Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:12:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549045.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_SRR1549045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:12:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,105,174
Mapped reads	2,696,053 / 86.82%
Unmapped reads	409,121 / 13.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	90,353 / 2.91%
Duplication rate	2.14%
Clipped reads	242,043 / 7.79%

2.2. ACGT Content

Number/percentage of A's	29,365,726 / 27.59%
Number/percentage of C's	23,420,688 / 22%
Number/percentage of T's	30,177,516 / 28.35%
Number/percentage of G's	23,478,166 / 22.06%
Number/percentage of N's	865 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0344
Standard Deviation	0.3425

2.4. Mapping Quality

Mean Mapping Quality	34.99

2.5. Mismatches and indels

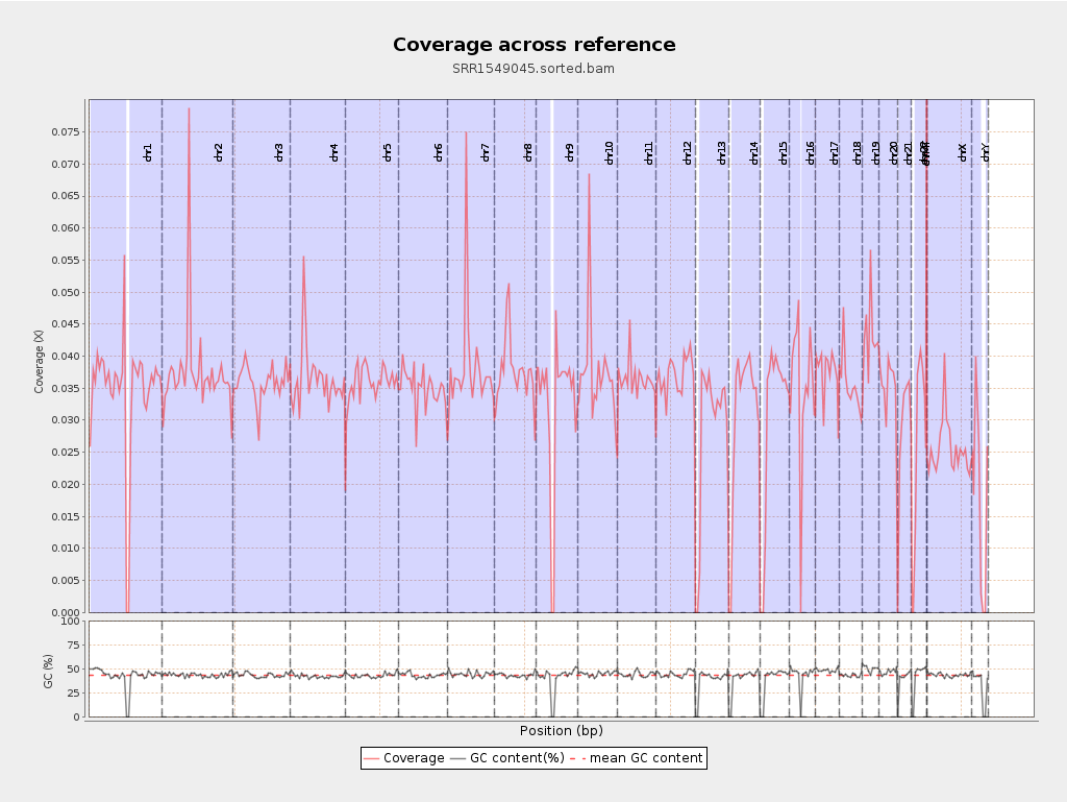
General error rate	0.33%
Mismatches	342,991
Insertions	3,583
Mapped reads with at least one insertion	0.13%
Deletions	7,488
Mapped reads with at least one deletion	0.28%
Homopolymer indels	37.87%

2.6. Chromosome stats

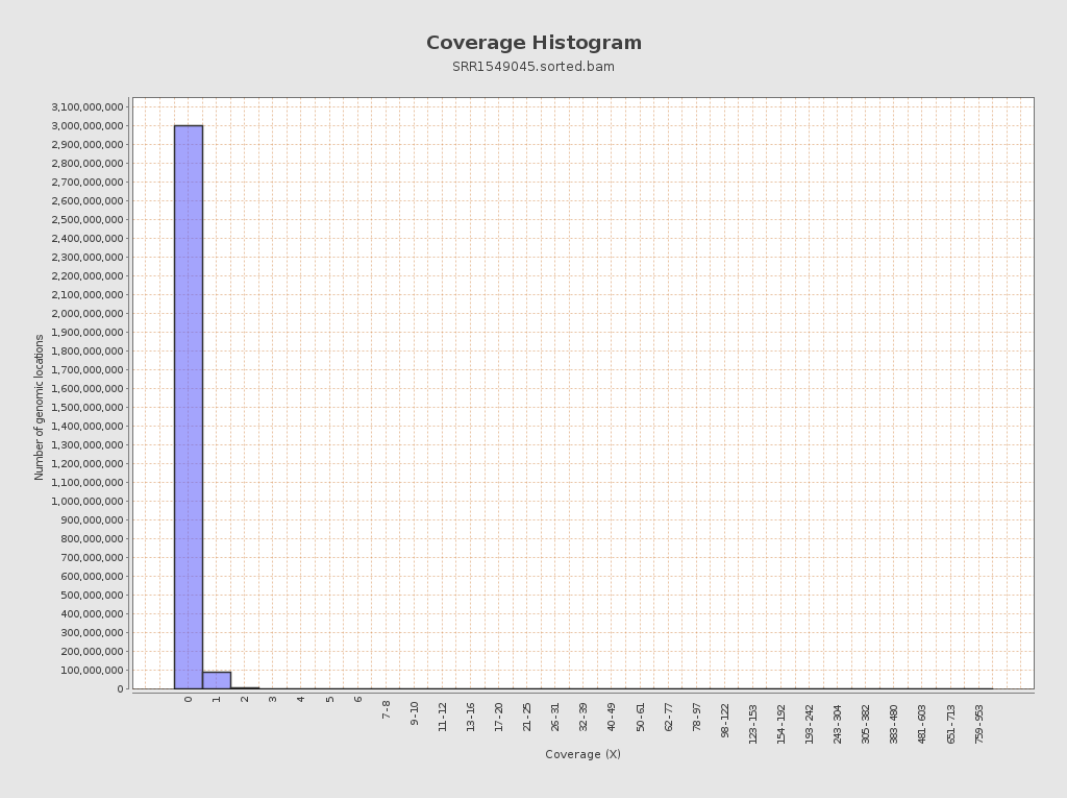
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8594791	0.0345	0.5301
chr2	243199373	9133855	0.0376	0.3812
chr3	198022430	7111637	0.0359	0.2052
chr4	191154276	6939677	0.0363	0.2277
chr5	180915260	6523809	0.0361	0.2101
chr6	171115067	5986662	0.035	0.2099
chr7	159138663	6100499	0.0383	0.4587
chr8	146364022	5490322	0.0375	0.5372

chr9	141213431	4565934	0.0323	0.3796
chr10	135534747	5070039	0.0374	0.316
chr11	135006516	4889424	0.0362	0.2678
chr12	133851895	4954511	0.037	0.2194
chr13	115169878	3251357	0.0282	0.1797
chr14	107349540	3296319	0.0307	0.2349
chr15	102531392	3089909	0.0301	0.1885
chr16	90354753	3174649	0.0351	0.2378
chr17	81195210	3034043	0.0374	0.2156
chr18	78077248	2798660	0.0358	0.6864
chr19	59128983	2553819	0.0432	0.5835
chr20	63025520	2223664	0.0353	0.2144
chr21	48129895	1371703	0.0285	0.2323
chr22	51304566	1314606	0.0256	0.2045
chrMT	16571	1602	0.0967	0.3417
chrX	155270560	3975269	0.0256	0.2428
chrY	59373566	1005689	0.0169	0.2005

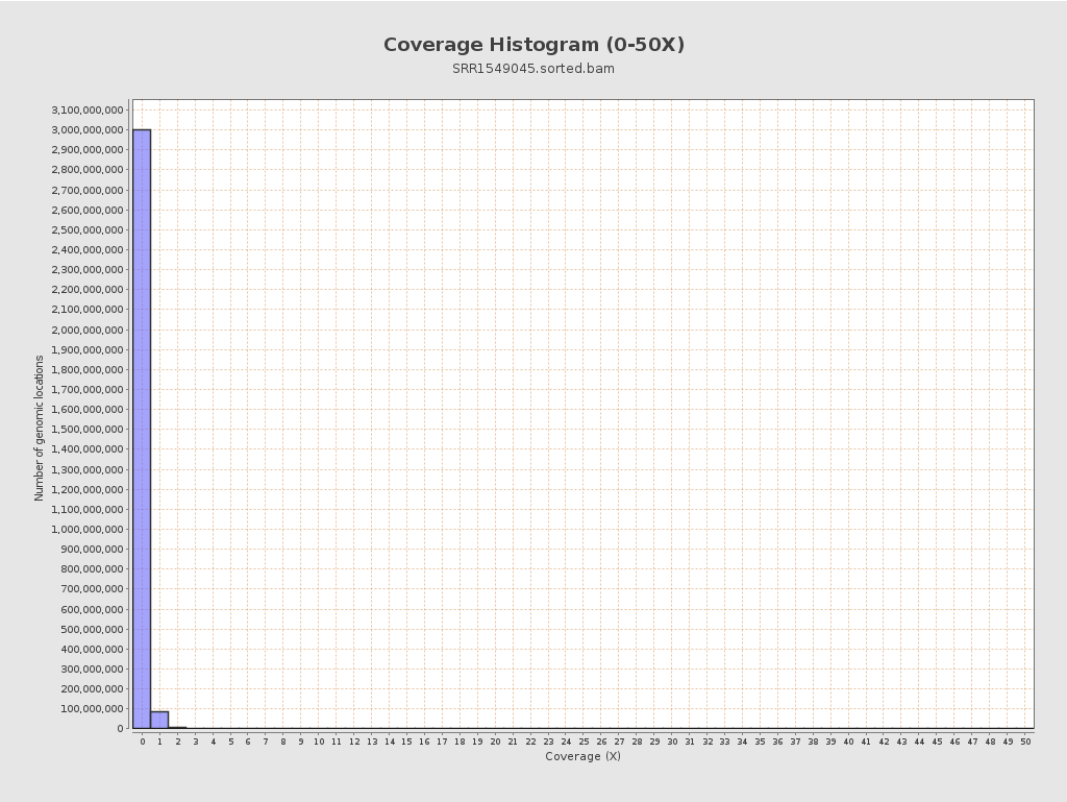
3. Results : Coverage across reference



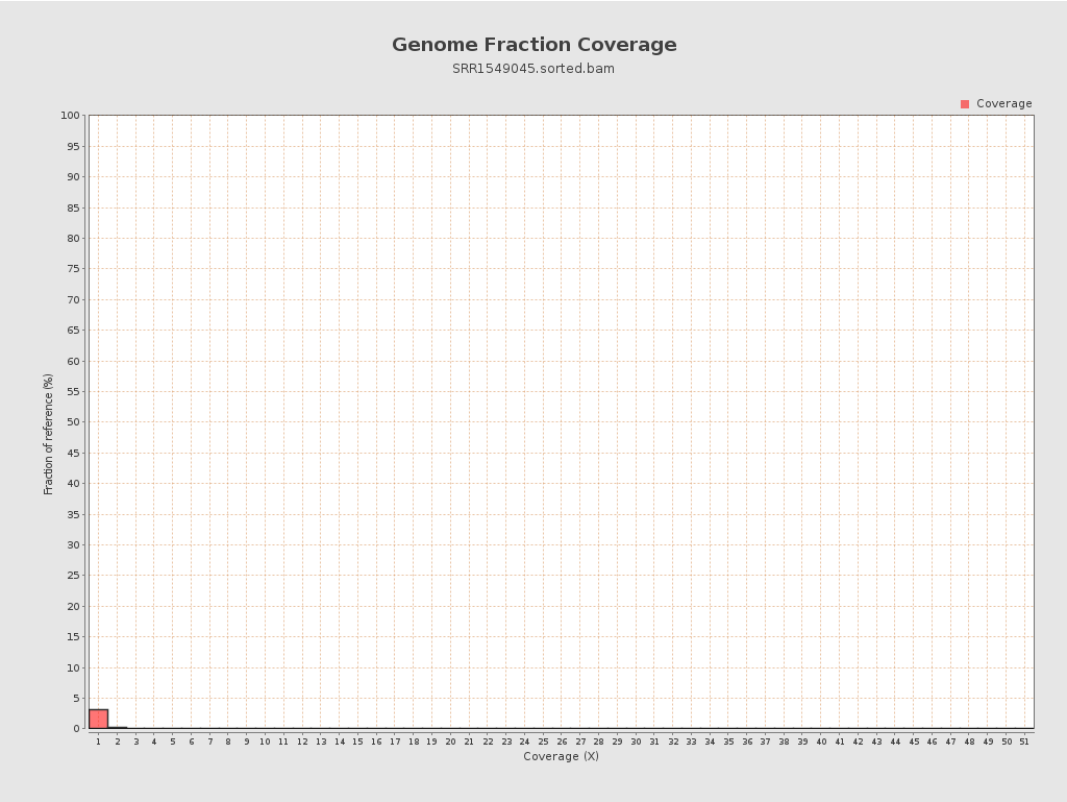
4. Results : Coverage Histogram



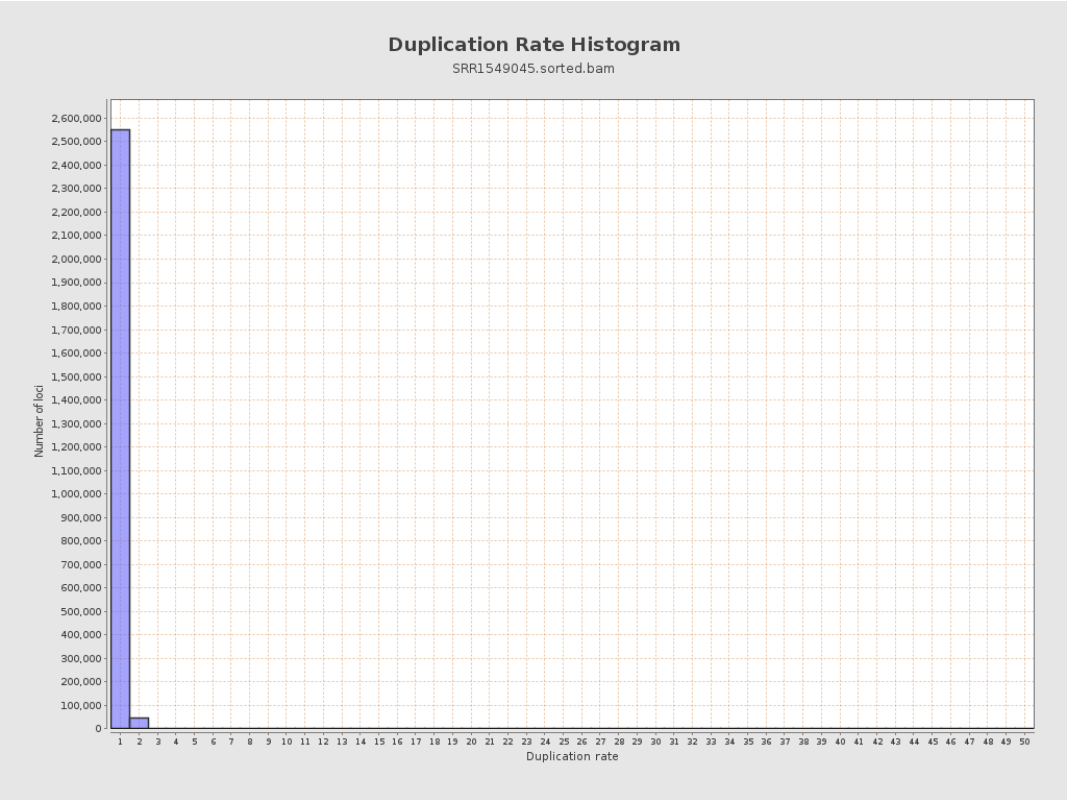
5. Results : Coverage Histogram (0-50X)



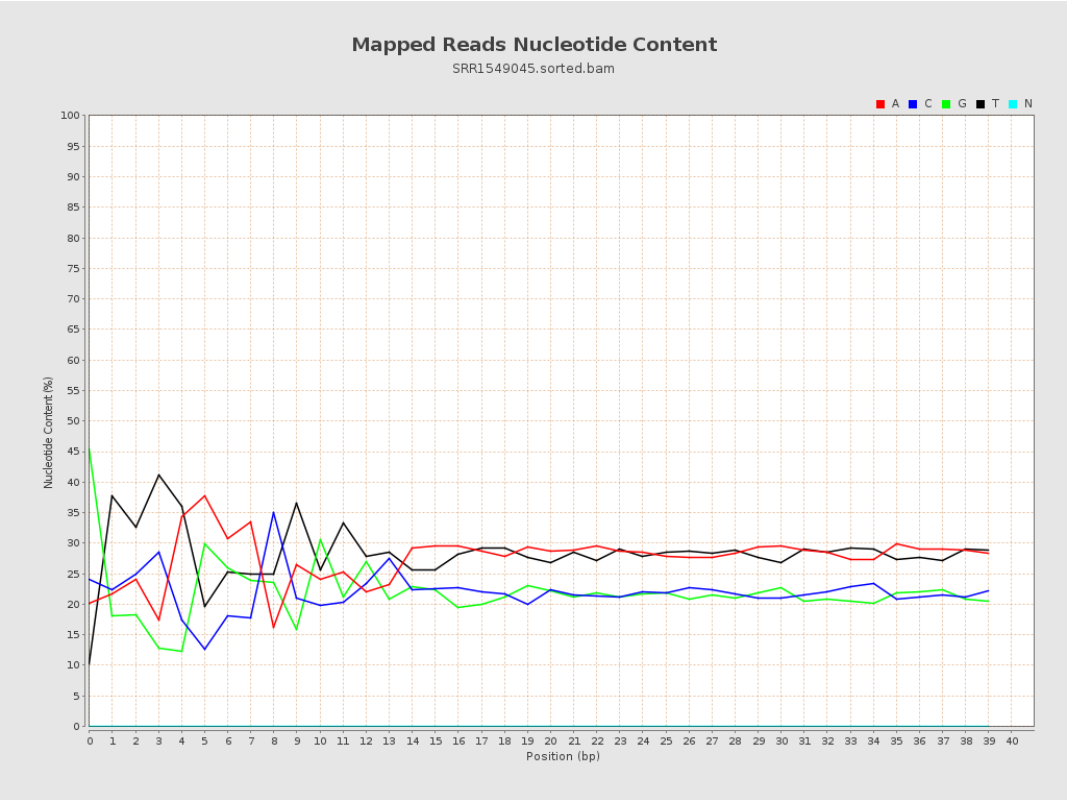
6. Results : Genome Fraction Coverage



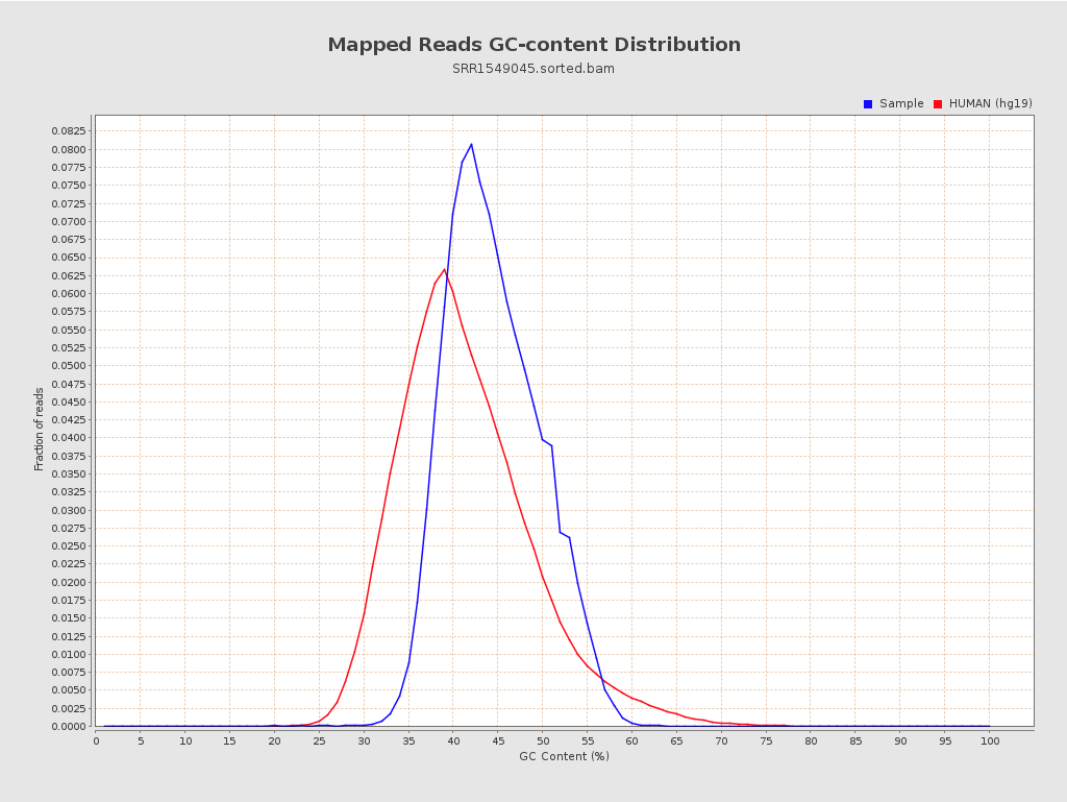
7. Results : Duplication Rate Histogram



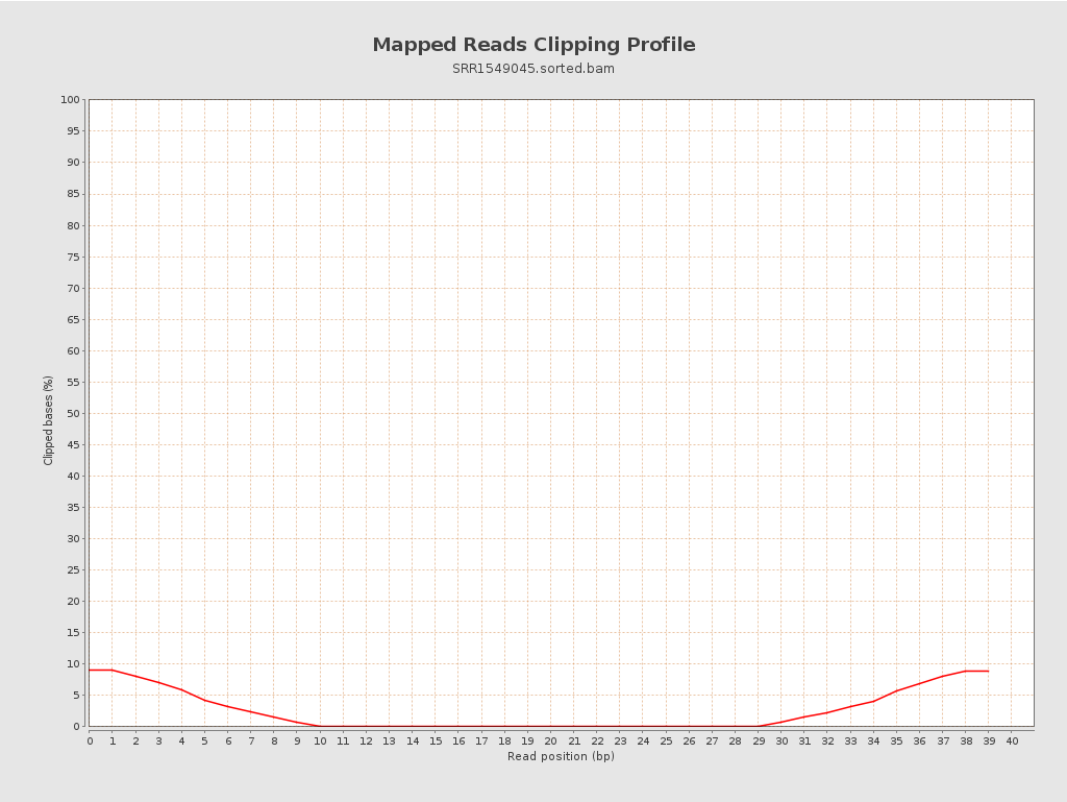
8. Results : Mapped Reads Nucleotide Content



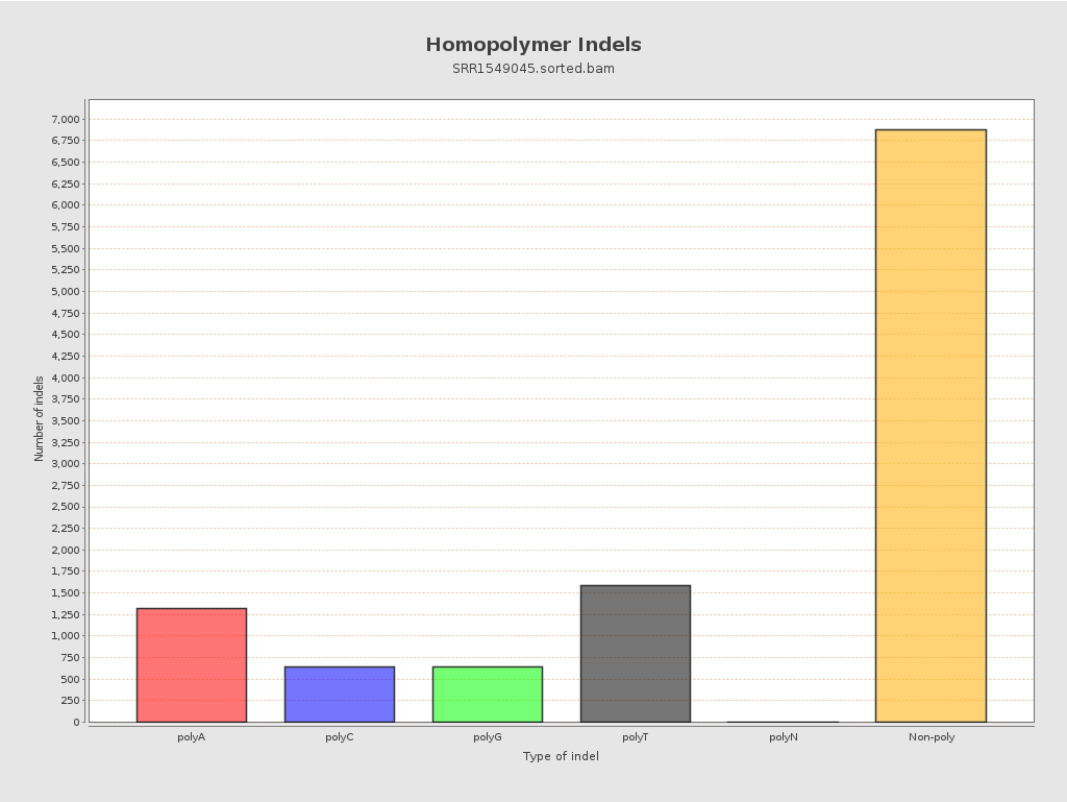
9. Results : Mapped Reads GC-content Distribution



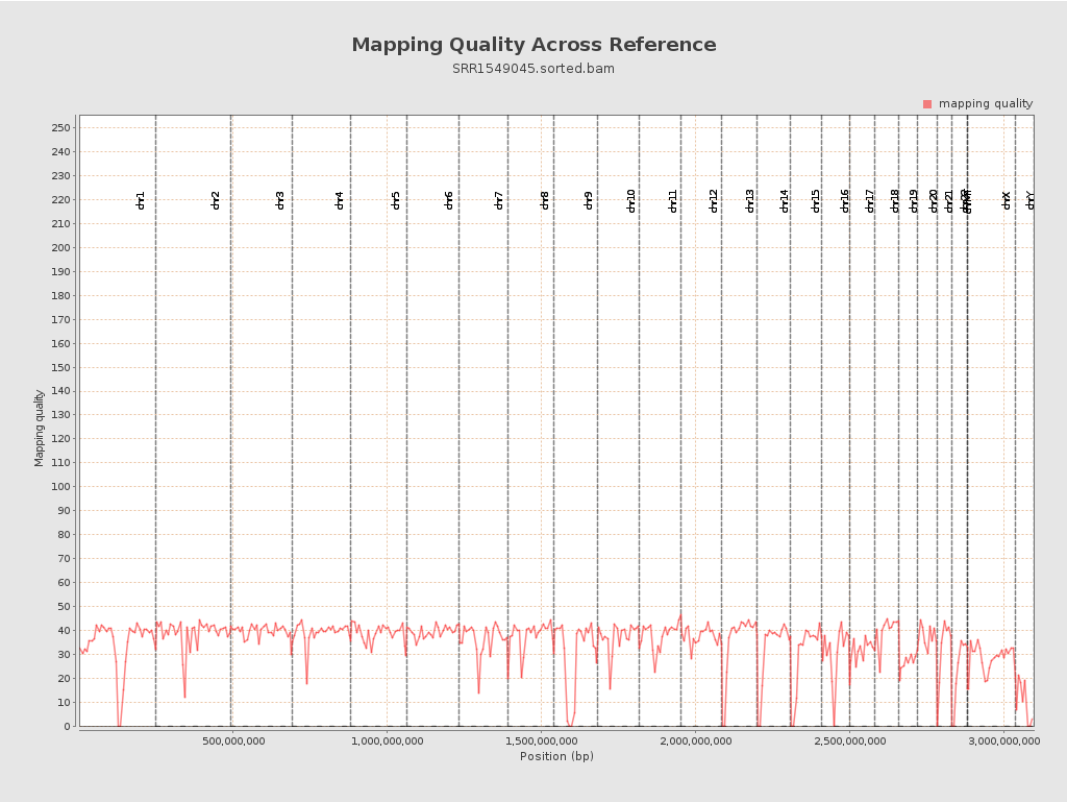
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram