Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:28:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505960.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_SRR1505960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:28:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,280,496
Mapped reads	5,427,382 / 74.55%
Unmapped reads	1,853,114 / 25.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	290 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	356,724 / 4.9%
Duplication rate	5.18%
Clipped reads	769,389 / 10.57%

2.2. ACGT Content

Number/percentage of A's	74,140,655 / 29.28%
Number/percentage of C's	52,609,506 / 20.78%
Number/percentage of T's	73,439,579 / 29.01%
Number/percentage of G's	52,979,481 / 20.93%
Number/percentage of N's	1,141 / 0%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0818

Standard Deviation	0.6329

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

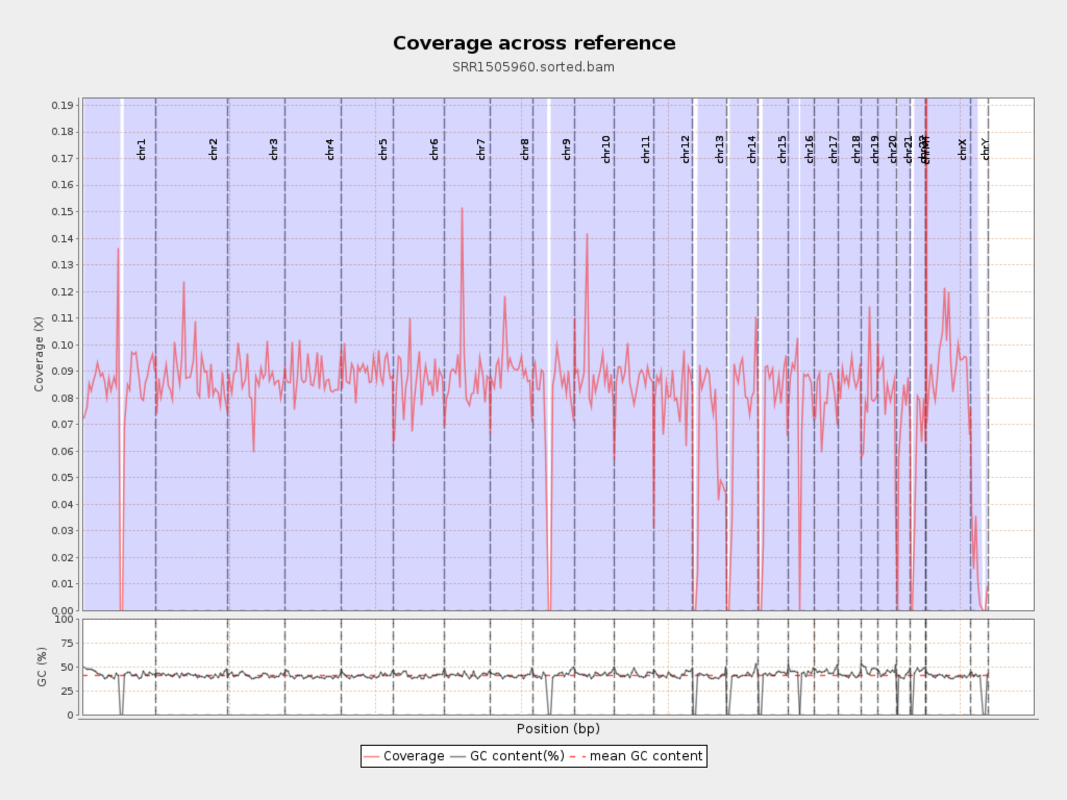
General error rate	0.51%
Mismatches	1,282,189
Insertions	11,607
Mapped reads with at least one insertion	0.21%
Deletions	35,825
Mapped reads with at least one deletion	0.66%
Homopolymer indels	44.26%

