

Table S1 The five-lncRNAs-associated target genes and miRNAs using online tools

target genes and miRNAs of five-lncRNAs					
	genes				miRNAs
A1CF	RBFOX1	PTBP1	HNRNPA2B1	U2AF2	hsa-mir-152-5p
BUD13	RBFOX2	PTBP2	HNRNPK	UCHL5	hsa-mir-216a-5p
CELF6	RBM15	PUM2	HNRNPL	UPF1	hsa-mir-2277-5p
CPEB2	RBM22	QKI	HNRNPLL	YBX3	hsa-mir-30b-3p
CPEB4	RBM24	RALY	HNRNPU	LIN28A	hsa-mir-4455
CPSF6	RBM27	METAP2	HNRNPUL1	LIN28B	hsa-mir-4477a
DDX3X	RBM28	PABPC1	IGF2BP1	LSM11	hsa-mir-4511
DDX55	RBM4	PABPC3	IGF2BP2	MATR3	hsa-mir-4645-3p
DDX6	RBM41	PABPC5	ILF3	SRSF9	hsa-mir-506-5p
EFTUD2	RBM42	PPIL4	KHDRBS1	SUB1	hsa-mir-6071
ELAVL1	RBM46	PPRC1	KHDRBS3	TARDBP	hsa-mir-7156-3p
ELAVL2	RBM4B	PRPF8	KHSRP	TIA1	hsa-mir-4703-5p
ENOX1	RBM5	TRA2A	RPS5	SRSF10	
FAM120A	RBM8A	TROVE2	SAFB2	SRSF12	
FUS	RBMS3	U2AF1	SART3	SRSF2	
SRSF1	SNRNP70	SND1	SF3B1	SF3B4	

Supplementary Figures Legends

Figure S1 Clinical features before and after propensity score matching between early BCR and long-term BCR survival groups.

Figure S2 The Enrichment Map of five-lncRNAs signature associated biological signaling pathway using GSEA (A, B). Circos plot showed the most correlated and co-expressed genes of PRKAG2-AS1 (C) and CRNDE (D) with respect to genomic coordinates.

Figure S3 Notable pathway enrichment of the target genes (A) and the enrichment in the GO terms: molecular function (B), biological process (C), cellular component (D).

Figure s1

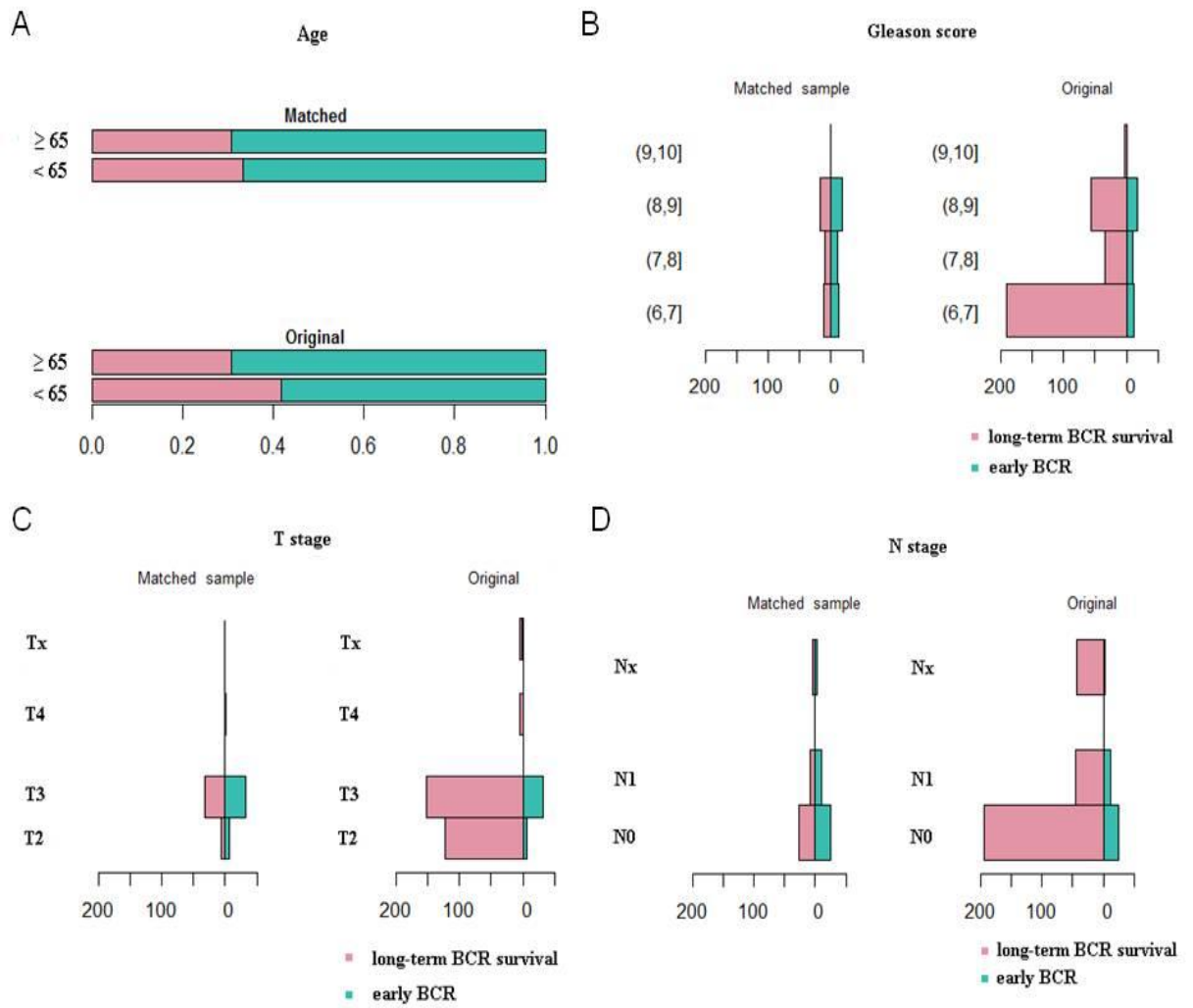


Figure s2

