Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:53:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236066.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_SRR6236066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236066.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:53:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,391,944
Mapped reads	1,236,912 / 88.86%
Unmapped reads	155,032 / 11.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,457 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	51,932 / 3.73%
Duplication rate	3.32%
Clipped reads	533,048 / 38.3%

2.2. ACGT Content

Number/percentage of A's	23,309,405 / 28.22%
Number/percentage of C's	14,590,778 / 17.66%
Number/percentage of T's	26,885,273 / 32.55%
Number/percentage of G's	17,780,893 / 21.53%
Number/percentage of N's	37,272 / 0.05%
GC Percentage	39.19%

2.3. Coverage

Mean	0.0267

Standard Deviation	0.2793

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

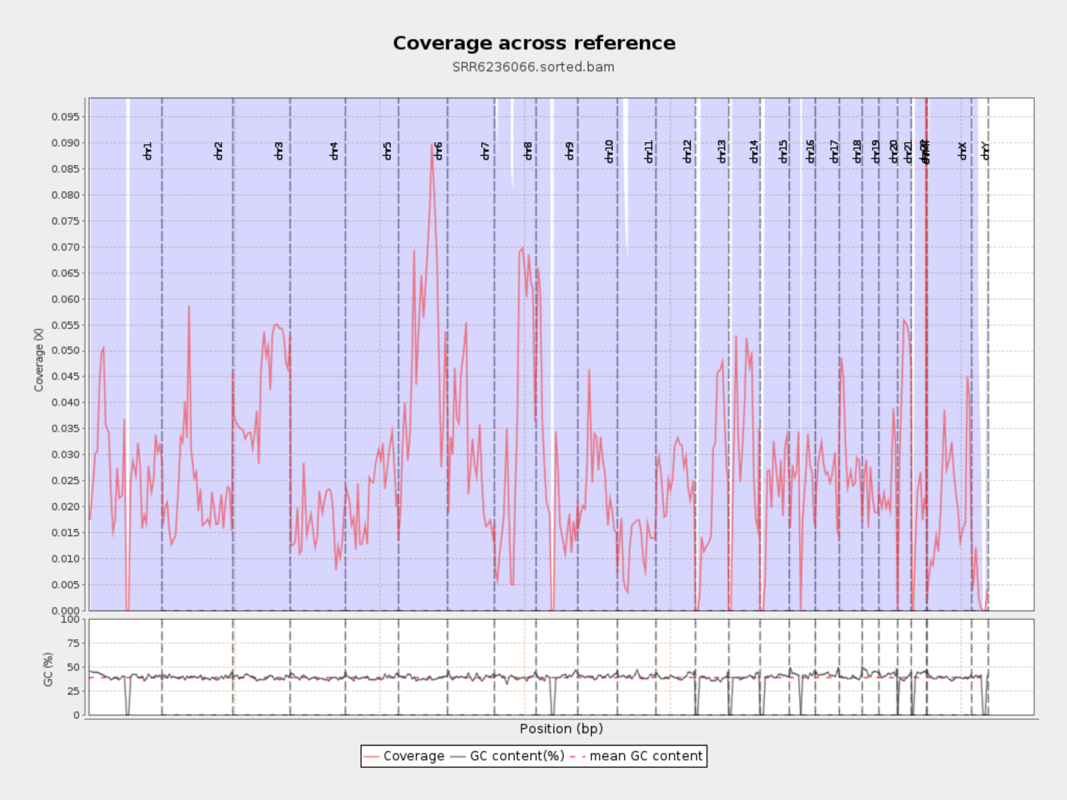
General error rate	0.84%
Mismatches	682,760
Insertions	6,203
Mapped reads with at least one insertion	0.5%
Deletions	26,473
Mapped reads with at least one deletion	2.11%
Homopolymer indels	46.05%

2.6. Chromosome stats

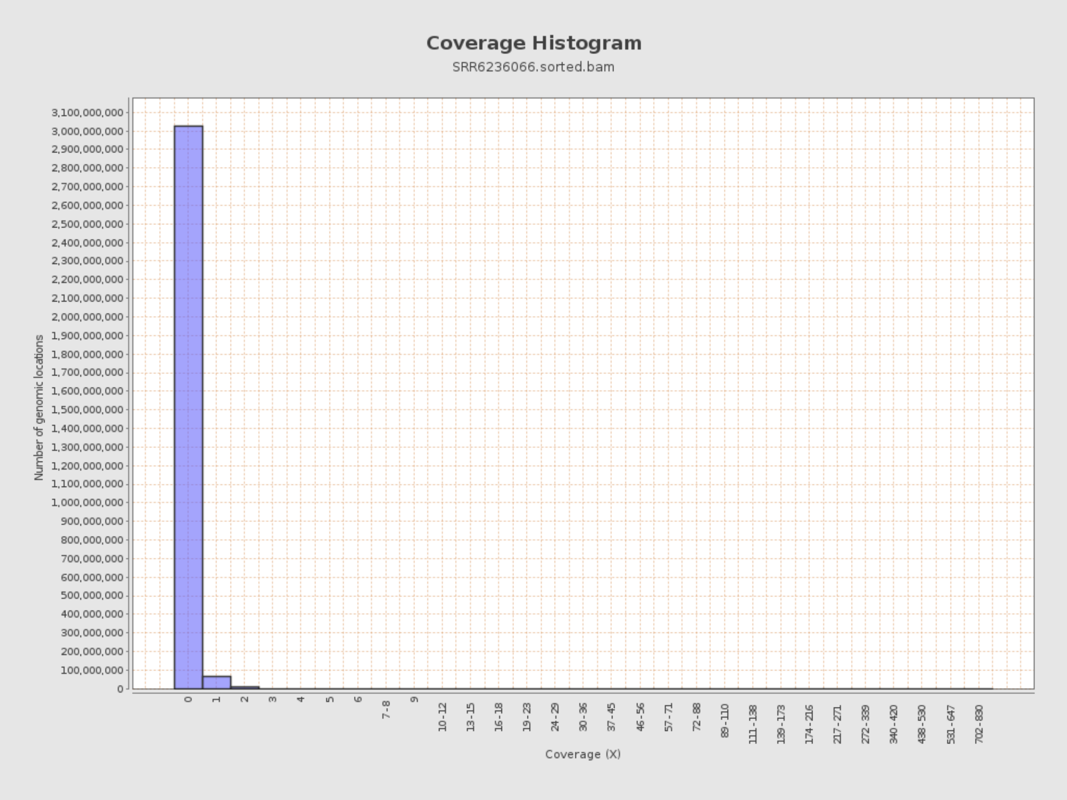
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6573455	0.0264	0.3728
chr2	243199373	5556695	0.0228	0.3034
chr3	198022430	8524014	0.043	0.2311
chr4	191154276	3189525	0.0167	0.155
chr5	180915260	4156340	0.023	0.1691
chr6	171115067	8734831	0.051	0.3536
chr7	159138663	4843590	0.0304	0.348

chr8	146364022	5189063	0.0355	0.572
chr9	141213431	3257082	0.0231	0.2629
chr10	135534747	3393813	0.025	0.2594
chr11	135006516	1681386	0.0125	0.1689
chr12	133851895	3512318	0.0262	0.1853
chr13	115169878	2649330	0.023	0.1682
chr14	107349540	3218459	0.03	0.1968
chr15	102531392	2208542	0.0215	0.1653
chr16	90354753	2133741	0.0236	0.1866
chr17	81195210	2081797	0.0256	0.2014
chr18	78077248	2421136	0.031	0.4339
chr19	59128983	1325982	0.0224	0.2993
chr20	63025520	1518120	0.0241	0.1751
chr21	48129895	2061292	0.0428	0.2412
chr22	51304566	825524	0.0161	0.139
chrMT	16571	23484	1.4172	1.423
chrX	155270560	3357247	0.0216	0.1791
chrY	59373566	213002	0.0036	0.0982

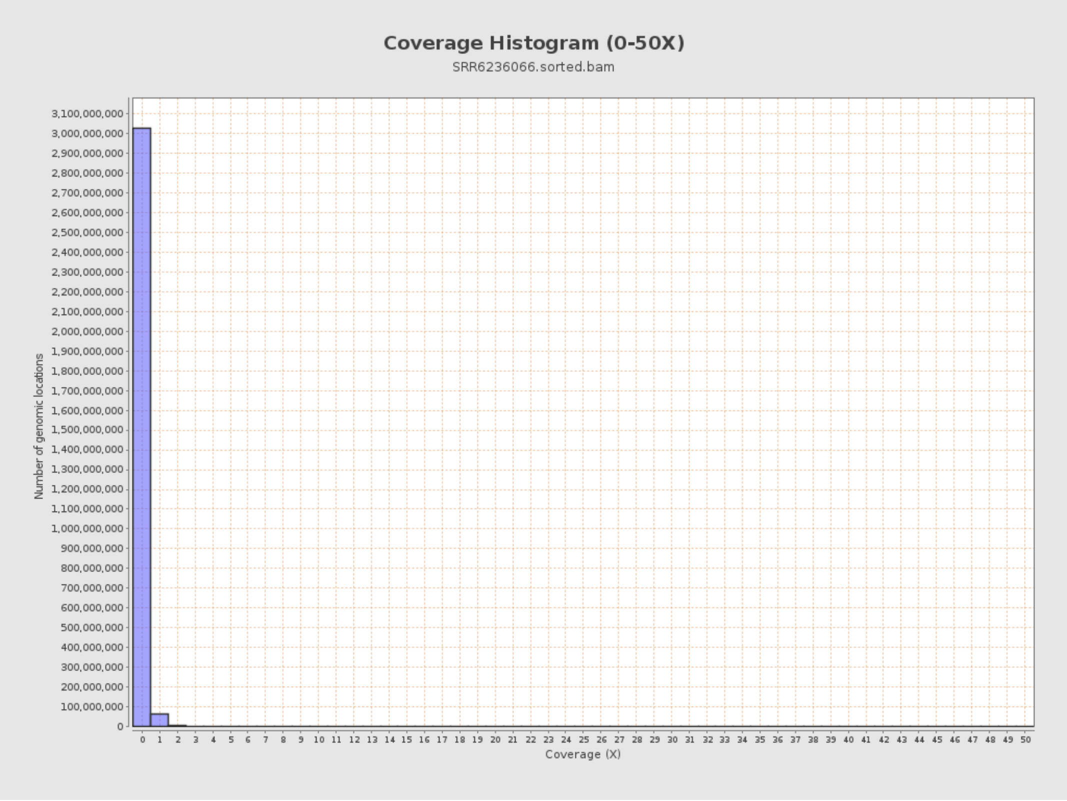
3. Results : Coverage across reference



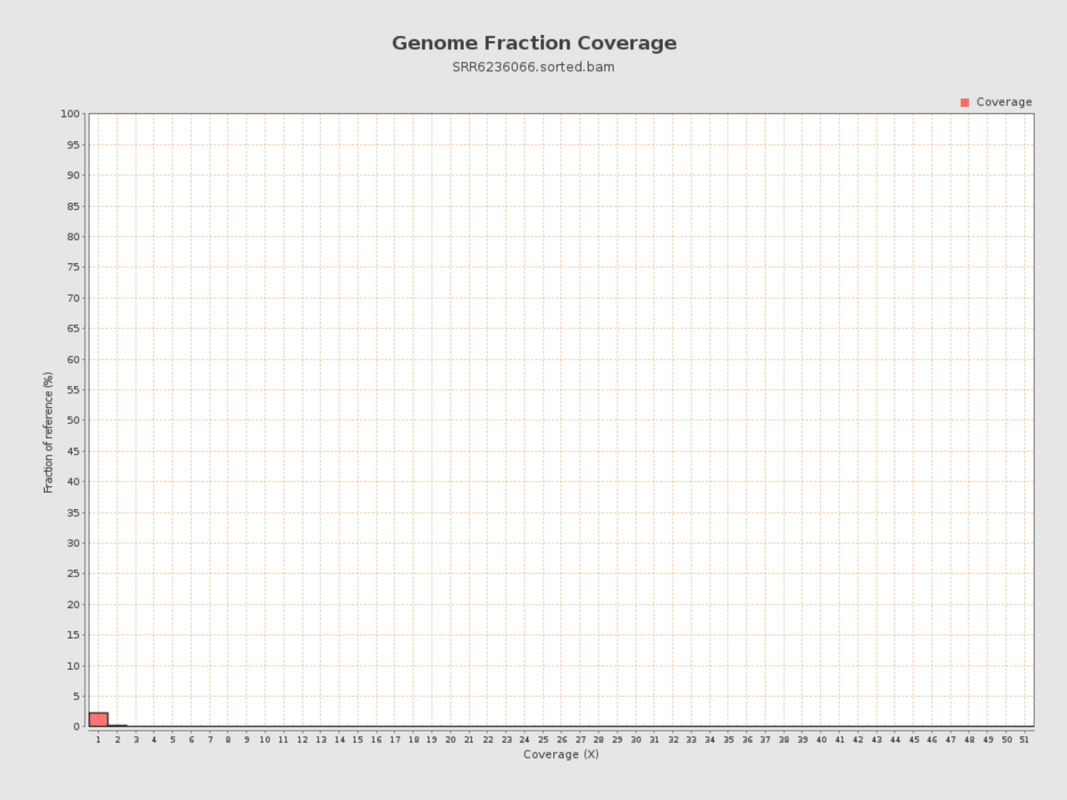
4. Results : Coverage Histogram



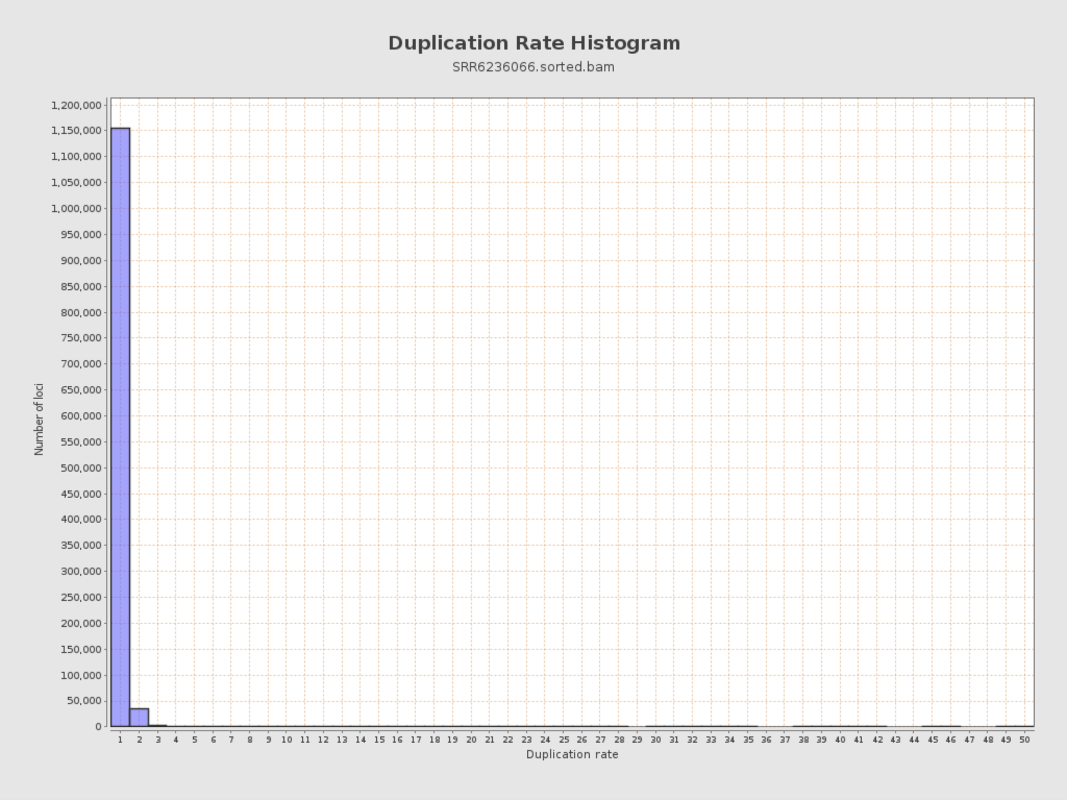
5. Results : Coverage Histogram (0-50X)



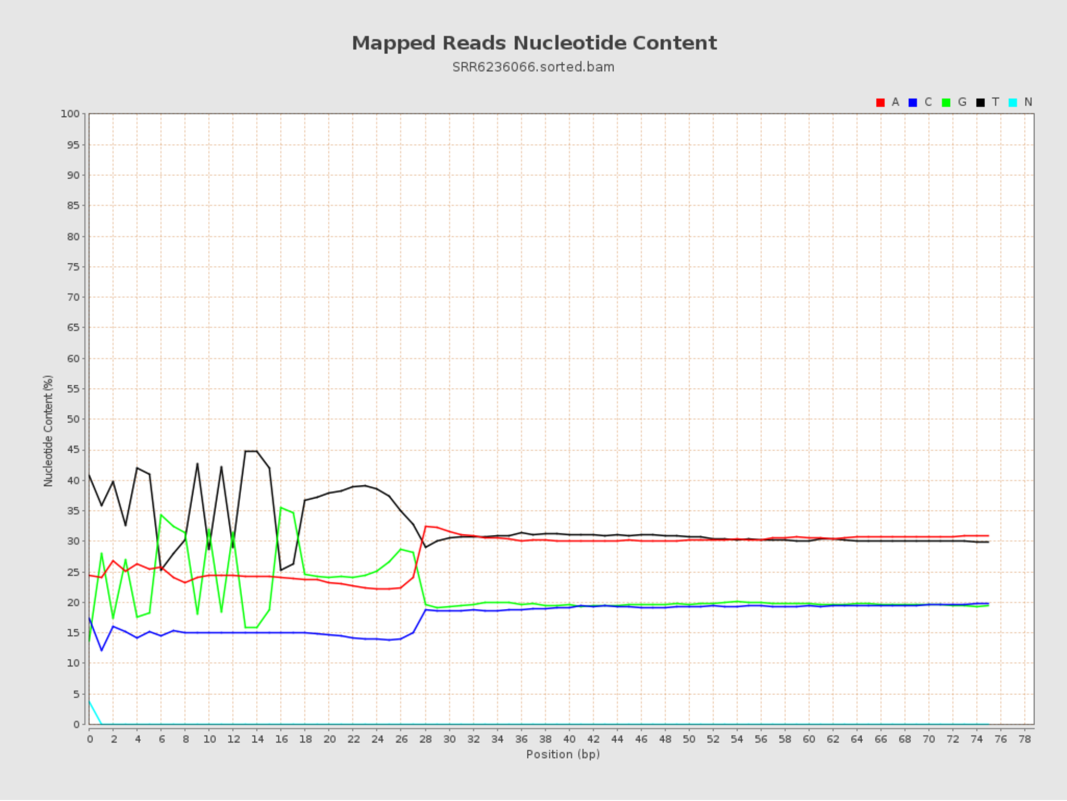
6. Results : Genome Fraction Coverage



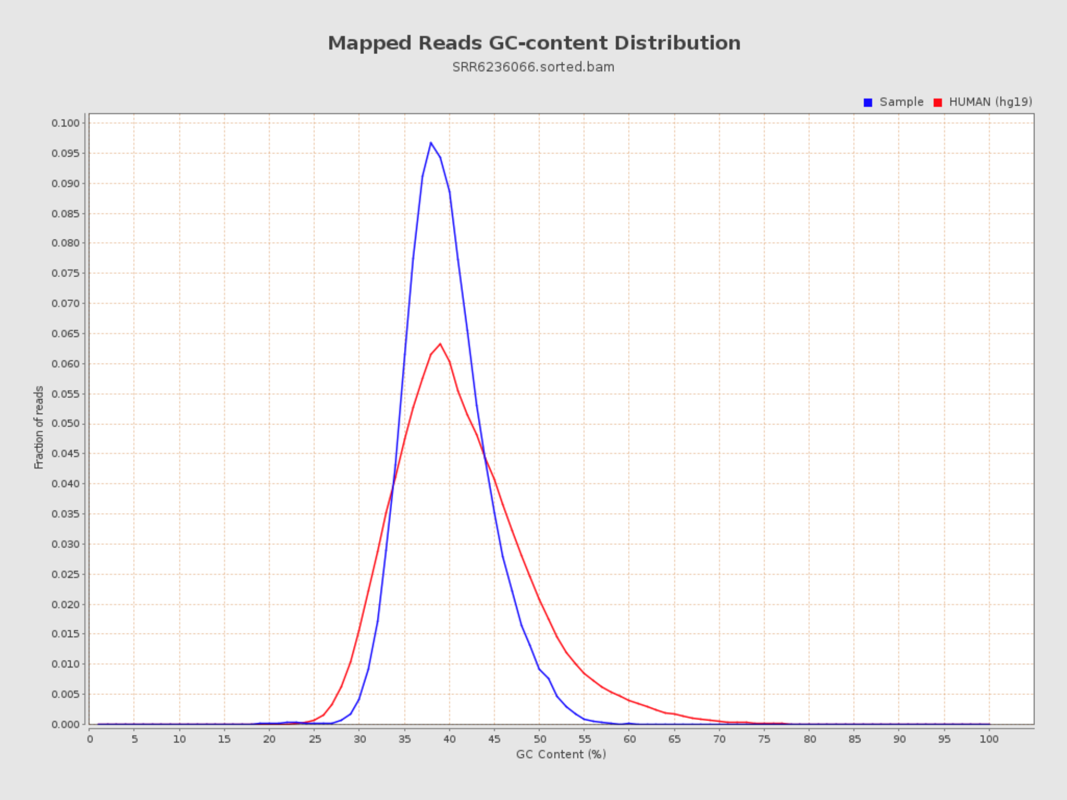
7. Results : Duplication Rate Histogram



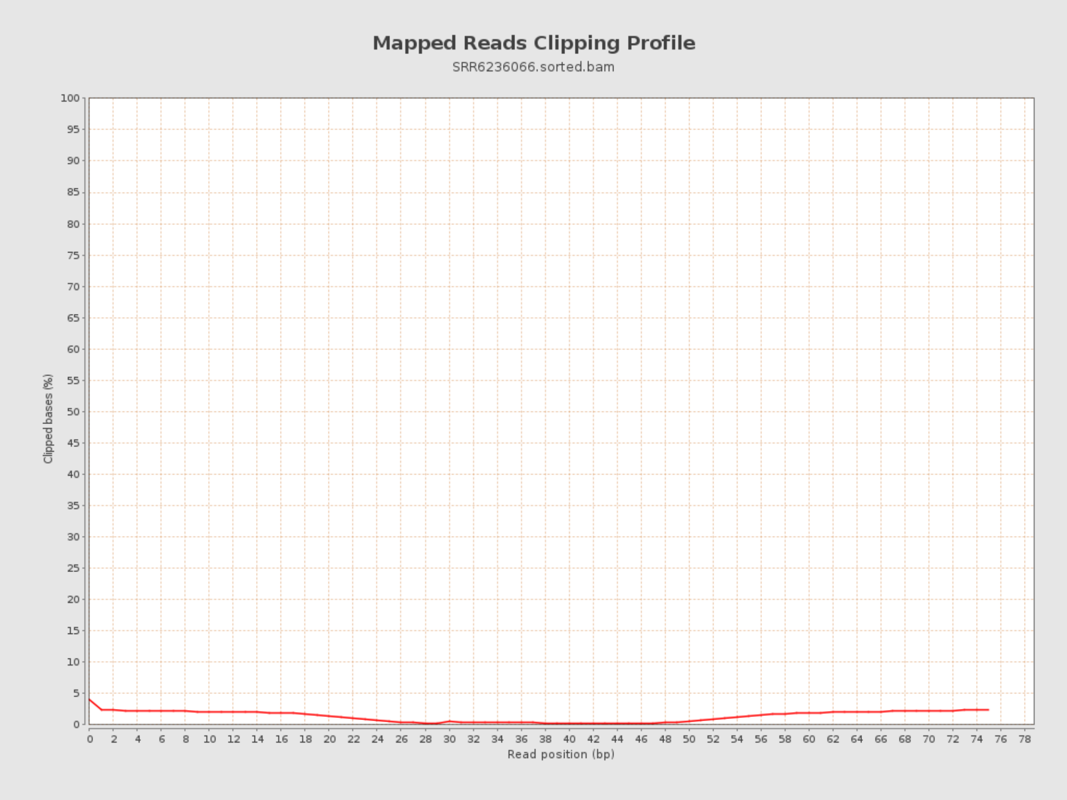
8. Results : Mapped Reads Nucleotide Content



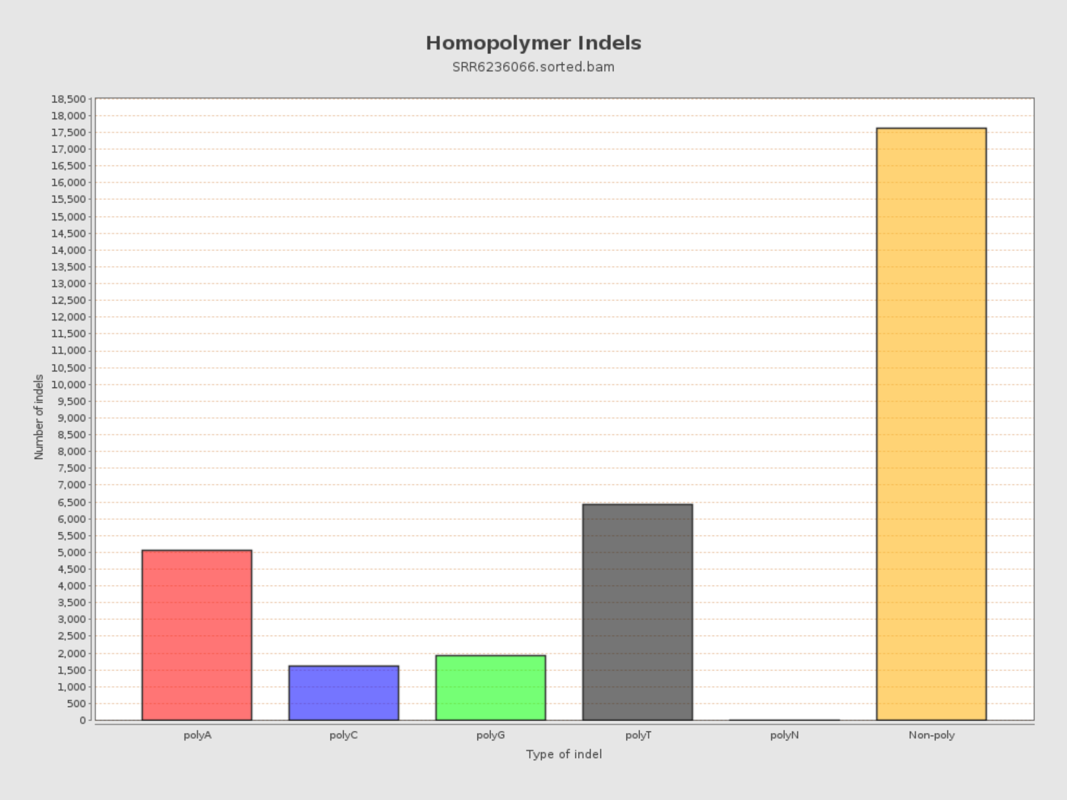
9. Results : Mapped Reads GC-content Distribution



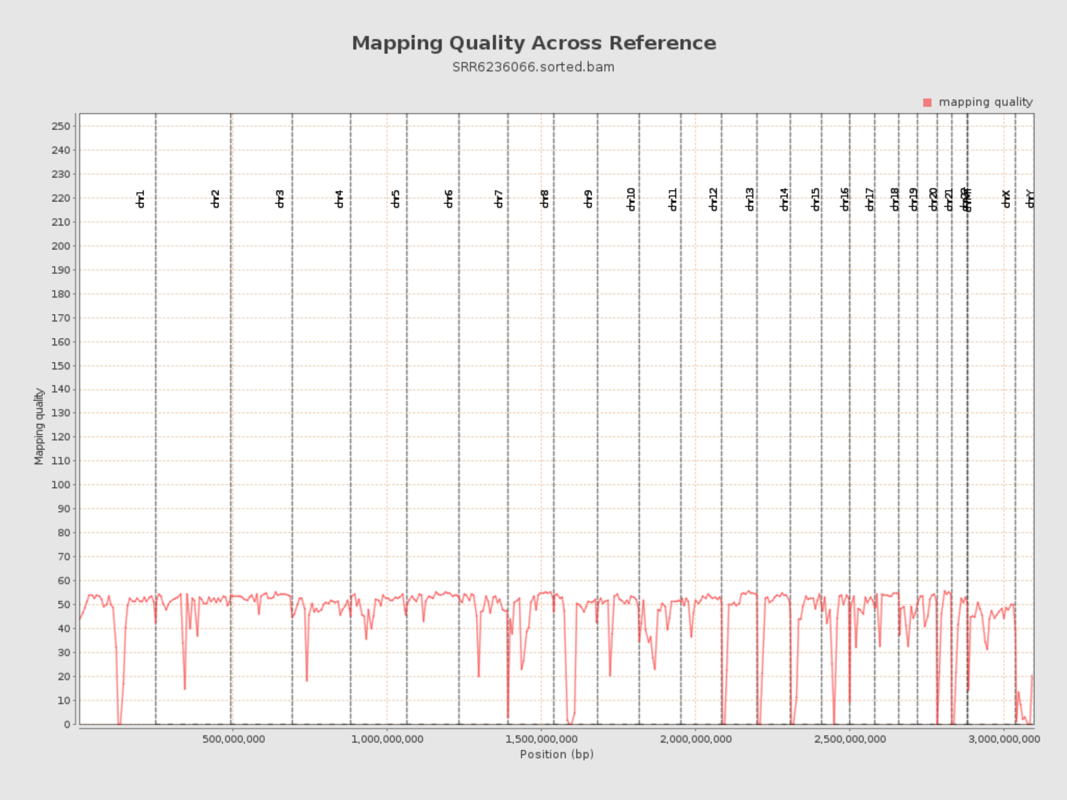
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram