



**Figure S3. Gene Ontology (GO) analysis of differentially expressed genes in stepwise tumorigenesis system. a,** Functional clustering by biological path using DAVID for each set of co-regulated genes (paths i to vii). **b,** Disease-related GO (DAVID) of differentially expressed genes. The x-axis (p-value) is given as  $-\log(p\text{-value})$ . Illustrated GO terms have  $p\text{-value} < 0,05$ .