Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004098.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_SRR6004098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004098.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:25:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,705,101
Mapped reads	3,208,857 / 86.61%
Unmapped reads	496,244 / 13.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,652 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	211,485 / 5.71%
Duplication rate	5.1%
Clipped reads	1,239,991 / 33.47%

2.2. ACGT Content

Number/percentage of A's	61,633,967 / 28.09%
Number/percentage of C's	41,144,724 / 18.75%
Number/percentage of T's	70,180,915 / 31.99%
Number/percentage of G's	46,414,169 / 21.15%
Number/percentage of N's	30,324 / 0.01%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0709

Standard Deviation	0.6843

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

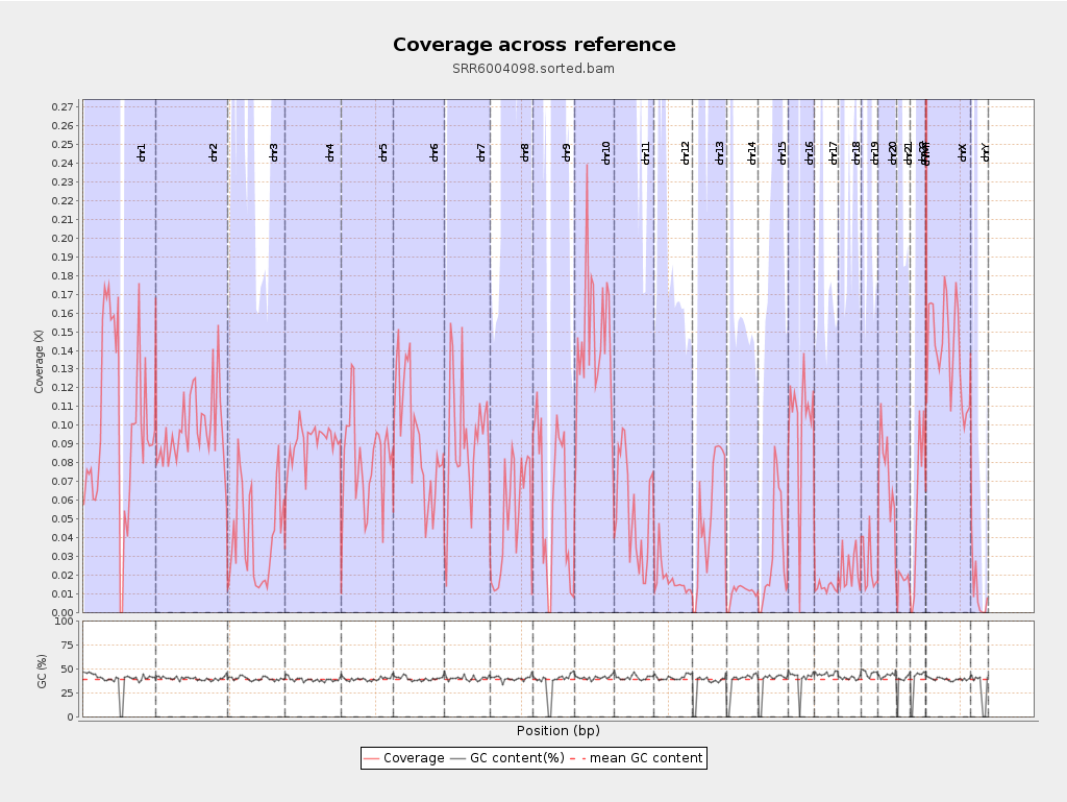
General error rate	0.92%
Mismatches	1,988,682
Insertions	17,274
Mapped reads with at least one insertion	0.53%
Deletions	51,655
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.54%

2.6. Chromosome stats

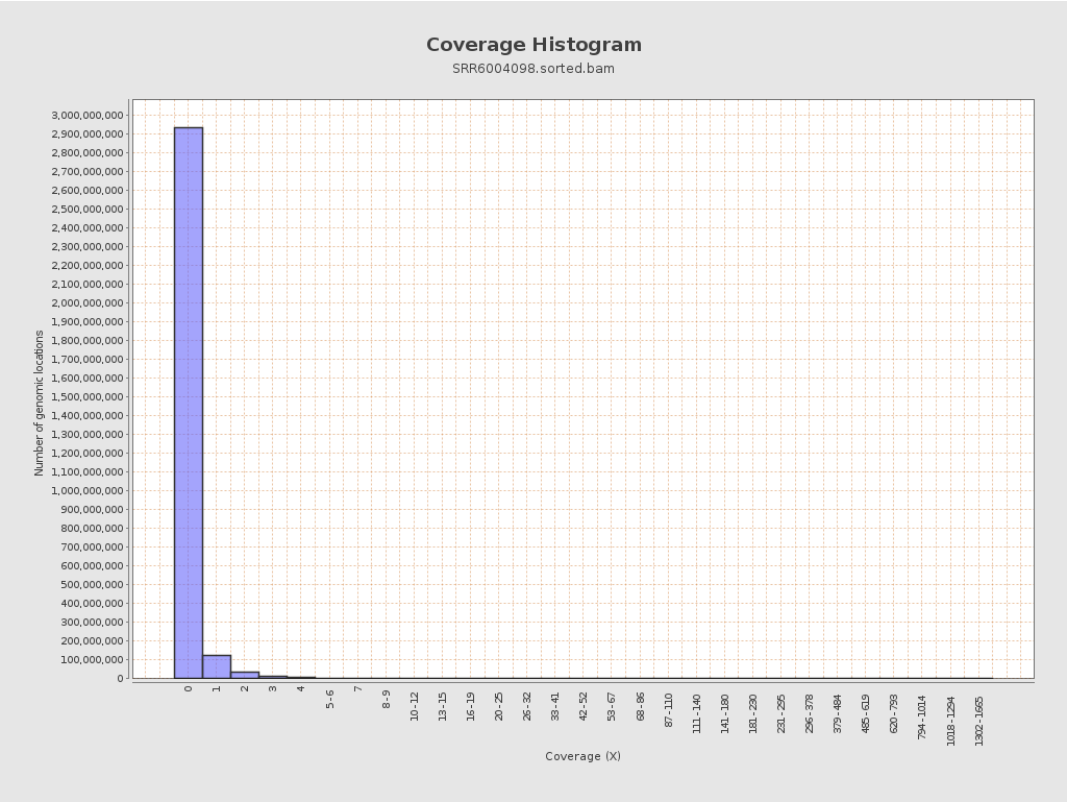
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24897625	0.0999	1.5128
chr2	243199373	23820126	0.0979	0.5933
chr3	198022430	8060739	0.0407	0.3156
chr4	191154276	17417429	0.0911	0.4447
chr5	180915260	14648090	0.081	0.3655
chr6	171115067	15961223	0.0933	0.5301
chr7	159138663	14482567	0.091	1.0911

chr8	146364022	7330757	0.0501	0.5885
chr9	141213431	8479572	0.06	0.4614
chr10	135534747	19687720	0.1453	1.0762
chr11	135006516	7310131	0.0541	0.3451
chr12	133851895	2338131	0.0175	0.1893
chr13	115169878	6197647	0.0538	0.2971
chr14	107349540	1138704	0.0106	0.1882
chr15	102531392	3237982	0.0316	0.2284
chr16	90354753	9216963	0.102	0.4963
chr17	81195210	1083030	0.0133	0.1727
chr18	78077248	1786311	0.0229	0.7004
chr19	59128983	1458037	0.0247	1.0311
chr20	63025520	4692476	0.0745	0.3662
chr21	48129895	802492	0.0167	0.2688
chr22	51304566	2973687	0.058	0.3044
chrMT	16571	118356	7.1424	4.6298
chrX	155270560	21721755	0.1399	0.5327
chrY	59373566	629289	0.0106	0.2611

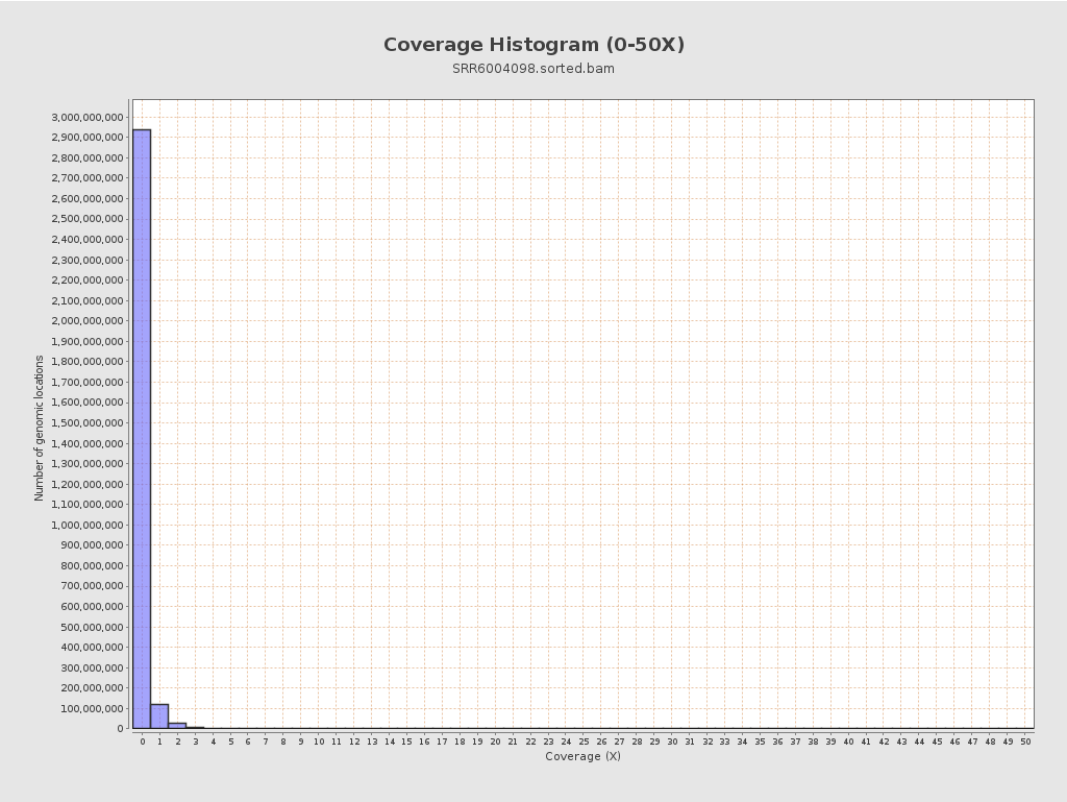
3. Results : Coverage across reference



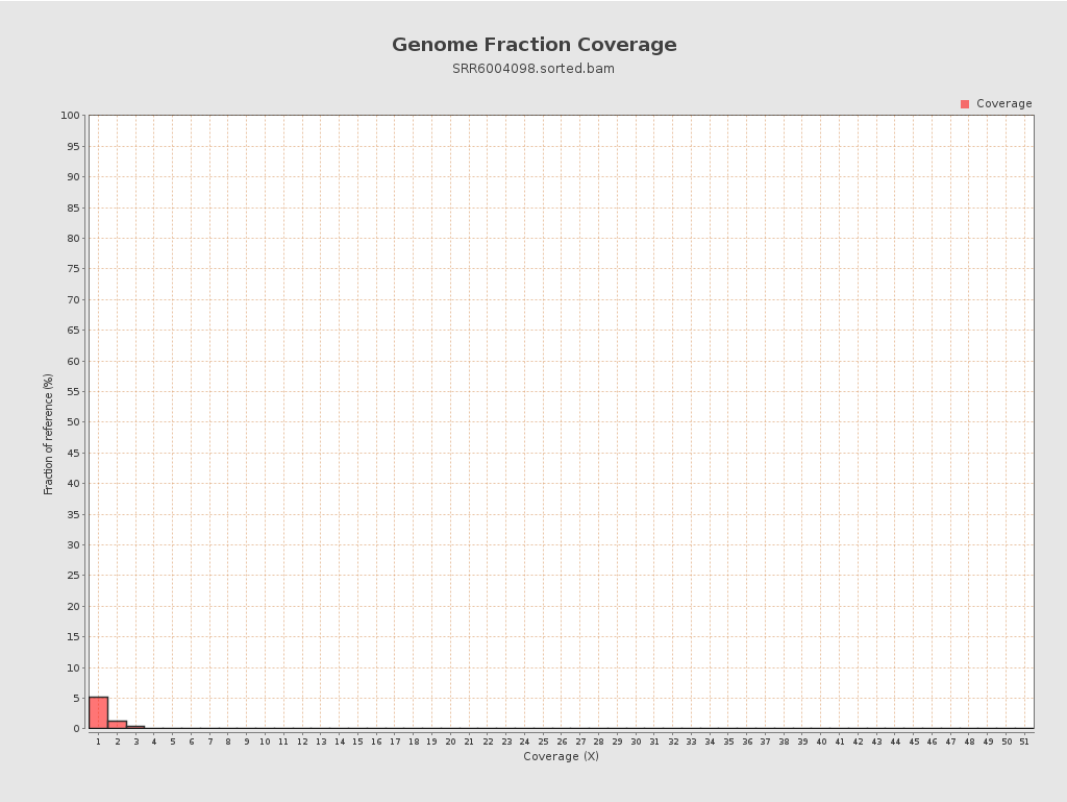
4. Results : Coverage Histogram



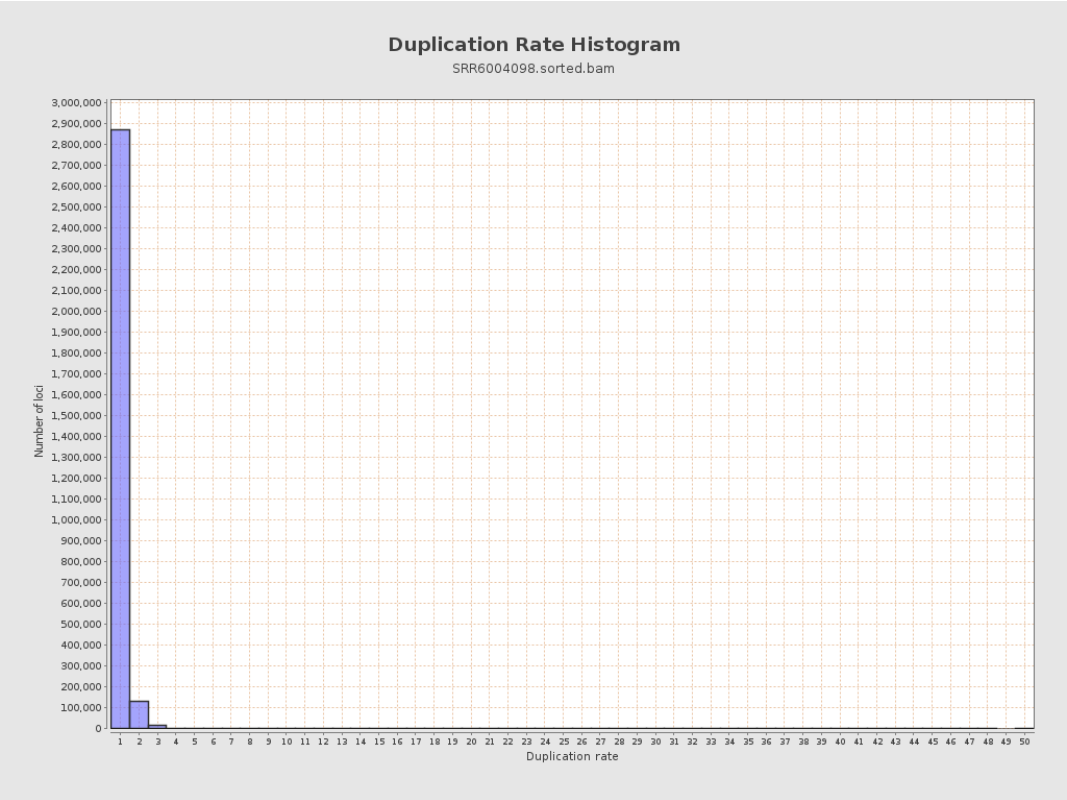
5. Results : Coverage Histogram (0-50X)



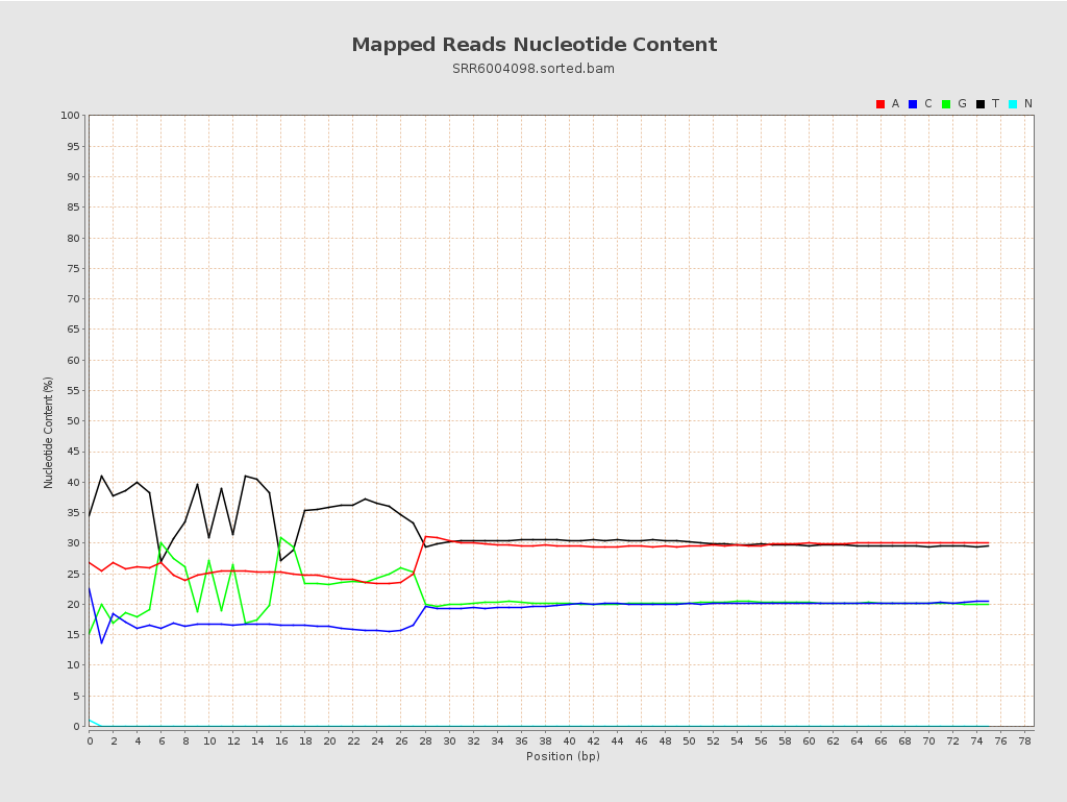
6. Results : Genome Fraction Coverage



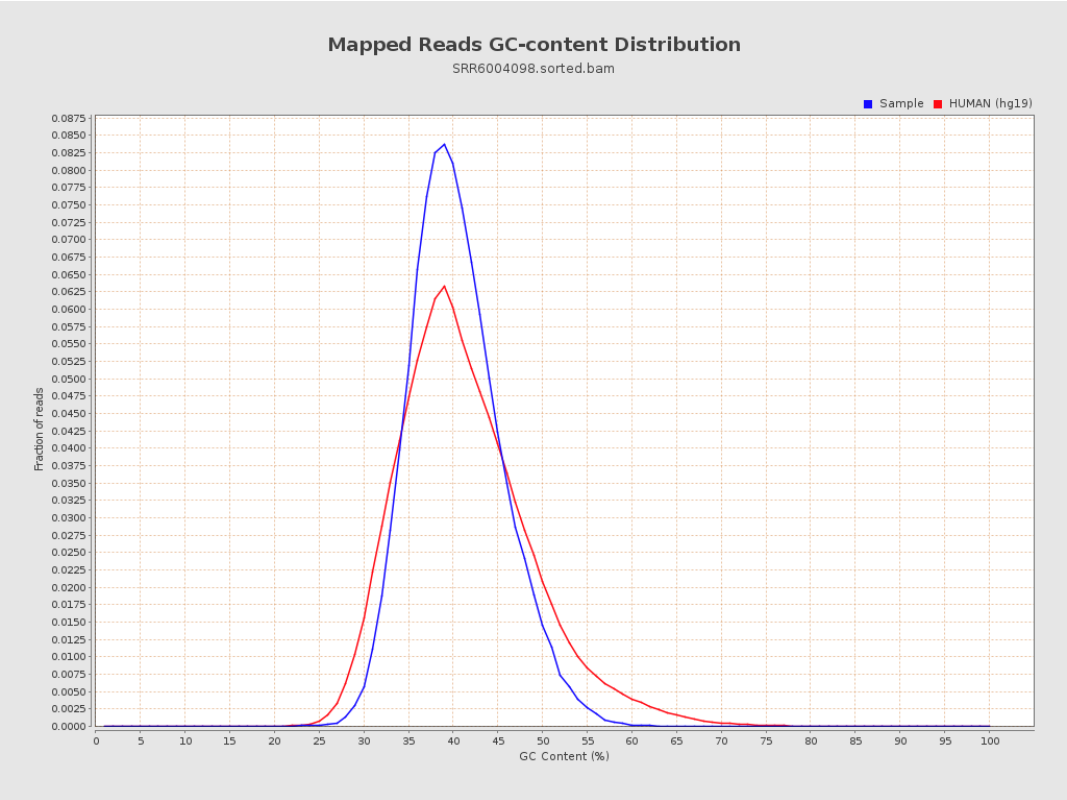
7. Results : Duplication Rate Histogram



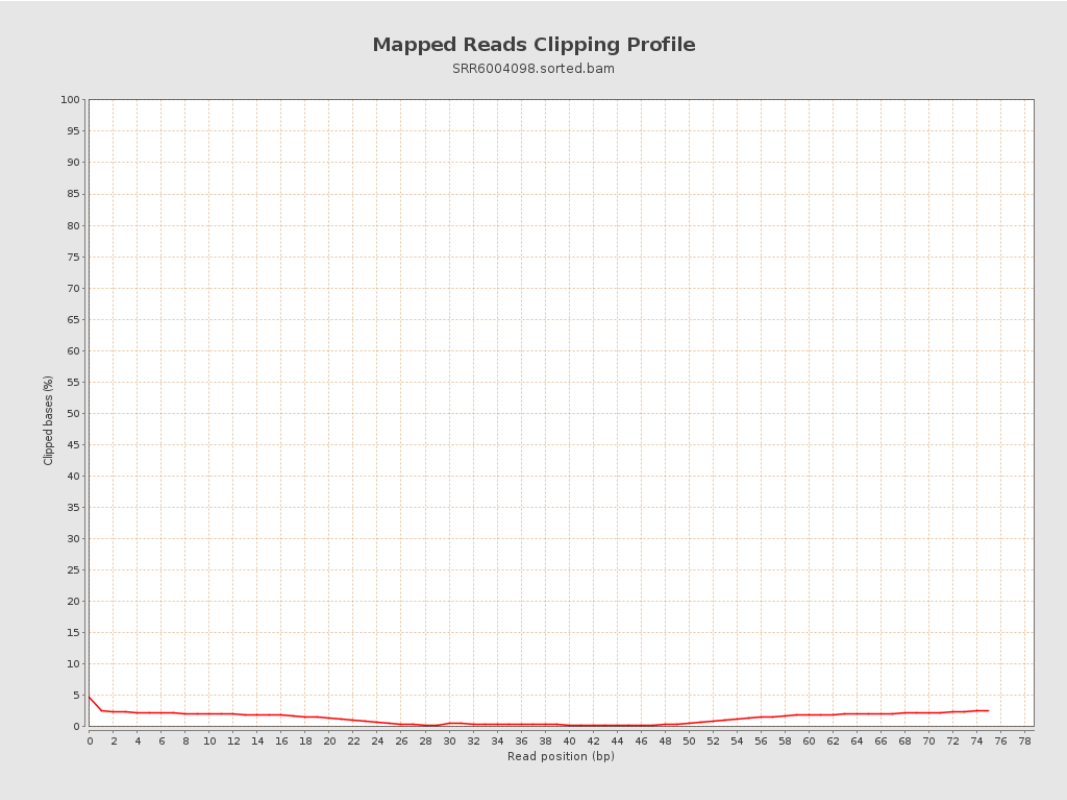
8. Results : Mapped Reads Nucleotide Content



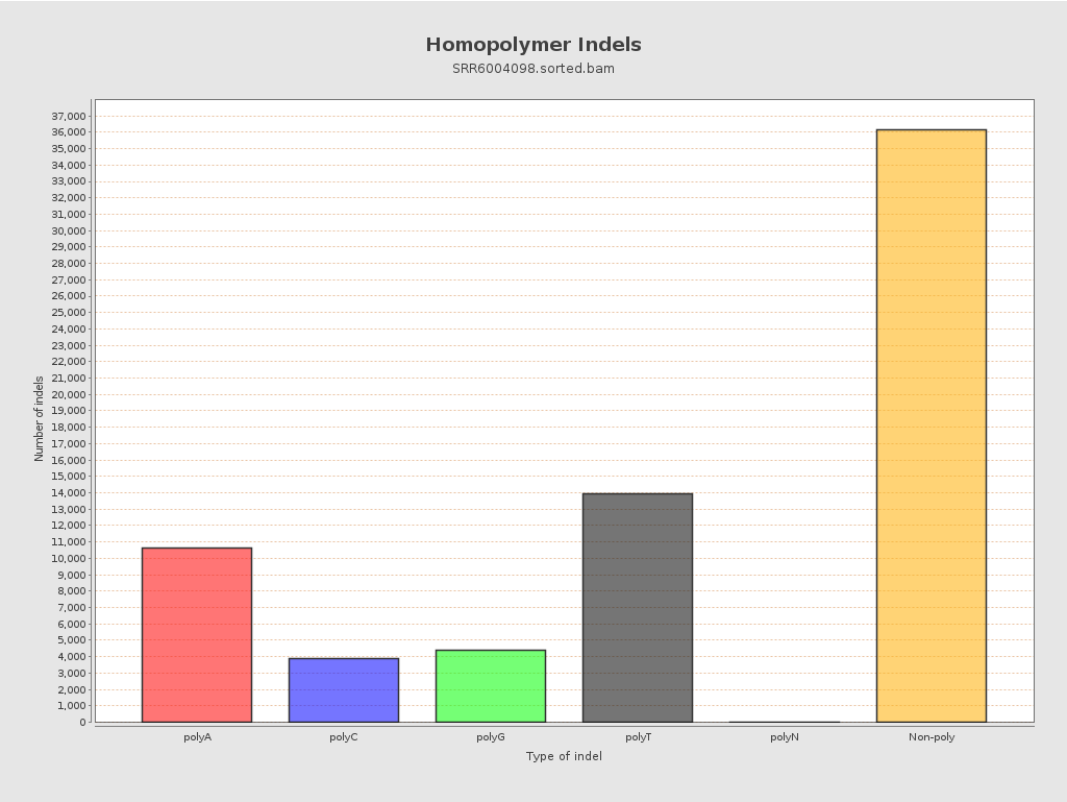
9. Results : Mapped Reads GC-content Distribution



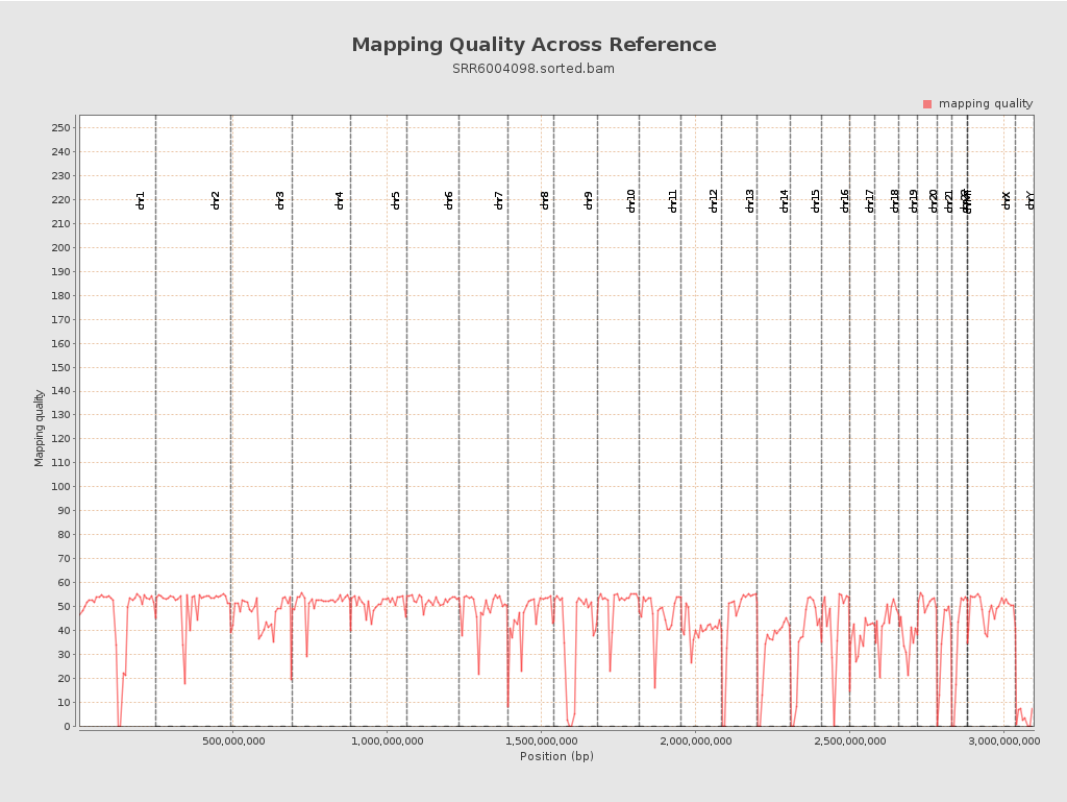
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram