

-N (read mismatches) 2 --read-gap-length 2 --read-edit-dist 2 (tophat parameters I used)

Total number of raw reads -12780994 after preprocessing

samtools flagstat (2-2-2) accepted_hits.bam

4295956 in total

0 QC failure

0 duplicates

4295956 mapped (100.00%)

4295956 paired in sequencing

2169131 read1

2126825 read2

3390786 properly paired (78.93%)

4142080 with itself and mate mapped

153876 singletons (3.58%)

0 with mate mapped to a different chr

0 with mate mapped to a different chr (mapQ>=5)

samtools flagstat 3-2-3/accepted_hits.bam

3425658 in total

0 QC failure

0 duplicates

3425658 mapped (100.00%)

3425658 paired in sequencing

1732807 read1

1692851 read2

2442650 properly paired (71.30%)

2973016 with itself and mate mapped

452642 singletons (13.21%)

7658 with mate mapped to a different chr

7658 with mate mapped to a different chr (mapQ>=5)

samtools flagstat 4-2-4/accepted_hits.bam

3633559 in total

0 QC failure

0 duplicates

3633559 mapped (100.00%)

3633559 paired in sequencing

1830021 read1

1803538 read2

2672708 properly paired (73.56%)

3262468 with itself and mate mapped

371091 singletons (10.21%)

8958 with mate mapped to a different chr

8956 with mate mapped to a different chr (mapQ>=5)

samtools flagstat 5-2-5/accepted_hits.bam

3757346 in total

0 QC failure

0 duplicates

3757346 mapped (100.00%)

3757346 paired in sequencing

1887598 read1

1869748 read2

2812130 properly paired (74.84%)

3436594 with itself and mate mapped

320752 singletons (8.54%)

9974 with mate mapped to a different chr

9968 with mate mapped to a different chr (mapQ>=5)

.....