Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548979.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_SRR1548979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548979.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:18:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,514,963
Mapped reads	3,321,565 / 44.2%
Unmapped reads	4,193,398 / 55.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	71,032 / 0.95%
Duplication rate	1.5%
Clipped reads	251,539 / 3.35%

2.2. ACGT Content

Number/percentage of A's	38,648,594 / 29.4%
Number/percentage of C's	26,693,553 / 20.31%
Number/percentage of T's	39,084,230 / 29.73%
Number/percentage of G's	27,014,853 / 20.55%
Number/percentage of N's	7,175 / 0.01%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0425
Standard Deviation	0.3039

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

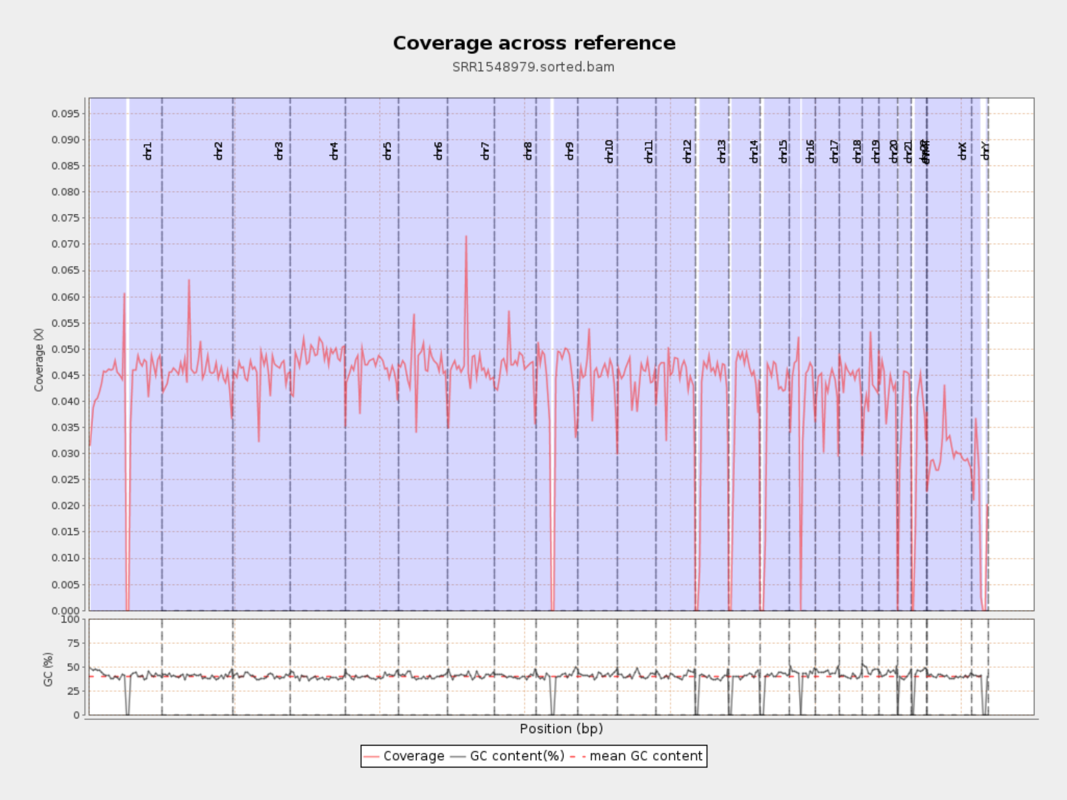
General error rate	0.28%
Mismatches	368,932
Insertions	4,418
Mapped reads with at least one insertion	0.13%
Deletions	11,620
Mapped reads with at least one deletion	0.35%
Homopolymer indels	44.7%

2.6. Chromosome stats

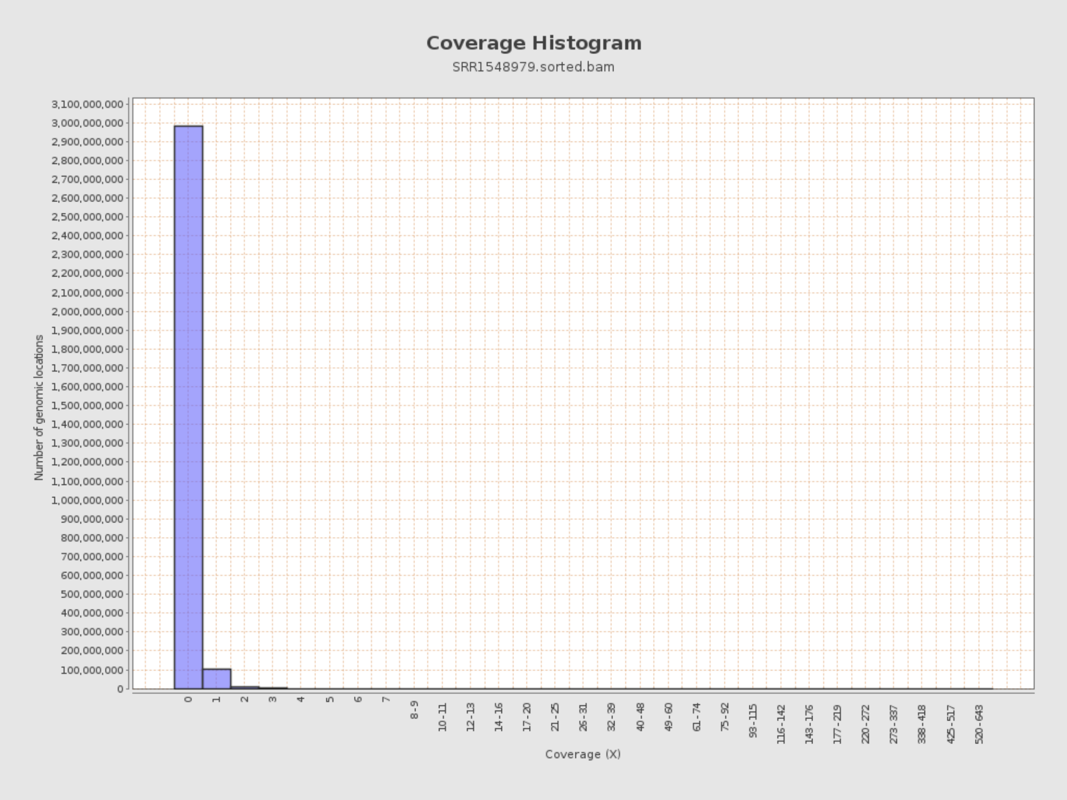
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10551667	0.0423	0.4762
chr2	243199373	11179878	0.046	0.3
chr3	198022430	9041290	0.0457	0.2354
chr4	191154276	9301030	0.0487	0.2469
chr5	180915260	8381116	0.0463	0.2387
chr6	171115067	8040427	0.047	0.2702
chr7	159138663	7482912	0.047	0.4513
chr8	146364022	6830291	0.0467	0.4078

chr9	141213431	5803282	0.0411	0.2811
chr10	135534747	6126350	0.0452	0.266
chr11	135006516	5996437	0.0444	0.277
chr12	133851895	6009739	0.0449	0.2381
chr13	115169878	4400861	0.0382	0.2144
chr14	107349540	4143117	0.0386	0.2445
chr15	102531392	3700406	0.0361	0.2089
chr16	90354753	3650593	0.0404	0.2321
chr17	81195210	3372735	0.0415	0.2399
chr18	78077248	3533395	0.0453	0.4063
chr19	59128983	2498754	0.0423	0.422
chr20	63025520	2651722	0.0421	0.2296
chr21	48129895	1720643	0.0357	0.2309
chr22	51304566	1447473	0.0282	0.2205
chrMT	16571	631	0.0381	0.197
chrX	155270560	4635522	0.0299	0.2191
chrY	59373566	962654	0.0162	0.163

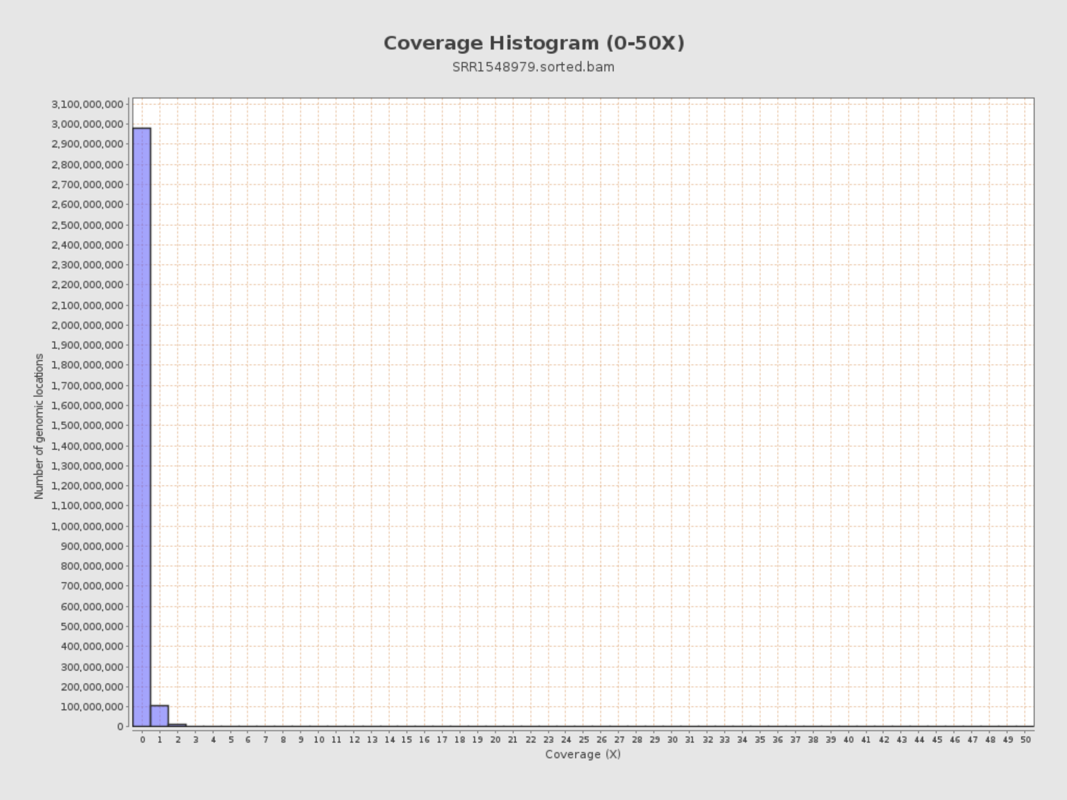
3. Results : Coverage across reference



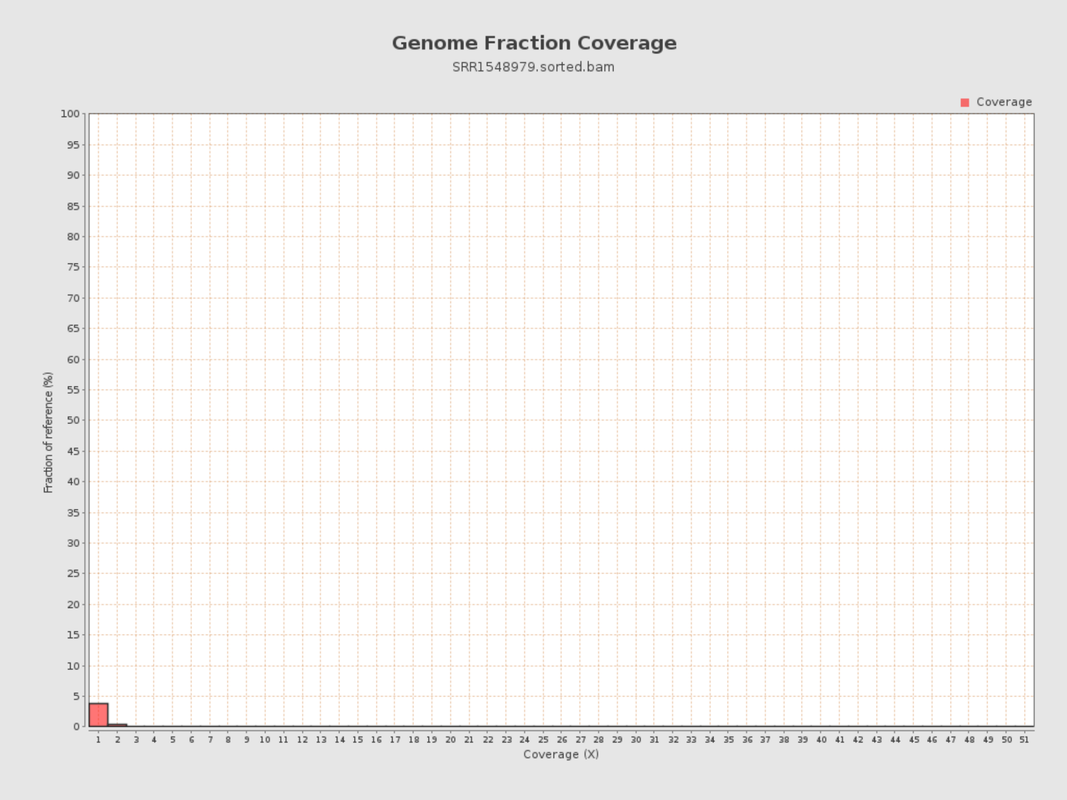
4. Results : Coverage Histogram



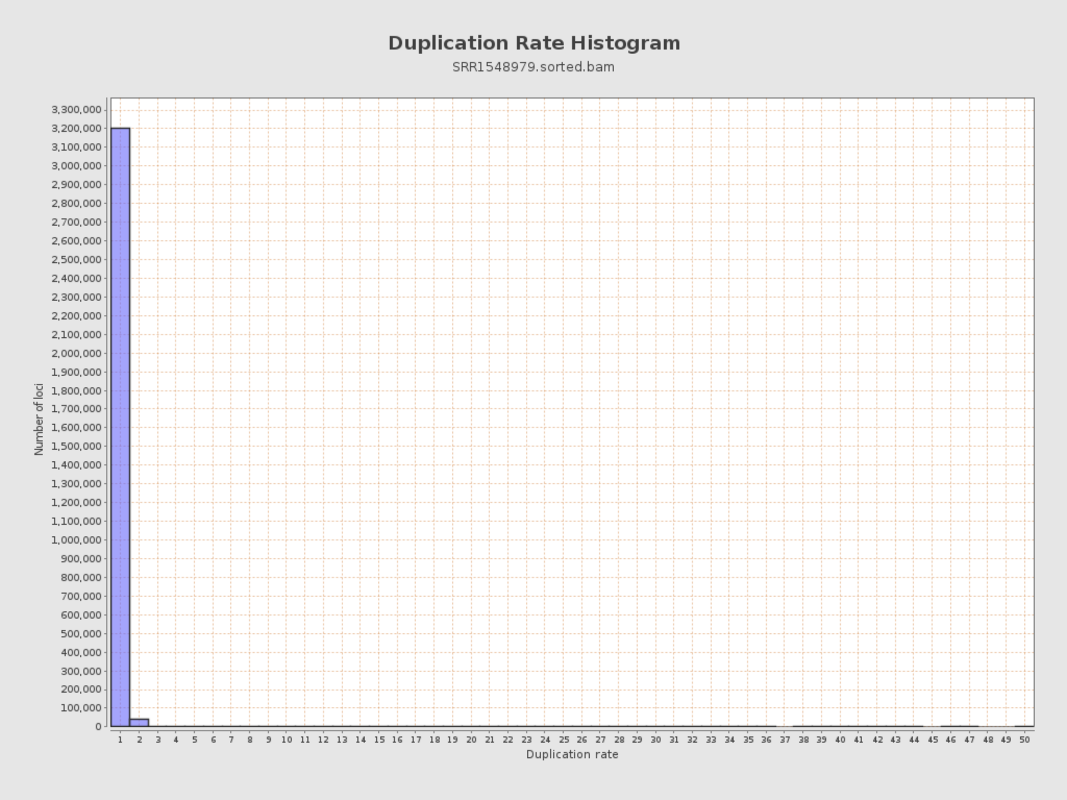
5. Results : Coverage Histogram (0-50X)



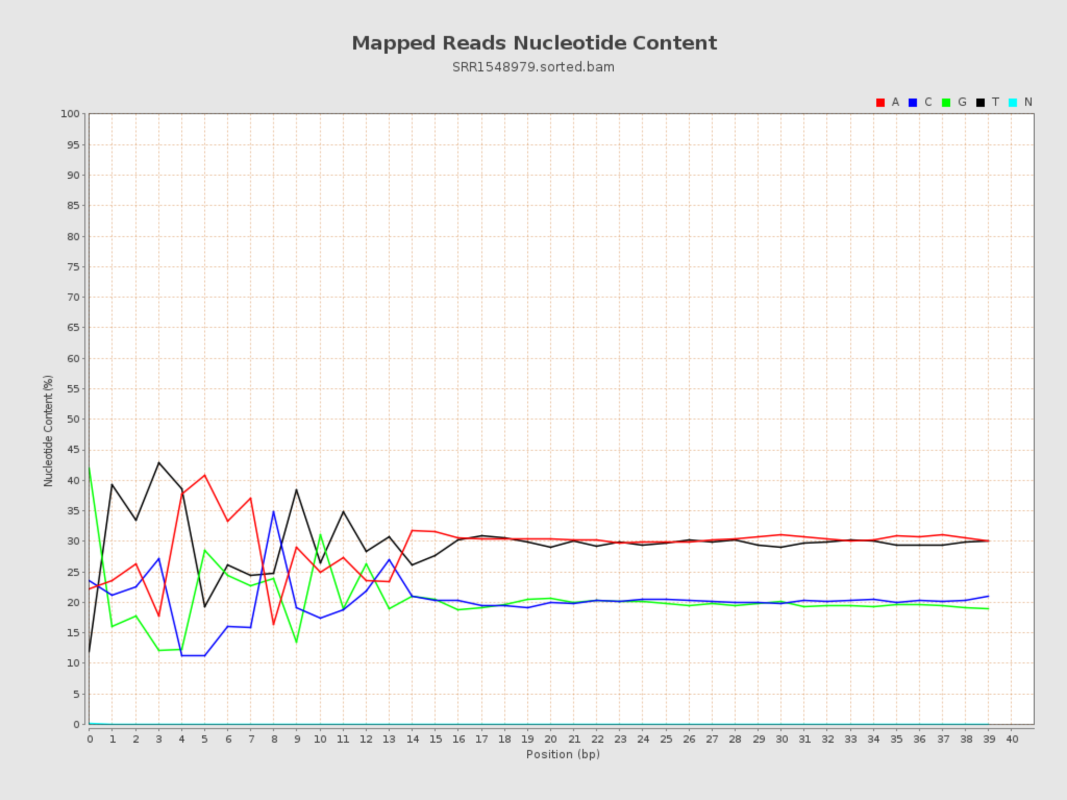
6. Results : Genome Fraction Coverage



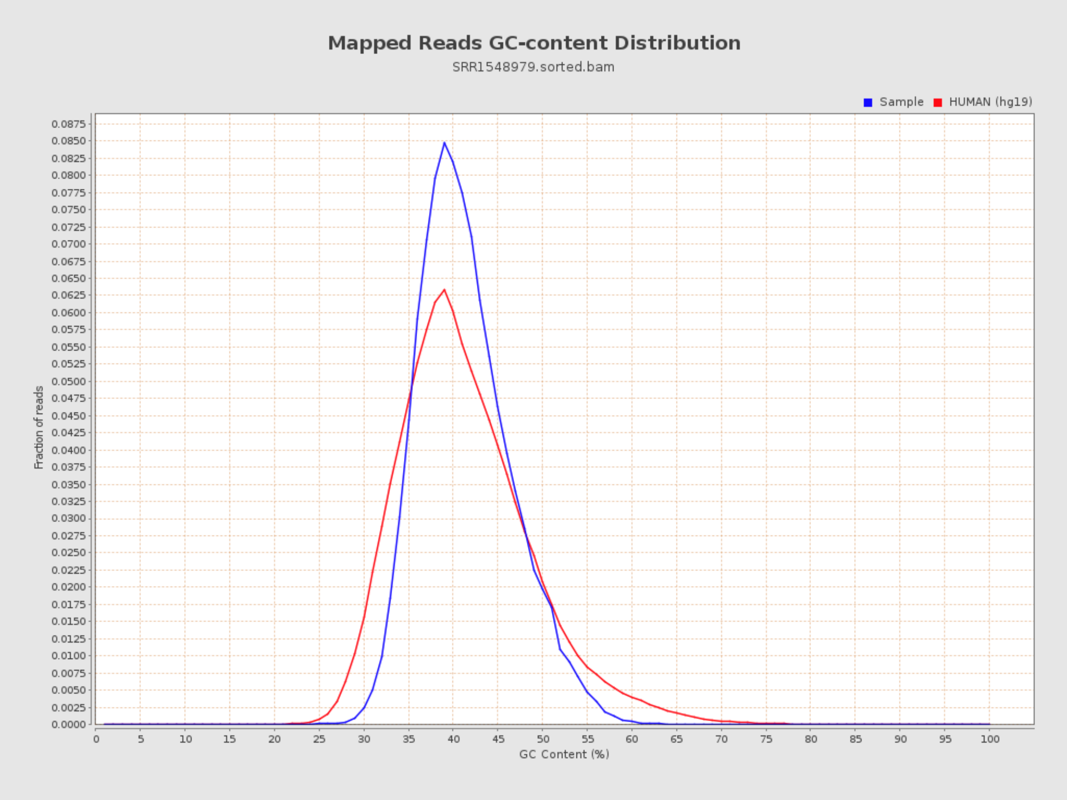
7. Results : Duplication Rate Histogram



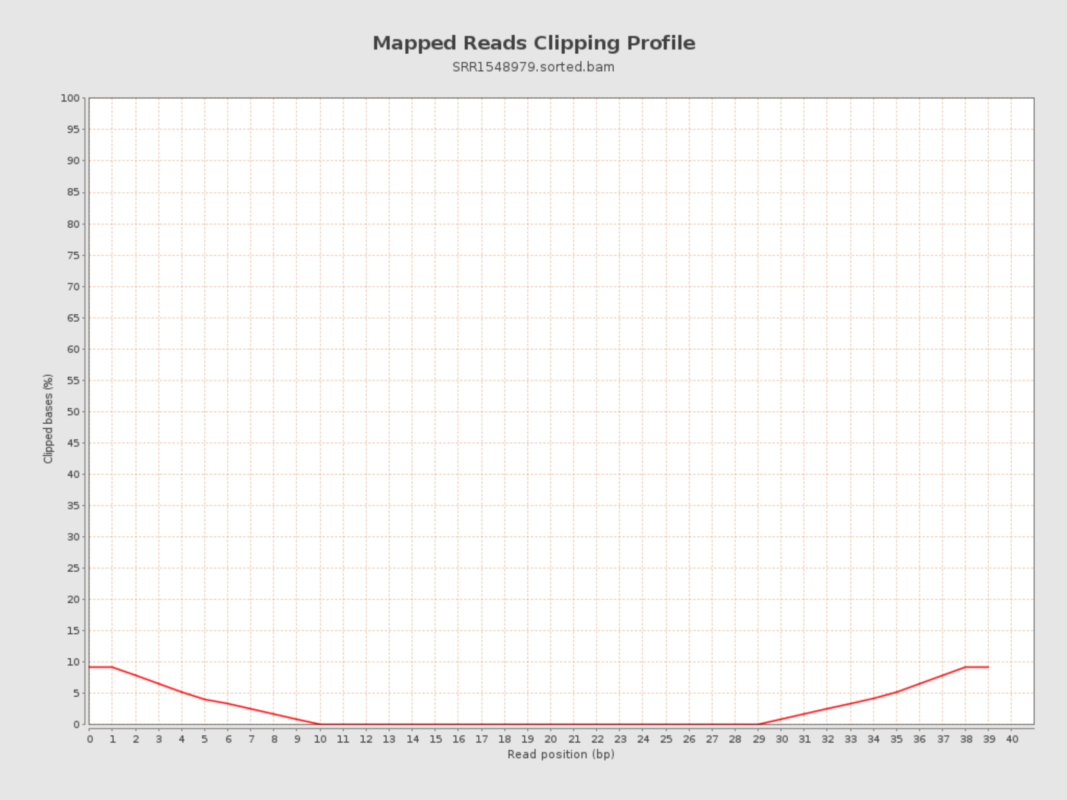
8. Results : Mapped Reads Nucleotide Content



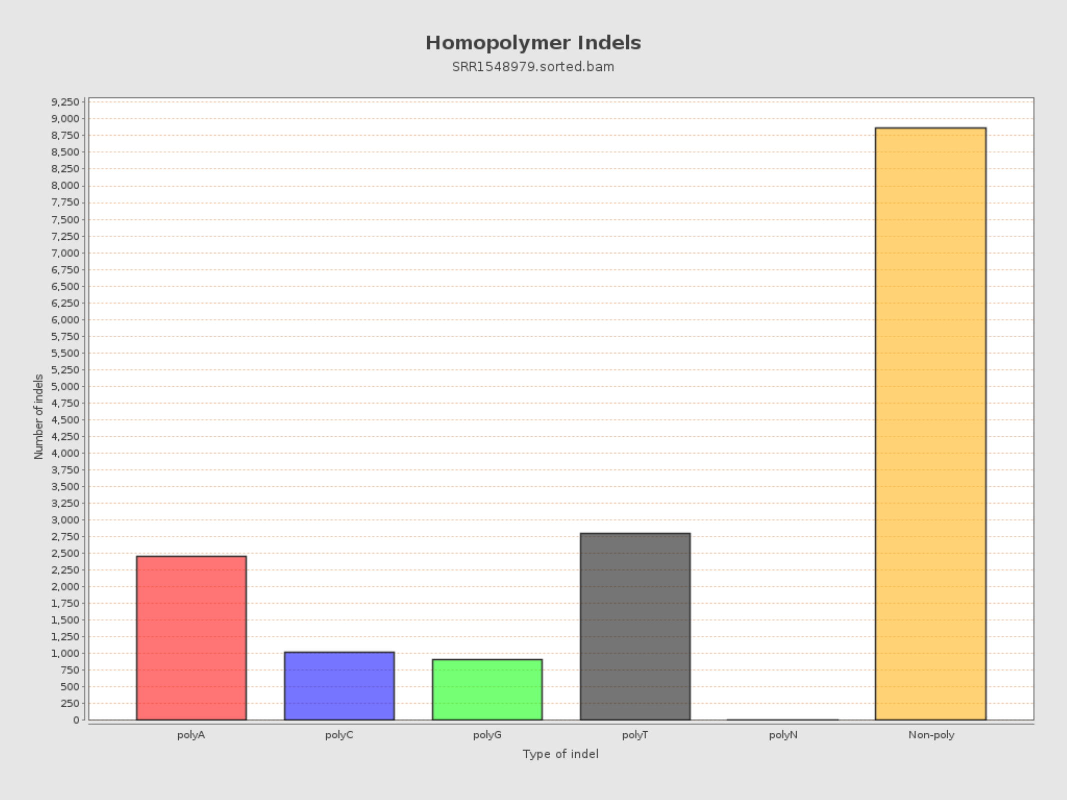
9. Results : Mapped Reads GC-content Distribution



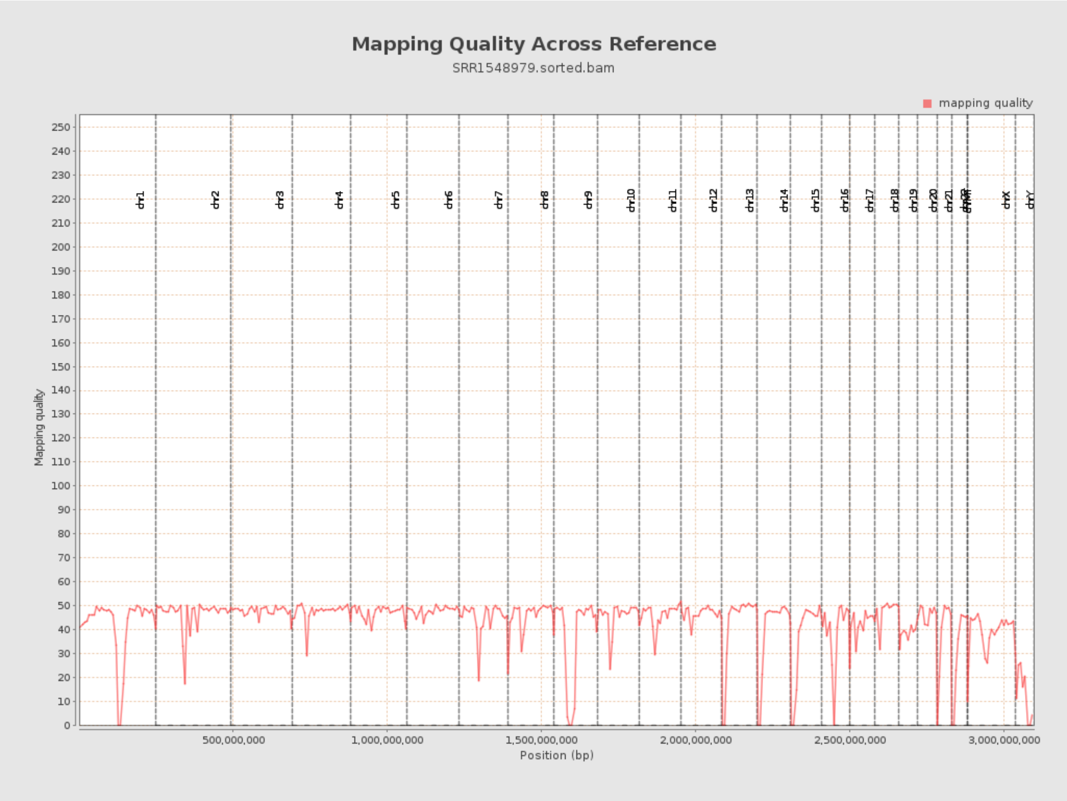
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram