Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:59:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506024.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_SRR1506024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:59:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,408,259
Mapped reads	5,031,218 / 78.51%
Unmapped reads	1,377,041 / 21.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	197 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	222,109 / 3.47%
Duplication rate	3.19%
Clipped reads	679,879 / 10.61%

2.2. ACGT Content

Number/percentage of A's	69,810,231 / 29.71%
Number/percentage of C's	48,120,301 / 20.48%
Number/percentage of T's	67,911,831 / 28.9%
Number/percentage of G's	48,377,450 / 20.59%
Number/percentage of N's	772,355 / 0.33%
GC Percentage	41.06%

2.3. Coverage

Mean	0.0759

Standard Deviation	0.629

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

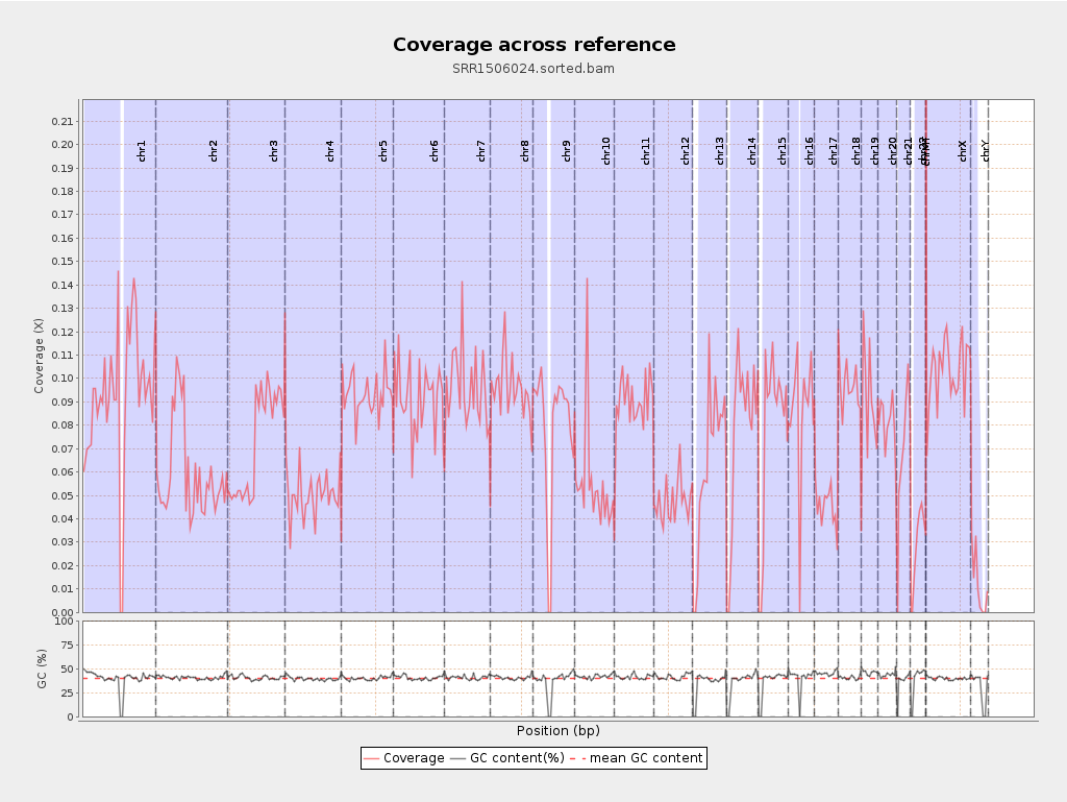
General error rate	0.78%
Mismatches	1,814,442
Insertions	9,605
Mapped reads with at least one insertion	0.19%
Deletions	34,317
Mapped reads with at least one deletion	0.68%
Homopolymer indels	46.29%

2.6. Chromosome stats

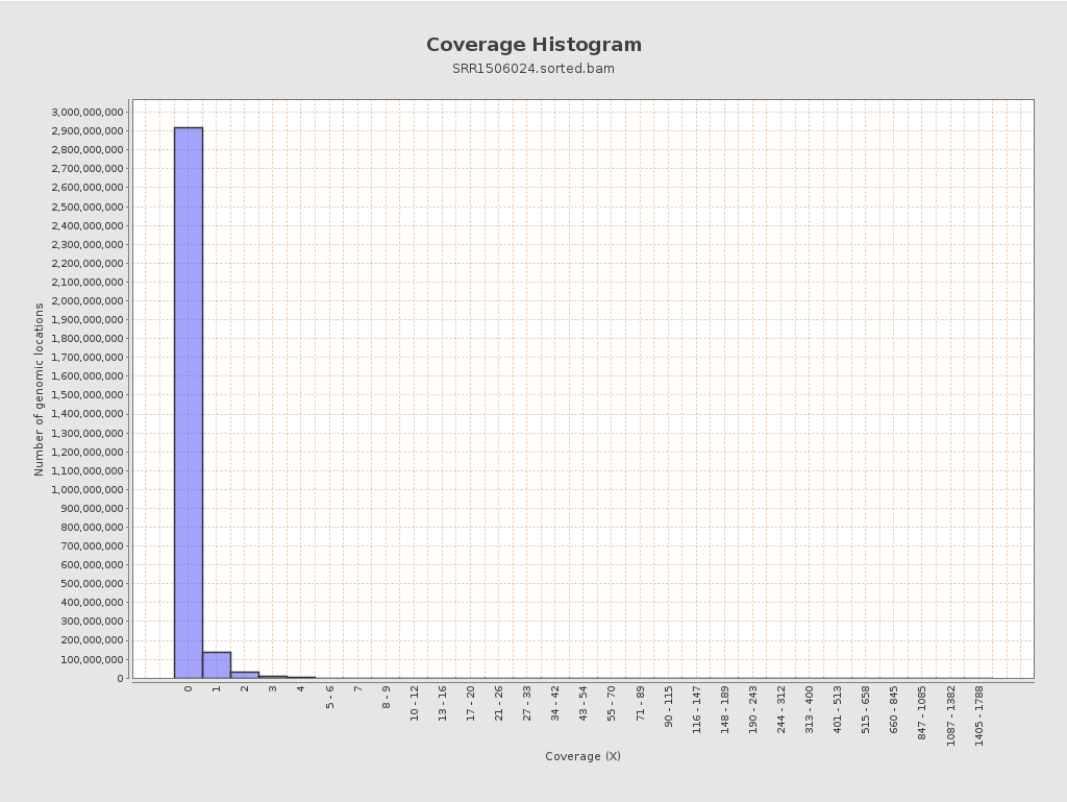
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23134656	0.0928	1.3569
chr2	243199373	14571549	0.0599	0.4883
chr3	198022430	14301341	0.0722	0.3476
chr4	191154276	9630663	0.0504	0.2959
chr5	180915260	16787983	0.0928	0.3887
chr6	171115067	15696682	0.0917	0.4564
chr7	159138663	15164315	0.0953	0.8044

chr8	146364022	13961753	0.0954	0.7856
chr9	141213431	11177589	0.0792	0.496
chr10	135534747	7350814	0.0542	0.7664
chr11	135006516	12137463	0.0899	0.509
chr12	133851895	6335754	0.0473	0.2977
chr13	115169878	7393074	0.0642	0.3152
chr14	107349540	8414783	0.0784	0.6193
chr15	102531392	7901964	0.0771	0.3468
chr16	90354753	7648419	0.0846	0.4283
chr17	81195210	3747054	0.0461	0.3075
chr18	78077248	7548797	0.0967	0.7768
chr19	59128983	5400490	0.0913	1.0097
chr20	63025520	5138674	0.0815	0.3638
chr21	48129895	3360663	0.0698	0.3672
chr22	51304566	1484657	0.0289	0.2185
chrMT	16571	6310	0.3808	0.7176
chrX	155270560	16035939	0.1033	0.4566
chrY	59373566	708428	0.0119	0.198

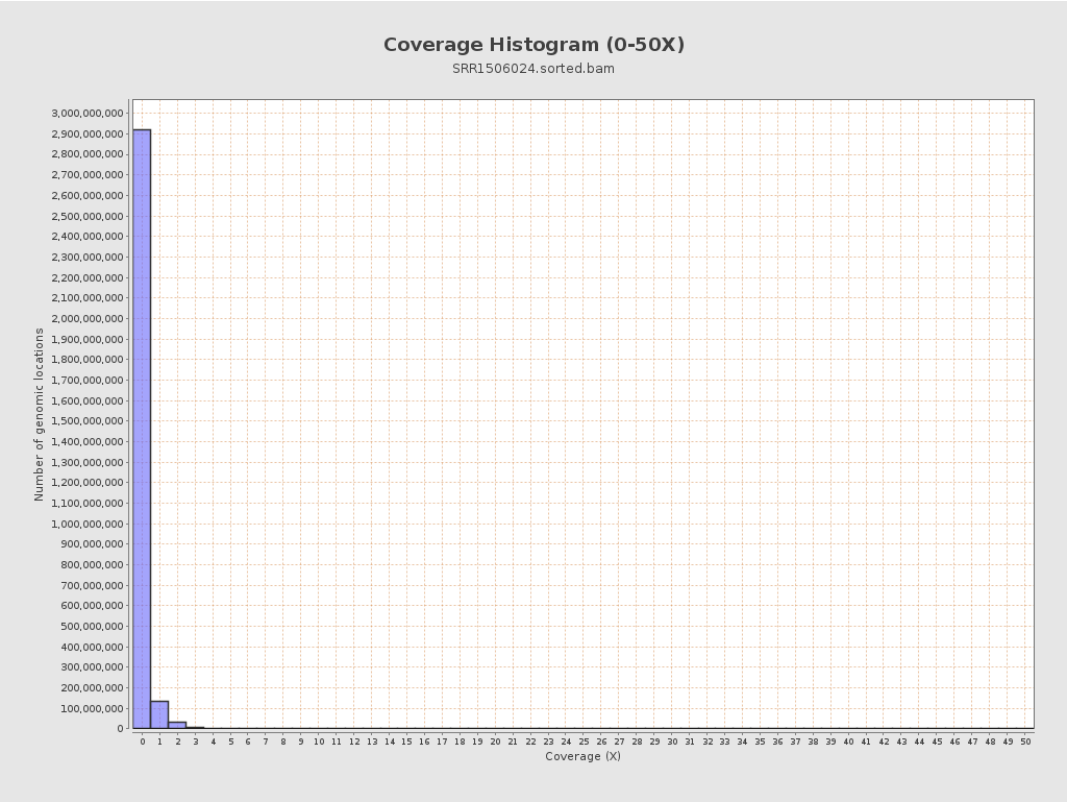
3. Results : Coverage across reference



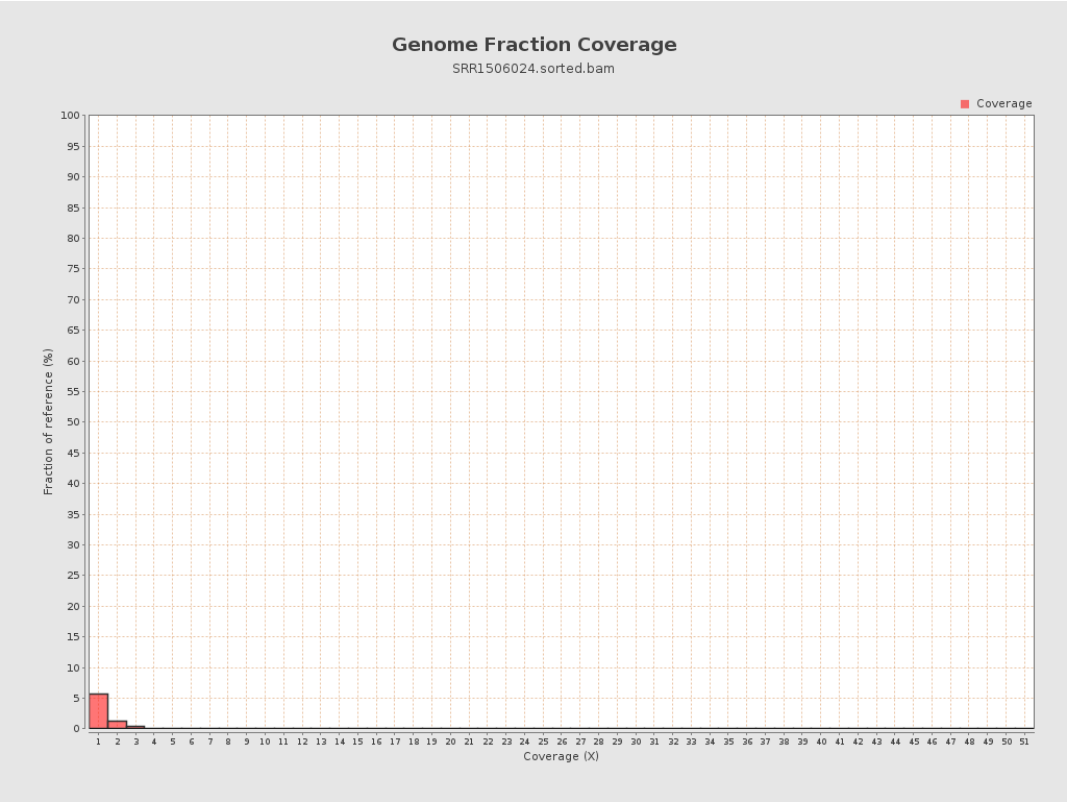
4. Results : Coverage Histogram



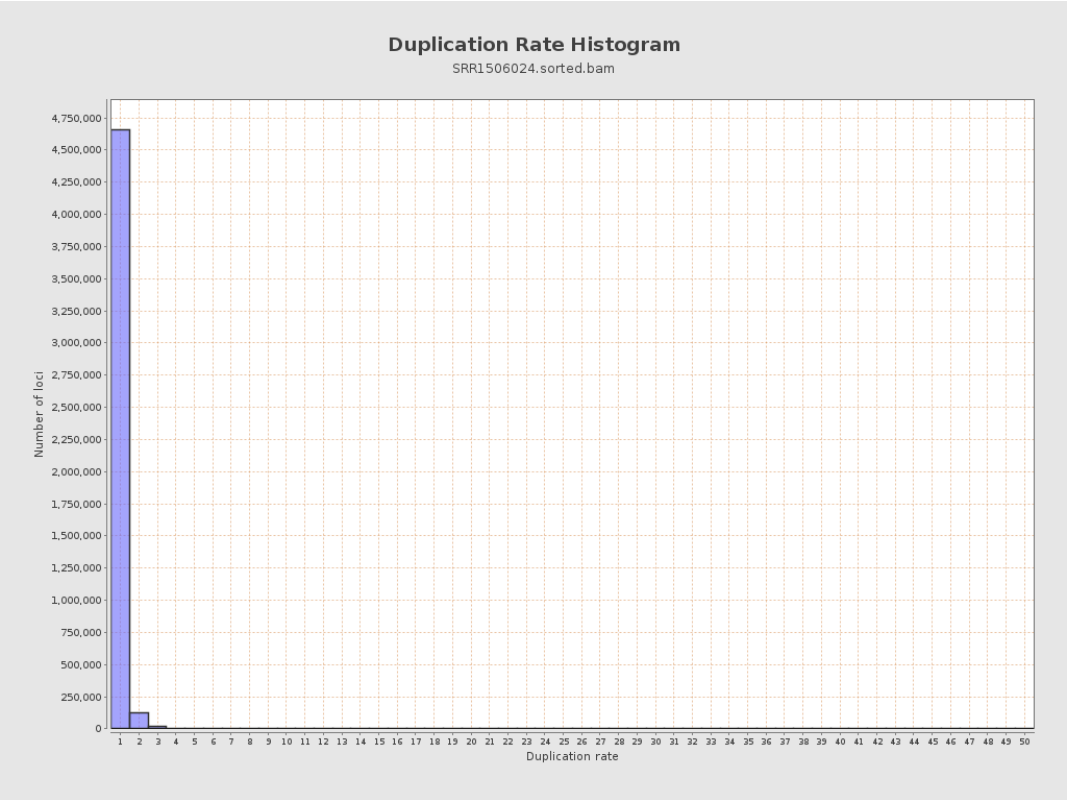
5. Results : Coverage Histogram (0-50X)



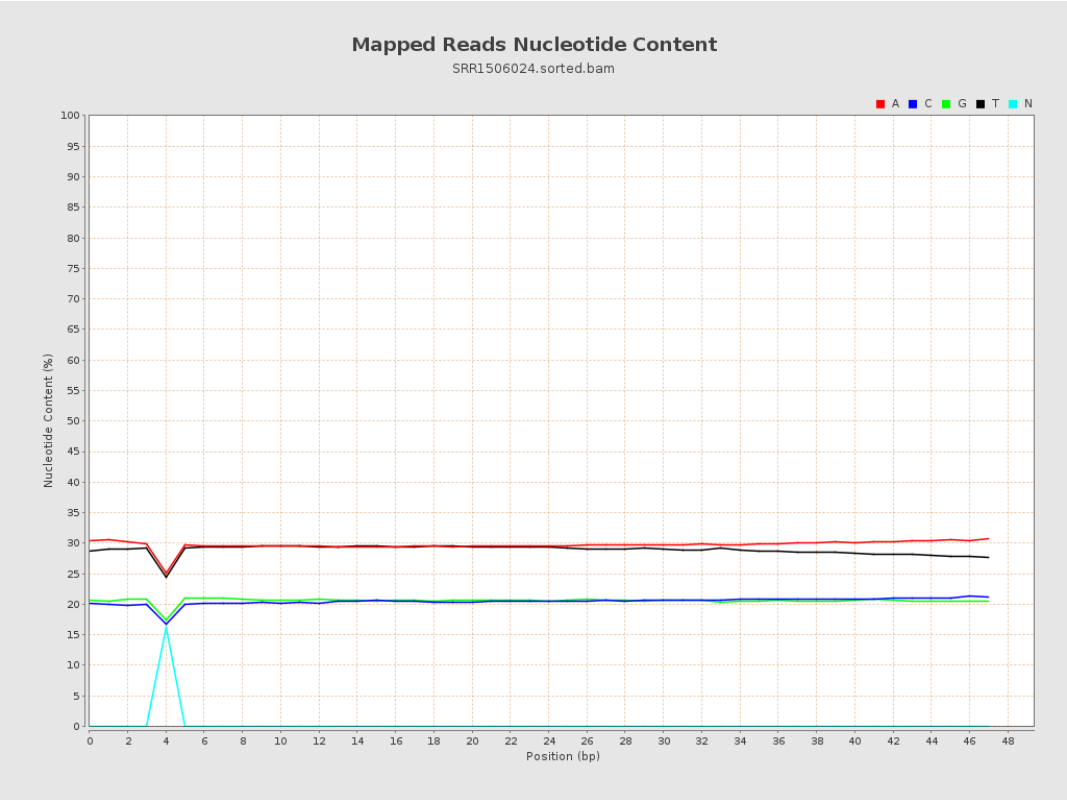
6. Results : Genome Fraction Coverage



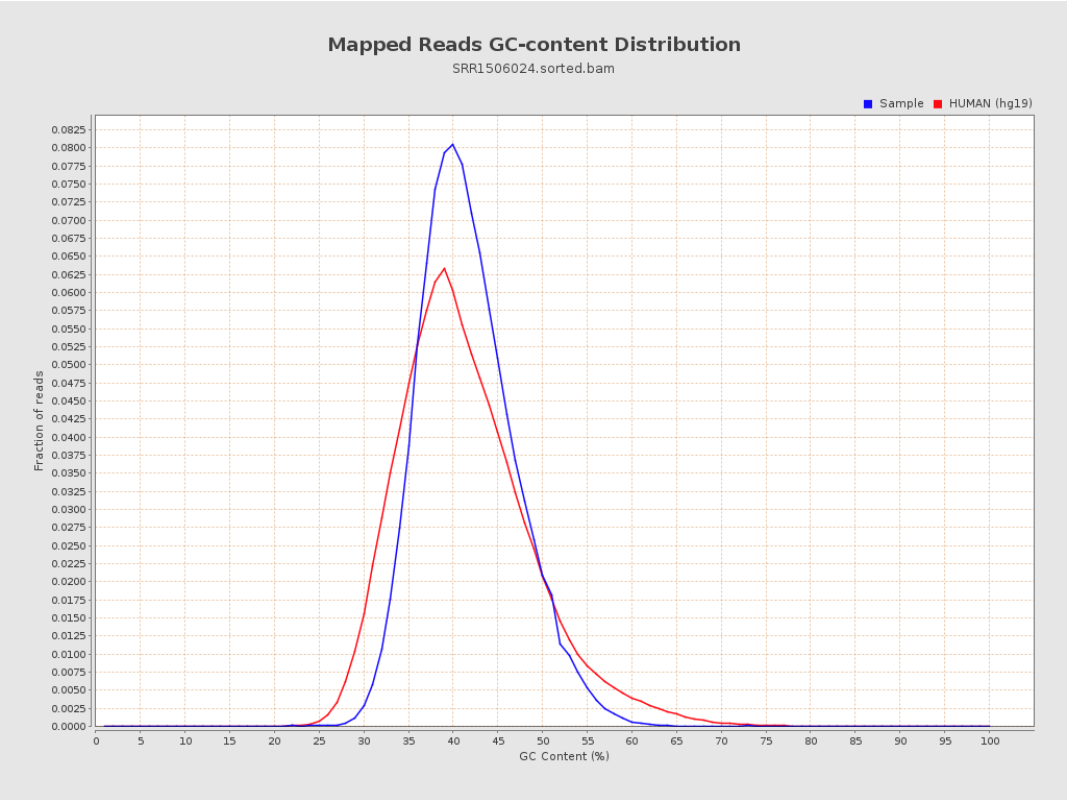
7. Results : Duplication Rate Histogram



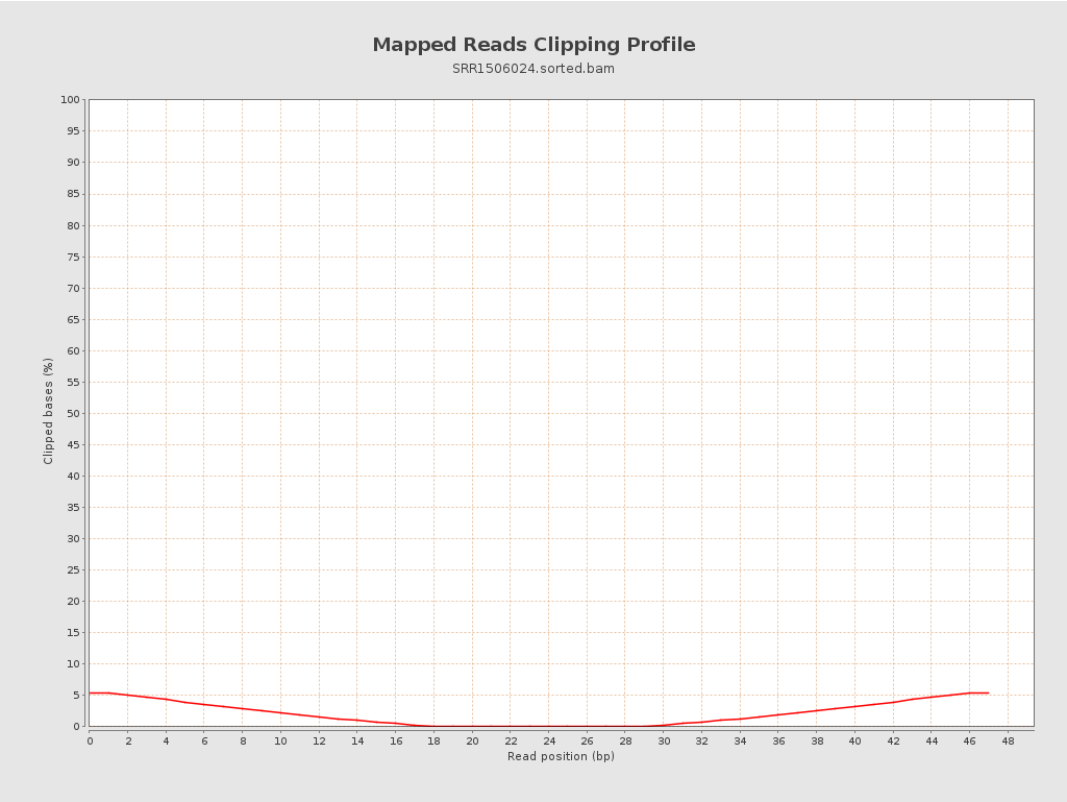
8. Results : Mapped Reads Nucleotide Content



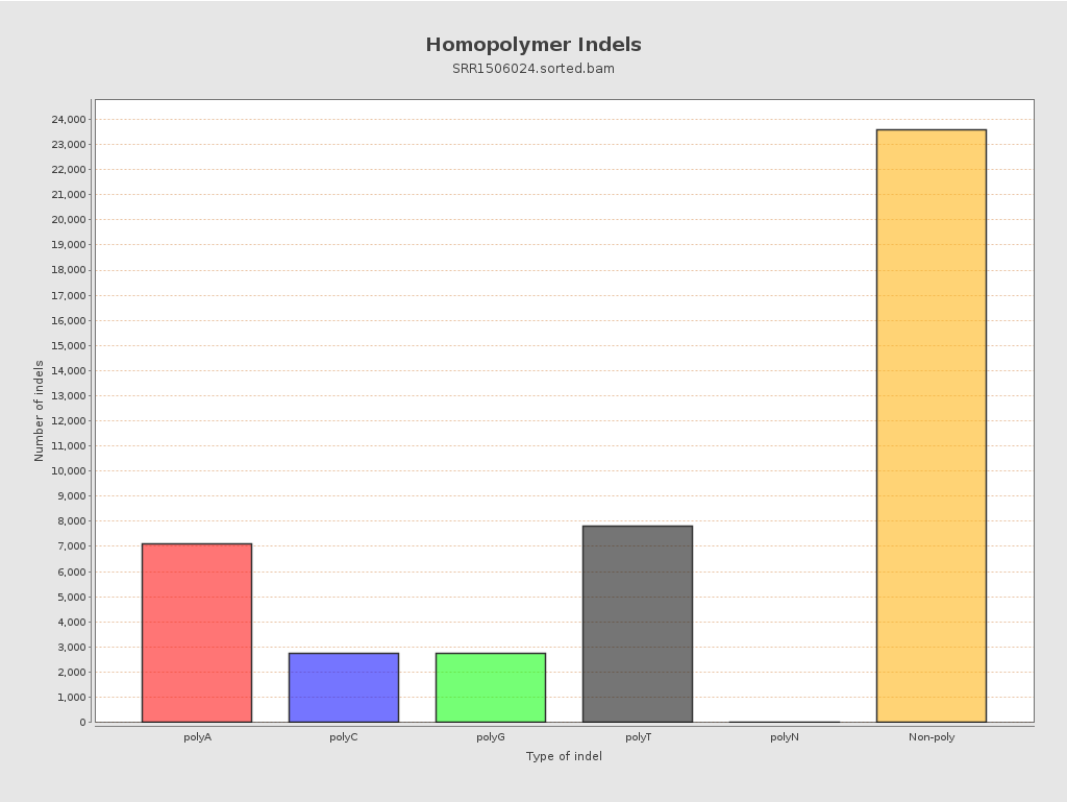
9. Results : Mapped Reads GC-content Distribution



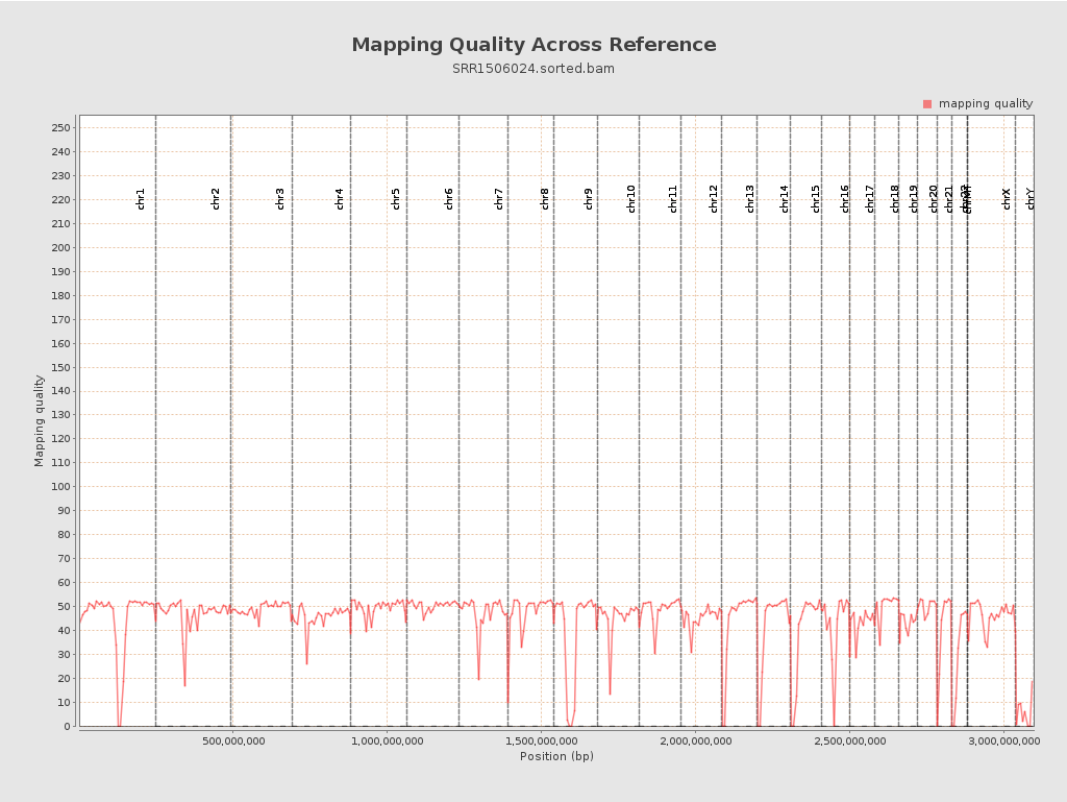
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram