Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:53:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238667.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_SRR6238667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238667.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:53:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,414,457
Mapped reads	2,980,137 / 87.28%
Unmapped reads	434,320 / 12.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,359 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	655,583 / 19.2%
Duplication rate	17.17%
Clipped reads	1,853,182 / 54.27%

2.2. ACGT Content

Number/percentage of A's	46,629,044 / 25.2%
Number/percentage of C's	33,250,408 / 17.97%
Number/percentage of T's	61,110,518 / 33.03%
Number/percentage of G's	44,009,255 / 23.79%
Number/percentage of N's	9,366 / 0.01%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.7626

2.4. Mapping Quality

Mean Mapping Quality	40.83

2.5. Mismatches and indels

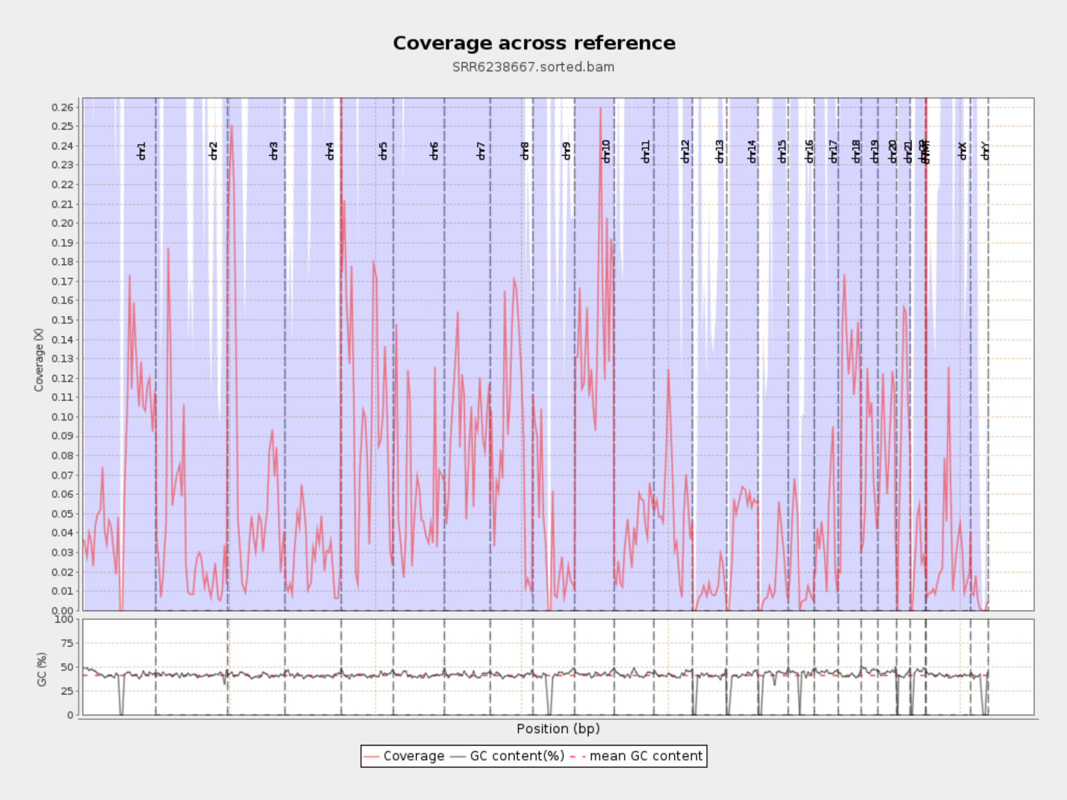
General error rate	0.59%
Mismatches	1,080,512
Insertions	11,060
Mapped reads with at least one insertion	0.37%
Deletions	48,998
Mapped reads with at least one deletion	1.63%
Homopolymer indels	41.51%

2.6. Chromosome stats

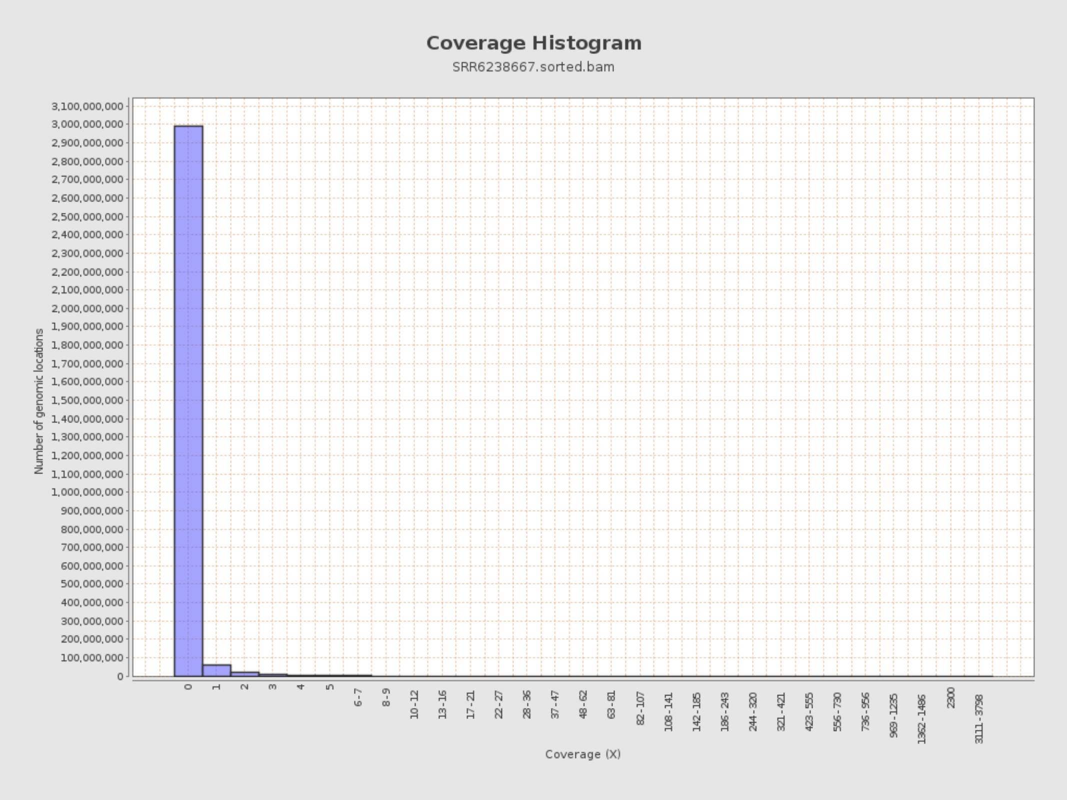
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17814515	0.0715	0.7483
chr2	243199373	9206167	0.0379	1.8009
chr3	198022430	14224452	0.0718	0.4444
chr4	191154276	5512233	0.0288	0.269
chr5	180915260	18880518	0.1044	0.5328
chr6	171115067	10499086	0.0614	0.6101
chr7	159138663	14975121	0.0941	0.9528

chr8	146364022	13019866	0.089	0.8071
chr9	141213431	4891071	0.0346	0.5613
chr10	135534747	19746206	0.1457	0.7794
chr11	135006516	5133135	0.038	0.3931
chr12	133851895	7300346	0.0545	0.3949
chr13	115169878	1260445	0.0109	0.3181
chr14	107349540	5106253	0.0476	0.3862
chr15	102531392	1714878	0.0167	0.3416
chr16	90354753	1805588	0.02	0.2894
chr17	81195210	3355174	0.0413	0.3399
chr18	78077248	9469790	0.1213	1.3782
chr19	59128983	4299548	0.0727	0.7223
chr20	63025520	5731220	0.0909	0.5131
chr21	48129895	4570850	0.095	0.51
chr22	51304566	1402151	0.0273	0.2687
chrMT	16571	77380	4.6696	5.2068
chrX	155270560	4767213	0.0307	0.3598
chrY	59373566	328652	0.0055	0.2065

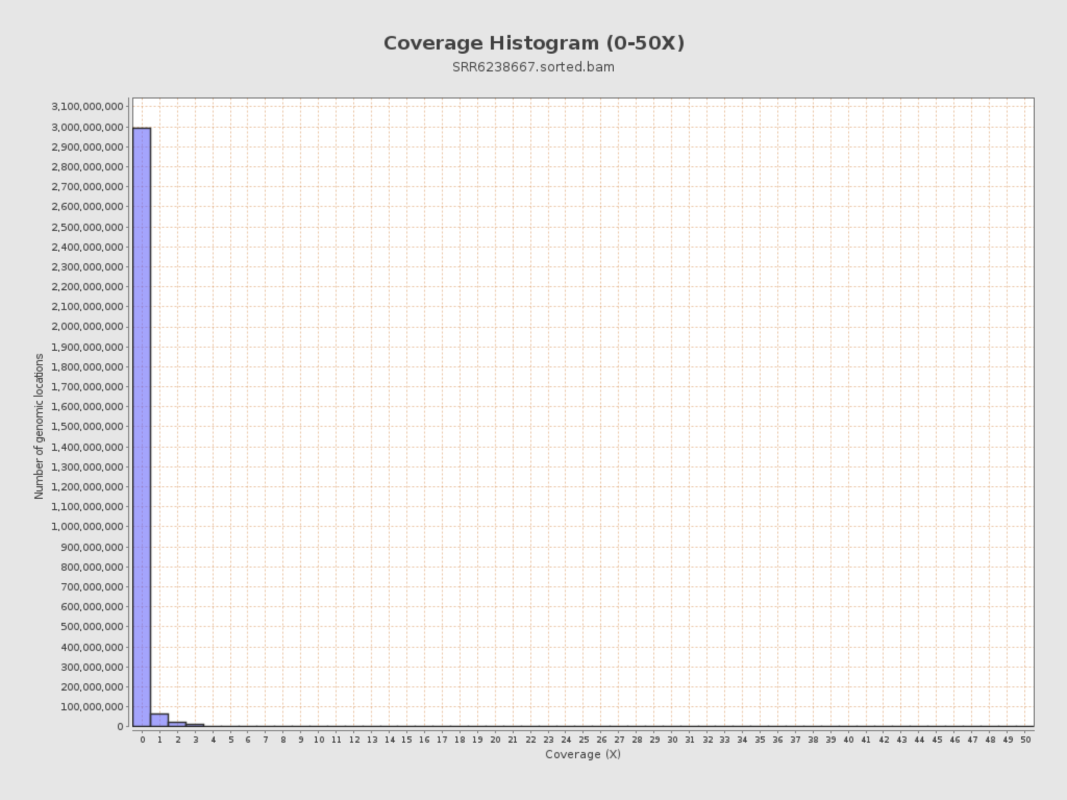
3. Results : Coverage across reference



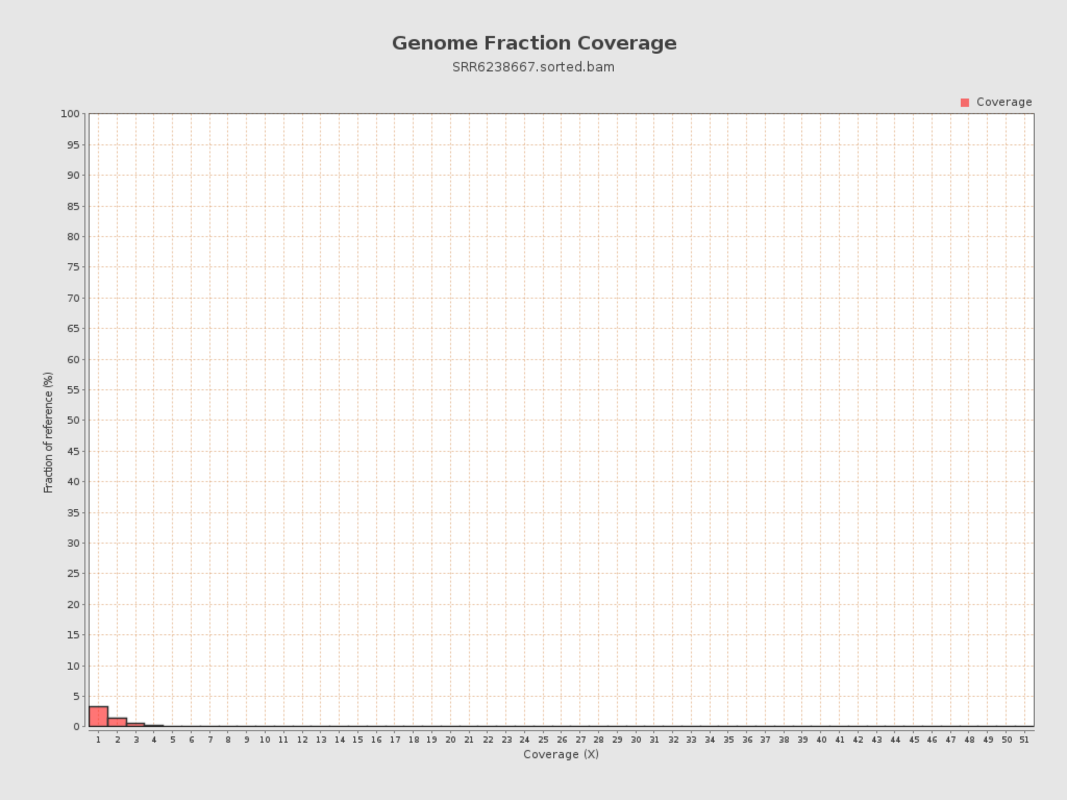
4. Results : Coverage Histogram



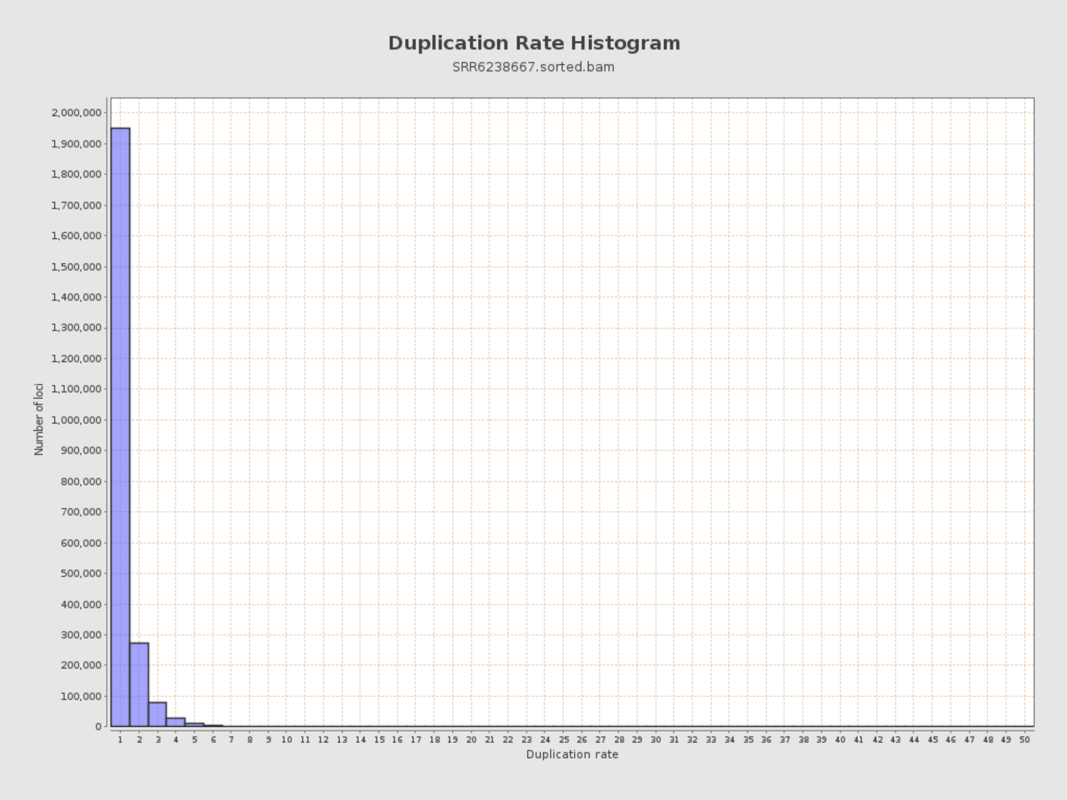
5. Results : Coverage Histogram (0-50X)



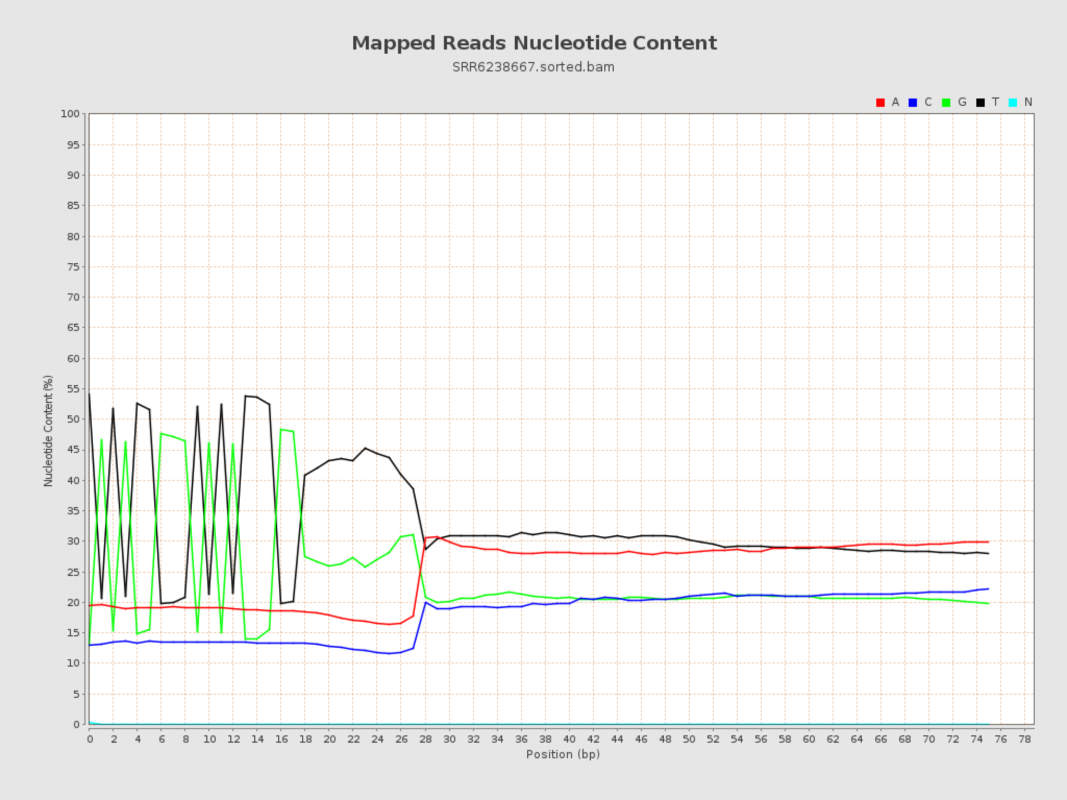
6. Results : Genome Fraction Coverage



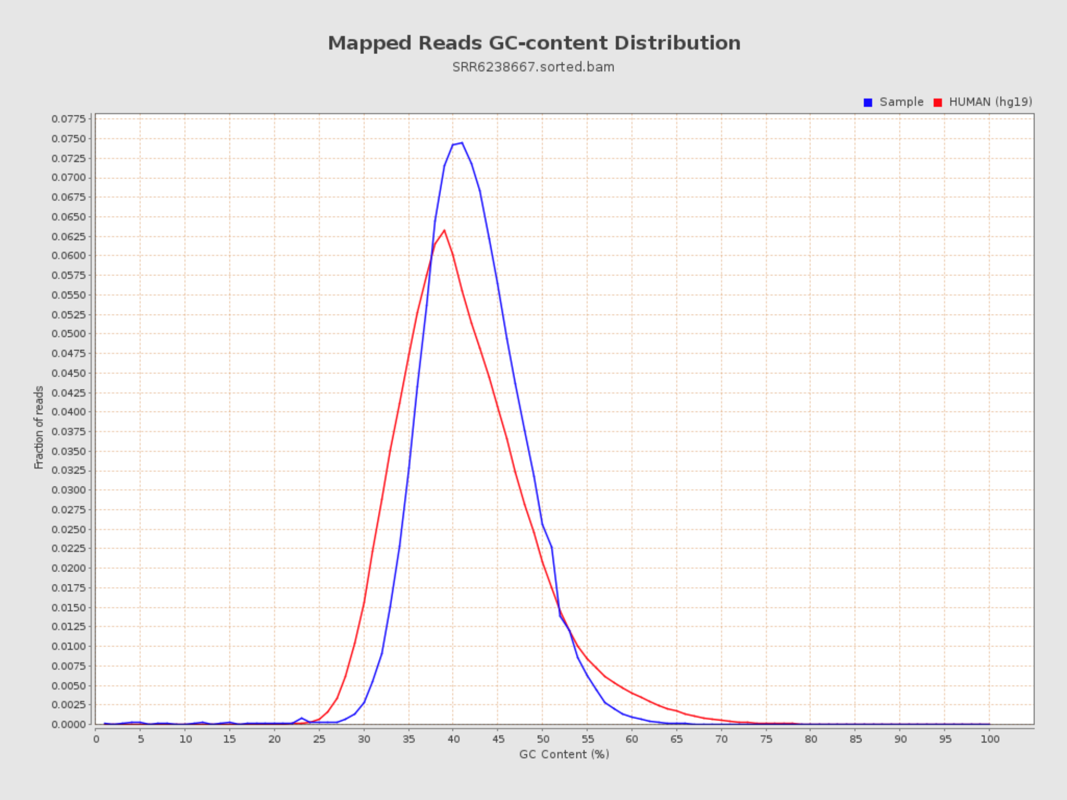
7. Results : Duplication Rate Histogram



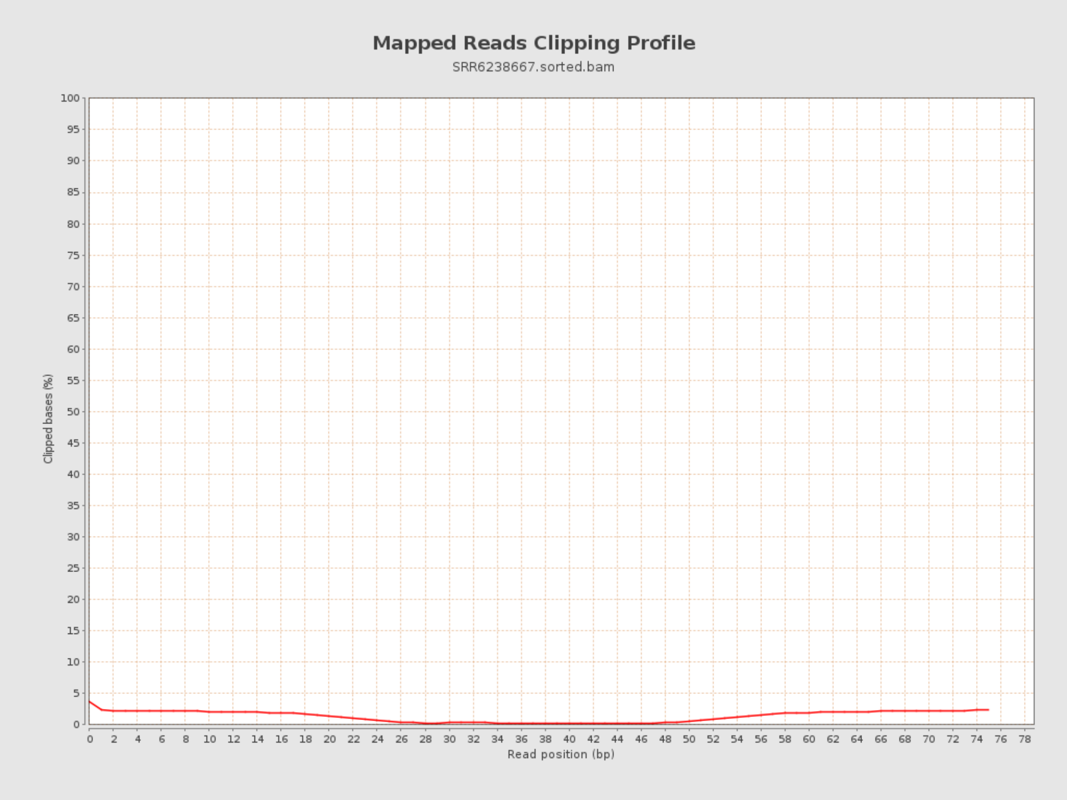
8. Results : Mapped Reads Nucleotide Content



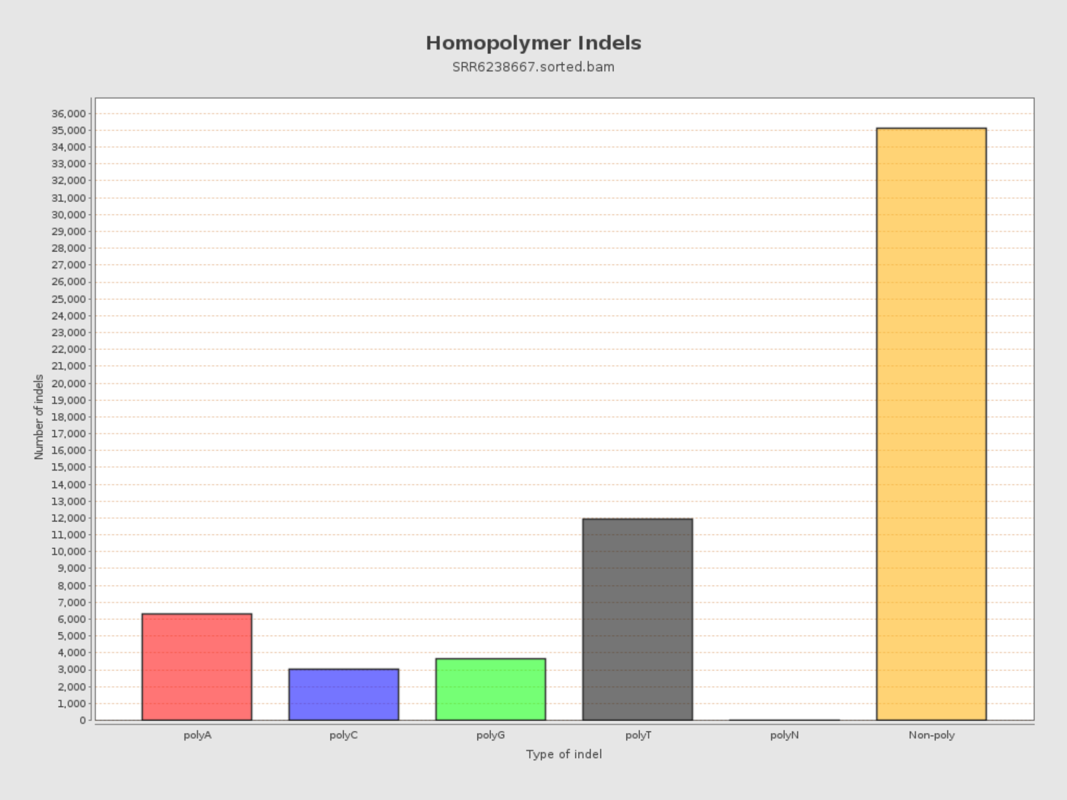
9. Results : Mapped Reads GC-content Distribution



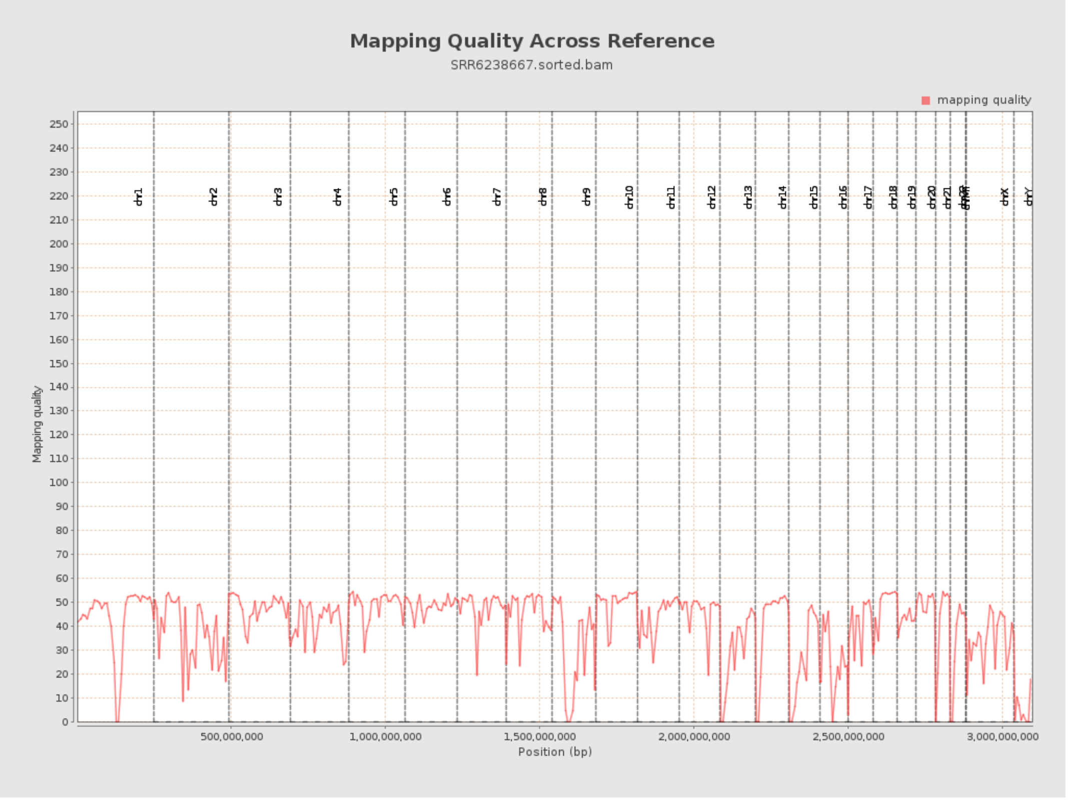
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram