

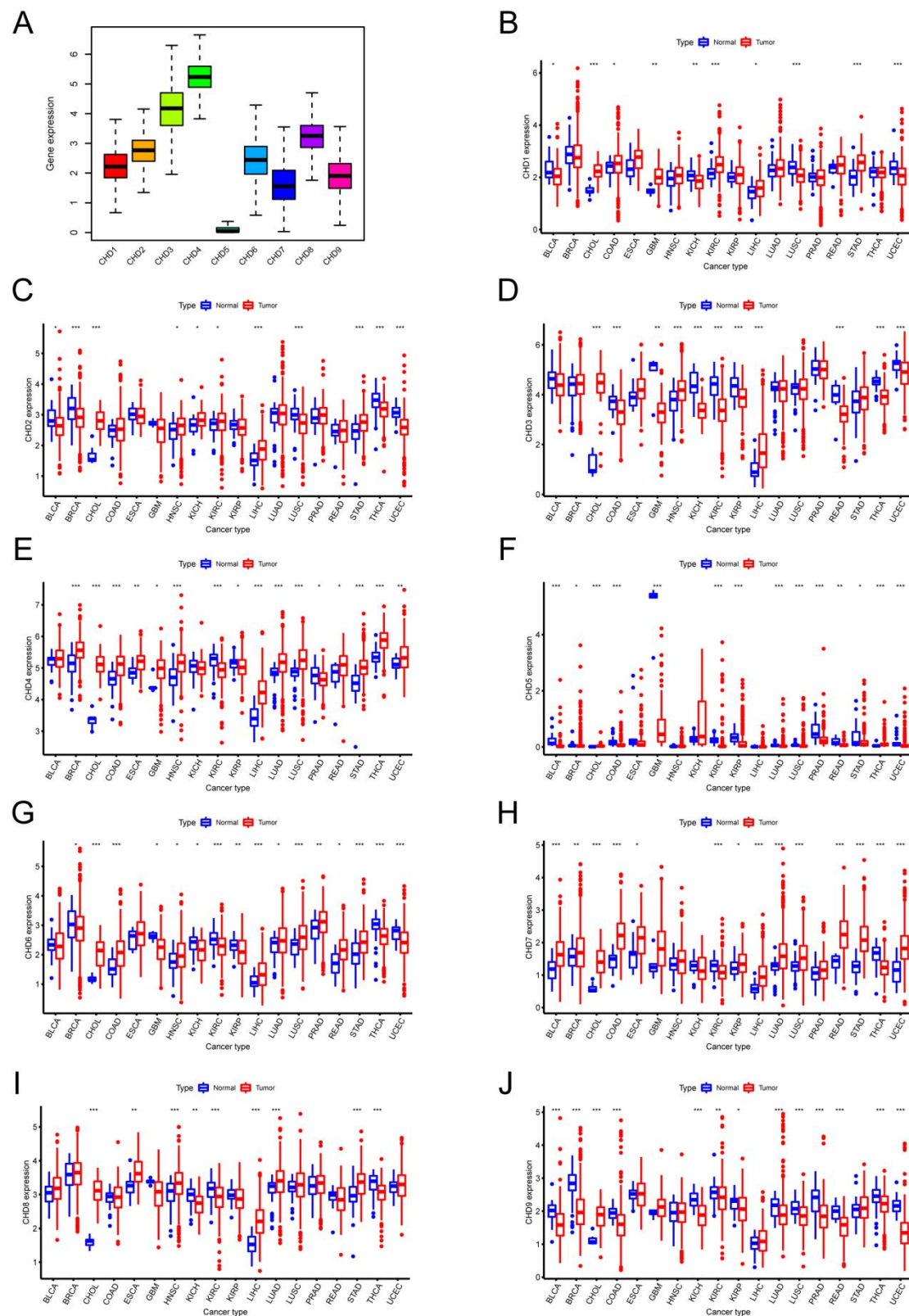


Figure S1. The expression of *CHD* gene family from TCGA. (A) The expression of *CHD* gene family in all the 33 cancers from TCGA. (B-J) The expression of *CHD1-CHD9* from TCGA. Only the cancer types which have at least 5 controls were calculated. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

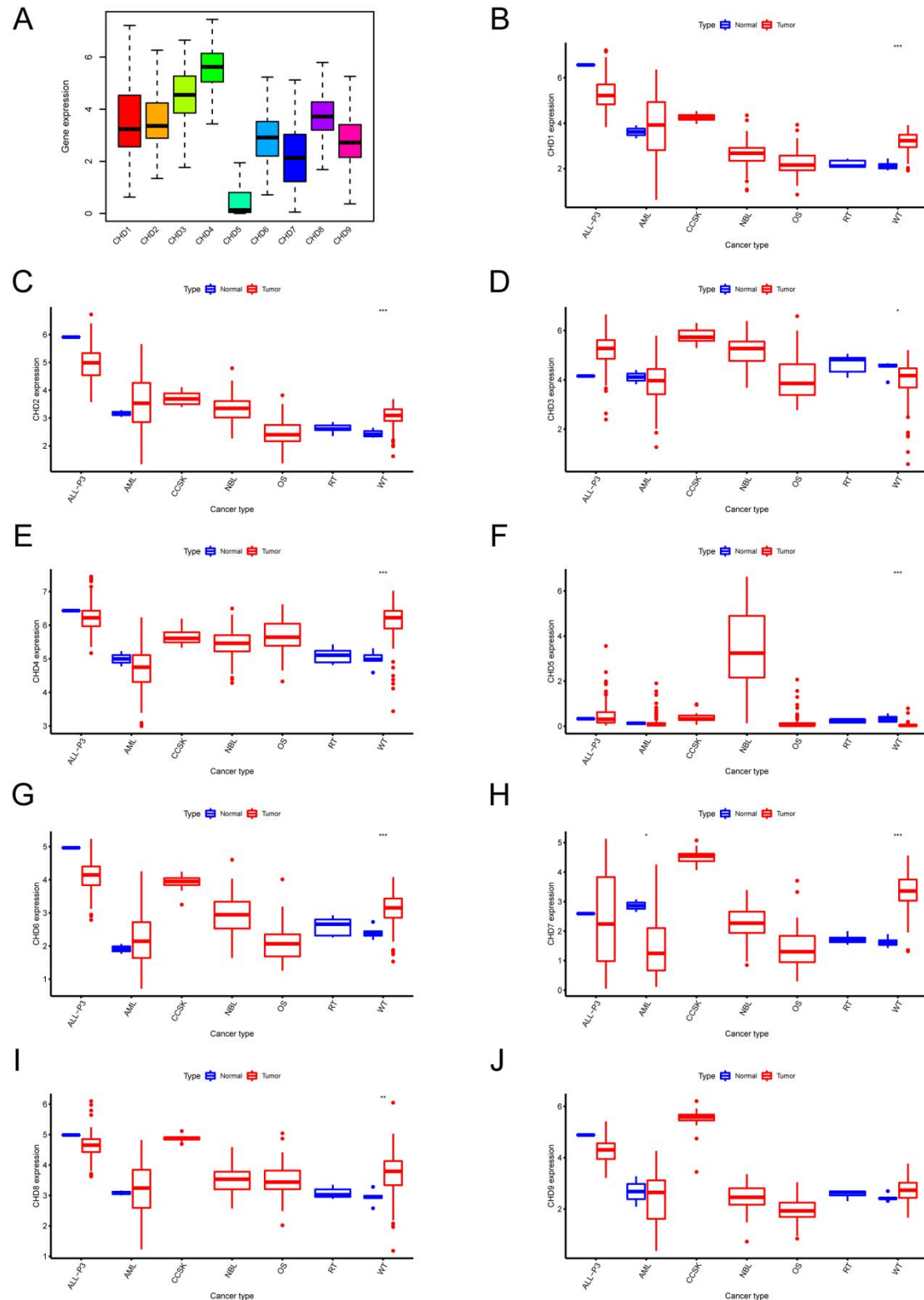


Figure S2. The expression of *CHD* gene family from TARGET. (A) The expression of *CHD* gene family in all the 7 cancer types from TARGET. (B-J) The expression of *CHD1-CHD9* from TARGET. All the cancer types were calculated ignoring the number of normal controls. OS, Osteosarcoma; RT, Rhabdoid Tumor; WT, Wilms tumor; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

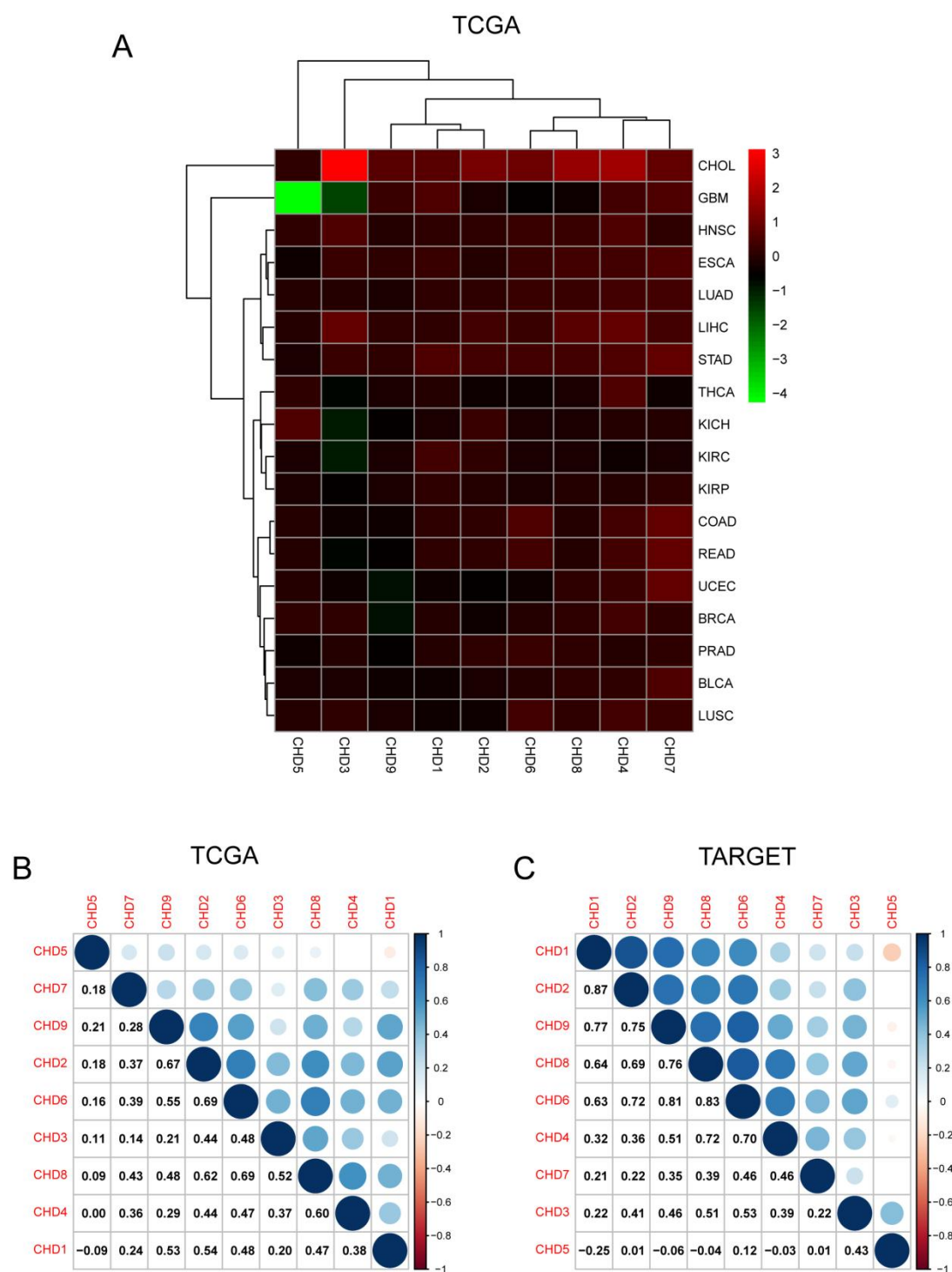


Figure S3. Correlation of gene expression between any two *CHD* members. (A) Heatmap for correlation of gene expression between any two *CHD* members. Only the cancer types which have at least 5 controls were calculated. (B) Correlation analysis of *CHD* gene expression in cancers from TCGA. (C) Correlation analysis of *CHD* gene expression in cancers from TARGET.

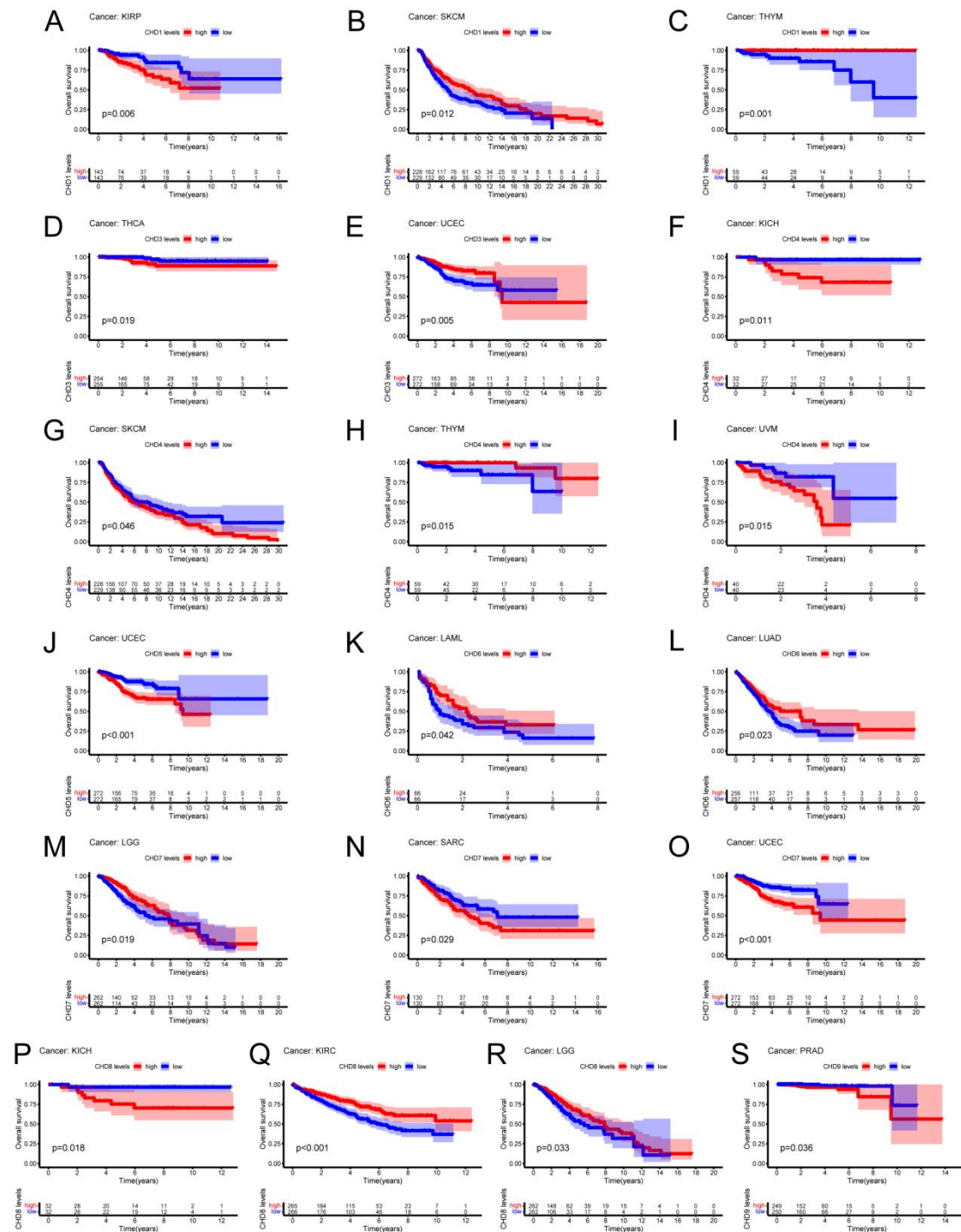


Figure S4. K-M plot of survival analysis for *CHD* gene family in 33 cancers of TCGA. Only significant results ($P < 0.05$) were shown. Group cut-offs were set at the median, creating high and low expression groups. Cancer types and survival time (years) were indicated at the top left and the bottom of each panel, respectively. Only those results with $P < 0.05$ were shown and P value was indicated above the abscissa axis.

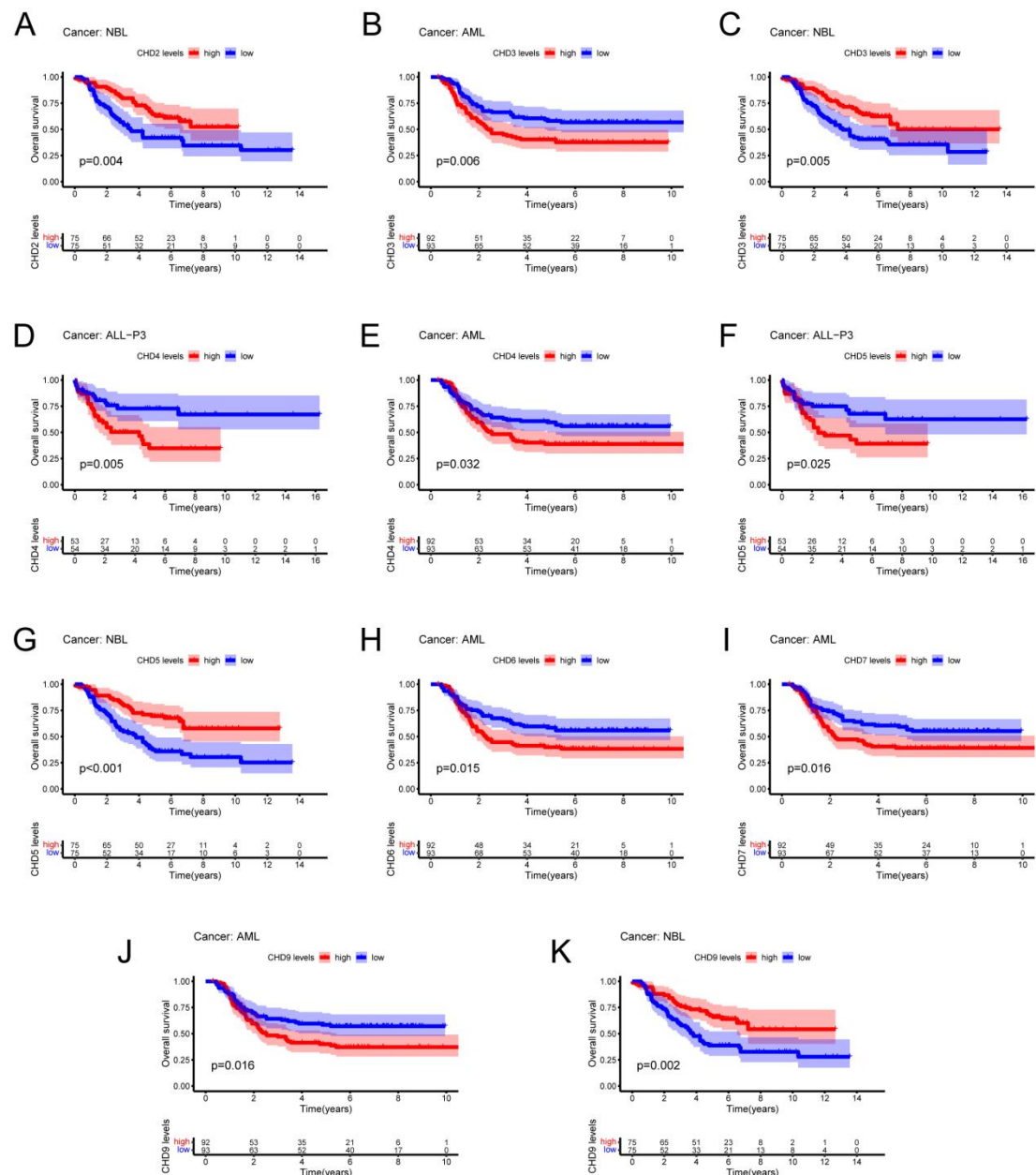


Figure S5. K-M plot of survival analysis for *CHD* gene family in 6 cancers of TARGET. Only significant results ($P < 0.05$) were shown. Group cut-offs were set at the median, creating high and low expression groups. Cancer types and survival time (years) were indicated at the top left and the bottom of each panel, respectively. Only those results with $P < 0.05$ were shown and P value was indicated above the abscissa axis.

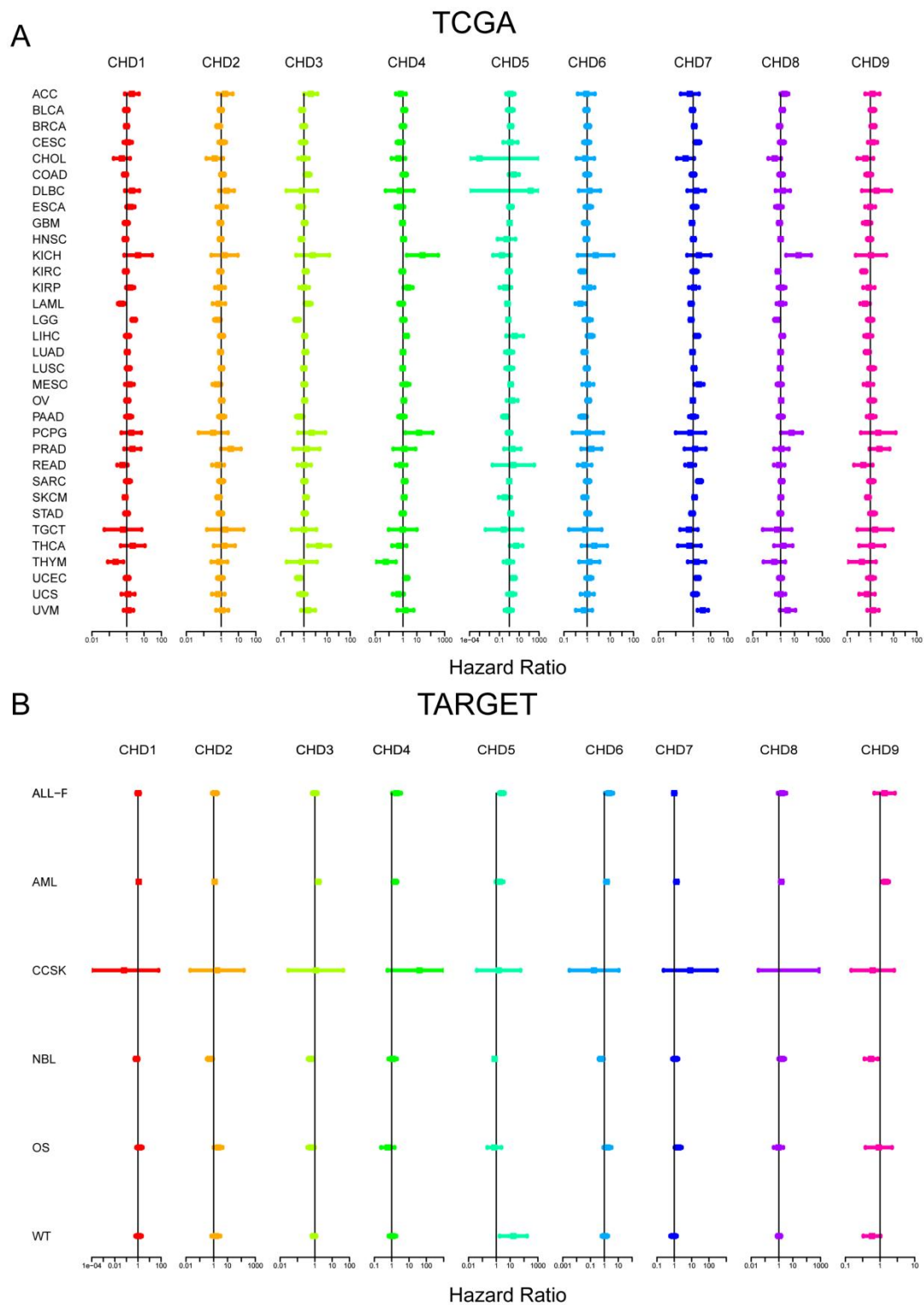


Figure S6. Forest plots of survival analysis for *CHD* gene family. All the cancers were shown in (A) for 33 cancers from TCGA and (B) 6 cancers for TAREGET.

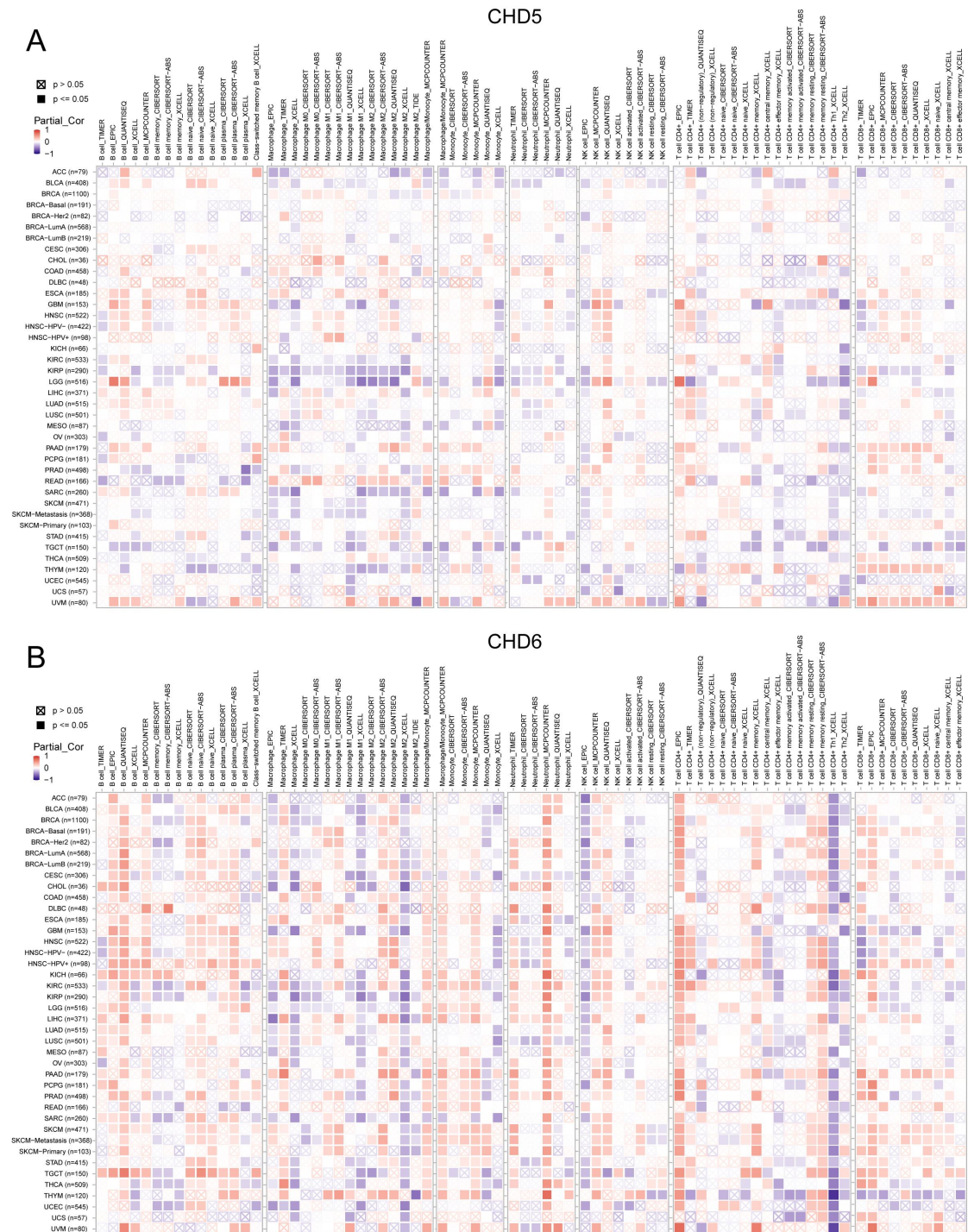


Figure S8. The correlation between the expression of *CHD* gene family and immune Infiltration. (A) The correlations between *CHD5* expression and immune infiltration in B cells, T cells, monocytes, macrophages, neutrophils and NK cells. (B) The correlations between *CHD6* expression and immune infiltration in B cells, T cells, monocytes, macrophages, neutrophils and NK cells. Cancer types and sample number were indicated on the left. Cell types and analyzing methods were indicated above. The results are represented in correlation matrices, highlighting positive (red rectangle) and negative (blue rectangle) partial correlations ($P < 0.05$).

CHD9

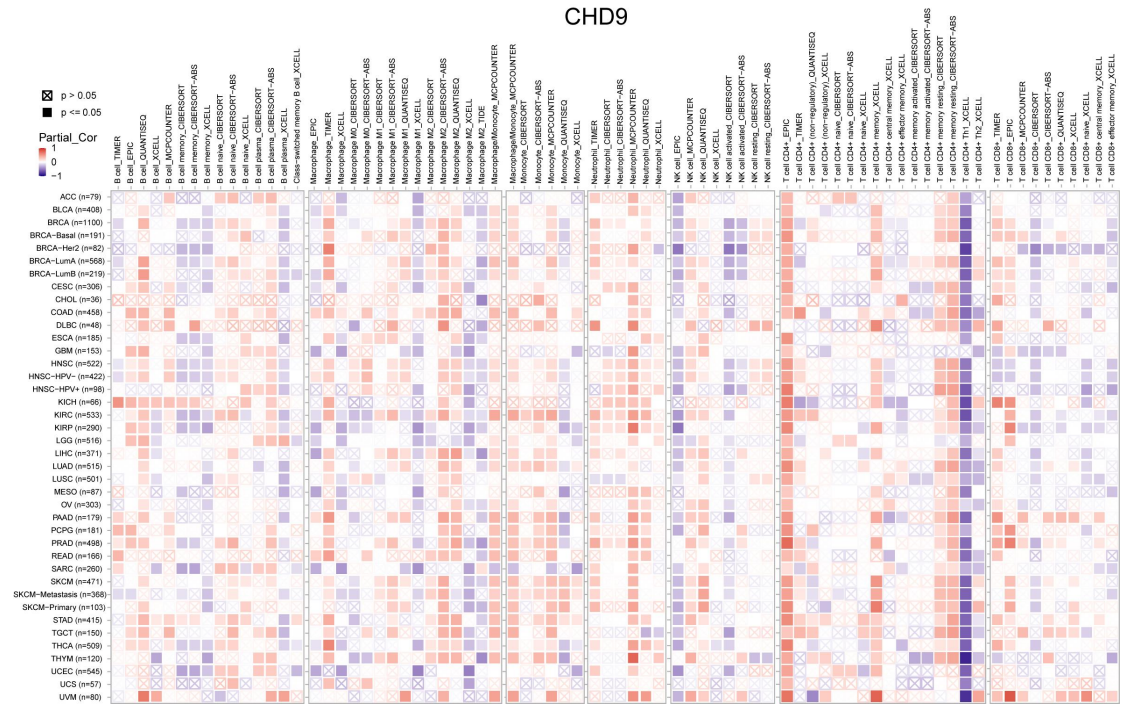


Figure S10. The correlations between *CHD9* expression and immune infiltration in B cells, T cells, monocytes, macrophages, neutrophils and NK cells. Cancer types and sample number were indicated on the left. Cell types and analyzing methods were indicated above. The results are represented in correlation matrices, highlighting positive (red rectangle) and negative (blue rectangle) partial correlations ($P < 0.05$).

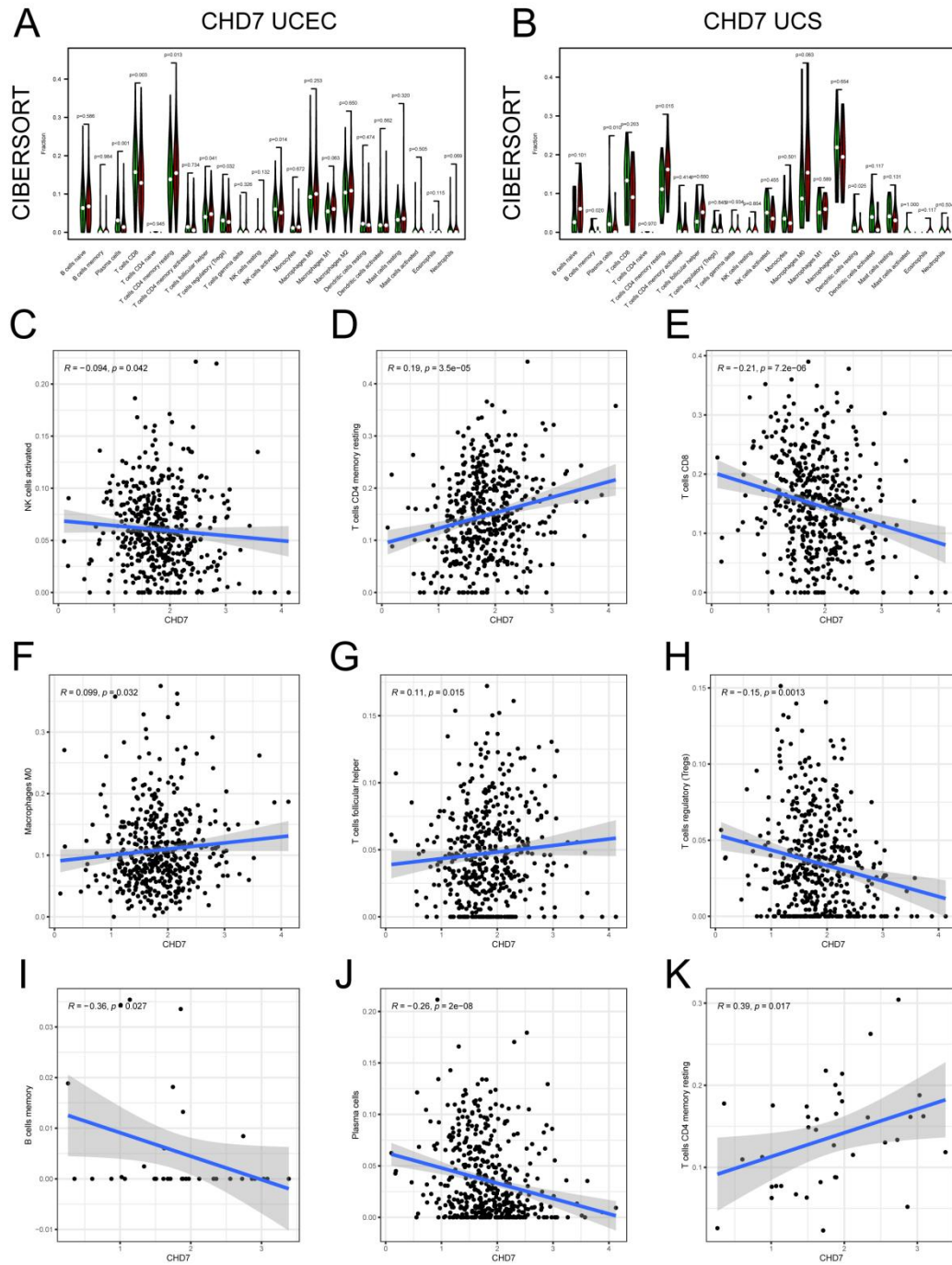


Figure S11. The correlation between *CHD7* expression and immune infiltration by CIBERSORT method. (A,B) *CHD7* expression of different types of immune cells in UCEC and UCS, respectively. (C-H) Different types of immune cells with significant difference ($P < 0.05$) in UCEC between higher expression and lower expression group, the cut-off of groups was set as median. (I-K) Different types of immune cells with significant difference ($P < 0.05$) in UCS between higher expression and lower expression group, the cut-off of groups was set as median.

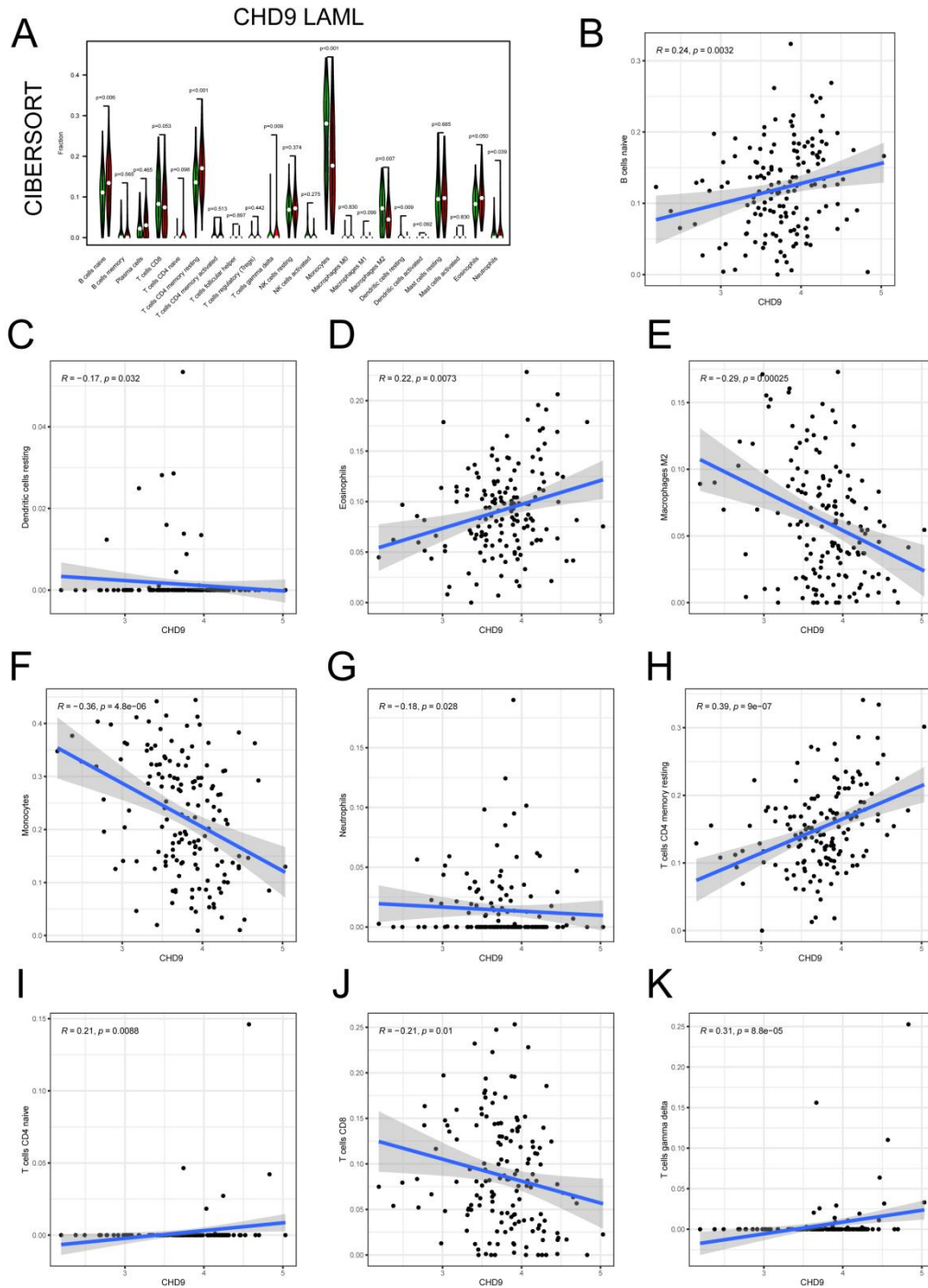


Figure S12. The correlation between *CHD9* expression and immune infiltration by CIBERSORT method. (A) Different types of immune cells in LAML. (B-K) Different types of immune cells with significant difference ($P < 0.05$) in LAML between higher expression and lower expression groups, the cut-off of which was set as median.

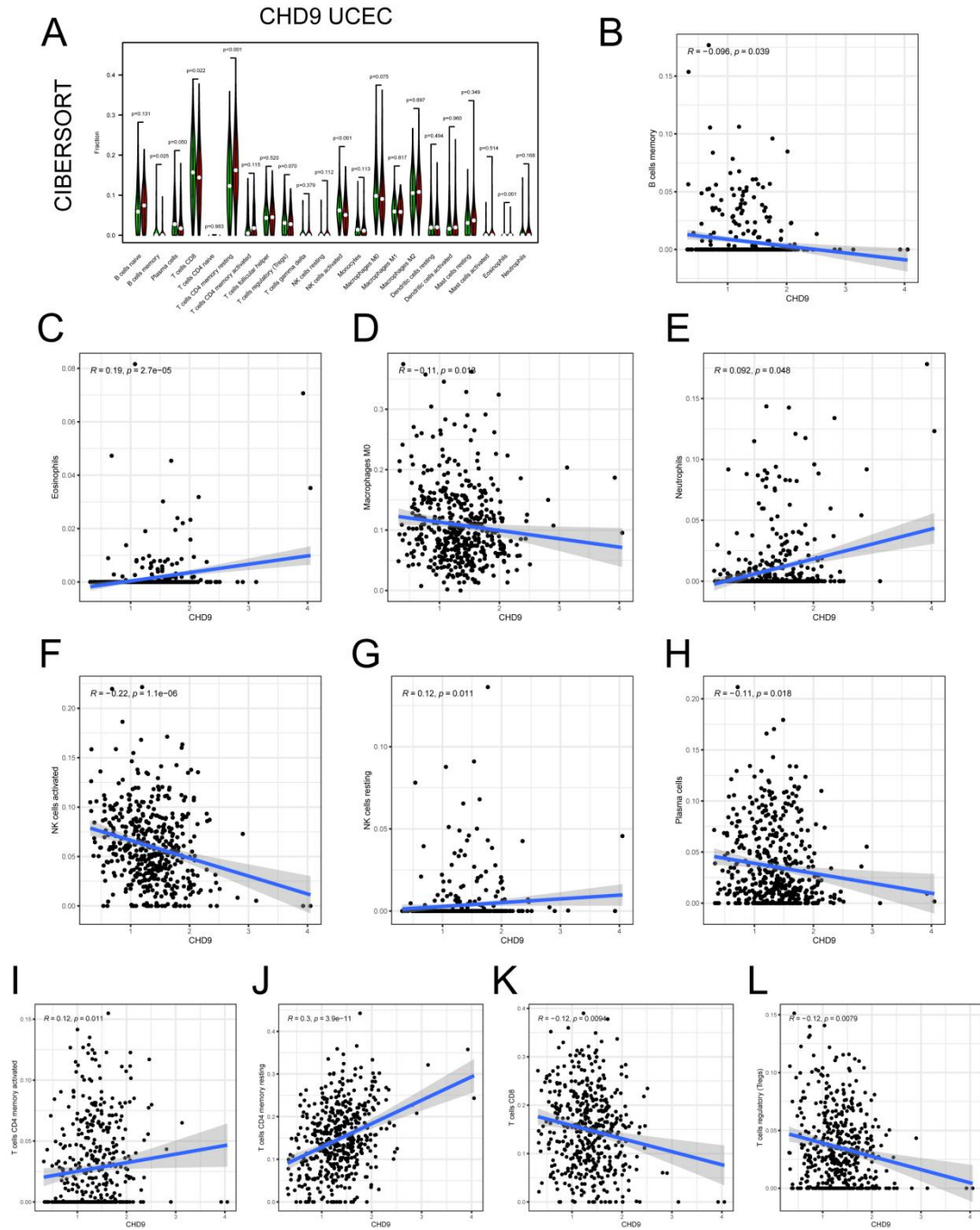


Figure S13. The correlation between *CHD9* expression and immune infiltration by CIBERSORT method. (A) *CHD9* expression of different types of immune cells in UCEC. (B-L) Different types of immune cells with significant difference ($P < 0.05$) in UCEC between higher expression and lower expression groups, the cut-off of which was set as median.

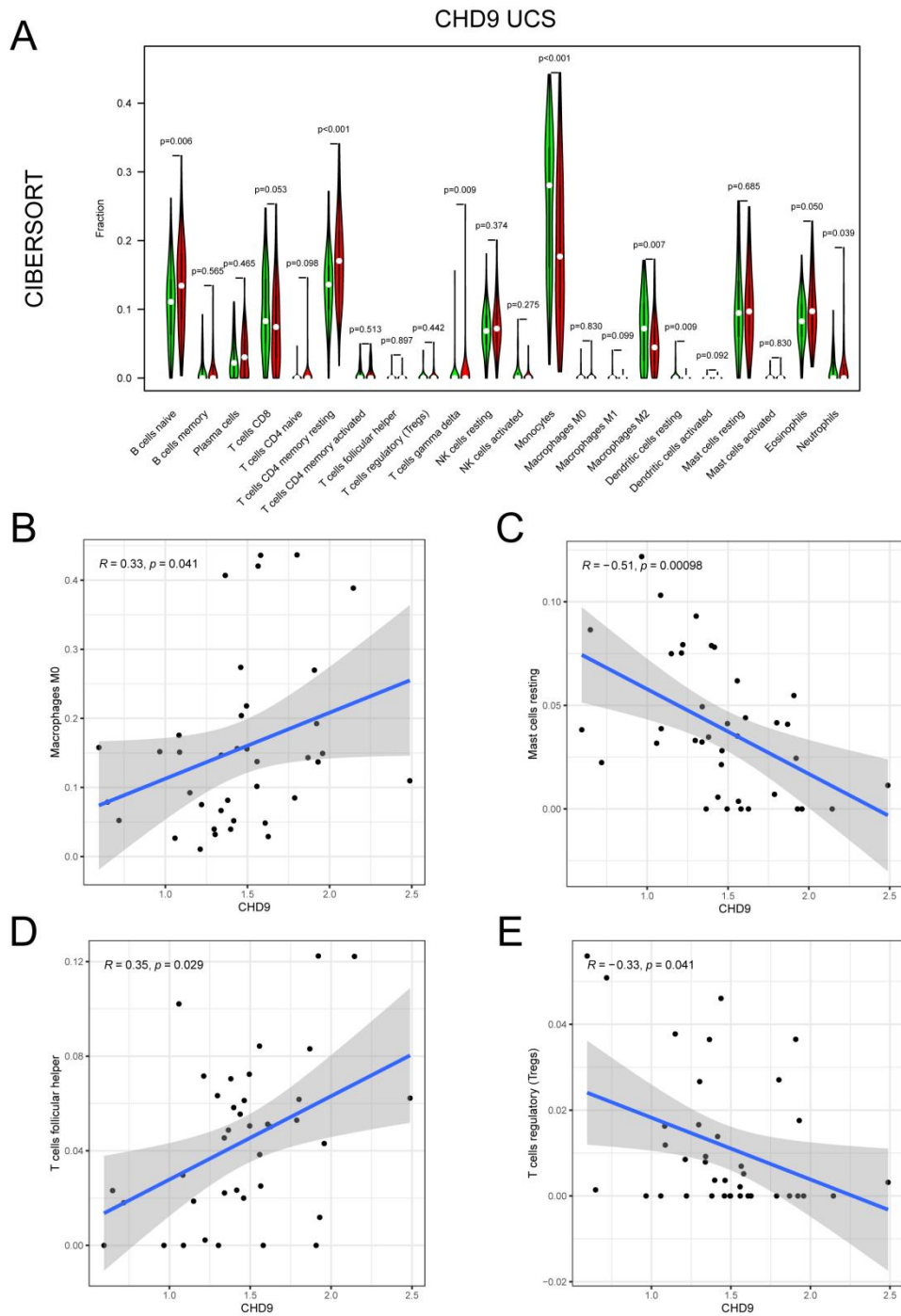


Figure S14. The correlation between *CHD9* expression and immune infiltration by CIBERSORT method. (A) *CHD9* expression of different types of immune cells in UCS. (B-E) Different types of immune cells with significant difference ($P < 0.05$) in UCS between higher expression and lower expression groups, the cut-off of which was set as median.

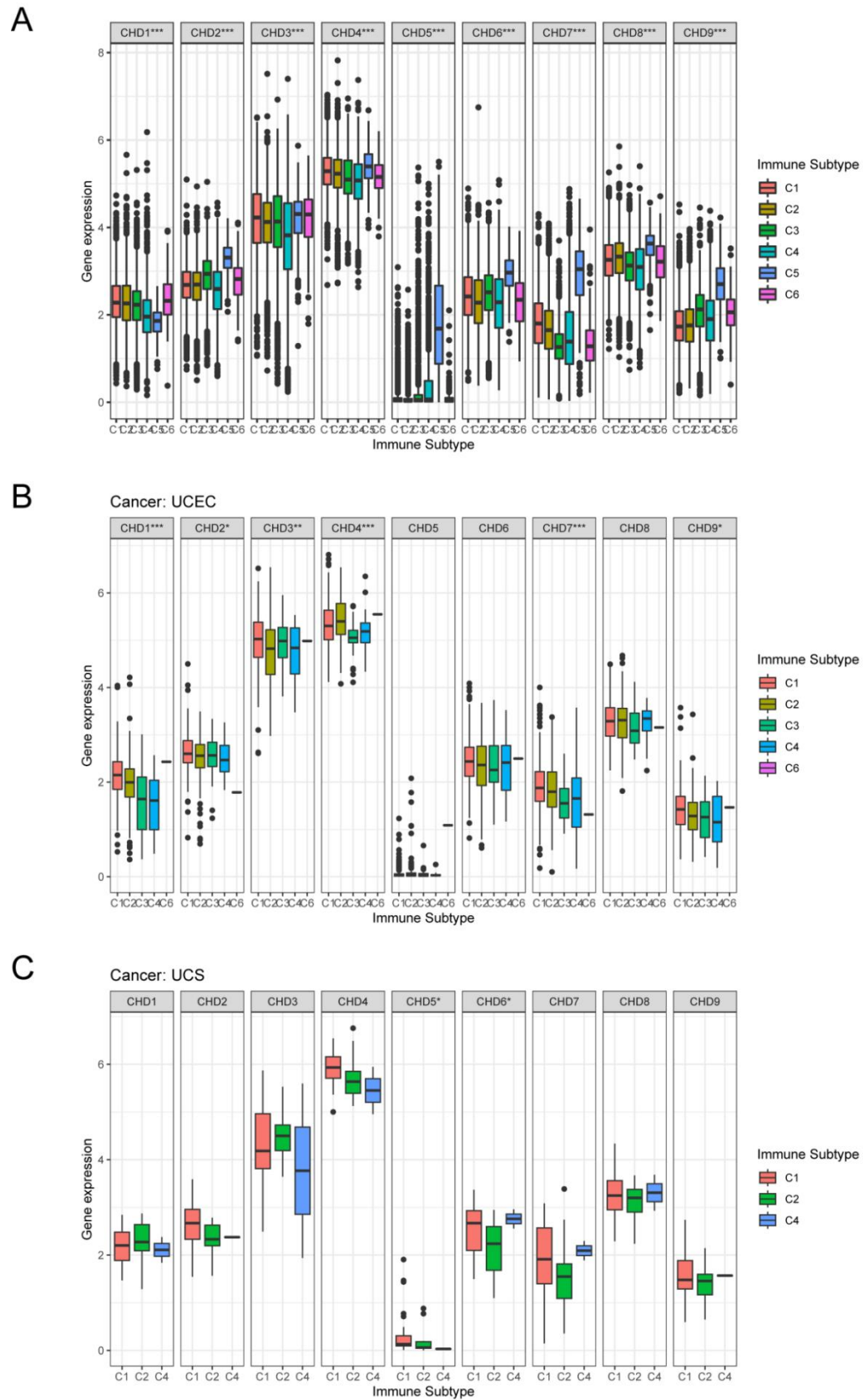


Figure S15. Expression of *CHD* gene family according to immune subtype of clinical parameter. (A-C) Expression of *CHD* gene family according to immune subtype of clinical parameter in LAML, UCEC and UCS, respectively.

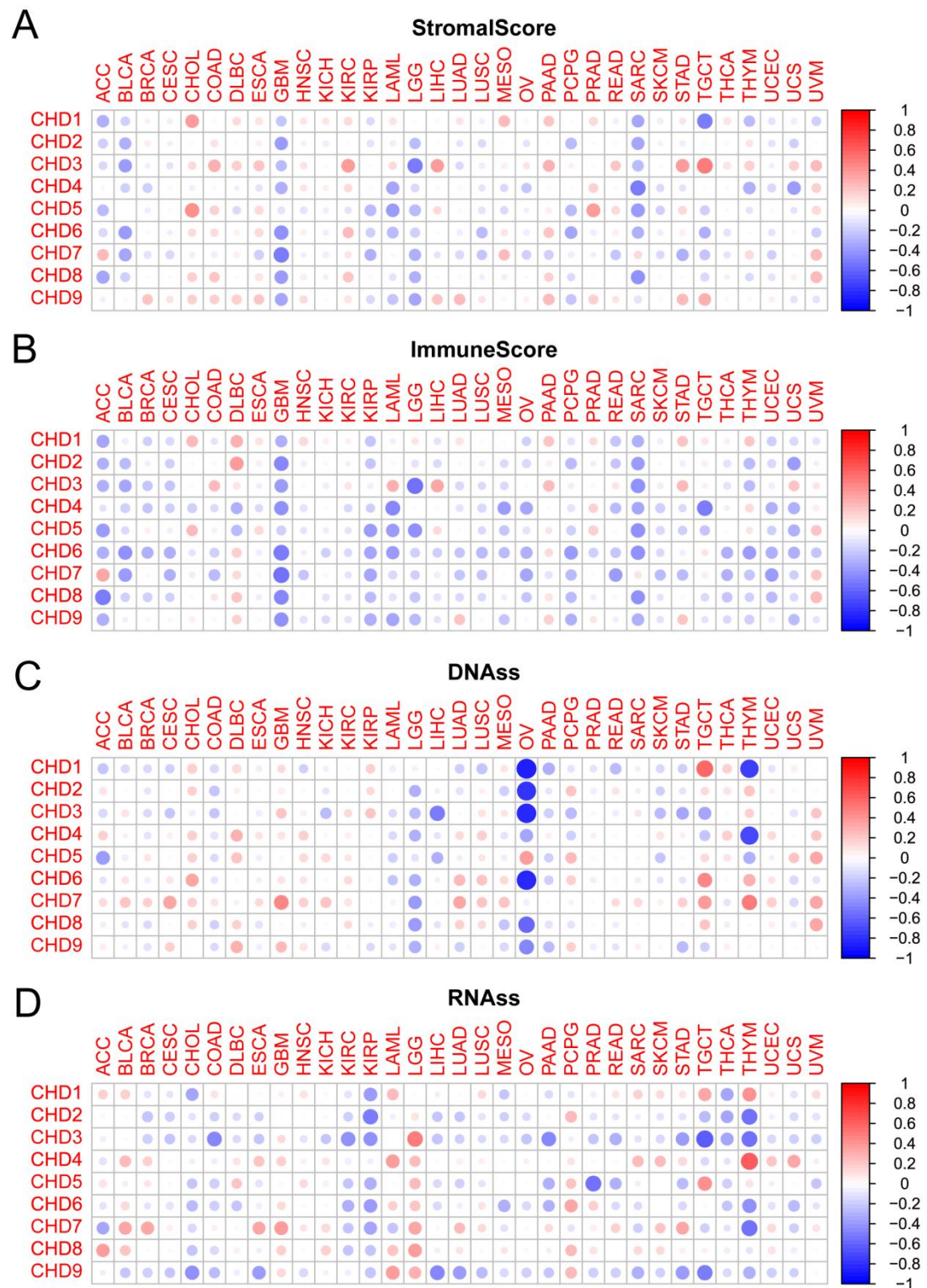


Figure S16. The micro-environment score and stemness score of *CHD* gene family in all the 33 types of cancers from TCGA. (A) Stromal score of *CHD* gene family. (B) Immune score of *CHD* gene family. (C) DNA methylation score of *CHD* gene family. (D) RNA expression score of *CHD* gene family.

Cancer: LAML

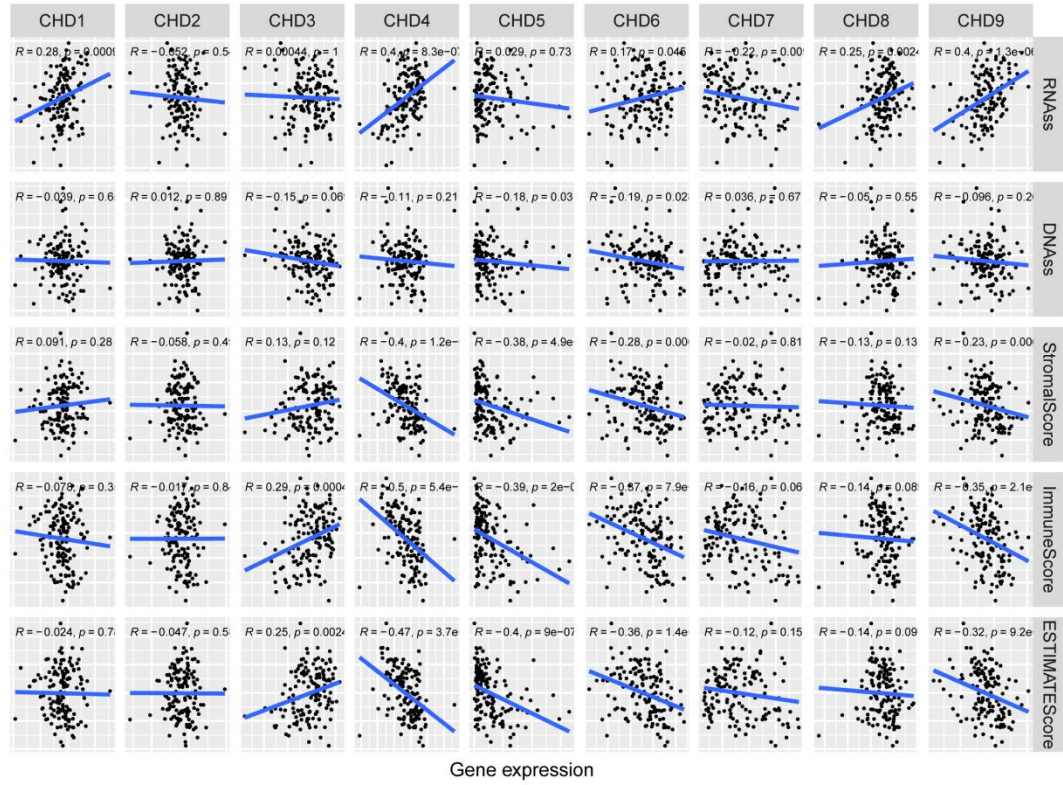
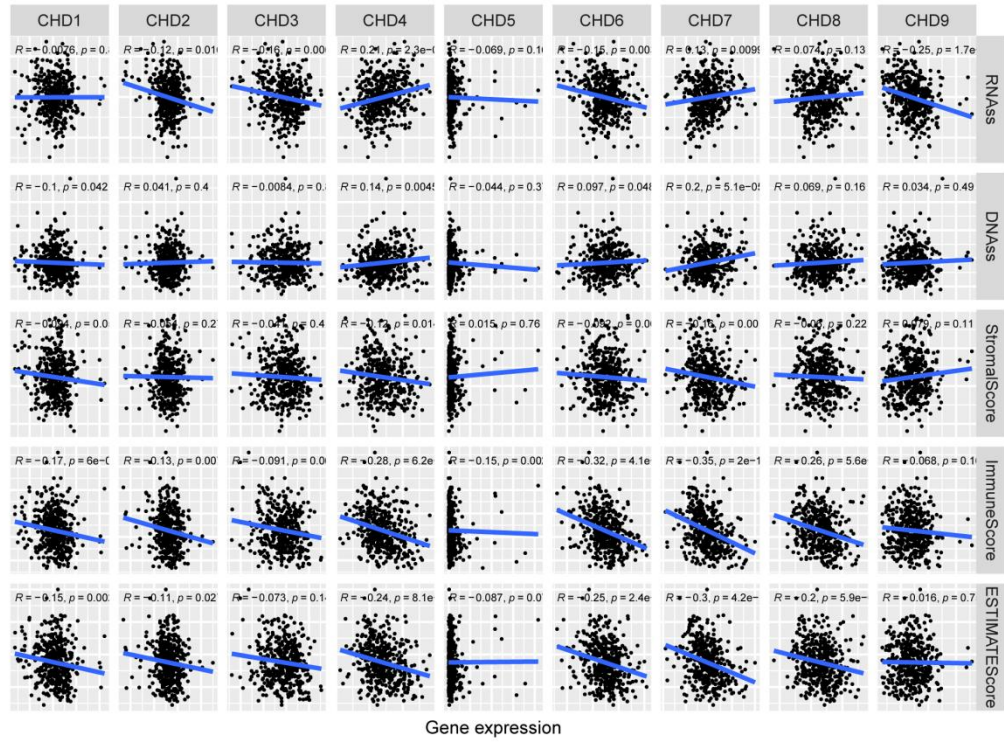


Figure S17. The micro-environment score and stemness score of *CHD* gene family in LAML.

A

Cancer: UCEC



B

Cancer: UCS

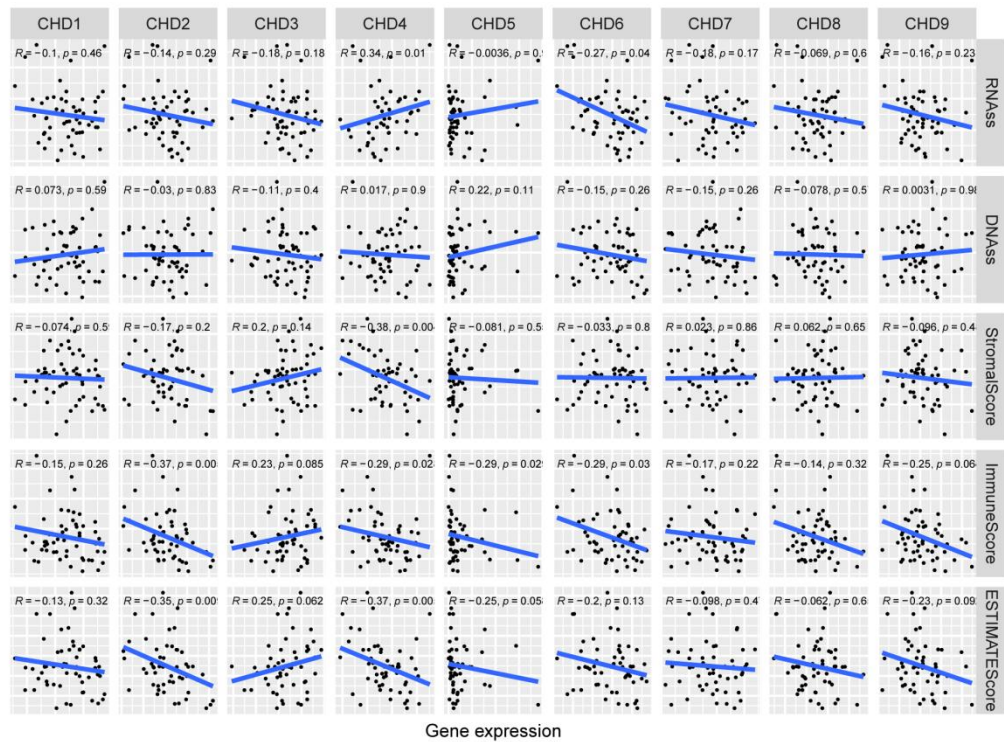


Figure S18. The micro-environment score and stemness score of *CHD* gene family in UCEC and UCS. (A) The micro-environment score and stemness score of *CHD* gene family in UCEC. (B) The micro-environment score and stemness score of *CHD* gene family in UCS.

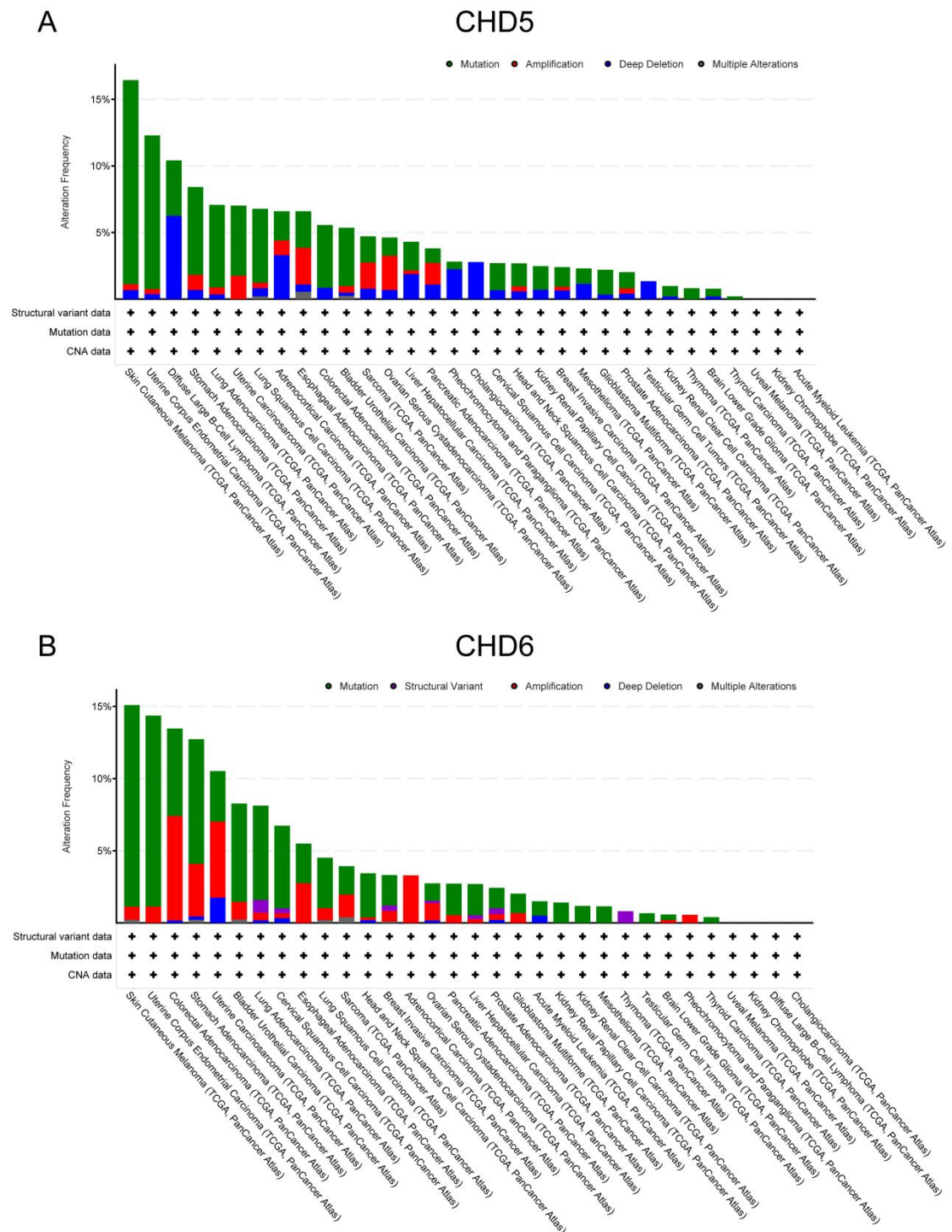


Figure S20. Mutation profiles of *CHD* gene family from cBioPortal. (A) Mutation frequency of *CHD5* in pan-cancer studies. (B) Mutation frequency of *CHD6* in pan-cancer studies. The mutation types of mutation, structural variant, amplification, deep deletion and multiple alternations were indicated in green, purple, red, blue and brown, respectively. Cancer types and data origin were indicated below the abscissa axis.

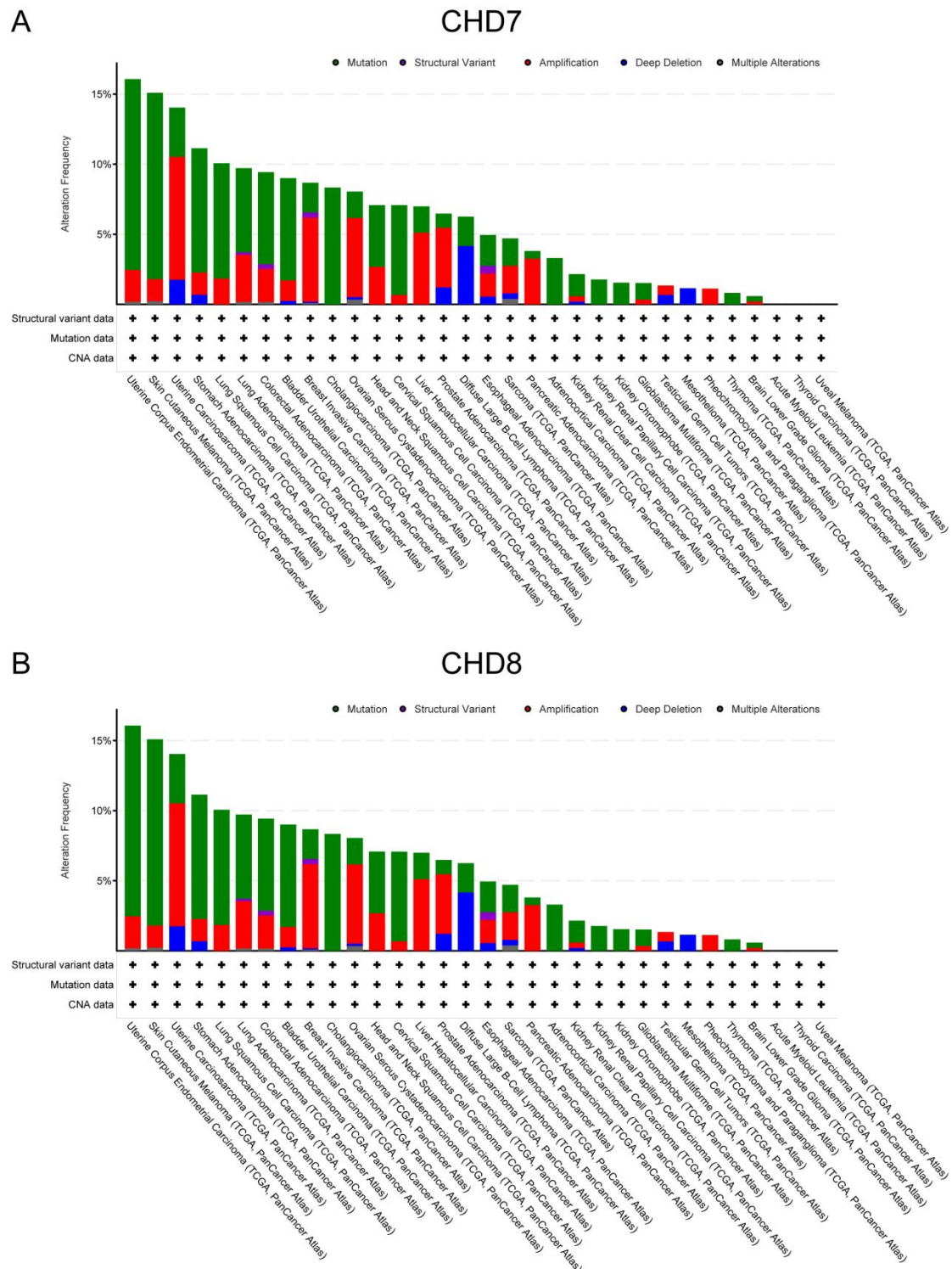


Figure S21. Mutation profiles of *CHD* gene family from cBioPortal. (A) Mutation frequency of *CHD7* in pan-cancer studies. (B) Mutation frequency of *CHD7* in pan-cancer studies. The mutation types of mutation, structural variant, amplification, deep deletion and multiple alternations were indicated in green, purple, red, blue and brown, respectively. Cancer types and data origin were indicated below the abscissa axis.

CHD9

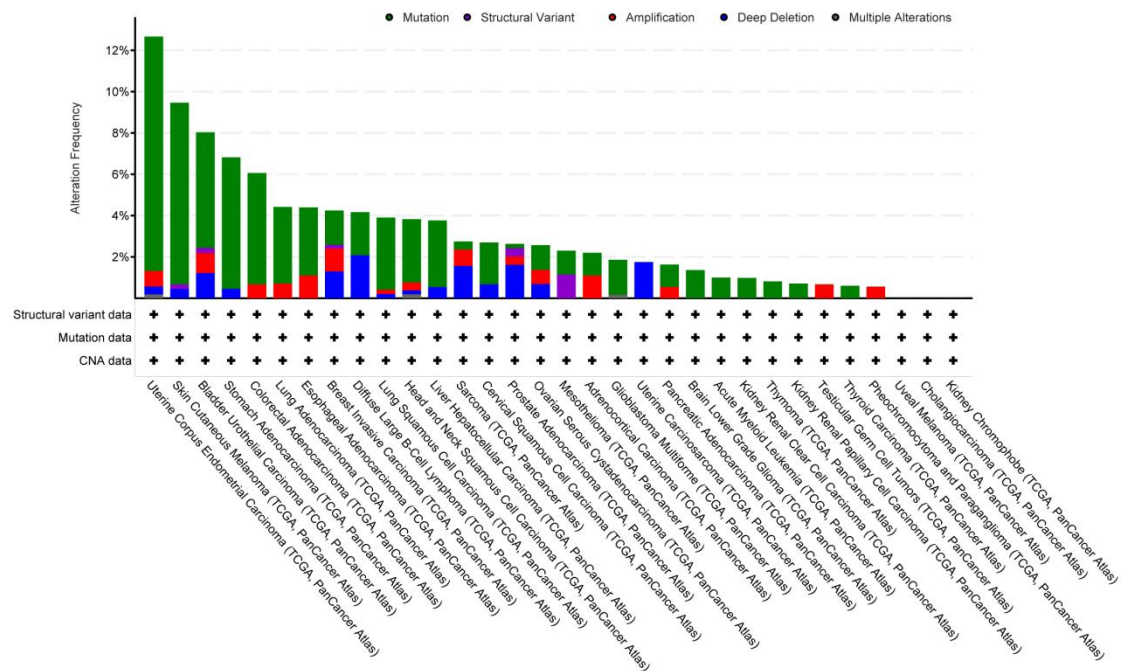


Figure S22. Mutation frequency of *CHD9* in pan-cancer studies. The mutation types of mutation, structural variant, amplification, deep deletion and multiple alternations were indicated in green, purple, red, blue and brown, respectively. Cancer tyeps and data origin were indicated below the abscissa axis.

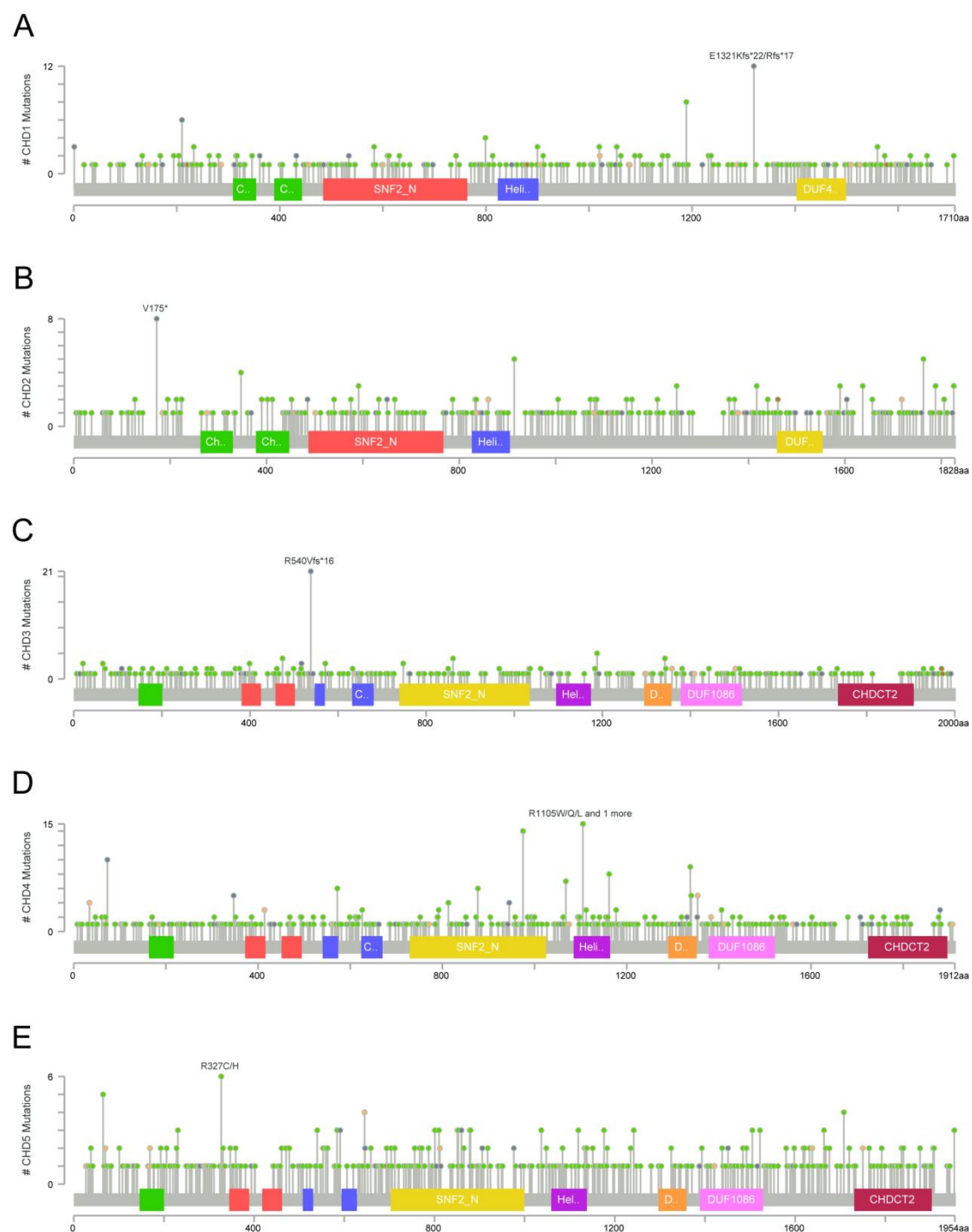


Figure S23. The mutation sites across the protein of *CHD* gene family in all cancer types from TCGA. (A-E) The general mutation count across the protein of *CHD1*, *CHD2*, *CHD3*, *CHD4*, *CHD5* in all cancer types from TCGA, respectively.

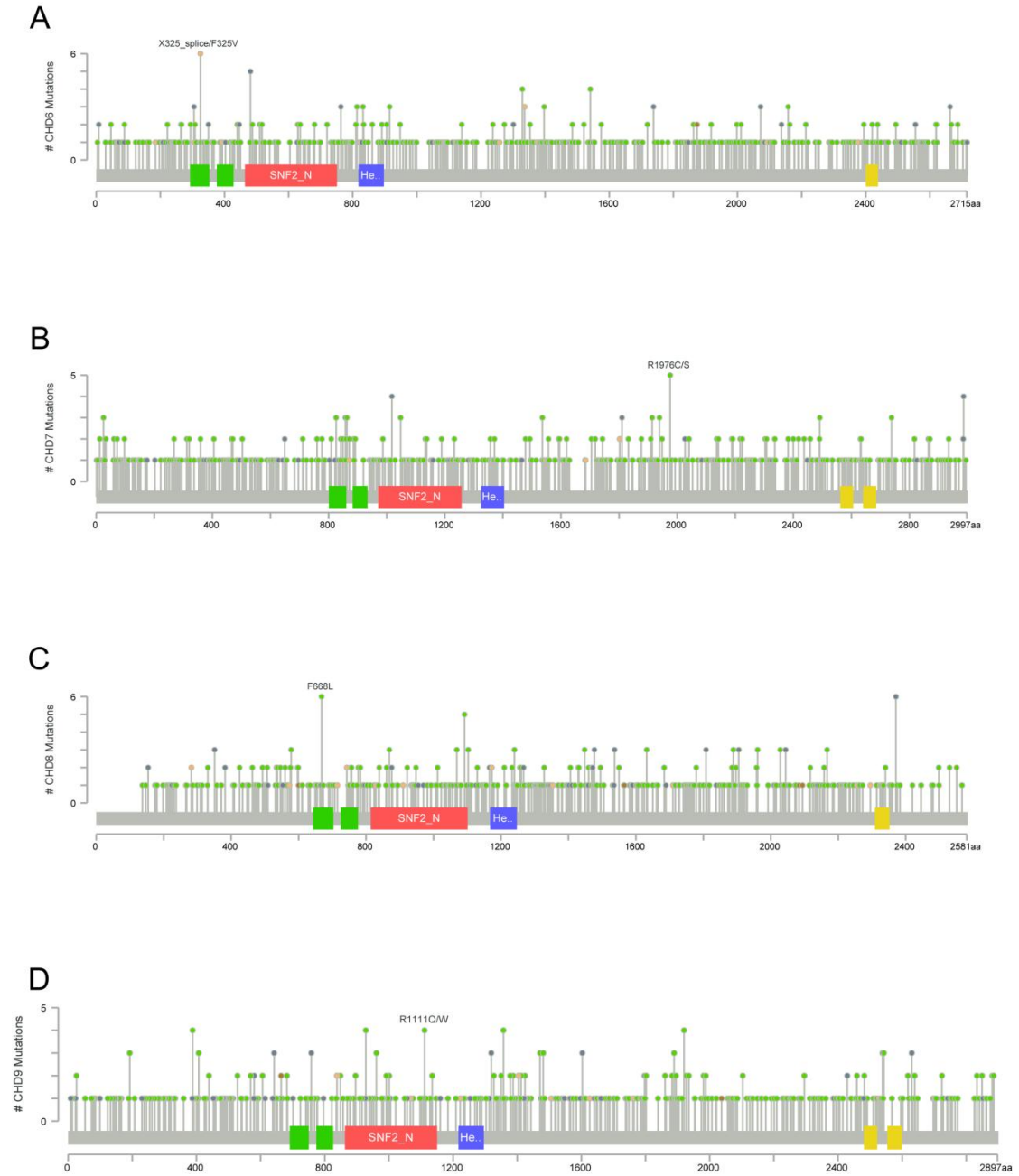


Figure S24. The mutation sites across the protein of *CHD* gene family in all cancer types from TCGA. (A-D) The general mutation count across the protein of *CHD6*, *CHD7*, *CHD8*, *CHD9* in all cancer types from TCGA, respectively.

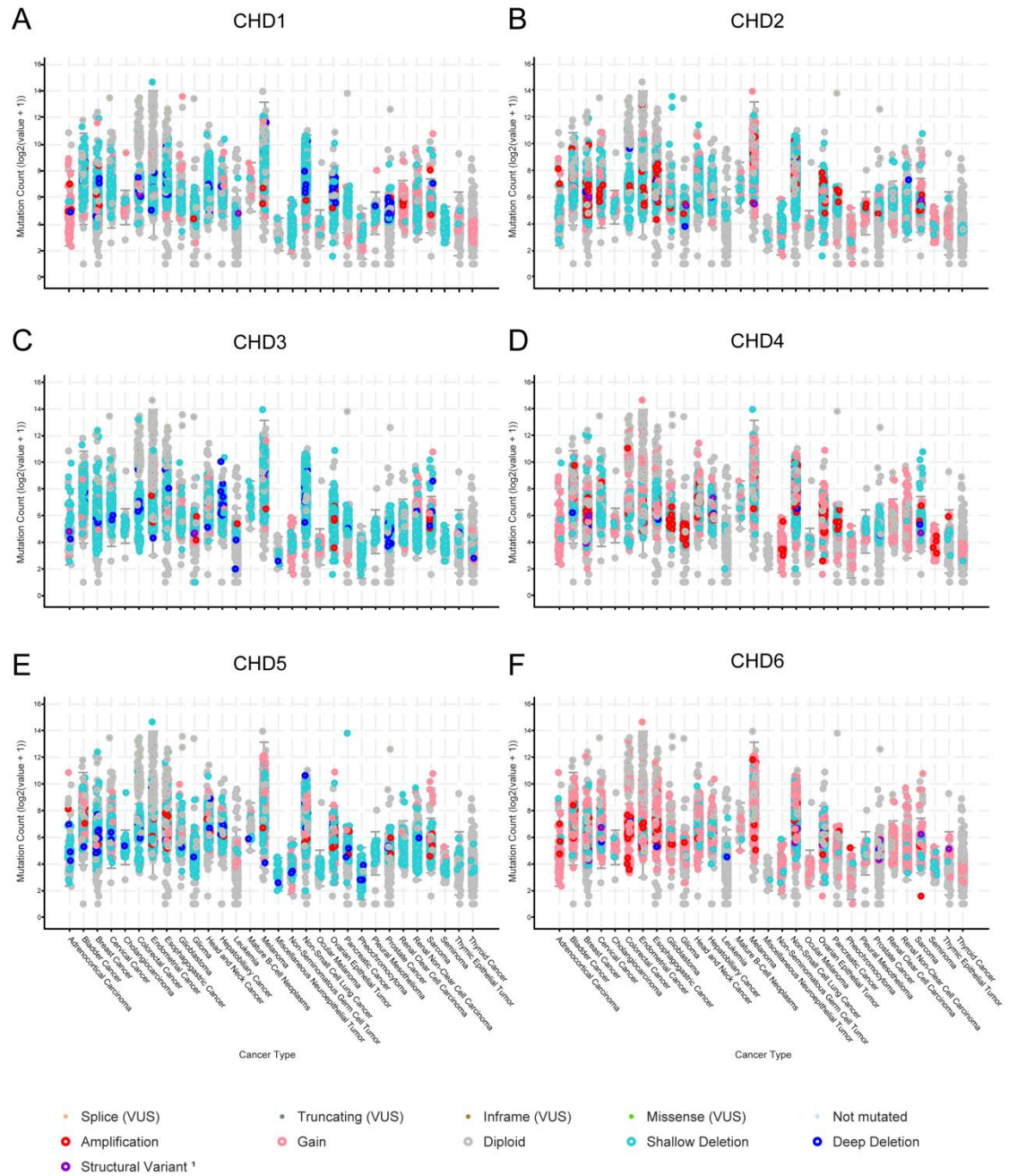


Figure S25. The different types of mutation count for *CHD* gene family in various cancer types. (A-F) The different types of mutation count for *CHD1*, *CHD2*, *CHD3*, *CHD4*, *CHD5* and *CHD6* in various cancer types, respectively.

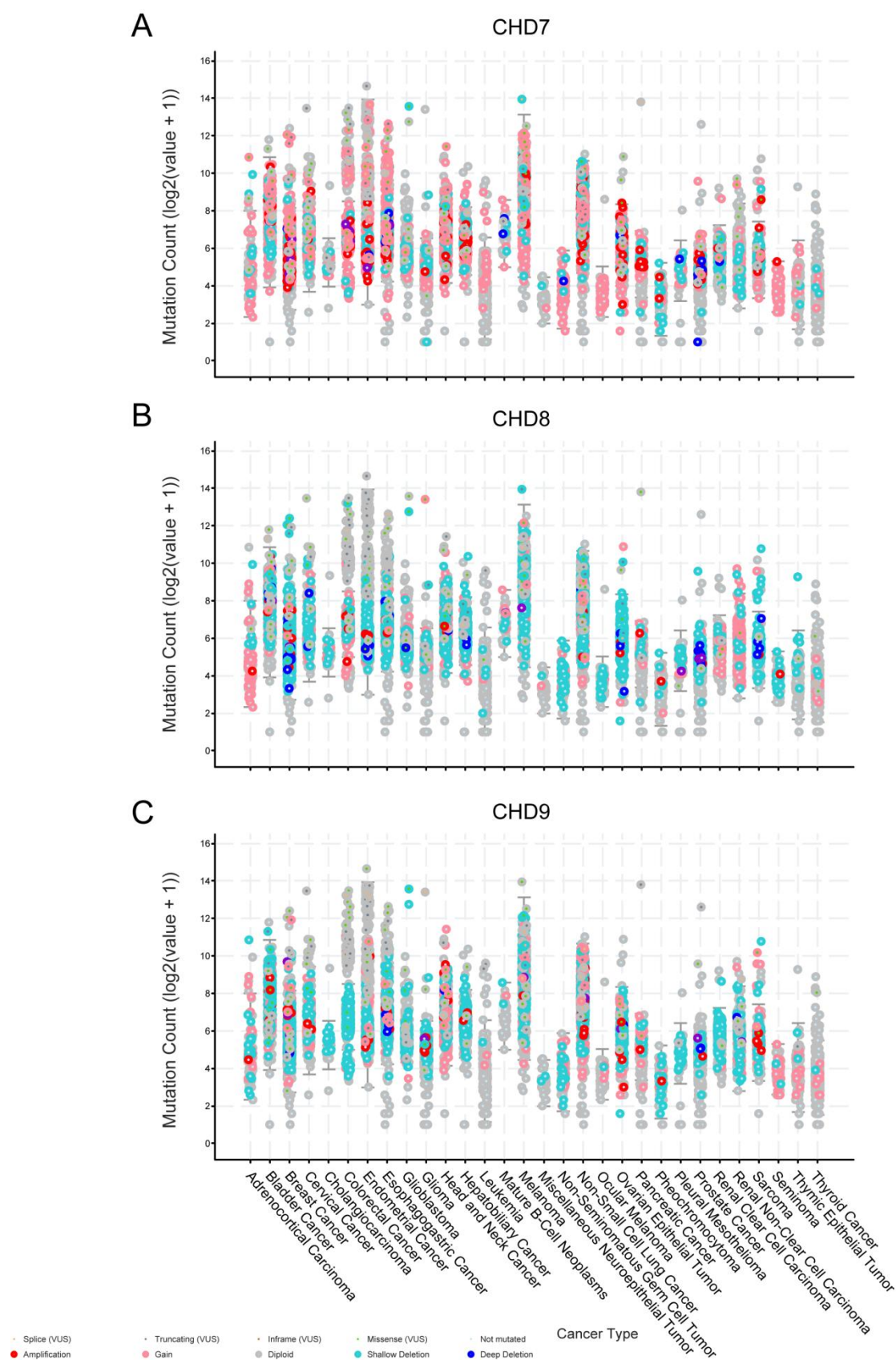


Figure S26. The different types of mutation count for *CHD* gene family in various cancer types. (A-C) The different types of mutation count for *CHD7*, *CHD8* and *CHD9* in various cancer types, respectively.

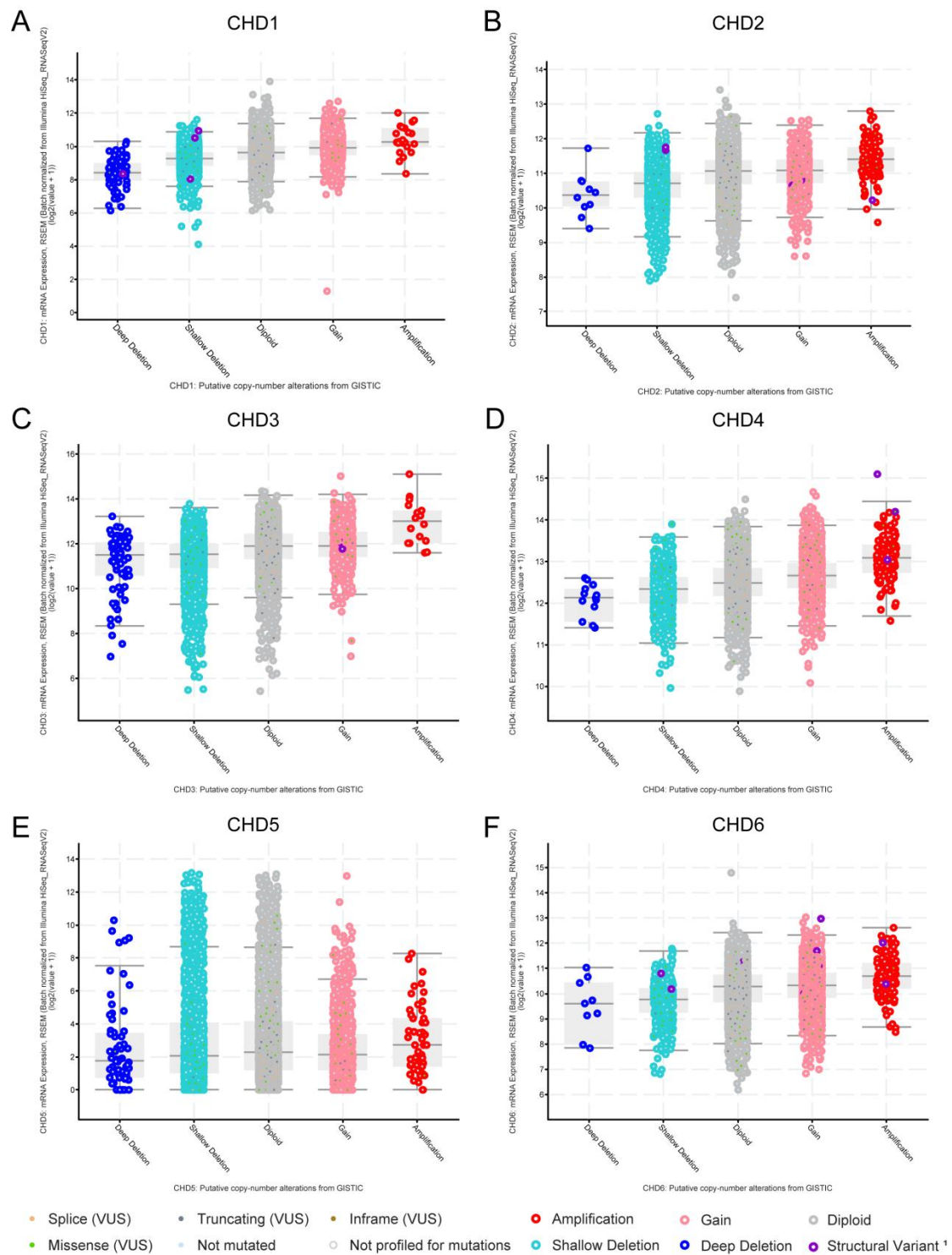


Figure S27. The correlation between mRNA expression of *CHD* gene family and putative copy-number alterations from GISTIC. (A-F) The correlation between mRNA expression of *CHD1*, *CHD2*, *CHD3*, *CHD4*, *CHD5*, *CHD6* and putative copy-number alterations from GISTIC, respectively.

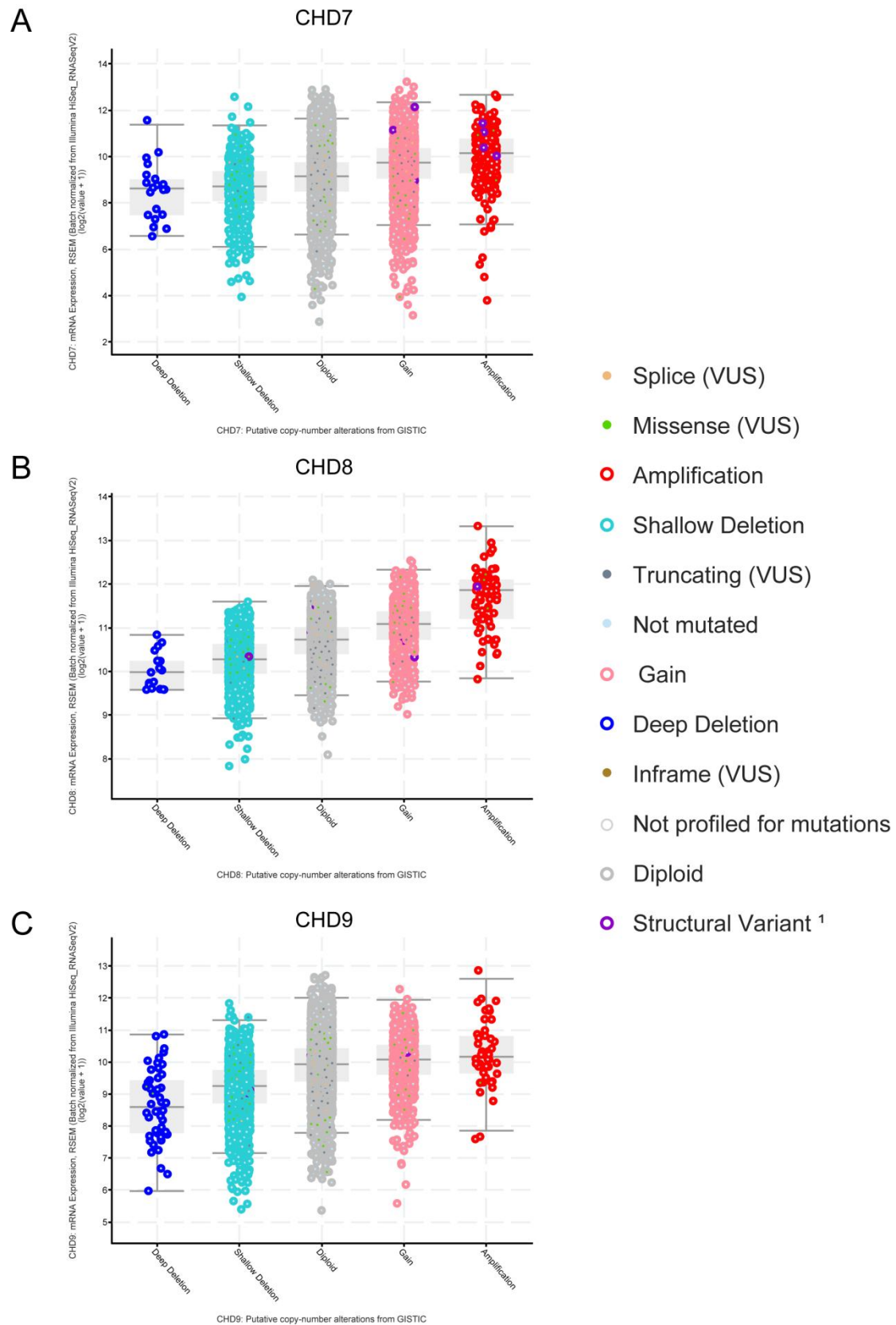


Figure S28. The correlation between mRNA expression of *CHD* gene family and putative copy-number alterations from GISTIC. (A-C)The correlation between mRNA expression of *CHD7*, *CHD8*, *CHD9* and putative copy-number alterations from GISTIC, respectively.

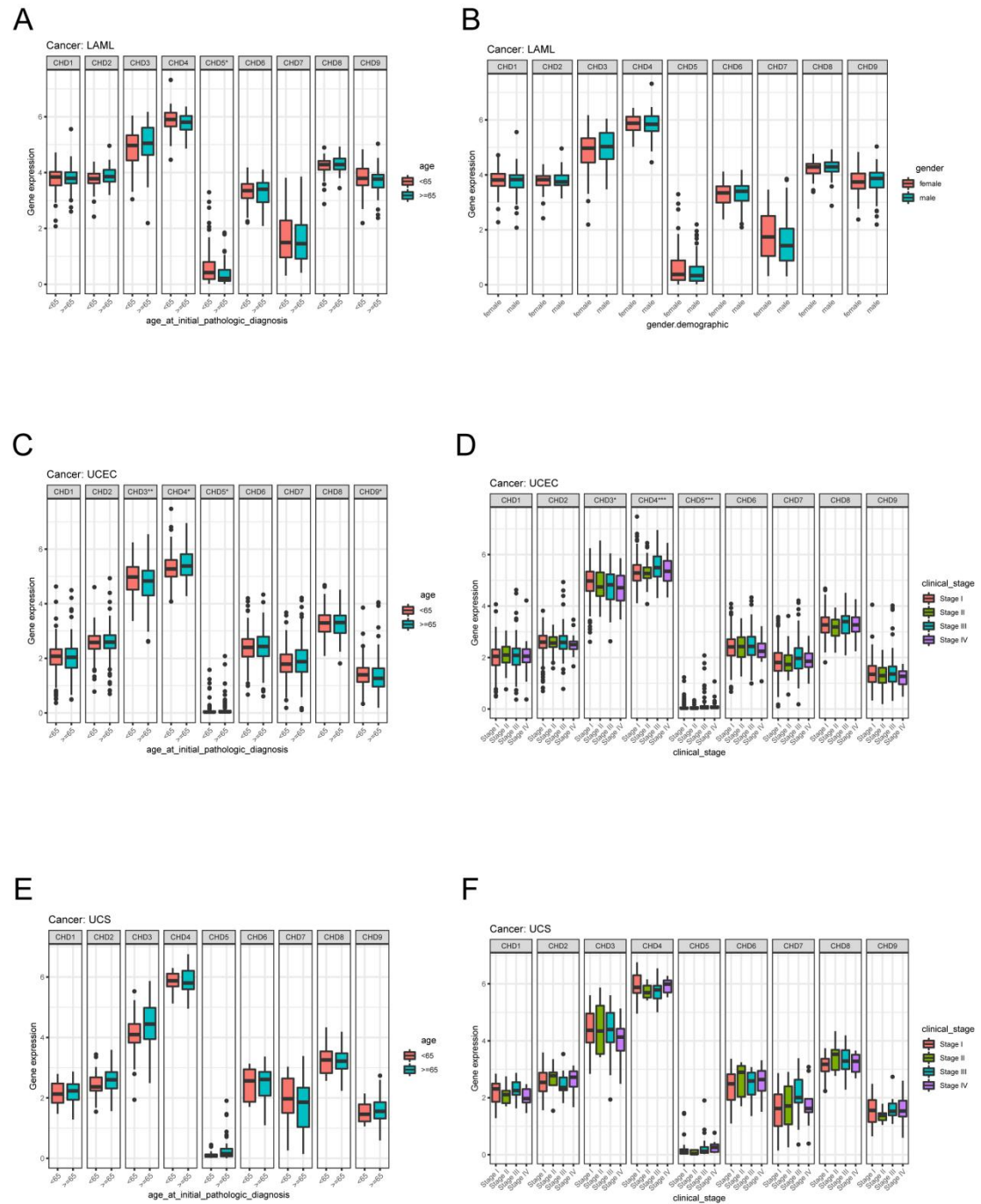


Figure S29. Expression of *CHD* gene family in LAML, UCEC and UCS according to clinical parameter. (A,B) Expression of *CHD* gene family in LAML based on age and gender, respectively. (C,D) Expression of *CHD* gene family in UCEC based on age and clinical stage, respectively. (E,F) Expression of *CHD* gene family in UCEC based on age and clinical stage, respectively. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

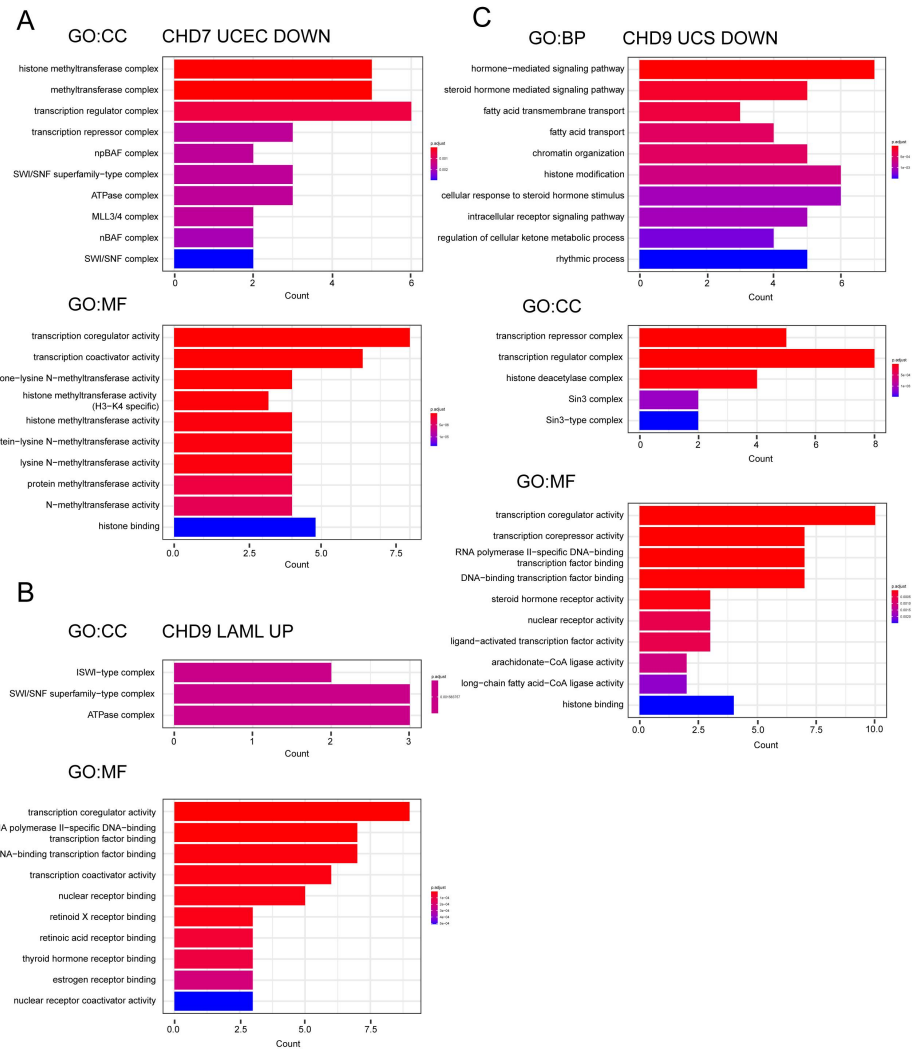


Figure S30. Gene Ontology analysis of *CHD7* and *CHD9* in LAML, UCEC and UCS. (A) Cellular component (CC) and molecular function (MF) of GO analysis for down-regulated DEGs interacting with *CHD7* in UCEC. (H) Cellular component (CC) and molecular function (MF) of GO analysis for down-regulated DEGs interacting with *CHD7* in UCS. (I) Cellular component(CC) and molecular function(MF) of GO analysis for up-regulated DEGs interacting with *CHD9* in LAML. (J) Biological progress(BP), cellular component(CC) and molecular function (MF) of GO analysis for down-regulated DEGs interacting with *CHD9* in UCS.