

Supplemental material

Supplemental Figures and Figure Legends

Fig. S1 Identification of cytokine-related genes as probable target genes of

SH3PXD2A-AS1. **A** Principal component analysis (PCA) shows the relationship and variation between samples. **B** The volcano map shows the gene/transcript expression differences between samples. The abscissa is the multiple of the difference in gene/transcript expression between the two samples, and the ordinate is the statistical test value of the difference in gene expression.

Fig. S2 Correlation analysis showed the correlations among FOXM1, CENPF,

KIF20A and SH3PXD2A-AS1. **A, B** The correlations among FOXM1, CENPF and KIF20A in LUAD tissue as assessed by GEPIA. **C, D, E** The correlations between SH3PXD2A-AS1 and FOXM1, SH3PXD2A-AS1 and CENPF, SH3PXD2A-AS1 and KIF20A in LUAD tissue as assessed by GEPIA. We used the nonlog scale for calculation and used the log-scale axis for visualization. Statistical analysis: Data were analysed using Pearson correlation analysis.

Fig. S3 SH3PXD2A-AS1 accelerates lung cancer cell cycle progression. A, B

The original FACS images for cell cycle analysis.

Fig. S4 Downregulation of DHX9 reverses the effects on cell cycle progression

induced by SH3PXD2A-AS1 overexpression. A, B The original FACS images for cell cycle analysis.

Fig. S5 Knockdown of SH3PXD2A-AS1 inhibits cell metastasis. A, B

Effects of SH3PXD2A-AS1 knockdown on migration and invasion of H292 and H23 cells. Lnc2(SH3PXD2A-AS1). ** $P < 0.01$, *** $P < 0.001$.

Fig. S6 Overexpression of SH3PXD2A-AS1 and DHX9 in LUAD correlates with

poor prognosis. A Kaplan–Meier survival curve analysis was performed to explore the

effects of SH3PXD2A-AS1 and DHX9 on the overall survival rate ($P<0.01$) or disease free survival ($P=0.05$) in LUAD.

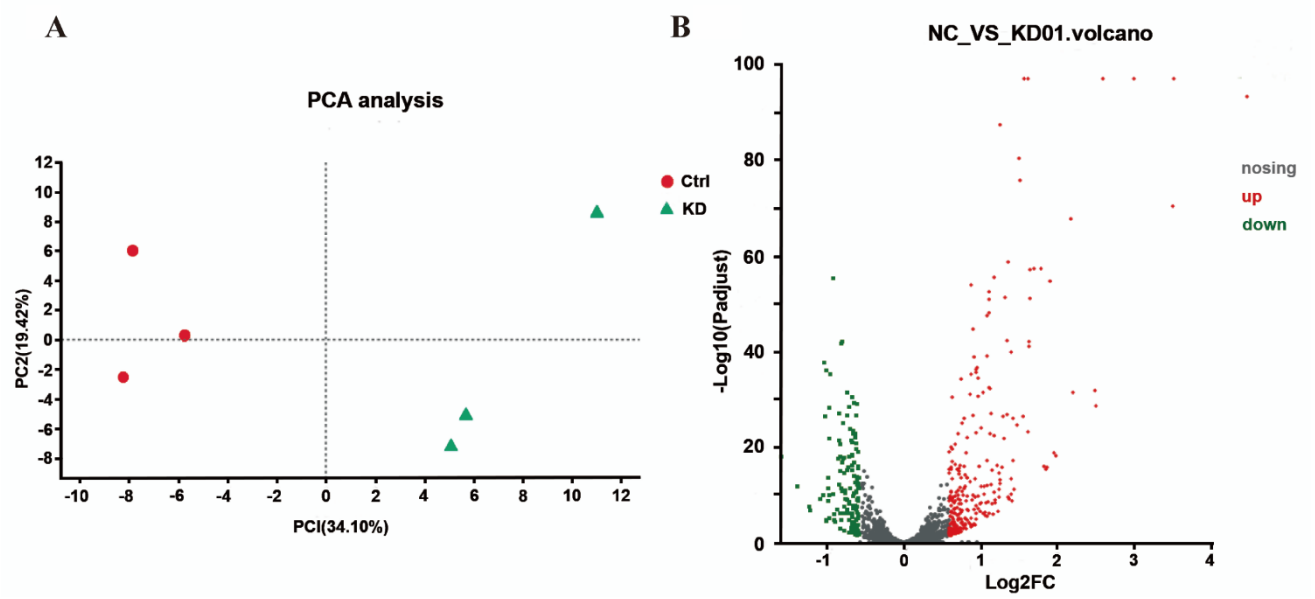
Fig. S7 Quantitative statistics of Western blottings. **A** Western blotting analysis for SH3PXD2A-AS1 OE in H1299 and A549 cells. **B** Western blotting analysis for SH3PXD2A-AS1 KD in H292 and H23 cells. **C** Western blotting analysis for DHX9 KD in H292 and H23 cells. **D** Western blotting analysis for SH3PXD2A-AS1 OE+DHX9 KD in H1299 and A549 cells. Lnc2(SH3PXD2A-AS1). Data are shown as the mean $\pm$ standard deviation from three independent experiments. $*P<0.05$, $**P<0.01$, $***P<0.001$.

Table S1 Text of mass spectrometry result.

Table S2 Text of RNA-Seq result.

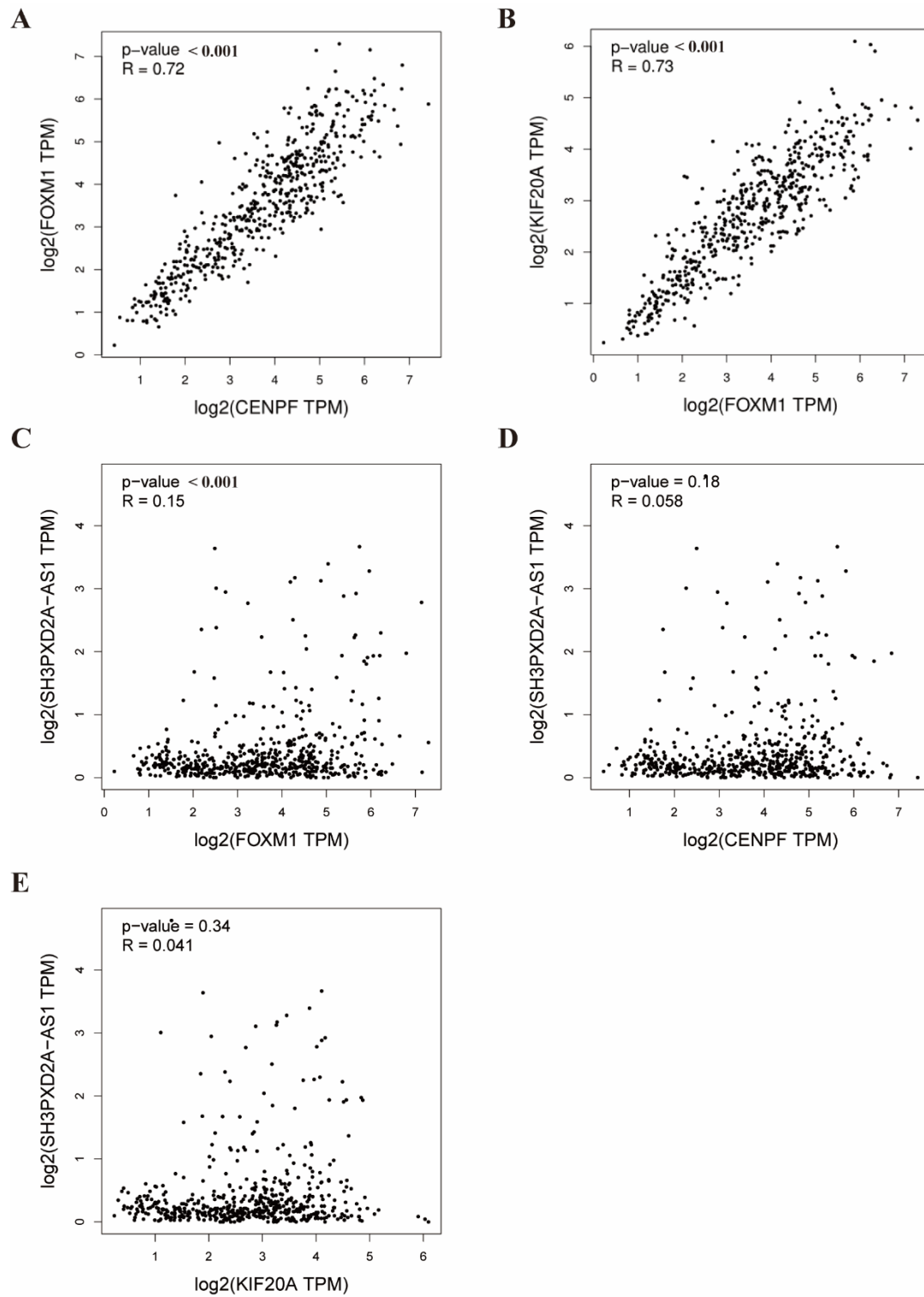
Table S3 Text of GO enrichment result.

Table S4 Text of KEGG enrichment result.



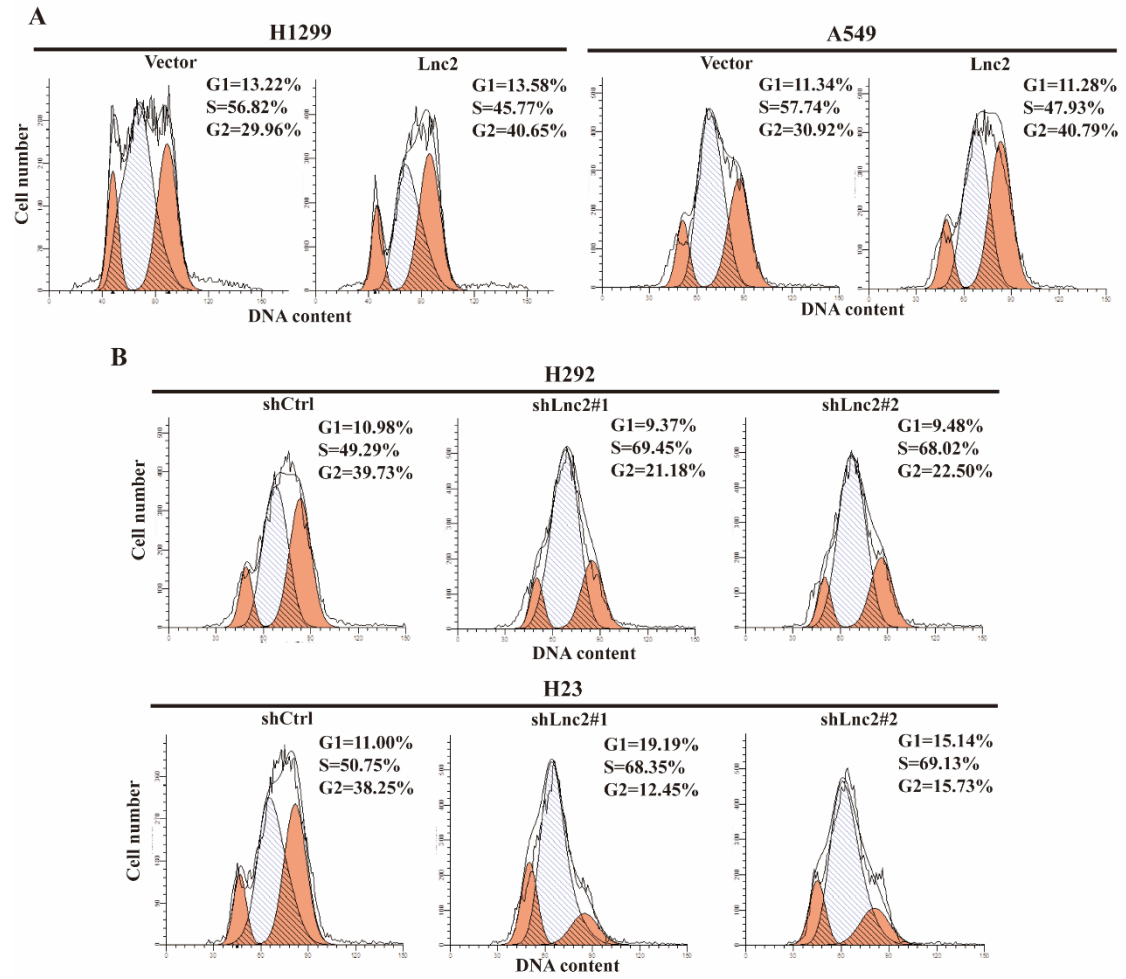
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51 **Figure S1**



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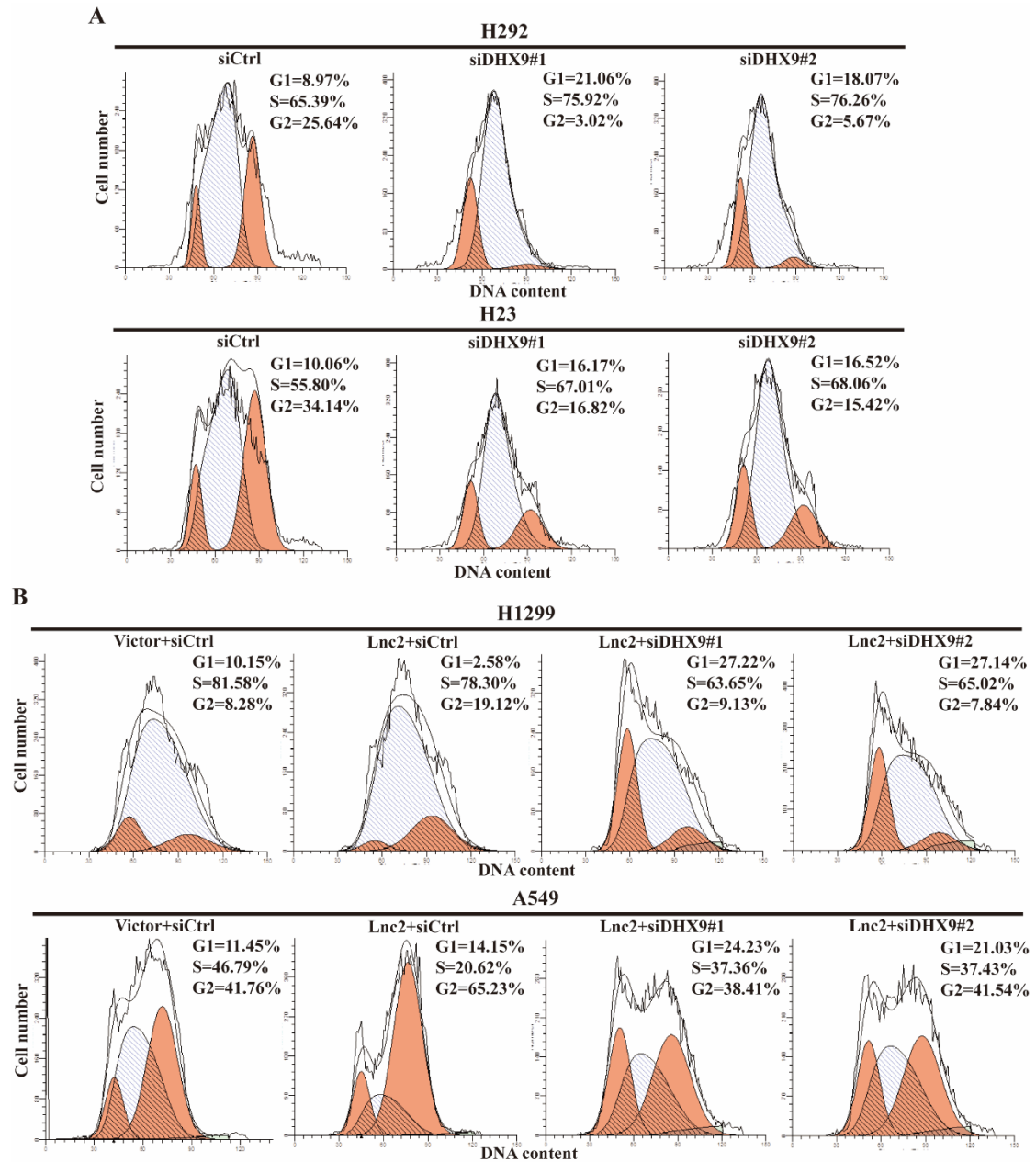


Figure S4

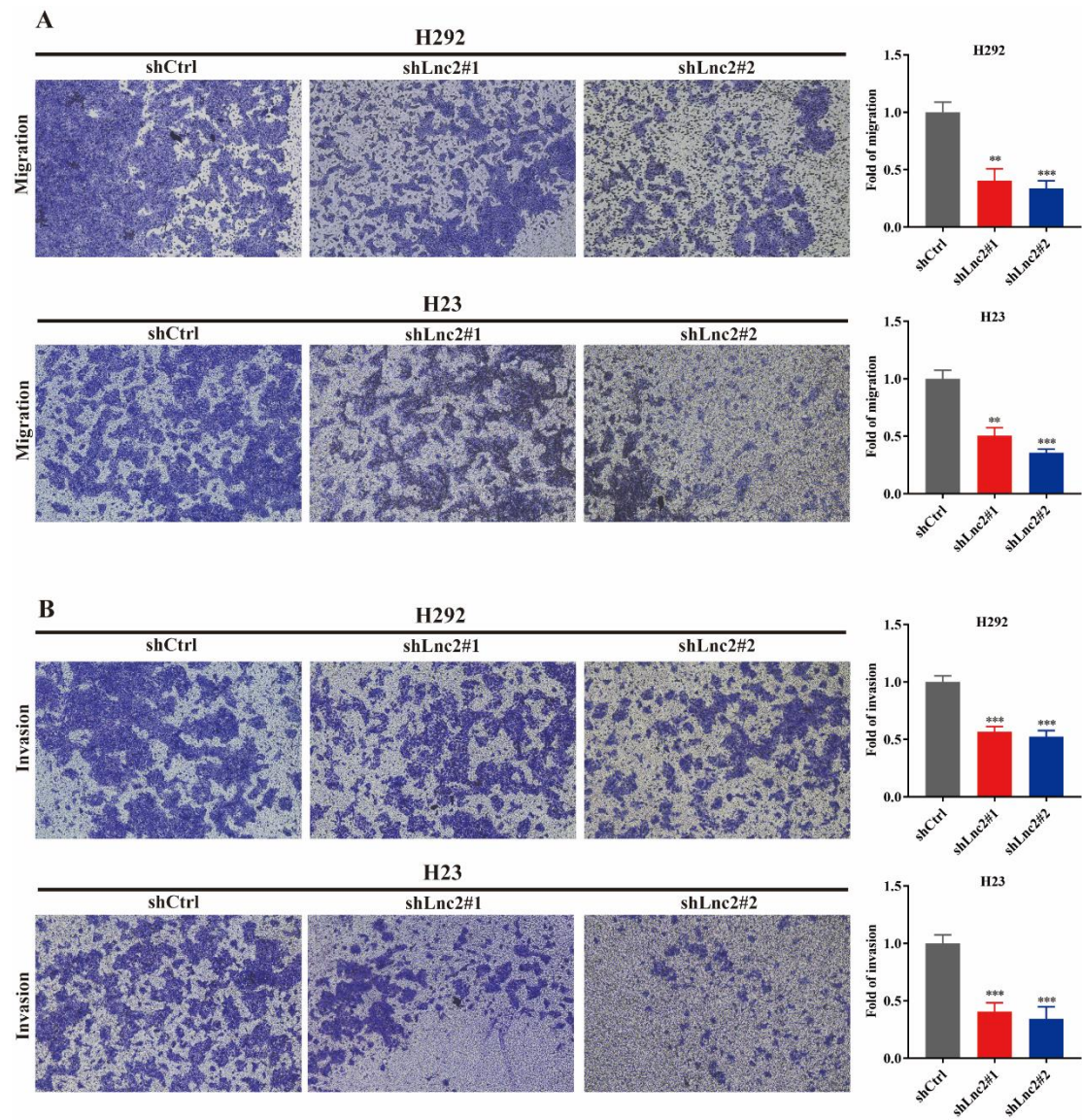
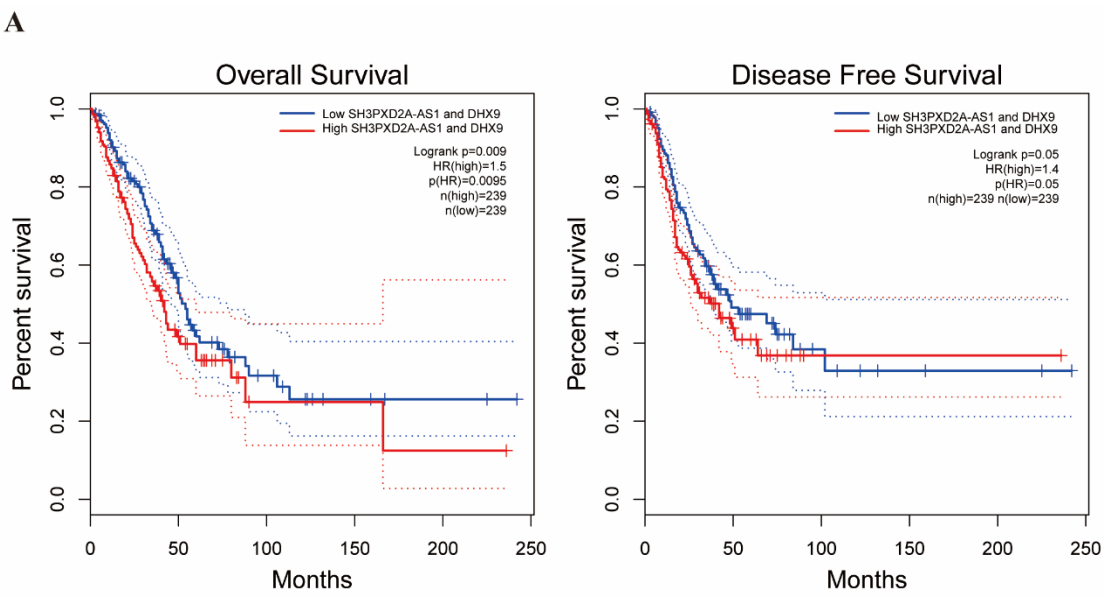


Figure S5

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Figure S6

