Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:55:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716124.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_SRR9716124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:55:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,404,223
Mapped reads	2,150,664 / 89.45%
Unmapped reads	253,559 / 10.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,808 / 1.82%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	101,472 / 4.22%
Duplication rate	3.38%
Clipped reads	2,189,659 / 91.08%

2.2. ACGT Content

Number/percentage of A's	43,657,204 / 25.74%
Number/percentage of C's	32,013,670 / 18.88%
Number/percentage of T's	53,251,807 / 31.4%
Number/percentage of G's	40,650,606 / 23.97%
Number/percentage of N's	11,992 / 0.01%
GC Percentage	42.85%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.5112

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

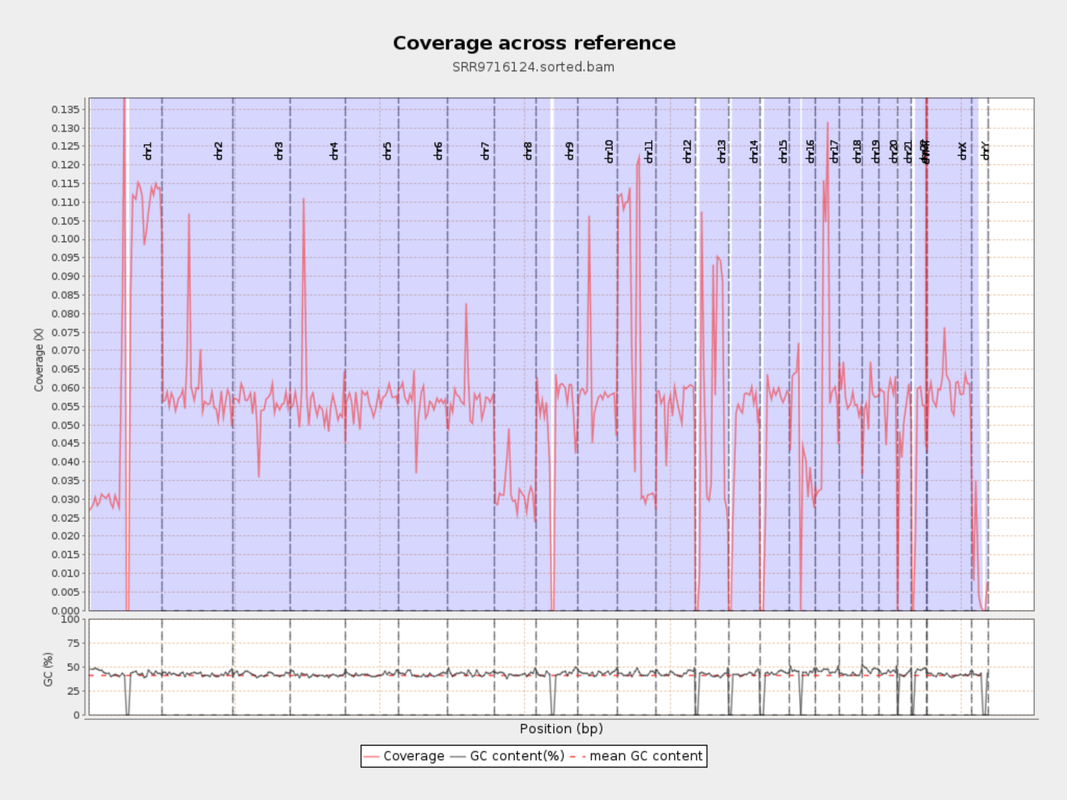
General error rate	0.68%
Mismatches	1,110,459
Insertions	15,359
Mapped reads with at least one insertion	0.7%
Deletions	40,025
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.59%

2.6. Chromosome stats

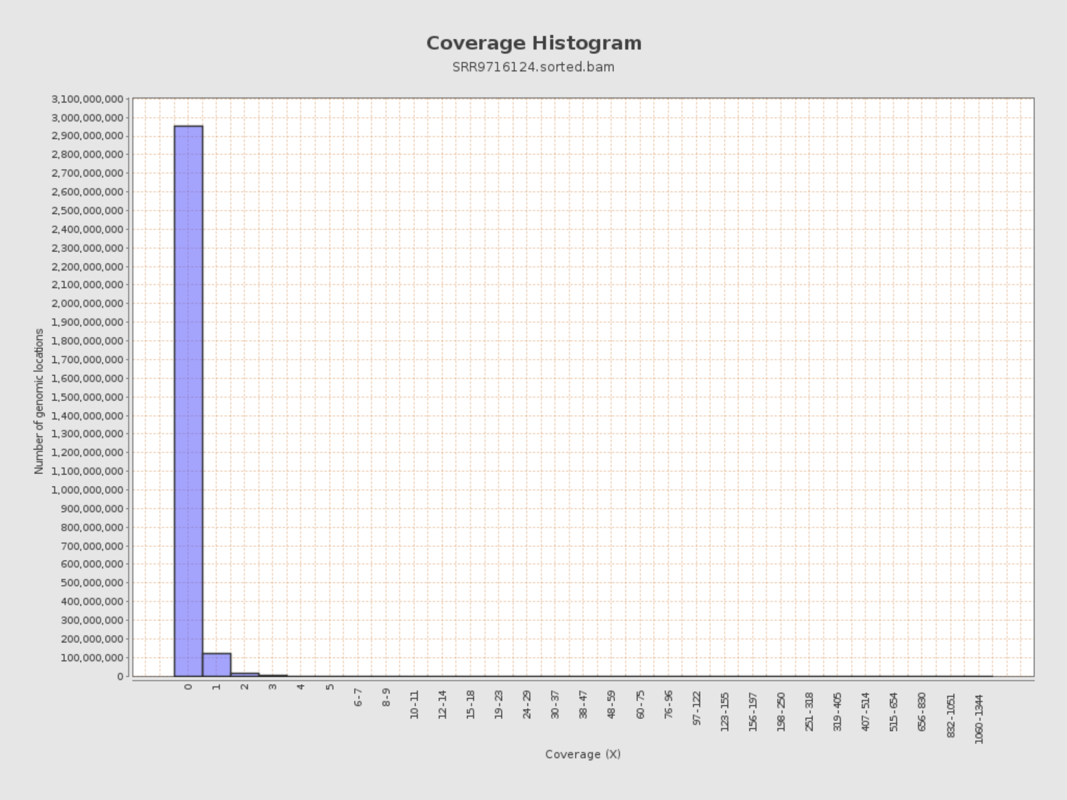
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16953362	0.068	1.1397
chr2	243199373	14320149	0.0589	0.5382
chr3	198022430	11028738	0.0557	0.2694
chr4	191154276	10882760	0.0569	0.3649
chr5	180915260	10191487	0.0563	0.274
chr6	171115067	9581849	0.056	0.3011
chr7	159138663	9114732	0.0573	0.5845

chr8	146364022	4619087	0.0316	0.5235
chr9	141213431	7005862	0.0496	0.4148
chr10	135534747	8057298	0.0594	0.5069
chr11	135006516	9713647	0.0719	0.5443
chr12	133851895	7513680	0.0561	0.2733
chr13	115169878	5950528	0.0517	0.2631
chr14	107349540	5019381	0.0468	0.2713
chr15	102531392	4898790	0.0478	0.2494
chr16	90354753	3903173	0.0432	0.2748
chr17	81195210	5429461	0.0669	0.3668
chr18	78077248	4499052	0.0576	0.6927
chr19	59128983	3320307	0.0562	0.7038
chr20	63025520	3603397	0.0572	0.2928
chr21	48129895	2248681	0.0467	0.299
chr22	51304566	2014975	0.0393	0.2285
chrMT	16571	8964	0.5409	0.8606
chrX	155270560	9255274	0.0596	0.3338
chrY	59373566	527655	0.0089	0.3056

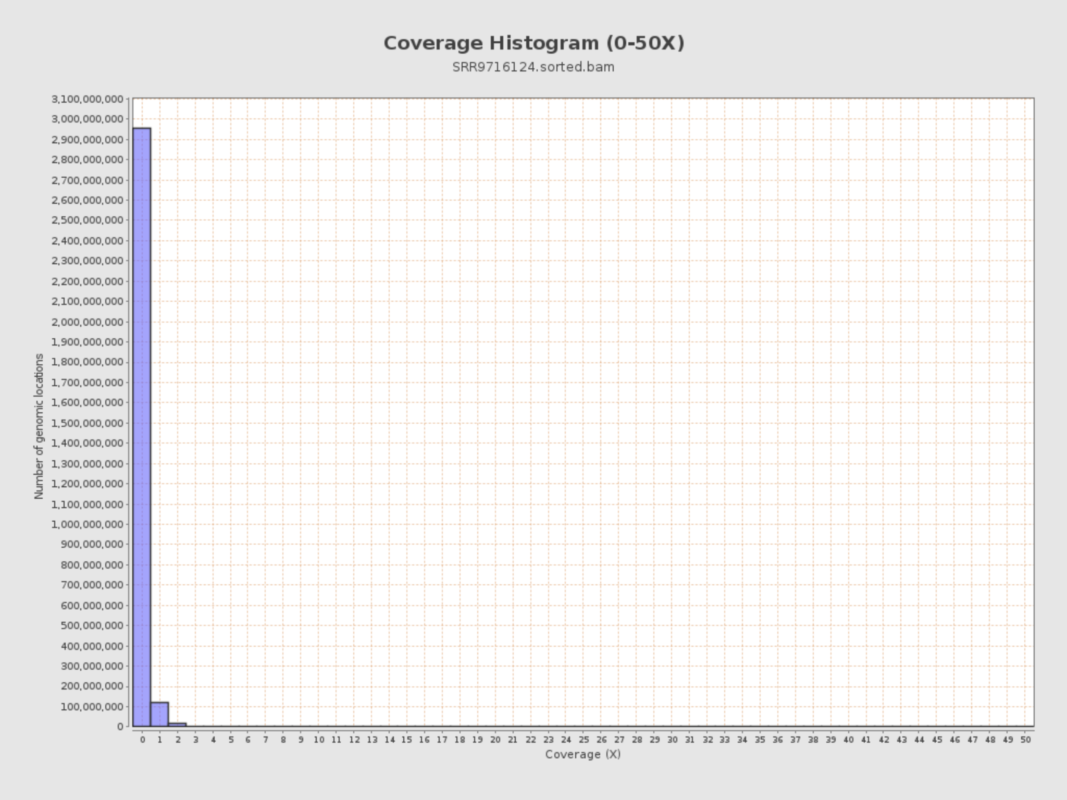
3. Results : Coverage across reference



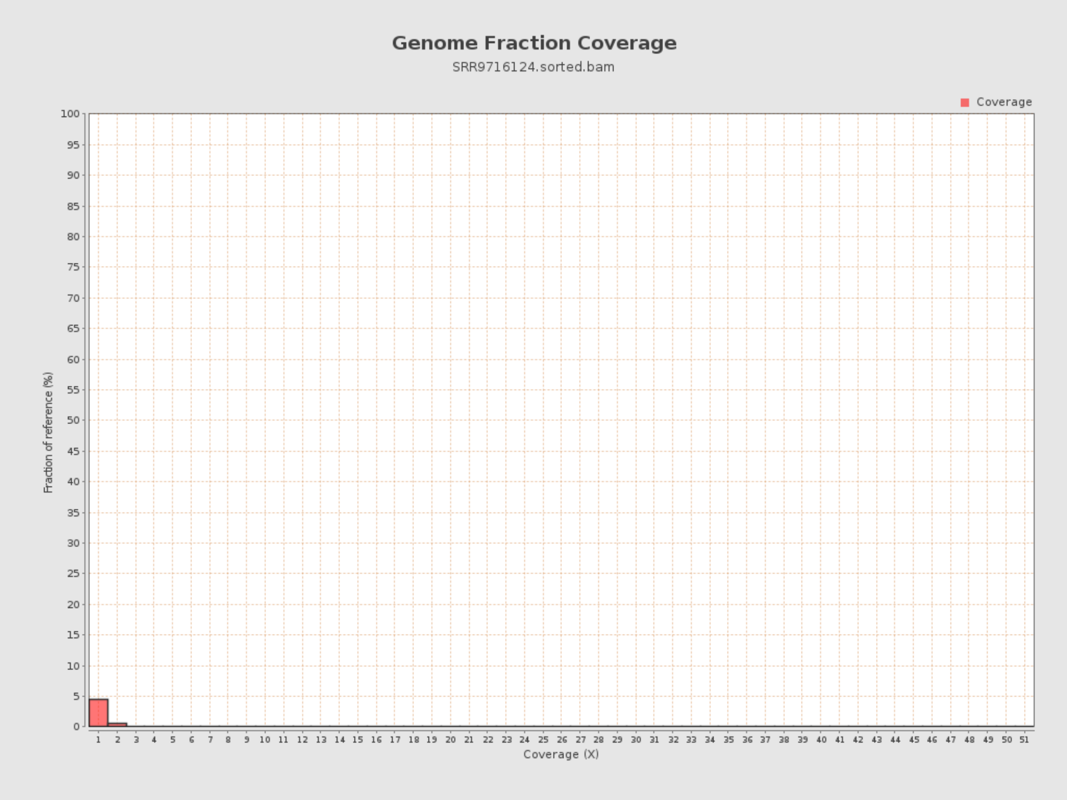
4. Results : Coverage Histogram



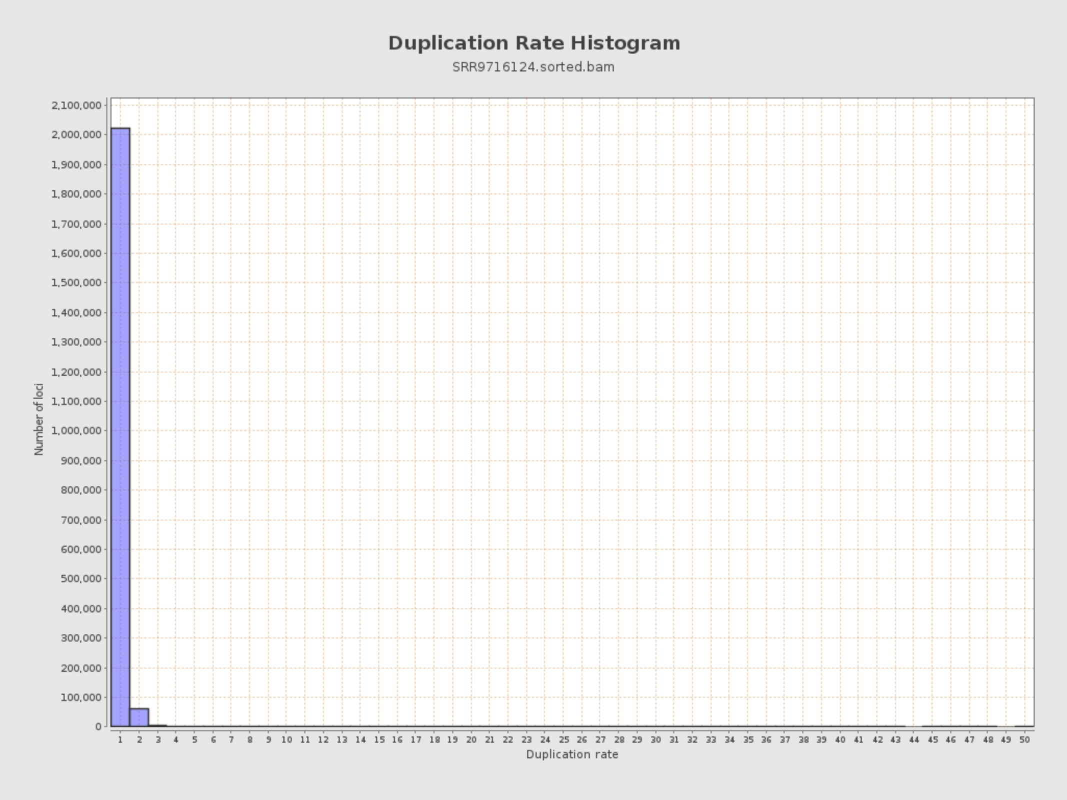
5. Results : Coverage Histogram (0-50X)



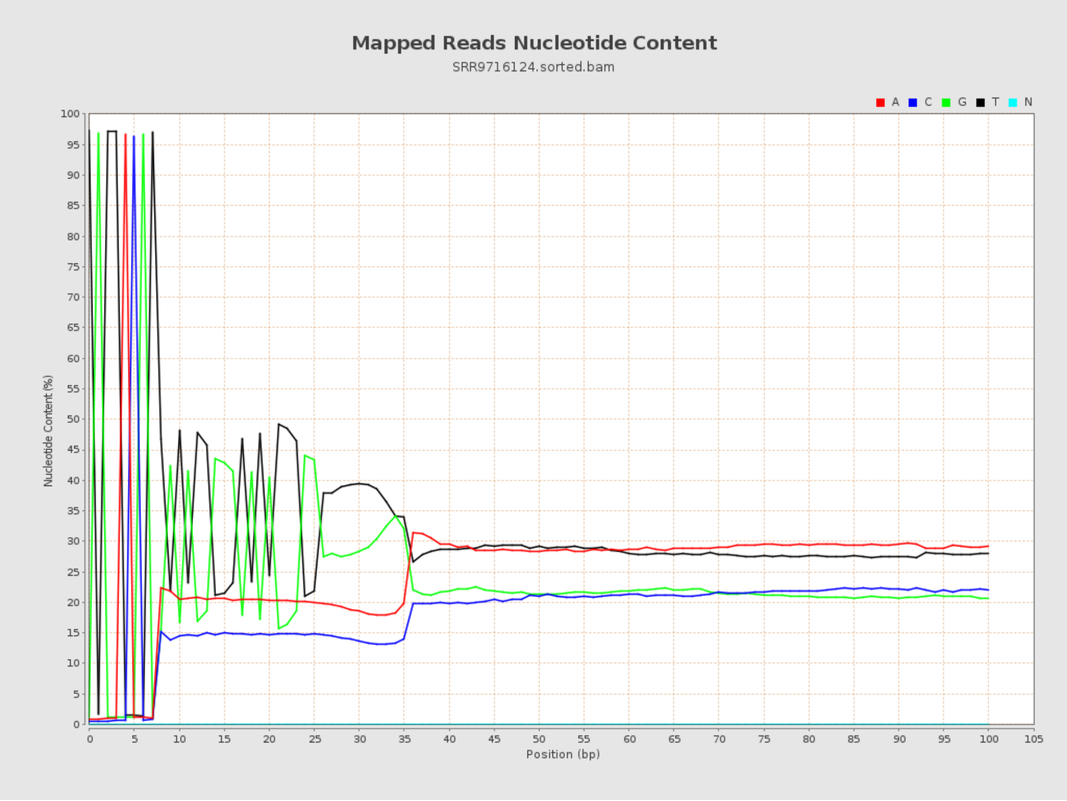
6. Results : Genome Fraction Coverage



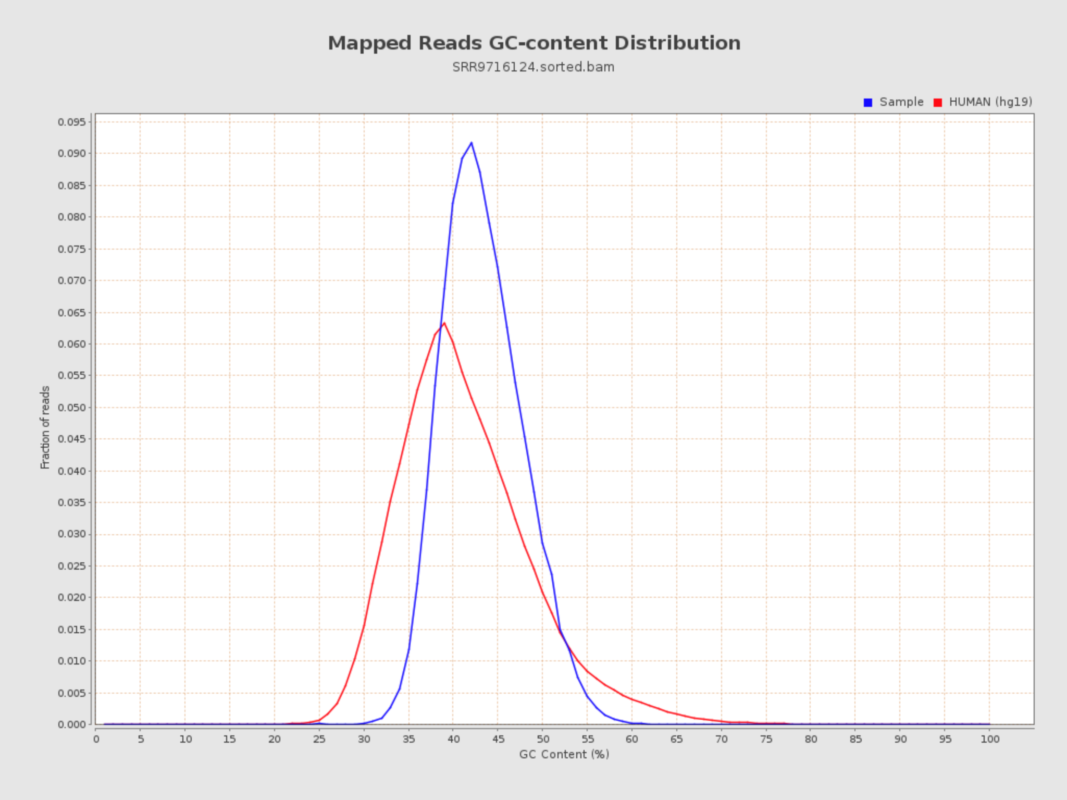
7. Results : Duplication Rate Histogram



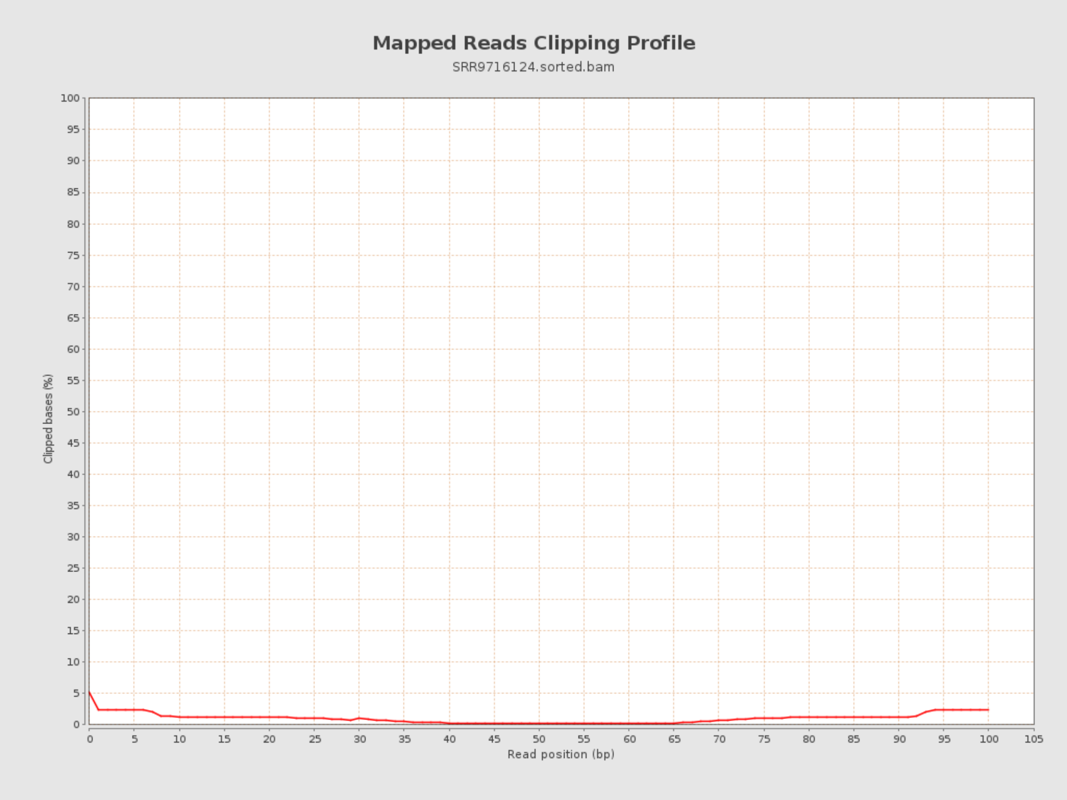
8. Results : Mapped Reads Nucleotide Content



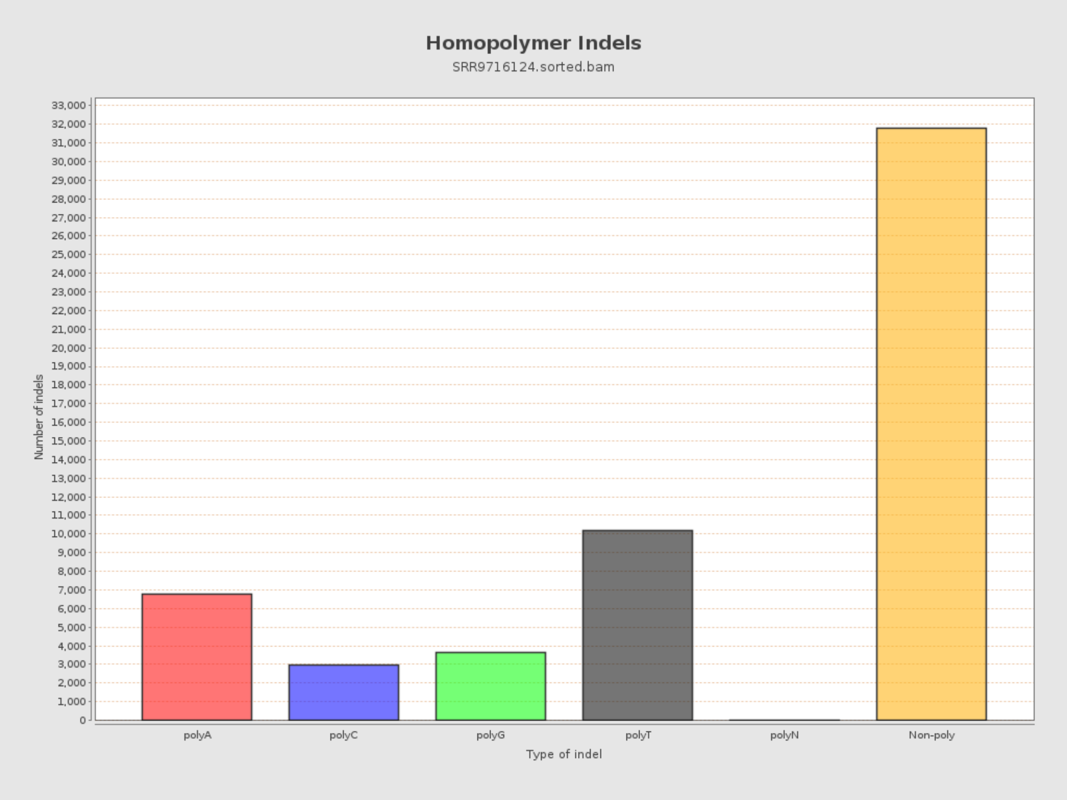
9. Results : Mapped Reads GC-content Distribution



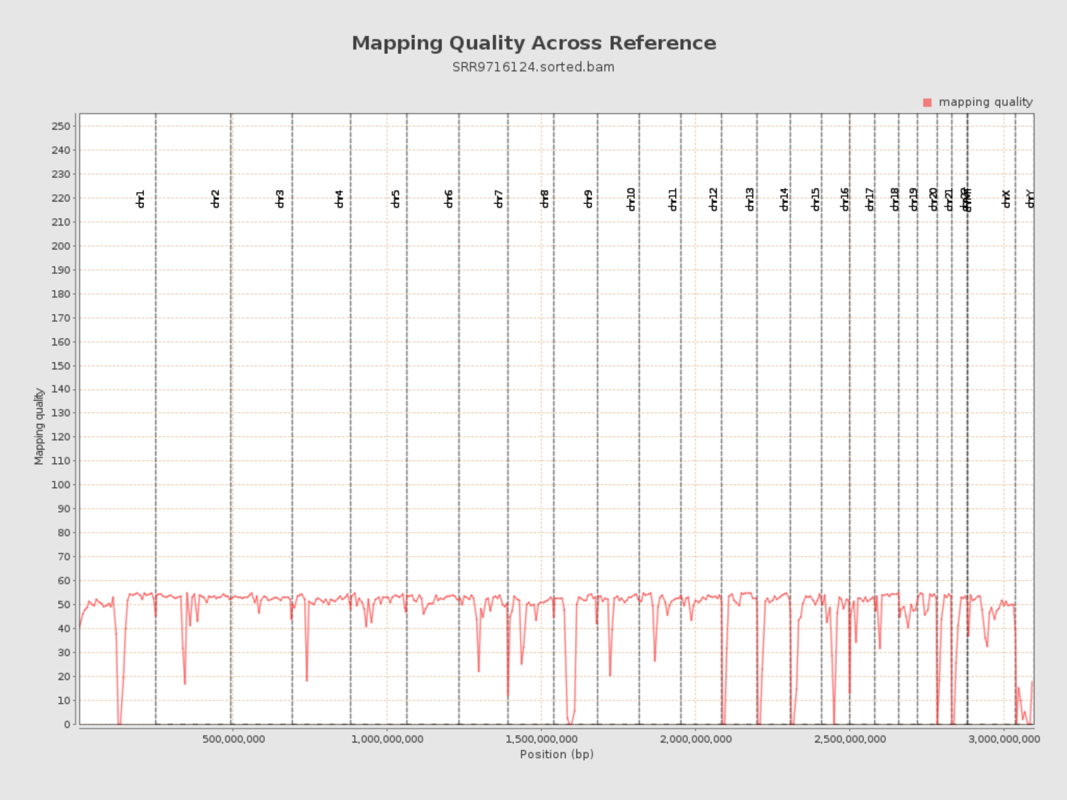
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram