Figure S1. The expression of H/ACA snoRNP gene family in HCC patient based on TCGA datasets. ***, P<0.001.
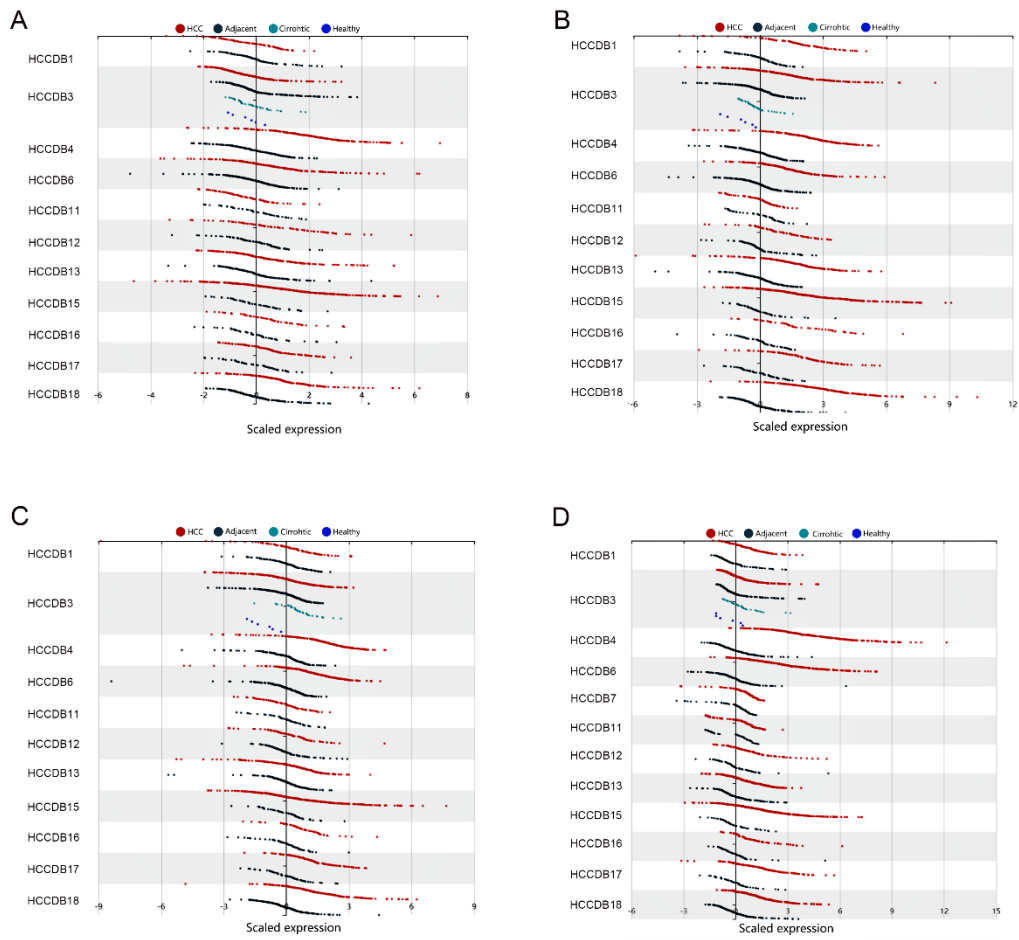

Figure S2. The expression of H/ACA snoRNP gene family in various tissues in the HCCDB database.

(A) The expression of GAR1 in different liver tissues. (B) The expression of NHP2 in different liver tissues. (C) The expression of NOP10 in different liver tissues. (D) The expression of DKC1in different liver tissues.
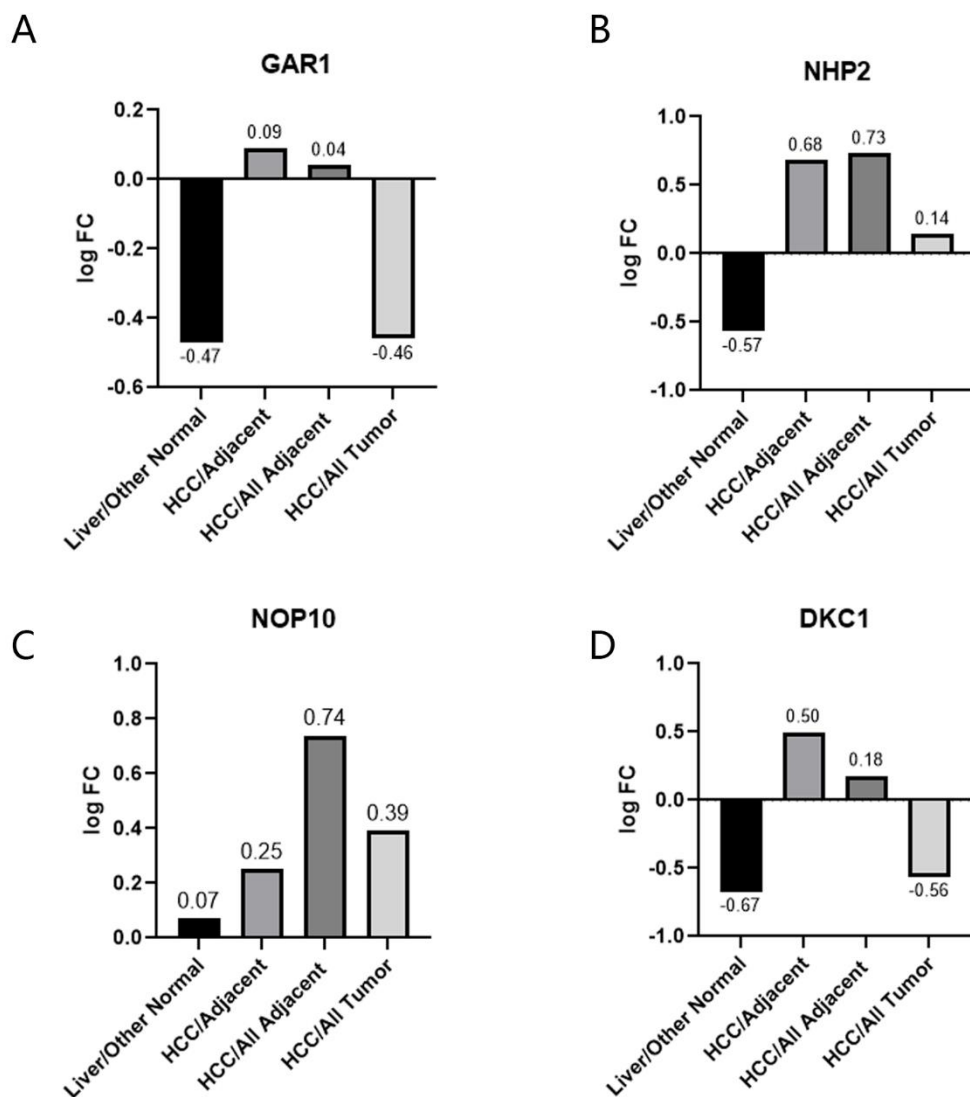

Figure S3. Chart bar of the overall expression of the H/ACA snoRNP gene family in various tissues in the HCCDB database. (A) The overall expression of GAR1 in different tissues. (B) The overall expression of NHP2 in different tissues. (C) The overall expression of NOP10 in different tissues. (D) The overall expression of DKC1 in different tissues.
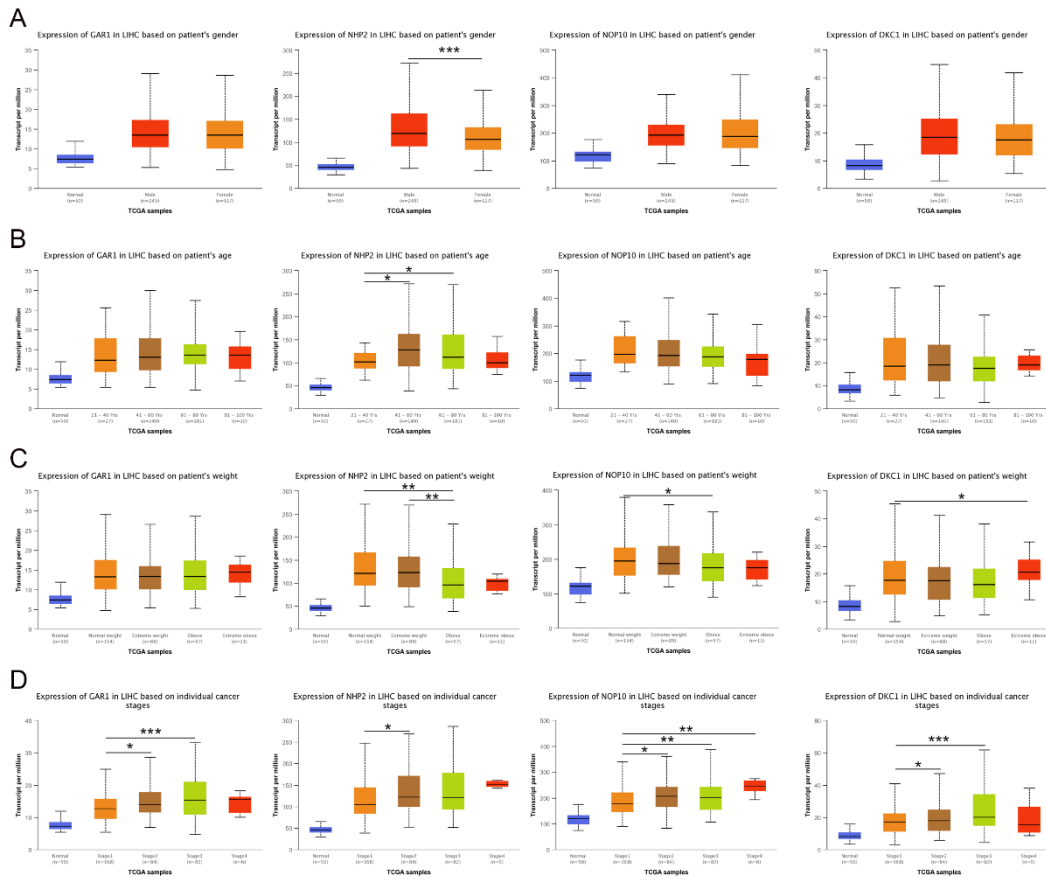
Figure S4. The mRNA expression of the H/ACA snoRNP gene family in the UALCAN database. (A) The expression of NHP2 had difference in gender, while the expression of GAR1, NOP10, DKC1 had no differences. (B) The expression of NHP2 had difference in age, while the expression of GAR1, NOP10, DKC1 had no differences. (C) The expression of NHP2, NOP10, DKC1 had differences in weight, while the expression of GAR1 had no difference. (D) The expression of GAR1, NHP2, NOP10, DKC1 had differences in cancer stage.

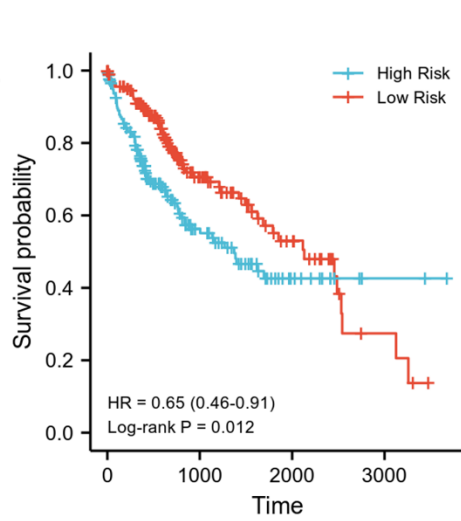 * represents P < 0.05, ** represents P < 0.01, *** represents P < 0.001.
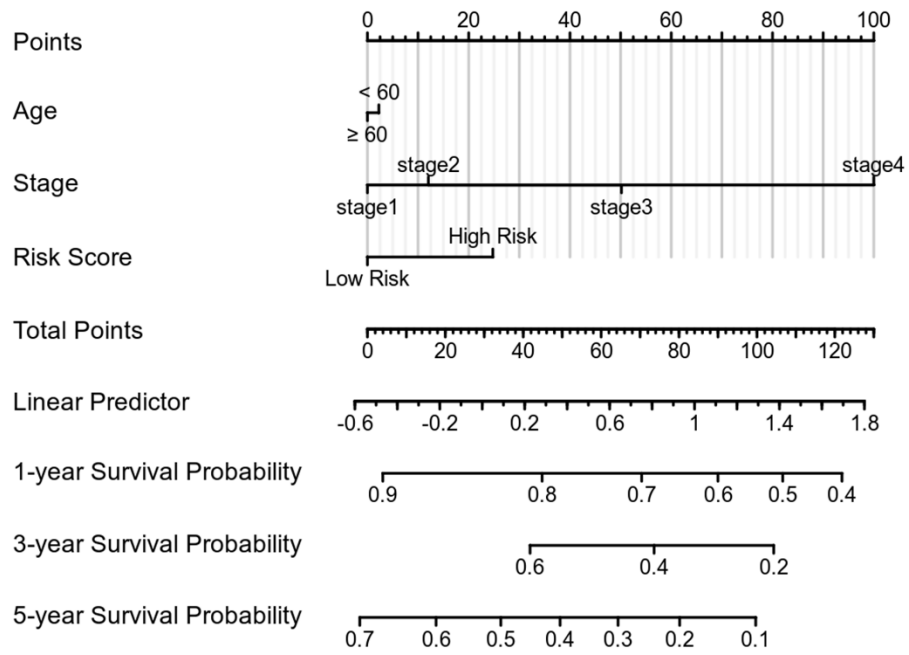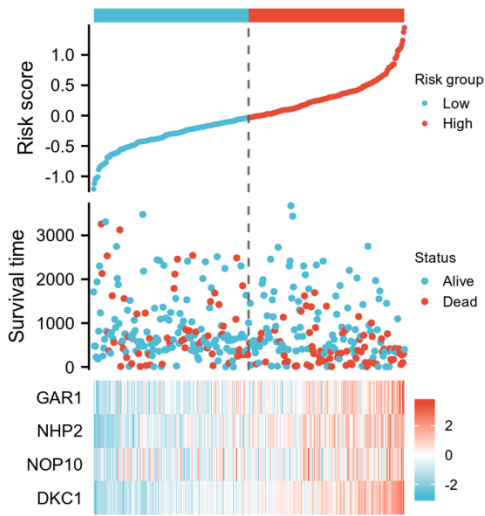
Figure S5. The prognostic value of the H/ACA snoRNP gene family in HCC. (A) The nomogram of clinical characteristics and risk score of the H/ACA snoRNP gene family. (B) The risk score map of the H/ACA snoRNP gene family. (C) The survival probability of the H/ACA snoRNP gene family grouped by risk score.
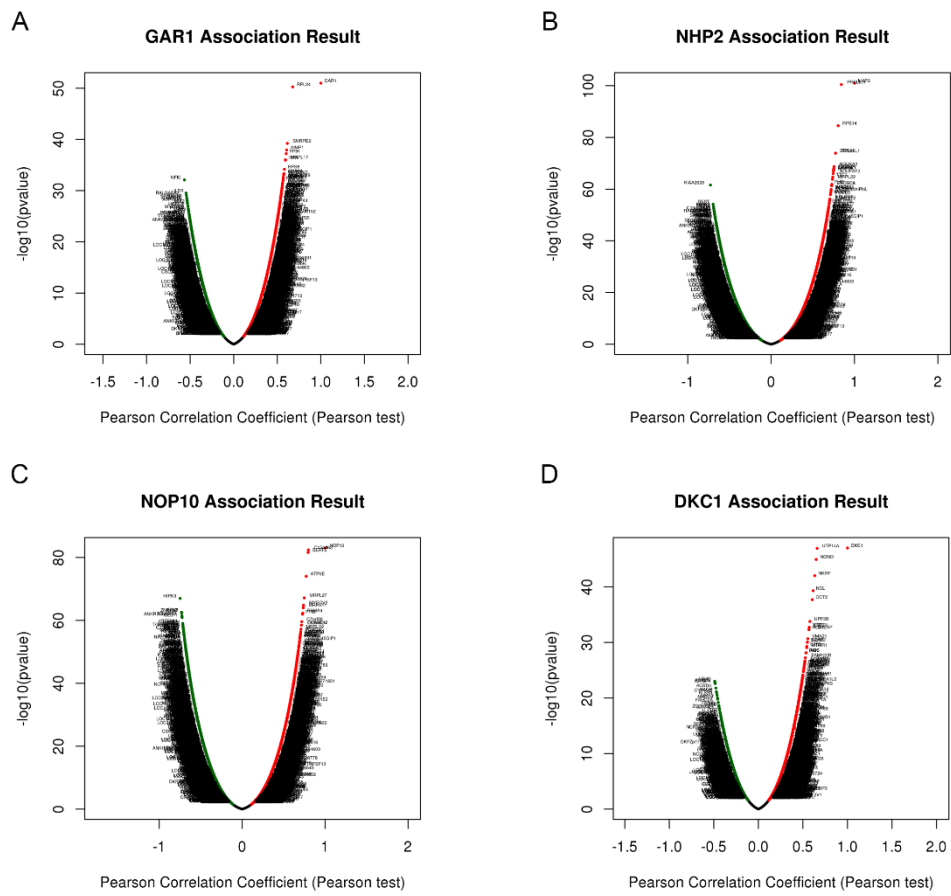
Figure S6. Volcano plot showing genes correlated with H/ACA snoRNPs gene family through Pearson's test analysis; red (positive), green (negative). (A) Genes correlated with GAR1. (B) Genes correlated with NHP2. (C) Genes correlated with NOP10. (D) Genes correlated with DKC1.
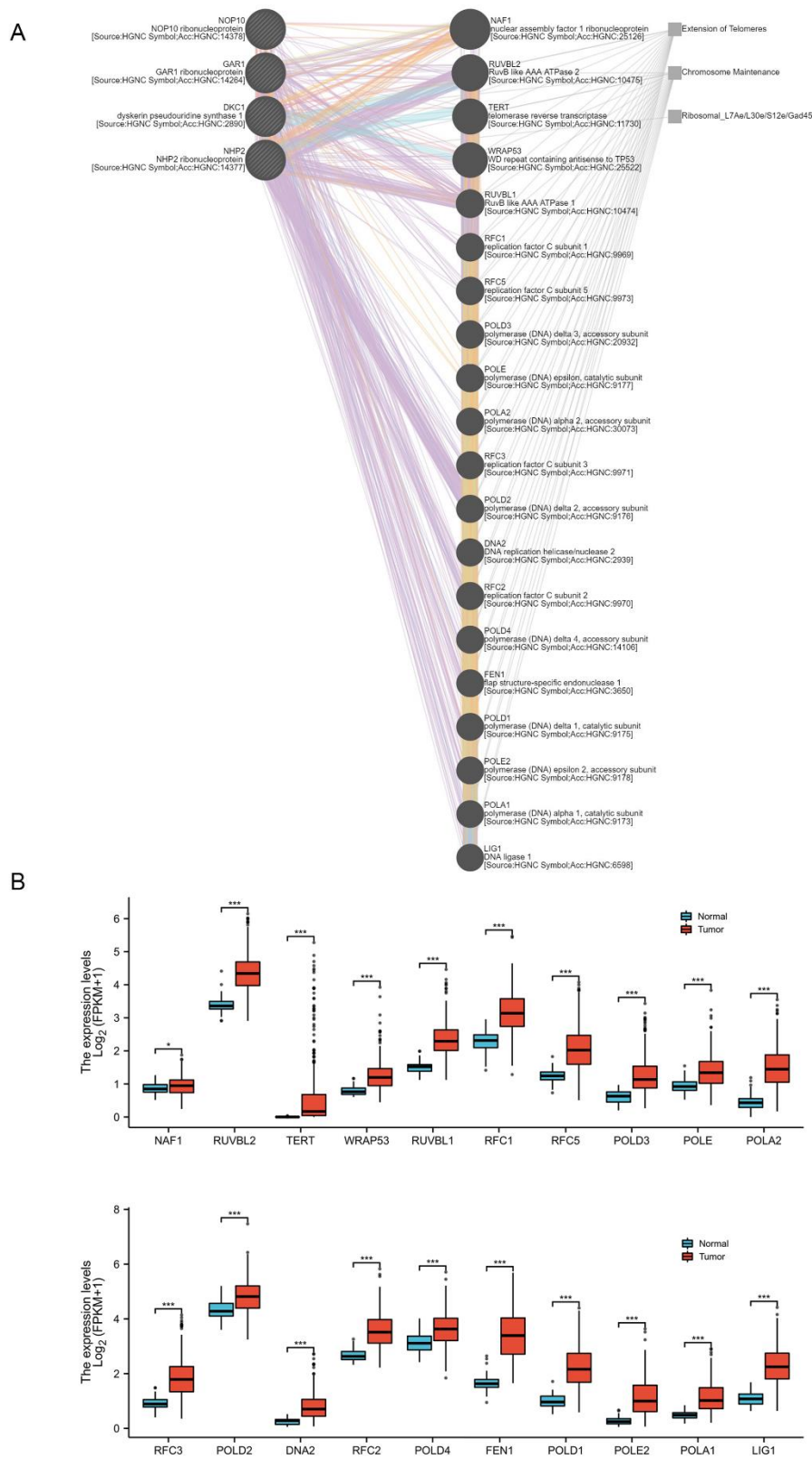
Figure S7. Genes interacted with the H/ACA snoRNP gene family and their expression differences between tumor tissues and normal liver tissues. (A) The Genes interacted with H/ACA snoRNP gene family in GeneMANIA. (B) The mRNA expression differences of the 20 co-expressed genes

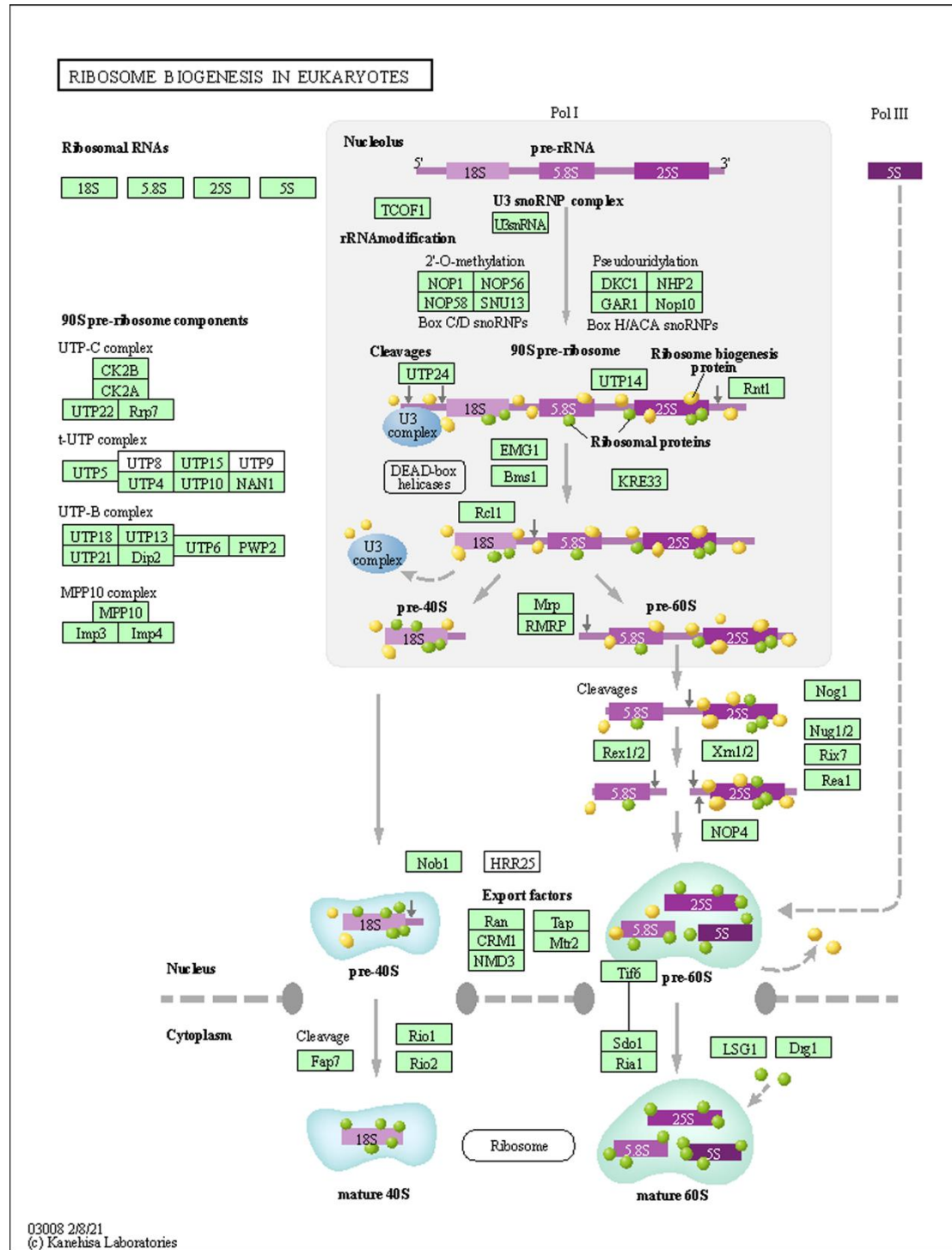between HCC tumor tissues and normal liver tissues. * represents P < 0.05, *** represents P < 0.001.

Figure S8. Ribosome biogenesis pathway from KEGG PATHWAY Database.