K-mer counting in TCGA-PRAD

Kmer counts were produced for each TCGA-PRAD Fastq file using Jellyfish V.2.2.6 using the command:

jellyfish count -L 2 -m 31 -s 10000 -t 10 -o $output -F 2 -C <(gunzip -c $r1) <(gunzip -c $r2)

$r1, $r2: Fastq files for reads R1 and R2 in fastq.gz format.

Counts for independent k-mers were then obtained with:

jellyfish query $file $list_kmer

file: Jellyfish count file (.jf)
list_kmer: file with list of k-mers to be queried

Counts were normalized by total read counts in each library.