Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:32:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549049.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_SRR1549049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:32:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,741,160
Mapped reads	3,050,414 / 81.54%
Unmapped reads	690,746 / 18.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	97,176 / 2.6%
Duplication rate	2.22%
Clipped reads	263,420 / 7.04%

2.2. ACGT Content

Number/percentage of A's	33,375,012 / 27.69%
Number/percentage of C's	26,322,874 / 21.84%
Number/percentage of T's	34,275,998 / 28.44%
Number/percentage of G's	26,545,519 / 22.03%
Number/percentage of N's	1,021 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0389
Standard Deviation	0.3451

2.4. Mapping Quality

Mean Mapping Quality	37.06

2.5. Mismatches and indels

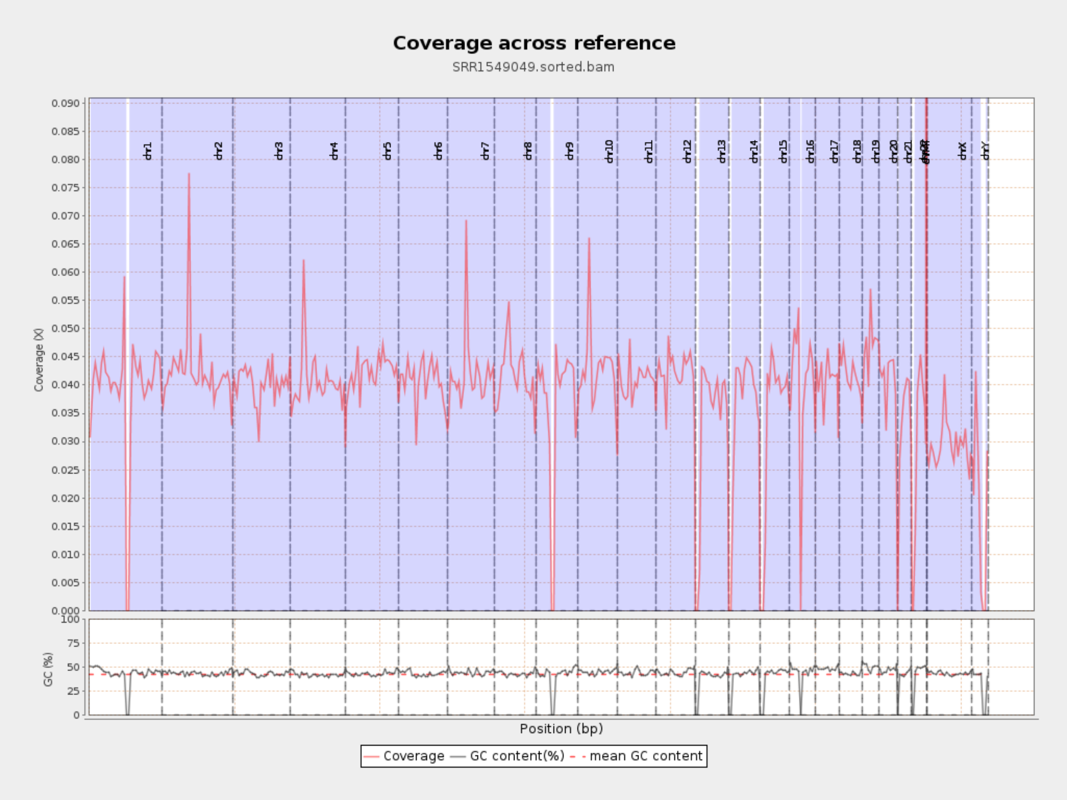
General error rate	0.3%
Mismatches	355,548
Insertions	4,035
Mapped reads with at least one insertion	0.13%
Deletions	8,284
Mapped reads with at least one deletion	0.27%
Homopolymer indels	38.53%

2.6. Chromosome stats

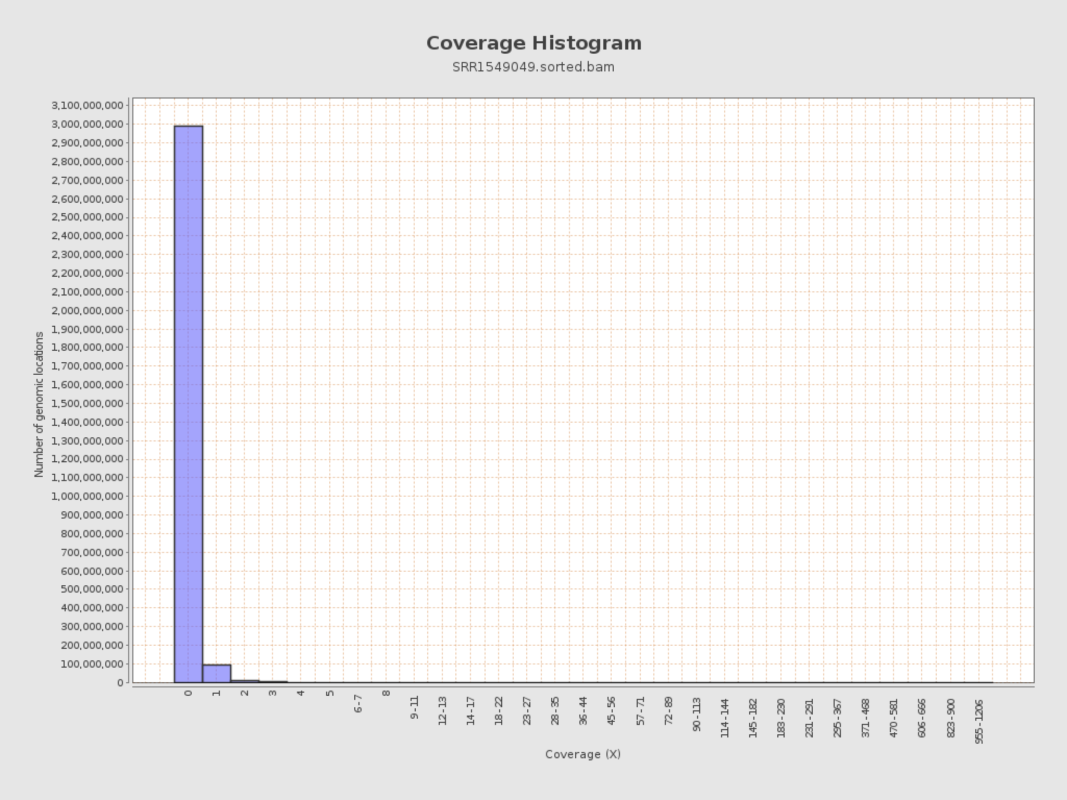
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9775967	0.0392	0.5029
chr2	243199373	10380201	0.0427	0.3776
chr3	198022430	7982936	0.0403	0.2238
chr4	191154276	7773945	0.0407	0.2426
chr5	180915260	7685886	0.0425	0.2316
chr6	171115067	6936472	0.0405	0.2354
chr7	159138663	6703682	0.0421	0.4181
chr8	146364022	6090841	0.0416	0.6489

chr9	141213431	5137404	0.0364	0.3692
chr10	135534747	5850795	0.0432	0.3069
chr11	135006516	5501780	0.0408	0.2753
chr12	133851895	5676608	0.0424	0.2343
chr13	115169878	3761498	0.0327	0.2002
chr14	107349540	3709532	0.0346	0.2408
chr15	102531392	3402433	0.0332	0.2031
chr16	90354753	3634119	0.0402	0.2449
chr17	81195210	3322636	0.0409	0.2341
chr18	78077248	3302346	0.0423	0.6012
chr19	59128983	2779930	0.047	0.545
chr20	63025520	2545109	0.0404	0.2306
chr21	48129895	1545840	0.0321	0.246
chr22	51304566	1414534	0.0276	0.266
chrMT	16571	9809	0.5919	0.9588
chrX	155270560	4562572	0.0294	0.2322
chrY	59373566	1044280	0.0176	0.2038

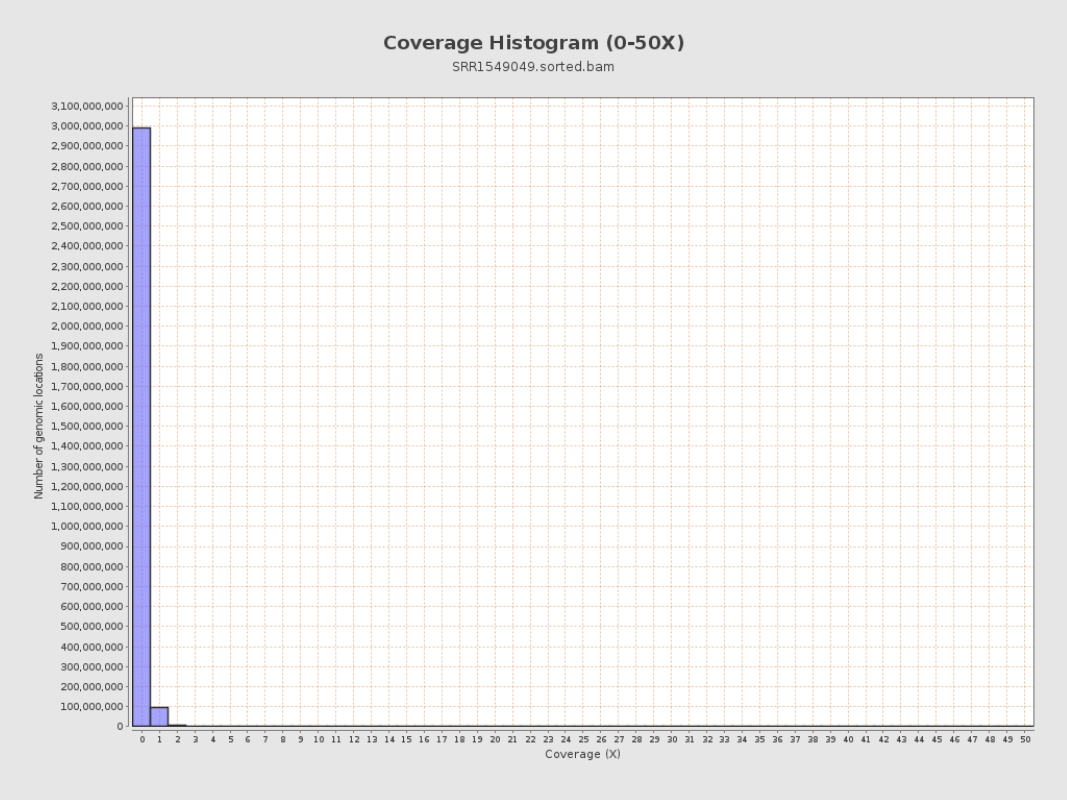
3. Results : Coverage across reference



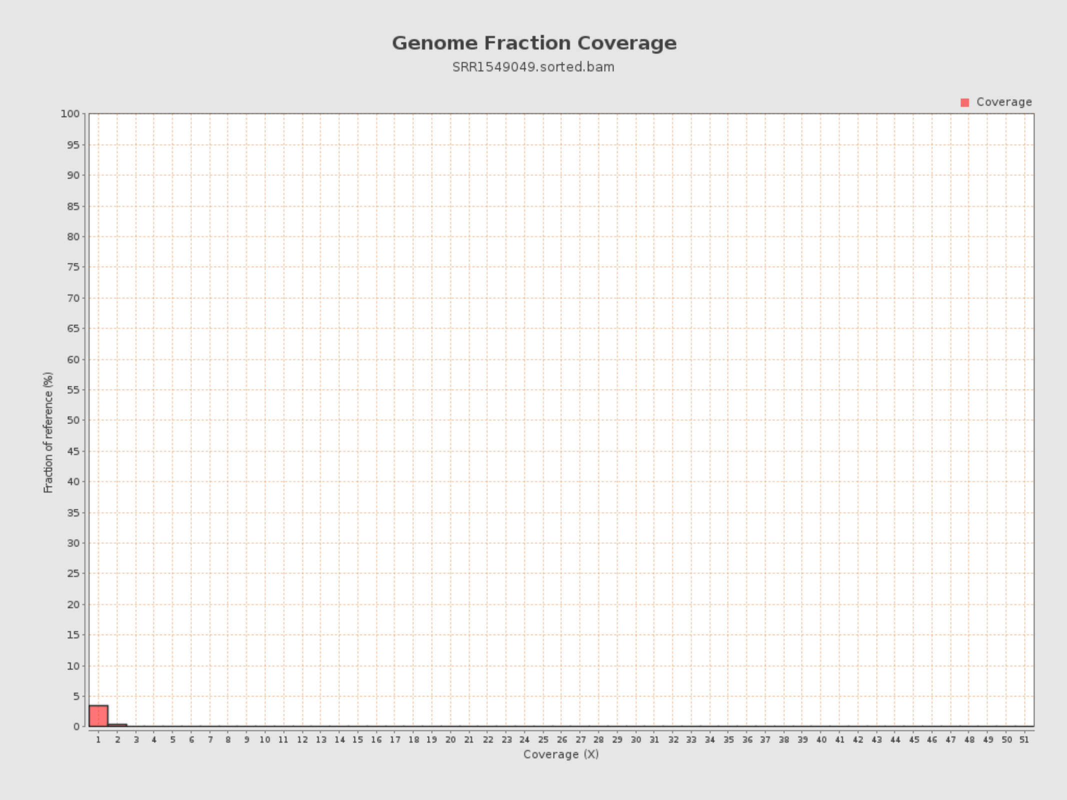
4. Results : Coverage Histogram



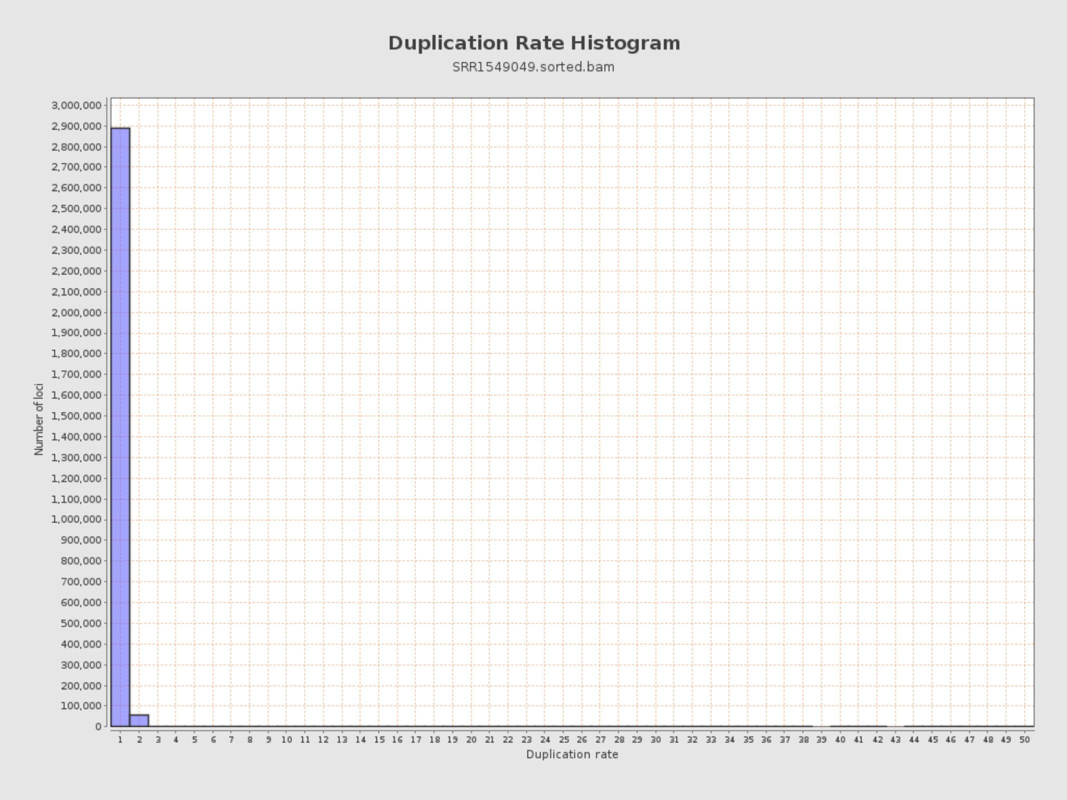
5. Results : Coverage Histogram (0-50X)



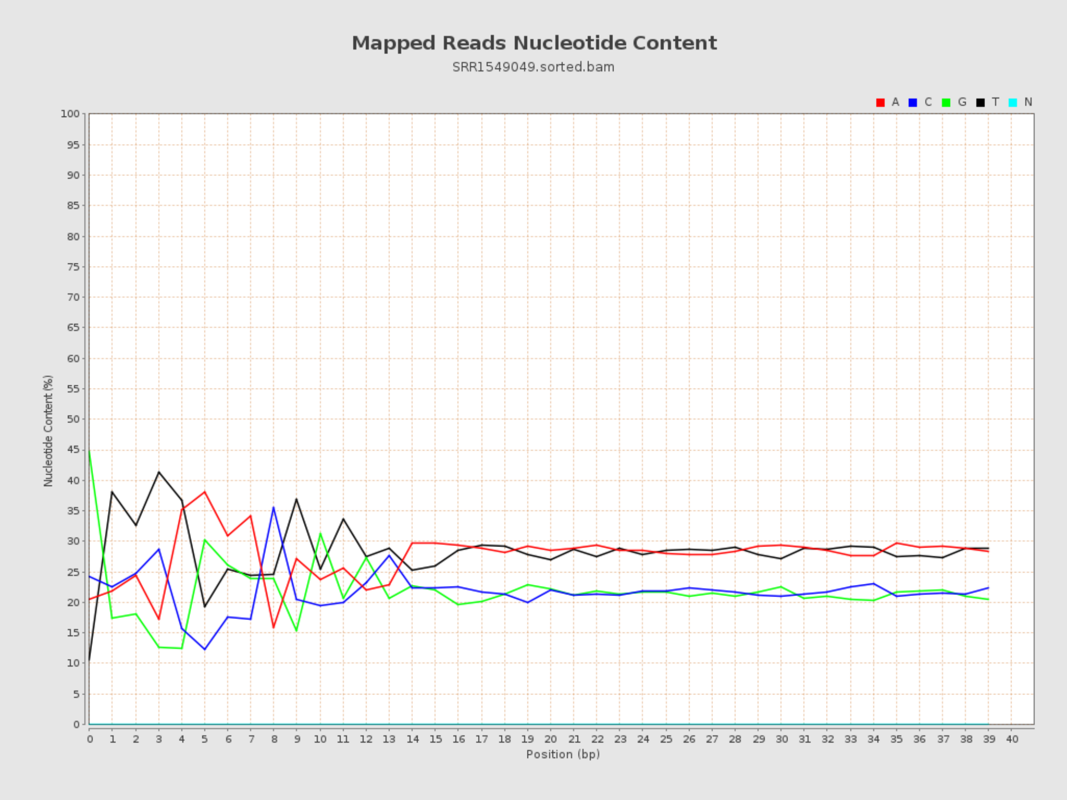
6. Results : Genome Fraction Coverage



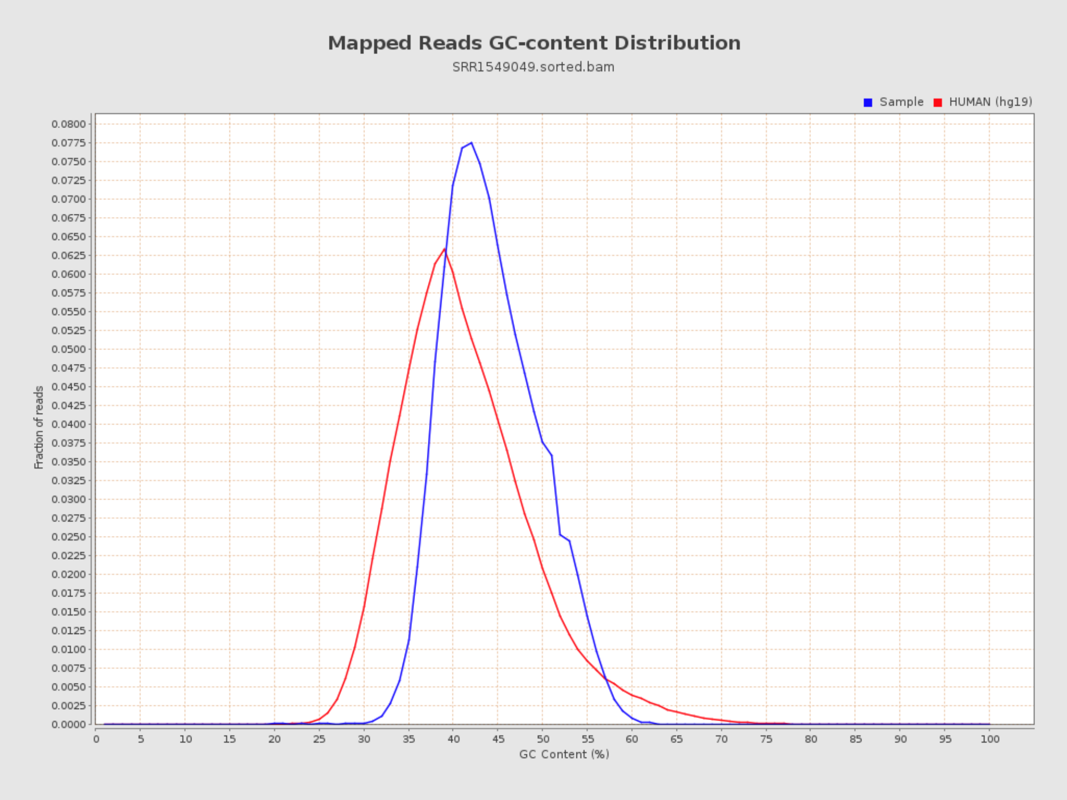
7. Results : Duplication Rate Histogram



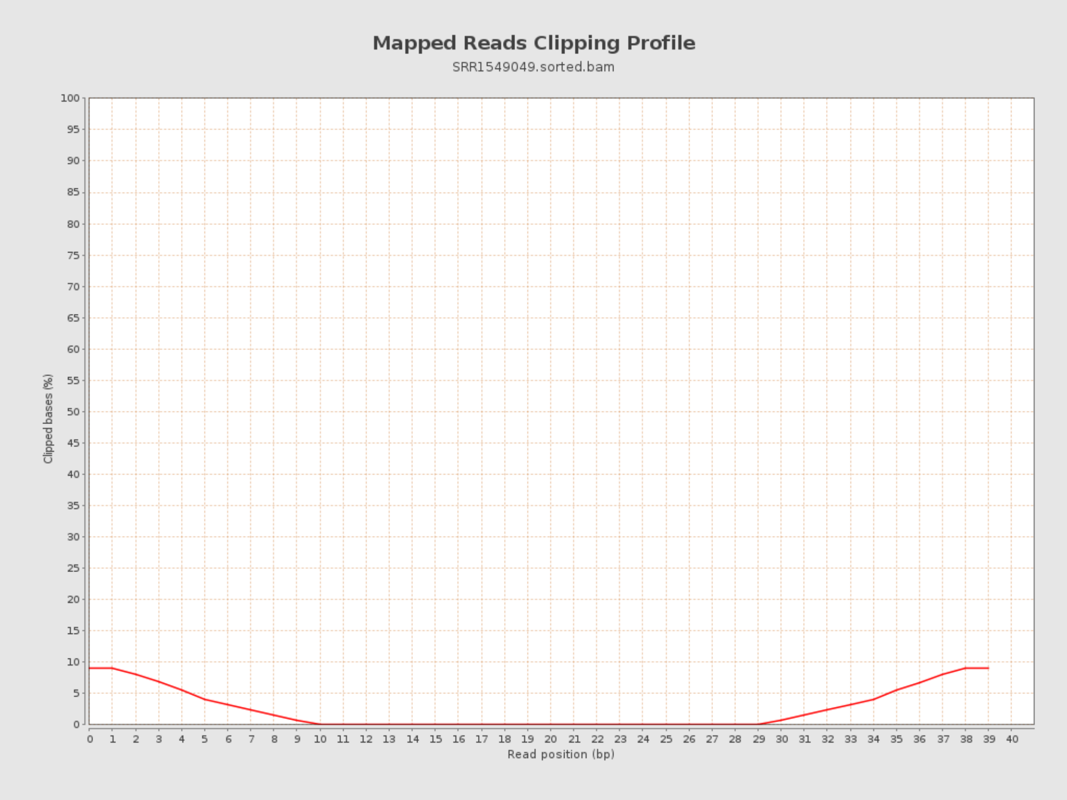
8. Results : Mapped Reads Nucleotide Content



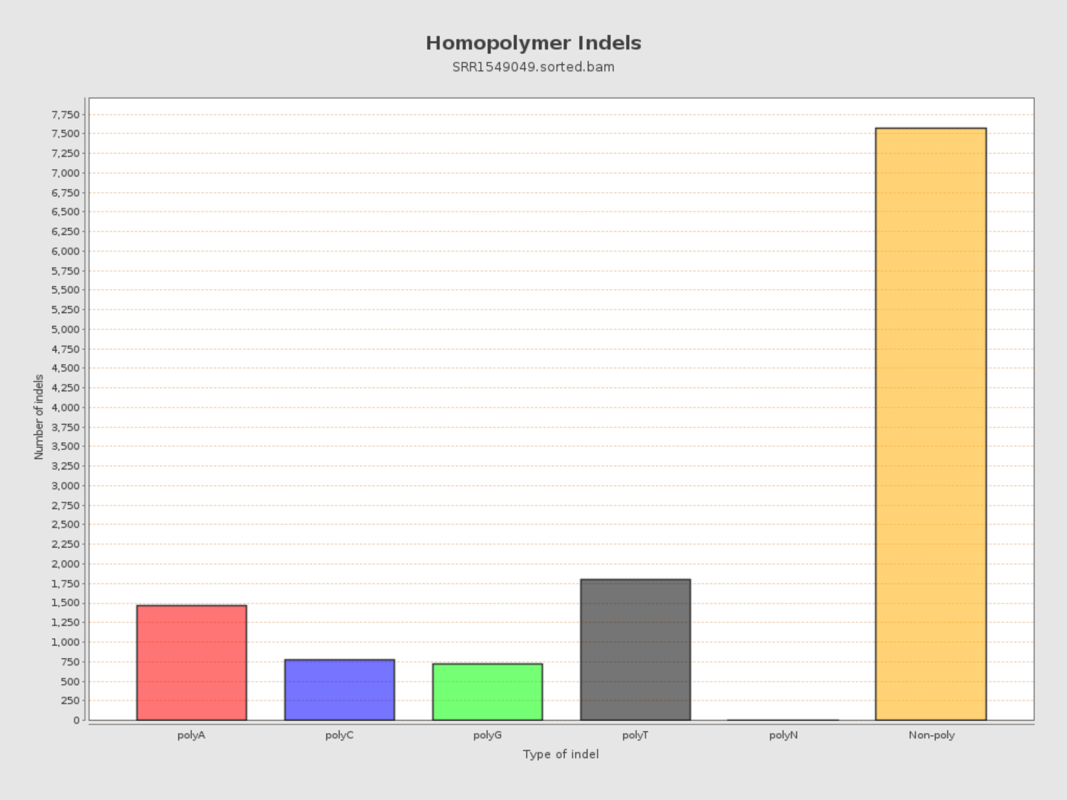
9. Results : Mapped Reads GC-content Distribution



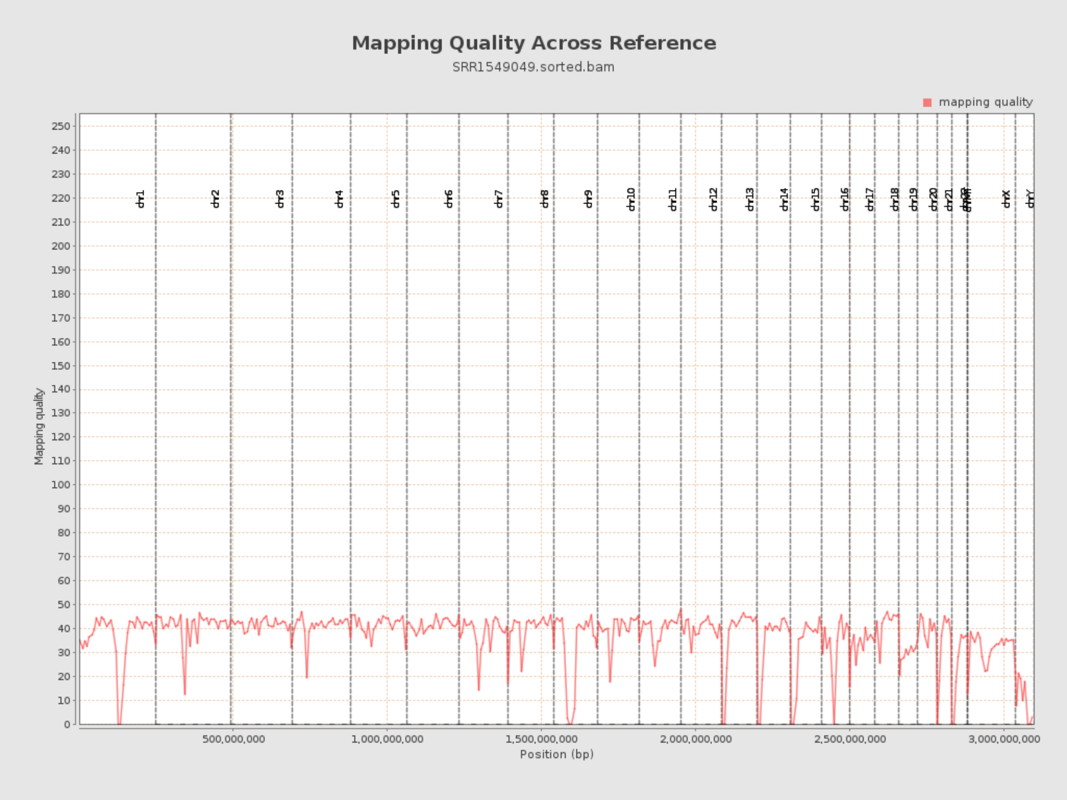
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram