Checking Databases

By checking the following databases before analyzing the datasets, we could have a basic understanding of the data in terms of estimated quantitative profiles, conservation, biological functions, annotation, and disease association of epi-transcriptome.

m6A_Atlas

m6A-Atlas is a comprehensive knowledgebase for unraveling the m6A epitranscriptome [3].

RMDisease

RMDisease is a database of genetic variants that affect RNA modifications, with implications for epitranscriptome pathogenesis [4].

WHISTLE

WHISTLE is a high-accuracy map of the human m6A epitranscriptome predicted using a machine learning approach [5].