Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:49:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819011.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_SRR1819011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819011.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:49:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,574,273
Mapped reads	1,545,759 / 98.19%
Unmapped reads	28,514 / 1.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,137 / 1.41%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	585,720 / 37.21%
Duplication rate	31.43%
Clipped reads	1,549,384 / 98.42%

2.2. ACGT Content

Number/percentage of A's	40,129,235 / 28.05%
Number/percentage of C's	29,496,301 / 20.62%
Number/percentage of T's	41,616,549 / 29.09%
Number/percentage of G's	31,814,862 / 22.24%
Number/percentage of N's	6,855 / 0%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.587

2.4. Mapping Quality

Mean Mapping Quality	49.25

2.5. Mismatches and indels

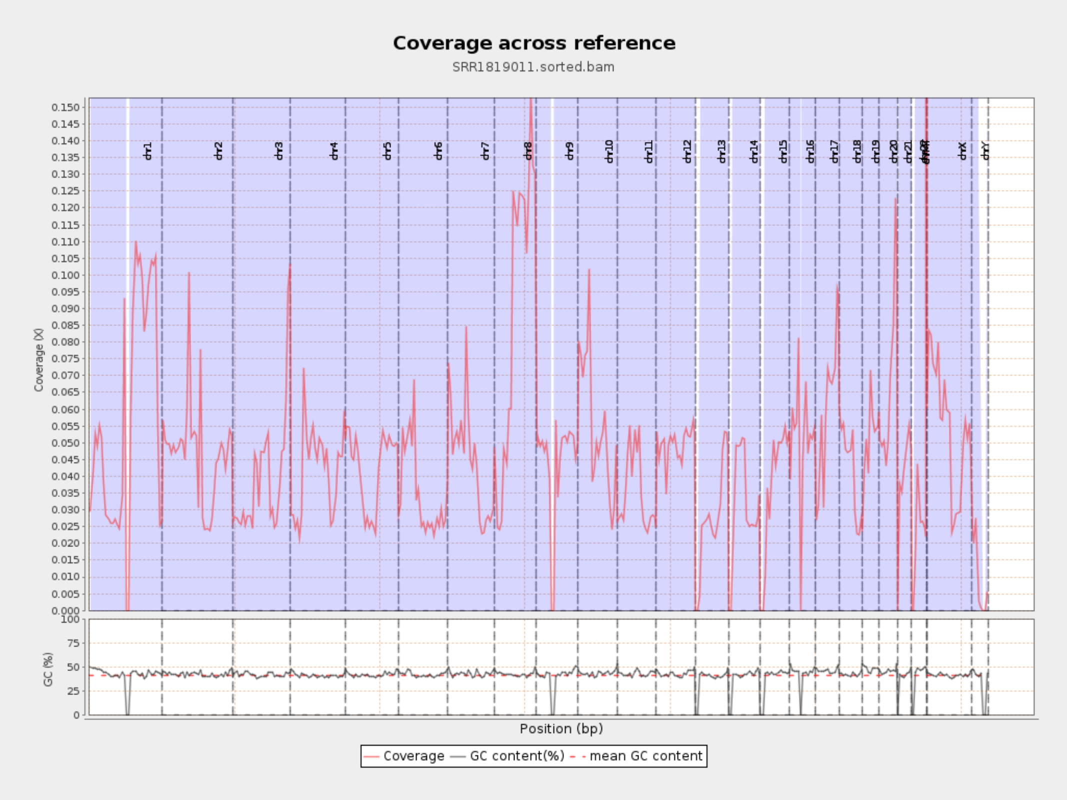
General error rate	0.68%
Mismatches	918,681
Insertions	23,890
Mapped reads with at least one insertion	1.5%
Deletions	47,373
Mapped reads with at least one deletion	3%
Homopolymer indels	39.64%

2.6. Chromosome stats

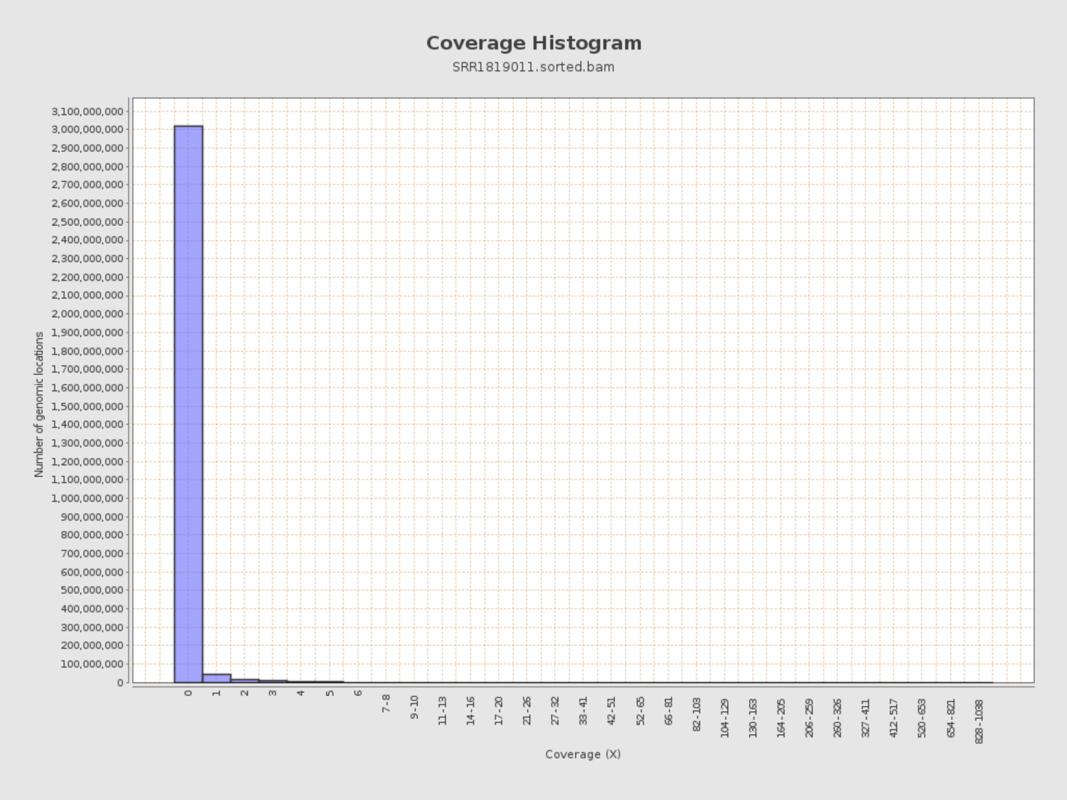
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14423198	0.0579	0.9998
chr2	243199373	11506512	0.0473	0.8743
chr3	198022430	7704350	0.0389	0.3314
chr4	191154276	7982039	0.0418	0.4037
chr5	180915260	7665488	0.0424	0.3597
chr6	171115067	5993208	0.035	0.3705
chr7	159138663	7126745	0.0448	0.7329

chr8	146364022	13118073	0.0896	0.5434
chr9	141213431	6135725	0.0435	0.5519
chr10	135534747	7511347	0.0554	0.7459
chr11	135006516	4808394	0.0356	0.3767
chr12	133851895	6629396	0.0495	0.38
chr13	115169878	3139836	0.0273	0.2785
chr14	107349540	3331723	0.031	0.3195
chr15	102531392	3752344	0.0366	0.3224
chr16	90354753	4613811	0.0511	0.7127
chr17	81195210	4890044	0.0602	0.473
chr18	78077248	3299918	0.0423	0.5517
chr19	59128983	3066656	0.0519	0.8582
chr20	63025520	4299488	0.0682	0.4787
chr21	48129895	1940698	0.0403	0.3611
chr22	51304566	1108584	0.0216	0.2683
chrMT	16571	21675	1.308	1.7752
chrX	155270560	8522583	0.0549	0.4469
chrY	59373566	561819	0.0095	0.689

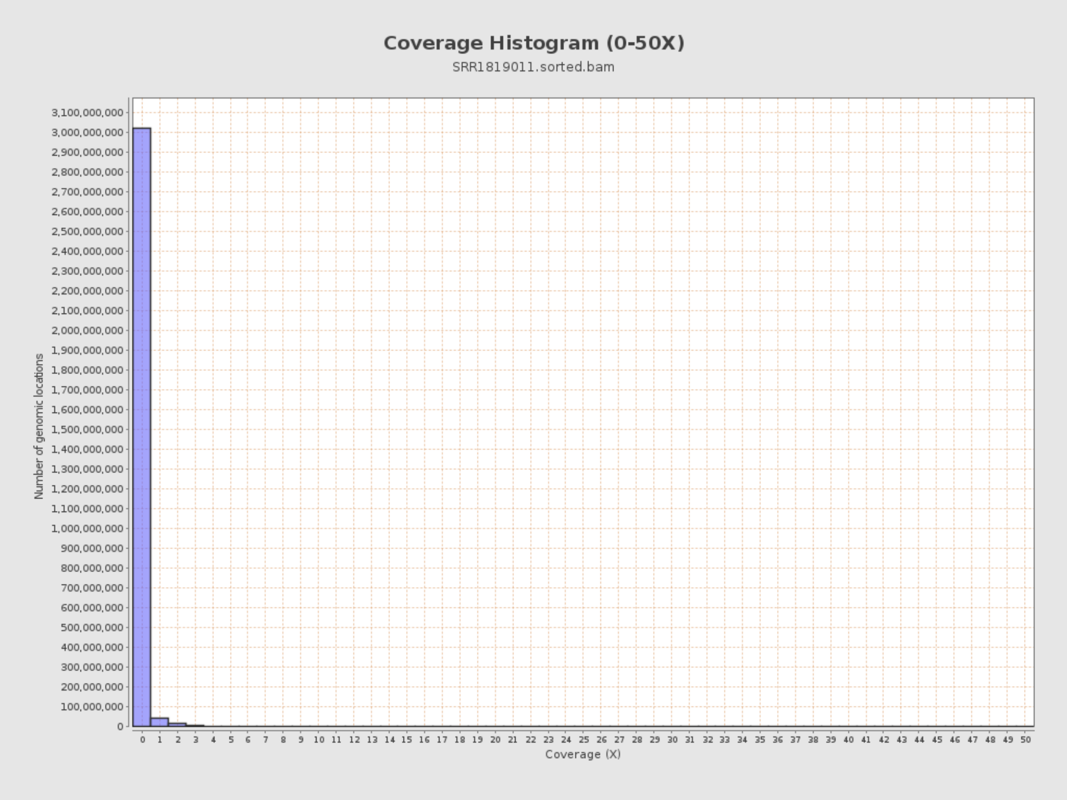
3. Results : Coverage across reference



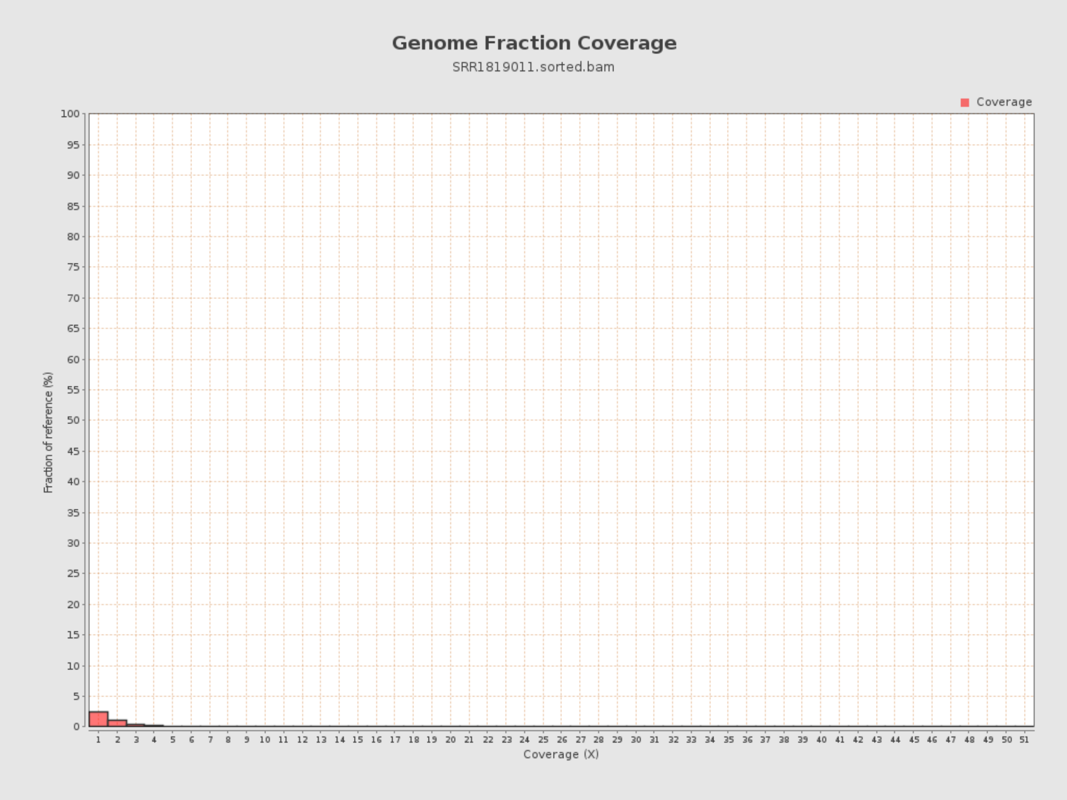
4. Results : Coverage Histogram



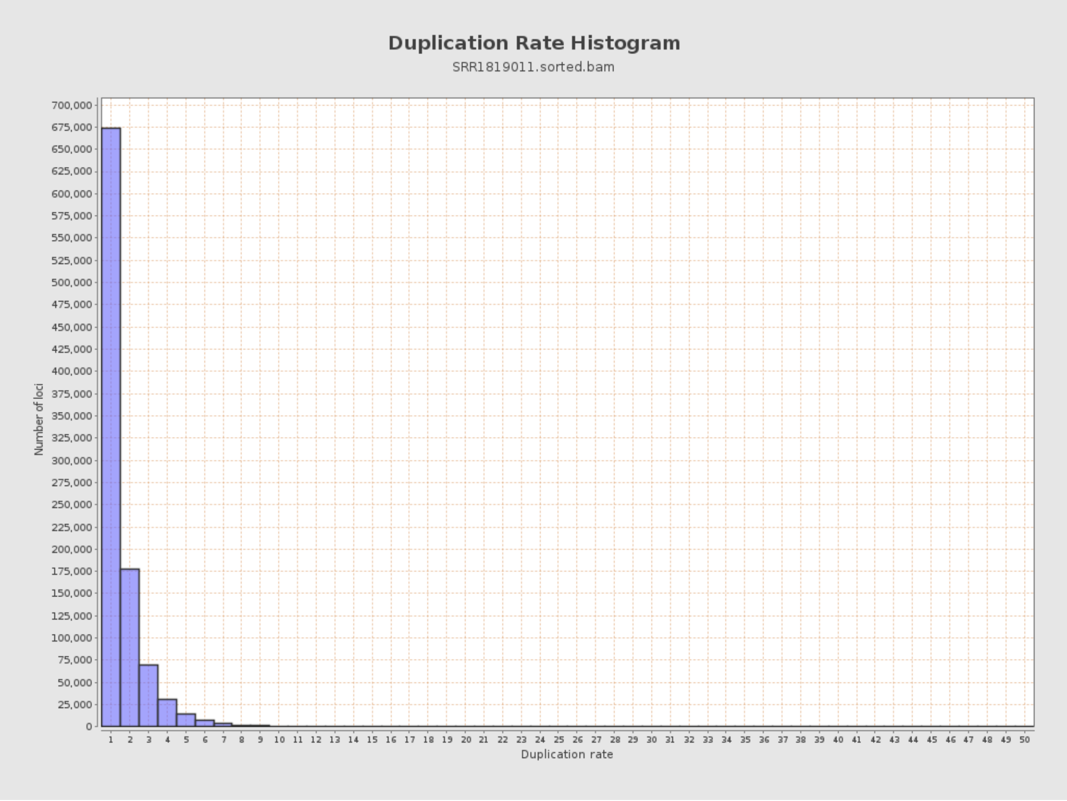
5. Results : Coverage Histogram (0-50X)



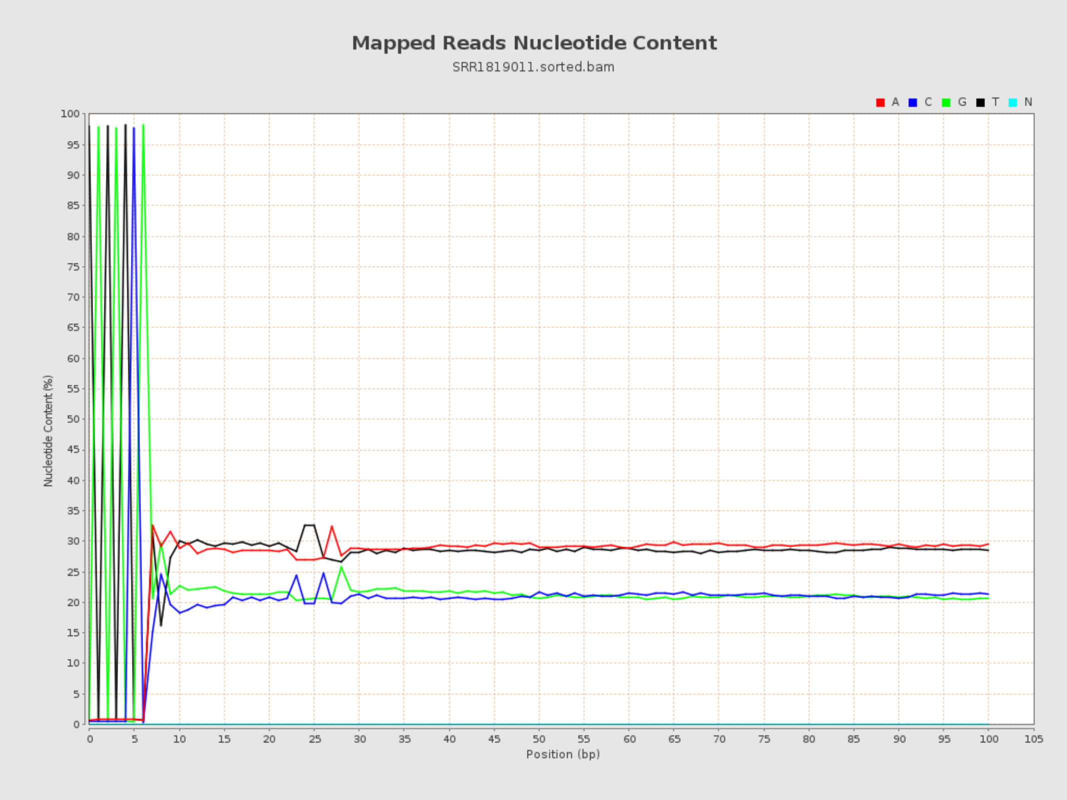
6. Results : Genome Fraction Coverage



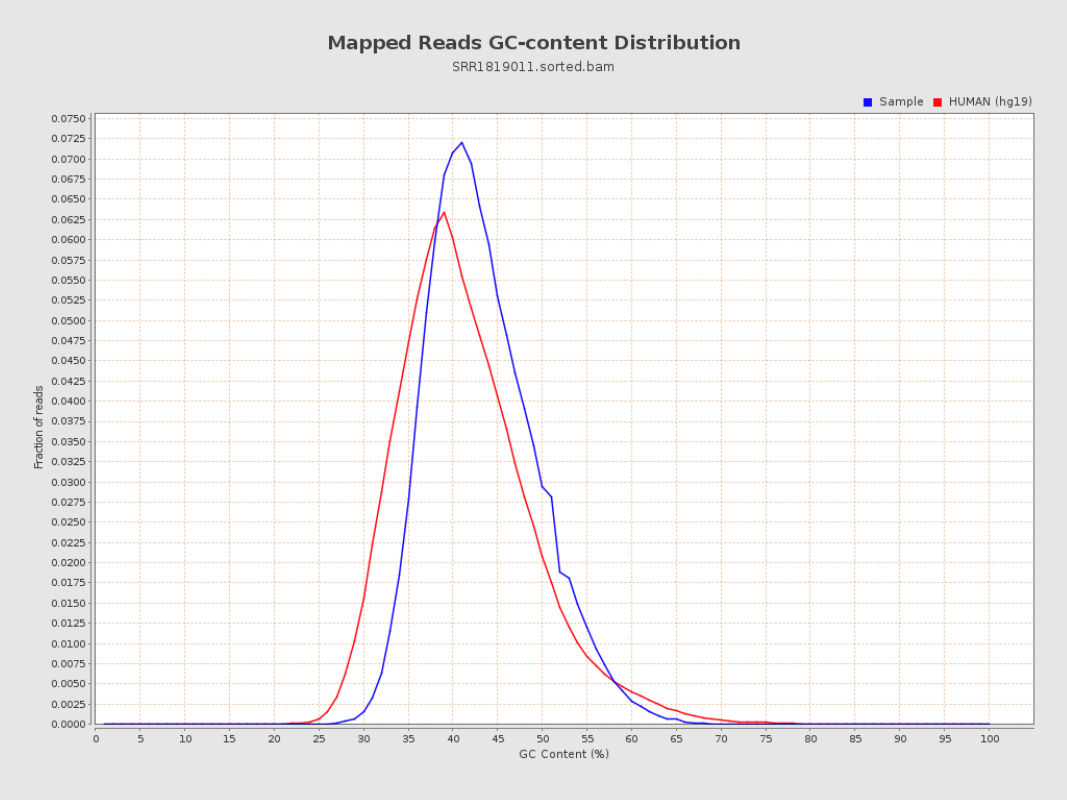
7. Results : Duplication Rate Histogram



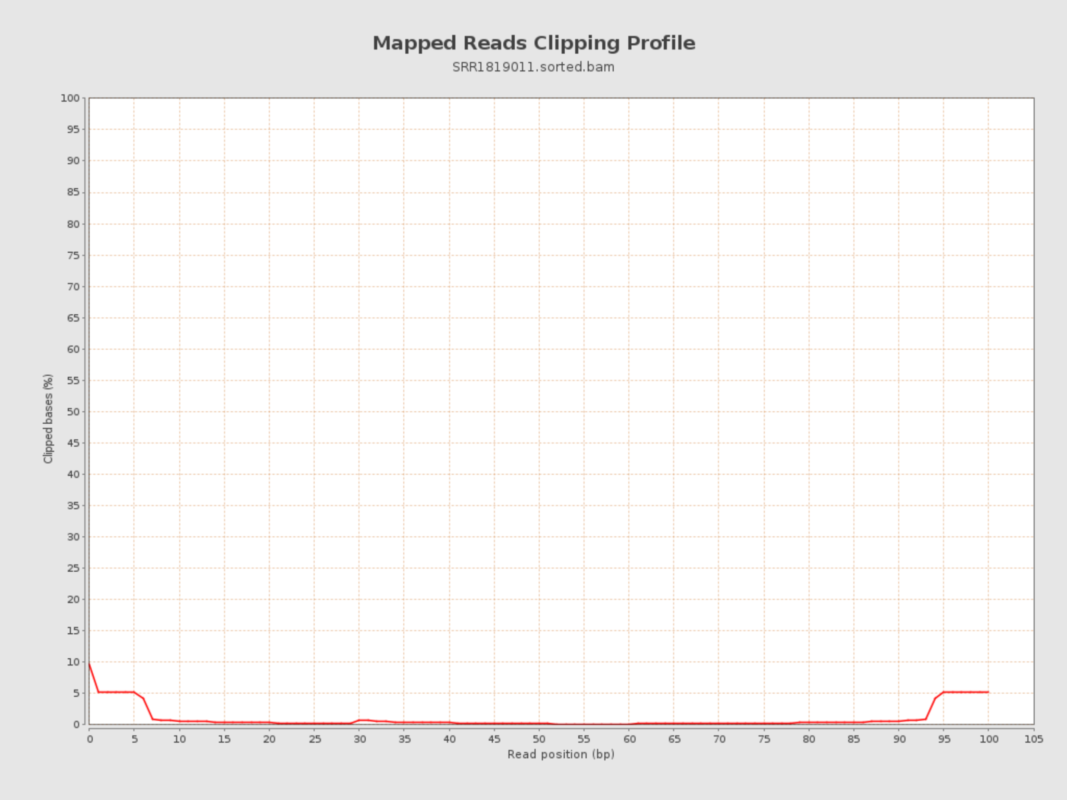
8. Results : Mapped Reads Nucleotide Content



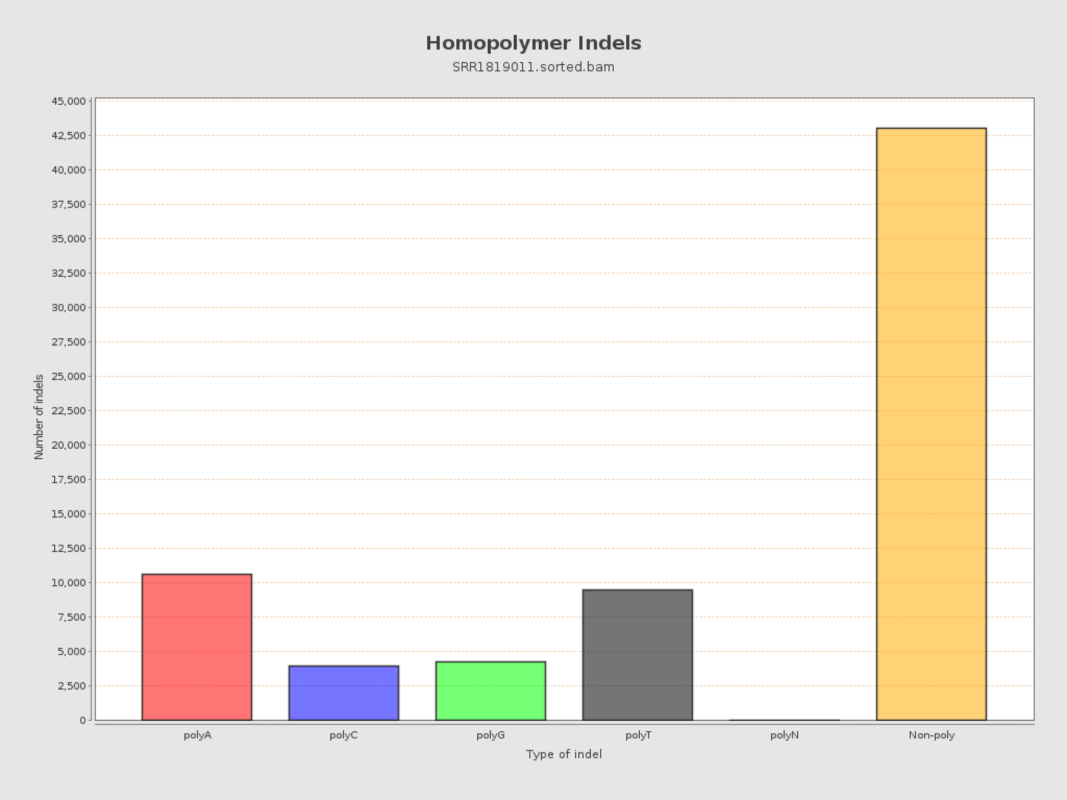
9. Results : Mapped Reads GC-content Distribution



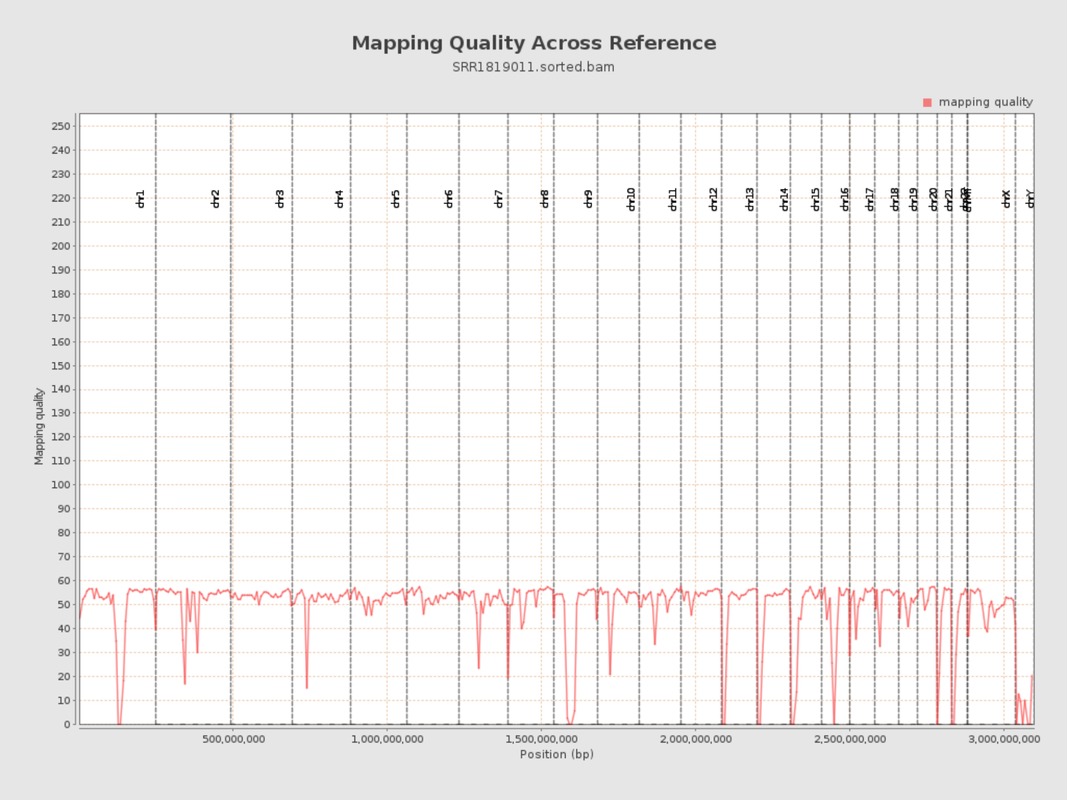
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram