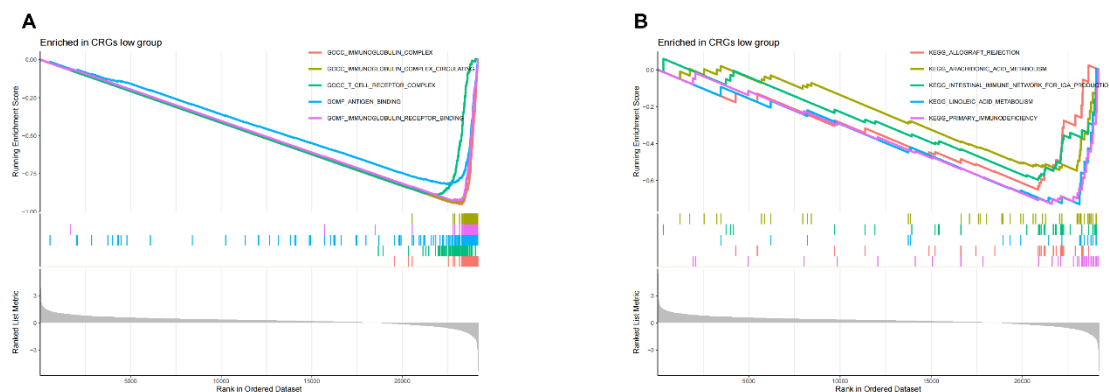# Supplementary information

Figure S1. A and B, Genomic enrichment analysis (GSEA) of high/low expression groups of centrosome-related genes
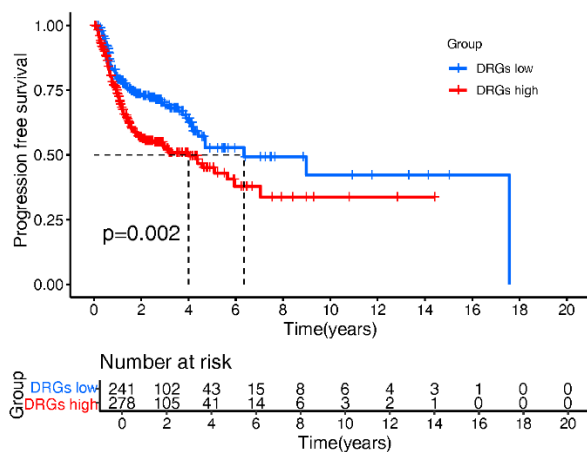

Figure S2. Kaplan-Meier analysis of progression free survival curves for TCGA patients in the DRGs high/low groups.
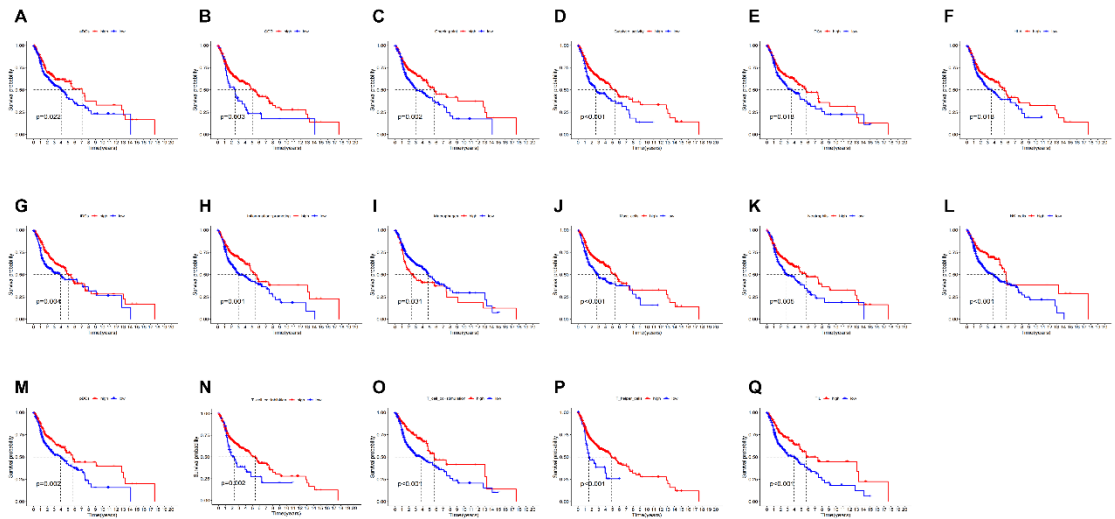
Figure S3. A to T, Kaplan-Meier analysis of OS curves in patients with high and low immunocompetence differences.
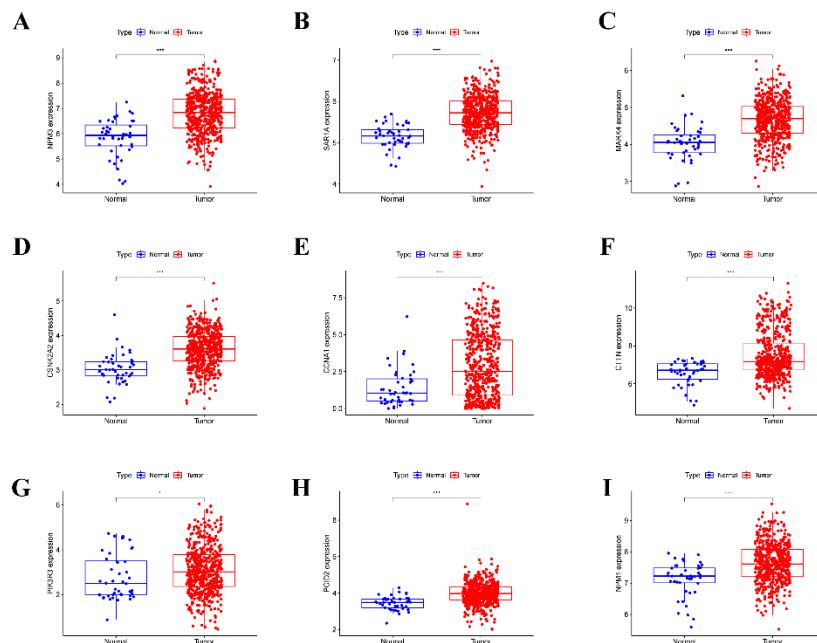

Figure S4. mRNA expression of SAR1A, NPM1, NMP3, CTTN, CSNK2A2, PIK3R3, PCID2, MARK4 and CCNA1 between normal and tumor in TCGA.

Table S1 Primer sequences used for Q-PCR and Real-time PCR

Gene Name	Primer	Sequence
CCNA1	Forward	GCACACTCAAGTCAGACCTGCA
	Reverse	ATCACATCTGTGCCAAGACTGGA
PIK3R3	Forward	CCACCTAAGCCAATGACTTCAGC
	Reverse	GTTGAGGCATCTCGGACCAAGA
CSNK2A2	Forward	CGACCATCAACAGAGACTGACTG
	Reverse	GTGAGACCACTGGAAAGCACAG
CTTN	Forward	AGGTGTCCTCTGCCTACCAGAA
	Reverse	CCTGCTCTTTCTCCTTAGCGAG
NMP3	Forward	TGACCATCAGGAGATCGCAGTC
	Reverse	TTCAGGCGGAAGGTTACAGGTG
NPM1	Forward	GCCAGTGCATATTAGTGGACAGC
	Reverse	GGAACCTTGCTACCACCTCCAG
PCID2	Forward	CTGCGGAATCTTCCTCATCCTG
	Reverse	GGCAACCAGAAAAGCATCCAGAG
SAR1A	Forward	GGGCTTTATGGACAGACCACAG
	Reverse	CCGTAACCTTGCCTCTTGAGCA
MARK4	Forward	GTCAACAGACTGTGAGAGCATCC
	Reverse	GCTCTGTGTATGGCTTCAACTCC
ACTB	Forward	CACCATTGGCAATGAGCGGTTC
	Reverse	AGGTCTTTGCGGATGTCCACGT