Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:31:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238535.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_SRR6238535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238535.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:31:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,680,376
Mapped reads	2,352,213 / 87.76%
Unmapped reads	328,163 / 12.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,414 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	860,331 / 32.1%
Duplication rate	22.21%
Clipped reads	1,540,114 / 57.46%

2.2. ACGT Content

Number/percentage of A's	35,026,341 / 24.31%
Number/percentage of C's	25,456,207 / 17.67%
Number/percentage of T's	48,498,998 / 33.66%
Number/percentage of G's	35,092,136 / 24.36%
Number/percentage of N's	9,276 / 0.01%
GC Percentage	42.02%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.9016

2.4. Mapping Quality

Mean Mapping Quality	38

2.5. Mismatches and indels

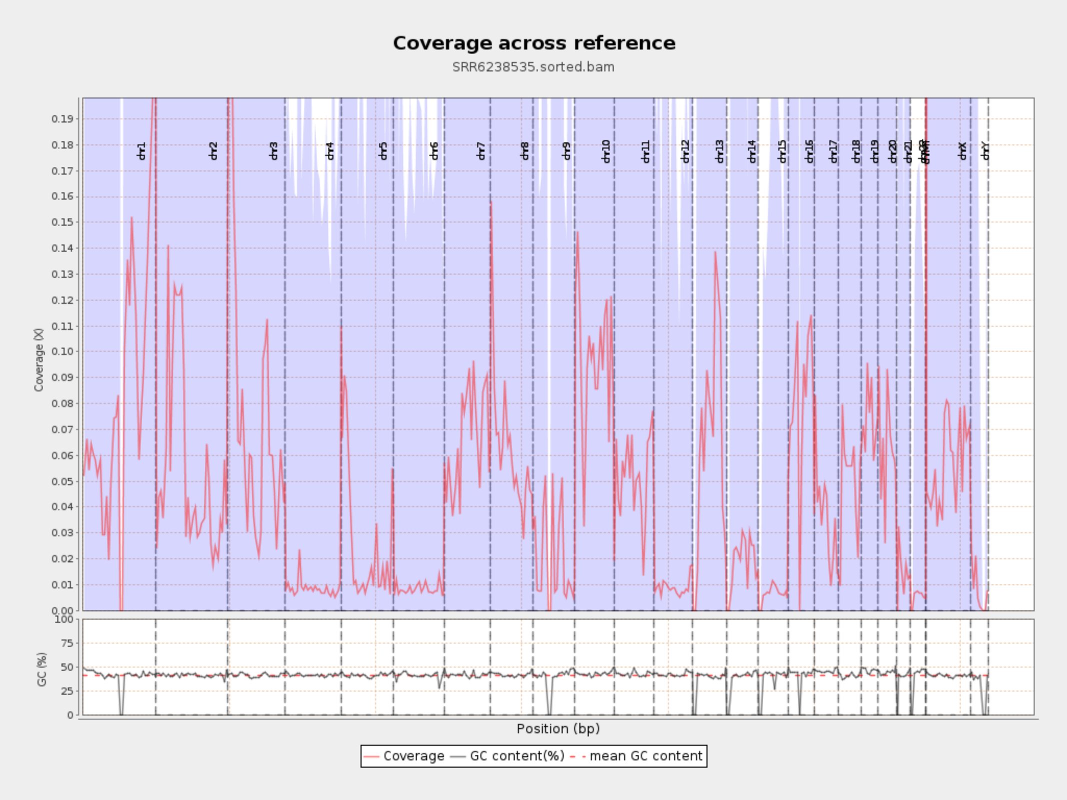
General error rate	0.66%
Mismatches	930,167
Insertions	9,443
Mapped reads with at least one insertion	0.4%
Deletions	52,763
Mapped reads with at least one deletion	2.22%
Homopolymer indels	40.29%

2.6. Chromosome stats

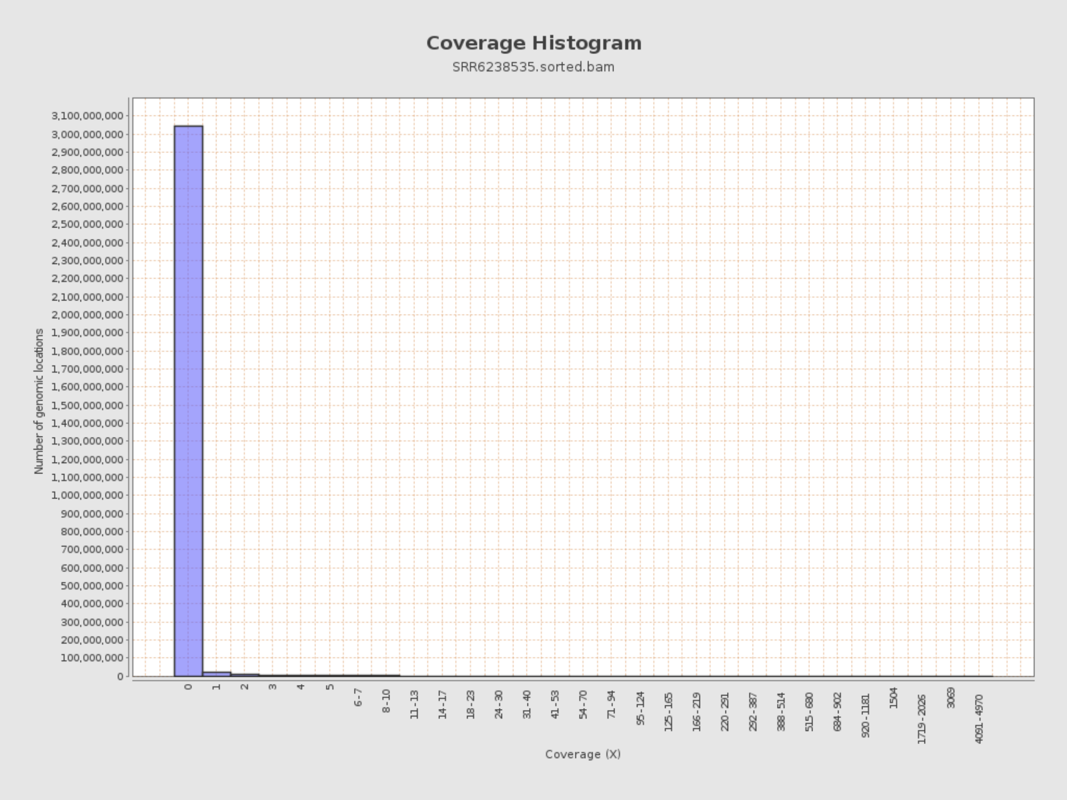
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21060216	0.0845	1.1396
chr2	243199373	13463931	0.0554	2.1959
chr3	198022430	15219552	0.0769	0.6877
chr4	191154276	1662633	0.0087	0.1852
chr5	180915260	4669807	0.0258	0.3927
chr6	171115067	1410401	0.0082	0.5967
chr7	159138663	10629921	0.0668	0.7746

chr8	146364022	9124945	0.0623	0.6852
chr9	141213431	2702201	0.0191	0.396
chr10	135534747	13394654	0.0988	0.8303
chr11	135006516	6910990	0.0512	0.5733
chr12	133851895	1187626	0.0089	0.2179
chr13	115169878	7554592	0.0656	0.7393
chr14	107349540	2026397	0.0189	0.3426
chr15	102531392	661005	0.0064	0.4402
chr16	90354753	7092072	0.0785	0.748
chr17	81195210	3007236	0.037	0.4709
chr18	78077248	3727453	0.0477	1.6129
chr19	59128983	4392190	0.0743	0.8382
chr20	63025520	3930285	0.0624	0.6379
chr21	48129895	752295	0.0156	0.2965
chr22	51304566	263763	0.0051	0.1266
chrMT	16571	37728	2.2767	3.5627
chrX	155270560	8839250	0.0569	0.5839
chrY	59373566	451416	0.0076	0.3045

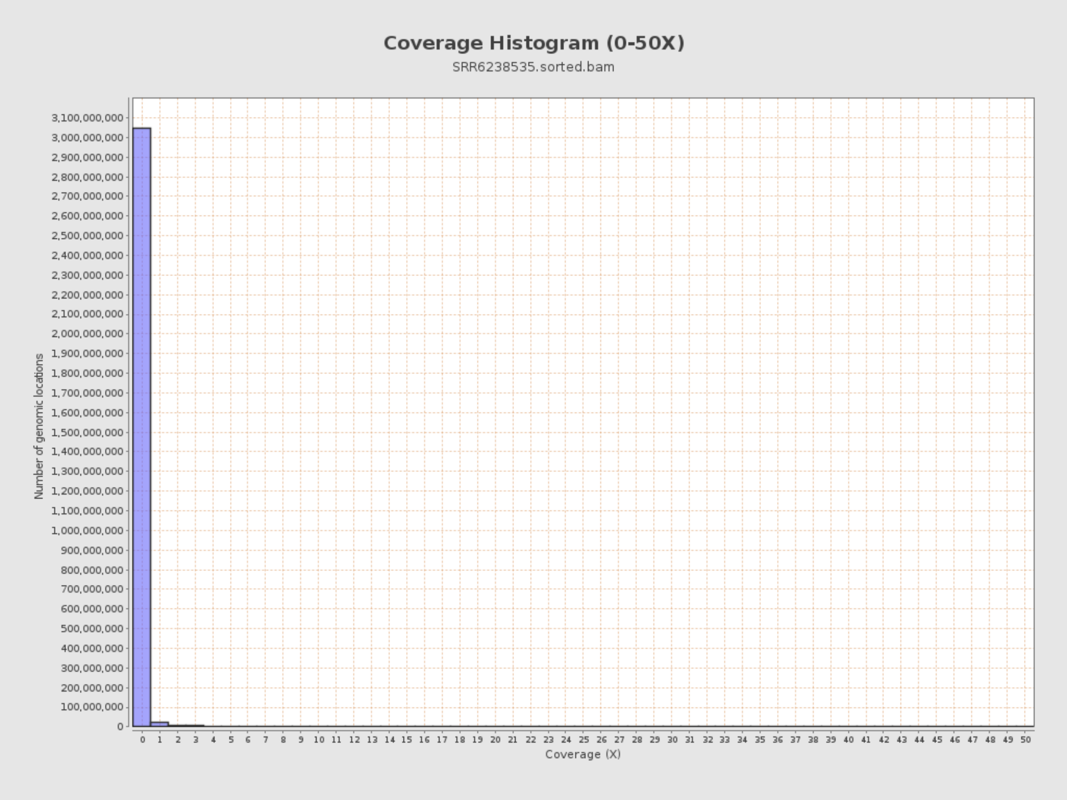
3. Results : Coverage across reference



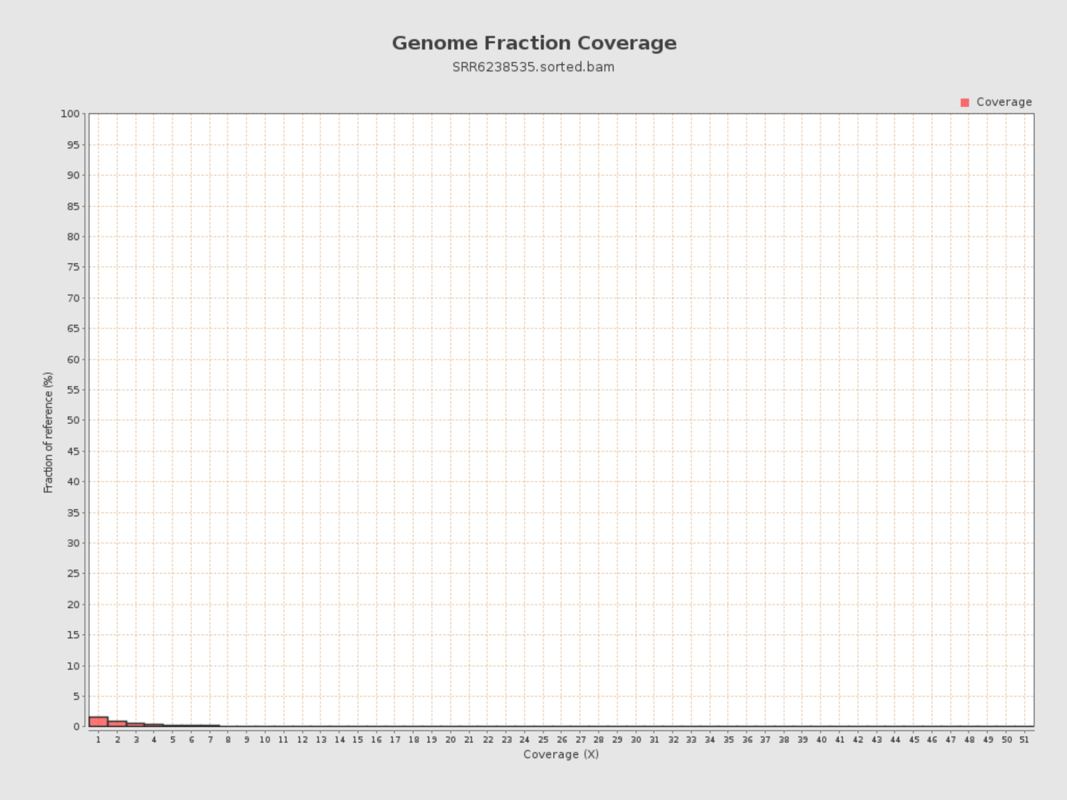
4. Results : Coverage Histogram



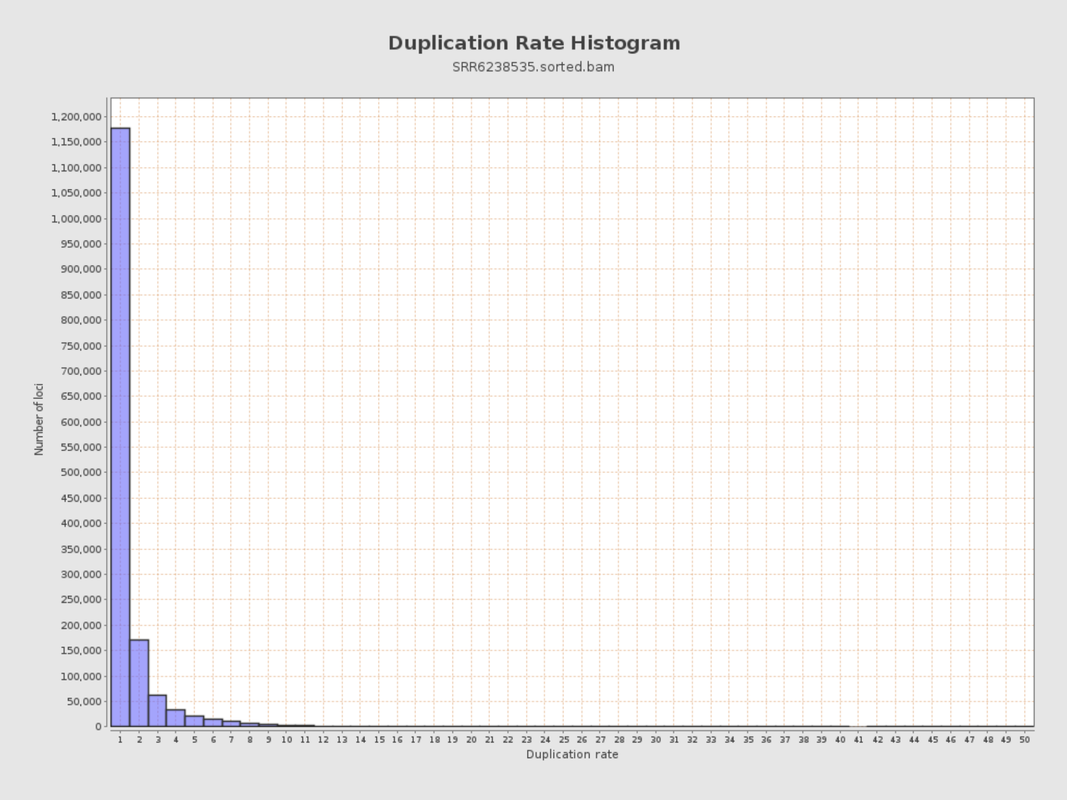
5. Results : Coverage Histogram (0-50X)



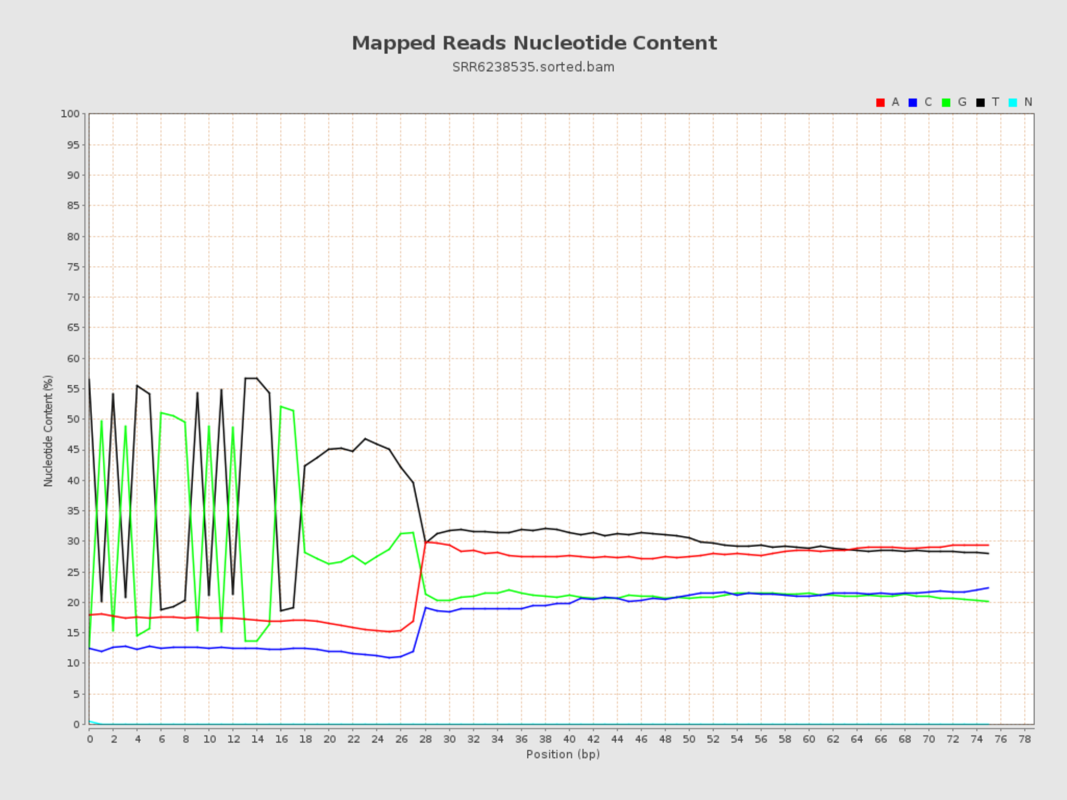
6. Results : Genome Fraction Coverage



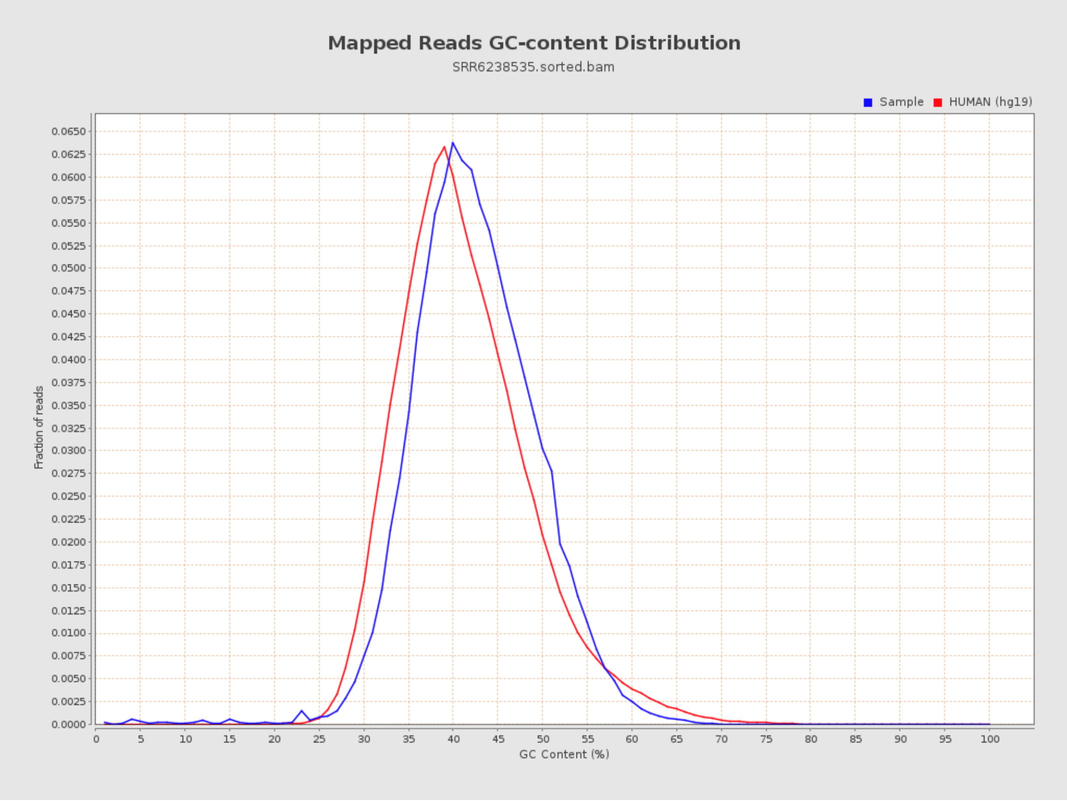
7. Results : Duplication Rate Histogram



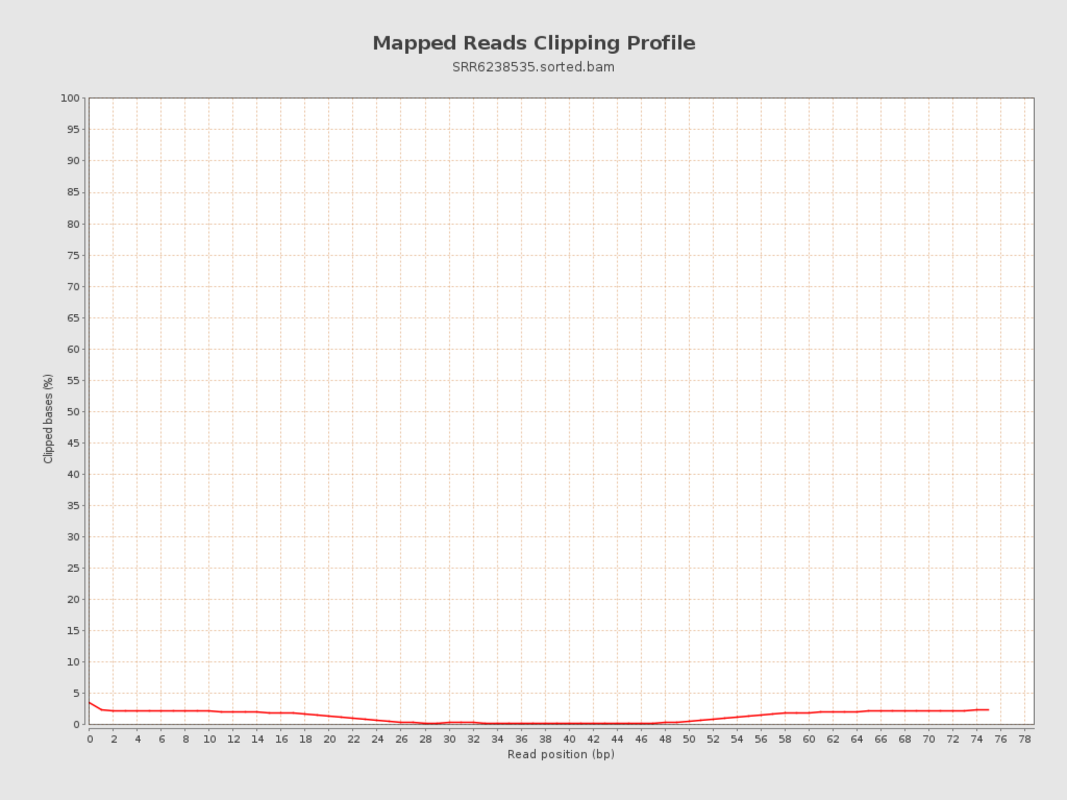
8. Results : Mapped Reads Nucleotide Content



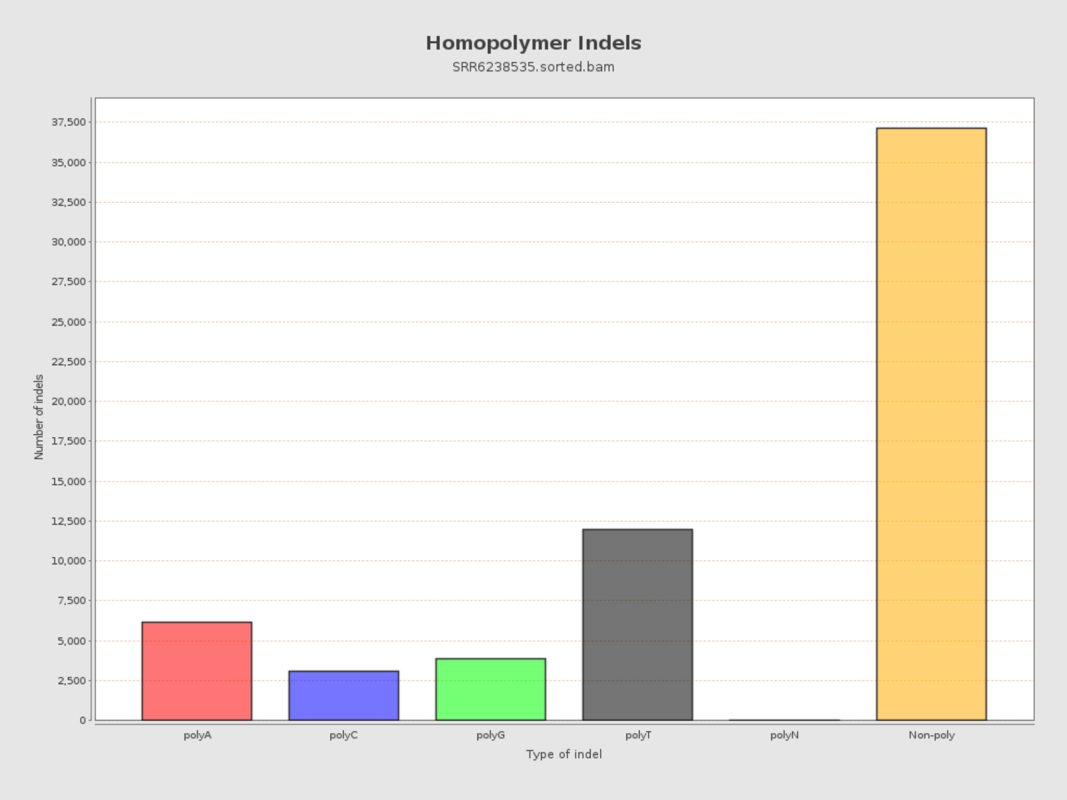
9. Results : Mapped Reads GC-content Distribution



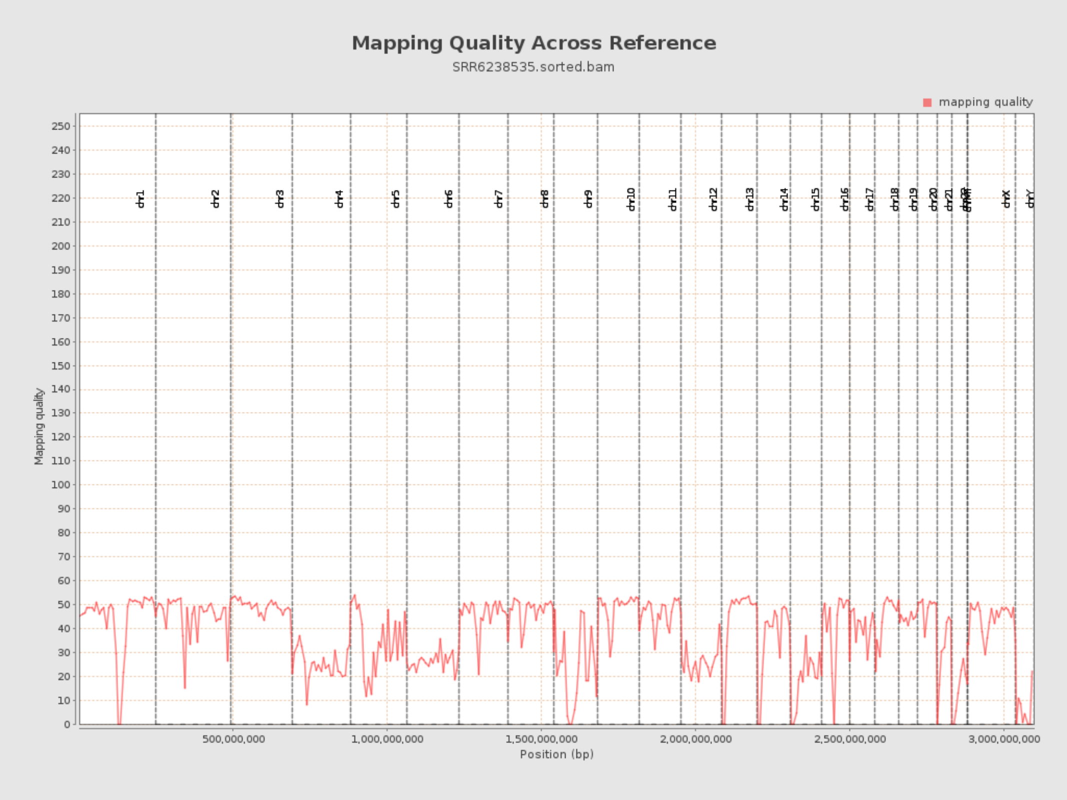
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram