Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:11:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819022.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_SRR1819022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:11:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,274,104
Mapped reads	1,255,276 / 98.52%
Unmapped reads	18,828 / 1.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,404 / 1.6%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	415,956 / 32.65%
Duplication rate	28.37%
Clipped reads	1,265,308 / 99.31%

2.2. ACGT Content

Number/percentage of A's	33,277,974 / 28.69%
Number/percentage of C's	24,515,213 / 21.14%
Number/percentage of T's	33,265,629 / 28.68%
Number/percentage of G's	24,920,423 / 21.49%
Number/percentage of N's	5,945 / 0.01%
GC Percentage	42.62%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.4805

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

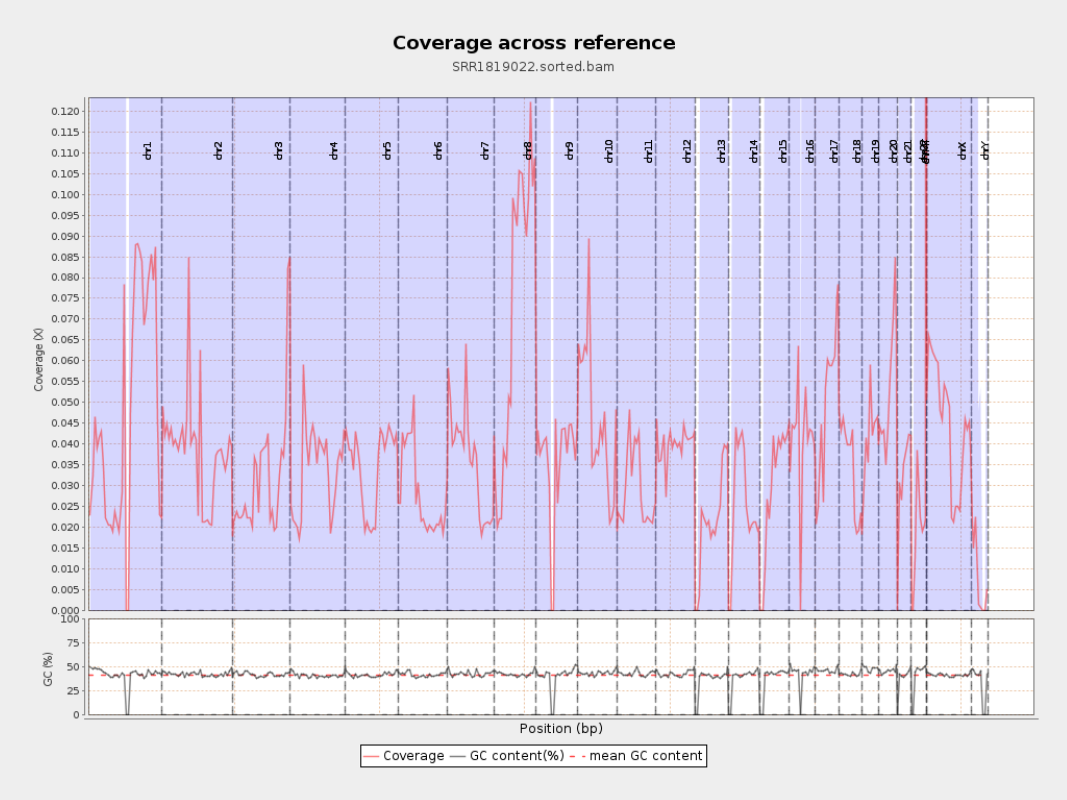
General error rate	0.68%
Mismatches	748,813
Insertions	18,905
Mapped reads with at least one insertion	1.46%
Deletions	38,715
Mapped reads with at least one deletion	3.01%
Homopolymer indels	40.16%

2.6. Chromosome stats

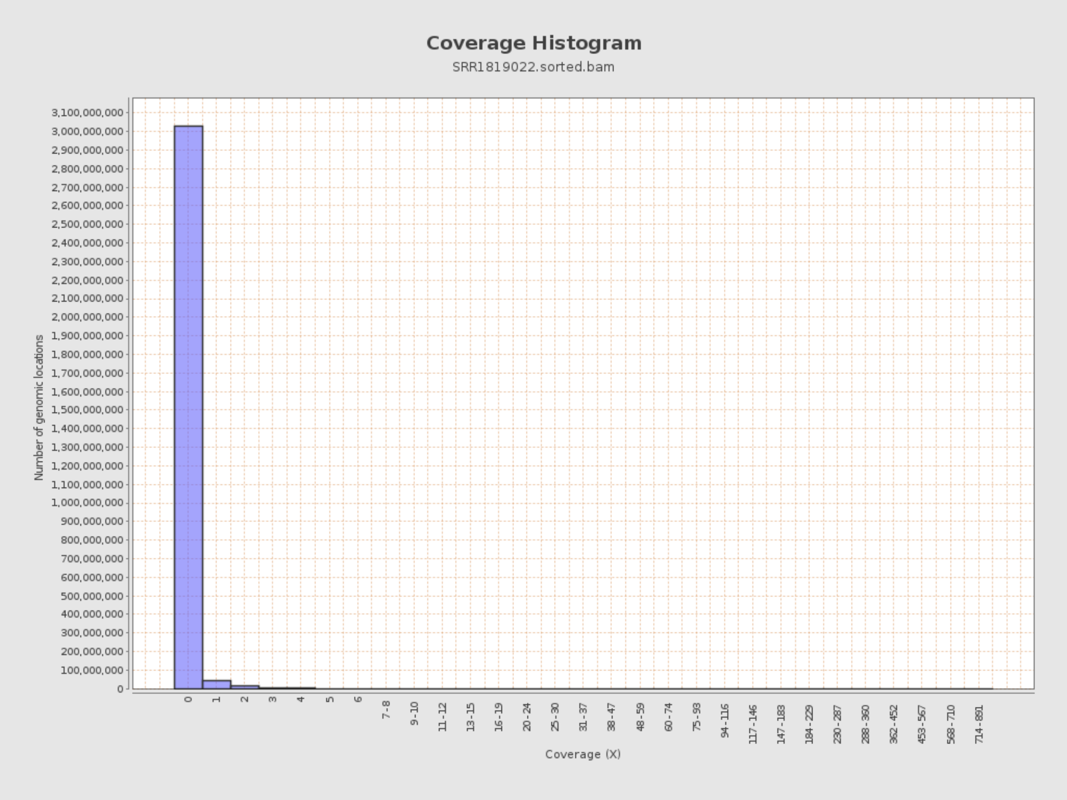
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11754363	0.0472	0.8464
chr2	243199373	9415353	0.0387	0.702
chr3	198022430	6209744	0.0314	0.2708
chr4	191154276	6433870	0.0337	0.3259
chr5	180915260	6226955	0.0344	0.2927
chr6	171115067	4813518	0.0281	0.3065
chr7	159138663	5702632	0.0358	0.5339

chr8	146364022	10629880	0.0726	0.4498
chr9	141213431	4956256	0.0351	0.4102
chr10	135534747	6188175	0.0457	0.6316
chr11	135006516	3935913	0.0292	0.3034
chr12	133851895	5348703	0.04	0.3101
chr13	115169878	2479591	0.0215	0.2218
chr14	107349540	2729727	0.0254	0.2642
chr15	102531392	2986956	0.0291	0.2626
chr16	90354753	3705763	0.041	0.5799
chr17	81195210	4069633	0.0501	0.384
chr18	78077248	2715836	0.0348	0.4992
chr19	59128983	2457392	0.0416	0.7587
chr20	63025520	3376825	0.0536	0.3829
chr21	48129895	1555024	0.0323	0.3019
chr22	51304566	918383	0.0179	0.2316
chrMT	16571	14161	0.8546	1.4807
chrX	155270560	6978849	0.0449	0.3753
chrY	59373566	454570	0.0077	0.5351

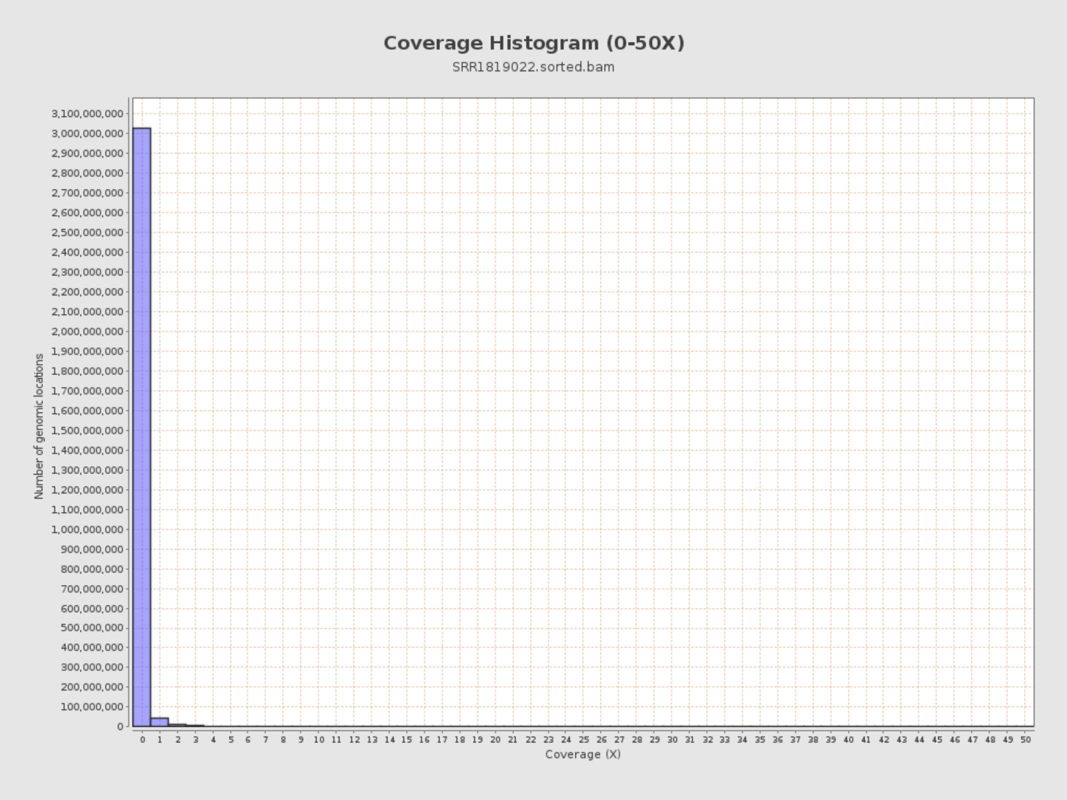
3. Results : Coverage across reference



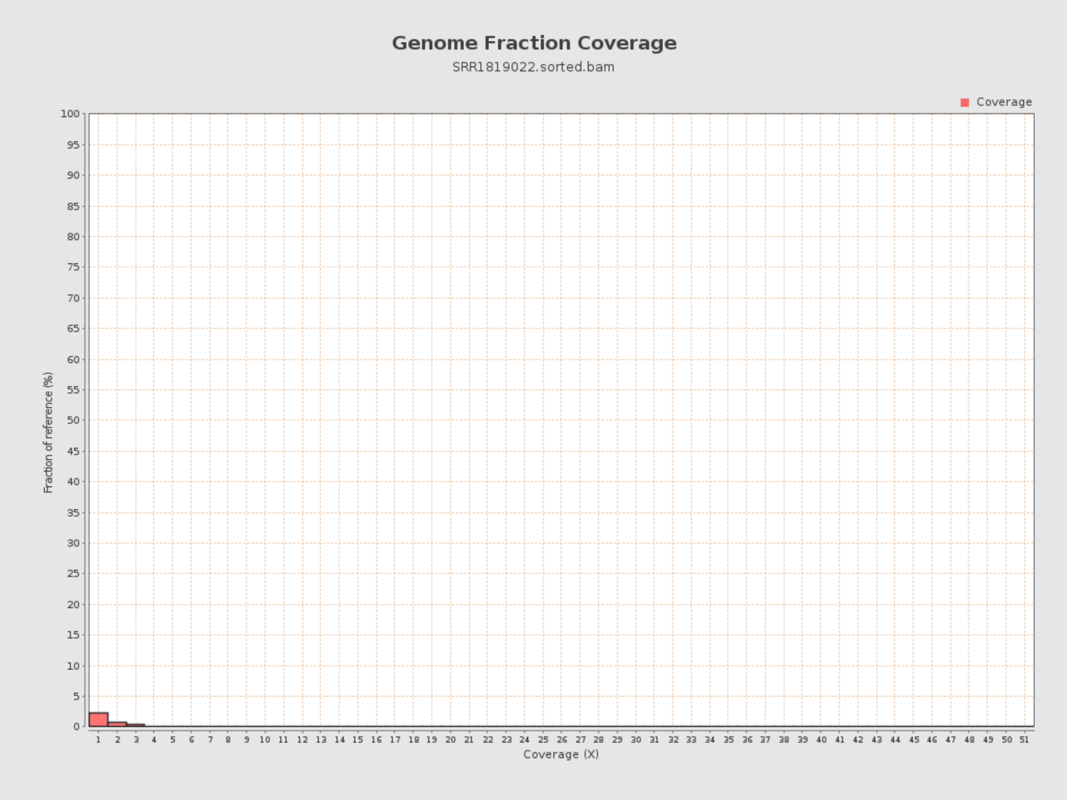
4. Results : Coverage Histogram



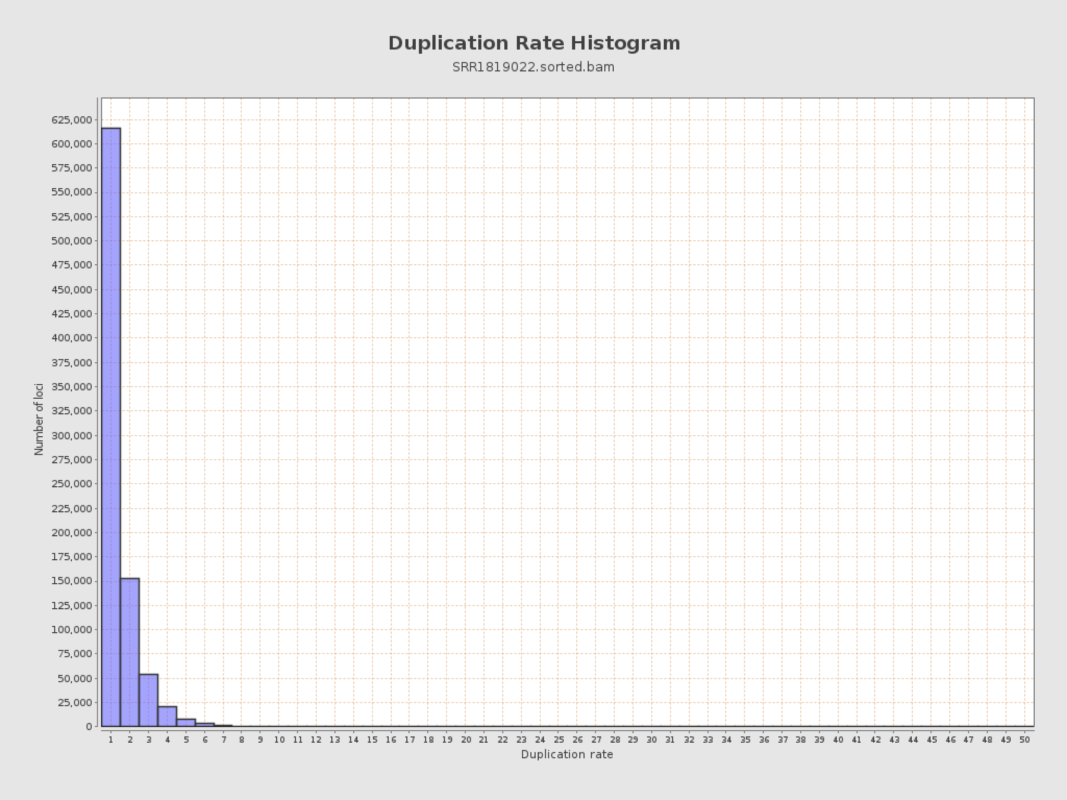
5. Results : Coverage Histogram (0-50X)



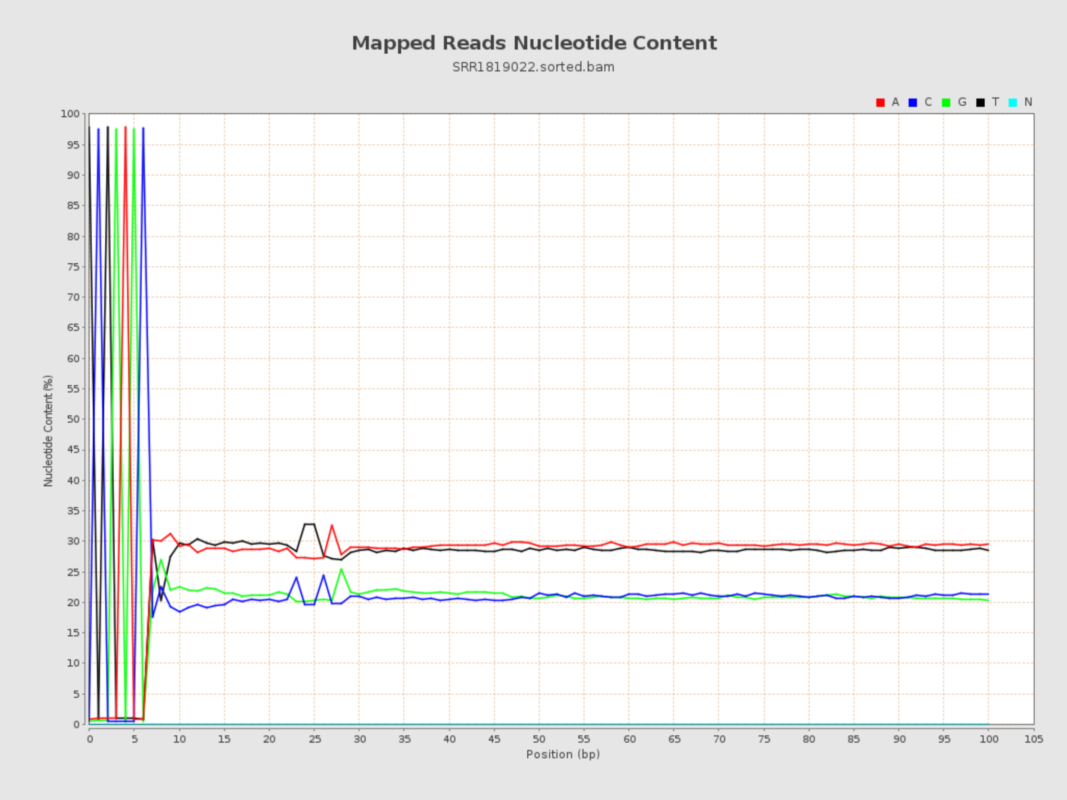
6. Results : Genome Fraction Coverage



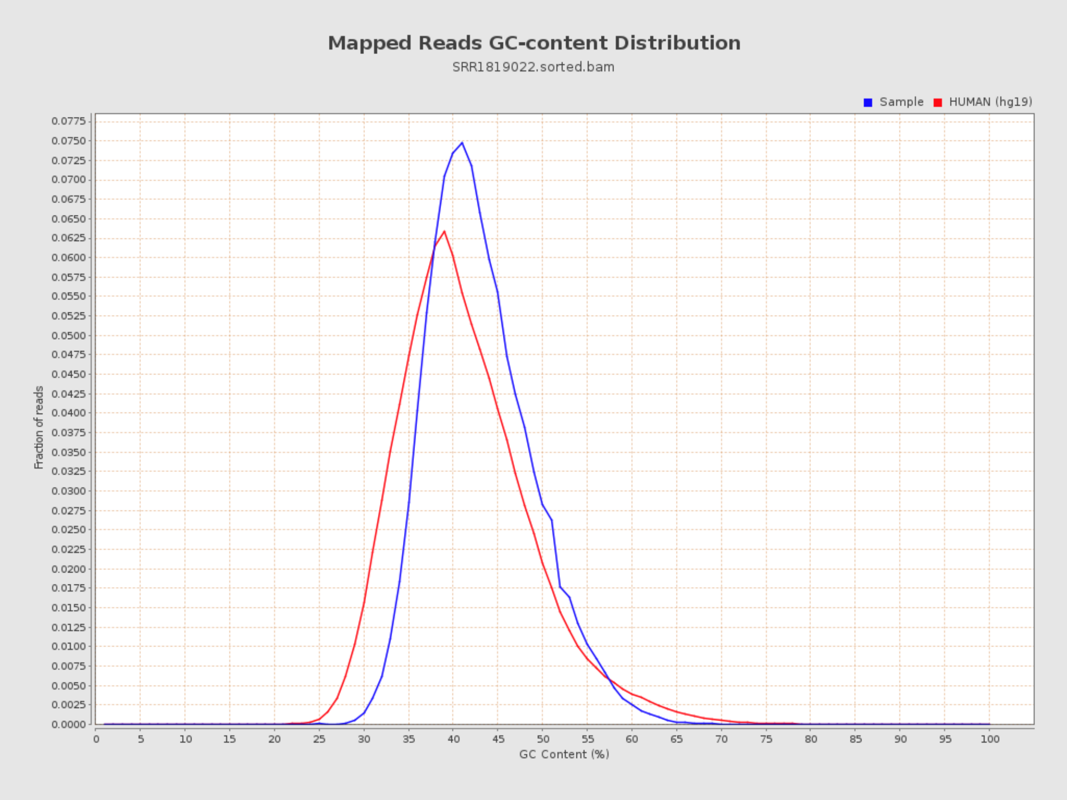
7. Results : Duplication Rate Histogram



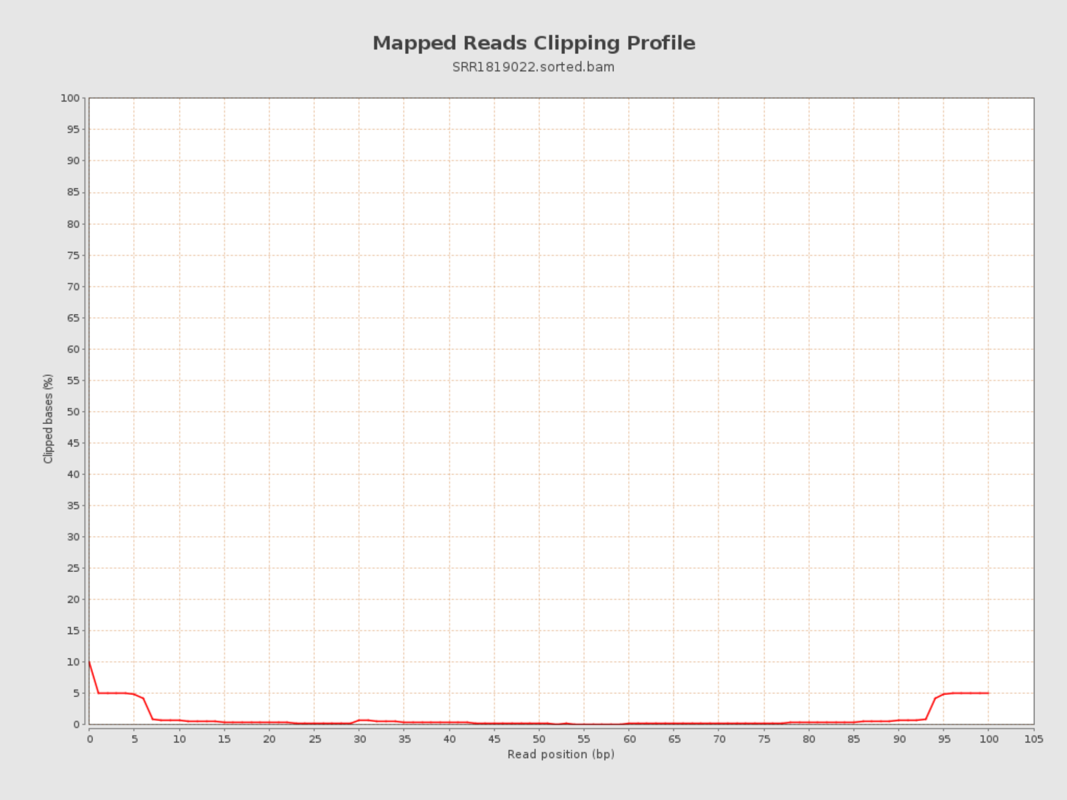
8. Results : Mapped Reads Nucleotide Content



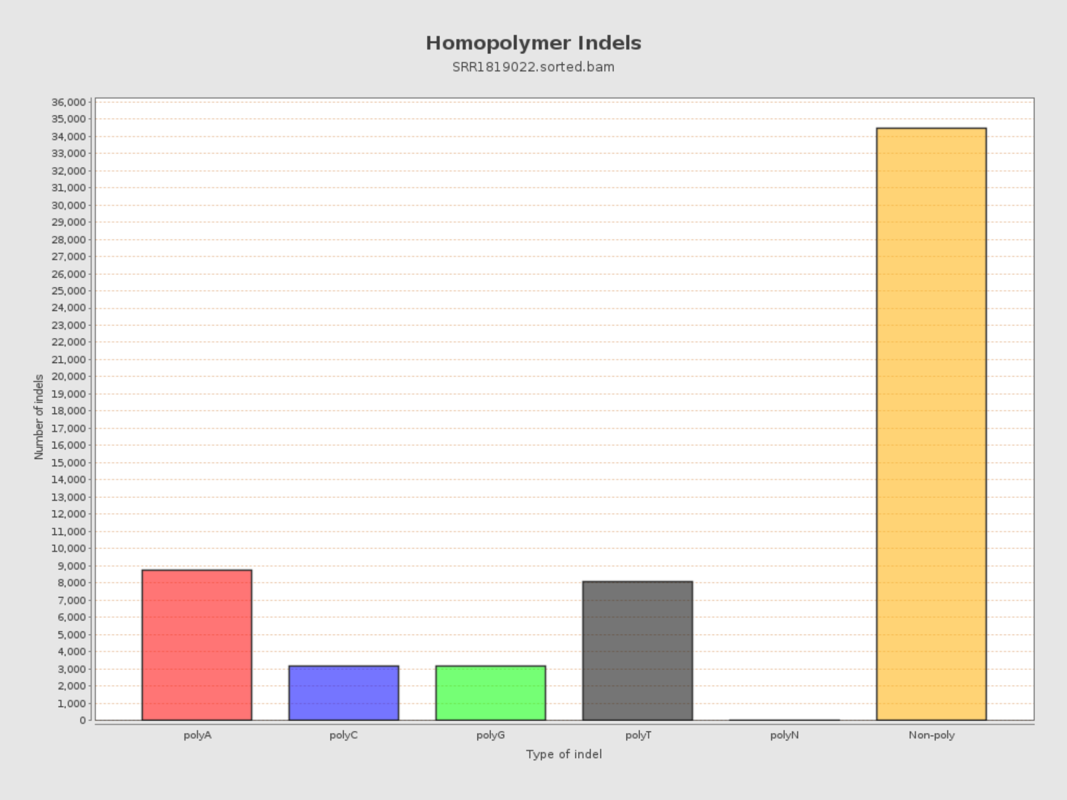
9. Results : Mapped Reads GC-content Distribution



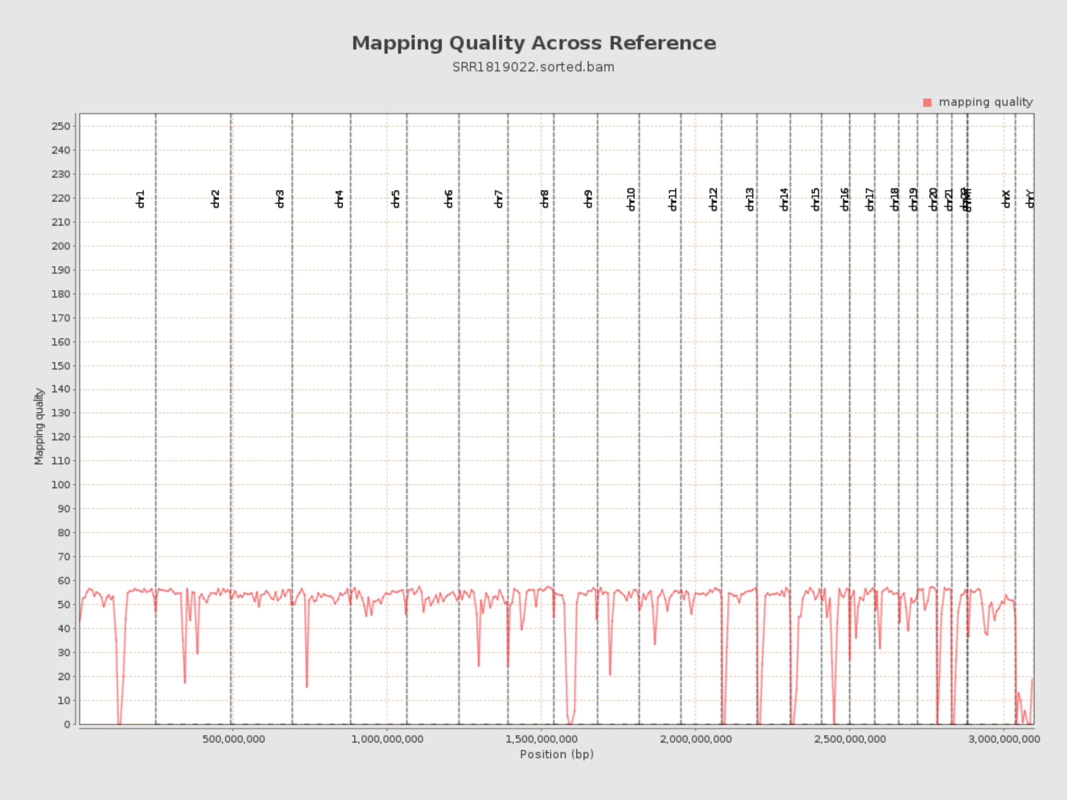
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram