Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:53:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238639.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_SRR6238639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238639.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:53:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,847,064
Mapped reads	3,513,652 / 91.33%
Unmapped reads	333,412 / 8.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,176 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,276,761 / 33.19%
Duplication rate	20.61%
Clipped reads	2,141,915 / 55.68%

2.2. ACGT Content

Number/percentage of A's	53,620,966 / 24.54%
Number/percentage of C's	38,550,671 / 17.64%
Number/percentage of T's	73,069,847 / 33.44%
Number/percentage of G's	53,253,164 / 24.37%
Number/percentage of N's	11,183 / 0.01%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0706

Standard Deviation	0.923

2.4. Mapping Quality

Mean Mapping Quality	43.88

2.5. Mismatches and indels

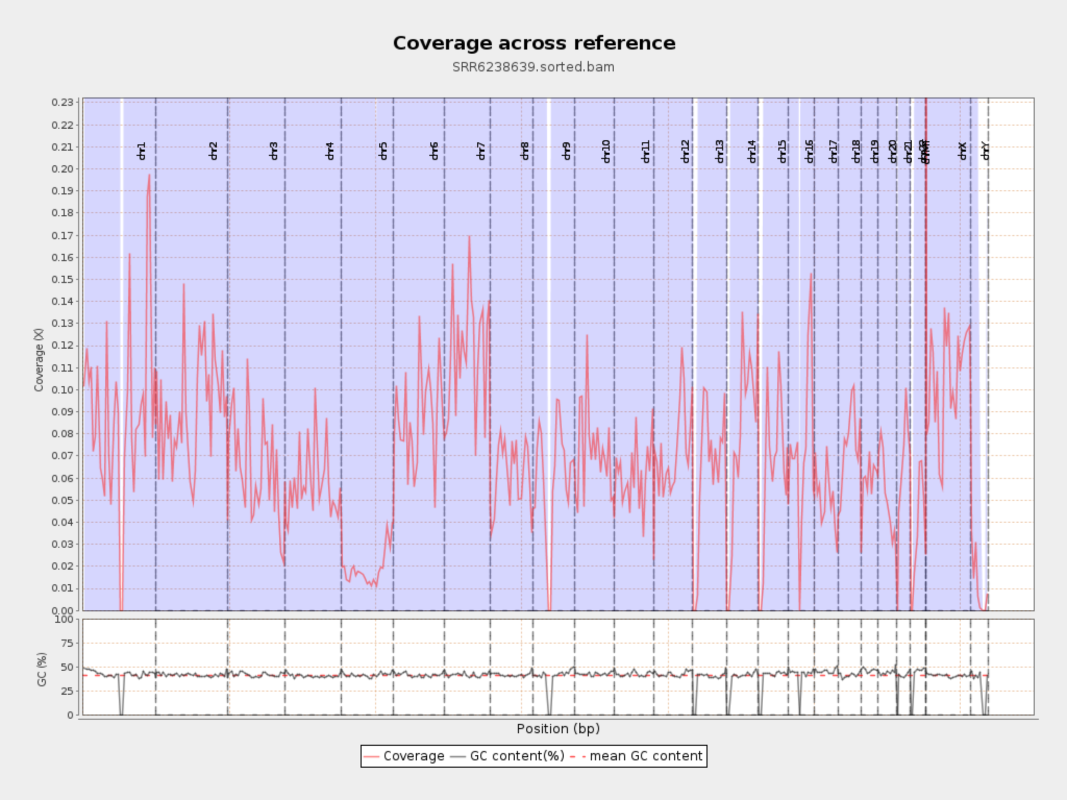
General error rate	0.53%
Mismatches	1,127,175
Insertions	13,906
Mapped reads with at least one insertion	0.39%
Deletions	48,701
Mapped reads with at least one deletion	1.37%
Homopolymer indels	43.89%

2.6. Chromosome stats

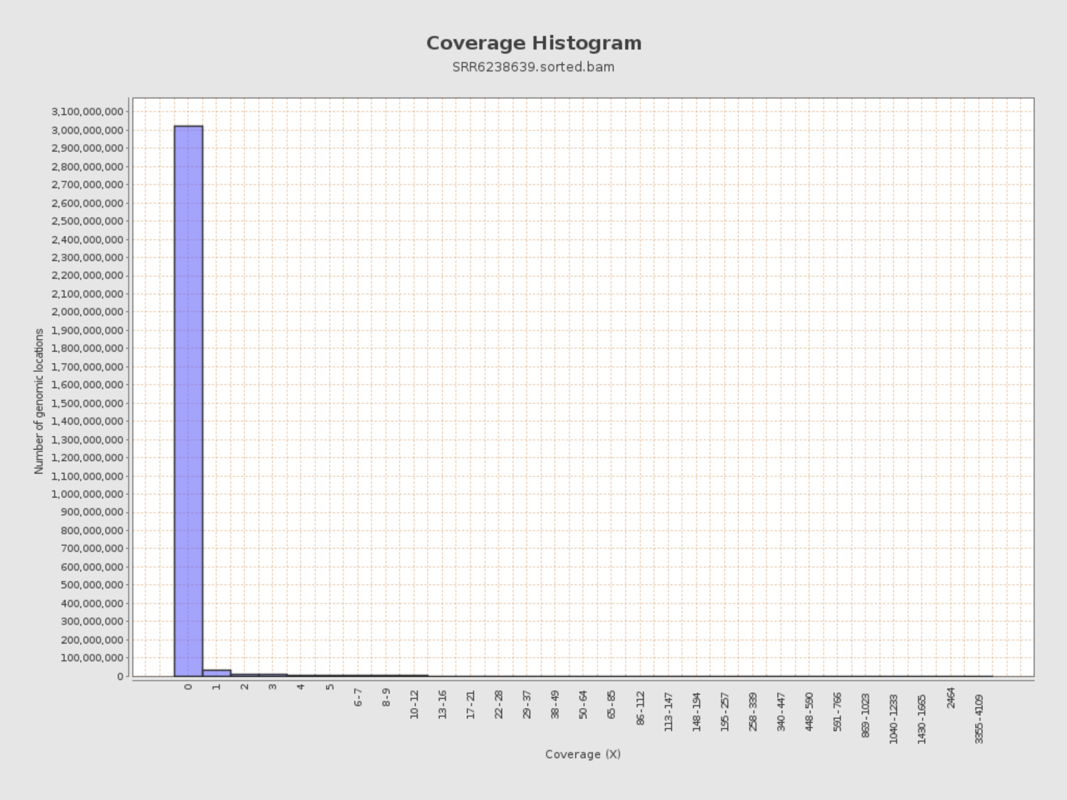
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22306587	0.0895	0.9965
chr2	243199373	22349569	0.0919	1.9398
chr3	198022430	12829858	0.0648	0.6298
chr4	191154276	11068031	0.0579	0.6062
chr5	180915260	3528994	0.0195	0.3219
chr6	171115067	15123368	0.0884	0.9378
chr7	159138663	18594445	0.1168	1.0632

chr8	146364022	9117156	0.0623	0.7299
chr9	141213431	8477558	0.06	0.6641
chr10	135534747	9798632	0.0723	0.7378
chr11	135006516	8260798	0.0612	0.6439
chr12	133851895	9736268	0.0727	0.6815
chr13	115169878	7233672	0.0628	0.7209
chr14	107349540	8267310	0.077	0.6986
chr15	102531392	6372049	0.0621	0.7106
chr16	90354753	6471638	0.0716	0.7106
chr17	81195210	4235203	0.0522	0.5891
chr18	78077248	5851716	0.0749	1.6191
chr19	59128983	3524716	0.0596	0.7066
chr20	63025520	3317290	0.0526	0.5781
chr21	48129895	3114526	0.0647	0.647
chr22	51304566	1881798	0.0367	0.4824
chrMT	16571	7870	0.4749	1.1039
chrX	155270560	16466539	0.1061	0.8405
chrY	59373566	654484	0.011	0.3683

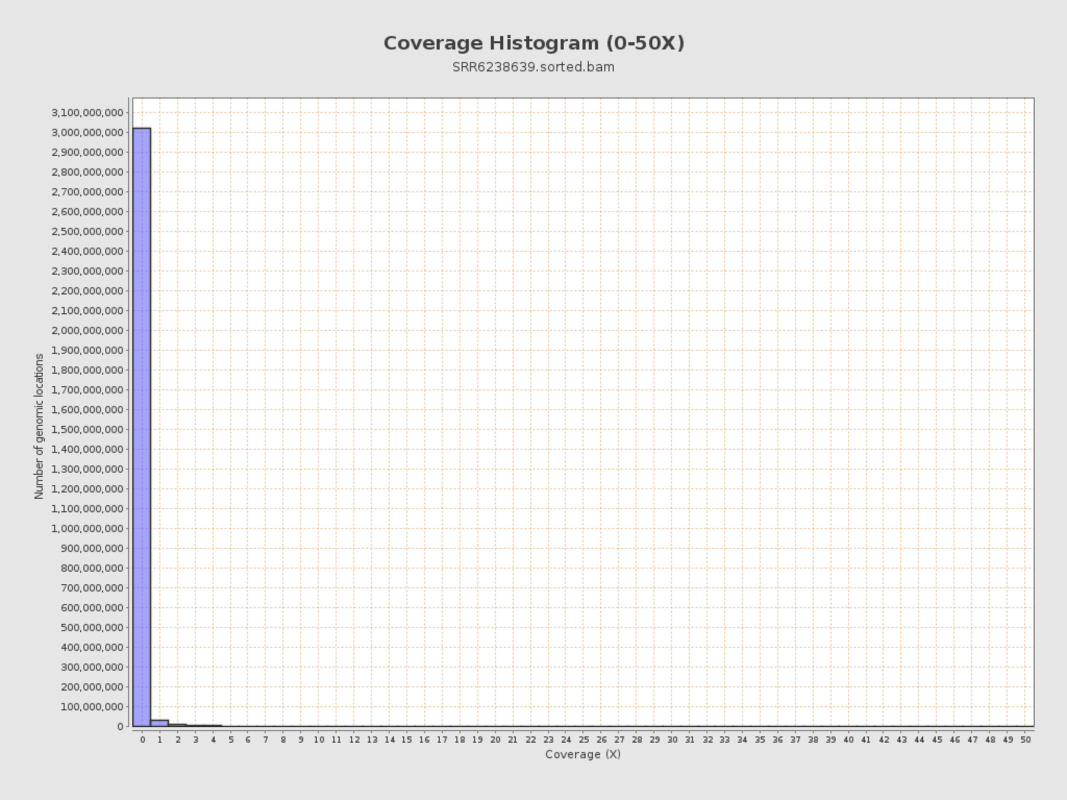
3. Results : Coverage across reference



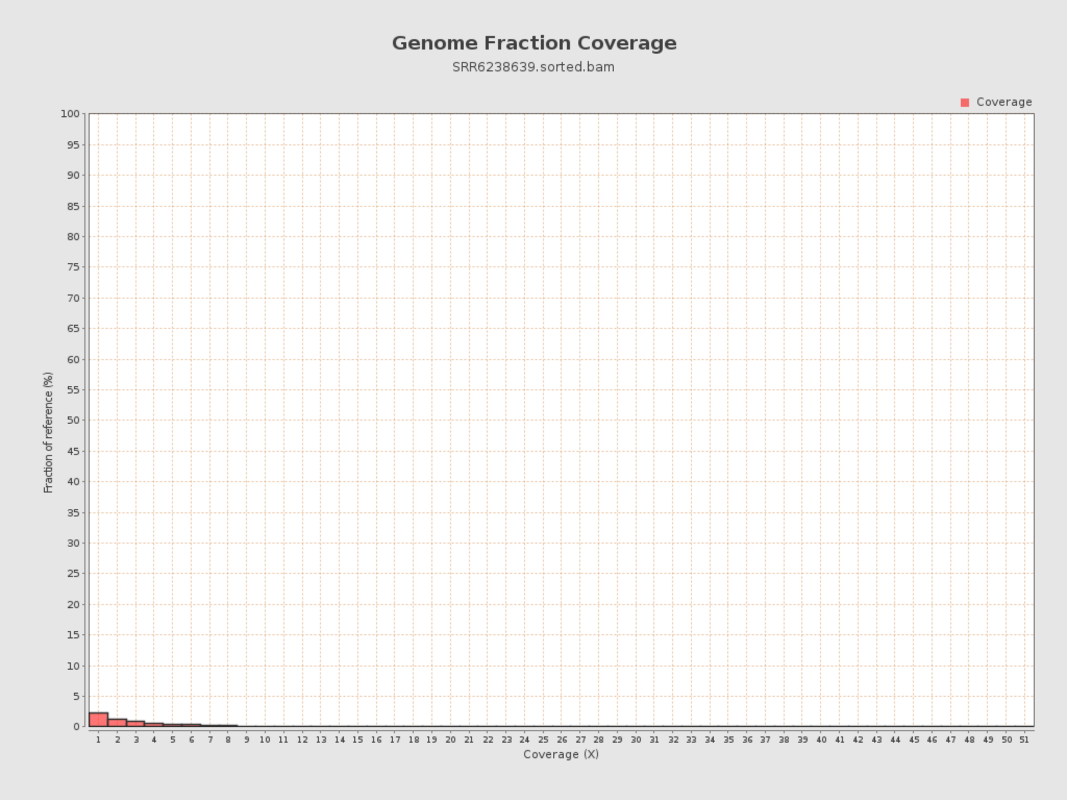
4. Results : Coverage Histogram



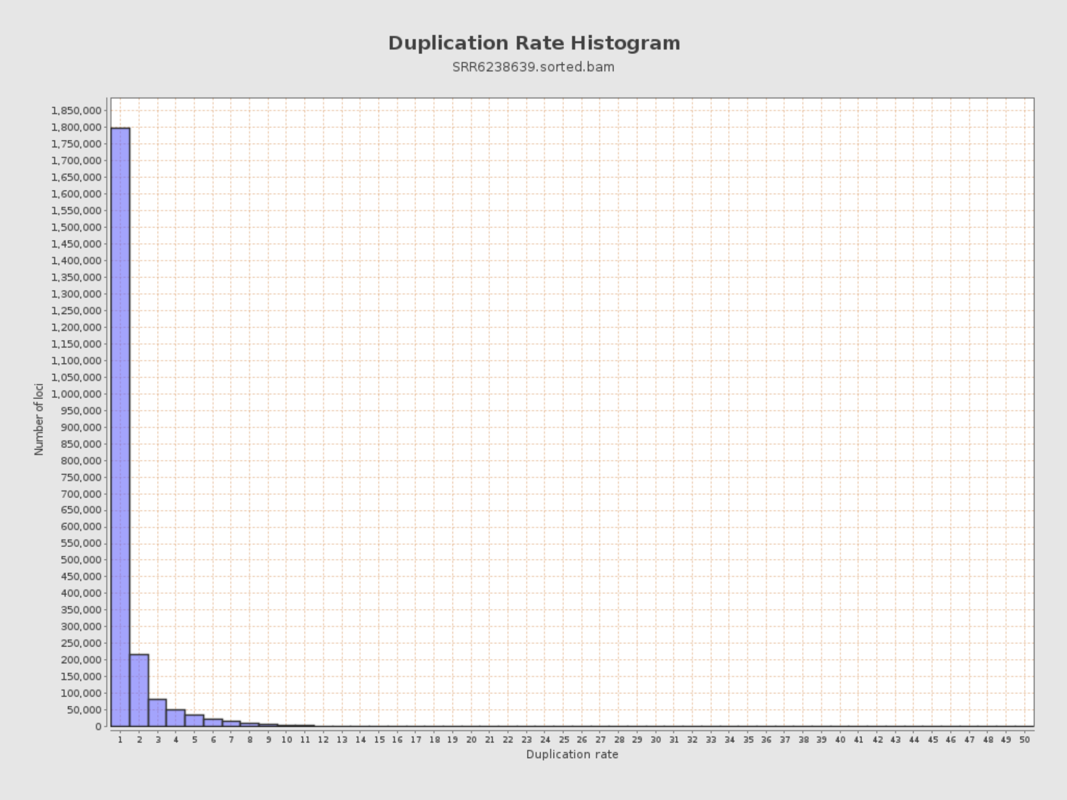
5. Results : Coverage Histogram (0-50X)



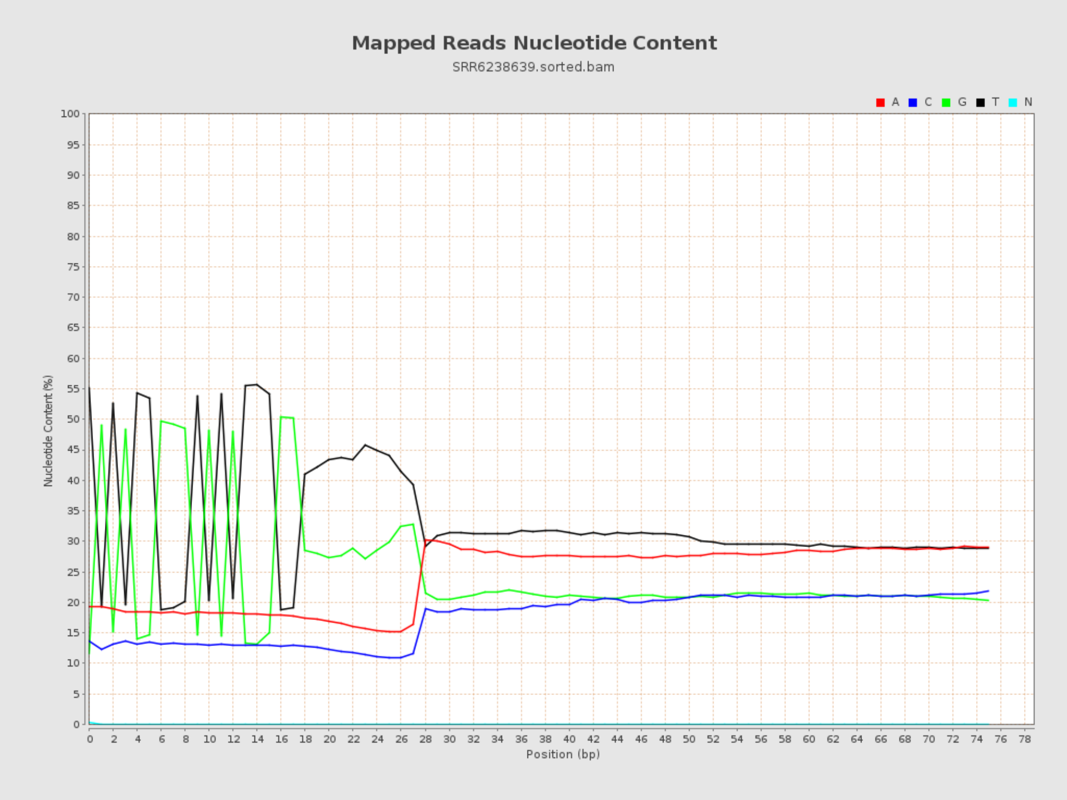
6. Results : Genome Fraction Coverage



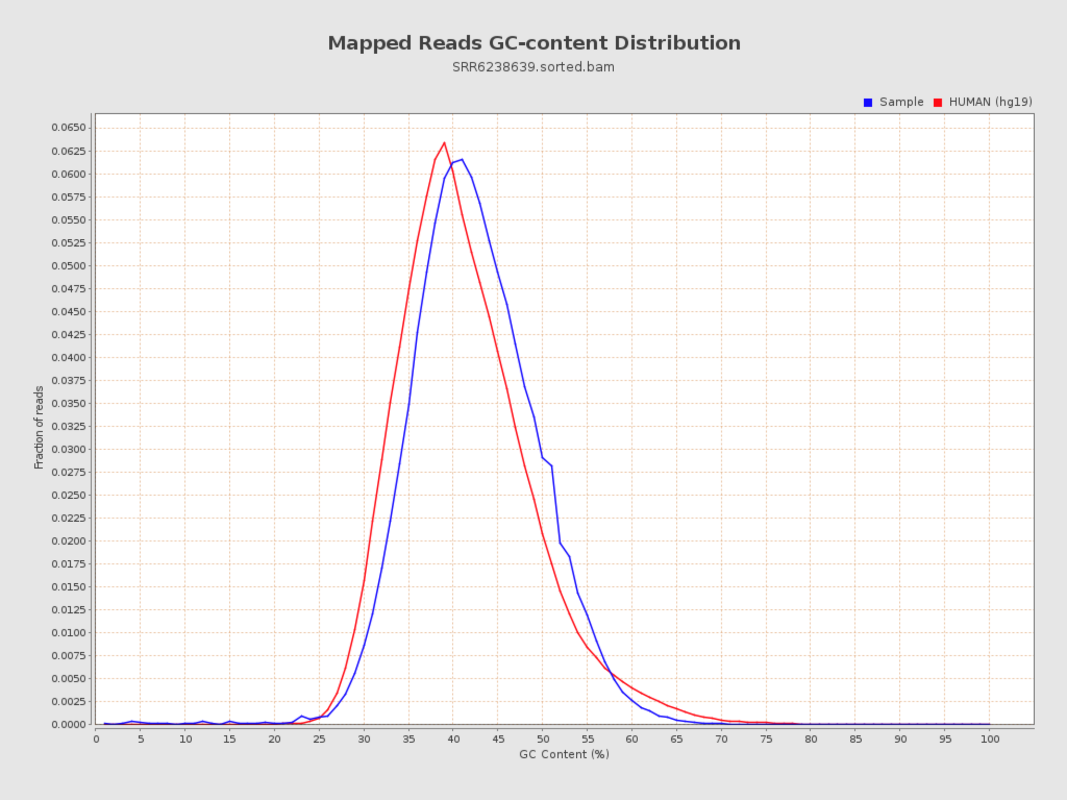
7. Results : Duplication Rate Histogram



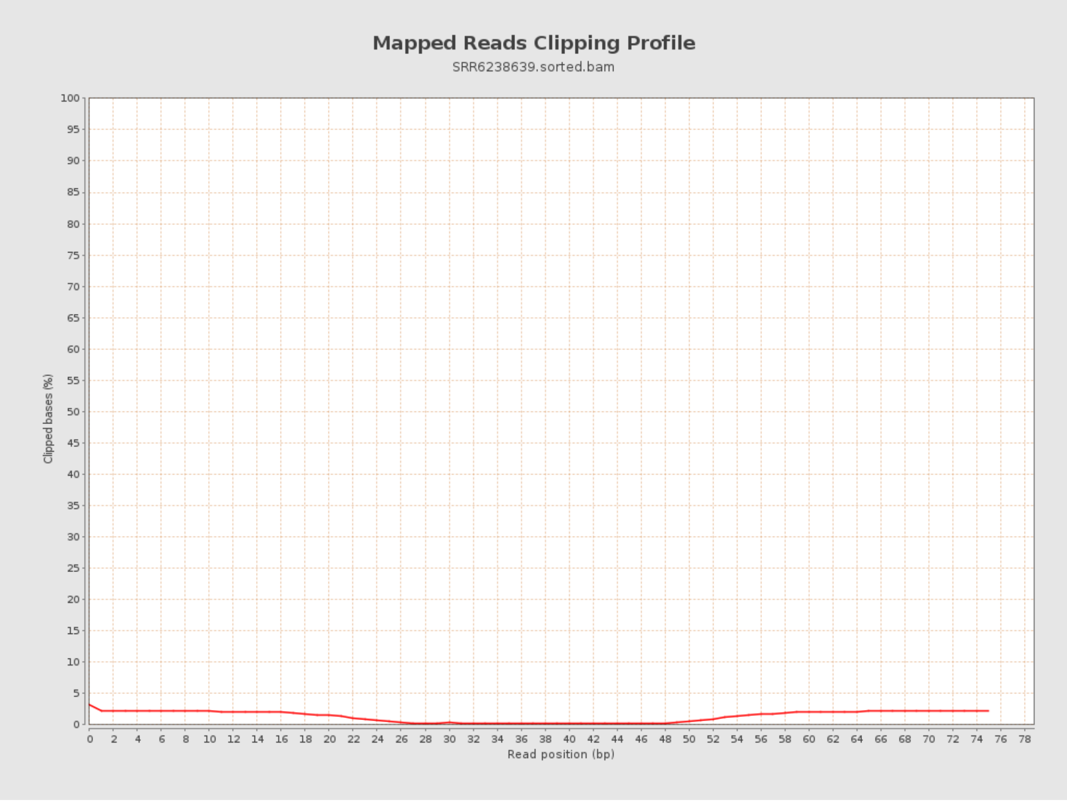
8. Results : Mapped Reads Nucleotide Content



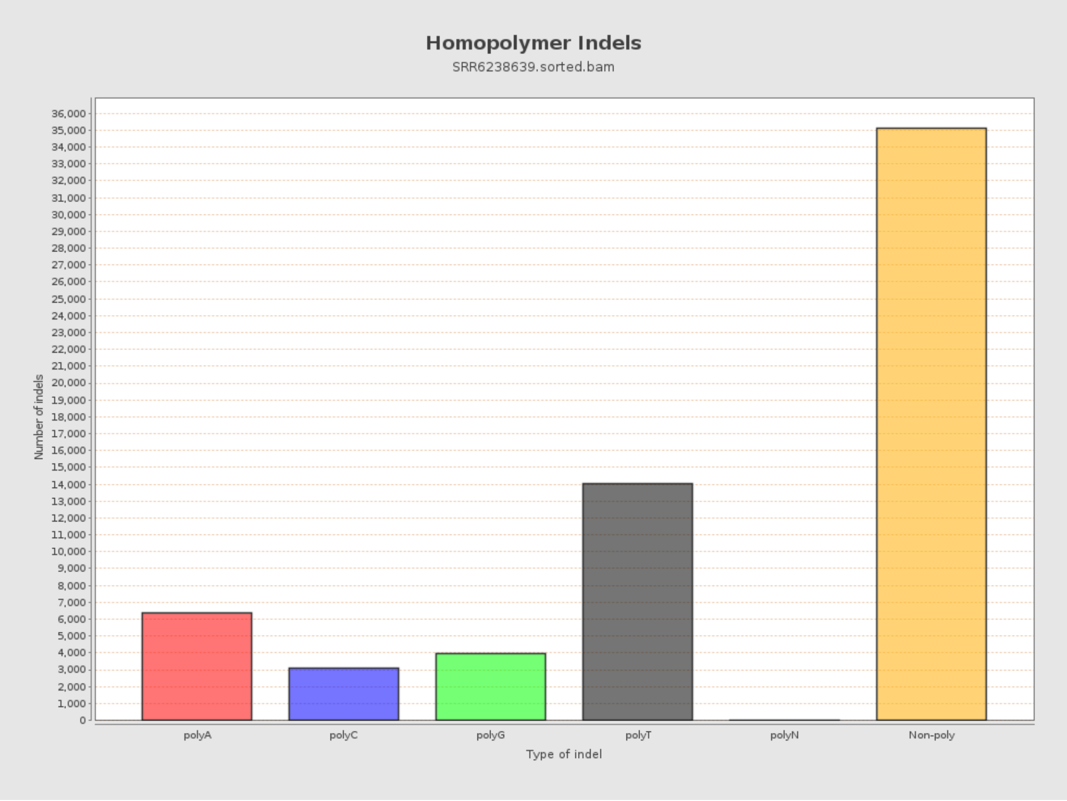
9. Results : Mapped Reads GC-content Distribution



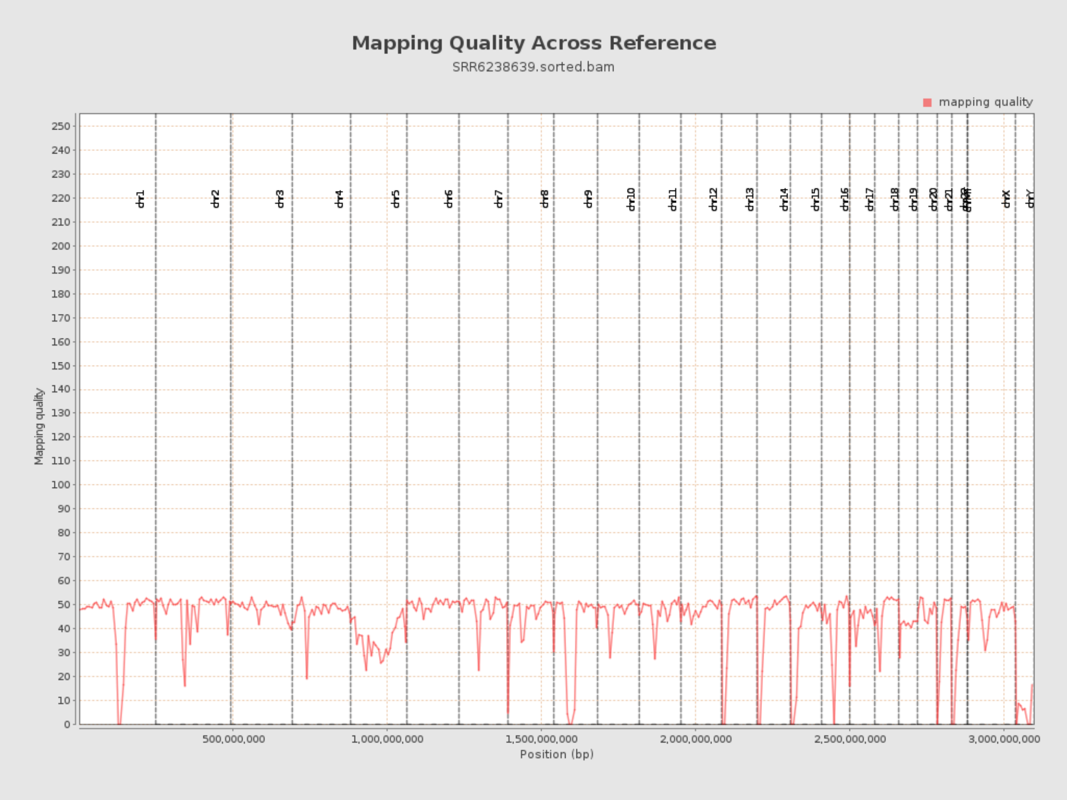
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram