

Figure S1. Heatmap of differentially expressed genes between ESCC and normal esophageal tissues from the GSE20347, GSE67269, and GSE38129 datasets.

Figure S2: Lipid peroxidation after transfection with siRNAs in ECA109 cells.

Figure S3: GSEA analysis of the prognostic signature.

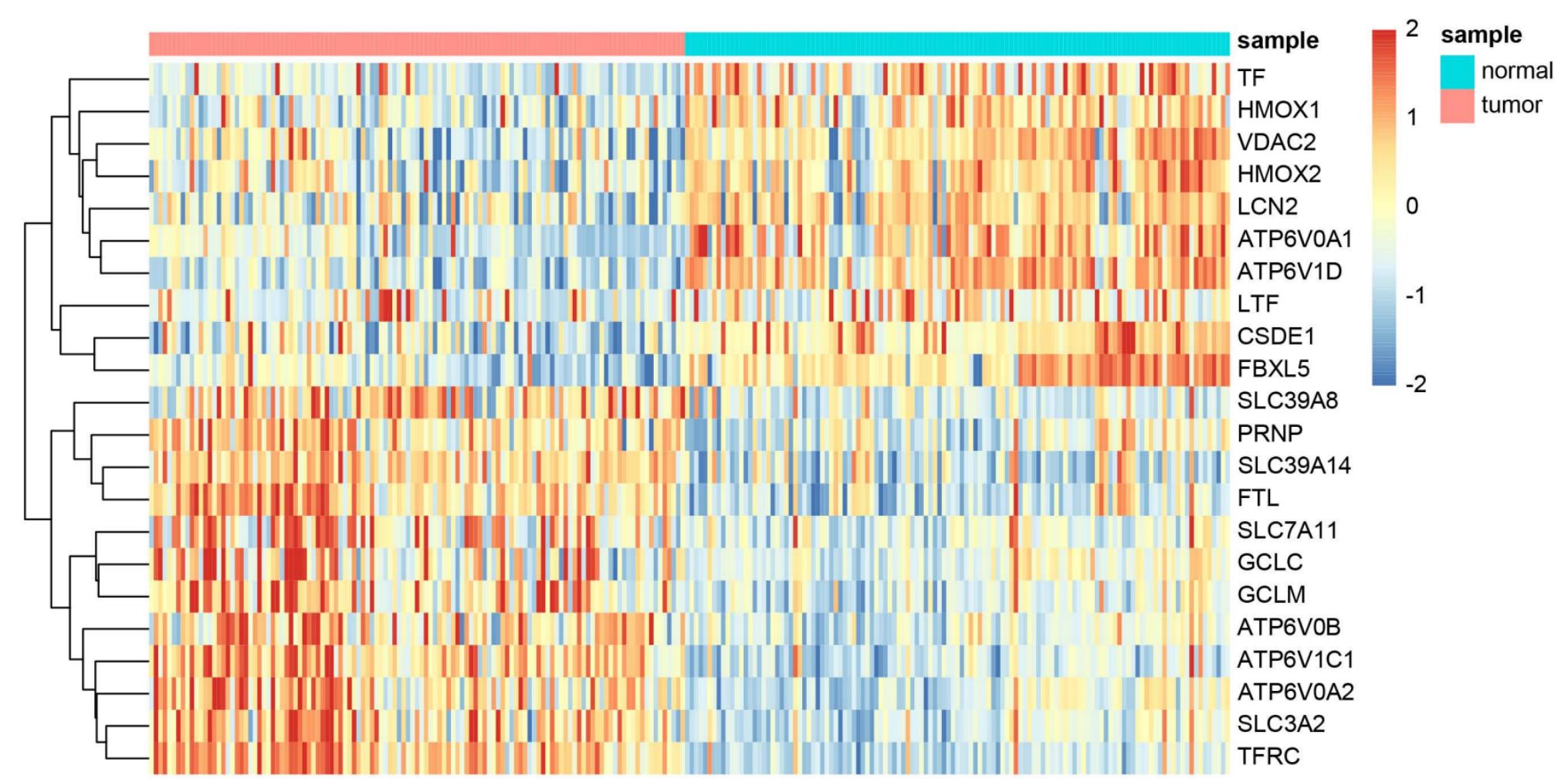
Figure S4: Kaplan-Meier curves of grade (A), T stage (B), stage (C), age (D), adjuvant therapy (E), and N stage (F) from the GSE53625 dataset.

Figure S5: Forest map of the 112 ESCC patients from Zhongshan Hospital, Fudan University.

Figure S6: Correlation of highly mutated genes in the low and high score group based on the TCGA database.

Figure S7: Correlation of key genes expressions and immune cell infiltration based on the TIMER database.

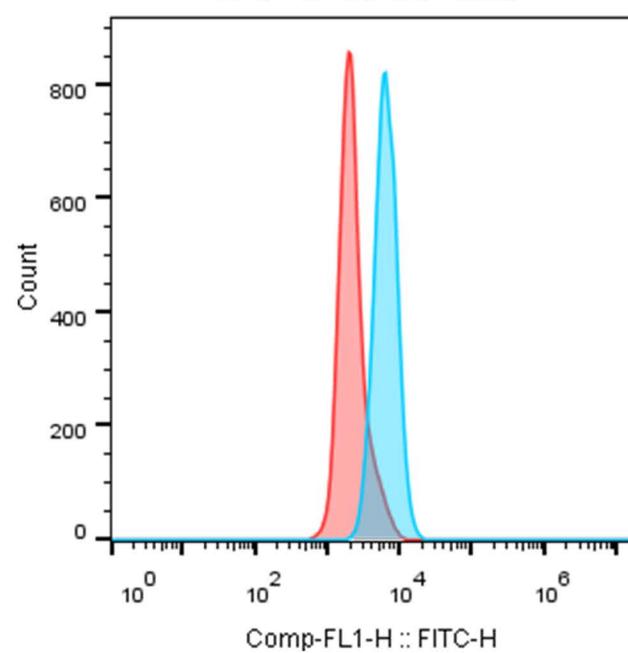
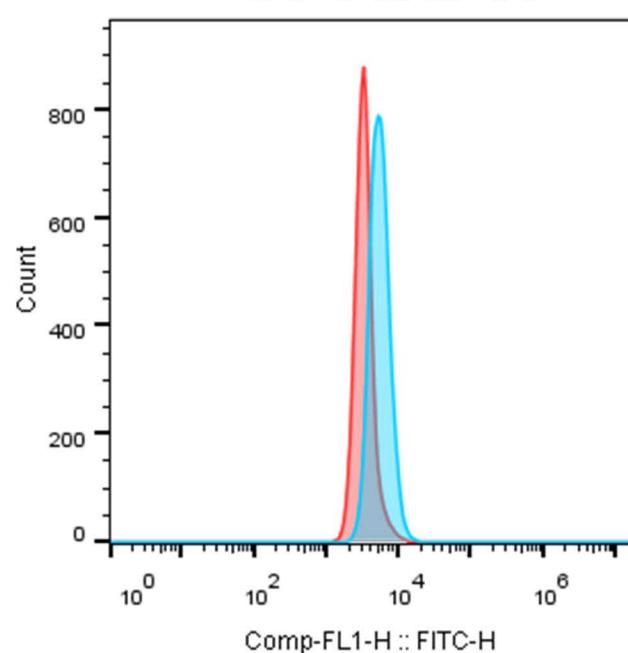
Figure S8: Anti-cancer drug sensitivity between the low and high score group based on the GDSC database.



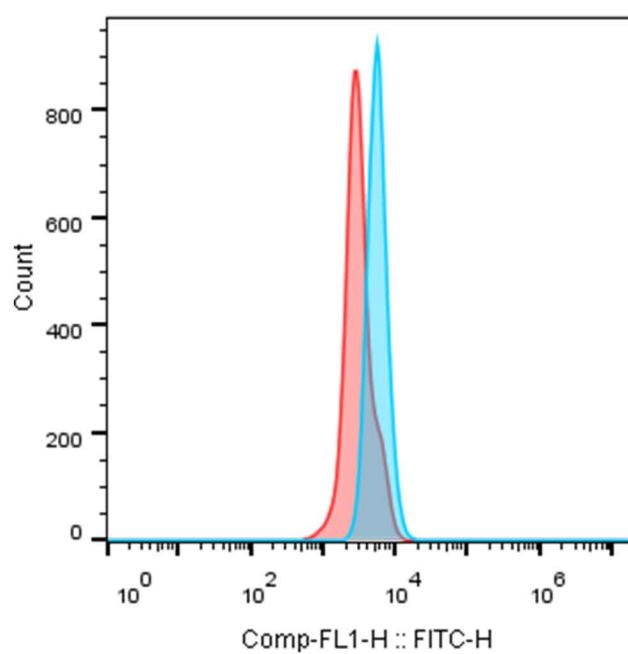
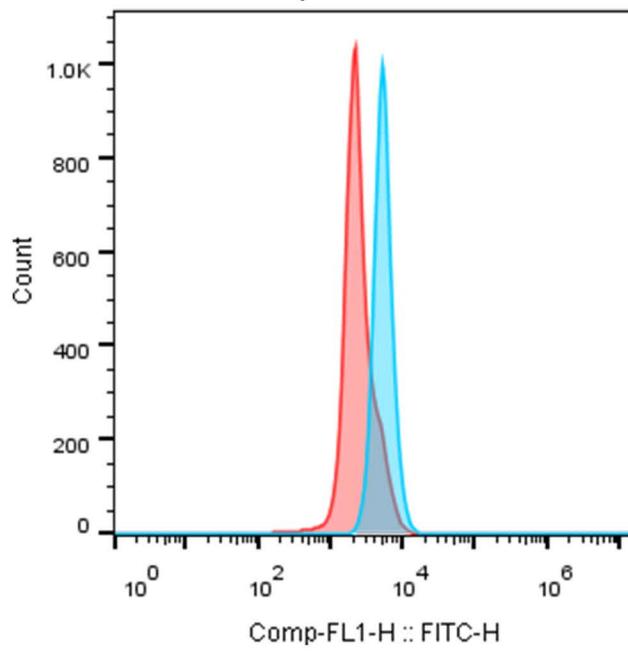


 si-RNA  
 NC

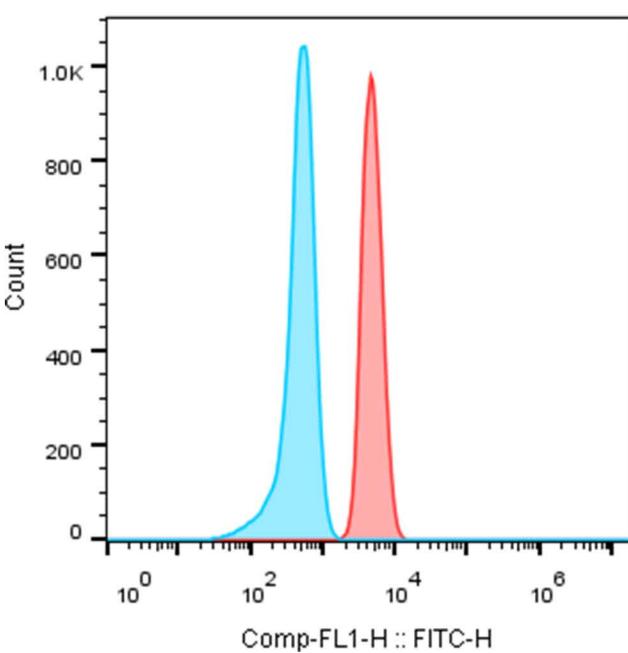
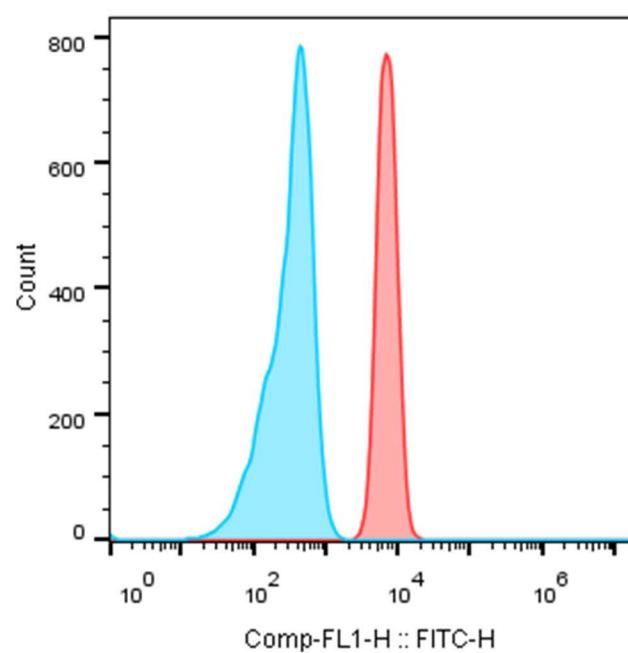
PRNP



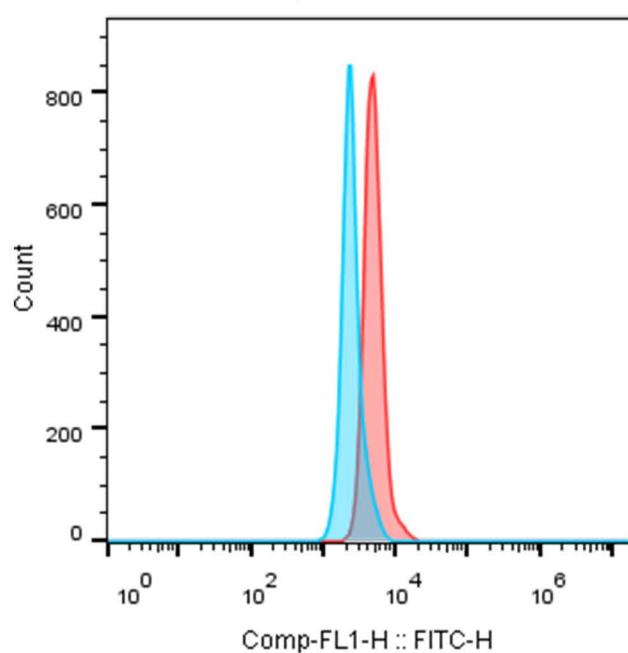
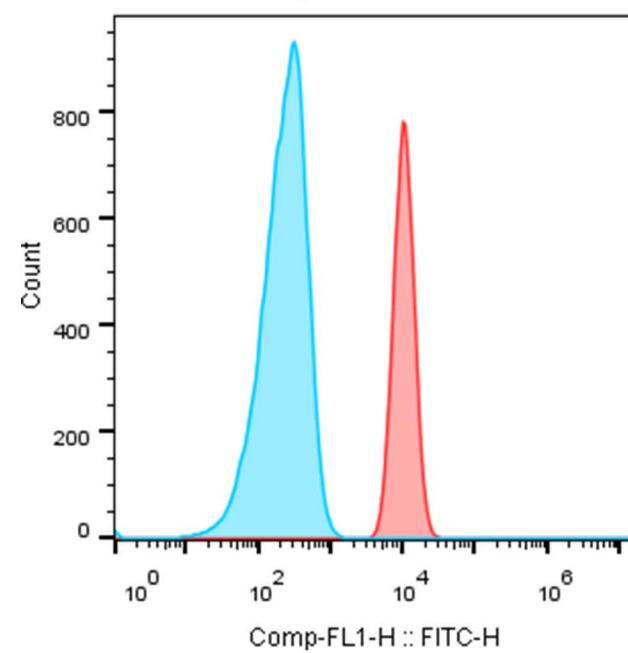
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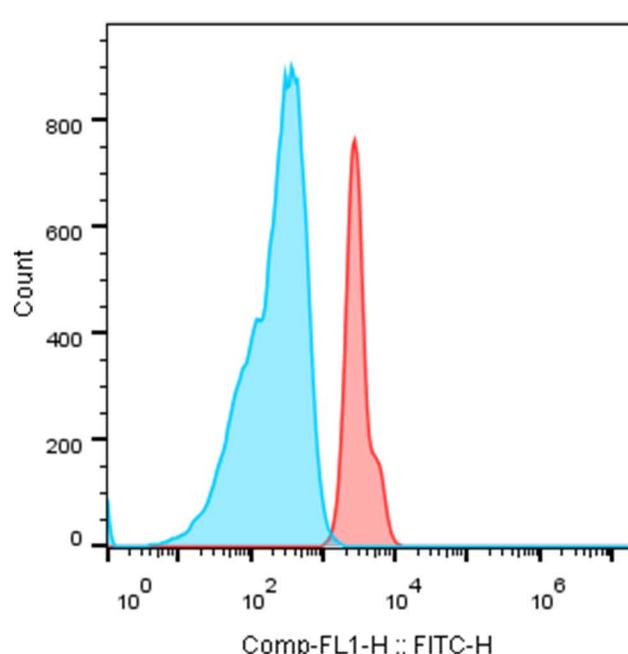
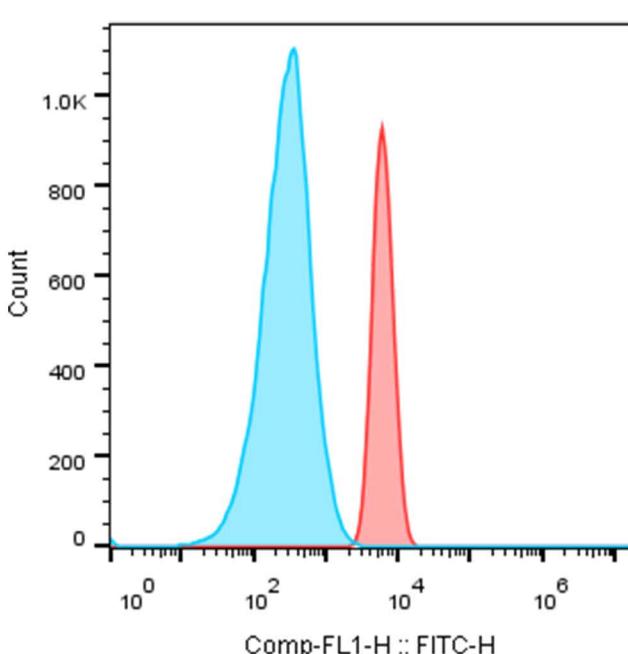
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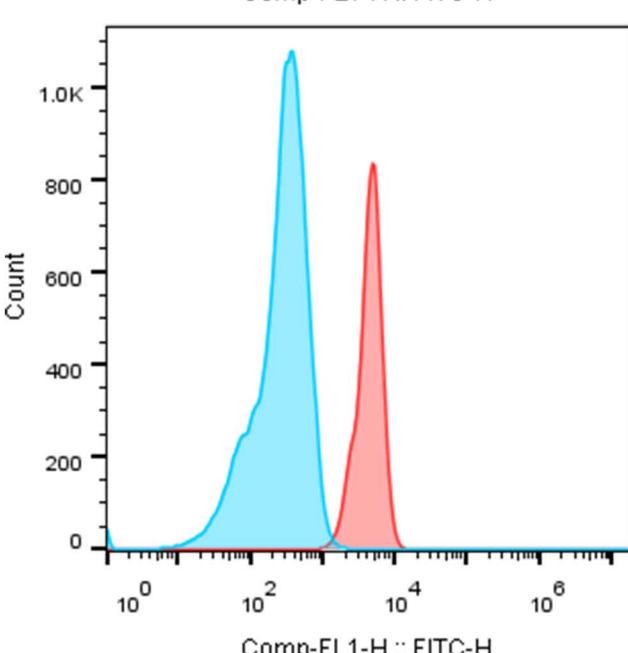
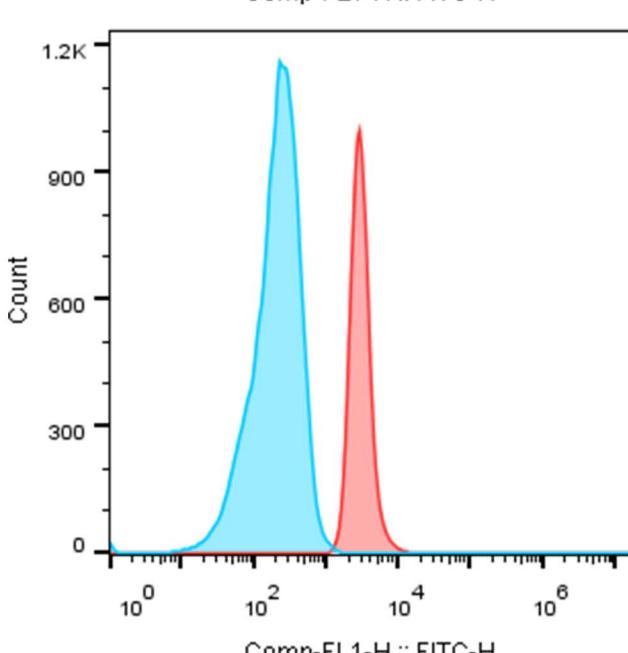
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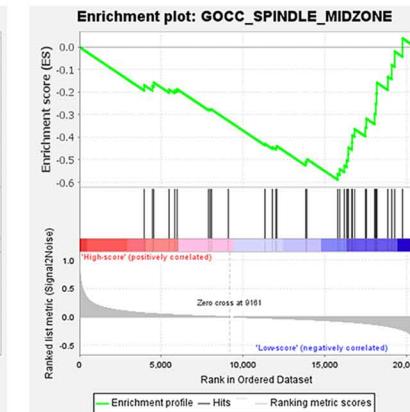
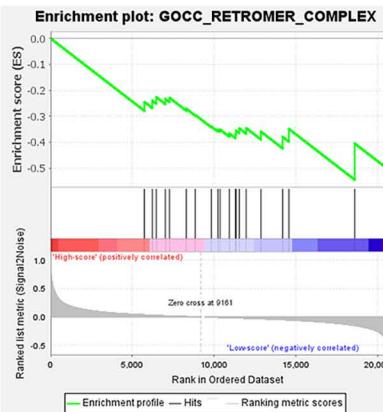
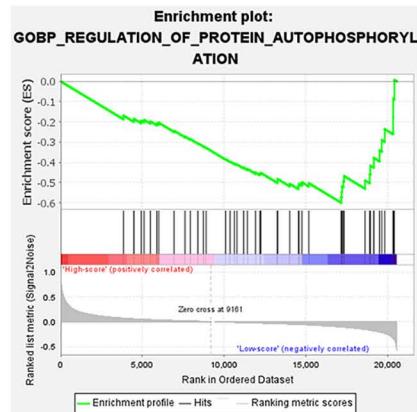
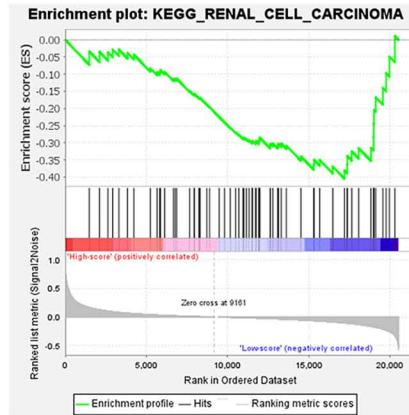
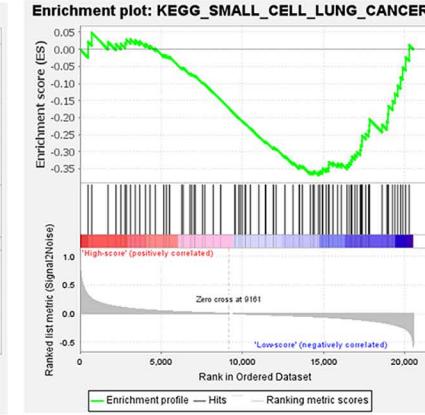
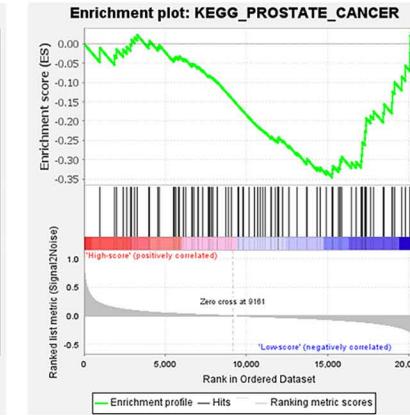
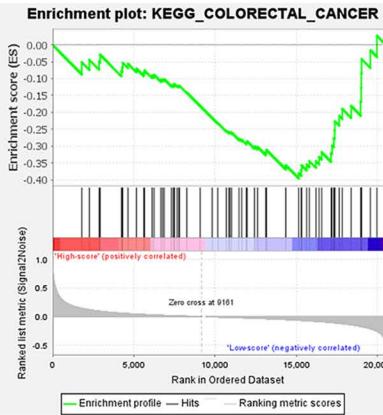
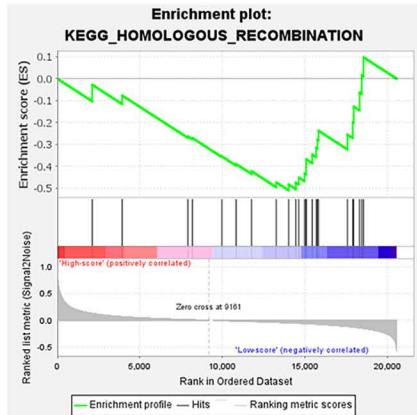
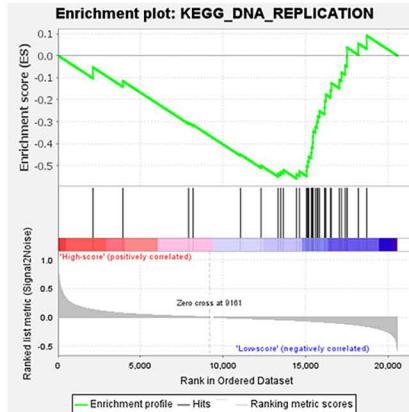
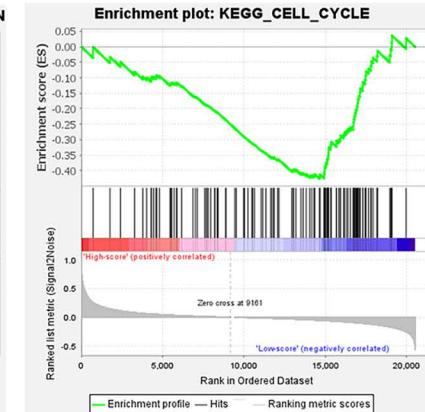
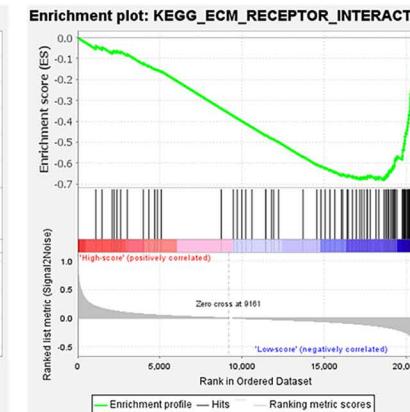
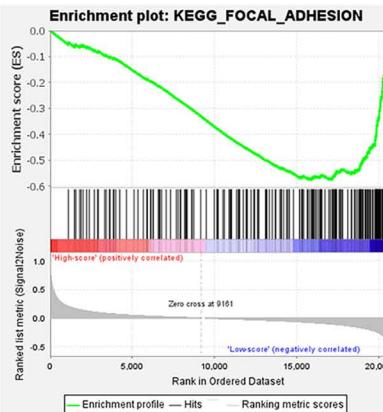
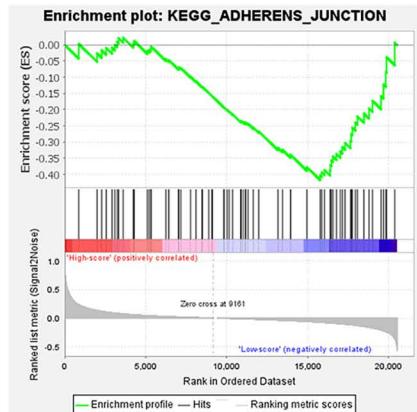


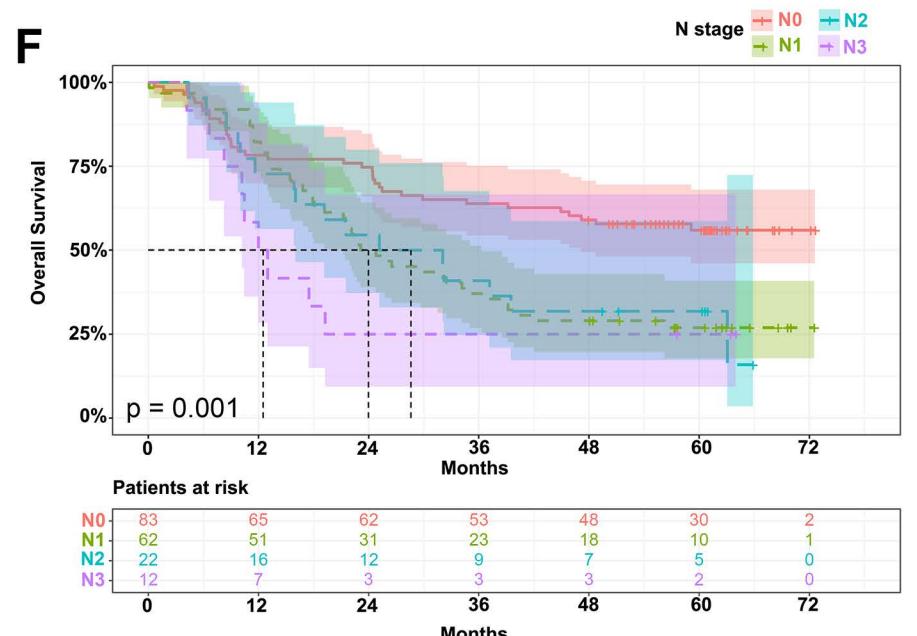
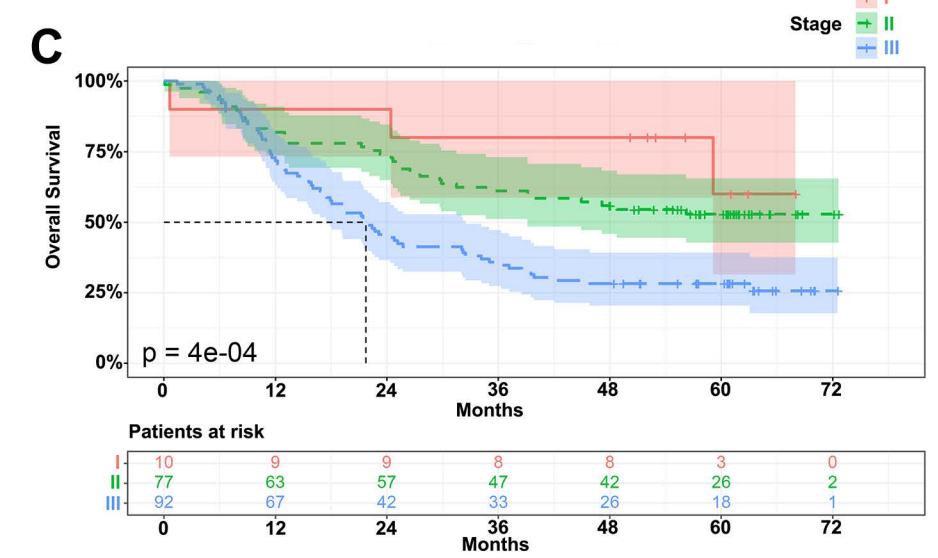
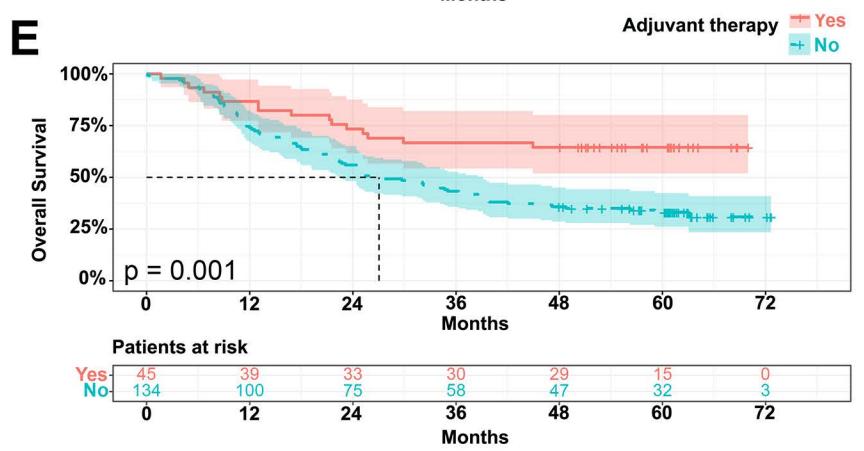
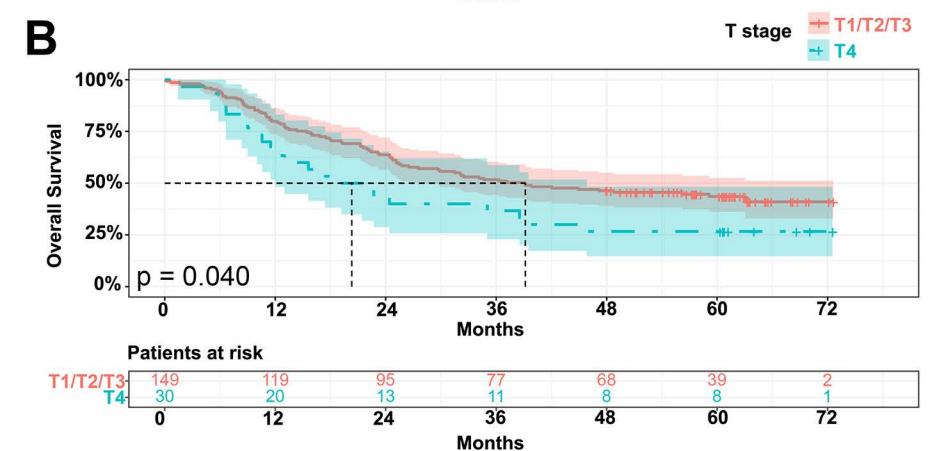
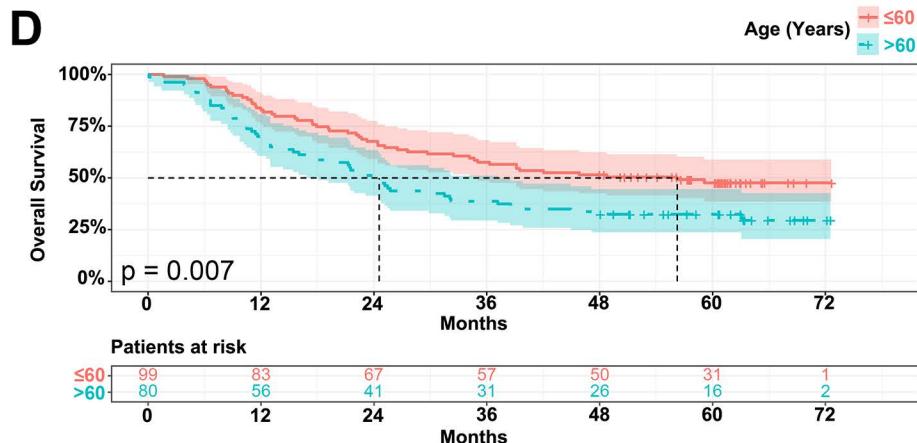
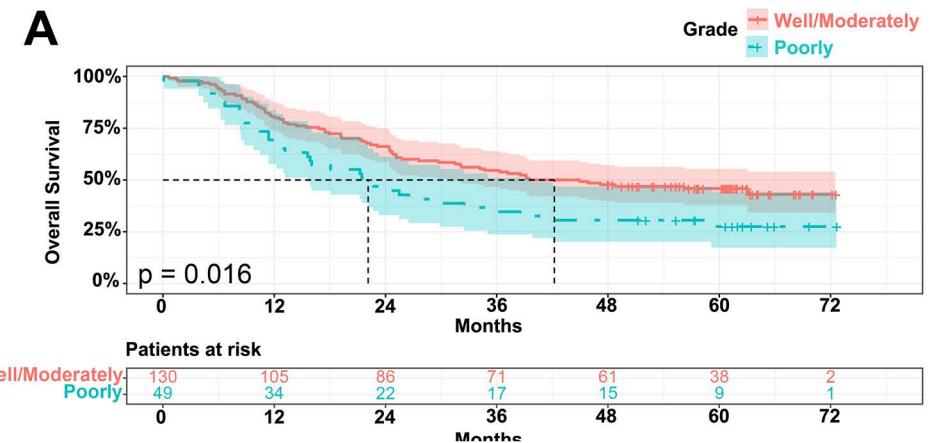
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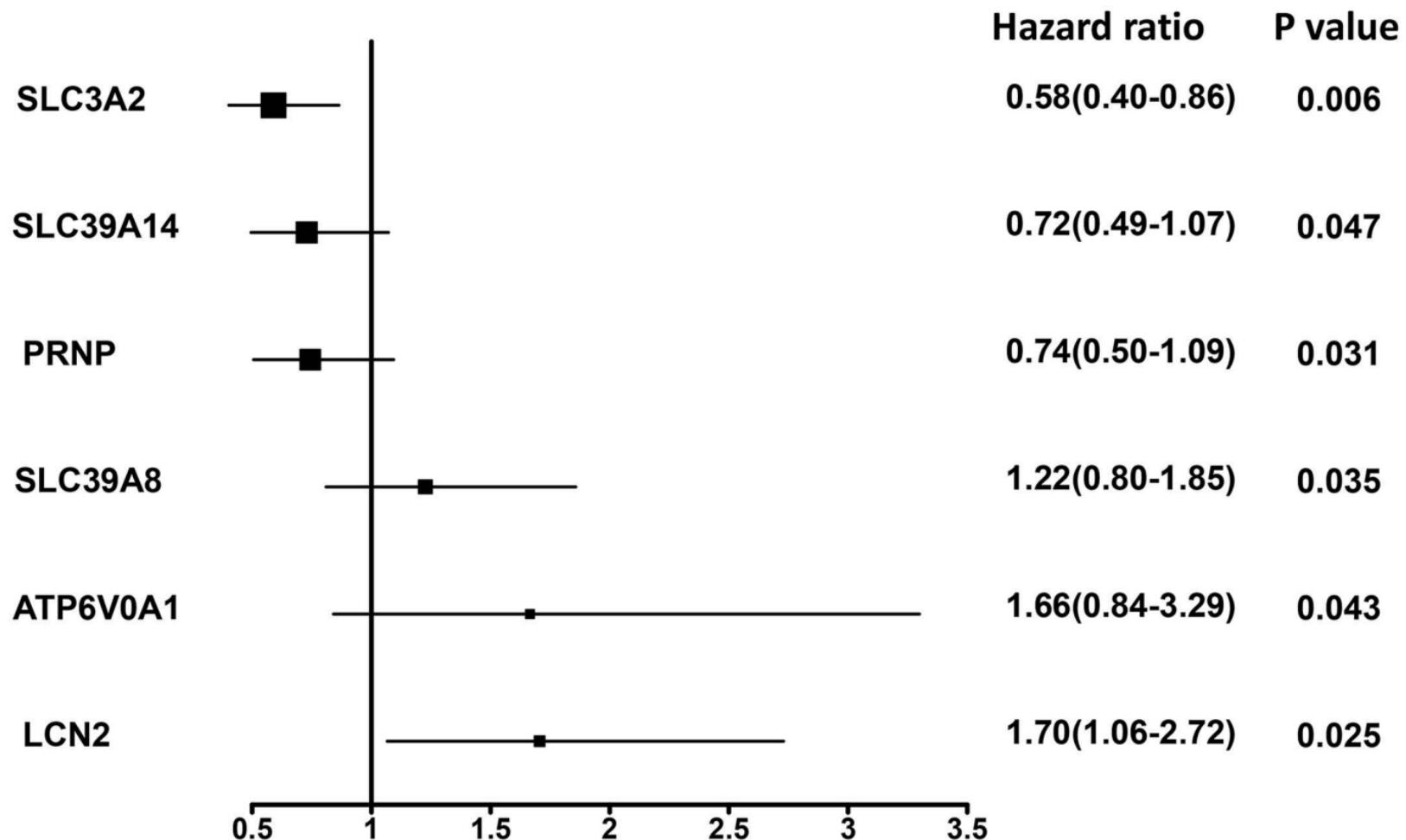


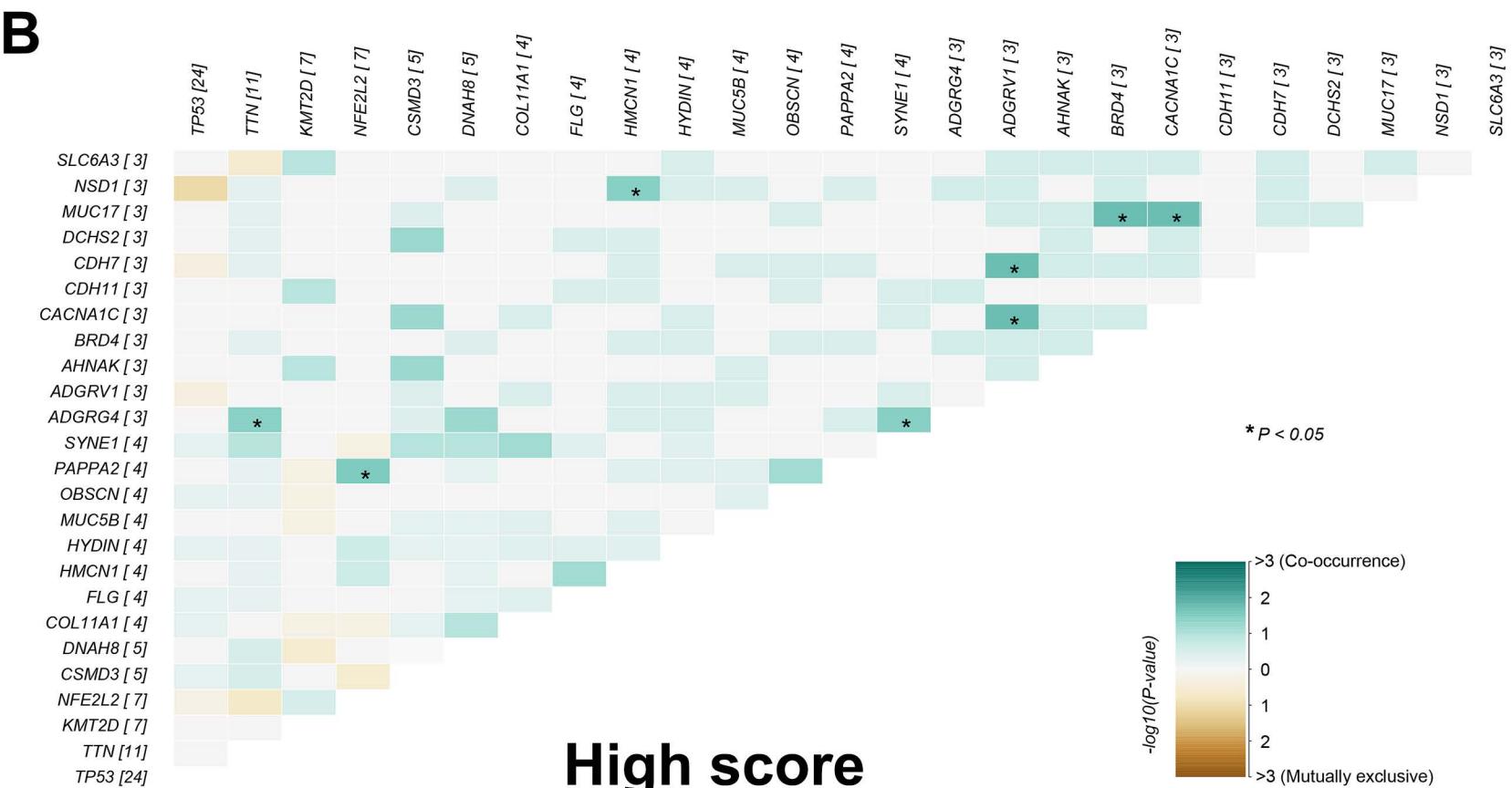
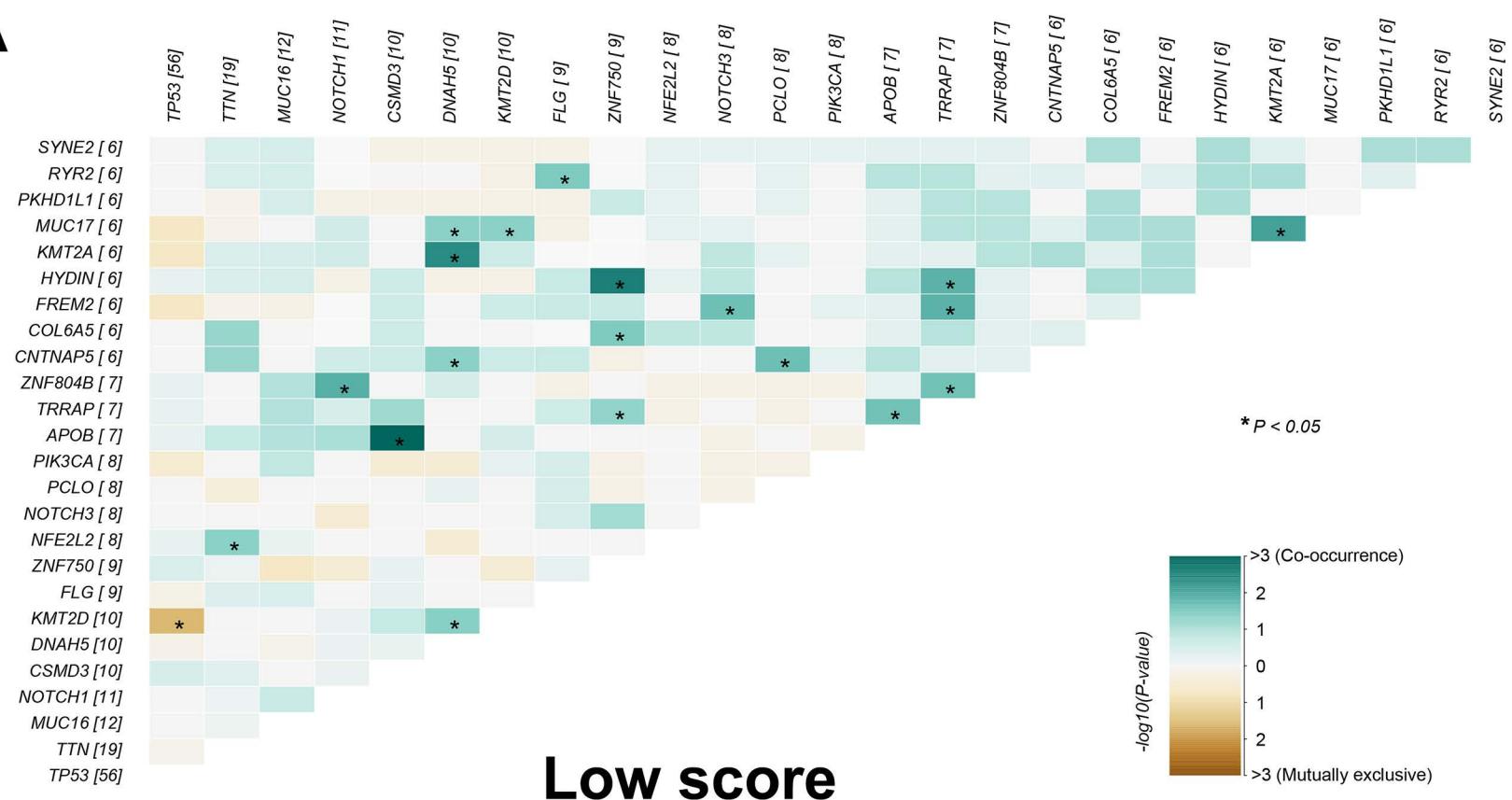
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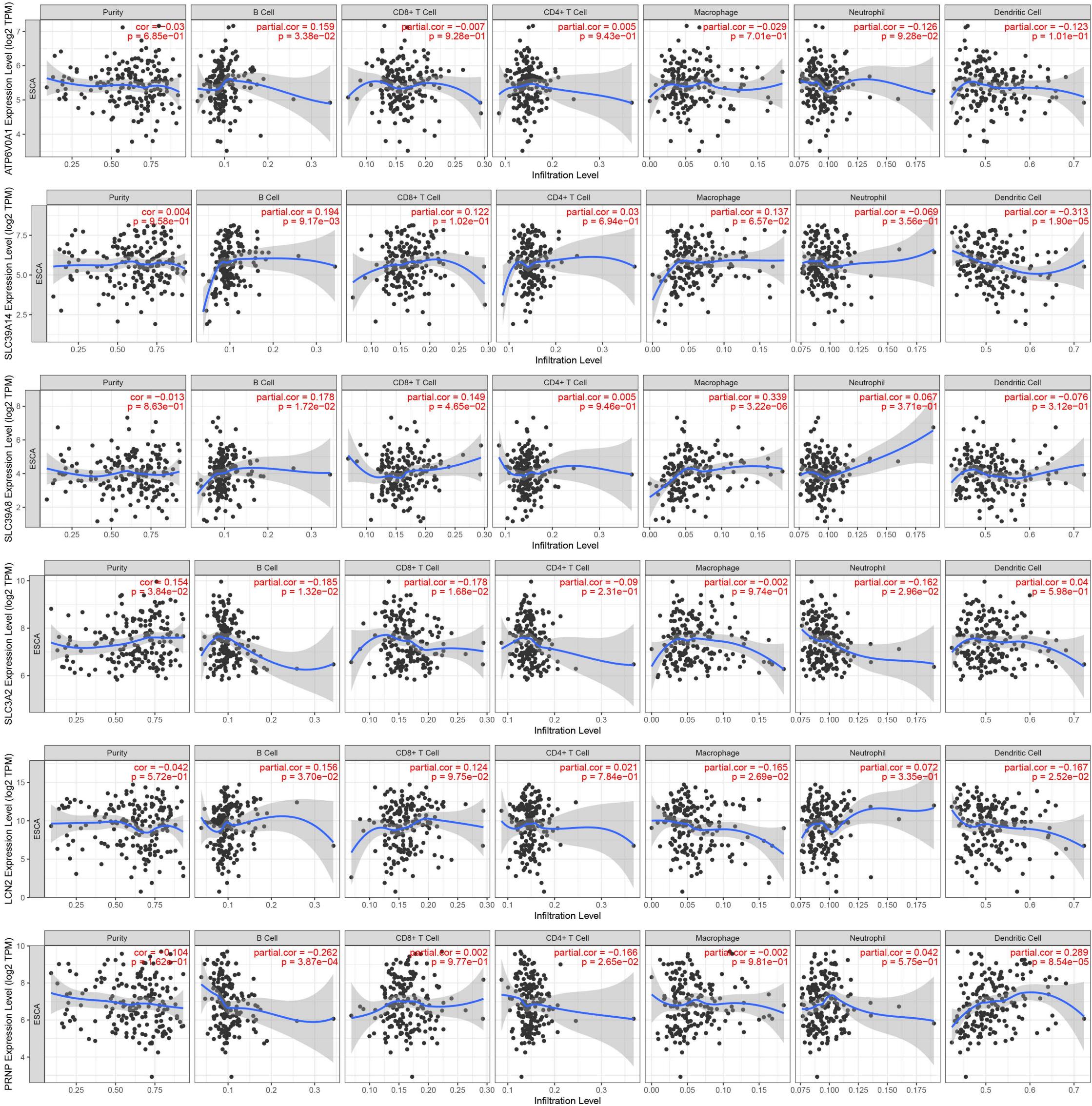


**A****B**









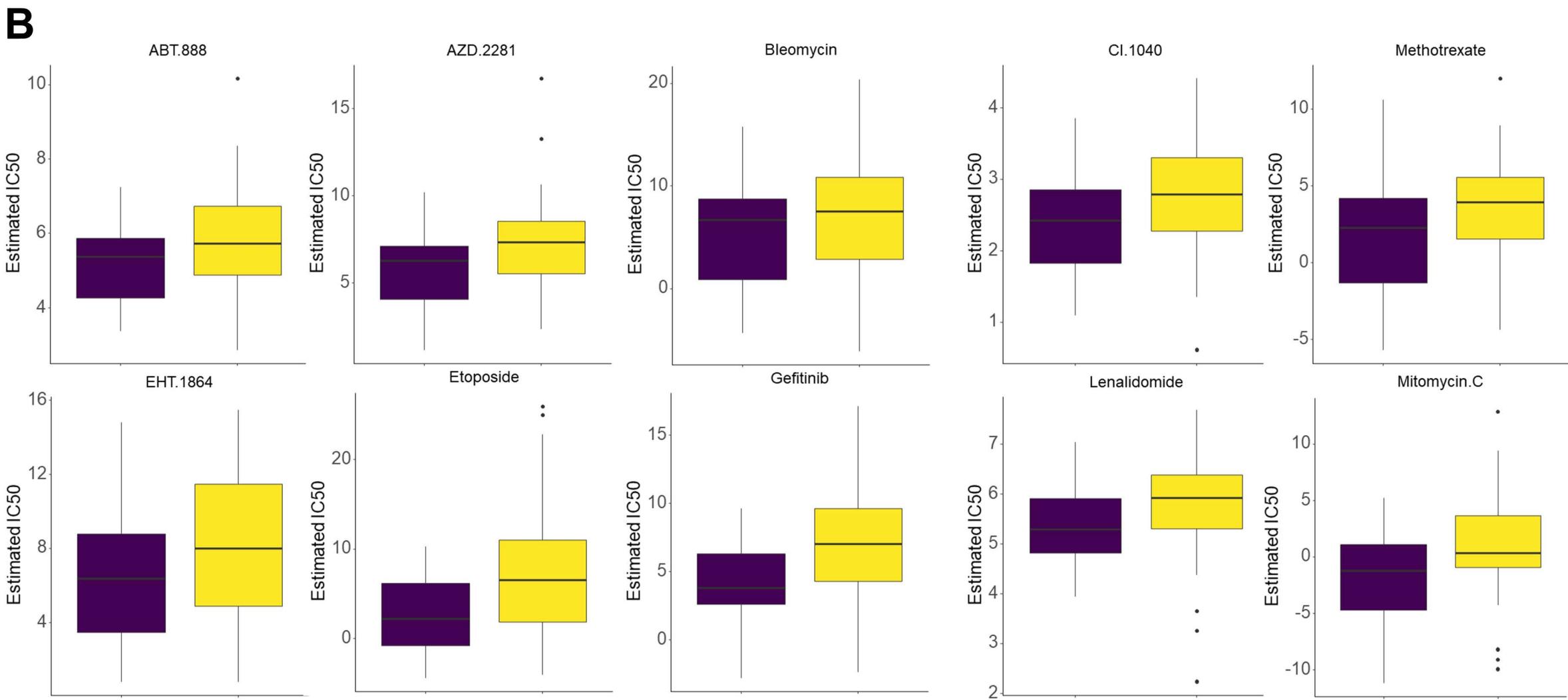
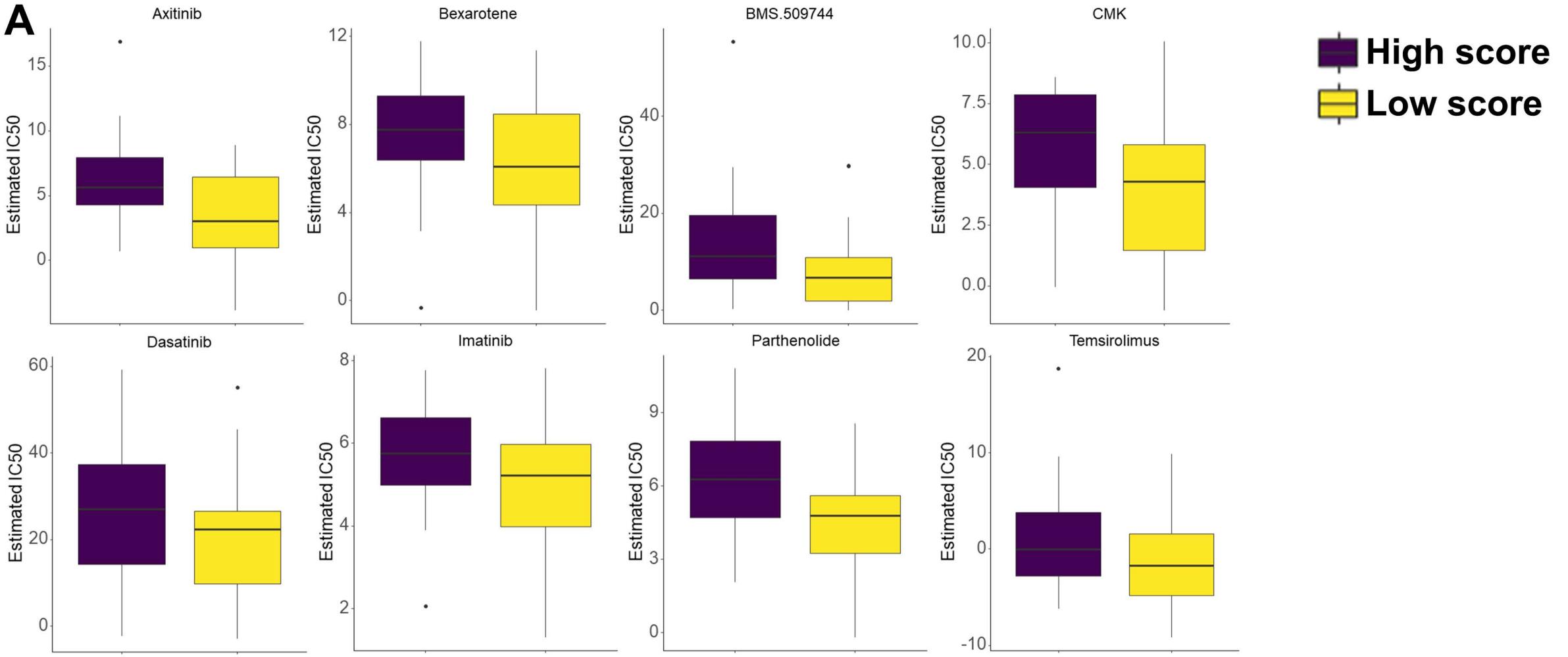


Table S1: Sequence of siRNAs and Primers of prognostic genes.

	siRNA1 (5'-3')	siRNA2 (5'-3')	Primer (5'-3')
PRNP	AUCAUUACAGCAGUG AACUG	AAACACUUCAAAUCA UAUGGG	F: AGTCAGTGGAACAAAG CCGAG R: CTGCCGAAATGTATGAT GGGC
SLC3A 2	UAGAUGUUUACCACA AACGAC	AUCUUCAUGAAUUG UAGCUA	F: TGAATGAGTTAGAGCC CGAGA R: GTCTCCGCCACCTTG ATCTT
SLC39 A8	UCAUAUACAAAGUGA AGUCUA	UAAGUAACUCAUCC UAUCUA	F: ATGCTACCCAAATAAC CAGCTC R: ACAGGAATCCATATCC CCAAACT
SLC39 A14	UGGUUAAGGAGAUCU AGUCUG	UUUCUUCUCUGAAGA AAUCAG	F: GAGGCTCACGCTTCAT CCC R: CCCTGCCATACCGAT GTATTA
ATP6V 0A1	UGAAGAACAGCAAU UCUGCA	UAUGAAGAACAGCA AUUCUG	F: GGGAGCGCATCCCTAC TTTT R: GGTTCTCGATTTCAGC CTGTC
LCN2	UGACAUUGUAGCUCU UGUCUU	UGUGCUALAACGUU GCUCUA	F: CCACCTCAGACCTGAT CCCA R: CCCCTGGAATTGGTTG TCCTG