2.6. Chromosome stats

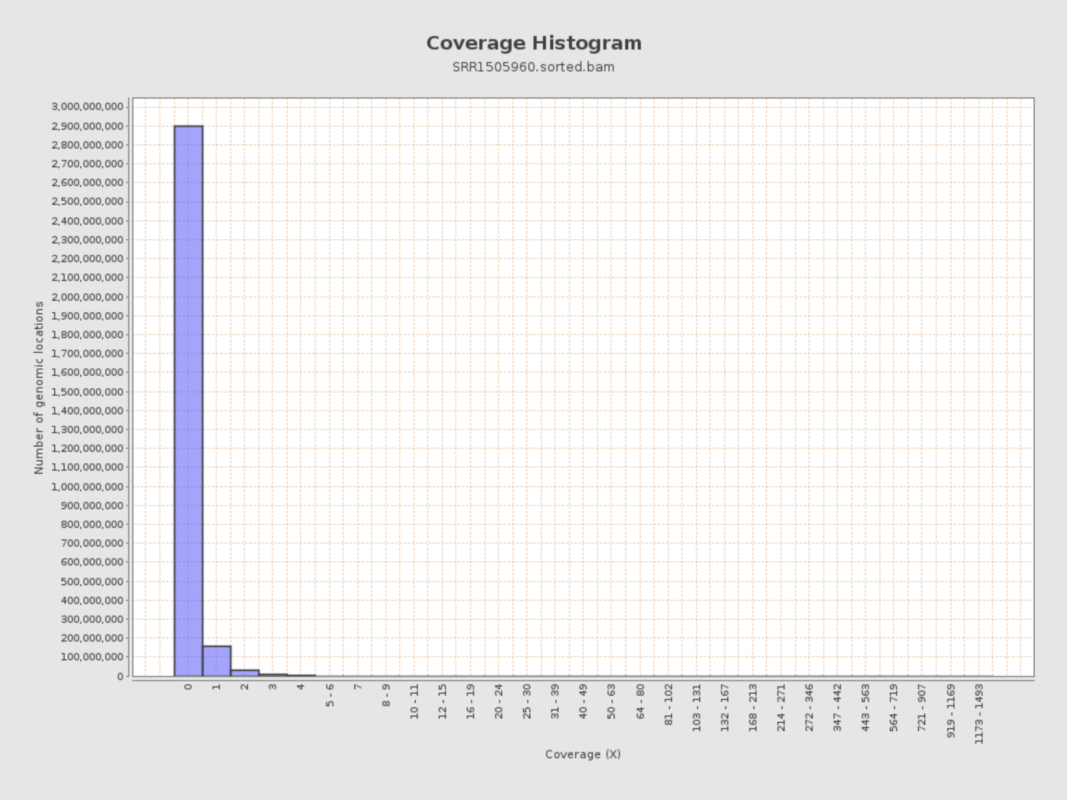
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20540049	0.0824	1.0588
chr2	243199373	21405745	0.088	0.547
chr3	198022430	17195305	0.0868	0.3675
chr4	191154276	16786548	0.0878	0.3768
chr5	180915260	16190153	0.0895	0.3742
chr6	171115067	14717571	0.086	0.4217
chr7	159138663	14119267	0.0887	0.9557

chr8	146364022	13301226	0.0909	0.8682
chr9	141213431	10740827	0.0761	0.4819
chr10	135534747	12123521	0.0894	0.6561
chr11	135006516	11711175	0.0867	0.5769
chr12	133851895	11047772	0.0825	0.3802
chr13	115169878	6870950	0.0597	0.3012
chr14	107349540	7777968	0.0725	1.1748
chr15	102531392	7149748	0.0697	0.3252
chr16	90354753	7090505	0.0785	0.4064
chr17	81195210	6510416	0.0802	0.4146
chr18	78077248	6823416	0.0874	0.998
chr19	59128983	4750013	0.0803	0.8104
chr20	63025520	5219593	0.0828	0.3765
chr21	48129895	3256211	0.0677	0.359
chr22	51304566	2686441	0.0524	0.2846
chrMT	16571	52758	3.1838	2.5802
chrX	155270560	14396252	0.0927	0.4382
chrY	59373566	756227	0.0127	0.1971

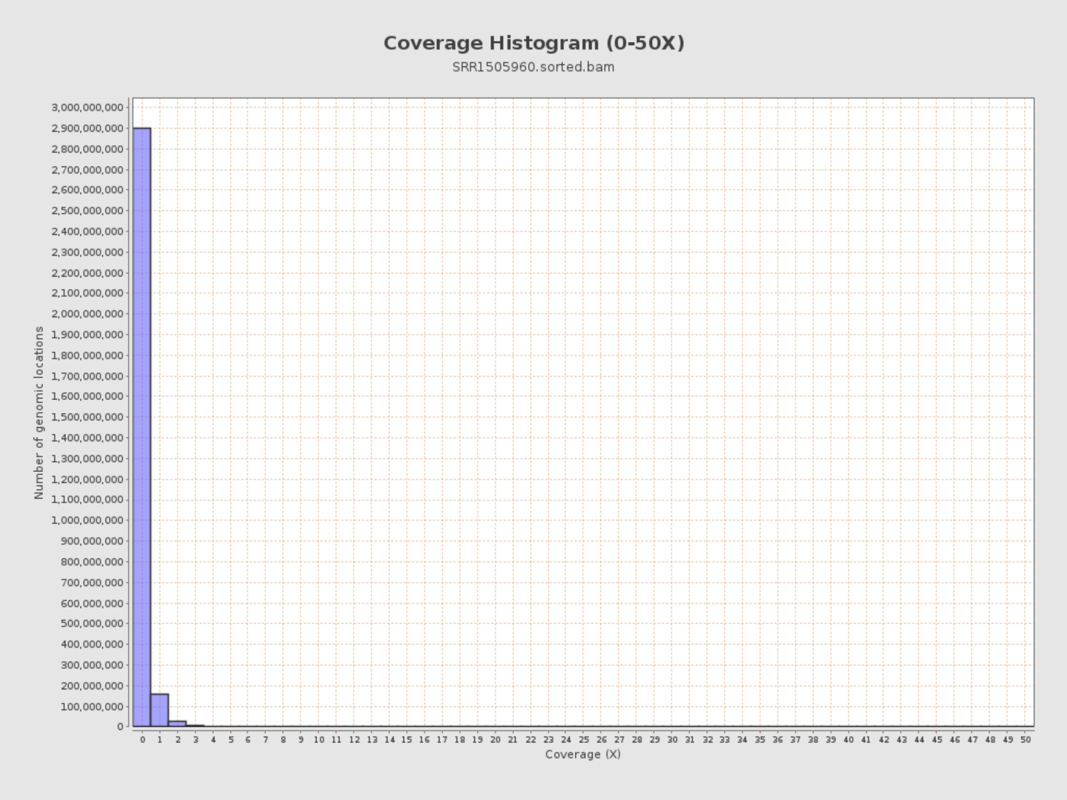
3. Results : Coverage across reference



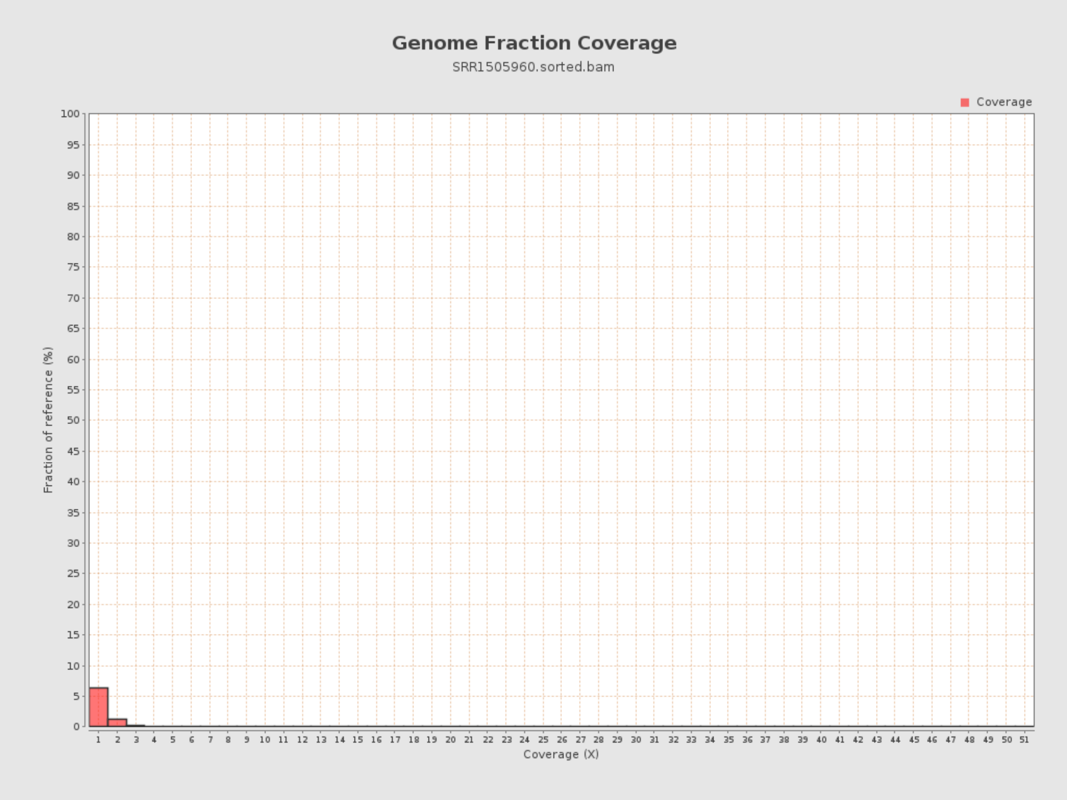
4. Results : Coverage Histogram



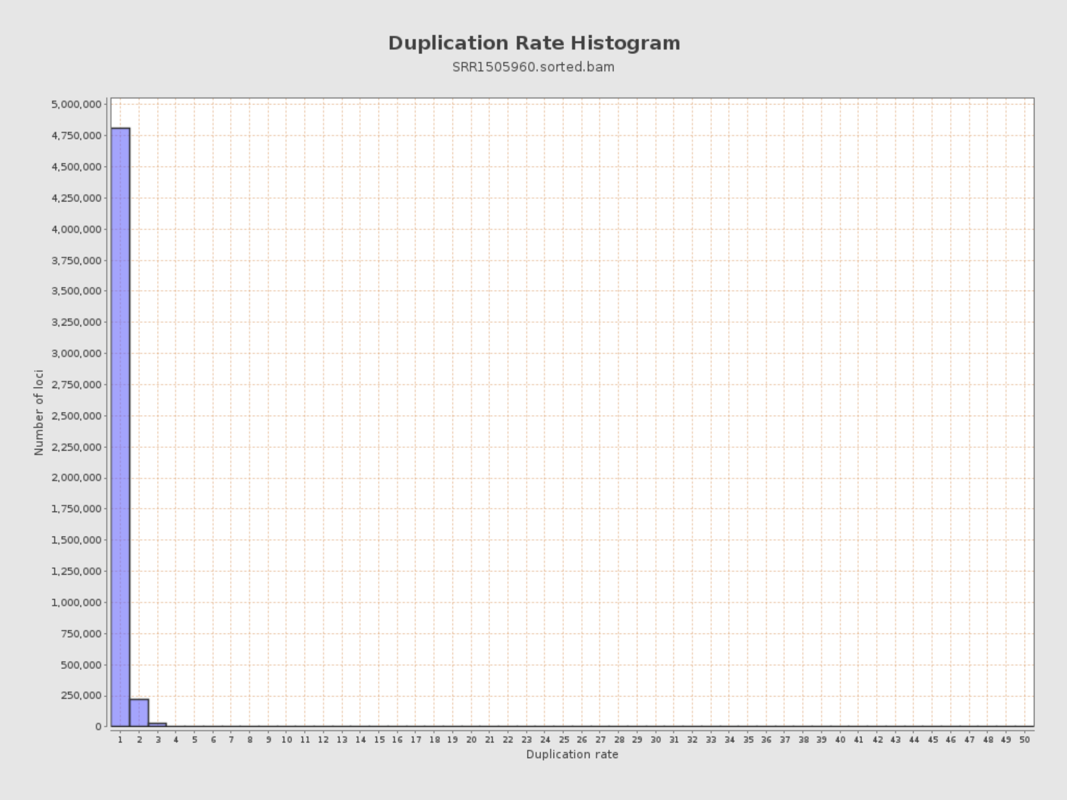
5. Results : Coverage Histogram (0-50X)



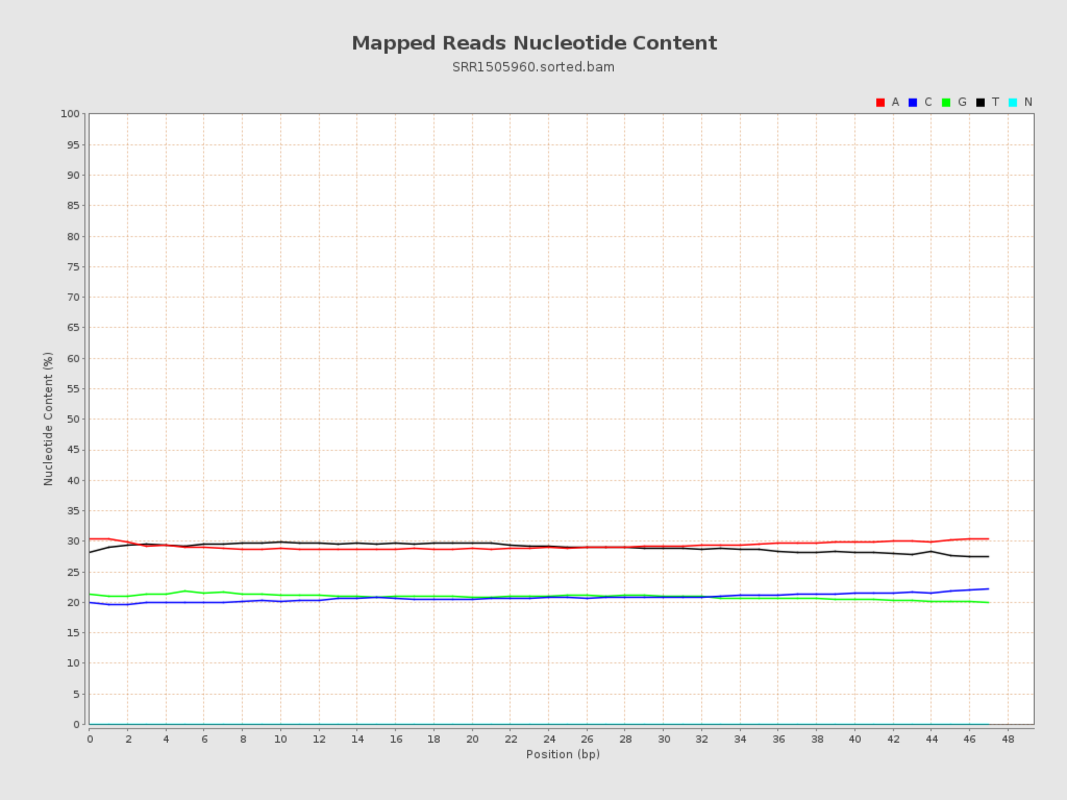
6. Results : Genome Fraction Coverage



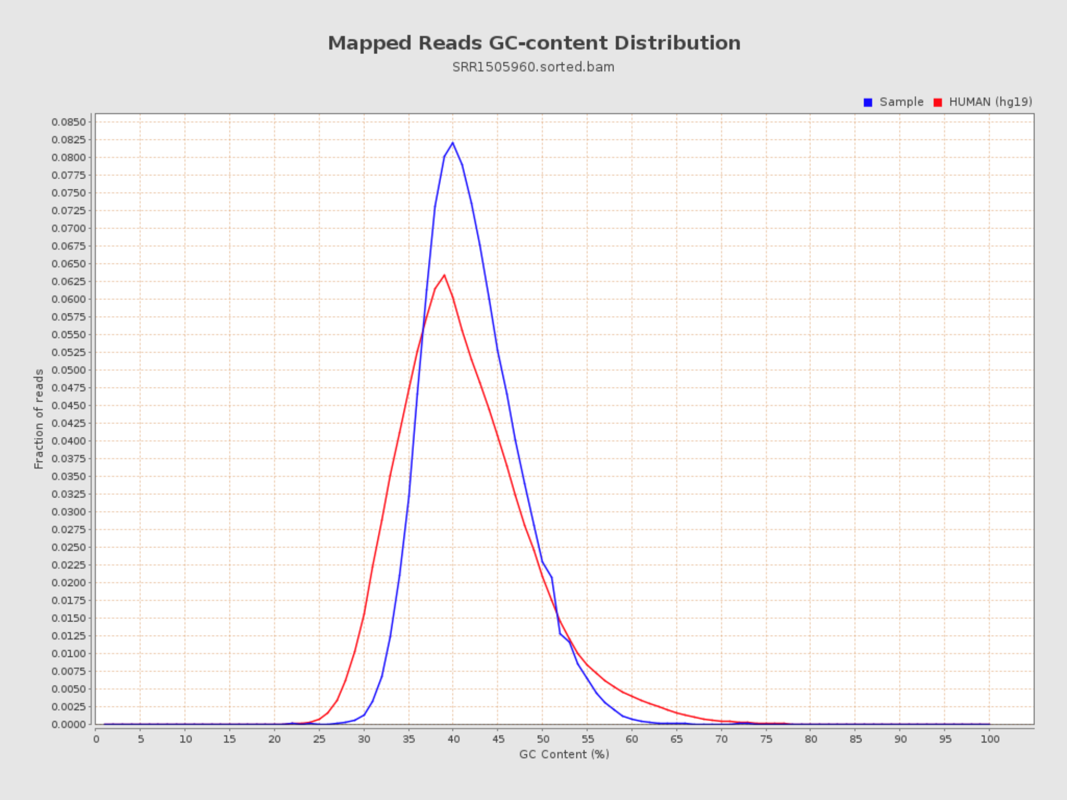
7. Results : Duplication Rate Histogram



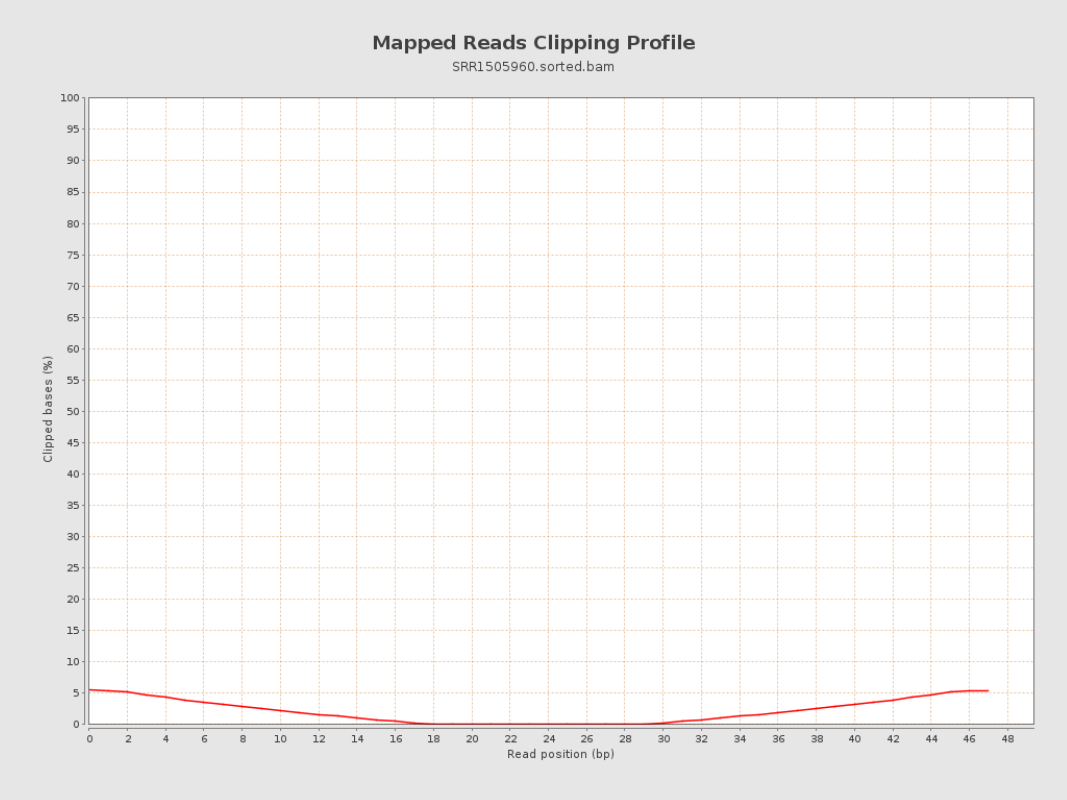
8. Results : Mapped Reads Nucleotide Content



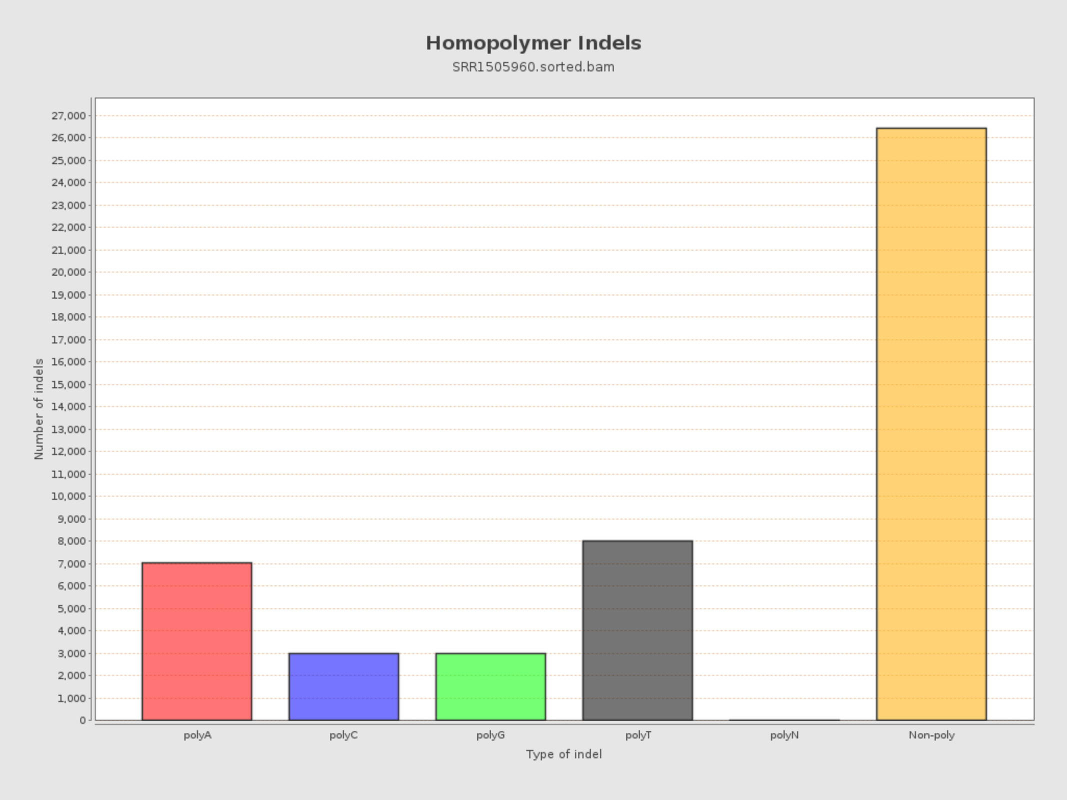
9. Results : Mapped Reads GC-content Distribution



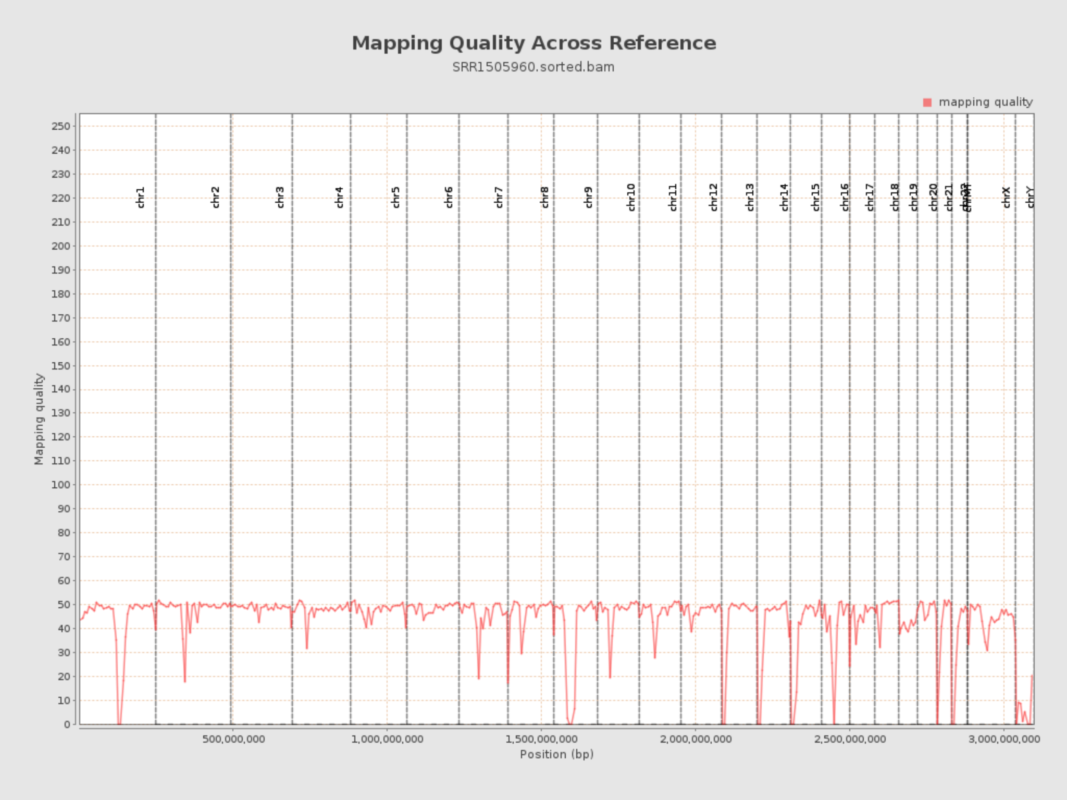
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram