Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:16:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236093.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_SRR6236093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:16:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	962,362
Mapped reads	811,537 / 84.33%
Unmapped reads	150,825 / 15.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,368 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	24,513 / 2.55%
Duplication rate	2.29%
Clipped reads	370,382 / 38.49%

2.2. ACGT Content

Number/percentage of A's	14,996,126 / 27.91%
Number/percentage of C's	9,476,353 / 17.64%
Number/percentage of T's	17,311,034 / 32.22%
Number/percentage of G's	11,924,032 / 22.19%
Number/percentage of N's	20,219 / 0.04%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.2072

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

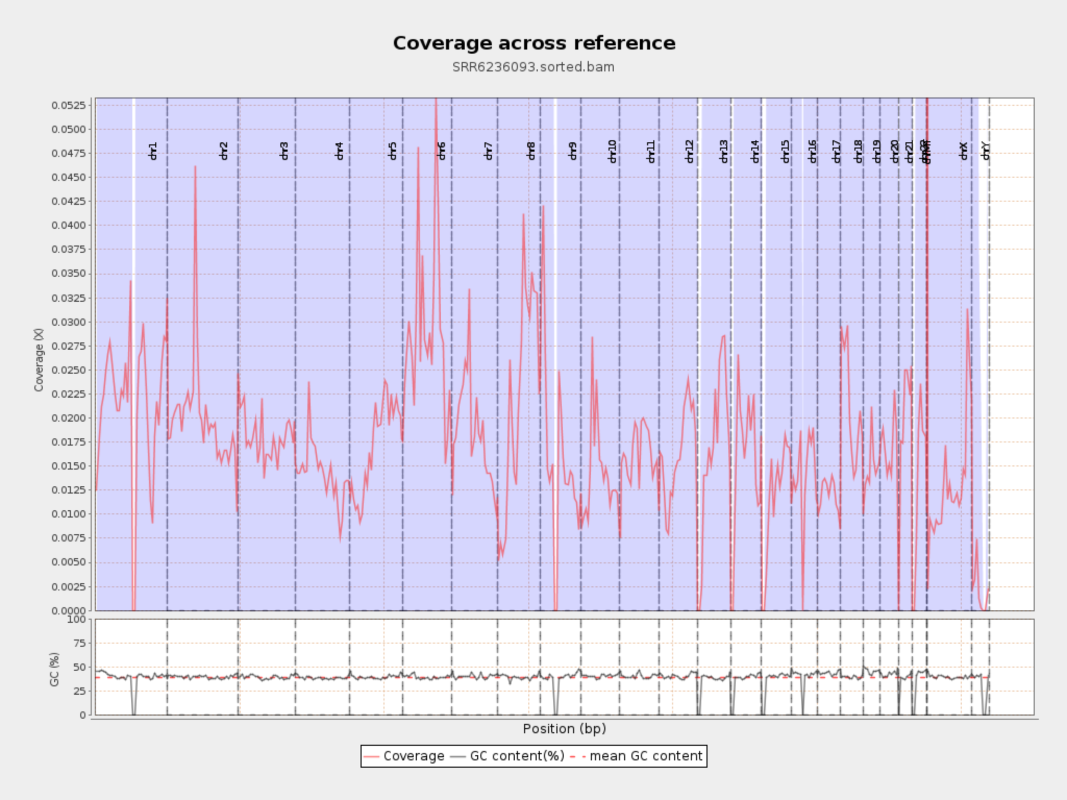
General error rate	0.86%
Mismatches	453,052
Insertions	4,155
Mapped reads with at least one insertion	0.51%
Deletions	15,943
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.4%

2.6. Chromosome stats

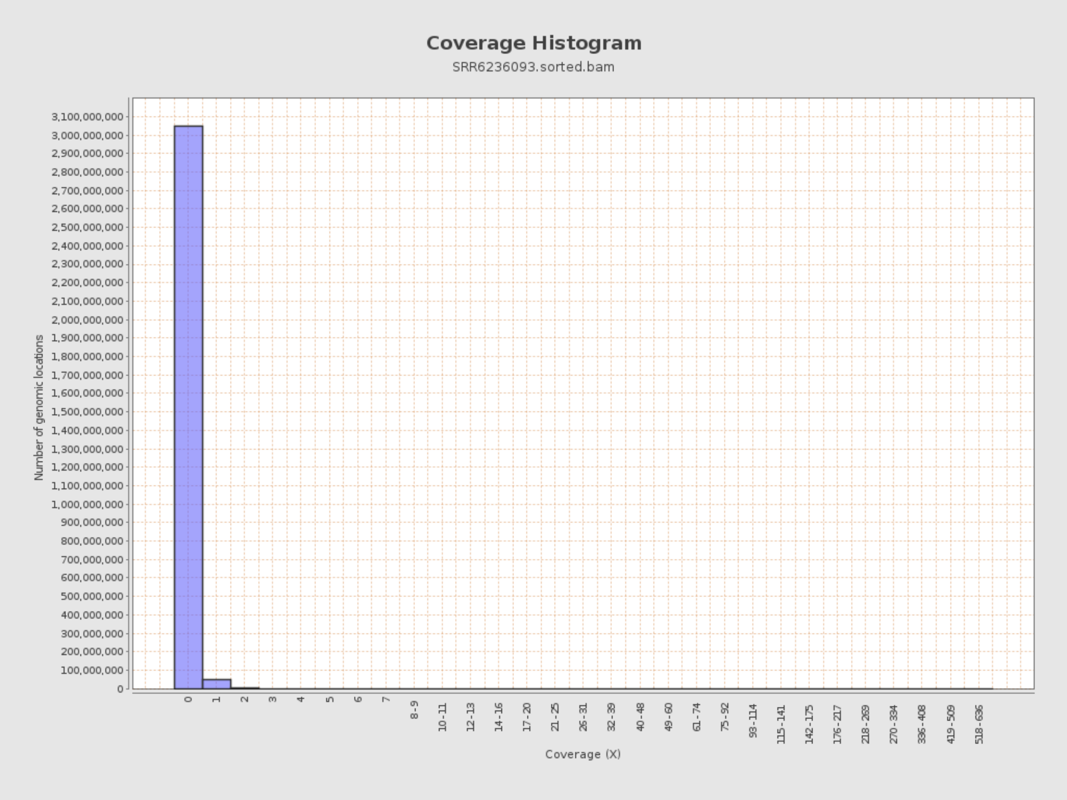
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5280141	0.0212	0.3092
chr2	243199373	4858313	0.02	0.2254
chr3	198022430	3566199	0.018	0.1416
chr4	191154276	2724614	0.0143	0.134
chr5	180915260	3121502	0.0173	0.1398
chr6	171115067	4972698	0.0291	0.2307
chr7	159138663	2977457	0.0187	0.2439

chr8	146364022	3256898	0.0223	0.4355
chr9	141213431	2295608	0.0163	0.1876
chr10	135534747	1922723	0.0142	0.1618
chr11	135006516	2208994	0.0164	0.1783
chr12	133851895	2174053	0.0162	0.1369
chr13	115169878	1912382	0.0166	0.1361
chr14	107349540	1639967	0.0153	0.138
chr15	102531392	1201233	0.0117	0.1186
chr16	90354753	1242608	0.0138	0.1352
chr17	81195210	975673	0.012	0.1249
chr18	78077248	1654387	0.0212	0.3
chr19	59128983	886969	0.015	0.2011
chr20	63025520	1065608	0.0169	0.1413
chr21	48129895	955901	0.0199	0.1569
chr22	51304566	687233	0.0134	0.1218
chrMT	16571	30849	1.8616	1.6988
chrX	155270560	2019293	0.013	0.1283
chrY	59373566	123984	0.0021	0.0703

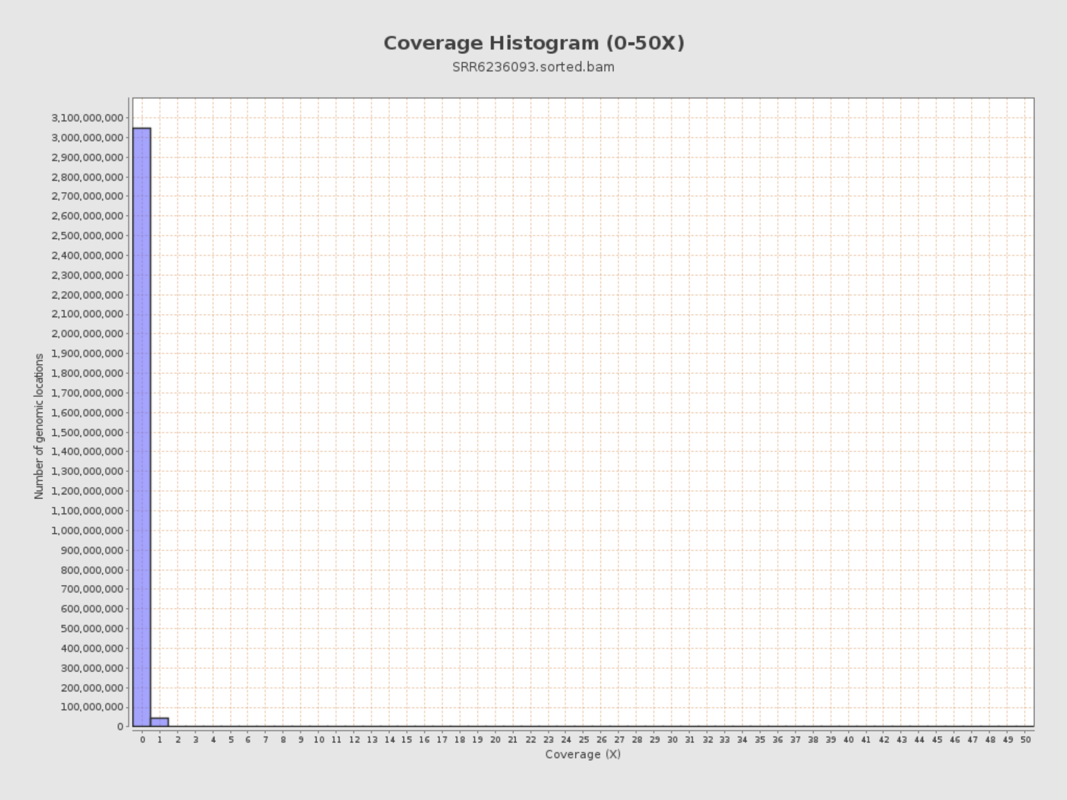
3. Results : Coverage across reference



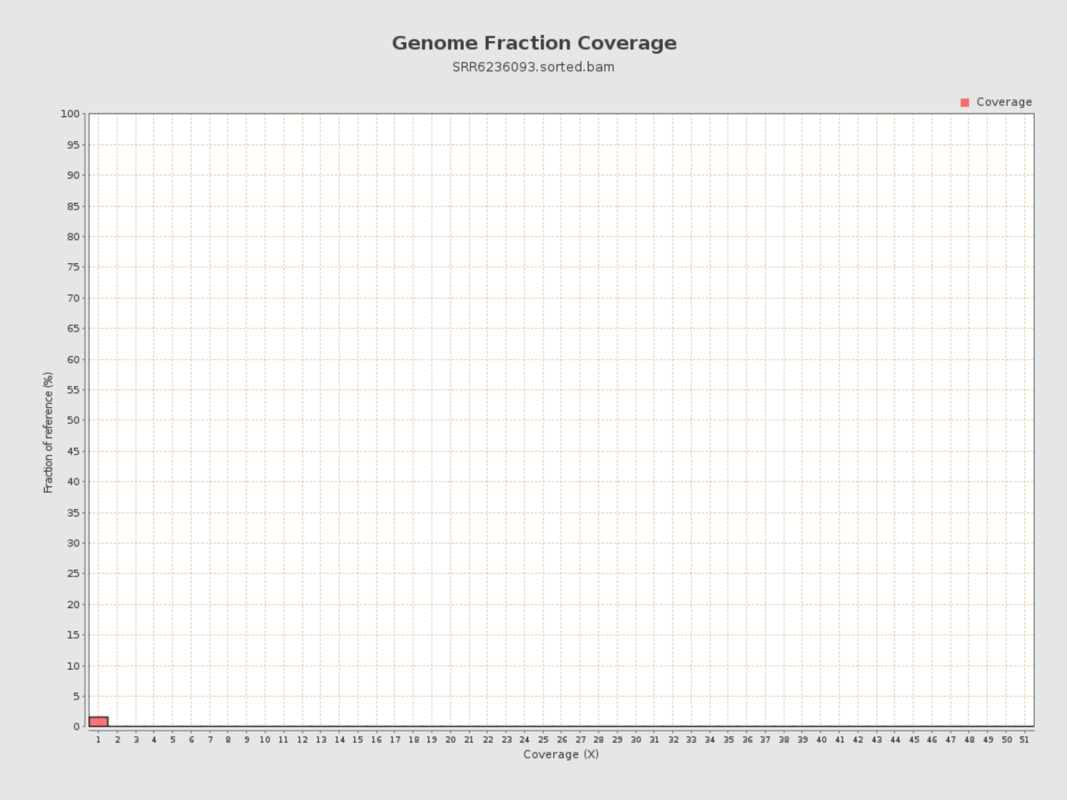
4. Results : Coverage Histogram



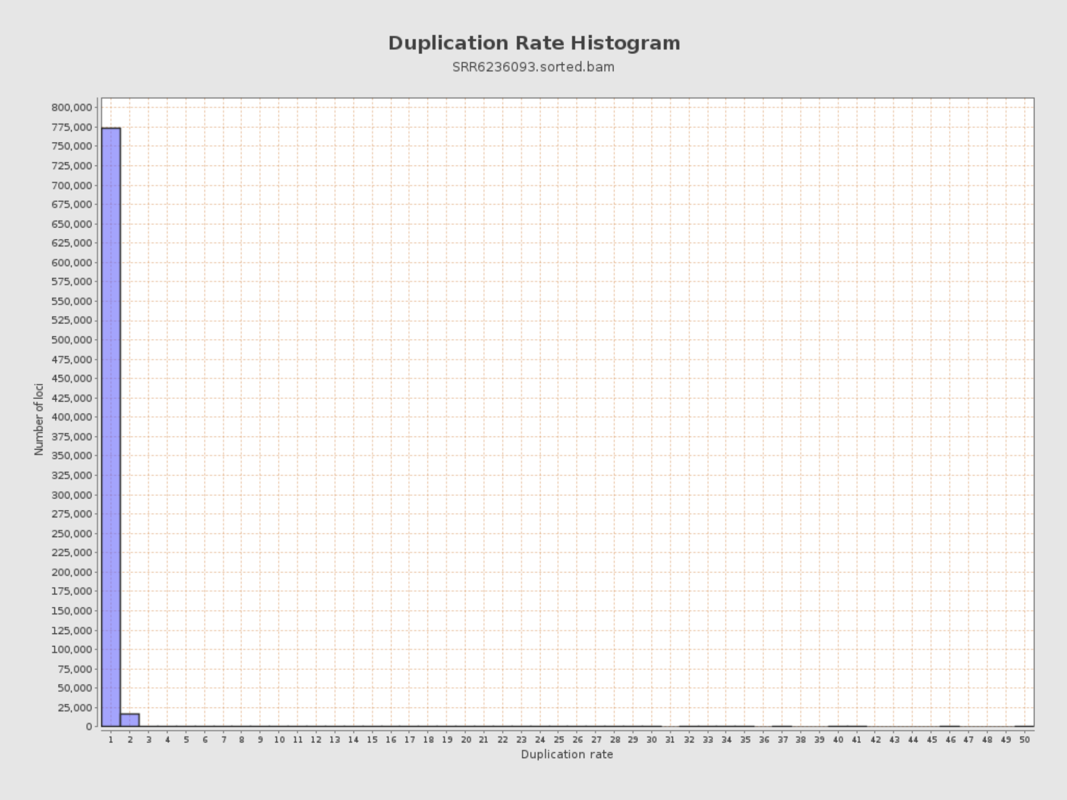
5. Results : Coverage Histogram (0-50X)



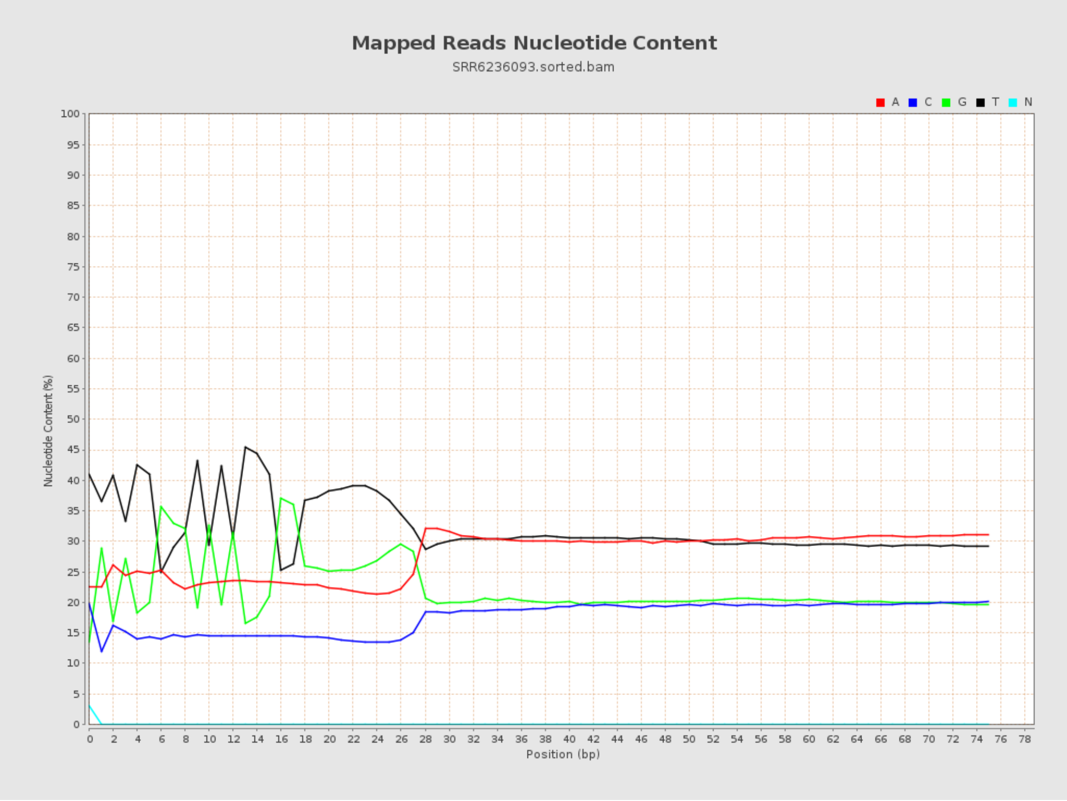
6. Results : Genome Fraction Coverage



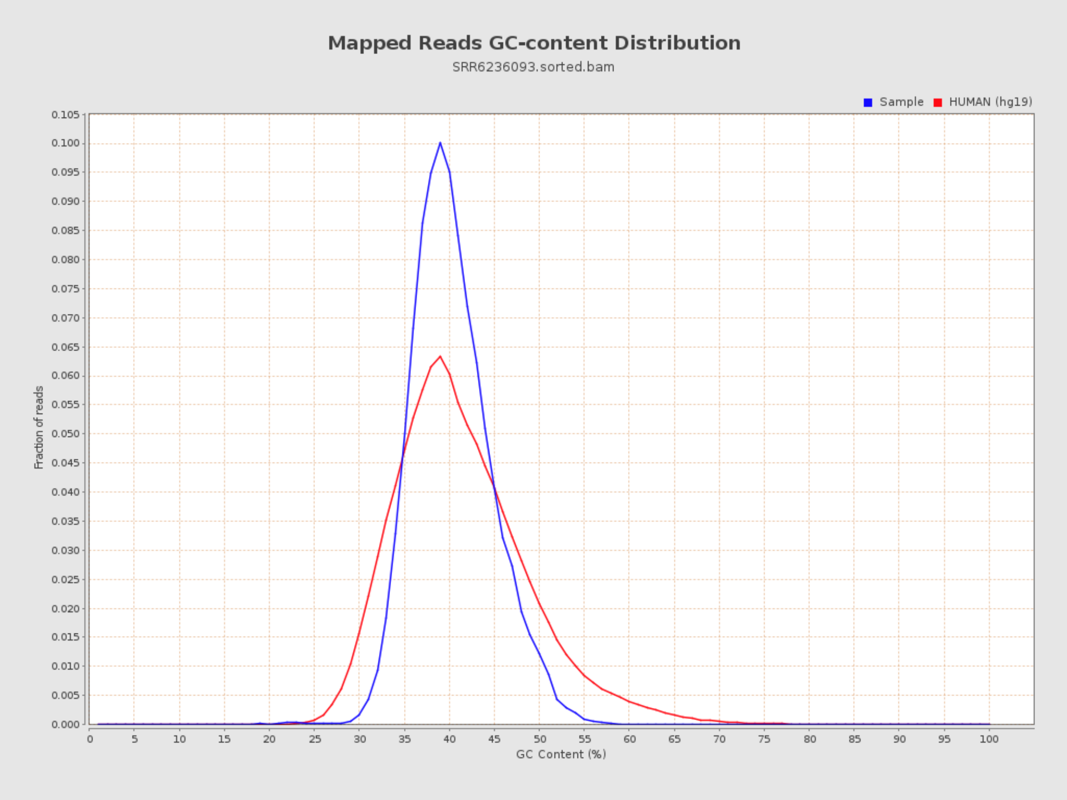
7. Results : Duplication Rate Histogram



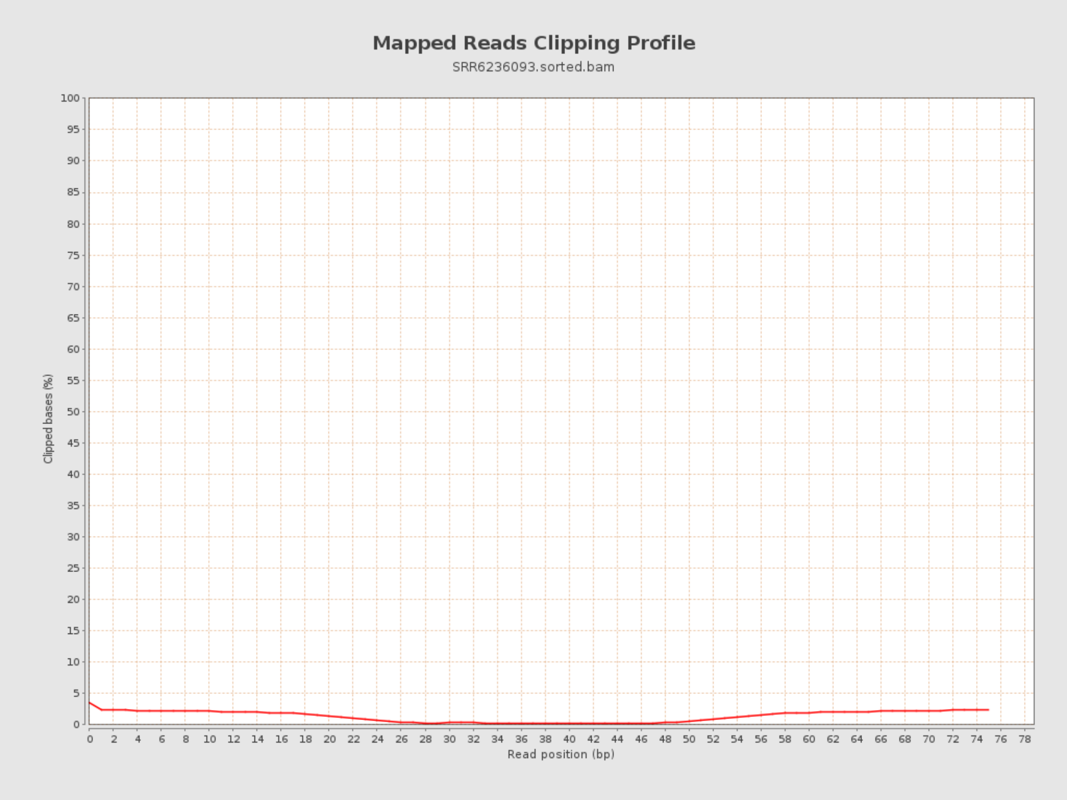
8. Results : Mapped Reads Nucleotide Content



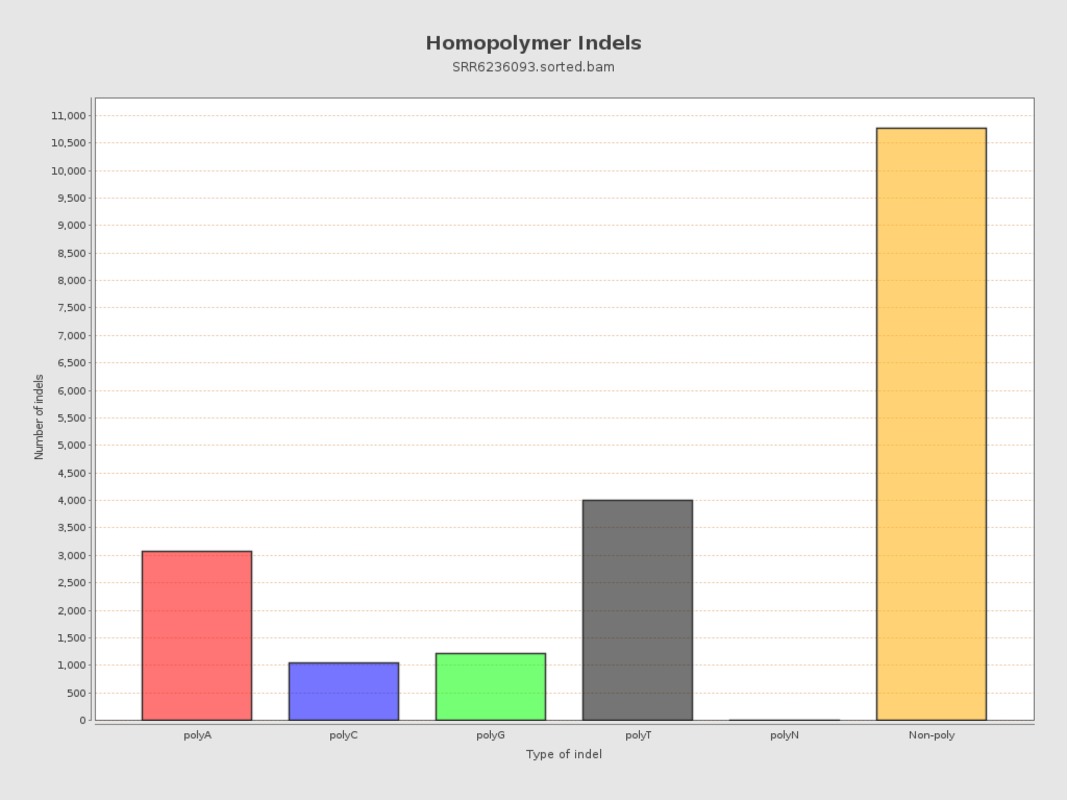
9. Results : Mapped Reads GC-content Distribution



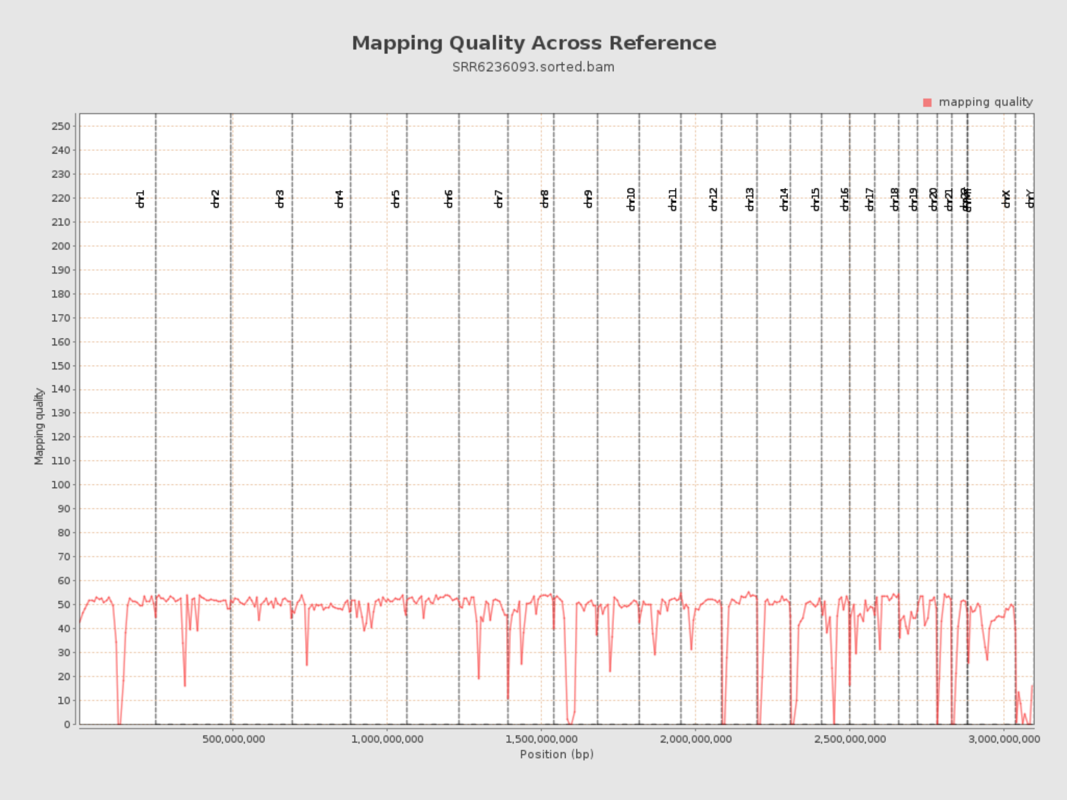
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram