Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:11:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236091.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_SRR6236091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,170,457
Mapped reads	1,880,933 / 86.66%
Unmapped reads	289,524 / 13.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,262 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	86,242 / 3.97%
Duplication rate	3.57%
Clipped reads	965,764 / 44.5%

2.2. ACGT Content

Number/percentage of A's	32,595,378 / 26.73%
Number/percentage of C's	21,949,884 / 18%
Number/percentage of T's	38,883,816 / 31.88%
Number/percentage of G's	28,470,449 / 23.34%
Number/percentage of N's	61,812 / 0.05%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.3671

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

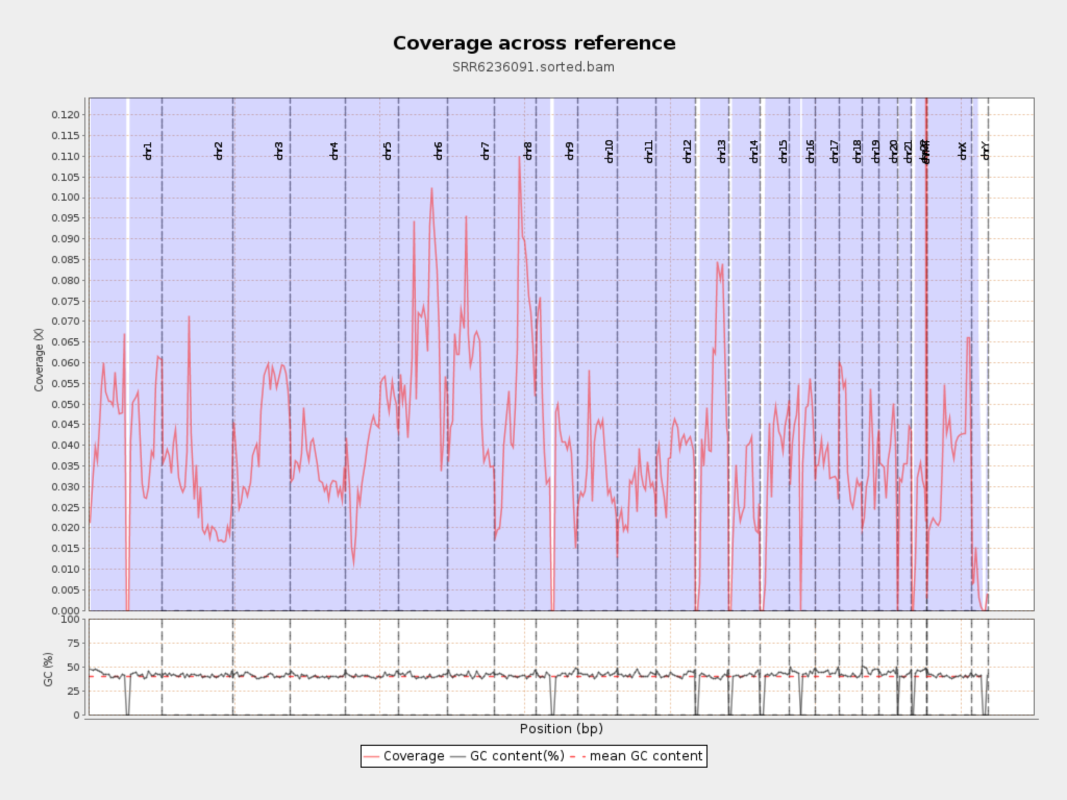
General error rate	0.84%
Mismatches	1,004,701
Insertions	8,559
Mapped reads with at least one insertion	0.45%
Deletions	33,984
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.38%

2.6. Chromosome stats

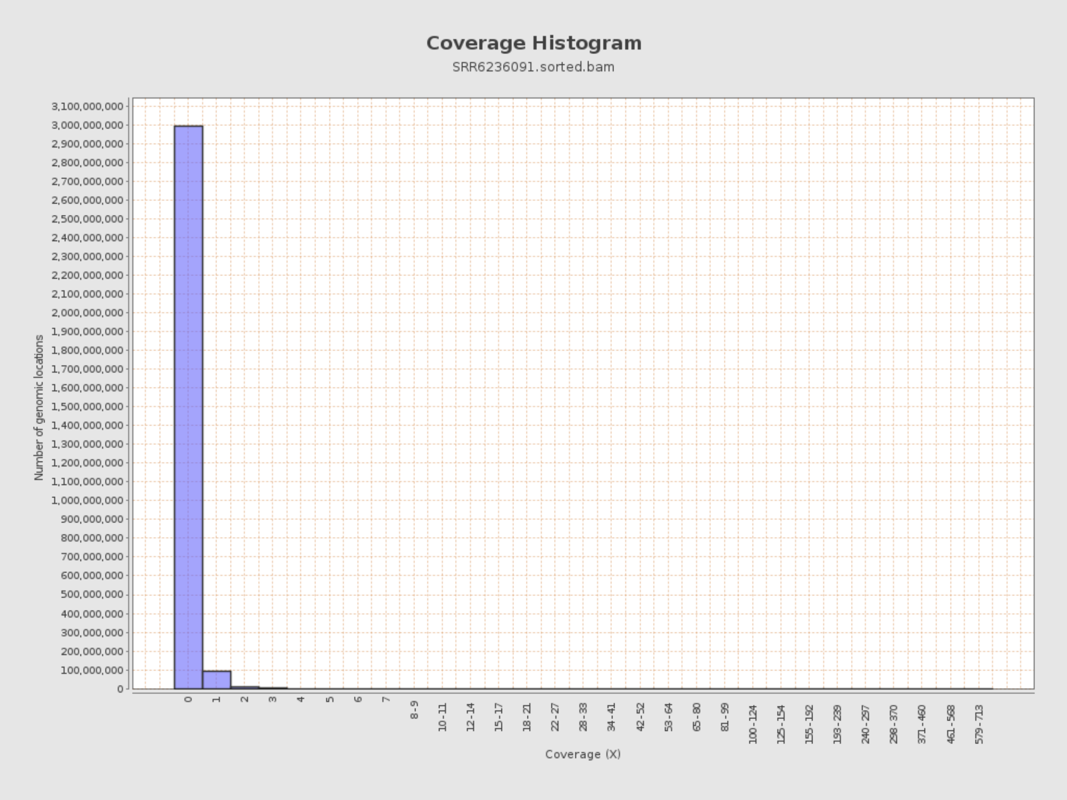
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10708987	0.043	0.6323
chr2	243199373	7006404	0.0288	0.4139
chr3	198022430	8976039	0.0453	0.2389
chr4	191154276	6491758	0.034	0.2252
chr5	180915260	7304604	0.0404	0.227
chr6	171115067	11097293	0.0649	0.3832
chr7	159138663	8918381	0.056	0.631

chr8	146364022	8113279	0.0554	0.4711
chr9	141213431	5383622	0.0381	0.346
chr10	135534747	4751267	0.0351	0.3203
chr11	135006516	3776038	0.028	0.248
chr12	133851895	5140174	0.0384	0.2275
chr13	115169878	5446590	0.0473	0.2448
chr14	107349540	2596330	0.0242	0.1895
chr15	102531392	3398448	0.0331	0.2154
chr16	90354753	3787263	0.0419	0.2526
chr17	81195210	2834767	0.0349	0.2323
chr18	78077248	3018950	0.0387	0.5296
chr19	59128983	2058686	0.0348	0.4552
chr20	63025520	2332126	0.037	0.221
chr21	48129895	1599474	0.0332	0.2283
chr22	51304566	1131611	0.0221	0.1637
chrMT	16571	121363	7.3238	4.8596
chrX	155270560	5759802	0.0371	0.2424
chrY	59373566	266997	0.0045	0.1216

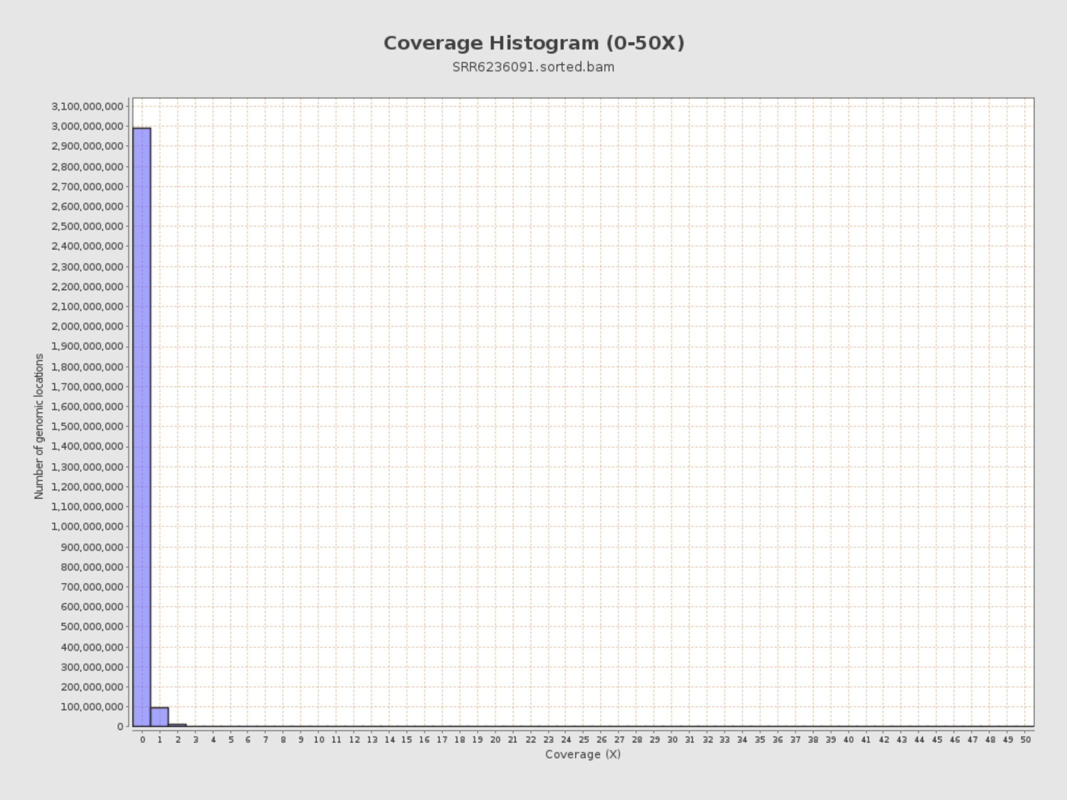
3. Results : Coverage across reference



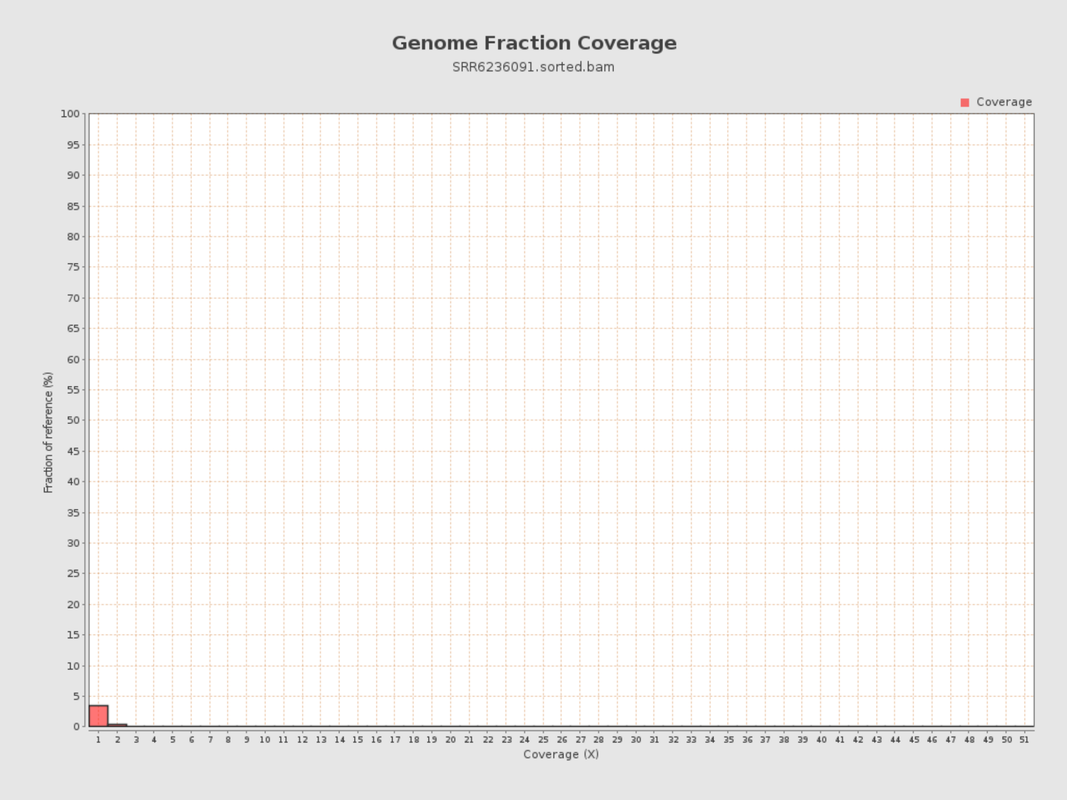
4. Results : Coverage Histogram



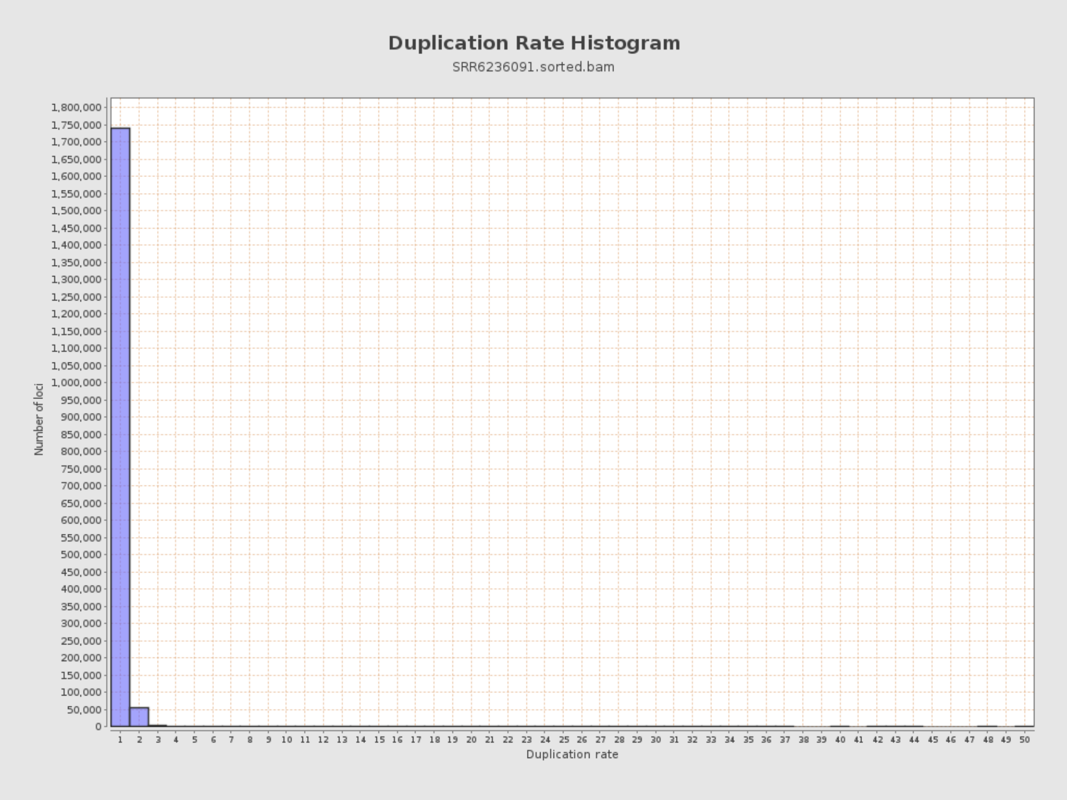
5. Results : Coverage Histogram (0-50X)



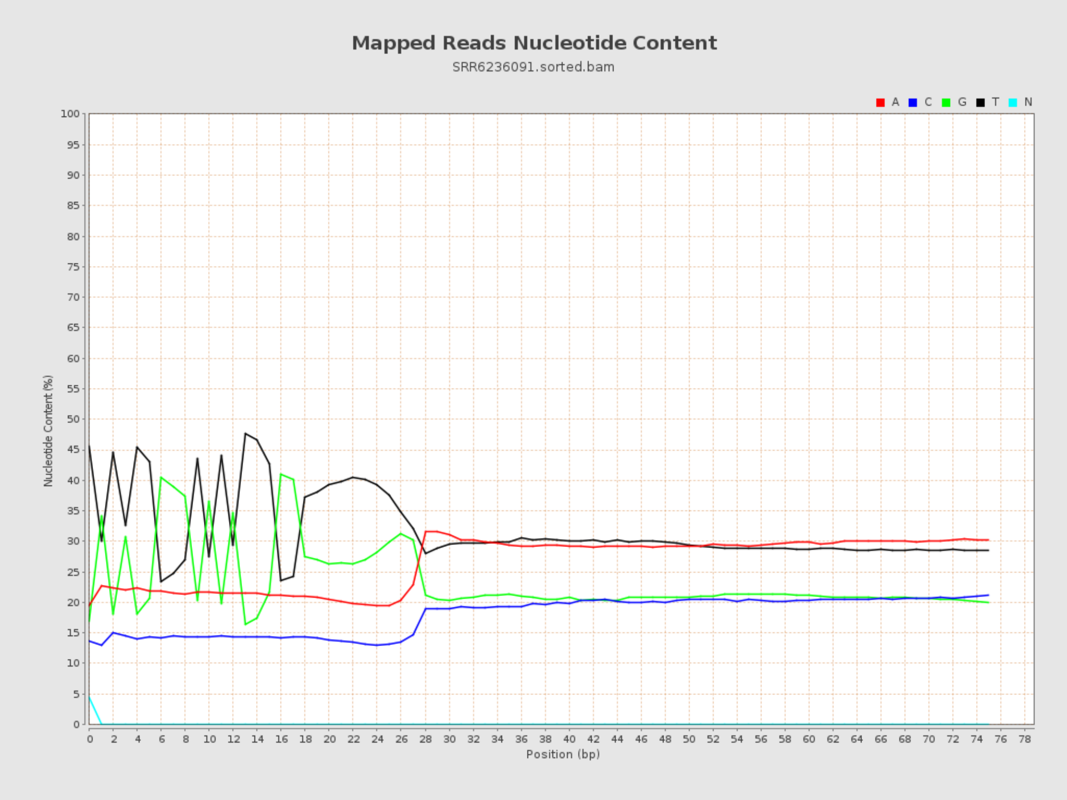
6. Results : Genome Fraction Coverage



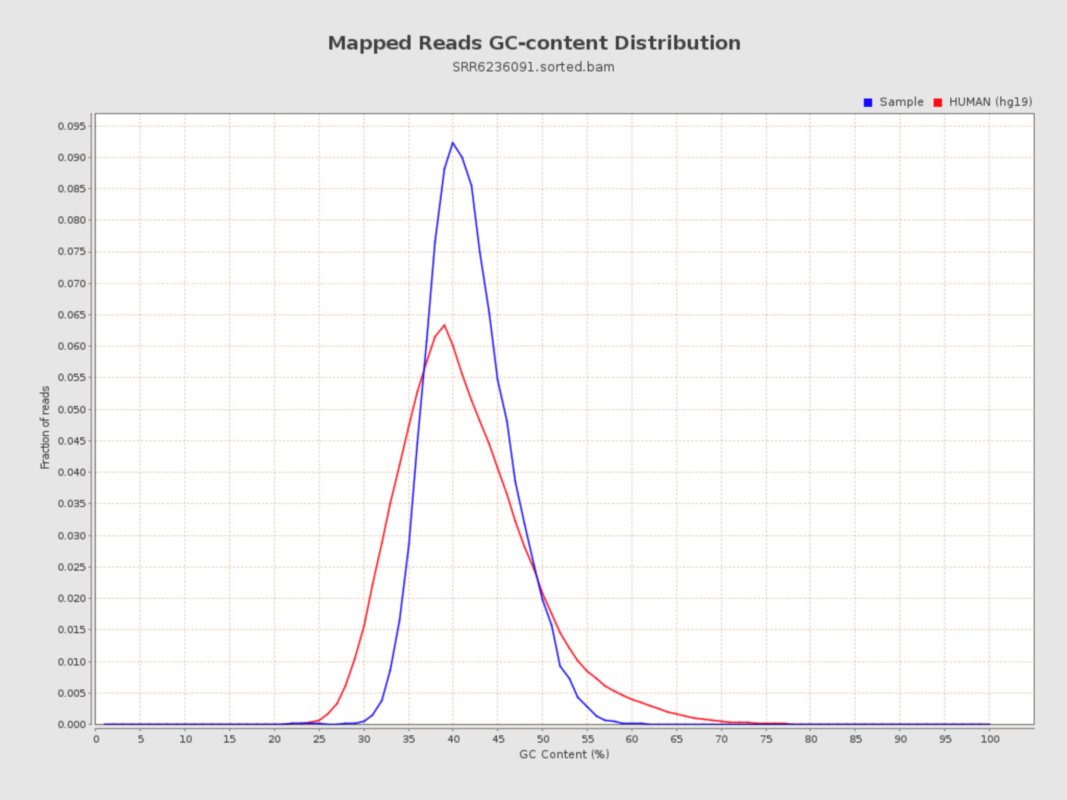
7. Results : Duplication Rate Histogram



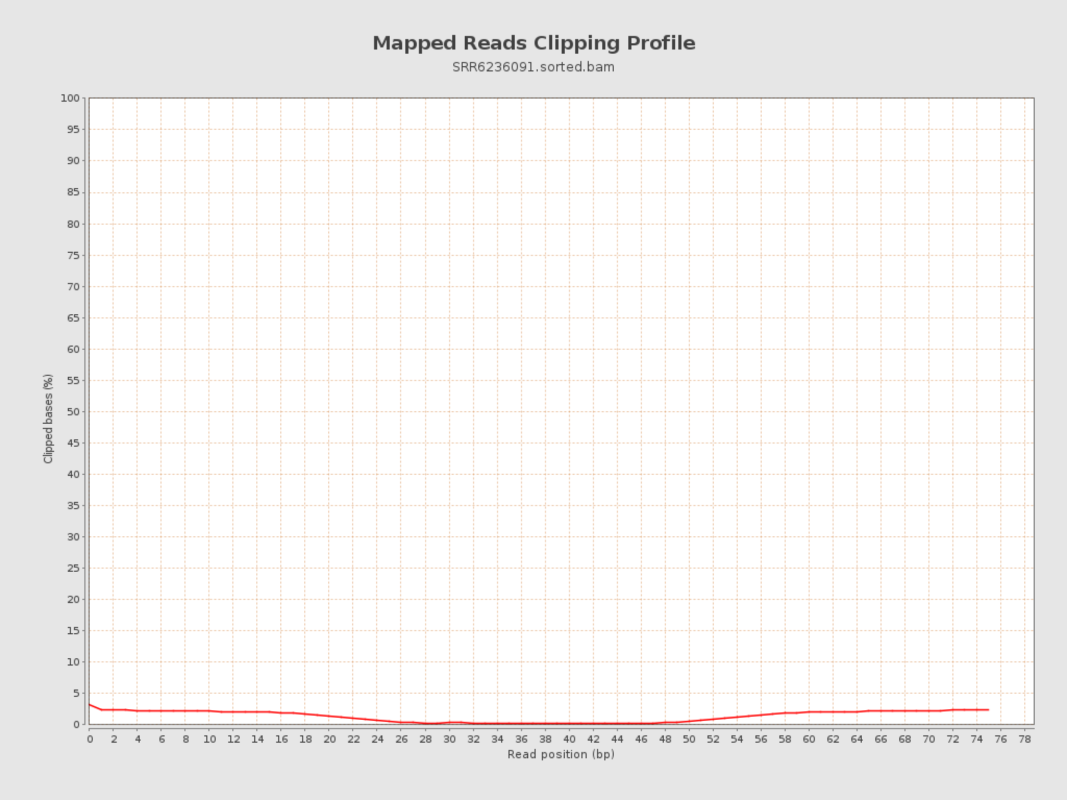
8. Results : Mapped Reads Nucleotide Content



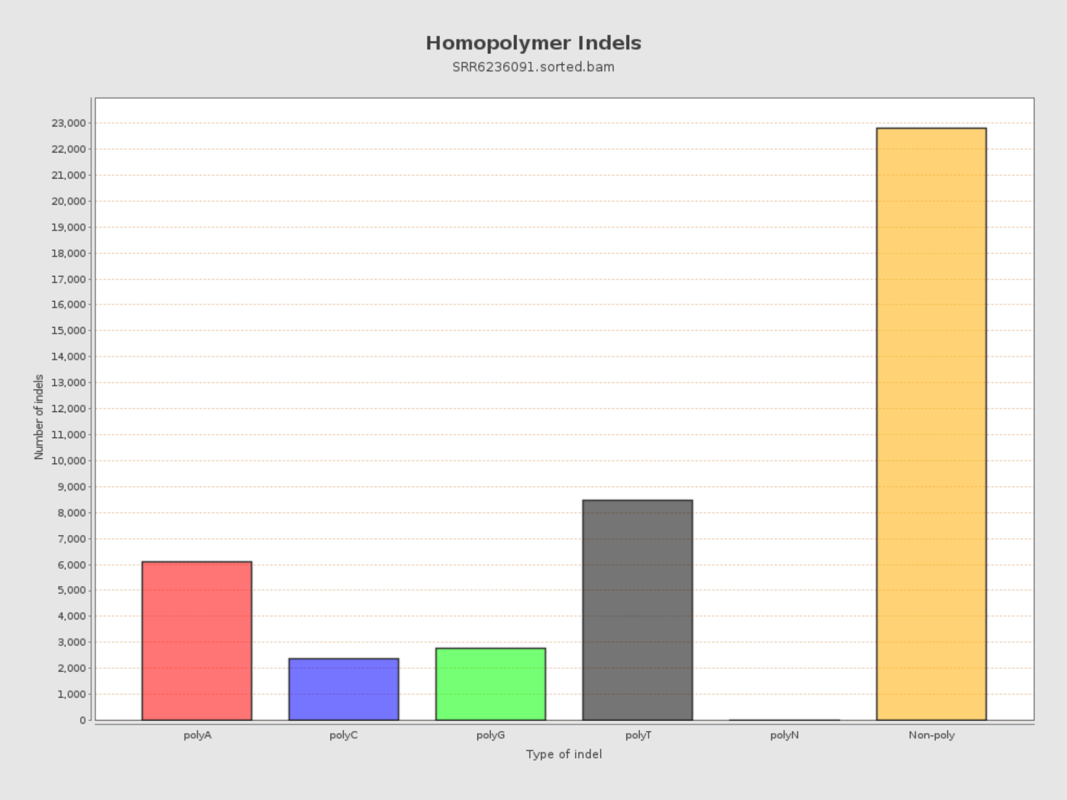
9. Results : Mapped Reads GC-content Distribution



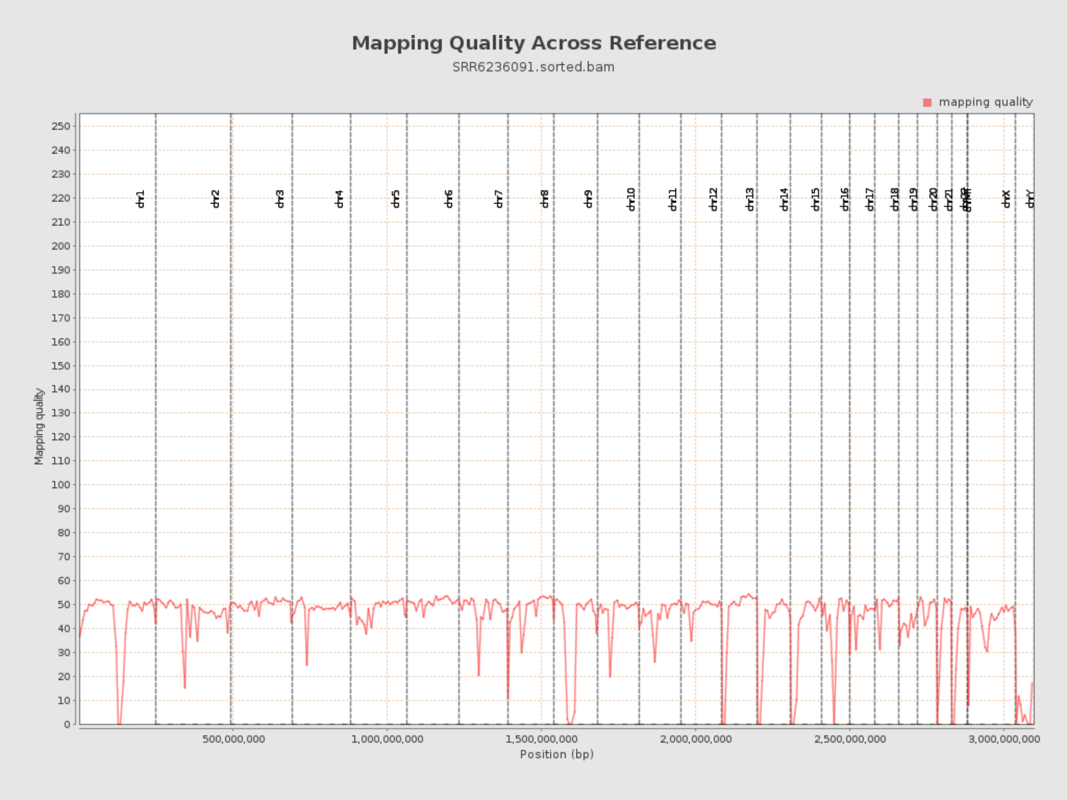
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram