

Supplemental Figure legends

Figure S1 Geminin expression levels increase in human ovarian cancer tissues compared with normal ovary tissues. (A) The Gene Expression Profile *GMNN* in human tumor tissues and normal tissues. Data are analysed with GEPIA 2 website, matched TCGA normal and GTEx data, using $\log_2(\text{TPM} + 1)$ for log-scale. VNOVA methods. (B) The RNA expression of geminin in human ovarian cancer tissues and normal ovary tissues based on TCGA database search. *** $p < 0.001$, Student's unpaired t-test were used for data analysis. (C) The RNA expression of geminin in different human ovarian cancer stages. (D) The RNA expression of geminin in different human ovarian cancer patient age distribution. The data was extracted from TCGA database. (E) IHC staining showing geminin expression. The data was extracted from HPA. Scale bar, 200 μM .

Figure S2 Aurora-A correlates with Geminin in RNA and protein levels. (A) Volcano-plot analysis for 20032 genes by RNAseq data based on attribute *GMNN* in TCGA ovarian cancer cohort, \log_2 fold changes of gene expression on the x-axis, FDR statistical significance ($-\log_{10} p$ value) on the y-axis; upregulated (red), downregulated (green) genes. Genes with at least a >1.5 fold change and $\text{FDR} < 0.01$ are displayed. (B) Heat map of part positively correlated significant genes and negatively correlated significant genes in TCGA ovarian cancer cohort. Gene expression ($n=20,032$) is normalized \log_2 counts/million. (C) Correlation of gene *GMNN* and *AURKA* in TCGA ovarian cancer cohort. \log_2 fold changes of gene expression on the axis, and the Spearman Method was used for calculating the correlation coefficient. (D) The protein-protein associations between Aurora-A and geminin protein. Data from STRING.

Figure S3 Aurora-A is overexpressed in ovarian cancer tissues and positively correlates with disease progression. (A) The Gene Expression Profile Aurora-A in human tumor tissues and normal tissues. Data are analysed with GEPIA 2 website, matched TCGA normal and GTEx data, using $\log_2(\text{TPM} + 1)$ for log-scale. VNOVA methods. (B) The RNA expression of Aurora-A in human ovarian cancer tissues and normal ovary tissues based on TCGA database. *** $p < 0.001$, Student's unpaired t-test were used for data analysis. (C) The RNA expression of Aurora-A in different human ovarian cancer stages. Data are analysed with GEPIA 2 website, using $\log_2(\text{TPM} + 1)$ for log-scale. (D) IHC staining showing Aurora-A expression. The data was extracted from HPA. Scale bar, 200 μM . (E) Kaplan-Meier curves are made to show the survival rate of 1676 ovarian cancer patients with high and low *Aurora-A* mRNA expression levels.

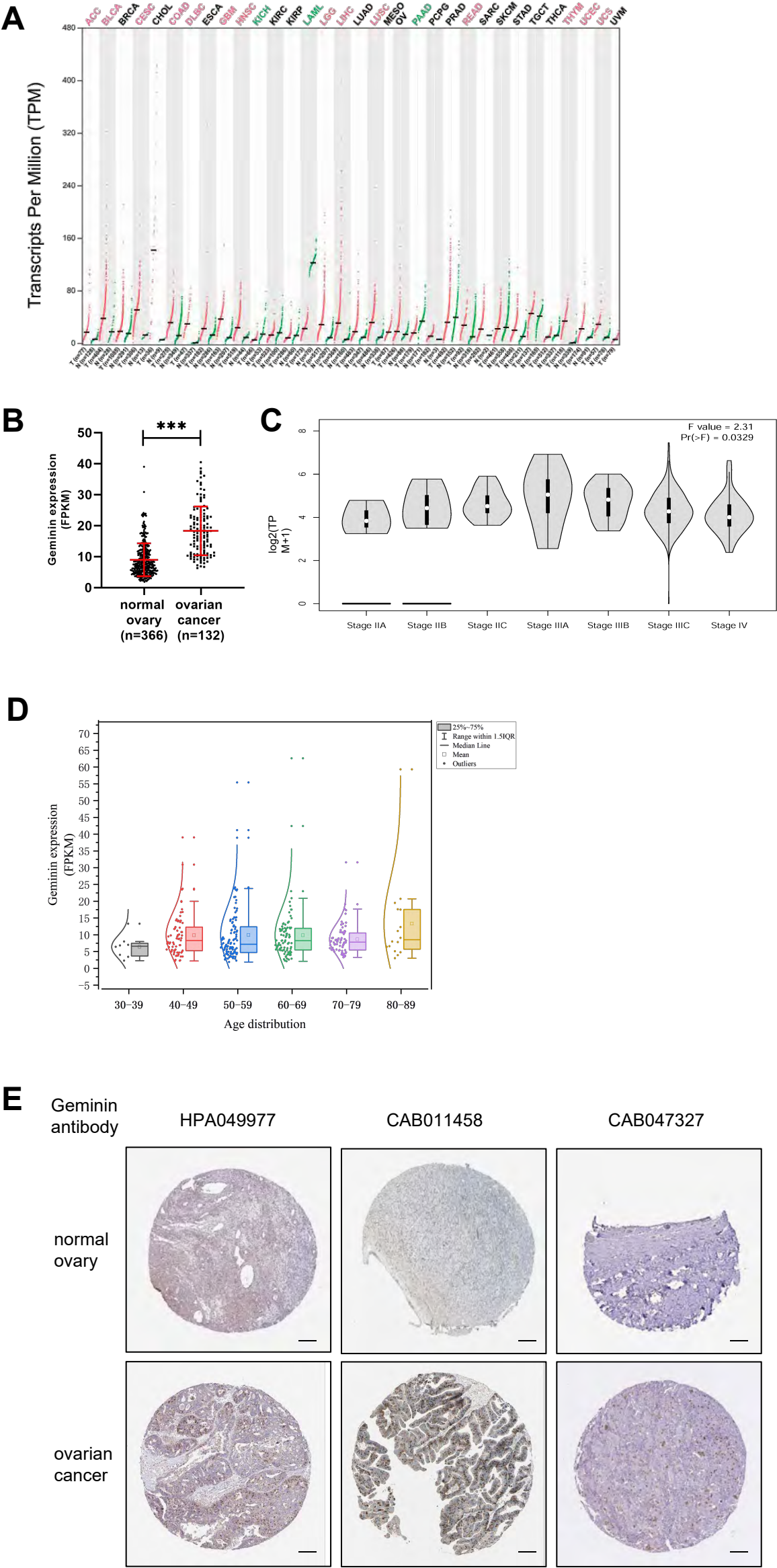
Figure S4 The GO Enrichment analysis on Biological Process category of gene *GMNN*. The results were extracted from LinkedOmics publicly portal, carried out with GSEA method and based upon the 17429 unique entrezgene IDs. The GO Slim summary (A) are based upon the 17429 unique entrezgene IDs and the height of the bar represents the number of IDs in the user list and also in the category. 25 positive related categories and 25 negative related categories are identified as enriched categories, in which 40 most significant categories and representatives in the reduced sets are shown in the Enrichment Results. The normalized enrichment score (NES) is used to evaluate the statistic for examining gene set enrichment results. The Enrichment Result bar chart (B) and DAG plot (C) are based upon the 13310 unique entrezgene IDs.

Figure S5 The GO Enrichment analysis on Molecular Function category of gene *GMNN*. The results were extracted from LinkedOmics publicly portal, carried out with GSEA method and based upon the 17429 unique entrezgene IDs. (A) The GO Slim summary are on Molecular Function category of *GMNN* based upon the 17429 unique entrezgene IDs and the height of the bar represents the number of IDs in the user list and also in the category. 25 positive related categories and 25 negative related categories are identified as enriched categories, in which 40 most significant categories and representatives in the reduced sets are shown in the Enrichment Results. The normalized enrichment score (NES) is used to evaluate the statistic for examining gene set enrichment results. The Enrichment Result bar chart (B) and DAG plot (C) are based upon the 11308 unique entrezgene IDs.

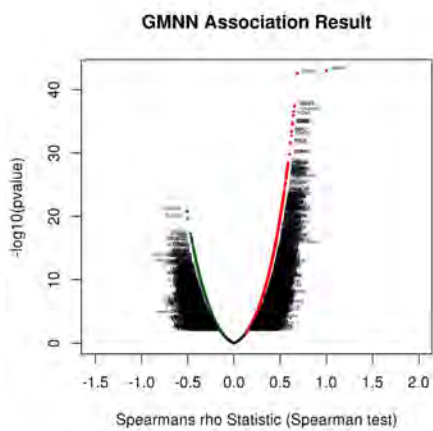
Figure S6 The KEGG Enrichment analysis of gene *GMNN*. The results were extracted from LinkedOmics publicly portal, carried out with GSEA method and based upon the 17429 unique entrezgene IDs. The normalized enrichment score (NES) is used to evaluate the statistic for examining gene set enrichment results. The Enrichment Result bar chart (A) and Volcano plot (B) are based upon the 11308 unique entrezgene IDs. (C) KEGG pathway analysis for cell cycle gene sets with *GMNN* based upon the annotated 6751 IDs.

Figure S7 The protein-protein associations of protein geminin. The top 50 proteins that had the strongest interaction with geminin were shown with the highest confidence 0.900. The edges indicate both functional and physical protein associations. Data from STRING.

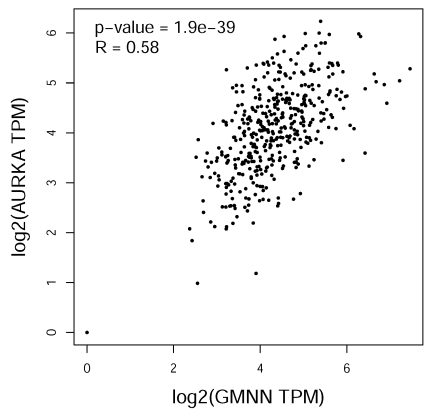
Figure S8 LPA signal mediates cell-cycle progression of HGSOC cells. (A) Cell cycle diagrams of the samples pretreated with 0.1% DMSO, 10 μM Ki16425, 10 μM BB94, 10 μM AG1478, 10 μM LY294002 or 100 nM Rapamycin for 30 minutes, and stimulated with 10 μM LPA up to 12 hours. (B) Quantification of DNA content in A. Data are analyzed with Origin 2021pro, One way VNOVA, Dunnett's Multiple Comparison Test, mean \pm SEM, $n=3$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



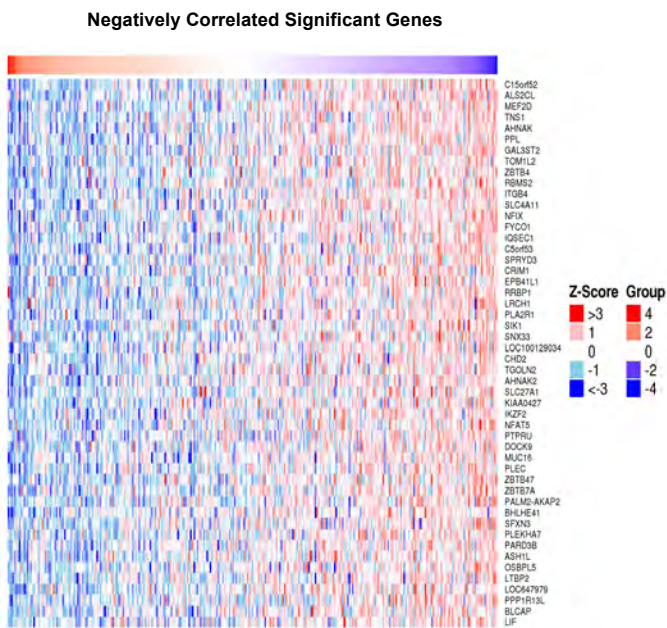
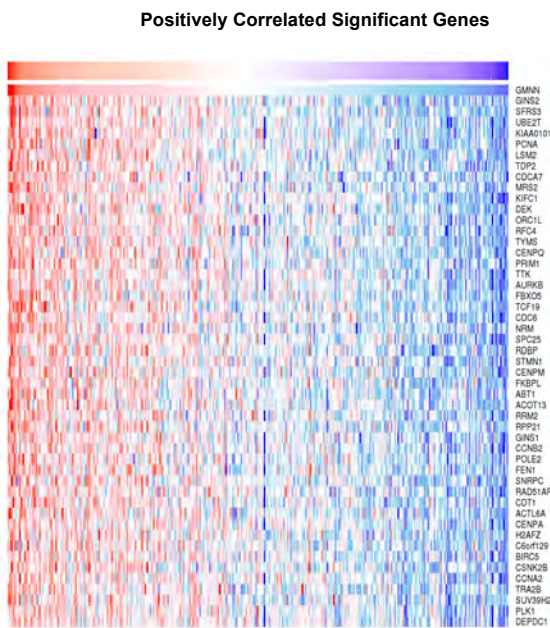
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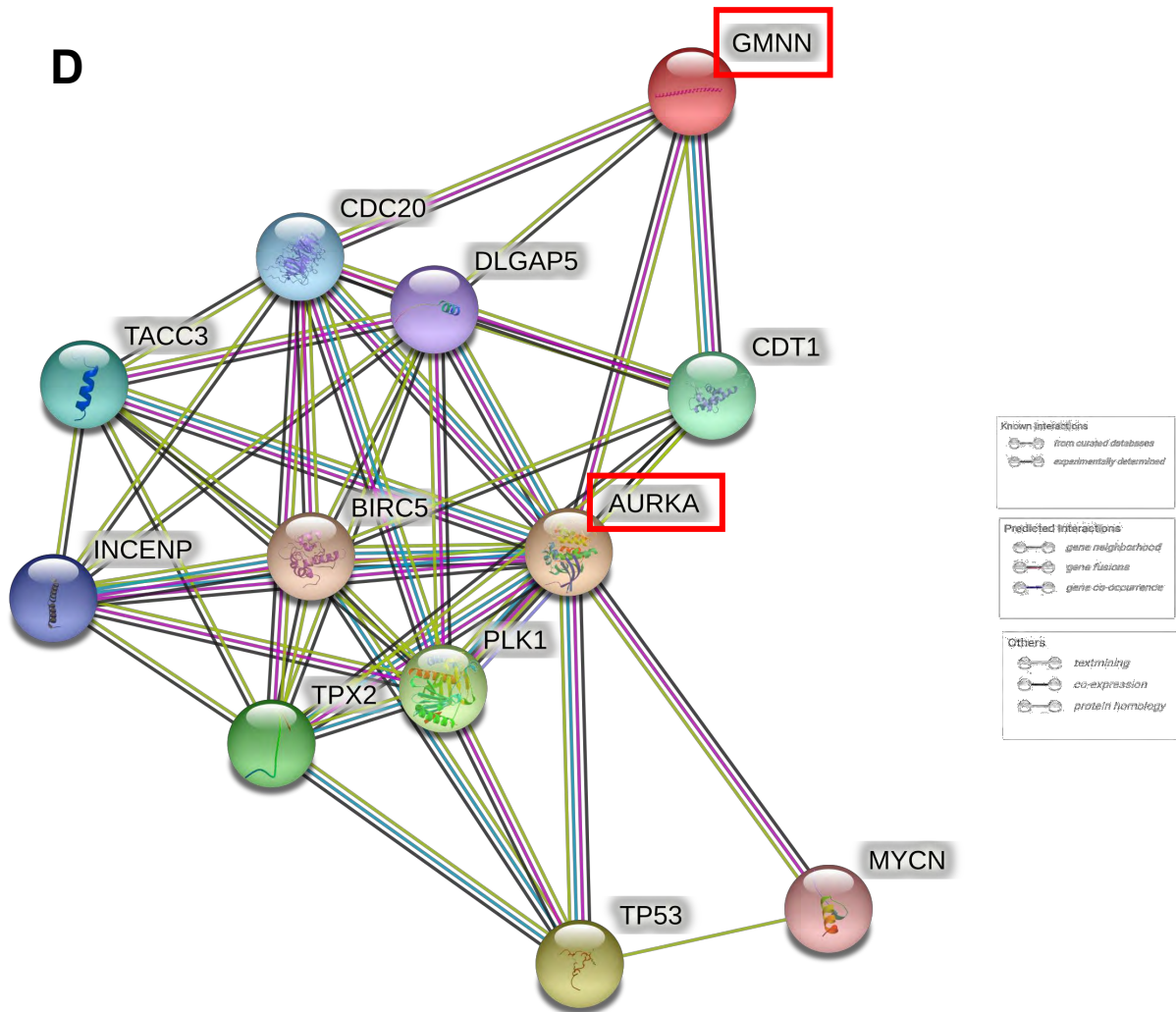
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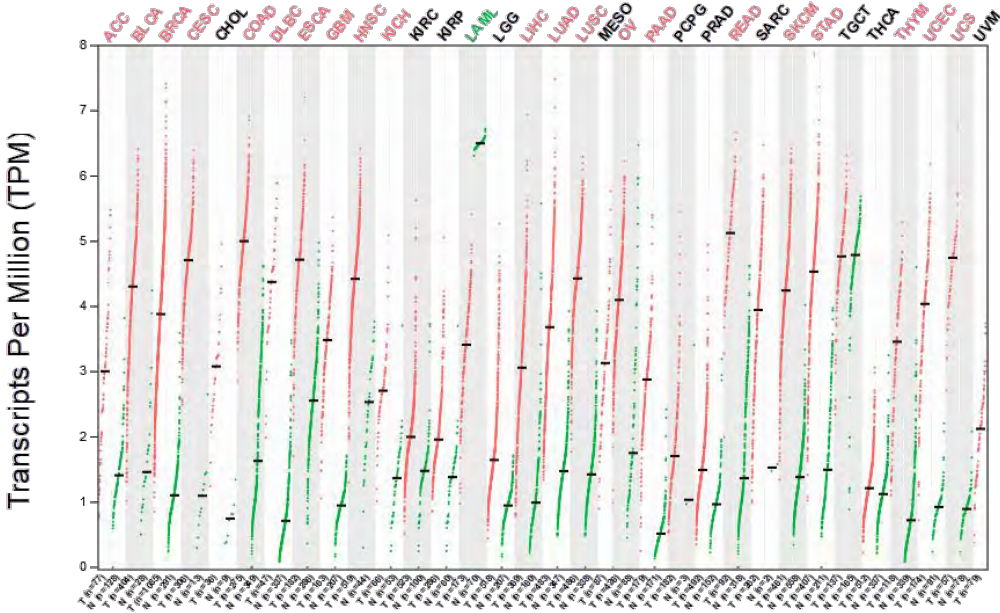
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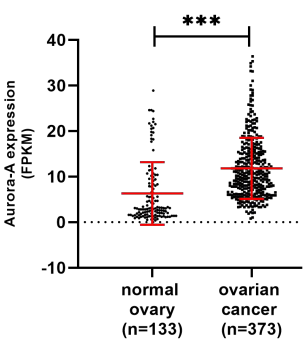
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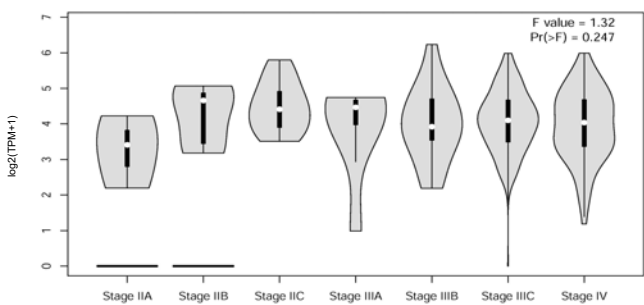
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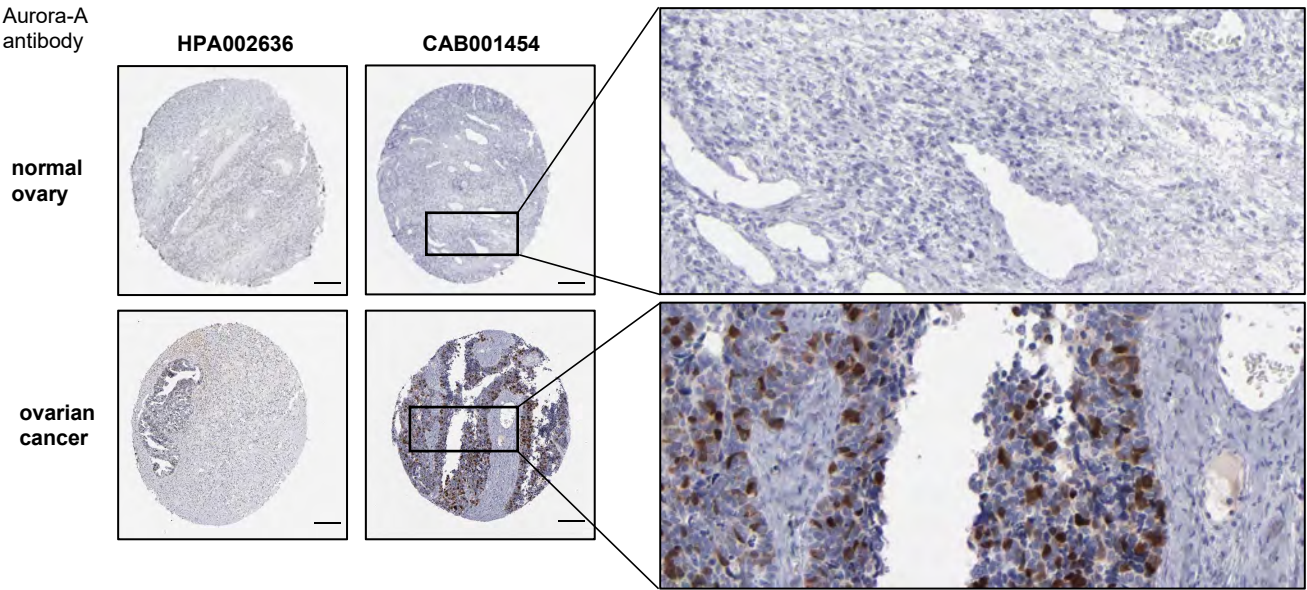
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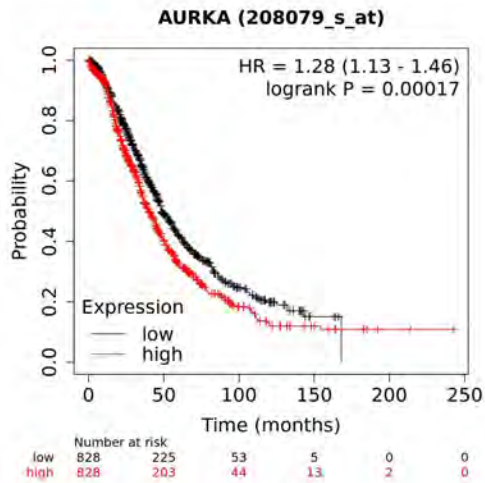
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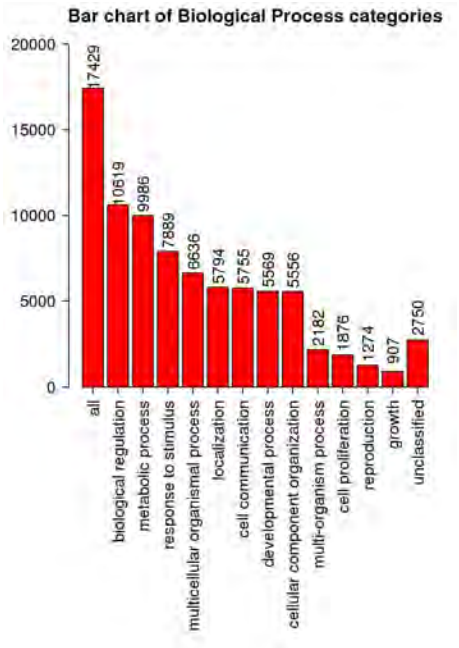
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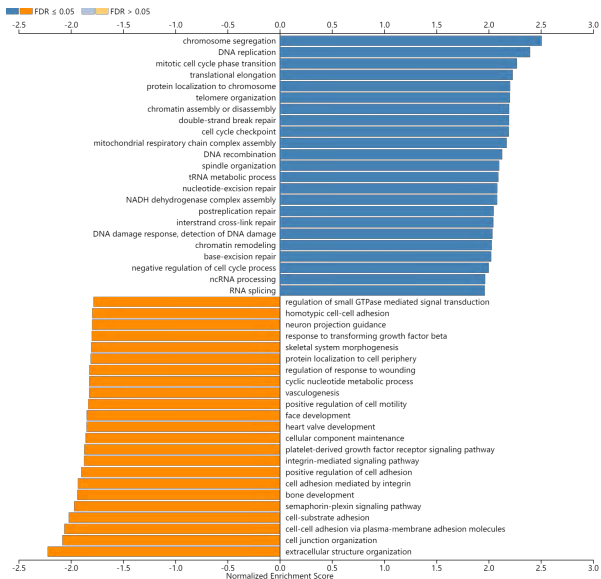
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A



B



C

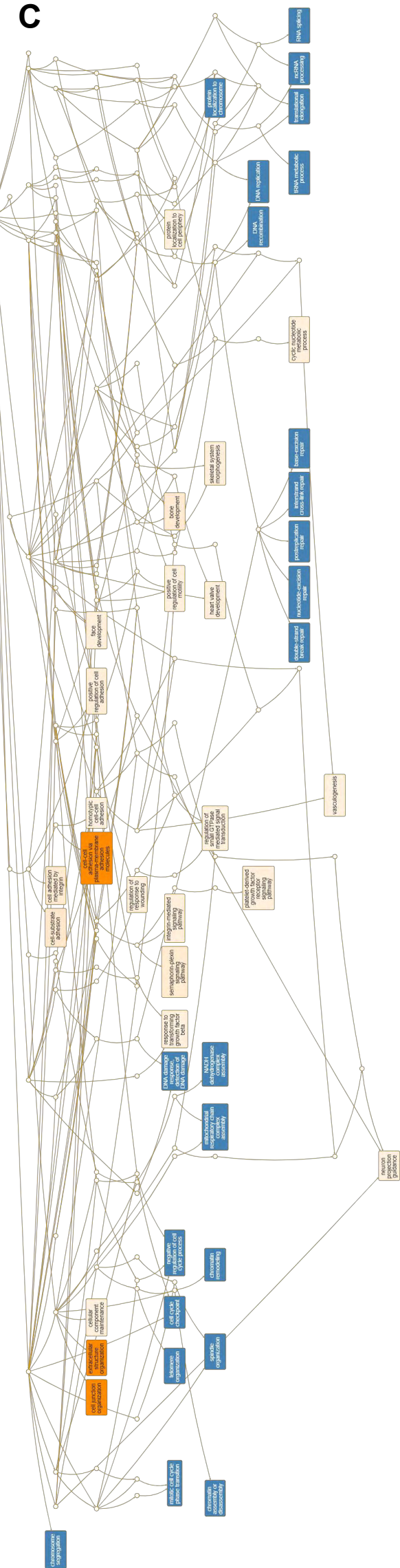
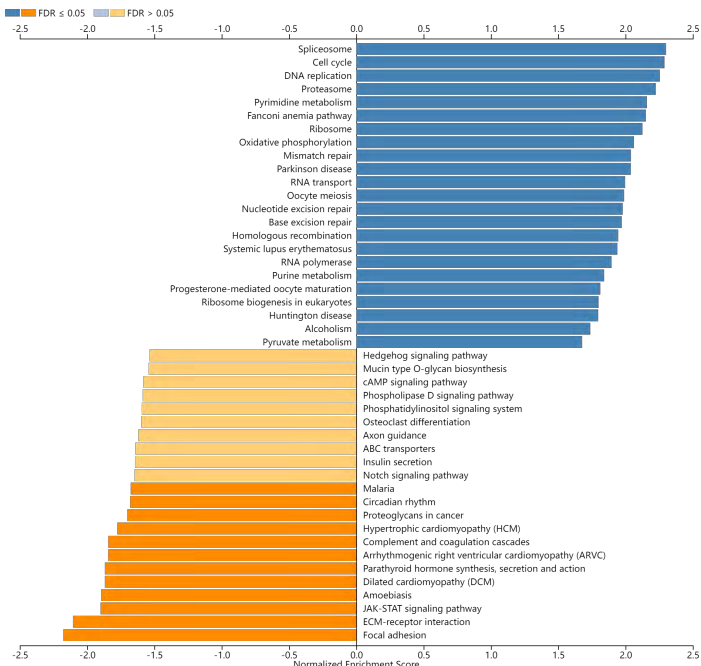
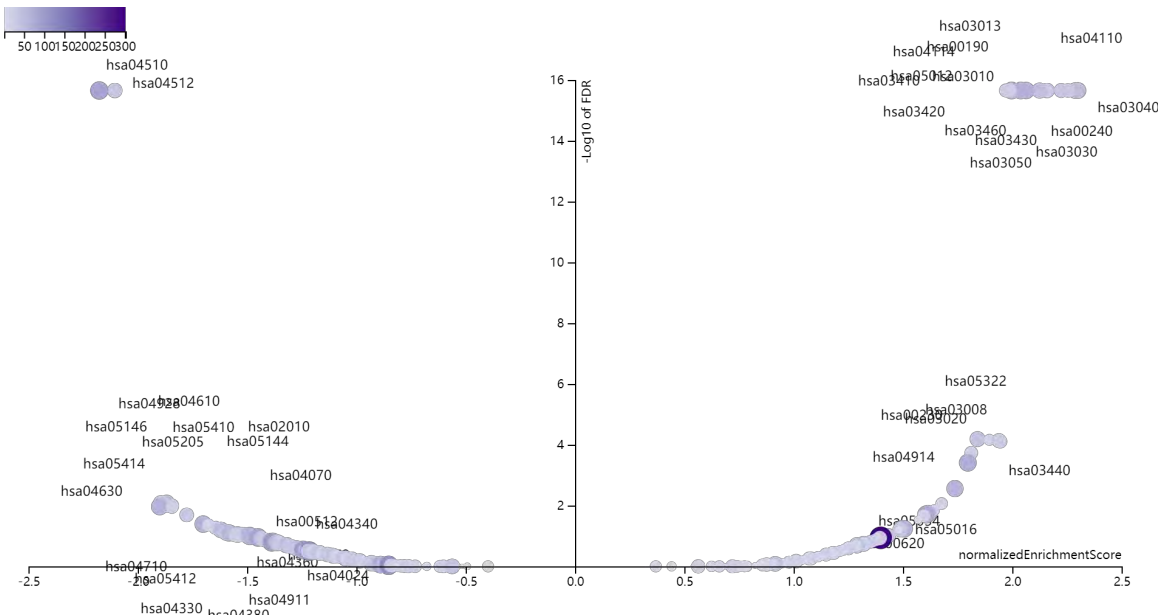


Fig S6

A



B



C

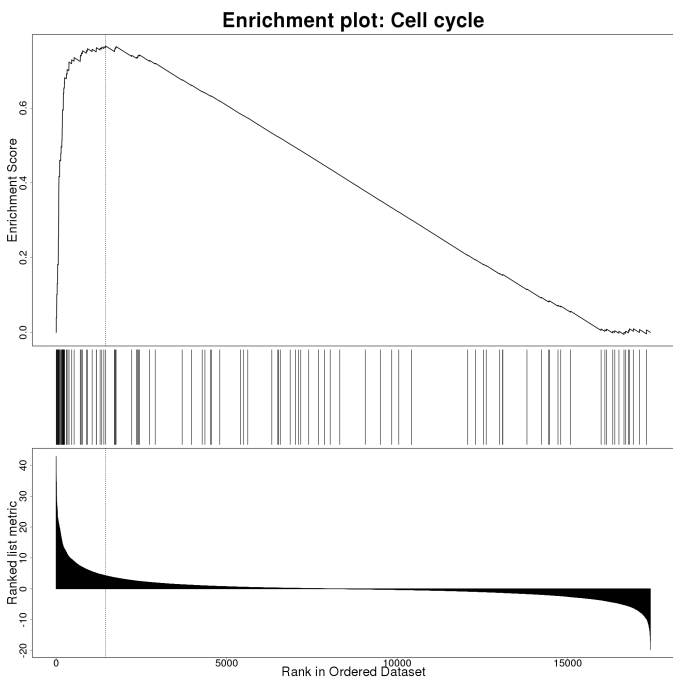
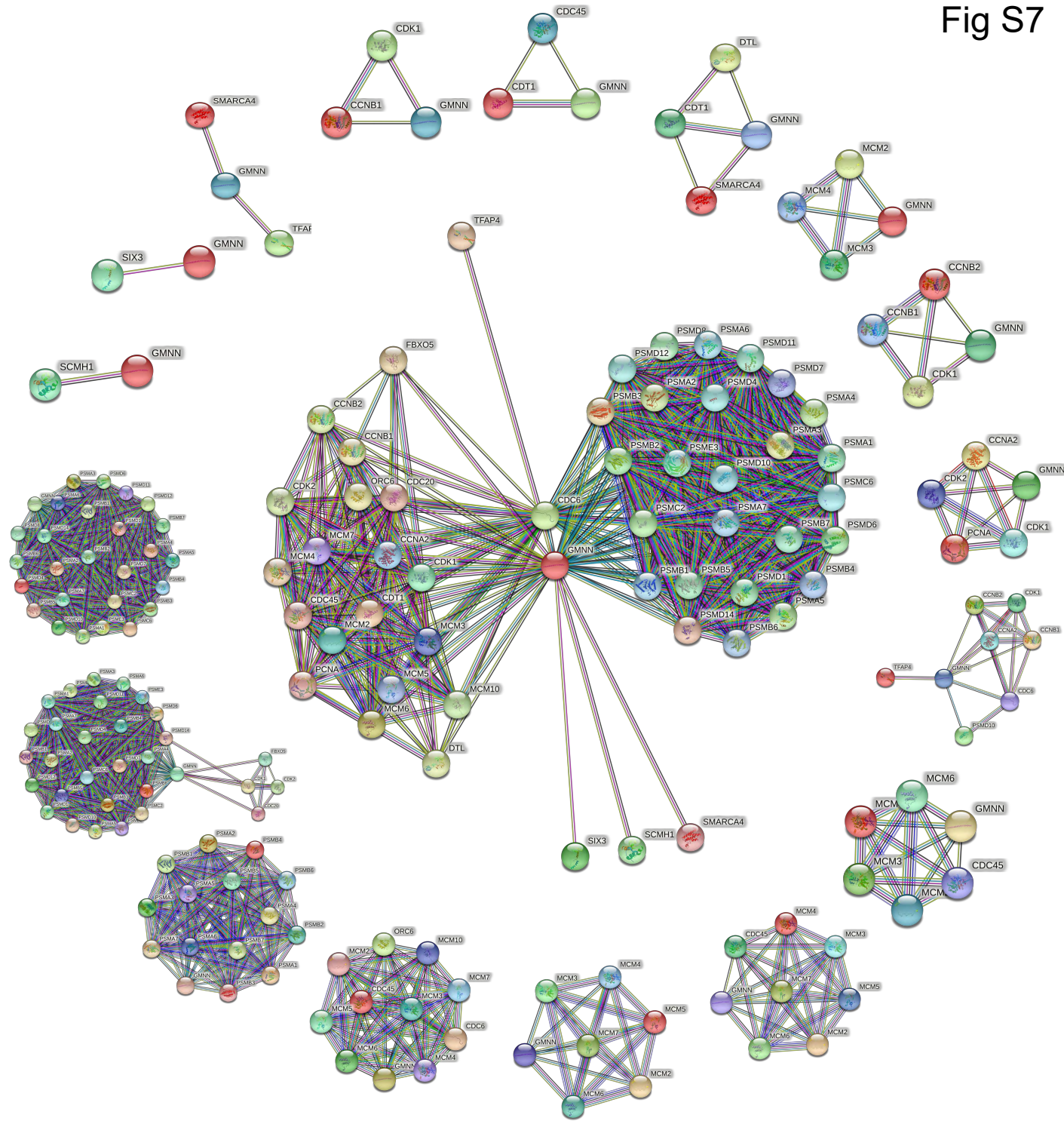






Fig S7



Nodes:

Network nodes represent proteins <i>splice isoforms or post-translational modifications are collapsed, i.e. each node represents all the proteins produced by a single, protein-coding gene locus.</i>	Node Color  <i>colored nodes: query proteins and first shell of interactors</i>  <i>white nodes: second shell of interactors</i>	Node Content  <i>empty nodes: proteins of unknown 3D structure</i>  <i>filled nodes: some 3D structure is known or predicted</i>
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Edges:









Edges represent protein-protein associations <i>associations are meant to be specific and meaningful, i.e. proteins jointly contribute to a shared function; this does not necessarily mean they are physically binding to each other.</i>	Known Interactions  <i>from curated databases</i>  <i>experimentally determined</i>	Predicted Interactions  <i>gene neighborhood</i>  <i>gene fusions</i>  <i>gene co-occurrence</i>	Others  <i>textmining</i>  <i>co-expression</i>  <i>protein homology</i>
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Fig S8

