Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:50:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230350.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_SRR6230350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230350.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:50:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230350.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,291,193
Mapped reads	1,822,330 / 79.54%
Unmapped reads	468,863 / 20.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,285 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	96,385 / 4.21%
Duplication rate	4.23%
Clipped reads	990,621 / 43.24%

2.2. ACGT Content

Number/percentage of A's	30,536,331 / 26.15%
Number/percentage of C's	19,988,864 / 17.12%
Number/percentage of T's	38,955,601 / 33.36%
Number/percentage of G's	27,061,392 / 23.18%
Number/percentage of N's	214,641 / 0.18%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3451

2.4. Mapping Quality

Mean Mapping Quality	46.66

2.5. Mismatches and indels

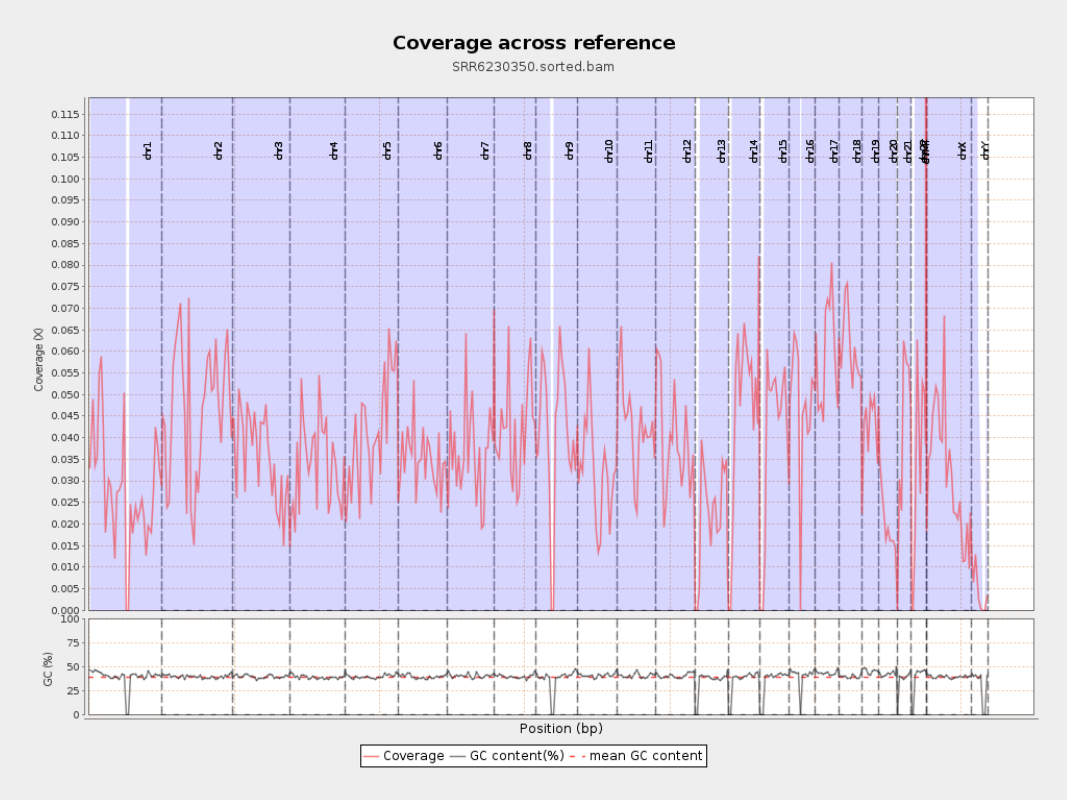
General error rate	0.91%
Mismatches	1,050,977
Insertions	9,845
Mapped reads with at least one insertion	0.54%
Deletions	29,038
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.32%

2.6. Chromosome stats

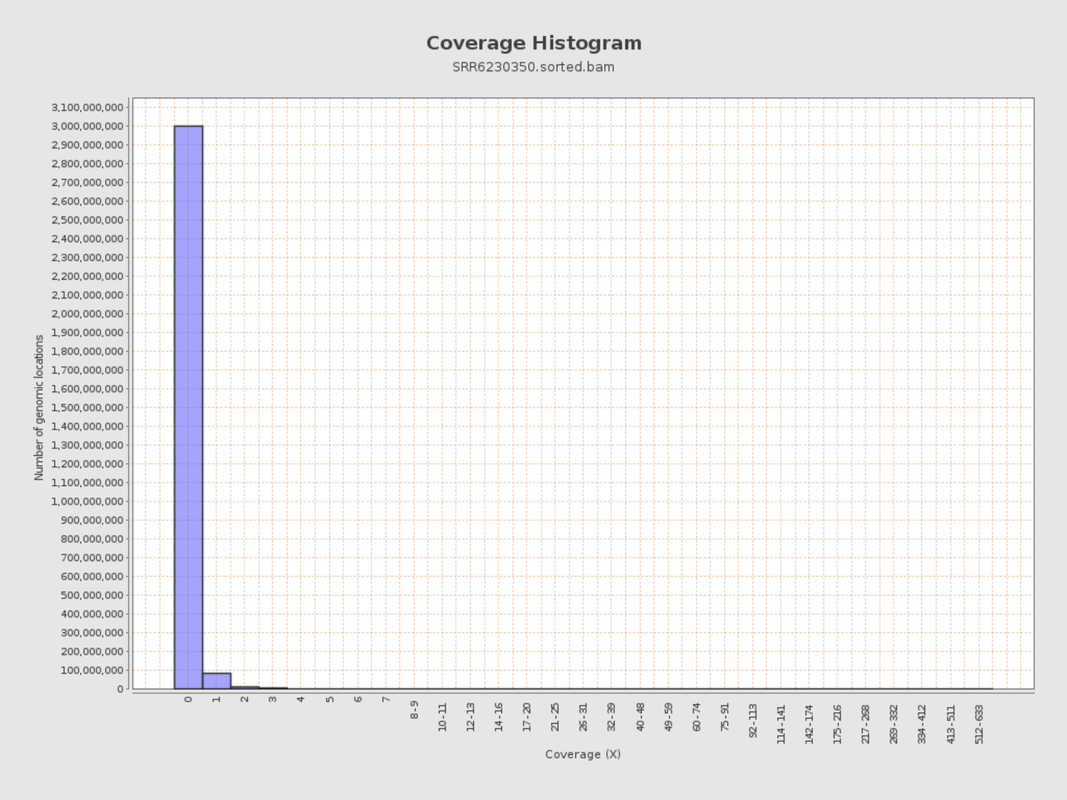
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7035474	0.0282	0.531
chr2	243199373	11439214	0.047	0.4586
chr3	198022430	7113301	0.0359	0.2203
chr4	191154276	6460762	0.0338	0.224
chr5	180915260	7474289	0.0413	0.2356
chr6	171115067	5974416	0.0349	0.3016
chr7	159138663	5806169	0.0365	0.4856

chr8	146364022	6160905	0.0421	0.3565
chr9	141213431	5744088	0.0407	0.3769
chr10	135534747	4293887	0.0317	0.2835
chr11	135006516	5780490	0.0428	0.3393
chr12	133851895	5237607	0.0391	0.2357
chr13	115169878	2588189	0.0225	0.1733
chr14	107349540	4901560	0.0457	0.2622
chr15	102531392	4137420	0.0404	0.232
chr16	90354753	4308056	0.0477	0.283
chr17	81195210	4839730	0.0596	0.3071
chr18	78077248	4773495	0.0611	0.6193
chr19	59128983	2536864	0.0429	0.4336
chr20	63025520	1261192	0.02	0.1737
chr21	48129895	2004941	0.0417	0.2518
chr22	51304566	1706977	0.0333	0.2108
chrMT	16571	97578	5.8885	6.2387
chrX	155270560	4875713	0.0314	0.263
chrY	59373566	251349	0.0042	0.1055

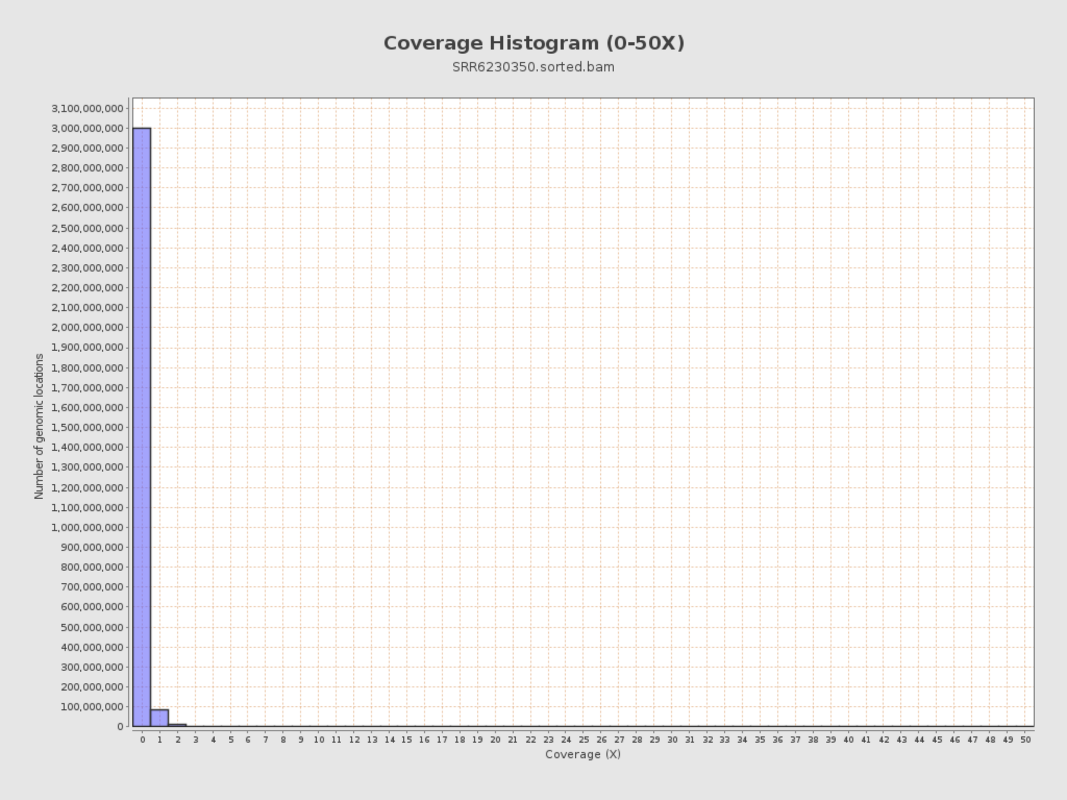
3. Results : Coverage across reference



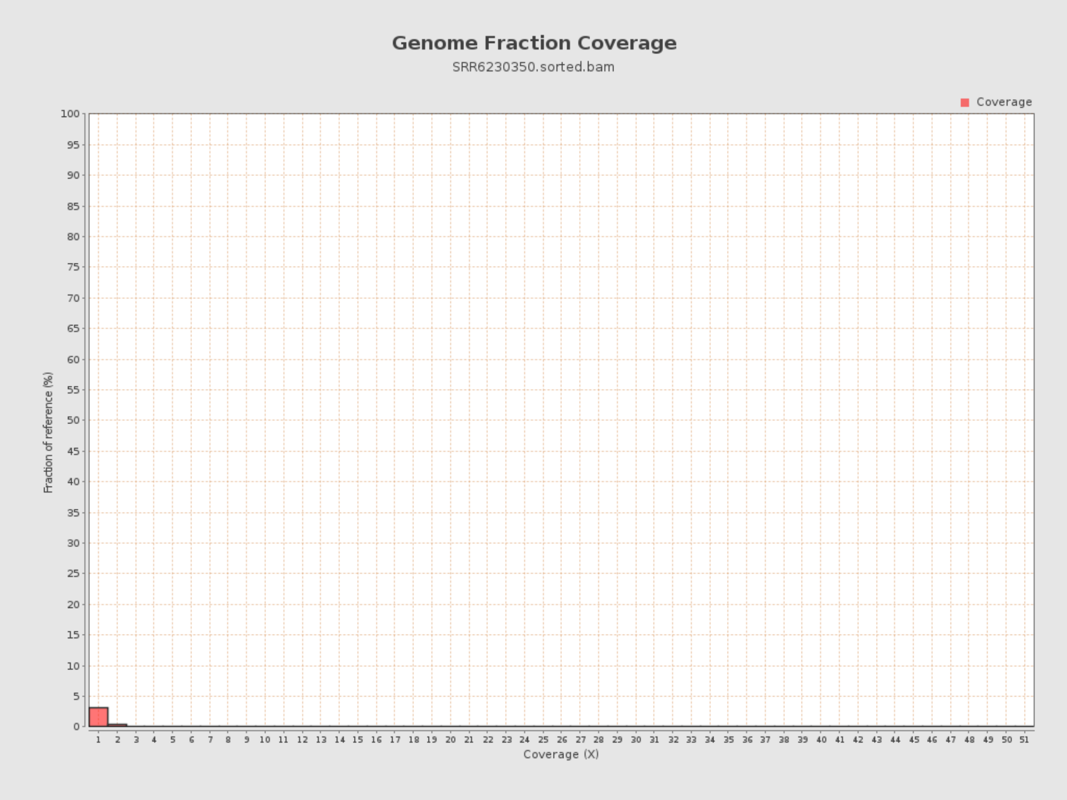
4. Results : Coverage Histogram



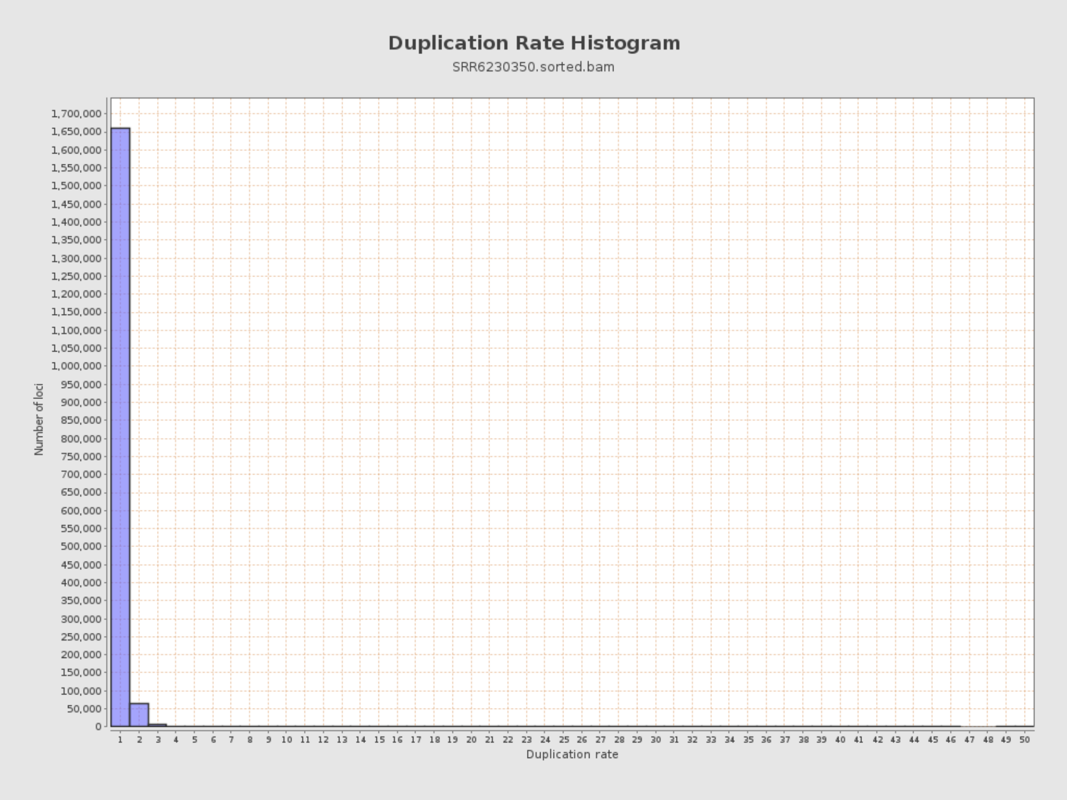
5. Results : Coverage Histogram (0-50X)



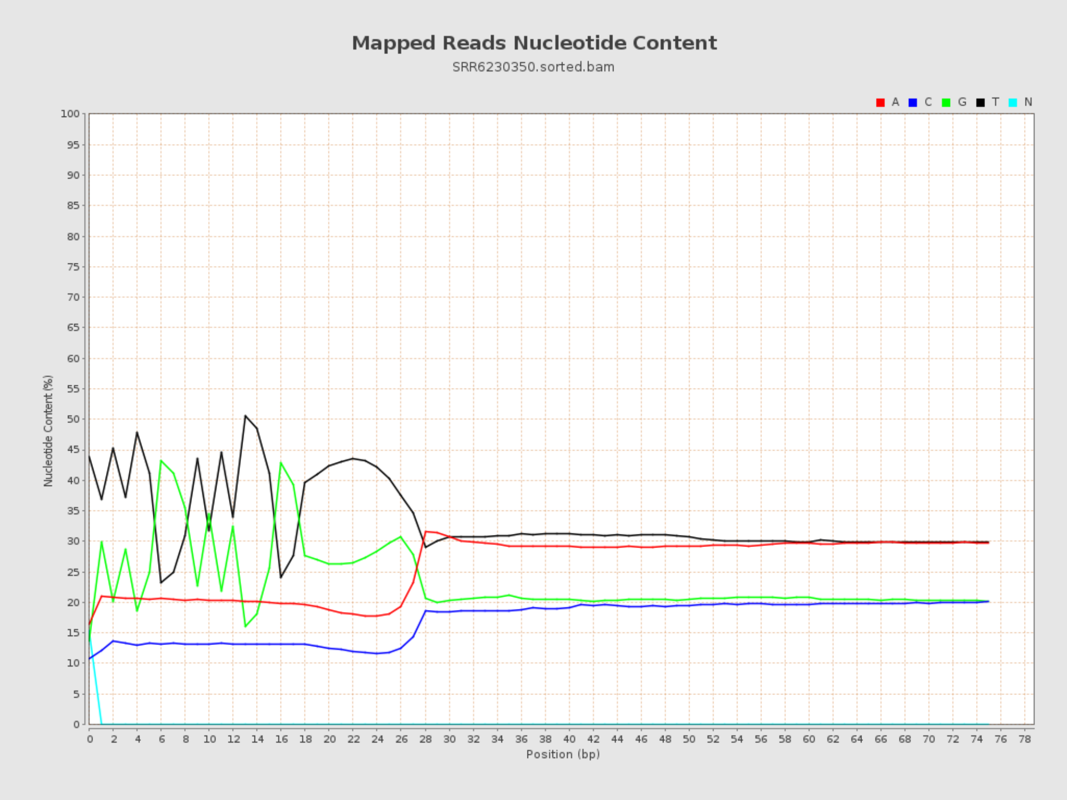
6. Results : Genome Fraction Coverage



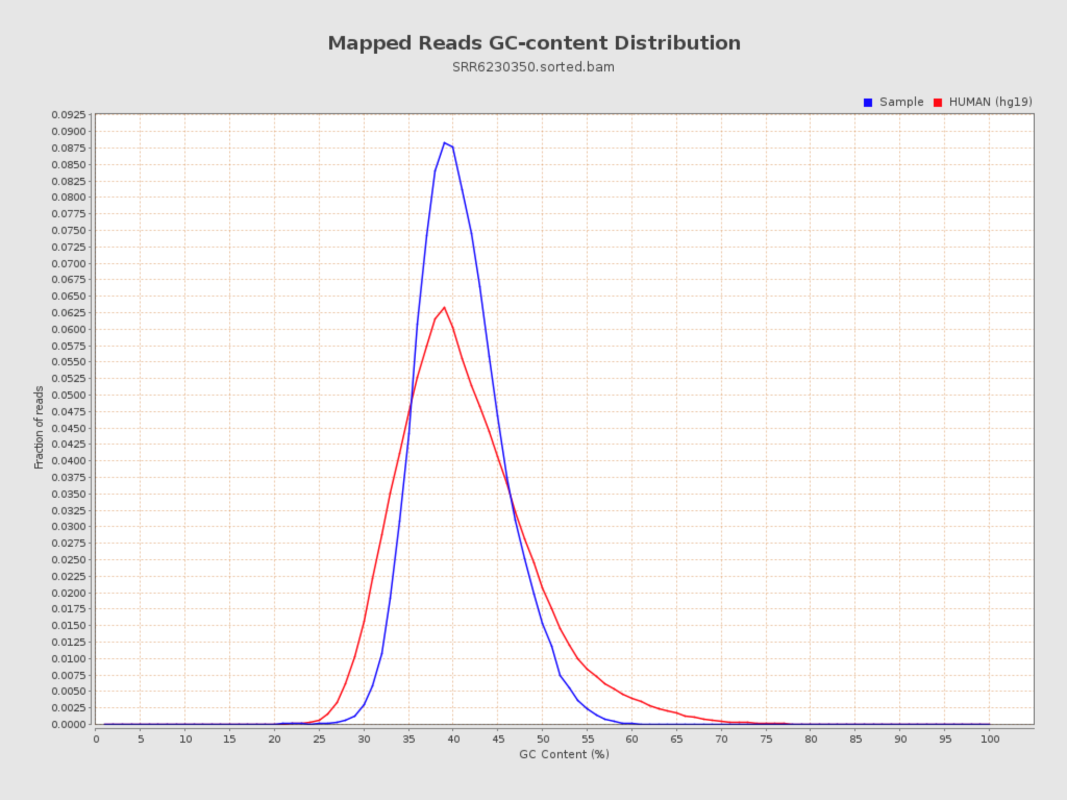
7. Results : Duplication Rate Histogram



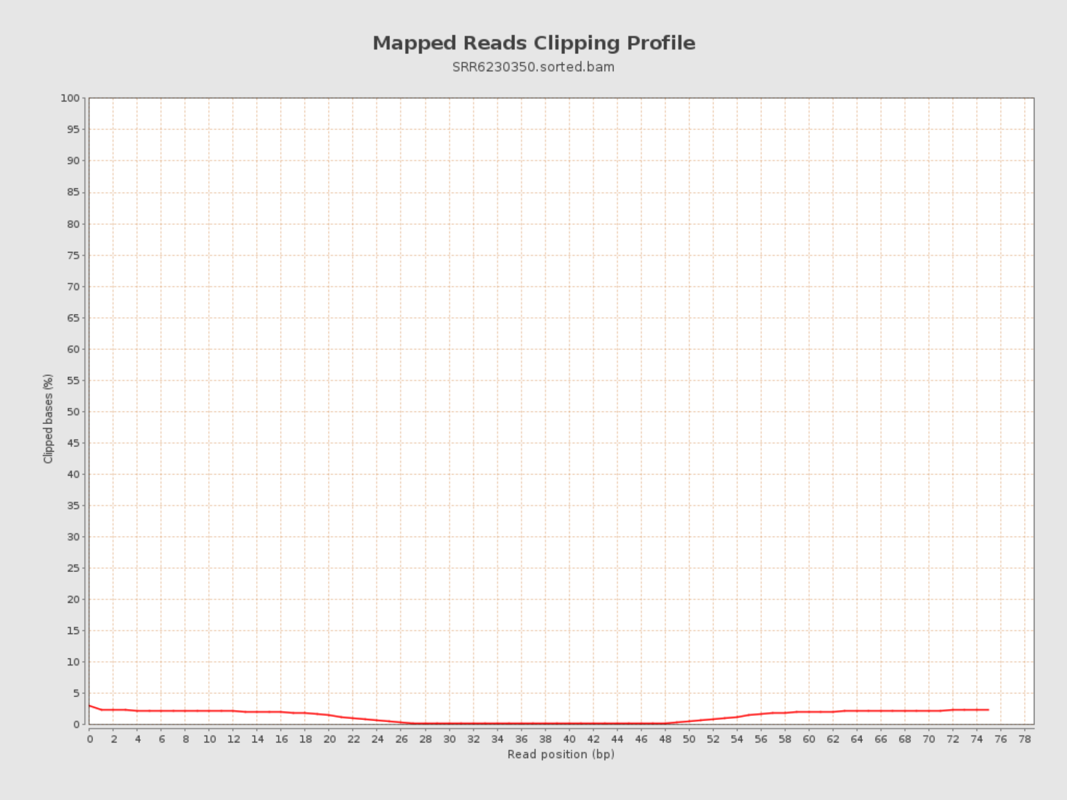
8. Results : Mapped Reads Nucleotide Content



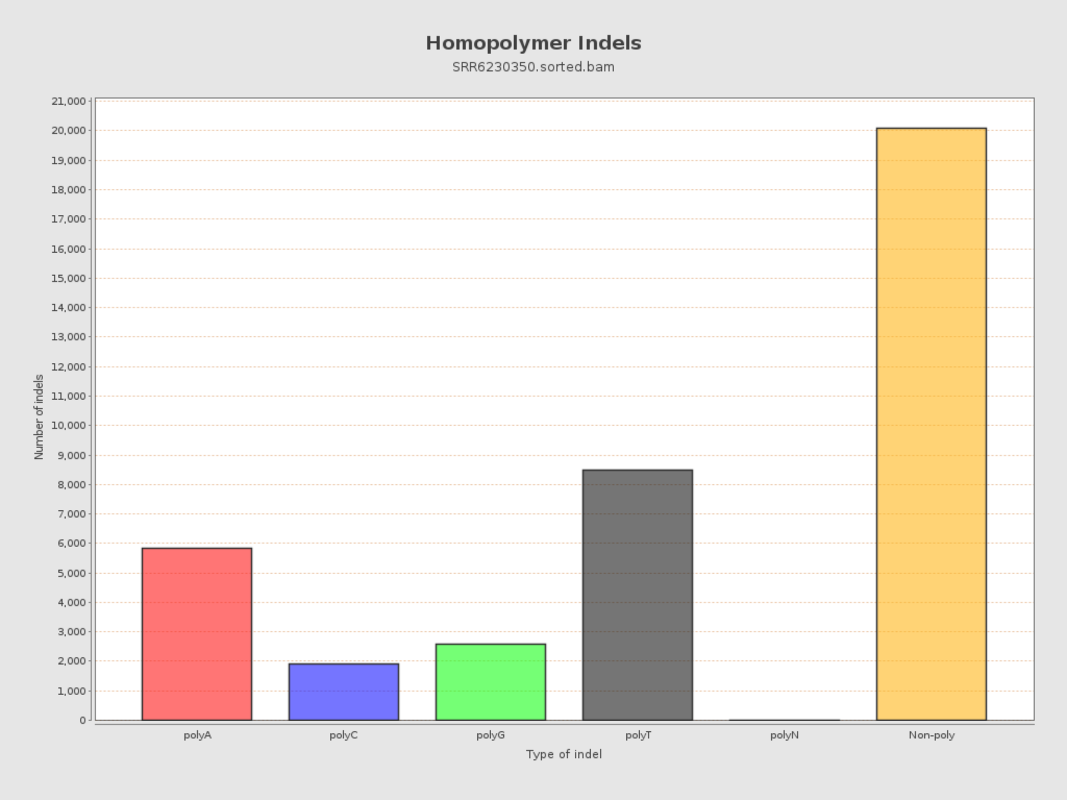
9. Results : Mapped Reads GC-content Distribution



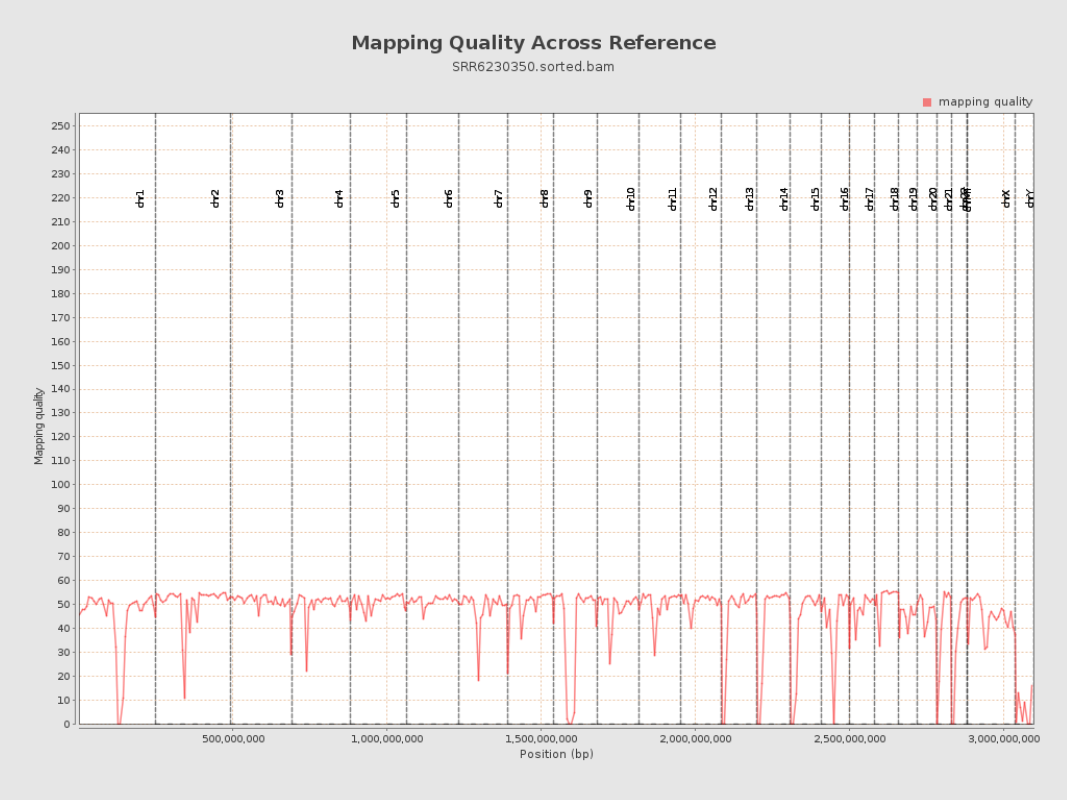
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram