Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:01:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238293.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_SRR6238293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238293.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:01:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,686,897
Mapped reads	2,407,922 / 89.62%
Unmapped reads	278,975 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,457 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	88,545 / 3.3%
Duplication rate	2.31%
Clipped reads	1,284,848 / 47.82%

2.2. ACGT Content

Number/percentage of A's	42,967,602 / 27.46%
Number/percentage of C's	30,563,342 / 19.53%
Number/percentage of T's	46,555,767 / 29.76%
Number/percentage of G's	36,338,540 / 23.23%
Number/percentage of N's	37,344 / 0.02%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.5156

2.4. Mapping Quality

Mean Mapping Quality	42.06

2.5. Mismatches and indels

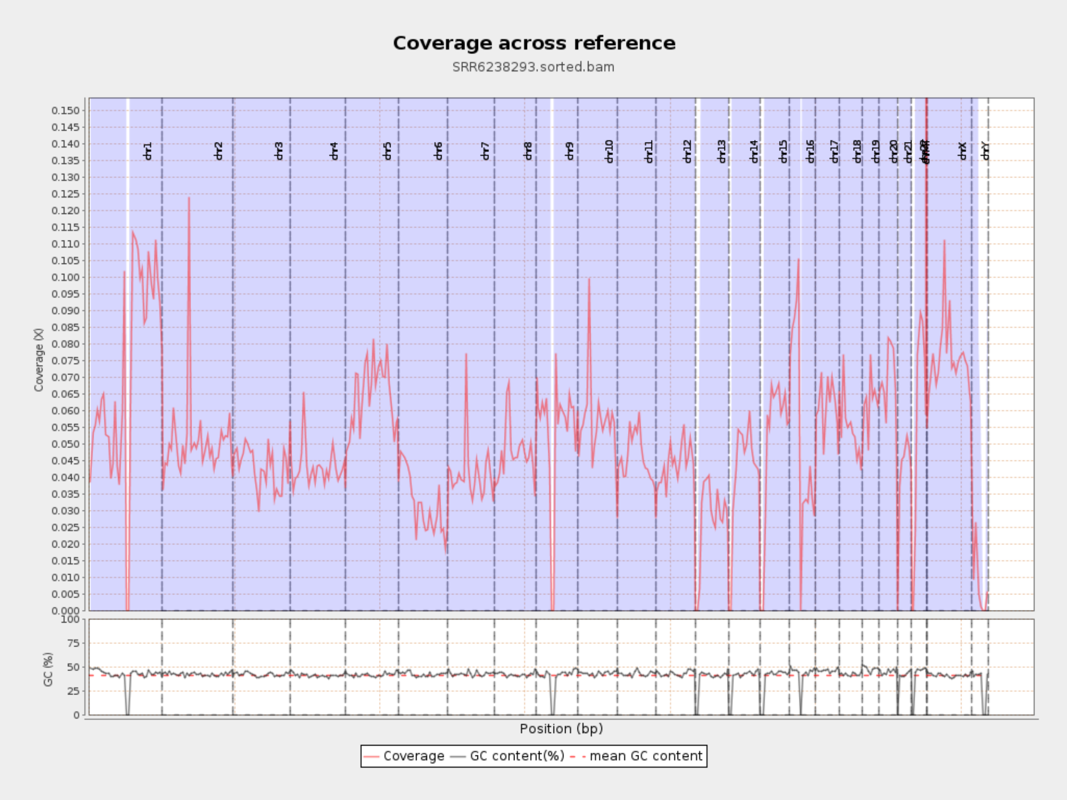
General error rate	0.91%
Mismatches	1,391,593
Insertions	13,468
Mapped reads with at least one insertion	0.55%
Deletions	44,042
Mapped reads with at least one deletion	1.81%
Homopolymer indels	44.23%

2.6. Chromosome stats

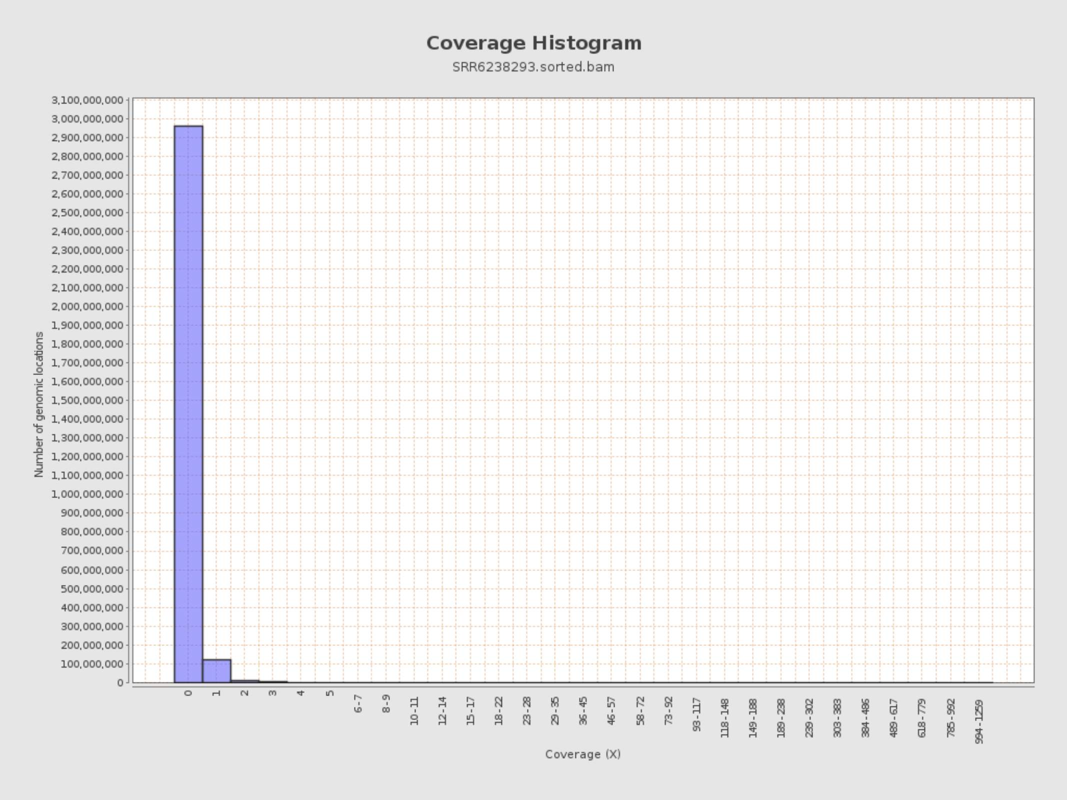
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17639506	0.0708	1.0344
chr2	243199373	12449749	0.0512	0.681
chr3	198022430	8493501	0.0429	0.2353
chr4	191154276	8176490	0.0428	0.2624
chr5	180915260	11742454	0.0649	0.2906
chr6	171115067	5432277	0.0317	0.2306
chr7	159138663	6553788	0.0412	0.5241

chr8	146364022	6876116	0.047	0.5885
chr9	141213431	7459759	0.0528	0.5728
chr10	135534747	7750288	0.0572	0.4719
chr11	135006516	6182076	0.0458	0.4147
chr12	133851895	5884692	0.044	0.2529
chr13	115169878	3088865	0.0268	0.1822
chr14	107349540	4437788	0.0413	0.3283
chr15	102531392	5169620	0.0504	0.2567
chr16	90354753	4829889	0.0535	0.337
chr17	81195210	4954453	0.061	0.3302
chr18	78077248	4276426	0.0548	0.9954
chr19	59128983	3686143	0.0623	0.7567
chr20	63025520	4371962	0.0694	0.3073
chr21	48129895	1985587	0.0413	0.2804
chr22	51304566	2840173	0.0554	0.2654
chrMT	16571	10683	0.6447	0.9585
chrX	155270560	11740314	0.0756	0.3885
chrY	59373566	503346	0.0085	0.2083

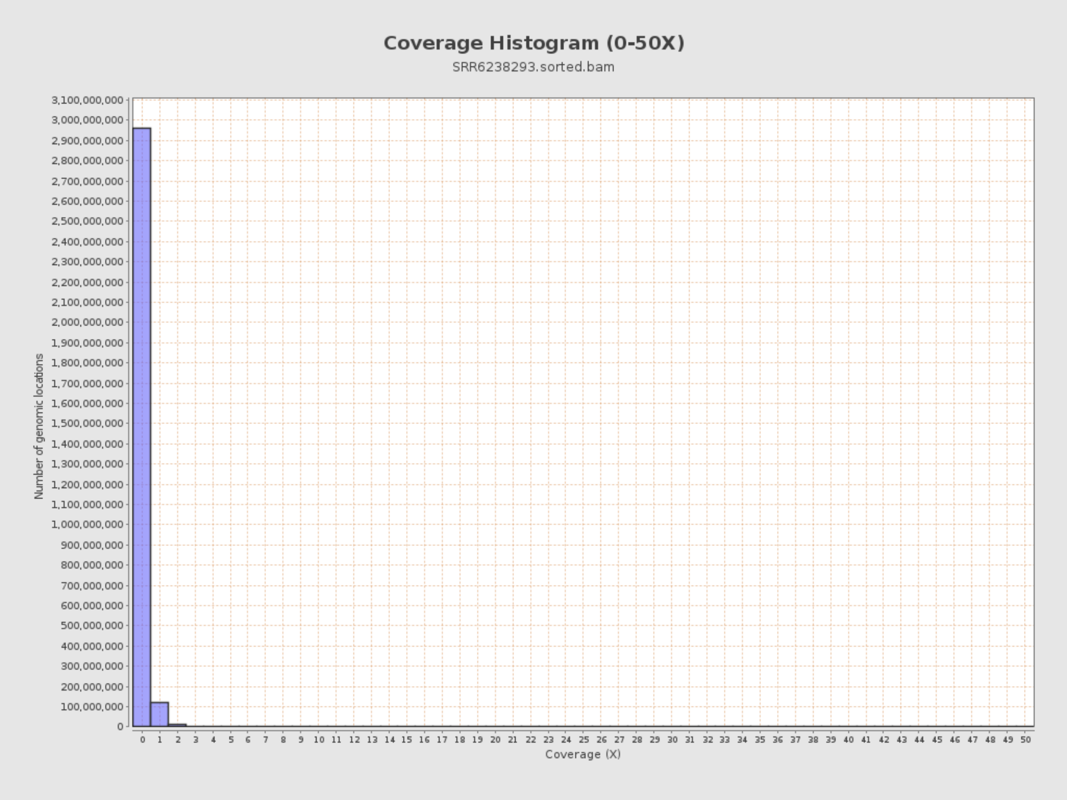
3. Results : Coverage across reference



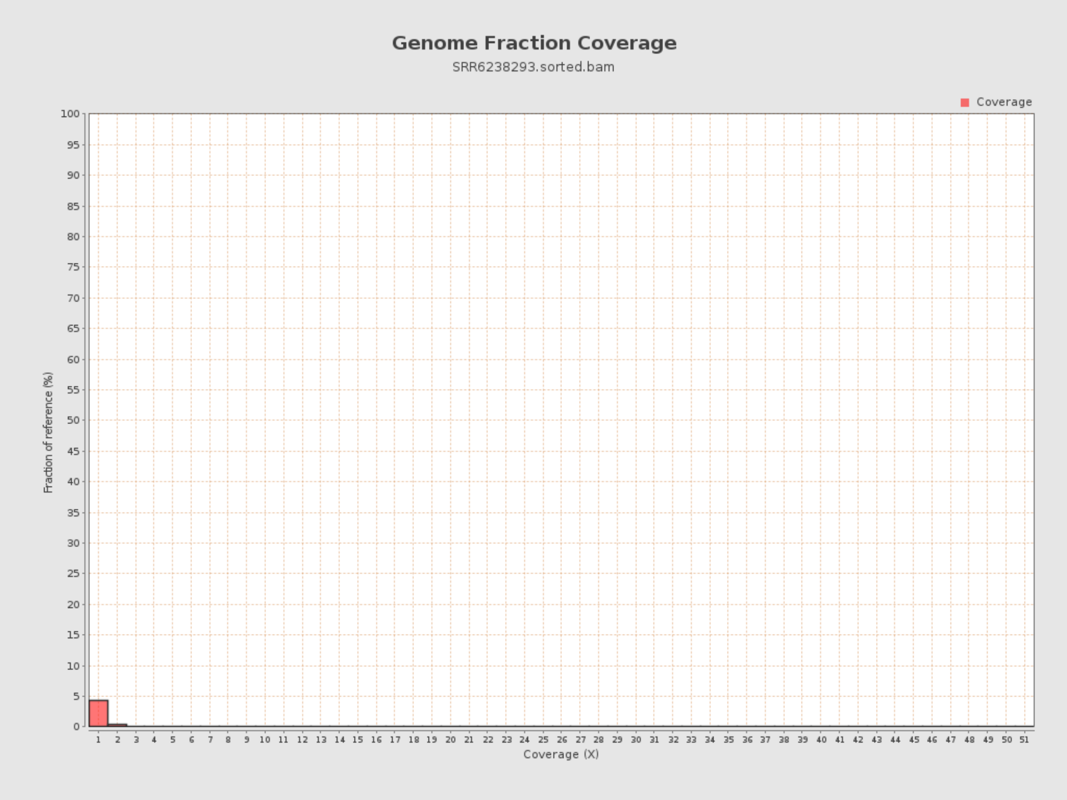
4. Results : Coverage Histogram



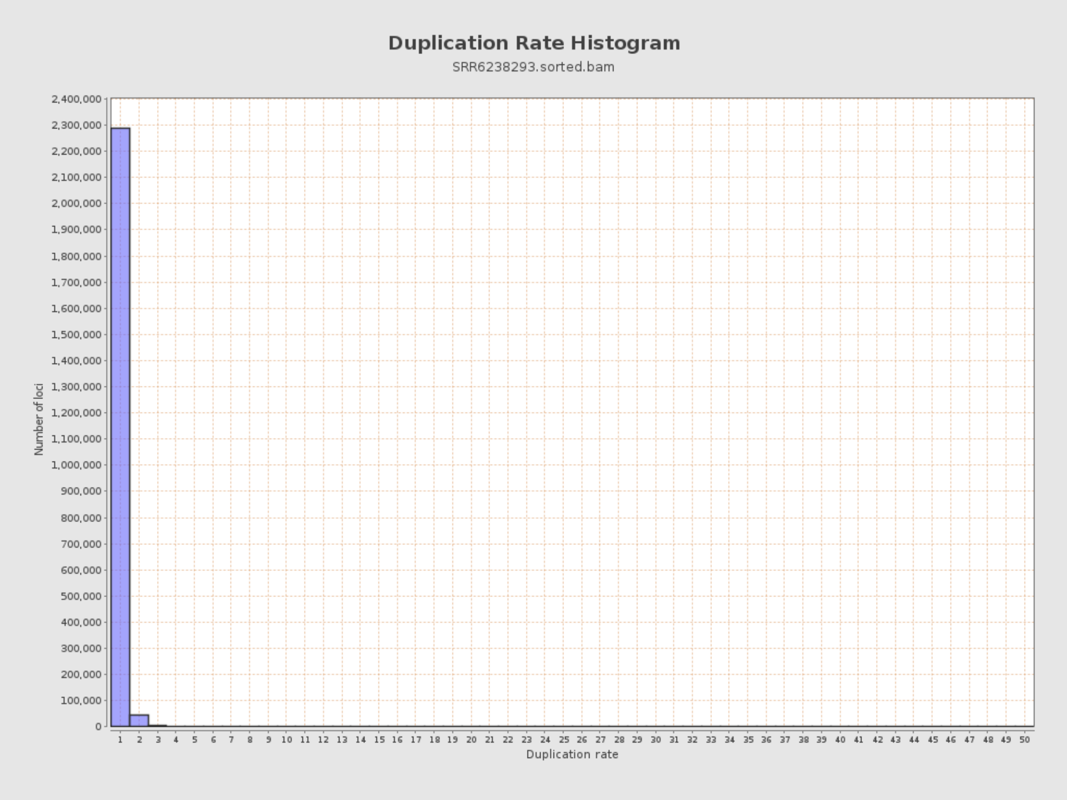
5. Results : Coverage Histogram (0-50X)



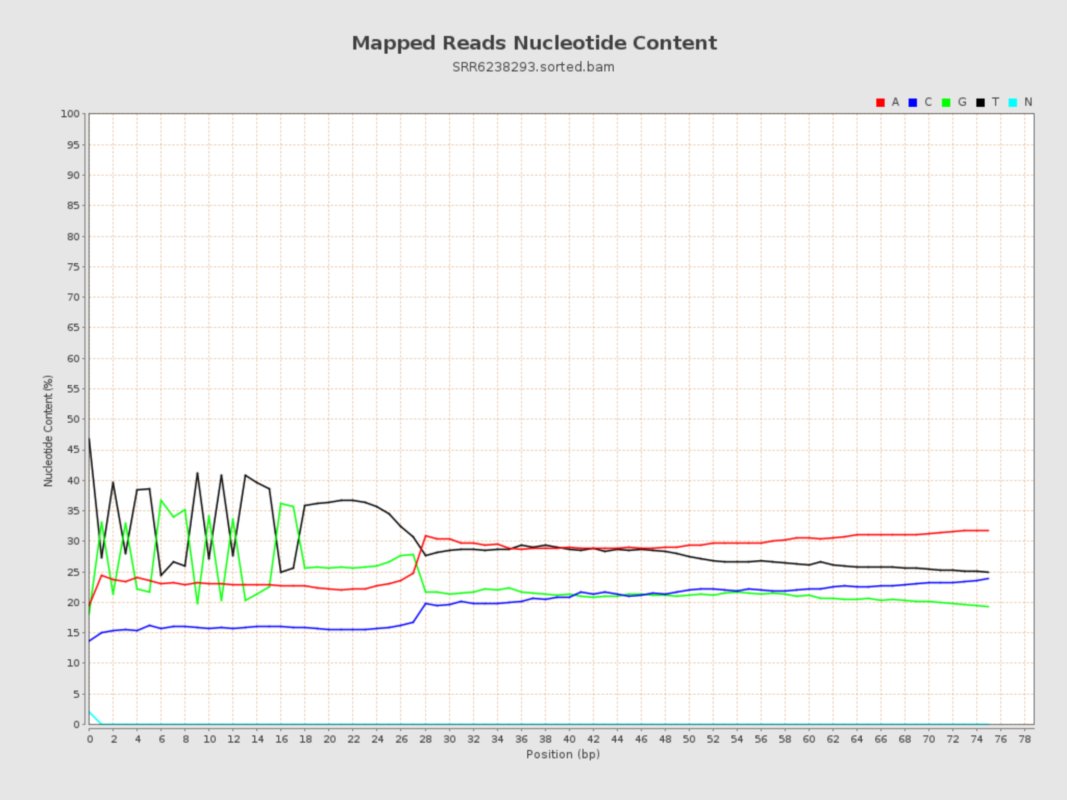
6. Results : Genome Fraction Coverage



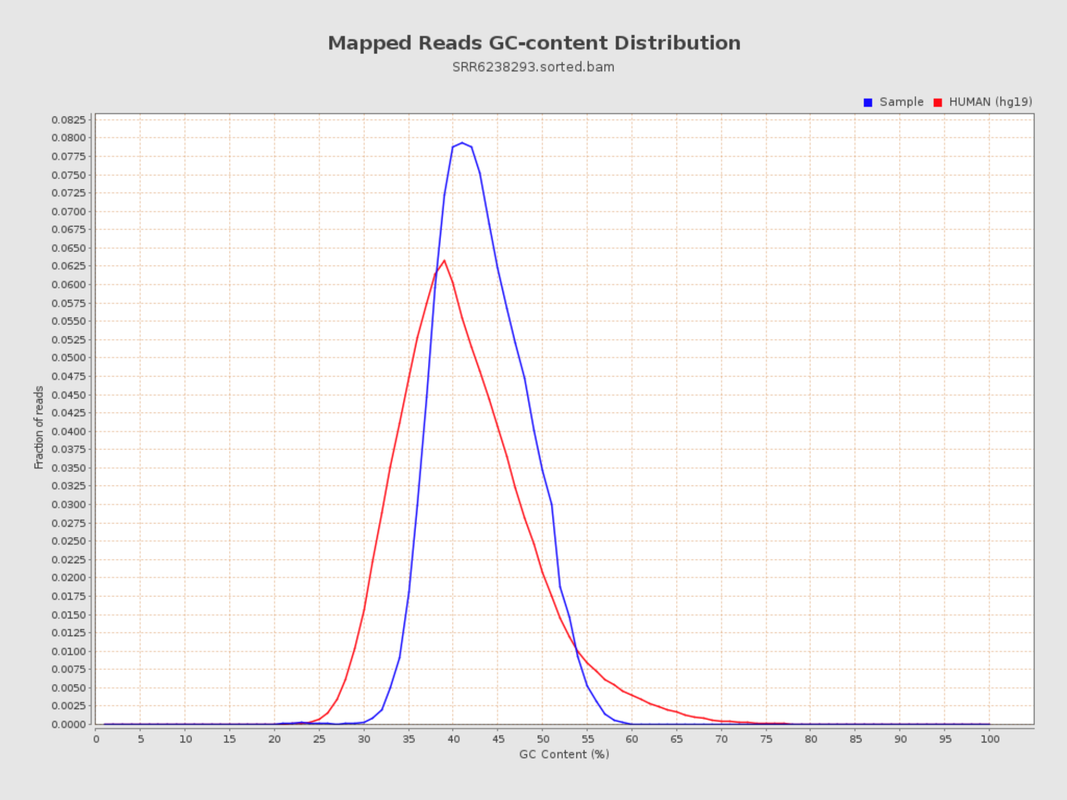
7. Results : Duplication Rate Histogram



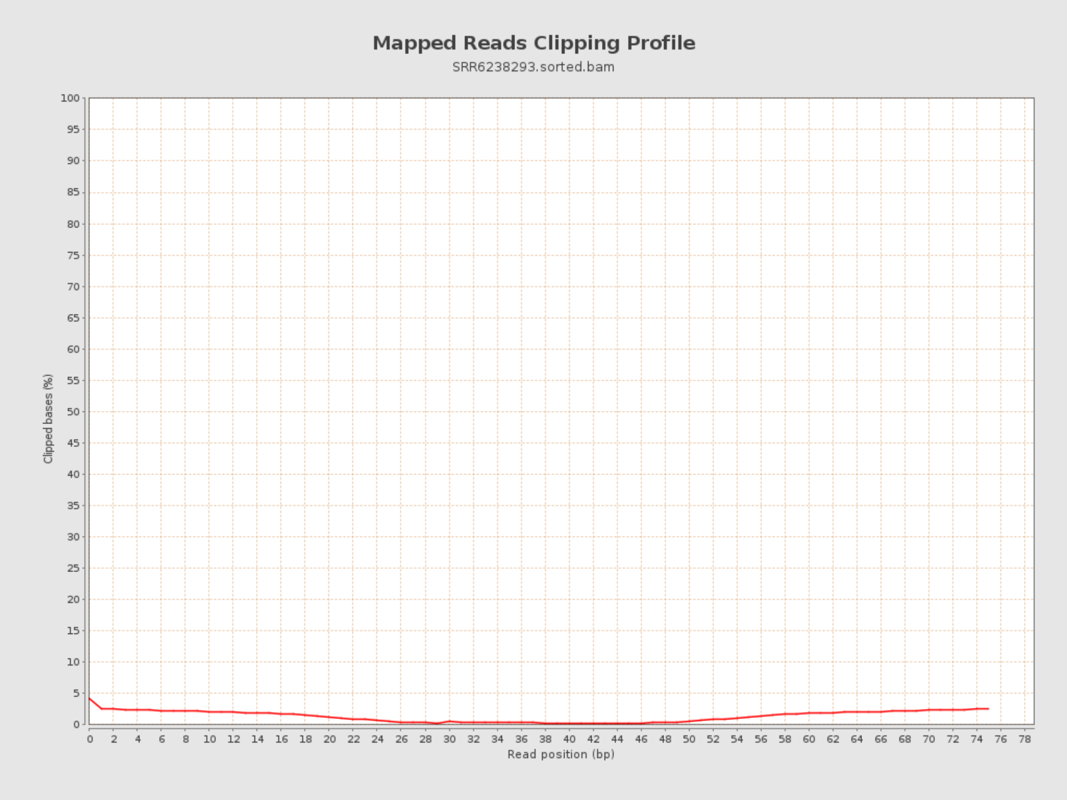
8. Results : Mapped Reads Nucleotide Content



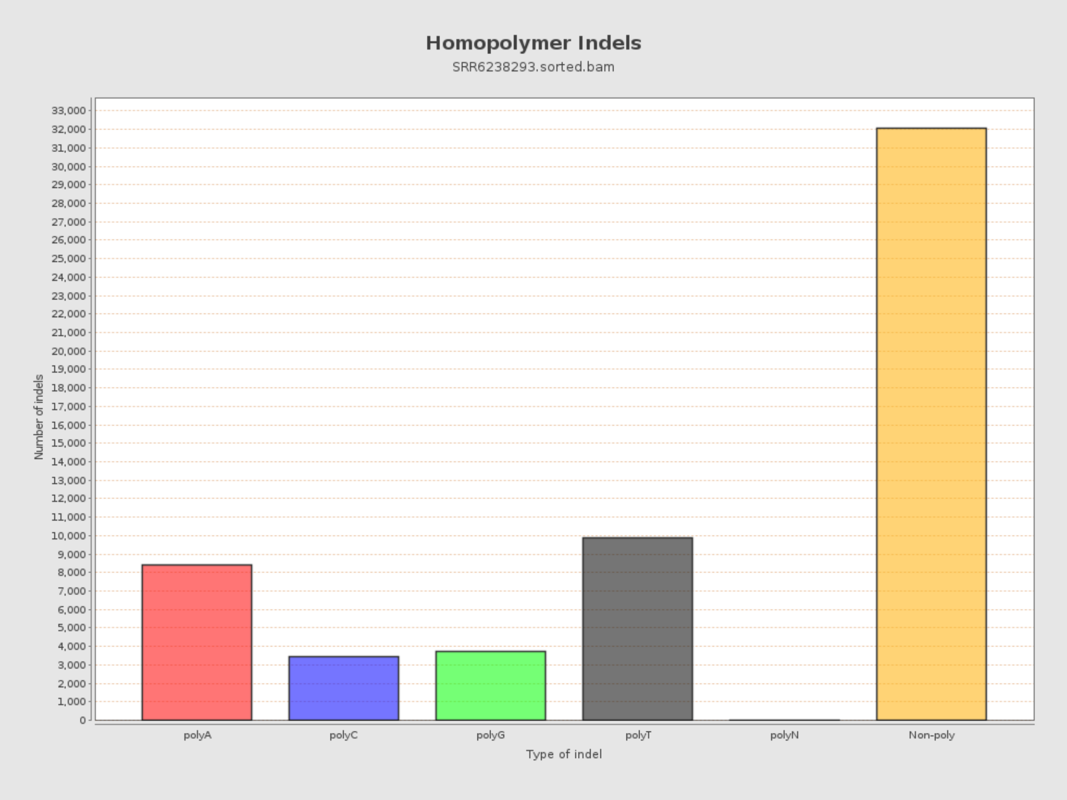
9. Results : Mapped Reads GC-content Distribution



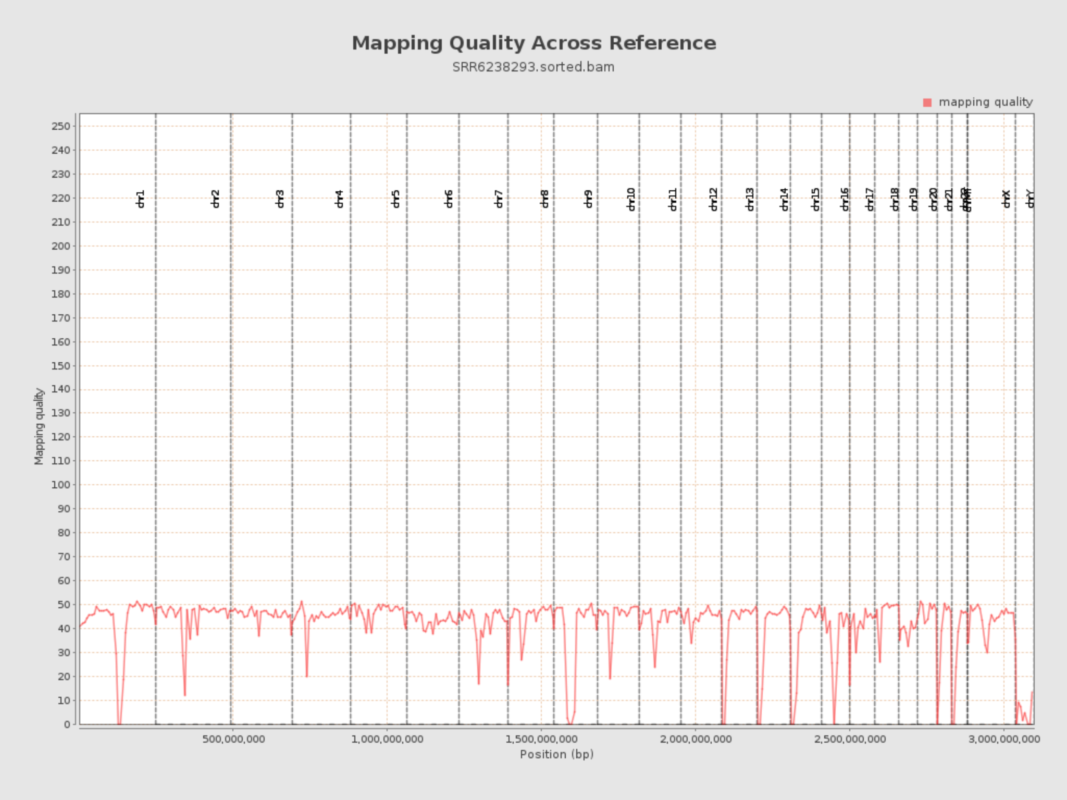
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram