Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:53:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004119.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_SRR6004119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:53:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,859,257
Mapped reads	4,123,279 / 84.85%
Unmapped reads	735,978 / 15.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,525 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	251,770 / 5.18%
Duplication rate	4.59%
Clipped reads	1,708,603 / 35.16%

2.2. ACGT Content

Number/percentage of A's	78,186,461 / 28.09%
Number/percentage of C's	50,414,027 / 18.11%
Number/percentage of T's	89,977,988 / 32.32%
Number/percentage of G's	59,754,321 / 21.47%
Number/percentage of N's	29,705 / 0.01%
GC Percentage	39.58%

2.3. Coverage

Mean	0.09

Standard Deviation	0.7967

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

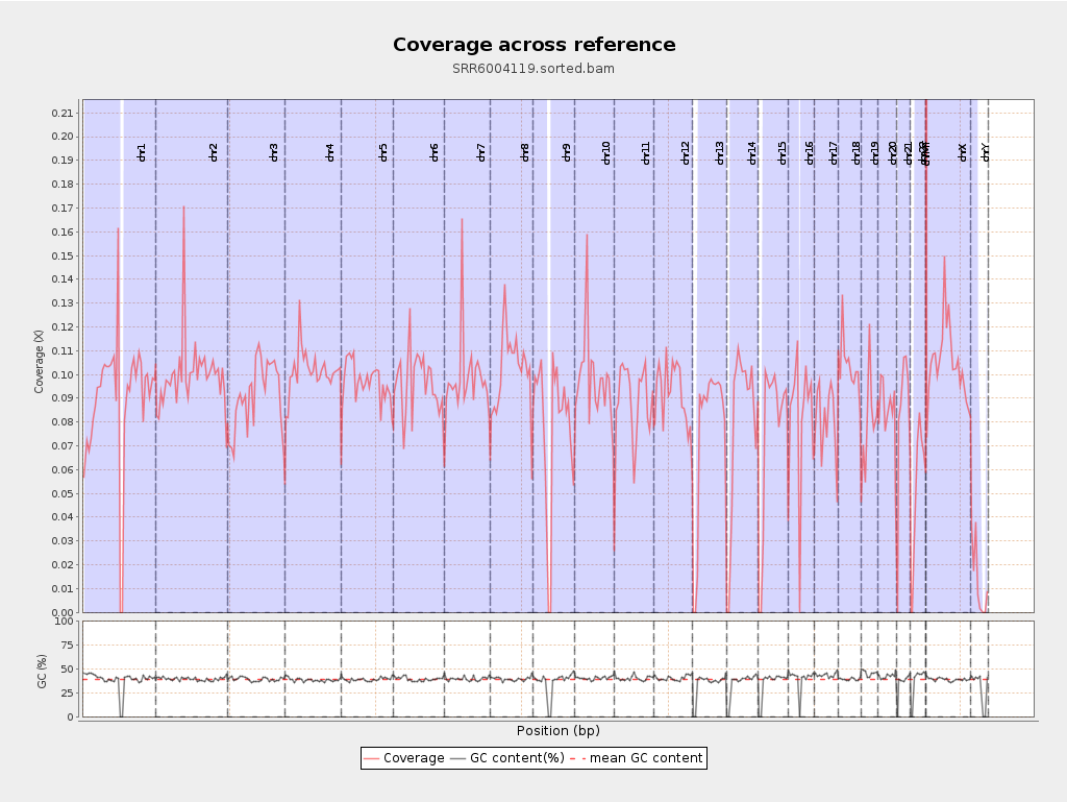
General error rate	0.95%
Mismatches	2,594,443
Insertions	24,719
Mapped reads with at least one insertion	0.59%
Deletions	70,283
Mapped reads with at least one deletion	1.69%
Homopolymer indels	47.42%

2.6. Chromosome stats

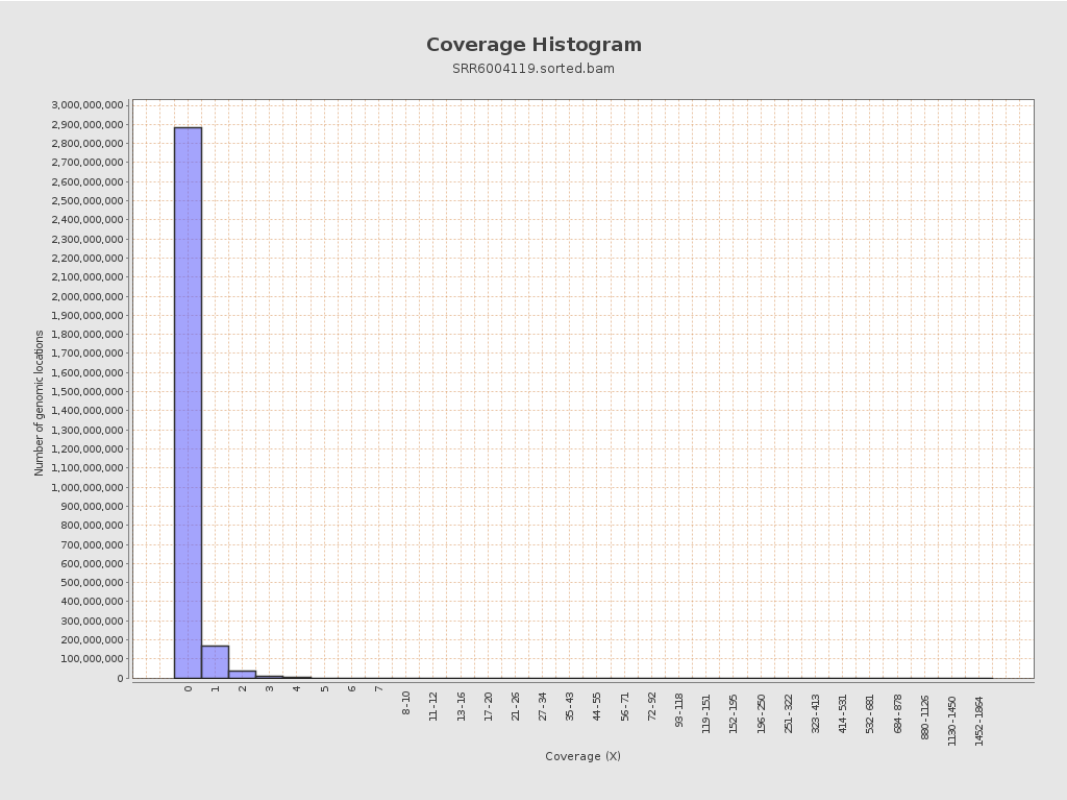
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22309936	0.0895	1.5652
chr2	243199373	24307691	0.0999	0.8779
chr3	198022430	17999921	0.0909	0.3822
chr4	191154276	19441850	0.1017	0.4317
chr5	180915260	17428397	0.0963	0.396
chr6	171115067	16544134	0.0967	0.4836
chr7	159138663	15604973	0.0981	1.0923

chr8	146364022	14909058	0.1019	1.2166
chr9	141213431	11104831	0.0786	0.7434
chr10	135534747	13260073	0.0978	0.7092
chr11	135006516	12028892	0.0891	0.6369
chr12	133851895	12282841	0.0918	0.403
chr13	115169878	8795820	0.0764	0.3425
chr14	107349540	8682586	0.0809	0.4207
chr15	102531392	7687873	0.075	0.3481
chr16	90354753	7272870	0.0805	0.4835
chr17	81195210	6668946	0.0821	0.4361
chr18	78077248	8125762	0.1041	1.6031
chr19	59128983	4784605	0.0809	0.9897
chr20	63025520	5431644	0.0862	0.3975
chr21	48129895	4043027	0.084	0.4343
chr22	51304566	2647307	0.0516	0.2774
chrMT	16571	58411	3.5249	2.7642
chrX	155270560	16304558	0.105	0.4865
chrY	59373566	754166	0.0127	0.2591

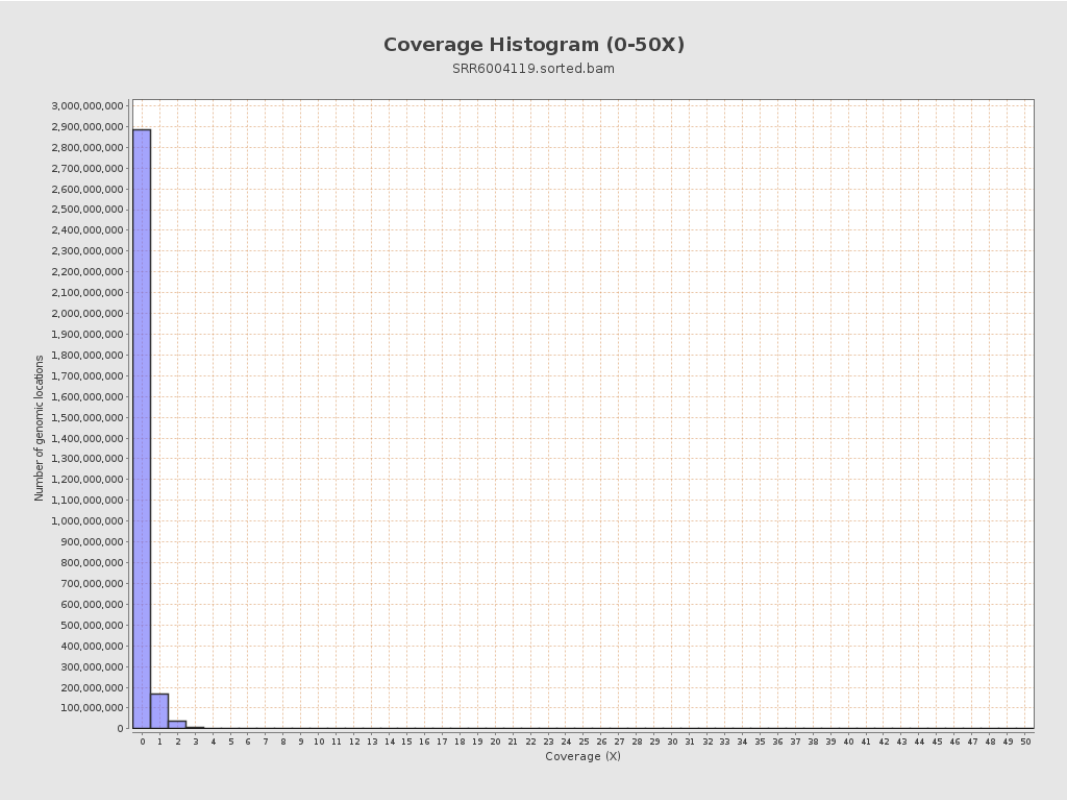
3. Results : Coverage across reference



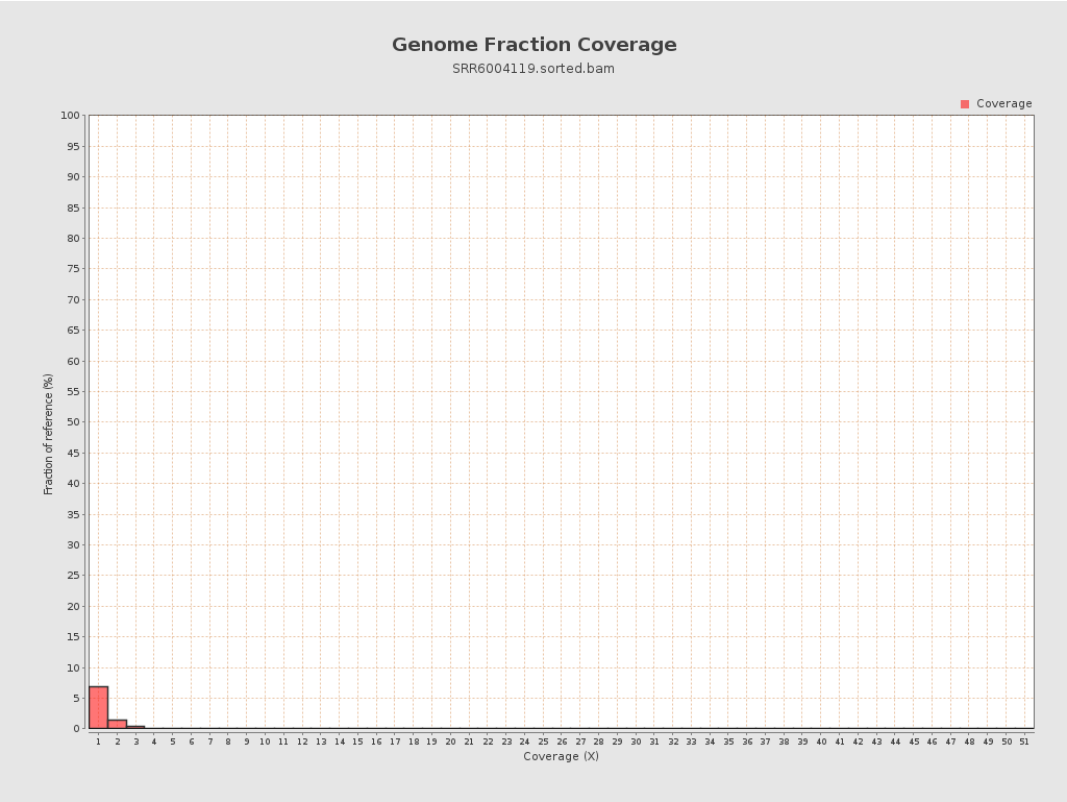
4. Results : Coverage Histogram



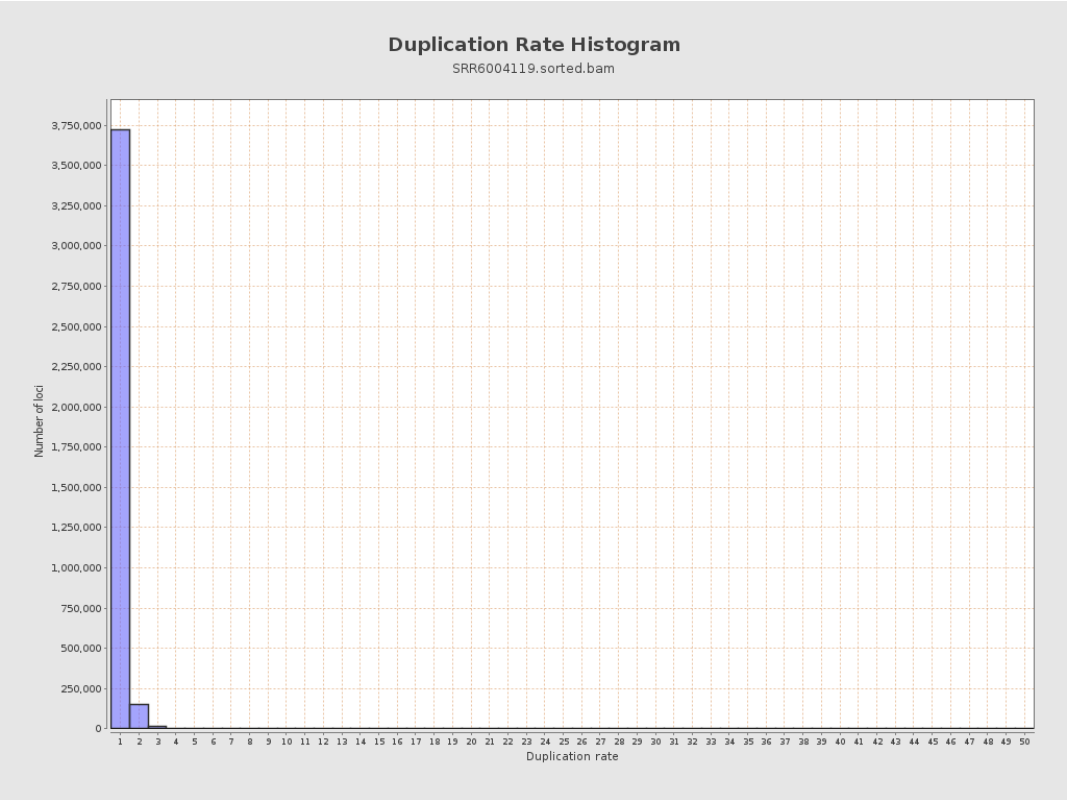
5. Results : Coverage Histogram (0-50X)



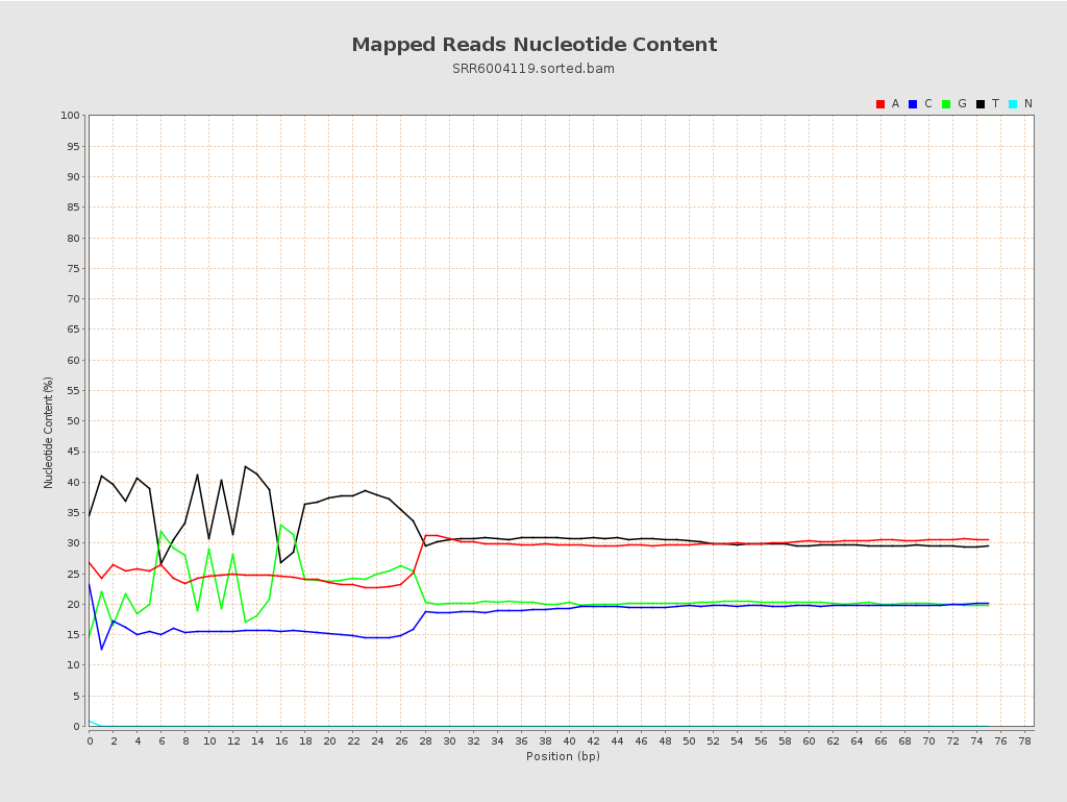
6. Results : Genome Fraction Coverage



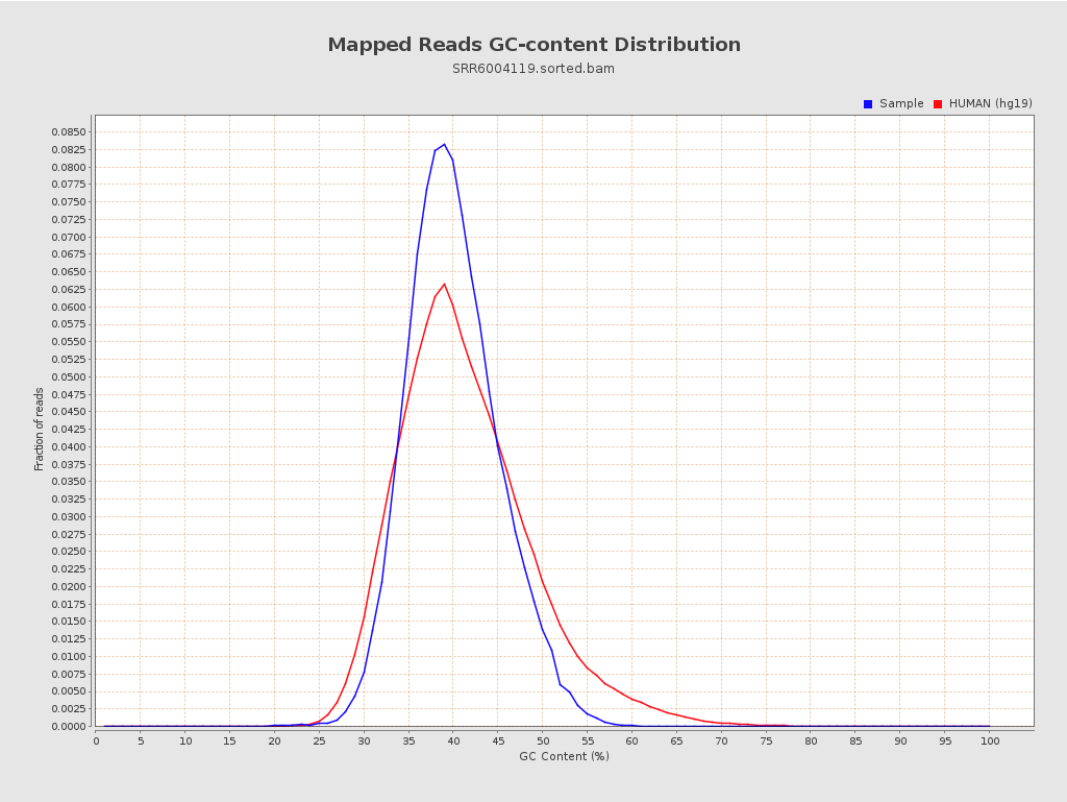
7. Results : Duplication Rate Histogram



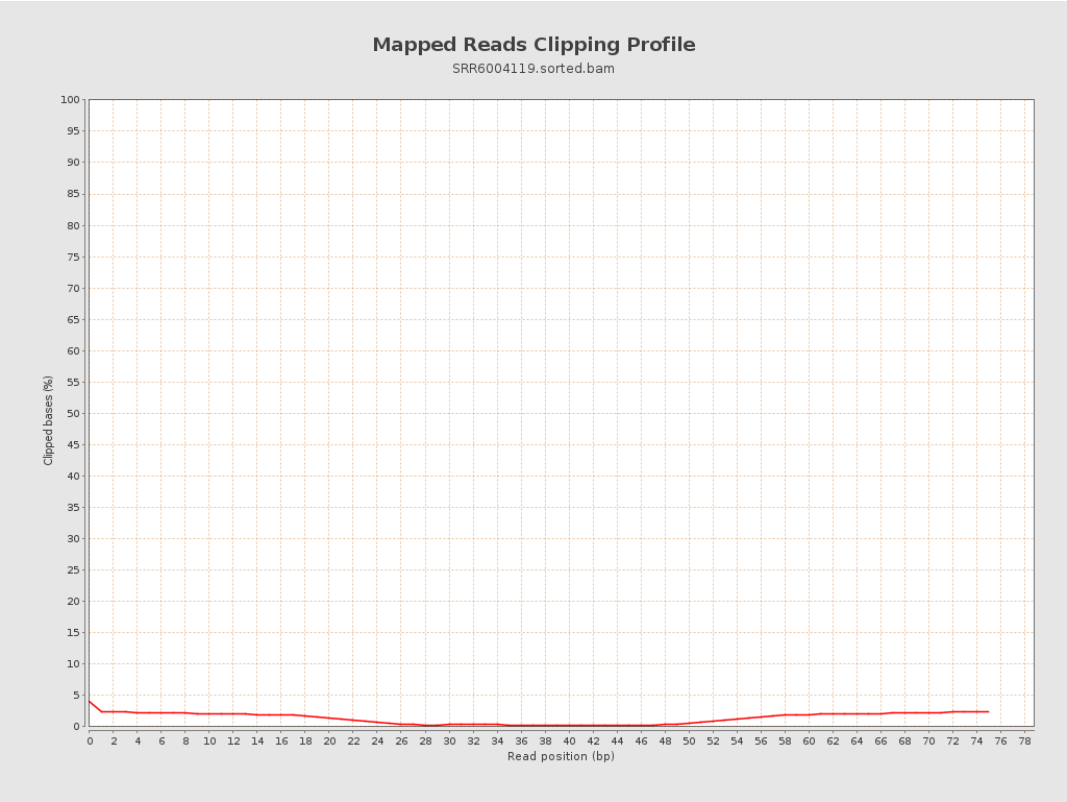
8. Results : Mapped Reads Nucleotide Content



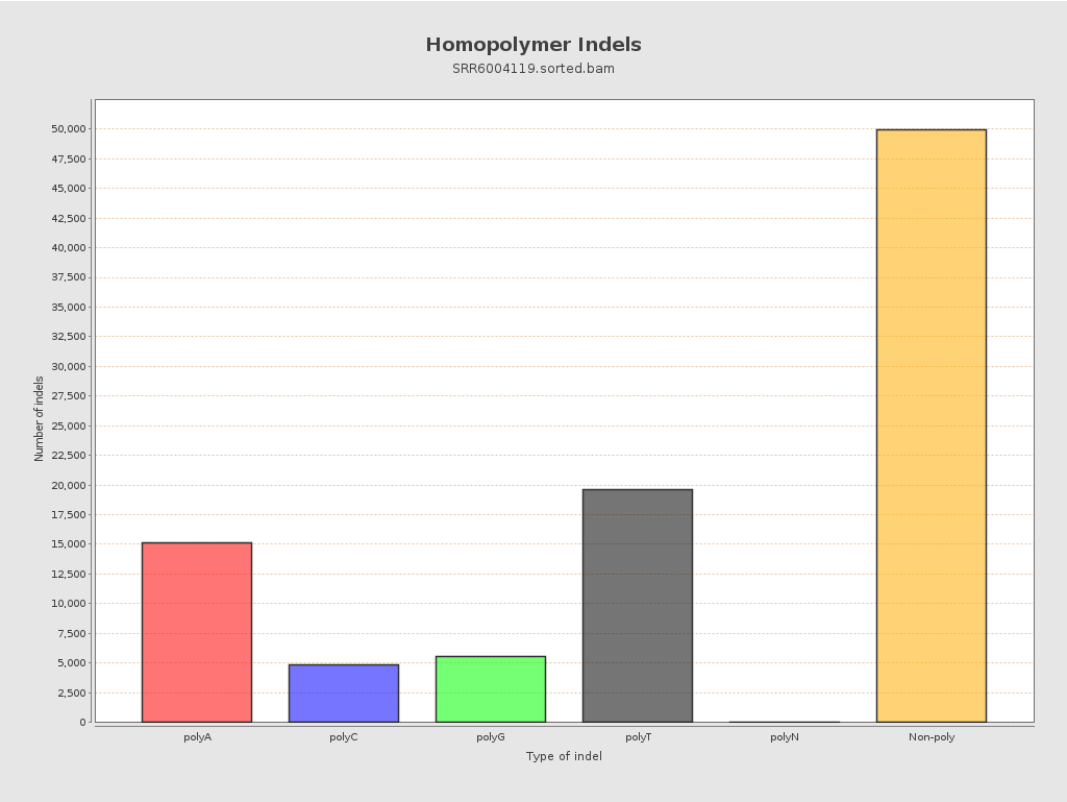
9. Results : Mapped Reads GC-content Distribution



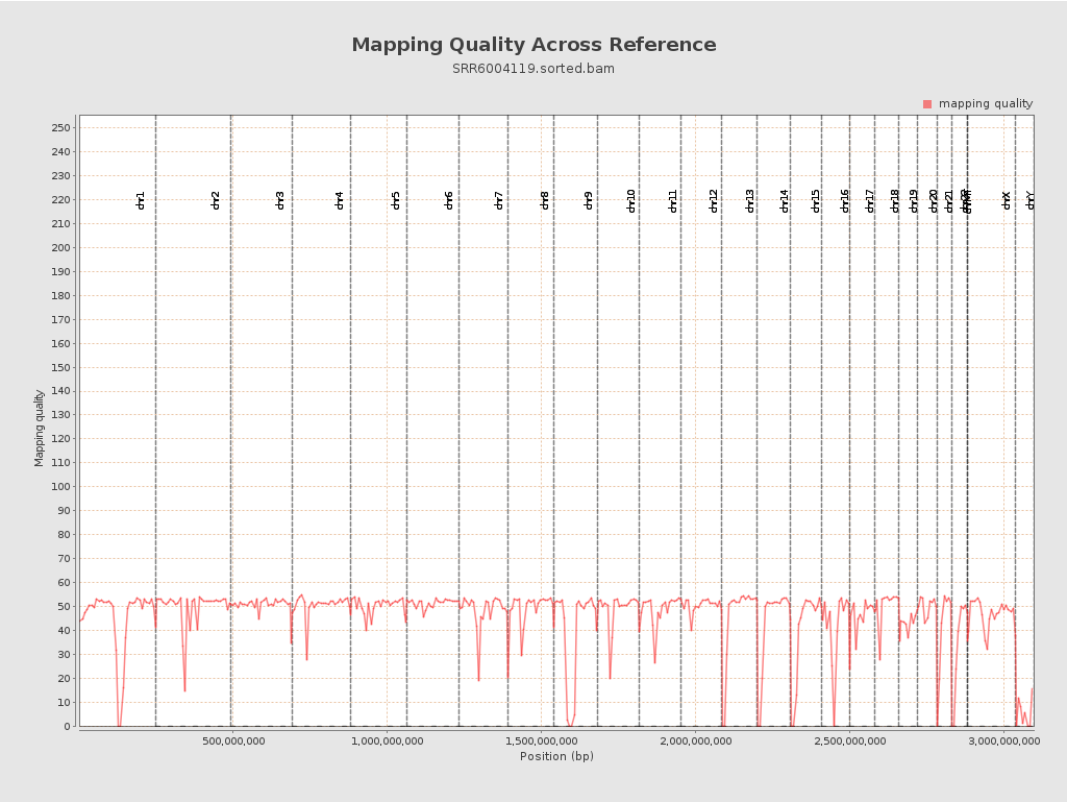
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram