# List of R and Perl scripts.

1. Extraction of UCHL5 mRNA expression data in pan-cancer
2. The UCHL5 mRNA data from 33 types of tumors in TCGA (Kruskal-Wallis test)
3. Differential expression analysis of UCHL5 mRNA between pan-cancer tumor tissues and normal tissues
4. Merging UCHL5 mRNA expression data and survival data in pan-cancer
5. Cox regression analysis of UCHL5 in pan-cancer and prognostic forest plots
6. Perform ESTIMATE analysis to obtain immune score, stromal score, and ESTIMATE Score of samples in pan-cancer.
7. Correlation analysis of UCHL5 expression with immune score, stromal score and ESTIMATE Score in pan-cancer.
8. CIBERSORT analysis of pan-cancer samples.
9. Correlation analysis of UCHL5 expression and CIBERSORT score in pan-cancer.
10. Correlation analysis of UCHL5 mRNA expression with tumor mutation burden (TMB) in different tumors.
11. Correlation analysis of UCHL5 mRNA expression with microsatellite instability (MSI) in different tumors.
12. Correlation analysis of UCHL5 mRNA expression with immunotherapy response in the validation cohorts.
13. TCGA gene symbol ID transformation script.
14. TMB data extraction script for samples.