Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230356.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_SRR6230356 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230356.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:09:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230356.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,158,569
Mapped reads	1,589,770 / 73.65%
Unmapped reads	568,799 / 26.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,888 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	75,443 / 3.5%
Duplication rate	3.7%
Clipped reads	805,432 / 37.31%

2.2. ACGT Content

Number/percentage of A's	27,704,488 / 26.81%
Number/percentage of C's	17,809,893 / 17.24%
Number/percentage of T's	34,422,865 / 33.31%
Number/percentage of G's	23,198,638 / 22.45%
Number/percentage of N's	195,101 / 0.19%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3339

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

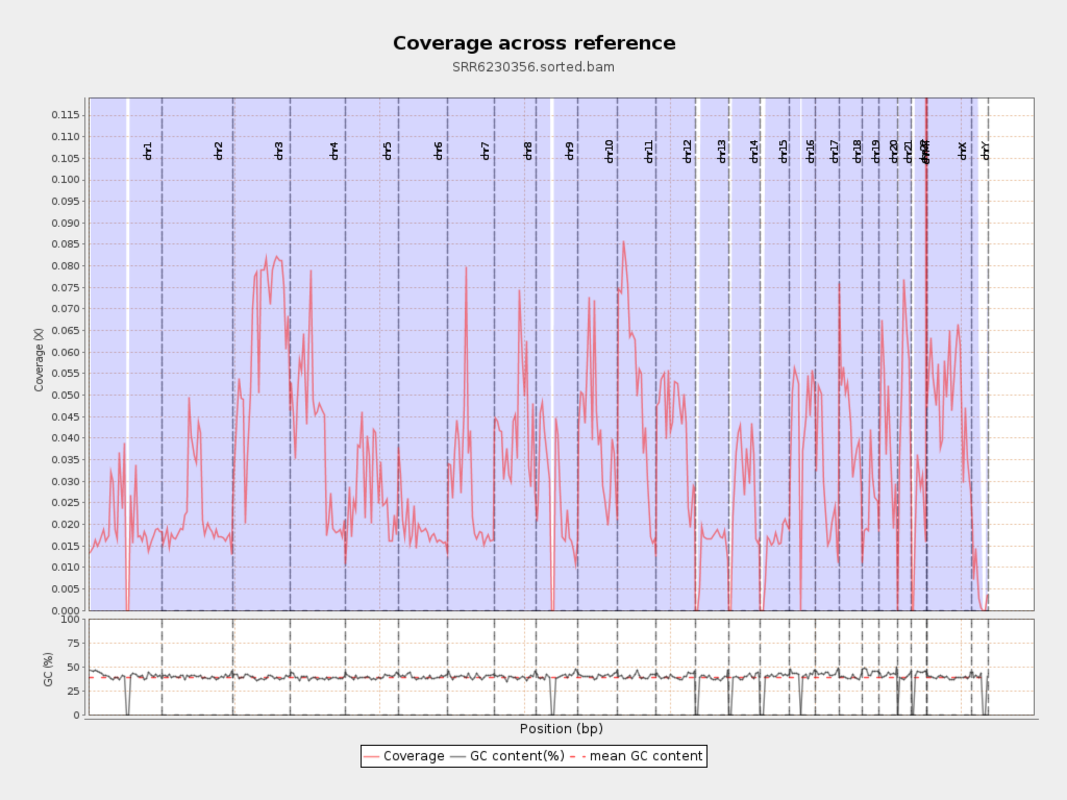
General error rate	0.96%
Mismatches	973,397
Insertions	9,378
Mapped reads with at least one insertion	0.58%
Deletions	27,383
Mapped reads with at least one deletion	1.71%
Homopolymer indels	48.57%

2.6. Chromosome stats

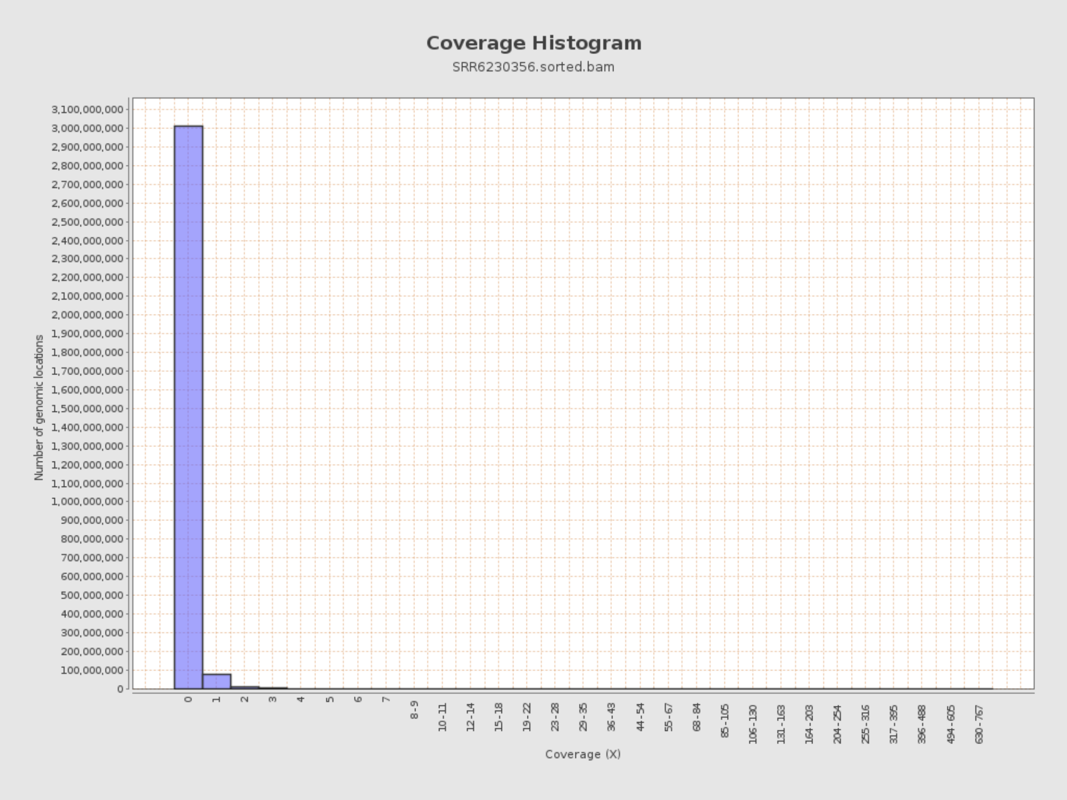
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4727143	0.019	0.4236
chr2	243199373	5442378	0.0224	0.3028
chr3	198022430	12599142	0.0636	0.2903
chr4	191154276	7672452	0.0401	0.2489
chr5	180915260	5011266	0.0277	0.1914
chr6	171115067	3288178	0.0192	0.2076
chr7	159138663	4698673	0.0295	0.6138

chr8	146364022	6241409	0.0426	0.5228
chr9	141213431	3572784	0.0253	0.2836
chr10	135534747	5750303	0.0424	0.3524
chr11	135006516	7049265	0.0522	0.419
chr12	133851895	5844542	0.0437	0.2416
chr13	115169878	1667141	0.0145	0.1372
chr14	107349540	2983607	0.0278	0.207
chr15	102531392	1462831	0.0143	0.1364
chr16	90354753	4076880	0.0451	0.273
chr17	81195210	2175879	0.0268	0.2295
chr18	78077248	3495760	0.0448	0.579
chr19	59128983	1469170	0.0248	0.3413
chr20	63025520	2612612	0.0415	0.247
chr21	48129895	2353596	0.0489	0.2734
chr22	51304566	1081607	0.0211	0.167
chrMT	16571	29394	1.7738	1.5725
chrX	155270560	7748034	0.0499	0.286
chrY	59373566	321881	0.0054	0.1259

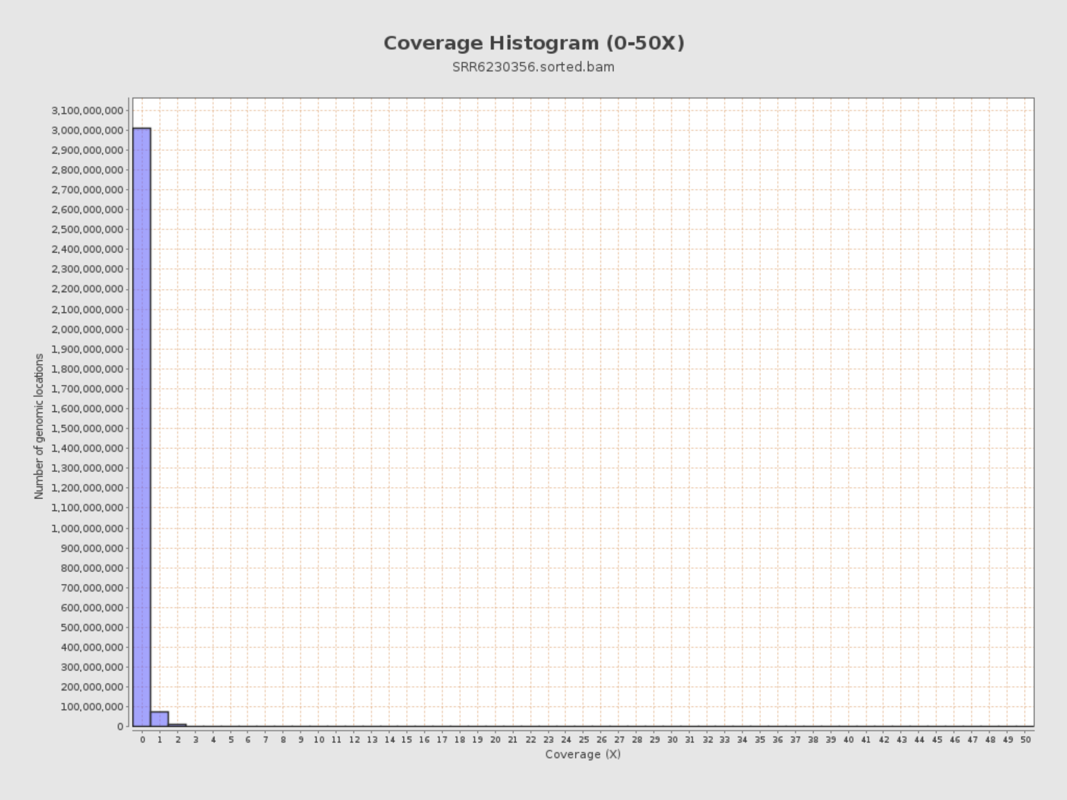
3. Results : Coverage across reference



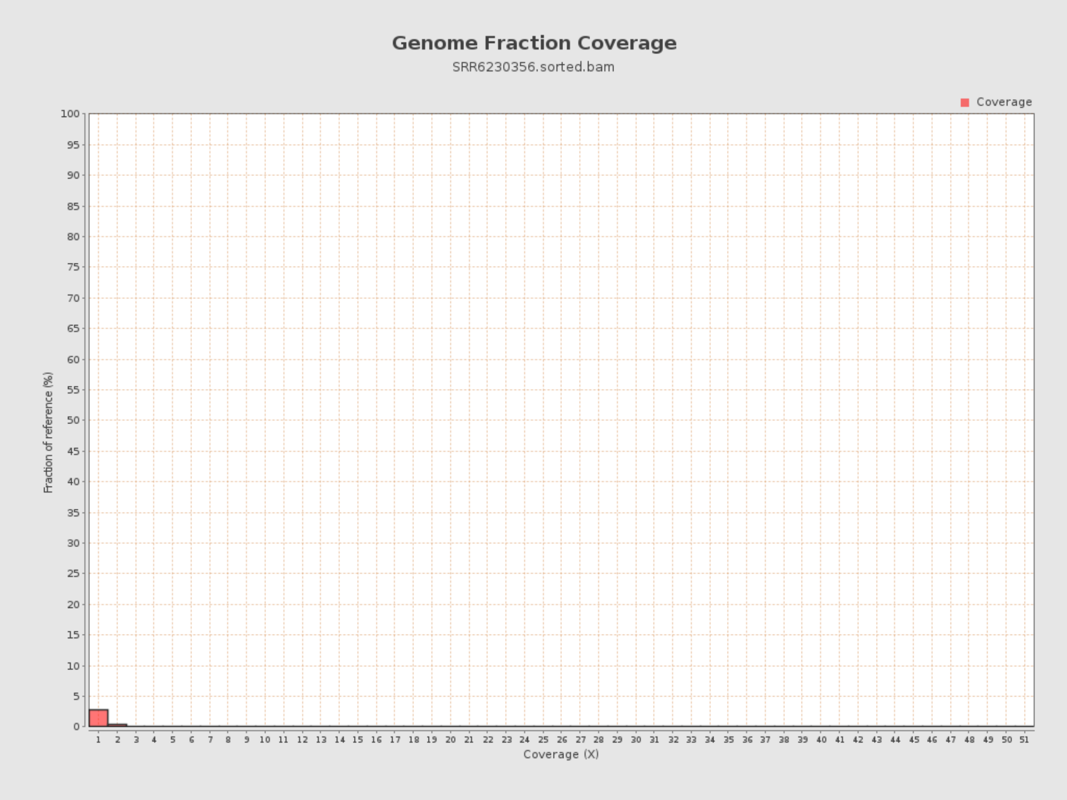
4. Results : Coverage Histogram



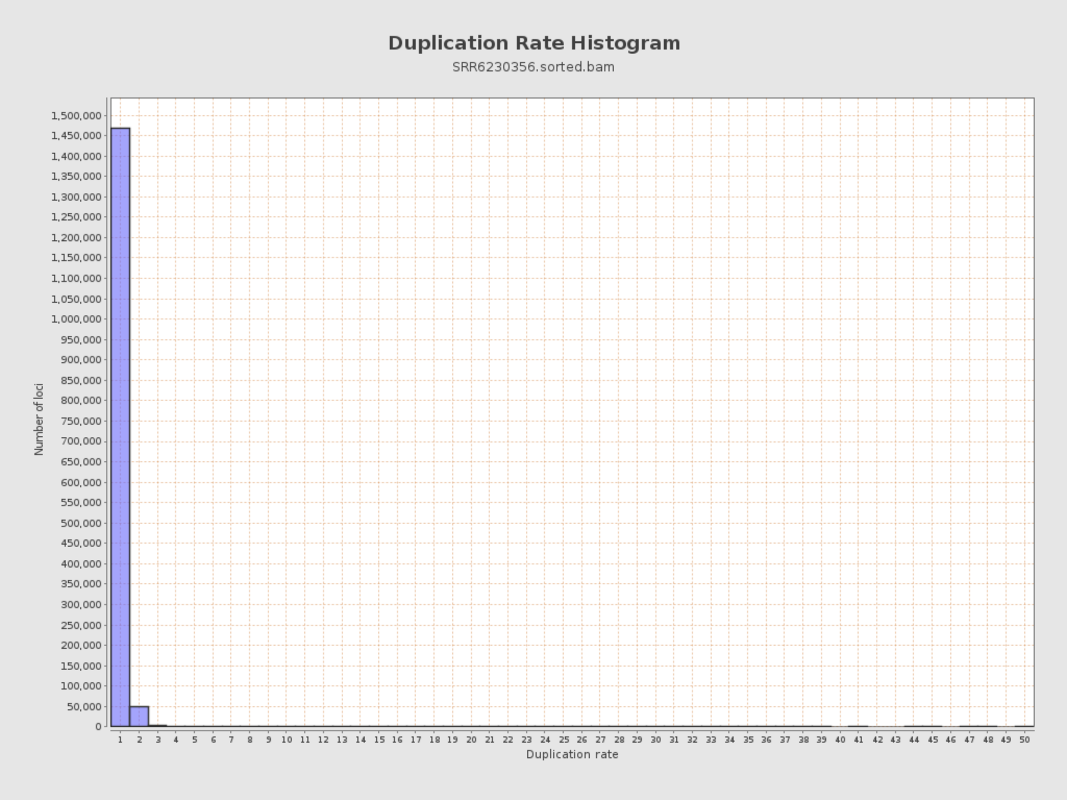
5. Results : Coverage Histogram (0-50X)



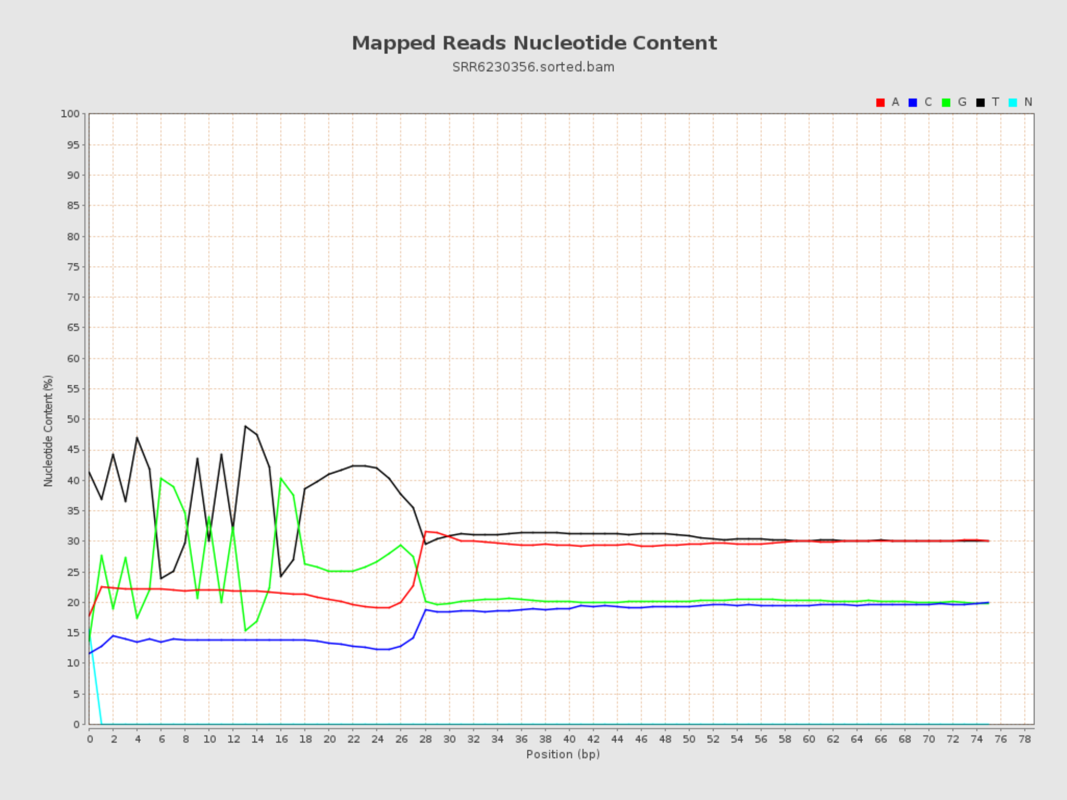
6. Results : Genome Fraction Coverage



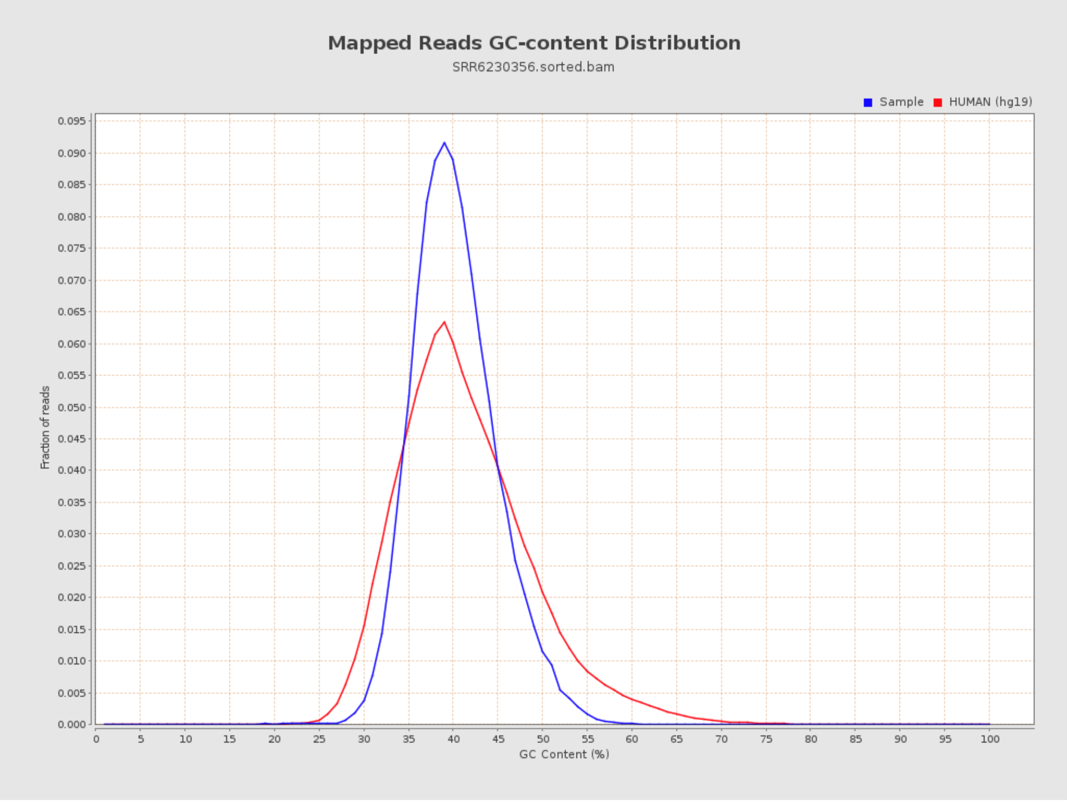
7. Results : Duplication Rate Histogram



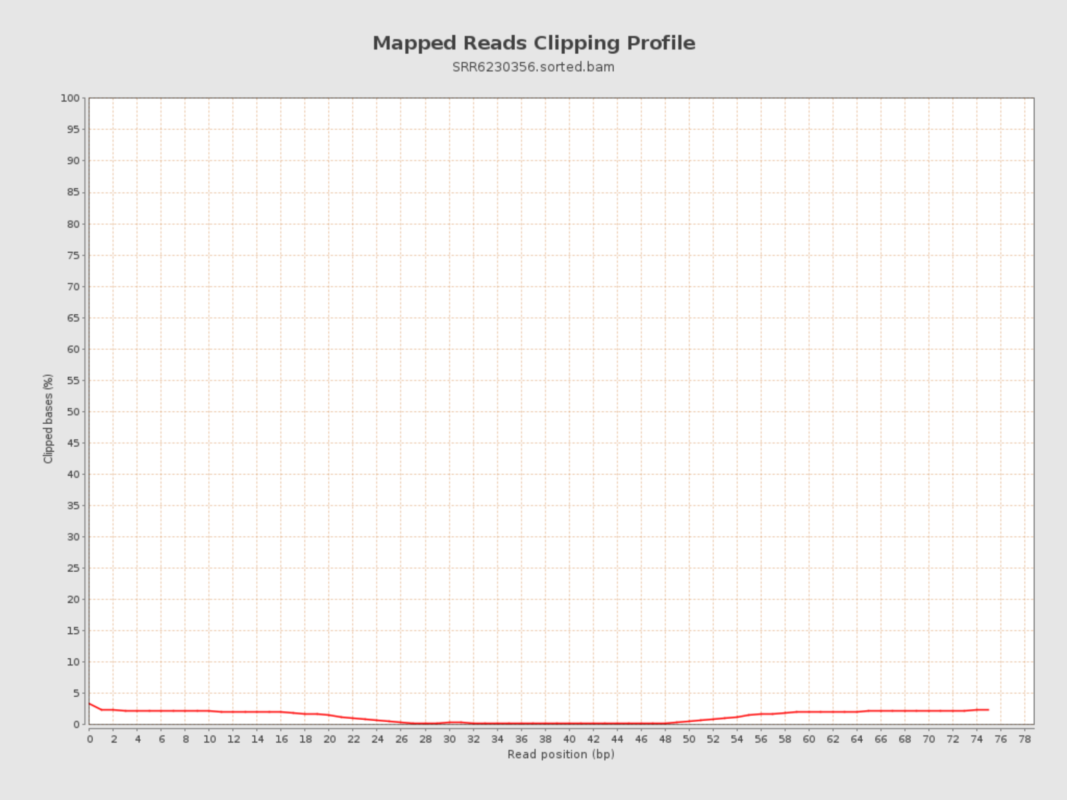
8. Results : Mapped Reads Nucleotide Content



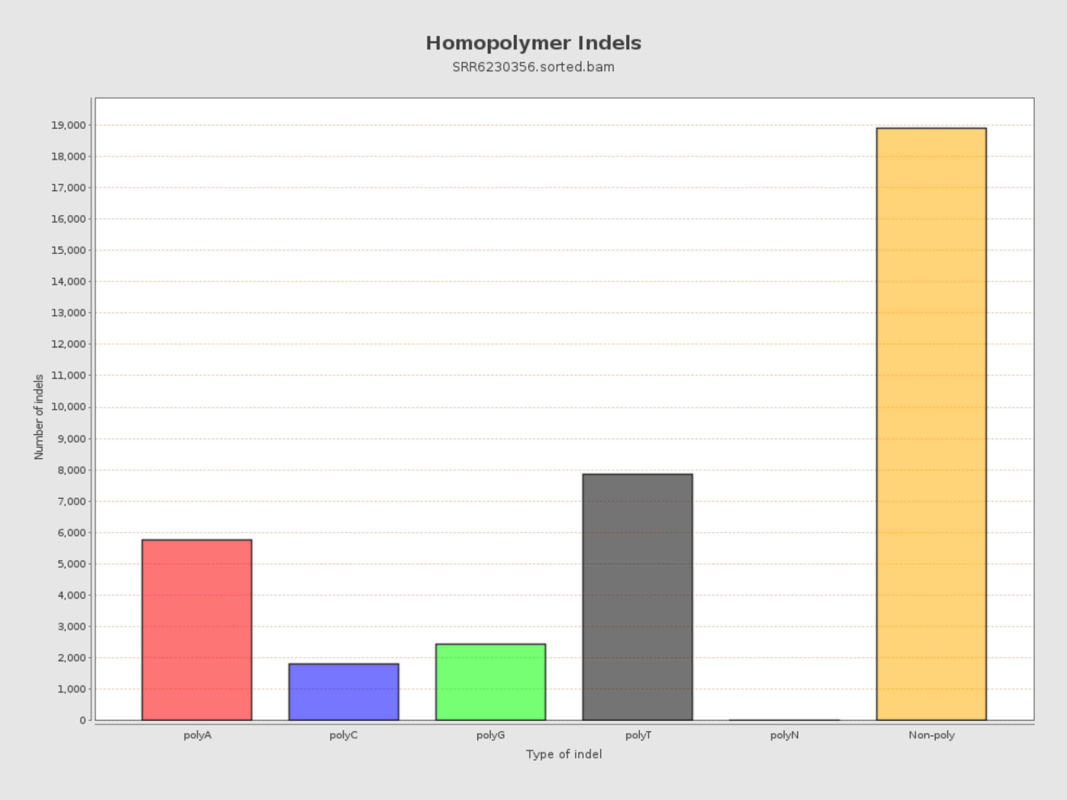
9. Results : Mapped Reads GC-content Distribution



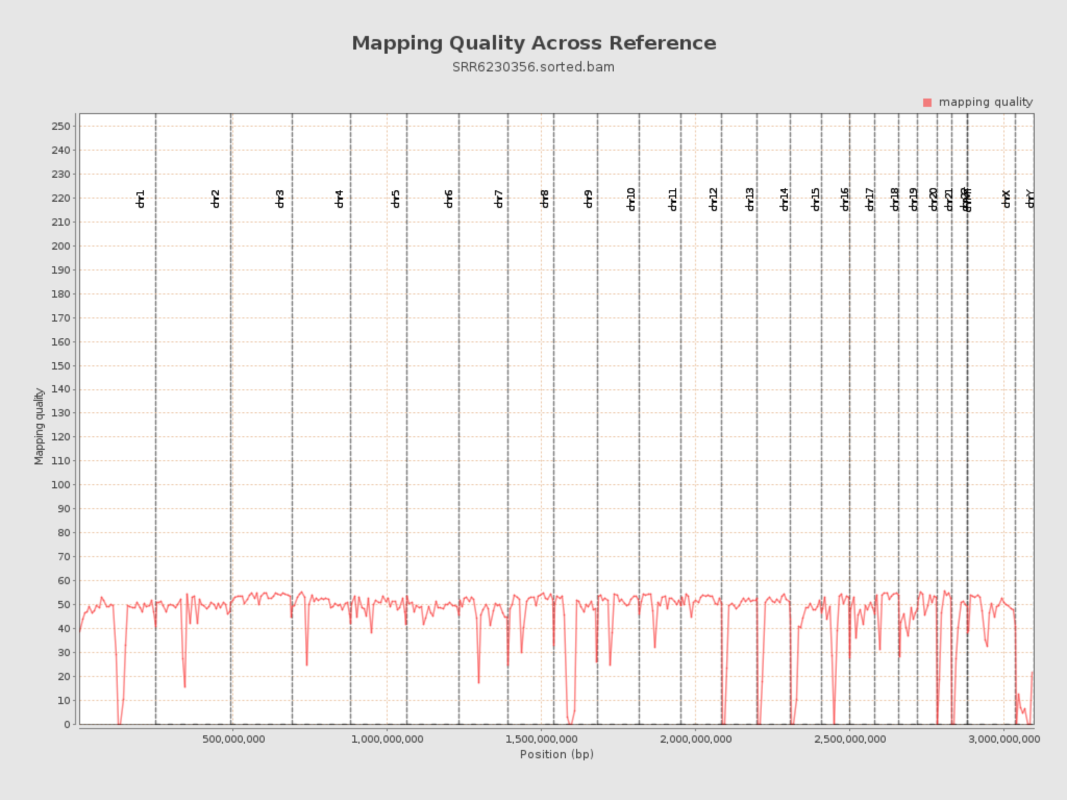
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram