Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:55:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238030.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_SRR6238030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:55:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,555,465
Mapped reads	2,269,937 / 88.83%
Unmapped reads	285,528 / 11.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,250 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	126,660 / 4.96%
Duplication rate	4.28%
Clipped reads	970,482 / 37.98%

2.2. ACGT Content

Number/percentage of A's	41,783,437 / 27.55%
Number/percentage of C's	28,399,553 / 18.73%
Number/percentage of T's	47,765,656 / 31.5%
Number/percentage of G's	33,673,038 / 22.21%
Number/percentage of N's	21,808 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.049

Standard Deviation	0.4453

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

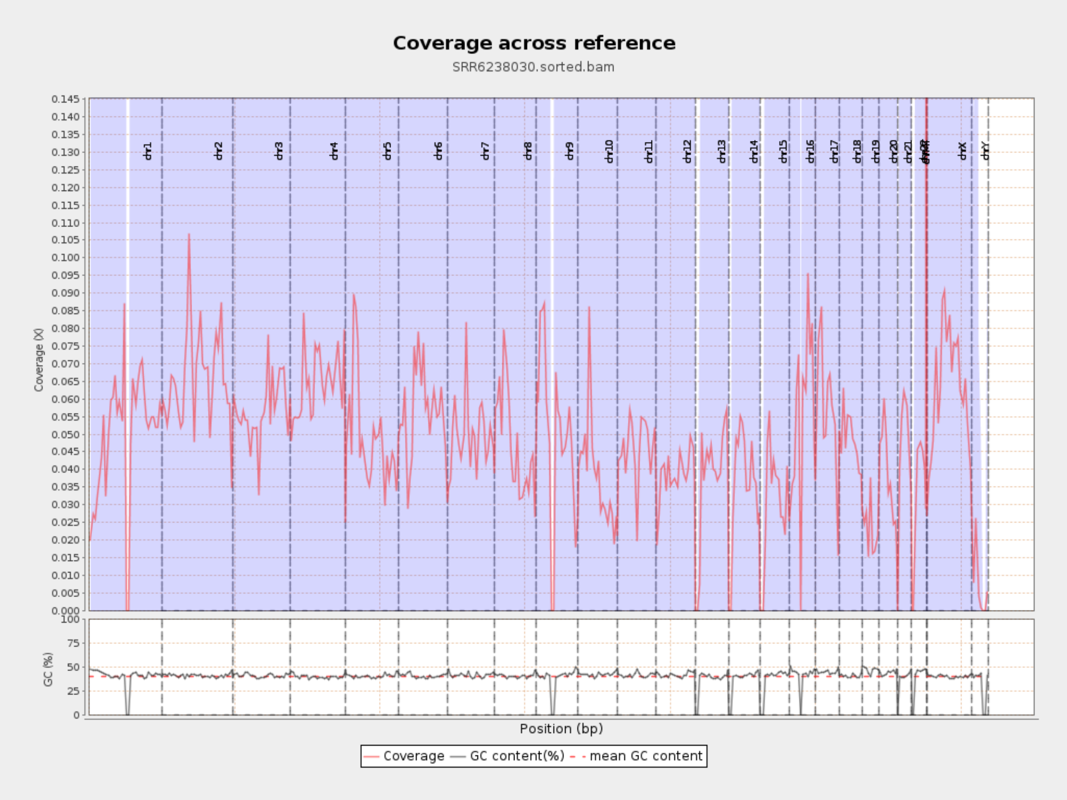
General error rate	0.8%
Mismatches	1,189,811
Insertions	11,090
Mapped reads with at least one insertion	0.48%
Deletions	44,730
Mapped reads with at least one deletion	1.95%
Homopolymer indels	45.08%

2.6. Chromosome stats

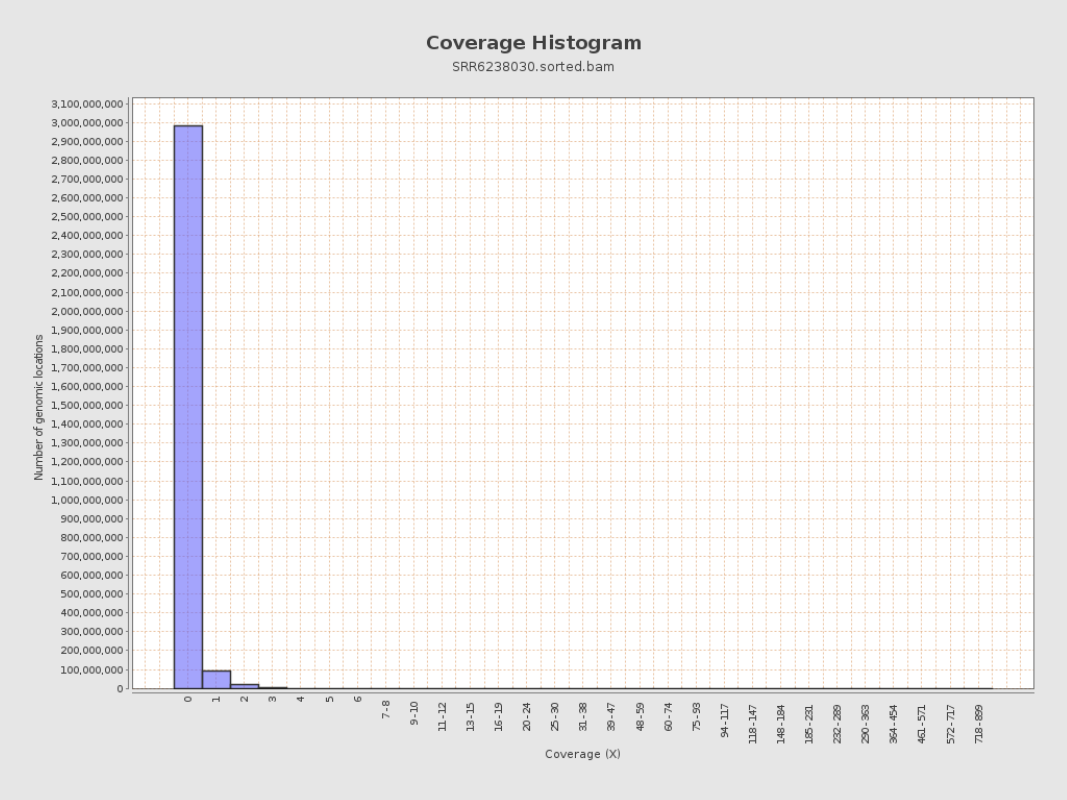
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12365832	0.0496	0.7218
chr2	243199373	16159466	0.0664	0.5479
chr3	198022430	11250030	0.0568	0.297
chr4	191154276	12318196	0.0644	0.3547
chr5	180915260	8882157	0.0491	0.2773
chr6	171115067	9665167	0.0565	0.3539
chr7	159138663	7970453	0.0501	0.5259

chr8	146364022	6897323	0.0471	0.6057
chr9	141213431	7052199	0.0499	0.4628
chr10	135534747	5215553	0.0385	0.4465
chr11	135006516	6178720	0.0458	0.3753
chr12	133851895	5115718	0.0382	0.2524
chr13	115169878	4304469	0.0374	0.2394
chr14	107349540	3855446	0.0359	0.2872
chr15	102531392	3119949	0.0304	0.219
chr16	90354753	5059497	0.056	0.3404
chr17	81195210	4548044	0.056	0.3588
chr18	78077248	3799005	0.0487	0.8345
chr19	59128983	1391189	0.0235	0.5748
chr20	63025520	2480052	0.0393	0.2639
chr21	48129895	2188989	0.0455	0.3125
chr22	51304566	1631031	0.0318	0.2217
chrMT	16571	14162	0.8546	1.1757
chrX	155270560	9828721	0.0633	0.3709
chrY	59373566	432474	0.0073	0.2189

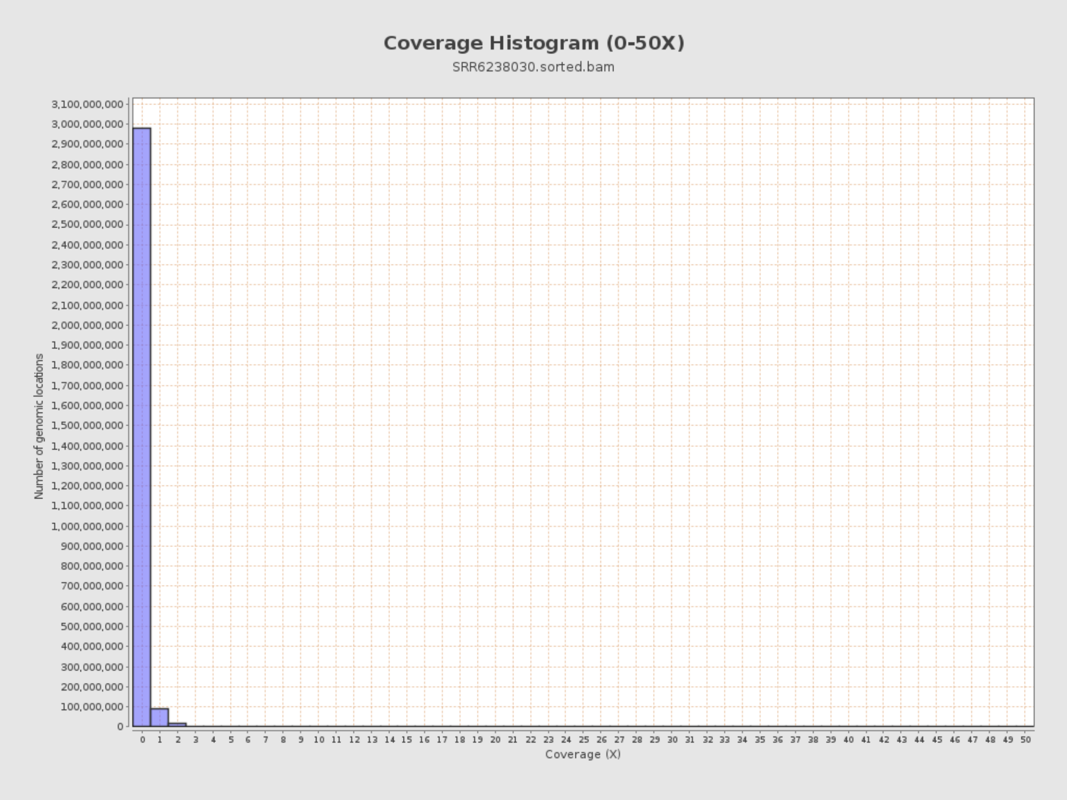
3. Results : Coverage across reference



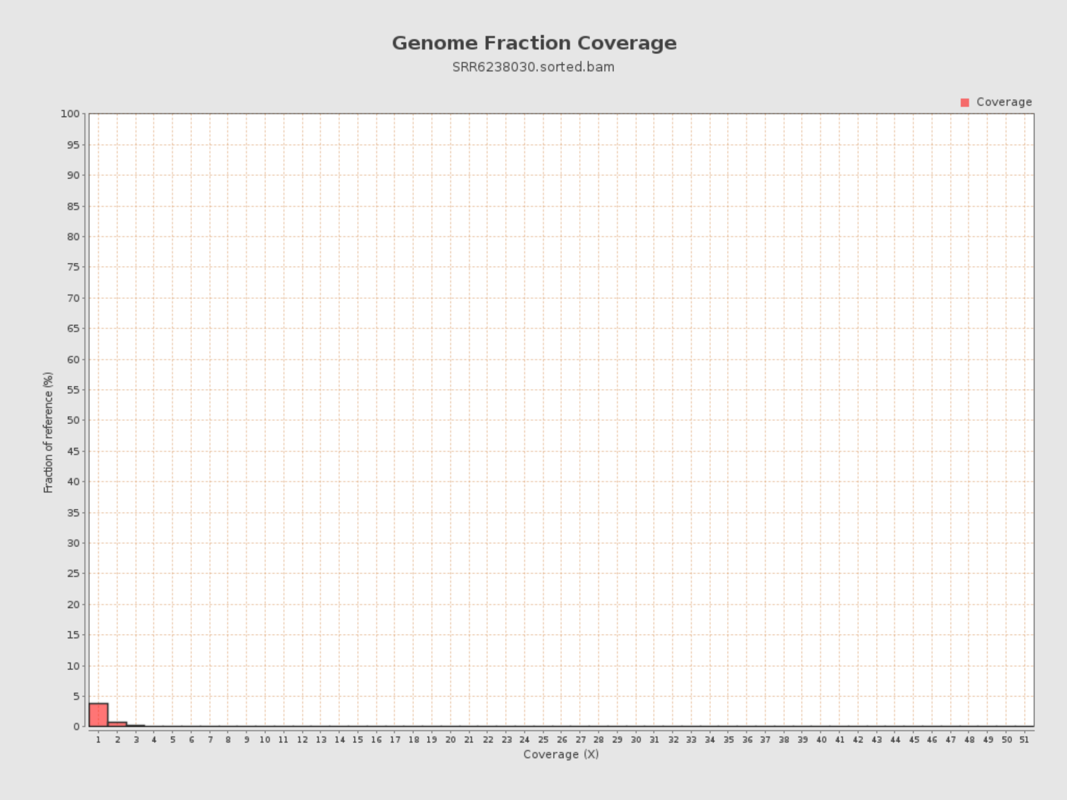
4. Results : Coverage Histogram



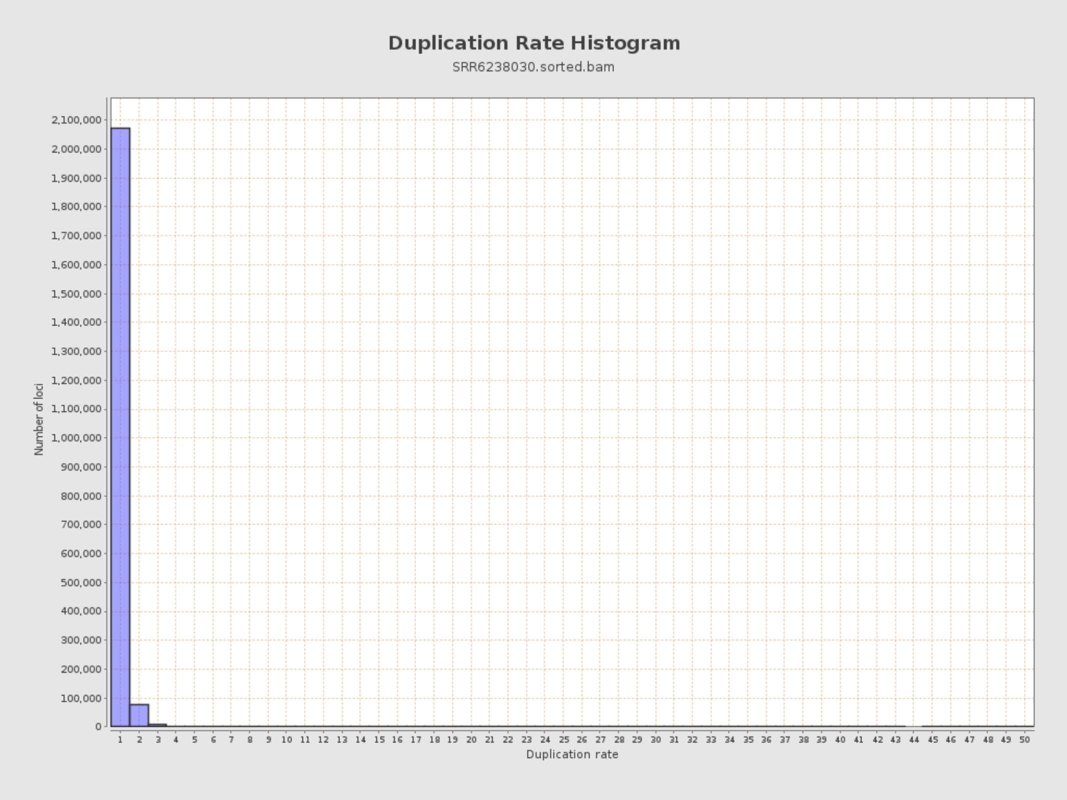
5. Results : Coverage Histogram (0-50X)



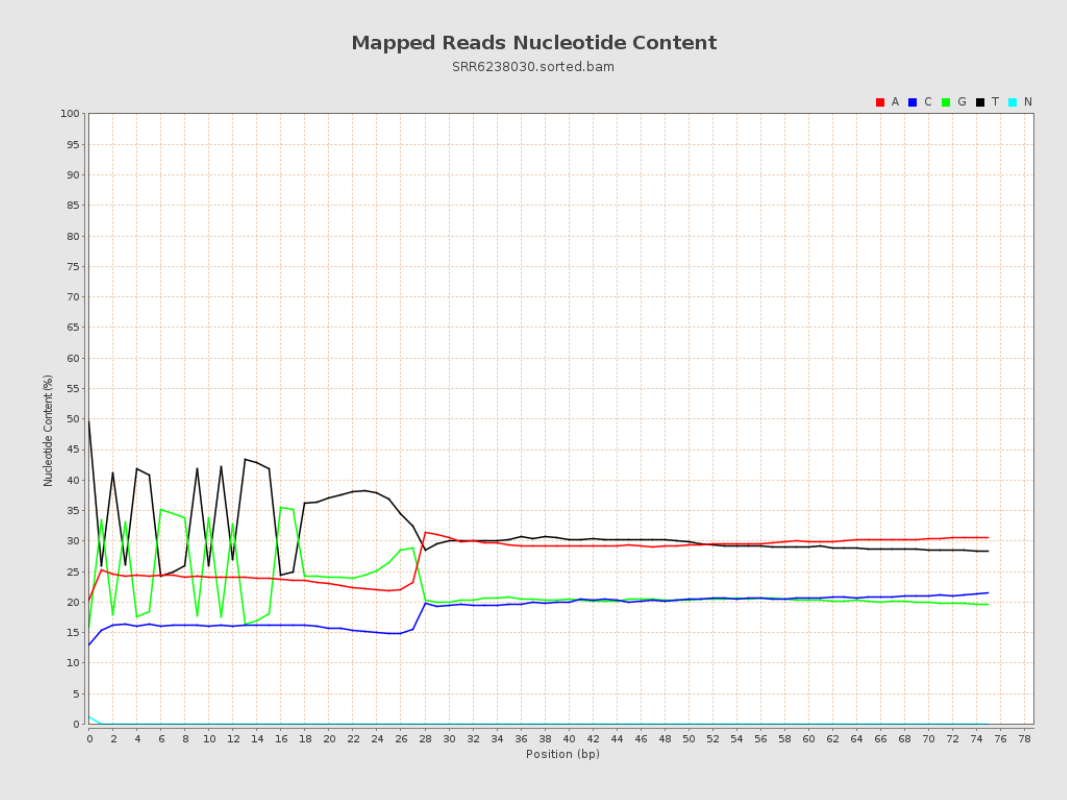
6. Results : Genome Fraction Coverage



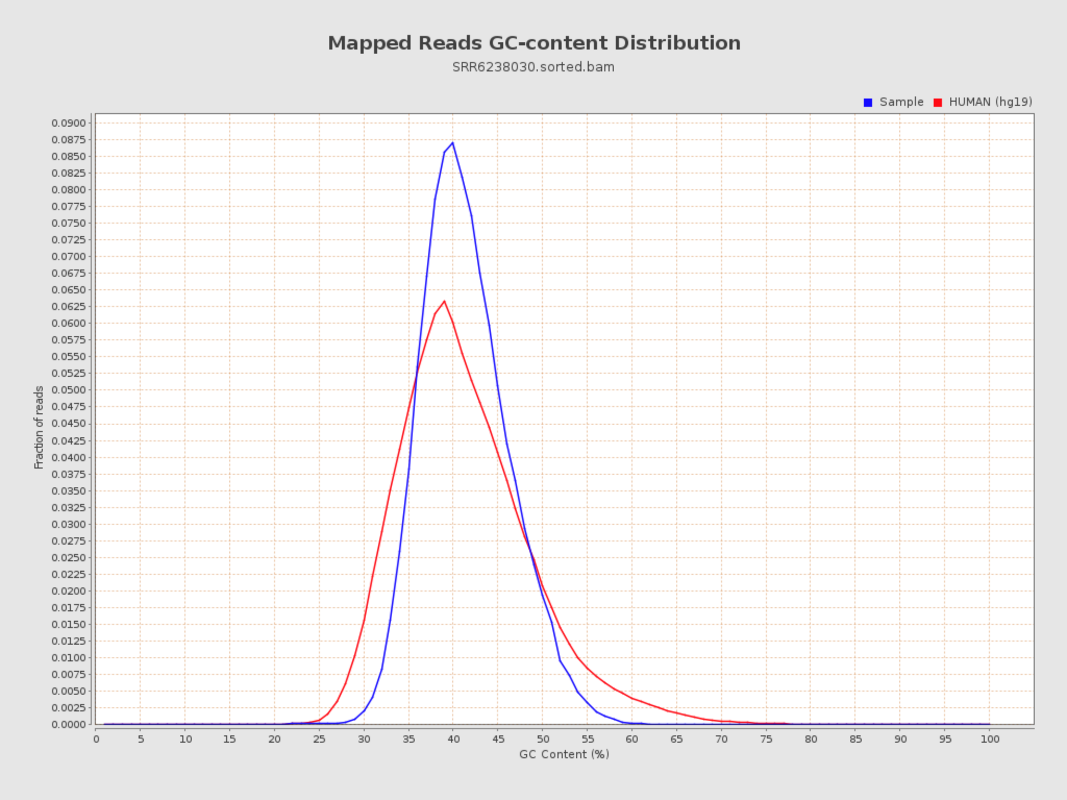
7. Results : Duplication Rate Histogram



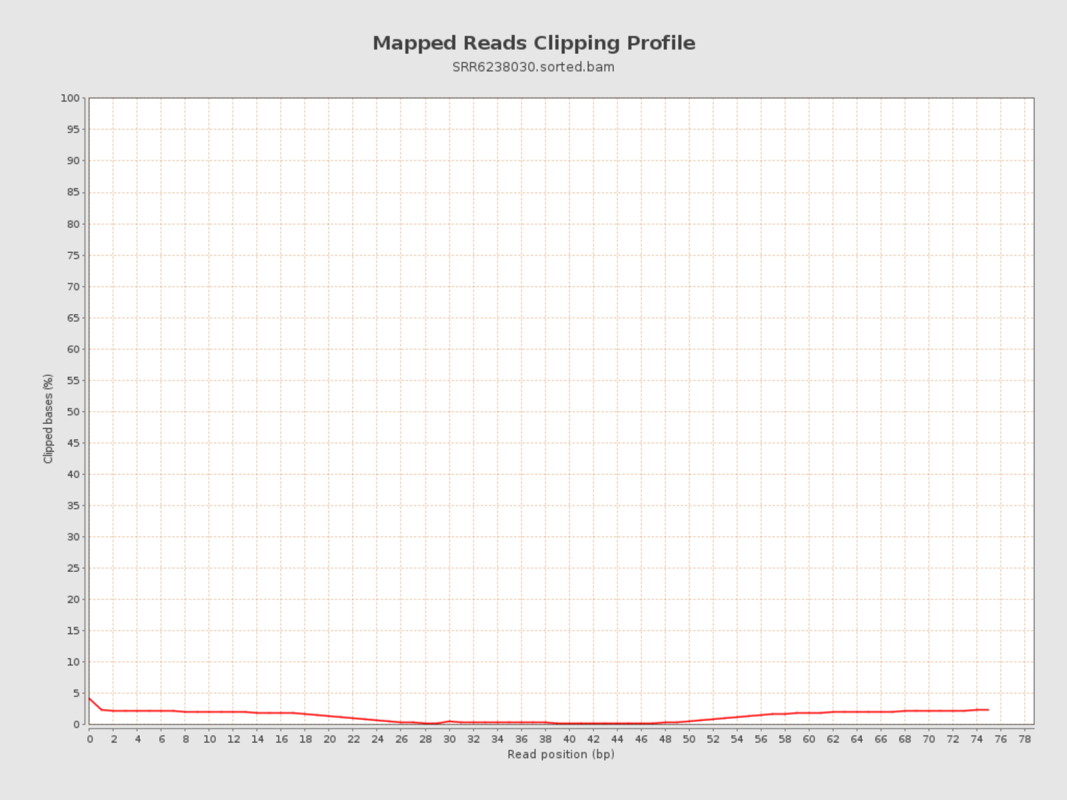
8. Results : Mapped Reads Nucleotide Content



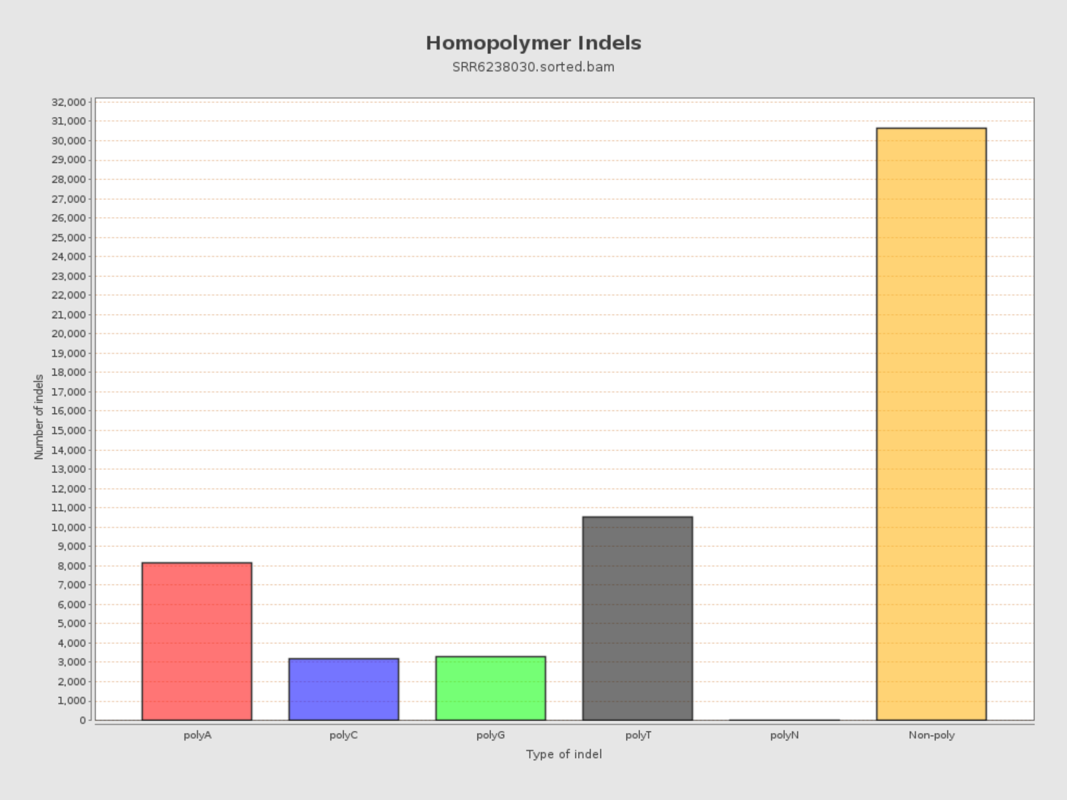
9. Results : Mapped Reads GC-content Distribution



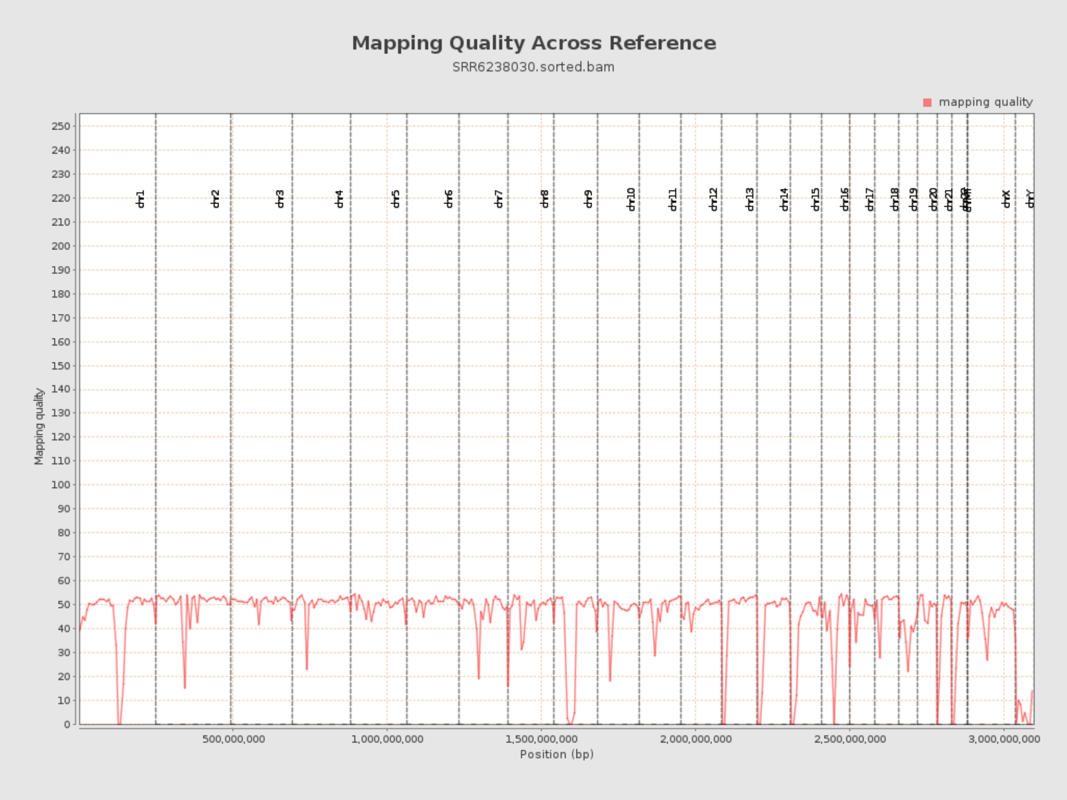
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram