**SUPPLEMENTARY MATERIAL**

**CXCL10 is a Tumor Microenvironment and Immune Infiltration Related Prognostic Biomarker in Pancreatic** **Adenocarcinoma**

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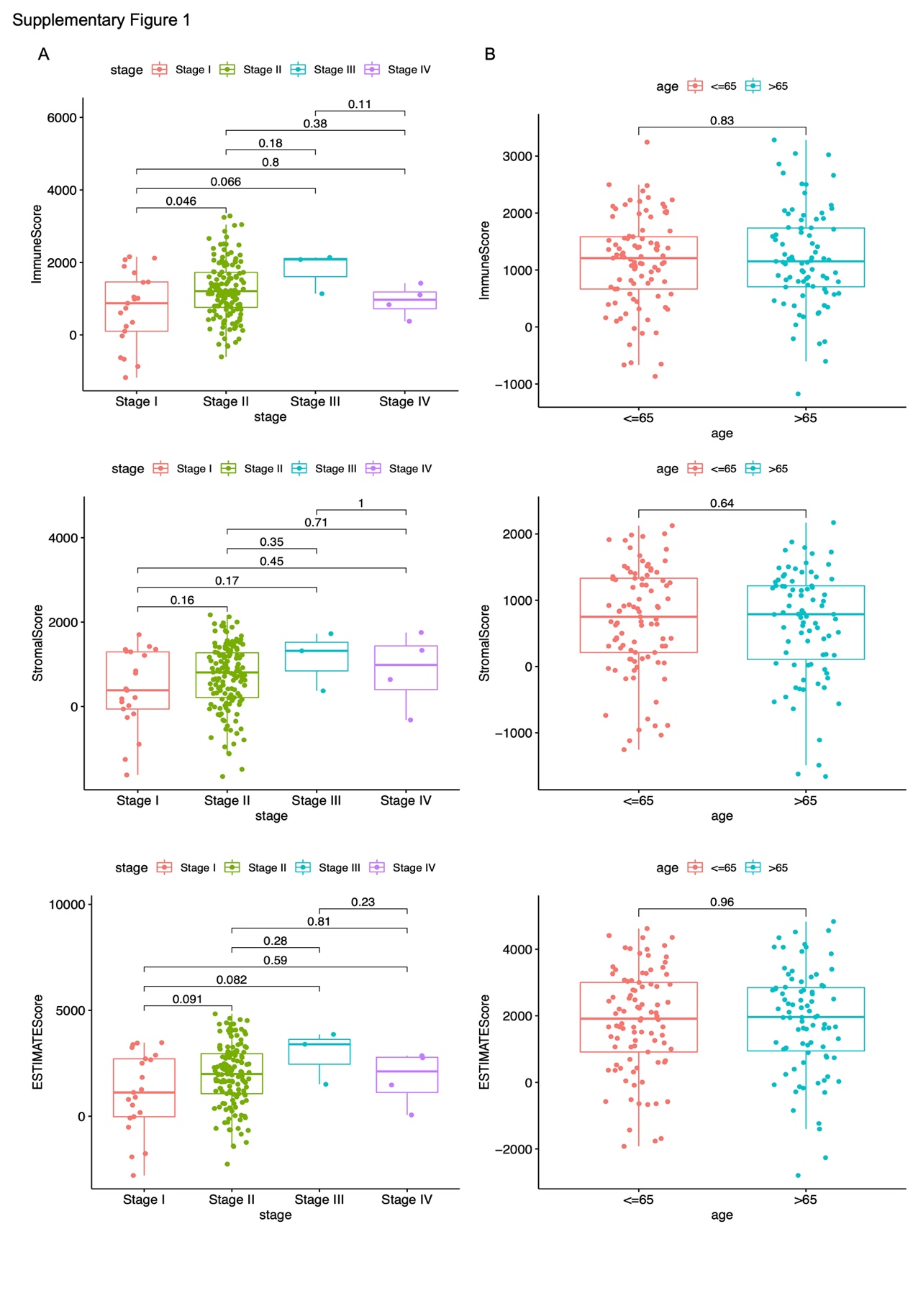
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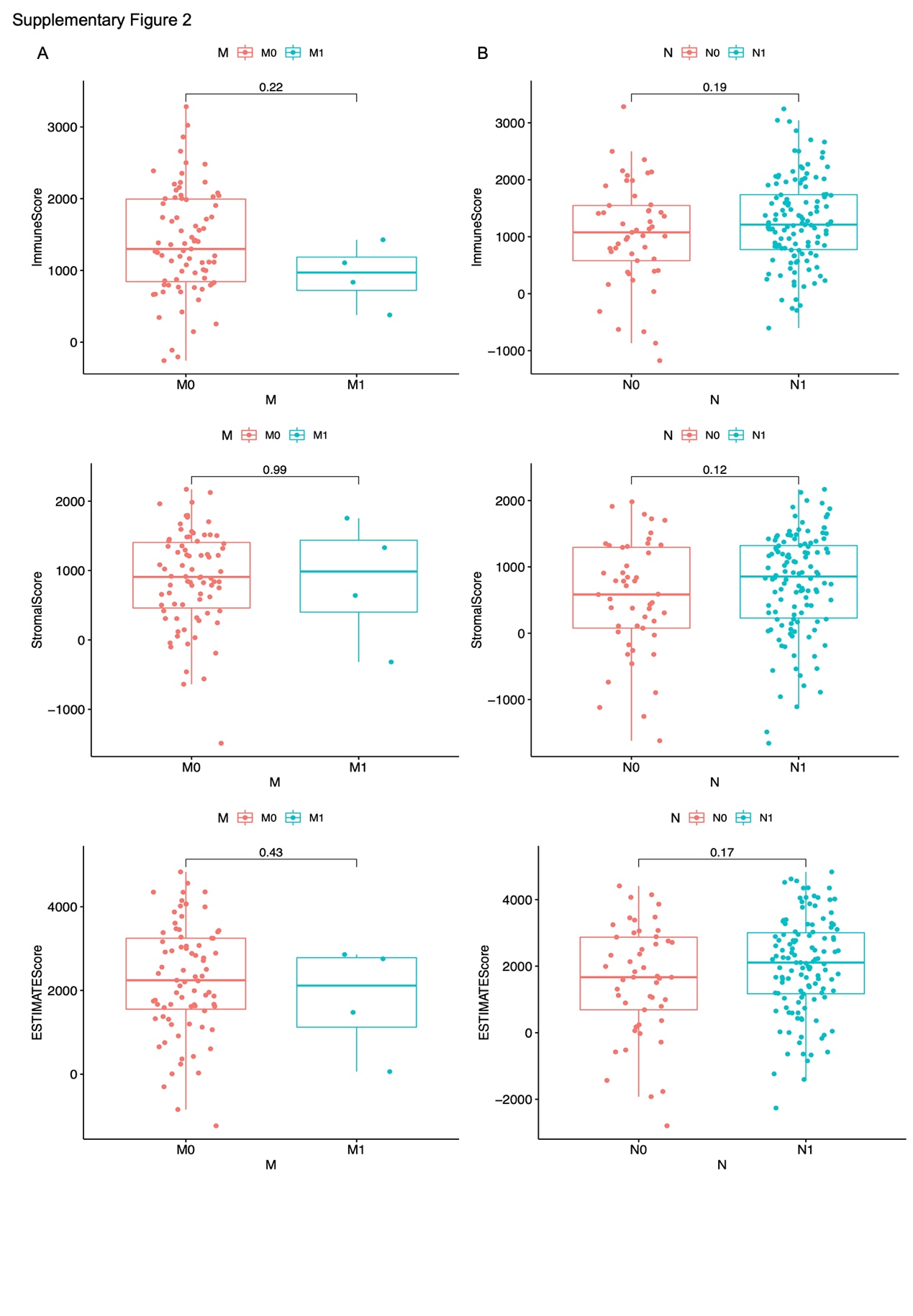
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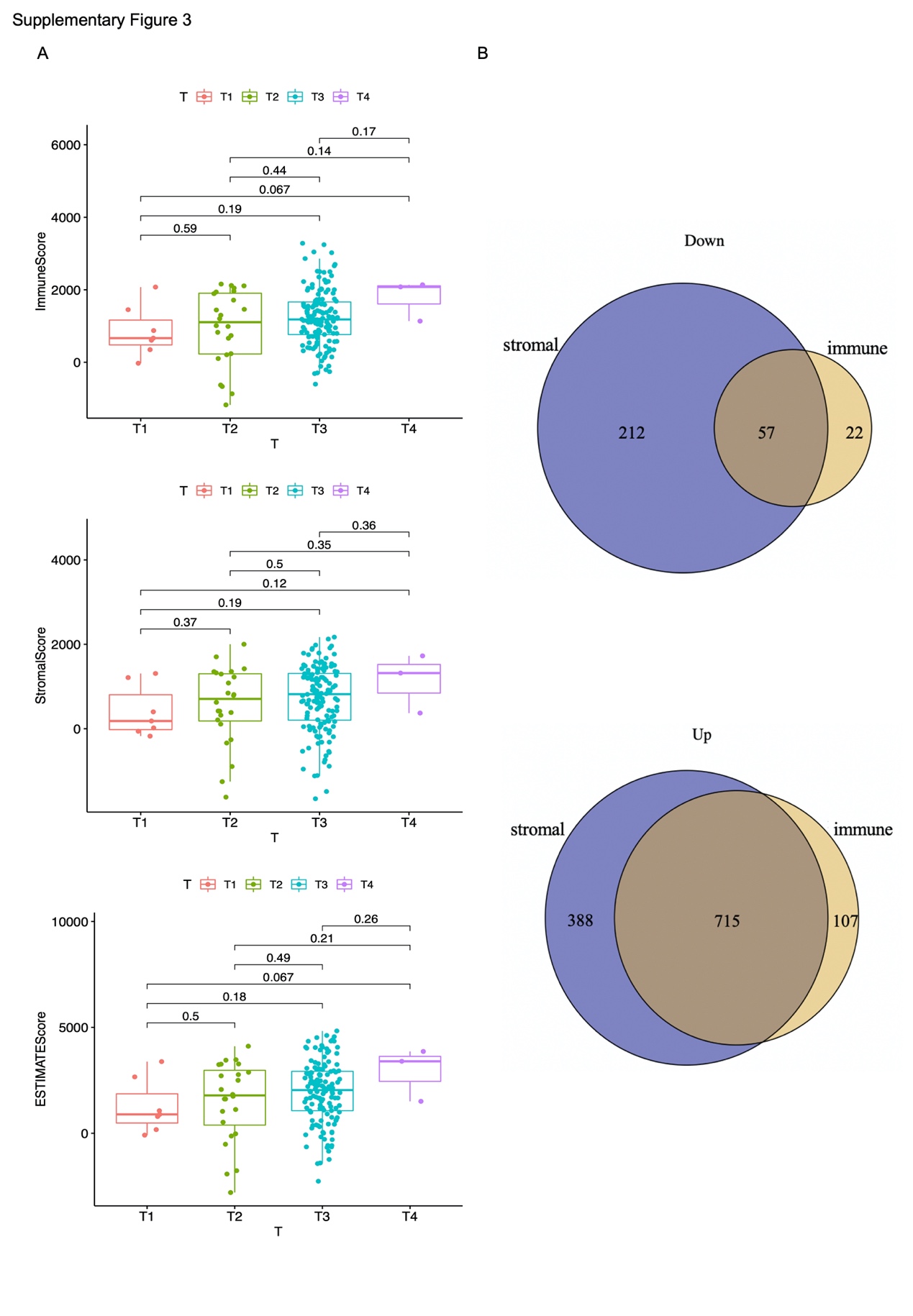
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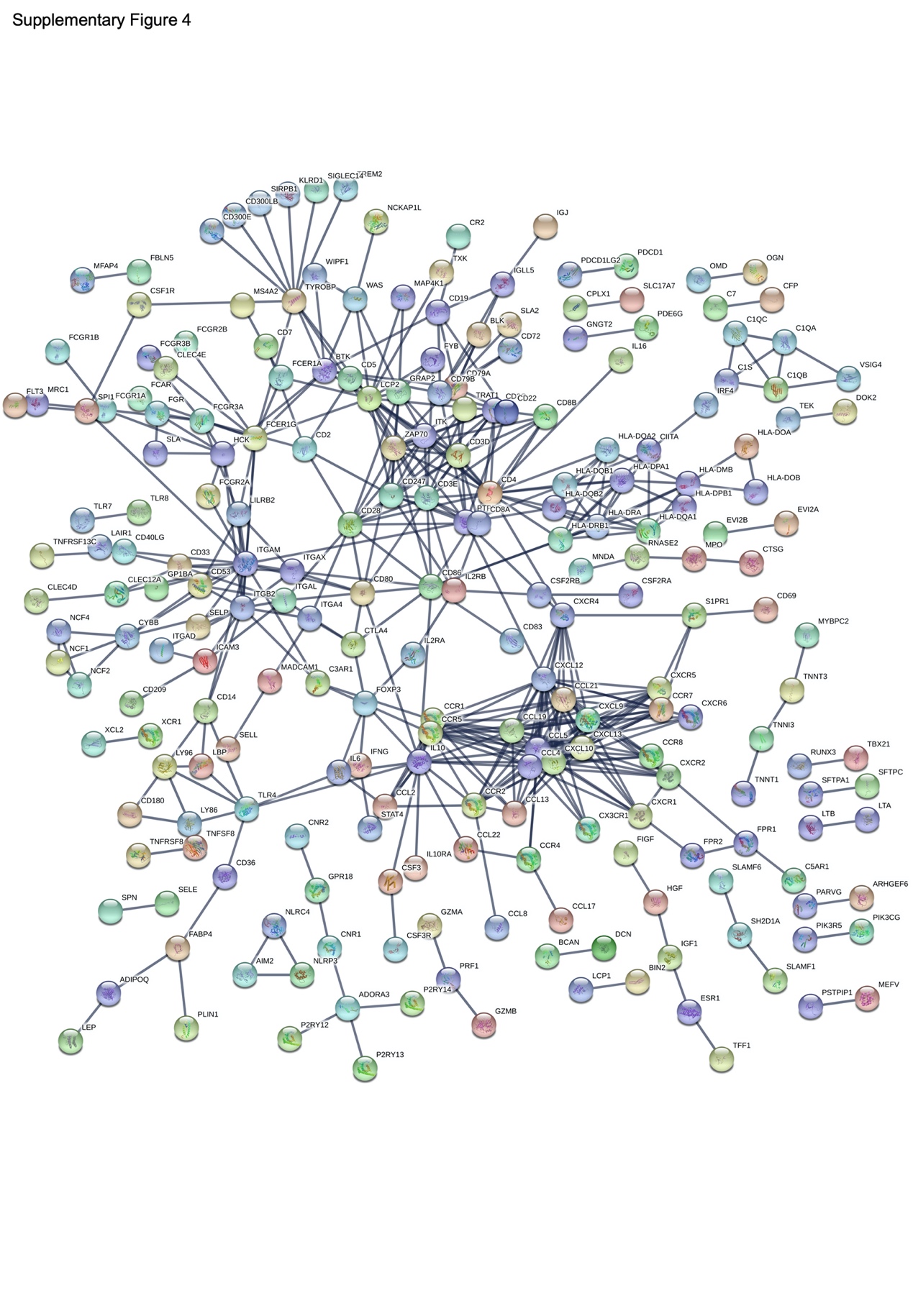
**Supplementary Figure 1.** Correlation between scores and pathology stage and age. **(A)** The immune scores were positively related to stage I and II disease (*p*=0.046). **(B)** No significance was found between the scores and age.



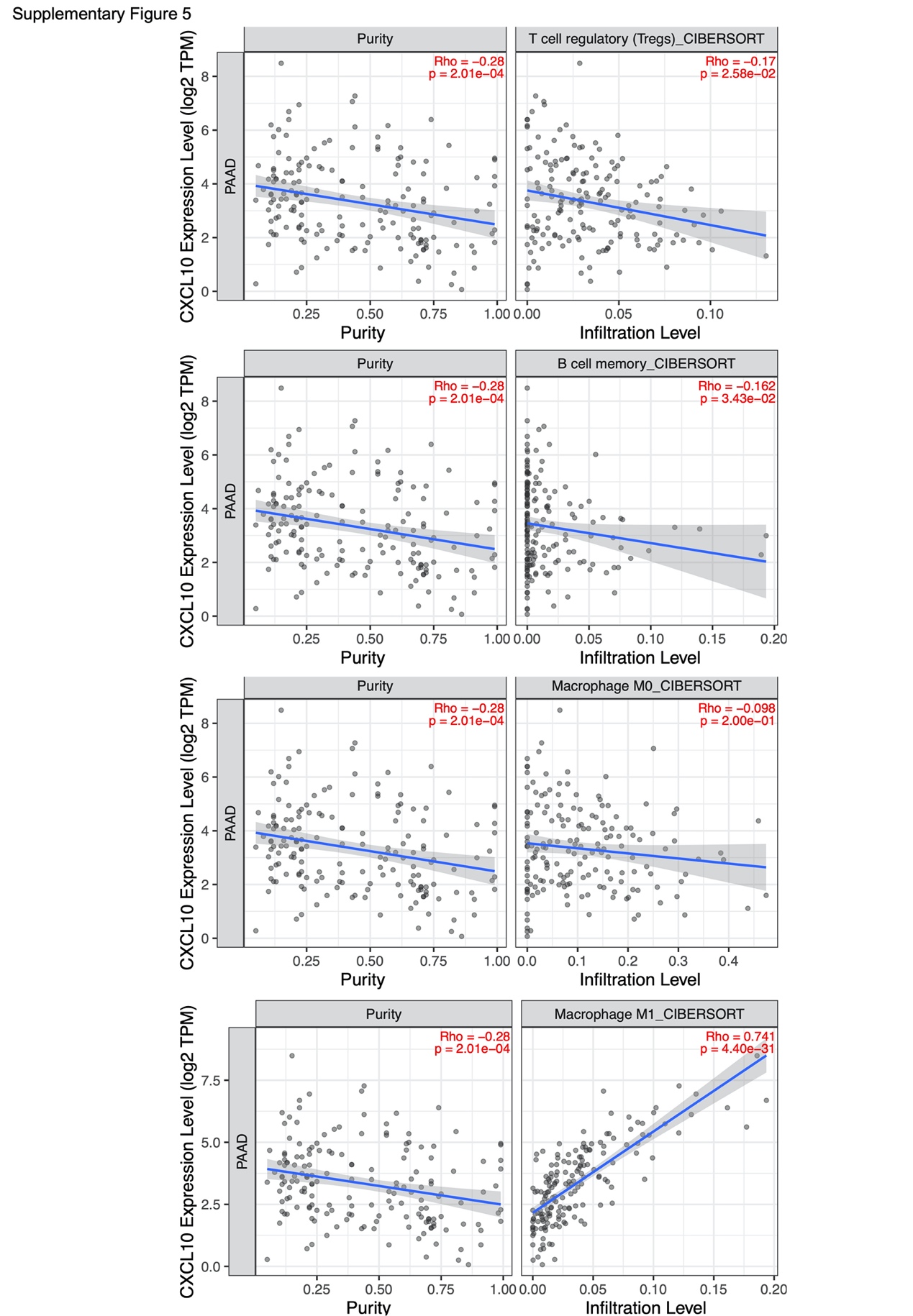
**Supplementary Figure 2.** Correlation between scores and M and N stage. **(A-B)** No significance was found between the scores and M and N stage.



**Supplementary Figure 3.** Correlation between scores and T stage and Venn diagram analysis. **(A)** No significance was found between the scores and T stage. **(B)** Venn diagram analysis of up-regulated and down-regulated differentially expressed genes based on immune scores and stromal scores.



**Supplementary Figure 4.** PPI network construction. PPI network construction based on the STRING database covered 222 nodes and 476 edges with interaction confidence value more than 0.99.

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**Supplementary Figure 5.** Cumulative survival analysis. Cumulative survival analysis was performed to validate the correlation of CXCL10 and four immune cells.

Supplementary Table 1. Clinico-pathological characteristics statistics of PAAD patients from TCGA database

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Clinical characteristics |  | | Total | | % |
| Age at diagnosis (year)  Gender  Grade  Stage  T classification  M classification  N classification | <=65  >65  Female  Male  G1  G2  G3  G4  Ⅰ  Ⅱ  Ⅲ  Ⅳ  T1  T2  T3  T4  M0  M1  N0  N1 | 93  83  80  96  30  94  48  2  21  145  3  4  7  24  140  3  79  4  49  122 | | 52.8  47.2  45.5  54.5  17.2  54.0  27.6  1.1  12.1  83.8  1.7  2.3  4.0  14.0  80.5  1.7  95.2  4.8  28.7  71.3 | |

Supplementary Table 2. Enriched gene sets

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| C7 collection | Gene set name | NES | | NOM p-val | |
| CXCL10 high expression    CXCL10 low expression | GSE13485\_CTRL\_VS\_DAY3\_YF17D\_VACCINE\_PBMC\_DN  GSE14000\_UNSTIM\_VS\_4H\_LPS\_DC\_TRANSLATED\_RNA\_DN  GSE14415\_INDUCED\_TREG\_VS\_FOXP3\_KO\_INDUCED\_TREG\_IL2\_CULTURE\_UP  GSE15330\_LYMPHOID\_MULTIPOTENT\_VS\_MEGAKARYOCYTE\_ERYTHROID\_PROGENITOR\_IKAROS\_KO\_DN  GSE19888\_ADENOSINE\_A3R\_INH\_VS\_ACT\_WITH\_INHIBITOR\_PRETREATMENT\_IN\_MAST\_CELL\_UP  GSE2706\_UNSTIM\_VS\_8H\_R848\_DC\_DN  GSE40685\_TREG\_VS\_FOXP3\_KO\_TREG\_PRECURSOR\_DN  GSE43863\_NAIVE\_VS\_MEMORY\_TH1\_CD4\_TCELL\_D150\_LCMV\_UP  GSE8835\_CD4\_VS\_CD8\_TCELL\_CLL\_PATIENT\_UP  GSE18791\_UNSTIM\_VS\_NEWCATSLE\_VIRUS\_DC\_1H\_UP  GSE21670\_UNTREATED\_VS\_TGFB\_TREATED\_STAT3\_KO\_CD4\_TCELL\_UP  GSE34156\_UNTREATED\_VS\_24H\_NOD2\_AND\_TLR1\_TLR2\_LIGAND\_TREATED\_MONOCYTE\_DN  GSE37533\_UNTREATED\_VS\_PIOGLIZATONE\_TREATED\_CD4\_TCELL\_PPARG2\_AND\_FOXP3\_TRASDUCED\_UP | 2.41  2.34  2.39  2.36  2.41  2.31  2.31  2.31  2.35  -1.47  -1.39  -1.56  -1.53 | 0  0  0  0  0  0  0  0  0  0.034  0.037  0.022  0.020 | |

C7 collection: c7.all.v.7.1symbols.gmt from MSigDB. NES: normalized enrichment score. NOM: nominal *p-*value. Gene sets with NOM *p*-value less than 0.05 was considered as statistical significance.

Supplementary Table 3. The intersection of difference analysis and correlation analysis

|  |  |  |  |
| --- | --- | --- | --- |
| Tumor infiltrated immune cells | Correlation test（*p*-value） | | Difference test（*p*-value） |
| B-cells memory  T-cells regulatory  macrophages M0  macrophages M1 | 0.004  <0.001  <0.001  <0.001 | 0.032  <0.001  0.013  <0.001 | |