Supplementary Fig. 1-6

for

Global characterization of extrachromosomal circular DNAs in advanced high grade serous ovarian cancer

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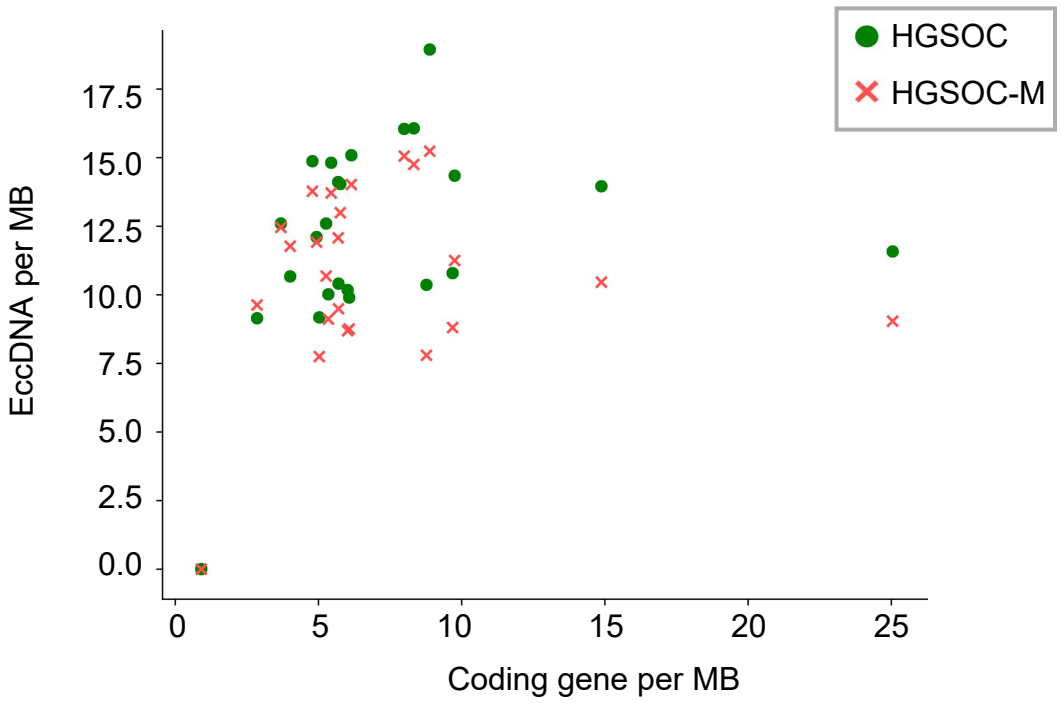
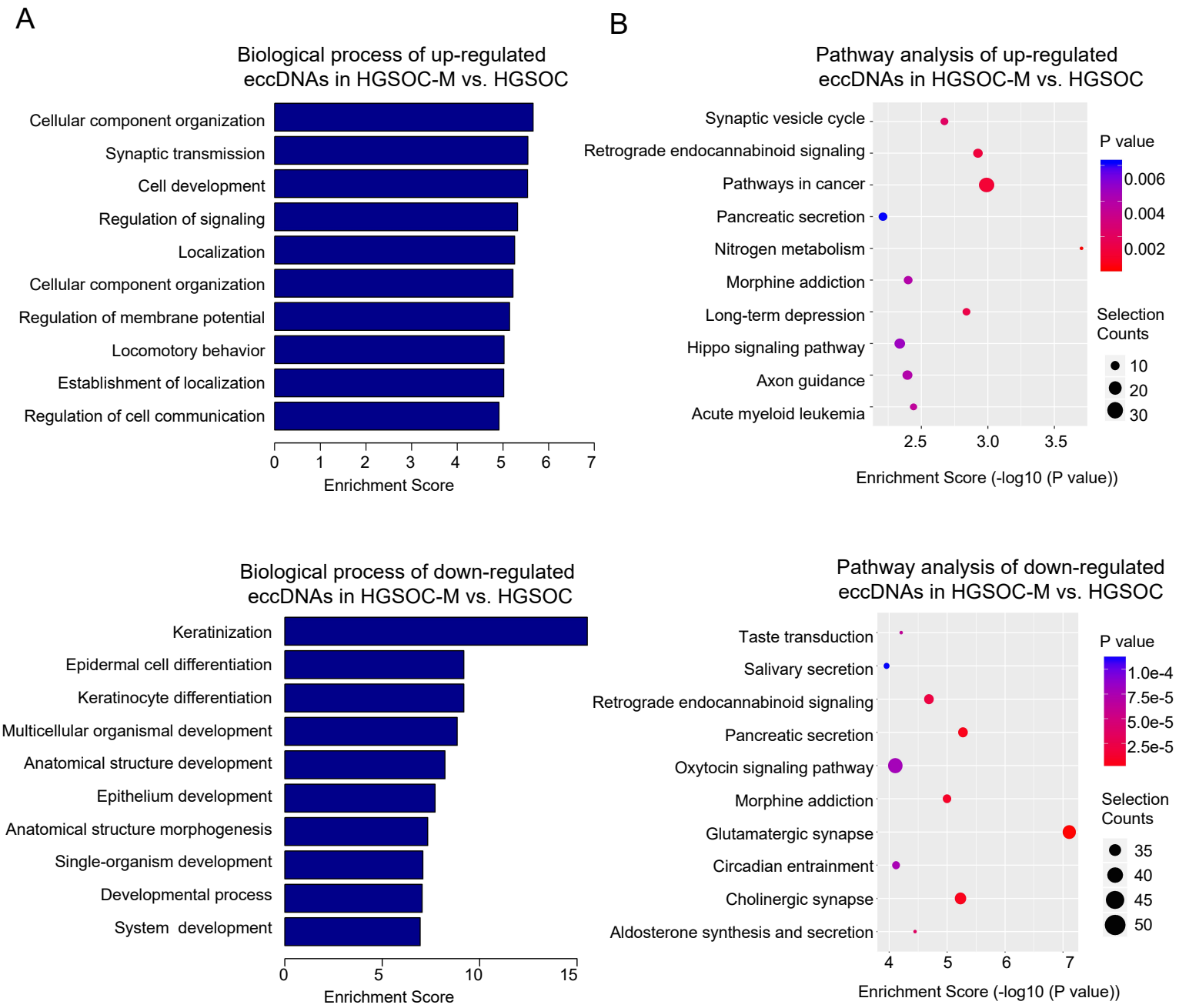
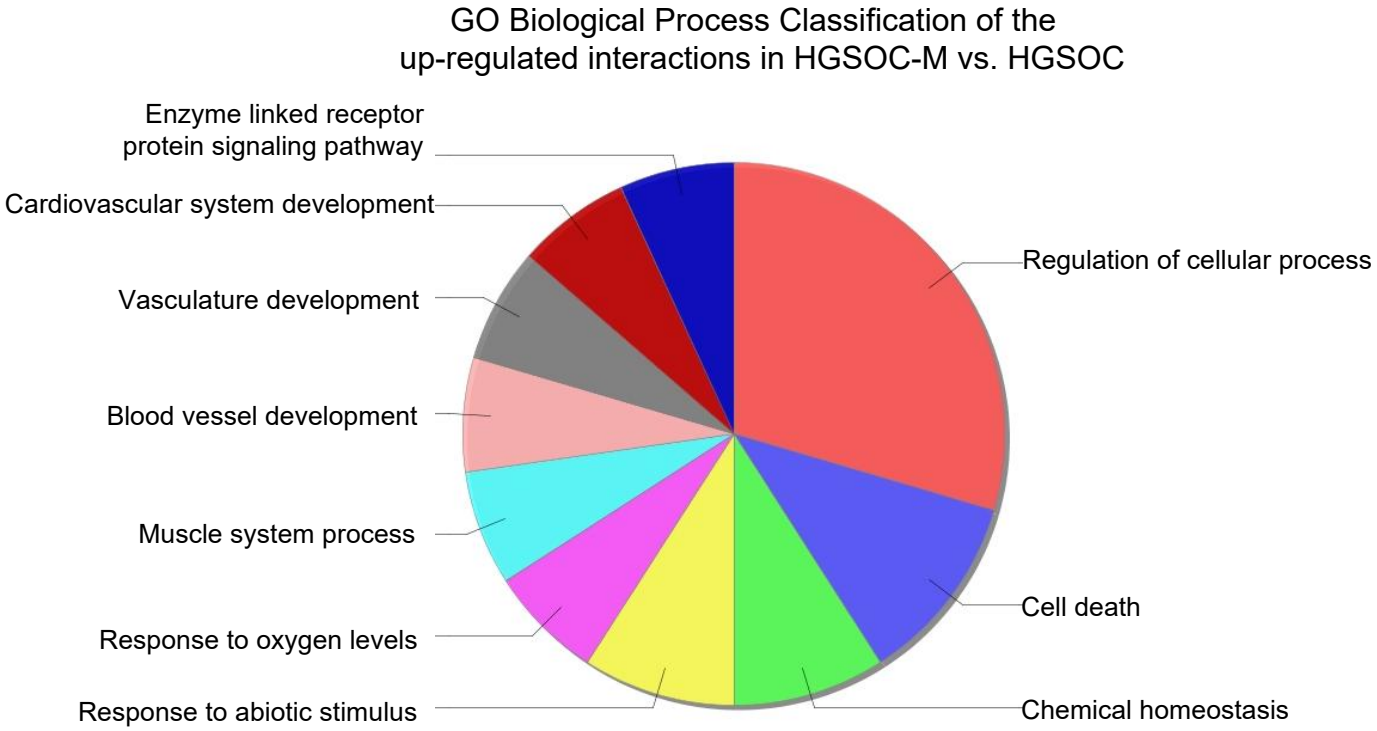
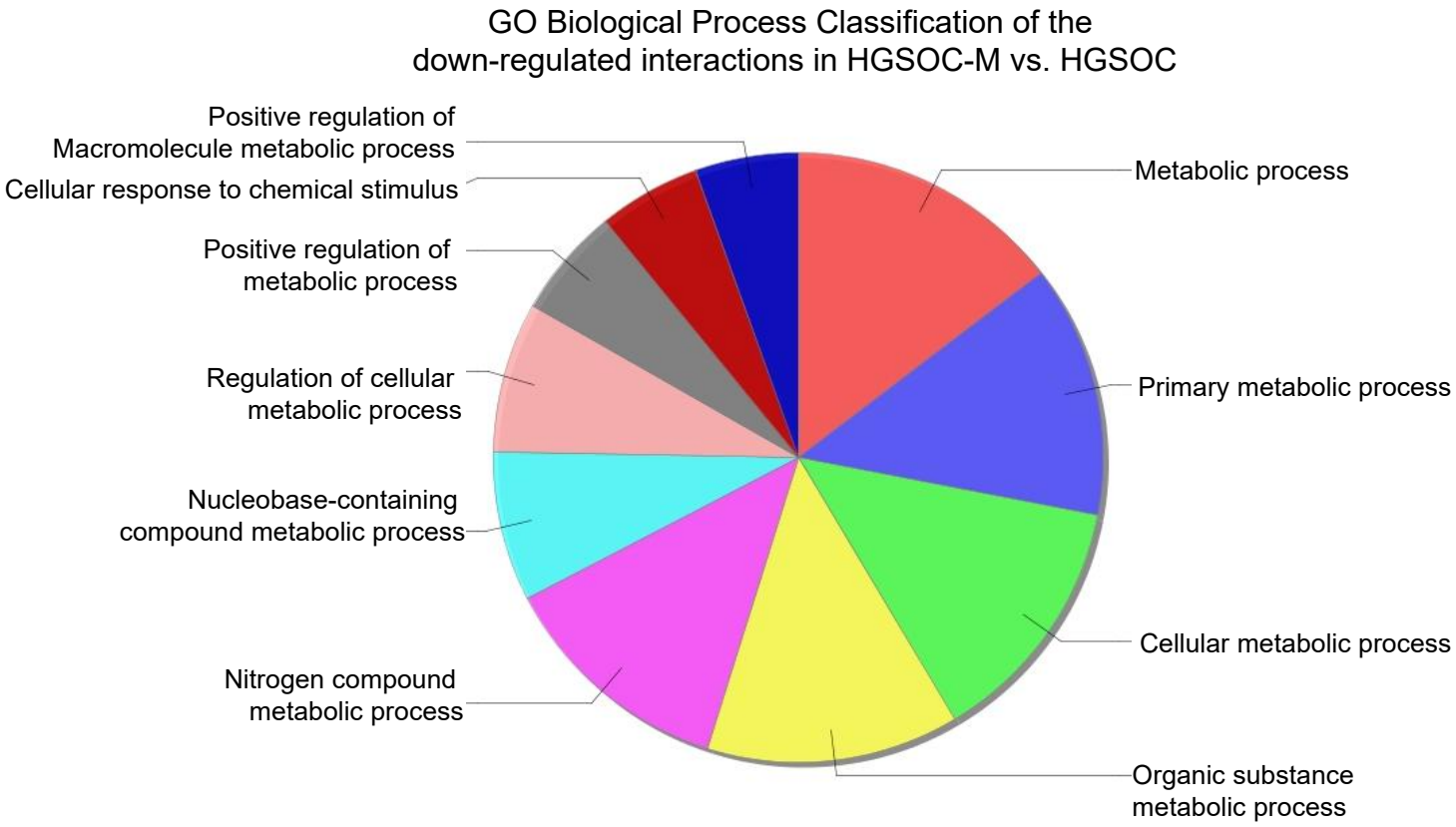


Supplementary Fig. 1 EccDNA counts per MB from HGSOC-M tissues (red cross, n=4) and HGSOC tissues (green dot, n=4) per coding genes per MB.

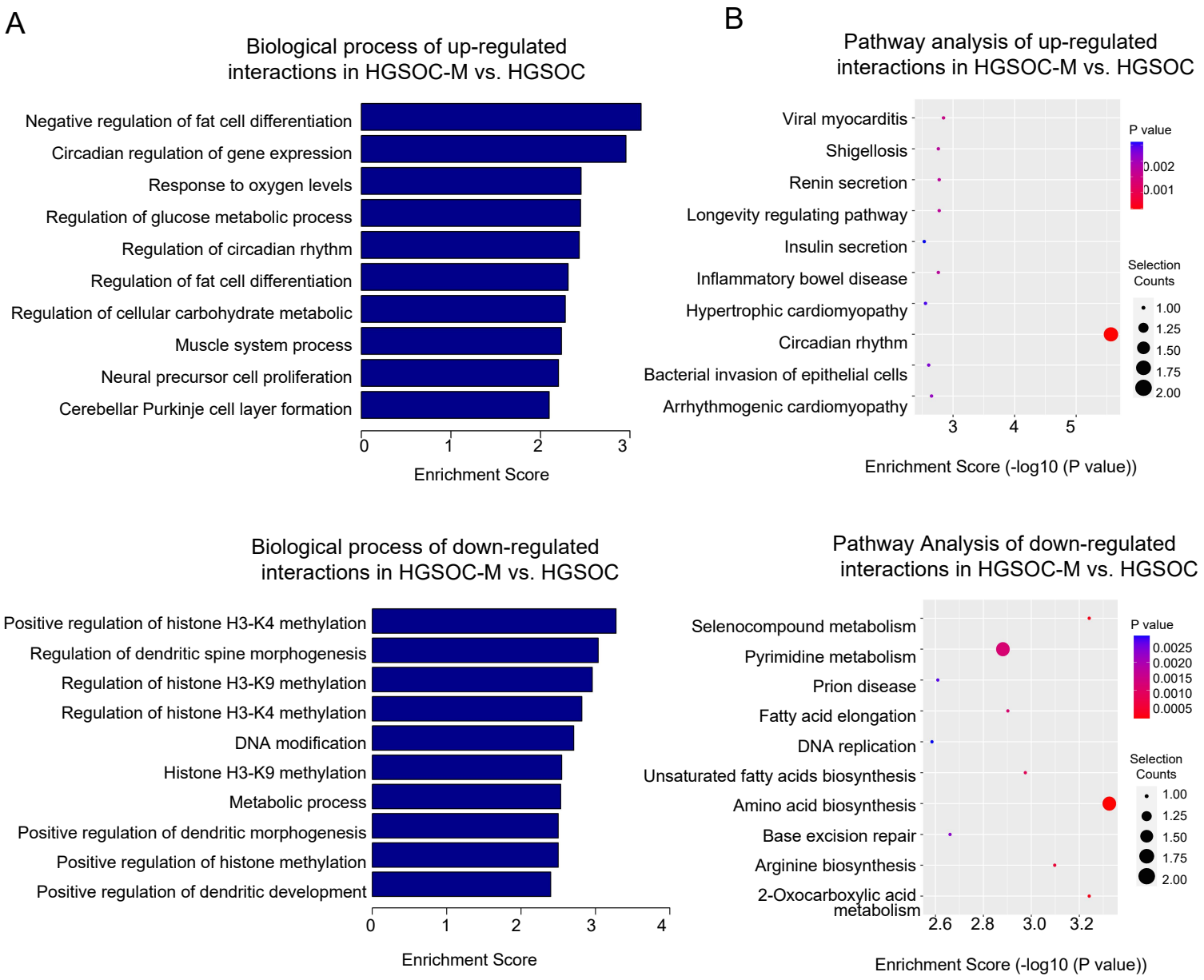


Supplementary Fig. 2 **A** The biological process analysis of differentially expressed eccDNAs between HGSOC-M and HGSOC group. Upper, differentially up-regulated in HGSOC-M; Lower, differentially down-regulated in HGSOC-M; **B** The enrichment pathway analysis of differentially expressed eccDNAs between HGSOC-M and HGSOC group. Upper, differentially up-regulated in HGSOC-M; Lower, differentially down-regulated in HGSOC-M;

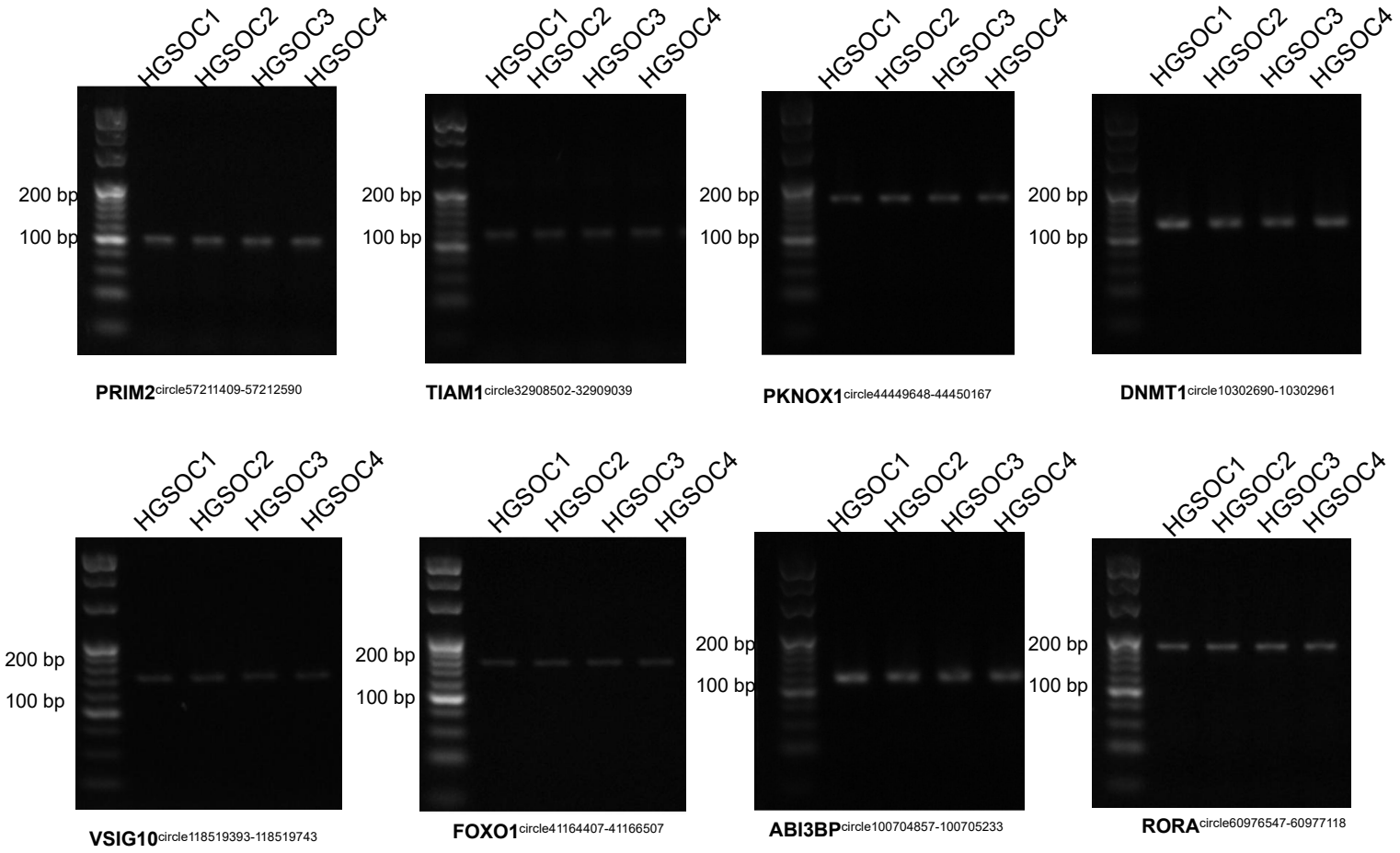




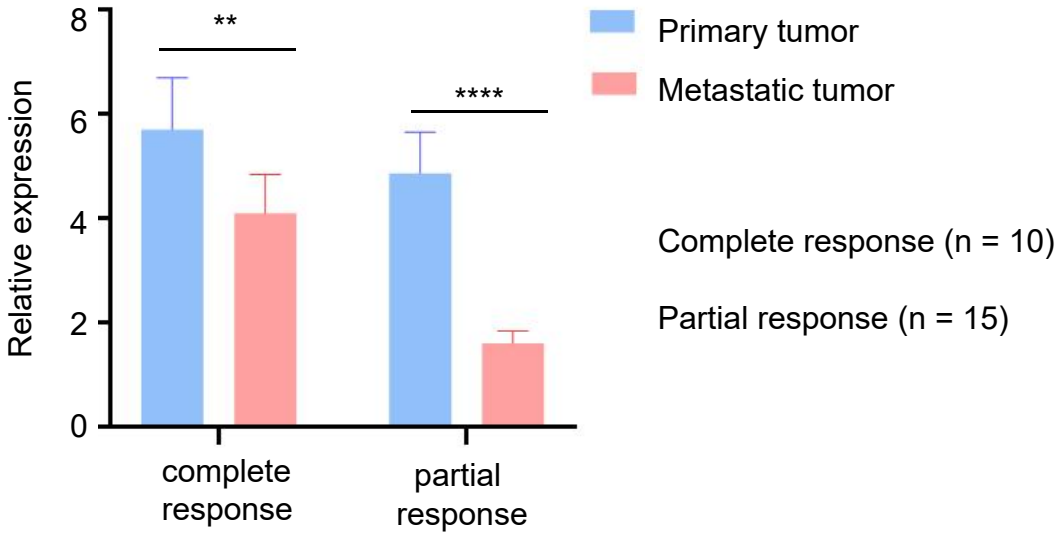
Supplementary Fig. 3 The classification of GO biological process of the overlap targets of Circle-Seq and RNA-Seq. Upper, differentially up-regulated in HGSOC-M; Lower, differentially down-regulated in HGSOC-M.



Supplementary Fig. 4 (A) The biological process analysis of overlap targets of Circle-Seq and RNA-Seq. Upper, differentially up-regulated in HGSOC-M; Lower, differentially down-regulated in HGSOC-M; **(B)** The enrichment pathway analysis of the overlap targets of Circle-Seq and RNA-Seq. Upper, differentially up-regulated in HGSOC-M; Lower, differentially down-regulated in HGSOC-M;



Supplementary Fig. 5 Gel electrophoresis analysis for a validated subset (n = 8) of eccDNAs by outward PCR using HGSOC1-4 tissues. EccDNAs were named according to gene content.



Supplementary Fig. 6 The DNMT1$^{circle10302690\text{-}10302961}$ expression of metastatic and primary tumors in 25 HGSOC patients who received NACT. The data were shown as mean ± SD. ** P < 0.01, **** P < 0.0001.