Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:31:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063579.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_SRR6063579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063579.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:31:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,118,158
Mapped reads	1,881,967 / 88.85%
Unmapped reads	236,191 / 11.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,012 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	71,610 / 3.38%
Duplication rate	2.48%
Clipped reads	756,998 / 35.74%

2.2. ACGT Content

Number/percentage of A's	36,037,618 / 28.43%
Number/percentage of C's	23,539,592 / 18.57%
Number/percentage of T's	39,188,021 / 30.91%
Number/percentage of G's	28,011,440 / 22.09%
Number/percentage of N's	3,539 / 0%
GC Percentage	40.66%

2.3. Coverage

Mean	0.041

Standard Deviation	0.5327

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

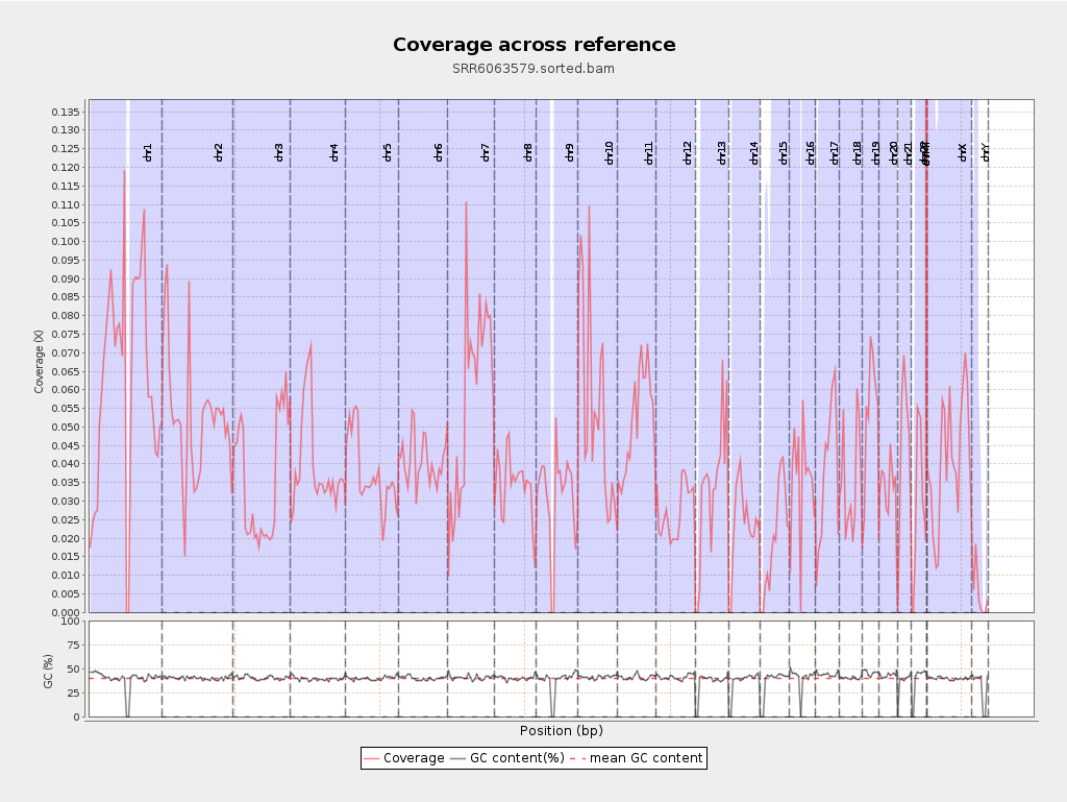
General error rate	0.87%
Mismatches	1,088,757
Insertions	9,589
Mapped reads with at least one insertion	0.51%
Deletions	33,483
Mapped reads with at least one deletion	1.76%
Homopolymer indels	46.75%

2.6. Chromosome stats

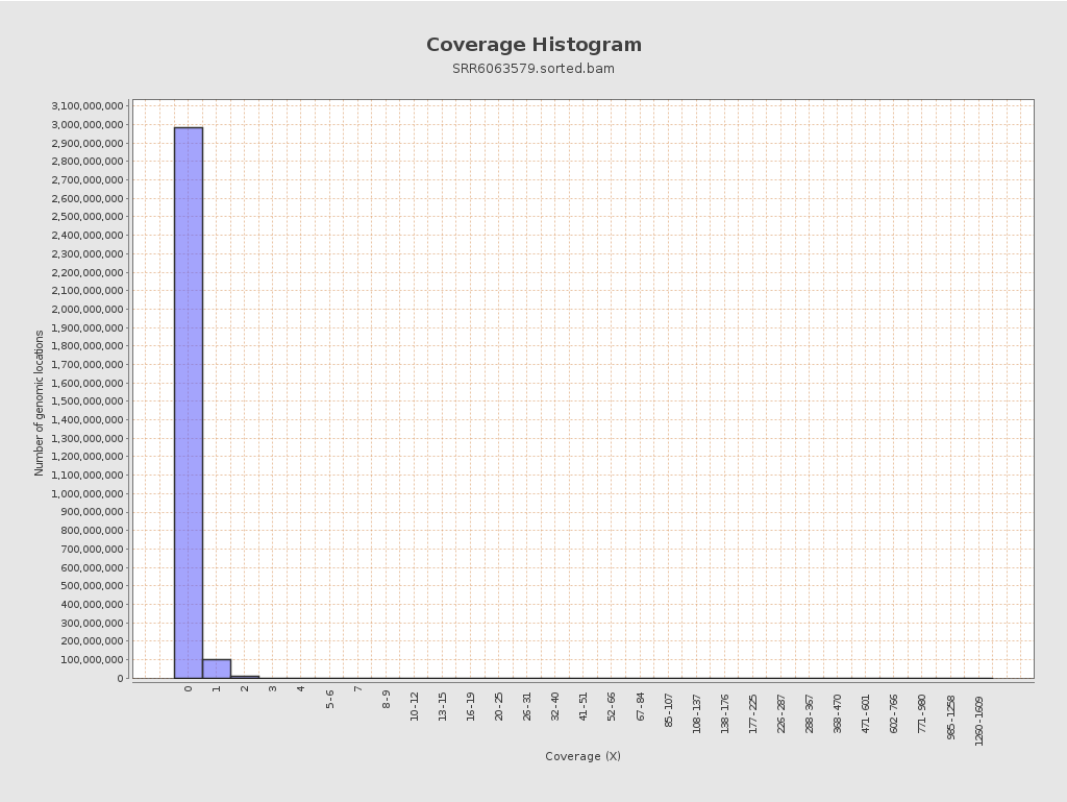
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15687006	0.0629	1.2652
chr2	243199373	12716028	0.0523	0.3965
chr3	198022430	7065436	0.0357	0.2322
chr4	191154276	7595569	0.0397	0.234
chr5	180915260	6740419	0.0373	0.2143
chr6	171115067	7054571	0.0412	0.2574
chr7	159138663	9280138	0.0583	0.8489

chr8	146364022	5029381	0.0344	0.6369
chr9	141213431	4422143	0.0313	0.4081
chr10	135534747	7526550	0.0555	0.5967
chr11	135006516	6898003	0.0511	0.3529
chr12	133851895	3666886	0.0274	0.1993
chr13	115169878	3810124	0.0331	0.1968
chr14	107349540	2547110	0.0237	0.2263
chr15	102531392	2052761	0.02	0.1532
chr16	90354753	3219443	0.0356	0.2704
chr17	81195210	3114541	0.0384	0.2417
chr18	78077248	2765756	0.0354	0.7896
chr19	59128983	3168218	0.0536	0.8059
chr20	63025520	2132374	0.0338	0.2267
chr21	48129895	2096574	0.0436	0.2646
chr22	51304566	1425658	0.0278	0.1808
chrMT	16571	51680	3.1187	2.6169
chrX	155270560	6469618	0.0417	0.2647
chrY	59373566	302835	0.0051	0.1764

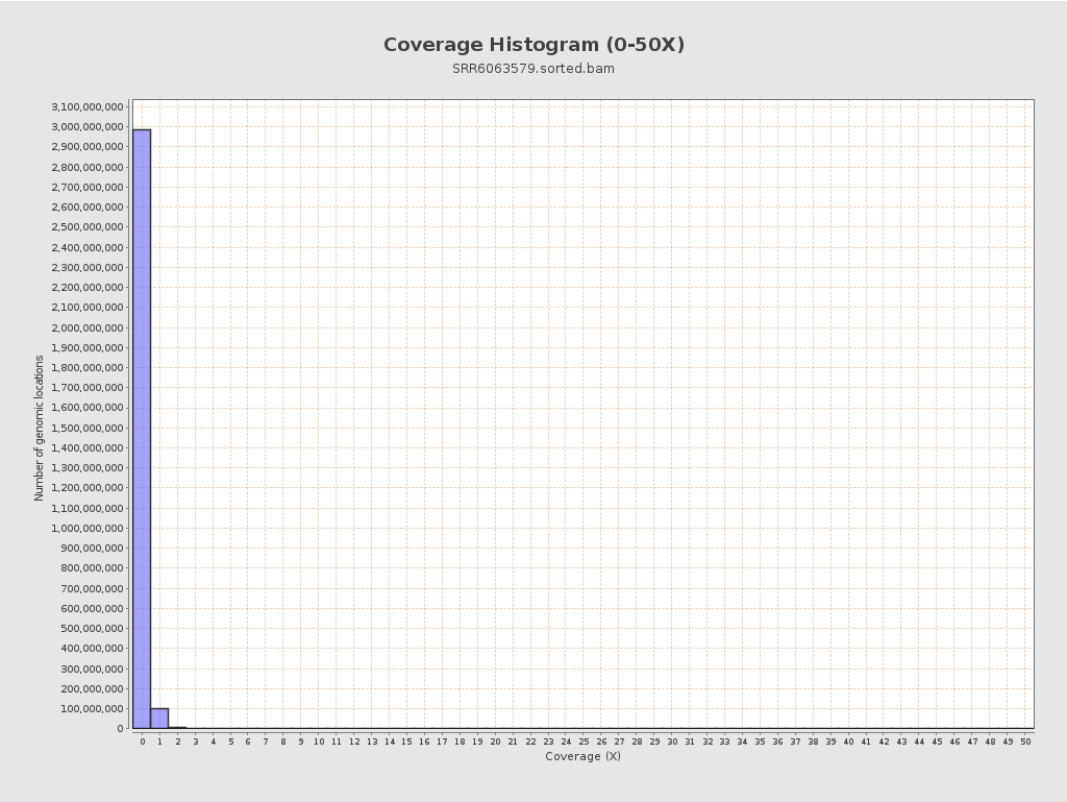
3. Results : Coverage across reference



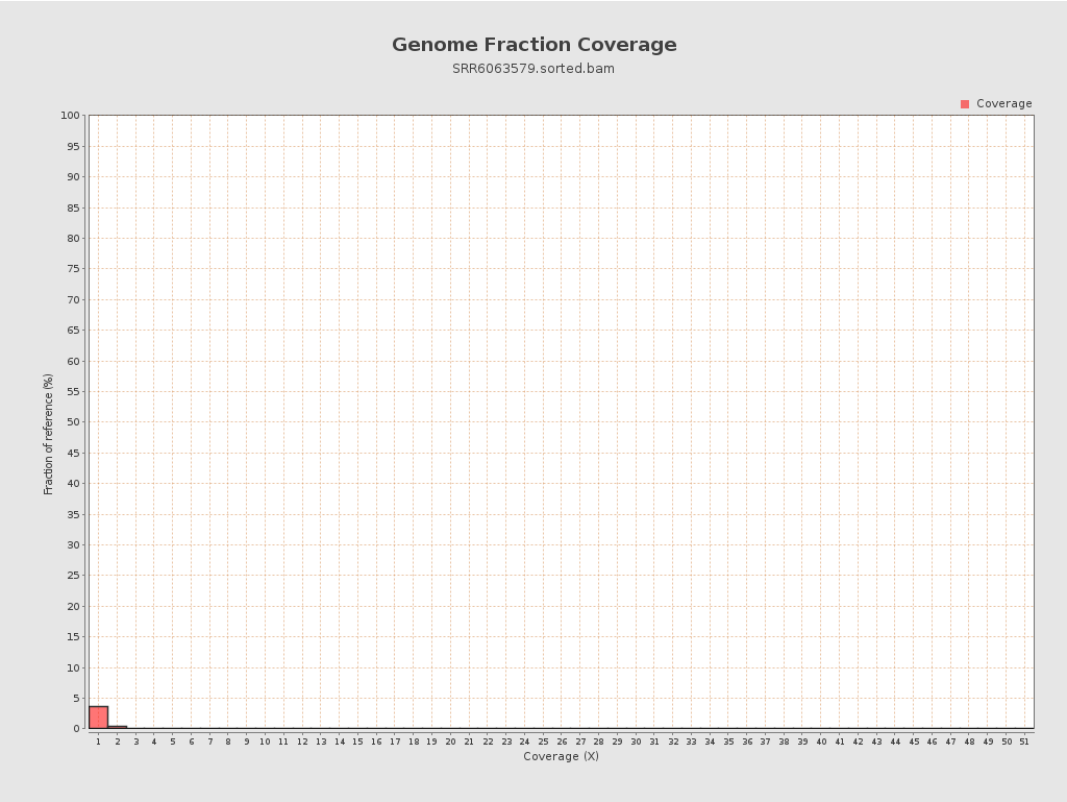
4. Results : Coverage Histogram



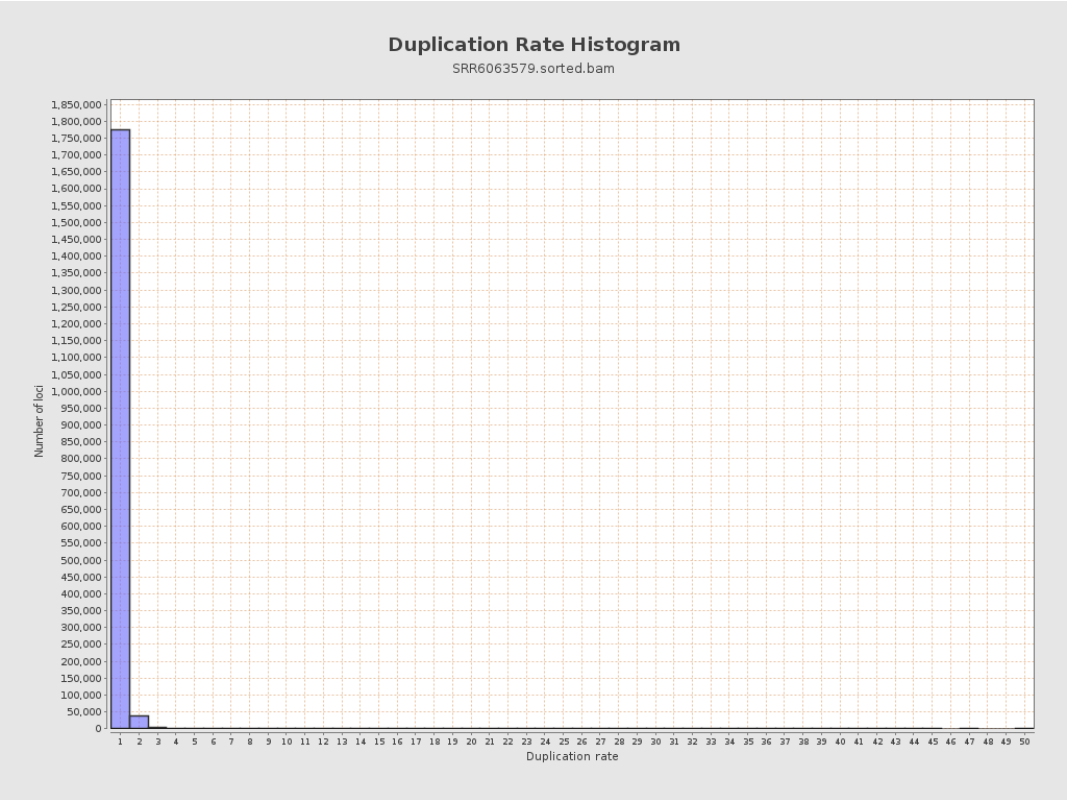
5. Results : Coverage Histogram (0-50X)



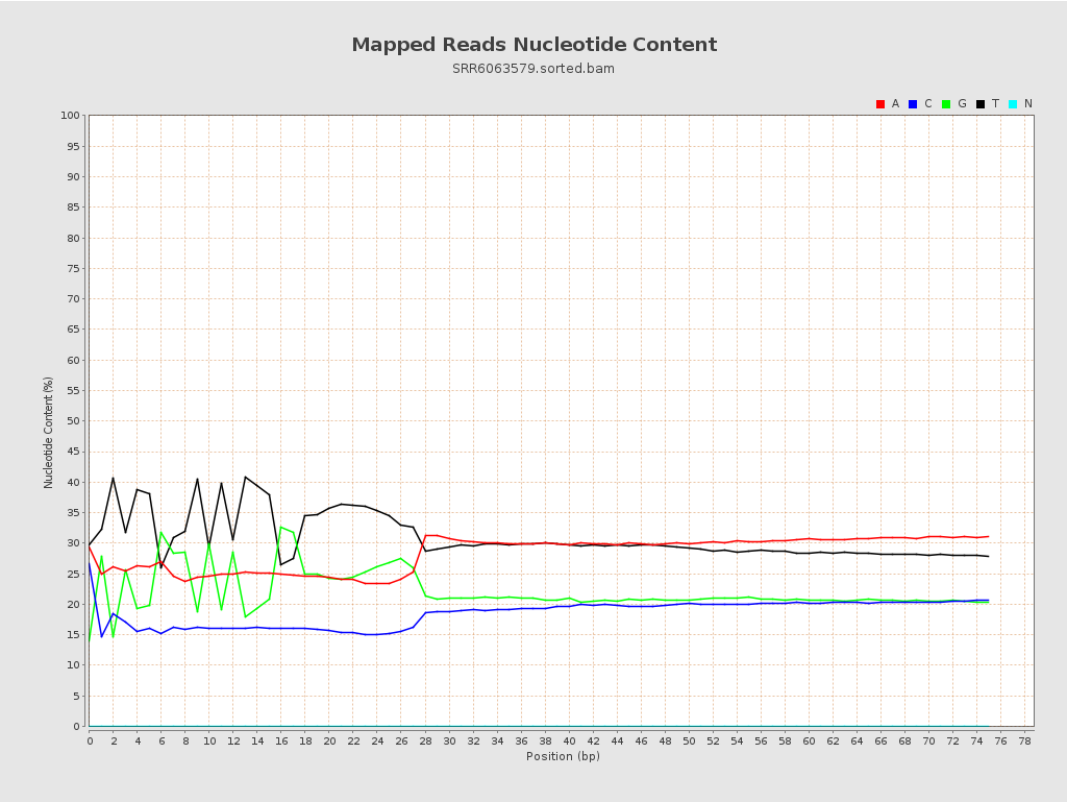
6. Results : Genome Fraction Coverage



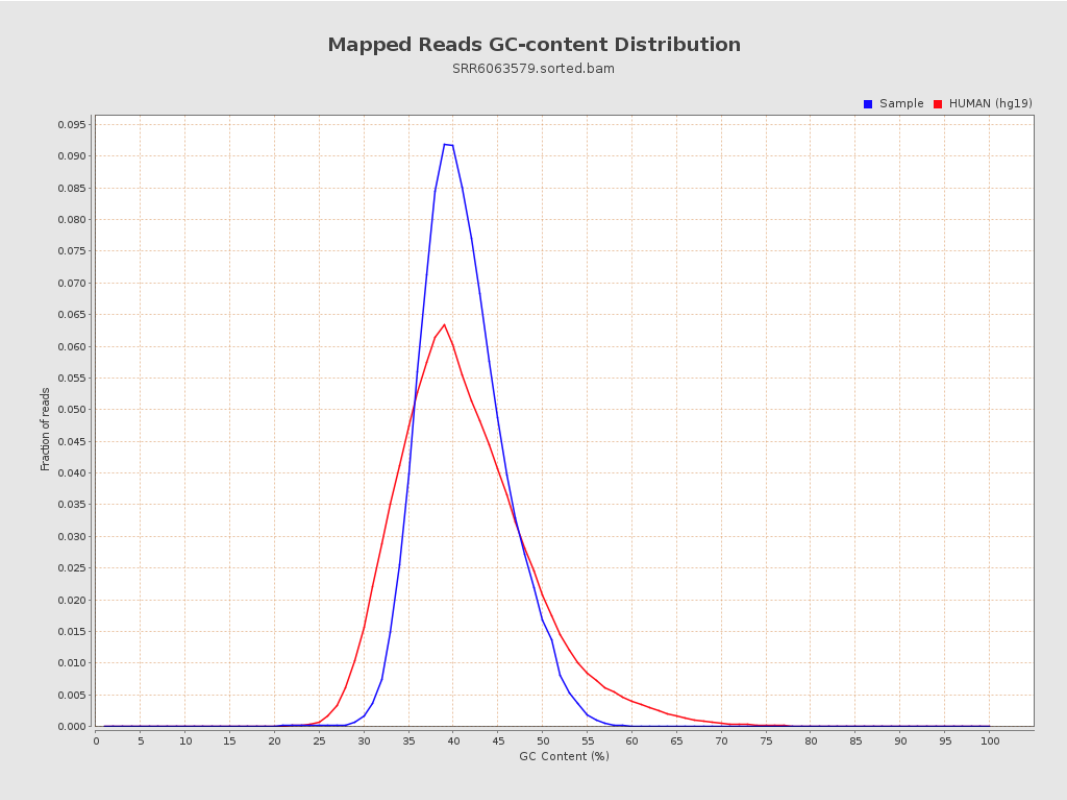
7. Results : Duplication Rate Histogram



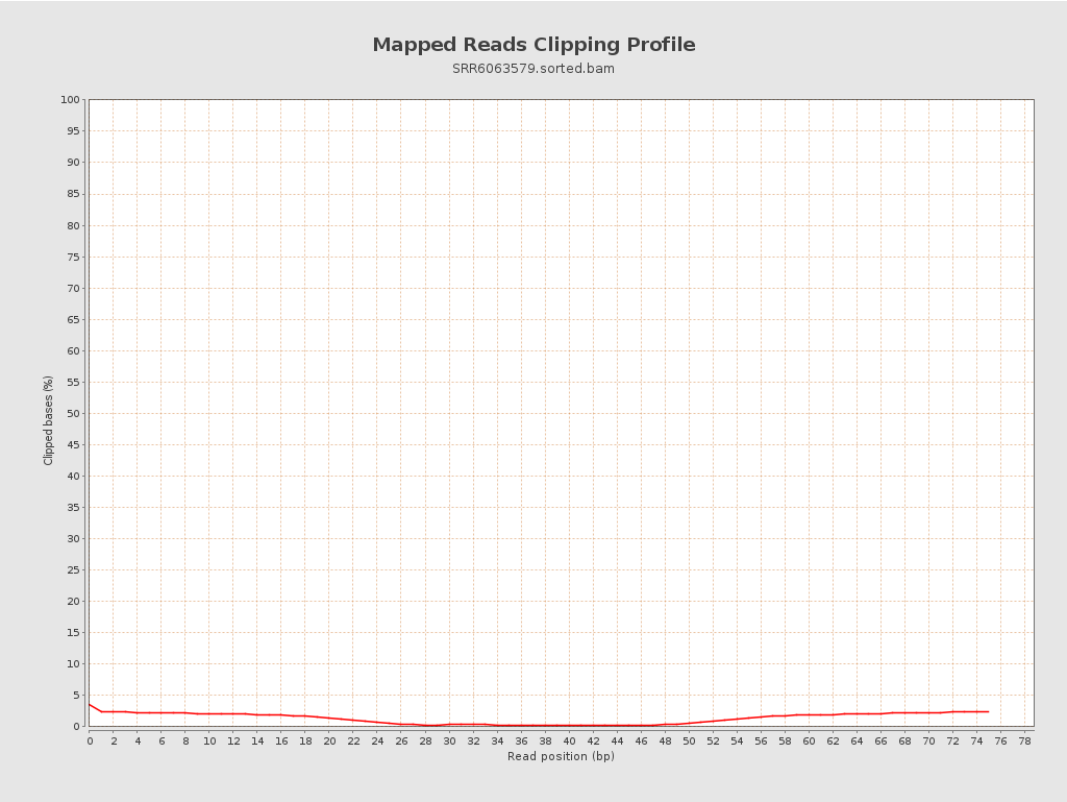
8. Results : Mapped Reads Nucleotide Content



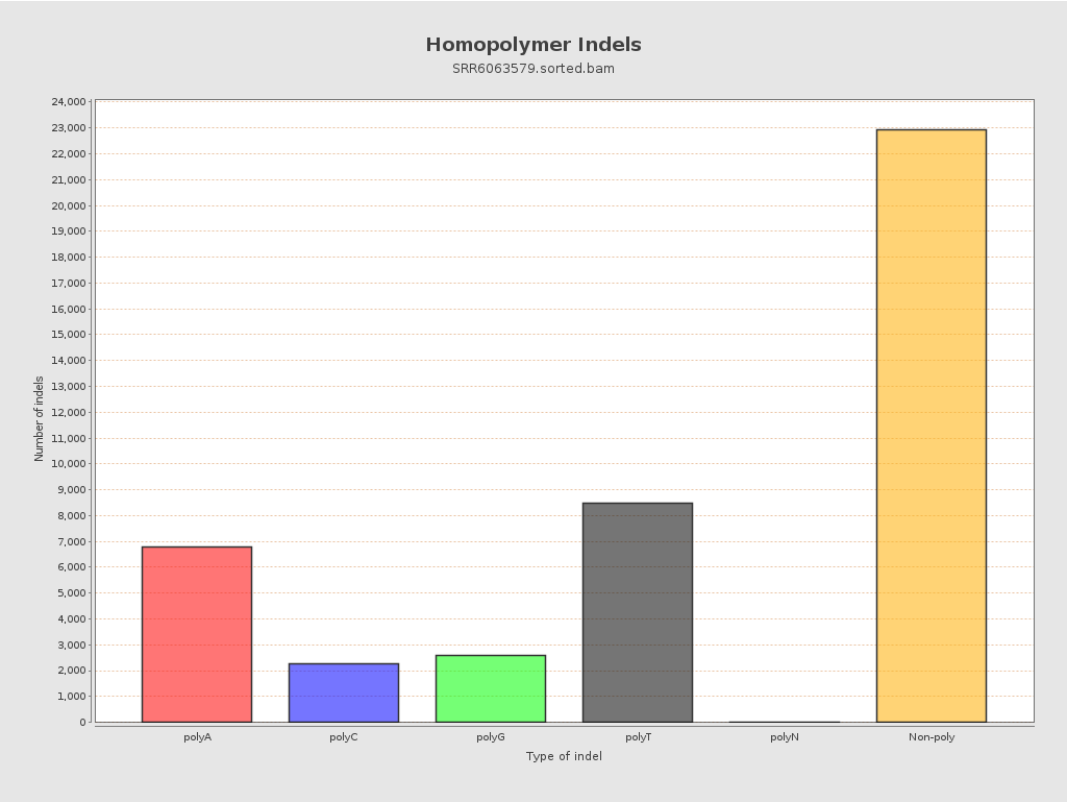
9. Results : Mapped Reads GC-content Distribution



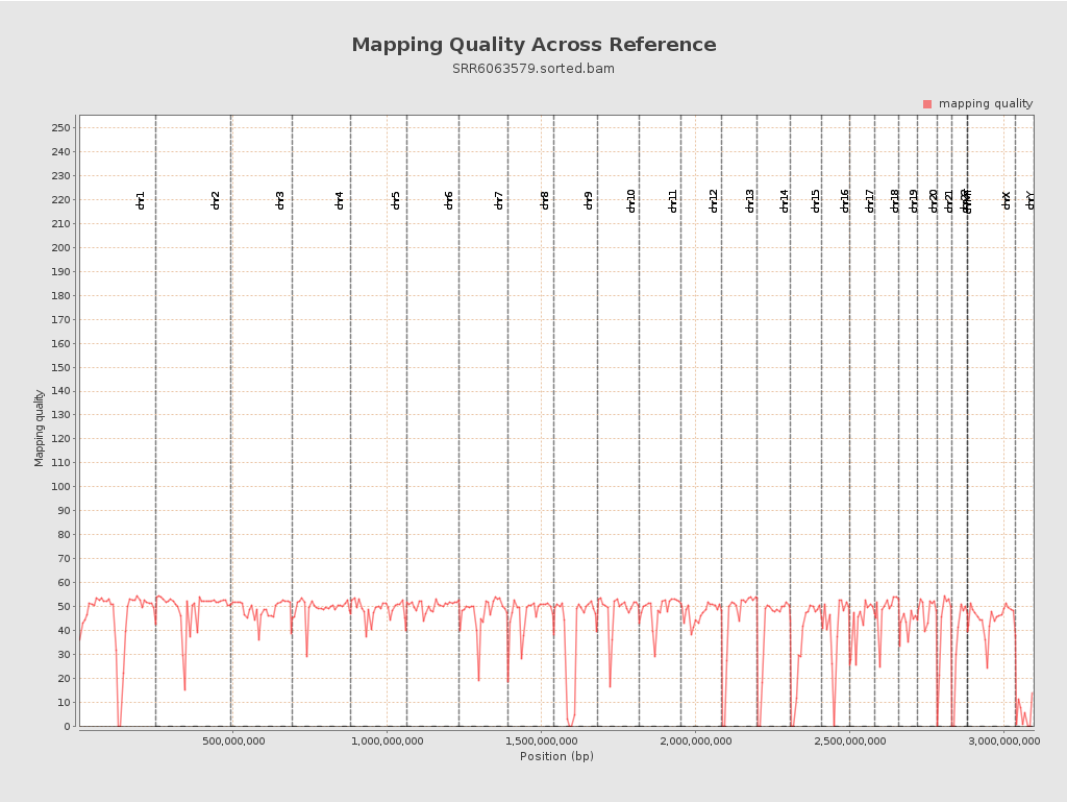
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram