Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:11:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004158.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_SRR6004158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:11:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,023,085
Mapped reads	1,790,782 / 88.52%
Unmapped reads	232,303 / 11.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,741 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	79,050 / 3.91%
Duplication rate	3.55%
Clipped reads	867,670 / 42.89%

2.2. ACGT Content

Number/percentage of A's	33,383,065 / 28.32%
Number/percentage of C's	21,353,273 / 18.12%
Number/percentage of T's	37,786,653 / 32.06%
Number/percentage of G's	25,331,242 / 21.49%
Number/percentage of N's	9,034 / 0.01%
GC Percentage	39.61%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3529

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

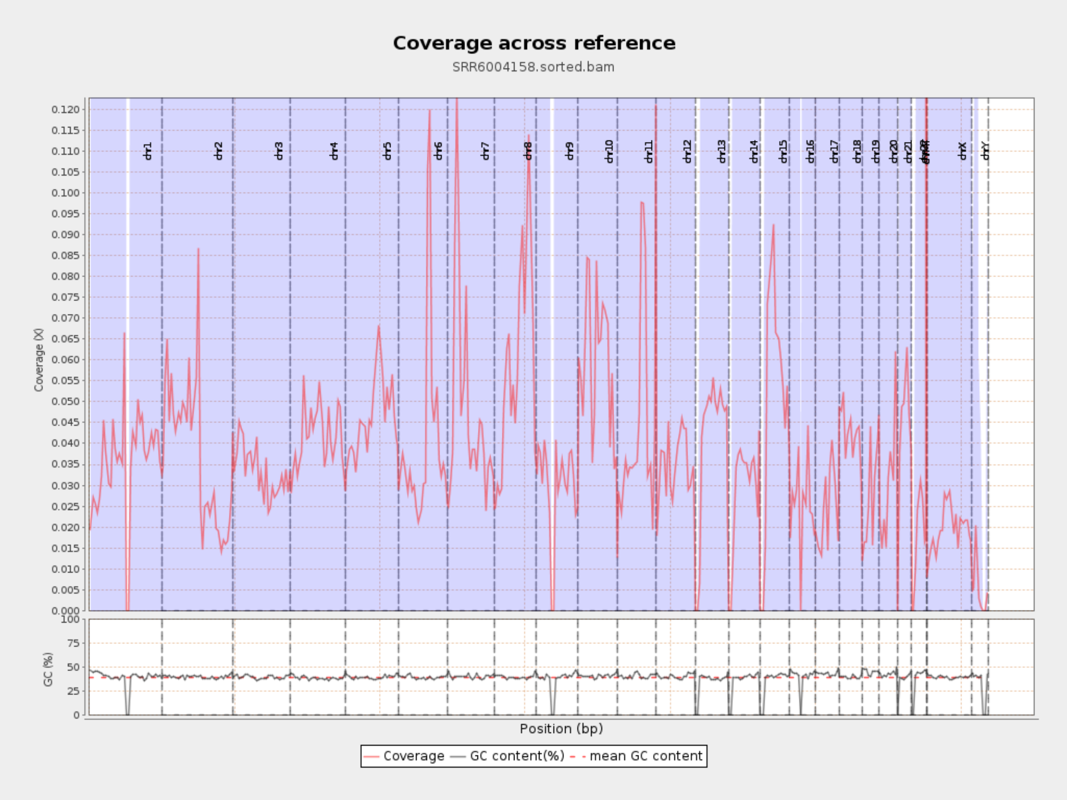
General error rate	0.98%
Mismatches	1,136,451
Insertions	9,043
Mapped reads with at least one insertion	0.5%
Deletions	46,688
Mapped reads with at least one deletion	2.57%
Homopolymer indels	43.69%

2.6. Chromosome stats

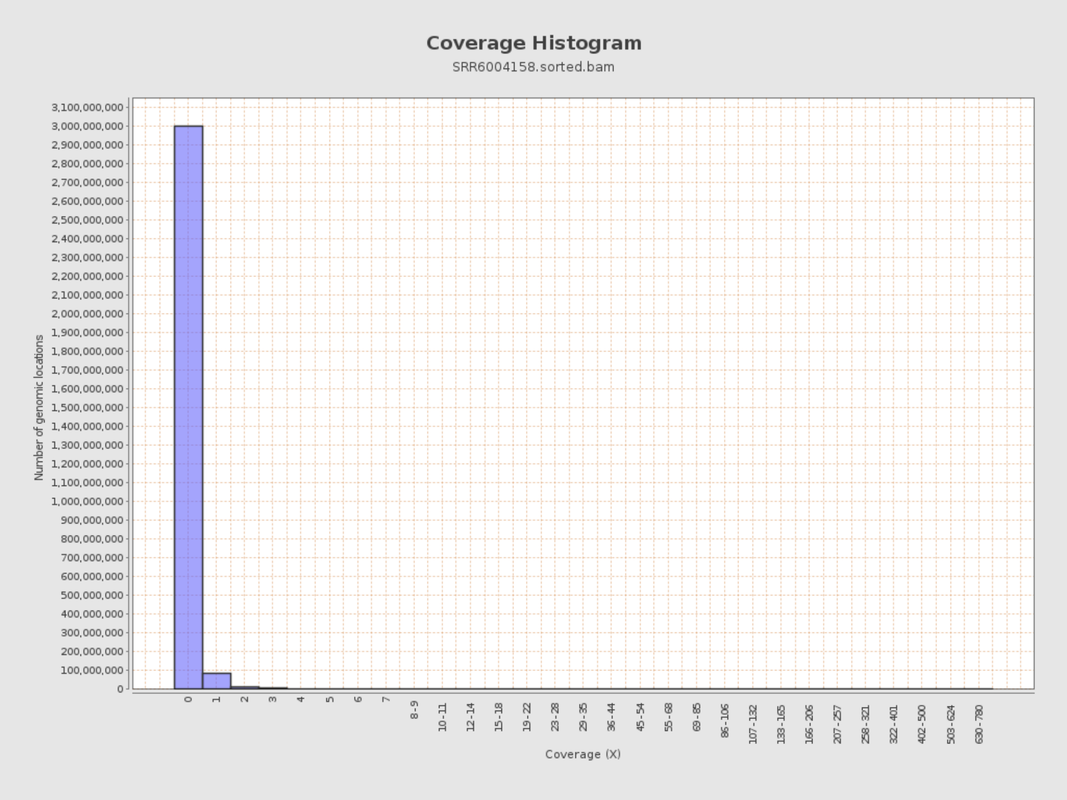
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8821587	0.0354	0.6791
chr2	243199373	9154270	0.0376	0.313
chr3	198022430	6609247	0.0334	0.2098
chr4	191154276	7951191	0.0416	0.2555
chr5	180915260	8414323	0.0465	0.2506
chr6	171115067	6957384	0.0407	0.2395
chr7	159138663	7789101	0.0489	0.5451

chr8	146364022	8771597	0.0599	0.5016
chr9	141213431	4195676	0.0297	0.2846
chr10	135534747	8132449	0.06	0.3998
chr11	135006516	5909781	0.0438	0.2956
chr12	133851895	4626378	0.0346	0.2181
chr13	115169878	4660299	0.0405	0.23
chr14	107349540	3029810	0.0282	0.2092
chr15	102531392	5439790	0.0531	0.2641
chr16	90354753	2296172	0.0254	0.2157
chr17	81195210	1957564	0.0241	0.1891
chr18	78077248	3340323	0.0428	0.4887
chr19	59128983	1606600	0.0272	0.4314
chr20	63025520	1944524	0.0309	0.2089
chr21	48129895	2098741	0.0436	0.2636
chr22	51304566	869575	0.0169	0.1462
chrMT	16571	53027	3.2	2.6824
chrX	155270560	3027152	0.0195	0.1823
chrY	59373566	286922	0.0048	0.1451

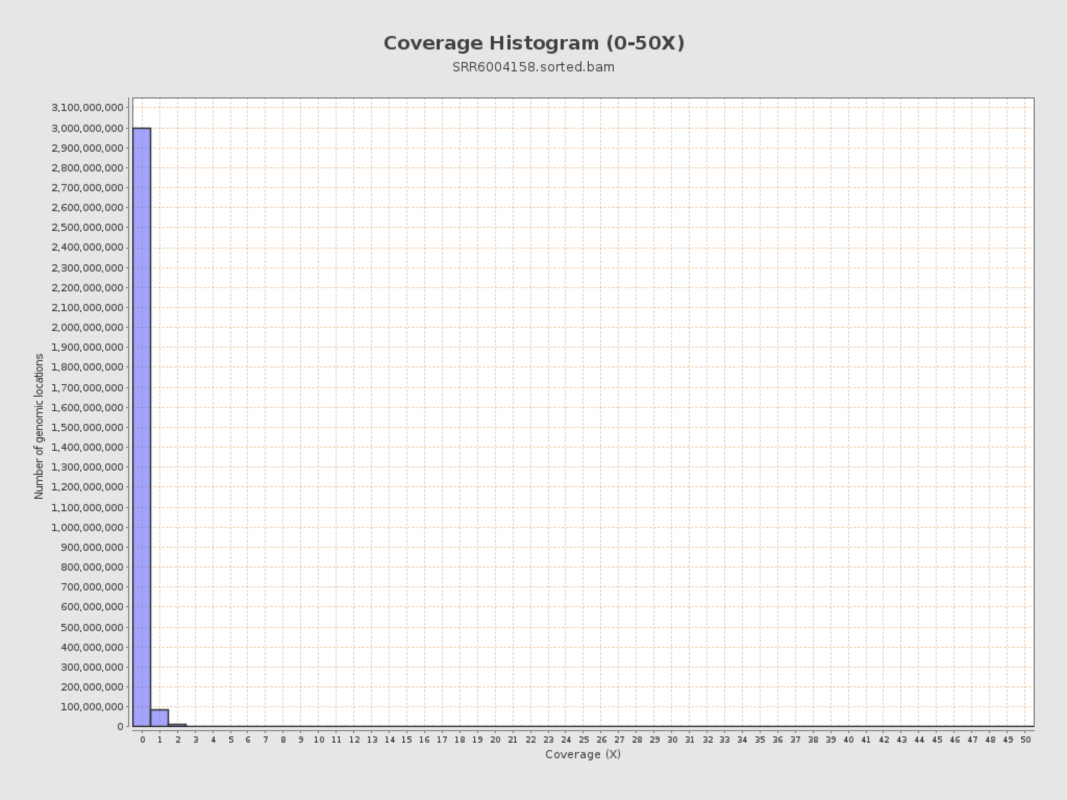
3. Results : Coverage across reference



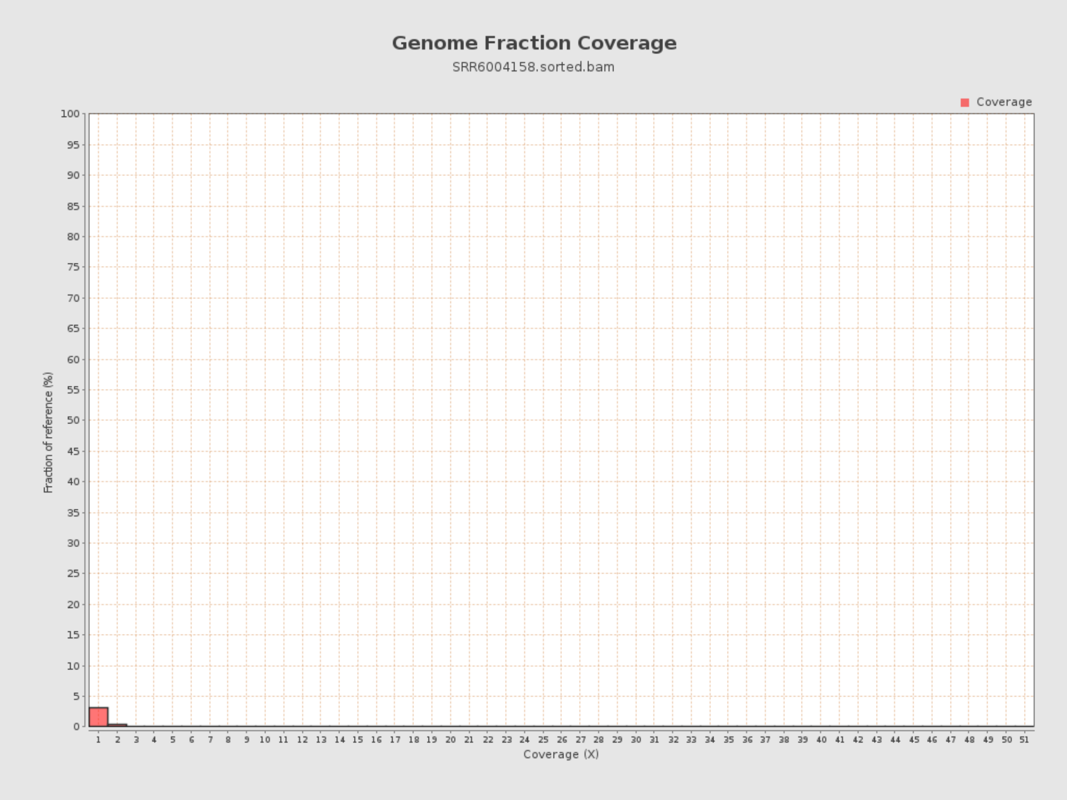
4. Results : Coverage Histogram



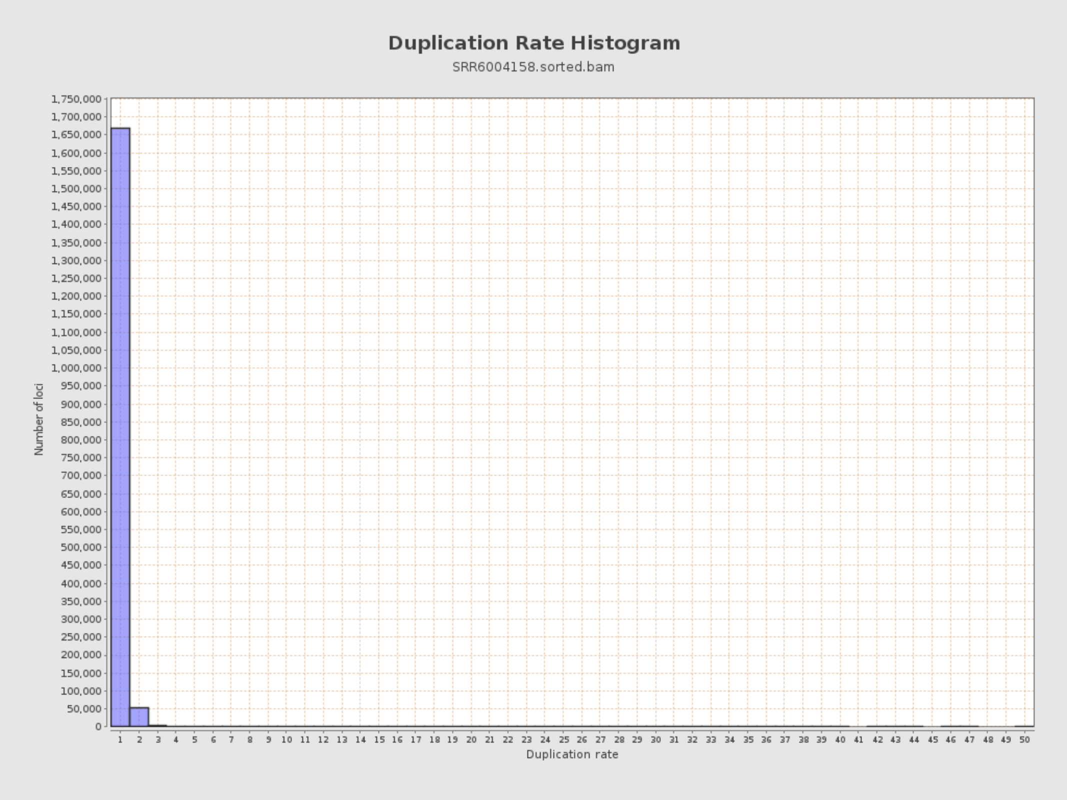
5. Results : Coverage Histogram (0-50X)



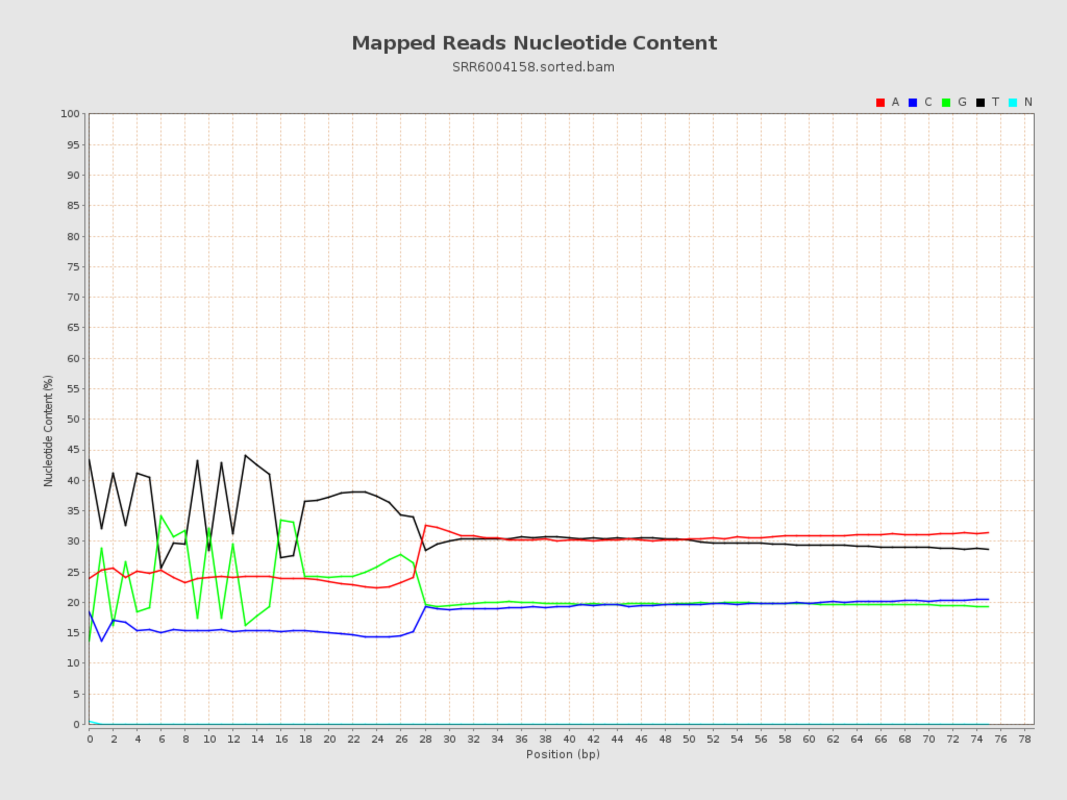
6. Results : Genome Fraction Coverage



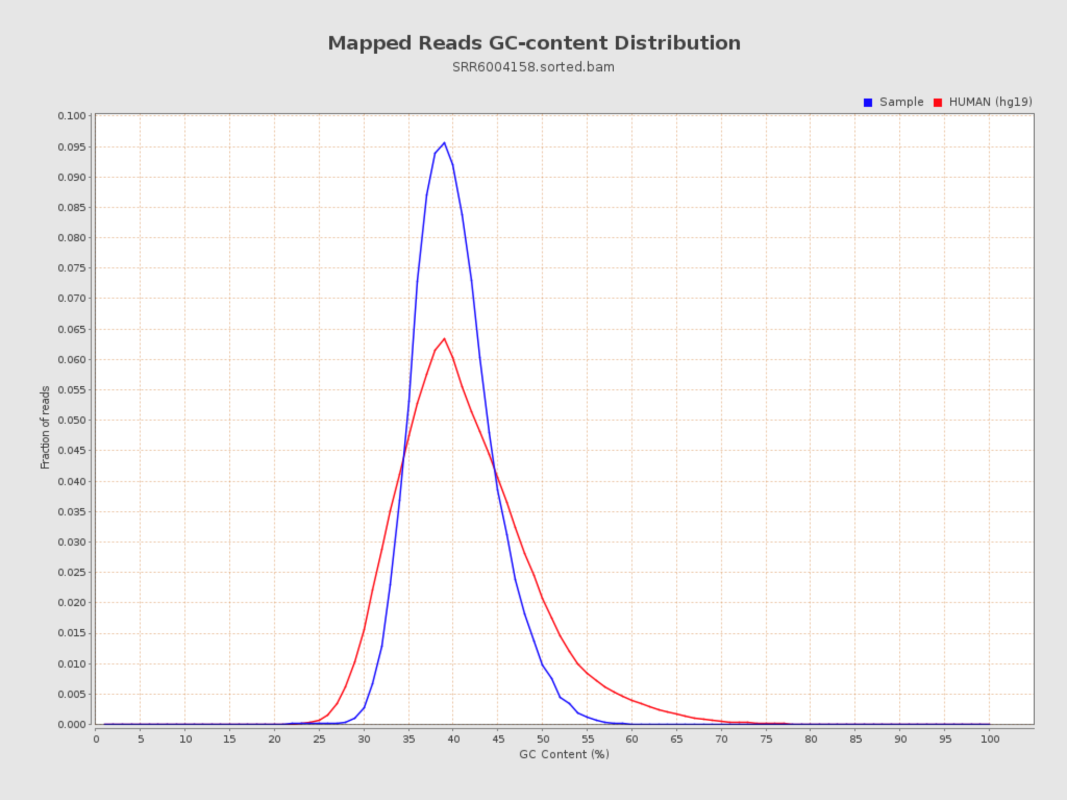
7. Results : Duplication Rate Histogram



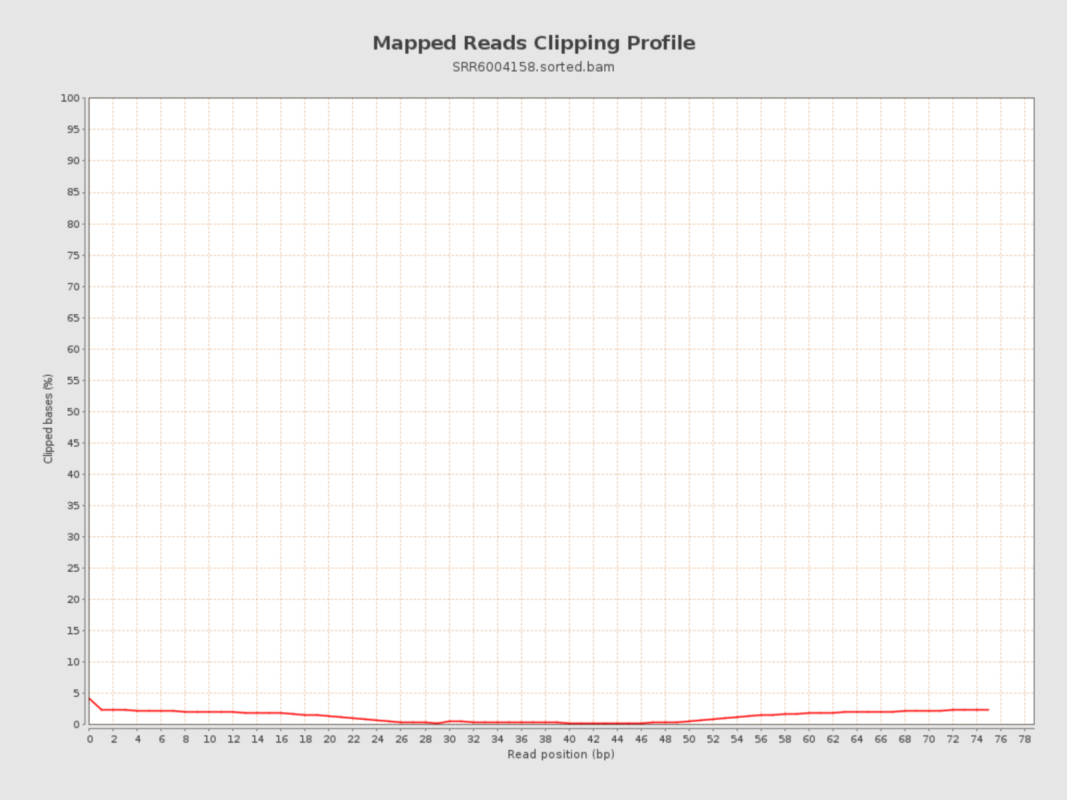
8. Results : Mapped Reads Nucleotide Content



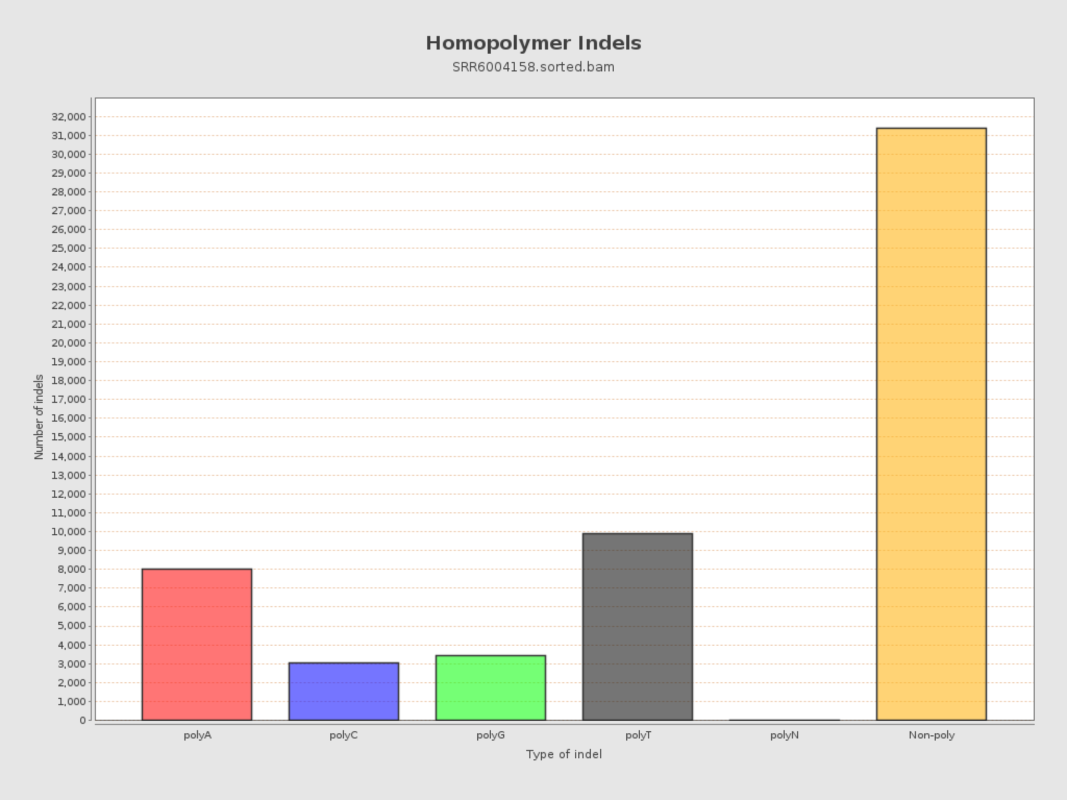
9. Results : Mapped Reads GC-content Distribution



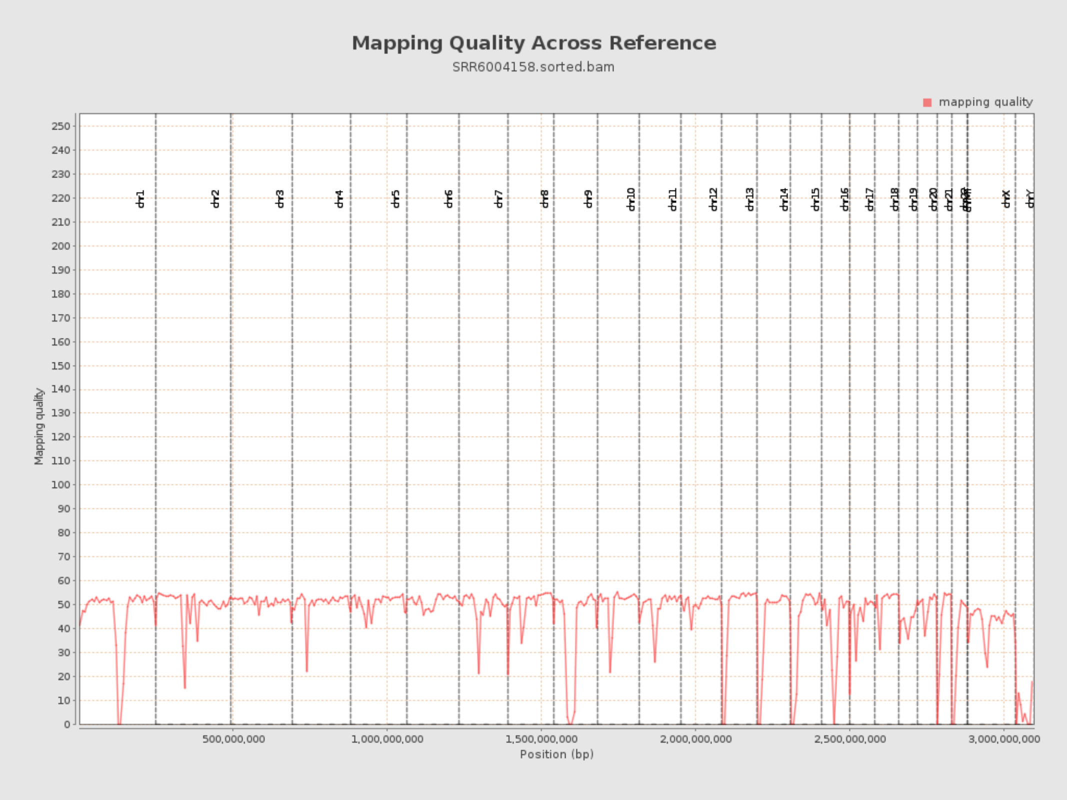
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram