Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:15:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819023.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_SRR1819023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:15:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,870,836
Mapped reads	1,750,291 / 93.56%
Unmapped reads	120,545 / 6.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,446 / 1.36%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	723,259 / 38.66%
Duplication rate	33.41%
Clipped reads	1,768,086 / 94.51%

2.2. ACGT Content

Number/percentage of A's	45,767,019 / 28.24%
Number/percentage of C's	34,058,901 / 21.02%
Number/percentage of T's	46,422,522 / 28.65%
Number/percentage of G's	35,797,369 / 22.09%
Number/percentage of N's	7,938 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0524

Standard Deviation	0.6089

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

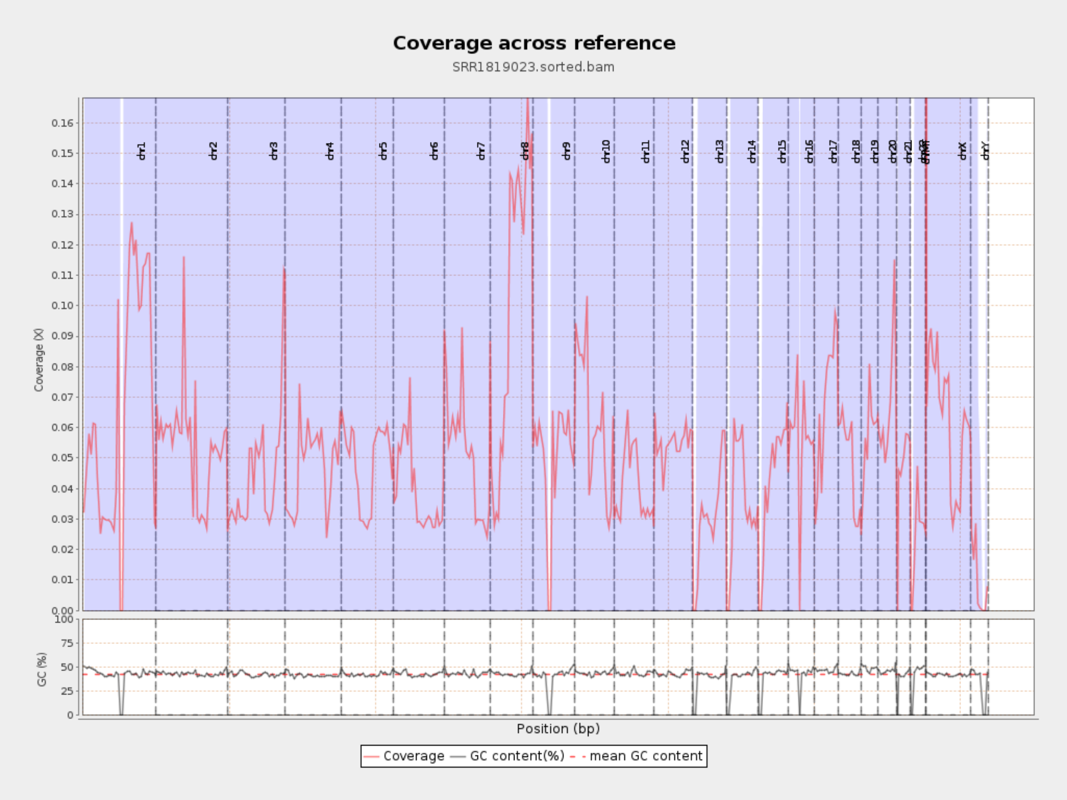
General error rate	0.64%
Mismatches	986,818
Insertions	24,536
Mapped reads with at least one insertion	1.37%
Deletions	51,798
Mapped reads with at least one deletion	2.9%
Homopolymer indels	42.76%

2.6. Chromosome stats

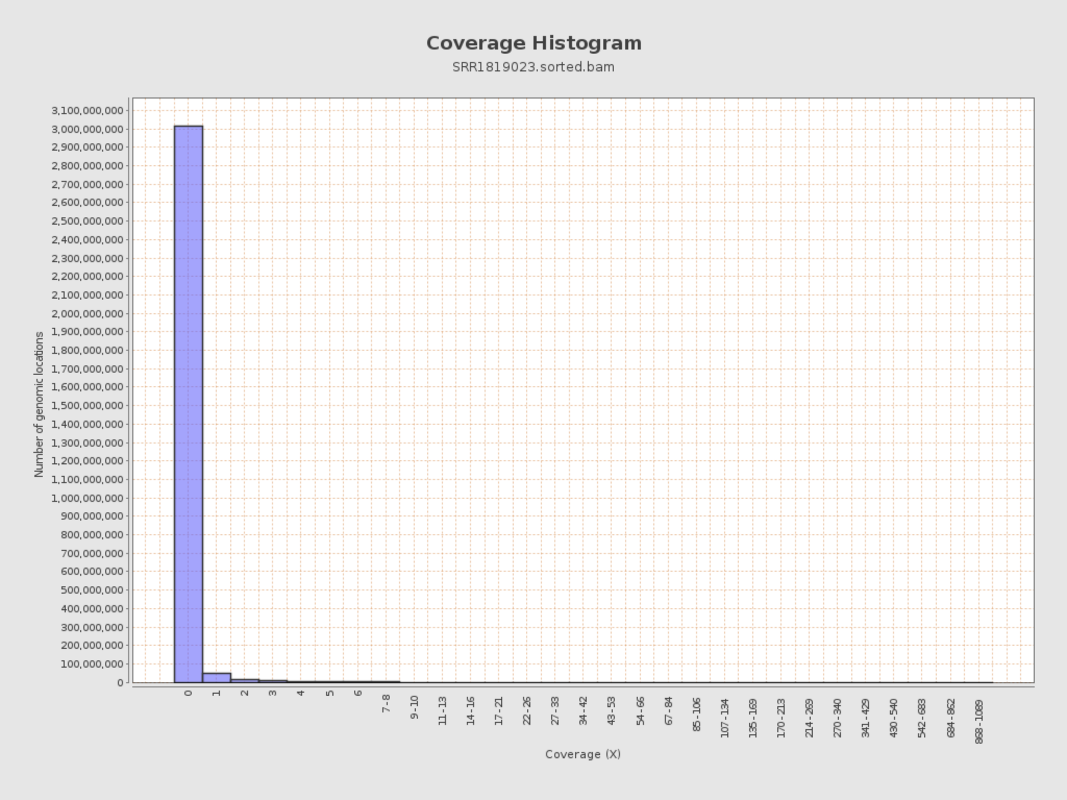
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16312816	0.0654	1.0184
chr2	243199373	13274103	0.0546	0.8357
chr3	198022430	8760831	0.0442	0.3716
chr4	191154276	9047136	0.0473	0.4326
chr5	180915260	8767648	0.0485	0.3996
chr6	171115067	6754062	0.0395	0.4225
chr7	159138663	8125845	0.0511	0.7725

chr8	146364022	14979139	0.1023	0.6299
chr9	141213431	7054234	0.05	0.5859
chr10	135534747	8424862	0.0622	0.7105
chr11	135006516	5540223	0.041	0.4247
chr12	133851895	7378619	0.0551	0.4244
chr13	115169878	3580157	0.0311	0.3097
chr14	107349540	3846892	0.0358	0.3566
chr15	102531392	4213531	0.0411	0.3589
chr16	90354753	5002265	0.0554	0.6493
chr17	81195210	5531056	0.0681	0.5239
chr18	78077248	3840036	0.0492	0.6769
chr19	59128983	3405155	0.0576	0.9721
chr20	63025520	4386391	0.0696	0.4955
chr21	48129895	2257673	0.0469	0.4102
chr22	51304566	1210436	0.0236	0.3067
chrMT	16571	45268	2.7318	3.1059
chrX	155270560	9841728	0.0634	0.5221
chrY	59373566	569117	0.0096	0.5304

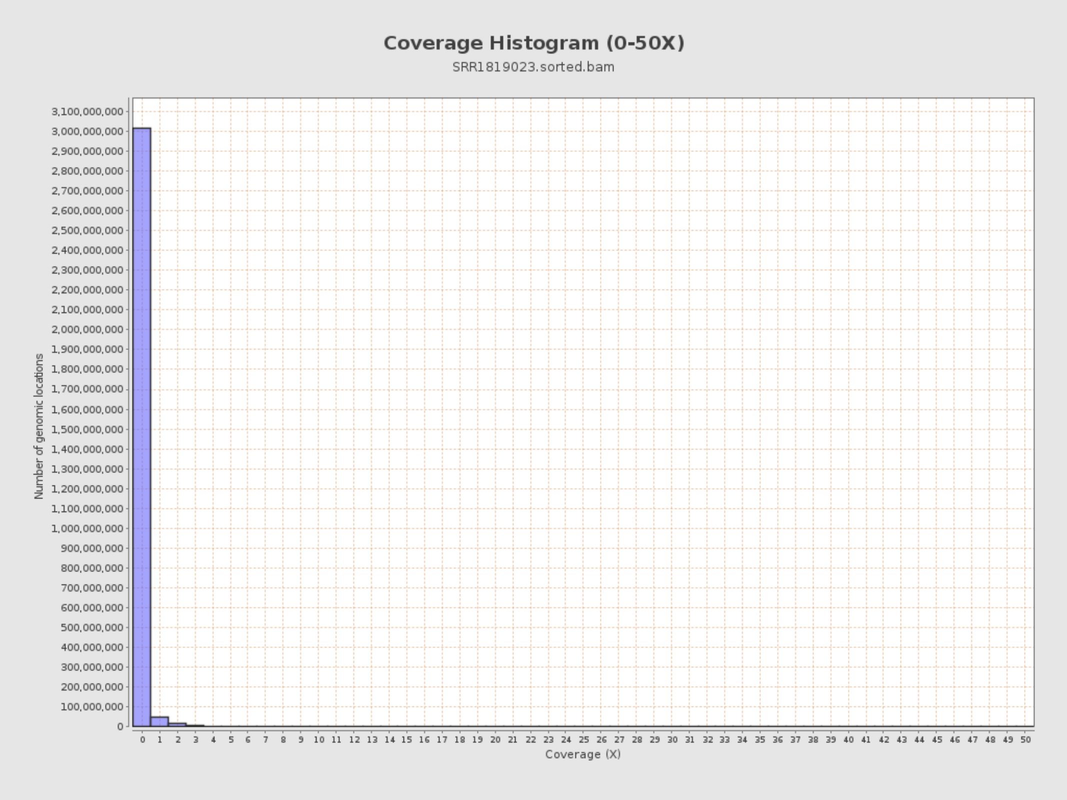
3. Results : Coverage across reference



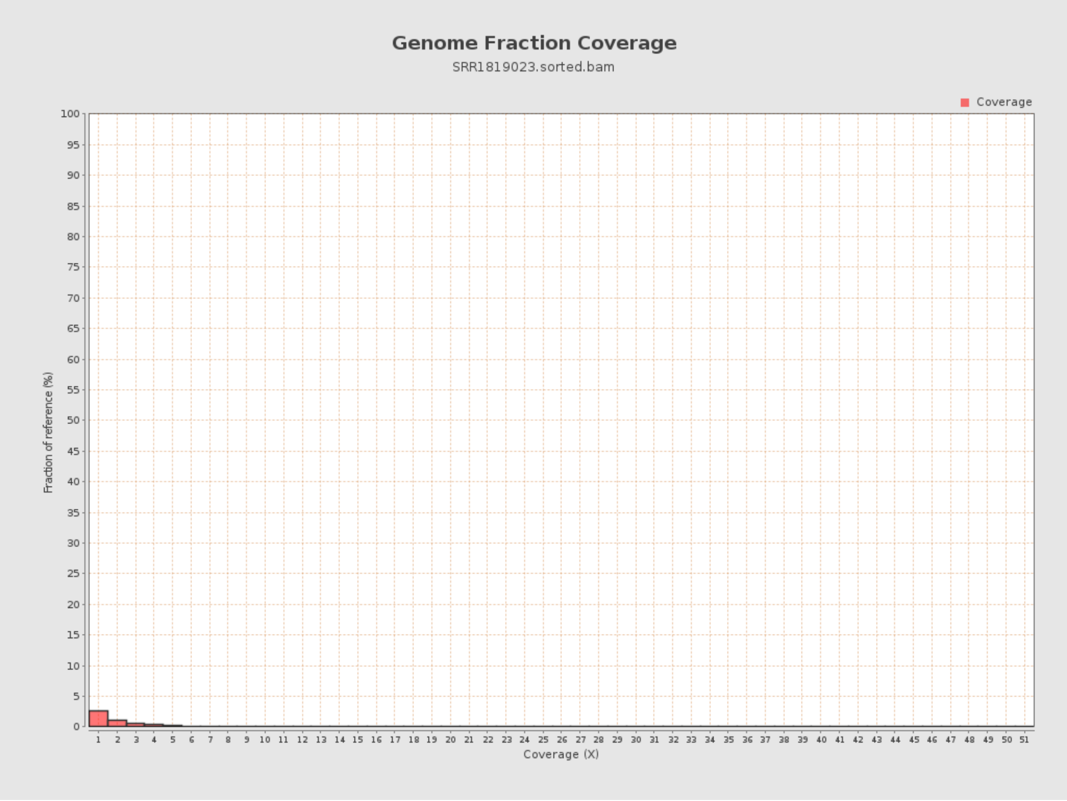
4. Results : Coverage Histogram



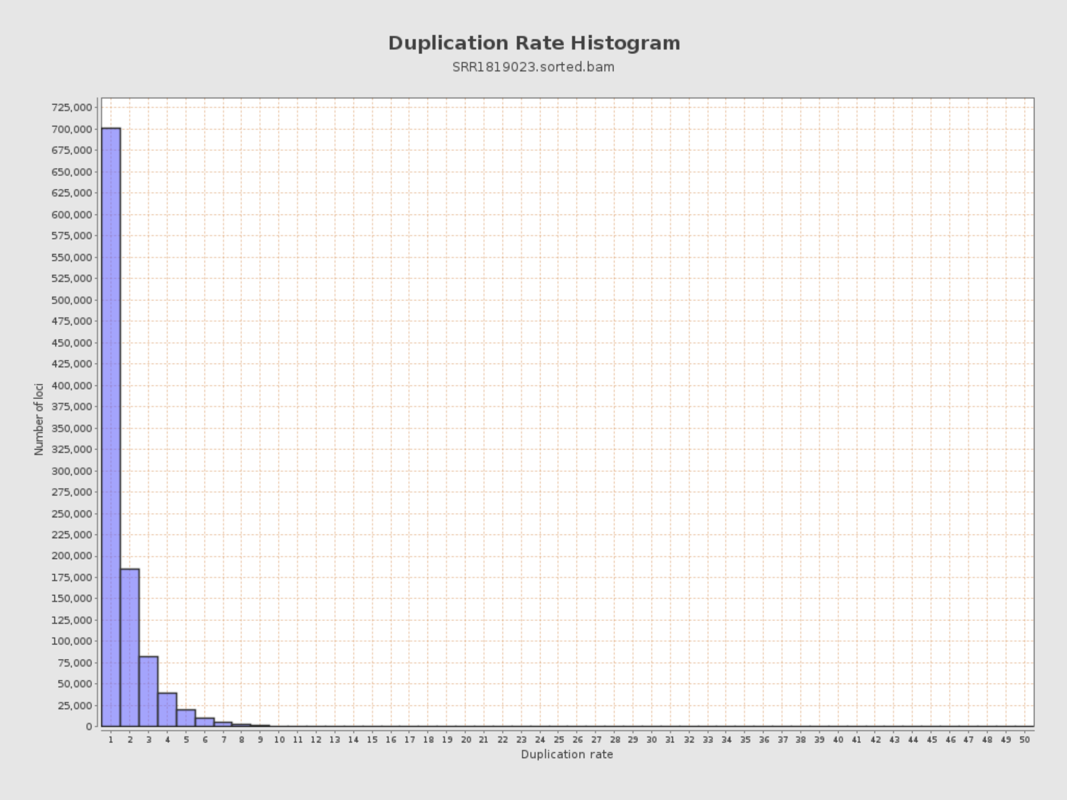
5. Results : Coverage Histogram (0-50X)



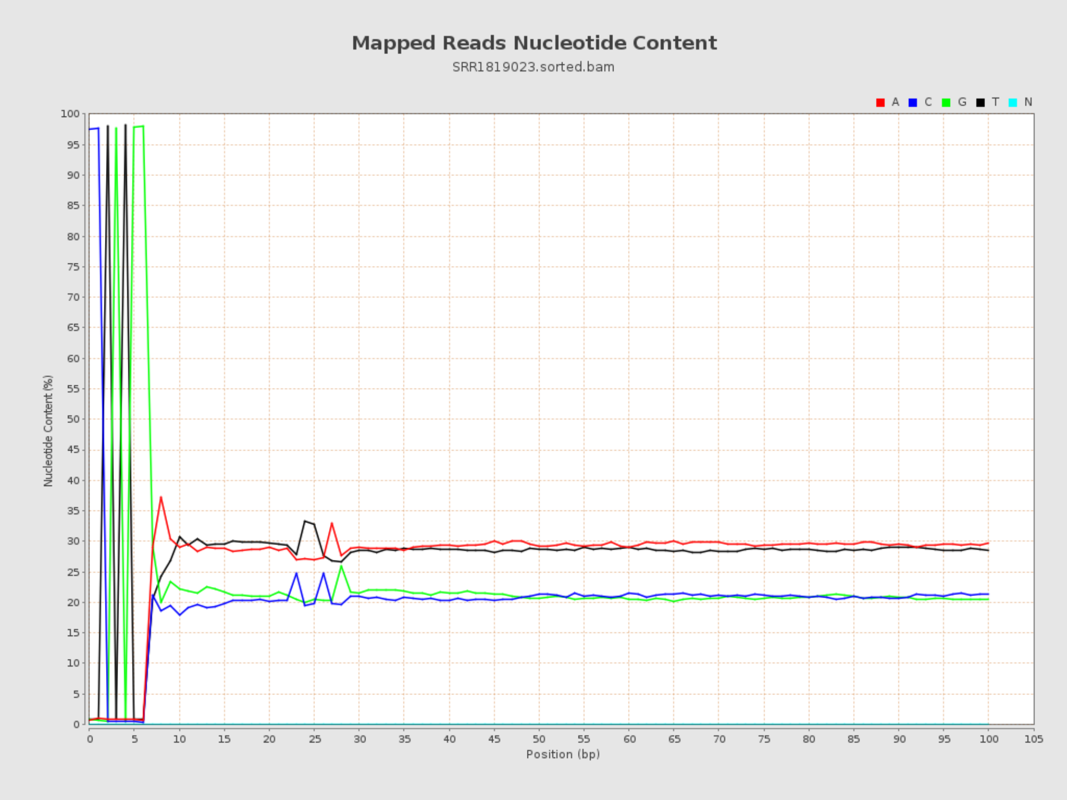
6. Results : Genome Fraction Coverage



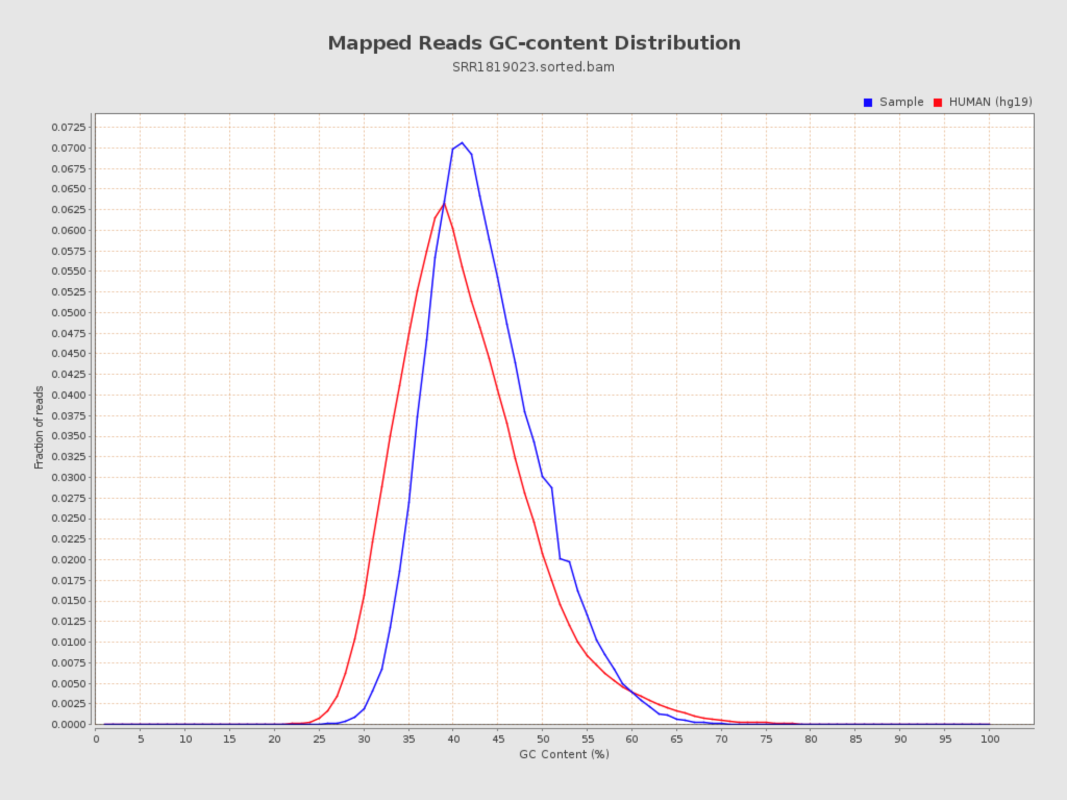
7. Results : Duplication Rate Histogram



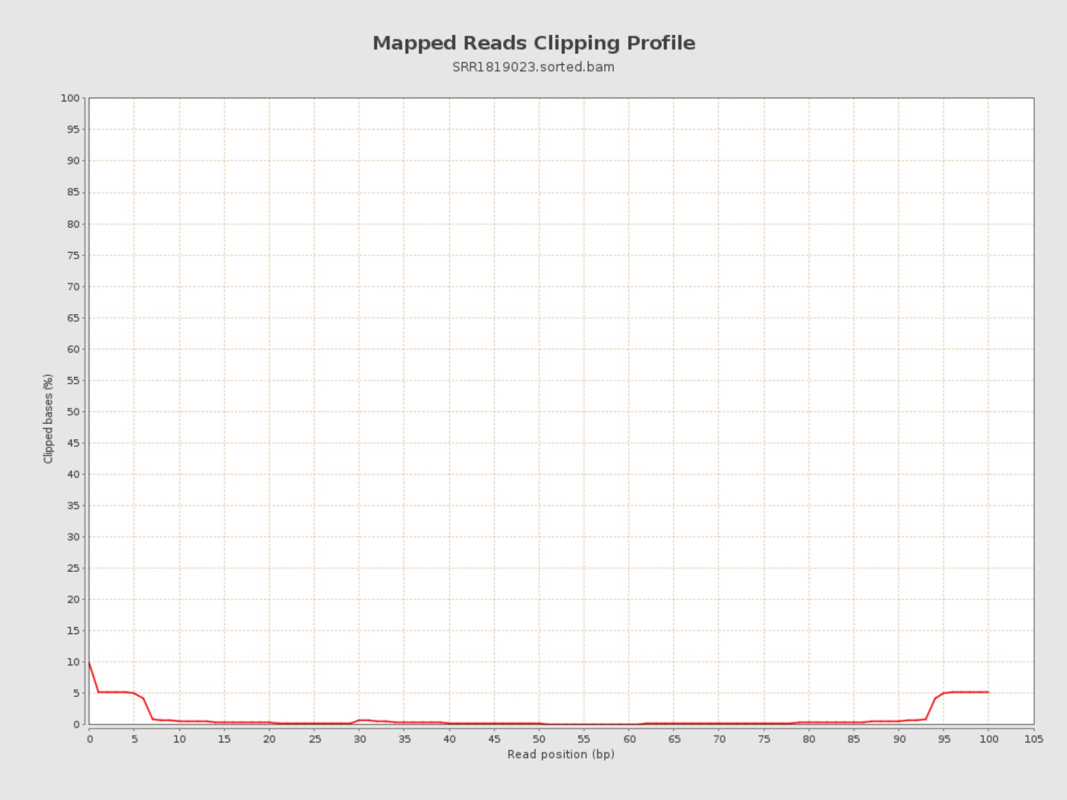
8. Results : Mapped Reads Nucleotide Content



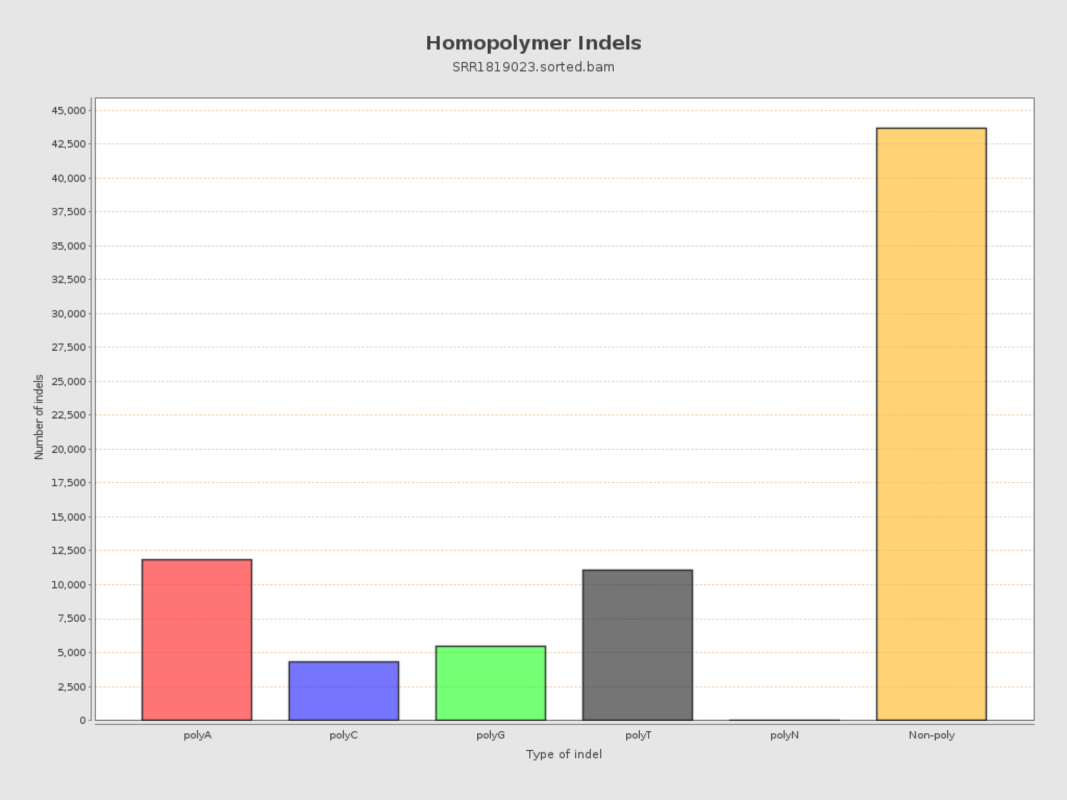
9. Results : Mapped Reads GC-content Distribution



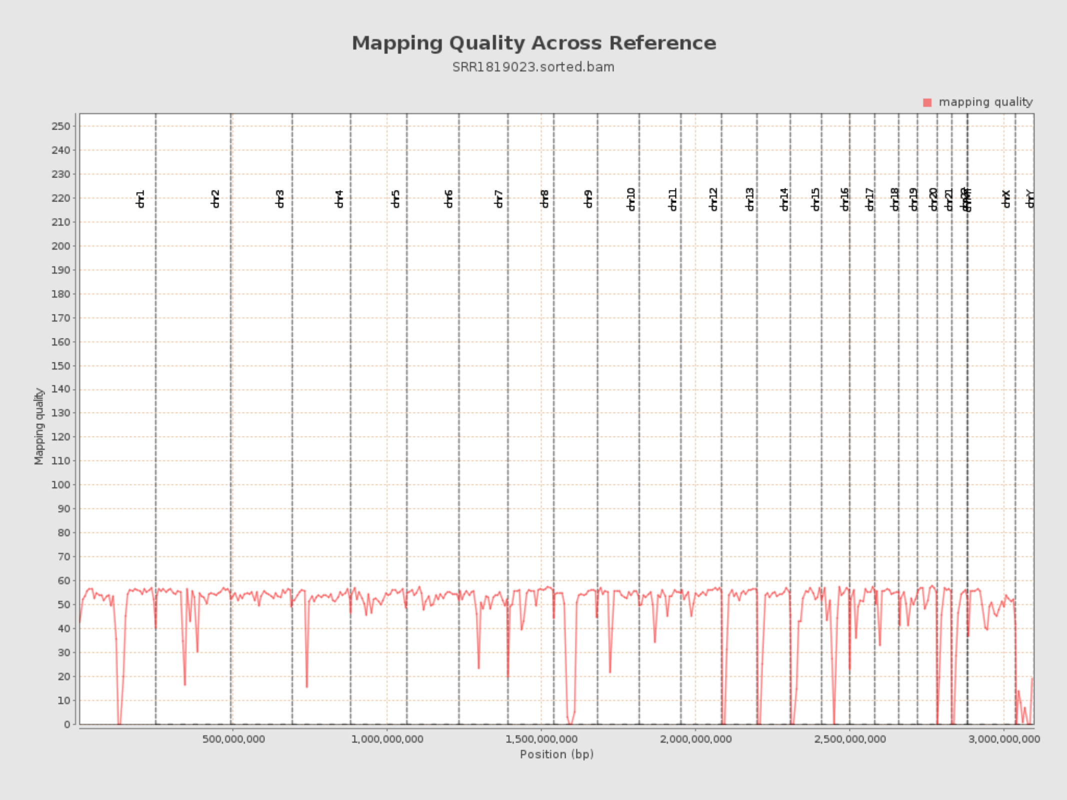
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram