Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:27:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716176.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_SRR9716176 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716176.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:27:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716176.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,471,991
Mapped reads	3,136,197 / 90.33%
Unmapped reads	335,794 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	78,419 / 2.26%
Read min/max/mean length	30 / 101 / 101.81
Duplicated reads (estimated)	141,942 / 4.09%
Duplication rate	3.14%
Clipped reads	3,209,550 / 92.44%

2.2. ACGT Content

Number/percentage of A's	61,795,085 / 26.33%
Number/percentage of C's	46,693,993 / 19.9%
Number/percentage of T's	71,925,419 / 30.65%
Number/percentage of G's	54,214,416 / 23.1%
Number/percentage of N's	27,202 / 0.01%
GC Percentage	43%

2.3. Coverage

Mean	0.0758

Standard Deviation	0.5921

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

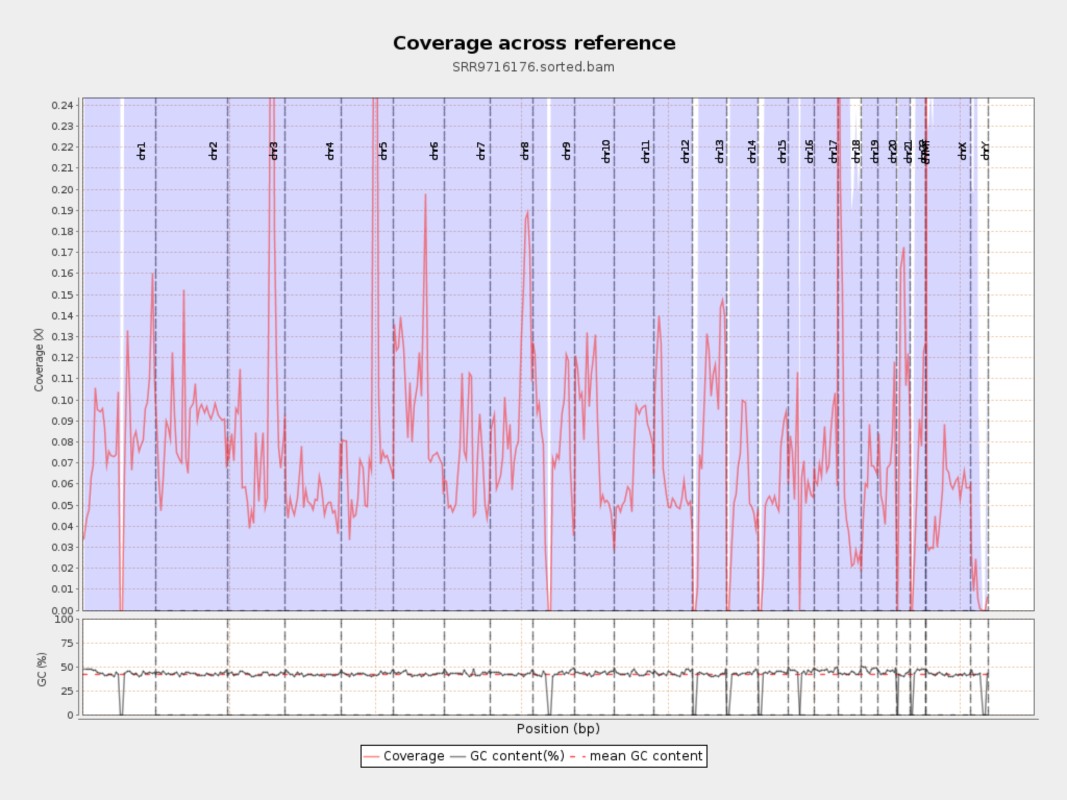
General error rate	0.74%
Mismatches	1,704,503
Insertions	20,869
Mapped reads with at least one insertion	0.66%
Deletions	50,287
Mapped reads with at least one deletion	1.58%
Homopolymer indels	39.02%

2.6. Chromosome stats

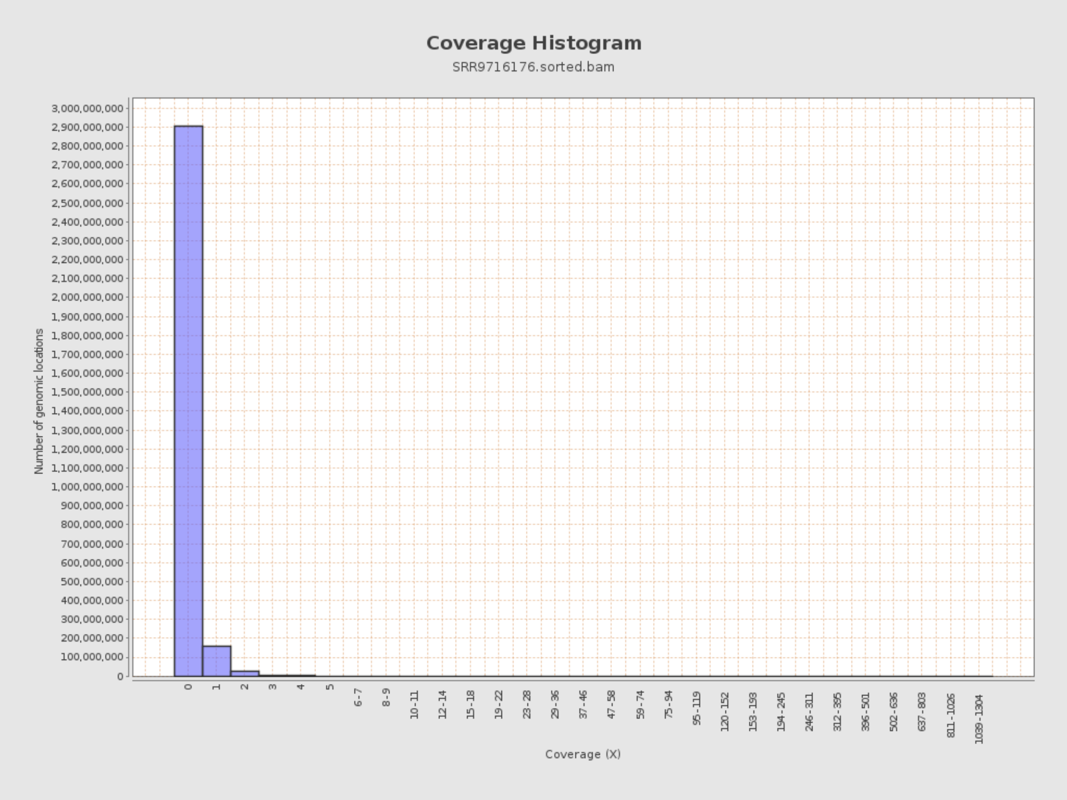
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19879459	0.0798	0.8085
chr2	243199373	21533431	0.0885	0.9727
chr3	198022430	18915575	0.0955	0.3903
chr4	191154276	10169379	0.0532	0.2941
chr5	180915260	15403493	0.0851	0.3606
chr6	171115067	17675141	0.1033	0.4563
chr7	159138663	10801834	0.0679	0.7824

chr8	146364022	14807682	0.1012	0.8031
chr9	141213431	10456627	0.074	0.5877
chr10	135534747	11740220	0.0866	0.5845
chr11	135006516	9567586	0.0709	0.4869
chr12	133851895	9198937	0.0687	0.3174
chr13	115169878	10727137	0.0931	0.3648
chr14	107349540	5819590	0.0542	0.3326
chr15	102531392	5200736	0.0507	0.2714
chr16	90354753	5576212	0.0617	0.3583
chr17	81195210	6132279	0.0755	0.3744
chr18	78077248	5935696	0.076	1.22
chr19	59128983	3714061	0.0628	0.7185
chr20	63025520	4408893	0.07	0.3813
chr21	48129895	5185332	0.1077	0.4152
chr22	51304566	3188182	0.0621	0.3025
chrMT	16571	10427	0.6292	1.557
chrX	155270560	8204081	0.0528	0.3883
chrY	59373566	489534	0.0082	0.2229

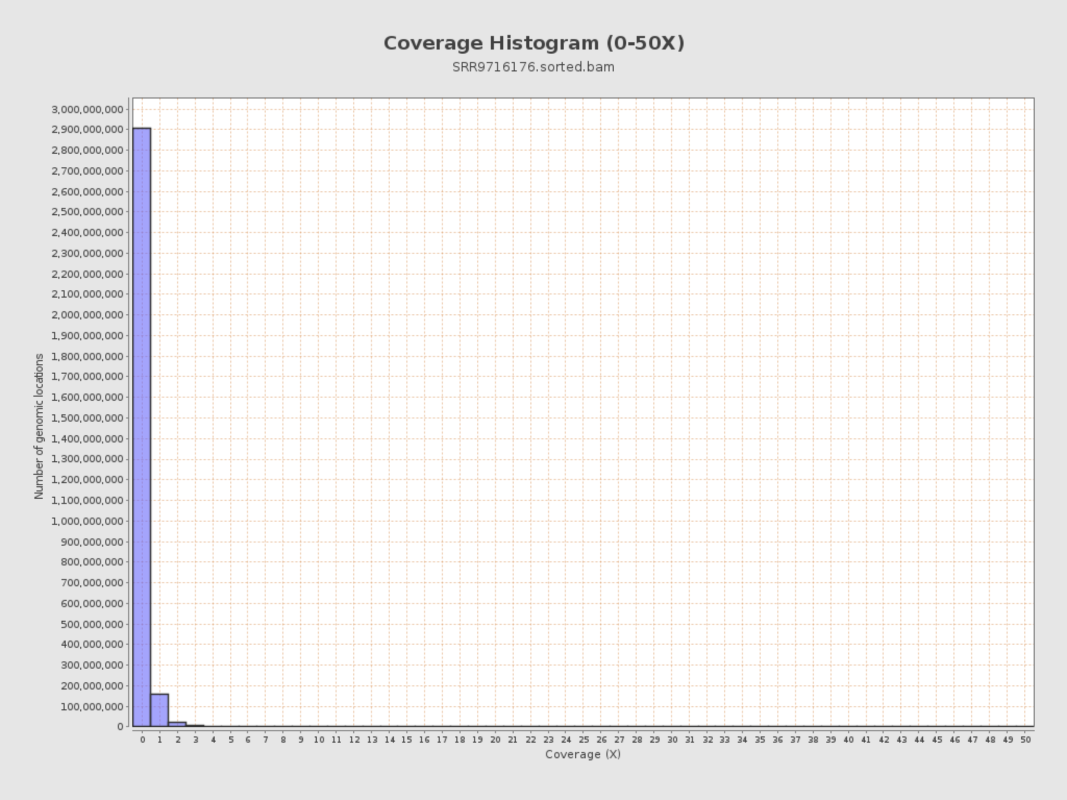
3. Results : Coverage across reference



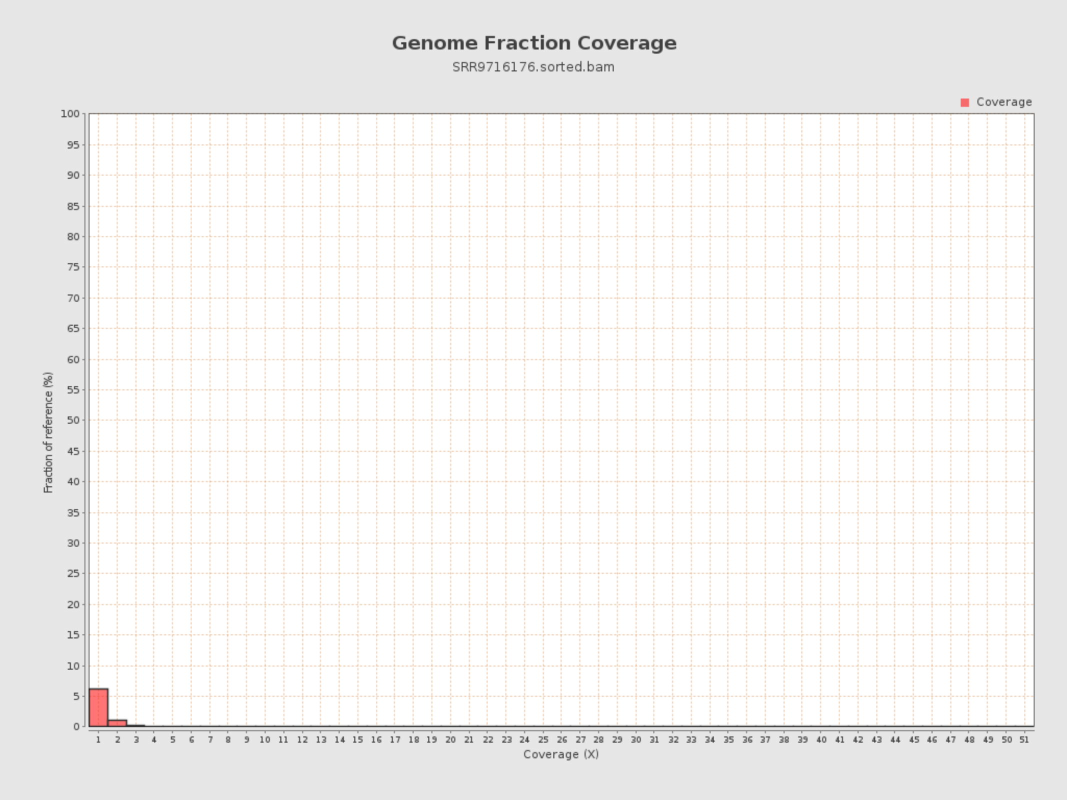
4. Results : Coverage Histogram



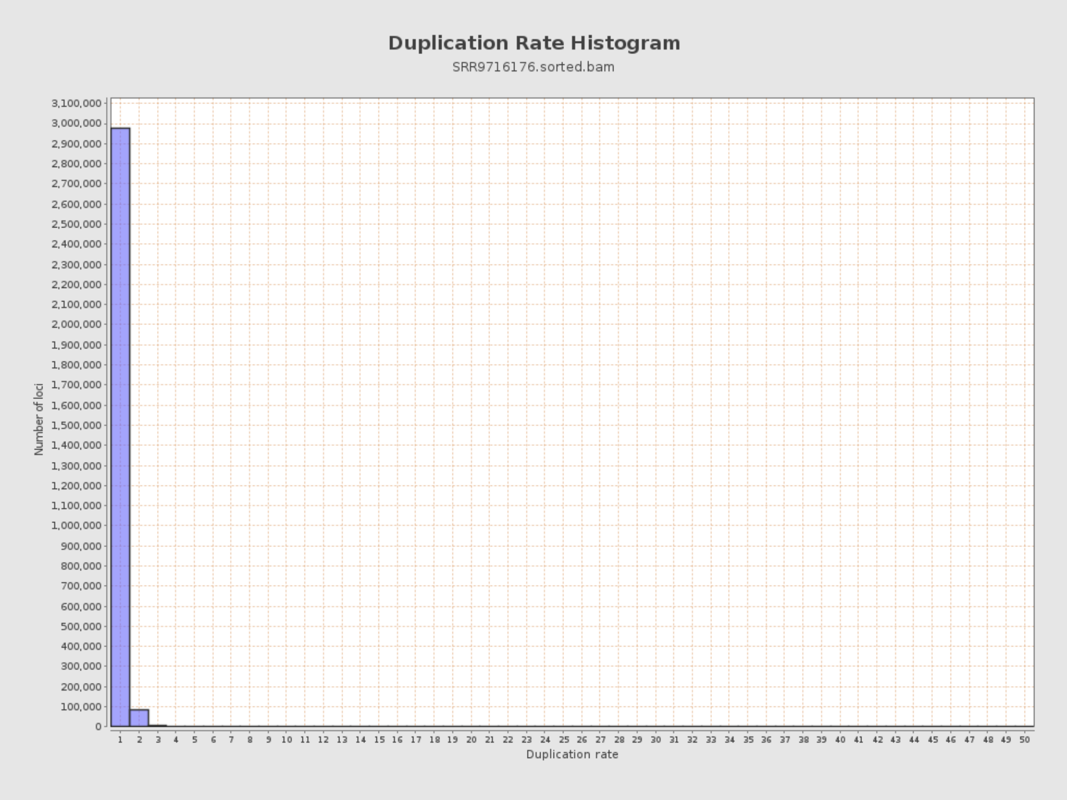
5. Results : Coverage Histogram (0-50X)



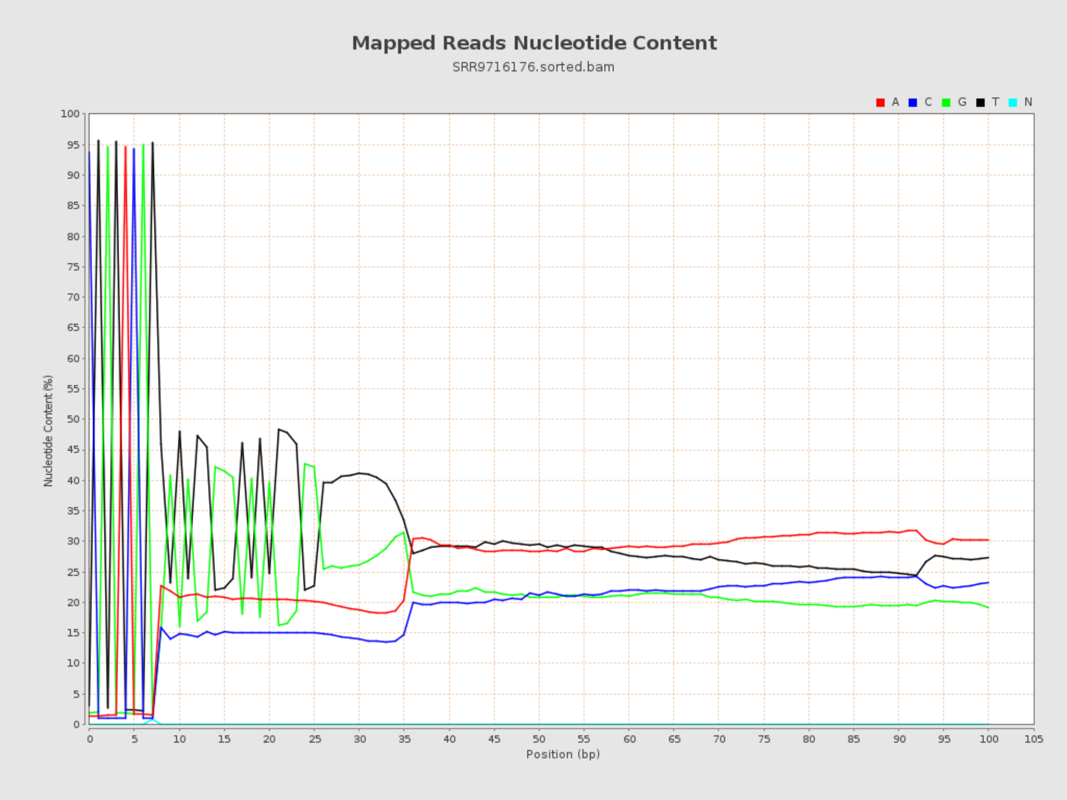
6. Results : Genome Fraction Coverage



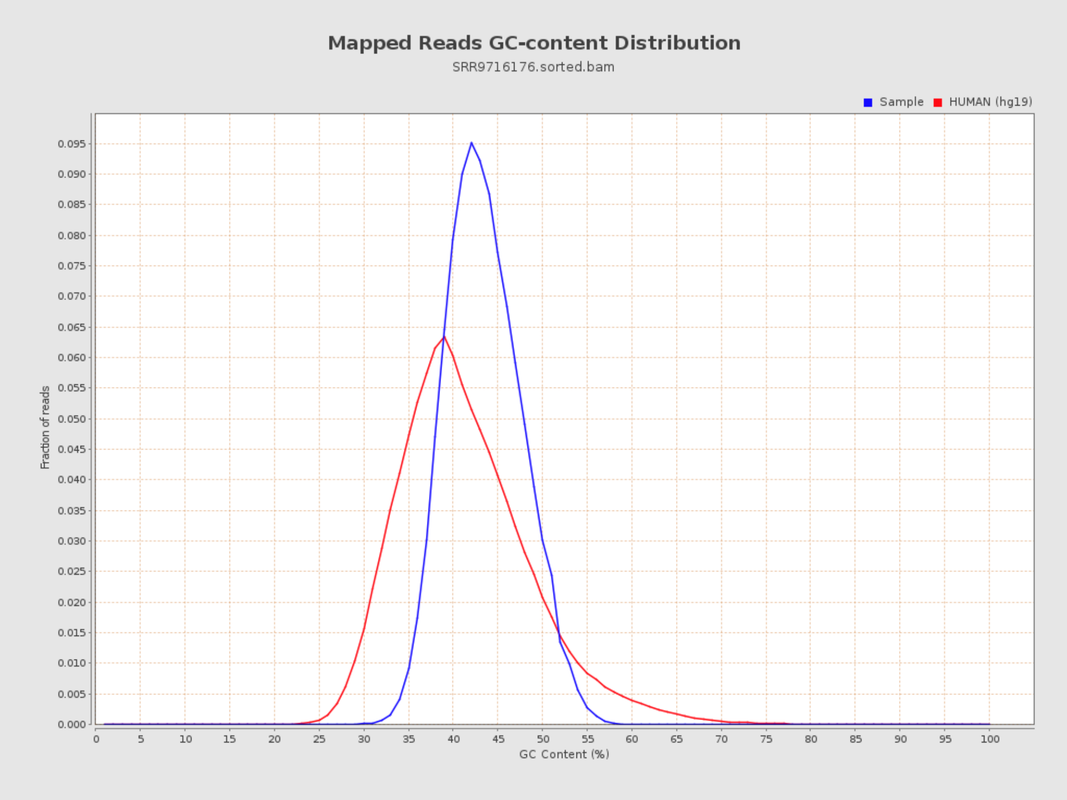
7. Results : Duplication Rate Histogram



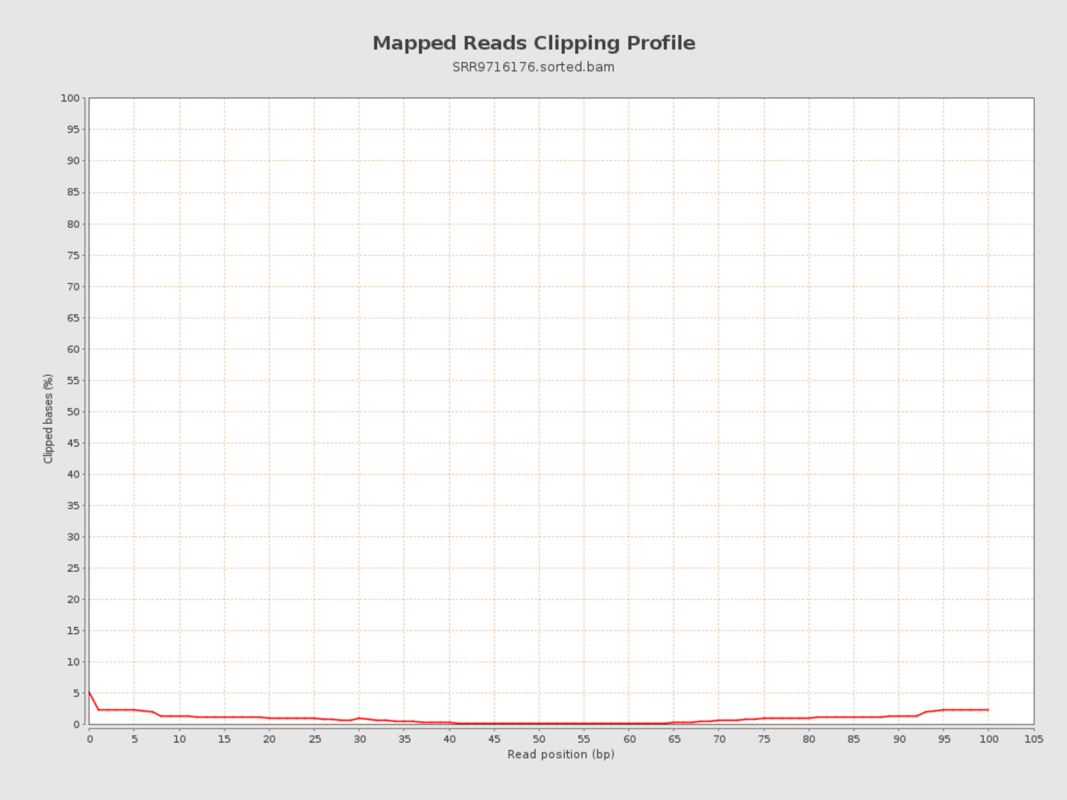
8. Results : Mapped Reads Nucleotide Content



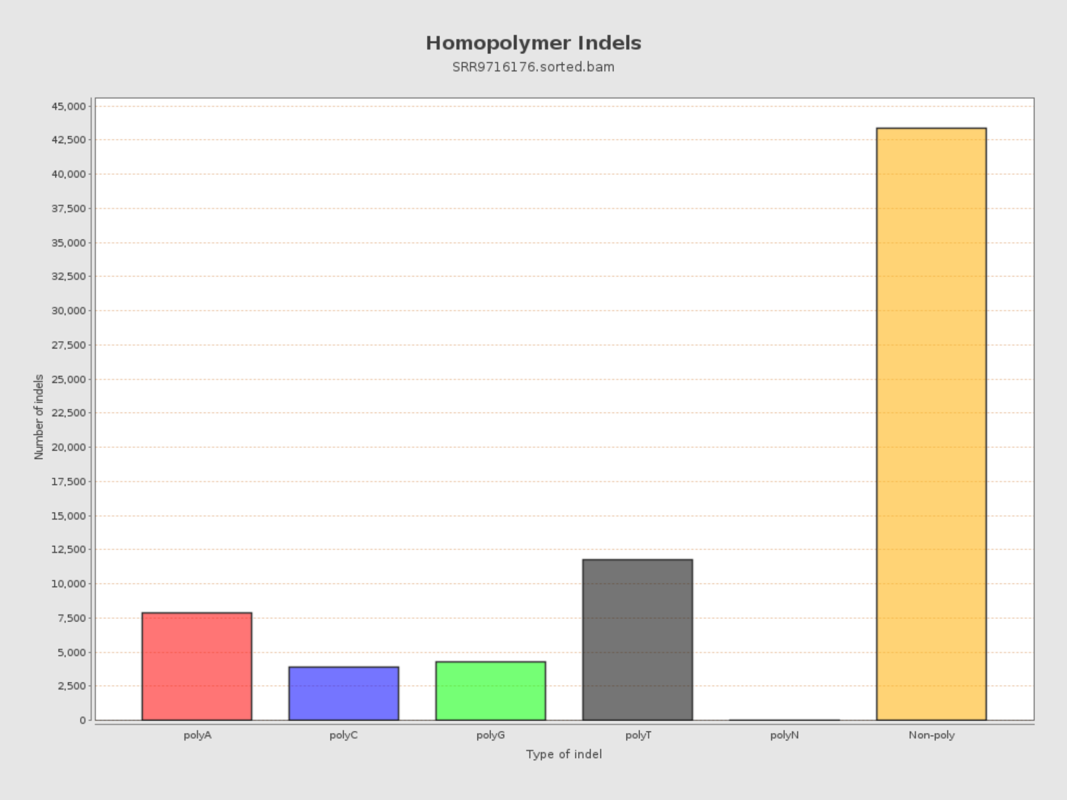
9. Results : Mapped Reads GC-content Distribution



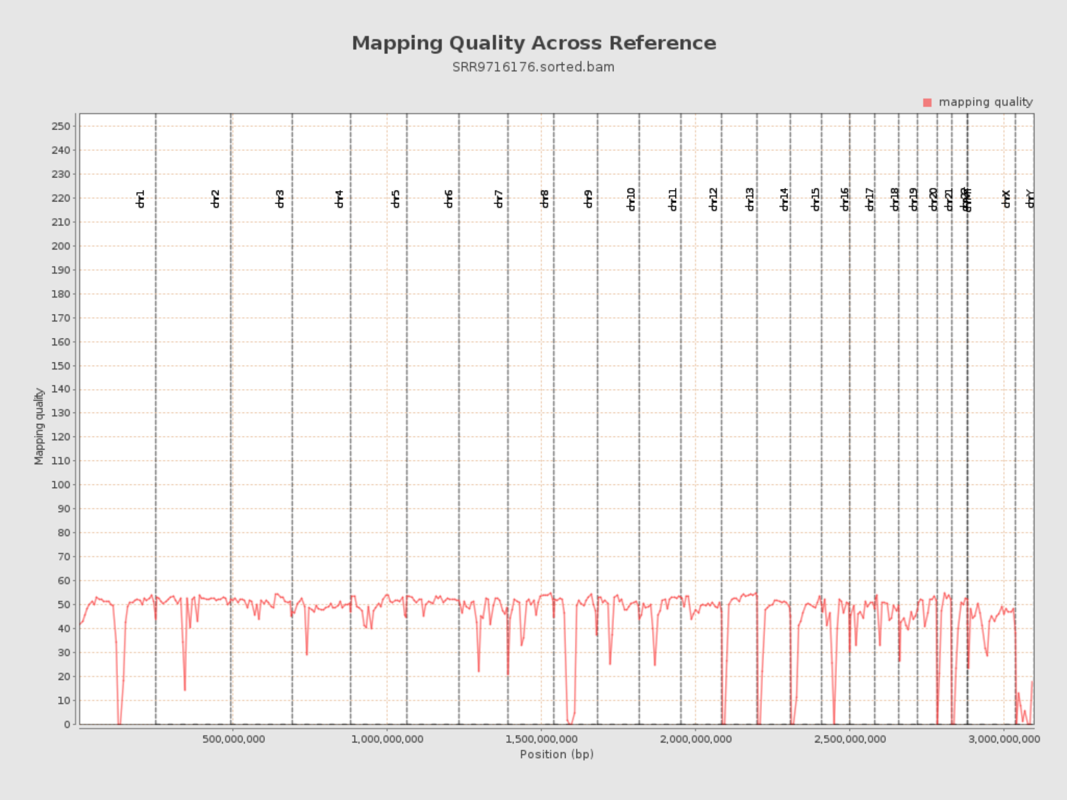
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram