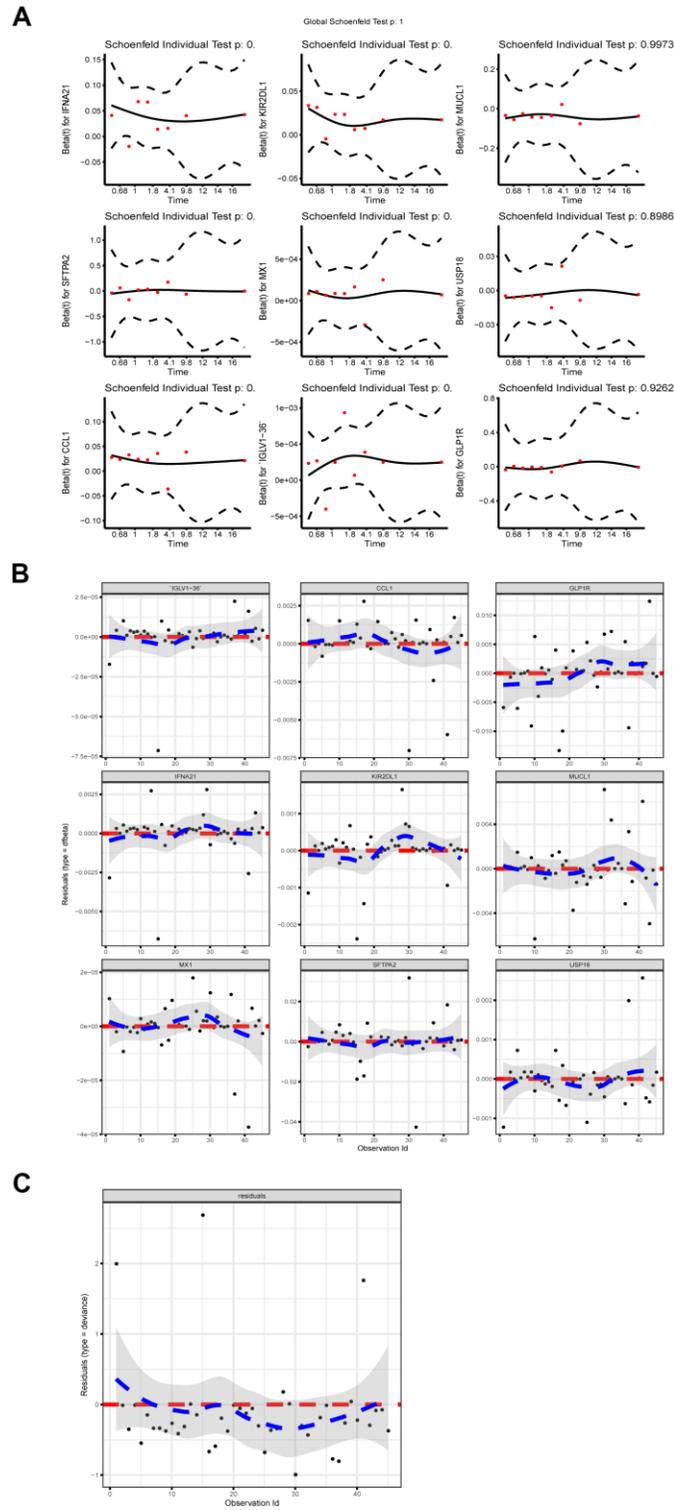
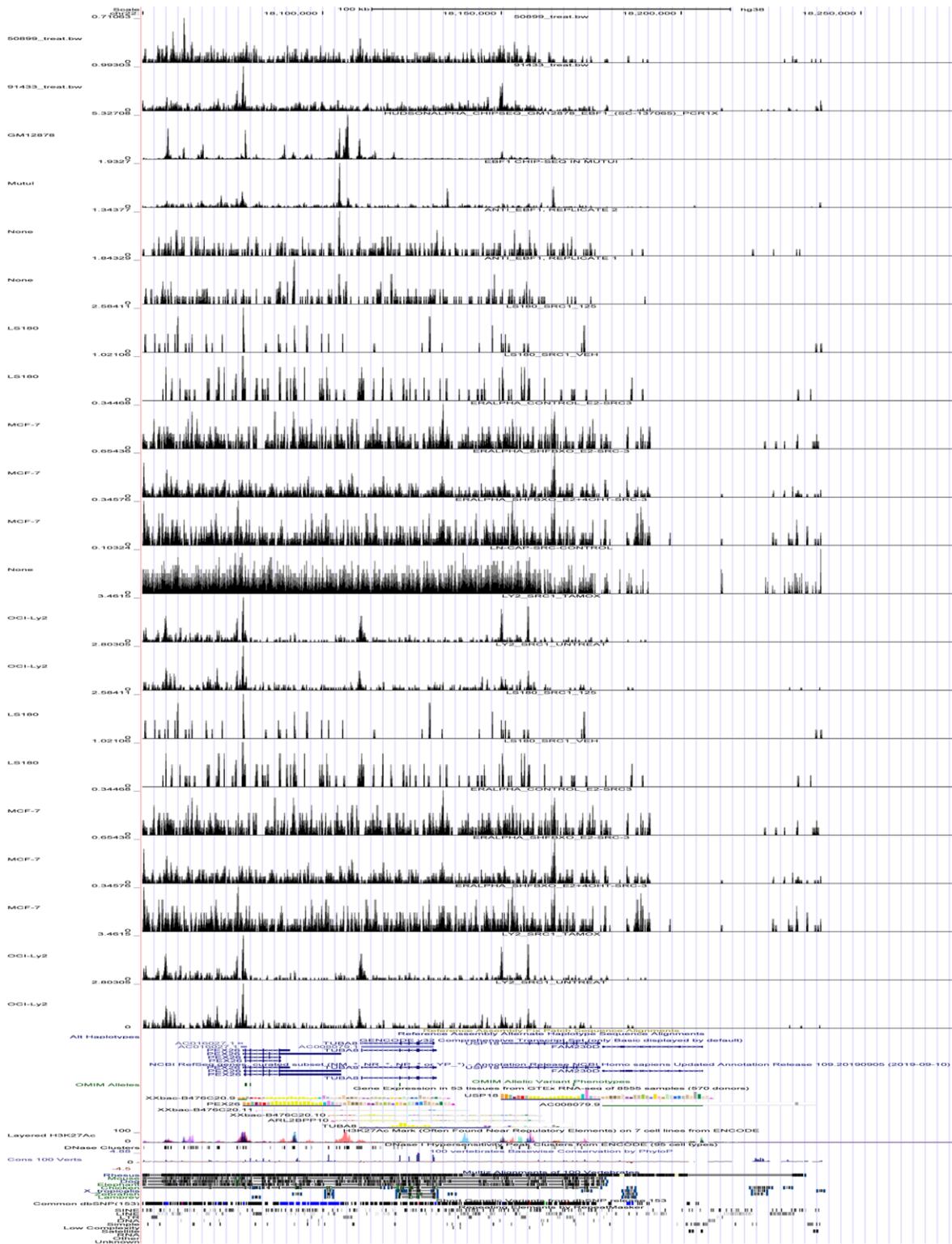


SUPPLEMENTARY FIGURES

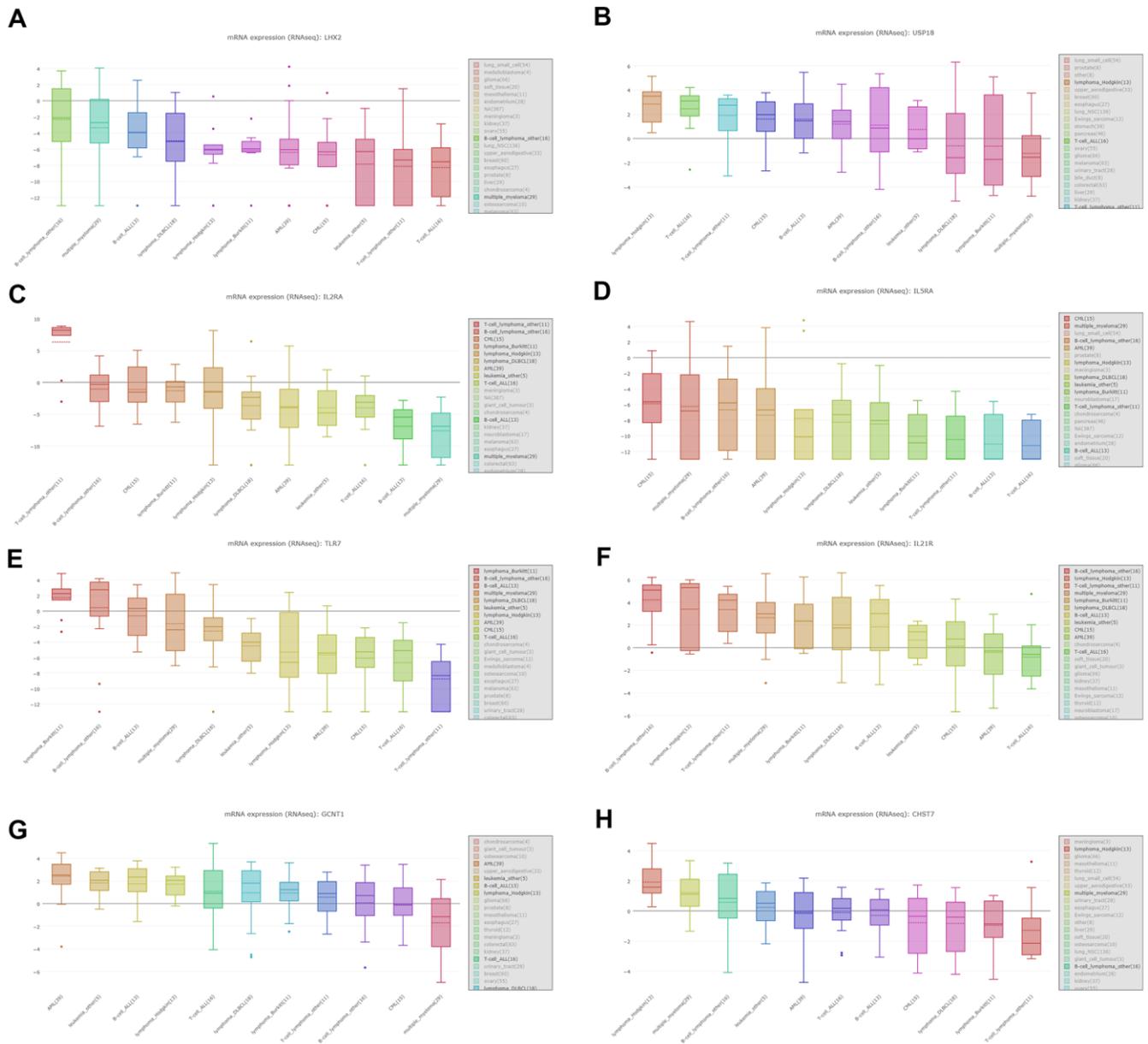


**Supplementary Figure 1. The result of Schoenfeld residuals test. (A)** The Schoenfeld residuals test of each key immune gene. **(B)** The residuals plot of each key immune gene. **(C)** The residuals plot of multivariable Cox regression analysis.

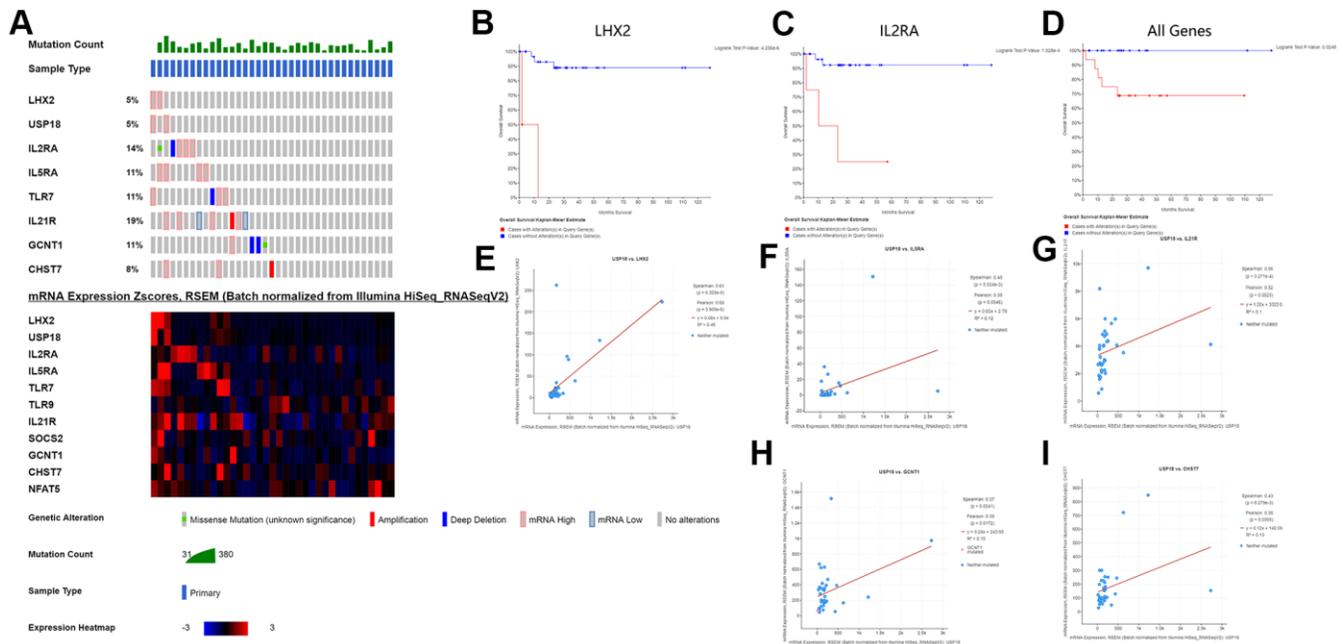


Supplementary Figure 2. The validation of regulatory mechanism between LHX2 and USP18 based on ChIP-Seq data from Cistrome database.

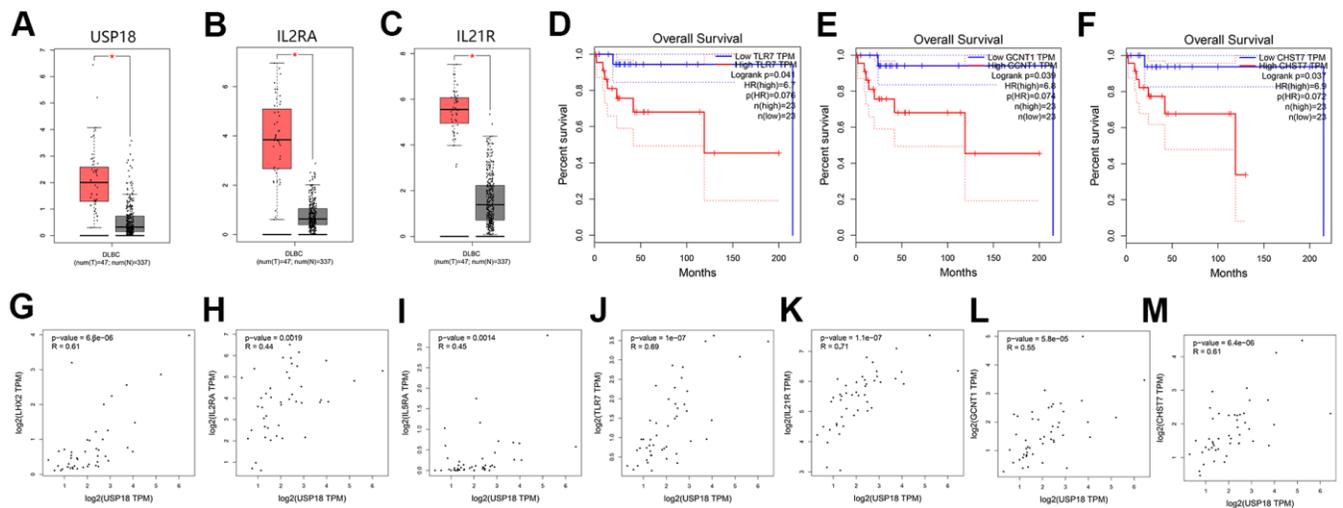




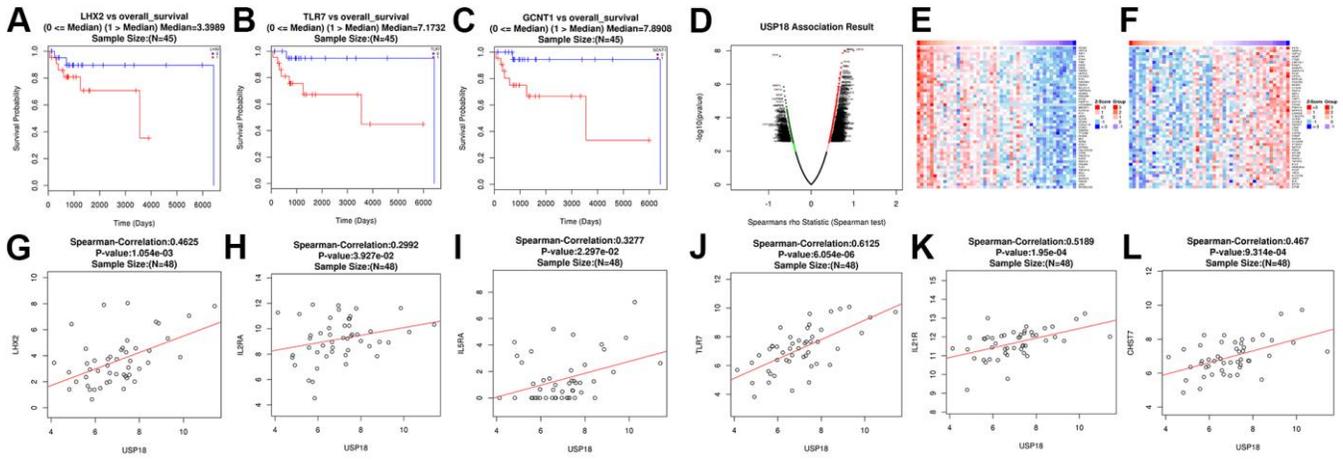
**Supplementary Figure 4.** The expression levels of LHX2, USP18, IL2RA, IL5RA, TLR7, IL21R, GCNT1 and CHST7 (A–H) in various hematologic malignancy cell lines in Cancer Cell Line Encyclopedia (CCLE).



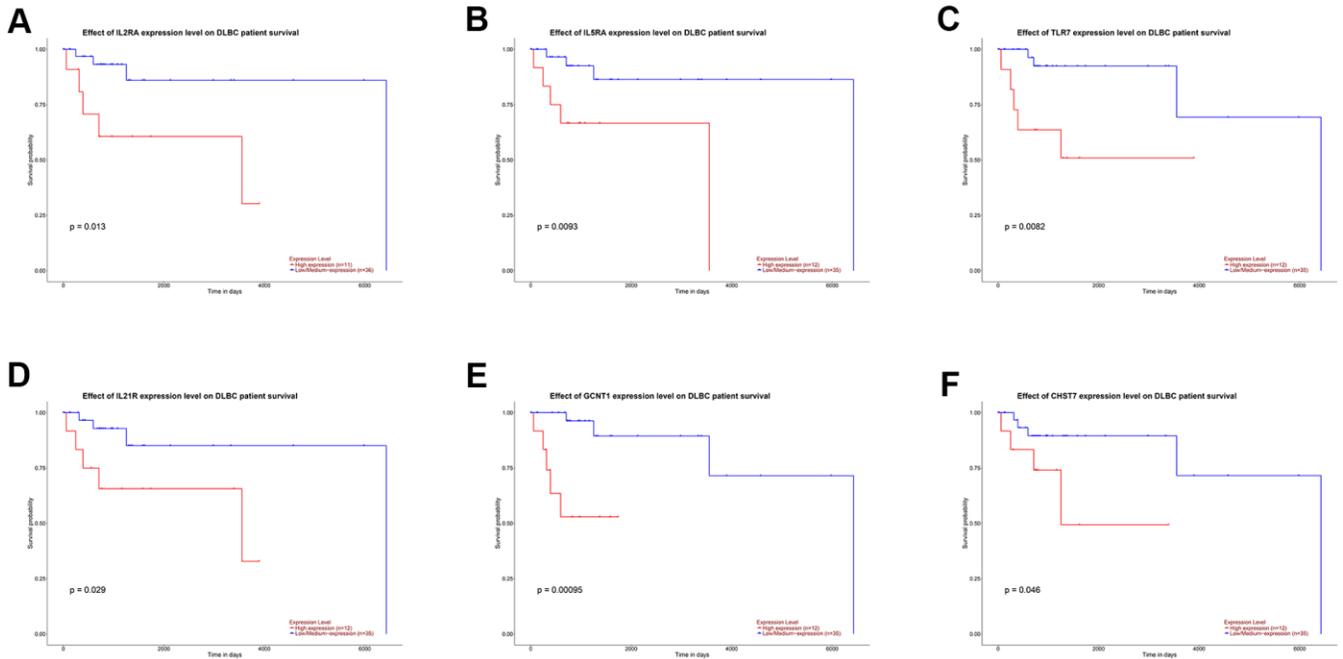
**Supplementary Figure 5. Integrative analysis of genomics and clinical profiles with the cBioPortal database. (A)** Alteration frequency of LHX2, USP18, IL2RA, IL5RA, TLR7, IL21R, GCNT1 and CHST7; **(B–D)** Kaplan-Meier survival curves of LHX2, IL2RA and all genes; **(E–I)** The co-expression between USP18 and LHX2, IL5RA, IL21R, GCNT1 and CHST7.



**Supplementary Figure 6. Integrative analysis of transcriptional and clinical profiles using the GEPIA database. (A–C)** The expression levels of USP18, IL2RA and IL21R between normal samples and DLBCL samples; **(D–F)** Kaplan-Meier survival curves of TLR7, GCNT1 and CHST7; **(G–M)** The co-expression between USP18 and LHX2, IL2RA, IL5RA, TLR7, IL21R, GCNT1 and CHST7.

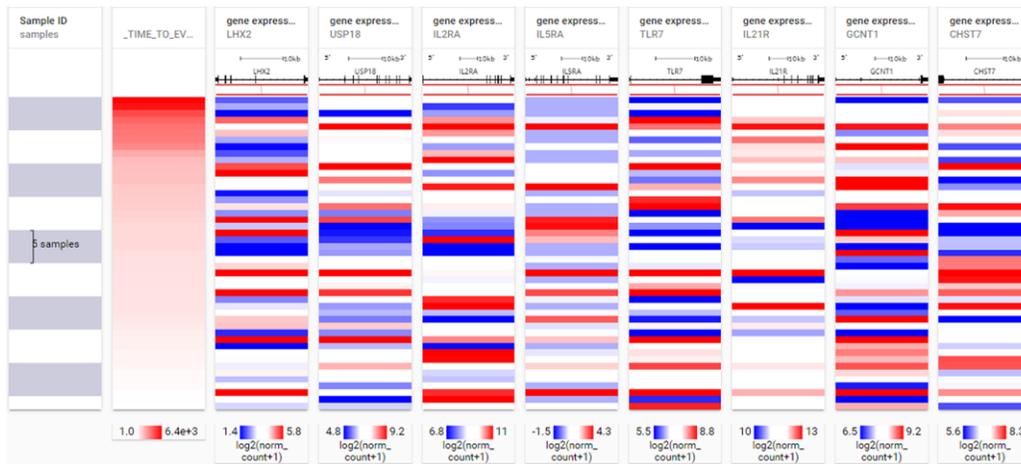


**Supplementary Figure 7. Evaluation prognostic value and relationship with USP18 of all the markers identified in the LinkedOmics database. (A–C)** Kaplan–Meier survival curves of LHX2, TLR7 and GCNT1; **(D–F)** The correlation relationship between USP18 and proteins in RPPA; **(G–L)** The co-expression between USP18 and LHX2, IL2RA, IL5RA, TLR7, IL21R and CHST7.

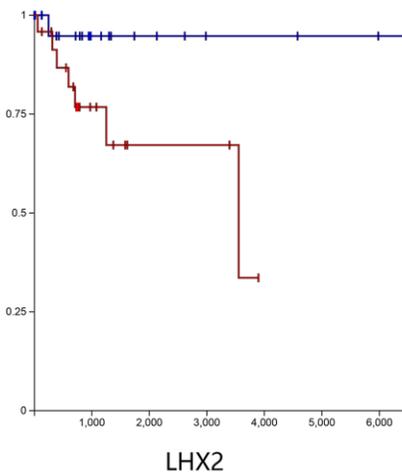


**Supplementary Figure 8.** Kaplan–Meier survival curves of IL2RA, IL5RA, TLR7, IL21R, GCNT1 and CHST7 **(A–F)** using the UALCAN database.

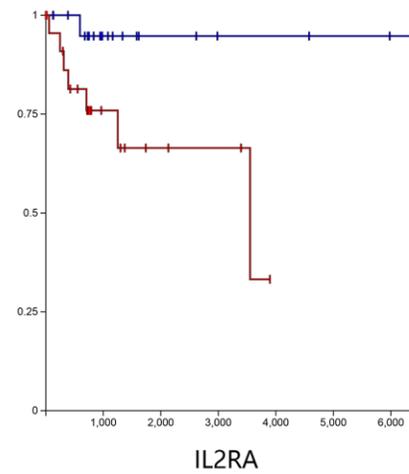
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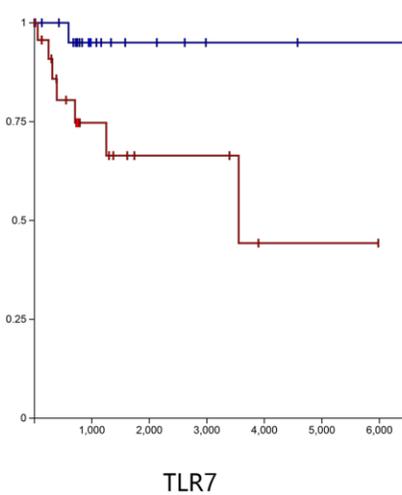
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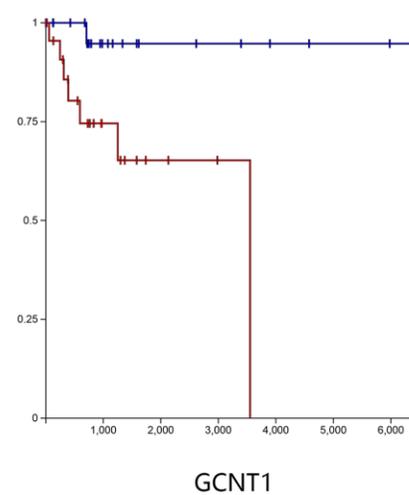
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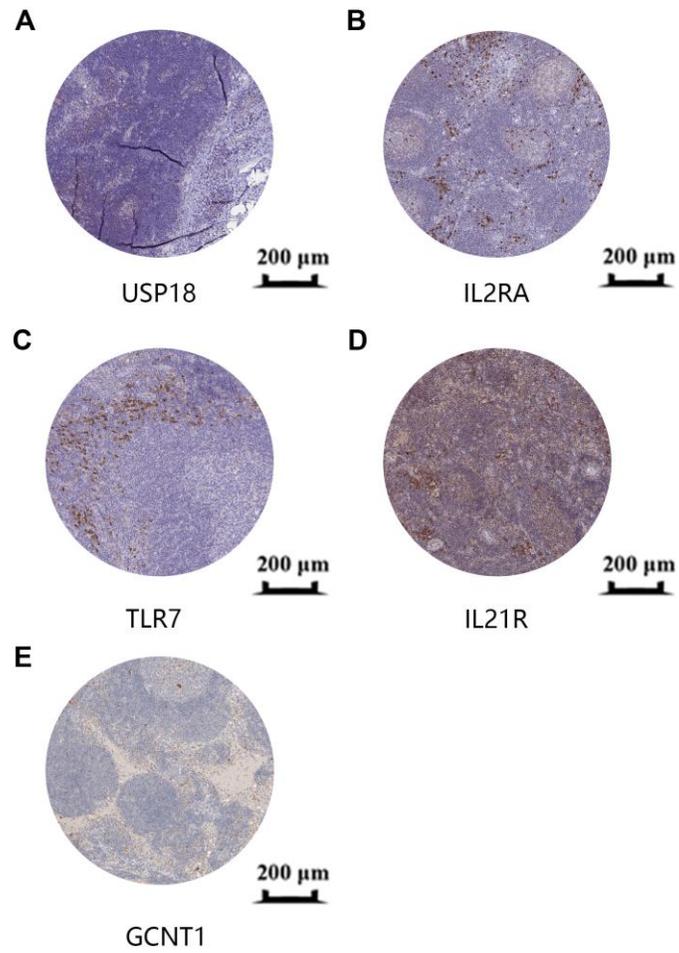
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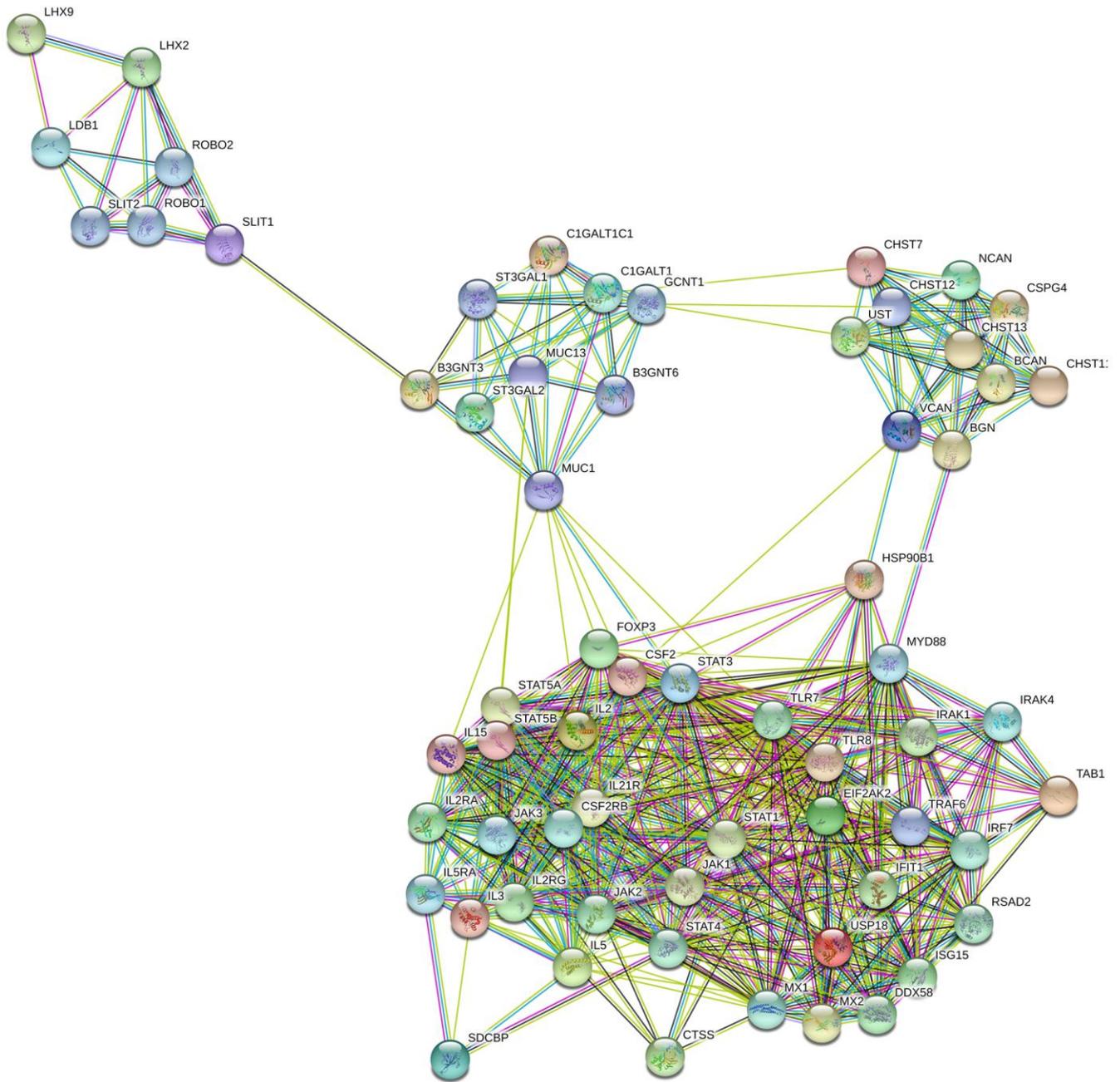
**E**



**Supplementary Figure 9. Integrative analysis of genomics and clinical profiles with the UCSC xena database. (A)** The expression level of LHX2, USP18, IL2RA, IL5RA, TLR7, IL21R, GCNT1 and CHST7 in DLBCL; **(B–E)** Kaplan-Meier survival curves of LHX2, IL2RA, TLR7 and GCNT1.

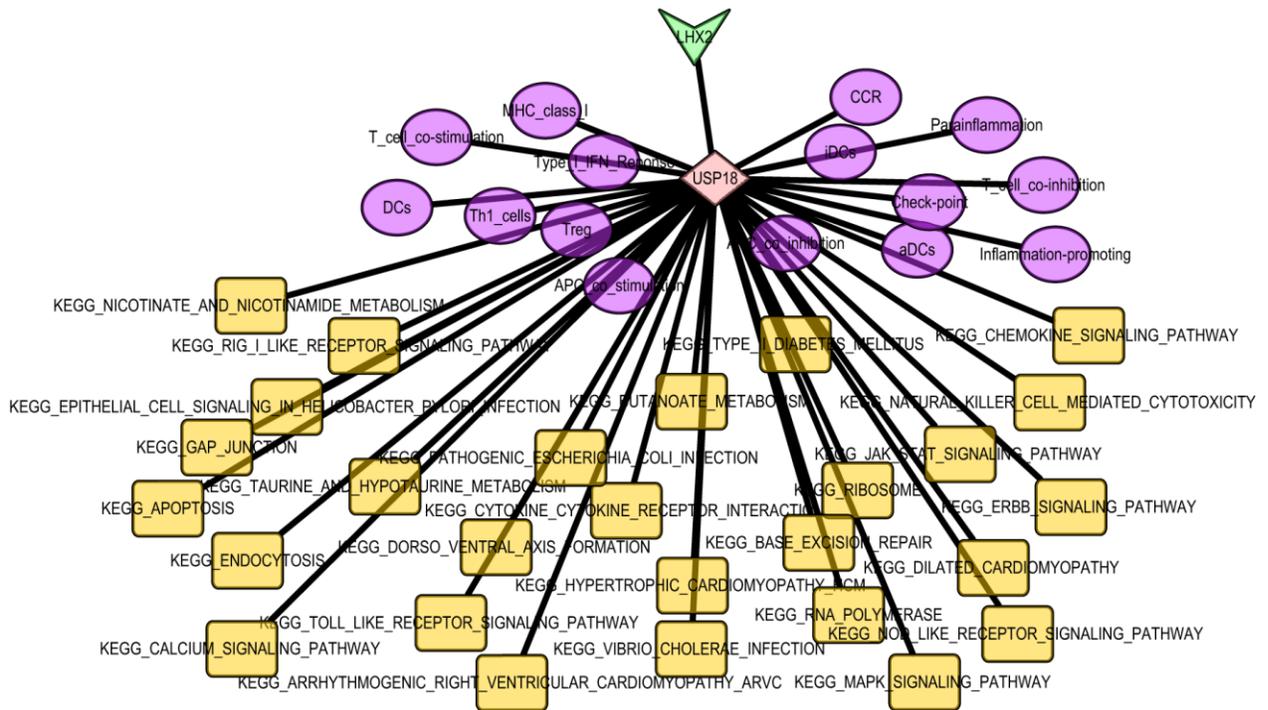


**Supplementary Figure 10.** Validation of USP18, IL2RA, TLR7, IL21R and GCNT1 (A–E) in the normal lymph node tissue on a translation level in the Human Protein Atlas database.

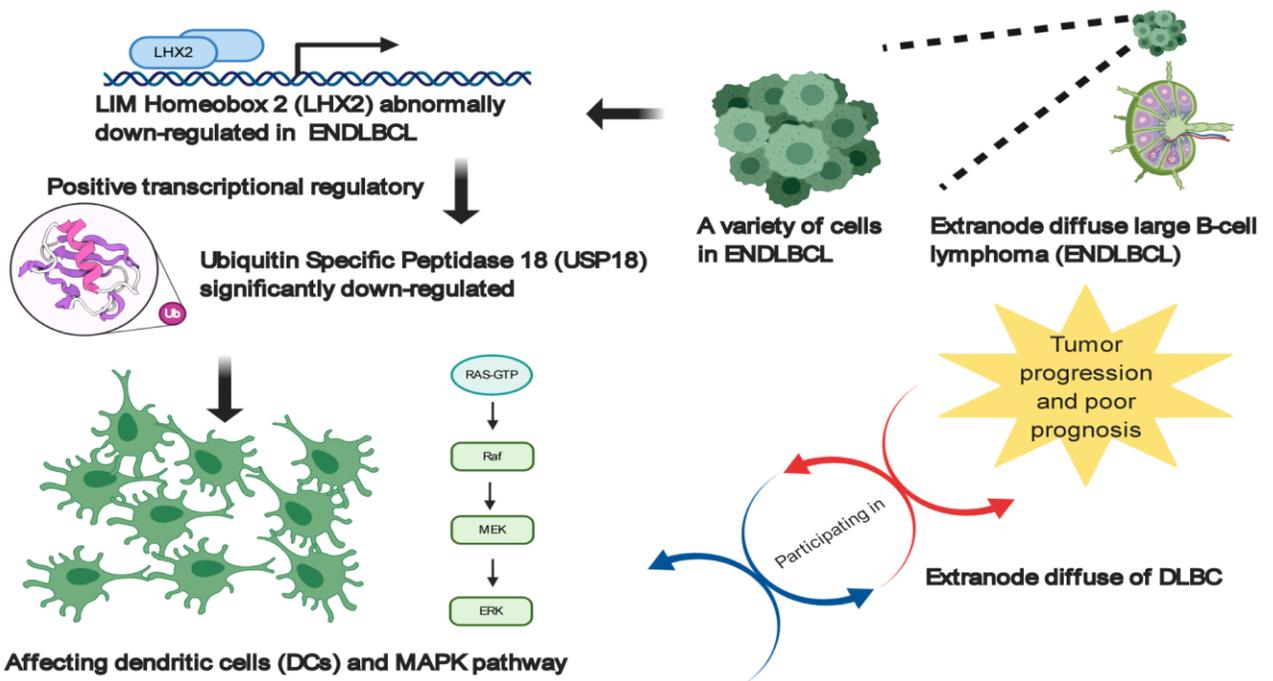


Supplementary Figure 11. The protein-protein interaction (PPI) network of all the markers in string.

**A**



**B**



Supplementary Figure 12. The network of this scientific hypothesis including key TF, immune gene, downstream KEGG pathways and immune gene sets. (A) The protein-protein interaction network among key TF, immune gene, KEGG pathways and immune gene sets by Cytoscape; (B) The schematic diagram of this scientific hypothesis.