**Supplementary Table S1.** Information for eight independent datasets in the study

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Lymphoma | Dataset | Platform | Number of samples | Application |
| DLBCL |  |  | n = 1490 |  |
|  | GS132929 | Affymetrix Human Genome U133 Plus 2.0 Array | 95 | Discovery cohort |
|  | GSE34171 | Affymetrix Human Genome U133 Plus 2.0 Array | 91 | Testing cohort |
|  | GSE25638 | Affymetrix Human Genome U133 Plus 2.0 Array | 26 | Testing cohort |
|  | GSE10846 | Affymetrix Human Genome U133 Plus 2.0 Array | 414 | Survival analysis |
|  | GSE117556 | Illumina HumanHT-12 WG-DASL V4.0 R2 expression beadchip | 928 | Survival analysis |
| FL |  |  | n = 268 |  |
|  | GS132929 | Affymetrix Human Genome U133 Plus 2.0 Array | 65 | Discovery cohort |
|  | GSE65135 | Affymetrix Human Genome U133 Plus 2.0 Array | 14 | Testing cohort |
|  | GSE93261 | Affymetrix Human Genome U133 Plus 2.0 Array | 147 | Testing cohort |
| BL |  |  | n = 92 |  |
|  | GS132929 | Affymetrix Human Genome U133 Plus 2.0 Array | 59 | Discovery cohort |
|  | LLMPP | Affymetrix Human Genome U133 Plus 2.0 Array | 33 | Testing cohort |

**Supplementary Table S2.** The log2 FC and *p*-value of 15 differentially expressed genes (DEGs) in the testing cohorts

|  |  |  |
| --- | --- | --- |
| DLBCLvsFL / BL | DLBCL(GSE34171, n=91) | DLBCL(GSE25638, n=26) |
| FL(GSE65135, n=14) | FL(GSE93261, n=147) | BL(LLMPP, n=33) | FL(GSE65135, n=14) | FL(GSE93261, n=147) | BL(LLMPP, n=33) |
| gene | log2 FC | *p* value | log2 FC | *p* value | log2 FC | *p* value | log2 FC | *p* value | log2 FC | *p* value | log2 FC | *p* value |
| *FDCSP* | -3.90 | 1.68E-06 | -2.37 | 2.38E-12 | 2.29 | 2.74E-04 | -2.72 | 9.08E-04 | -3.23 | 2.00E-12 | 1.21 | 3.38E-02 |
| *CCL21* | -3.82 | 1.11E-07 | -1.39 | 2.37E-07 | 1.71 | 5.23E-04 | -2.05 | 1.11E-03 | -1.42 | 1.34E-04 | 1.30 | 4.51E-03 |
| *CLU* | -2.43 | 6.61E-08 | -1.19 | 1.54E-12 | 1.60 | 1.48E-07 | -1.31 | 1.35E-03 | -1.14 | 2.00E-06 | 1.14 | 8.74E-04 |
| *ITM2A* | -0.94 | 2.04E-02 | -1.41 | 6.79E-18 | 2.43 | 7.08E-13 | -1.33 | 1.62E-04 | -1.78 | 4.69E-13 | 1.81 | 1.77E-07 |
| *ICOS* | -1.09 | 8.47E-04 | -1.66 | 3.80E-21 | 1.80 | 1.42E-12 | -2.01 | 9.11E-05 | -2.60 | 5.58E-11 | 0.93 | 9.29E-05 |
| *TRBC1* | -1.35 | 8.14E-05 | -1.06 | 2.19E-12 | 1.53 | 1.22E-08 | -1.26 | 7.19E-05 | -0.97 | 8.89E-08 | 1.44 | 4.70E-07 |
| *CD3D* | -1.17 | 8.19E-04 | -1.06 | 1.25E-11 | 2.49 | 4.88E-13 | -1.31 | 3.07E-05 | -1.19 | 1.72E-10 | 2.12 | 2.38E-09 |
| *BTLA* | -1.07 | 7.22E-03 | -1.21 | 1.14E-11 | 1.88 | 1.53E-09 | -1.04 | 1.36E-02 | -1.16 | 1.04E-05 | 1.69 | 8.88E-06 |
| *CHN1* | -0.99 | 2.20E-04 | -1.57 | 1.07E-27 | 1.39 | 4.59E-12 | -0.84 | 1.23E-03 | -1.38 | 2.88E-12 | 1.50 | 1.79E-09 |
| *LAT* | -1.18 | 6.68E-05 | -1.03 | 7.60E-16 | 1.08 | 3.06E-08 | -1.21 | 1.62E-04 | -1.13 | 1.35E-08 | 0.86 | 8.18E-05 |
| *BANK1* | -2.11 | 2.78E-07 | -1.04 | 1.42E-10 | 1.84 | 9.07E-09 | -1.59 | 1.02E-04 | -1.51 | 1.62E-09 | 0.98 | 1.75E-03 |
| *CXCL13* | -1.32 | 7.02E-03 | -0.93 | 4.51E-07 | 3.71 | 3.08E-12 | -1.22 | 2.00E-03 | -1.78 | 1.87E-10 | 1.28 | 9.87E-03 |
| *KLRB1* | -1.47 | 5.41E-04 | -1.31 | 2.07E-12 | 1.82 | 2.58E-09 | -2.14 | 5.66E-05 | -2.01 | 1.03E-09 | 1.10 | 1.75E-03 |
| *ITK* | -0.87 | 3.81E-02 | -1.41 | 2.84E-15 | 2.82 | 7.58E-14 | -1.01 | 2.65E-03 | -1.54 | 1.01E-10 | 2.52 | 1.63E-09 |
| *HJURP* | 1.07 | 1.33E-05 | 1.12 | 3.60E-22 | -0.91 | 7.54E-10 | 1.16 | 1.02E-04 | 1.17 | 6.56E-10 | -0.82 | 1.30E-06 |

**Abbreviations:** FC, fold change.

**Supplementary Table S3.** Clinical characteristics of the patients in GSE10846 and GSE117556 datasets

|  |  |  |
| --- | --- | --- |
| Characteristics | GSE10846n=414 | GSE117556n=928  |
| Age, No. (%) |  |  |
| <60 | 179(43.2) | 332(35.8) |
| >=60 | 235(56.8) | 595(64.1) |
| NA |  | 1(0.1) |
| Sex, No (%) |  |  |
| Female | 172(41.6) | 411(44.3) |
| Male | 224(54.1) | 517(55.7) |
| NA | 18(4.3) |  |
| Subtype, No. (%) |  |  |
| ABC | 167(40.3) | 274(26.3) |
| GCB | 183(44.2) | 475(51.2) |
| UC | 64(15.5) | 209(22.5) |
| Stage, No. (%) |  |  |
| I-II | 189(45.7) | 268(30.8) |
| III-IV | 217(52.4) | 638(68.8) |
| NA | 8(1.9) | 4(0.4) |
| ECOG, No. (%) |  |  |
| <2 | 296(71.5) | 823(88.7) |
| >=2 | 93(22.5) | 105(11.3) |
| NA | 25(6) |  |
| IPI, No. (%) |  |  |
| <=2 |  | 482(51.9) |
| >2 |  | 446(48.1) |

**Abbreviations:** UC: unclassified; NA: not available; ECOG: Eastern Cooperative Oncology Group score; IPI: international prognostic index, GCB: germinal center B-cell-like; ABC: activated B-cell-like.

**Supplementary Table S4.** Correlation between *CHN1* expression and clinical features in GSE10846 and GSE117556 datasets

|  |  |  |
| --- | --- | --- |
|  | GSE10846 | GSE117556 |
| Parameters | *CHN1* expression | *p*-value | *CHN1* expression | *p*-value |
|  | low expression(n=156) | high expression(n=157) |  | low expression(n=357) | high expression(n=358) |  |
| Age, No. (%) |  |  | 0.9945 |  |  | 0.1216 |
| <60 | 69(44.2) | 65(41.4) |  | 121(33.9) | 113(31.6) |  |
| ≥60 | 87(55.8) | 92(58.6) |  | 236(66.1) | 245(68.4) |  |
| Sex, No. (%) |  |  | 0.6683 |  |  | 0.0019 |
| Female | 68(43.6) | 74(47.1) |  | 143(40.1) | 179(50.0) |  |
| Male | 88(56.4) | 83(52.9) |  | 214(59.9) | 179(50.0) |  |
| Subtype, No. (%) |  |  | 5.8E-05 |  |  | 1.7E-05 |
| ABC | 94(60.3) | 58(36.9) |  | 146(40.9) | 98(27.4) |  |
| GCB | 62(30.7) | 99(63.1) |  | 211(59.1) | 260(72.6) |  |
| Stage, No. (%) |  |  | 0.7876 |  |  | 0.4744 |
| I-II | 74(47.4) | 76(48.4) |  | 110(30.8) | 120(33.5) |  |
| III-IV | 82(52.6) | 81(51.6) |  | 247(69.2) | 238(66.5) |  |
| ECOG, No. (%) |  |  | 0.0296 |  |  | 0.0306 |
| <1 | 111(71.2) | 130(82.8) |  | 305(85.4) | 328(91.6) |  |
| ≥1 | 45(28.8) | 27(17.2) |  | 52(14.6) | 30(8.4) |  |
| IPI, No. (%) |  |  |  |  |  | 0.4490 |
| ≤2 |  |  |  | 184(51.5) | 193(53.9) |  |
| >2 |  |  |  | 173(48.5) | 165(46.1) |  |

**Abbreviations:** ECOG: Eastern Cooperative Oncology Group score; IPI: international prognostic index, GCB: germinal center B-cell-like; ABC: activated B-cell-like.

**Supplementary Figure S1.** **The correlation between *CHN1* expression and clinical features in GSE117556.**

(a) Association between clinical features and *CHN1* expression. (b, c) Distribution of *CHN1* expression in patients stratified by the molecular subtype and ECOG performance status.



**Supplementary Figure S2. Enrichment plots from GSEA in GSE117556.**

Significantly enriched GO terms (a, b) and KEGG pathways (c, d) in the high *CHN1* expression group.



**Supplementary Figure S3. Enrichment plots from GSEA in GSE10846 and GSE117556.**

Significant enrichment of genes in PI3K signaling pathways for the high expression phenotype of *CHN1* in GSE10846 (a) and GSE117556 (b).

