Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:38:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716965.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_SRR9716965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:38:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,028,961
Mapped reads	953,384 / 92.66%
Unmapped reads	75,577 / 7.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,812 / 2.12%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	40,578 / 3.94%
Duplication rate	3.34%
Clipped reads	972,686 / 94.53%

2.2. ACGT Content

Number/percentage of A's	18,730,268 / 25.15%
Number/percentage of C's	15,006,671 / 20.15%
Number/percentage of T's	22,535,638 / 30.26%
Number/percentage of G's	18,201,366 / 24.44%
Number/percentage of N's	3,061 / 0%
GC Percentage	44.59%

2.3. Coverage

Mean	0.0241

Standard Deviation	0.2385

2.4. Mapping Quality

Mean Mapping Quality	46.62

2.5. Mismatches and indels

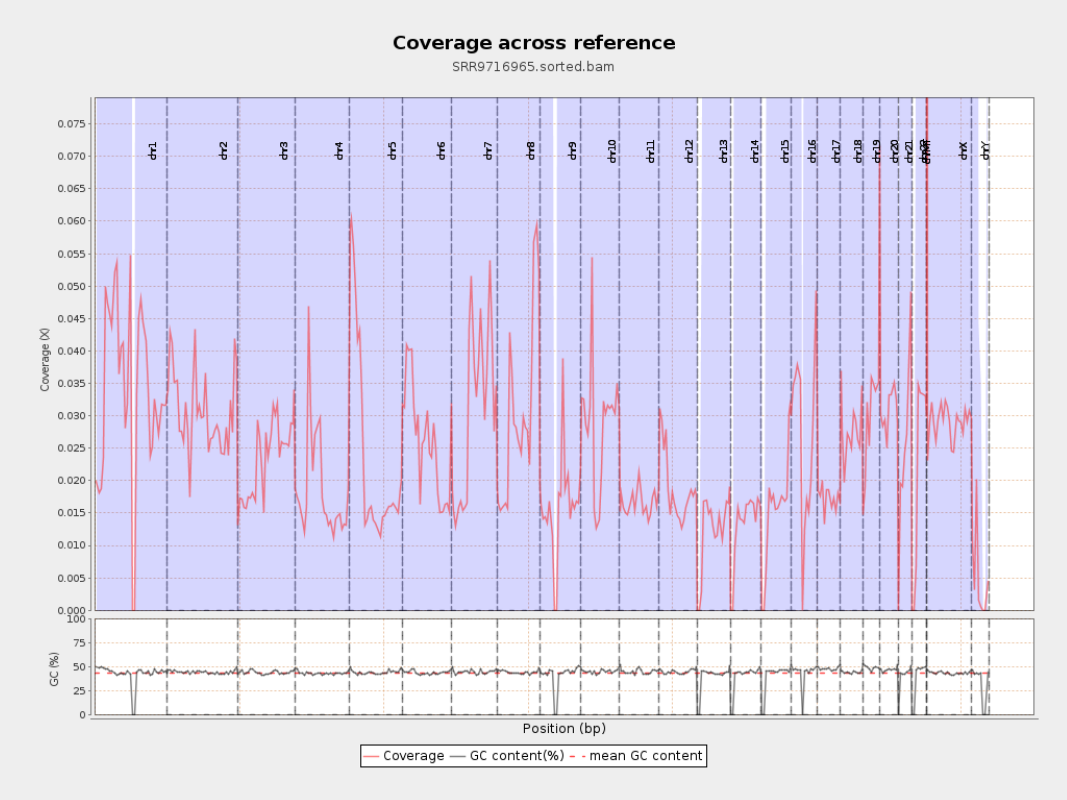
General error rate	0.7%
Mismatches	504,971
Insertions	7,176
Mapped reads with at least one insertion	0.74%
Deletions	14,934
Mapped reads with at least one deletion	1.54%
Homopolymer indels	39.04%

2.6. Chromosome stats

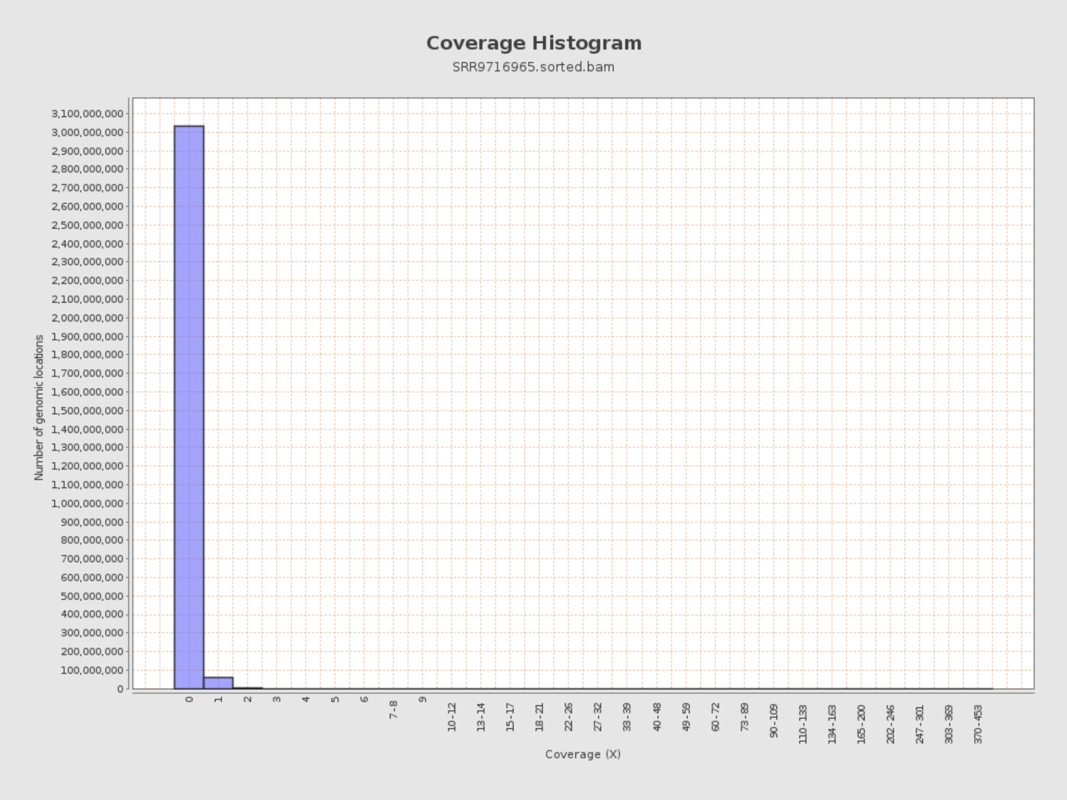
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8462515	0.034	0.457
chr2	243199373	7460415	0.0307	0.2524
chr3	198022430	4621456	0.0233	0.1692
chr4	191154276	3561898	0.0186	0.2067
chr5	180915260	4240171	0.0234	0.1727
chr6	171115067	4439642	0.0259	0.1871
chr7	159138663	4890353	0.0307	0.2826

chr8	146364022	4452964	0.0304	0.2538
chr9	141213431	2214529	0.0157	0.1647
chr10	135534747	3932519	0.029	0.2774
chr11	135006516	2243589	0.0166	0.1912
chr12	133851895	2537873	0.019	0.1529
chr13	115169878	1399618	0.0122	0.1221
chr14	107349540	1410910	0.0131	0.1348
chr15	102531392	1556164	0.0152	0.1356
chr16	90354753	2381237	0.0264	0.191
chr17	81195210	1402503	0.0173	0.1598
chr18	78077248	2140348	0.0274	0.2476
chr19	59128983	1868983	0.0316	0.3399
chr20	63025520	1941966	0.0308	0.2027
chr21	48129895	1273701	0.0265	0.2108
chr22	51304566	1156389	0.0225	0.1738
chrMT	16571	123354	7.444	6.1092
chrX	155270560	4506179	0.029	0.1981
chrY	59373566	288772	0.0049	0.1965

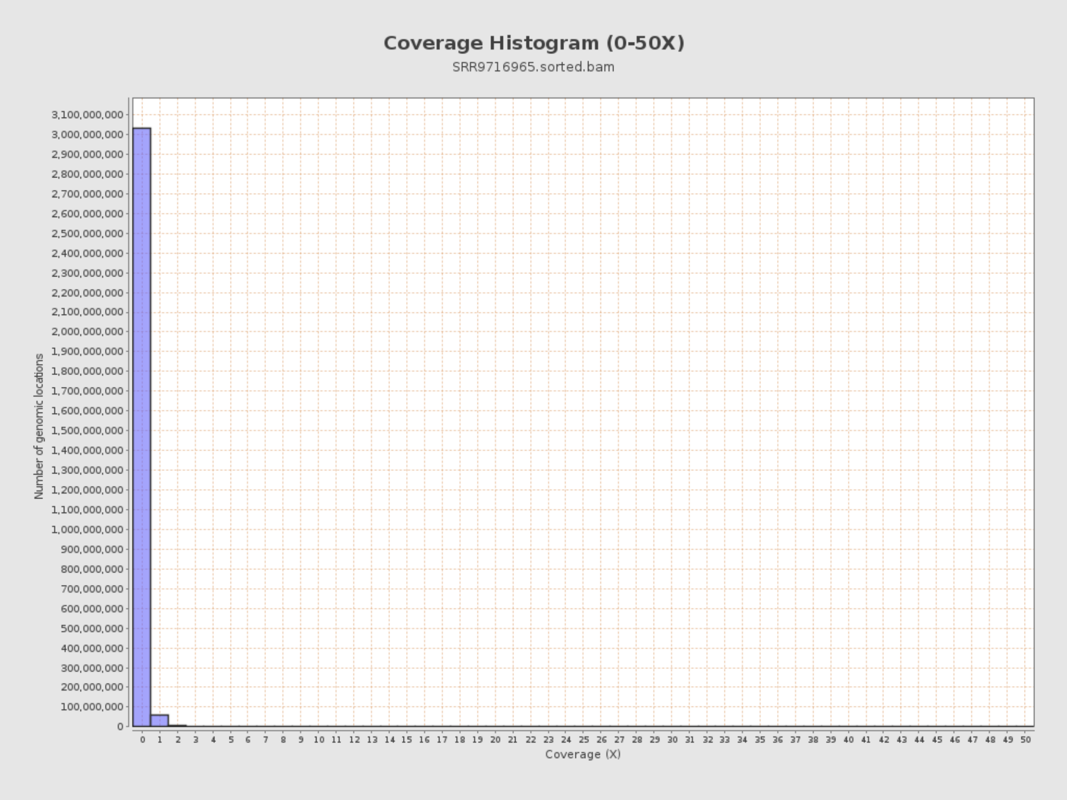
3. Results : Coverage across reference



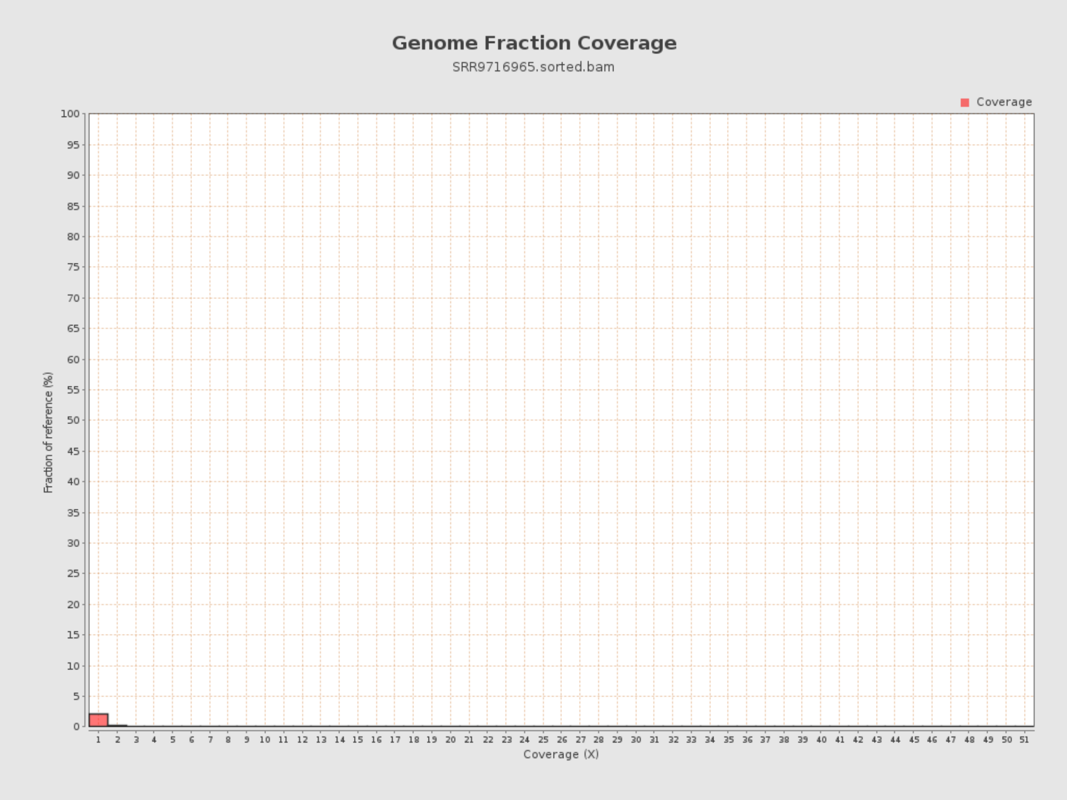
4. Results : Coverage Histogram



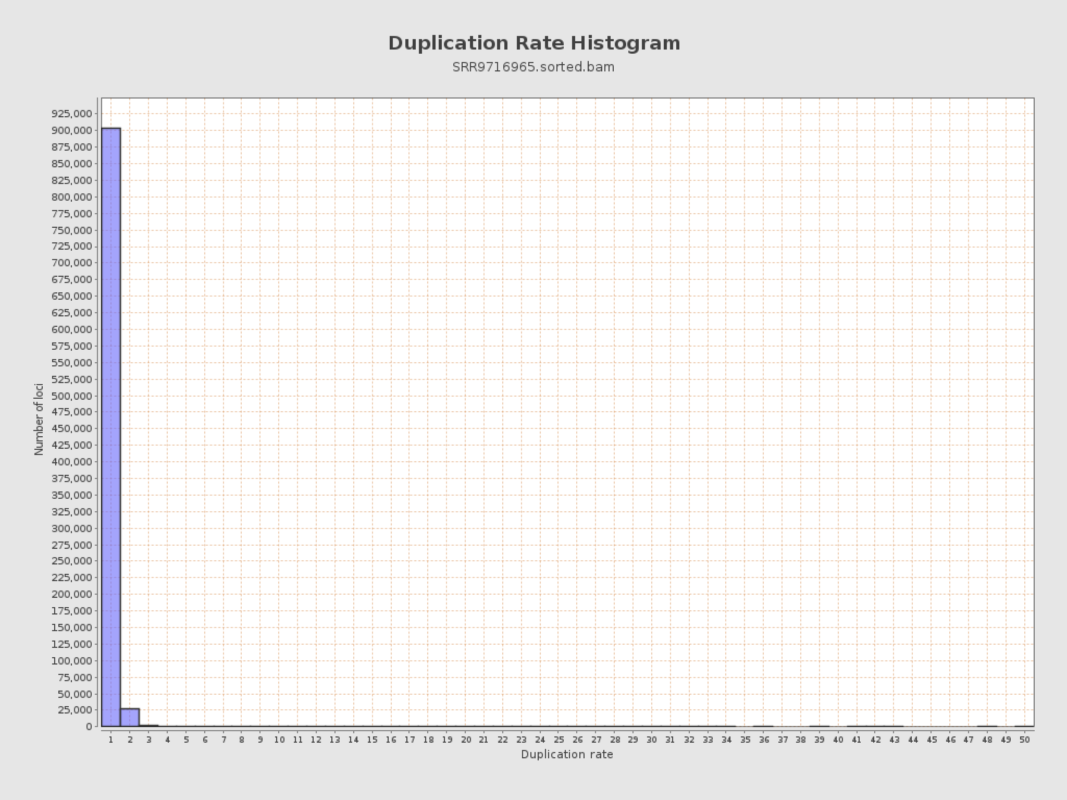
5. Results : Coverage Histogram (0-50X)



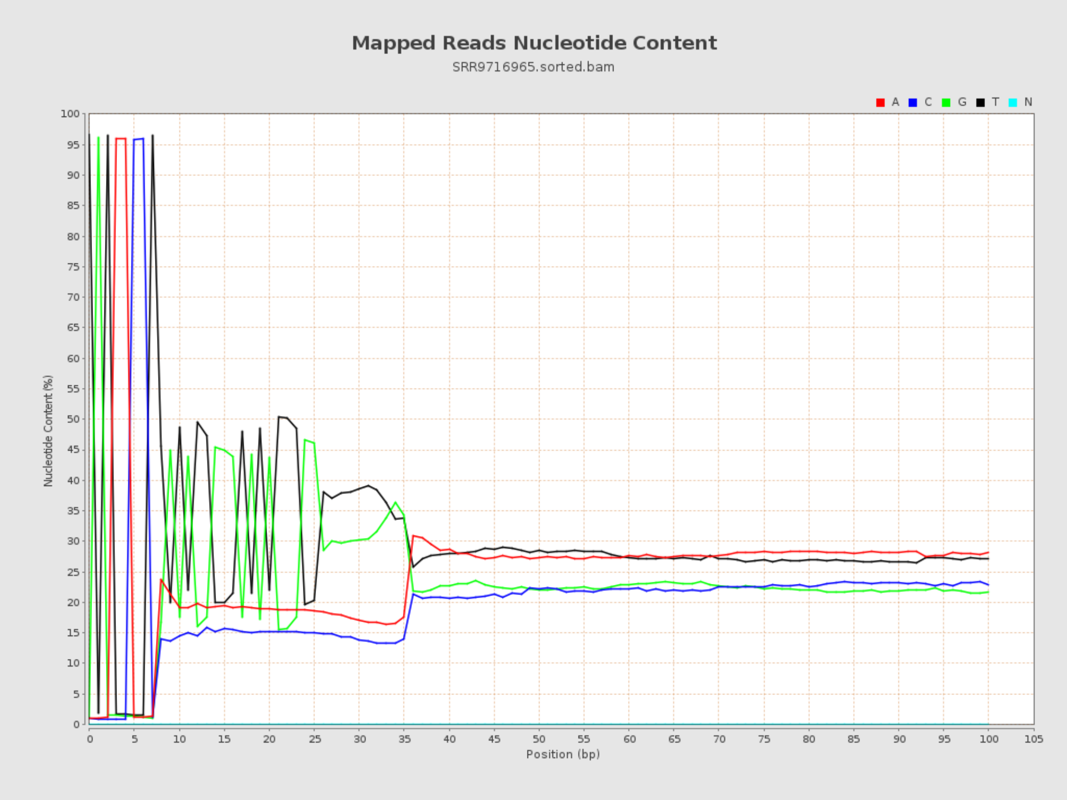
6. Results : Genome Fraction Coverage



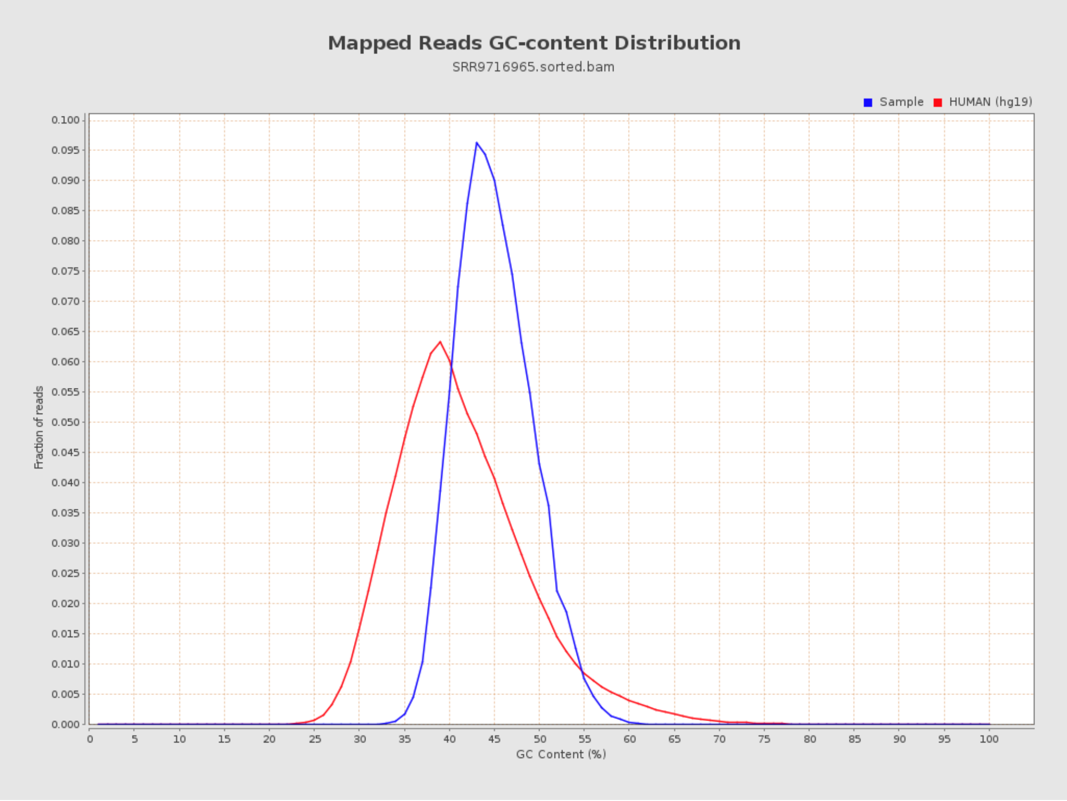
7. Results : Duplication Rate Histogram



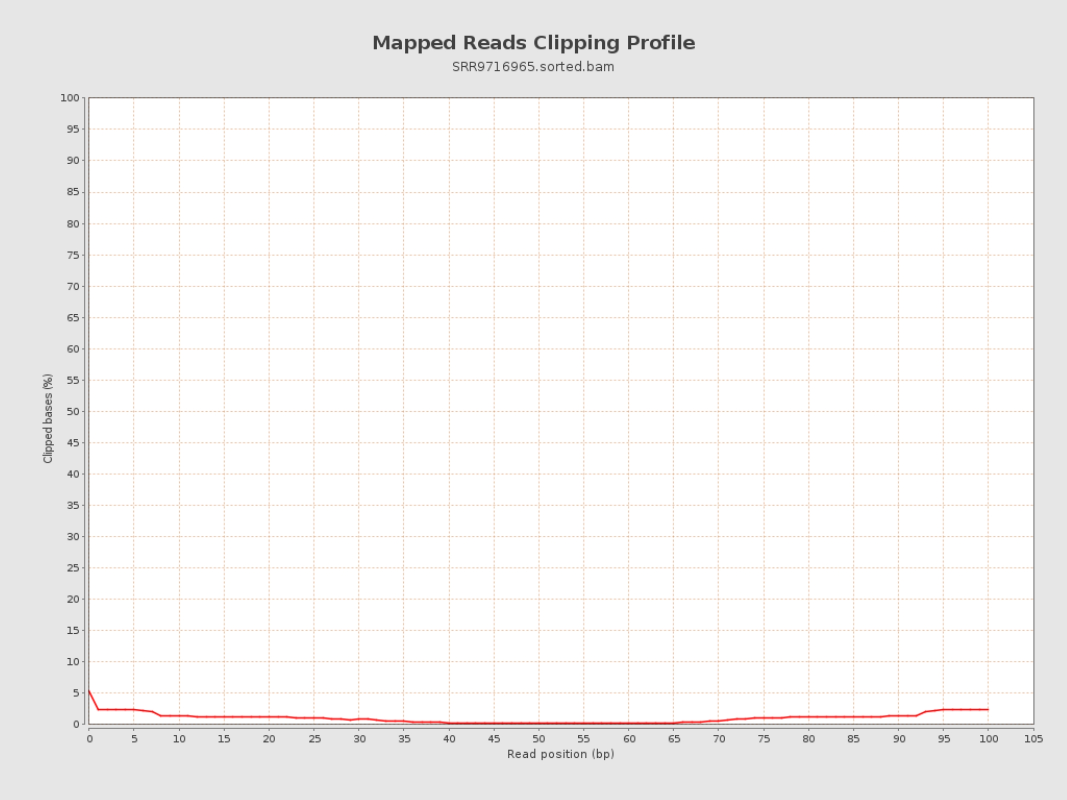
8. Results : Mapped Reads Nucleotide Content



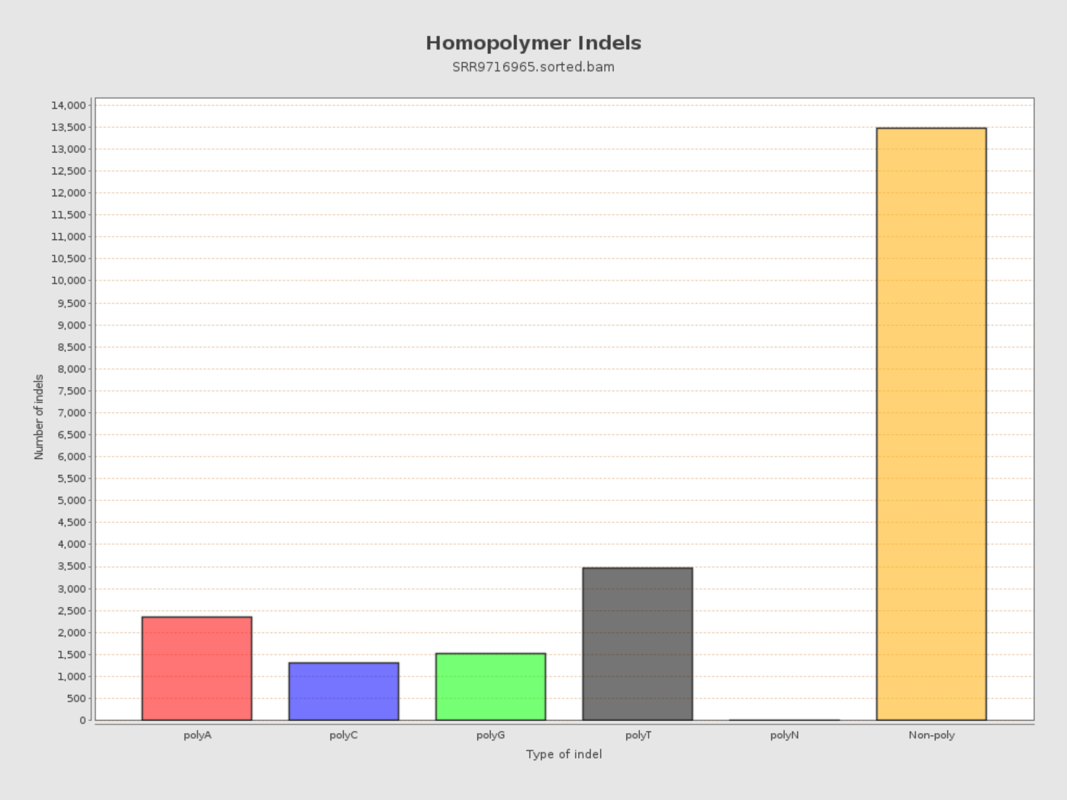
9. Results : Mapped Reads GC-content Distribution



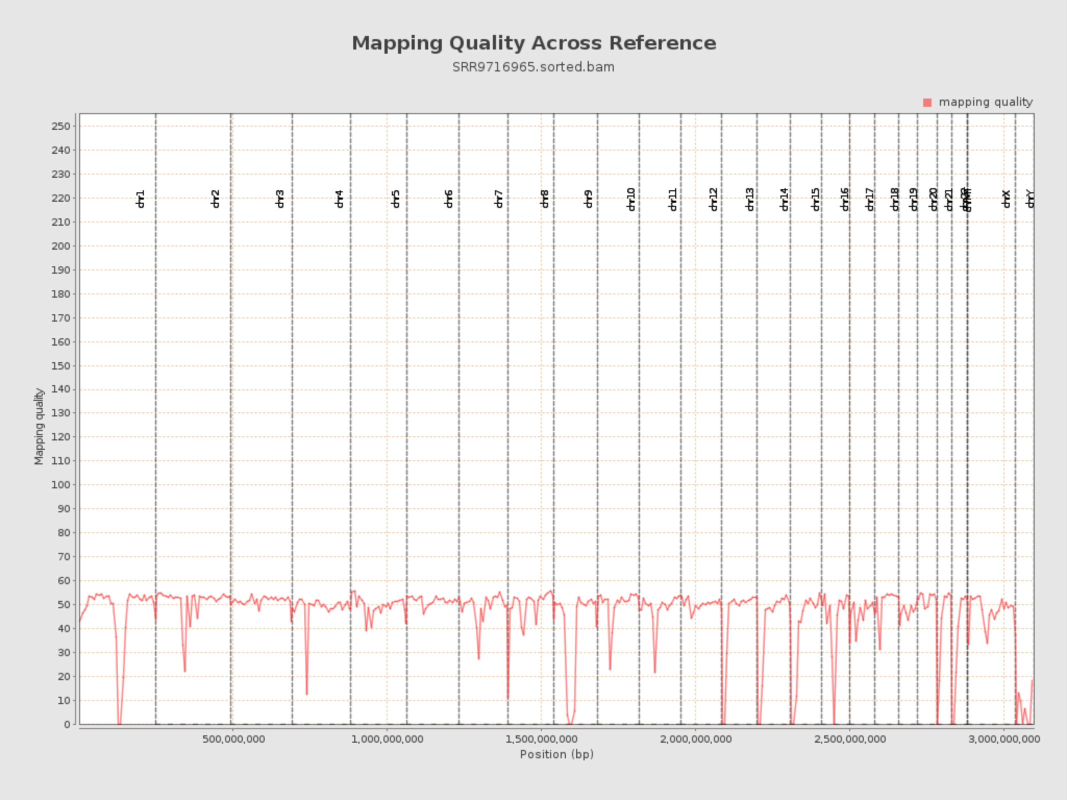
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram