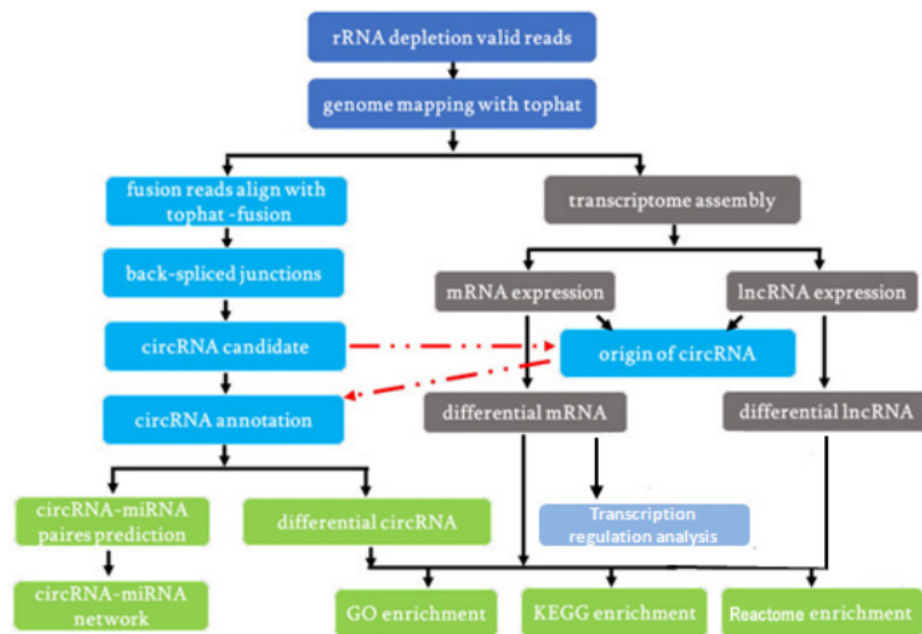
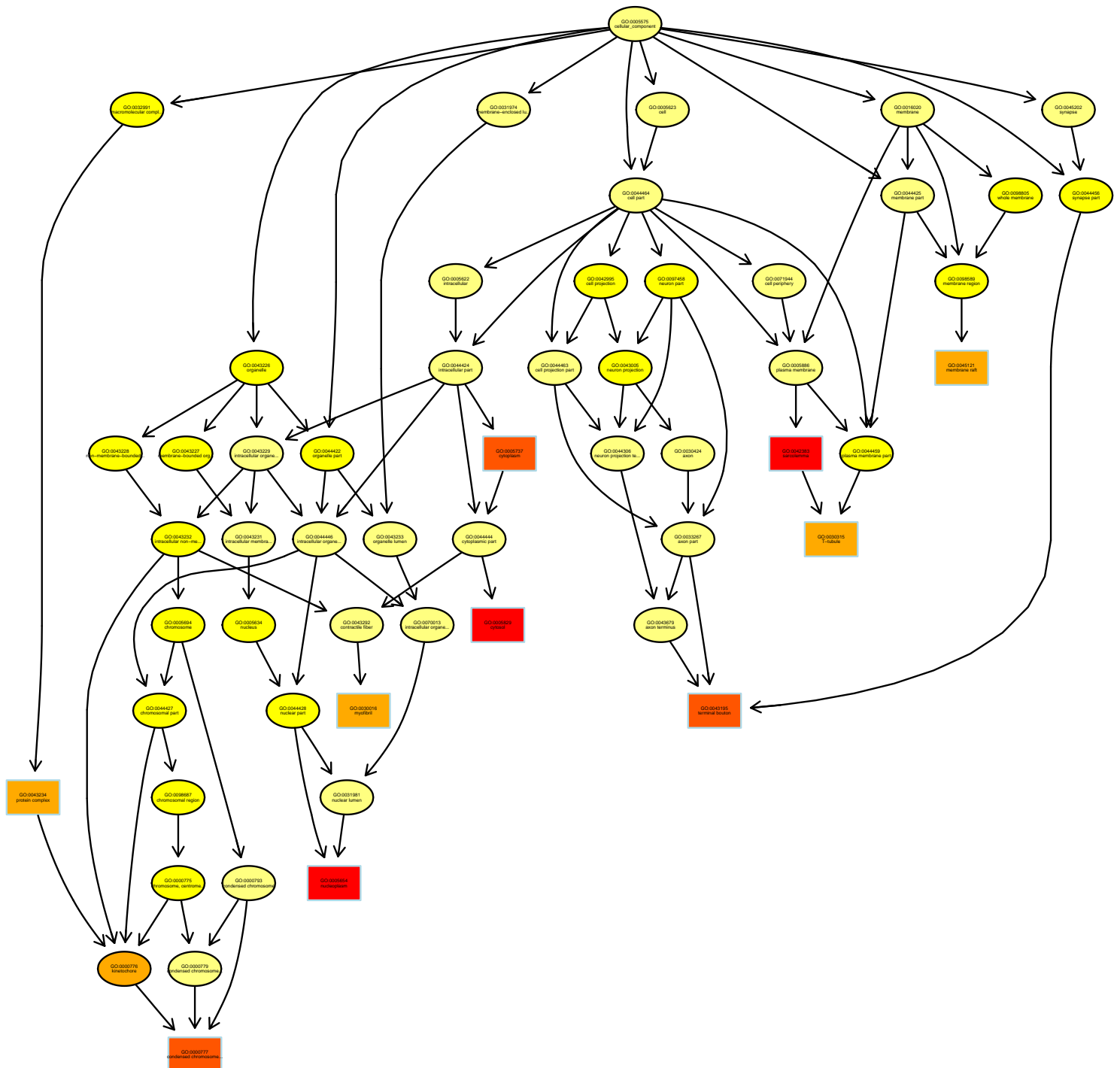


sFigure 1

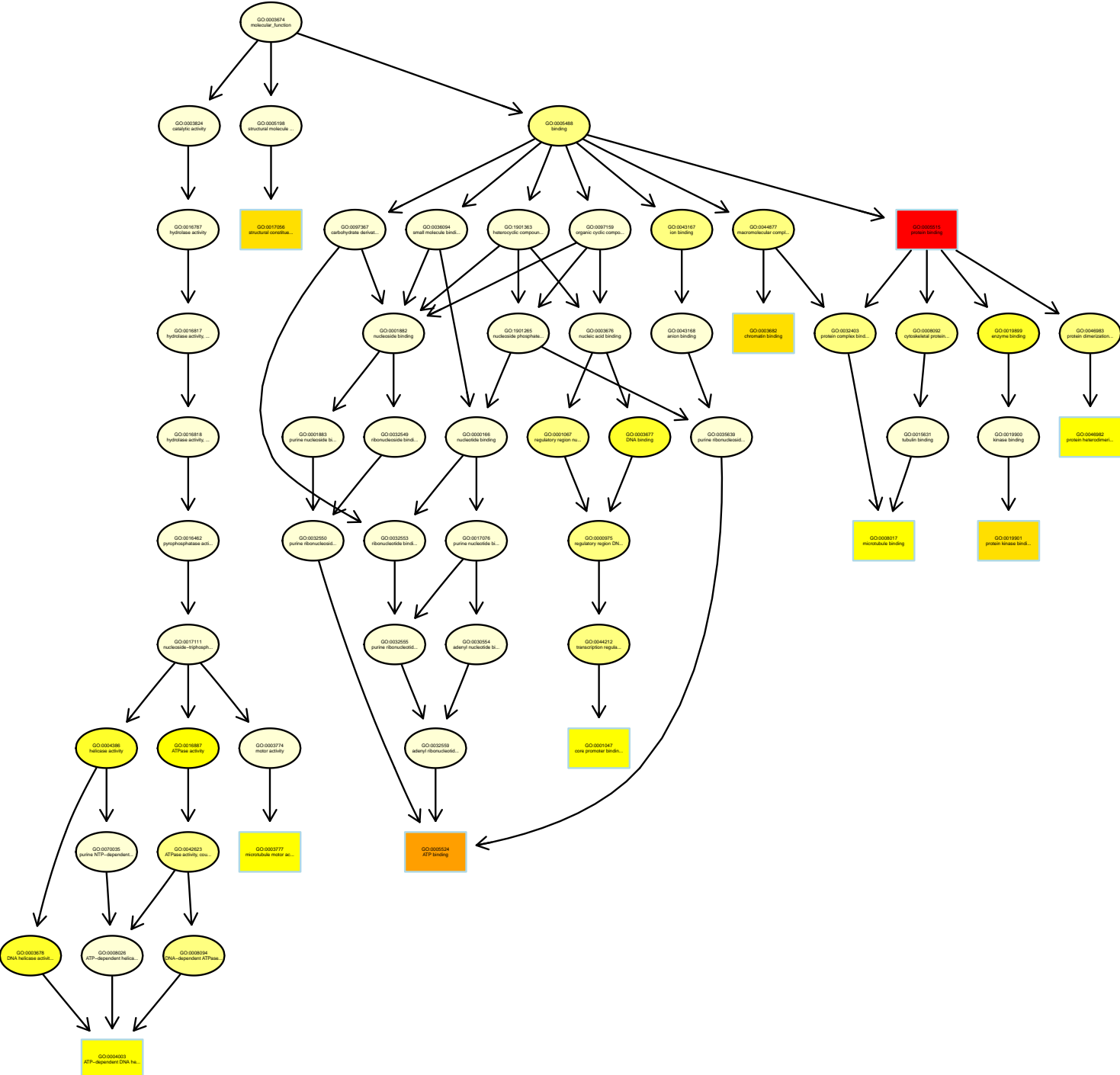


sFigure 1 The experiment workflow and data analysis flowchart.

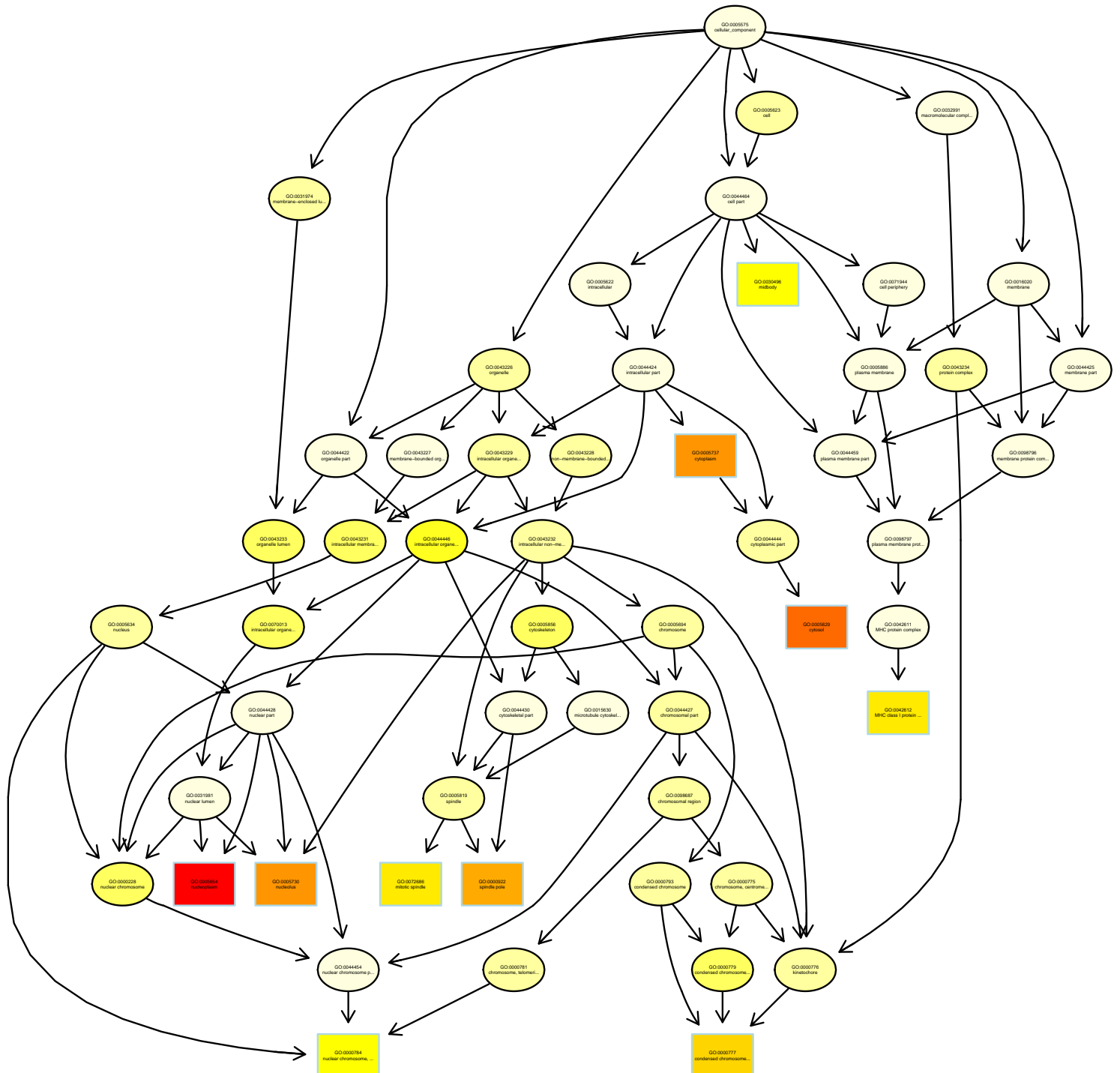
sFigure 2A



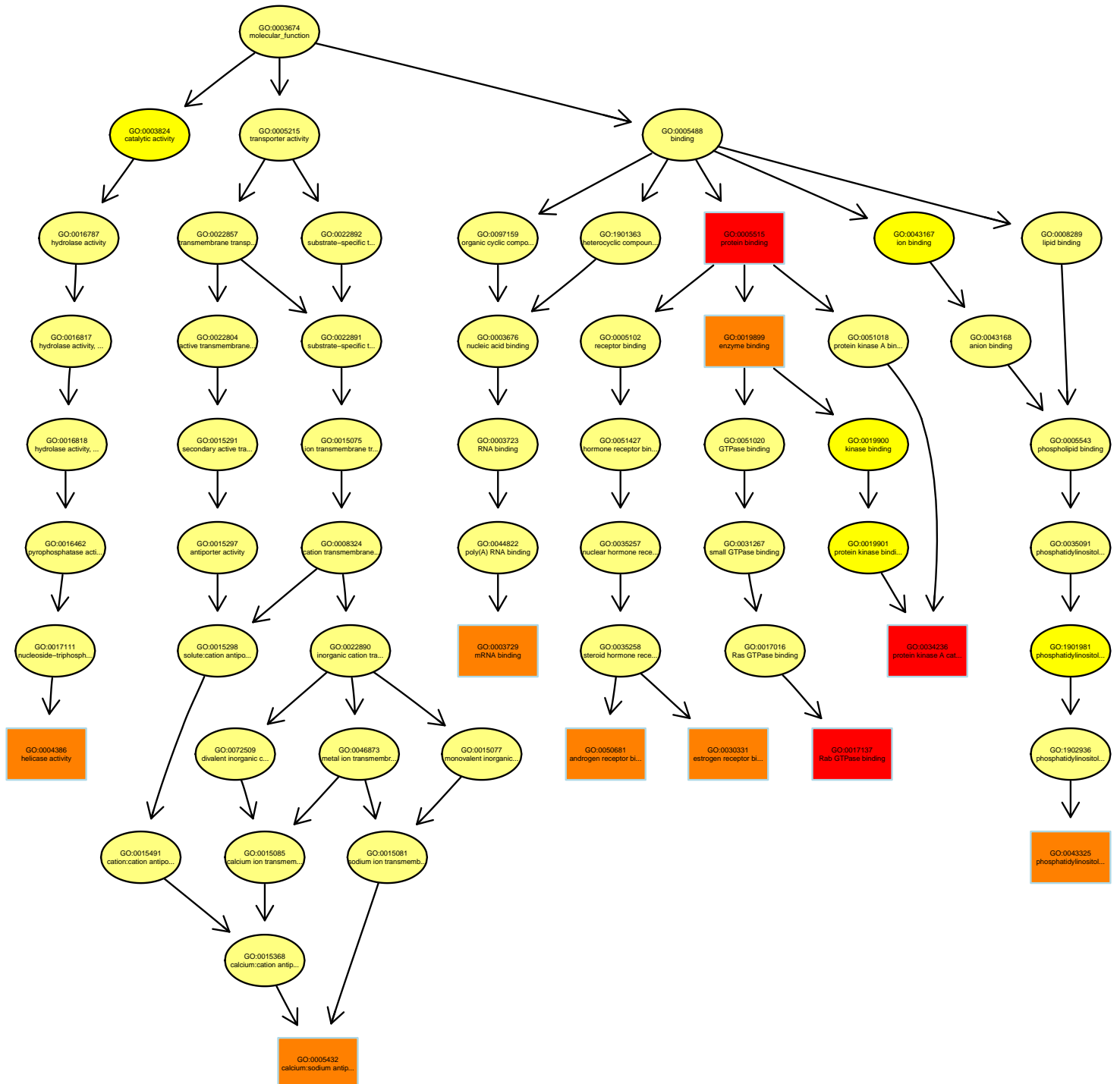
sFigure 2B



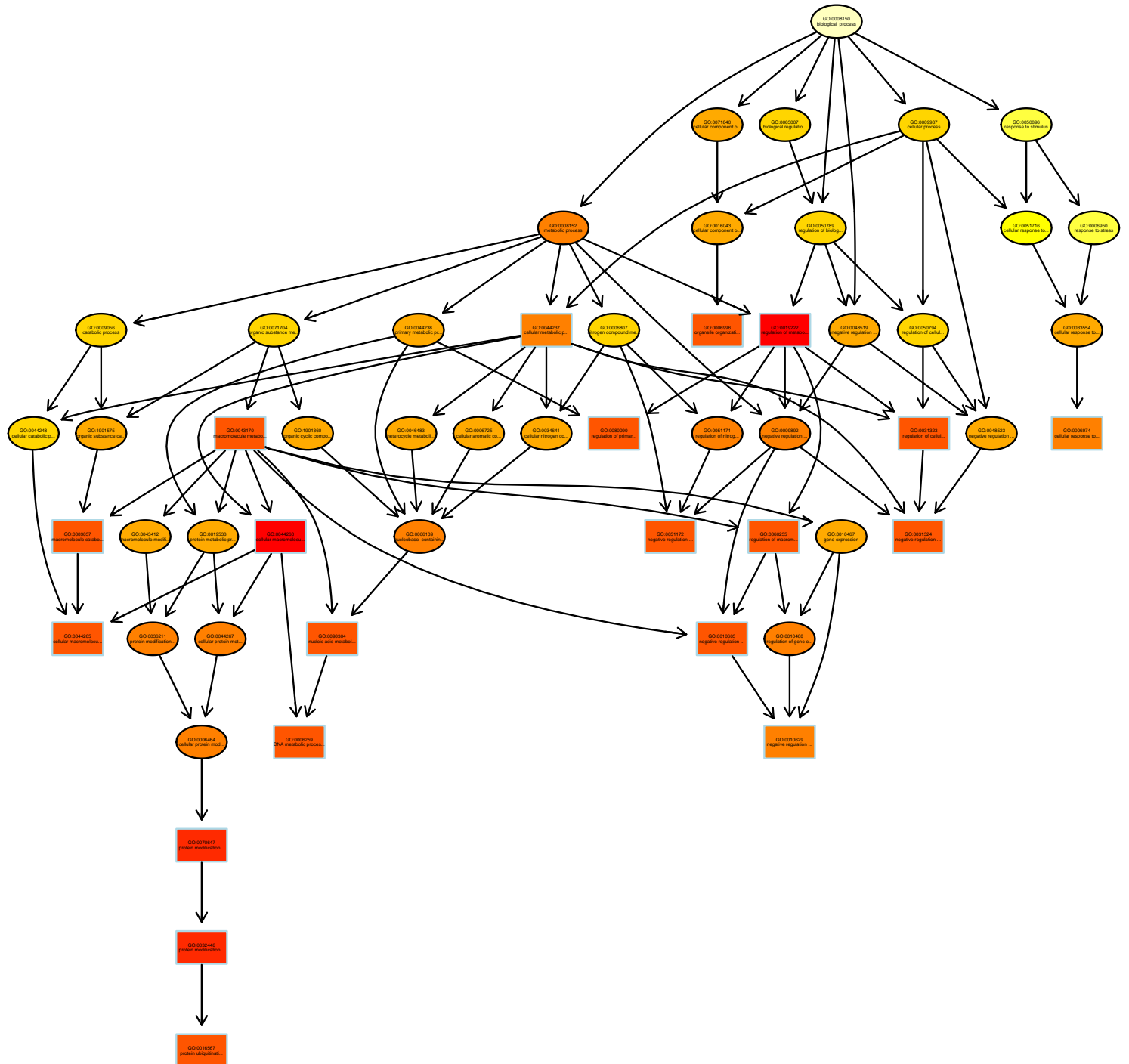
sFigure 2C



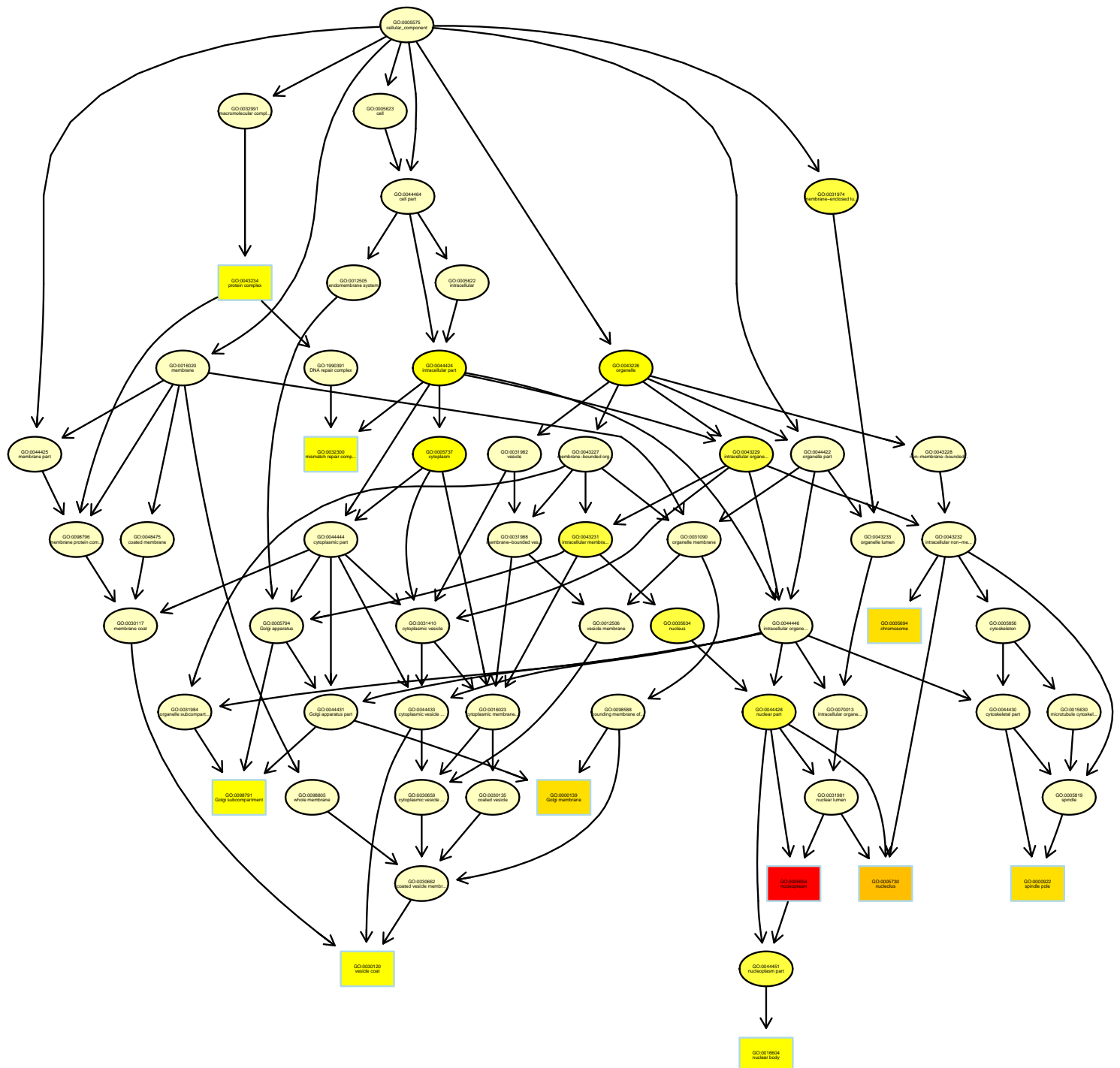
sFigure 2D



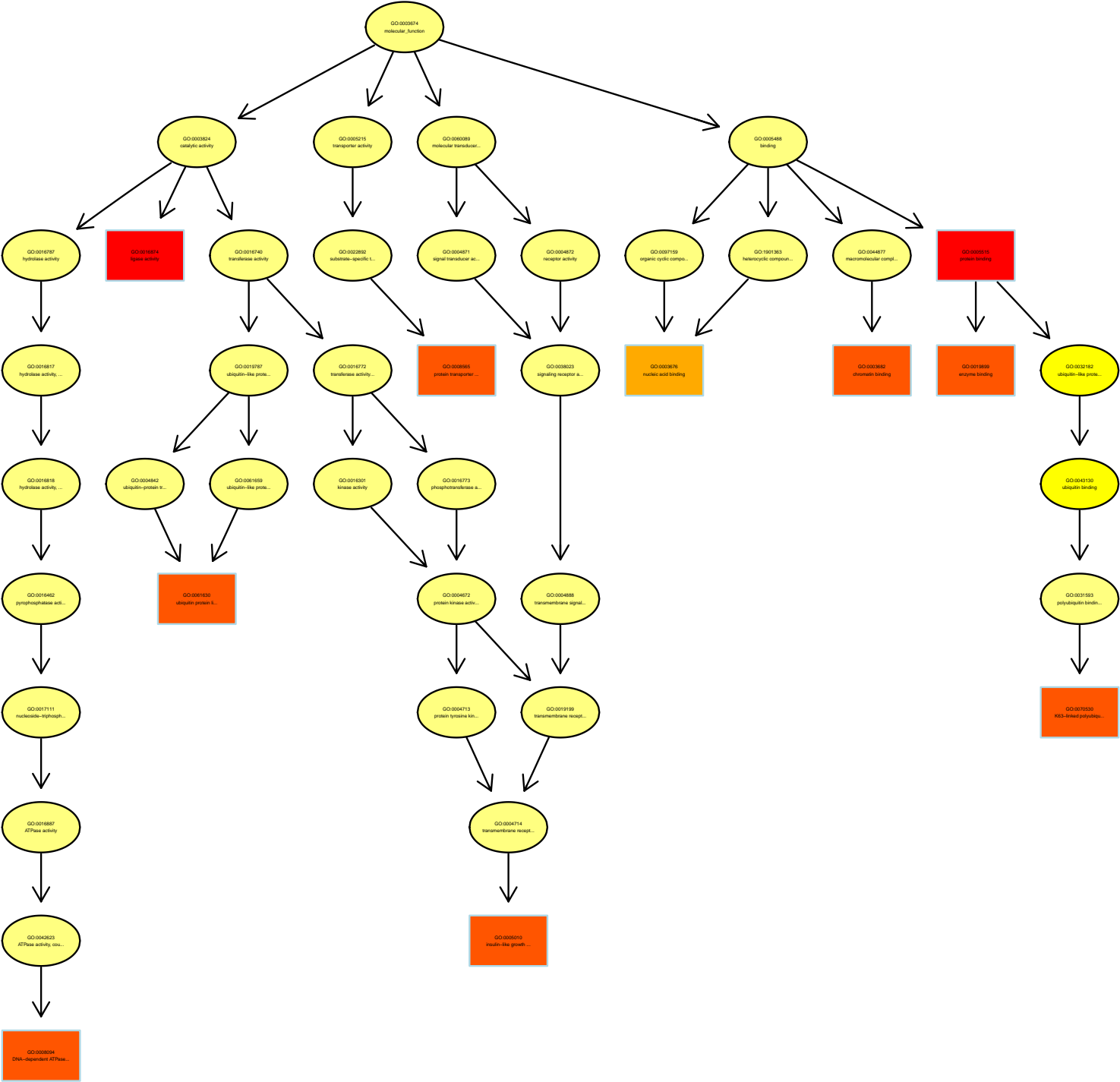
sFigure 2E



sFigure 2F

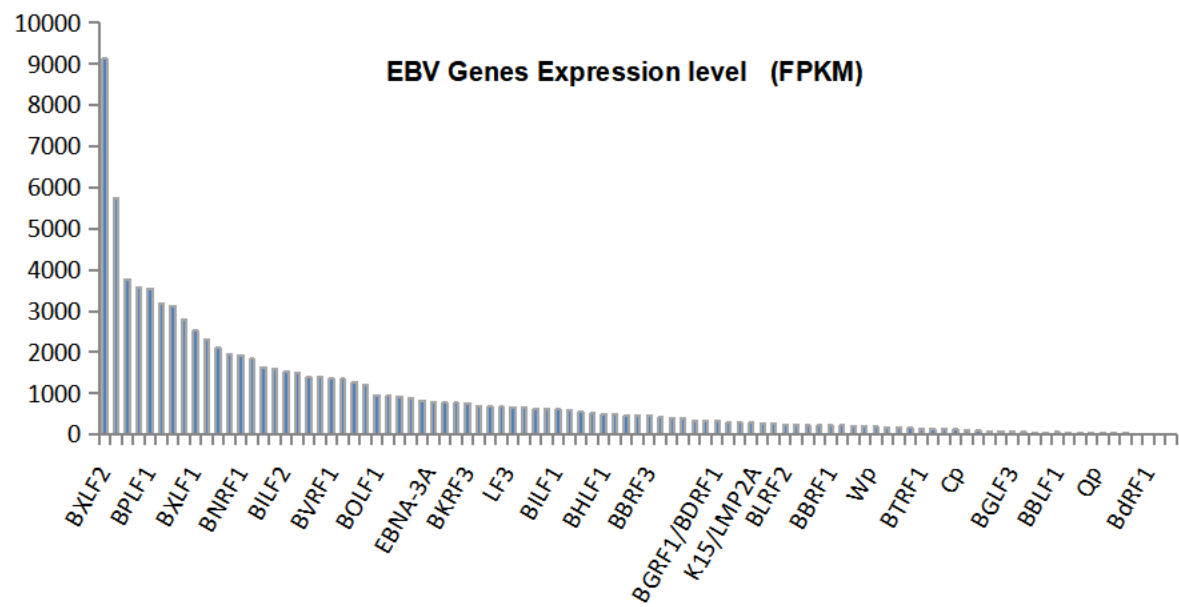


sFigure 2G



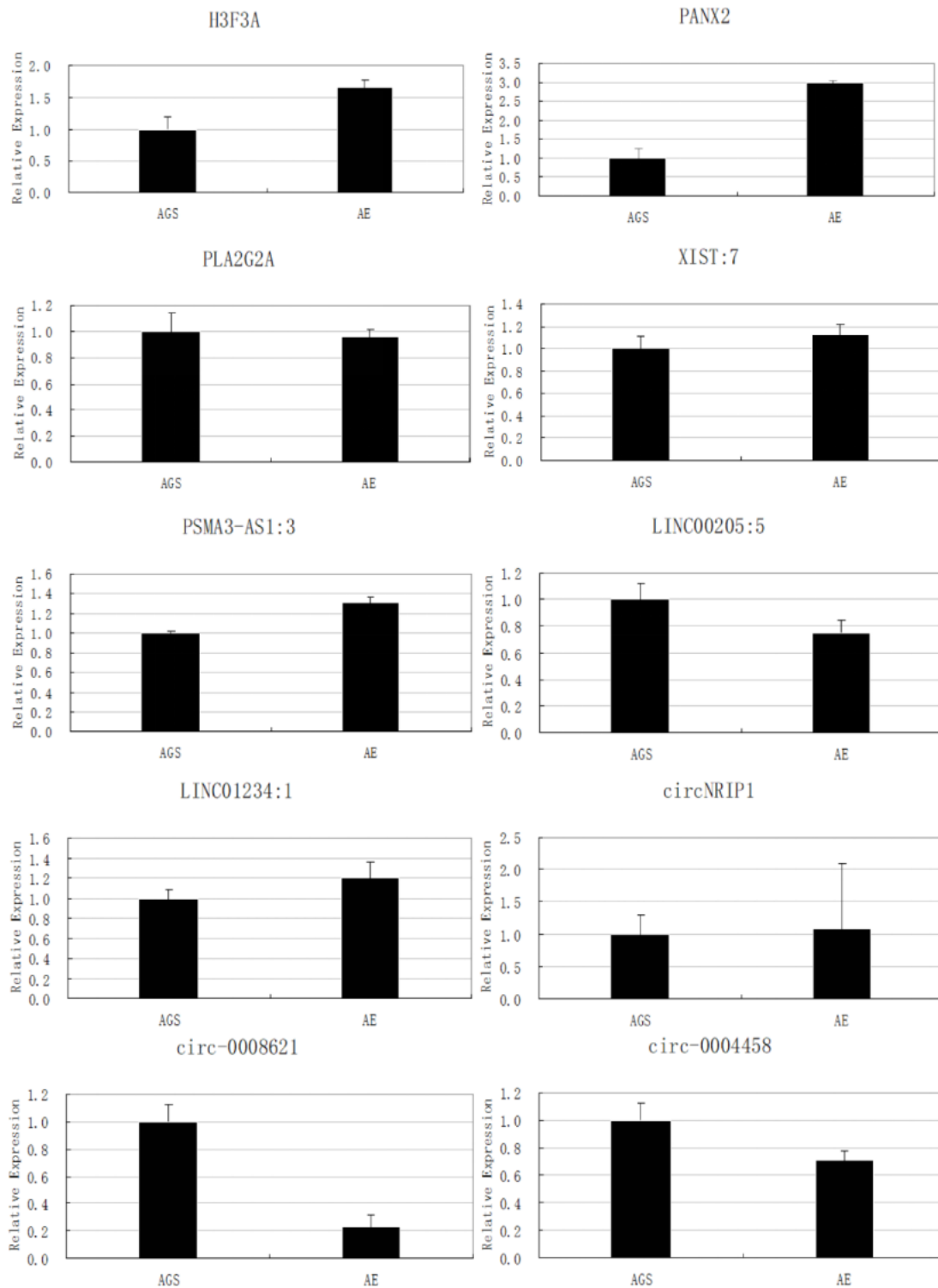
sFigure 2 GO tree illustrating the top 10 GO terms (boxes) related to biological process (BP) and cell component (CC) molecular function (MF). The colour of the box indicates the enrichment degree, with the red box representing the highest degree of enrichment, followed by the orange and yellow boxes in descending order. (A, B) Representative GO tree in mRNA CC and MF. (C, D) Representative GO tree in lncRNA CC and MF. (E-G) Representative GO tree in circRNA BP, CC, and MF.

sFigure 3



sFigure 3 The expression of viral gene in AGS-EBV.

sFigure 4



sFigure 4 Verification of differentially expressed genes by qRT-PCR, P value < 0.05 .

AE=AGS-EBV cell line. DE mRNA: H3F3A, PANX2, PLA2G2A; DE lncRNA: XIST:7, PSMA3-AS1:3, LINC00205:5, LINC01234:1; DE circRNA: circNRIP1, circ-0008621, circ-0004458.