Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:49:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524669.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_SRR10524669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:49:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,291,707
Mapped reads	2,114,427 / 92.26%
Unmapped reads	177,280 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,032 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	101,246 / 4.42%
Duplication rate	3.56%
Clipped reads	2,115,782 / 92.32%

2.2. ACGT Content

Number/percentage of A's	33,323,393 / 26.73%
Number/percentage of C's	23,333,947 / 18.72%
Number/percentage of T's	37,889,709 / 30.4%
Number/percentage of G's	30,087,311 / 24.14%
Number/percentage of N's	17,232 / 0.01%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3629

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

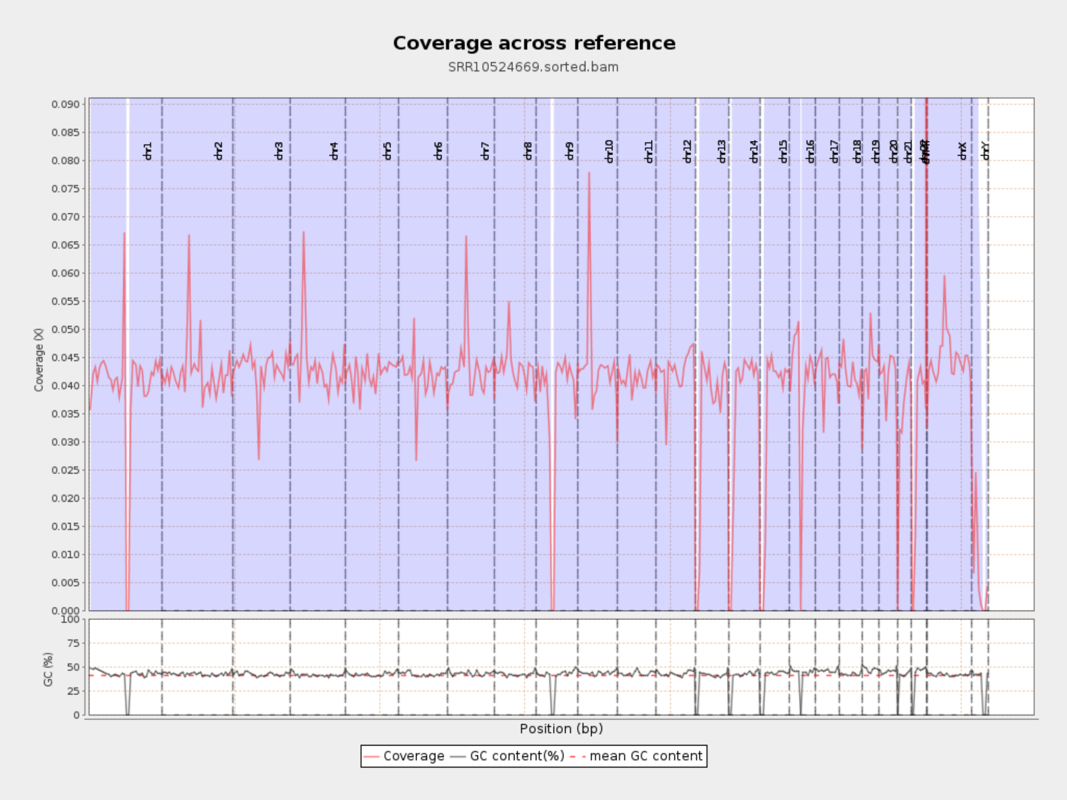
General error rate	0.52%
Mismatches	621,555
Insertions	10,588
Mapped reads with at least one insertion	0.5%
Deletions	23,383
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.13%

2.6. Chromosome stats

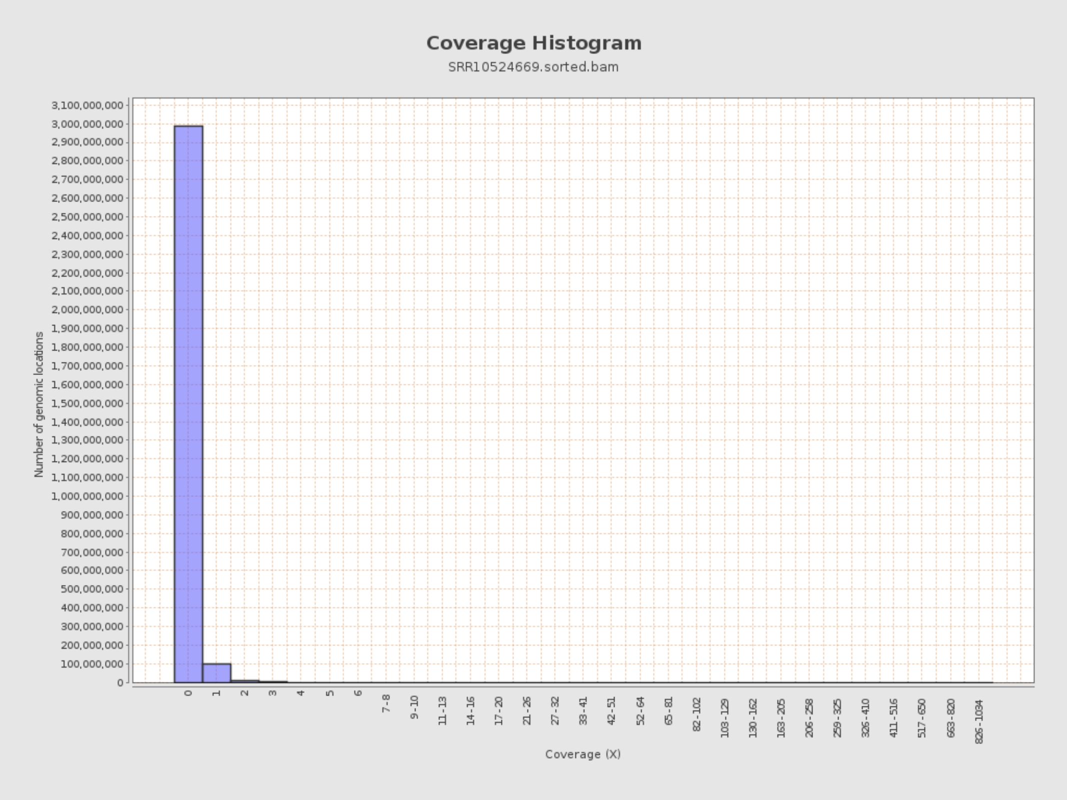
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9879761	0.0396	0.6631
chr2	243199373	10360092	0.0426	0.504
chr3	198022430	8494653	0.0429	0.2343
chr4	191154276	8319291	0.0435	0.2662
chr5	180915260	7620776	0.0421	0.2305
chr6	171115067	7170589	0.0419	0.2676
chr7	159138663	6890727	0.0433	0.4372

chr8	146364022	6321069	0.0432	0.395
chr9	141213431	5173534	0.0366	0.2951
chr10	135534747	5948953	0.0439	0.3633
chr11	135006516	5576092	0.0413	0.3083
chr12	133851895	5693733	0.0425	0.2317
chr13	115169878	3942542	0.0342	0.2086
chr14	107349540	3801735	0.0354	0.2194
chr15	102531392	3517363	0.0343	0.209
chr16	90354753	3624163	0.0401	0.2464
chr17	81195210	3397056	0.0418	0.2448
chr18	78077248	3291073	0.0422	0.5592
chr19	59128983	2580546	0.0436	0.504
chr20	63025520	2624651	0.0416	0.2303
chr21	48129895	1632901	0.0339	0.2445
chr22	51304566	1453795	0.0283	0.1865
chrMT	16571	18572	1.1208	1.2745
chrX	155270560	6956330	0.0448	0.2659
chrY	59373566	398894	0.0067	0.2249

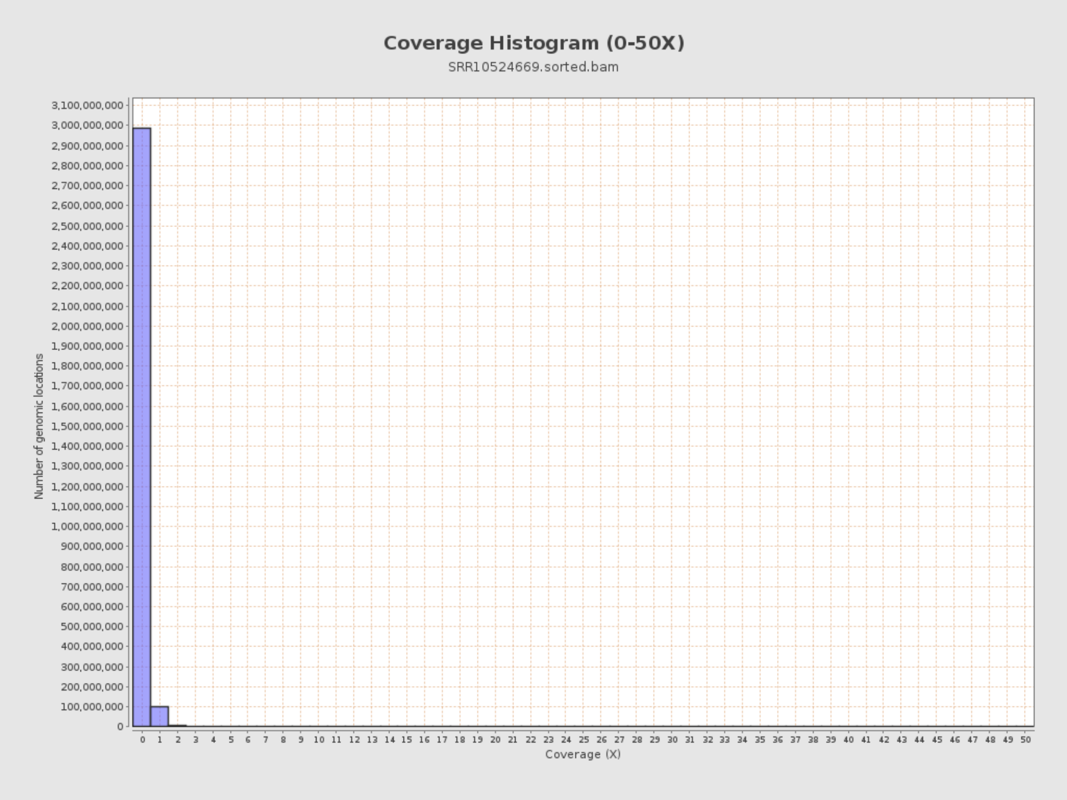
3. Results : Coverage across reference



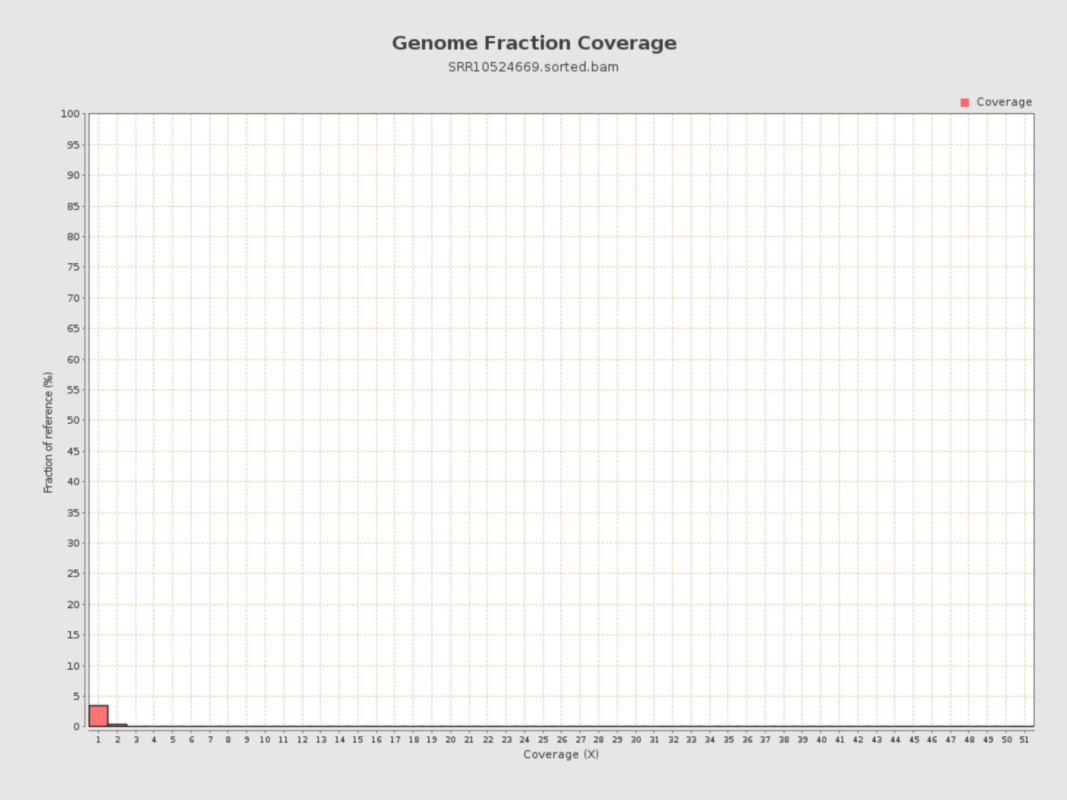
4. Results : Coverage Histogram



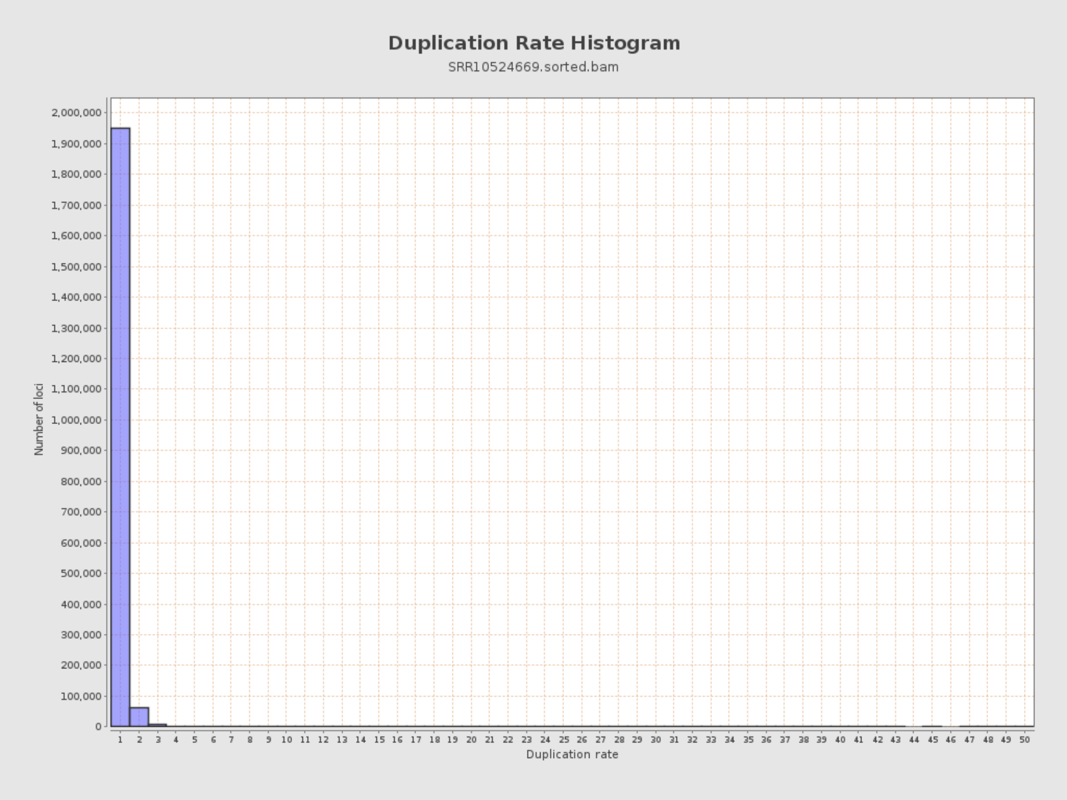
5. Results : Coverage Histogram (0-50X)



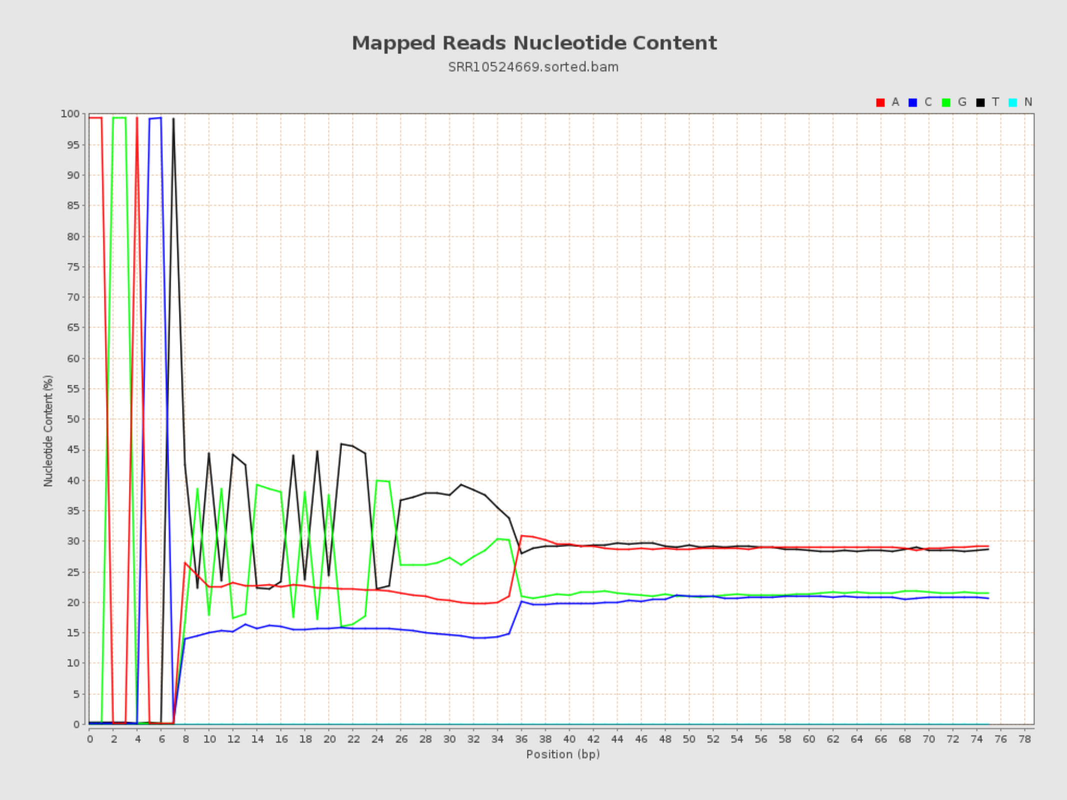
6. Results : Genome Fraction Coverage



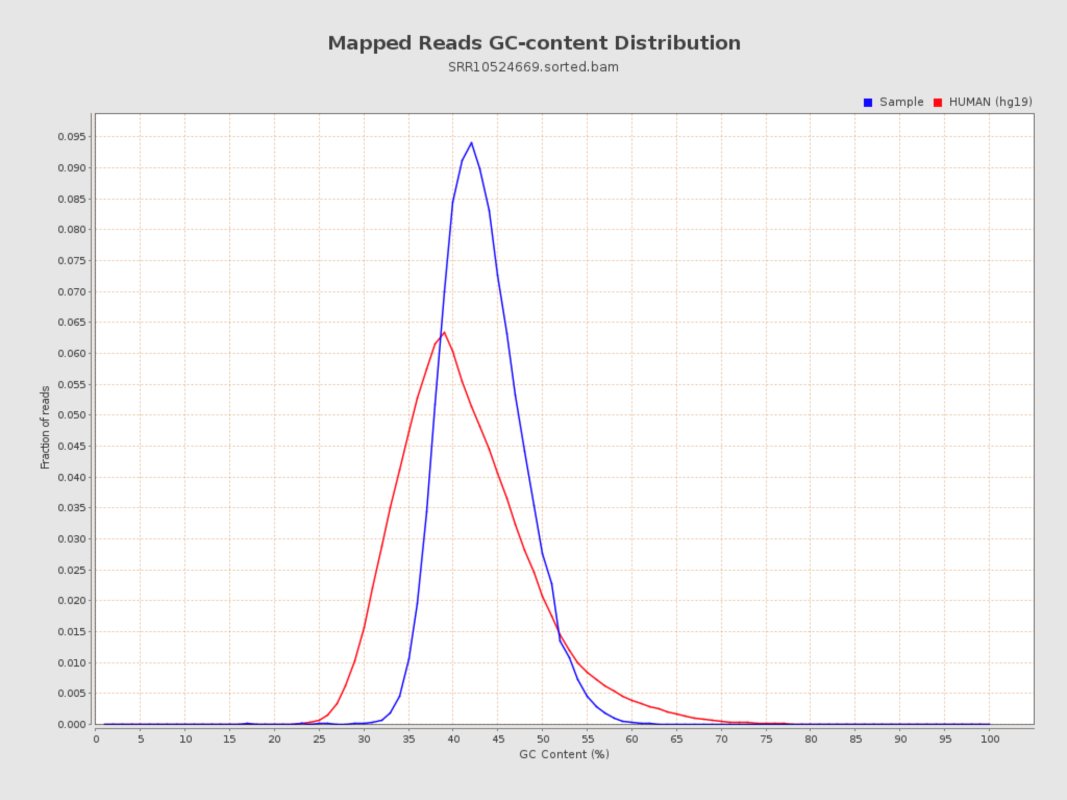
7. Results : Duplication Rate Histogram



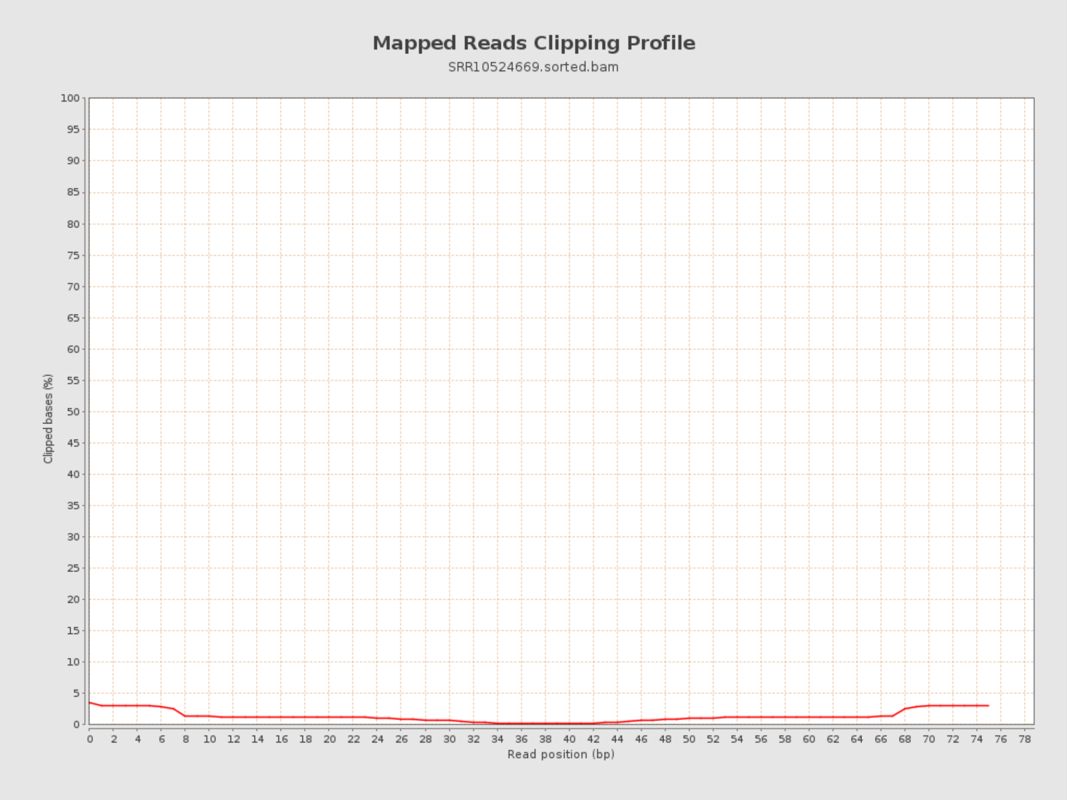
8. Results : Mapped Reads Nucleotide Content



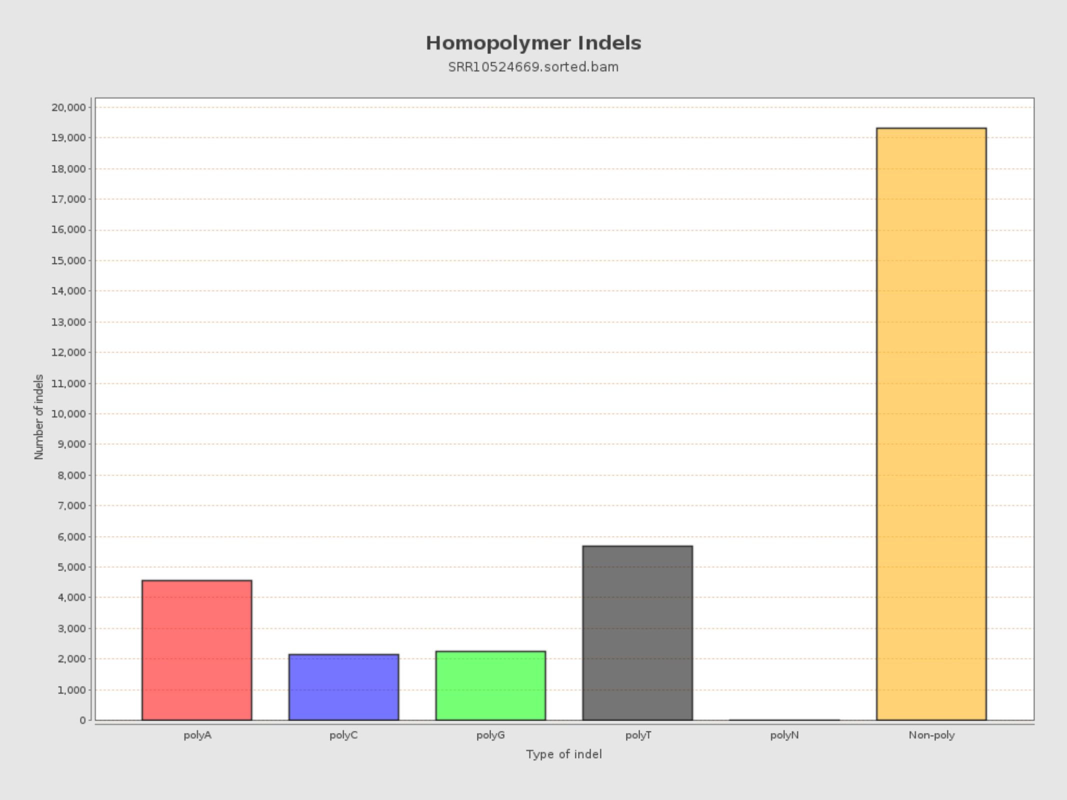
9. Results : Mapped Reads GC-content Distribution



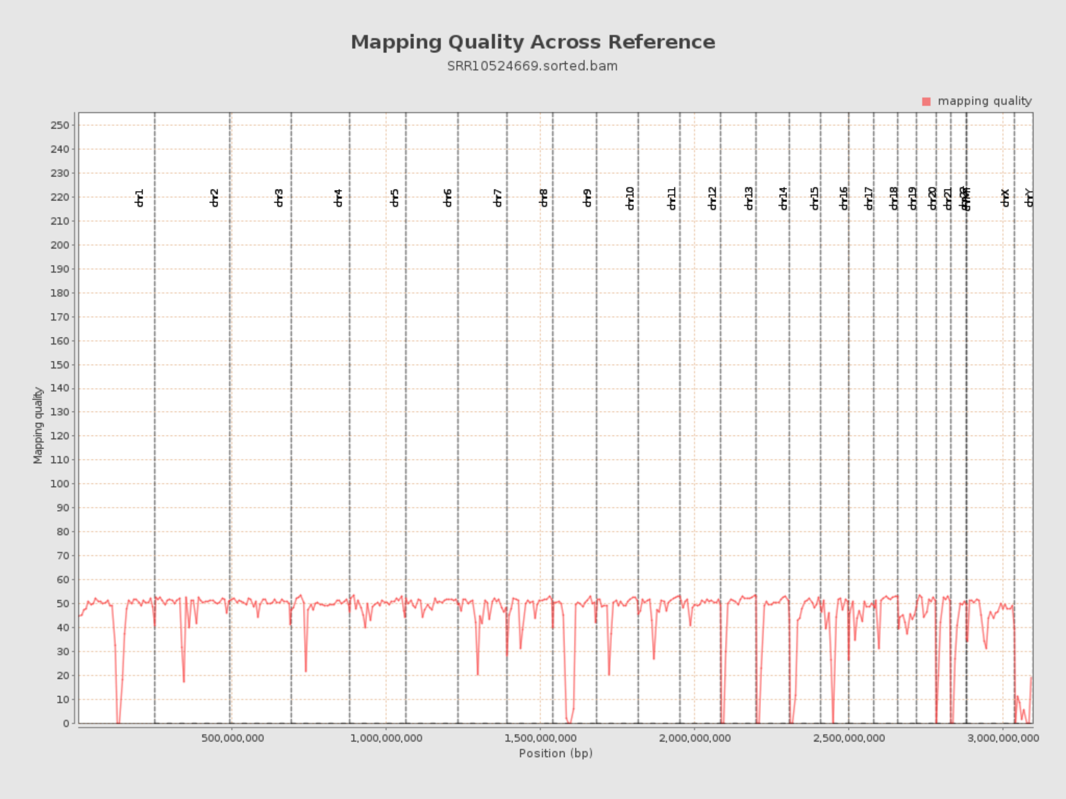
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram