Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716530.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_SRR9716530 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716530.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716530.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,444,549
Mapped reads	2,314,076 / 94.66%
Unmapped reads	130,473 / 5.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,693 / 1.87%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	106,423 / 4.35%
Duplication rate	3.38%
Clipped reads	2,357,250 / 96.43%

2.2. ACGT Content

Number/percentage of A's	46,120,879 / 25%
Number/percentage of C's	36,443,499 / 19.75%
Number/percentage of T's	56,443,826 / 30.59%
Number/percentage of G's	45,478,235 / 24.65%
Number/percentage of N's	12,561 / 0.01%
GC Percentage	44.4%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.4705

2.4. Mapping Quality

Mean Mapping Quality	47.78

2.5. Mismatches and indels

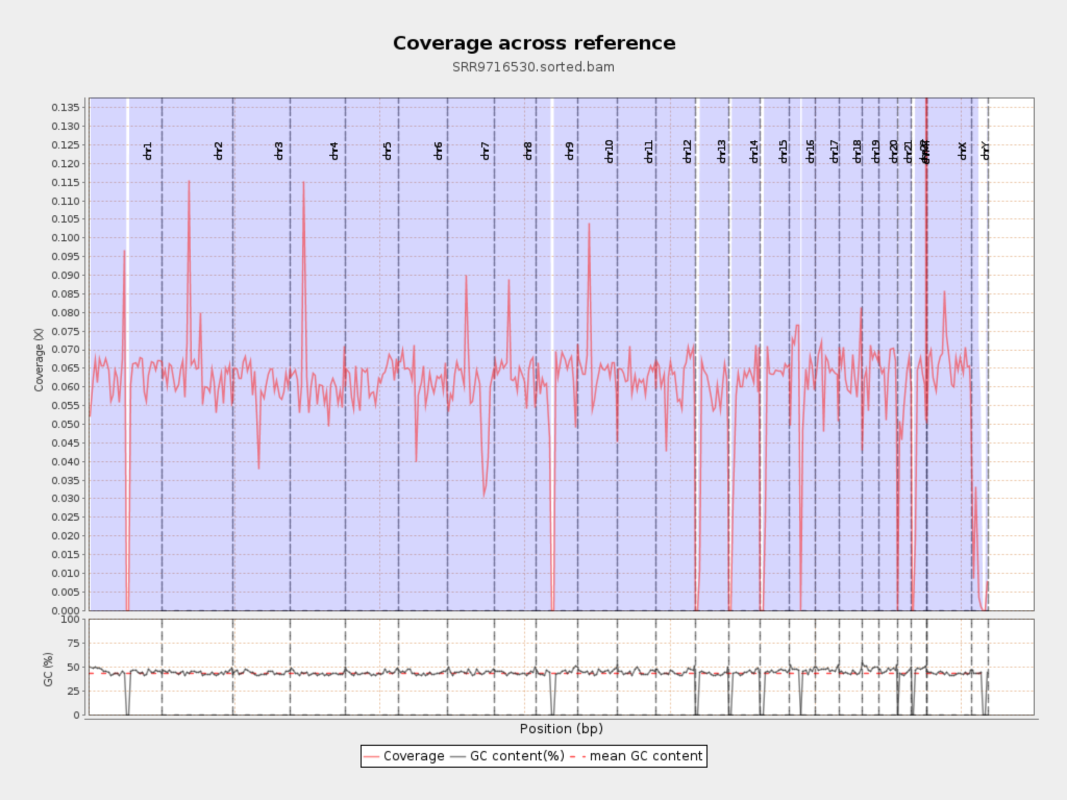
General error rate	0.64%
Mismatches	1,156,623
Insertions	14,215
Mapped reads with at least one insertion	0.6%
Deletions	43,125
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.96%

2.6. Chromosome stats

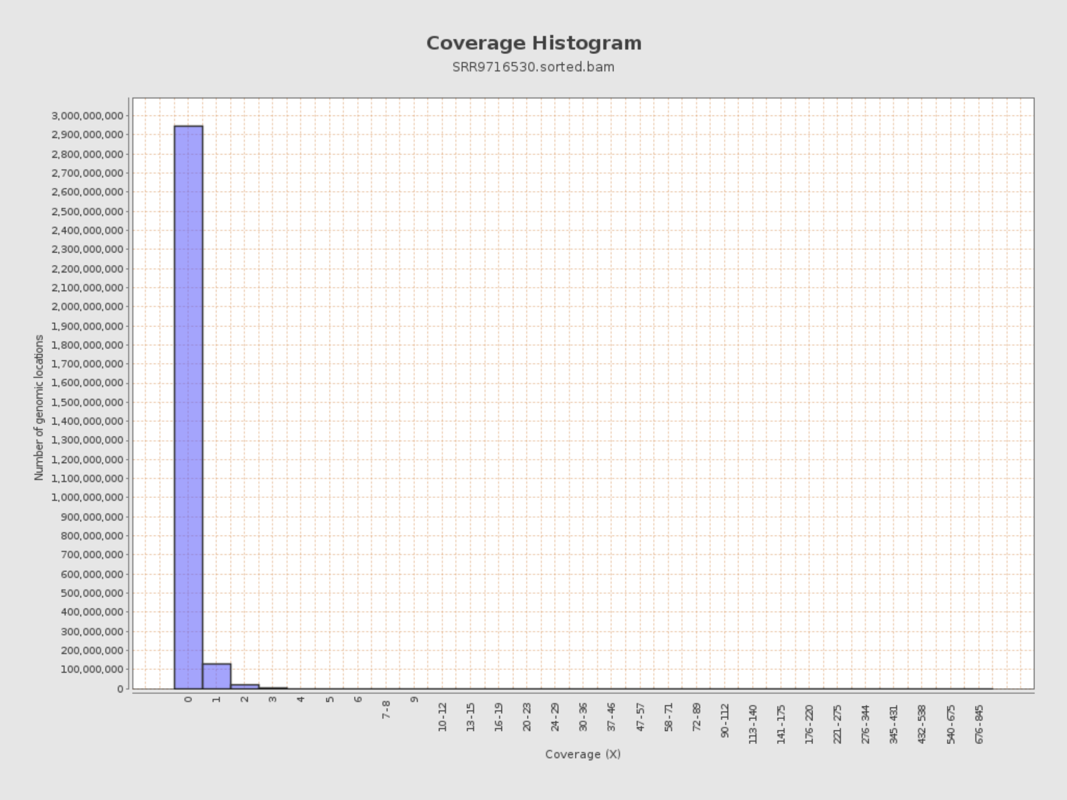
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15108454	0.0606	0.804
chr2	243199373	15713664	0.0646	0.5947
chr3	198022430	12037700	0.0608	0.2852
chr4	191154276	11826394	0.0619	0.3787
chr5	180915260	11193333	0.0619	0.2935
chr6	171115067	10592632	0.0619	0.3226
chr7	159138663	9249556	0.0581	0.6363

chr8	146364022	9446574	0.0645	0.5817
chr9	141213431	7866542	0.0557	0.4439
chr10	135534747	8924391	0.0658	0.4974
chr11	135006516	8442056	0.0625	0.4562
chr12	133851895	8352410	0.0624	0.2937
chr13	115169878	5783239	0.0502	0.2601
chr14	107349540	5612763	0.0523	0.2903
chr15	102531392	5400725	0.0527	0.2668
chr16	90354753	5400909	0.0598	0.3166
chr17	81195210	5167249	0.0636	0.3535
chr18	78077248	5068021	0.0649	0.7344
chr19	59128983	3796985	0.0642	0.5877
chr20	63025520	4024966	0.0639	0.3137
chr21	48129895	2487087	0.0517	0.3227
chr22	51304566	2233385	0.0435	0.2427
chrMT	16571	10613	0.6405	0.9813
chrX	155270560	10302470	0.0664	0.3648
chrY	59373566	539771	0.0091	0.2956

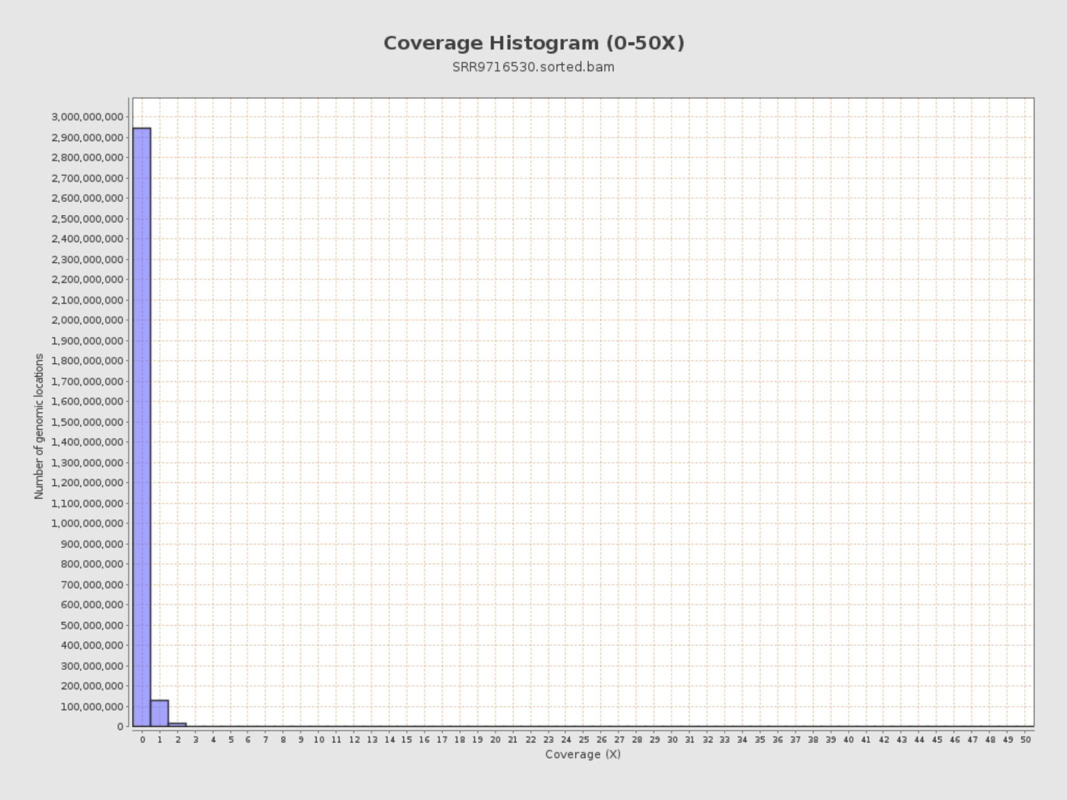
3. Results : Coverage across reference



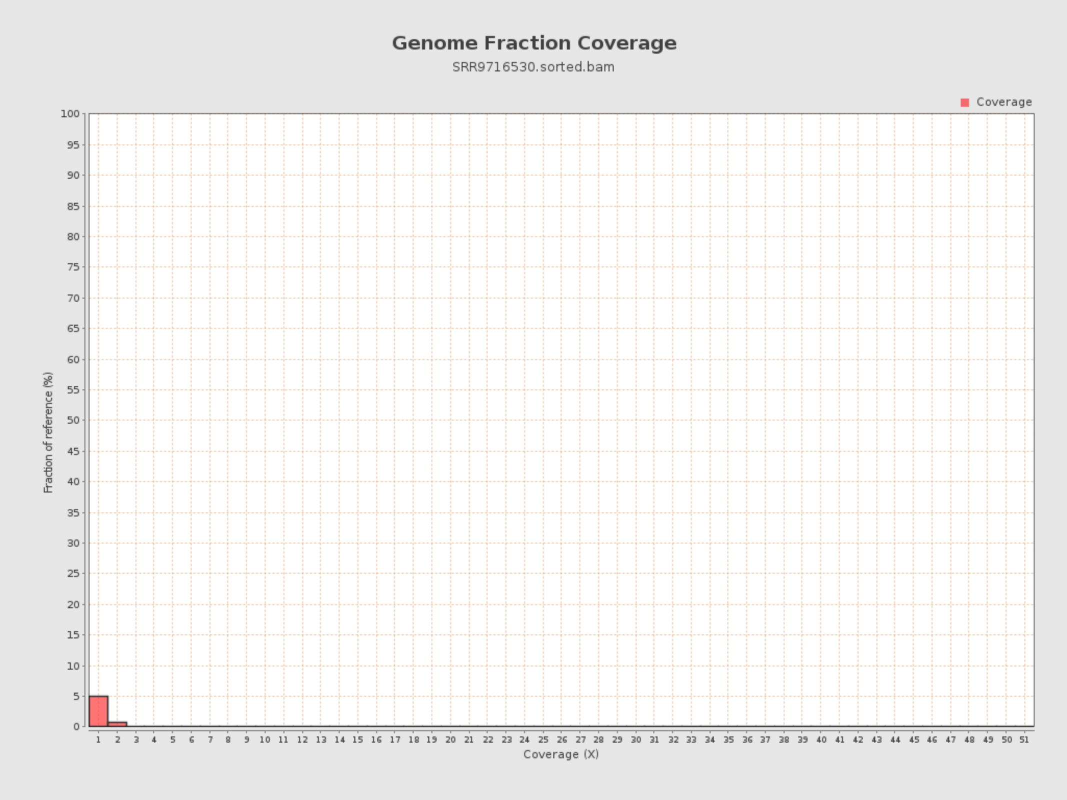
4. Results : Coverage Histogram



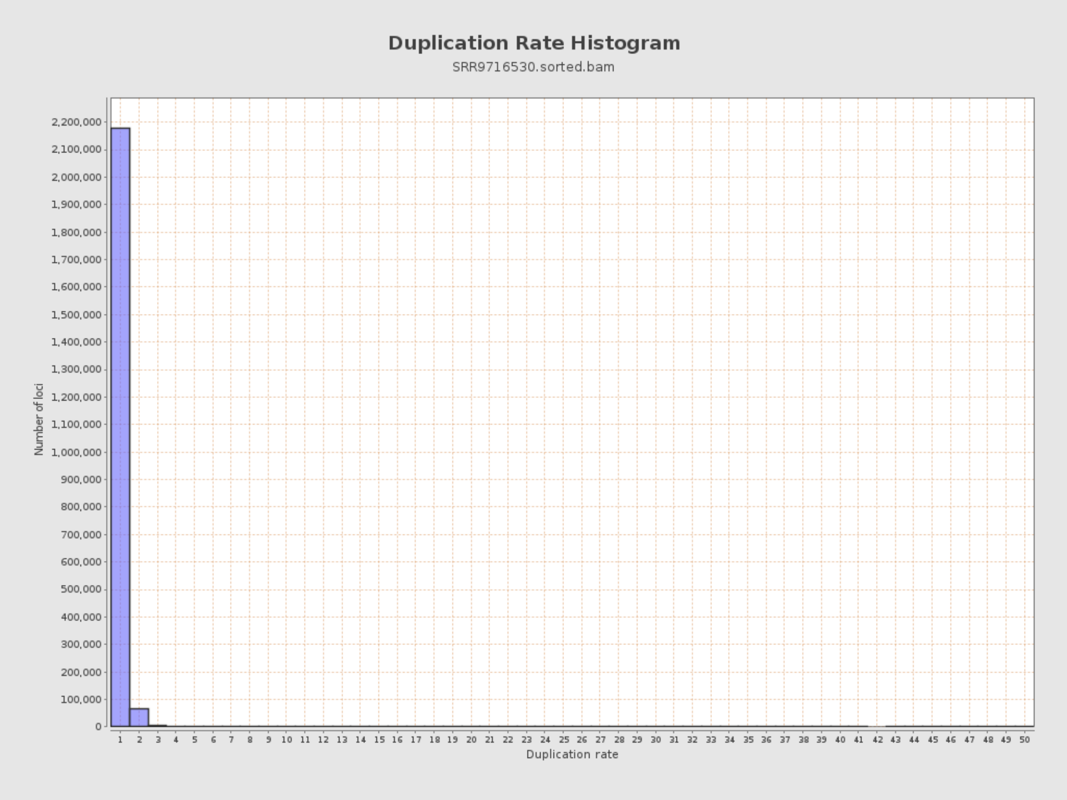
5. Results : Coverage Histogram (0-50X)



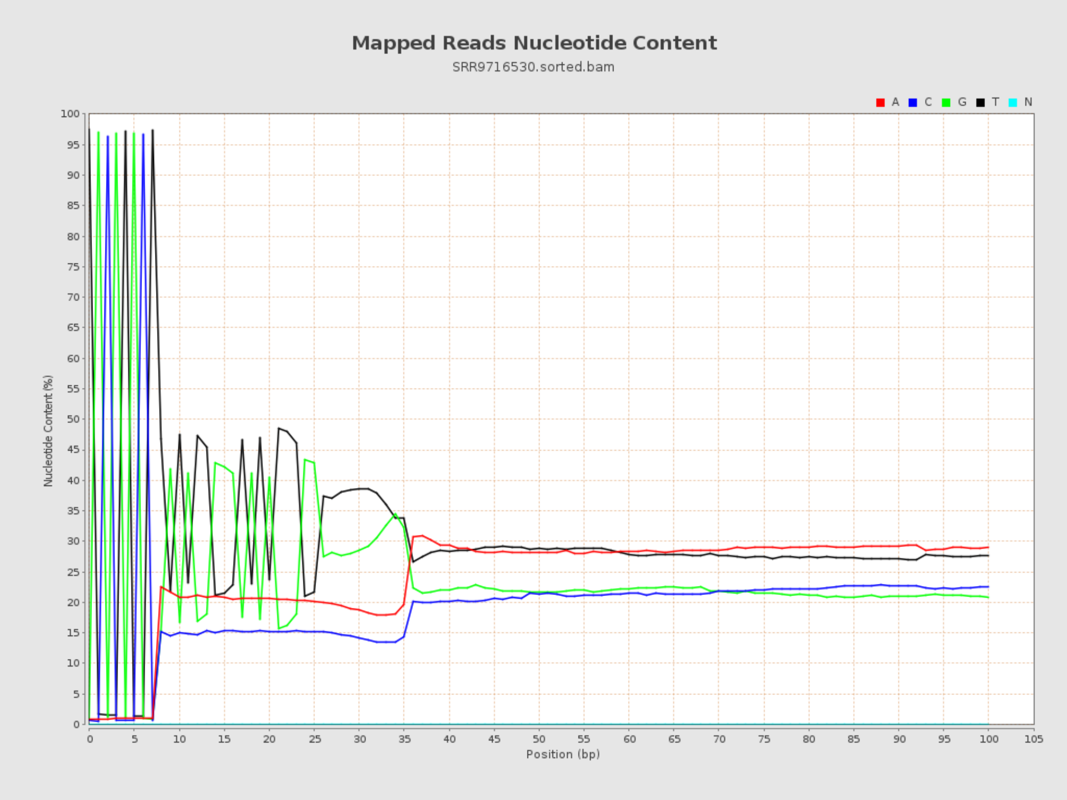
6. Results : Genome Fraction Coverage



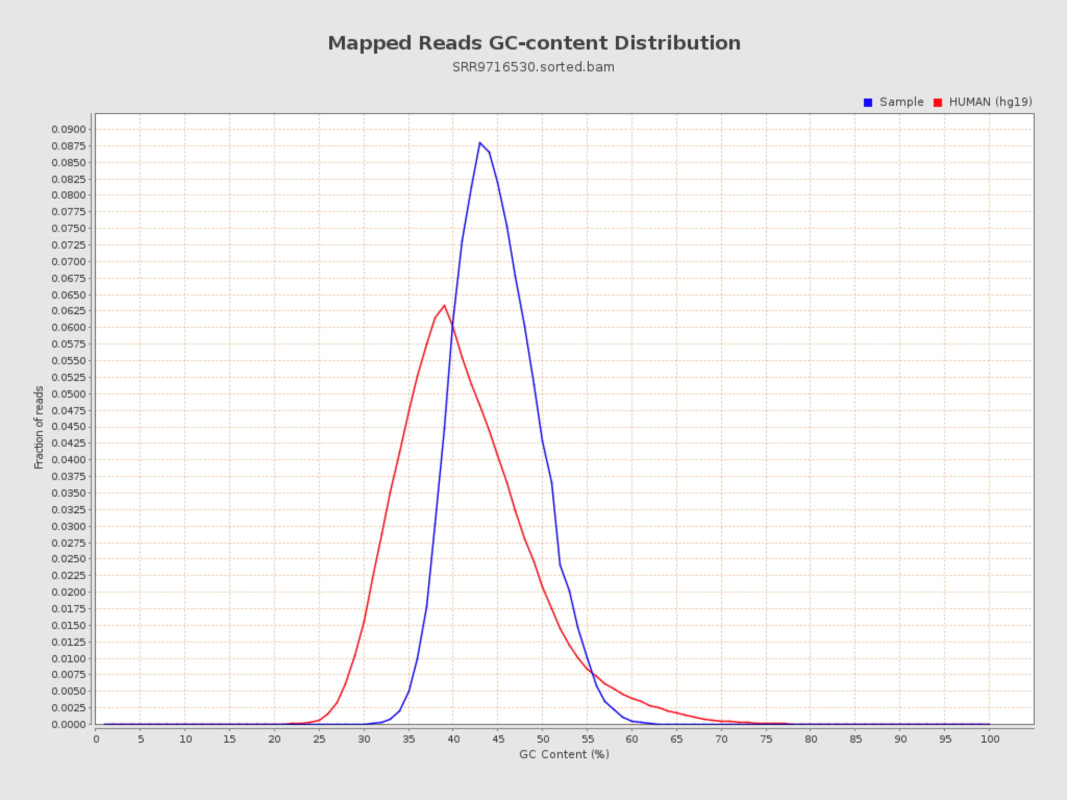
7. Results : Duplication Rate Histogram



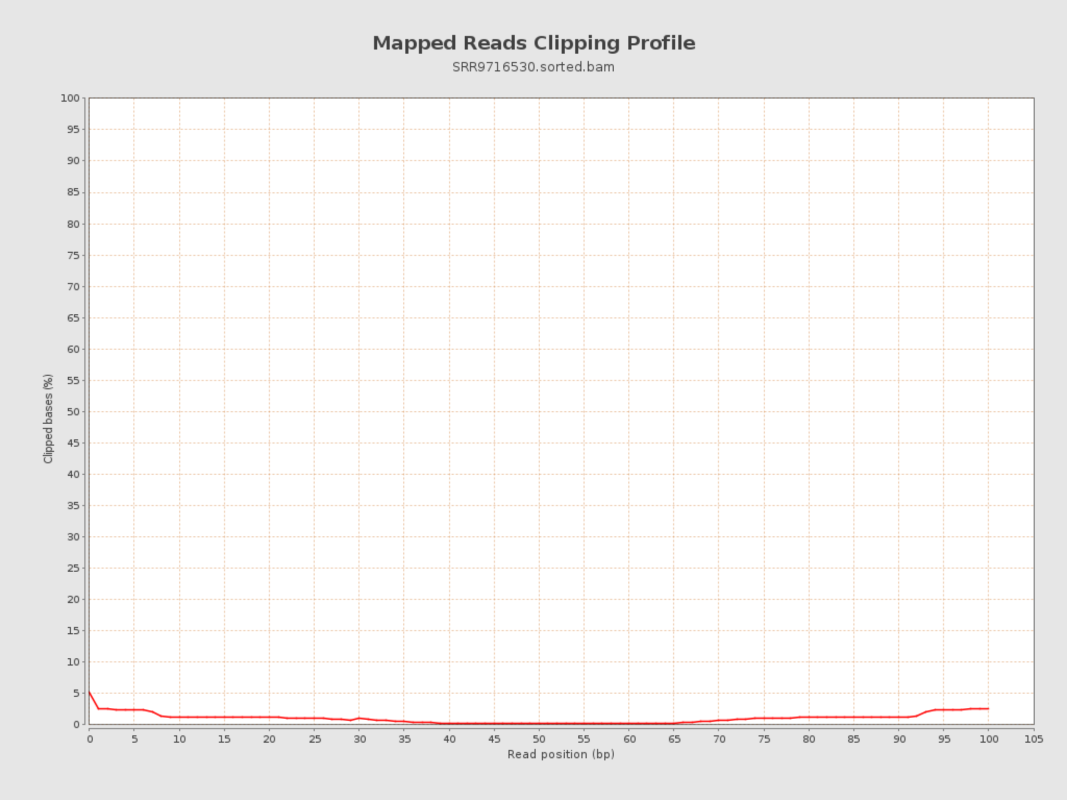
8. Results : Mapped Reads Nucleotide Content



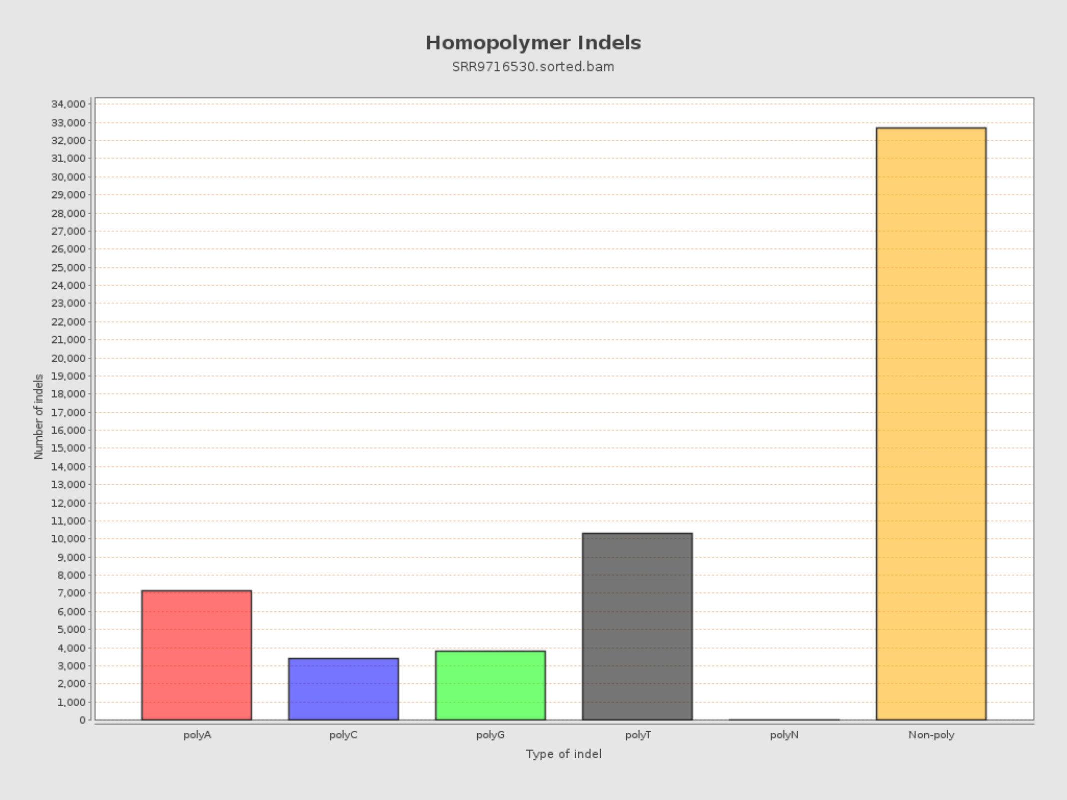
9. Results : Mapped Reads GC-content Distribution



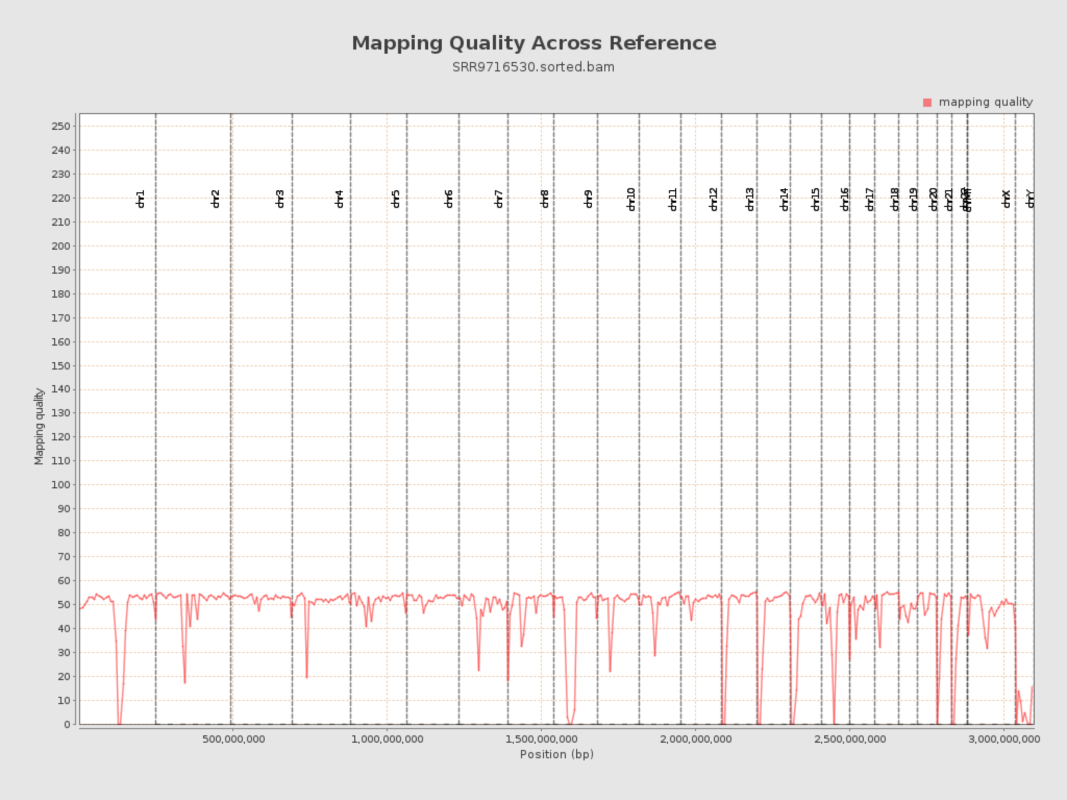
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram