

Supplemental Data

- [Supplementary figures S1-S11, text S1-S2 and table S1, S3, S18, and S19. \(.pdf, 12.8 MB\)](#) - Supplementary figures S1-S11, text S1-S2 and table S1, S3, S18, and S19.
- [Table S2 \(.xlsx, 88 KB\)](#) - This spreadsheet lists Gold-standard GO biological process and KEGG pathway terms for individual cancer types.
- [Table S4-S9 \(.xlsx, 1.3 MB\)](#) - This spreadsheet lists mRNA and protein co-expression networks for breast cancer, colorectal cancer and ovarian cancer.
- [Table S10-S15 \(.xlsx, 79 KB\)](#) - This spreadsheet lists functional enrichment results and cytogenetic band results for mRNA and protein co-expression modules of breast cancer, colorectal cancer and ovarian cancer.
- [Table S16-S17 \(.xlsx, 236 KB\)](#) - This spreadsheet lists AUROCs for the gold-standard GO biological process terms and KEGG pathways in the three cancer types.
- [Table S20-S22 \(.xlsx, 69 KB\)](#) - This spreadsheet lists the detailed information of function prediction for the driver genes in the three cancer types based on the Gene2Net.