Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:11:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004109.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_SRR6004109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:11:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,863,485
Mapped reads	4,367,531 / 89.8%
Unmapped reads	495,954 / 10.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,274 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	216,506 / 4.45%
Duplication rate	3.08%
Clipped reads	1,879,193 / 38.64%

2.2. ACGT Content

Number/percentage of A's	80,927,930 / 27.35%
Number/percentage of C's	59,447,788 / 20.09%
Number/percentage of T's	88,703,769 / 29.98%
Number/percentage of G's	66,772,805 / 22.57%
Number/percentage of N's	39,168 / 0.01%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0956

Standard Deviation	1.0212

2.4. Mapping Quality

Mean Mapping Quality	42.3

2.5. Mismatches and indels

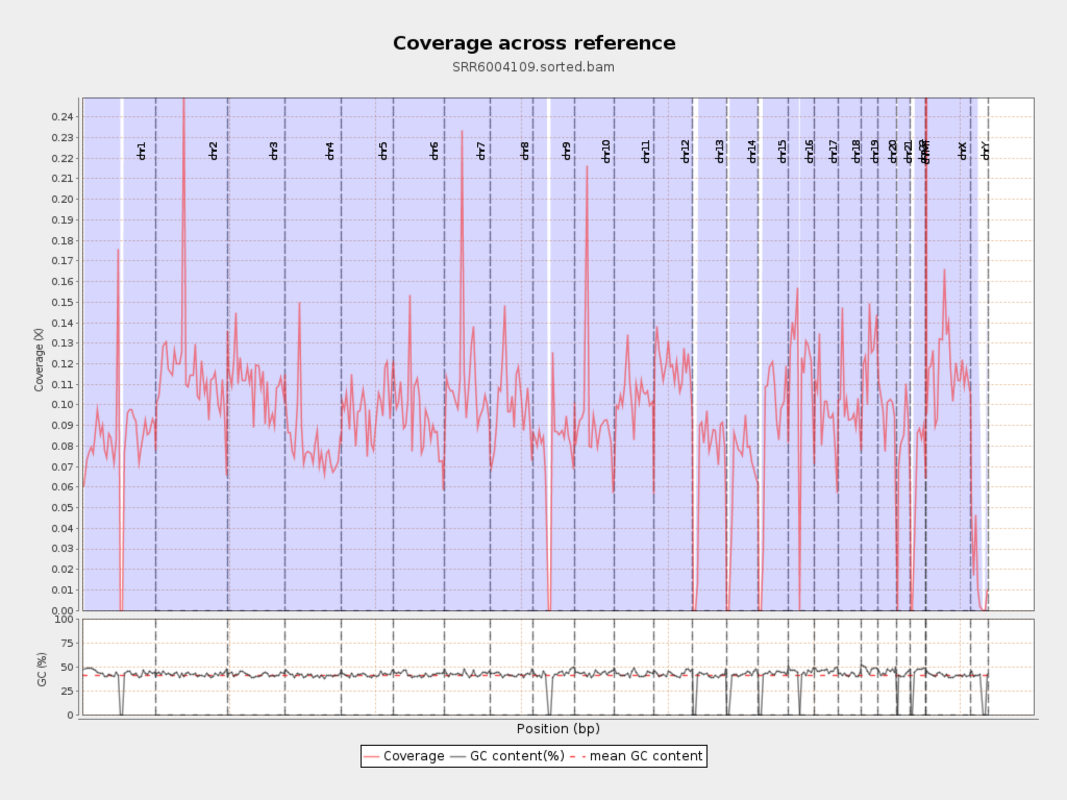
General error rate	1%
Mismatches	2,914,632
Insertions	27,016
Mapped reads with at least one insertion	0.61%
Deletions	72,655
Mapped reads with at least one deletion	1.64%
Homopolymer indels	44.56%

2.6. Chromosome stats

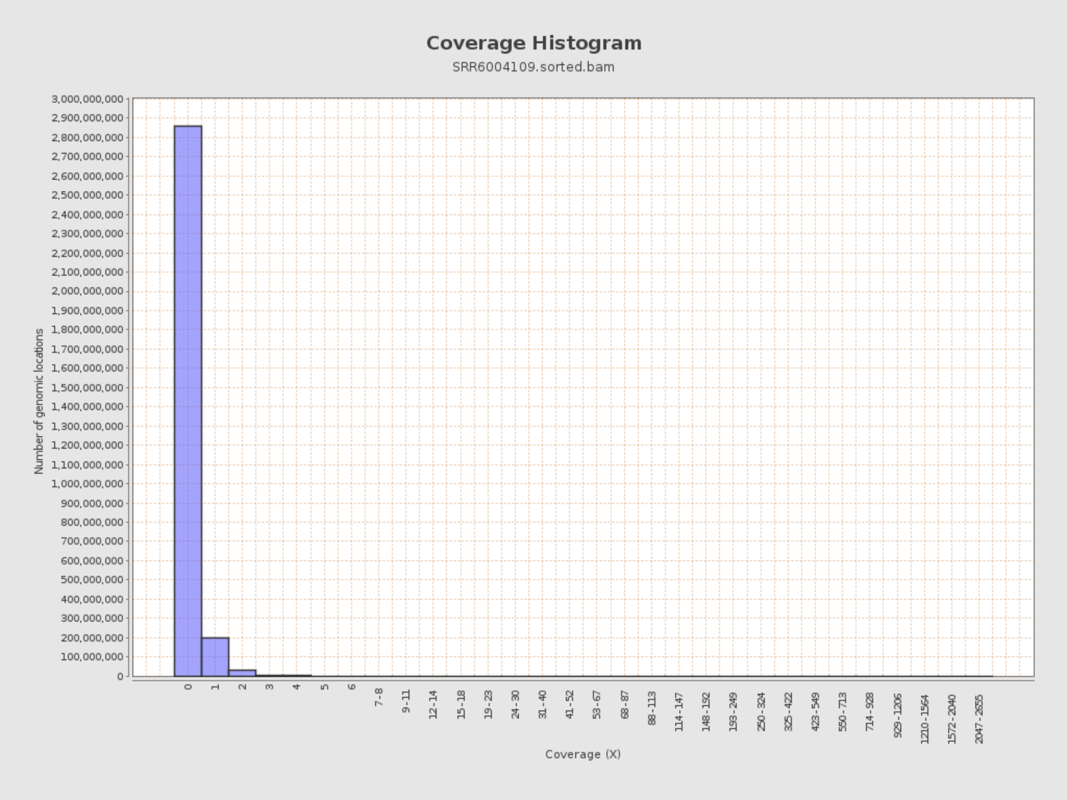
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20383955	0.0818	2.1847
chr2	243199373	28341207	0.1165	1.1916
chr3	198022430	21962905	0.1109	0.4209
chr4	191154276	15556100	0.0814	0.4533
chr5	180915260	17850294	0.0987	0.3819
chr6	171115067	16183725	0.0946	0.6733
chr7	159138663	17812858	0.1119	1.7187

chr8	146364022	14698419	0.1004	0.9328
chr9	141213431	10783448	0.0764	0.8555
chr10	135534747	12779938	0.0943	1.0504
chr11	135006516	14014943	0.1038	0.8156
chr12	133851895	15975559	0.1194	0.4302
chr13	115169878	8179752	0.071	0.3112
chr14	107349540	7057240	0.0657	0.4239
chr15	102531392	8746341	0.0853	0.3659
chr16	90354753	10216252	0.1131	0.5776
chr17	81195210	7932246	0.0977	0.5392
chr18	78077248	7905303	0.1012	1.8349
chr19	59128983	7361127	0.1245	1.3687
chr20	63025520	6065993	0.0962	0.4468
chr21	48129895	3720421	0.0773	0.4403
chr22	51304566	3065558	0.0598	0.2921
chrMT	16571	141738	8.5534	6.247
chrX	155270560	18374995	0.1183	0.5248
chrY	59373566	903900	0.0152	0.3331

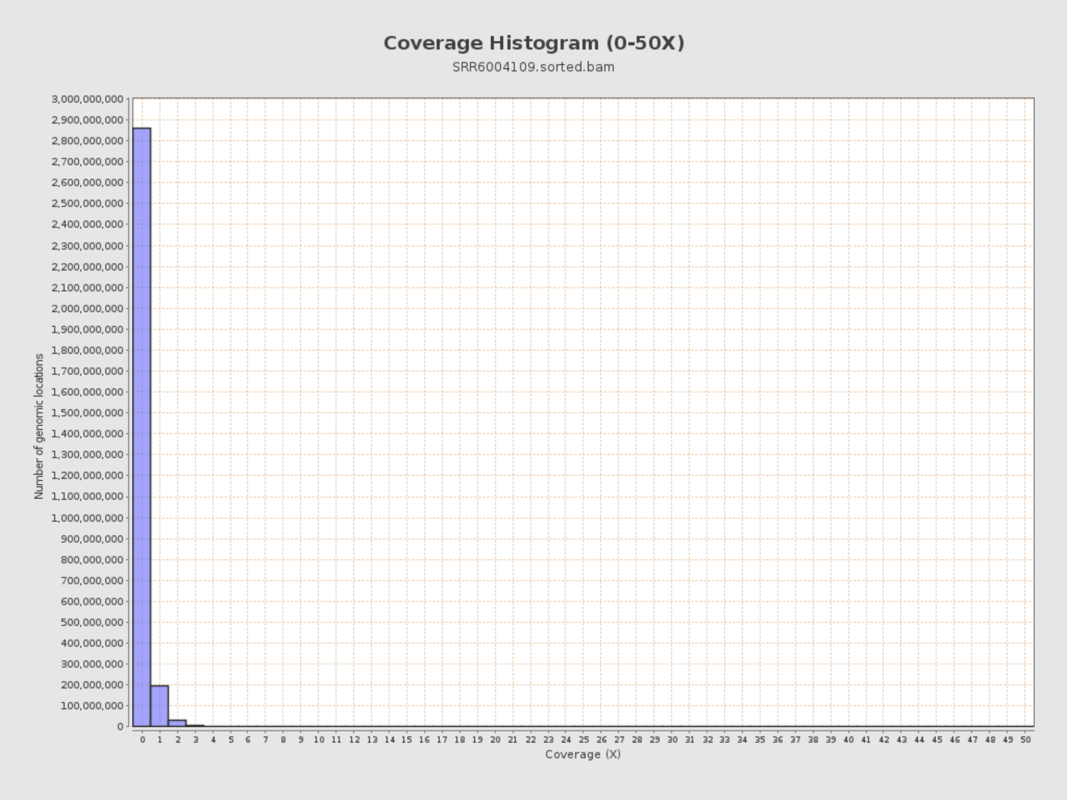
3. Results : Coverage across reference



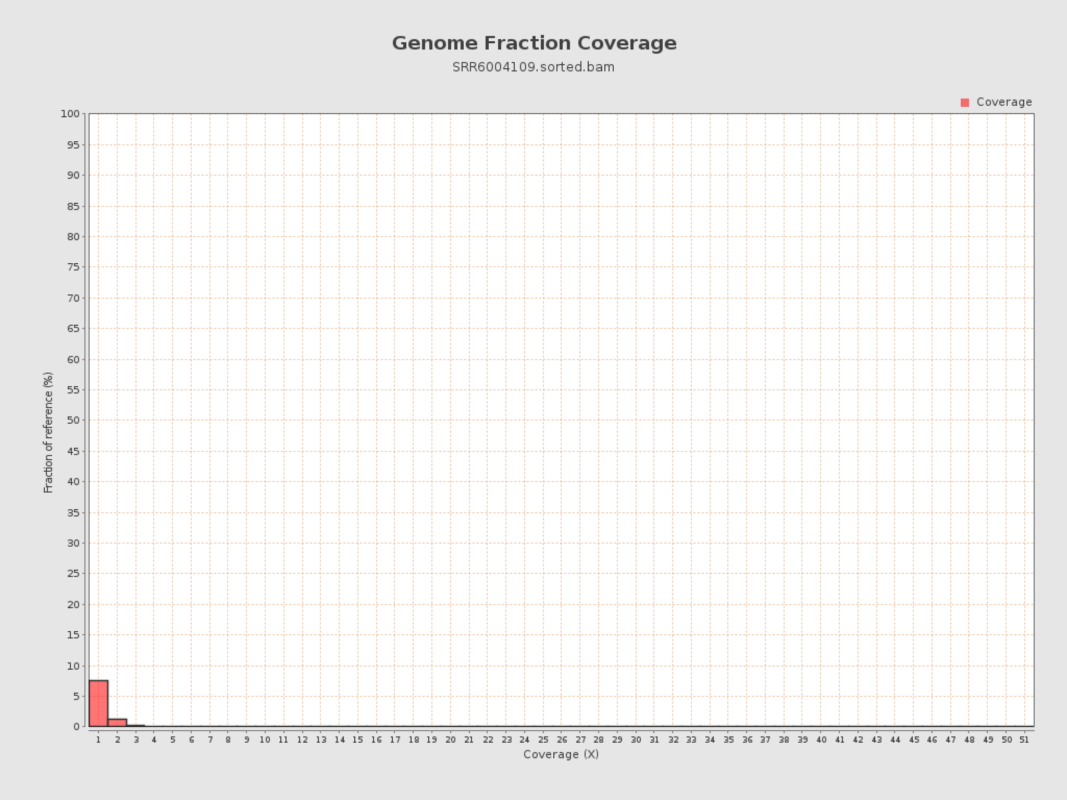
4. Results : Coverage Histogram



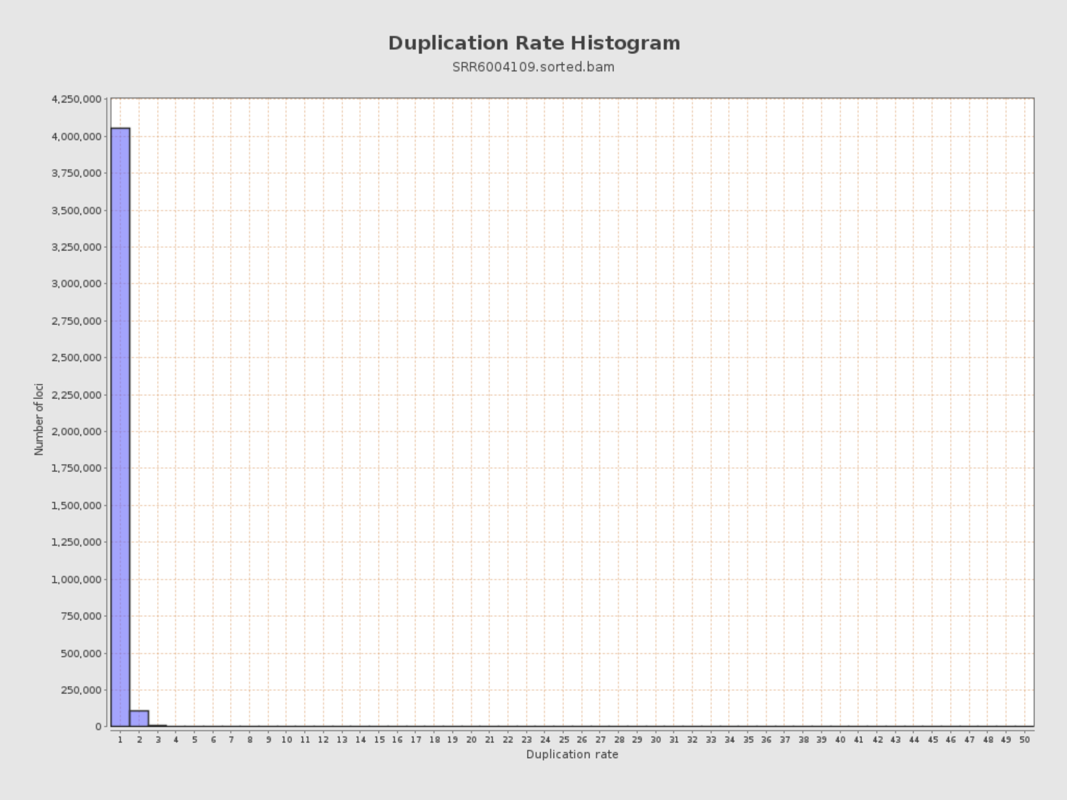
5. Results : Coverage Histogram (0-50X)



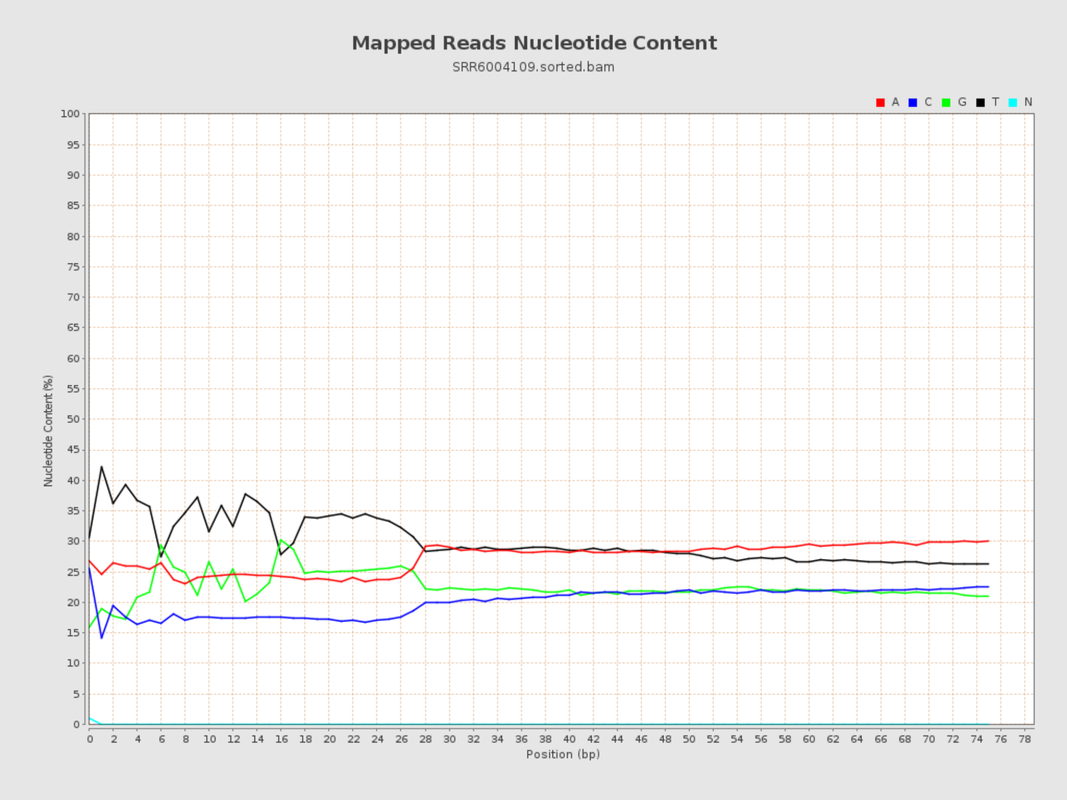
6. Results : Genome Fraction Coverage



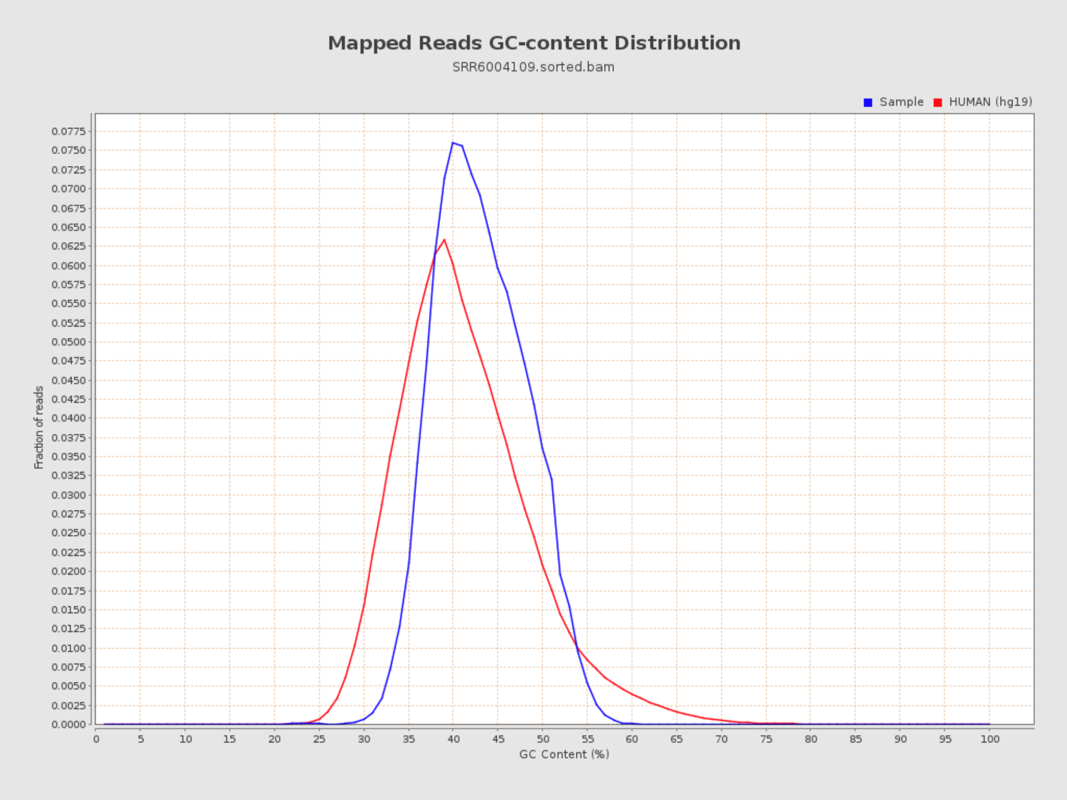
7. Results : Duplication Rate Histogram



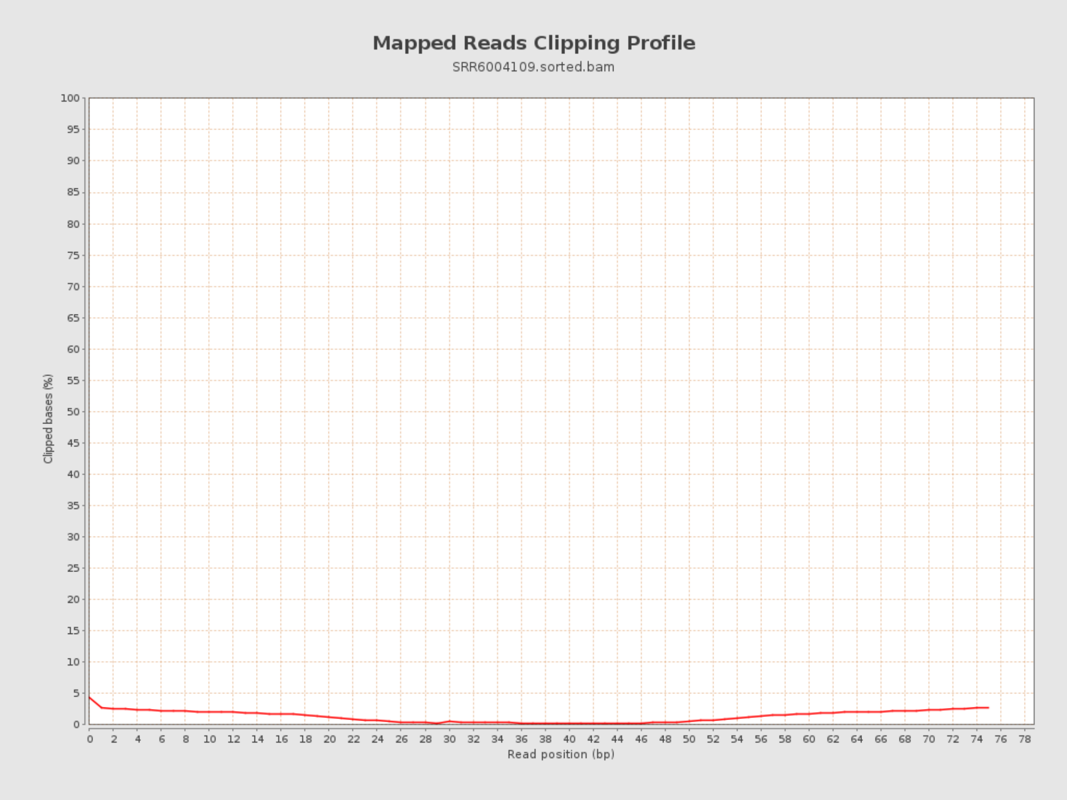
8. Results : Mapped Reads Nucleotide Content



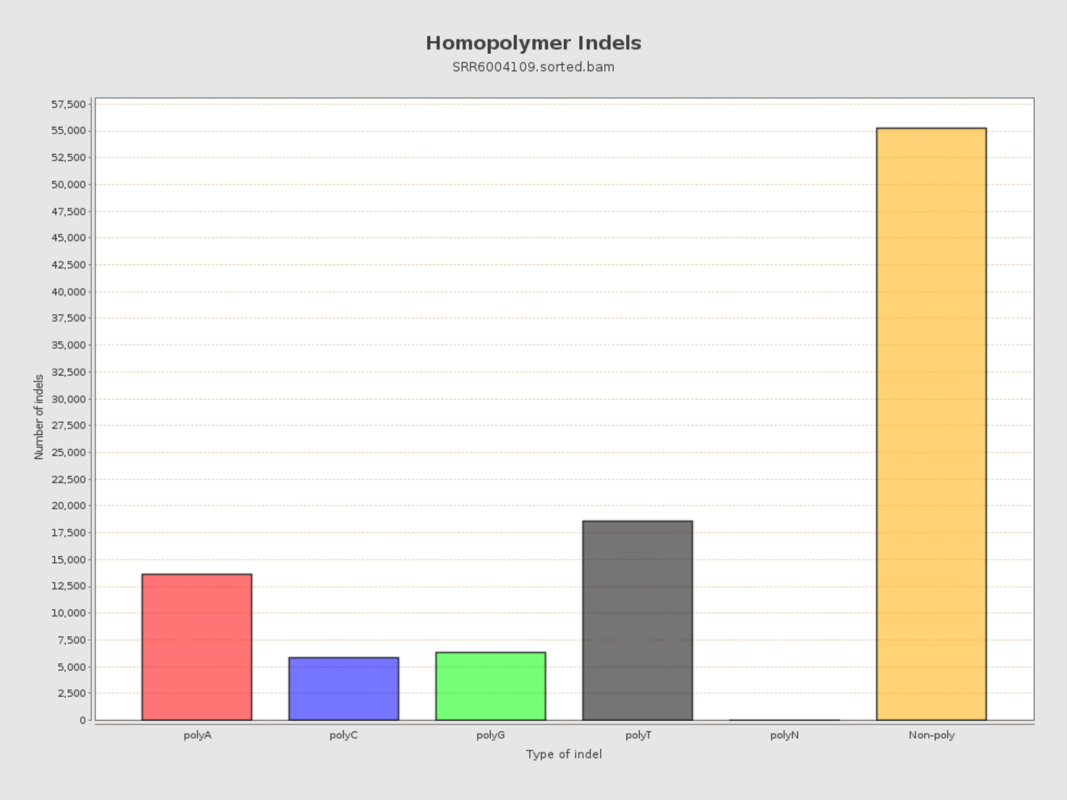
9. Results : Mapped Reads GC-content Distribution



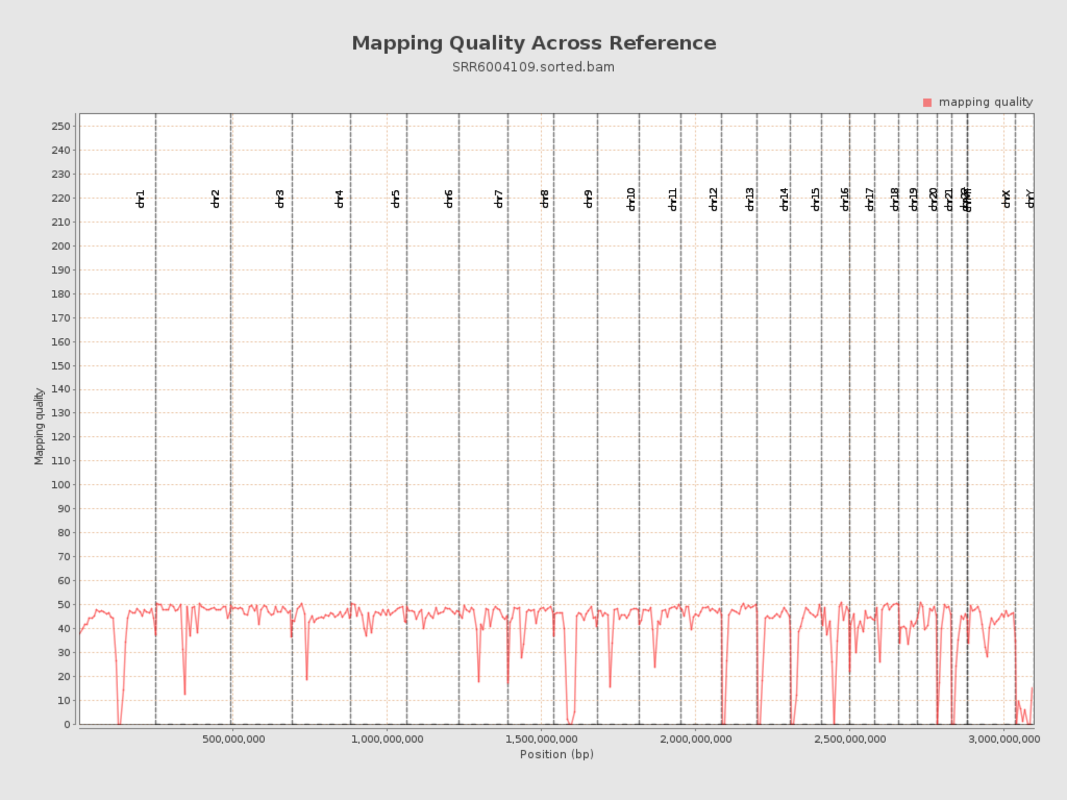
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram