Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:15:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819000.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_SRR1819000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819000.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:15:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,451,457
Mapped reads	1,427,460 / 98.35%
Unmapped reads	23,997 / 1.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,405 / 1.68%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	499,854 / 34.44%
Duplication rate	30.37%
Clipped reads	1,437,886 / 99.07%

2.2. ACGT Content

Number/percentage of A's	37,307,250 / 28.3%
Number/percentage of C's	27,685,639 / 21%
Number/percentage of T's	38,112,255 / 28.91%
Number/percentage of G's	28,728,154 / 21.79%
Number/percentage of N's	6,202 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.5467

2.4. Mapping Quality

Mean Mapping Quality	49.12

2.5. Mismatches and indels

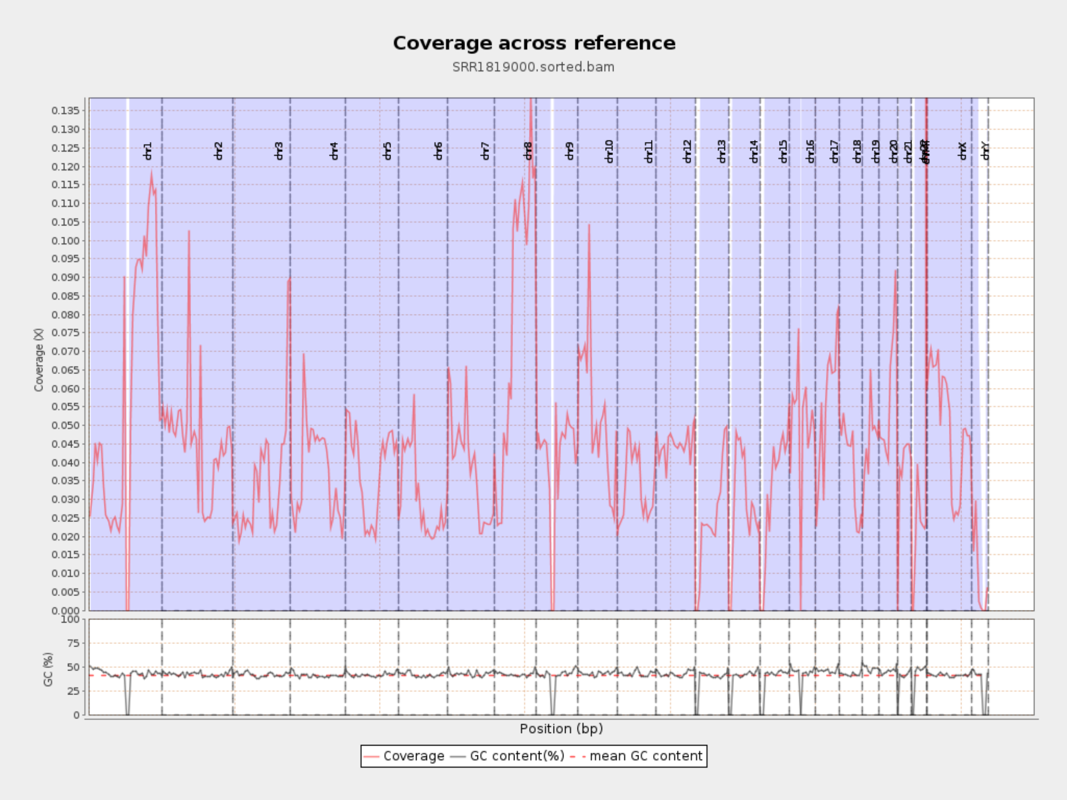
General error rate	0.67%
Mismatches	835,686
Insertions	21,089
Mapped reads with at least one insertion	1.44%
Deletions	43,285
Mapped reads with at least one deletion	2.96%
Homopolymer indels	41.38%

2.6. Chromosome stats

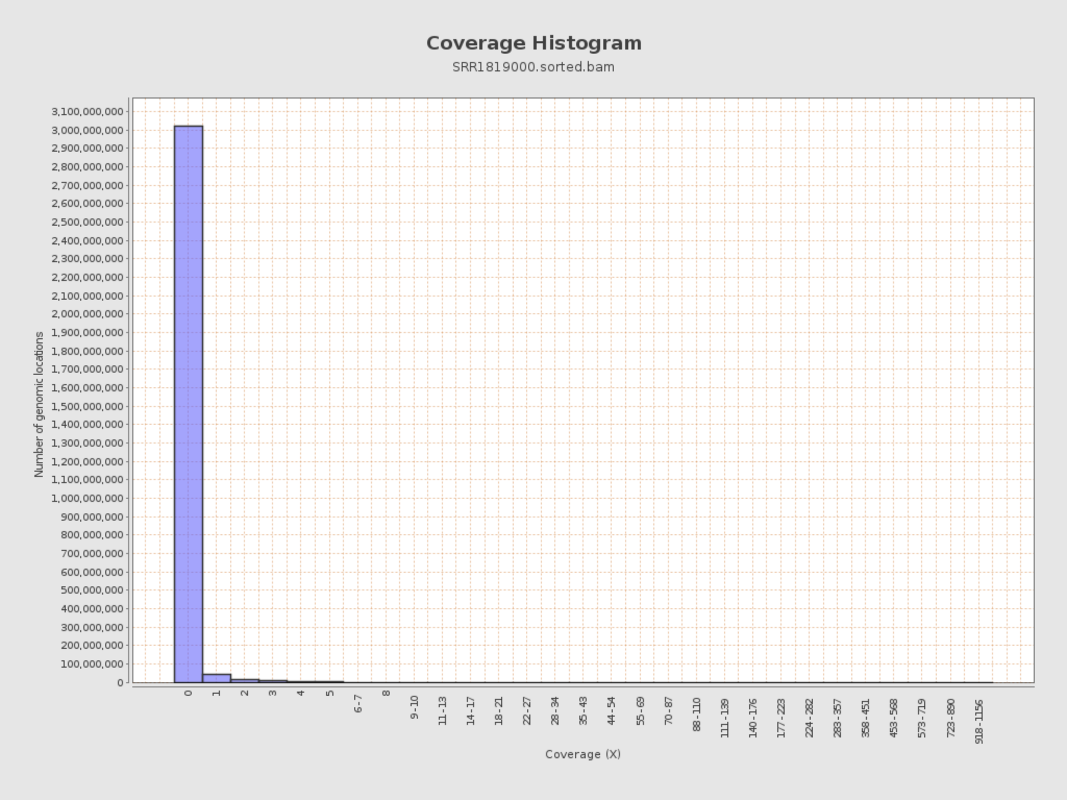
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14321629	0.0575	1.0636
chr2	243199373	11145759	0.0458	0.7708
chr3	198022430	6746130	0.0341	0.2904
chr4	191154276	7033607	0.0368	0.3644
chr5	180915260	6903328	0.0382	0.3178
chr6	171115067	5227110	0.0305	0.3313
chr7	159138663	6152745	0.0387	0.5385

chr8	146364022	11875569	0.0811	0.5112
chr9	141213431	5729707	0.0406	0.4748
chr10	135534747	7178070	0.053	0.6803
chr11	135006516	4566561	0.0338	0.3603
chr12	133851895	5993940	0.0448	0.3403
chr13	115169878	2879645	0.025	0.2447
chr14	107349540	3081970	0.0287	0.2819
chr15	102531392	3291820	0.0321	0.2802
chr16	90354753	4510365	0.0499	0.6074
chr17	81195210	4526945	0.0558	0.411
chr18	78077248	3079880	0.0394	0.559
chr19	59128983	2709160	0.0458	0.8404
chr20	63025520	3677885	0.0584	0.4035
chr21	48129895	1812473	0.0377	0.3285
chr22	51304566	1015499	0.0198	0.2488
chrMT	16571	49379	2.9798	3.428
chrX	155270560	7864526	0.0507	0.4323
chrY	59373566	547118	0.0092	0.6129

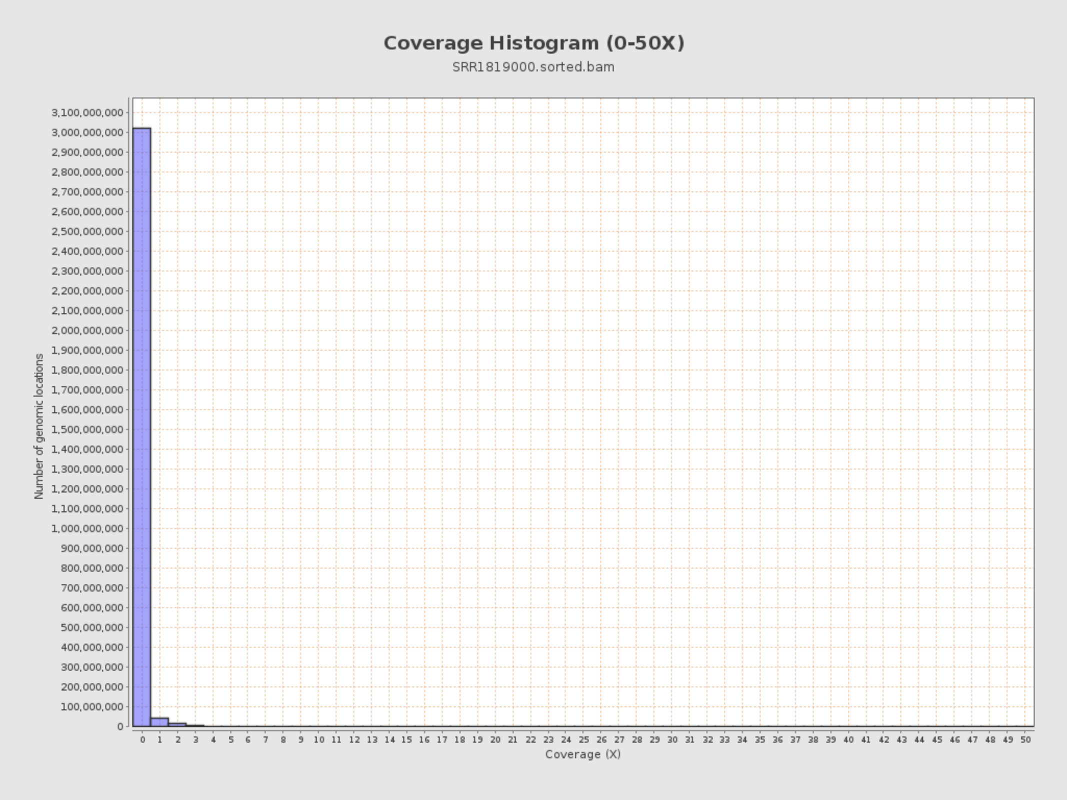
3. Results : Coverage across reference



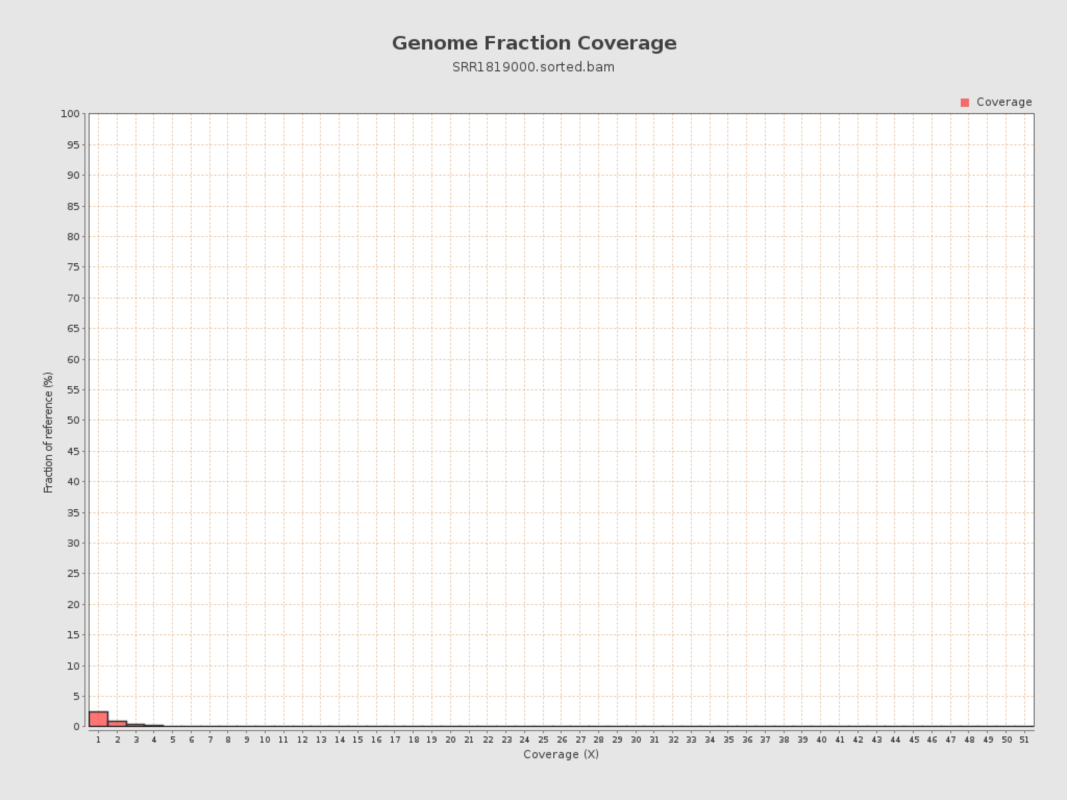
4. Results : Coverage Histogram



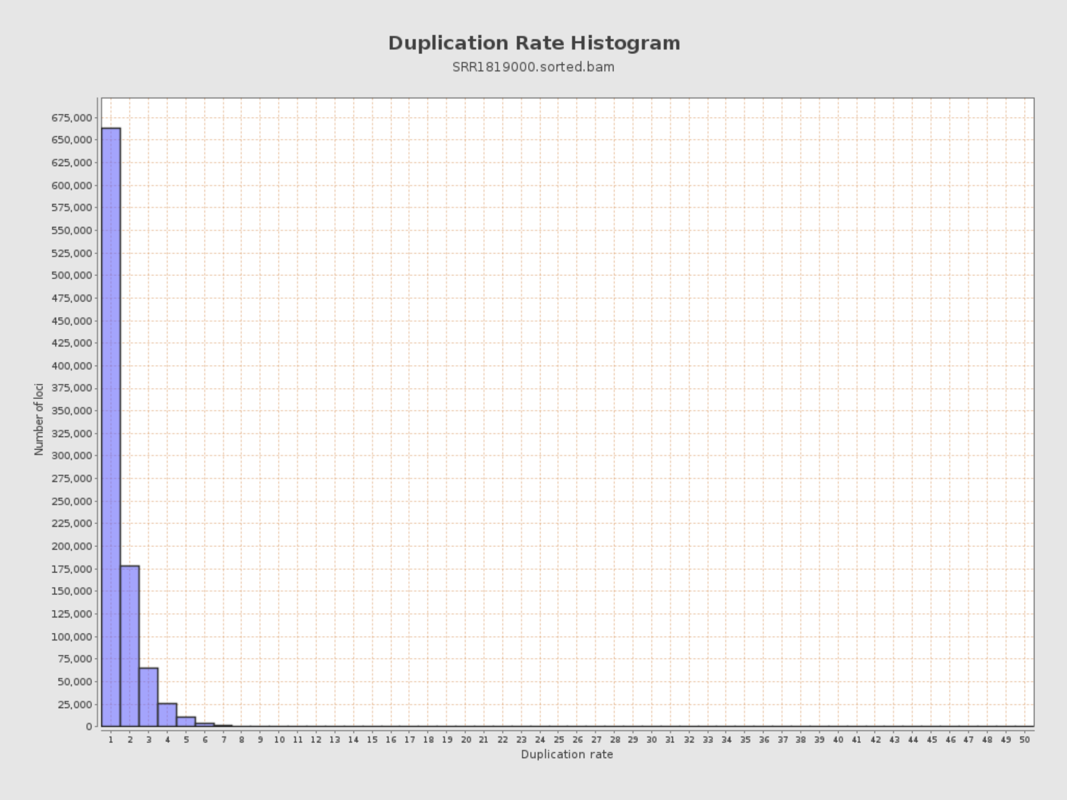
5. Results : Coverage Histogram (0-50X)



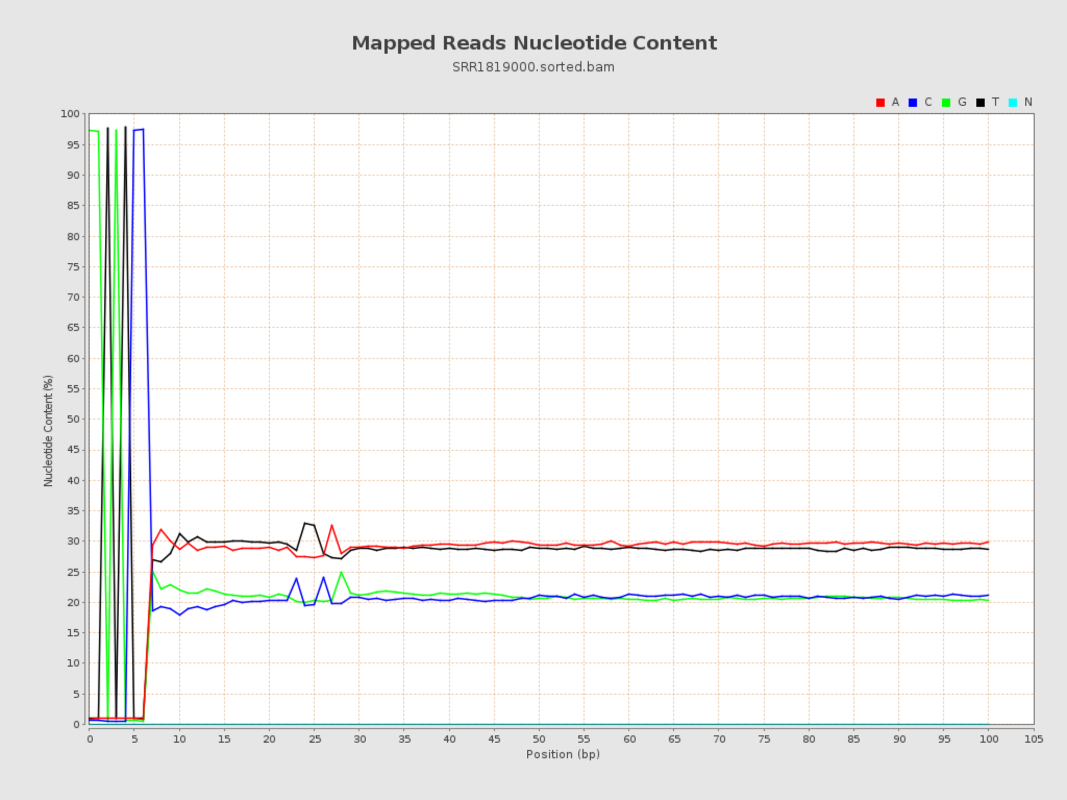
6. Results : Genome Fraction Coverage



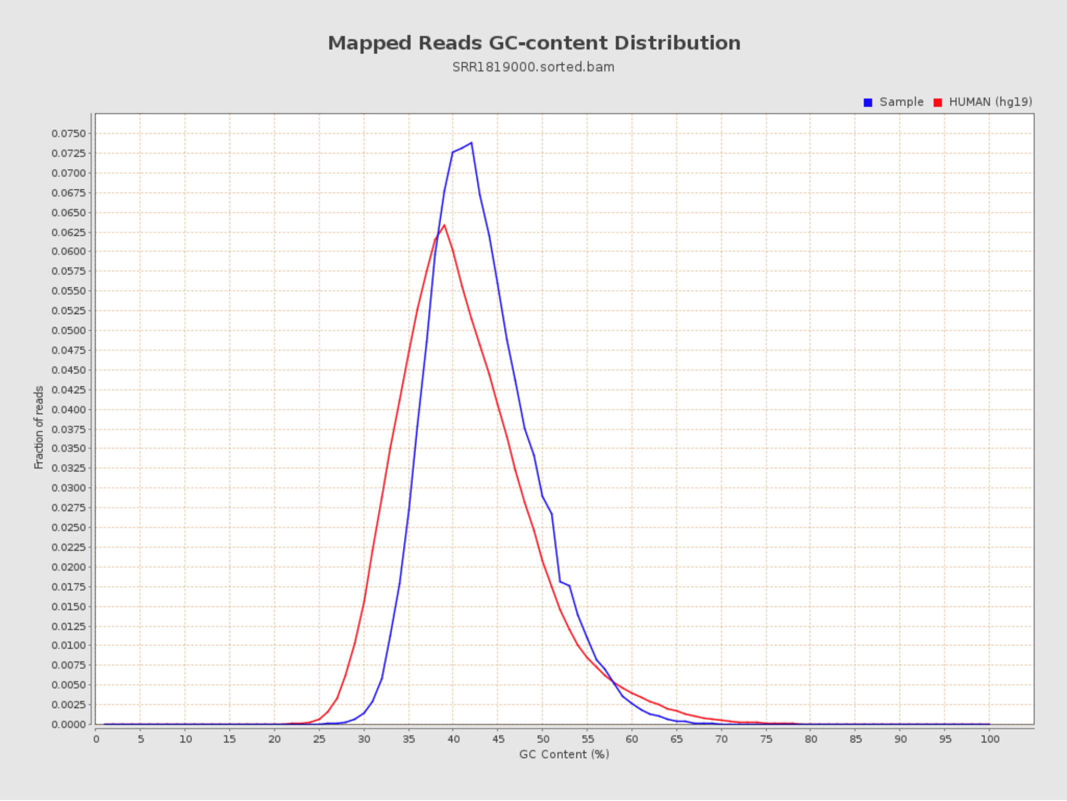
7. Results : Duplication Rate Histogram



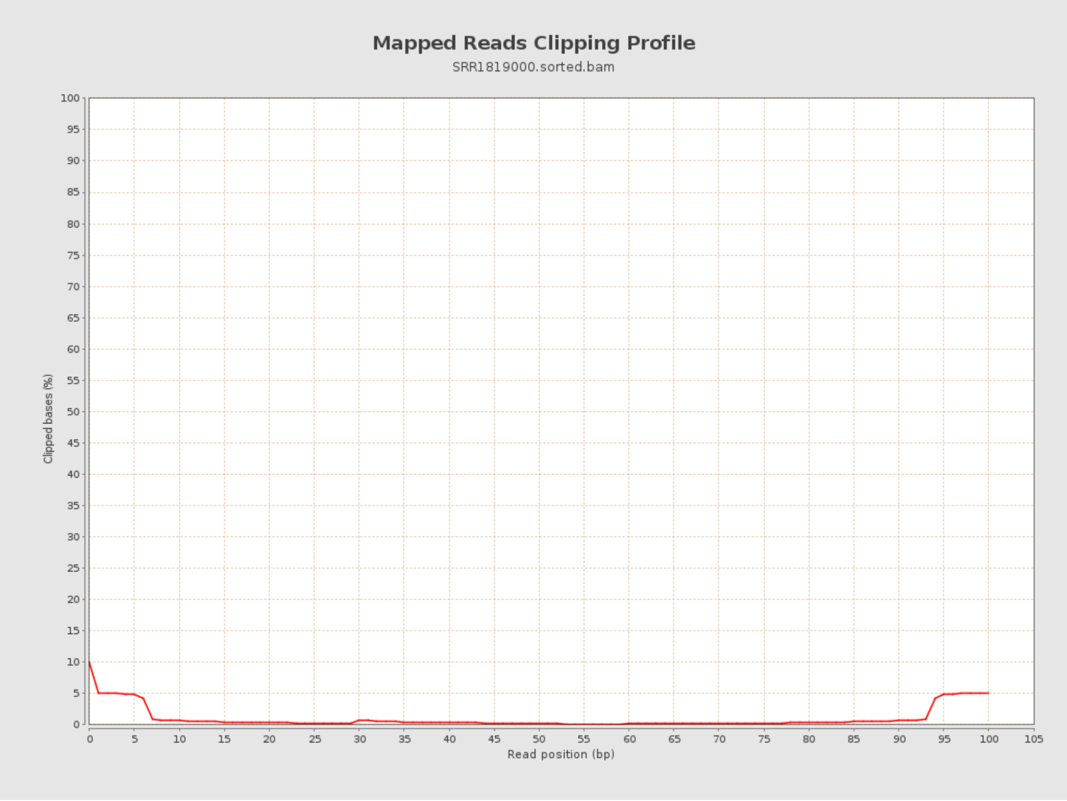
8. Results : Mapped Reads Nucleotide Content



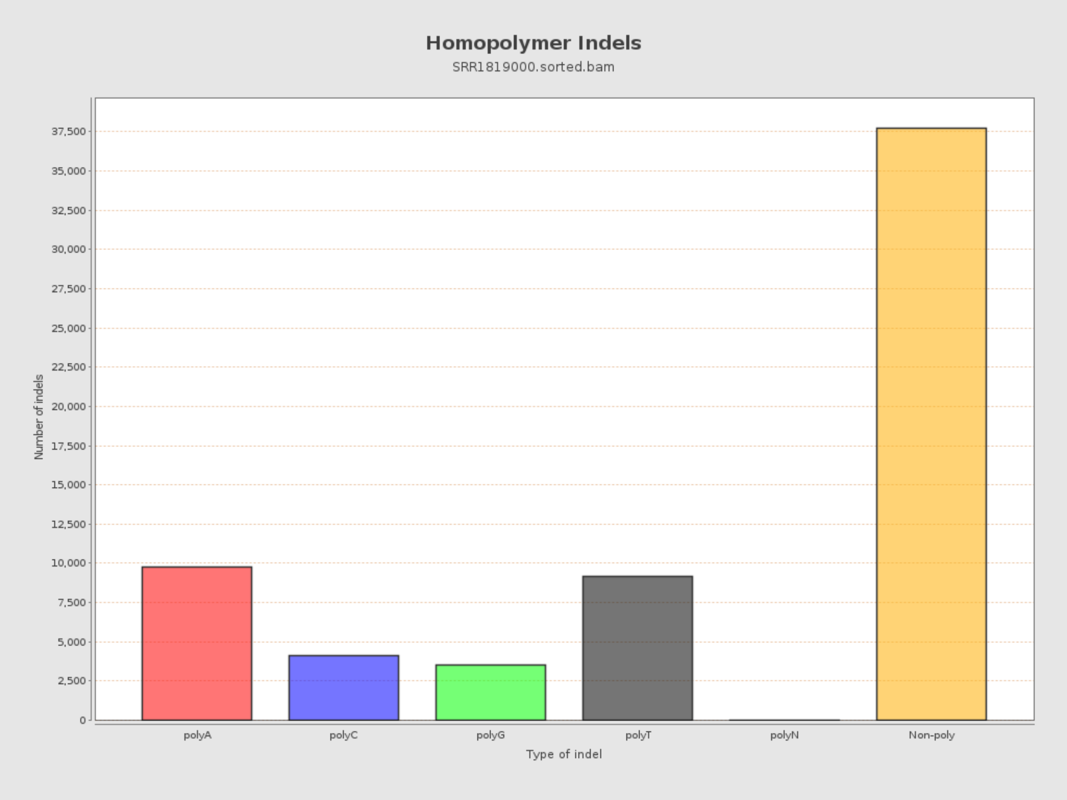
9. Results : Mapped Reads GC-content Distribution



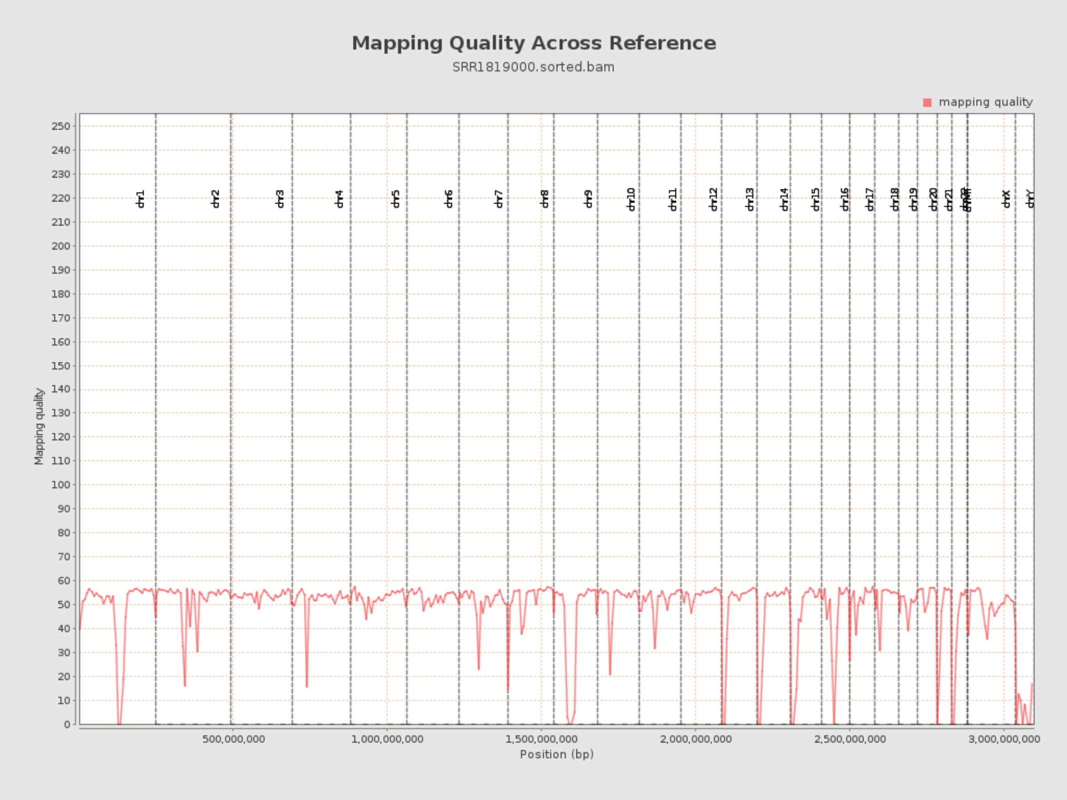
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram