Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:24:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716197.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_SRR9716197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716197.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:24:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,227,830
Mapped reads	2,695,334 / 51.56%
Unmapped reads	2,532,496 / 48.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	70,114 / 1.34%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	109,031 / 2.09%
Duplication rate	2.91%
Clipped reads	2,761,625 / 52.83%

2.2. ACGT Content

Number/percentage of A's	53,490,314 / 26.62%
Number/percentage of C's	39,958,846 / 19.89%
Number/percentage of T's	59,785,168 / 29.76%
Number/percentage of G's	47,665,032 / 23.72%
Number/percentage of N's	24,034 / 0.01%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0649

Standard Deviation	0.4599

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

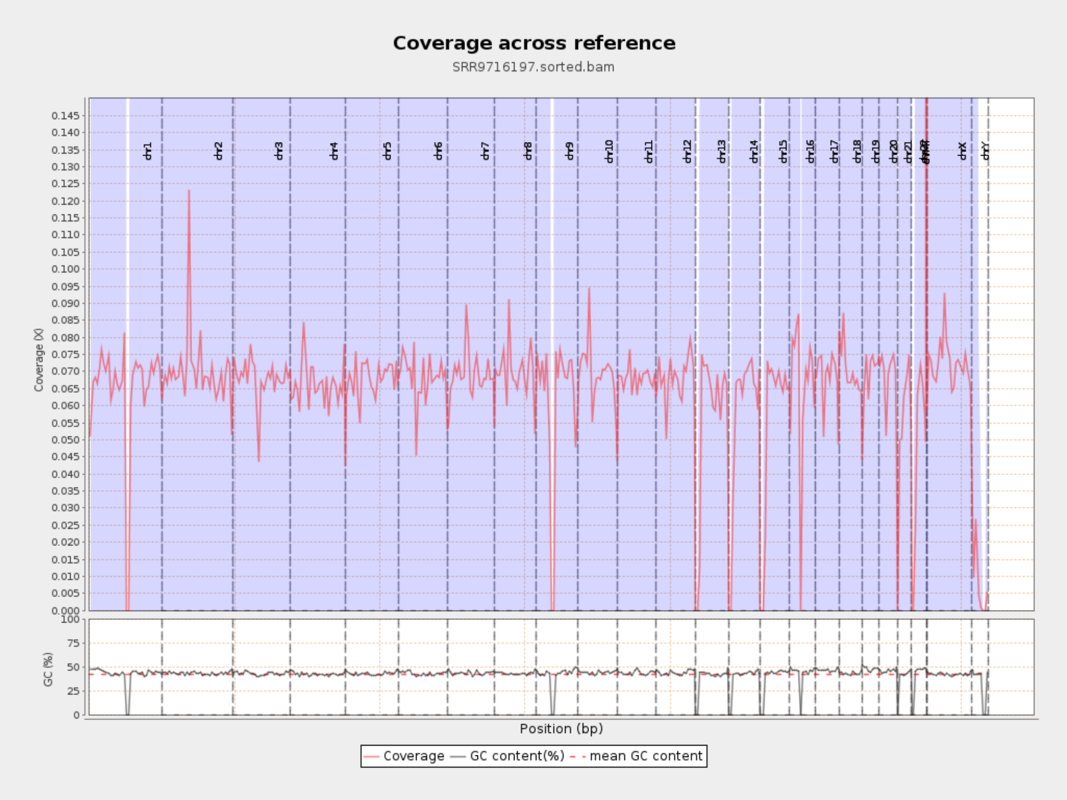
General error rate	0.75%
Mismatches	1,480,193
Insertions	16,417
Mapped reads with at least one insertion	0.6%
Deletions	40,655
Mapped reads with at least one deletion	1.49%
Homopolymer indels	40.21%

2.6. Chromosome stats

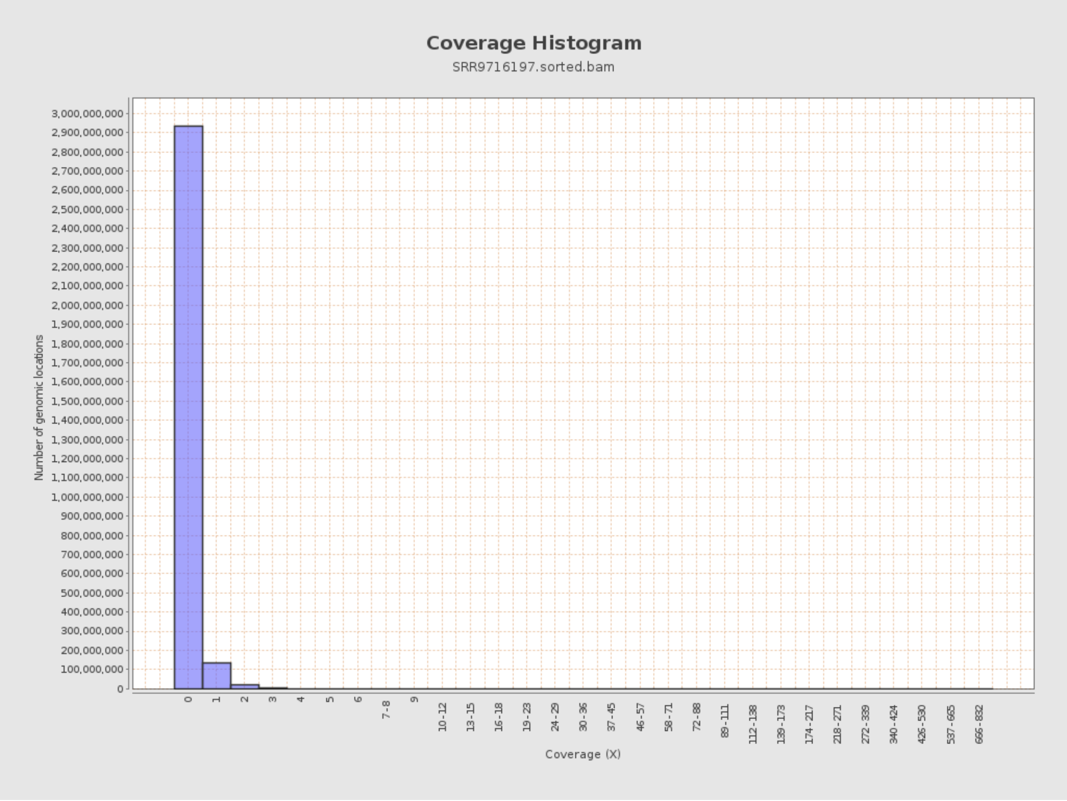
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16042815	0.0644	0.5361
chr2	243199373	17116773	0.0704	0.7193
chr3	198022430	13421442	0.0678	0.308
chr4	191154276	12665736	0.0663	0.3389
chr5	180915260	12285004	0.0679	0.3132
chr6	171115067	11681533	0.0683	0.3488
chr7	159138663	11071656	0.0696	0.5337

chr8	146364022	10264827	0.0701	0.5929
chr9	141213431	8574250	0.0607	0.49
chr10	135534747	9489797	0.07	0.4536
chr11	135006516	9143967	0.0677	0.5
chr12	133851895	9112412	0.0681	0.3166
chr13	115169878	6357350	0.0552	0.2783
chr14	107349540	6054167	0.0564	0.3521
chr15	102531392	5634523	0.055	0.2833
chr16	90354753	5941070	0.0658	0.3463
chr17	81195210	5525031	0.068	0.3433
chr18	78077248	5526019	0.0708	0.8965
chr19	59128983	4109259	0.0695	0.4988
chr20	63025520	4296064	0.0682	0.3303
chr21	48129895	2634940	0.0547	0.3151
chr22	51304566	2283516	0.0445	0.2551
chrMT	16571	27461	1.6572	1.7862
chrX	155270560	11233036	0.0723	0.4069
chrY	59373566	501009	0.0084	0.2221

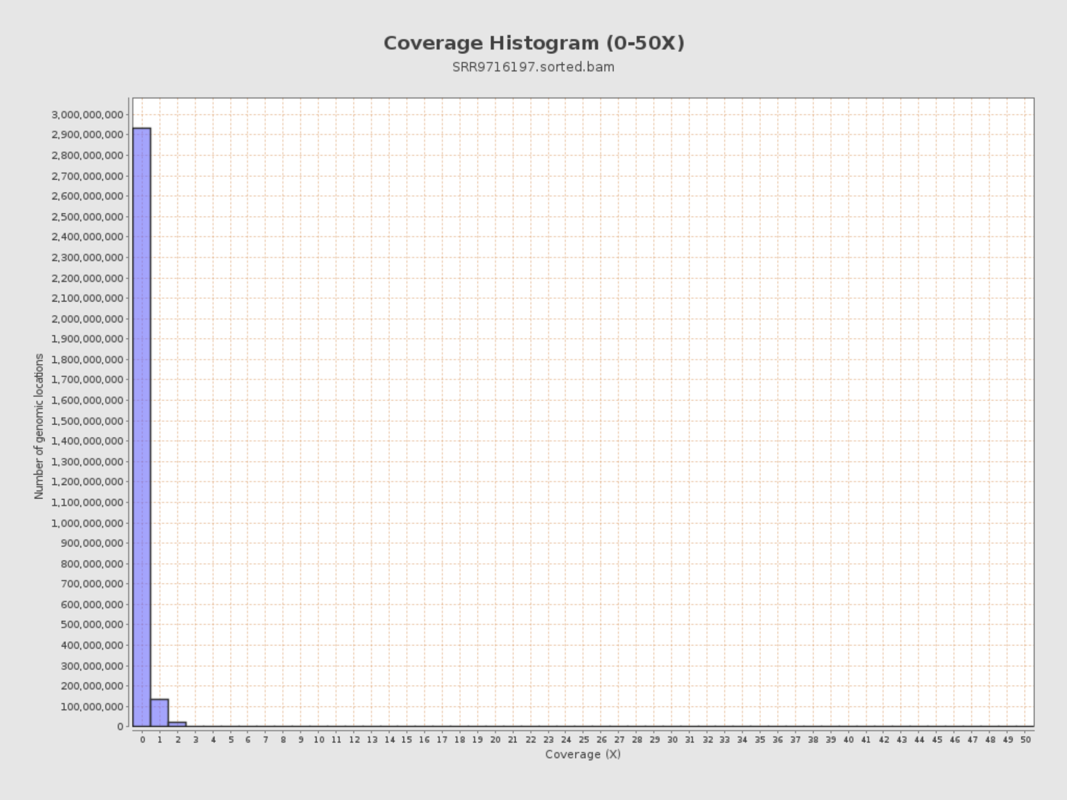
3. Results : Coverage across reference



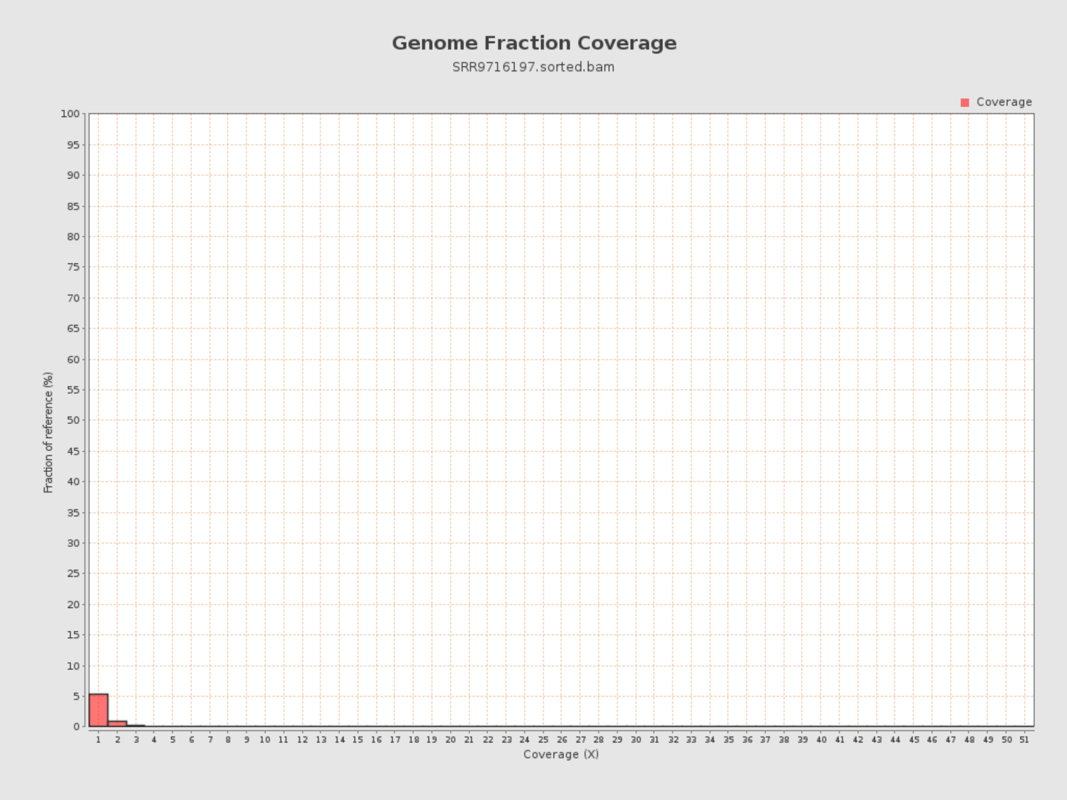
4. Results : Coverage Histogram



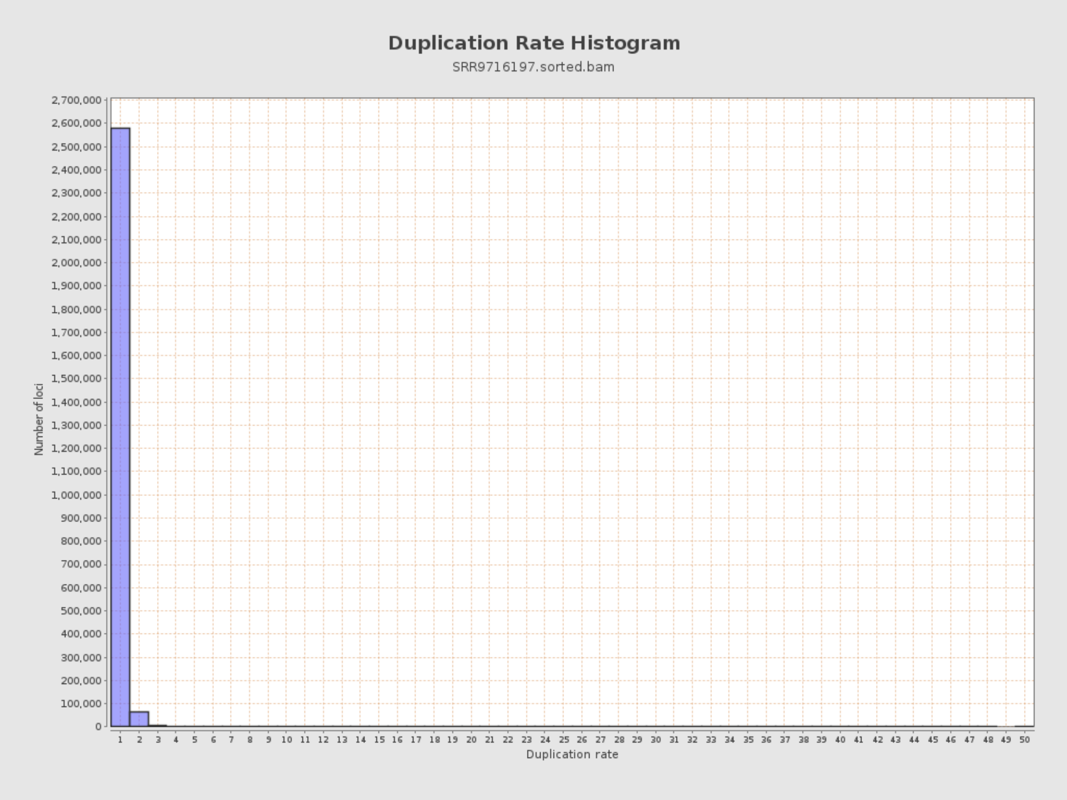
5. Results : Coverage Histogram (0-50X)



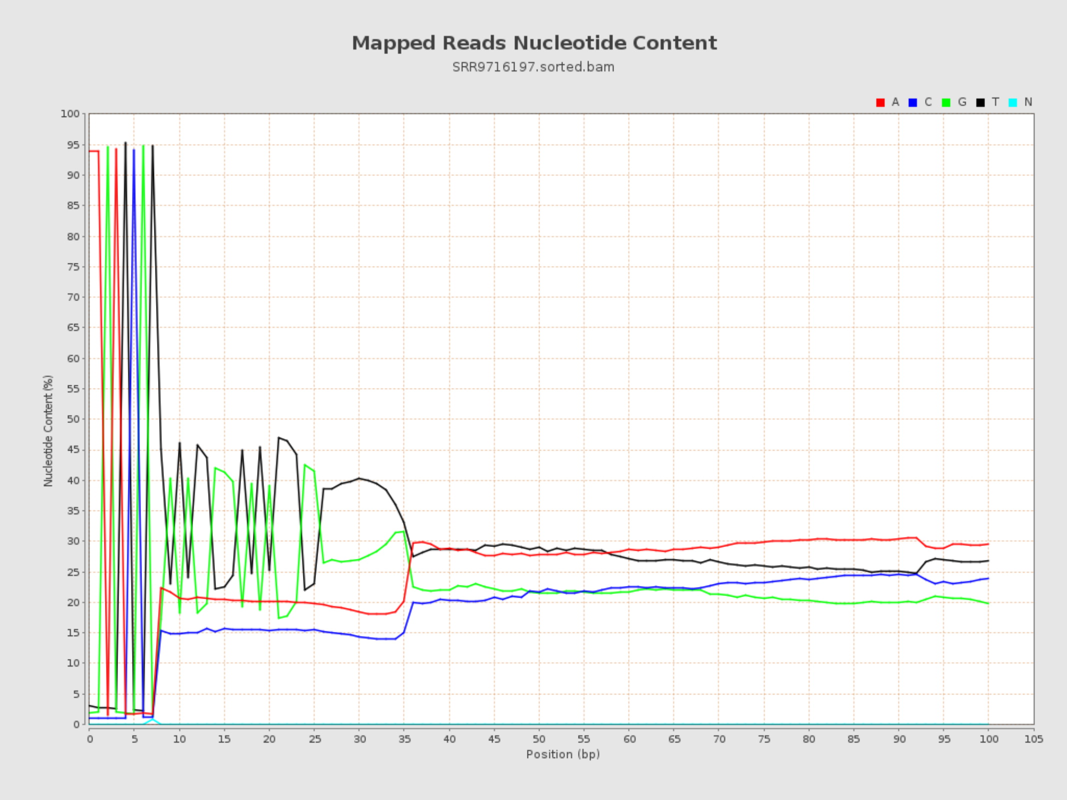
6. Results : Genome Fraction Coverage



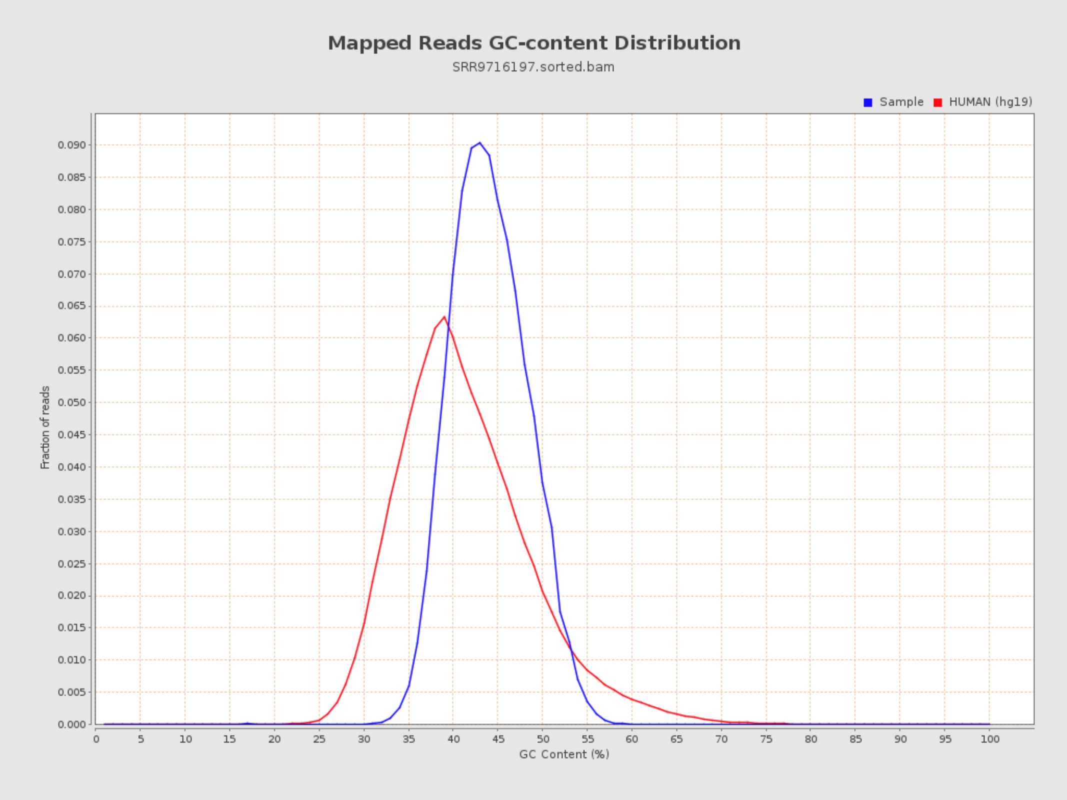
7. Results : Duplication Rate Histogram



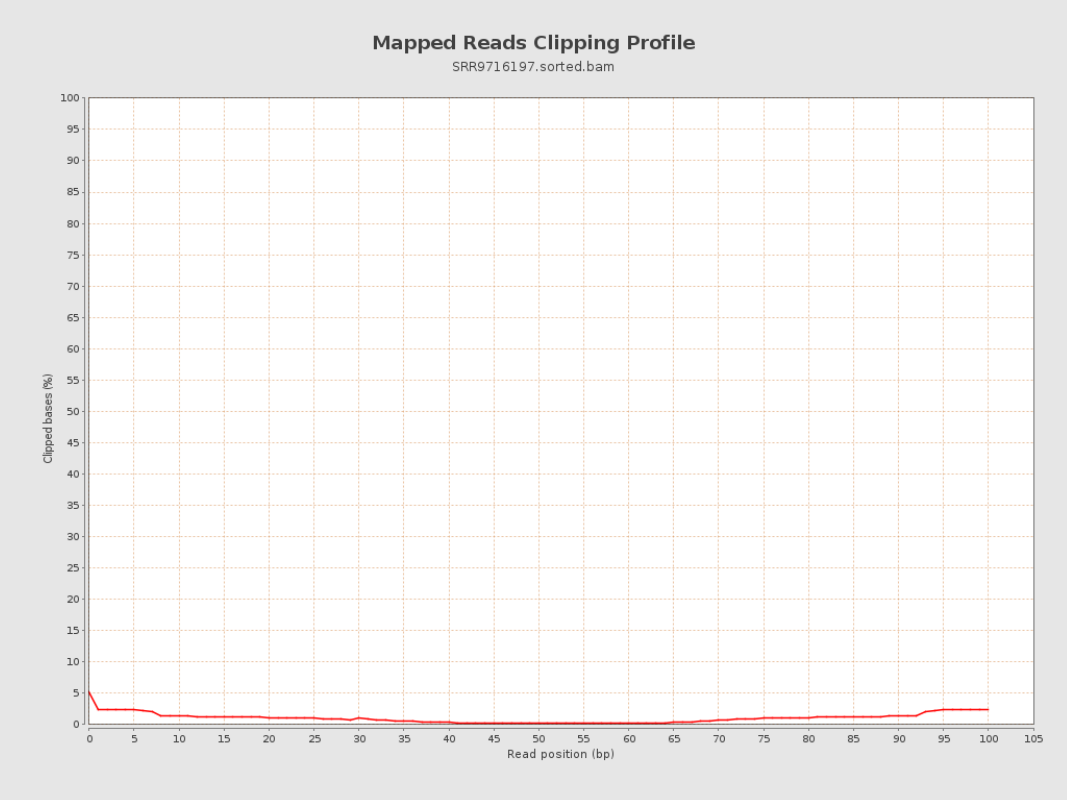
8. Results : Mapped Reads Nucleotide Content



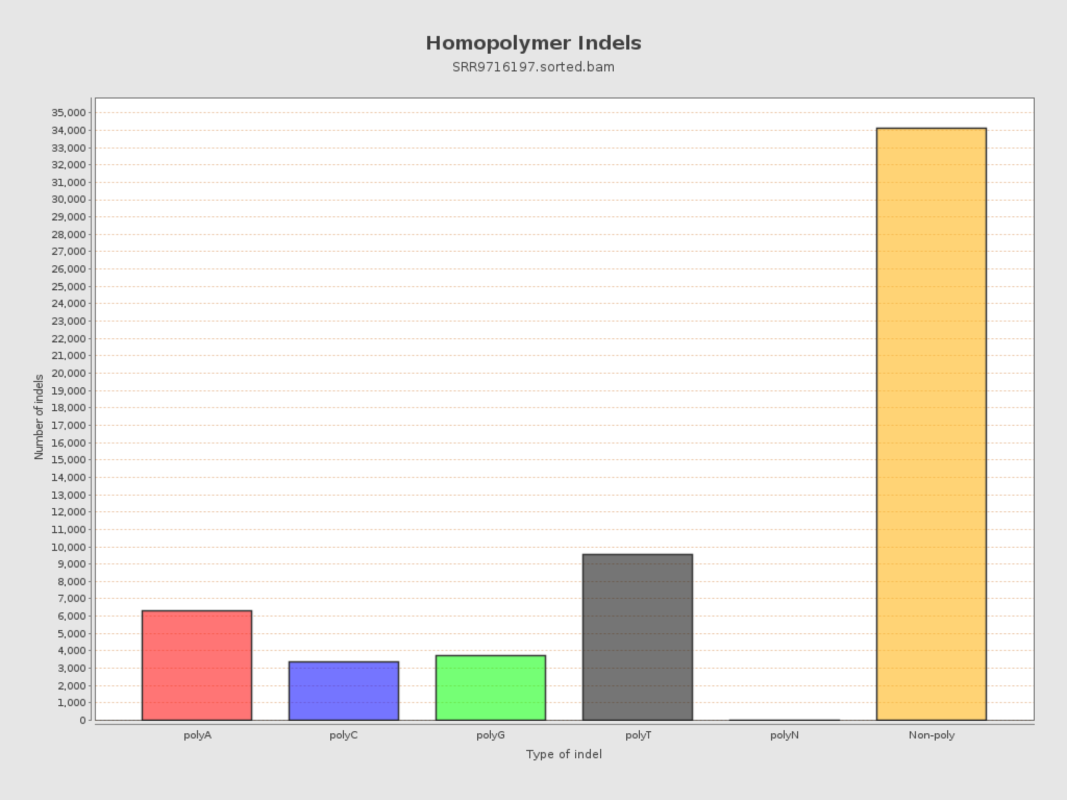
9. Results : Mapped Reads GC-content Distribution



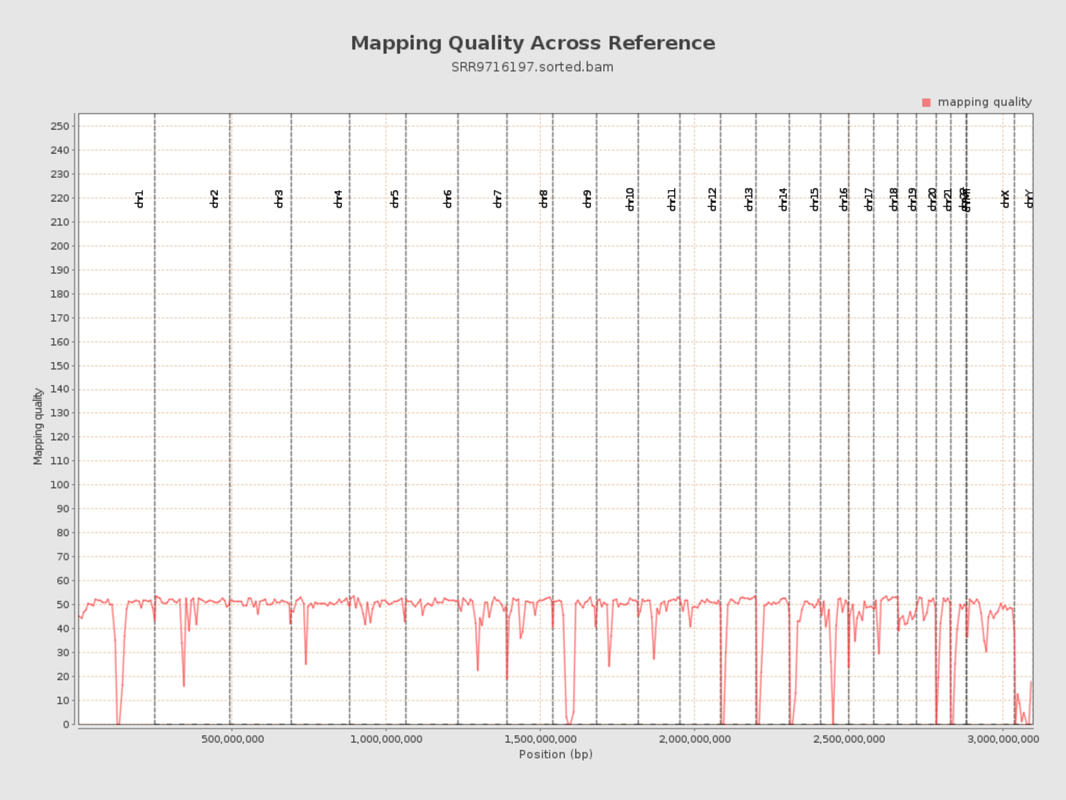
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram