Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:05:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716432.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_SRR9716432 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716432.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:05:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716432.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,907,819
Mapped reads	3,512,738 / 89.89%
Unmapped reads	395,081 / 10.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	70,430 / 1.8%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	197,194 / 5.05%
Duplication rate	4.14%
Clipped reads	3,576,195 / 91.51%

2.2. ACGT Content

Number/percentage of A's	67,748,134 / 25.29%
Number/percentage of C's	55,911,723 / 20.87%
Number/percentage of T's	81,457,191 / 30.41%
Number/percentage of G's	62,699,098 / 23.41%
Number/percentage of N's	33,837 / 0.01%
GC Percentage	44.28%

2.3. Coverage

Mean	0.0866

Standard Deviation	0.6046

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

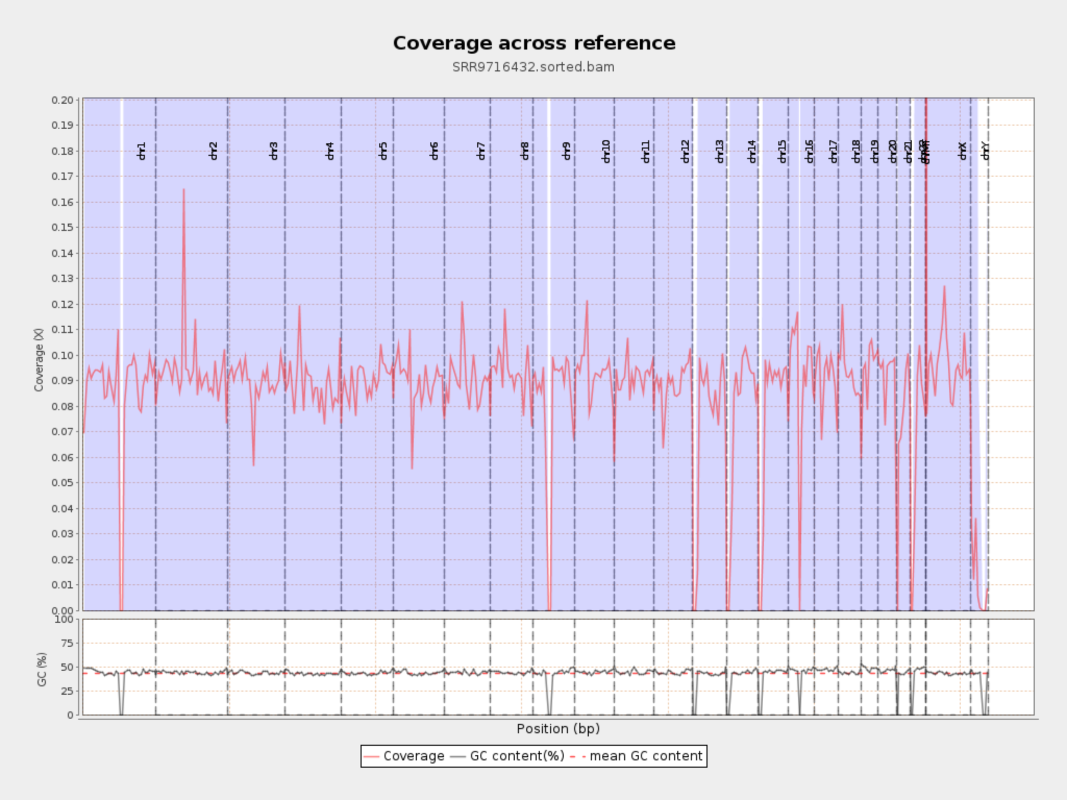
General error rate	0.74%
Mismatches	1,939,466
Insertions	22,296
Mapped reads with at least one insertion	0.63%
Deletions	55,371
Mapped reads with at least one deletion	1.56%
Homopolymer indels	41.31%

2.6. Chromosome stats

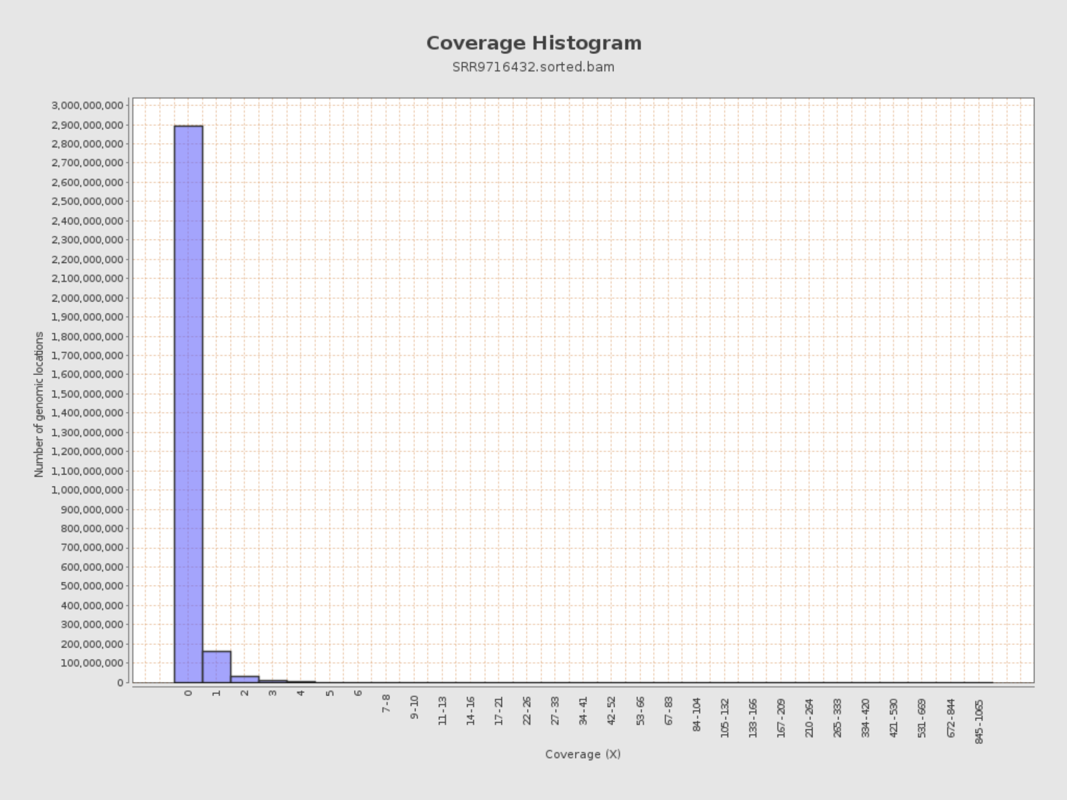
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21270881	0.0853	0.696
chr2	243199373	22944892	0.0943	0.9189
chr3	198022430	17755071	0.0897	0.3753
chr4	191154276	17004295	0.089	0.4263
chr5	180915260	16315310	0.0902	0.3824
chr6	171115067	15360937	0.0898	0.4505
chr7	159138663	14489231	0.091	0.7723

chr8	146364022	13640993	0.0932	0.7923
chr9	141213431	11252774	0.0797	0.6763
chr10	135534747	12690662	0.0936	0.5547
chr11	135006516	12290473	0.091	0.6634
chr12	133851895	11908823	0.089	0.3875
chr13	115169878	8411895	0.073	0.3387
chr14	107349540	8241700	0.0768	0.4387
chr15	102531392	7690007	0.075	0.3481
chr16	90354753	8025427	0.0888	0.4336
chr17	81195210	7444937	0.0917	0.4264
chr18	78077248	7340088	0.094	1.2947
chr19	59128983	5634313	0.0953	0.6567
chr20	63025520	5812968	0.0922	0.4112
chr21	48129895	3556575	0.0739	0.395
chr22	51304566	3229418	0.0629	0.319
chrMT	16571	35096	2.1179	2.3288
chrX	155270560	14935533	0.0962	0.5424
chrY	59373566	662583	0.0112	0.2926

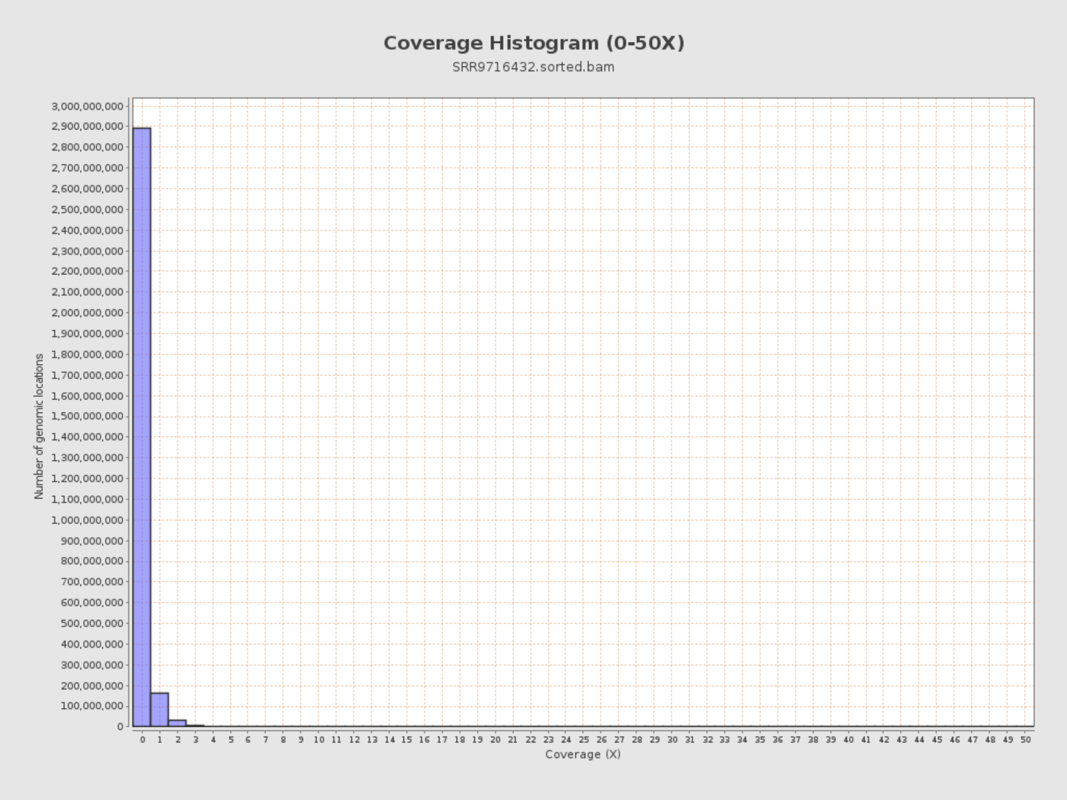
3. Results : Coverage across reference



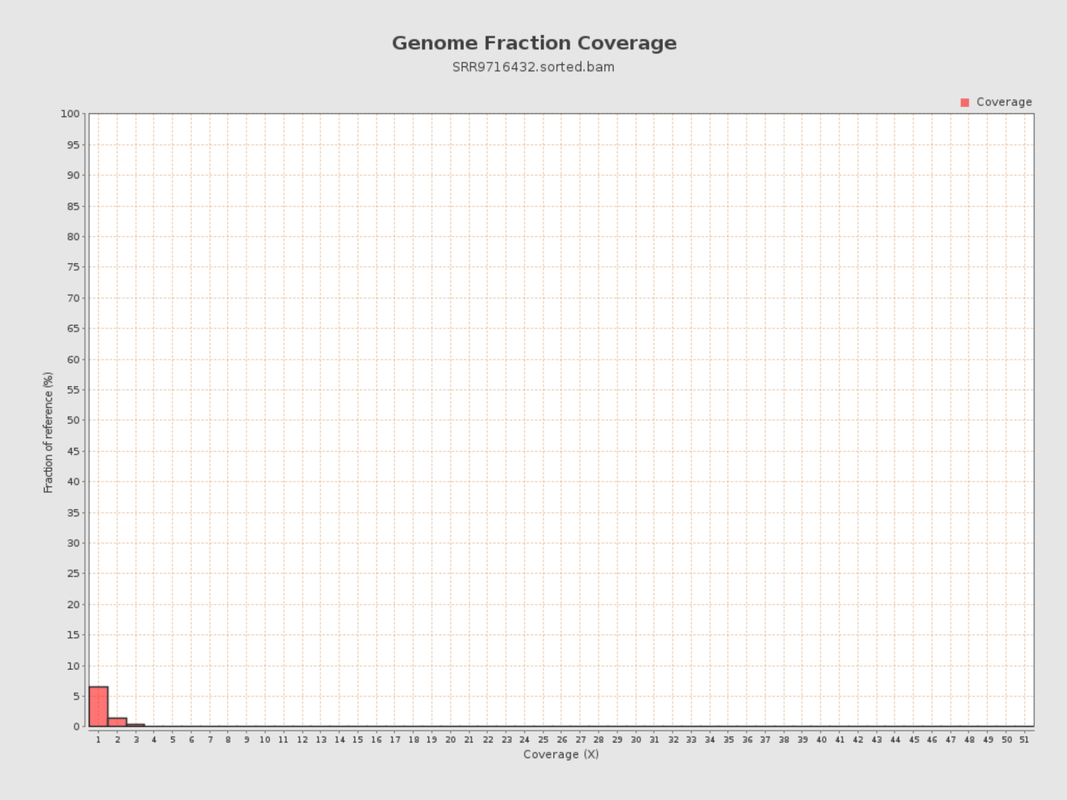
4. Results : Coverage Histogram



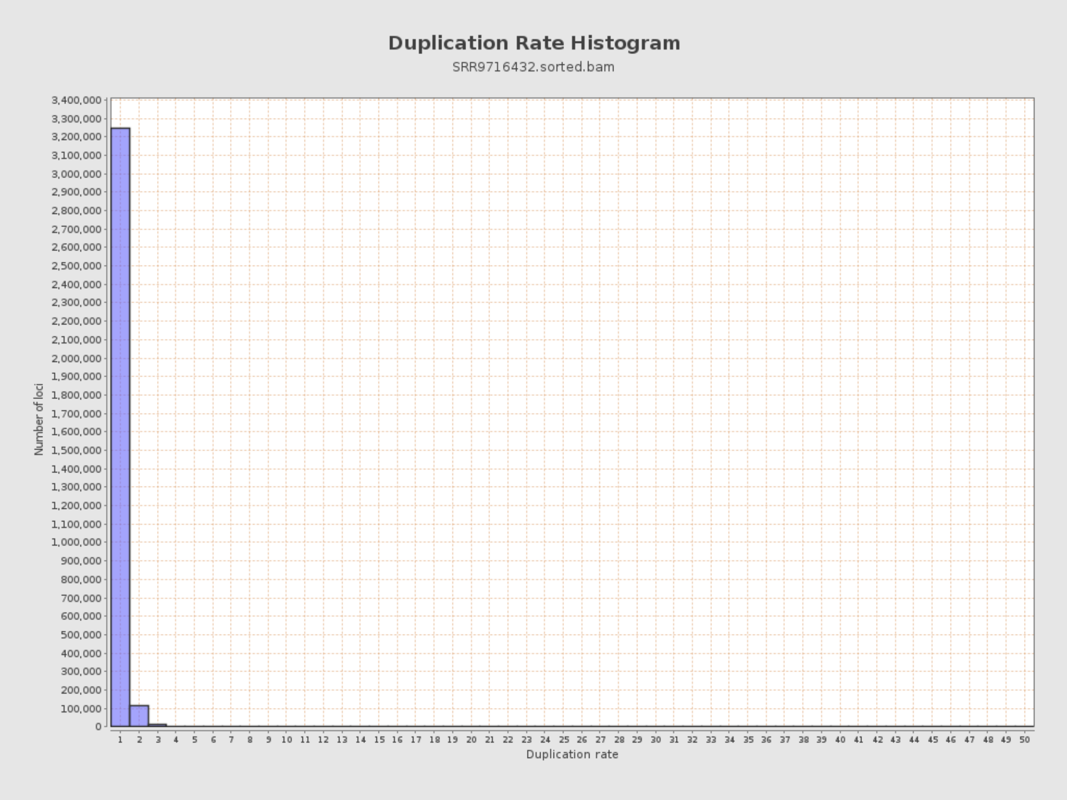
5. Results : Coverage Histogram (0-50X)



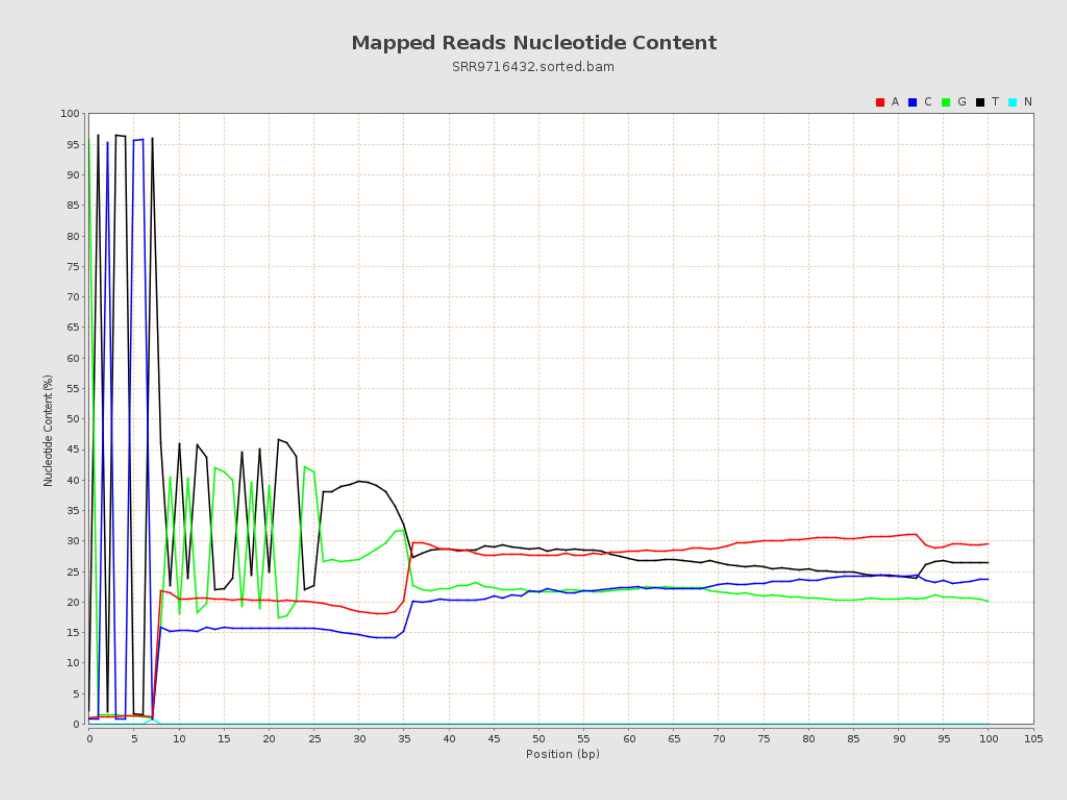
6. Results : Genome Fraction Coverage



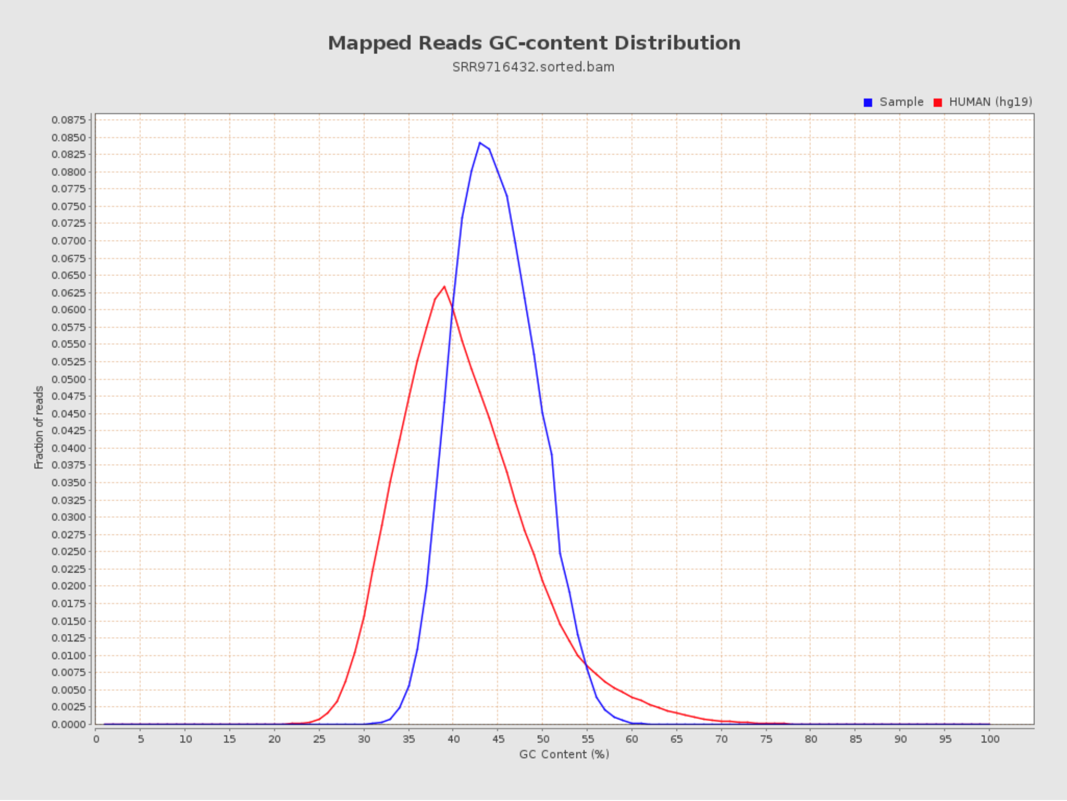
7. Results : Duplication Rate Histogram



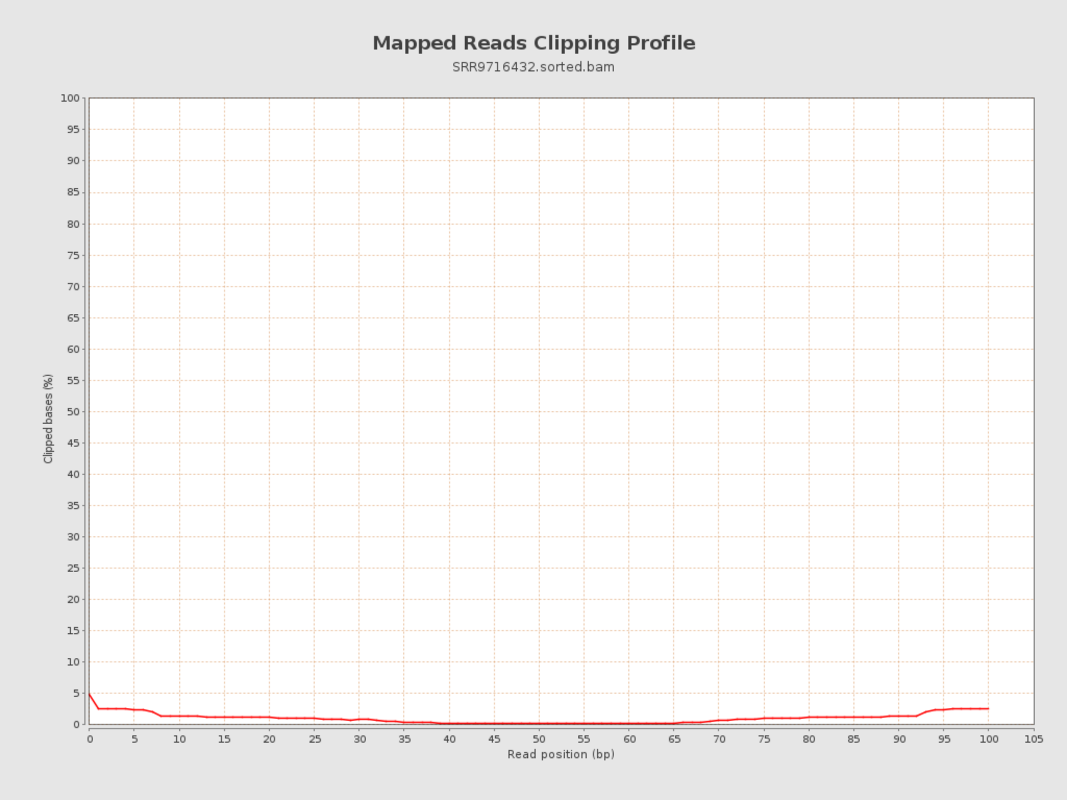
8. Results : Mapped Reads Nucleotide Content



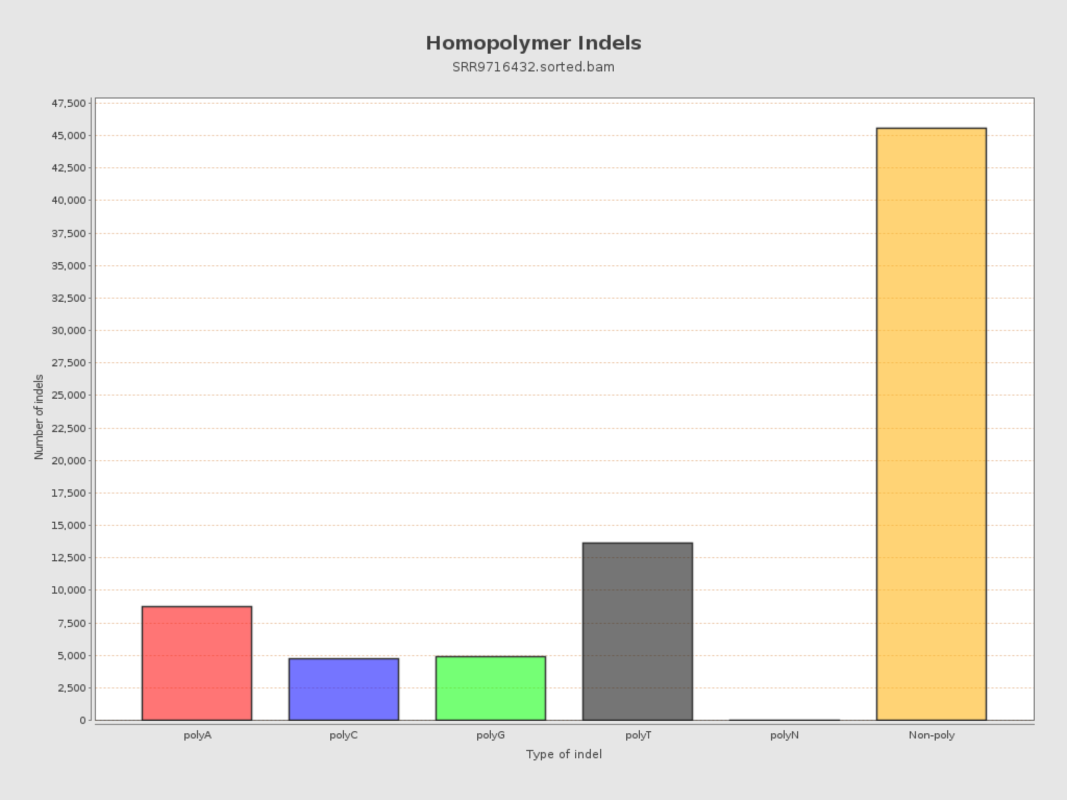
9. Results : Mapped Reads GC-content Distribution



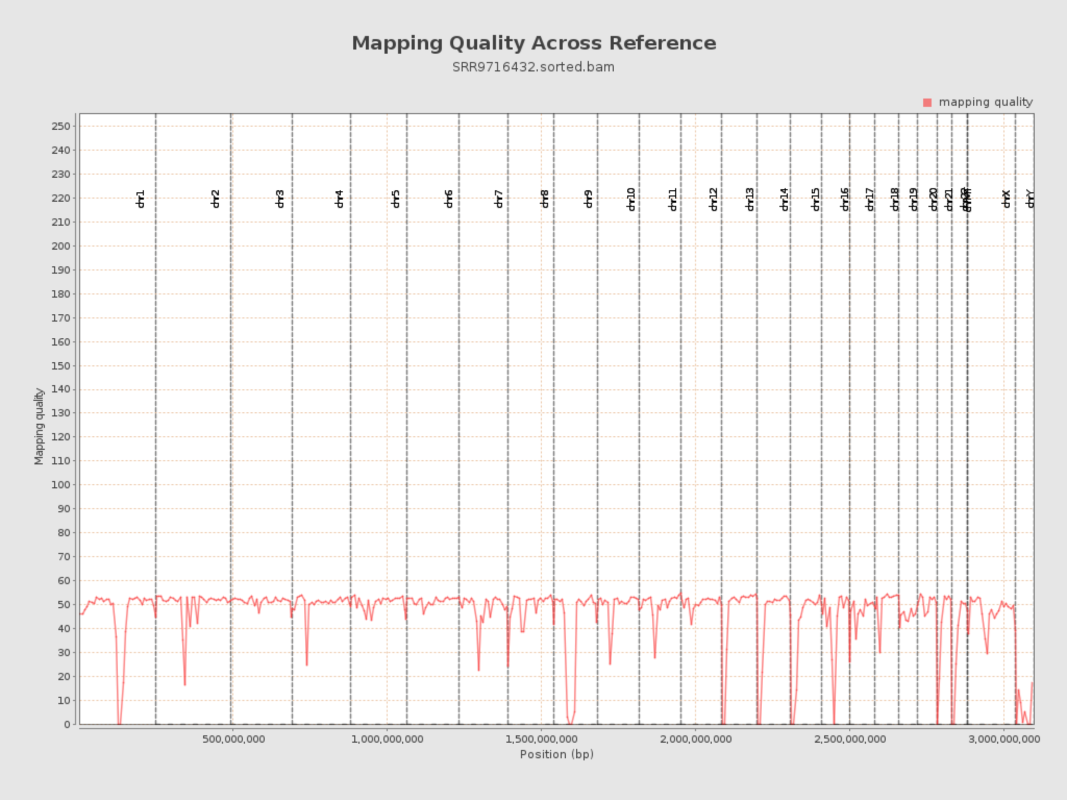
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram