**Supplementary Figure Legends**

**Supplementary Table\_1b：**ISLR gene expression in 11 up-regulated tumors and 18 down-regulated tumors in TCGA + GTEx. x ± S represents mean ± standard deviation. P-value < 0.05.

**Supplementary Table\_1c:** ISLR gene expression in 34 tumors and normal tissues in TCGA + GTEx. T means tumor, N means Normal.

**Supplementary Figure 2**: COX regression analysis between ISLR mRNA expression and OS in pan-cancer. The first column is tumor type, the second column is forest plot, the third column is pvalue, and the fourth column is Hazard Ratio (95% CI).

**Supplementary Figure DFS:** COX regression analysis between ISLR mRNA expression and DFS in pan-cancer. The first column is tumor type, the second column is forest plot, the third column is pvalue, and the fourth column is Hazard Ratio (95% CI).

**Supplementary Figure DSS:** COX regression analysis between ISLR mRNA expression and DSS in pan-cancer. The first column is tumor type, the second column is forest plot, the third column is pvalue, and the fourth column is Hazard Ratio (95% CI).

**Supplementary Figure PFS:** COX regression analysis between ISLR mRNA expression and PFS in pan-cancer. The first column is tumor type, the second column is forest plot, the third column is pvalue, and the fourth column is Hazard Ratio (95% CI).