Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:31:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082323.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_SRR3082323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:31:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,104,331
Mapped reads	1,826,413 / 86.79%
Unmapped reads	277,918 / 13.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,891 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	66,955 / 3.18%
Duplication rate	2.65%
Clipped reads	876,290 / 41.64%

2.2. ACGT Content

Number/percentage of A's	33,303,634 / 27.54%
Number/percentage of C's	22,902,228 / 18.94%
Number/percentage of T's	36,924,207 / 30.54%
Number/percentage of G's	27,776,007 / 22.97%
Number/percentage of N's	2,343 / 0%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3636

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

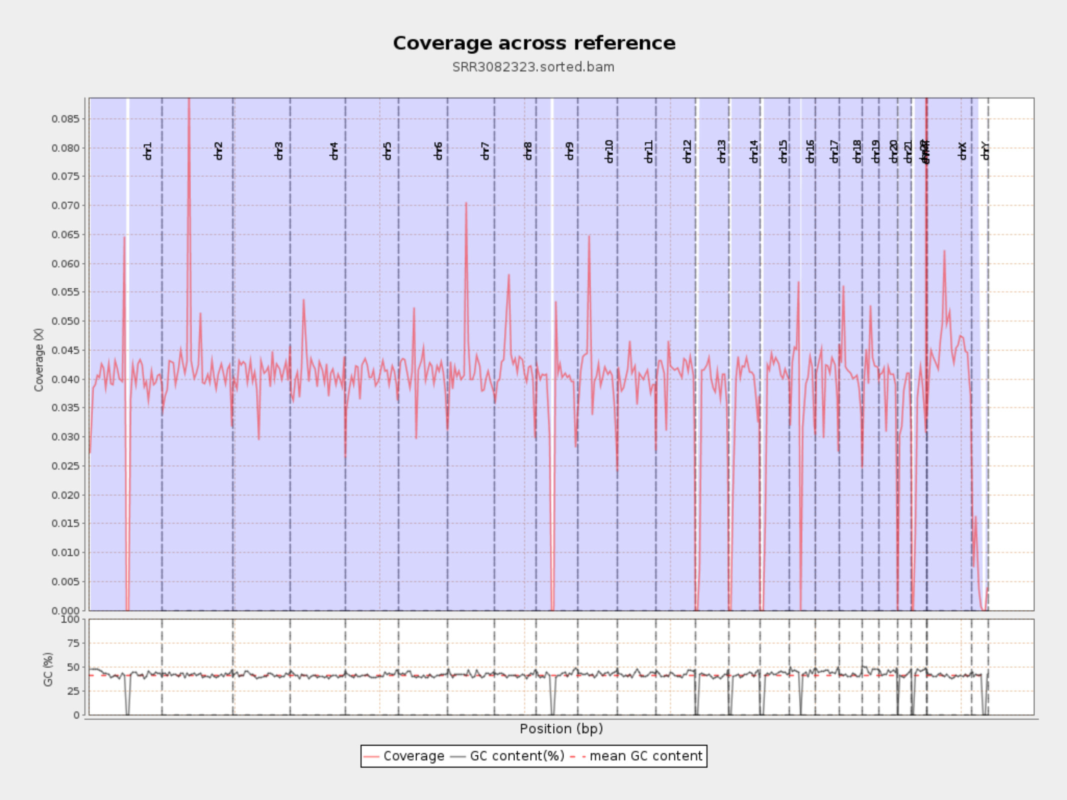
General error rate	0.89%
Mismatches	1,060,119
Insertions	10,223
Mapped reads with at least one insertion	0.55%
Deletions	27,751
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.24%

2.6. Chromosome stats

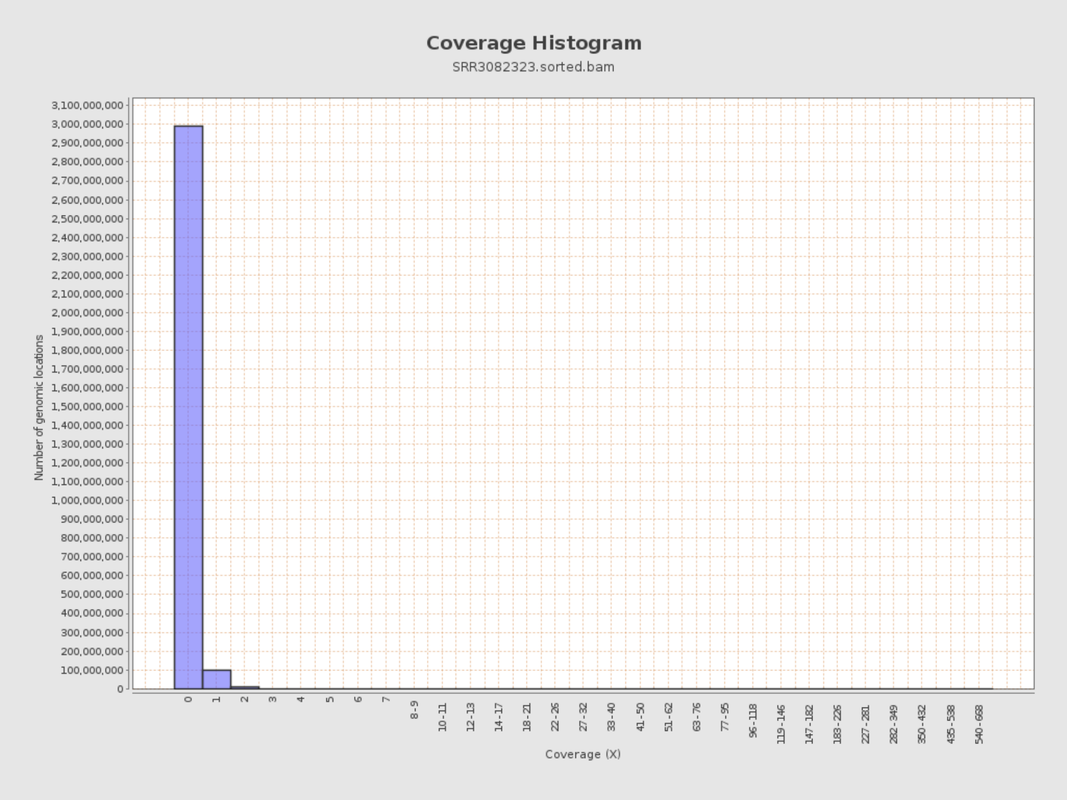
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9522964	0.0382	0.5465
chr2	243199373	10411112	0.0428	0.5378
chr3	198022430	8085538	0.0408	0.2226
chr4	191154276	7855281	0.0411	0.2383
chr5	180915260	7313400	0.0404	0.2229
chr6	171115067	7067746	0.0413	0.2676
chr7	159138663	6695551	0.0421	0.4875

chr8	146364022	6225797	0.0425	0.4605
chr9	141213431	5033331	0.0356	0.3786
chr10	135534747	5623546	0.0415	0.3257
chr11	135006516	5395344	0.04	0.3438
chr12	133851895	5539708	0.0414	0.227
chr13	115169878	3832629	0.0333	0.1992
chr14	107349540	3637986	0.0339	0.2331
chr15	102531392	3489620	0.034	0.2122
chr16	90354753	3414664	0.0378	0.2468
chr17	81195210	3251182	0.04	0.2452
chr18	78077248	3294334	0.0422	0.6983
chr19	59128983	2517785	0.0426	0.4619
chr20	63025520	2448641	0.0389	0.2244
chr21	48129895	1566831	0.0326	0.218
chr22	51304566	1339146	0.0261	0.1765
chrMT	16571	6177	0.3728	0.6602
chrX	155270560	7054661	0.0454	0.2775
chrY	59373566	330565	0.0056	0.1276

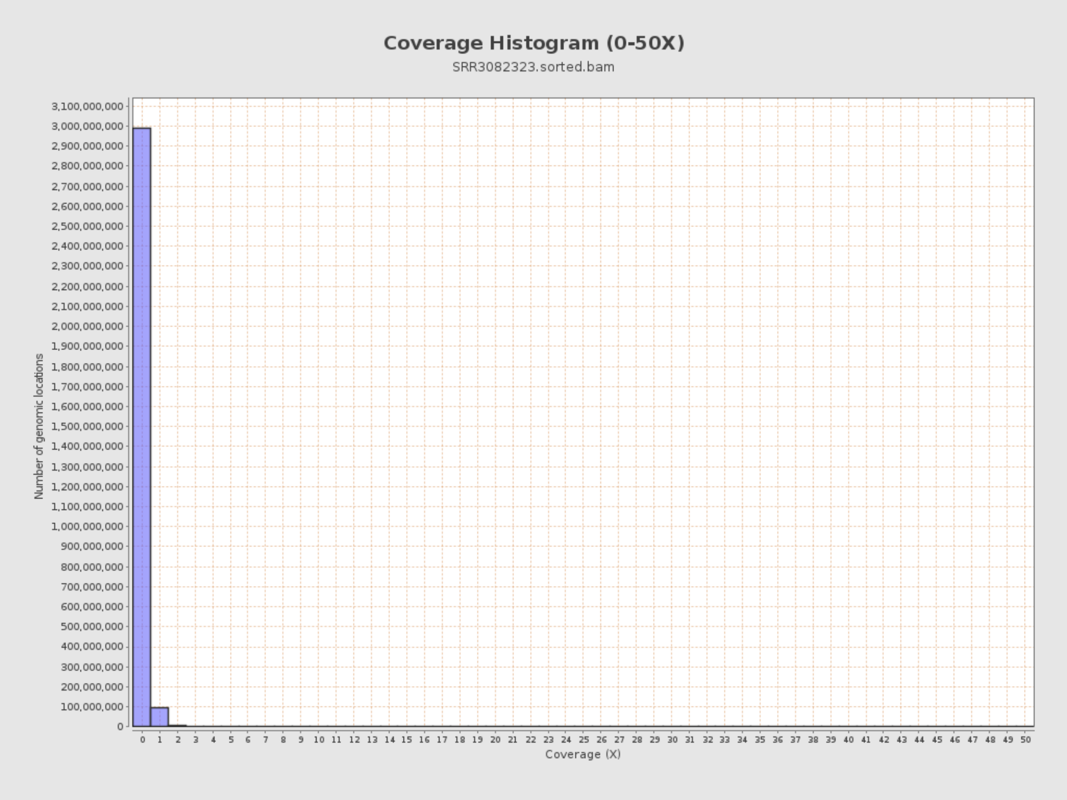
3. Results : Coverage across reference



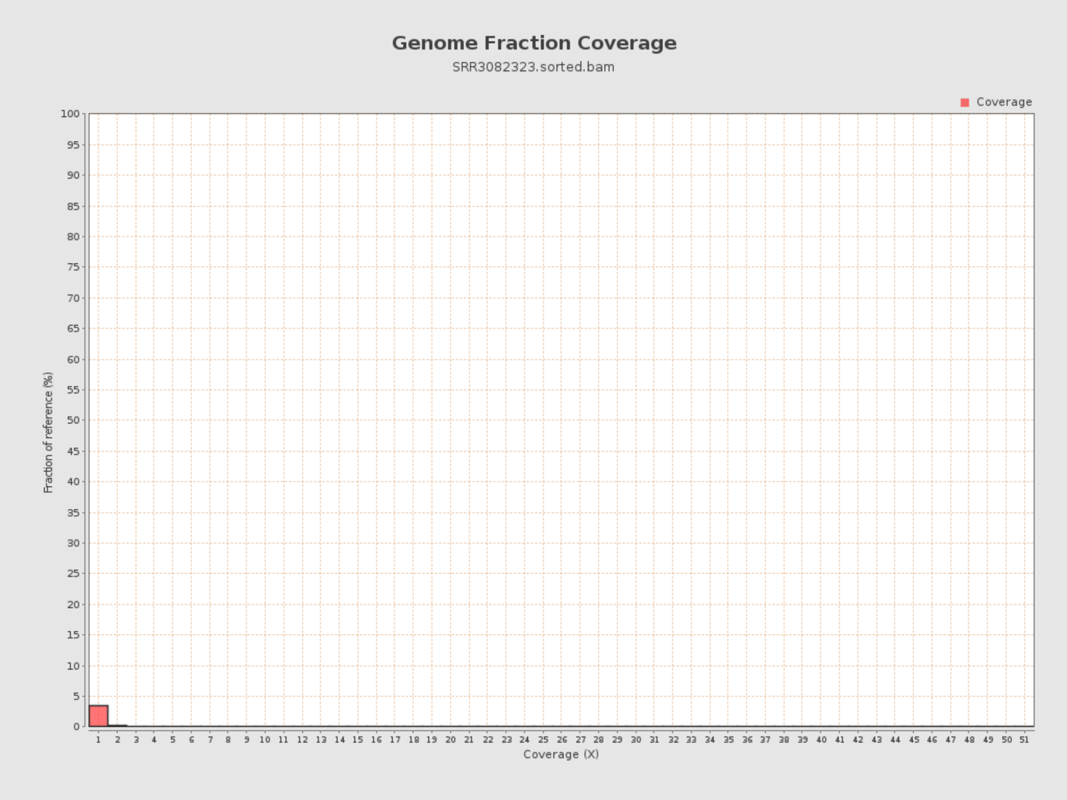
4. Results : Coverage Histogram



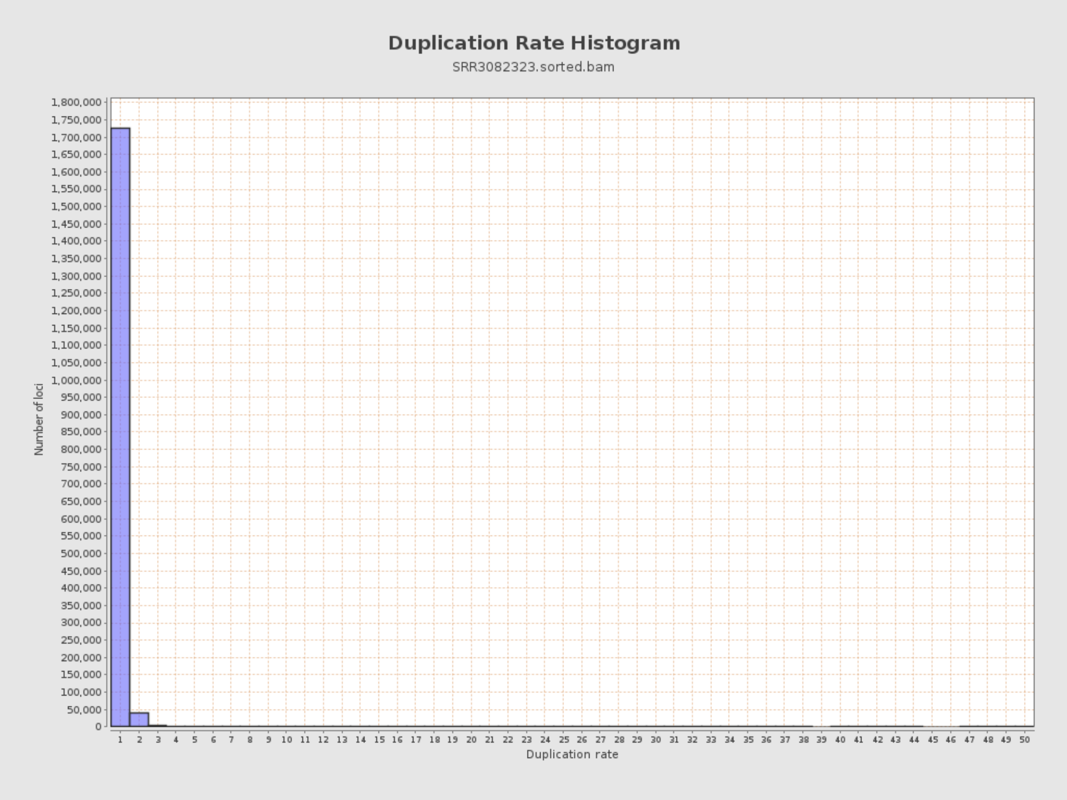
5. Results : Coverage Histogram (0-50X)



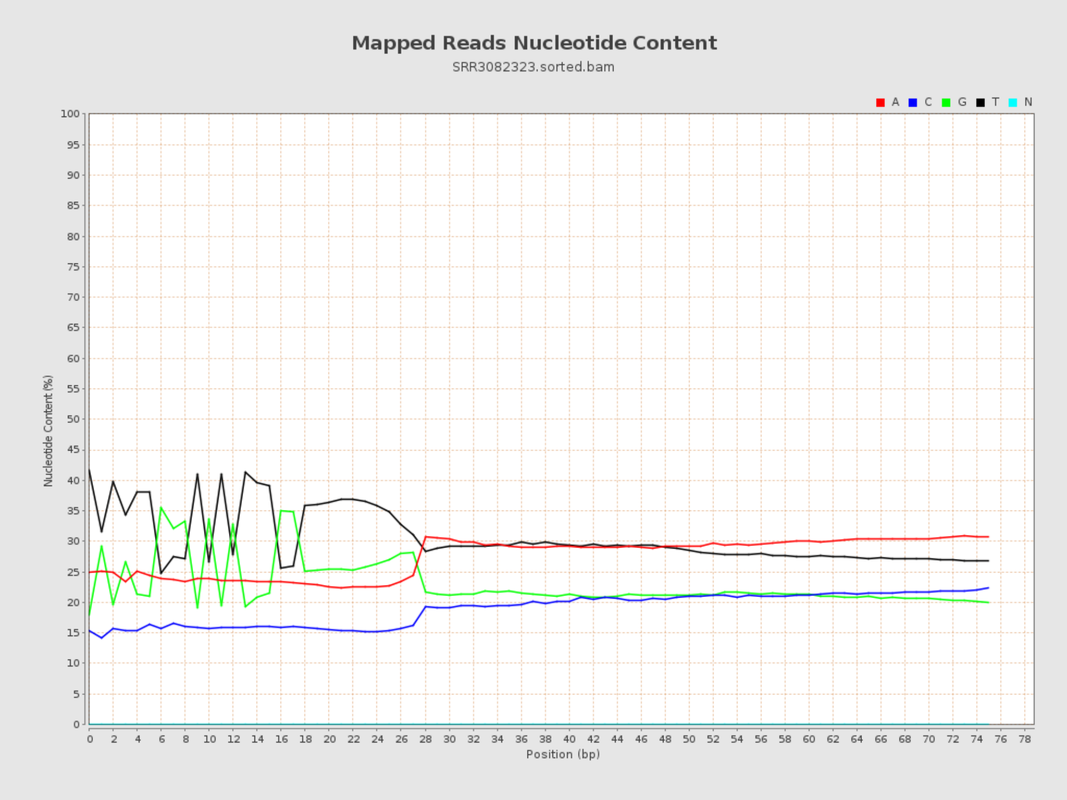
6. Results : Genome Fraction Coverage



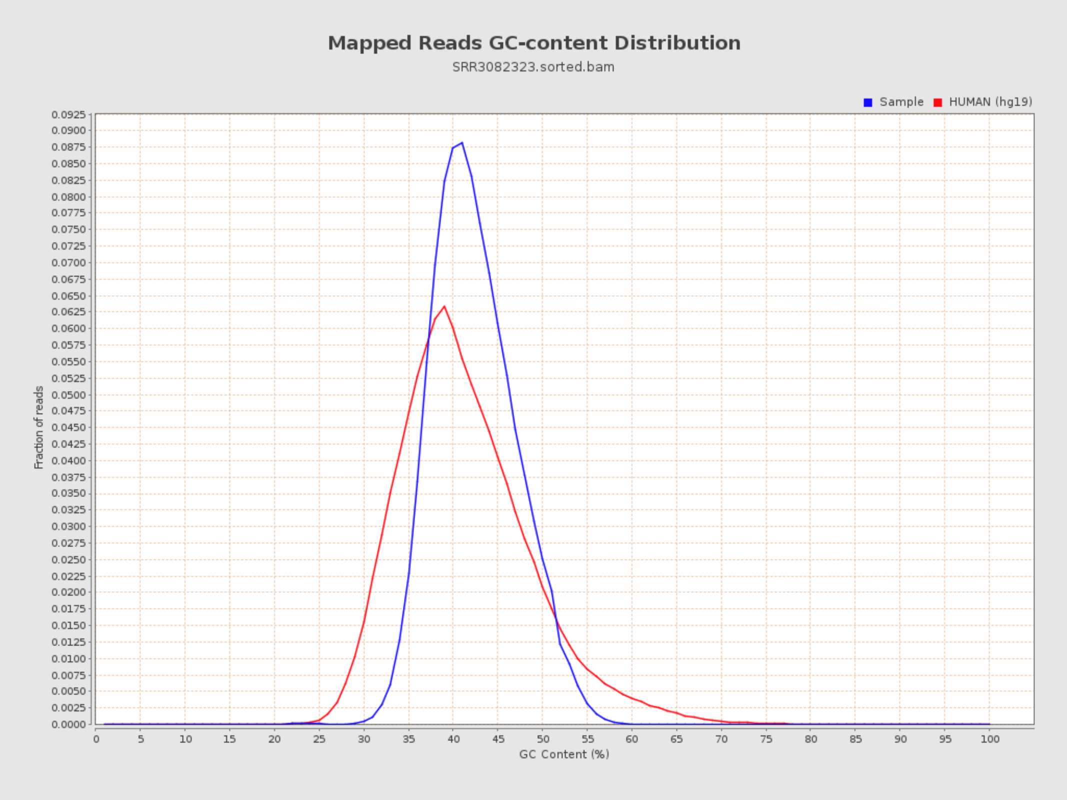
7. Results : Duplication Rate Histogram



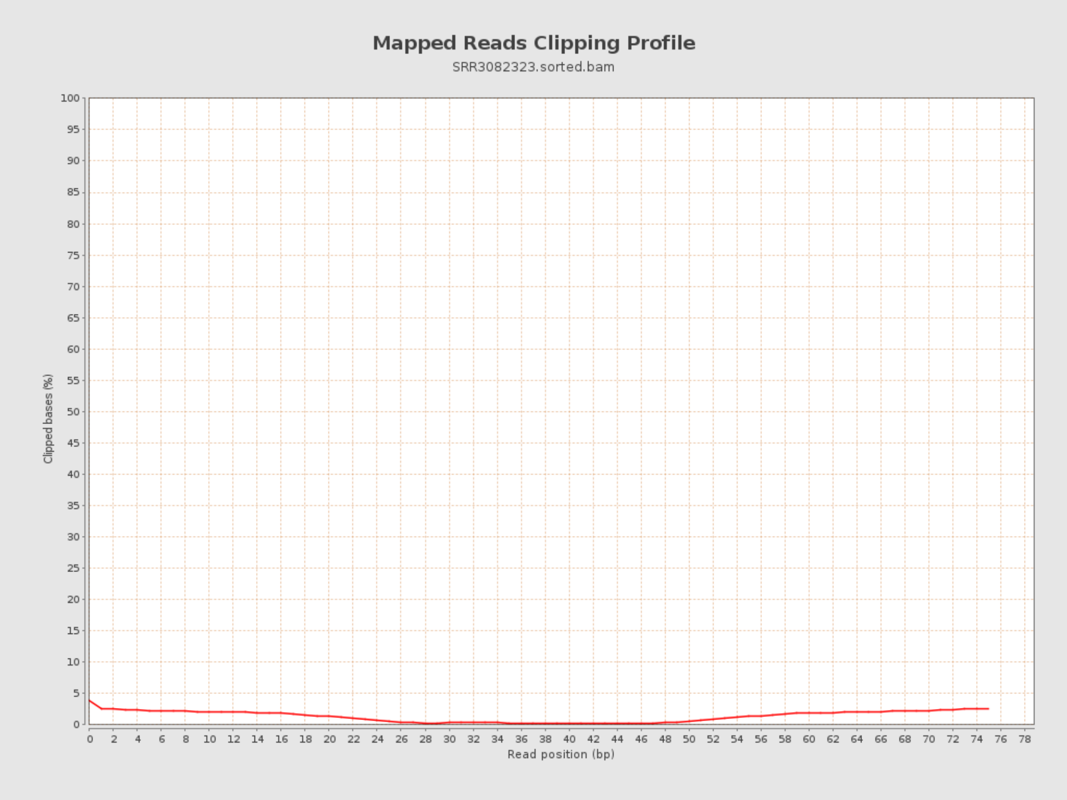
8. Results : Mapped Reads Nucleotide Content



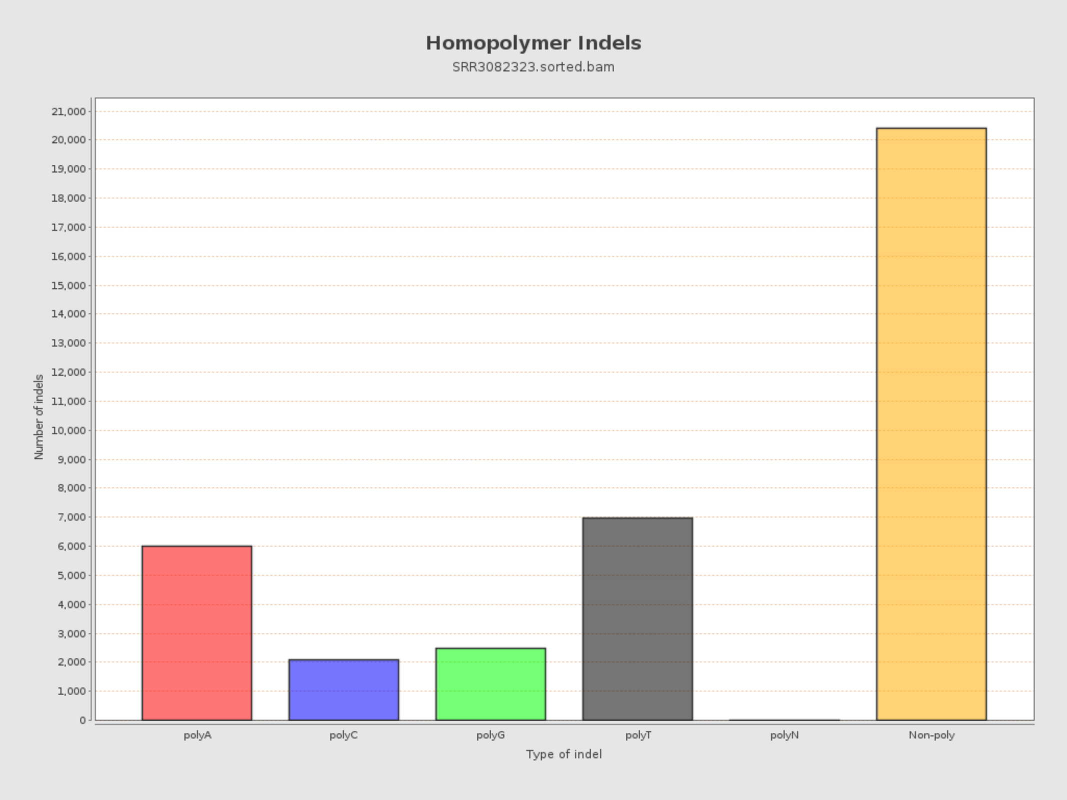
9. Results : Mapped Reads GC-content Distribution



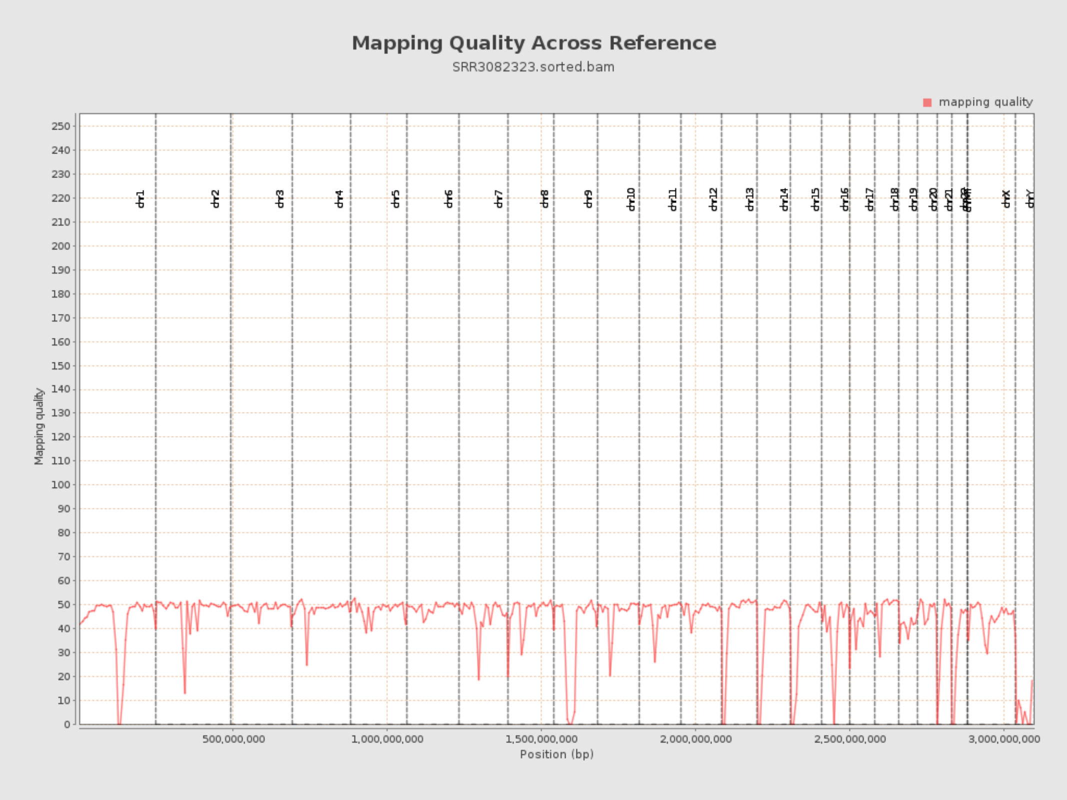
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram