Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:20:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084279.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_SRR3084279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084279.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:20:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,781,750
Mapped reads	2,526,440 / 90.82%
Unmapped reads	255,310 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,118 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	84,138 / 3.02%
Duplication rate	2.73%
Clipped reads	1,251,375 / 44.99%

2.2. ACGT Content

Number/percentage of A's	46,244,092 / 27.71%
Number/percentage of C's	32,529,982 / 19.49%
Number/percentage of T's	50,522,448 / 30.27%
Number/percentage of G's	37,412,930 / 22.41%
Number/percentage of N's	206,022 / 0.12%
GC Percentage	41.9%

2.3. Coverage

Mean	0.0539

Standard Deviation	0.3544

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

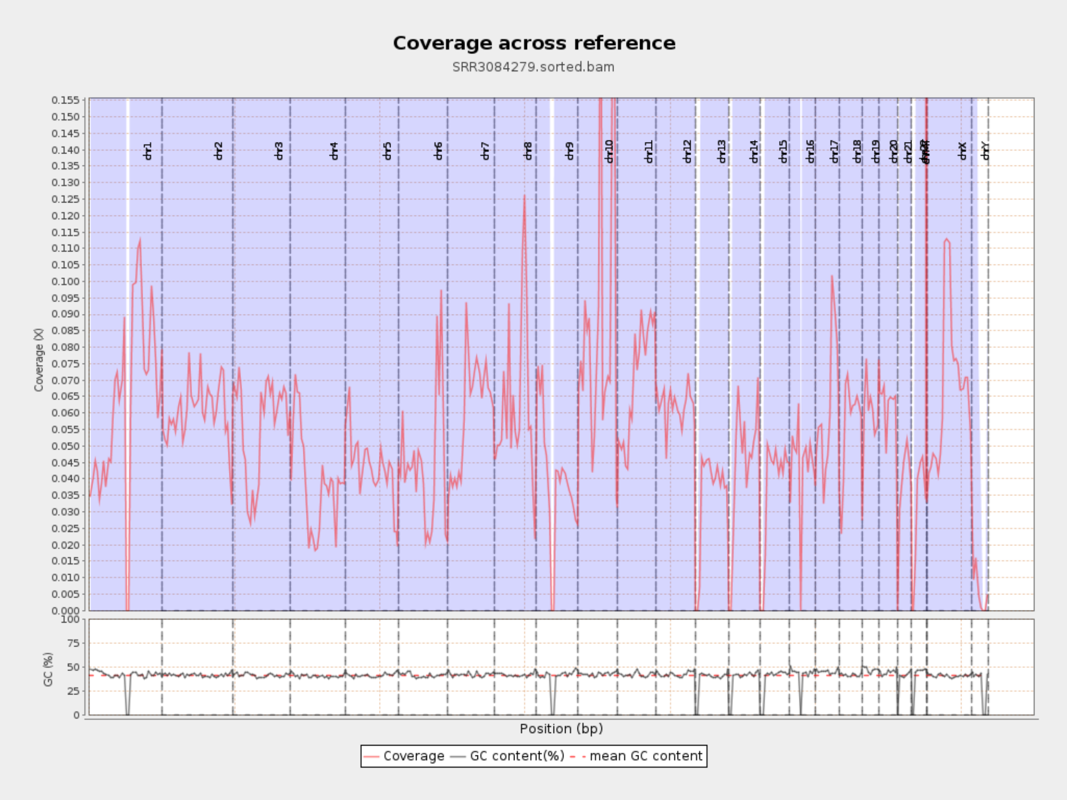
General error rate	1.05%
Mismatches	1,724,264
Insertions	12,867
Mapped reads with at least one insertion	0.5%
Deletions	35,674
Mapped reads with at least one deletion	1.4%
Homopolymer indels	45.75%

2.6. Chromosome stats

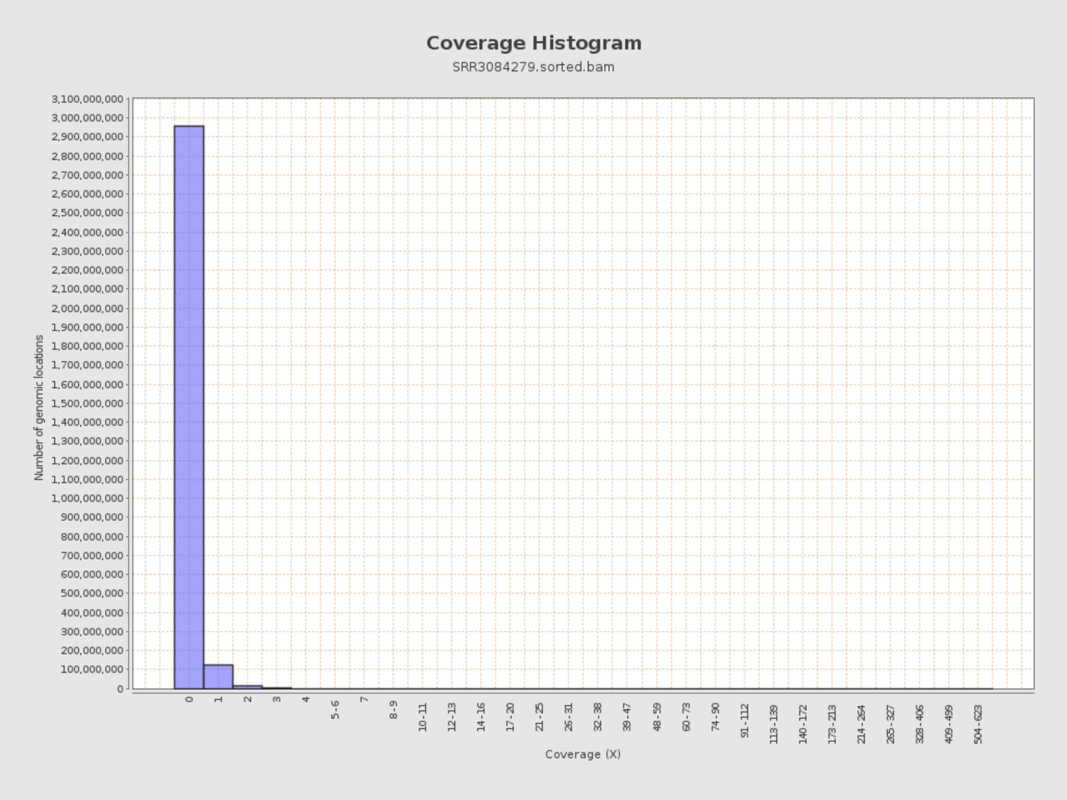
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15755013	0.0632	0.545
chr2	243199373	14706257	0.0605	0.423
chr3	198022430	11113965	0.0561	0.2754
chr4	191154276	7441849	0.0389	0.2316
chr5	180915260	7890998	0.0436	0.2387
chr6	171115067	7646710	0.0447	0.2671
chr7	159138663	9672456	0.0608	0.5262

chr8	146364022	9239458	0.0631	0.3782
chr9	141213431	5666754	0.0401	0.272
chr10	135534747	12356266	0.0912	0.5146
chr11	135006516	9417373	0.0698	0.3555
chr12	133851895	8334042	0.0623	0.2847
chr13	115169878	3993450	0.0347	0.2122
chr14	107349540	4791349	0.0446	0.2493
chr15	102531392	3823835	0.0373	0.229
chr16	90354753	3966868	0.0439	0.2682
chr17	81195210	5031461	0.062	0.3064
chr18	78077248	4407653	0.0565	0.4299
chr19	59128983	3607693	0.061	0.4271
chr20	63025520	3913742	0.0621	0.2877
chr21	48129895	1833502	0.0381	0.2292
chr22	51304566	1502256	0.0293	0.1939
chrMT	16571	39008	2.354	2.1814
chrX	155270560	10436136	0.0672	0.3234
chrY	59373566	384800	0.0065	0.1156

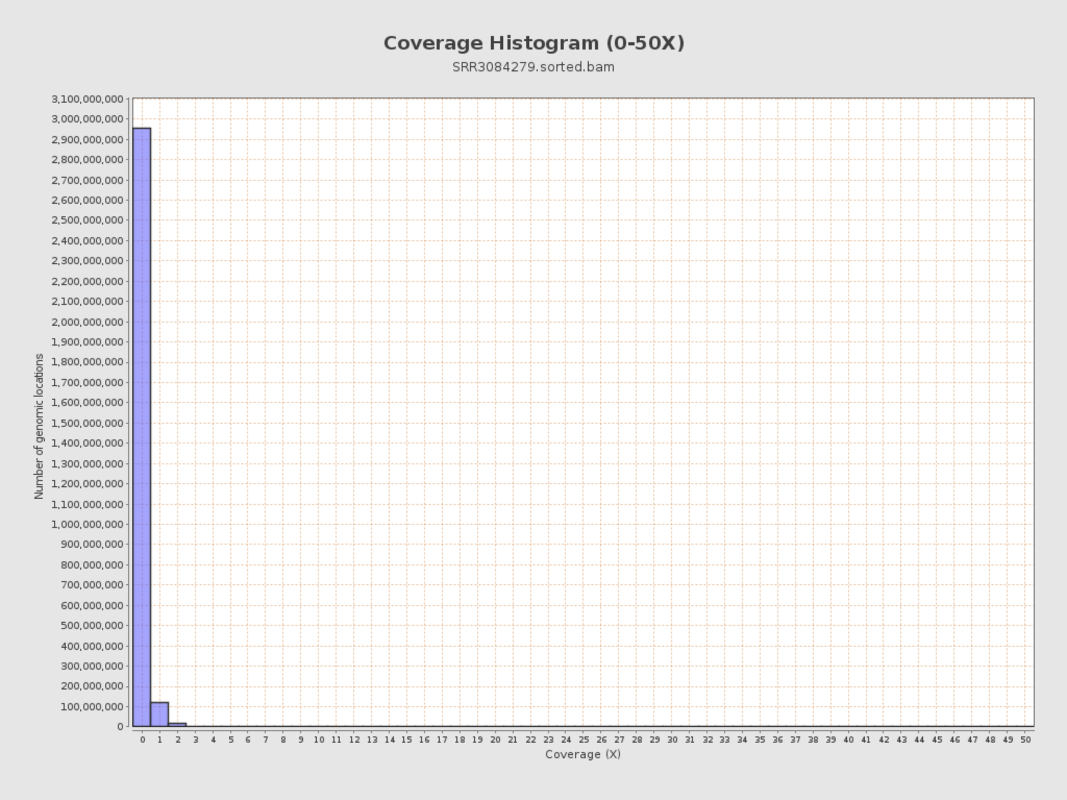
3. Results : Coverage across reference



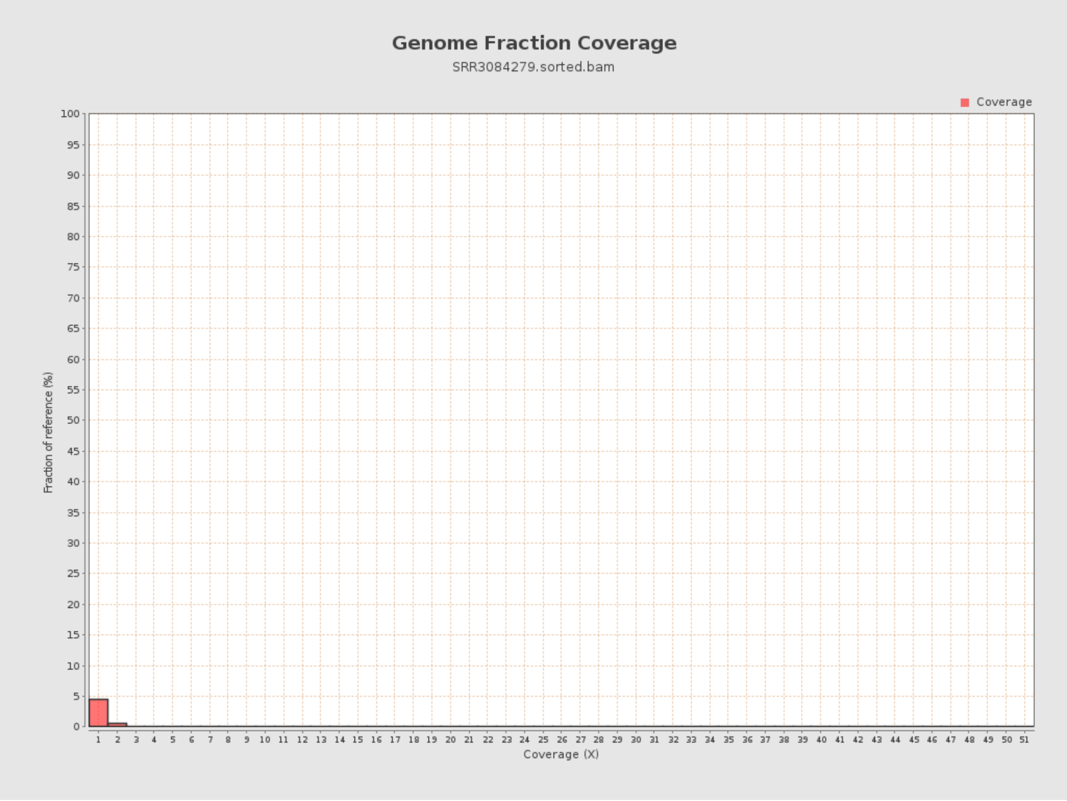
4. Results : Coverage Histogram



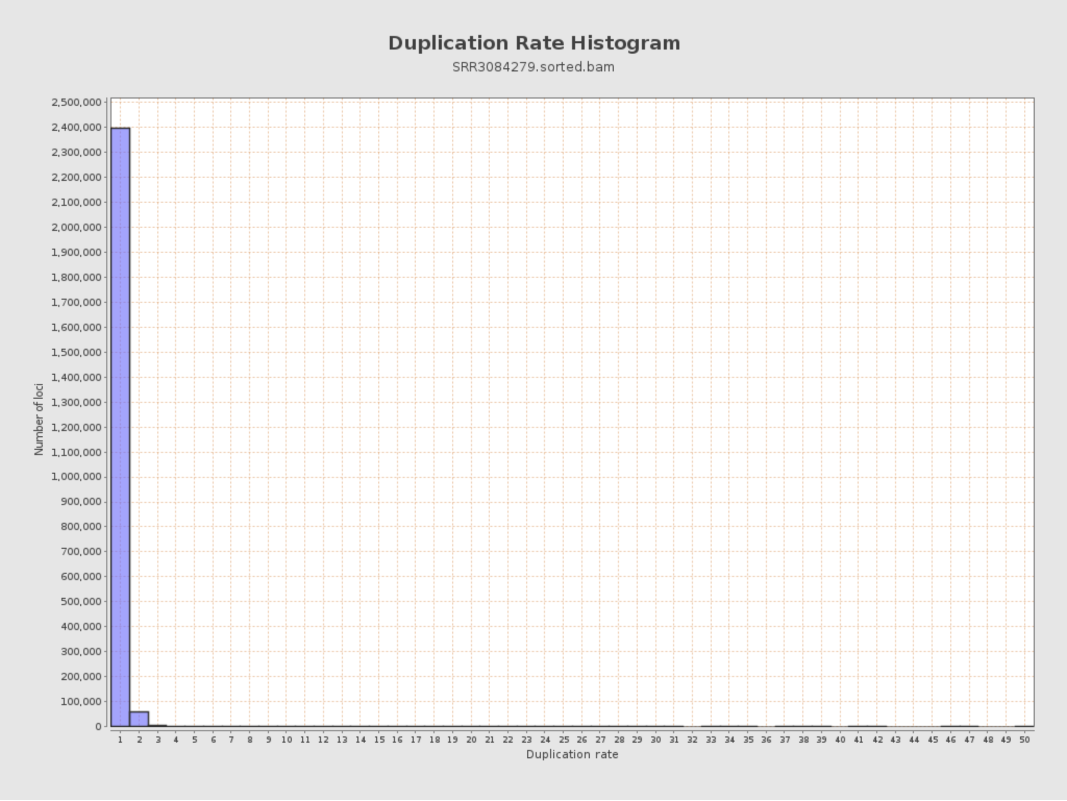
5. Results : Coverage Histogram (0-50X)



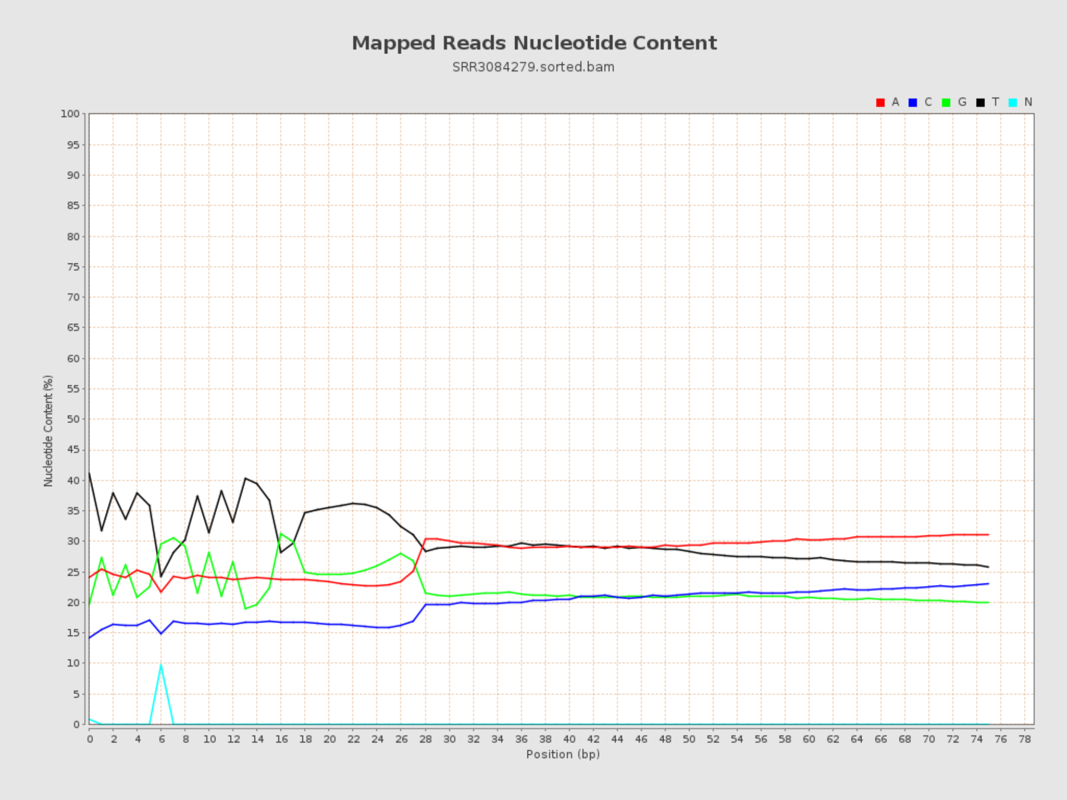
6. Results : Genome Fraction Coverage



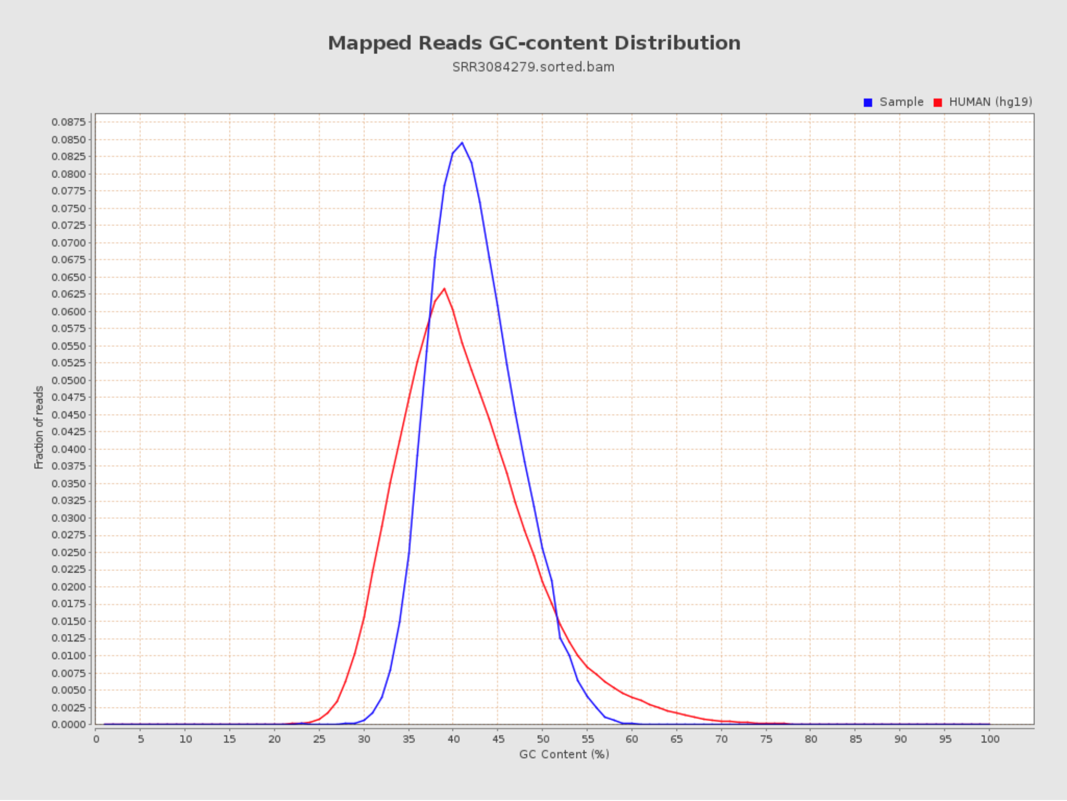
7. Results : Duplication Rate Histogram



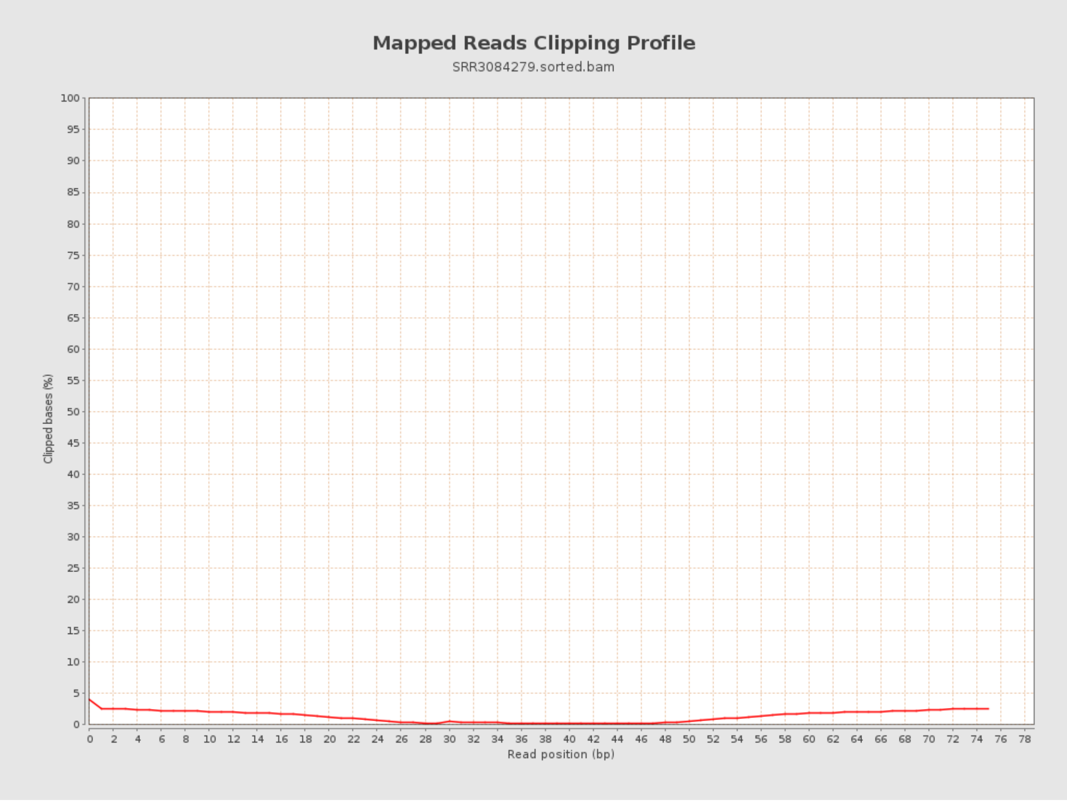
8. Results : Mapped Reads Nucleotide Content



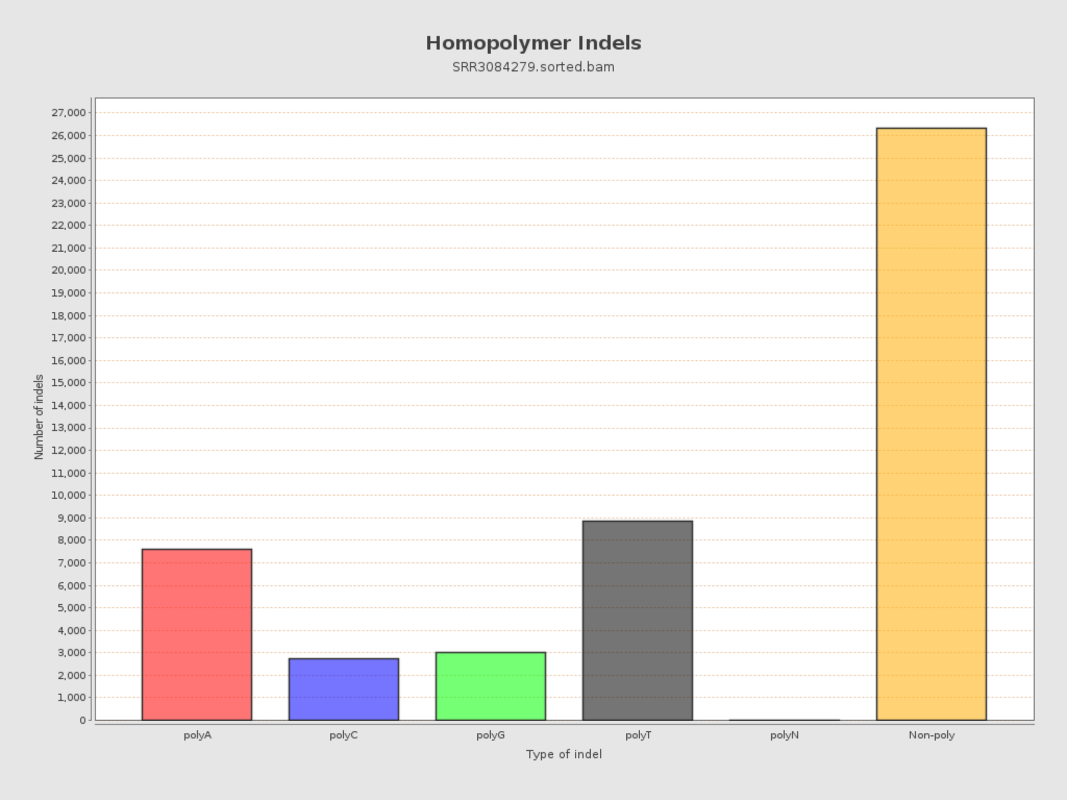
9. Results : Mapped Reads GC-content Distribution



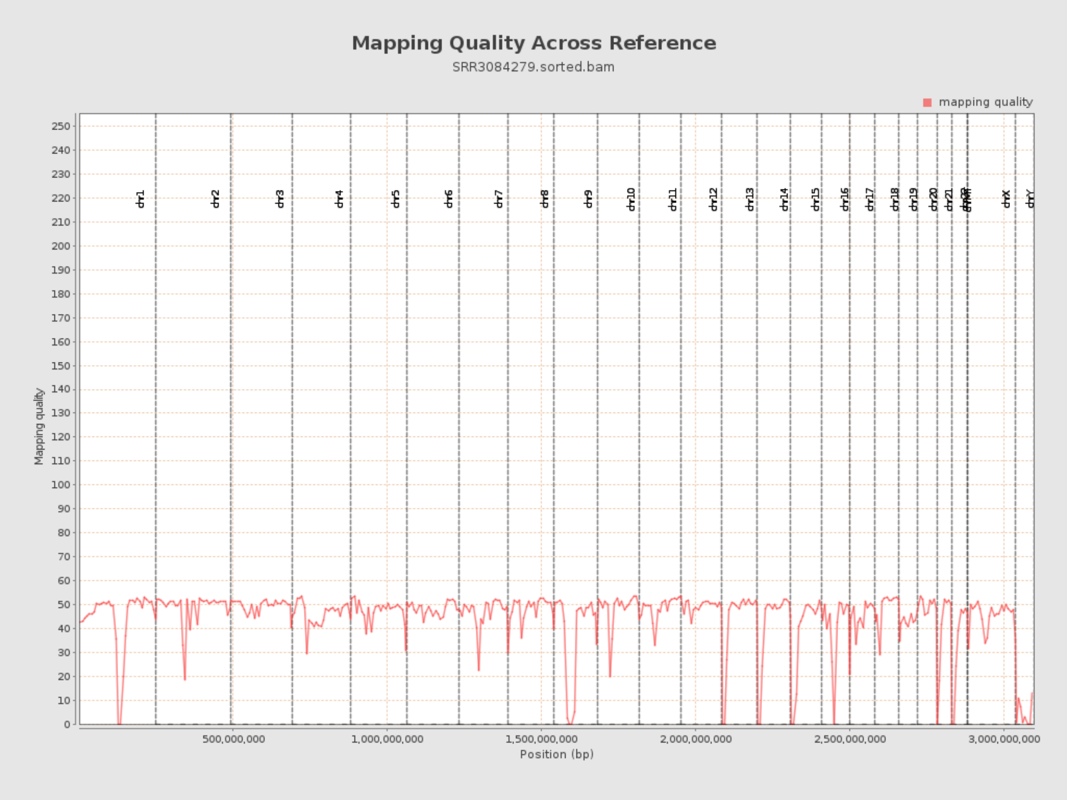
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram