

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 23:21:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163026.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1163026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 23:21:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	85,335,396
Mapped reads	83,687,695 / 98.07%
Unmapped reads	1,647,701 / 1.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	459,712 / 0.54%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	46,631,887 / 54.65%
Duplication rate	45.04%
Clipped reads	11,184,529 / 13.11%

2.2. ACGT Content

Number/percentage of A's	1,943,365,629 / 23.79%
Number/percentage of C's	2,141,802,933 / 26.22%
Number/percentage of T's	1,942,505,421 / 23.78%
Number/percentage of G's	2,138,195,920 / 26.18%
Number/percentage of N's	1,851,899 / 0.02%
GC Percentage	52.4%

2.3. Coverage

Mean	2.6388

Standard Deviation	34.4485
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2.4. Mapping Quality

Mean Mapping Quality	48.94
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2.5. Mismatches and indels

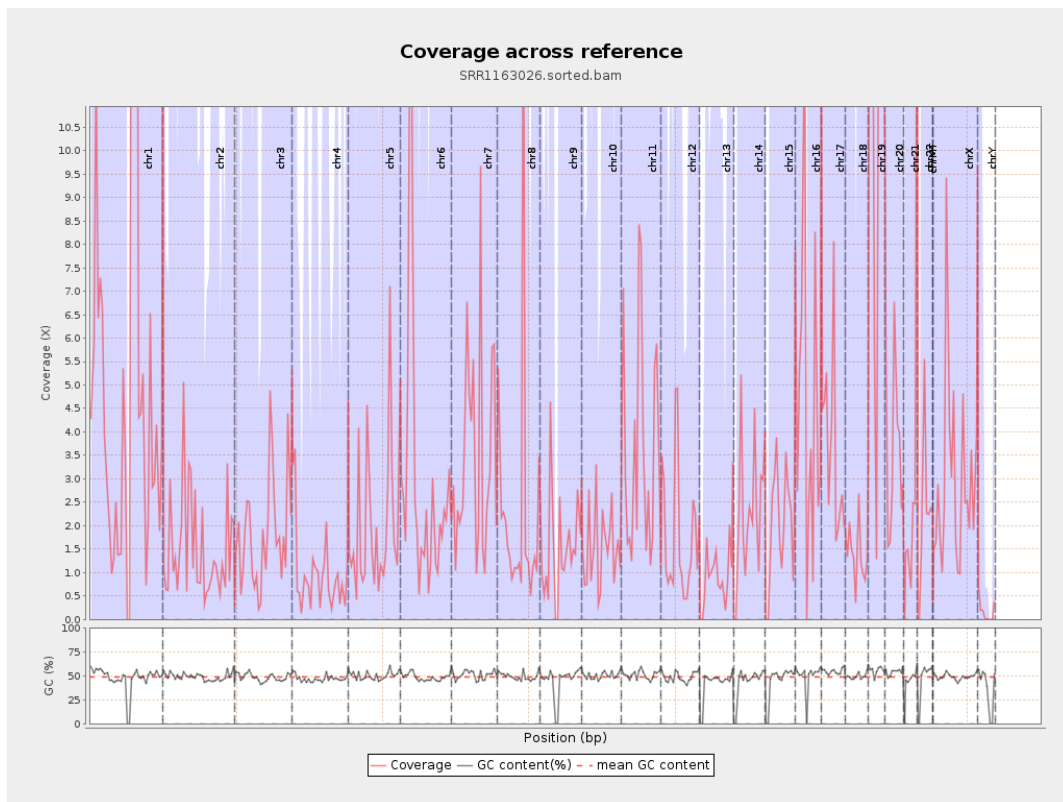
General error rate	0.45%
Mismatches	35,655,977
Insertions	541,566
Mapped reads with at least one insertion	0.64%
Deletions	465,938
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.97%

2.6. Chromosome stats

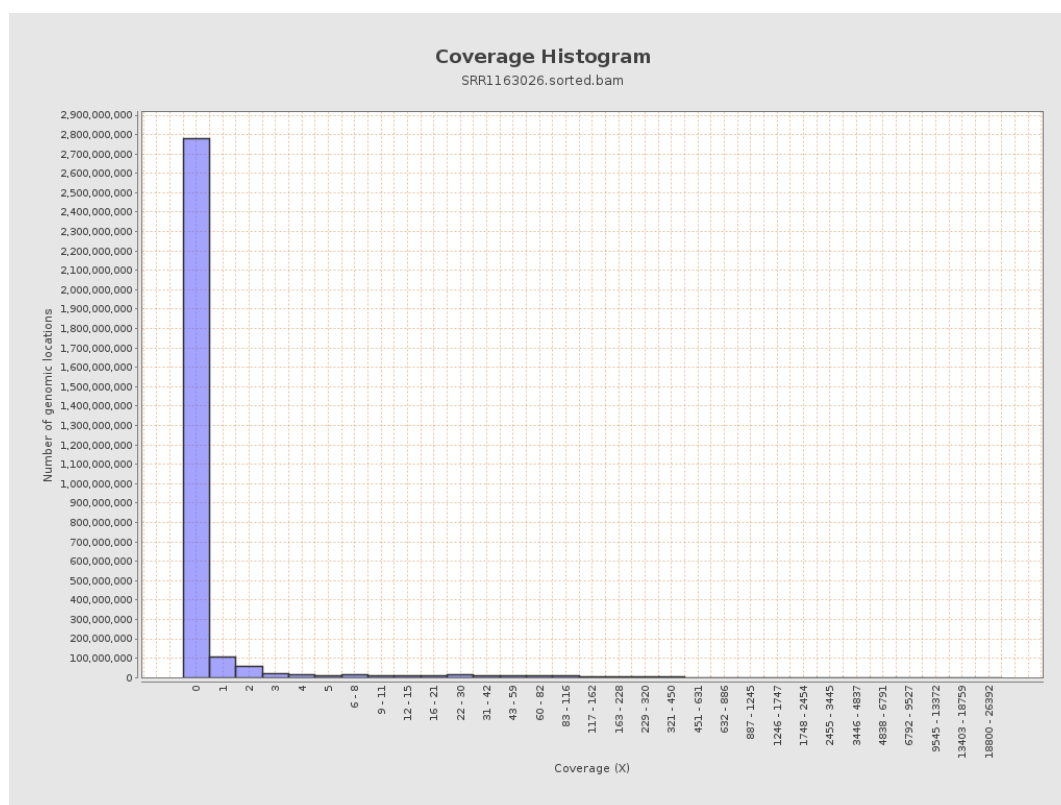
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1316278624	5.2809	47.7627
chr2	243199373	365010659	1.5009	17.3432
chr3	198022430	359534260	1.8156	18.4759
chr4	191154276	182700855	0.9558	17.4451
chr5	180915260	374181161	2.0683	34.5966
chr6	171115067	496663990	2.9025	31.2451
chr7	159138663	554976535	3.4874	41.3814

chr8	146364022	338466680	2.3125	44.1273
chr9	141213431	211270257	1.4961	17.3541
chr10	135534747	207583223	1.5316	21.6119
chr11	135006516	488947740	3.6217	30.4674
chr12	133851895	242786515	1.8138	18.2139
chr13	115169878	107528607	0.9337	13.3576
chr14	107349540	237193783	2.2095	21.4751
chr15	102531392	199974417	1.9504	17.855
chr16	90354753	415390022	4.5973	37.0432
chr17	81195210	298342459	3.6744	29.6778
chr18	78077248	108379612	1.3881	15.342
chr19	59128983	705245209	11.9272	85.9707
chr20	63025520	221174210	3.5093	30.9337
chr21	48129895	149220673	3.1004	117.7373
chr22	51304566	112032984	2.1837	20.7367
chrMT	16571	5429	0.3276	0.6718
chrX	155270560	466382114	3.0037	33.3281
chrY	59373566	9492976	0.1599	7.9695

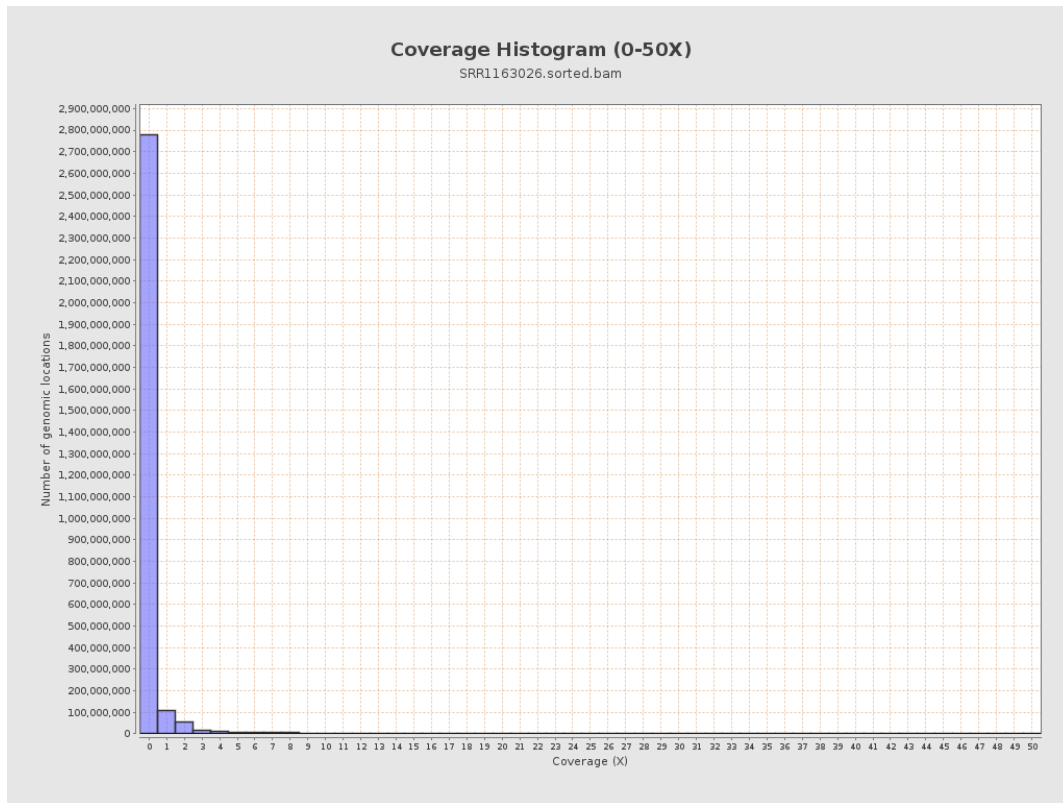
3. Results : Coverage across reference



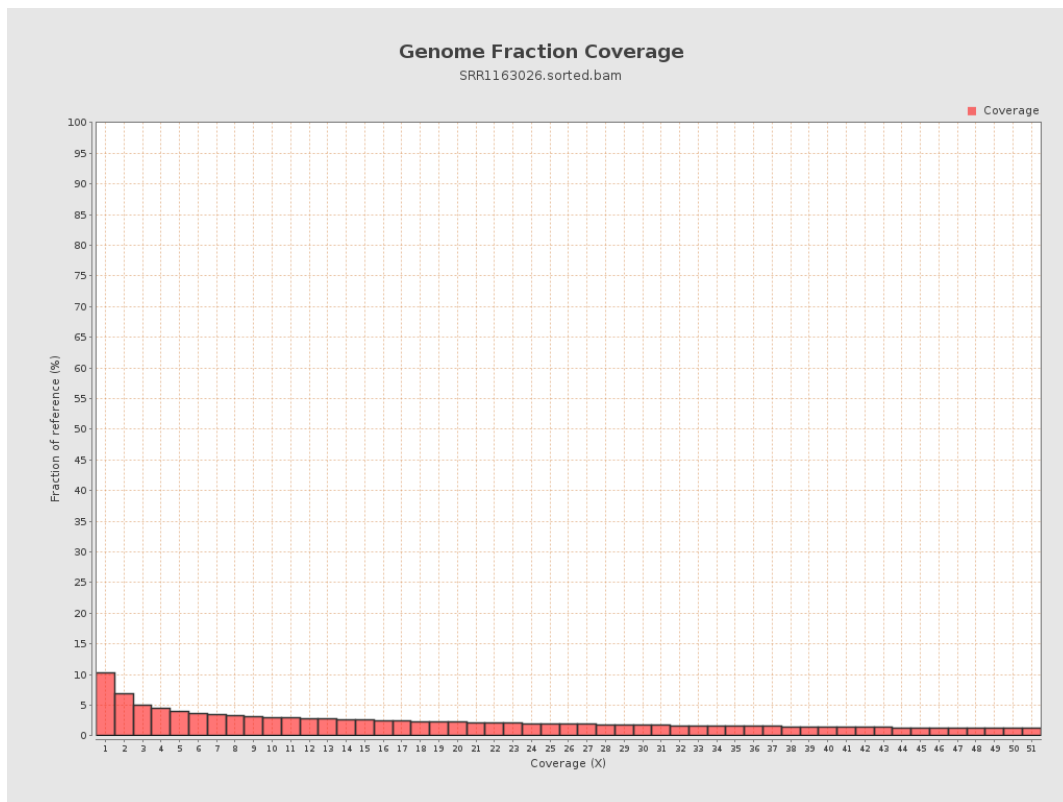
4. Results : Coverage Histogram



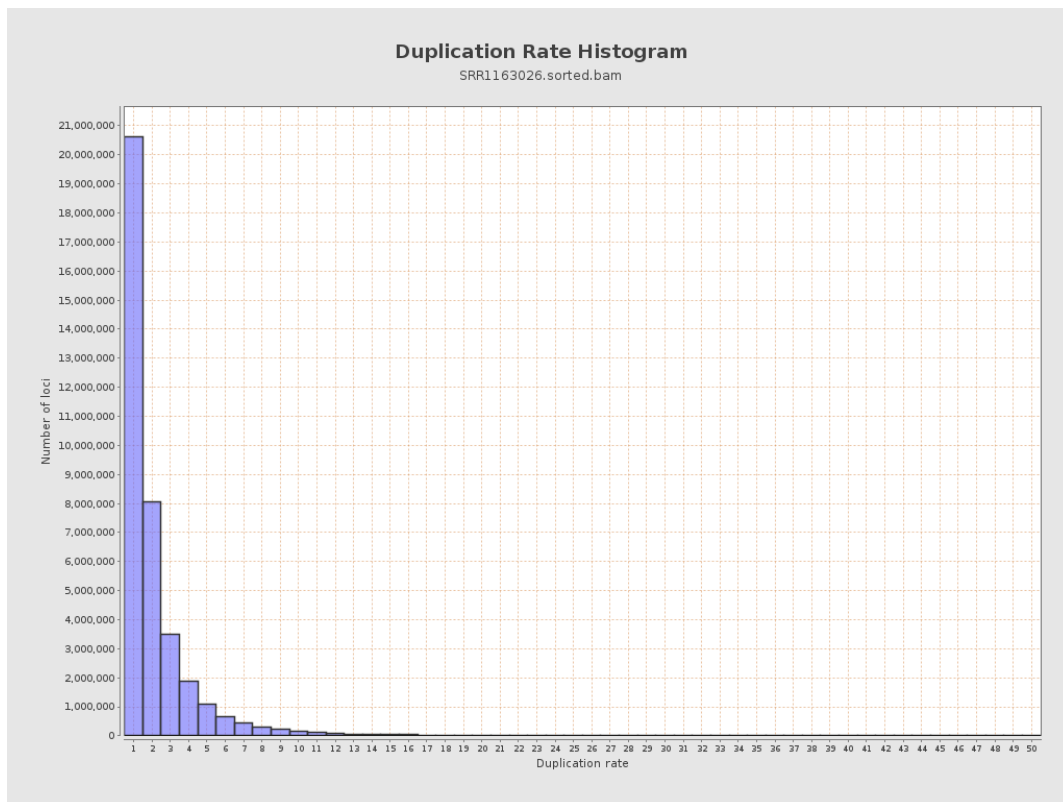
5. Results : Coverage Histogram (0-50X)



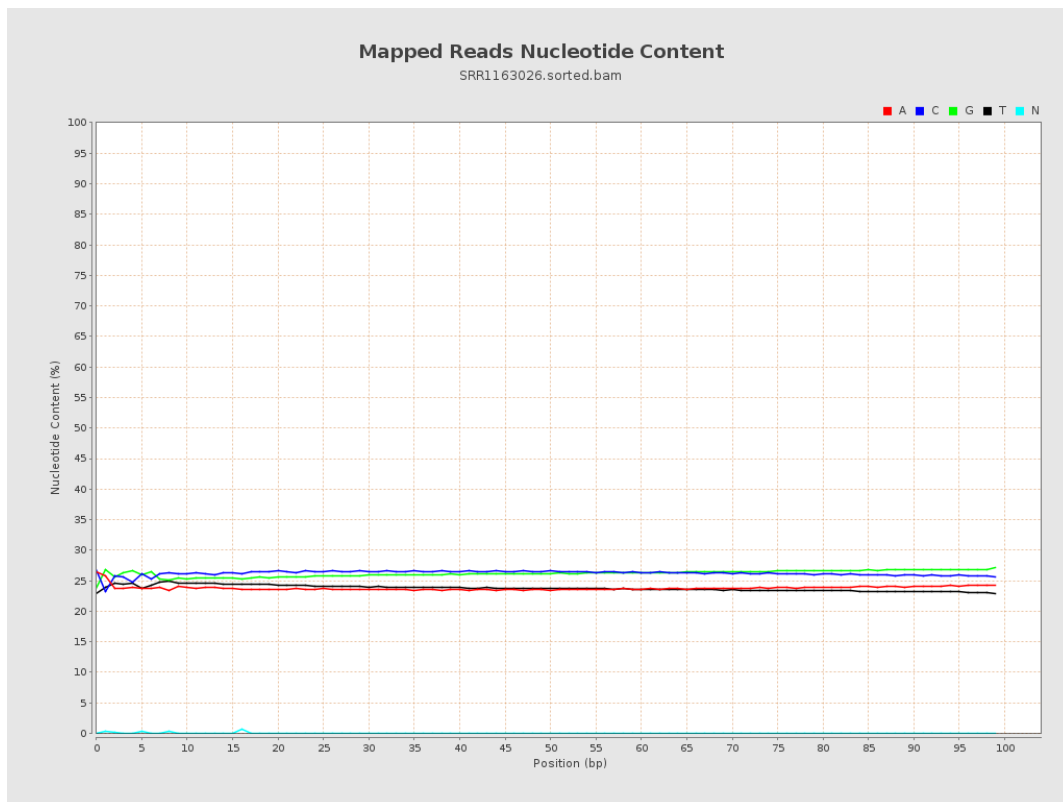
6. Results : Genome Fraction Coverage



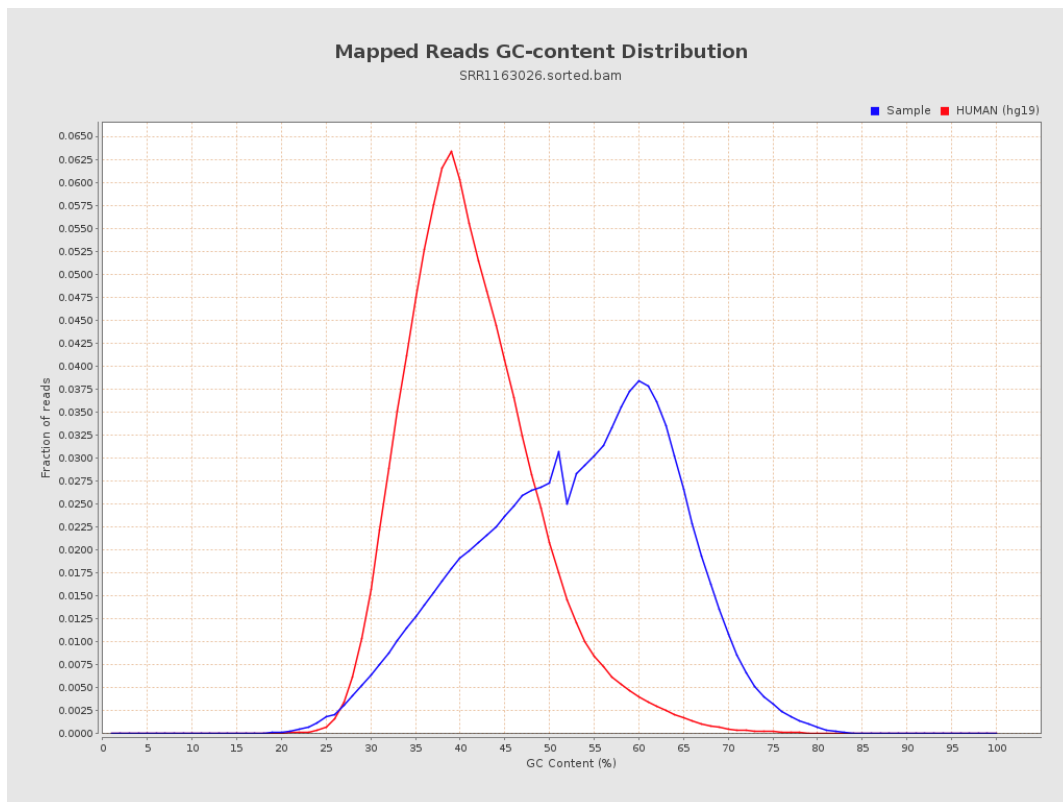
7. Results : Duplication Rate Histogram



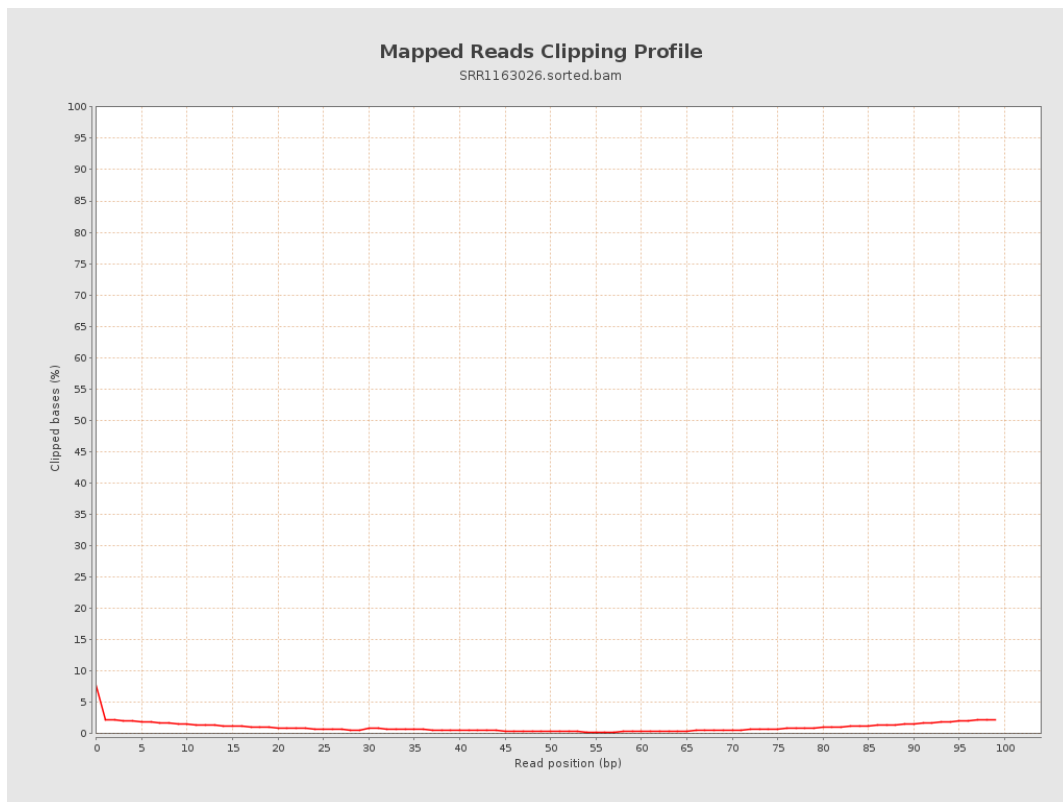
8. Results : Mapped Reads Nucleotide Content



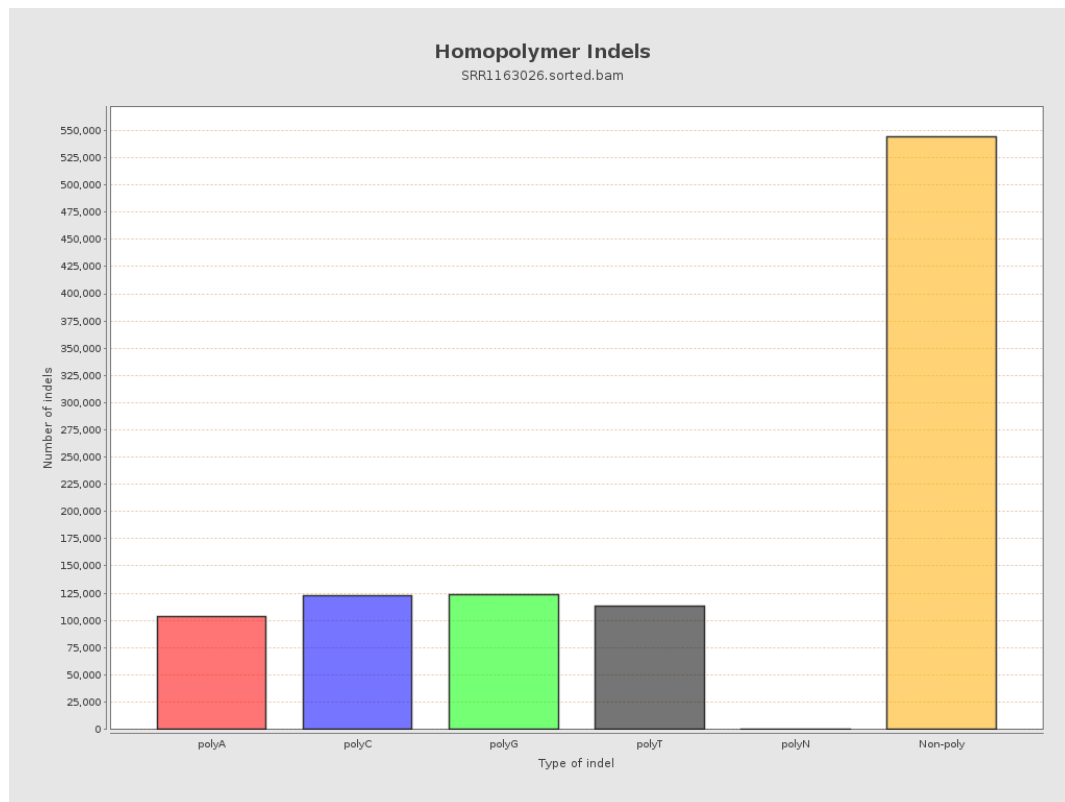
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

