Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:06:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004020.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_SRR6004020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:06:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,637,065
Mapped reads	2,141,772 / 81.22%
Unmapped reads	495,293 / 18.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,298 / 1.22%
Read min/max/mean length	30 / 76 / 76.43
Duplicated reads (estimated)	213,450 / 8.09%
Duplication rate	7.74%
Clipped reads	1,136,205 / 43.09%

2.2. ACGT Content

Number/percentage of A's	39,163,716 / 28.13%
Number/percentage of C's	25,737,304 / 18.49%
Number/percentage of T's	43,872,008 / 31.51%
Number/percentage of G's	30,395,616 / 21.83%
Number/percentage of N's	45,898 / 0.03%
GC Percentage	40.32%

2.3. Coverage

Mean	0.045

Standard Deviation	0.5335

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

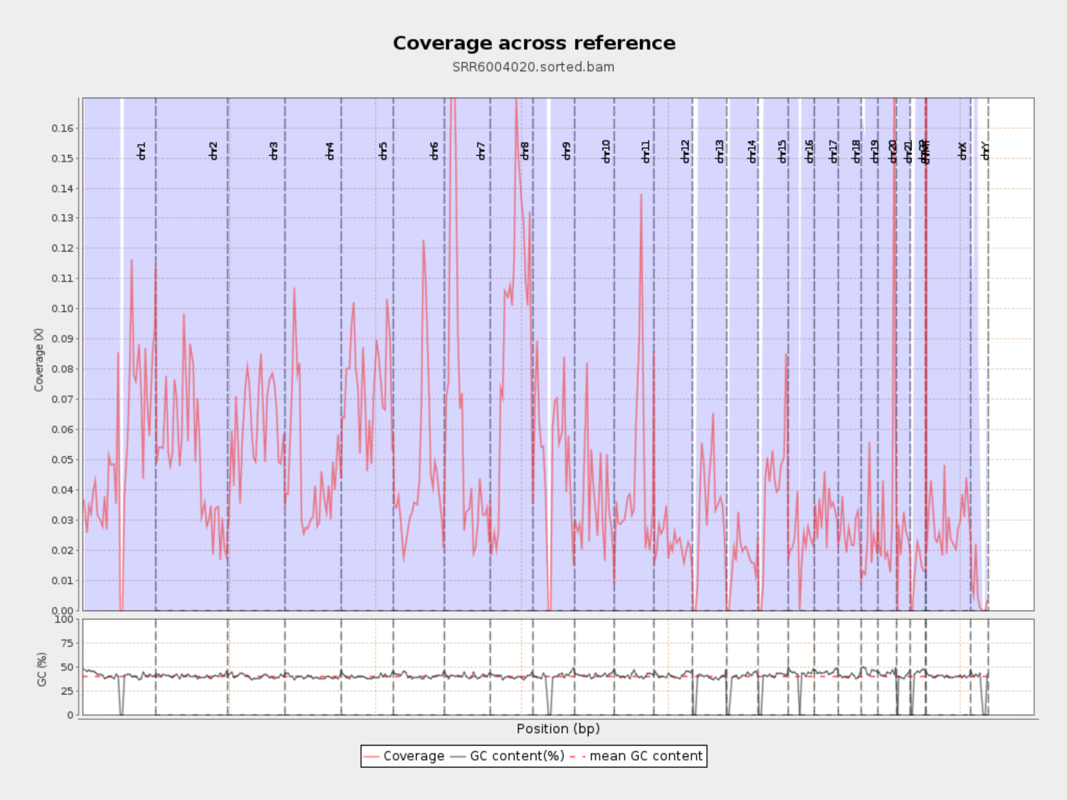
General error rate	0.87%
Mismatches	1,189,236
Insertions	10,239
Mapped reads with at least one insertion	0.47%
Deletions	43,003
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.02%

2.6. Chromosome stats

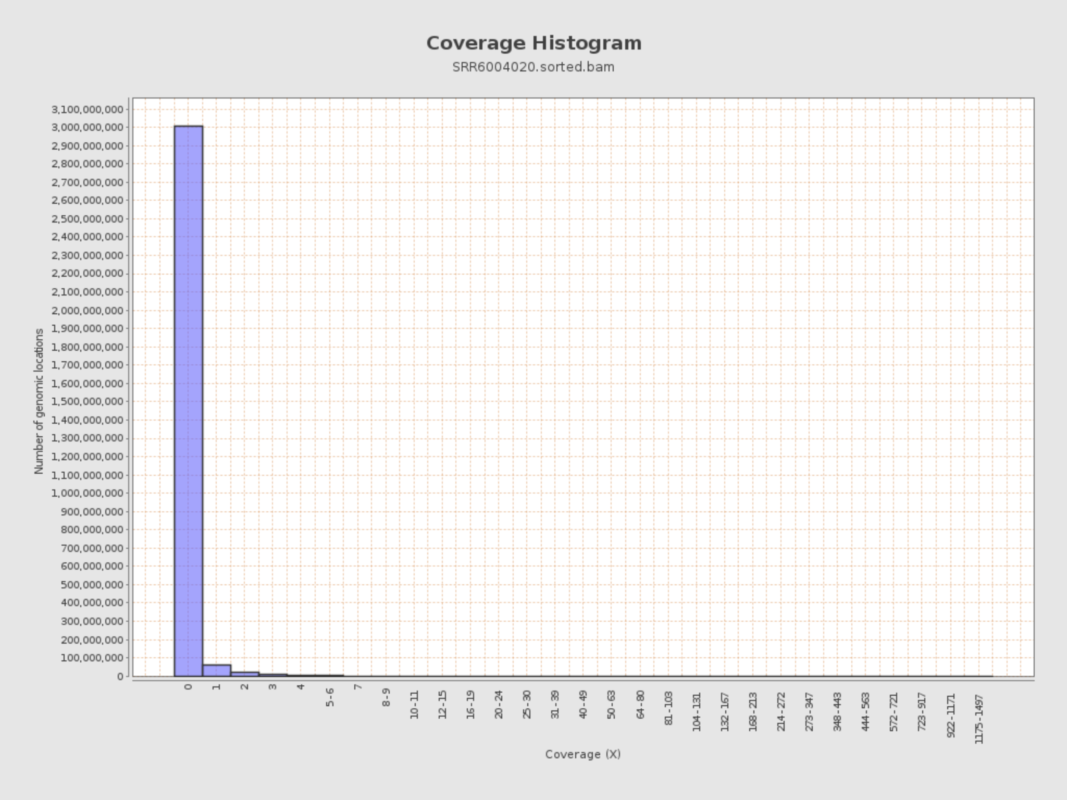
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13156044	0.0528	1.2414
chr2	243199373	12297848	0.0506	0.4816
chr3	198022430	12031790	0.0608	0.3566
chr4	191154276	8647093	0.0452	0.3371
chr5	180915260	13382429	0.074	0.4012
chr6	171115067	7776114	0.0454	0.33
chr7	159138663	9927878	0.0624	0.595

chr8	146364022	13553349	0.0926	0.7691
chr9	141213431	7212899	0.0511	0.4323
chr10	135534747	4872244	0.0359	0.435
chr11	135006516	5927469	0.0439	0.3446
chr12	133851895	2987088	0.0223	0.2374
chr13	115169878	3914412	0.034	0.2667
chr14	107349540	1776009	0.0165	0.2491
chr15	102531392	4137889	0.0404	0.294
chr16	90354753	1953058	0.0216	0.251
chr17	81195210	2697854	0.0332	0.2788
chr18	78077248	2062484	0.0264	0.5919
chr19	59128983	1368655	0.0231	0.8094
chr20	63025520	2925278	0.0464	0.3353
chr21	48129895	1103983	0.0229	0.2446
chr22	51304566	654689	0.0128	0.1555
chrMT	16571	46171	2.7863	2.7656
chrX	155270560	4547001	0.0293	0.2686
chrY	59373566	327591	0.0055	0.1813

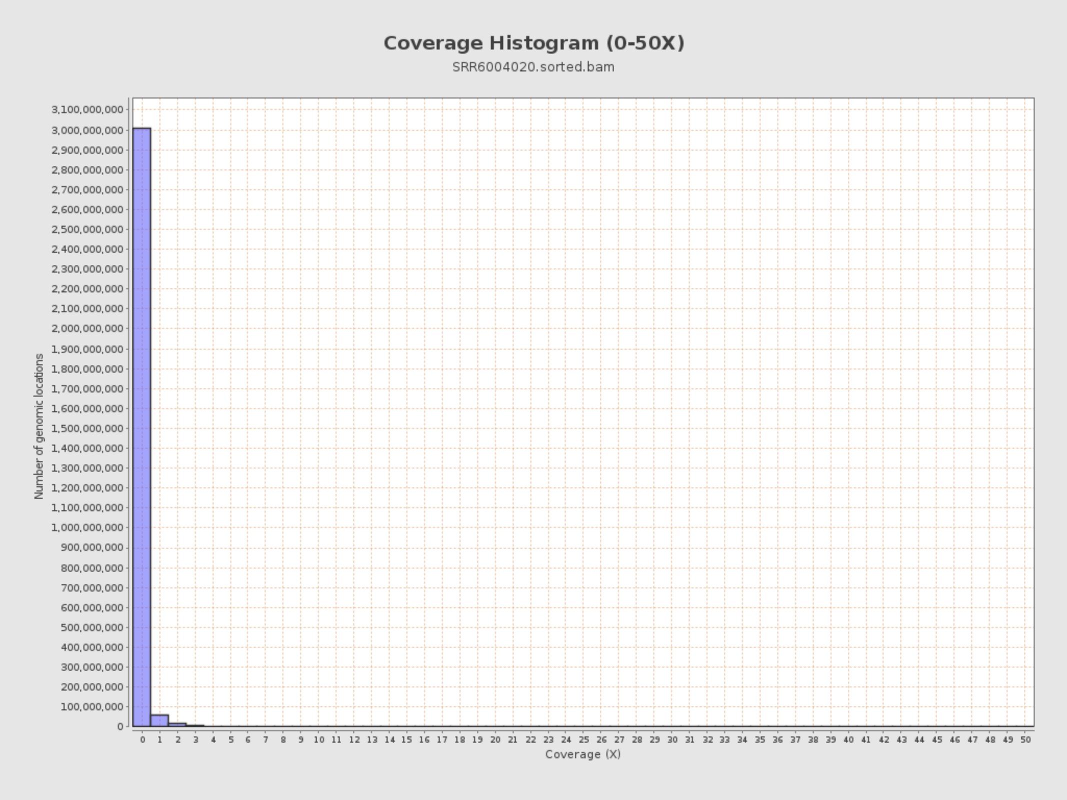
3. Results : Coverage across reference



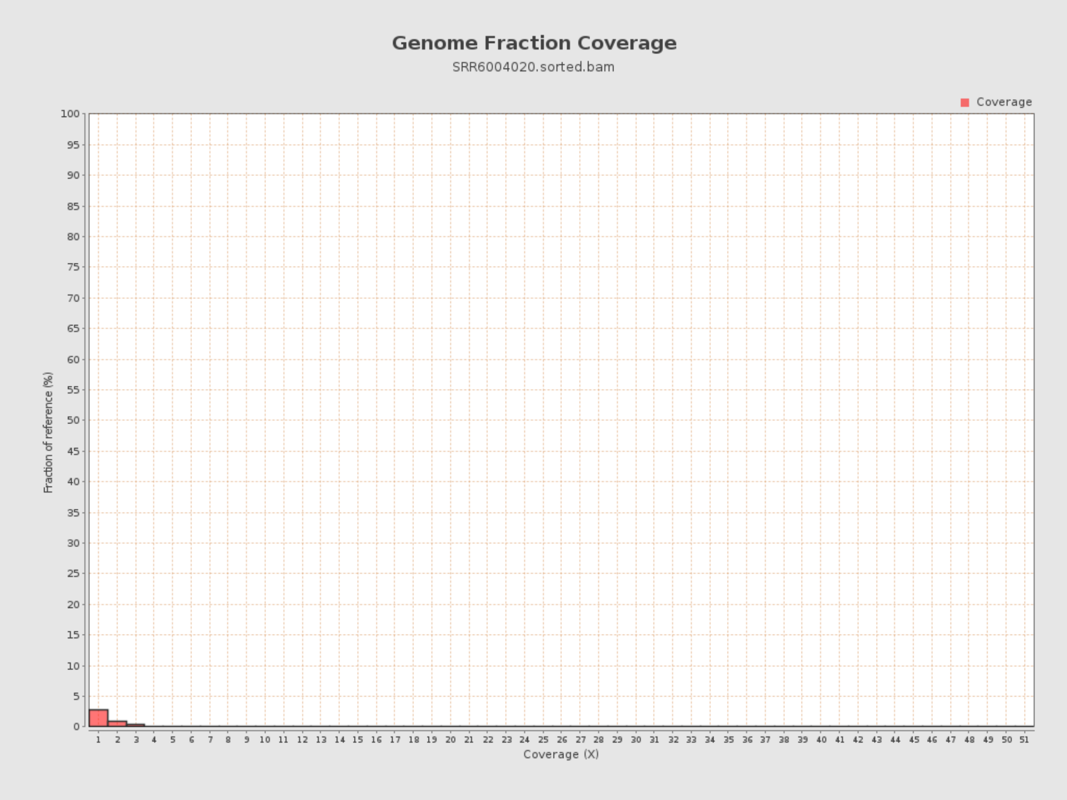
4. Results : Coverage Histogram



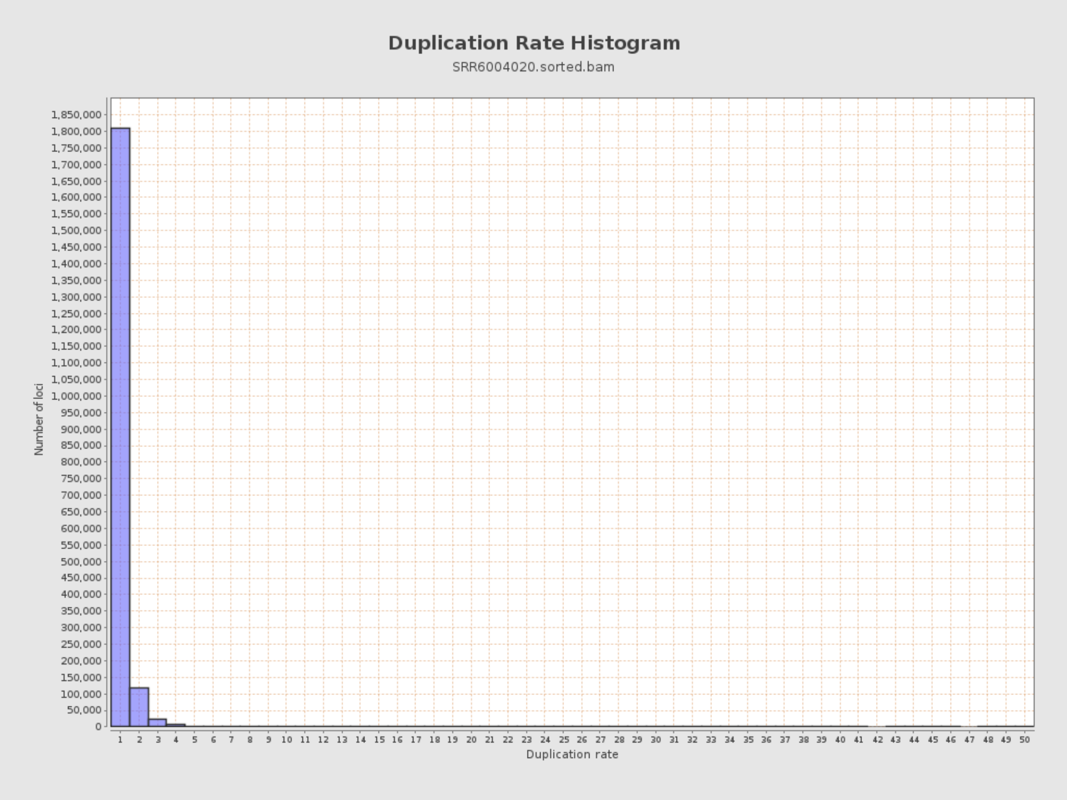
5. Results : Coverage Histogram (0-50X)



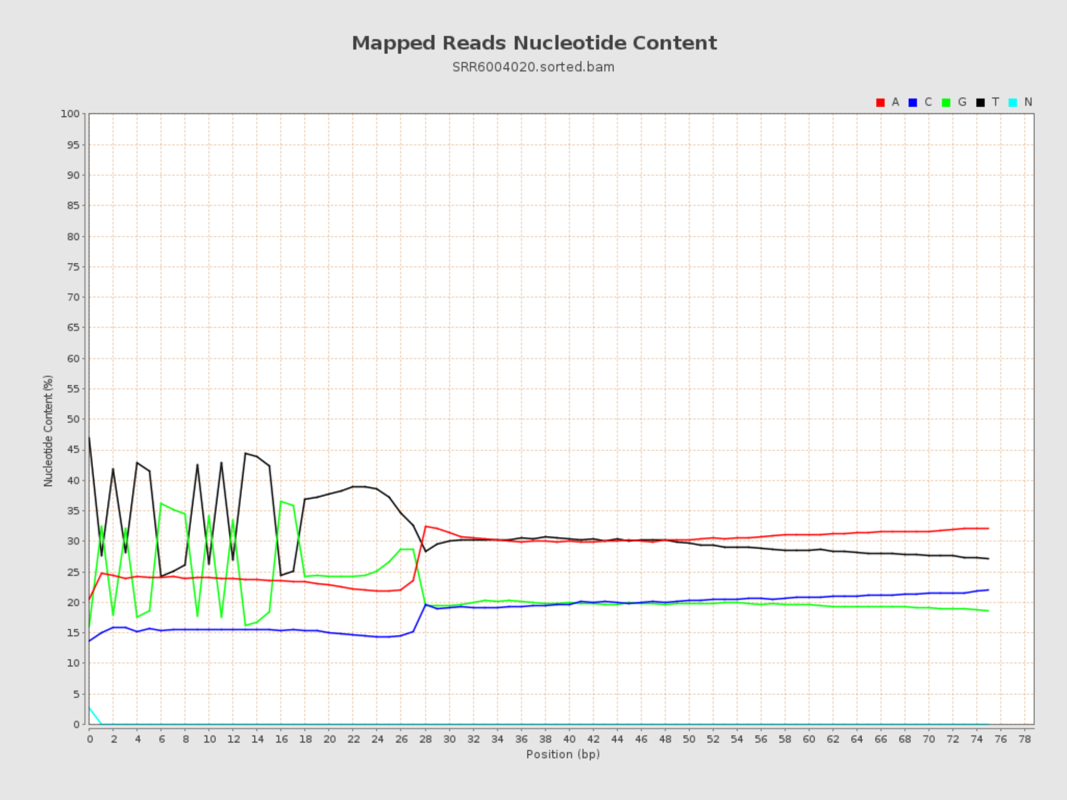
6. Results : Genome Fraction Coverage



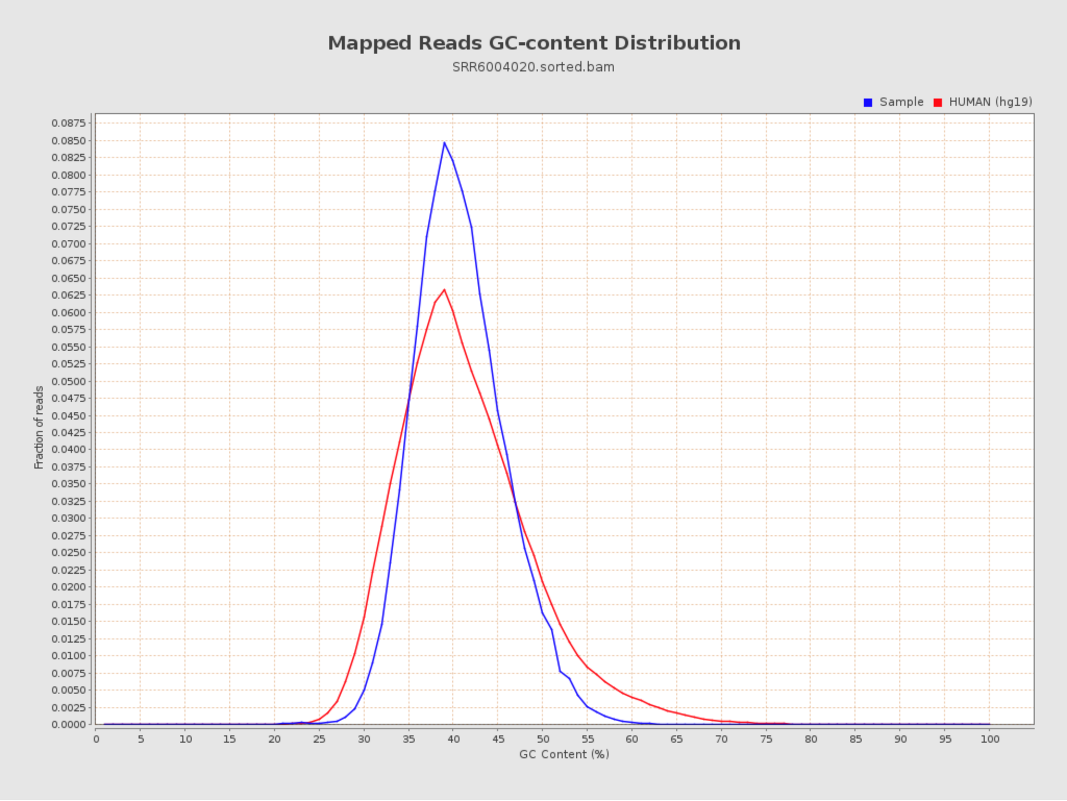
7. Results : Duplication Rate Histogram



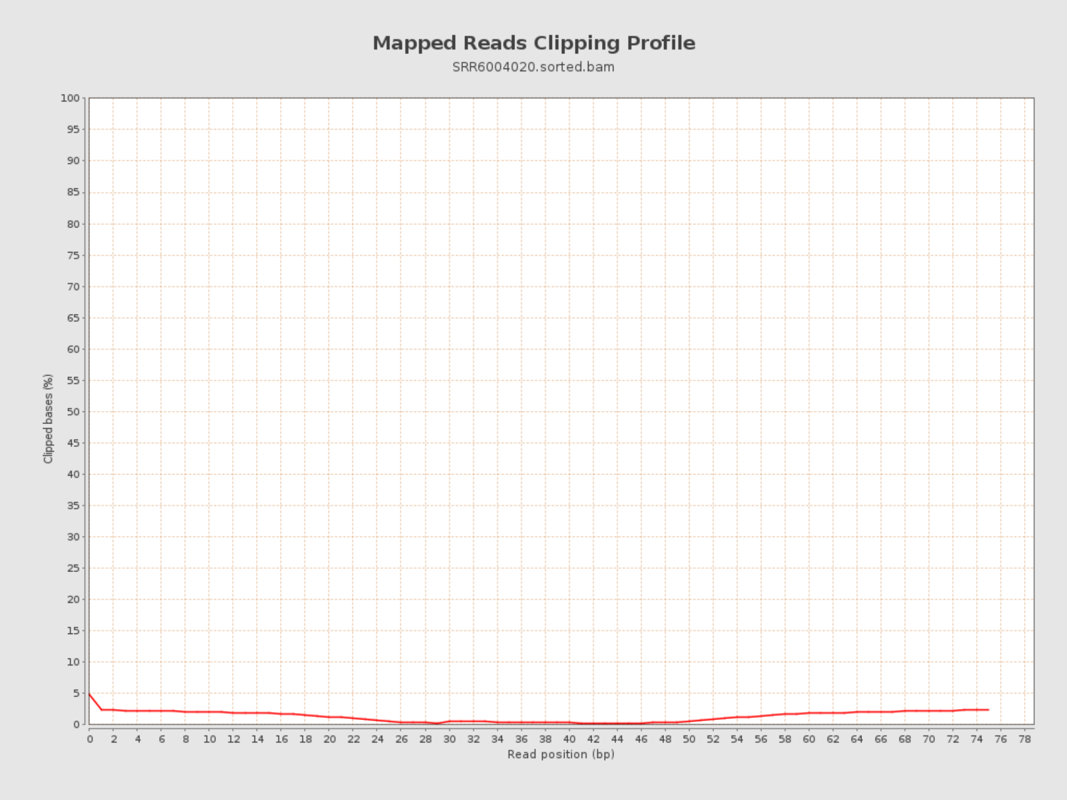
8. Results : Mapped Reads Nucleotide Content



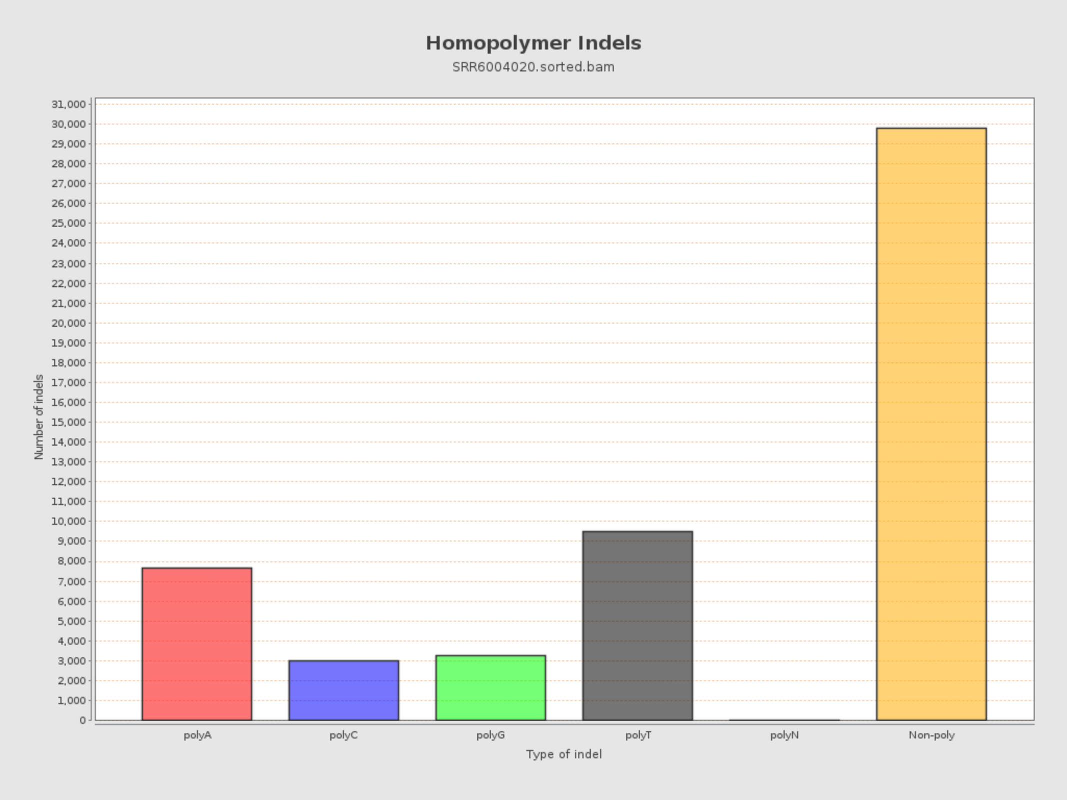
9. Results : Mapped Reads GC-content Distribution



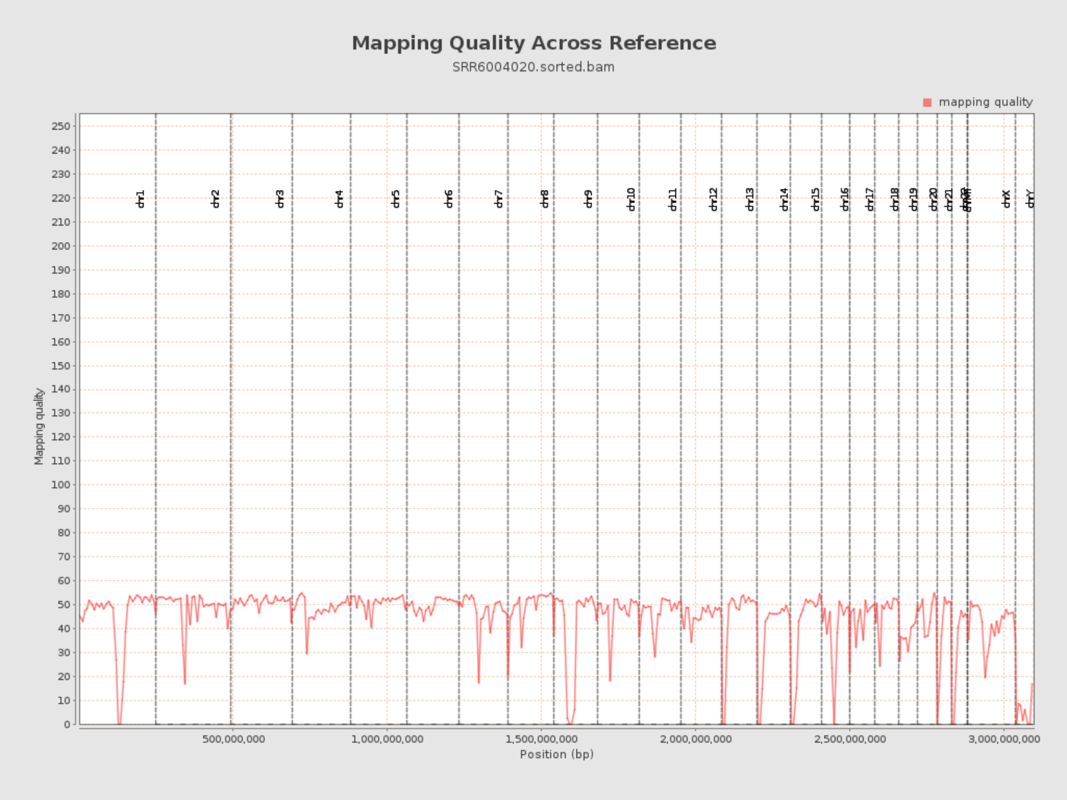
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram