Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:29:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716466.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_SRR9716466 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716466.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:29:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716466.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,495,792
Mapped reads	3,177,582 / 90.9%
Unmapped reads	318,210 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,405 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	171,680 / 4.91%
Duplication rate	4.11%
Clipped reads	3,186,870 / 91.16%

2.2. ACGT Content

Number/percentage of A's	49,543,441 / 26.36%
Number/percentage of C's	38,201,896 / 20.33%
Number/percentage of T's	57,158,963 / 30.41%
Number/percentage of G's	43,029,952 / 22.9%
Number/percentage of N's	5,248 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0607

Standard Deviation	0.4765

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

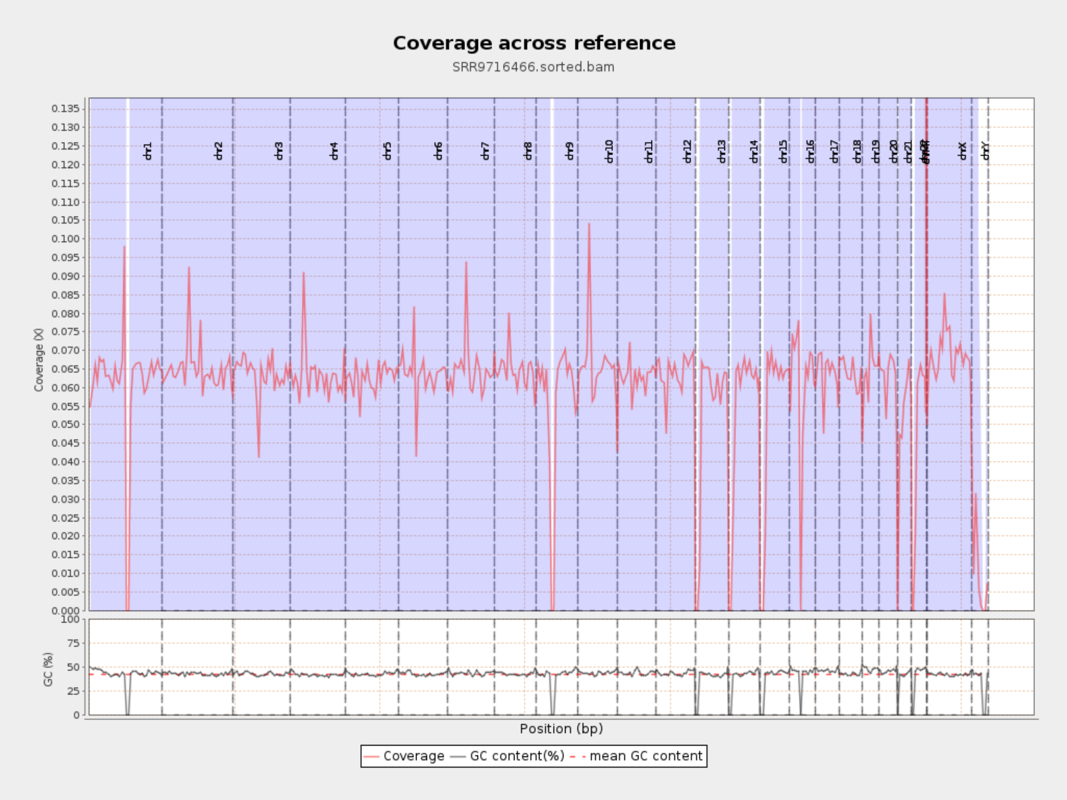
General error rate	0.51%
Mismatches	932,637
Insertions	14,291
Mapped reads with at least one insertion	0.45%
Deletions	34,915
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.04%

2.6. Chromosome stats

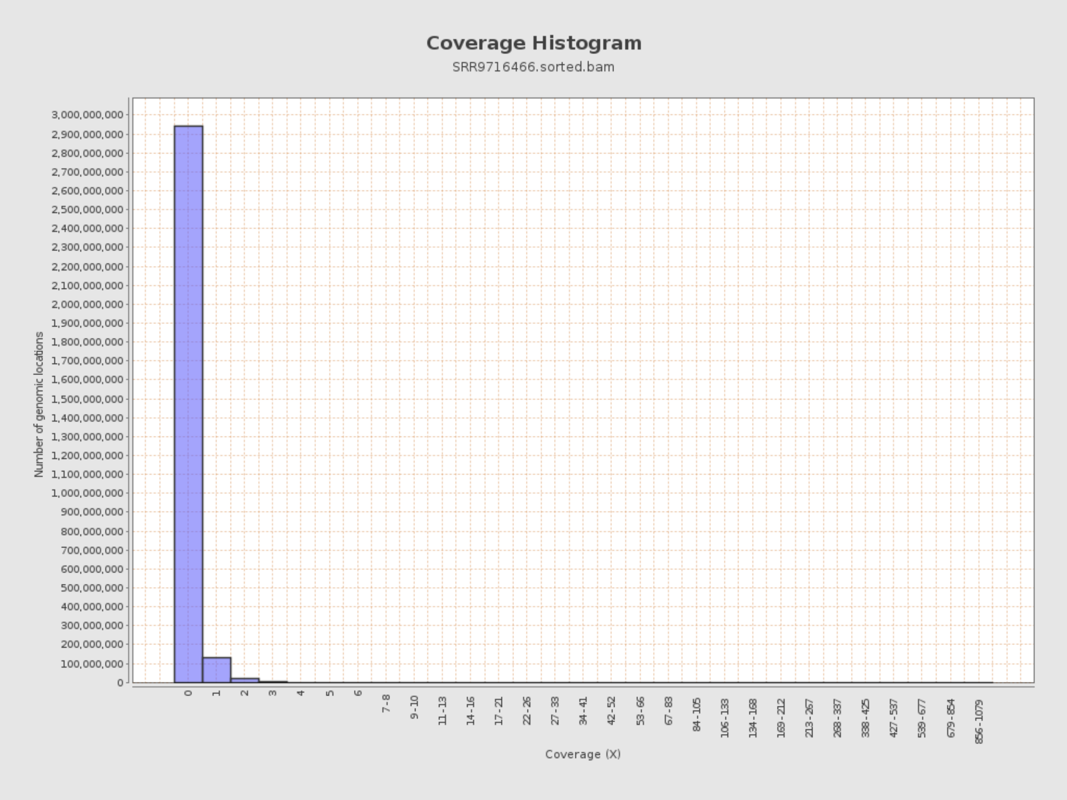
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15131212	0.0607	0.9436
chr2	243199373	15861777	0.0652	0.5666
chr3	198022430	12559860	0.0634	0.3007
chr4	191154276	12093035	0.0633	0.3321
chr5	180915260	11349170	0.0627	0.2994
chr6	171115067	10931581	0.0639	0.3812
chr7	159138663	10322863	0.0649	0.5946

chr8	146364022	9459838	0.0646	0.4401
chr9	141213431	7812766	0.0553	0.3926
chr10	135534747	9016555	0.0665	0.461
chr11	135006516	8484090	0.0628	0.407
chr12	133851895	8543922	0.0638	0.3074
chr13	115169878	5956896	0.0517	0.2671
chr14	107349540	5715917	0.0532	0.3076
chr15	102531392	5409464	0.0528	0.2795
chr16	90354753	5482566	0.0607	0.3205
chr17	81195210	5144229	0.0634	0.3277
chr18	78077248	4998097	0.064	0.7513
chr19	59128983	3856361	0.0652	0.6836
chr20	63025520	3969996	0.063	0.3054
chr21	48129895	2444878	0.0508	0.3099
chr22	51304566	2227213	0.0434	0.2454
chrMT	16571	27779	1.6764	1.5907
chrX	155270560	10633573	0.0685	0.3526
chrY	59373566	561205	0.0095	0.2322

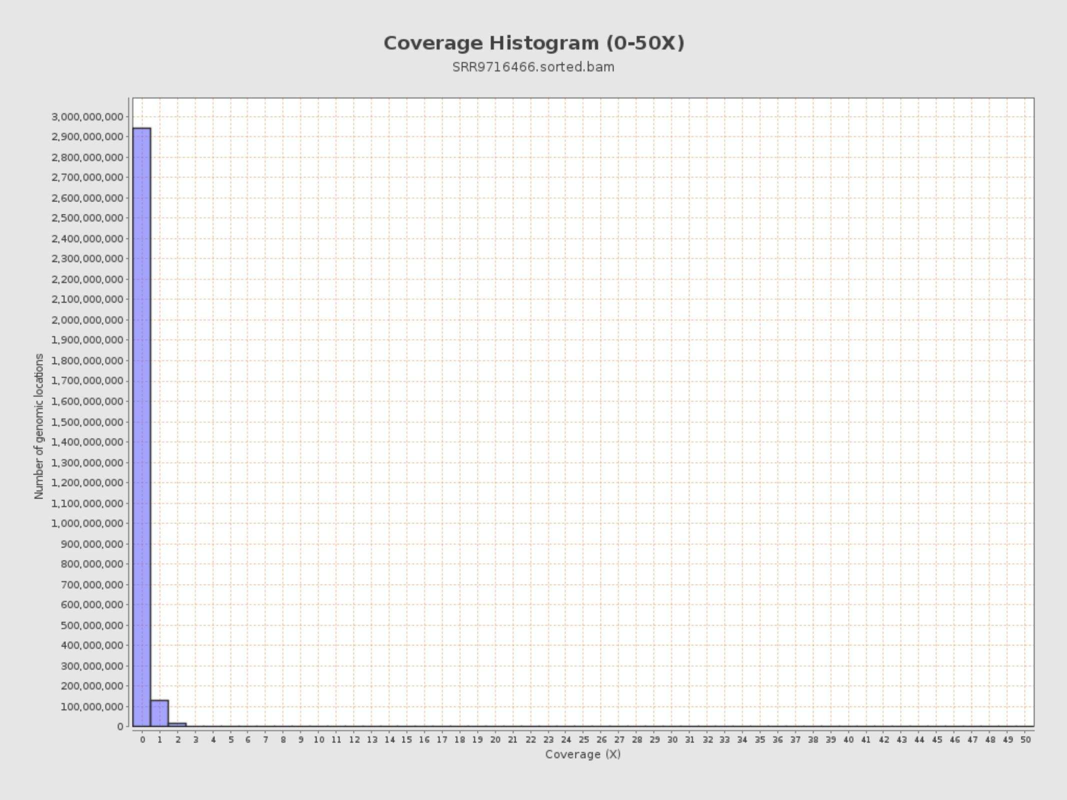
3. Results : Coverage across reference



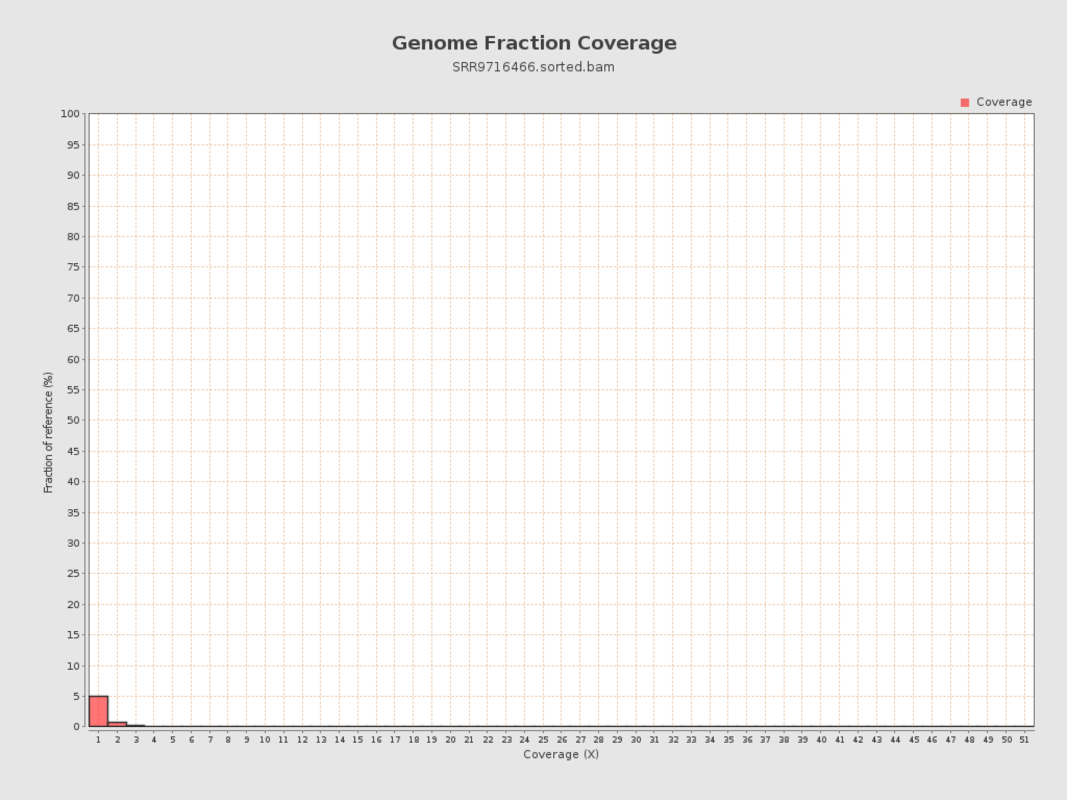
4. Results : Coverage Histogram



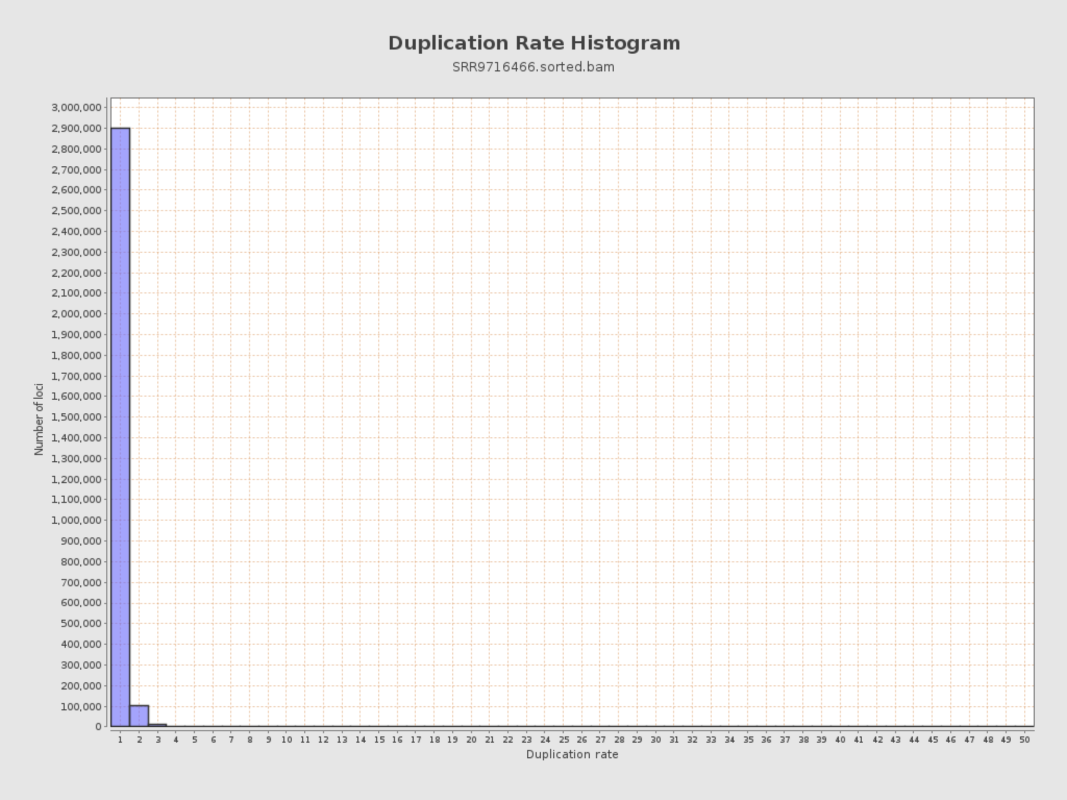
5. Results : Coverage Histogram (0-50X)



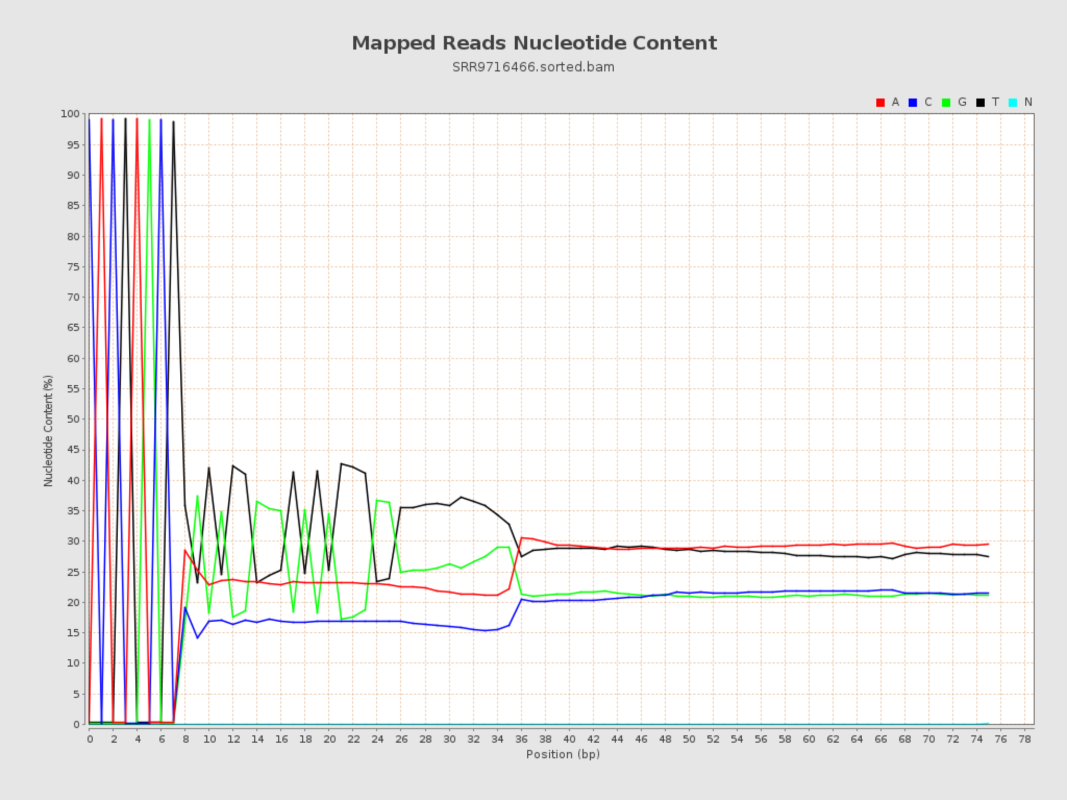
6. Results : Genome Fraction Coverage



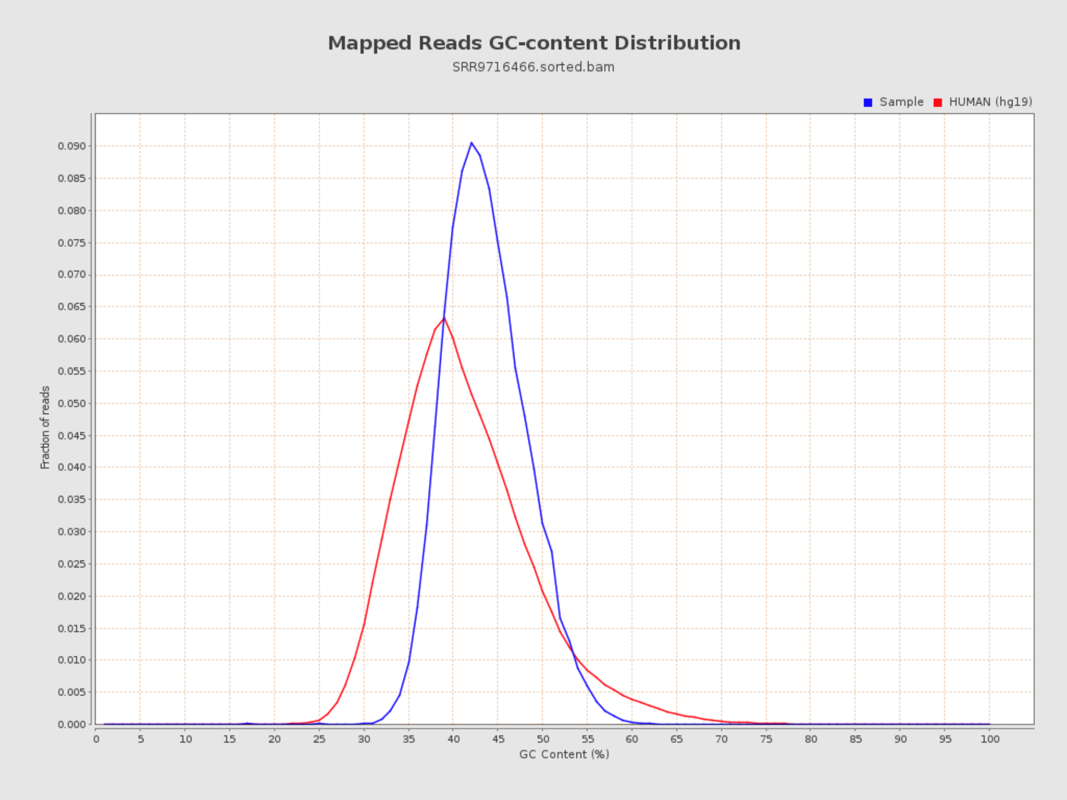
7. Results : Duplication Rate Histogram



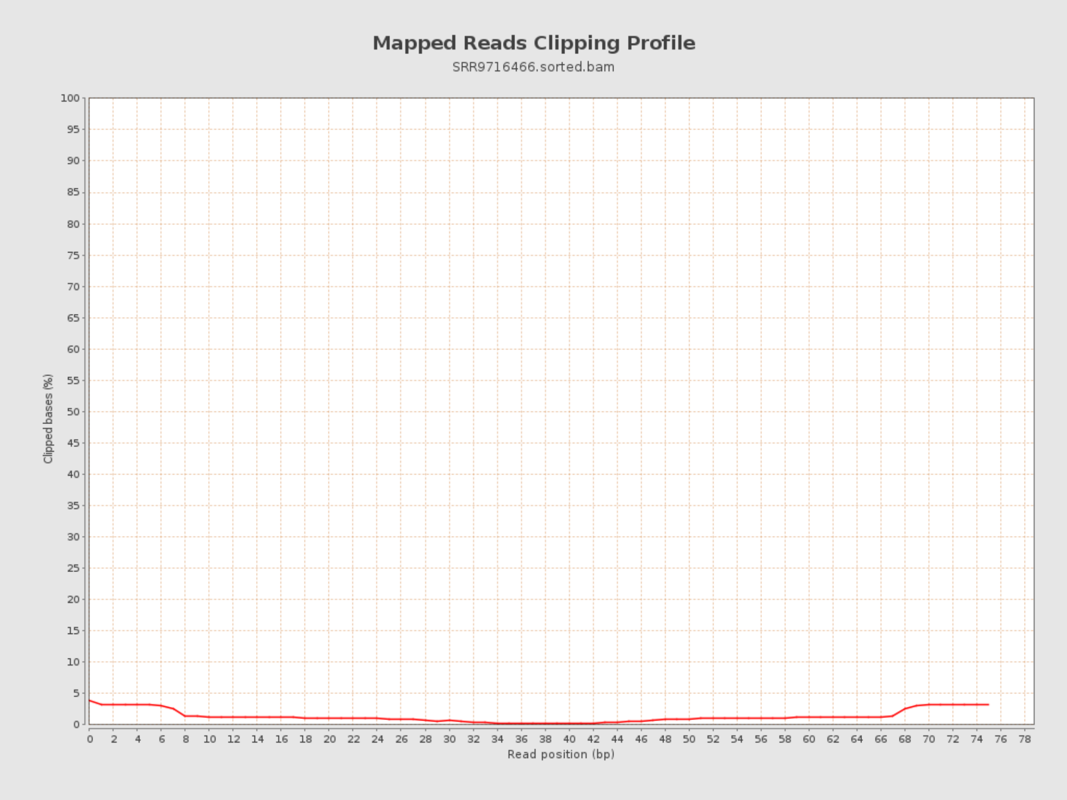
8. Results : Mapped Reads Nucleotide Content



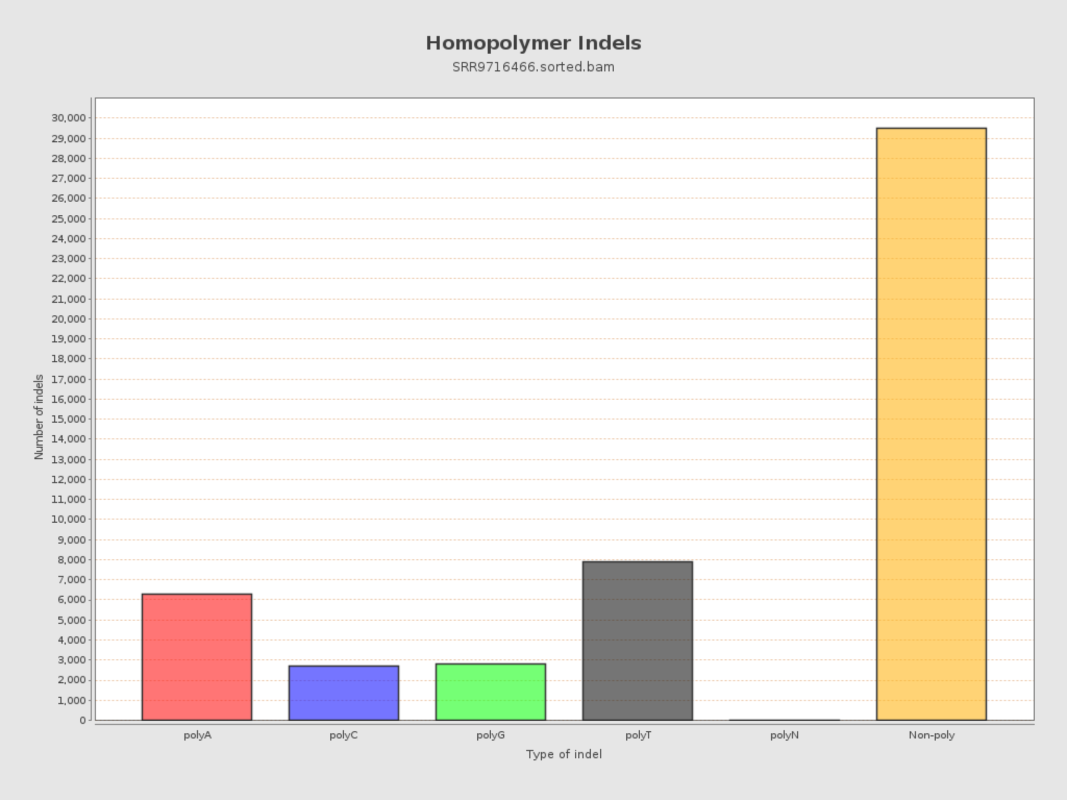
9. Results : Mapped Reads GC-content Distribution



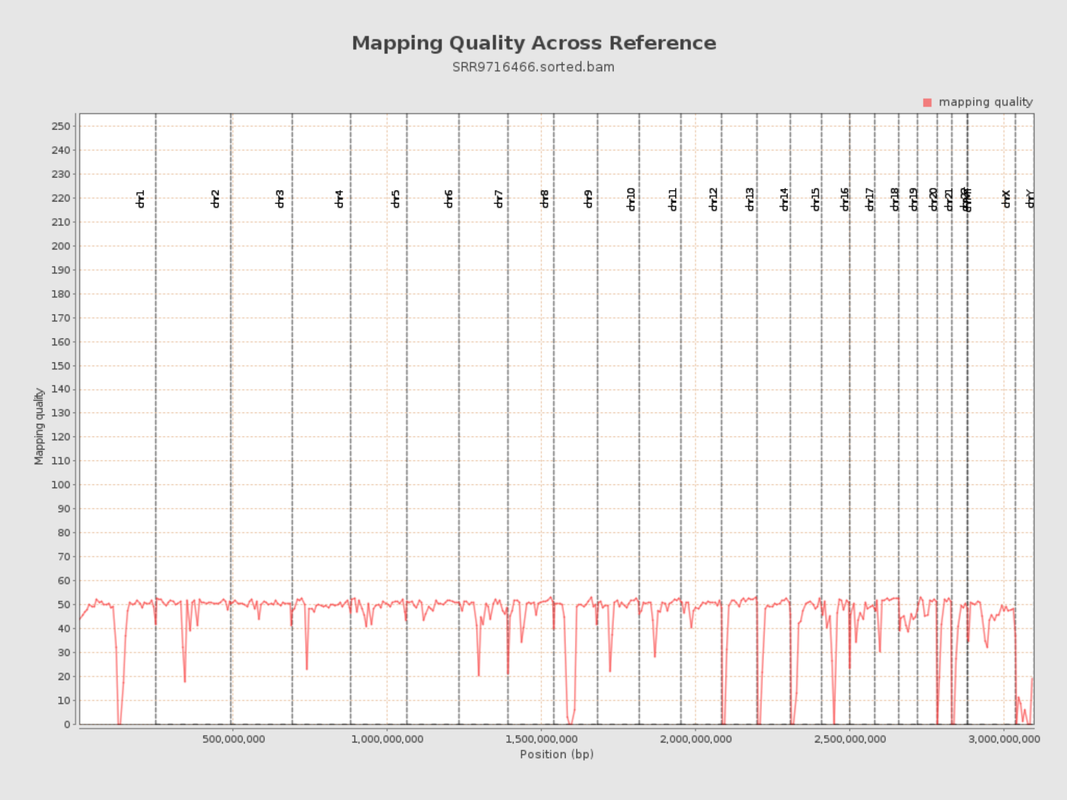
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram