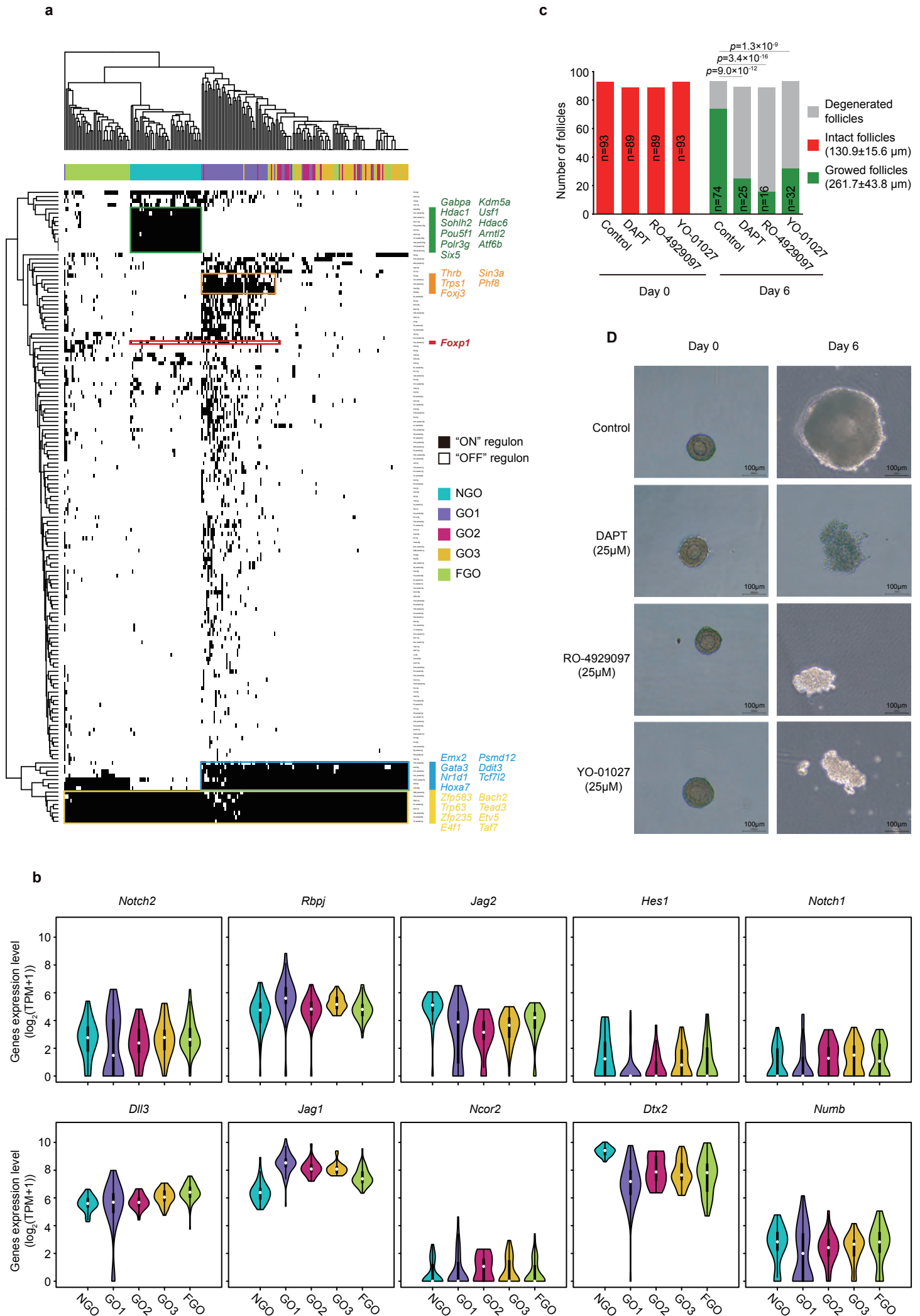




Supplementary information, Fig. S11 Featured gene expression and chromatin accessibility involved in oocyte growth. **(a)** A SCENIC (Aibar *et al. Nature Methods*. 2017) heatmap showed the clustering of growing oocytes and potentially active transcription factors during oocyte maturation. scRNA-seq data was used here. **(b)** Expression levels of representative Notch signalling pathway genes in single oocytes. **(c)** Statistics of *in vitro* cultured mouse follicles either under normal condition or in the presence of notch signaling inhibitors (DAPT, RO-4929097, YO-01027). For each replicate, experiments for control and three of inhibitors groups were conducted in parallel. A total 364 of follicles from 4 replicated experiments were analysed, and the number of follicles for each group was: n = 93 for control group, n = 89 for DAPT group, n = 89 for RO-4929097 group, n = 93 for YO-01027 group. **(d)** Representative images of *in vitro* cultured mouse follicles. Scale bar indicates 100 μ m. P-values were defined by the chi square test.