Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004093.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_SRR6004093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:07:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,707,655
Mapped reads	3,395,625 / 91.58%
Unmapped reads	312,030 / 8.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,579 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	151,289 / 4.08%
Duplication rate	3.19%
Clipped reads	1,602,303 / 43.22%

2.2. ACGT Content

Number/percentage of A's	61,471,568 / 27.31%
Number/percentage of C's	42,861,316 / 19.04%
Number/percentage of T's	69,112,307 / 30.7%
Number/percentage of G's	51,608,637 / 22.93%
Number/percentage of N's	47,257 / 0.02%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0727

Standard Deviation	0.6205

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

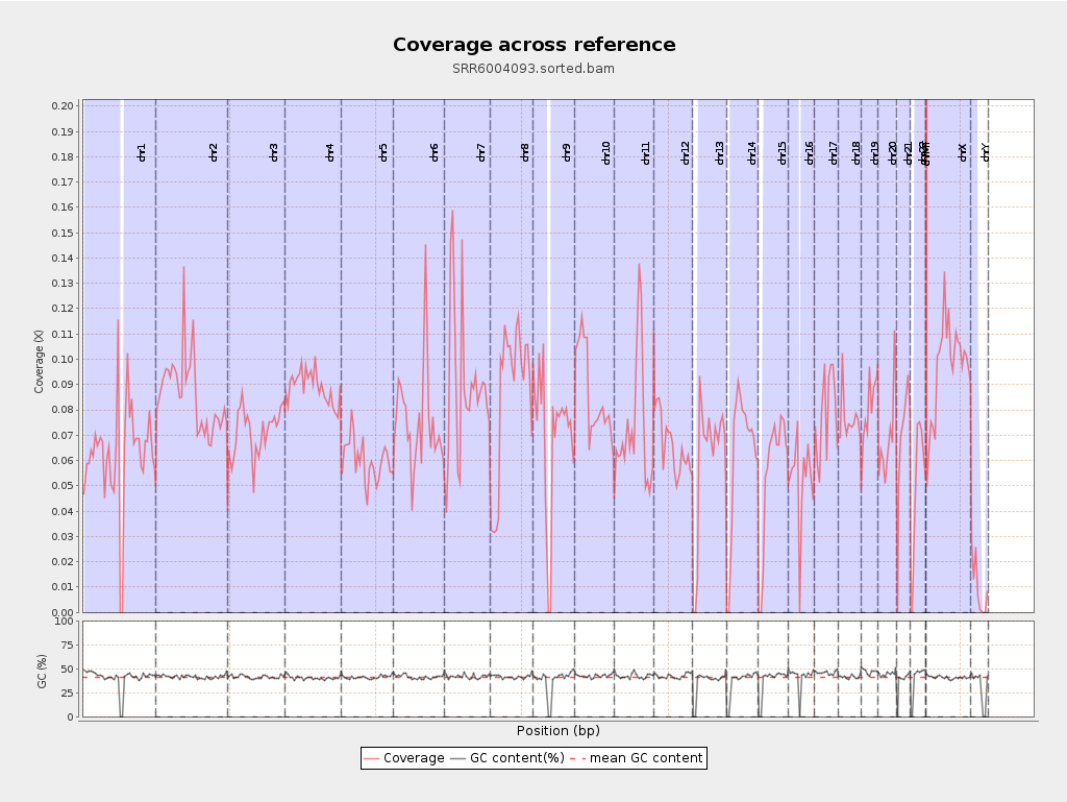
General error rate	0.85%
Mismatches	1,874,789
Insertions	17,657
Mapped reads with at least one insertion	0.52%
Deletions	64,349
Mapped reads with at least one deletion	1.87%
Homopolymer indels	46.01%

2.6. Chromosome stats

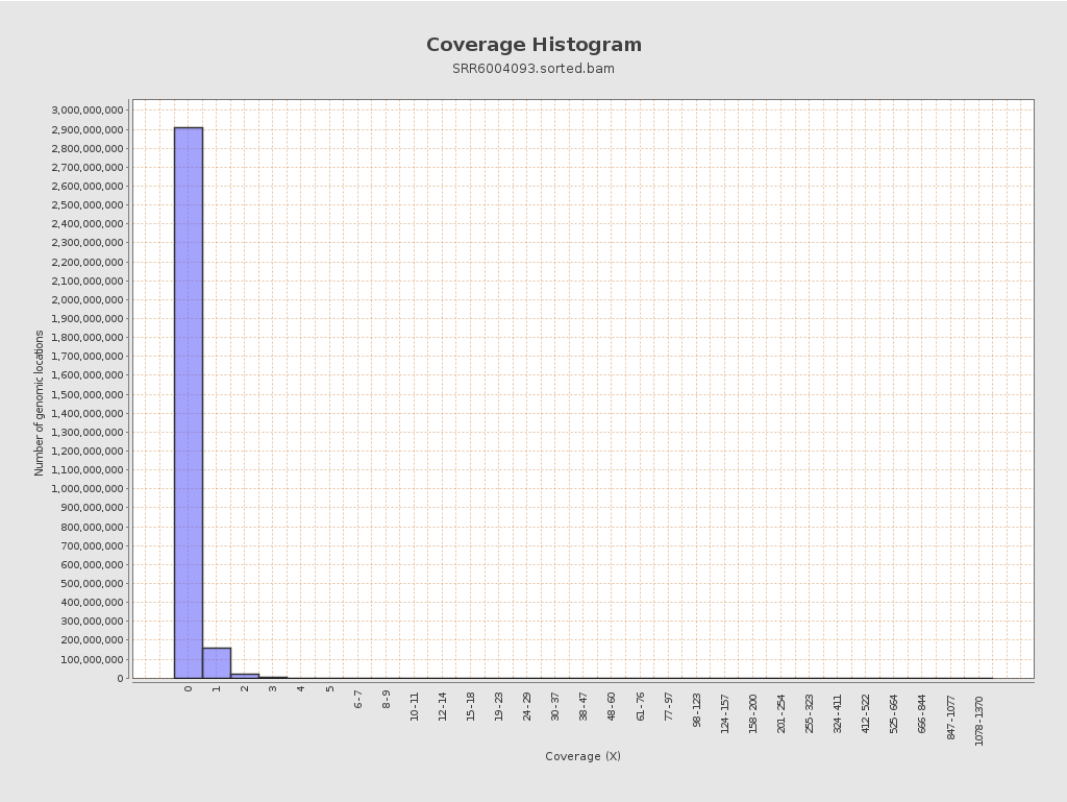
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15509732	0.0622	1.2002
chr2	243199373	20875449	0.0858	0.7649
chr3	198022430	14065038	0.071	0.31
chr4	191154276	17011101	0.089	0.3622
chr5	180915260	10845765	0.0599	0.2945
chr6	171115067	12913341	0.0755	0.3773
chr7	159138663	14056836	0.0883	0.9888

chr8	146364022	12609543	0.0862	0.6378
chr9	141213431	9841981	0.0697	0.5614
chr10	135534747	11635169	0.0858	0.528
chr11	135006516	9797160	0.0726	0.5183
chr12	133851895	8854236	0.0661	0.3219
chr13	115169878	7043647	0.0612	0.2891
chr14	107349540	6837344	0.0637	0.3605
chr15	102531392	5510135	0.0537	0.2808
chr16	90354753	4654937	0.0515	0.3513
chr17	81195210	6410017	0.0789	0.371
chr18	78077248	5960659	0.0763	1.2257
chr19	59128983	4780452	0.0808	0.798
chr20	63025520	4410715	0.07	0.3293
chr21	48129895	3305213	0.0687	0.34
chr22	51304566	2547548	0.0497	0.2577
chrMT	16571	171616	10.3564	6.4019
chrX	155270560	14987616	0.0965	0.4326
chrY	59373566	570998	0.0096	0.1762

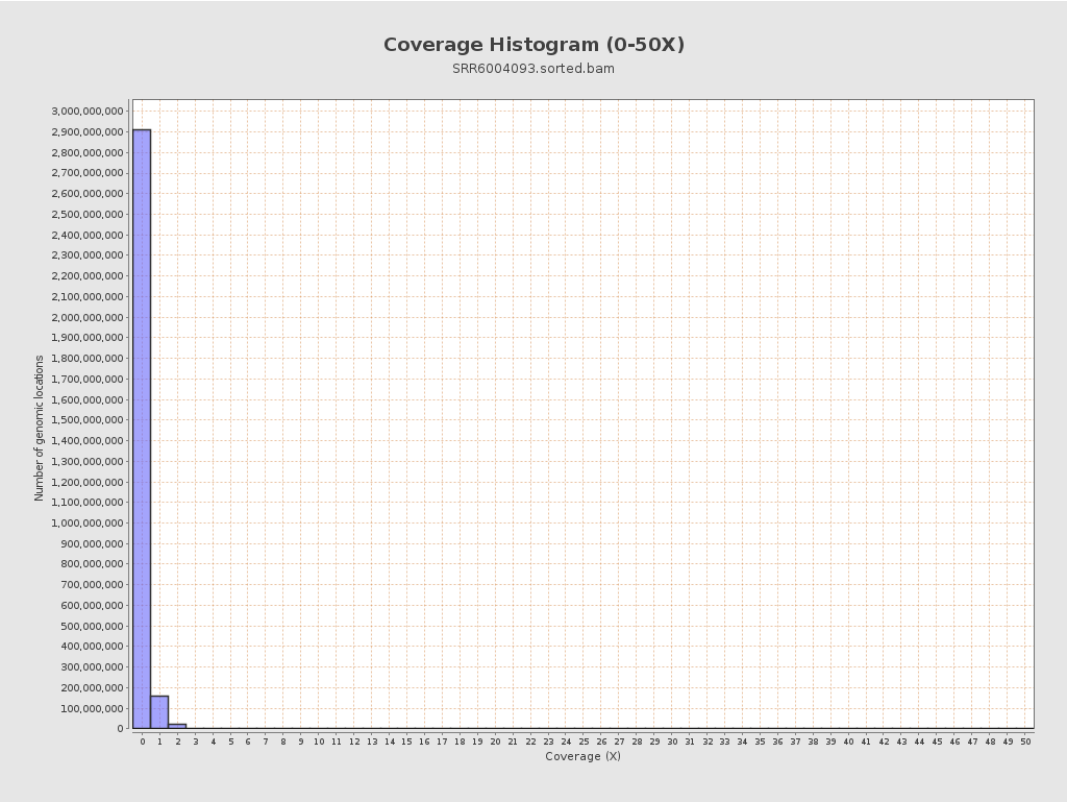
3. Results : Coverage across reference



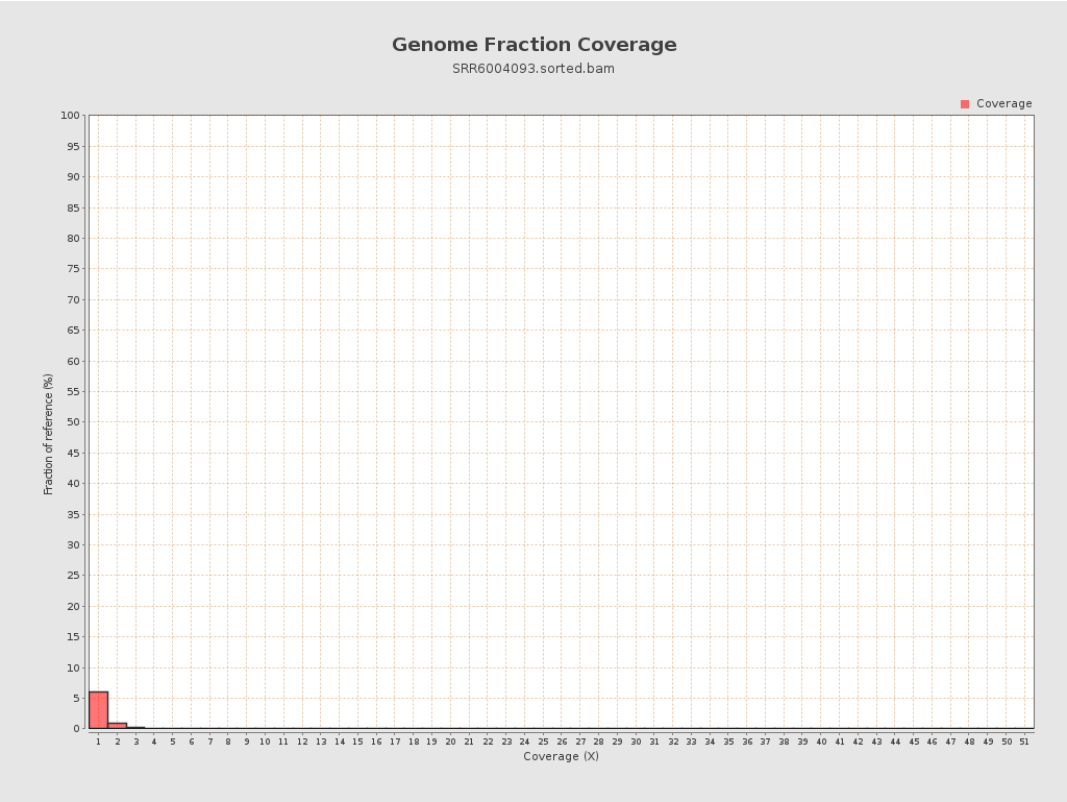
4. Results : Coverage Histogram



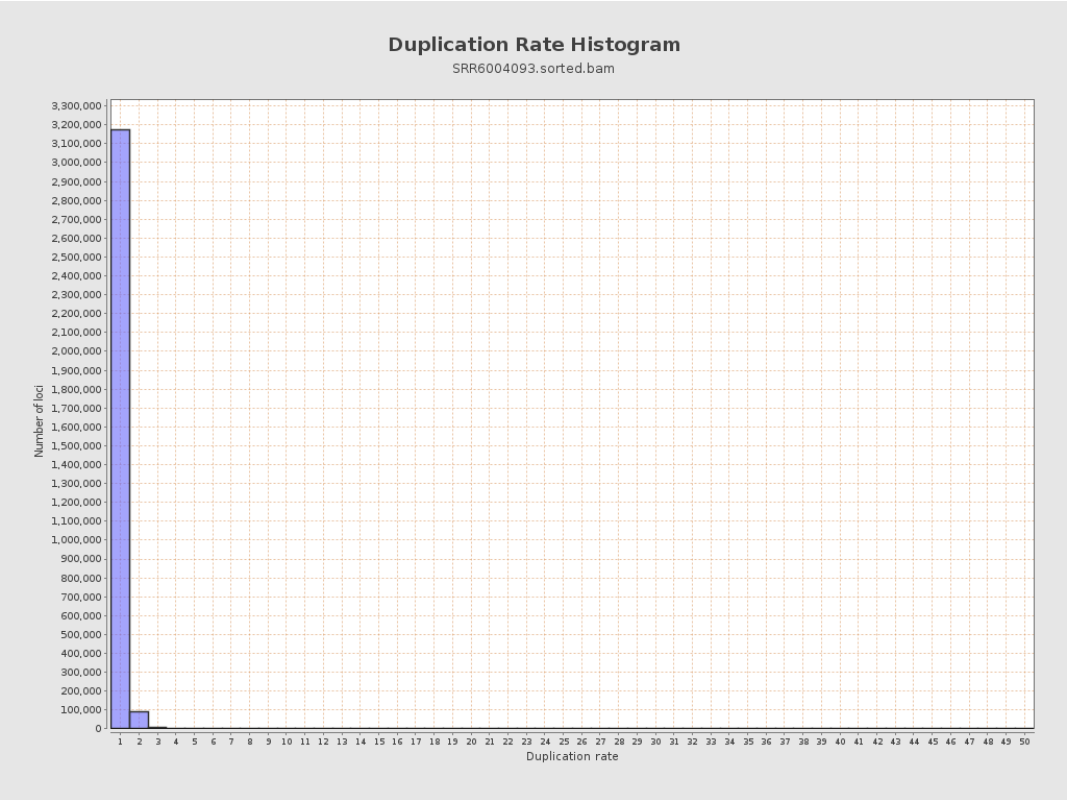
5. Results : Coverage Histogram (0-50X)



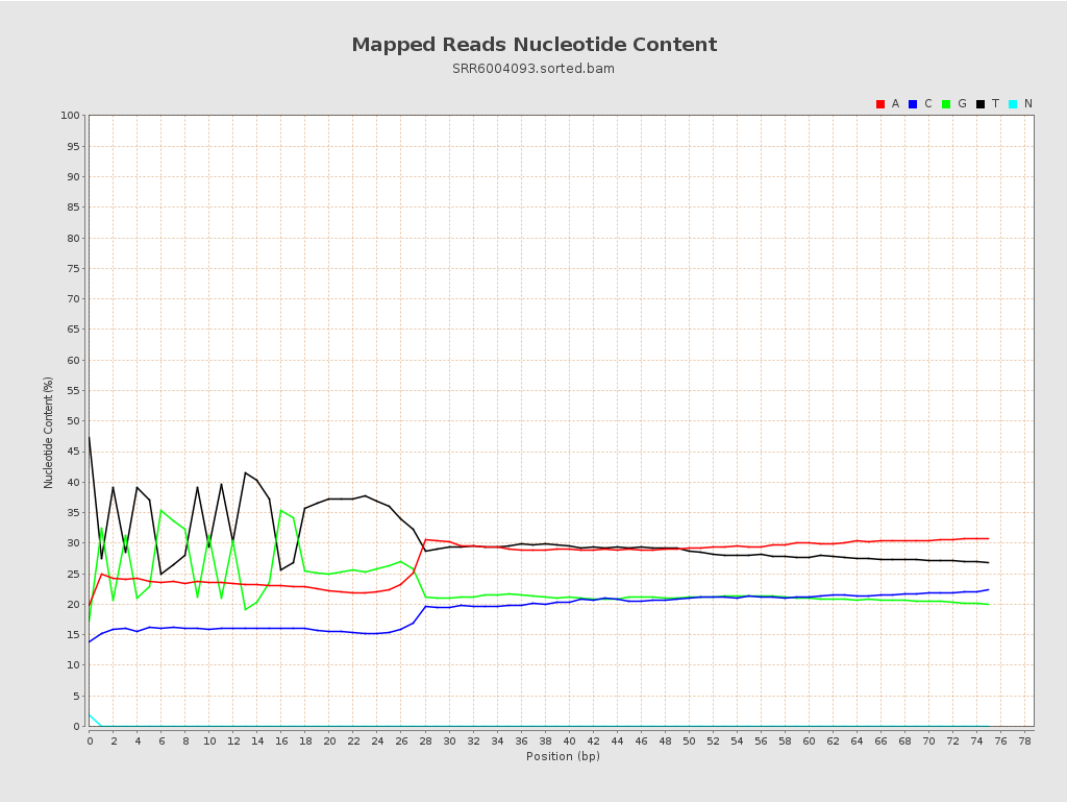
6. Results : Genome Fraction Coverage



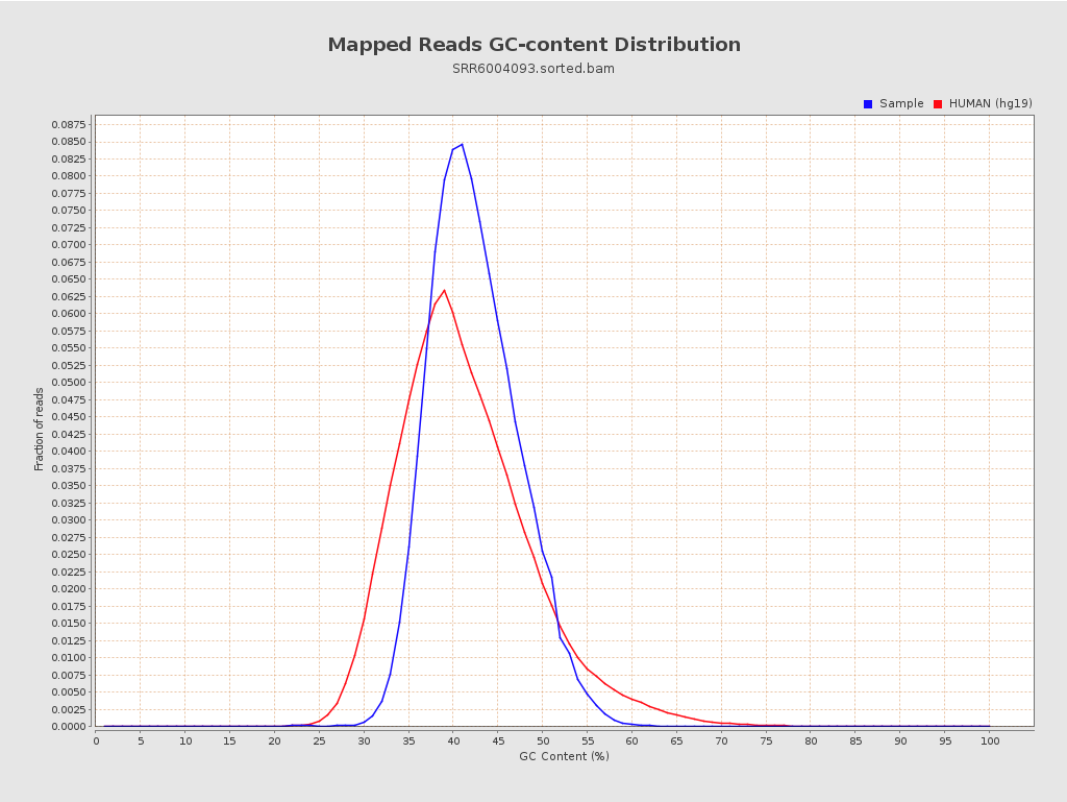
7. Results : Duplication Rate Histogram



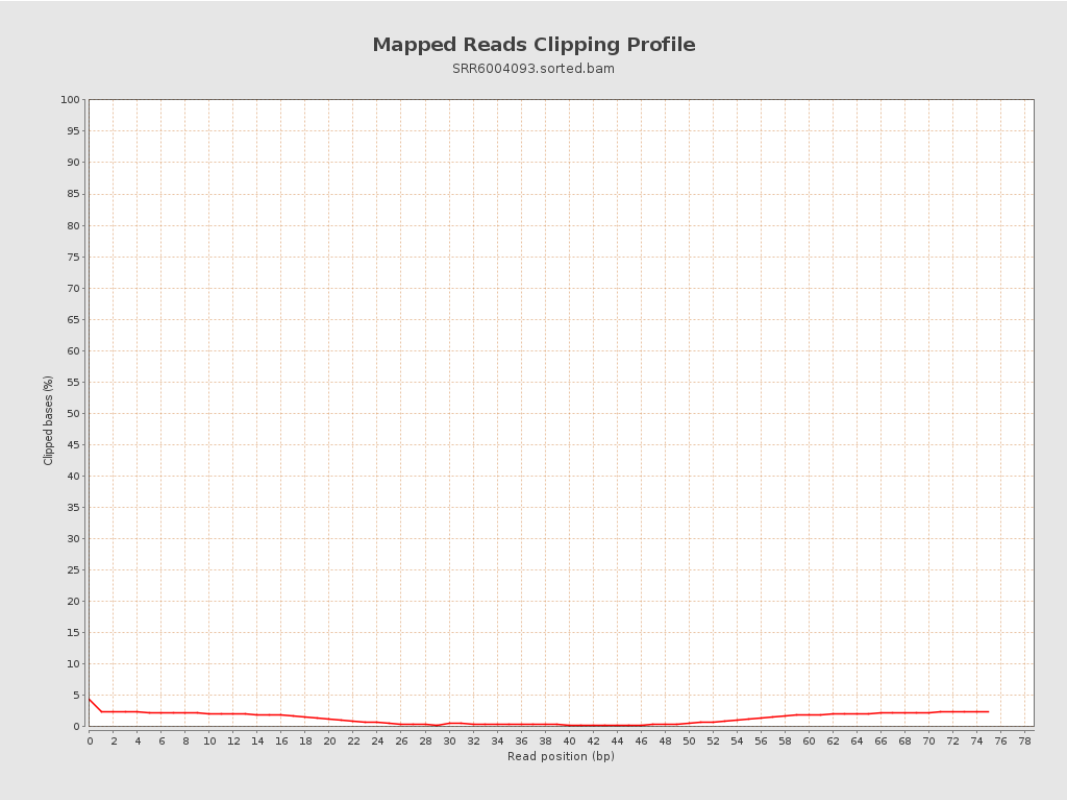
8. Results : Mapped Reads Nucleotide Content



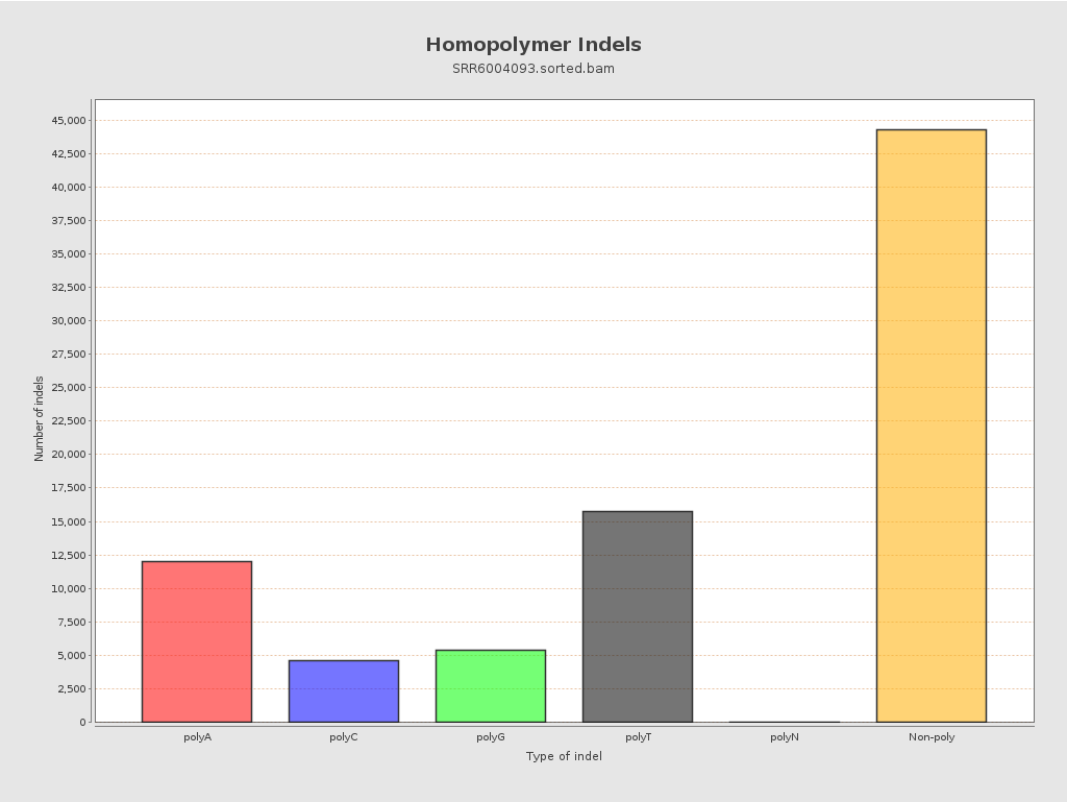
9. Results : Mapped Reads GC-content Distribution



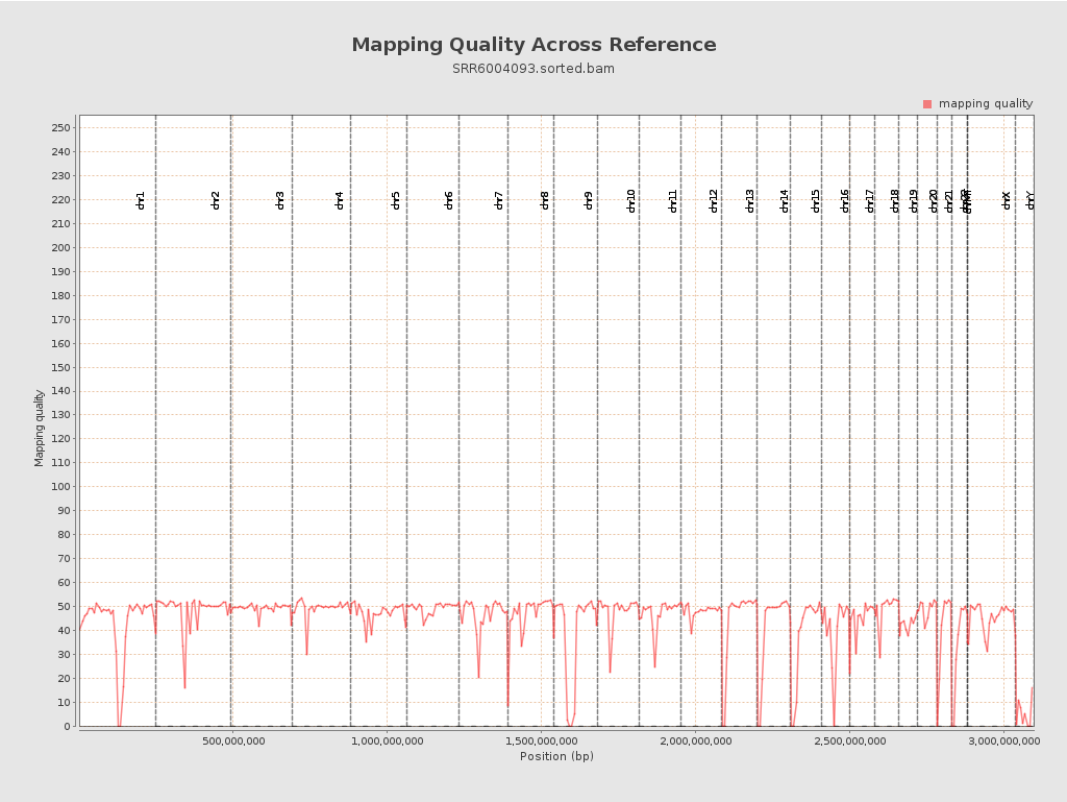
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram