Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:32:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238304.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_SRR6238304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238304.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:32:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,331,181
Mapped reads	2,143,053 / 91.93%
Unmapped reads	188,128 / 8.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,390 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	90,345 / 3.88%
Duplication rate	3.18%
Clipped reads	977,734 / 41.94%

2.2. ACGT Content

Number/percentage of A's	40,685,946 / 28.49%
Number/percentage of C's	26,693,148 / 18.69%
Number/percentage of T's	44,762,675 / 31.34%
Number/percentage of G's	30,633,389 / 21.45%
Number/percentage of N's	47,253 / 0.03%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.4211

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

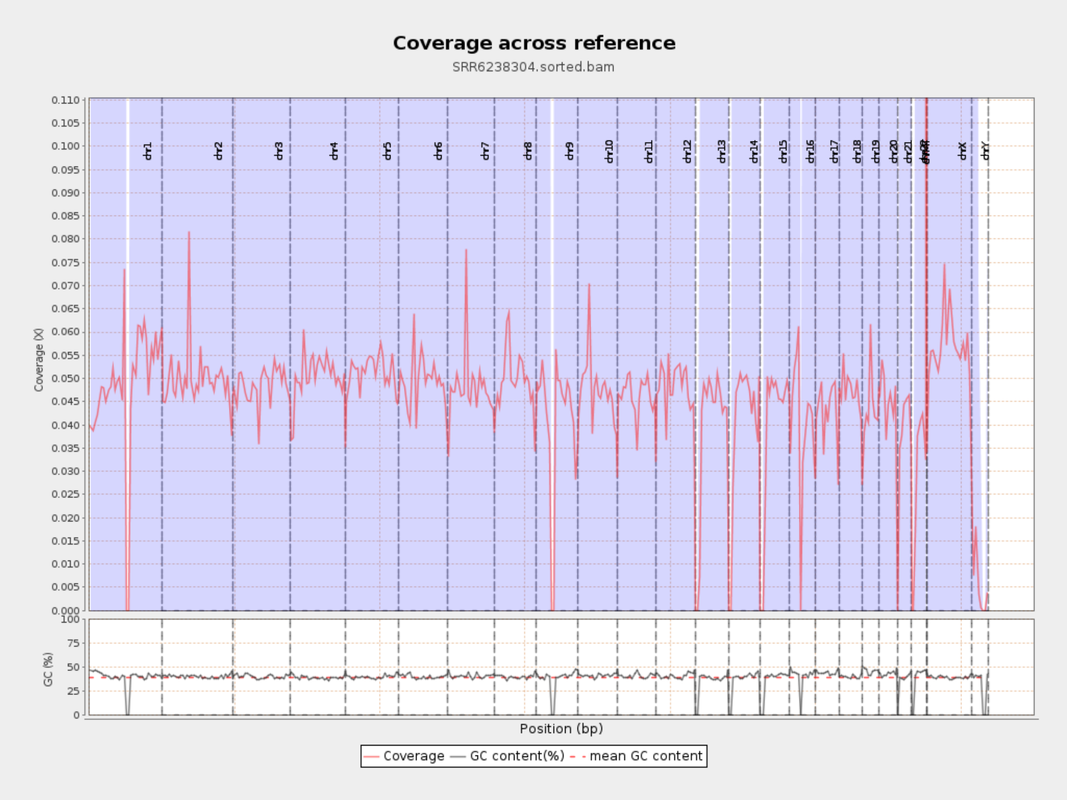
General error rate	0.83%
Mismatches	1,161,044
Insertions	10,547
Mapped reads with at least one insertion	0.49%
Deletions	36,212
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.72%

2.6. Chromosome stats

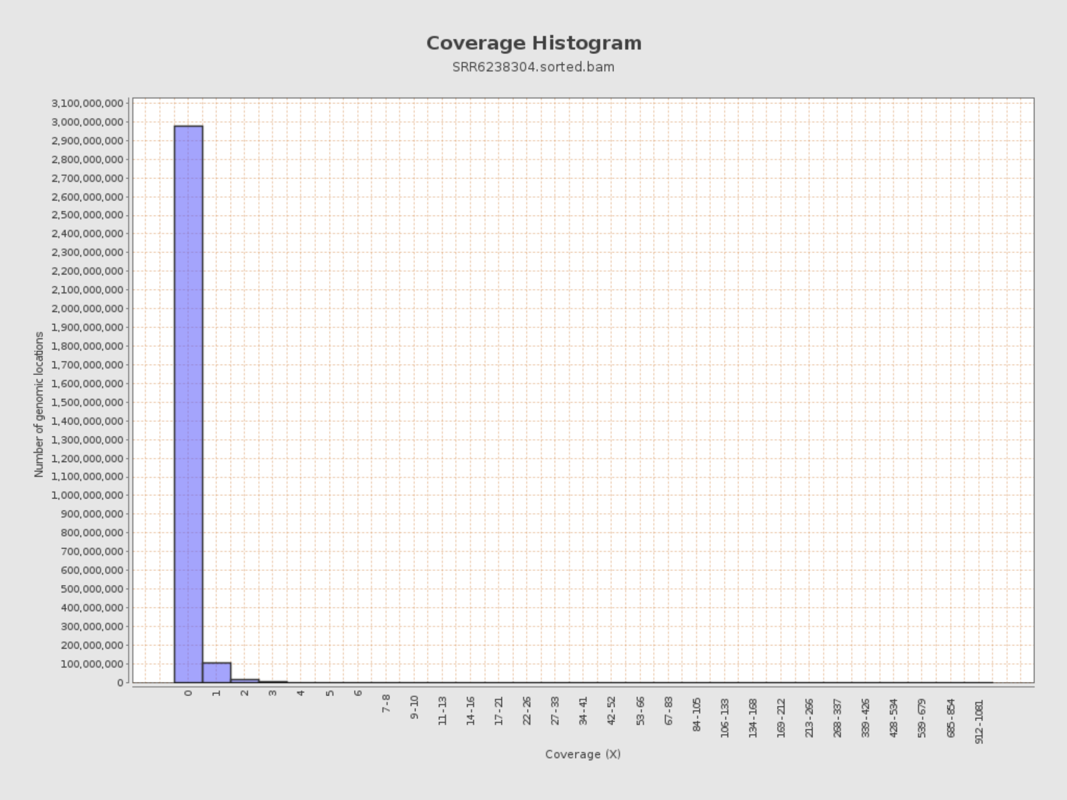
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12027346	0.0483	0.7276
chr2	243199373	12159651	0.05	0.4428
chr3	198022430	9606486	0.0485	0.2527
chr4	191154276	9644838	0.0505	0.2742
chr5	180915260	9321985	0.0515	0.2655
chr6	171115067	8435257	0.0493	0.3069
chr7	159138663	7714931	0.0485	0.5385

chr8	146364022	7246516	0.0495	0.69
chr9	141213431	5757904	0.0408	0.368
chr10	135534747	6495042	0.0479	0.369
chr11	135006516	6217936	0.0461	0.346
chr12	133851895	6463696	0.0483	0.2647
chr13	115169878	4401958	0.0382	0.2277
chr14	107349540	4206972	0.0392	0.2582
chr15	102531392	4013179	0.0391	0.2322
chr16	90354753	3654037	0.0404	0.2546
chr17	81195210	3452460	0.0425	0.2643
chr18	78077248	3707292	0.0475	0.6586
chr19	59128983	2587849	0.0438	0.5237
chr20	63025520	2841281	0.0451	0.2508
chr21	48129895	1795040	0.0373	0.2467
chr22	51304566	1415605	0.0276	0.189
chrMT	16571	596195	35.9782	22.476
chrX	155270560	8775570	0.0565	0.3038
chrY	59373566	346486	0.0058	0.1481

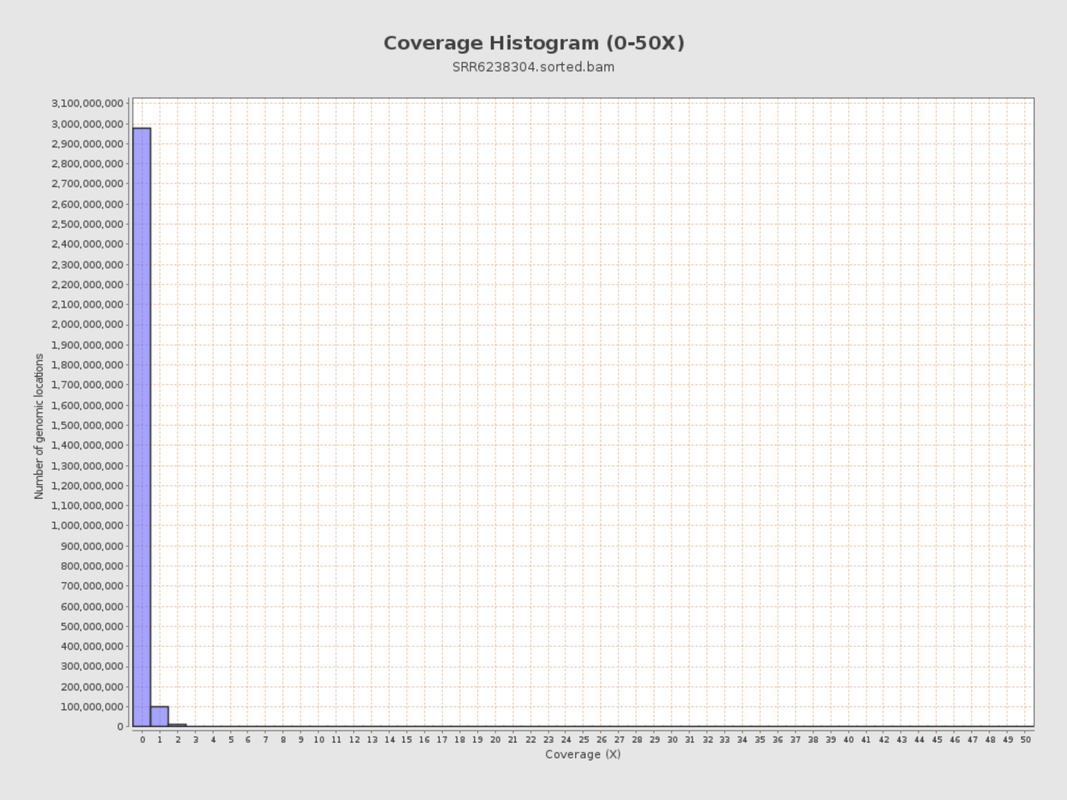
3. Results : Coverage across reference



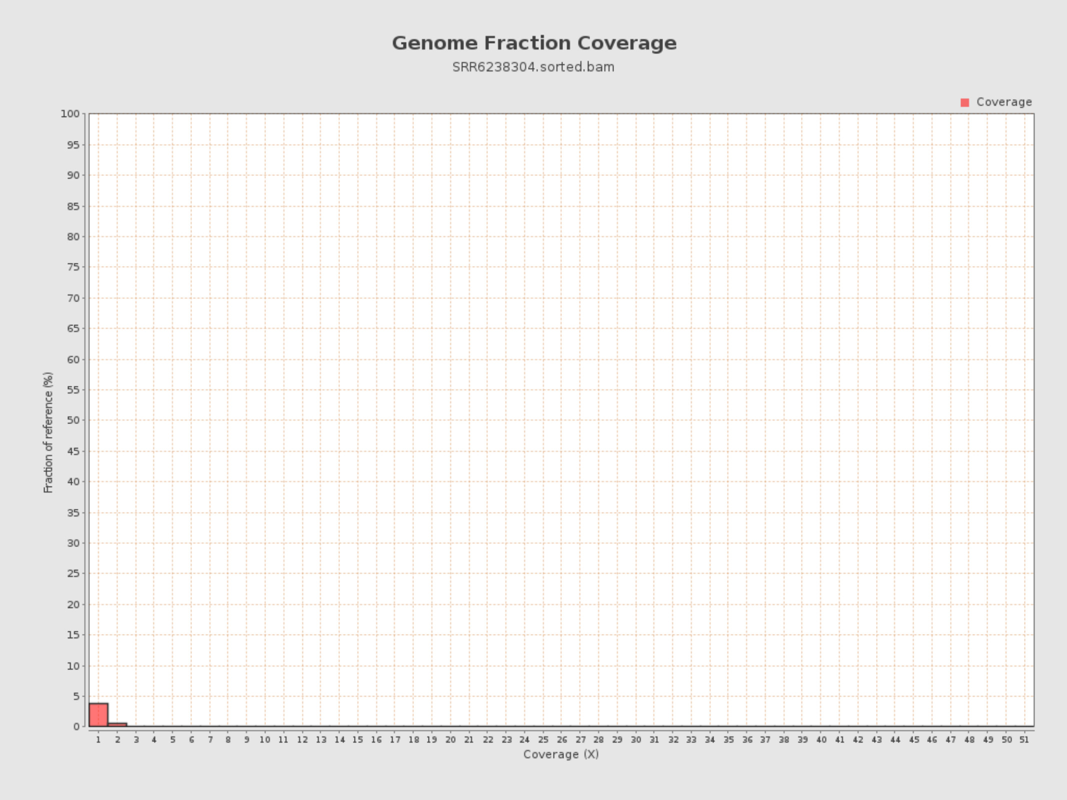
4. Results : Coverage Histogram



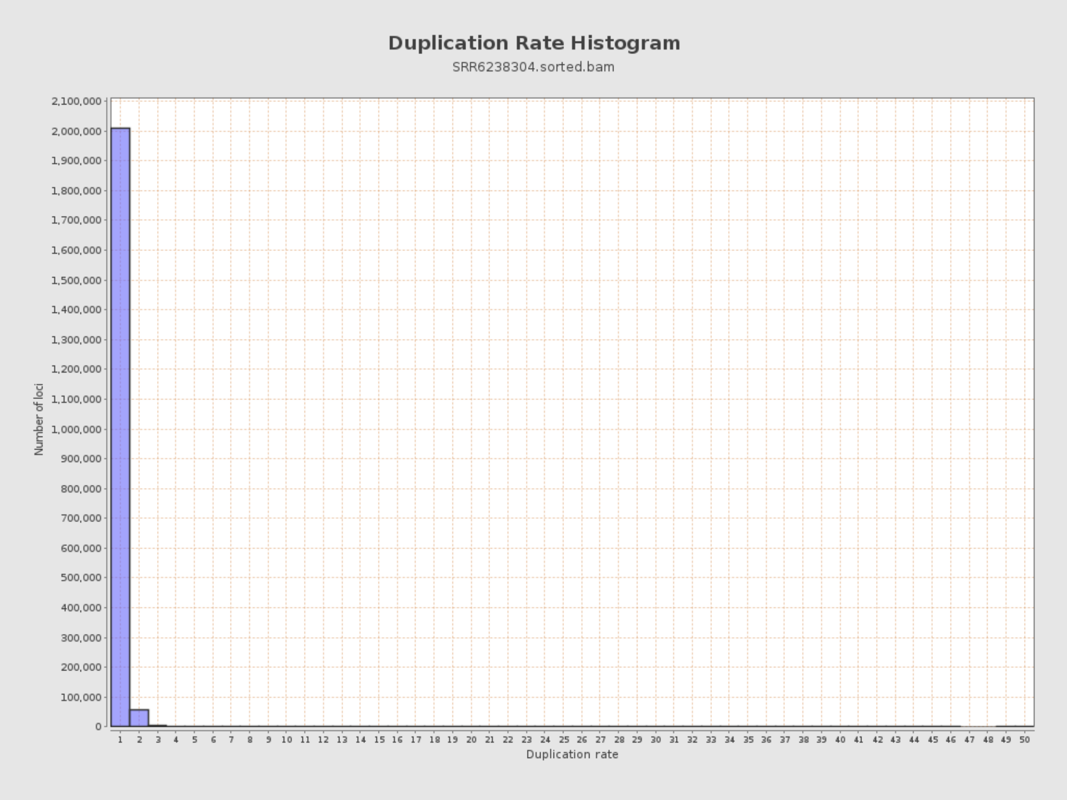
5. Results : Coverage Histogram (0-50X)



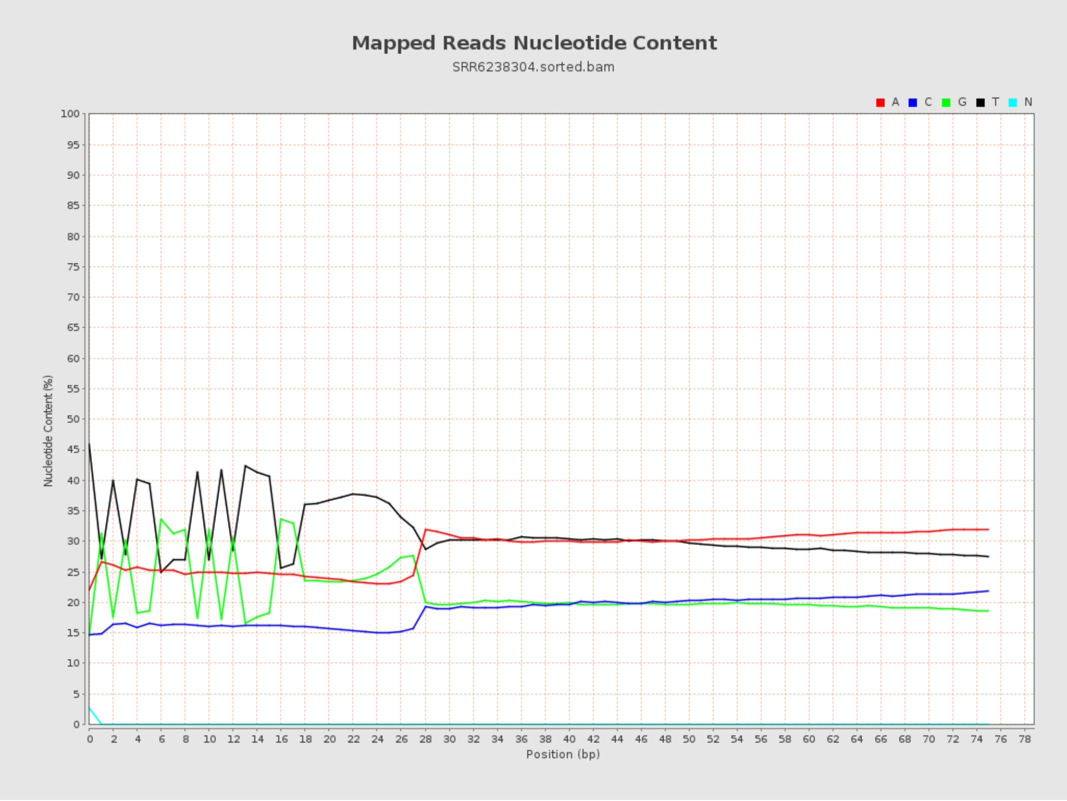
6. Results : Genome Fraction Coverage



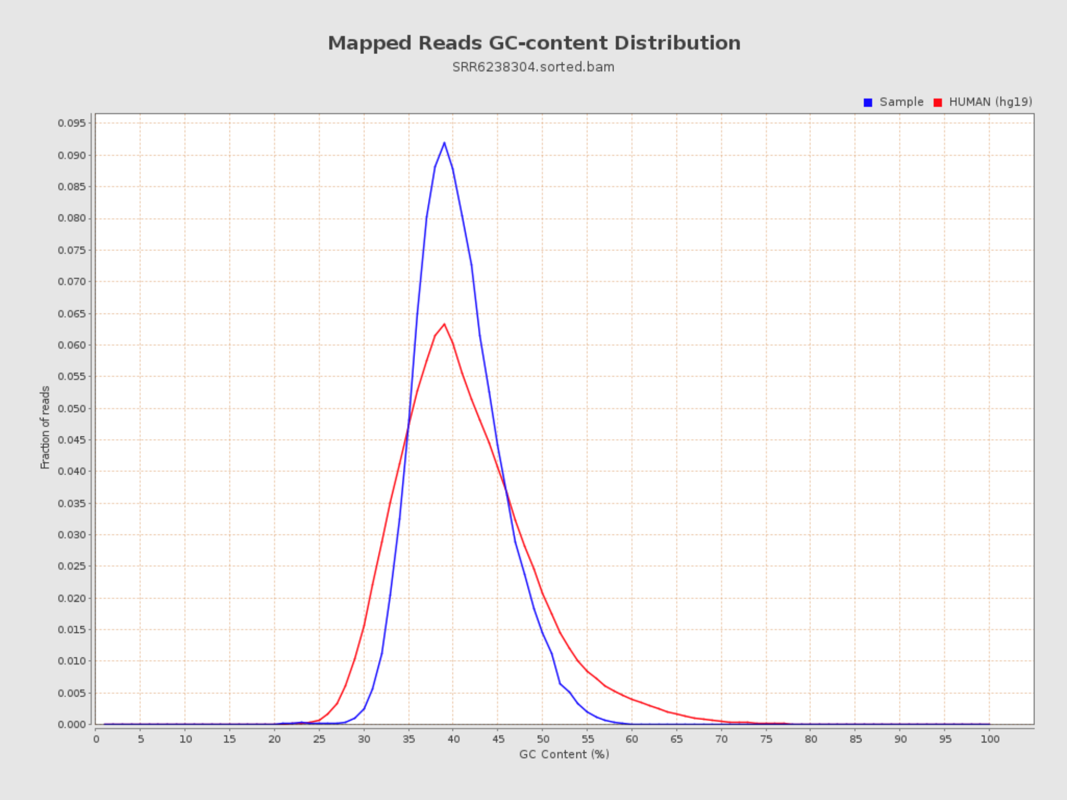
7. Results : Duplication Rate Histogram



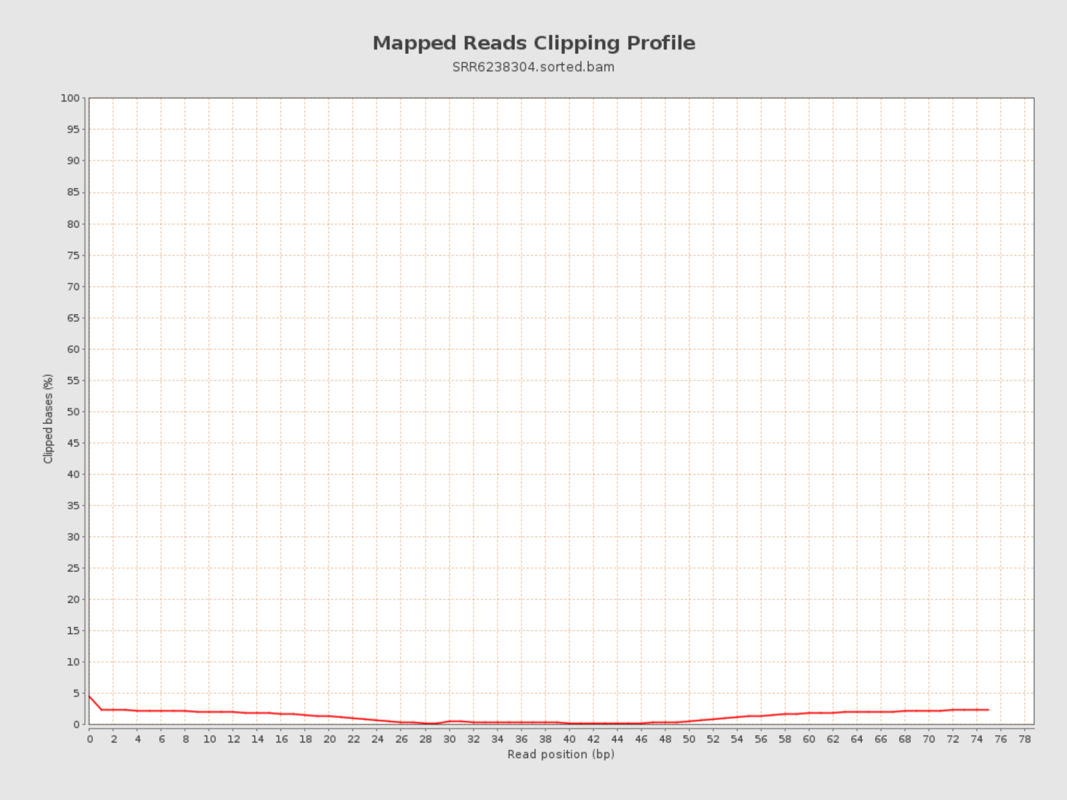
8. Results : Mapped Reads Nucleotide Content



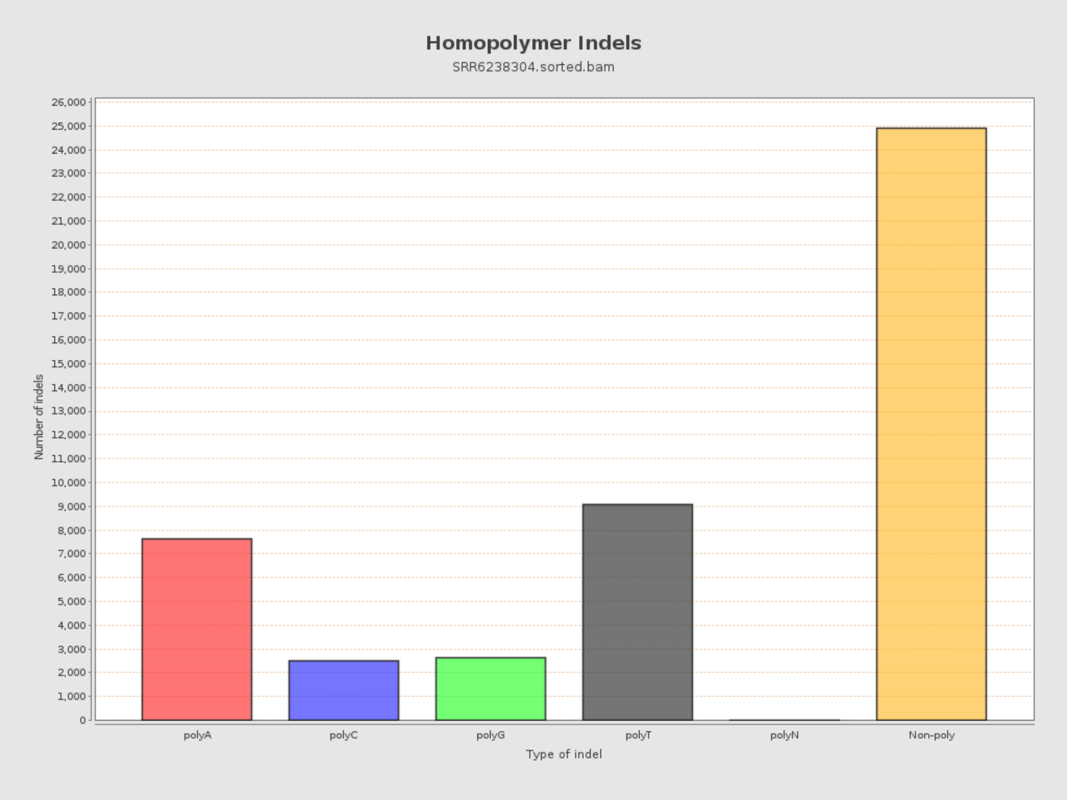
9. Results : Mapped Reads GC-content Distribution



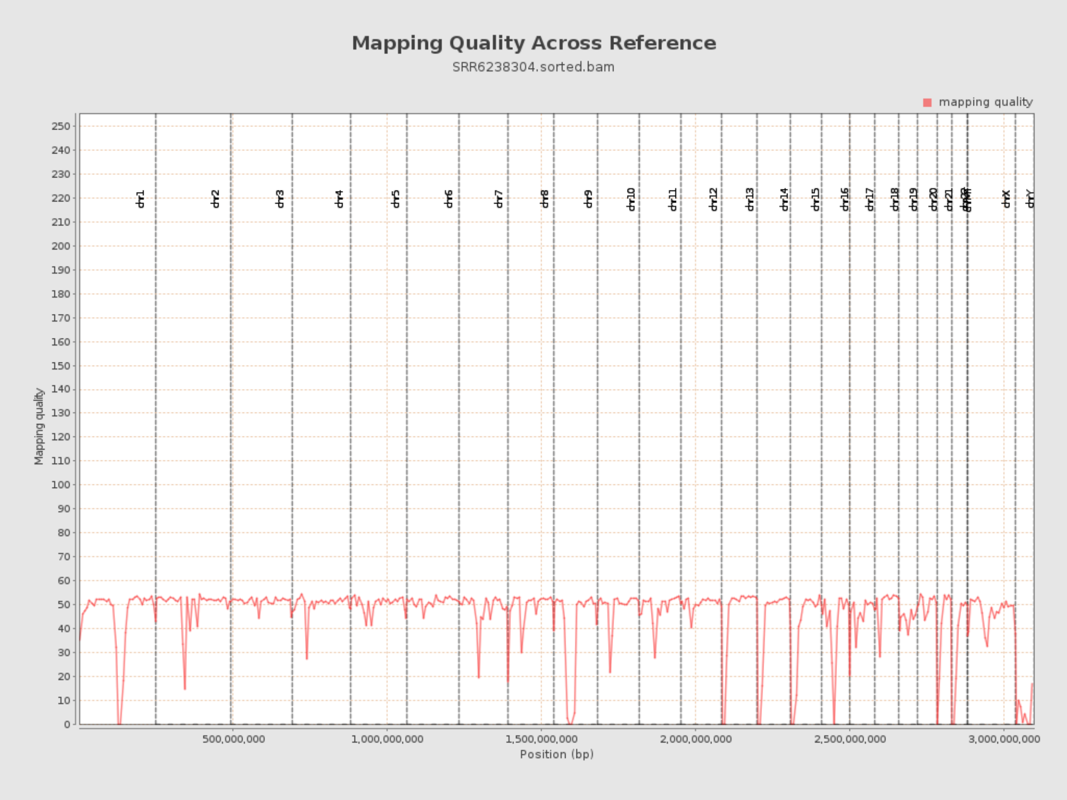
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram