Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:11:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084907.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_SRR3084907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:11:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,601,632
Mapped reads	1,420,226 / 88.67%
Unmapped reads	181,406 / 11.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,508 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	80,820 / 5.05%
Duplication rate	3.15%
Clipped reads	576,700 / 36.01%

2.2. ACGT Content

Number/percentage of A's	27,604,183 / 28.44%
Number/percentage of C's	18,364,736 / 18.92%
Number/percentage of T's	29,356,431 / 30.25%
Number/percentage of G's	21,712,665 / 22.37%
Number/percentage of N's	14,903 / 0.02%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.64

2.4. Mapping Quality

Mean Mapping Quality	42.14

2.5. Mismatches and indels

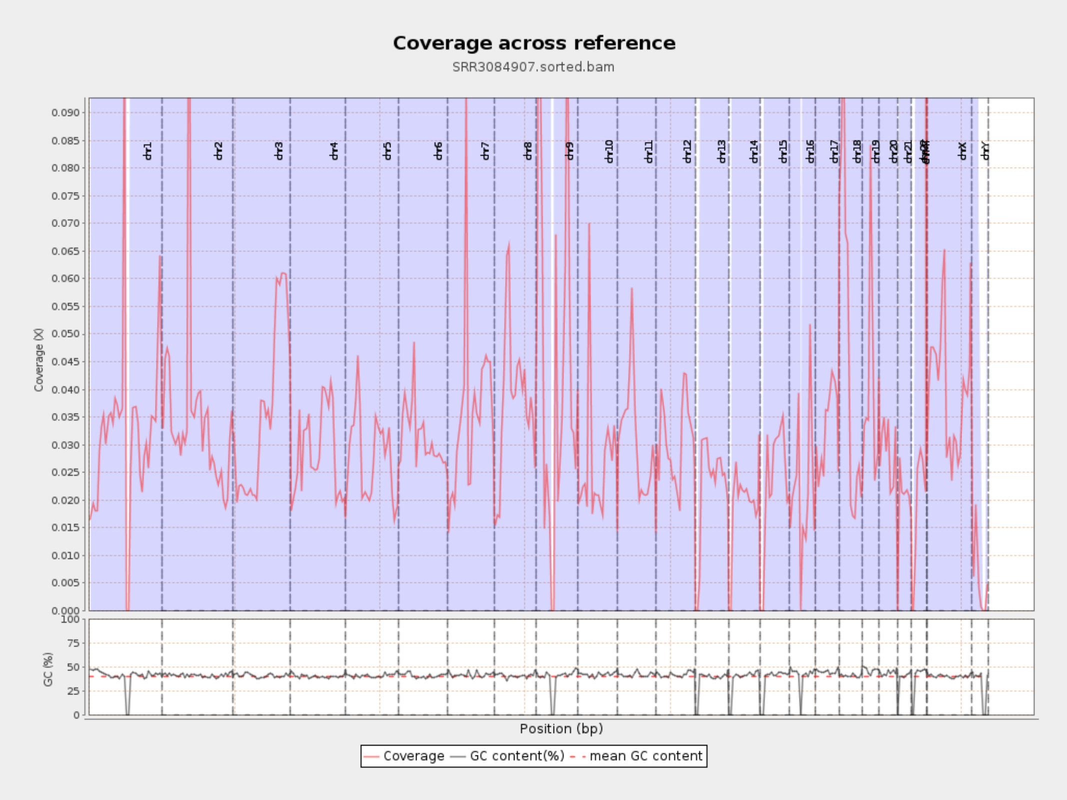
General error rate	1%
Mismatches	952,472
Insertions	9,159
Mapped reads with at least one insertion	0.64%
Deletions	20,702
Mapped reads with at least one deletion	1.44%
Homopolymer indels	44.12%

2.6. Chromosome stats

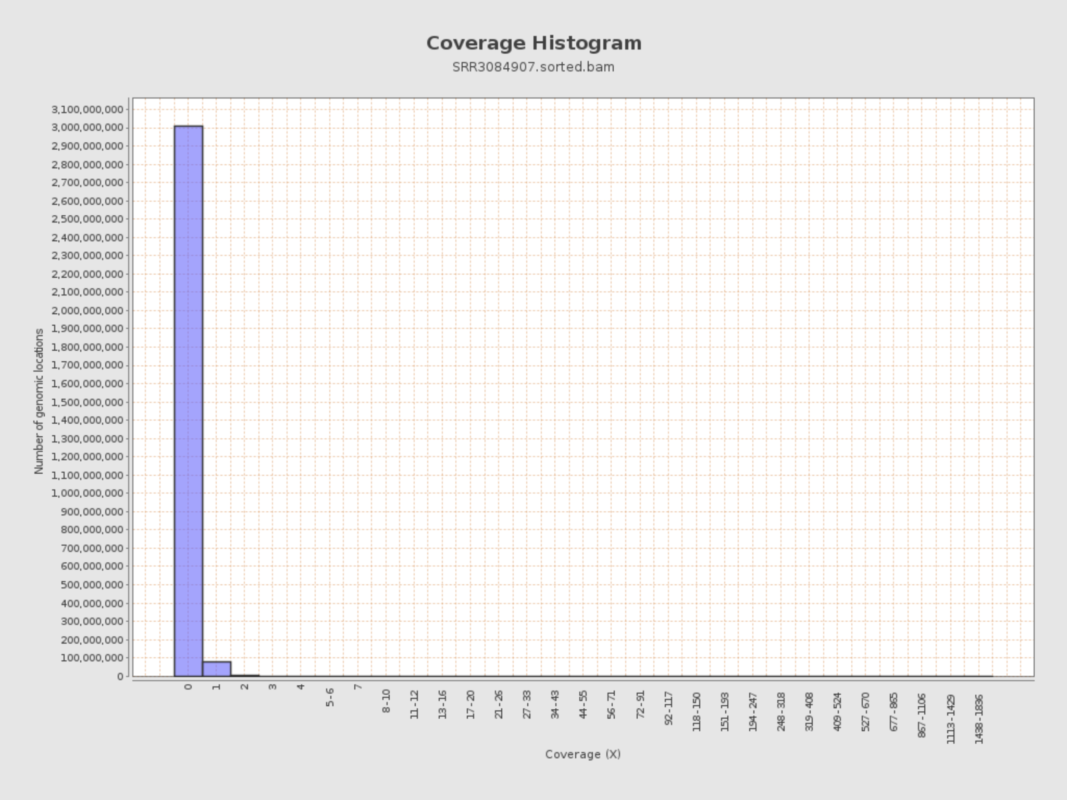
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8108543	0.0325	1.5243
chr2	243199373	8568400	0.0352	0.7756
chr3	198022430	7094564	0.0358	0.2067
chr4	191154276	5474189	0.0286	0.1911
chr5	180915260	5071832	0.028	0.214
chr6	171115067	5352367	0.0313	0.2247
chr7	159138663	5768916	0.0363	0.6924

chr8	146364022	5491524	0.0375	0.7424
chr9	141213431	6349311	0.045	0.6632
chr10	135534747	3558931	0.0263	0.4408
chr11	135006516	4111889	0.0305	0.4913
chr12	133851895	4113453	0.0307	0.2191
chr13	115169878	2543490	0.0221	0.1558
chr14	107349540	1972253	0.0184	0.2331
chr15	102531392	2371091	0.0231	0.1676
chr16	90354753	2028606	0.0225	0.2865
chr17	81195210	2716229	0.0335	0.264
chr18	78077248	3710442	0.0475	1.2916
chr19	59128983	2409698	0.0408	0.8756
chr20	63025520	1814302	0.0288	0.2296
chr21	48129895	955710	0.0199	0.2125
chr22	51304566	936210	0.0182	0.1411
chrMT	16571	50381	3.0403	2.4765
chrX	155270560	6193072	0.0399	0.3228
chrY	59373566	323192	0.0054	0.2062

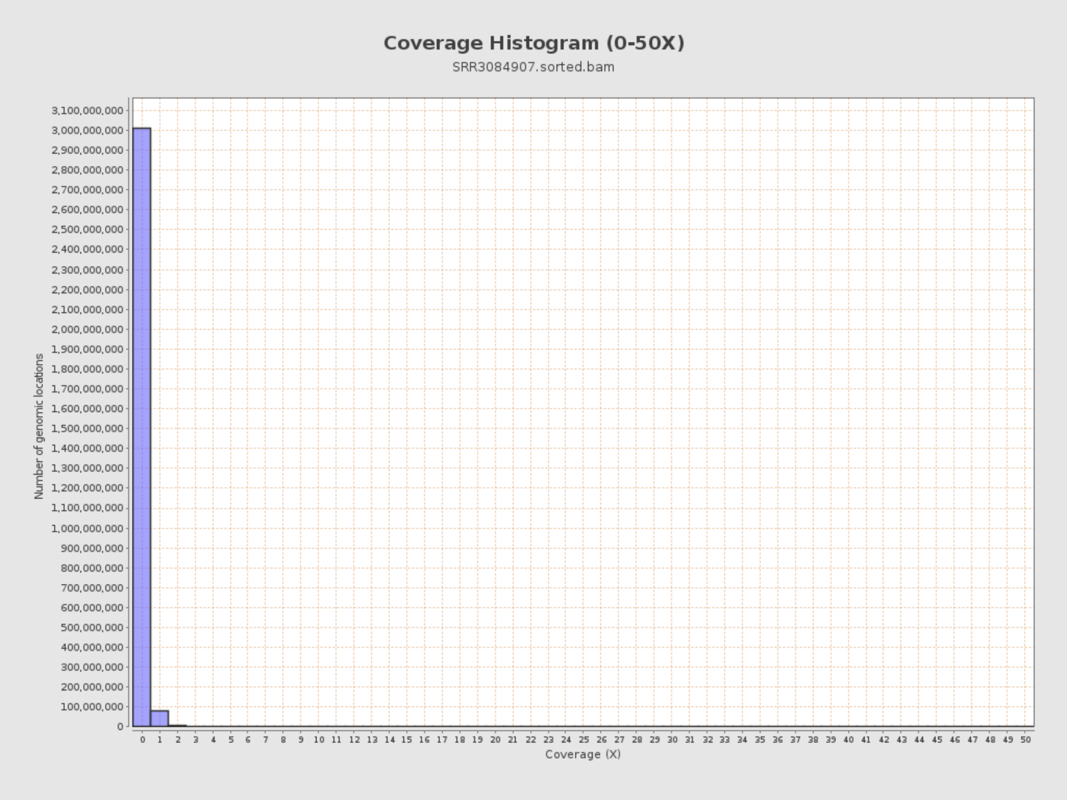
3. Results : Coverage across reference



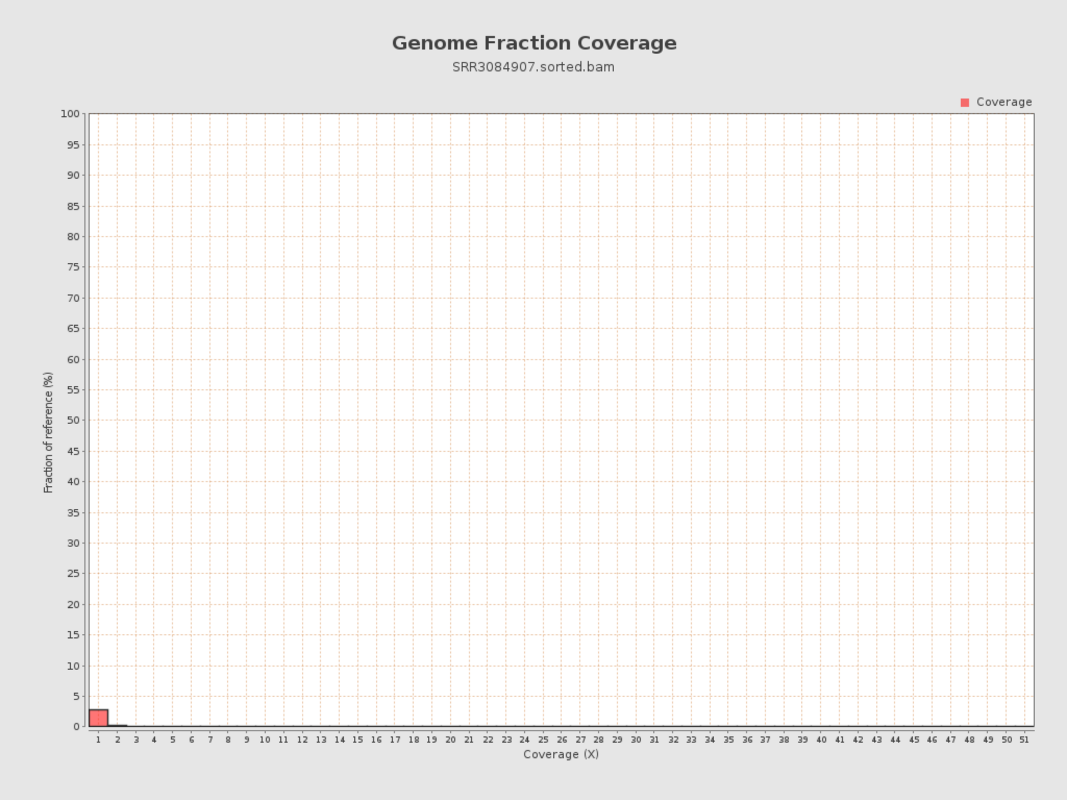
4. Results : Coverage Histogram



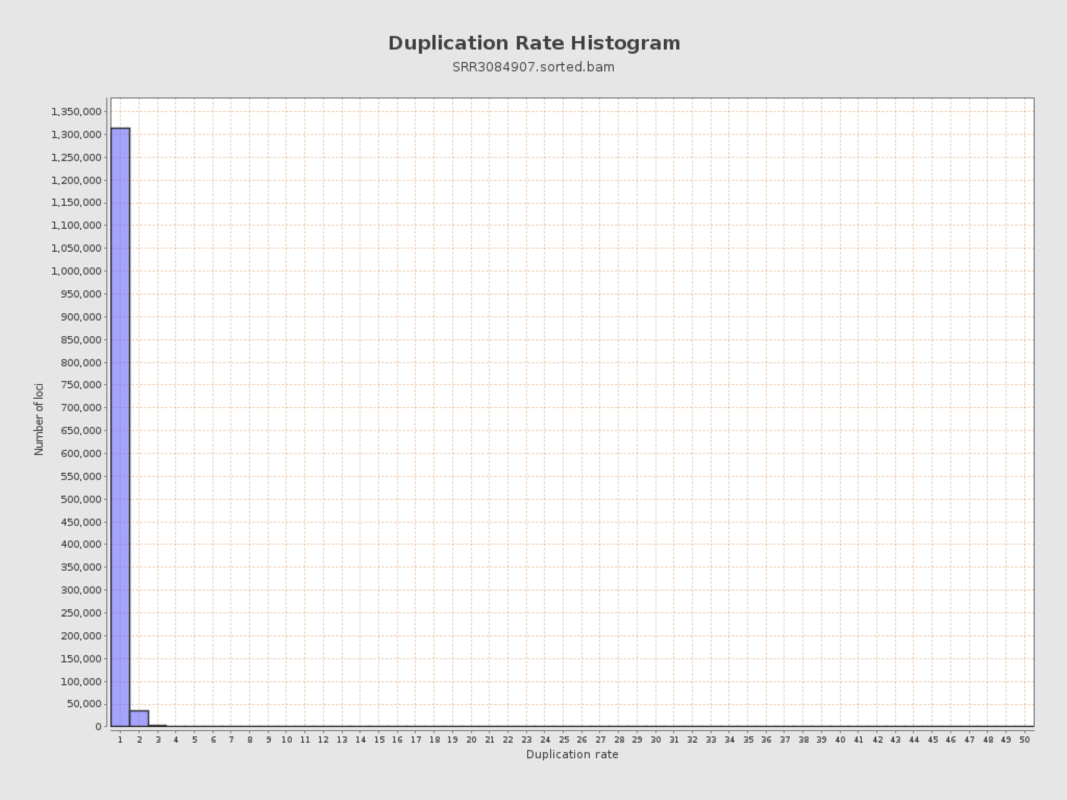
5. Results : Coverage Histogram (0-50X)



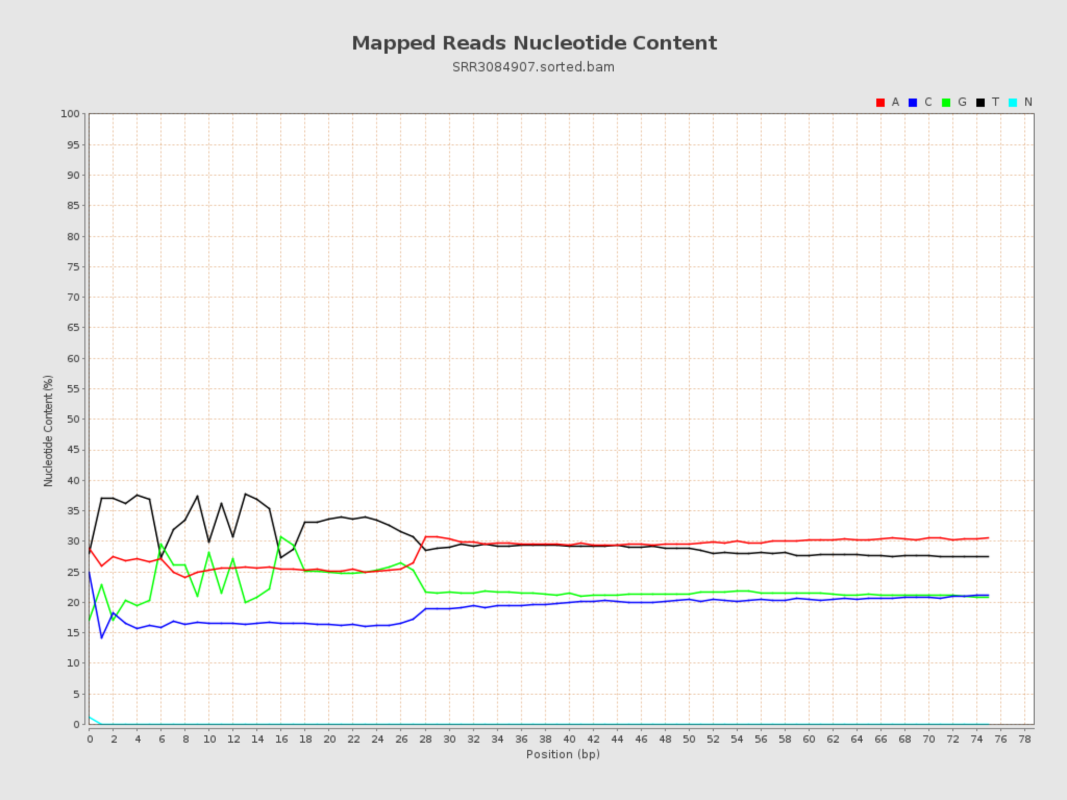
6. Results : Genome Fraction Coverage



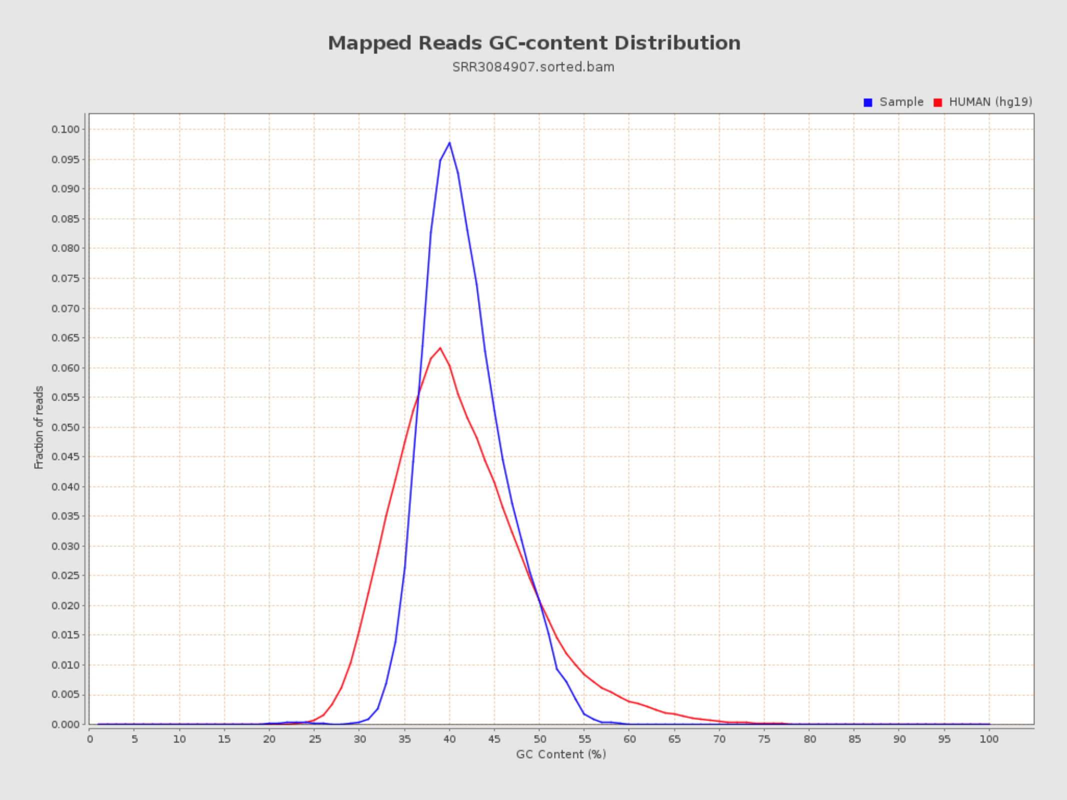
7. Results : Duplication Rate Histogram



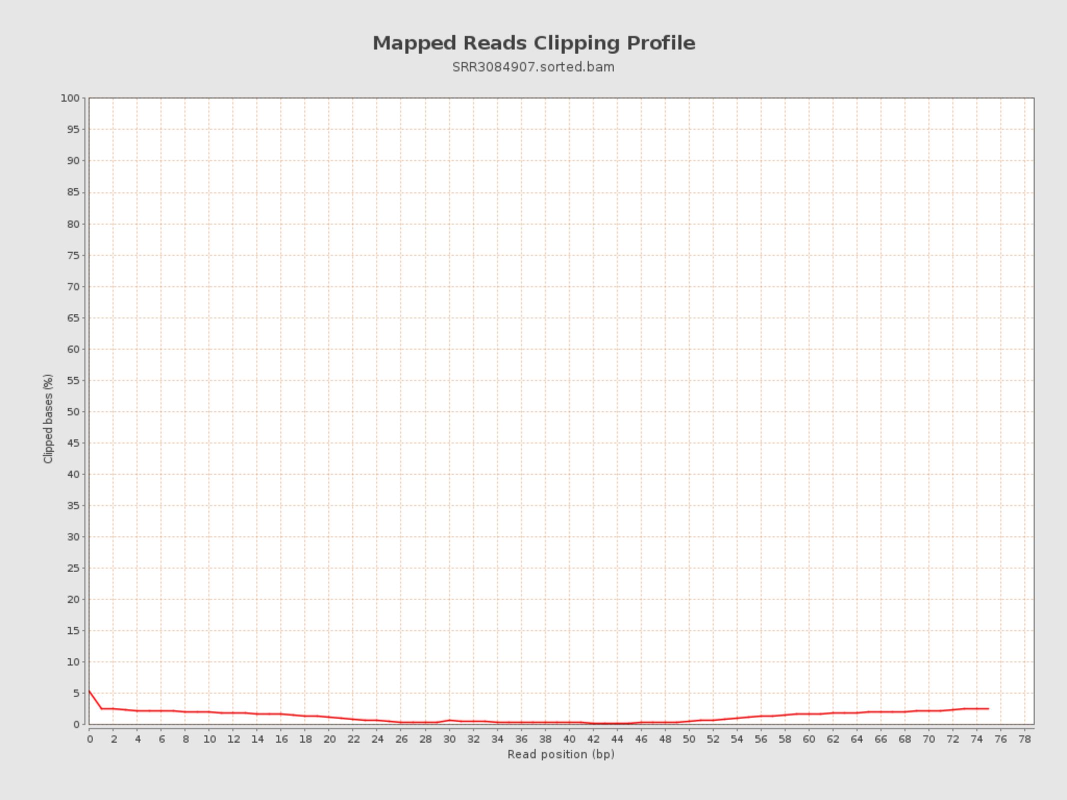
8. Results : Mapped Reads Nucleotide Content



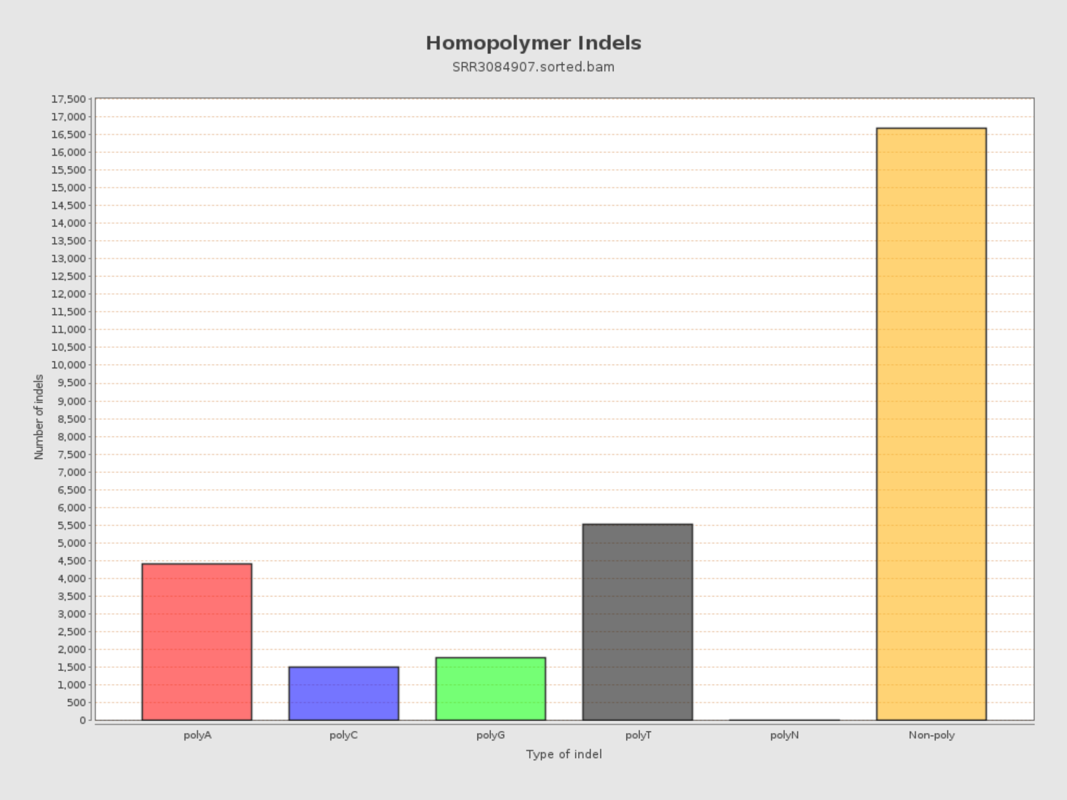
9. Results : Mapped Reads GC-content Distribution



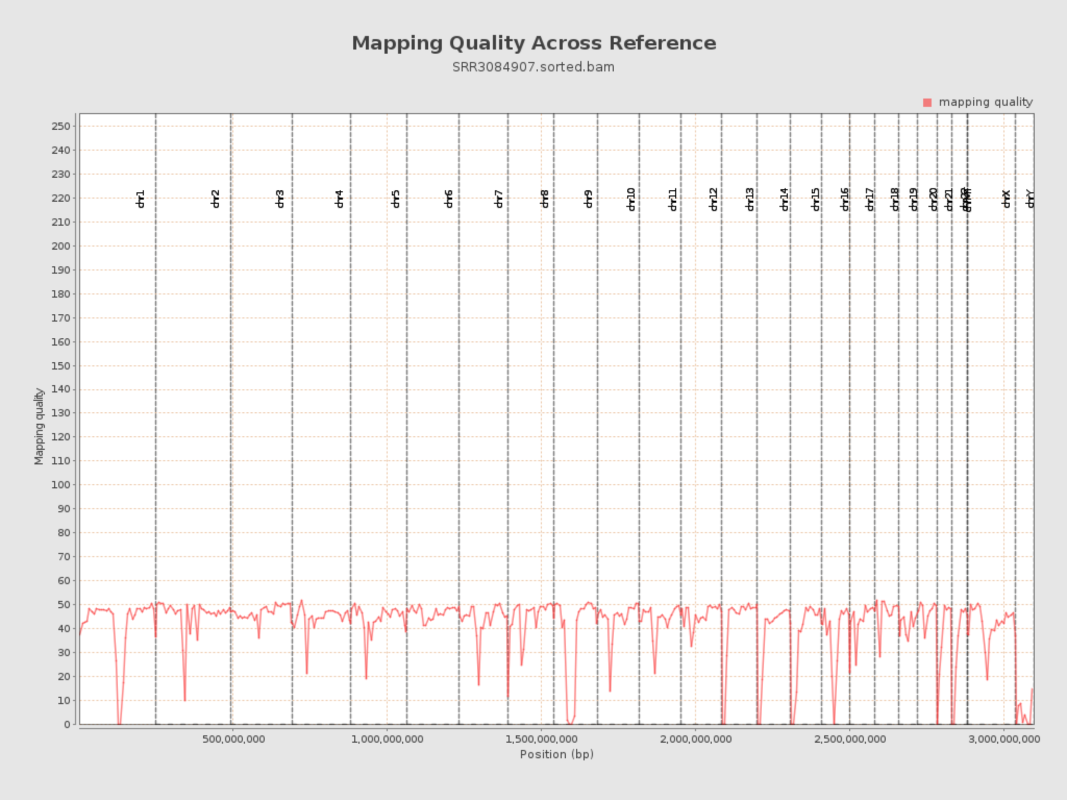
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram