Introduction

Transfer RNAs (tRNAs) play essential roles in the protein translational process, and changes in expression of tRNAs play multiple roles in tumorigenesis. The database tRNA in Cancer (tRiC) show the global expression landscape of tRNAs among 31 cancer types and more than 10000 samples from The Cancer Genome Atlas. Here we systematically analyzed tRNA expression profiles at gene codon and amino acid levels and the functional consequence (e.g. patient tumor stage, subtype, and survival). We also try to link the differentially expression of tRNA the translational control in tumor.

What we can do

1. Search tRNA expression profile in different cancer types;
2. Analyze the expression alteration of tRNAs between tumor and normal samples;
3. Analyze the tRNA related clinically relevant events;
4. Comparative analyze the expression and expression alteration at tRNA, codon and amino acid levels;
5. Analyzed codon usage among whole genome;
6. Download all expression data to independently validate a pattern of interest.