Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:04:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524592.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_SRR10524592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:04:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,660,432
Mapped reads	1,541,814 / 92.86%
Unmapped reads	118,618 / 7.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,163 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	66,020 / 3.98%
Duplication rate	3.3%
Clipped reads	1,539,663 / 92.73%

2.2. ACGT Content

Number/percentage of A's	23,376,890 / 25.93%
Number/percentage of C's	15,076,233 / 16.73%
Number/percentage of T's	29,023,052 / 32.2%
Number/percentage of G's	22,663,219 / 25.14%
Number/percentage of N's	603 / 0%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.2595

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

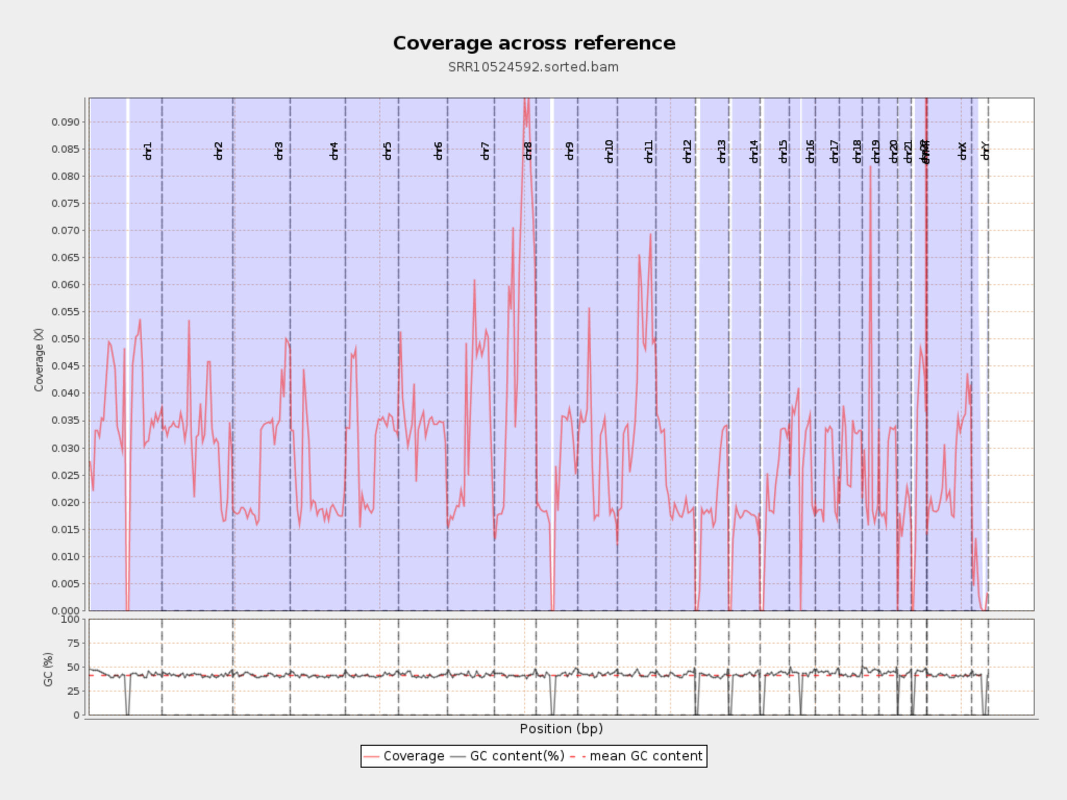
General error rate	0.48%
Mismatches	418,331
Insertions	6,238
Mapped reads with at least one insertion	0.4%
Deletions	16,845
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.42%

2.6. Chromosome stats

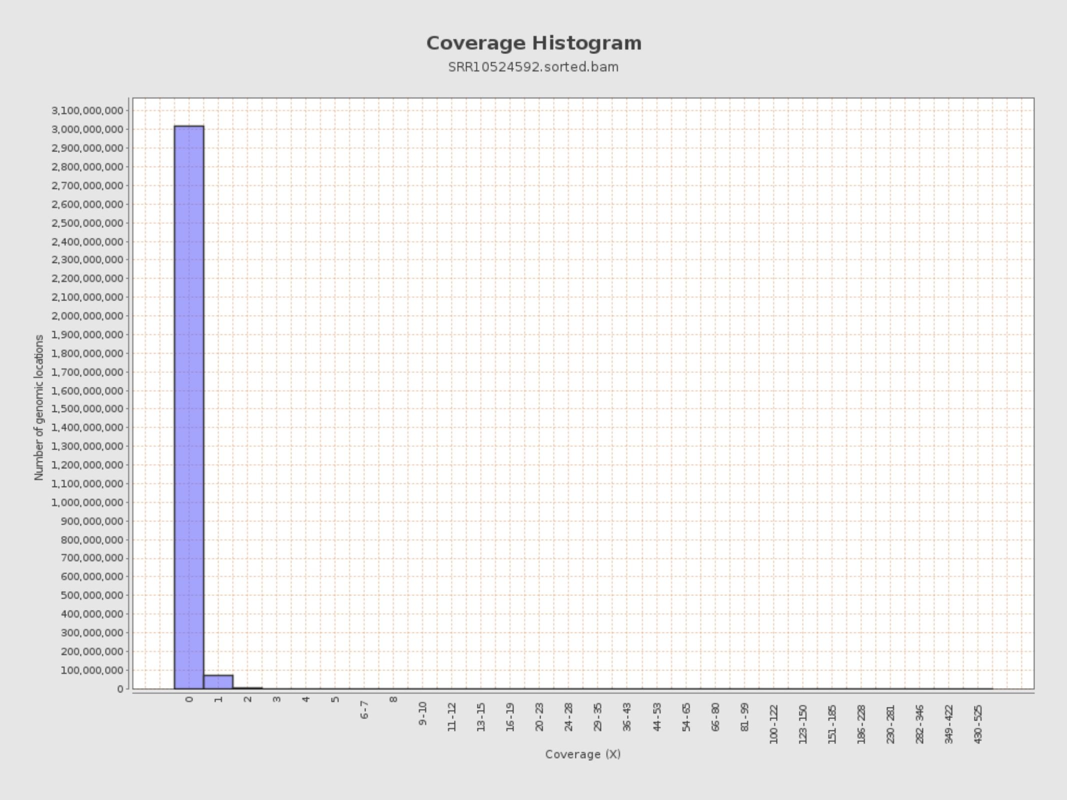
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8869819	0.0356	0.4347
chr2	243199373	7868468	0.0324	0.2989
chr3	198022430	5583141	0.0282	0.1868
chr4	191154276	4222619	0.0221	0.1874
chr5	180915260	5654064	0.0313	0.1965
chr6	171115067	5956318	0.0348	0.2219
chr7	159138663	5479445	0.0344	0.3488

chr8	146364022	7904157	0.054	0.3482
chr9	141213431	3275790	0.0232	0.2313
chr10	135534747	3850070	0.0284	0.2725
chr11	135006516	5625247	0.0417	0.2691
chr12	133851895	2986316	0.0223	0.1712
chr13	115169878	2223247	0.0193	0.1545
chr14	107349540	1616951	0.0151	0.1431
chr15	102531392	2236877	0.0218	0.1684
chr16	90354753	2609358	0.0289	0.202
chr17	81195210	1955063	0.0241	0.1767
chr18	78077248	2393157	0.0307	0.3546
chr19	59128983	1680535	0.0284	0.3115
chr20	63025520	1601682	0.0254	0.1797
chr21	48129895	791988	0.0165	0.1614
chr22	51304566	1516205	0.0296	0.1912
chrMT	16571	8566	0.5169	0.8787
chrX	155270560	4033889	0.026	0.2031
chrY	59373566	225760	0.0038	0.1078

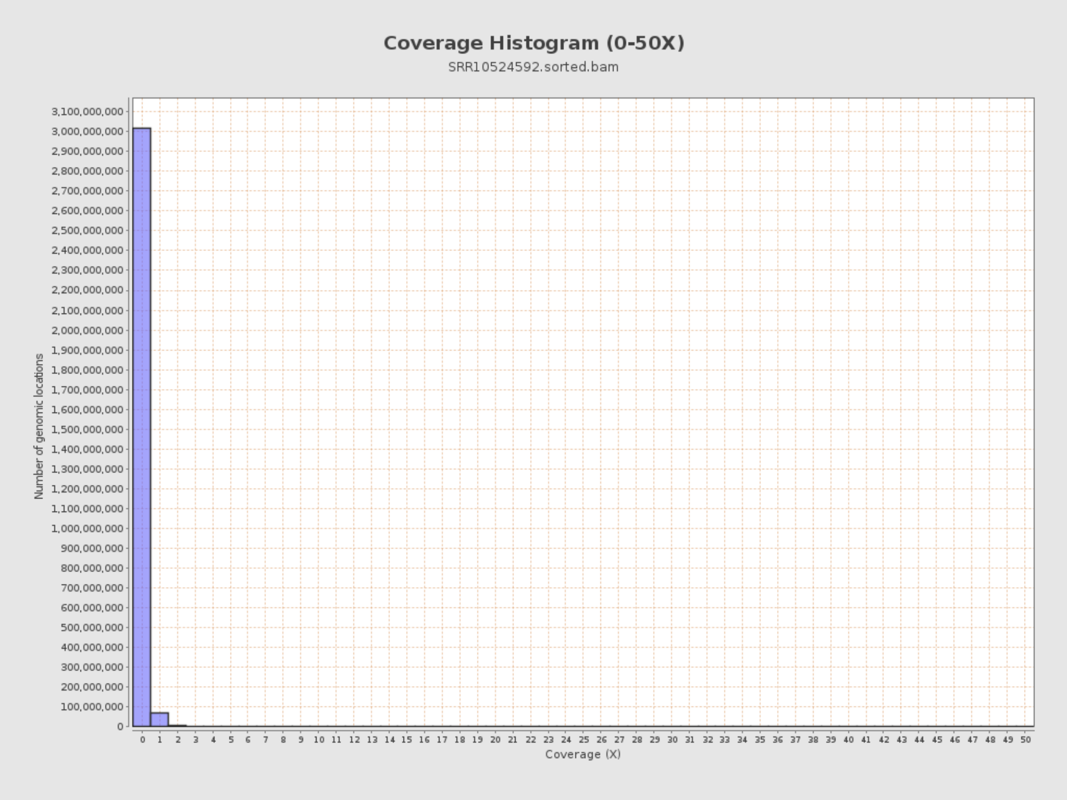
3. Results : Coverage across reference



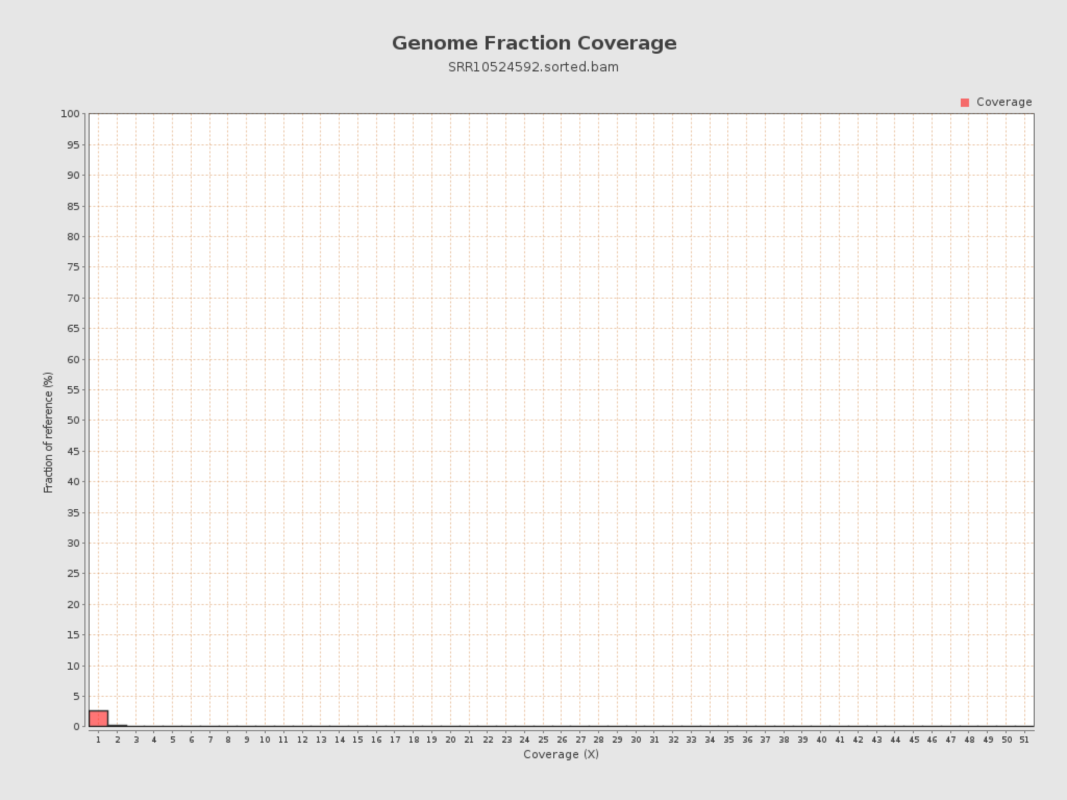
4. Results : Coverage Histogram



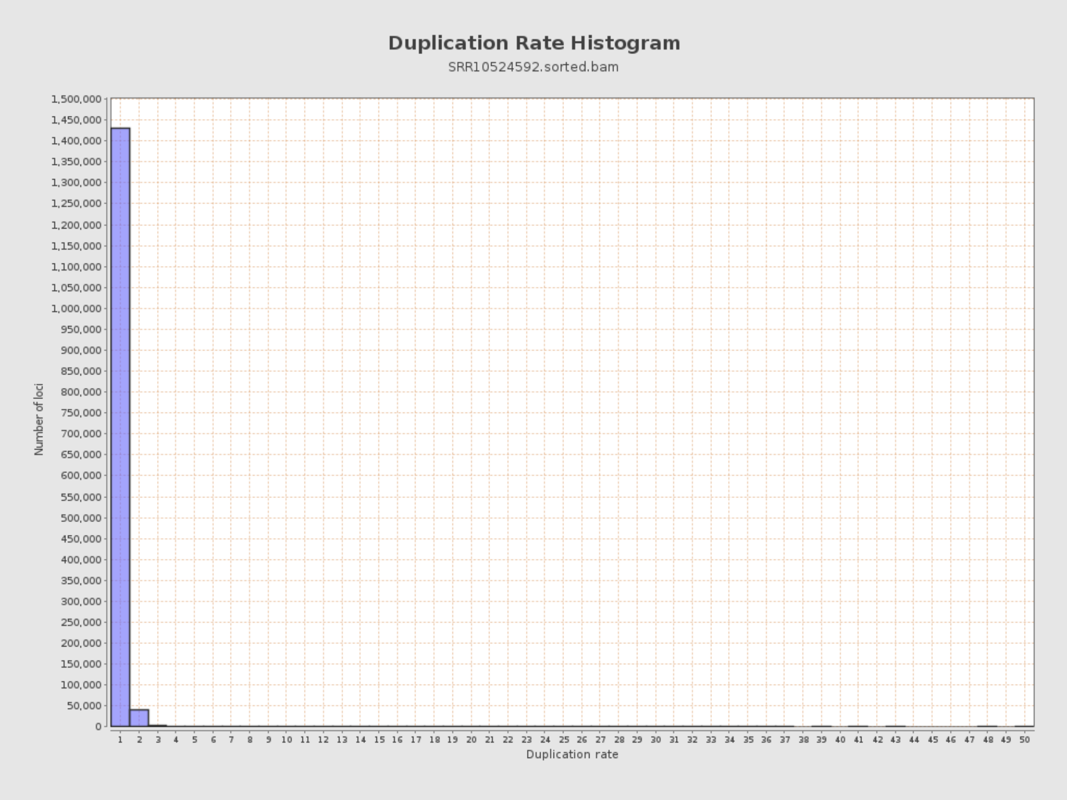
5. Results : Coverage Histogram (0-50X)



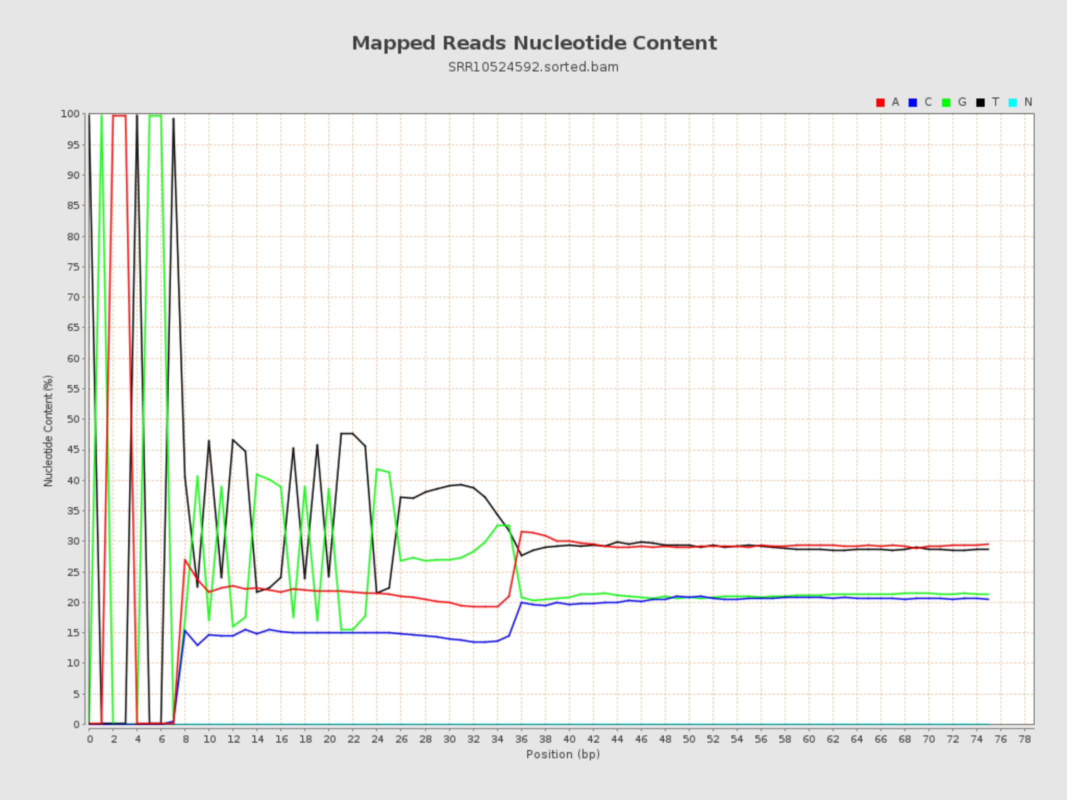
6. Results : Genome Fraction Coverage



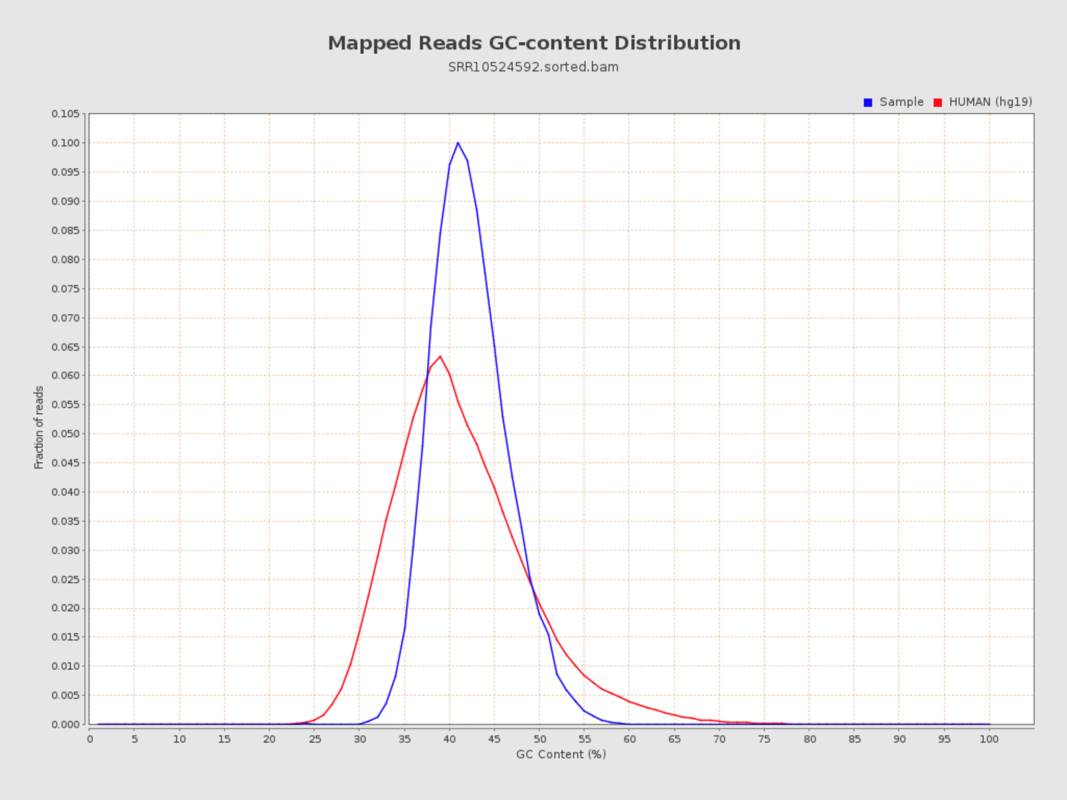
7. Results : Duplication Rate Histogram



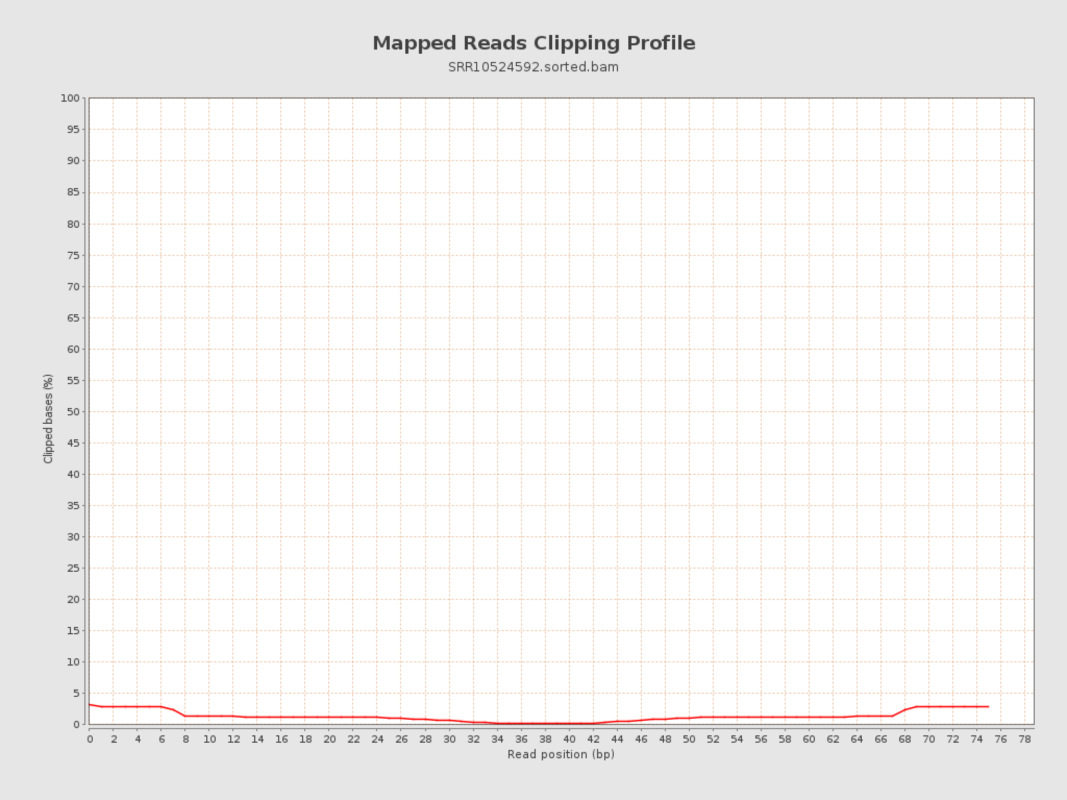
8. Results : Mapped Reads Nucleotide Content



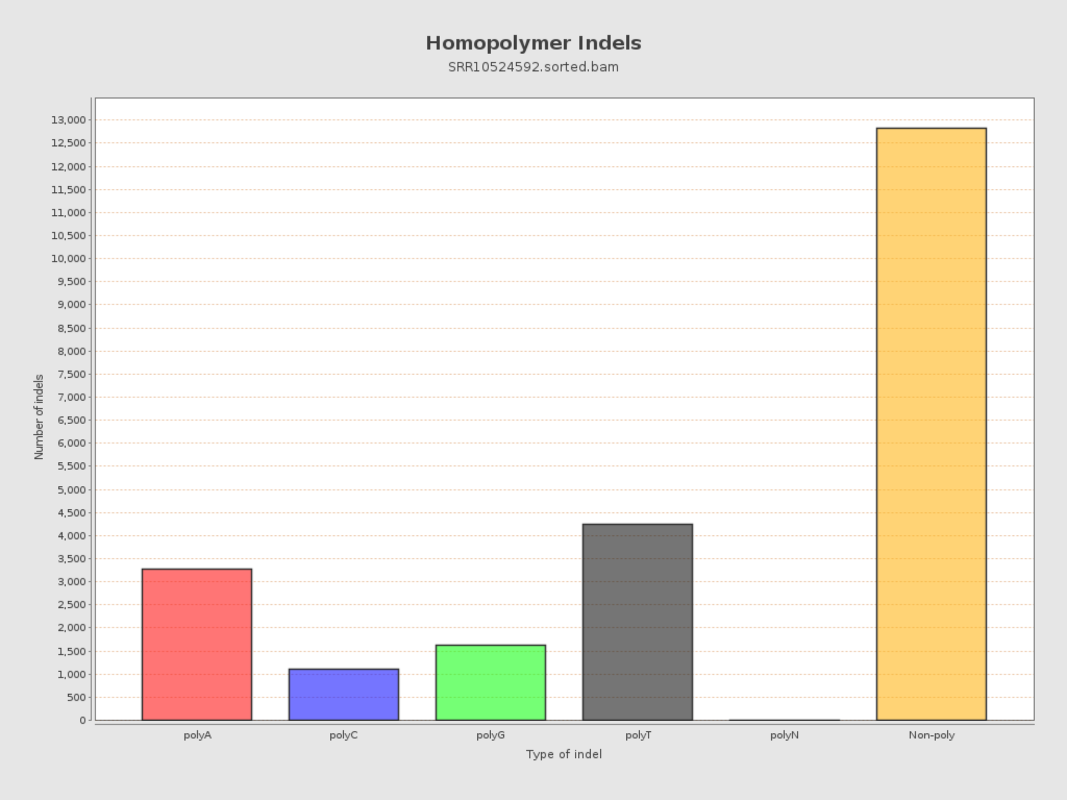
9. Results : Mapped Reads GC-content Distribution



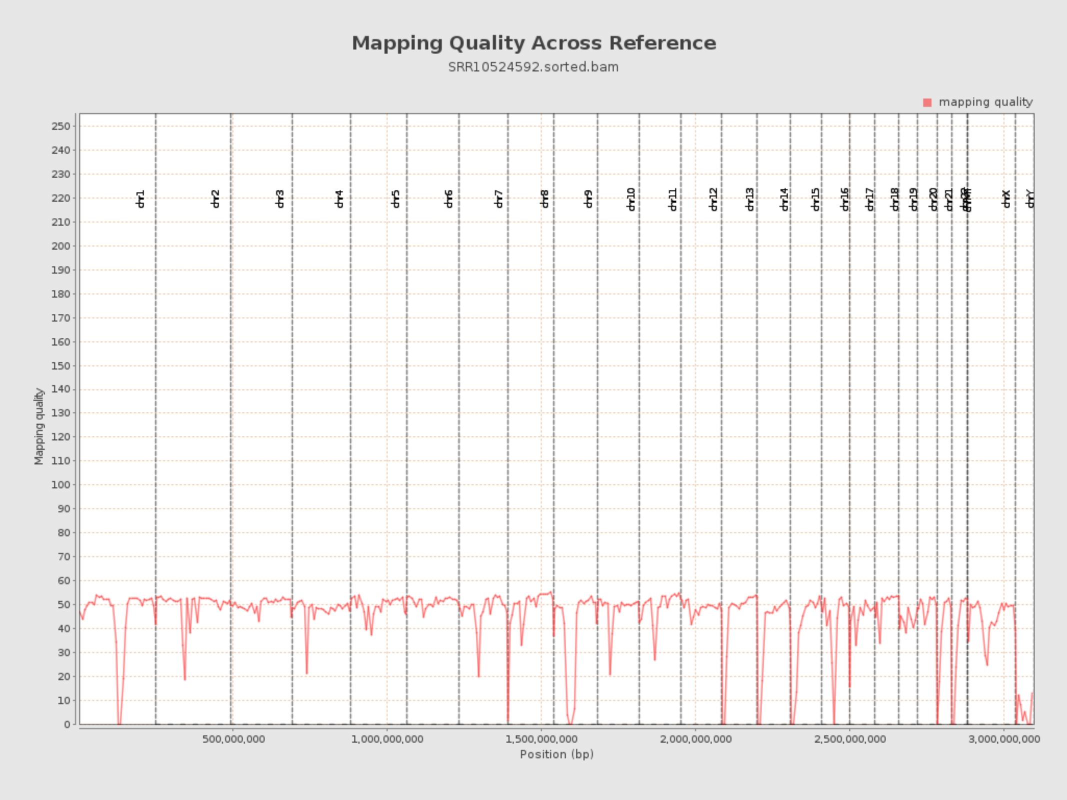
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram