

Supplementary Table S1

Supplementary table S1: RTqPCR primers used (5' to 3')

Meis1 Fwd	GATGGCGCAAAGGTACGAC
Meis1 Rev	GGTACTGATGCGAGTGCAGA
hsa-mir-499a-5p	GTTAAGACTTGCAGTGATGTTTAAAA
Universal Reverse primer for miRNAs GT19	GAATCGAGCACCAGTTACG
RNU6B	ACGCAAATTCGTGAAGCGTT
Malat1 Fwd	GGGGGAATGGGGGCAAAATA
Malat1 Rev	AACTACCAGCAATTCCGCCA
SRSF4 Fwd	TGCAGCTGGCAAGACCTAAA
SRSF4 Rev	TTTTTGCGTCCCTTGTGAGC

Supplementary Figure S1

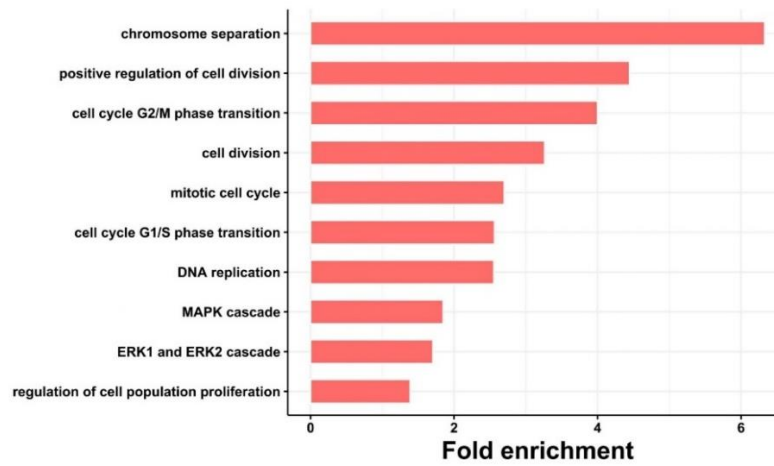
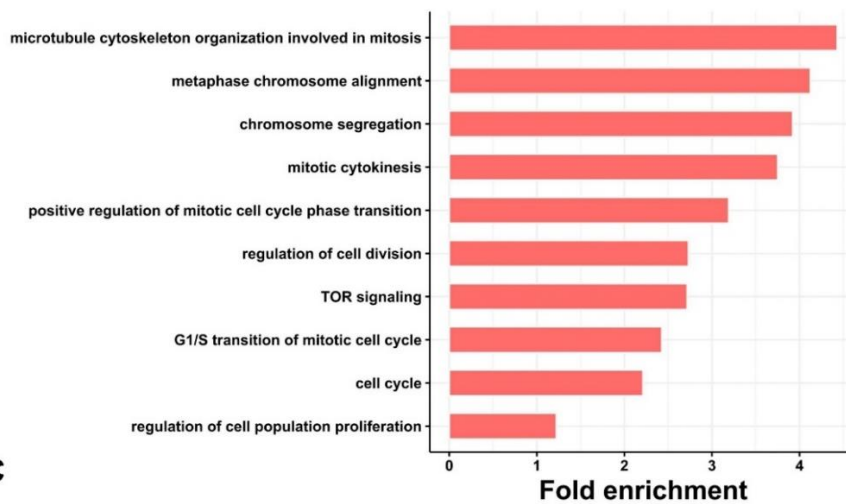
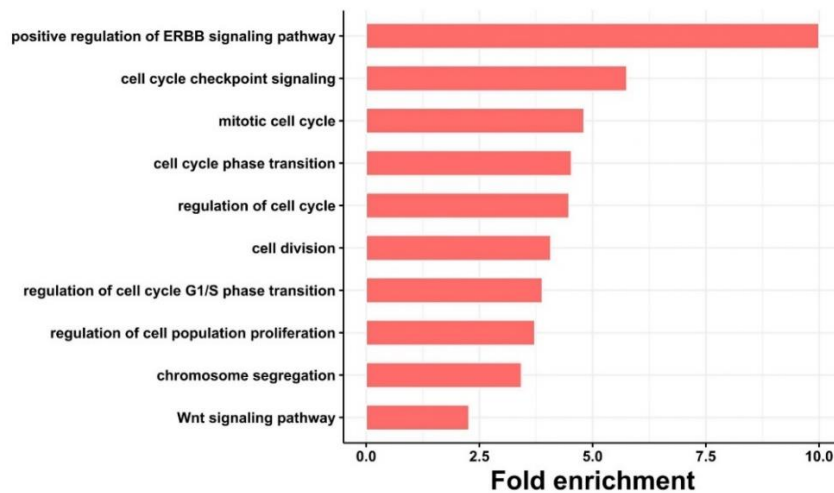
A**B****C**

Figure S1. Gene Ontology functional enrichment analysis. Gene Ontology (GO) functional enrichment analysis of differentially expressed proteins involved in different biological processes (BP) upon (A) knockdown of Malat1 (n=3), (B) mimicking of miR-499-5p (n=3), and (C) knockdown of Meis1 (n=3) in C166 cells. All terms were significantly enriched, *P < 0.05.

Supplementary Figure S2

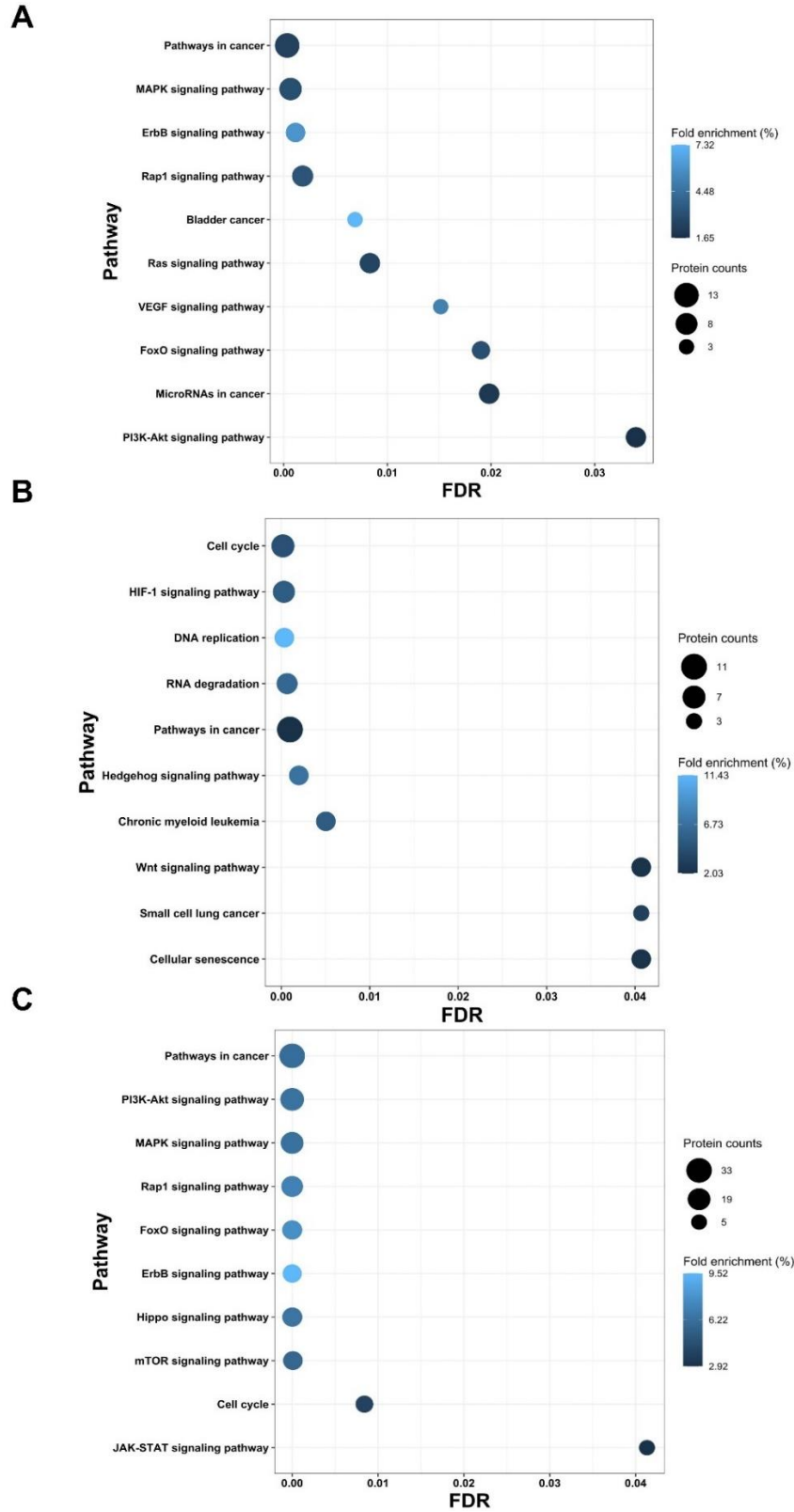


Figure S2. KEGG enrichment analysis. KEGG enrichment analysis of differentially expressed proteins involved in various pathways upon (A) knockdown of Malat1 (n=3), (B) mimicking of miR-499-5p (n=3), and (C) knockdown of Meis1 (n=3) in C166 cells.

Supplementary Figure S3

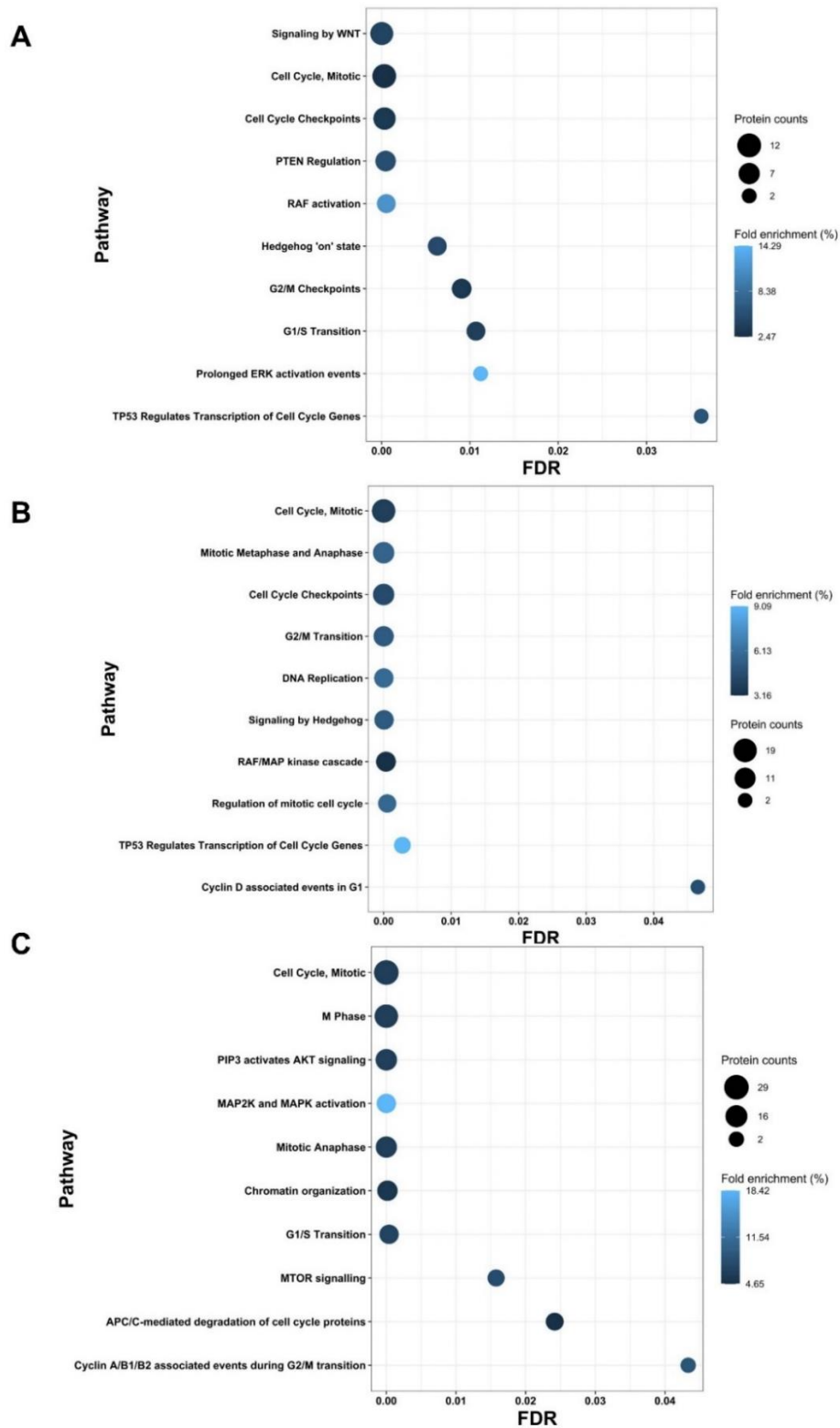


Figure 8. Reactome enrichment analysis. Reactome enrichment analysis of differentially expressed proteins involved in various pathways upon (A) knockdown of Malat1 (n=3), (B) mimicking of miR-499-5p (n=3), and (C) knockdown of Meis1 (n=3) in C166 cells.