

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 04:20:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231806.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_SRR6231806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 04:20:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,482,564
Mapped reads	9,993,385 / 87.03%
Unmapped reads	1,489,179 / 12.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	79,437 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	865,674 / 7.54%
Duplication rate	5.13%
Clipped reads	5,172,528 / 45.05%

2.2. ACGT Content

Number/percentage of A's	188,841,053 / 28.97%
Number/percentage of C's	128,214,301 / 19.67%
Number/percentage of T's	188,735,344 / 28.95%
Number/percentage of G's	146,063,405 / 22.41%
Number/percentage of N's	49,210 / 0.01%
GC Percentage	42.07%

2.3. Coverage

Mean	0.2107

Standard Deviation	17.5659
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2.4. Mapping Quality

Mean Mapping Quality	44.57
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2.5. Mismatches and indels

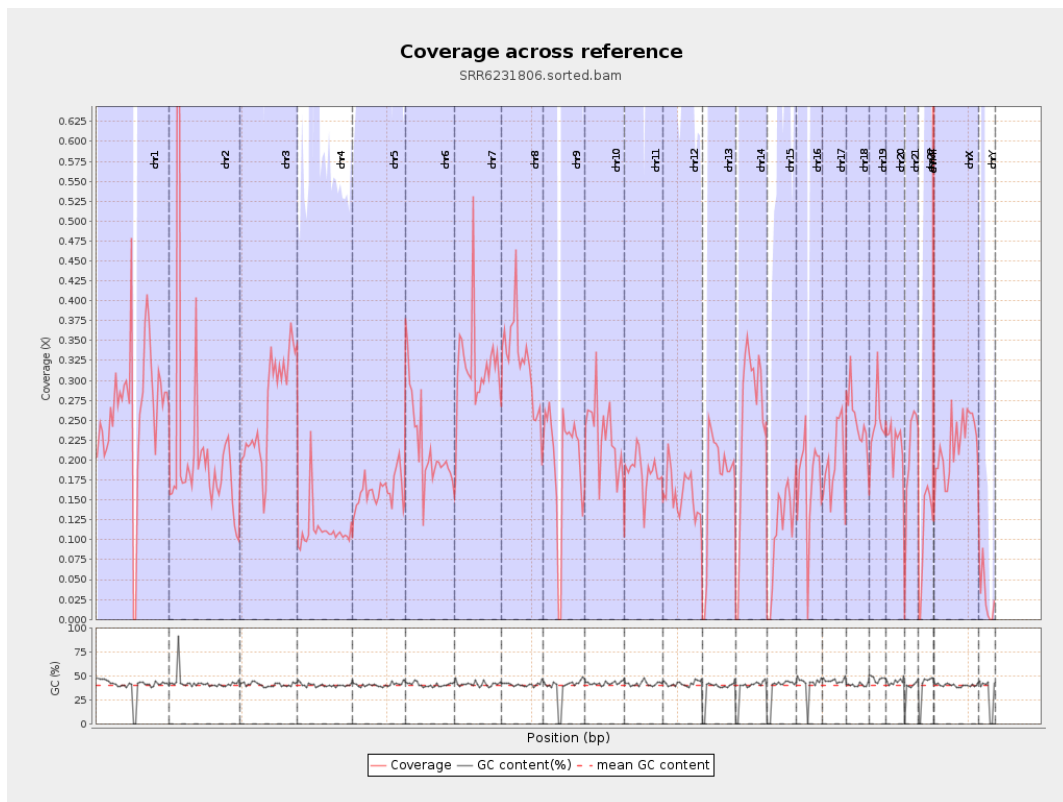
General error rate	0.63%
Mismatches	4,031,278
Insertions	47,994
Mapped reads with at least one insertion	0.48%
Deletions	144,139
Mapped reads with at least one deletion	1.43%
Homopolymer indels	45.41%

2.6. Chromosome stats

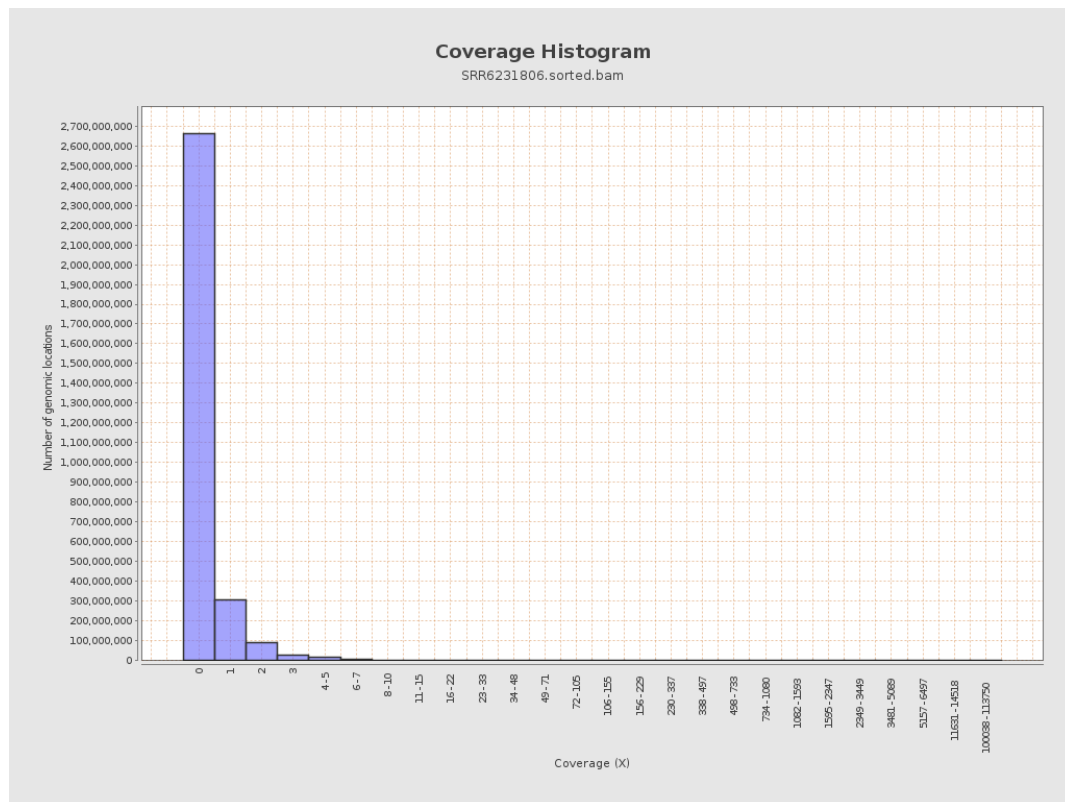
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	65825258	0.2641	4.655
chr2	243199373	54008622	0.2221	62.285
chr3	198022430	52366553	0.2644	0.7149
chr4	191154276	21331587	0.1116	0.7143
chr5	180915260	29119611	0.161	0.5967
chr6	171115067	37458740	0.2189	0.9142
chr7	159138663	50796524	0.3192	3.4688

chr8	146364022	46647910	0.3187	2.5326
chr9	141213431	28301246	0.2004	1.6024
chr10	135534747	31375379	0.2315	1.5424
chr11	135006516	24773032	0.1835	1.6689
chr12	133851895	21001974	0.1569	0.6444
chr13	115169878	19907618	0.1729	0.5706
chr14	107349540	27048984	0.252	1.0323
chr15	102531392	11495879	0.1121	0.4668
chr16	90354753	15785043	0.1747	0.9172
chr17	81195210	15762354	0.1941	0.8871
chr18	78077248	19619292	0.2513	3.5421
chr19	59128983	14629835	0.2474	2.5951
chr20	63025520	13857952	0.2199	0.7476
chr21	48129895	9845003	0.2046	0.7772
chr22	51304566	5545283	0.1081	0.4308
chrMT	16571	224865	13.5698	9.8227
chrX	155270560	33798251	0.2177	0.9926
chrY	59373566	1616685	0.0272	0.5751

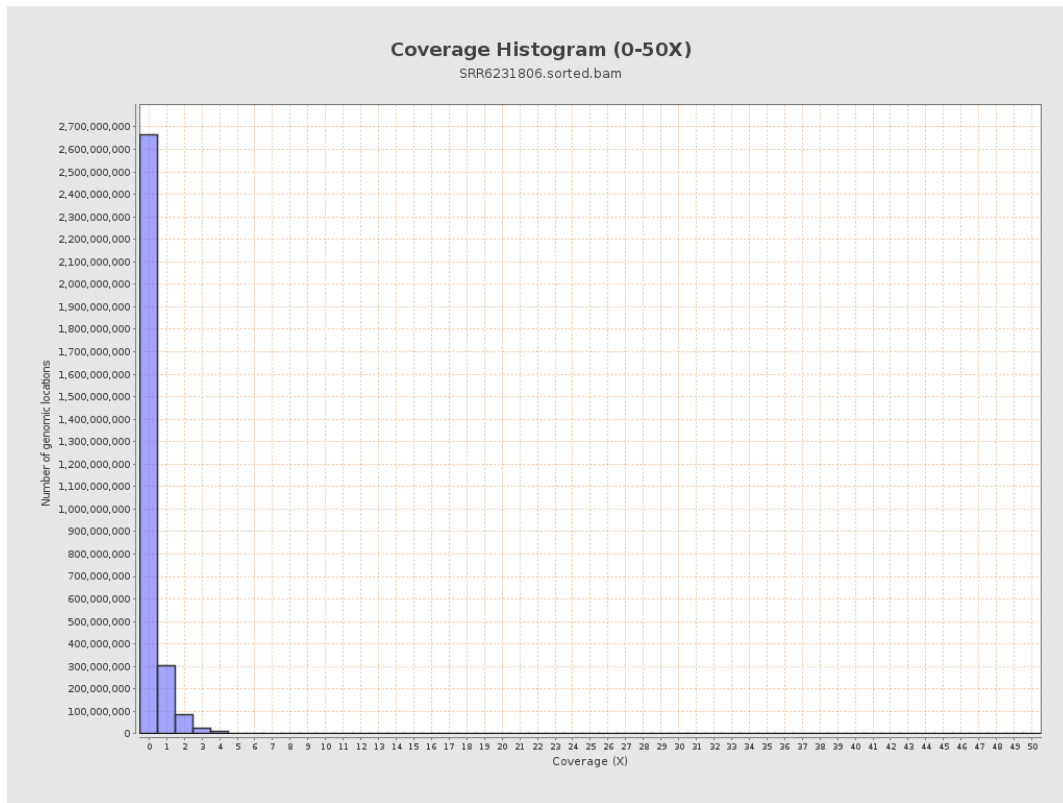
3. Results : Coverage across reference



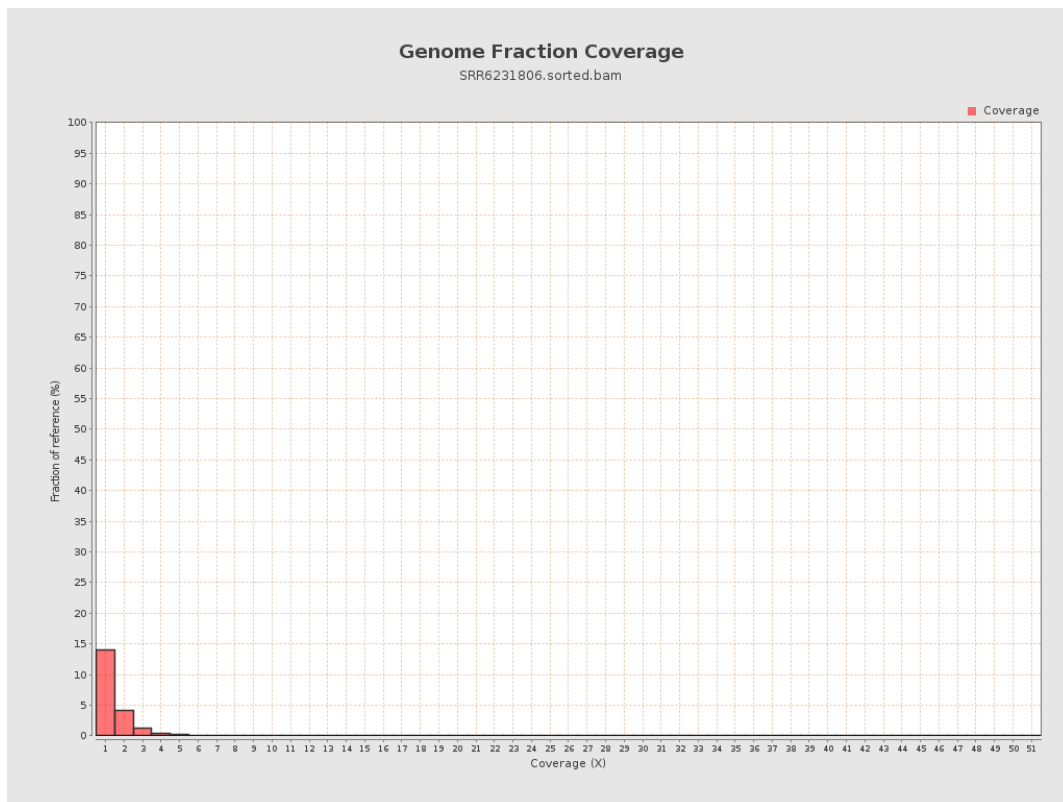
4. Results : Coverage Histogram



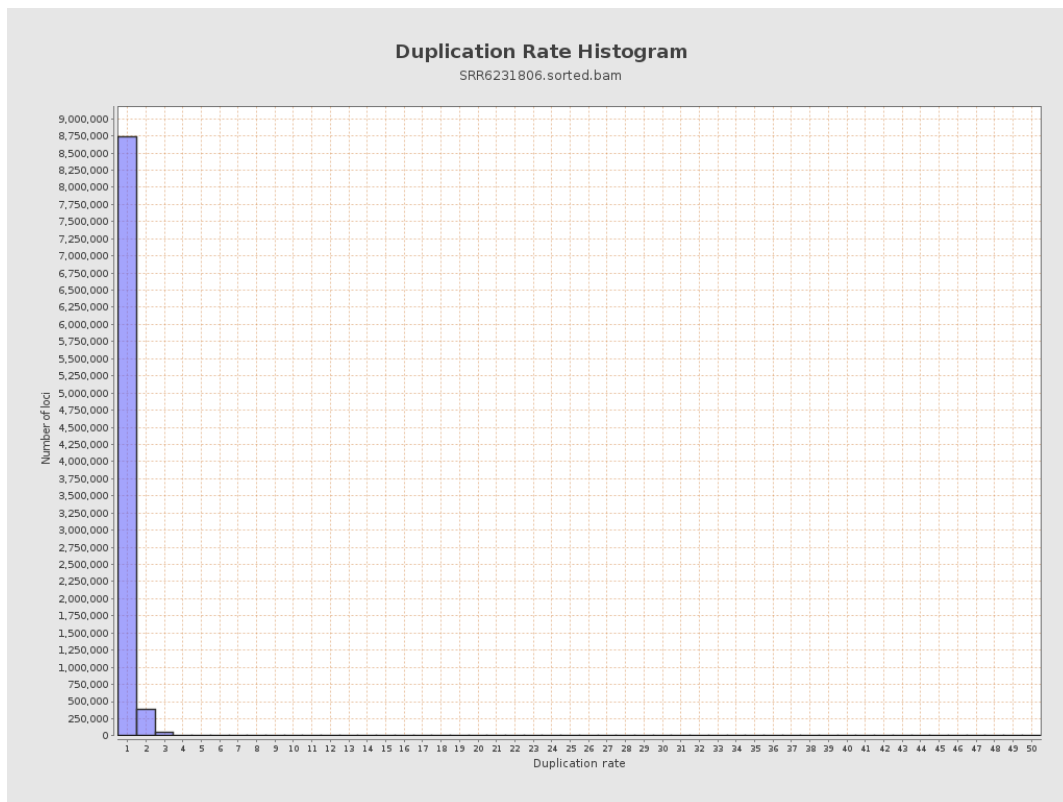
5. Results : Coverage Histogram (0-50X)



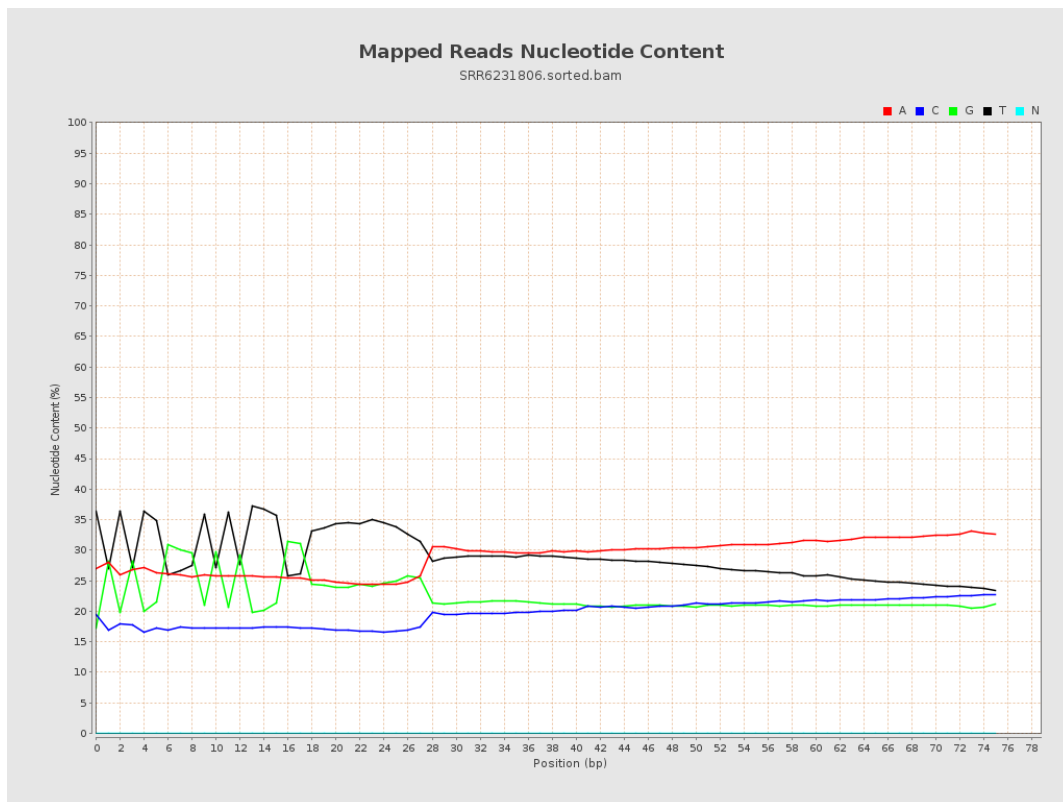
6. Results : Genome Fraction Coverage



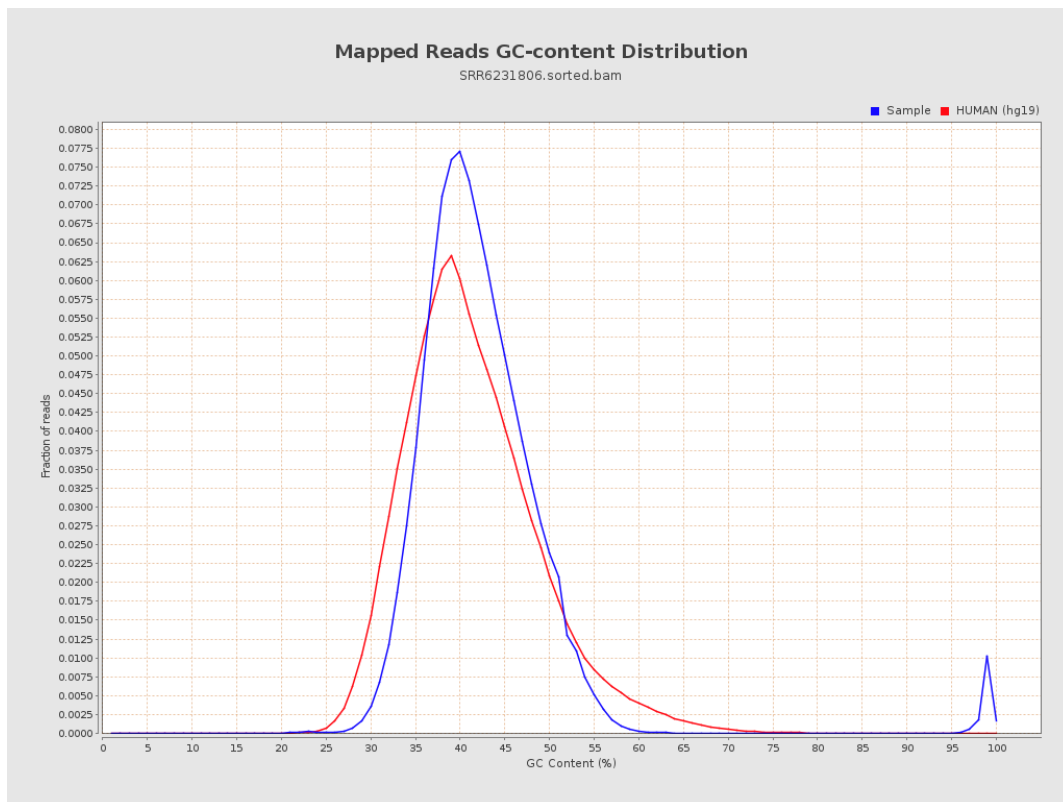
7. Results : Duplication Rate Histogram



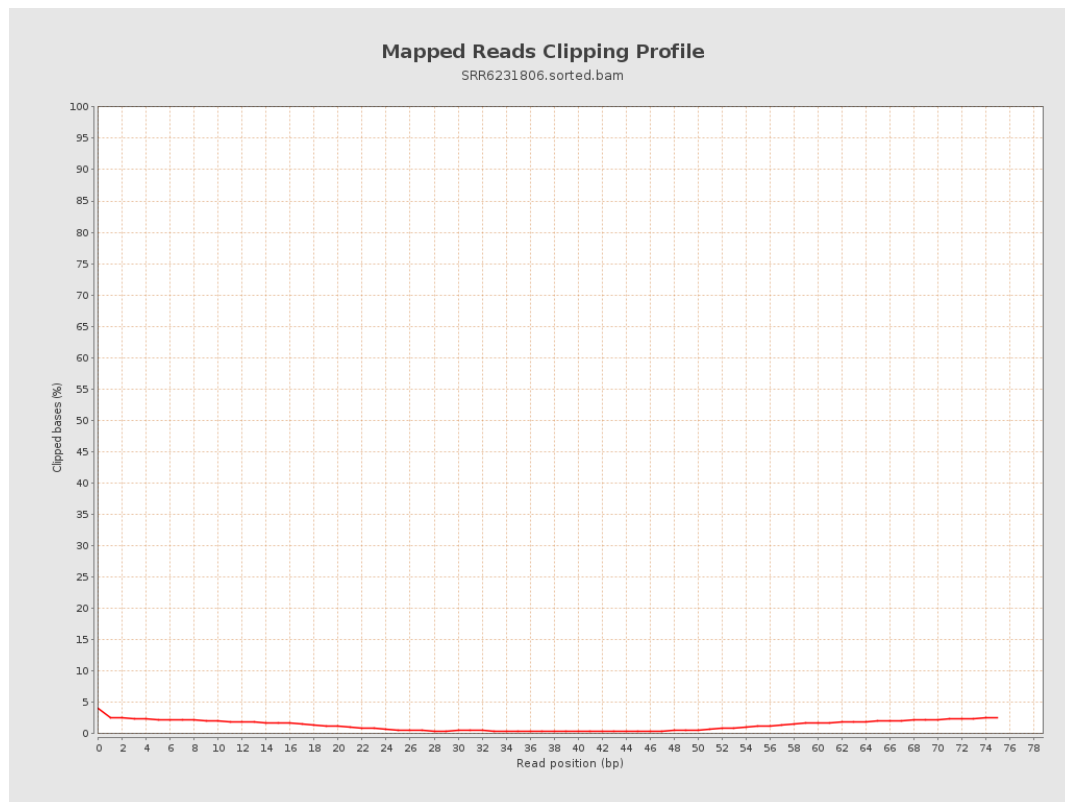
8. Results : Mapped Reads Nucleotide Content



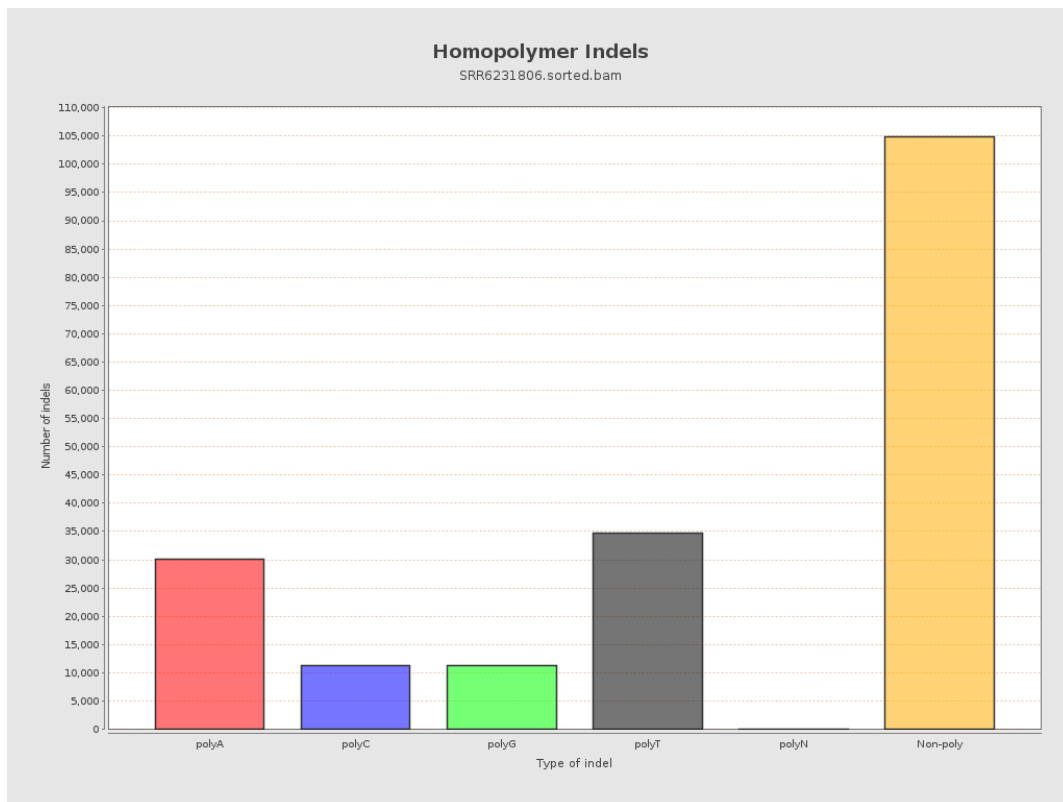
9. Results : Mapped Reads GC-content Distribution



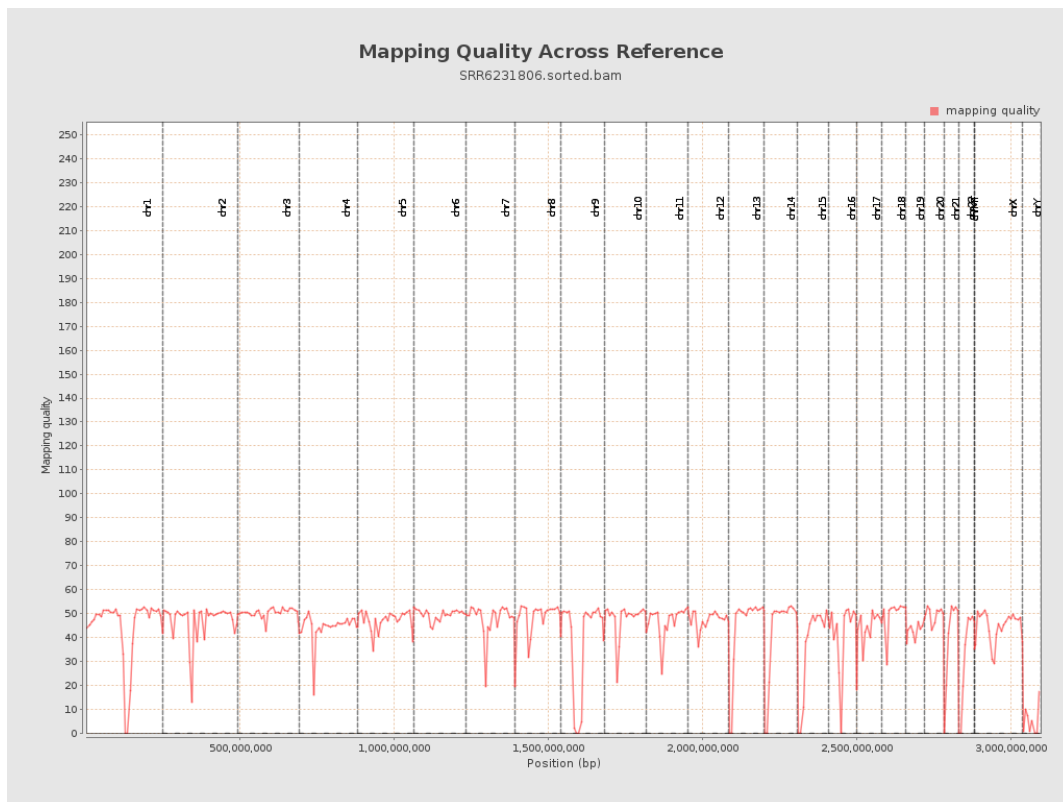
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

