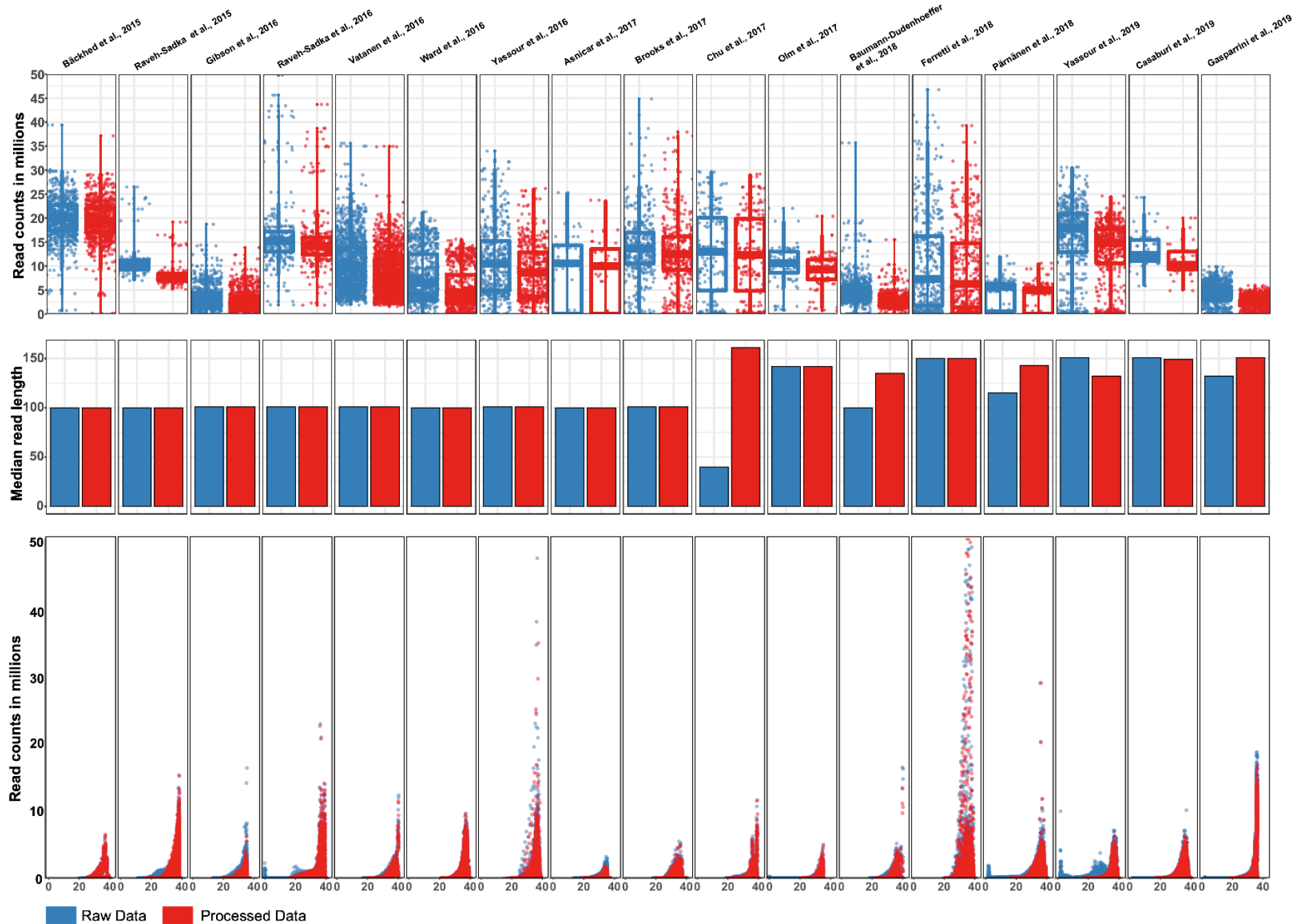




Supplementary Figure 1. The attributions (counts, lengths, and qualities) of raw and processed sequencing reads. The first-row depicting the distribution of the read counts of raw data (Raw) and the clean data (Clean) within a study. Raw: raw data; Clean: clean data following quality control (after Trimmomatic and BMTagger); the second-row depicting descriptive information about the median read length range of each sample reads for each study included in our analysis. *: All reads in Brooks et al., 2017 are single-ended reads; the third-row depicting the distribution of the read quality of raw data and the clean data within a study. Blue dots refer to raw data, and red dots refer to clean data after quality control (after Trimmomatic and BMTagger). X axis refers to the read quality and Y axis refers to the number of read count. Color in blue refers to raw data, and red refers to processed data