Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:44:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505952.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_SRR1505952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:44:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,381,008
Mapped reads	4,556,865 / 71.41%
Unmapped reads	1,824,143 / 28.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	280 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	313,386 / 4.91%
Duplication rate	5.21%
Clipped reads	758,677 / 11.89%

2.2. ACGT Content

Number/percentage of A's	62,093,122 / 29.38%
Number/percentage of C's	44,129,779 / 20.88%
Number/percentage of T's	60,791,322 / 28.76%
Number/percentage of G's	44,329,187 / 20.97%
Number/percentage of N's	667 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0683

Standard Deviation	0.639

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

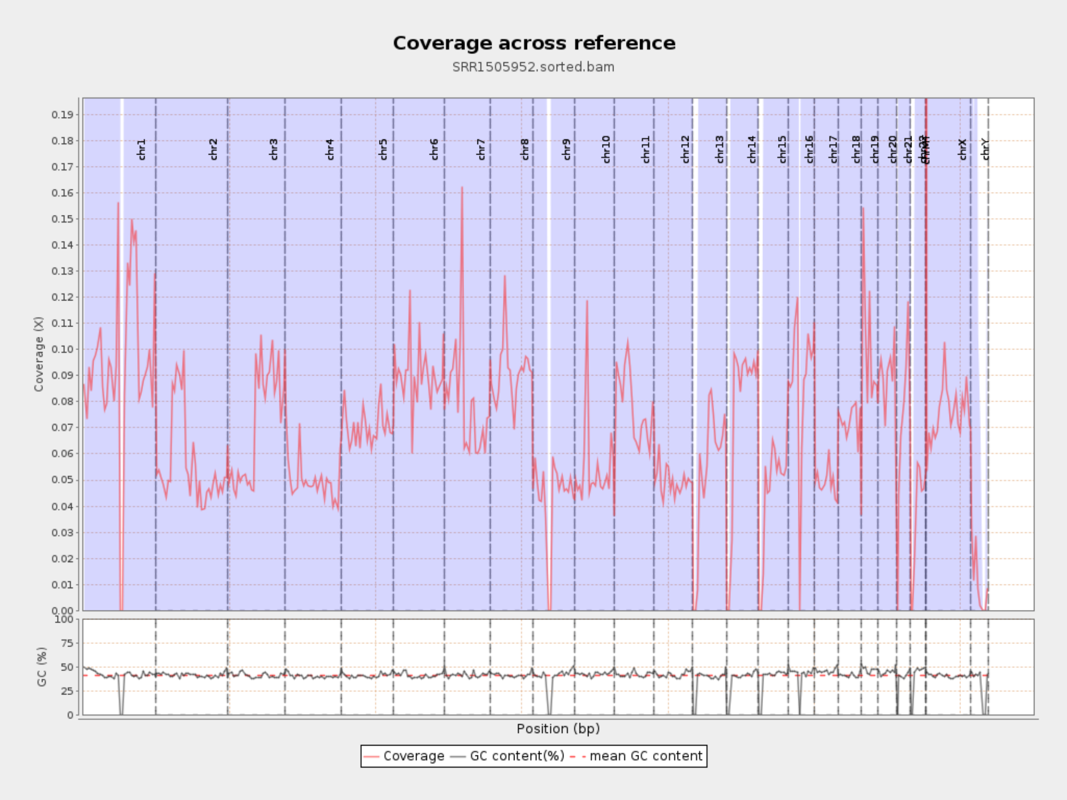
General error rate	0.51%
Mismatches	1,069,037
Insertions	9,308
Mapped reads with at least one insertion	0.2%
Deletions	30,947
Mapped reads with at least one deletion	0.68%
Homopolymer indels	45.6%

2.6. Chromosome stats

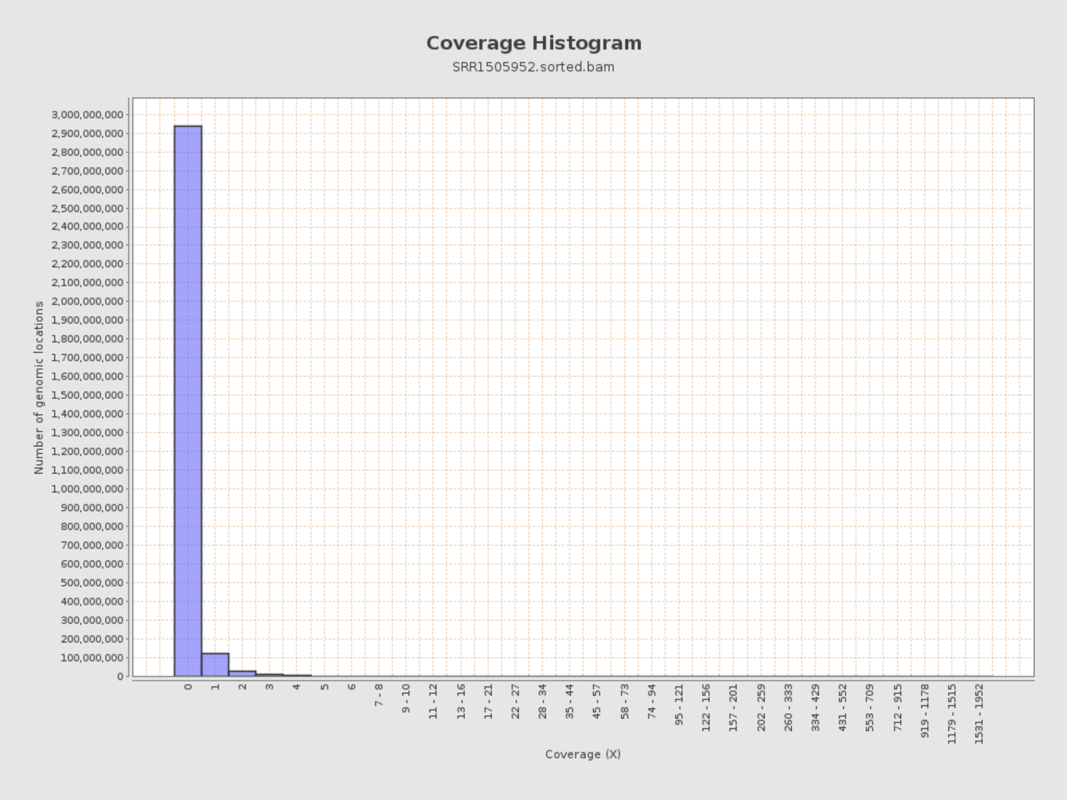
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23553994	0.0945	1.3564
chr2	243199373	13725041	0.0564	0.4574
chr3	198022430	13962977	0.0705	0.3419
chr4	191154276	9558095	0.05	0.2965
chr5	180915260	12769783	0.0706	0.3455
chr6	171115067	15452355	0.0903	0.4907
chr7	159138663	12738686	0.08	1.1288

chr8	146364022	13329657	0.0911	0.8826
chr9	141213431	6112180	0.0433	0.3947
chr10	135534747	7374983	0.0544	0.5696
chr11	135006516	10511658	0.0779	0.6098
chr12	133851895	6637245	0.0496	0.3051
chr13	115169878	6265848	0.0544	0.2941
chr14	107349540	8223912	0.0766	0.3664
chr15	102531392	4529563	0.0442	0.2638
chr16	90354753	7793984	0.0863	0.4096
chr17	81195210	4009826	0.0494	0.3335
chr18	78077248	5672905	0.0727	0.731
chr19	59128983	5854775	0.099	1.0078
chr20	63025520	5668960	0.0899	0.3939
chr21	48129895	3461352	0.0719	0.3787
chr22	51304566	1822759	0.0355	0.2375
chrMT	16571	22164	1.3375	1.721
chrX	155270560	11720961	0.0755	0.4143
chrY	59373566	613162	0.0103	0.1666

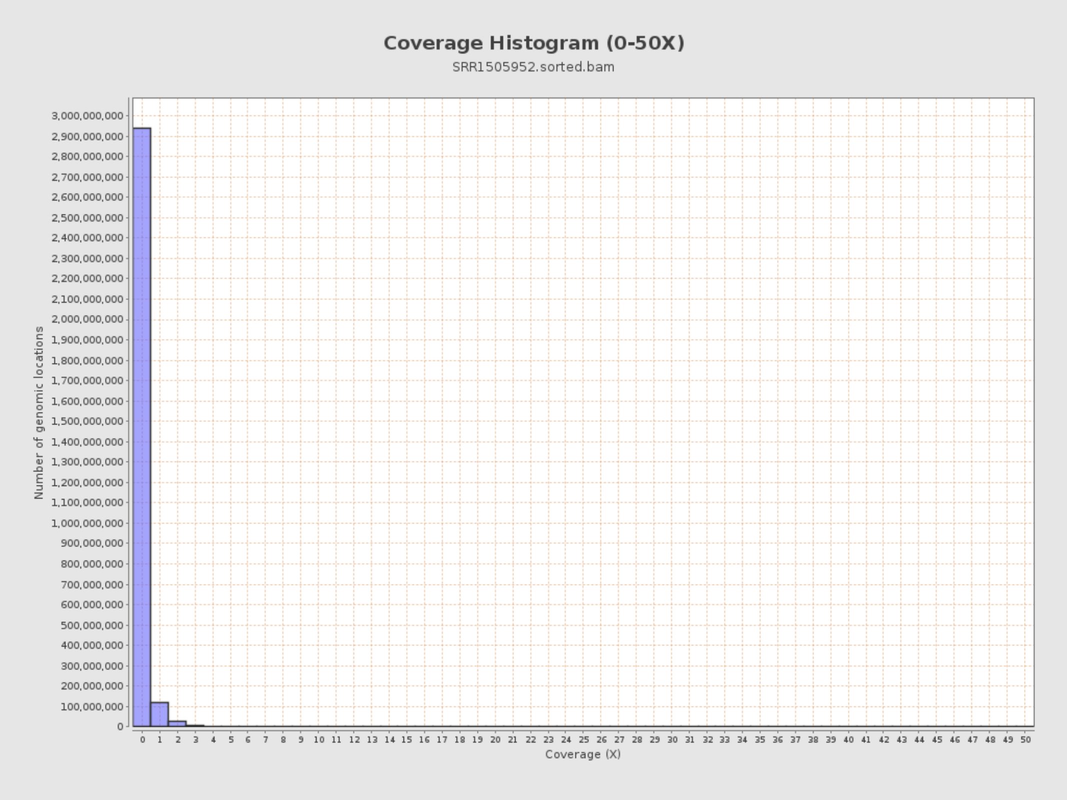
3. Results : Coverage across reference



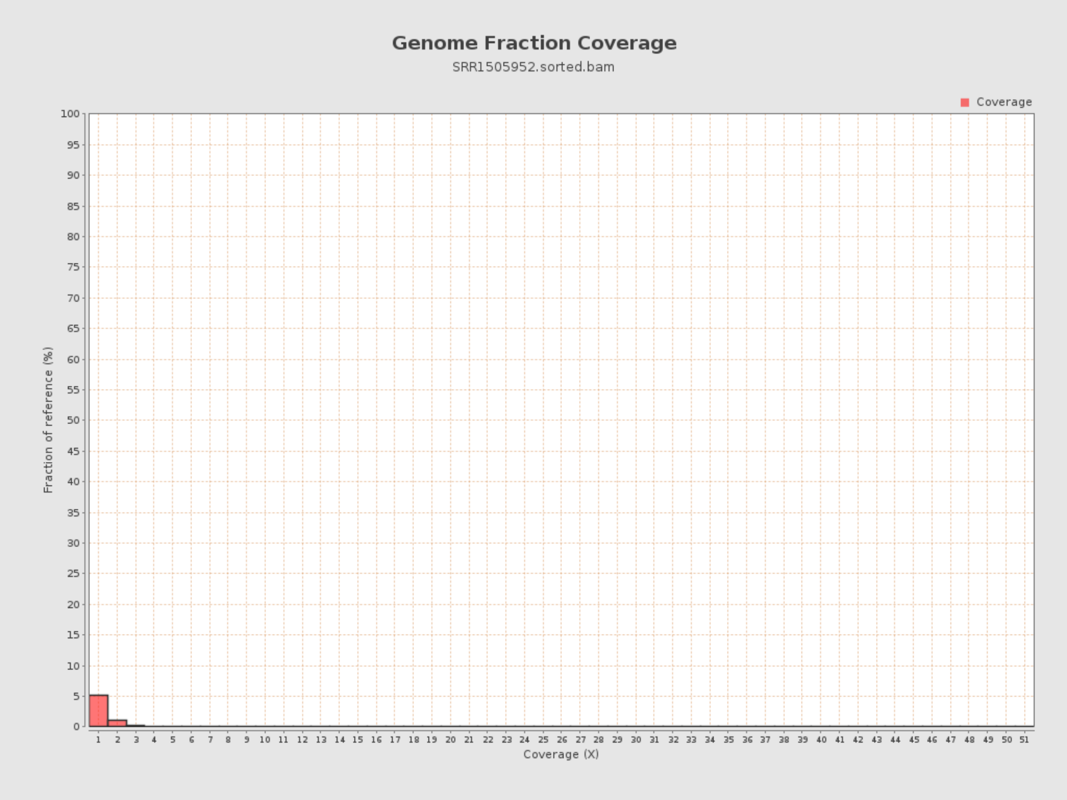
4. Results : Coverage Histogram



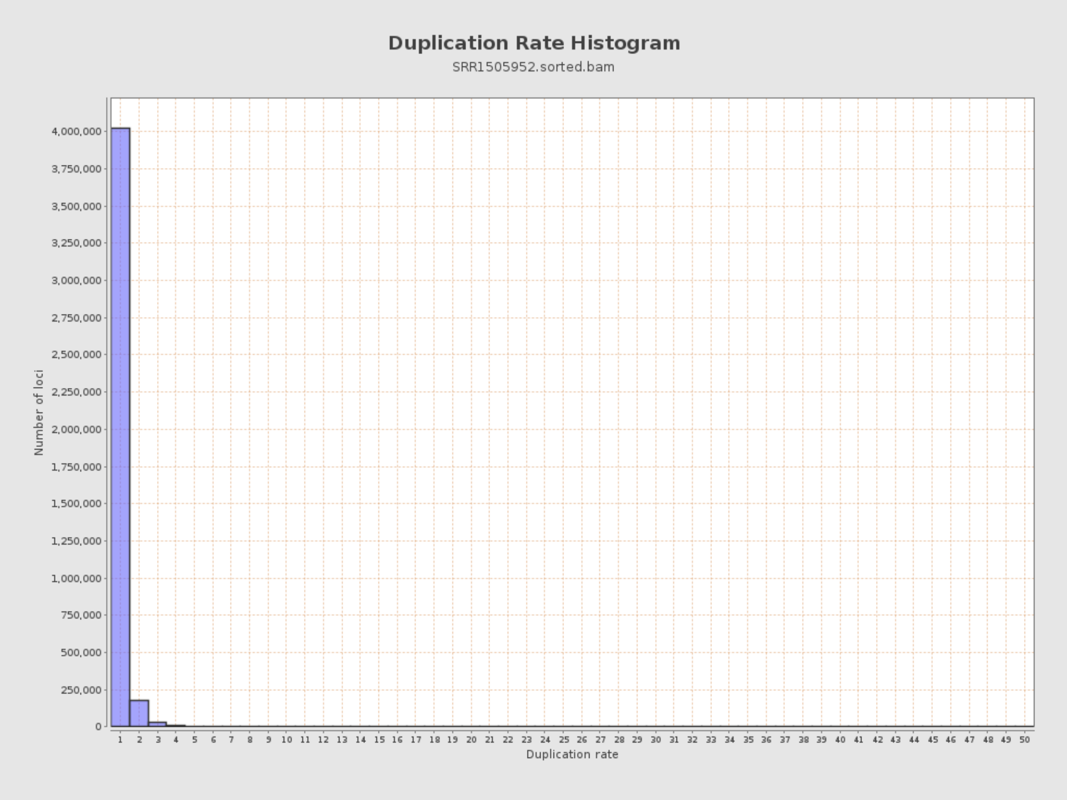
5. Results : Coverage Histogram (0-50X)



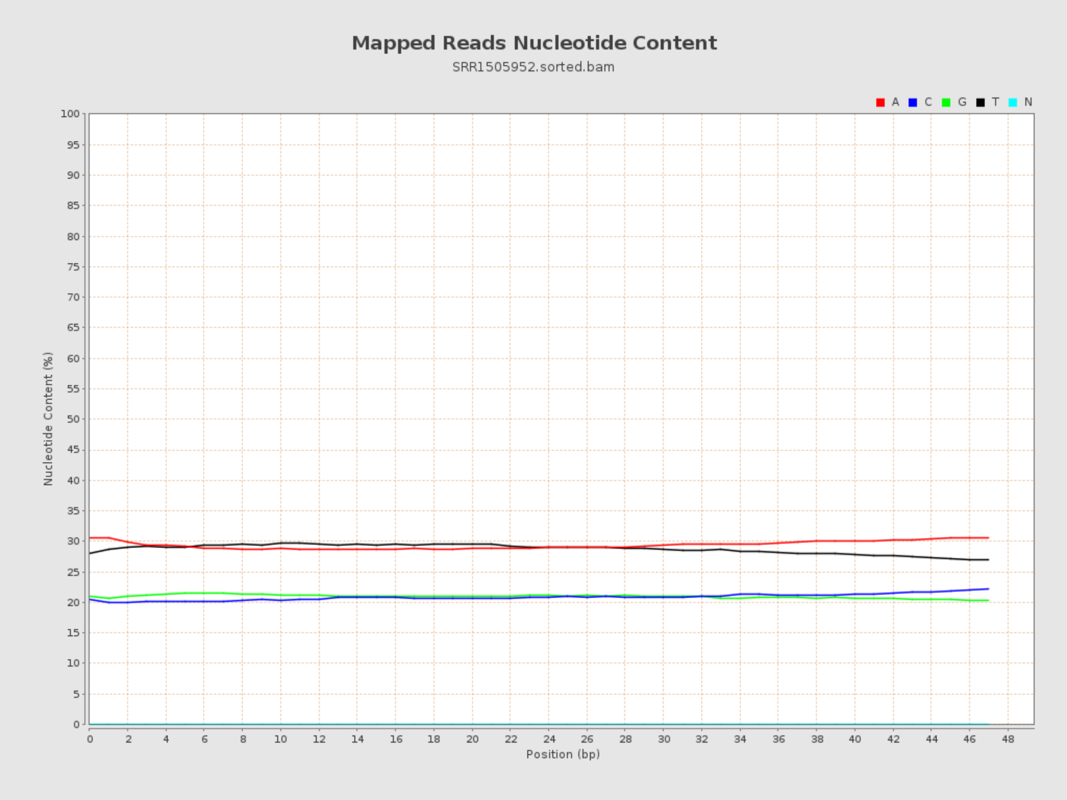
6. Results : Genome Fraction Coverage



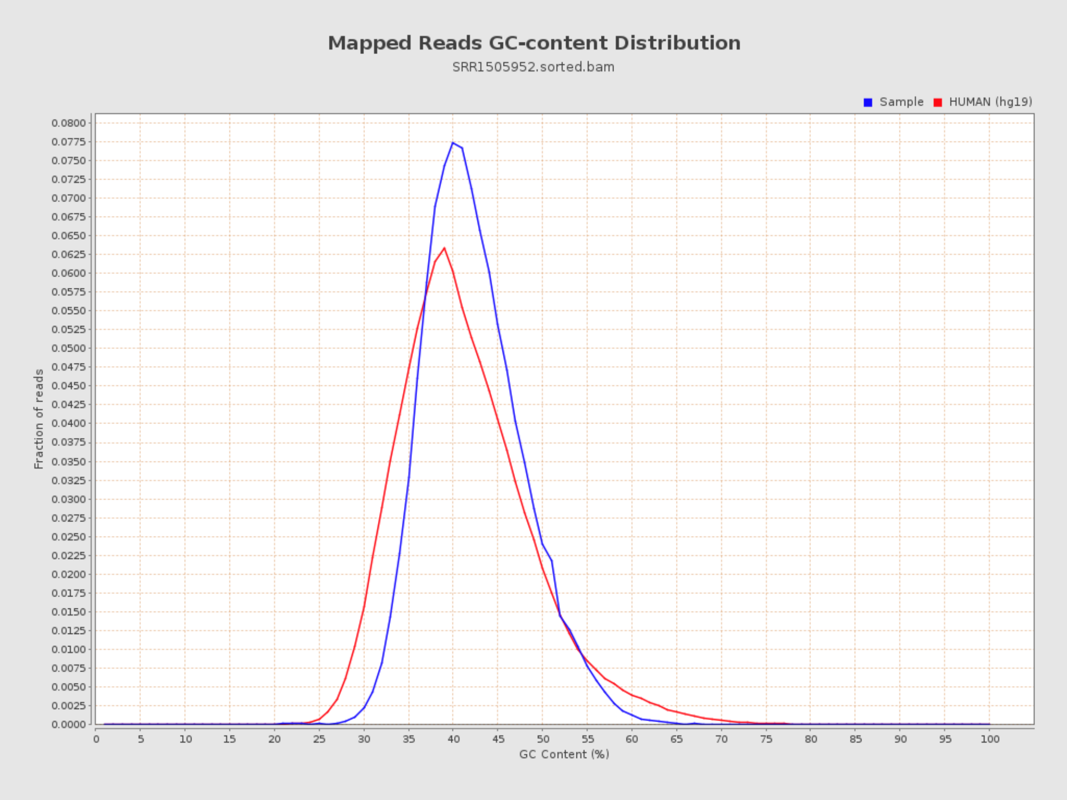
7. Results : Duplication Rate Histogram



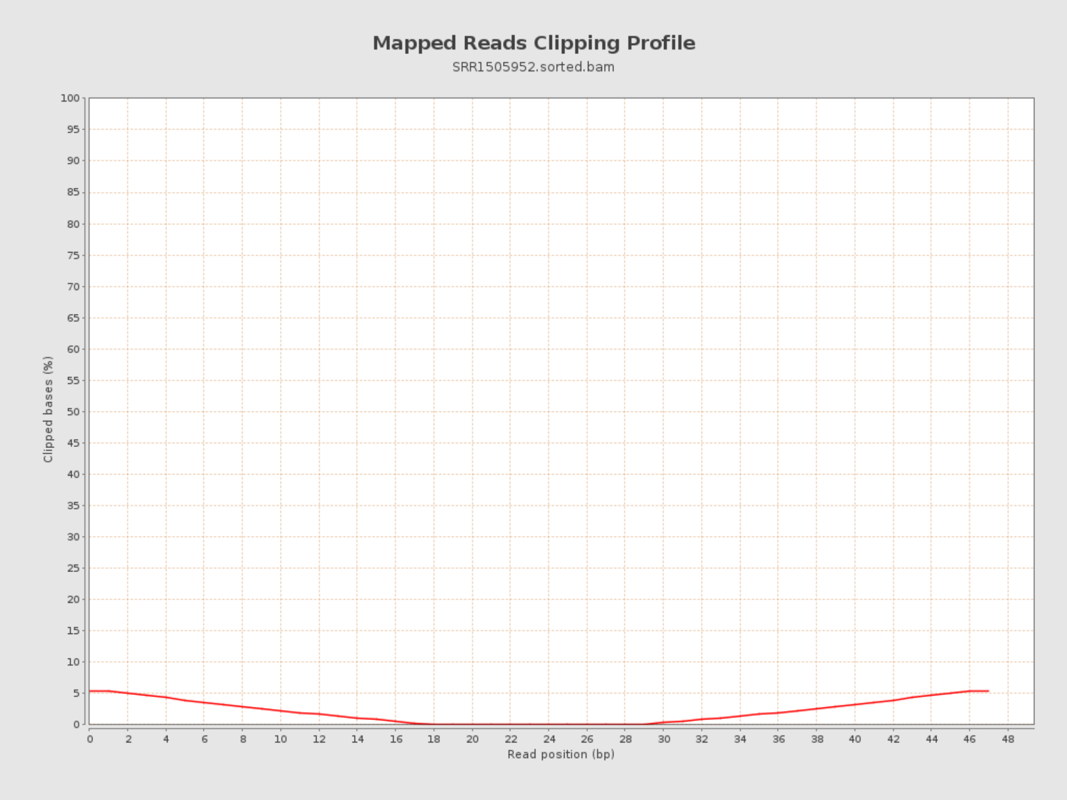
8. Results : Mapped Reads Nucleotide Content



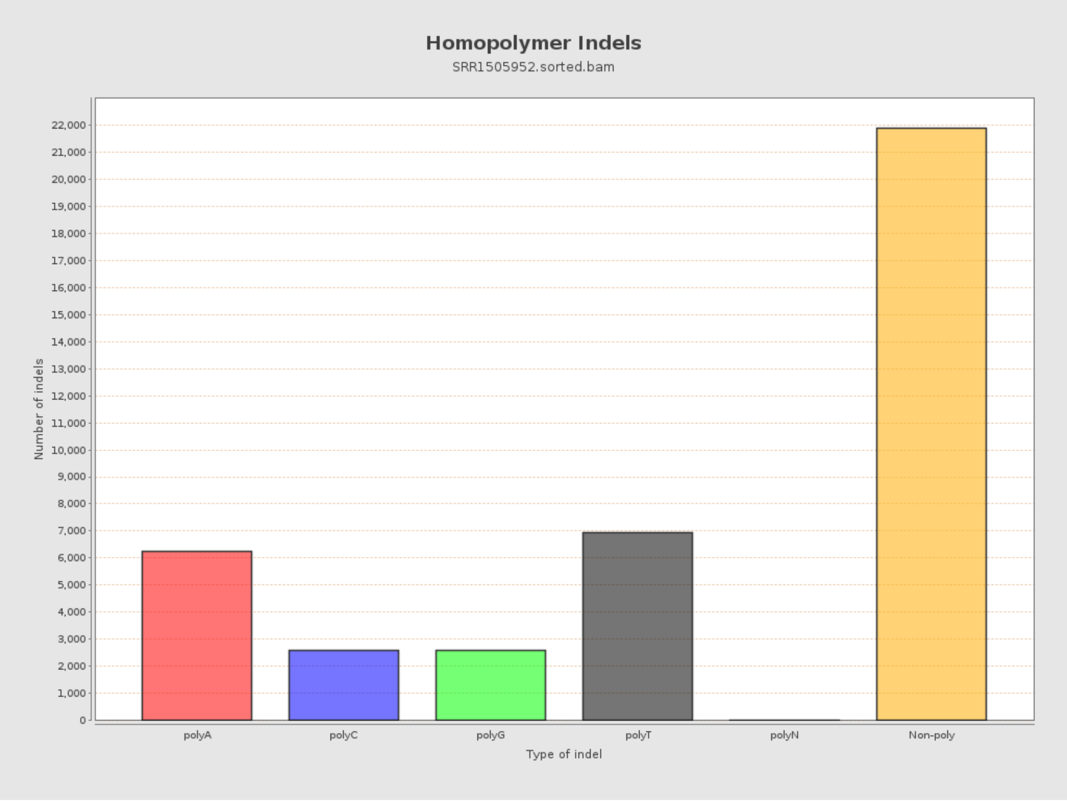
9. Results : Mapped Reads GC-content Distribution



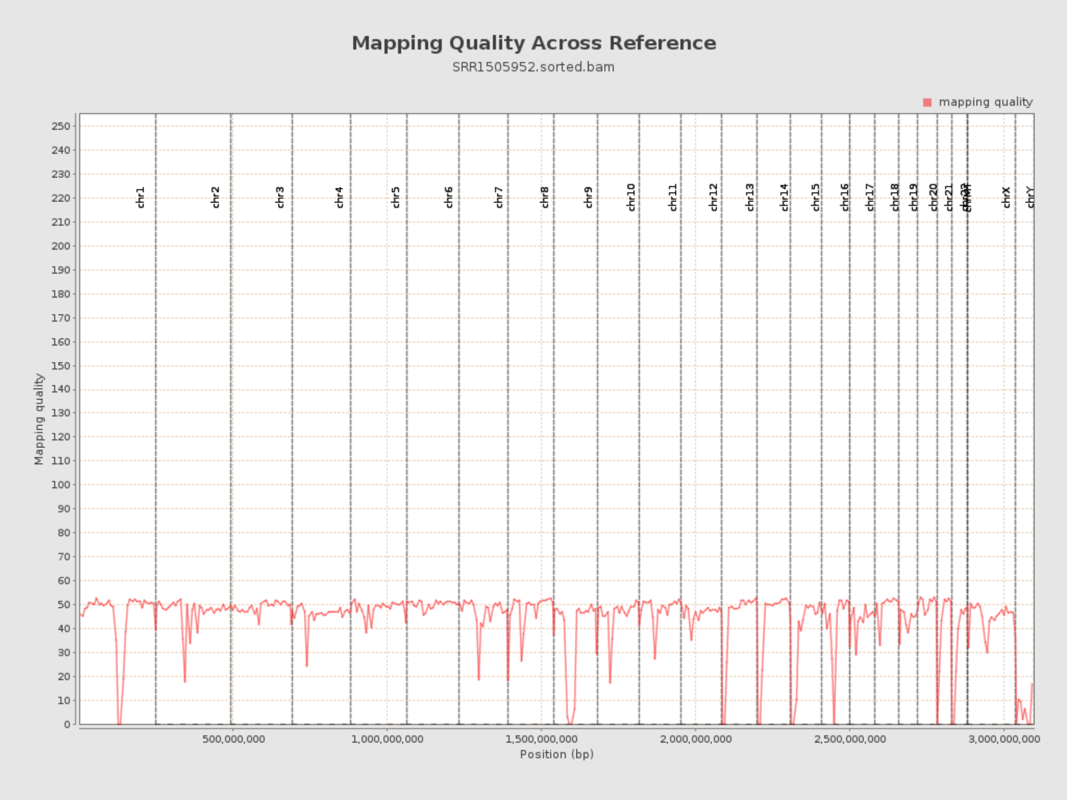
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram