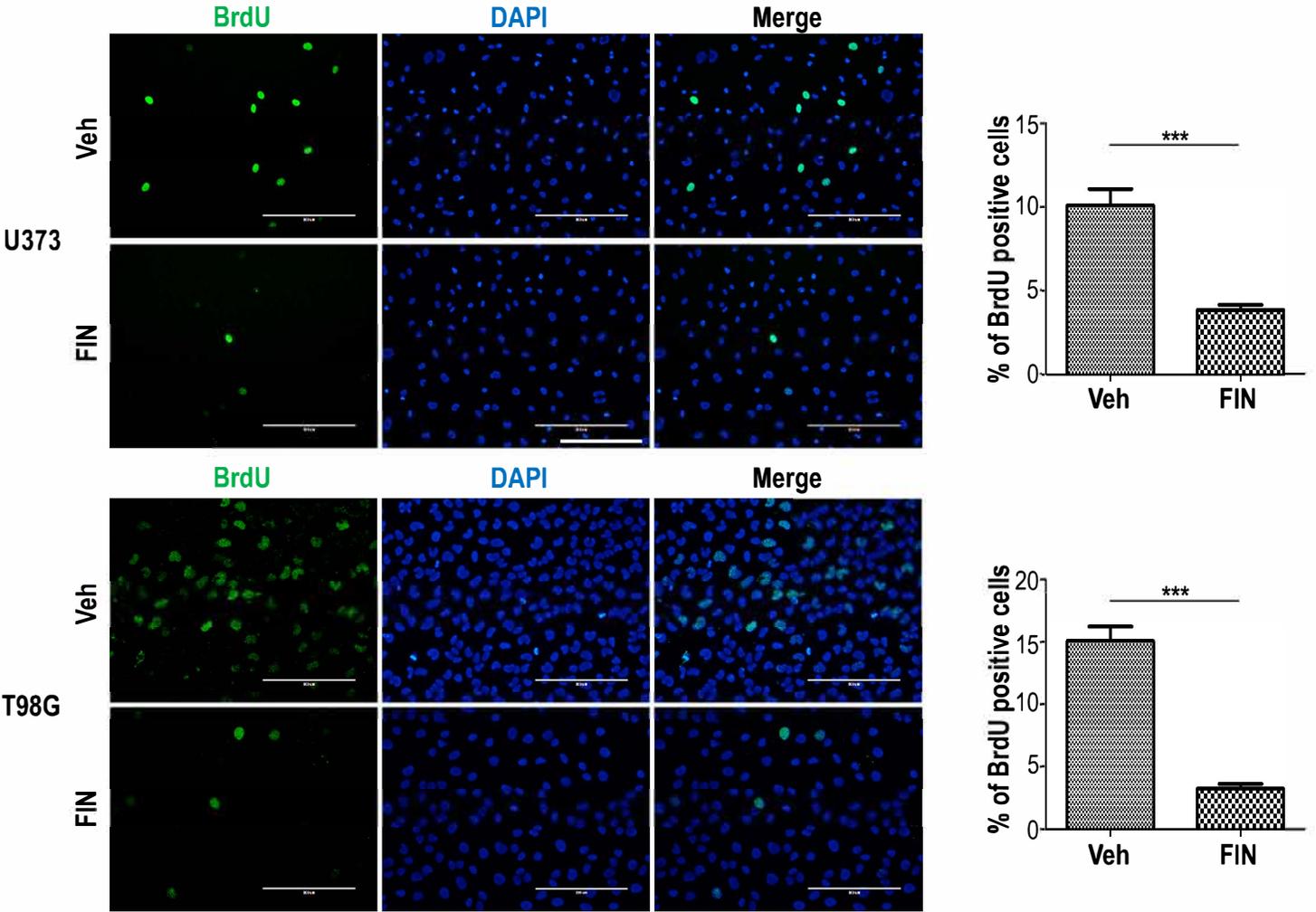
**A**



**B**



**Supplementary Figure S1. Transcriptome analysis of finasteride-treated glioblastoma cells.** (A and B) mRNA profiles of corn oil or finasteride administrated rat livers were extracted and analyzed from NCBI GEO profile database (GEO accession: GSE8251). Determination of upregulated genes was based on fold-change of the expression level > 2 and a *p*-value < 0.05. Determination of downregulated genes was based on fold-change of the expression level < 0.5 and a *p*-value < 0.05. GO enrichment analysis for the biological process (A) and biological pathway analysis (B) of up- or down-regulated genes post finasteride treatment were conducted by utilizing g:Profiler.



**Supplementary Figure S2. The effect of finasteride on cell cycle progression.** BrdU staining was performed in vehicle- or FIN-treated cells. Green signals indicated BrdU-positive cells. Nuclear DAPI (4',6-diamidino-2-phenylindole) staining is shown in blue (left). The quantification of BrdU-positive cell proportions in vehicle- or FIN-treated cells (right).