Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:10:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238057.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_SRR6238057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:10:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,388,094
Mapped reads	2,166,484 / 90.72%
Unmapped reads	221,610 / 9.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,153 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	87,129 / 3.65%
Duplication rate	3.08%
Clipped reads	899,949 / 37.68%

2.2. ACGT Content

Number/percentage of A's	39,797,465 / 27.38%
Number/percentage of C's	27,688,256 / 19.05%
Number/percentage of T's	45,232,735 / 31.12%
Number/percentage of G's	32,600,498 / 22.43%
Number/percentage of N's	19,234 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.047

Standard Deviation	0.3911

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

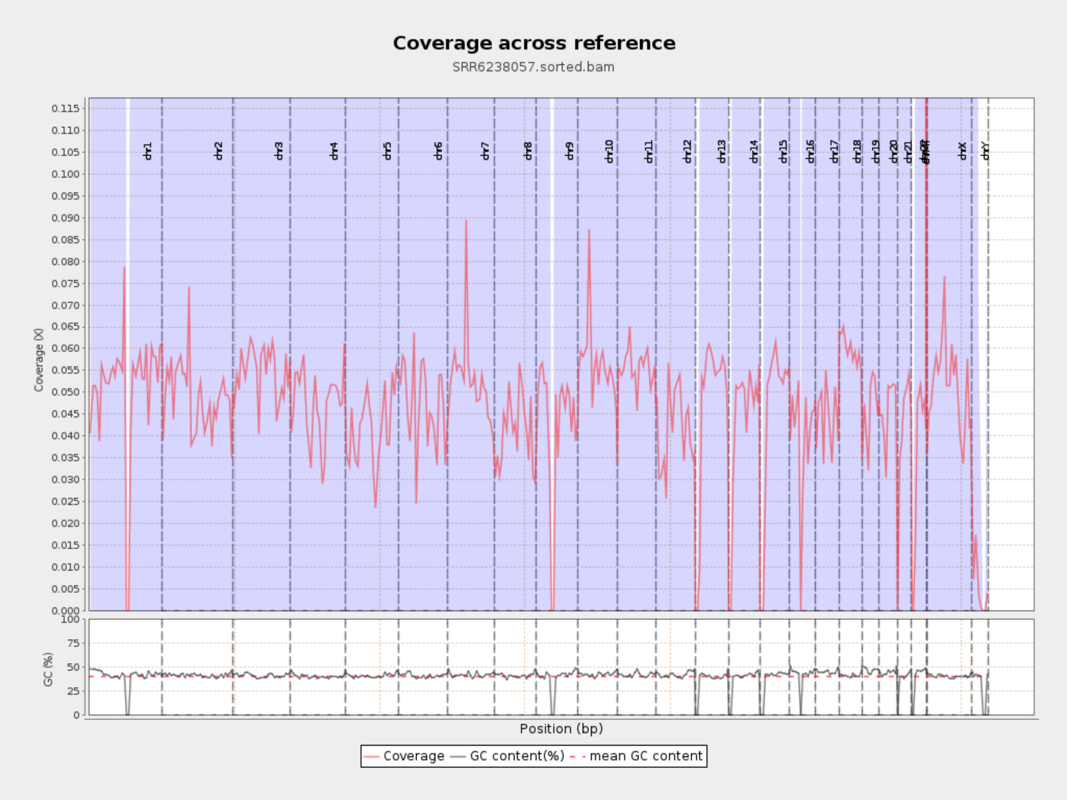
General error rate	0.76%
Mismatches	1,089,856
Insertions	9,831
Mapped reads with at least one insertion	0.45%
Deletions	39,279
Mapped reads with at least one deletion	1.79%
Homopolymer indels	45.94%

2.6. Chromosome stats

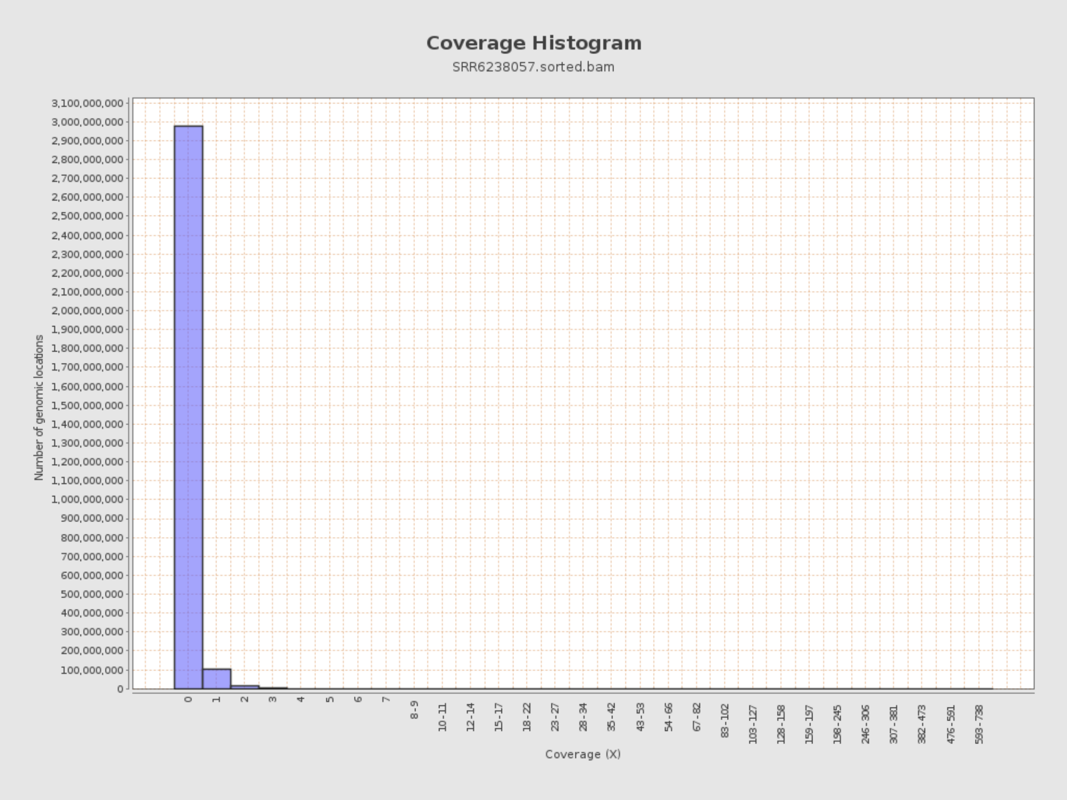
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12679234	0.0509	0.6666
chr2	243199373	11933782	0.0491	0.4282
chr3	198022430	10822887	0.0547	0.2712
chr4	191154276	9048819	0.0473	0.2666
chr5	180915260	7612542	0.0421	0.2402
chr6	171115067	8081480	0.0472	0.3116
chr7	159138663	8482678	0.0533	0.6037

chr8	146364022	5977095	0.0408	0.4399
chr9	141213431	5968257	0.0423	0.3411
chr10	135534747	7727715	0.057	0.4405
chr11	135006516	7482523	0.0554	0.3861
chr12	133851895	5608961	0.0419	0.2418
chr13	115169878	5336494	0.0463	0.2495
chr14	107349540	4539886	0.0423	0.2646
chr15	102531392	4619004	0.045	0.2487
chr16	90354753	3572954	0.0395	0.2564
chr17	81195210	3577557	0.0441	0.2833
chr18	78077248	4686758	0.06	0.6603
chr19	59128983	2708396	0.0458	0.4765
chr20	63025520	2847706	0.0452	0.2532
chr21	48129895	1984873	0.0412	0.2575
chr22	51304566	1695192	0.033	0.2092
chrMT	16571	35582	2.1472	2.1492
chrX	155270560	8031900	0.0517	0.2995
chrY	59373566	345338	0.0058	0.1424

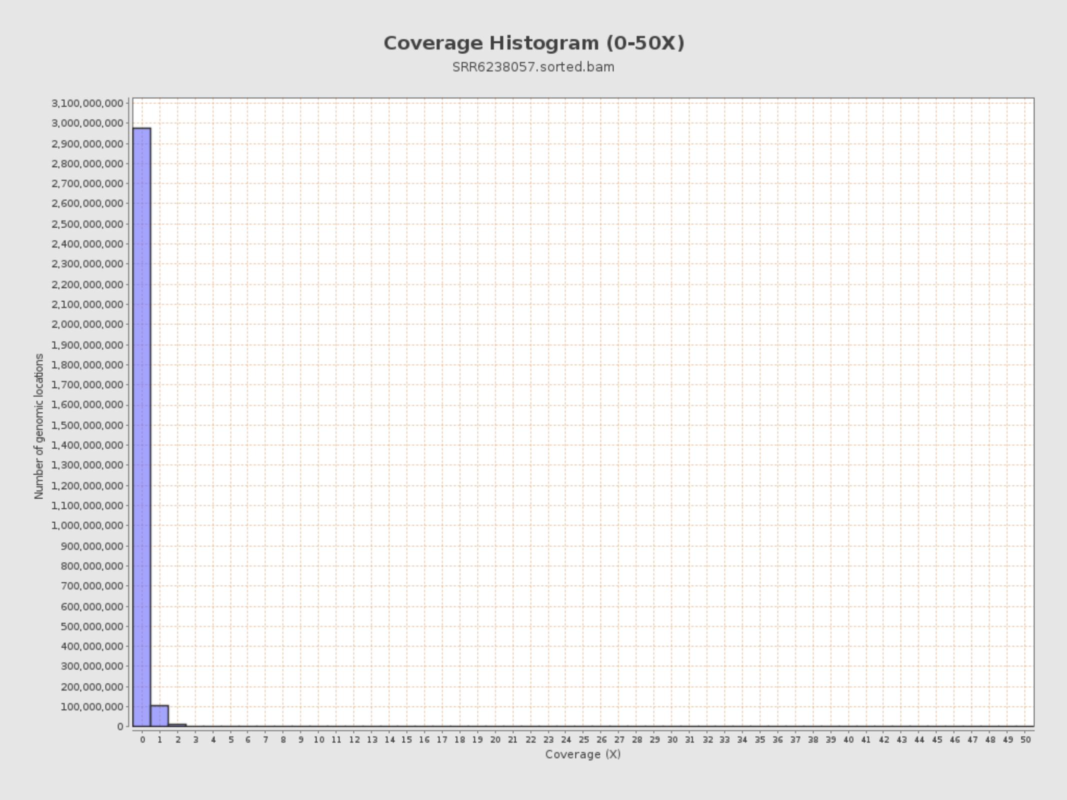
3. Results : Coverage across reference



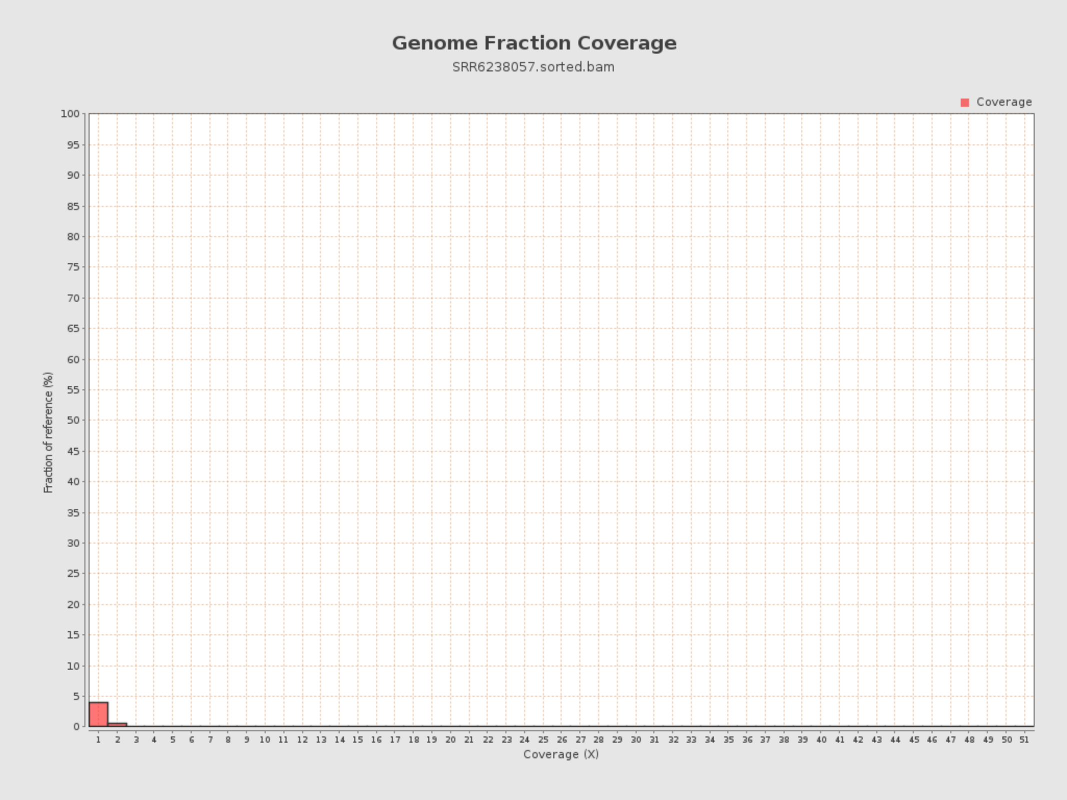
4. Results : Coverage Histogram



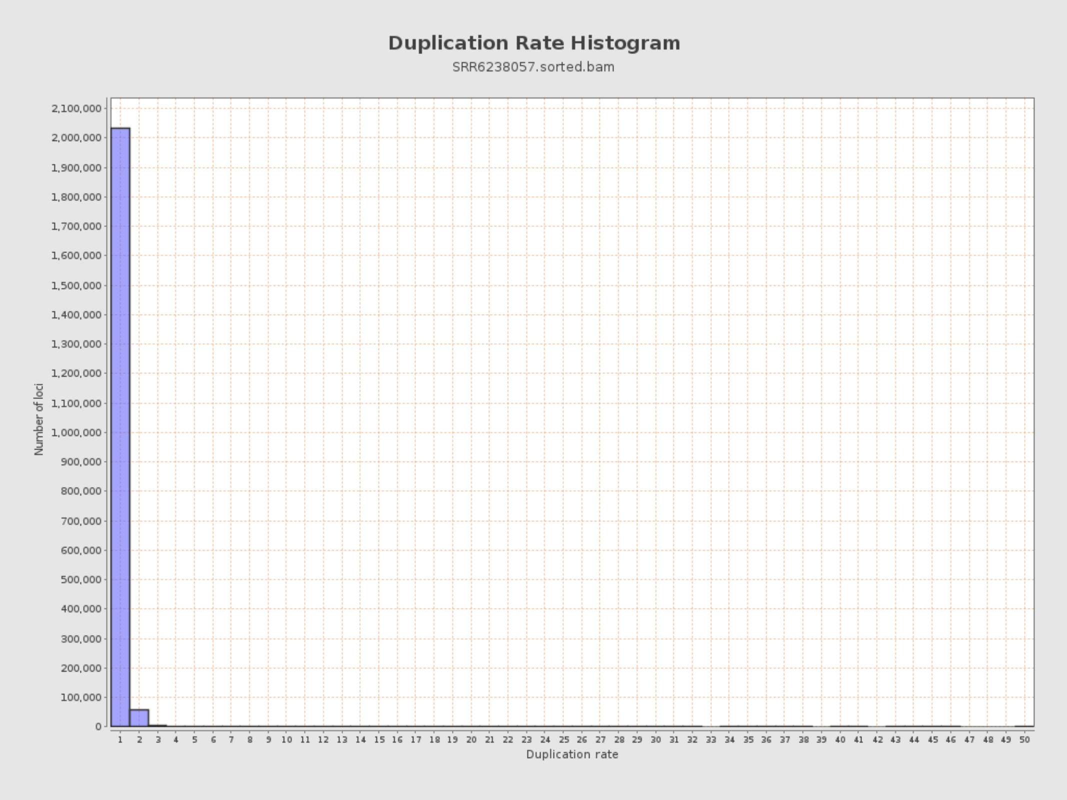
5. Results : Coverage Histogram (0-50X)



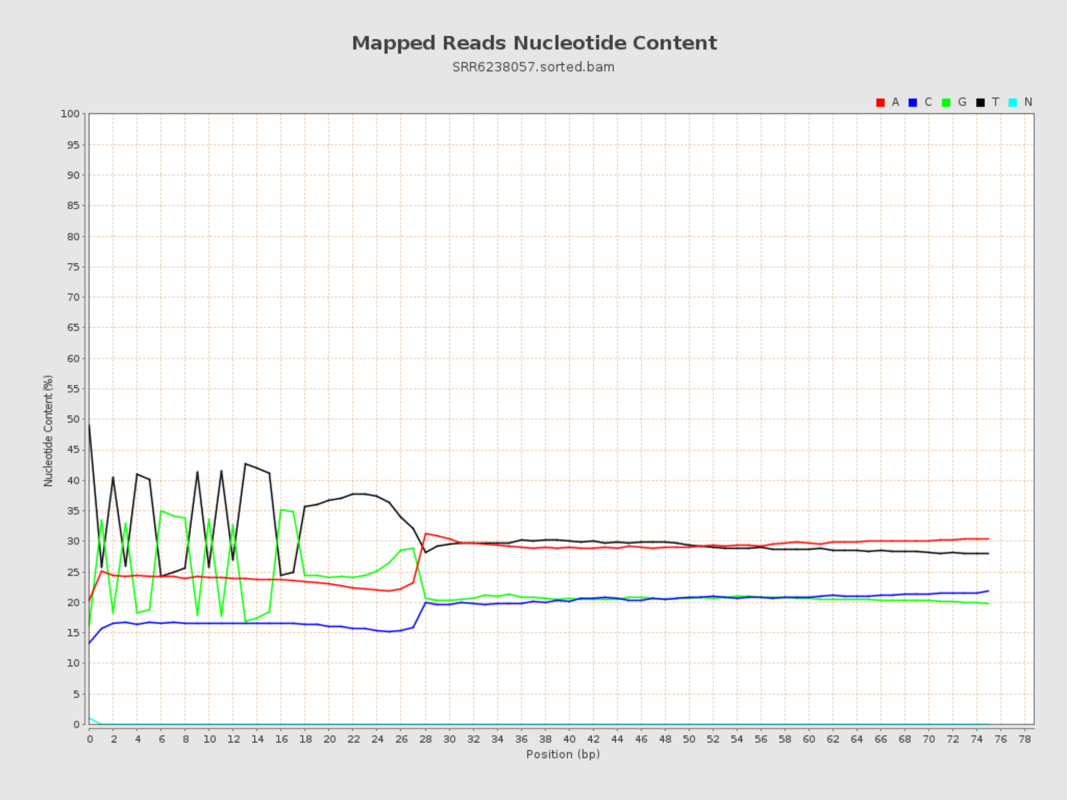
6. Results : Genome Fraction Coverage



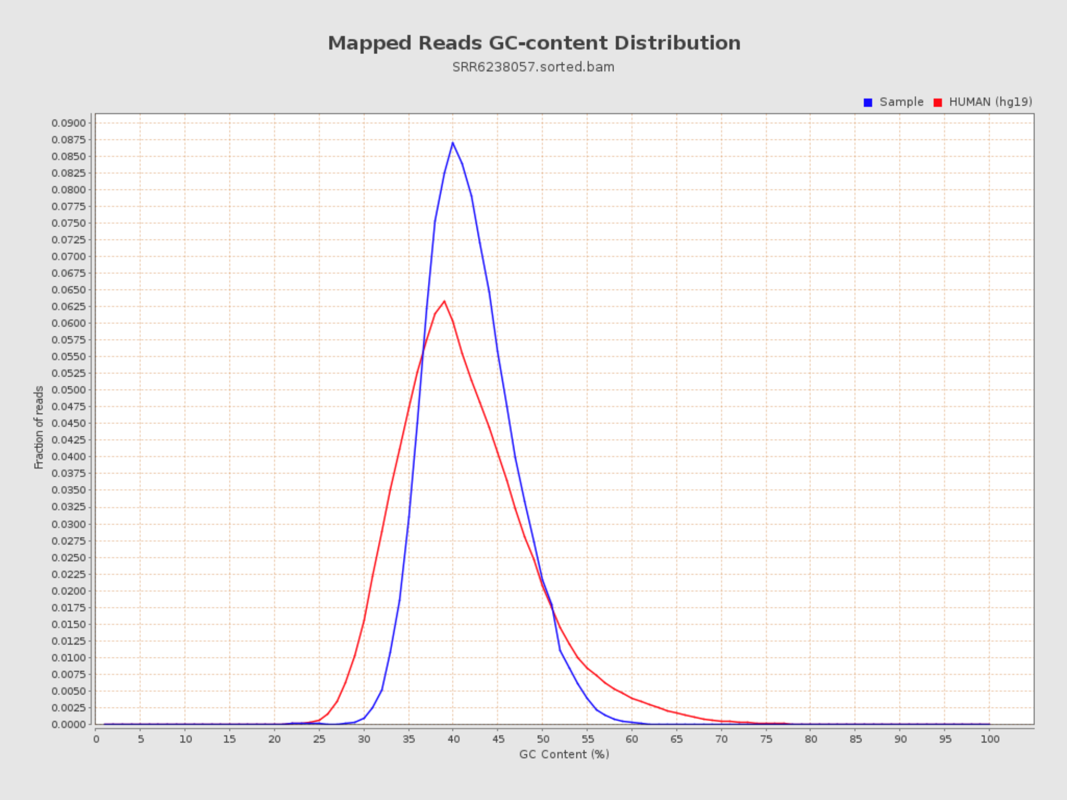
7. Results : Duplication Rate Histogram



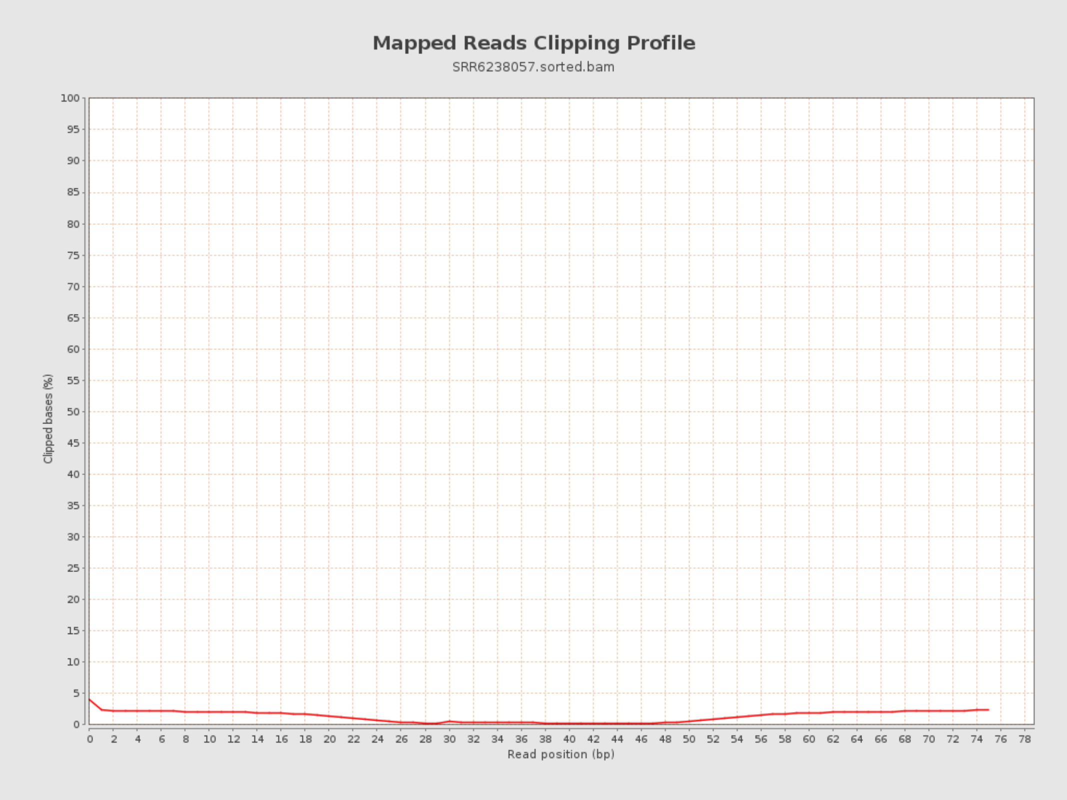
8. Results : Mapped Reads Nucleotide Content



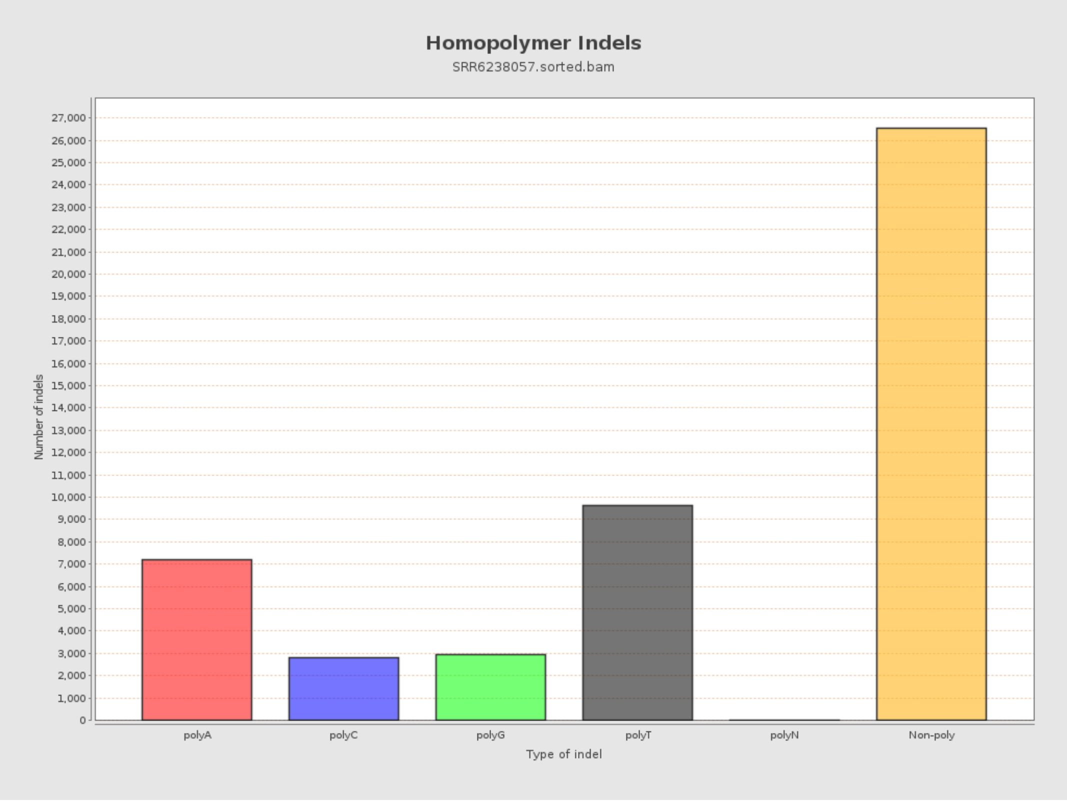
9. Results : Mapped Reads GC-content Distribution



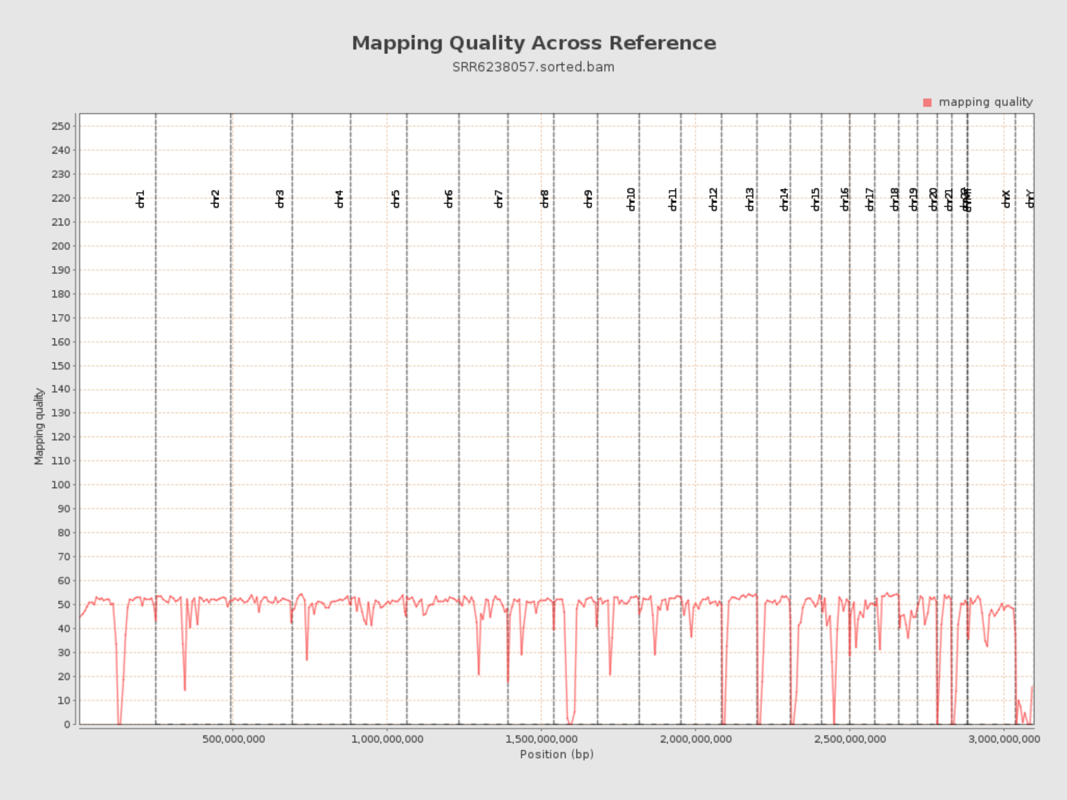
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram