Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:14:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819014.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_SRR1819014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:14:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,265,720
Mapped reads	3,069,204 / 93.98%
Unmapped reads	196,516 / 6.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	48,160 / 1.47%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	1,572,120 / 48.14%
Duplication rate	43.13%
Clipped reads	3,093,998 / 94.74%

2.2. ACGT Content

Number/percentage of A's	82,877,586 / 29.21%
Number/percentage of C's	59,580,615 / 21%
Number/percentage of T's	82,051,430 / 28.92%
Number/percentage of G's	59,223,337 / 20.87%
Number/percentage of N's	14,203 / 0.01%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0917

Standard Deviation	1.0568

2.4. Mapping Quality

Mean Mapping Quality	49.12

2.5. Mismatches and indels

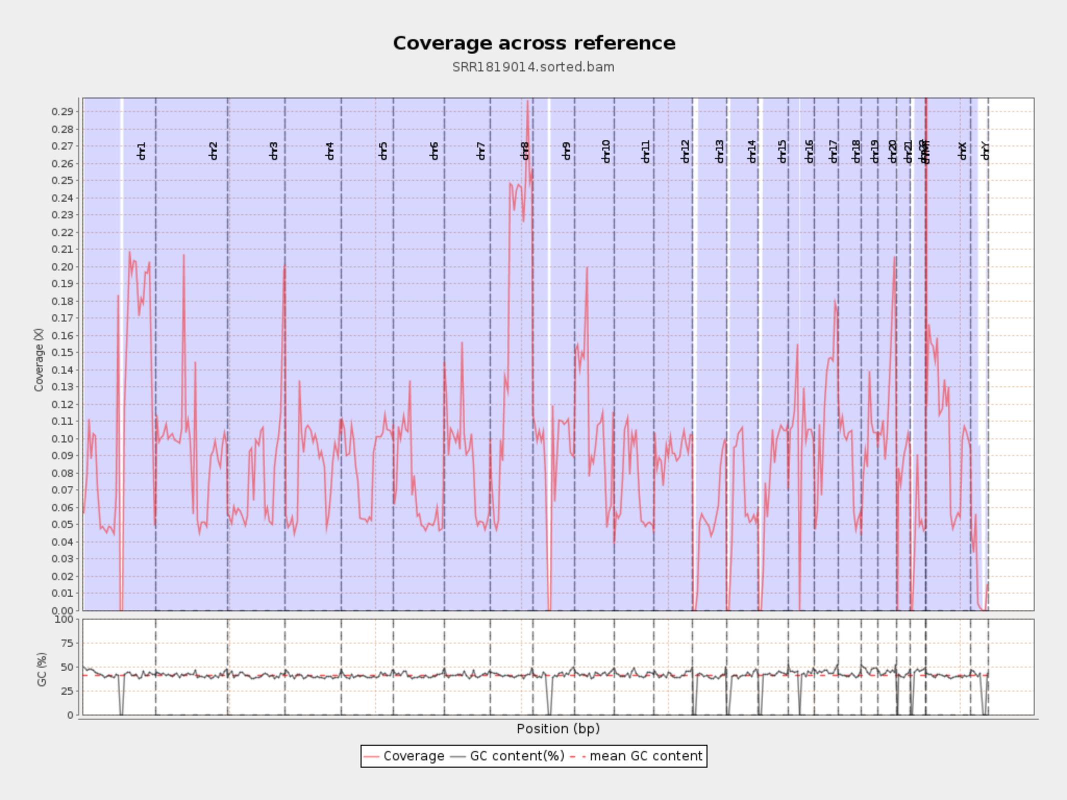
General error rate	0.67%
Mismatches	1,793,180
Insertions	45,987
Mapped reads with at least one insertion	1.46%
Deletions	91,970
Mapped reads with at least one deletion	2.93%
Homopolymer indels	40.99%

2.6. Chromosome stats

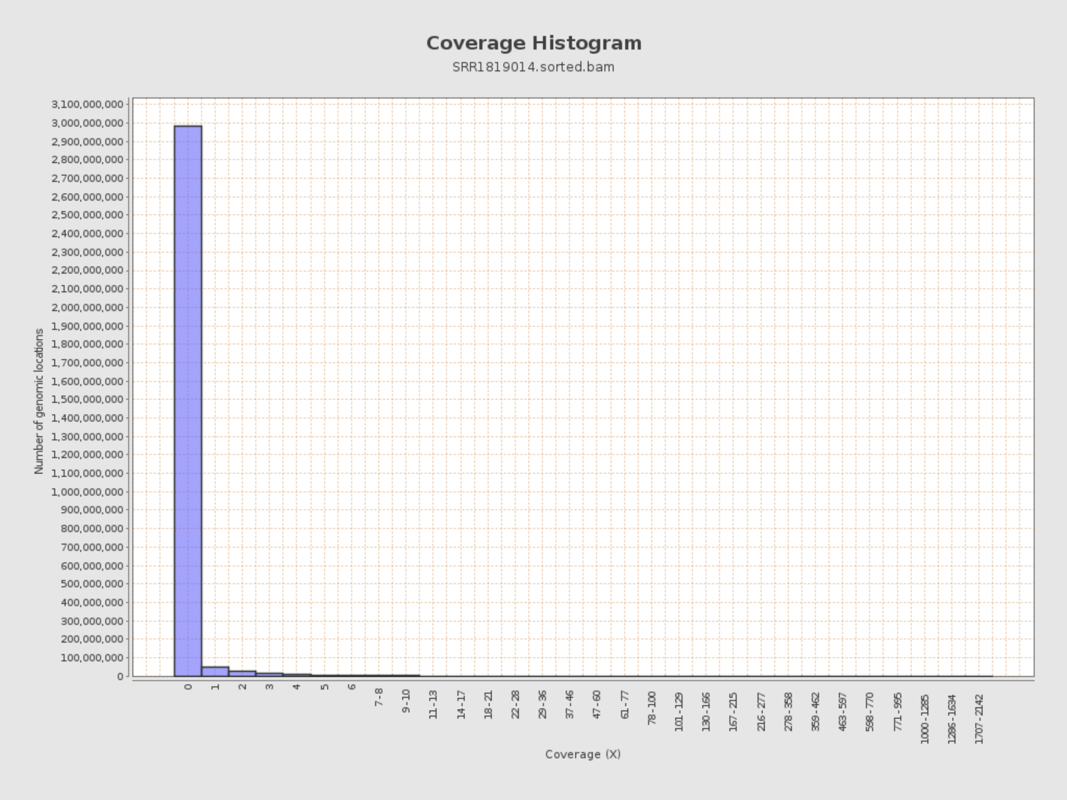
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27769928	0.1114	1.9266
chr2	243199373	22940272	0.0943	1.4714
chr3	198022430	15707046	0.0793	0.5715
chr4	191154276	15857154	0.083	0.6816
chr5	180915260	15825892	0.0875	0.6189
chr6	171115067	12117857	0.0708	0.682
chr7	159138663	13925731	0.0875	1.2522

chr8	146364022	26248075	0.1793	0.9906
chr9	141213431	12557990	0.0889	1.0078
chr10	135534747	14945885	0.1103	1.3476
chr11	135006516	9551647	0.0707	0.6881
chr12	133851895	12421238	0.0928	0.6352
chr13	115169878	6014195	0.0522	0.4582
chr14	107349540	6752636	0.0629	0.5513
chr15	102531392	7559114	0.0737	0.5513
chr16	90354753	9003176	0.0996	1.1918
chr17	81195210	9653172	0.1189	0.7904
chr18	78077248	6781727	0.0869	1.1373
chr19	59128983	5814929	0.0983	1.7559
chr20	63025520	8326635	0.1321	0.8061
chr21	48129895	3899011	0.081	0.6536
chr22	51304566	2174678	0.0424	0.4657
chrMT	16571	50321	3.0367	4.0051
chrX	155270560	16927705	0.109	0.7854
chrY	59373566	1092310	0.0184	1.1693

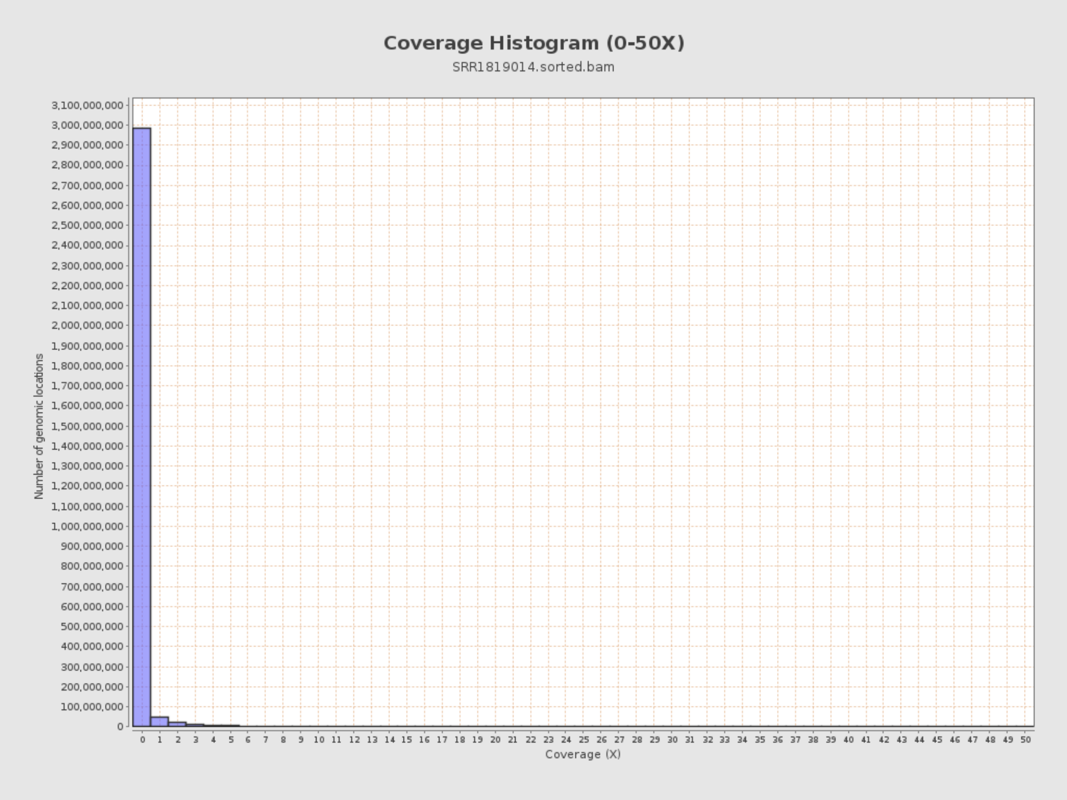
3. Results : Coverage across reference



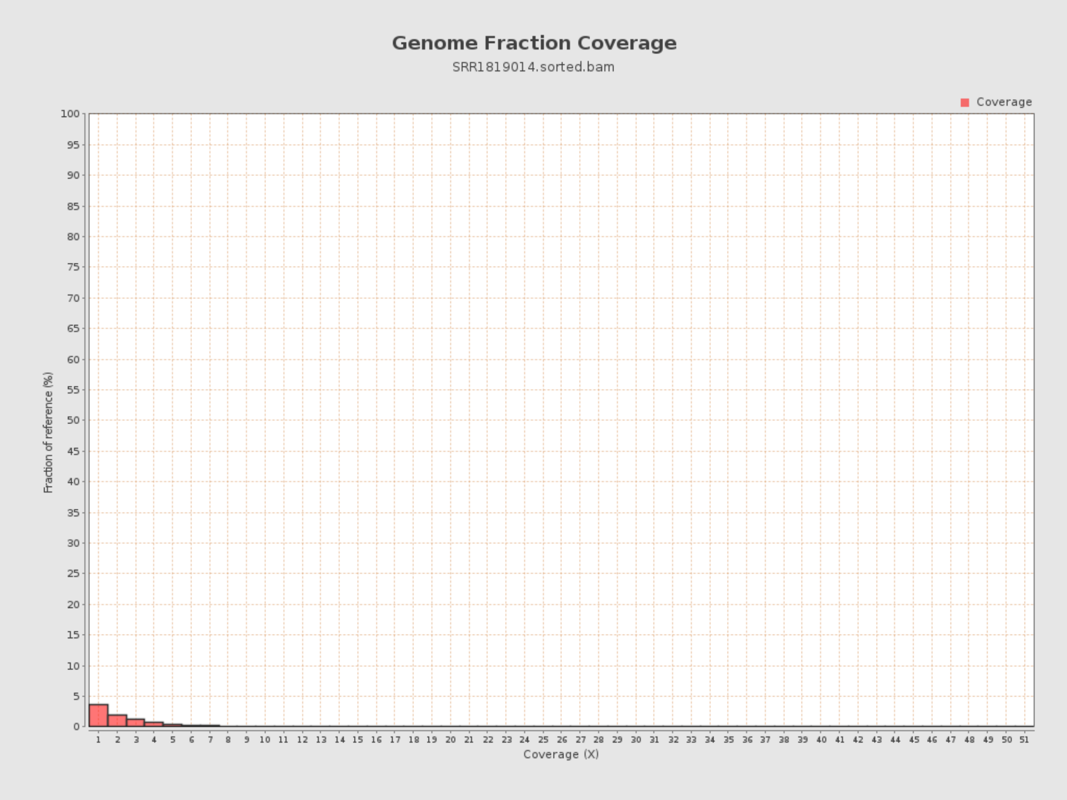
4. Results : Coverage Histogram



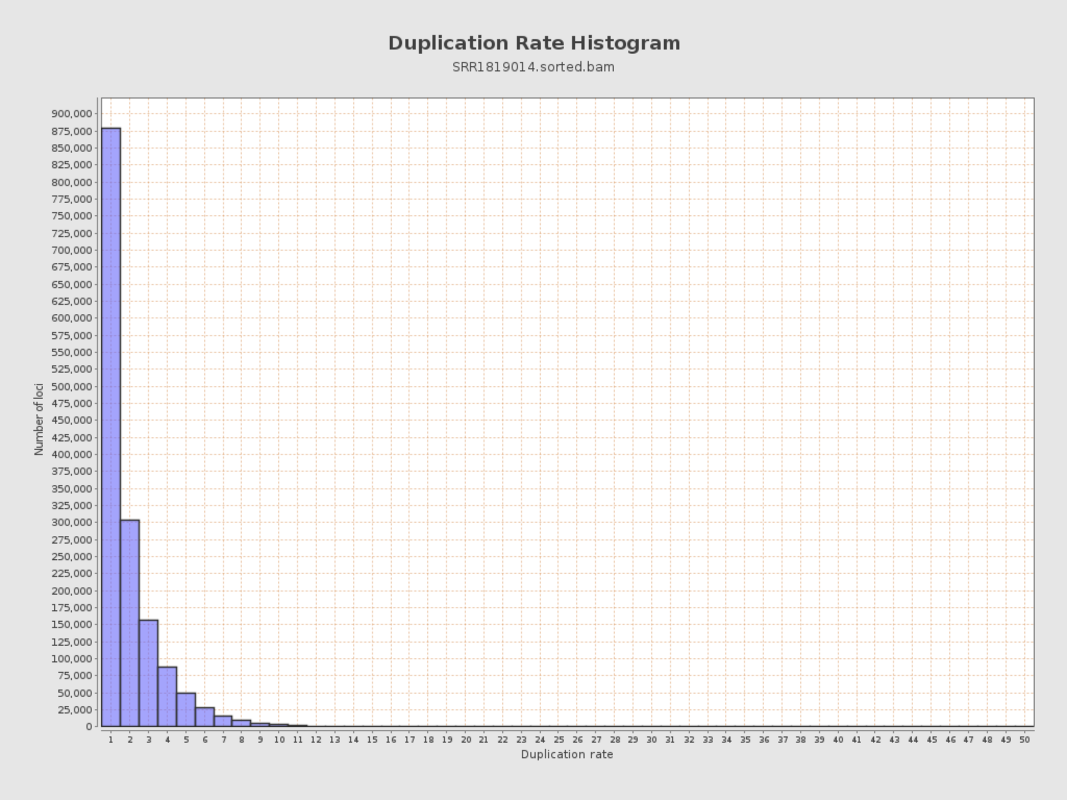
5. Results : Coverage Histogram (0-50X)



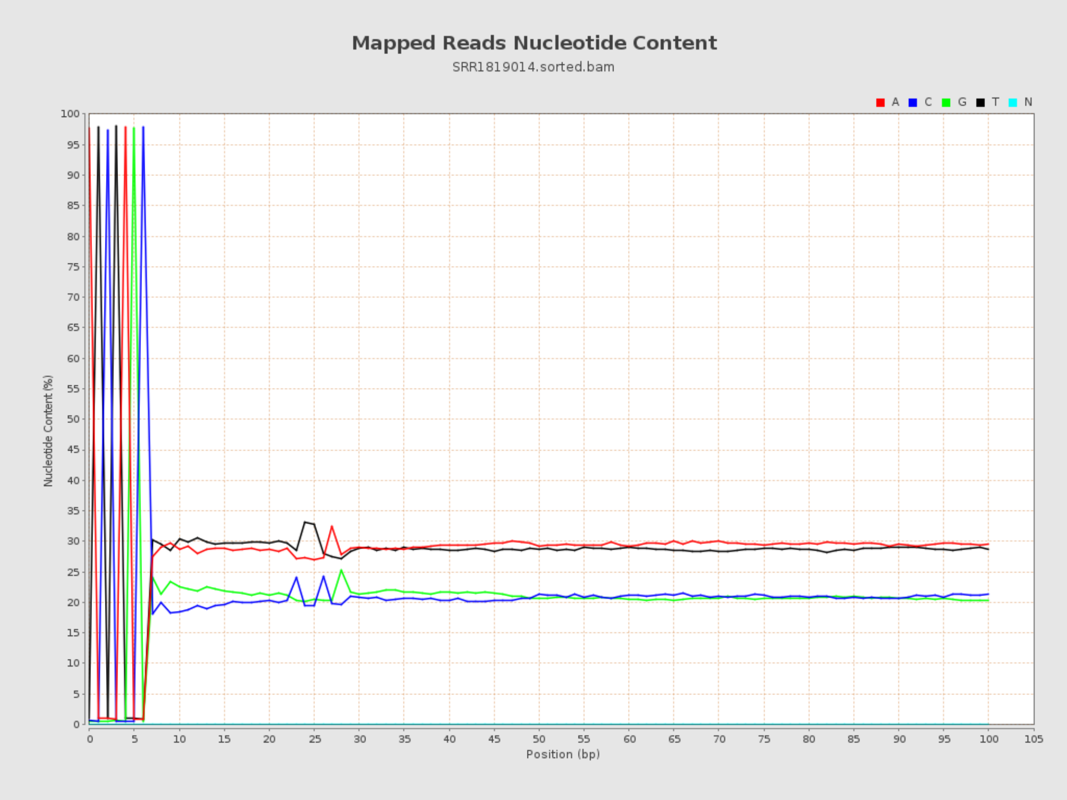
6. Results : Genome Fraction Coverage



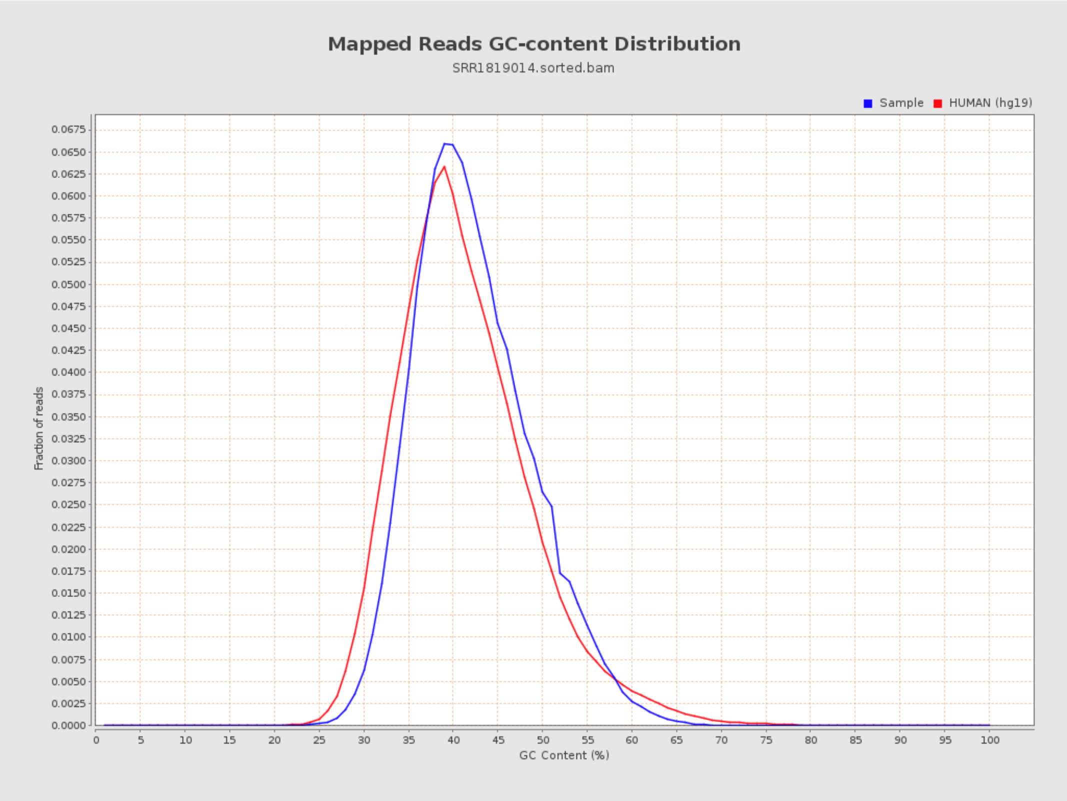
7. Results : Duplication Rate Histogram



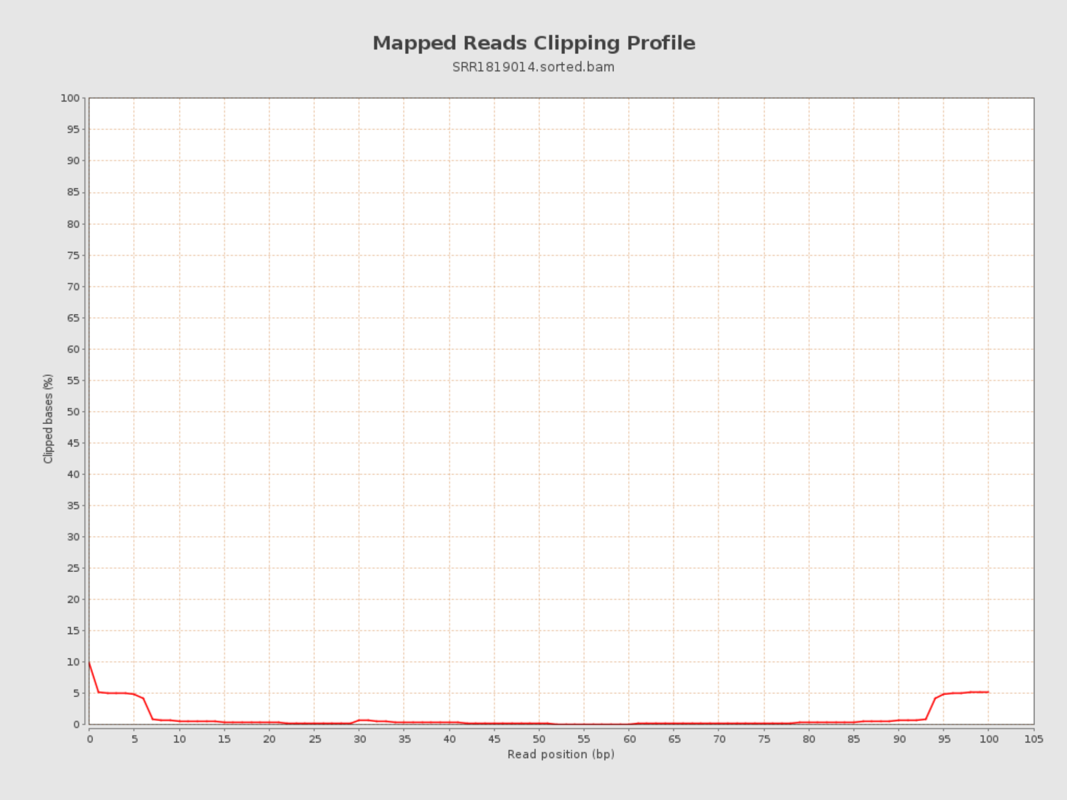
8. Results : Mapped Reads Nucleotide Content



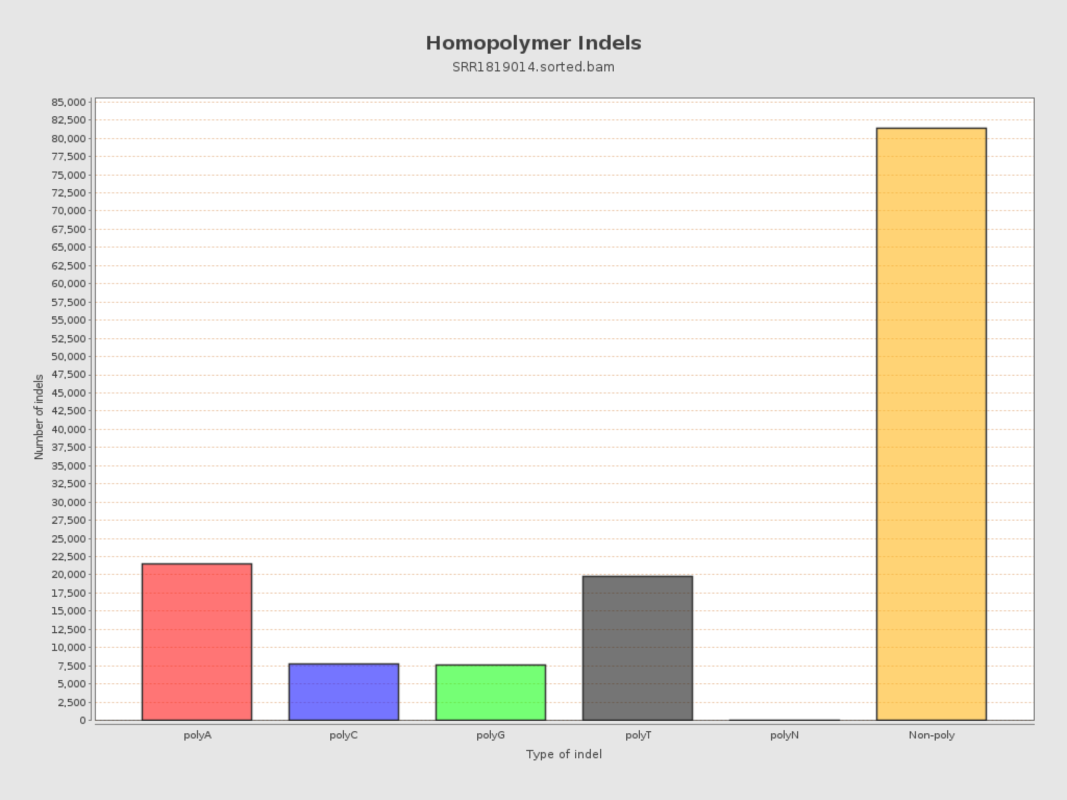
9. Results : Mapped Reads GC-content Distribution



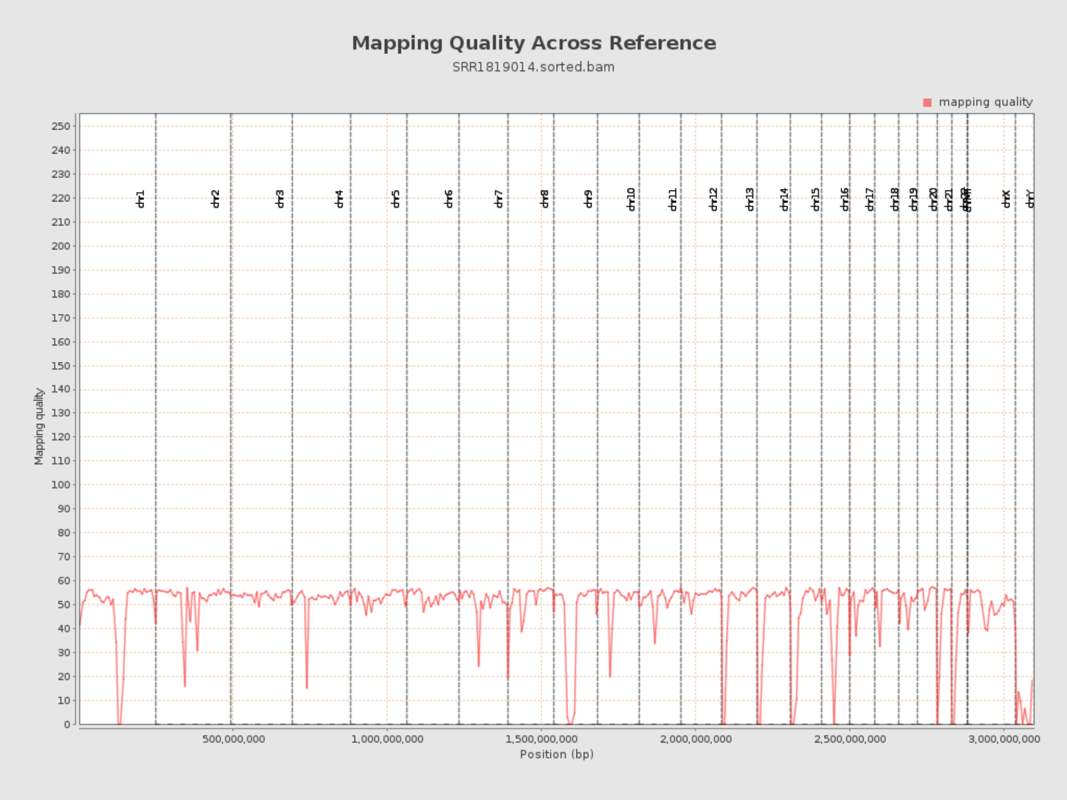
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram