Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:09:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238035.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_SRR6238035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:09:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,222,807
Mapped reads	1,987,446 / 89.41%
Unmapped reads	235,361 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,378 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	96,840 / 4.36%
Duplication rate	3.79%
Clipped reads	835,175 / 37.57%

2.2. ACGT Content

Number/percentage of A's	36,097,109 / 27.09%
Number/percentage of C's	25,711,314 / 19.3%
Number/percentage of T's	41,167,136 / 30.9%
Number/percentage of G's	30,246,477 / 22.7%
Number/percentage of N's	18,877 / 0.01%
GC Percentage	42%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.3959

2.4. Mapping Quality

Mean Mapping Quality	43

2.5. Mismatches and indels

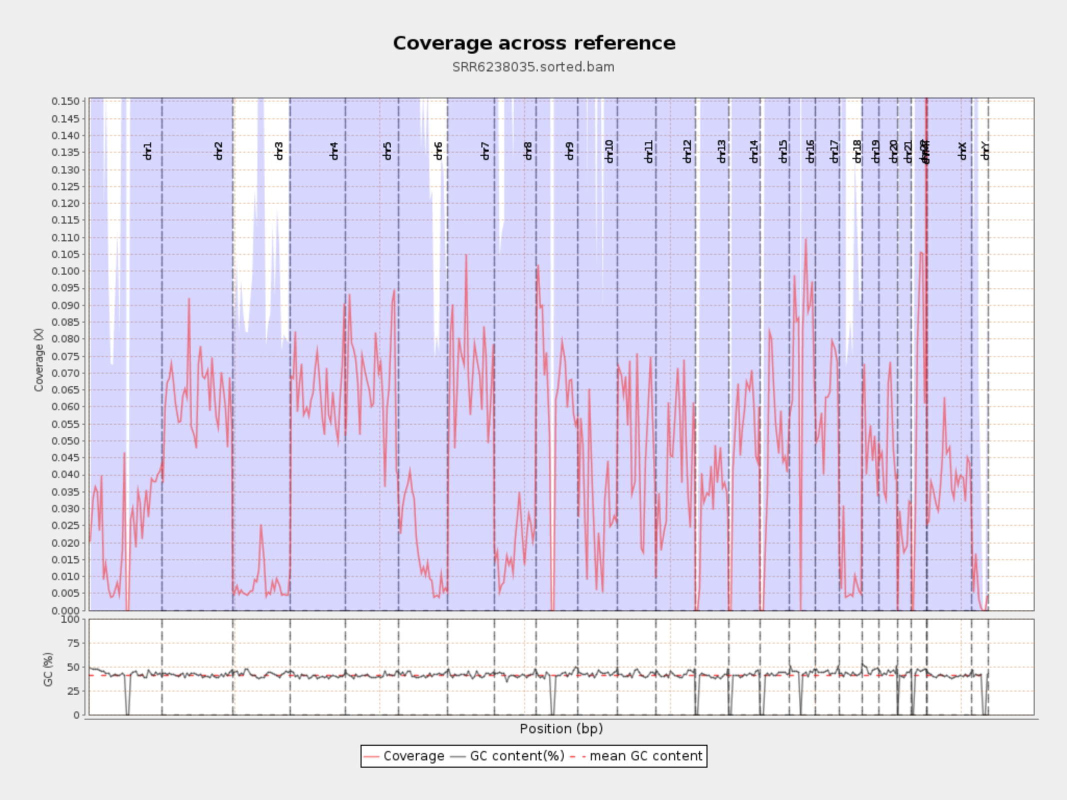
General error rate	0.75%
Mismatches	984,307
Insertions	9,134
Mapped reads with at least one insertion	0.46%
Deletions	31,332
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.55%

2.6. Chromosome stats

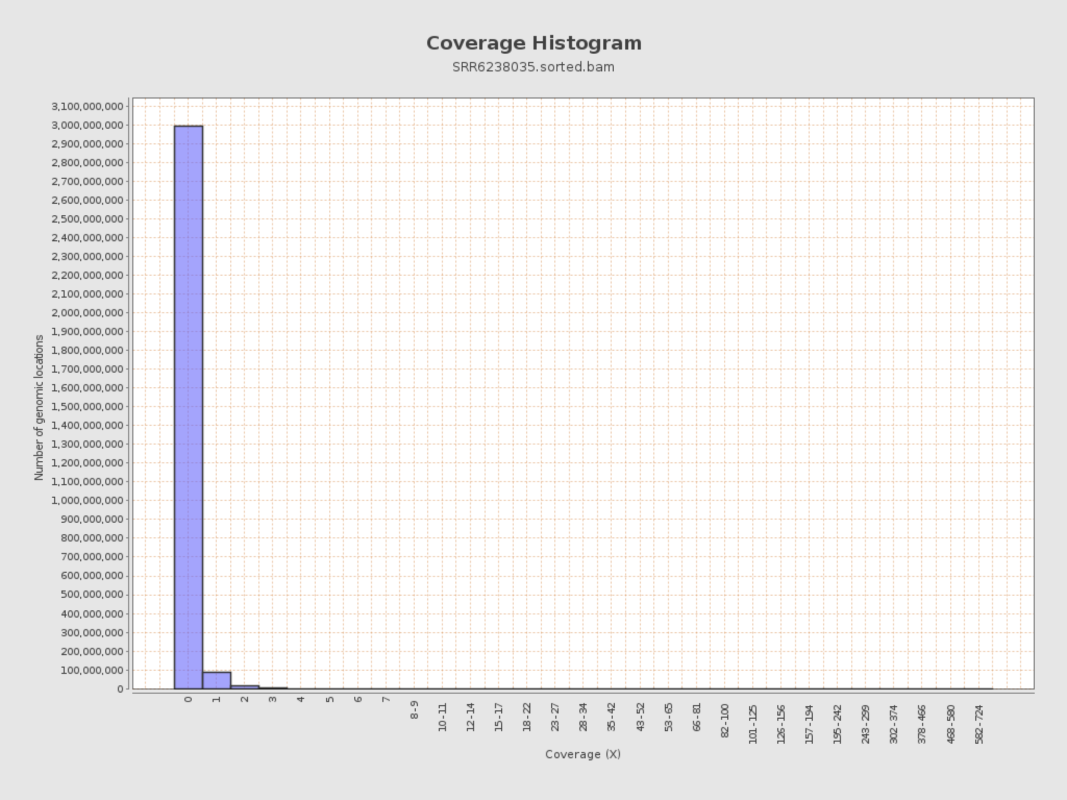
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5967517	0.0239	0.6413
chr2	243199373	15403915	0.0633	0.4571
chr3	198022430	1456251	0.0074	0.1038
chr4	191154276	12380905	0.0648	0.3314
chr5	180915260	12295535	0.068	0.3209
chr6	171115067	3093233	0.0181	0.1837
chr7	159138663	11332581	0.0712	0.7207

chr8	146364022	2684057	0.0183	0.3249
chr9	141213431	8952433	0.0634	0.4158
chr10	135534747	3937518	0.0291	0.3462
chr11	135006516	7114675	0.0527	0.3637
chr12	133851895	5902081	0.0441	0.2629
chr13	115169878	3640700	0.0316	0.2137
chr14	107349540	5312276	0.0495	0.3232
chr15	102531392	4584052	0.0447	0.2575
chr16	90354753	7020081	0.0777	0.3761
chr17	81195210	5018440	0.0618	0.3758
chr18	78077248	687786	0.0088	0.6336
chr19	59128983	2951228	0.0499	0.4712
chr20	63025520	3022725	0.048	0.2752
chr21	48129895	1077501	0.0224	0.2196
chr22	51304566	3079733	0.06	0.3027
chrMT	16571	54412	3.2836	2.938
chrX	155270560	6020639	0.0388	0.2755
chrY	59373566	307006	0.0052	0.1365

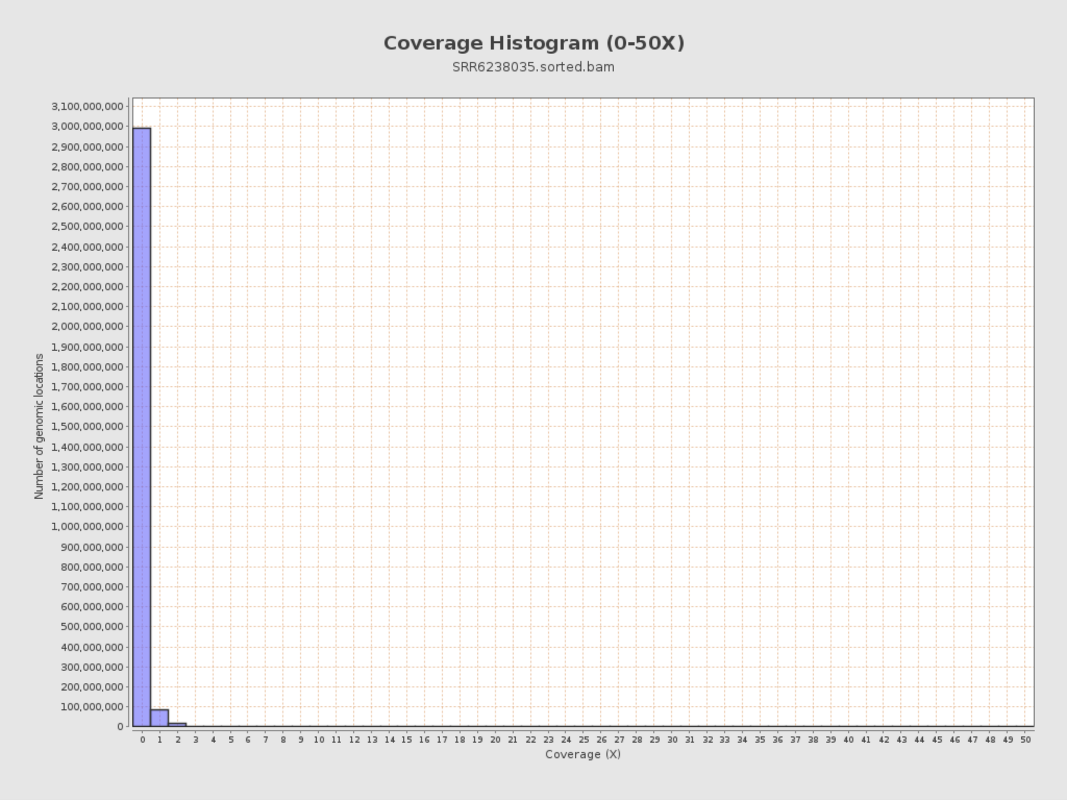
3. Results : Coverage across reference



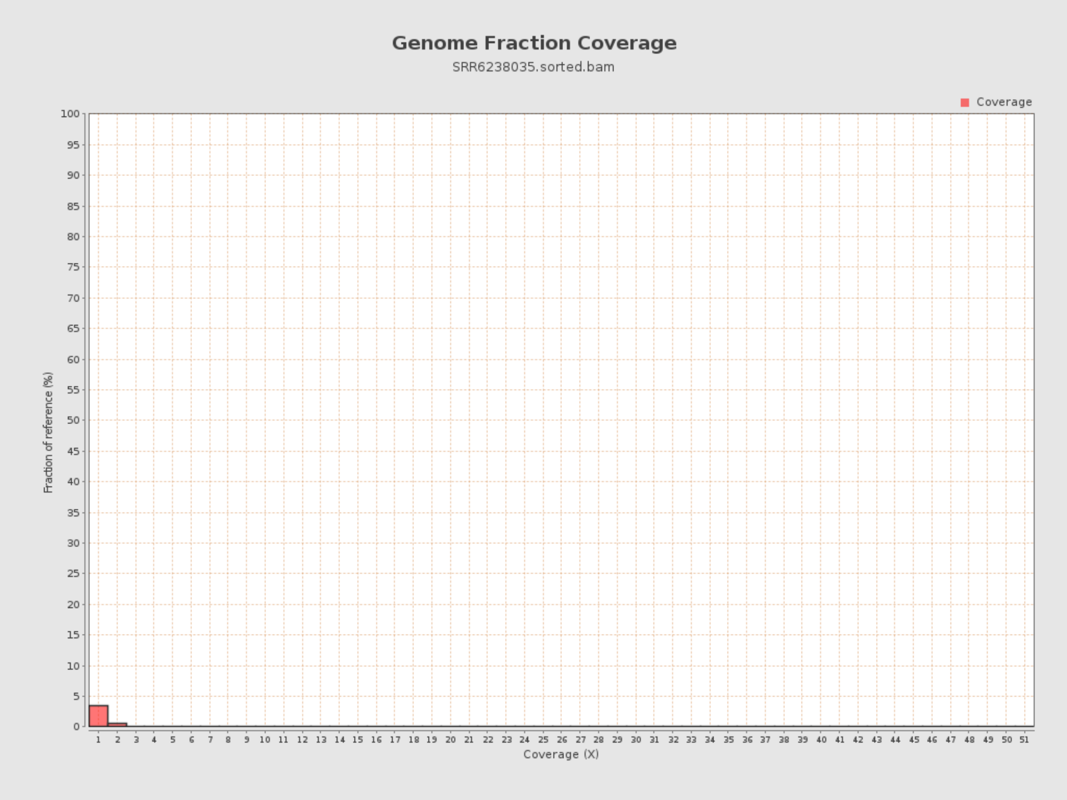
4. Results : Coverage Histogram



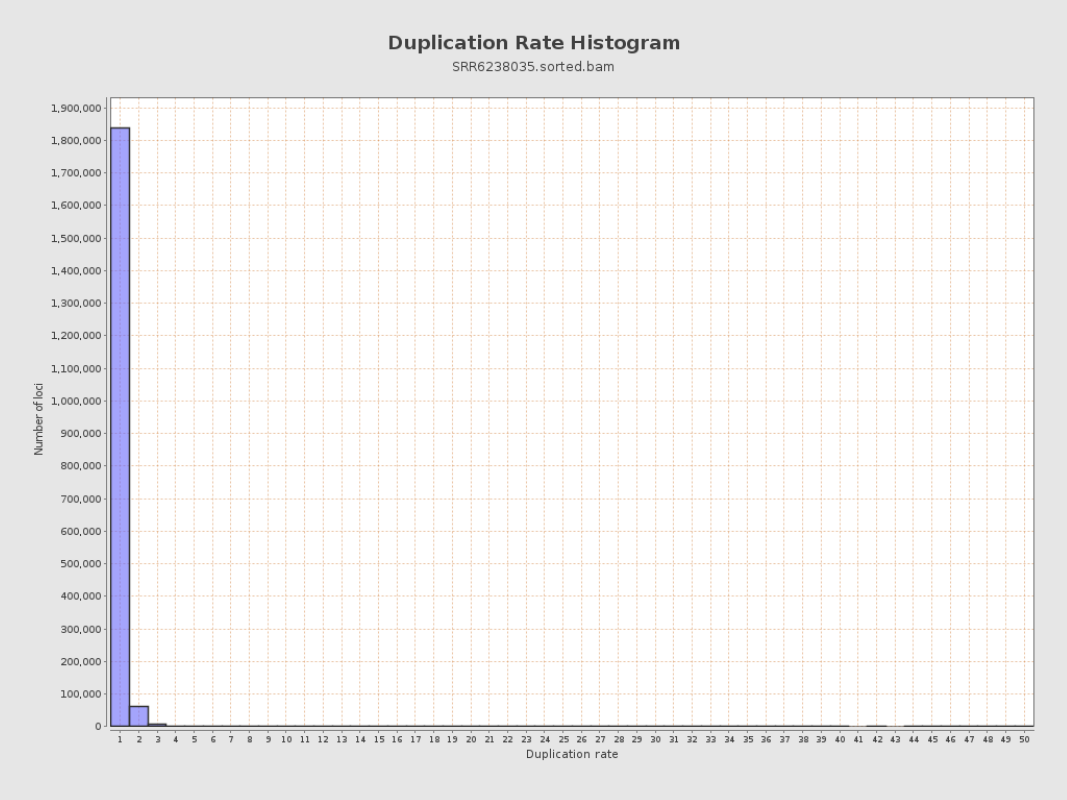
5. Results : Coverage Histogram (0-50X)



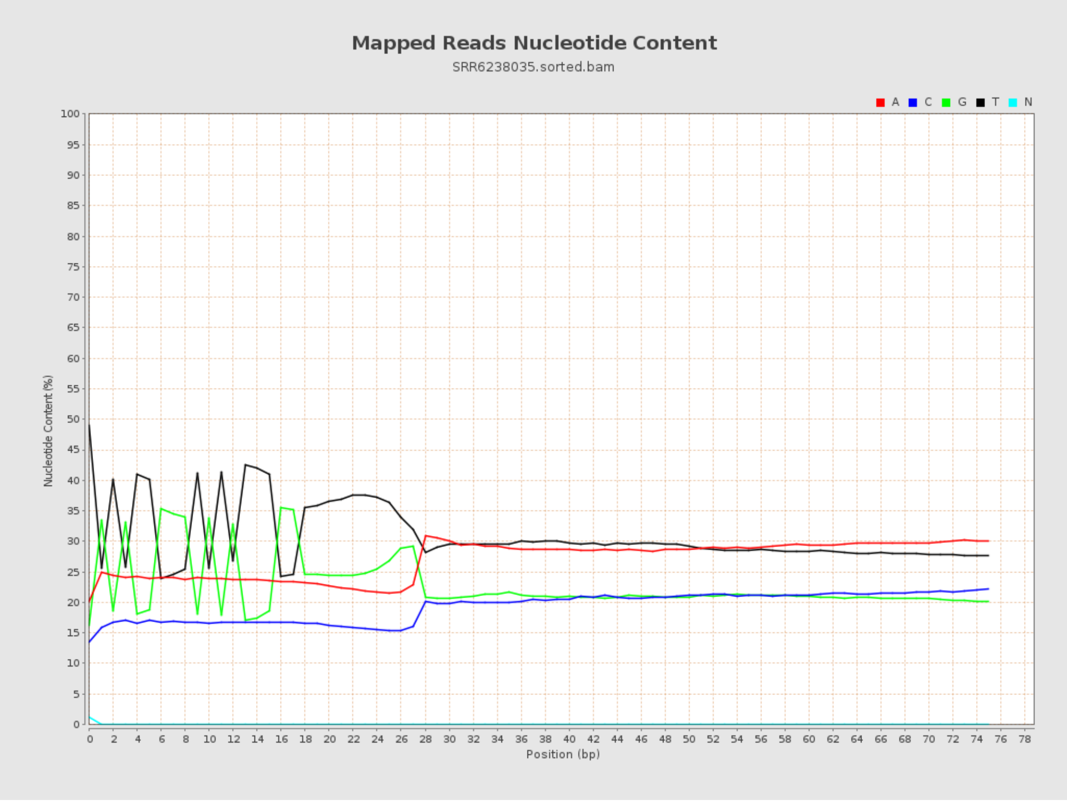
6. Results : Genome Fraction Coverage



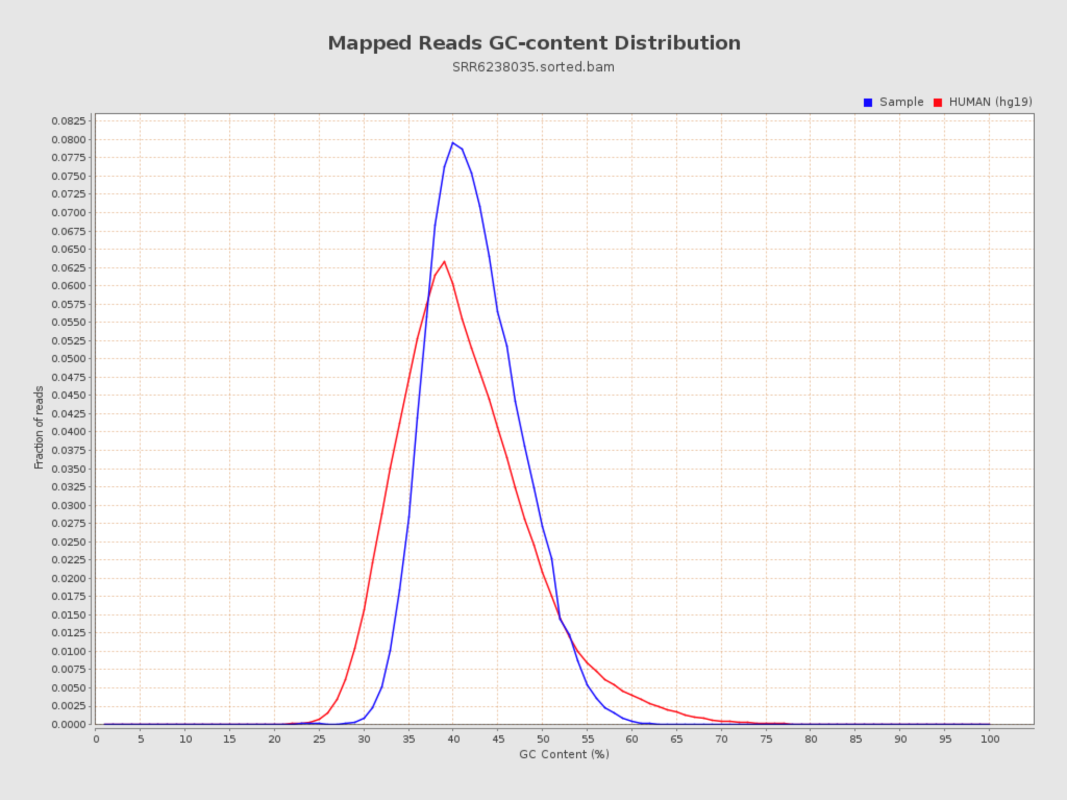
7. Results : Duplication Rate Histogram



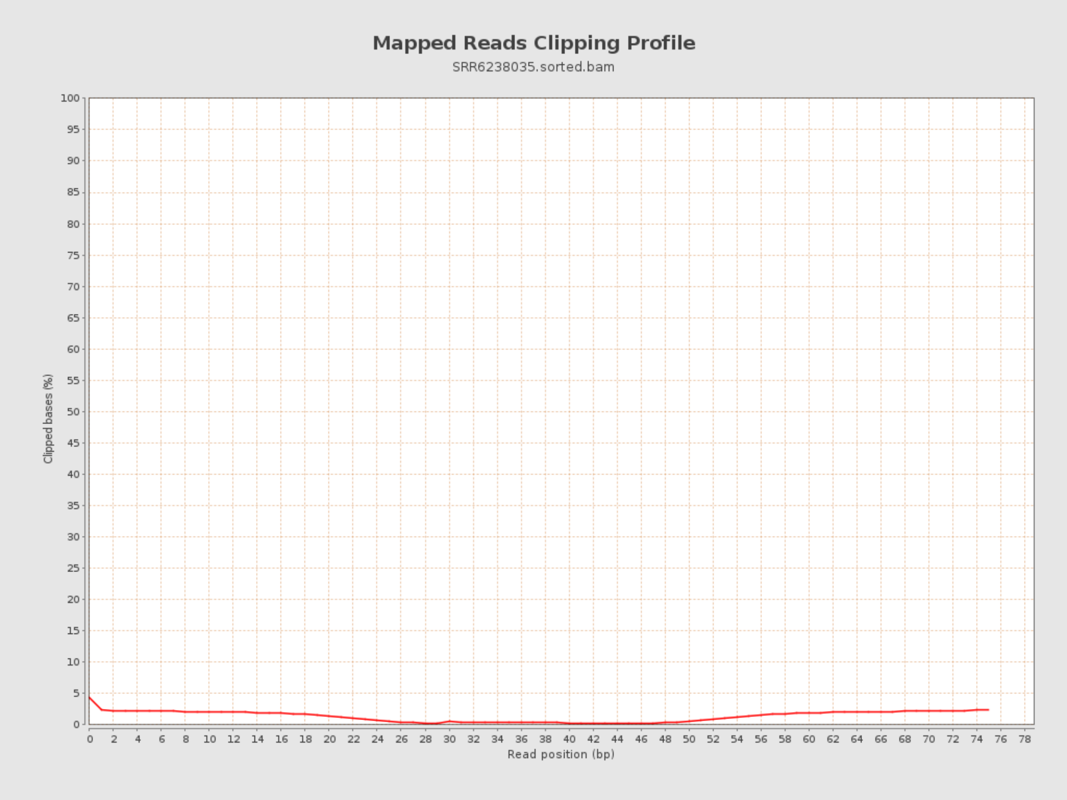
8. Results : Mapped Reads Nucleotide Content



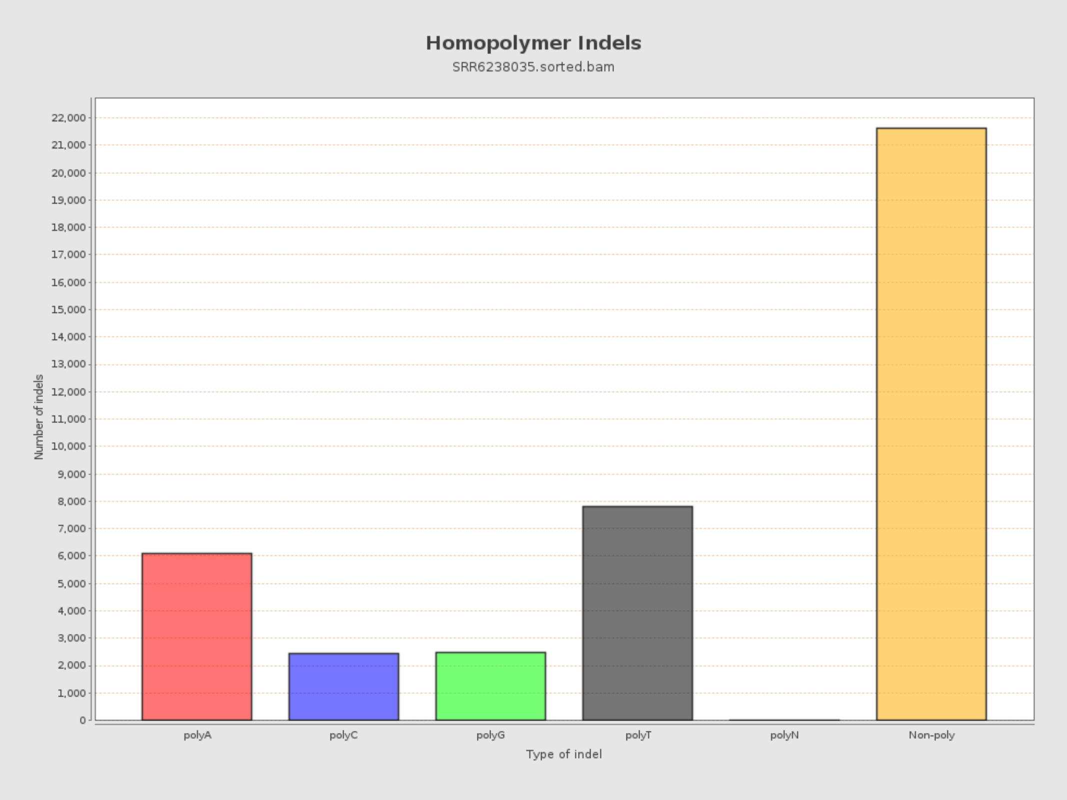
9. Results : Mapped Reads GC-content Distribution



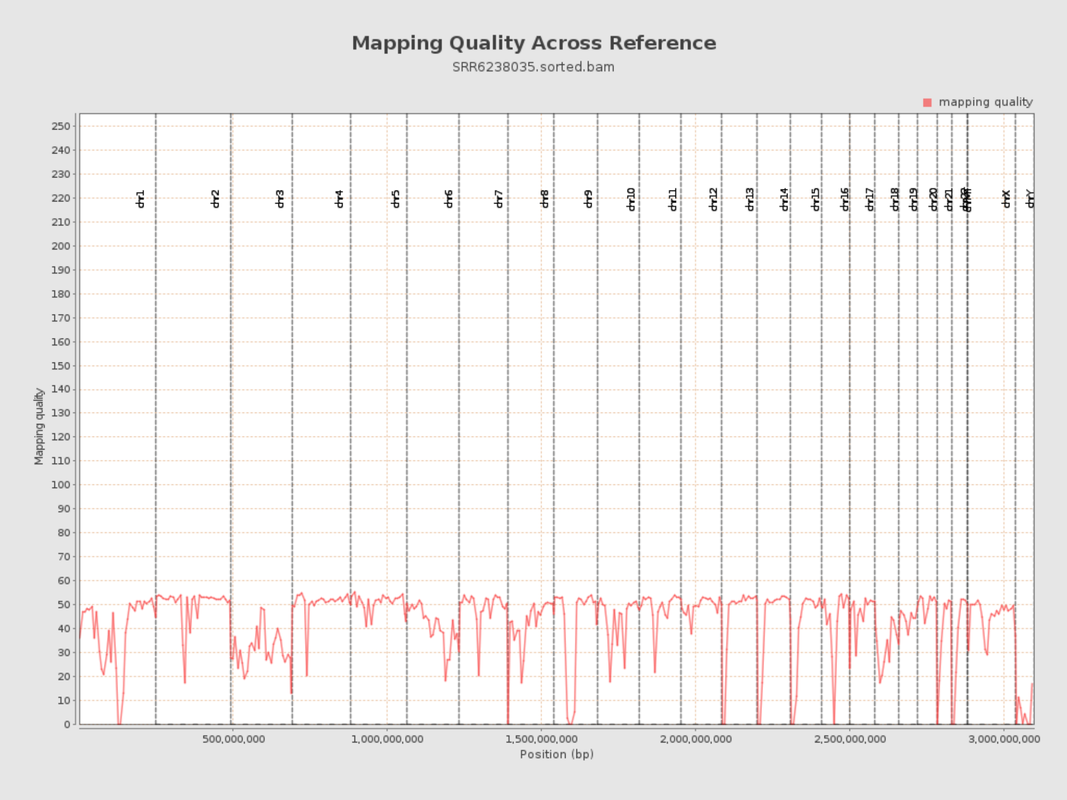
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram