Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:26:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716303.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_SRR9716303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:26:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,796,268
Mapped reads	4,328,674 / 90.25%
Unmapped reads	467,594 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,414 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	243,426 / 5.08%
Duplication rate	3.98%
Clipped reads	4,336,386 / 90.41%

2.2. ACGT Content

Number/percentage of A's	62,965,665 / 25.36%
Number/percentage of C's	46,795,994 / 18.85%
Number/percentage of T's	78,669,238 / 31.69%
Number/percentage of G's	59,843,884 / 24.1%
Number/percentage of N's	3,871 / 0%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0802

Standard Deviation	0.6995

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

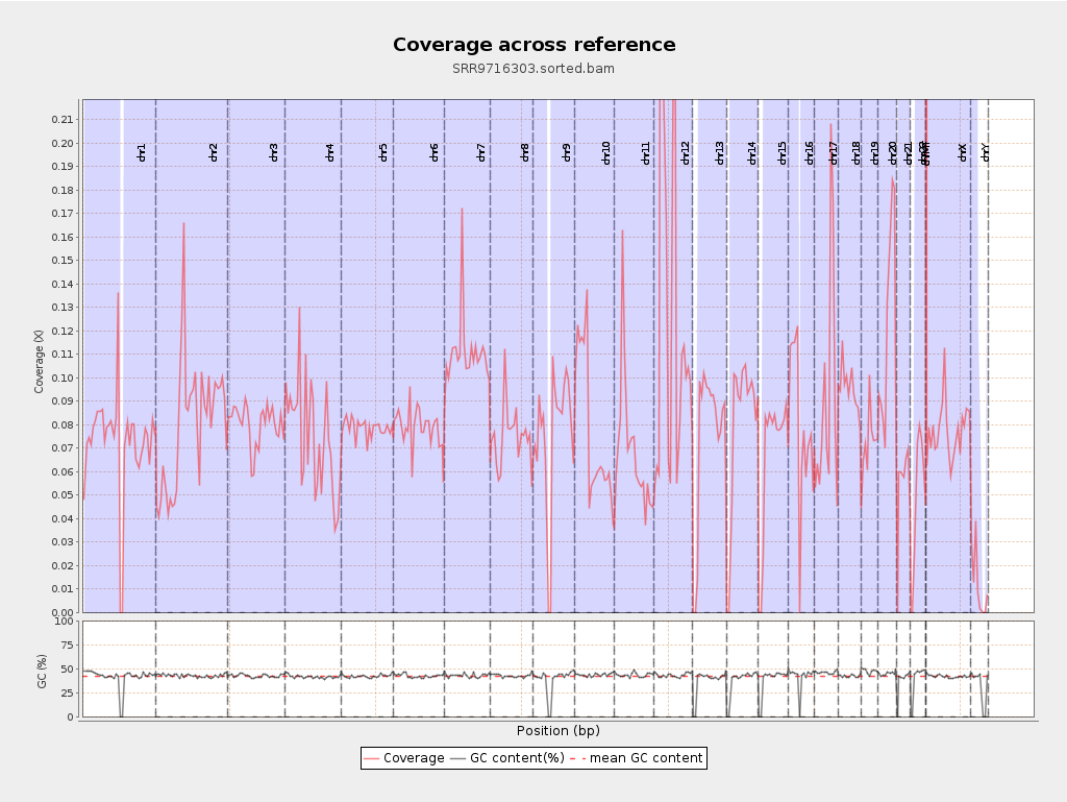
General error rate	0.56%
Mismatches	1,342,438
Insertions	19,350
Mapped reads with at least one insertion	0.45%
Deletions	41,547
Mapped reads with at least one deletion	0.95%
Homopolymer indels	39.59%

2.6. Chromosome stats

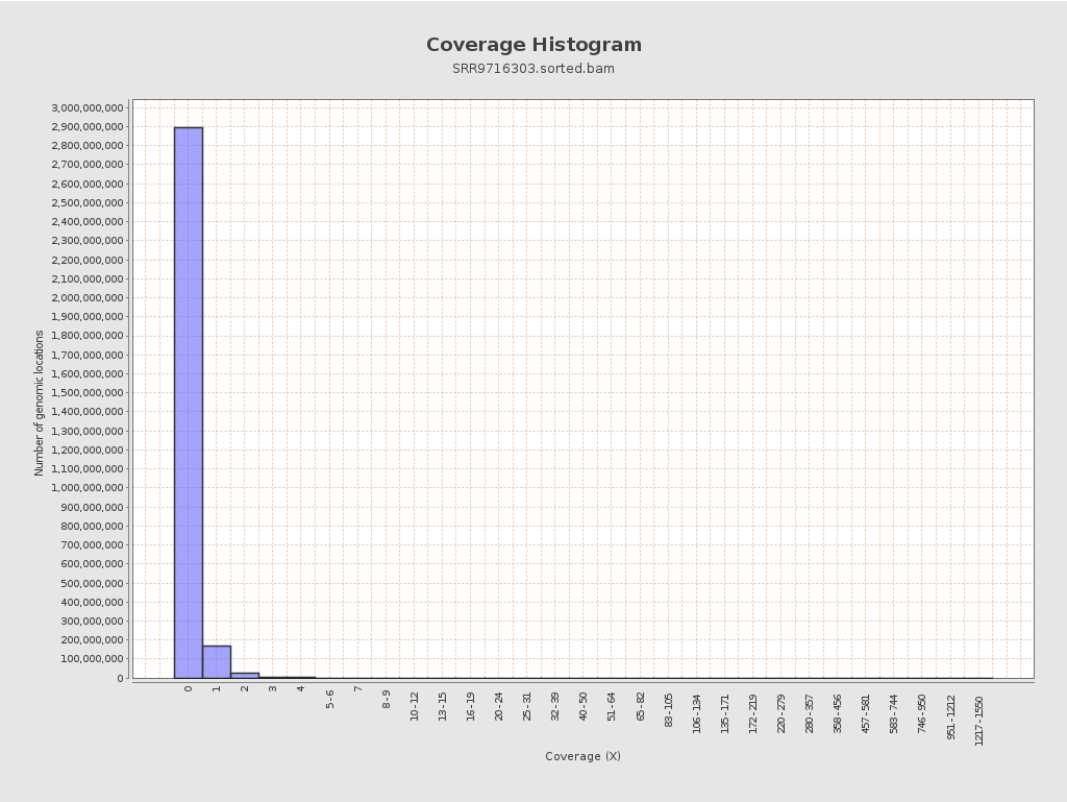
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18059644	0.0725	1.32
chr2	243199373	19505720	0.0802	0.7717
chr3	198022430	15890281	0.0802	0.3359
chr4	191154276	14251330	0.0746	0.3907
chr5	180915260	14192925	0.0785	0.3438
chr6	171115067	13516906	0.079	0.422
chr7	159138663	17579664	0.1105	1.0982

chr8	146364022	10948611	0.0748	0.6183
chr9	141213431	10752749	0.0761	0.7737
chr10	135534747	10379868	0.0766	0.6461
chr11	135006516	9305518	0.0689	0.5702
chr12	133851895	17927197	0.1339	0.5383
chr13	115169878	8621118	0.0749	0.321
chr14	107349540	8628564	0.0804	0.473
chr15	102531392	6759189	0.0659	0.3071
chr16	90354753	7032620	0.0778	0.4153
chr17	81195210	7439406	0.0916	0.3935
chr18	78077248	7491573	0.096	1.4274
chr19	59128983	4332776	0.0733	1.0151
chr20	63025520	7826702	0.1242	0.4507
chr21	48129895	2631759	0.0547	0.3965
chr22	51304566	2505279	0.0488	0.2566
chrMT	16571	113289	6.8366	4.7913
chrX	155270560	11966581	0.0771	0.4885
chrY	59373566	688398	0.0116	0.2487

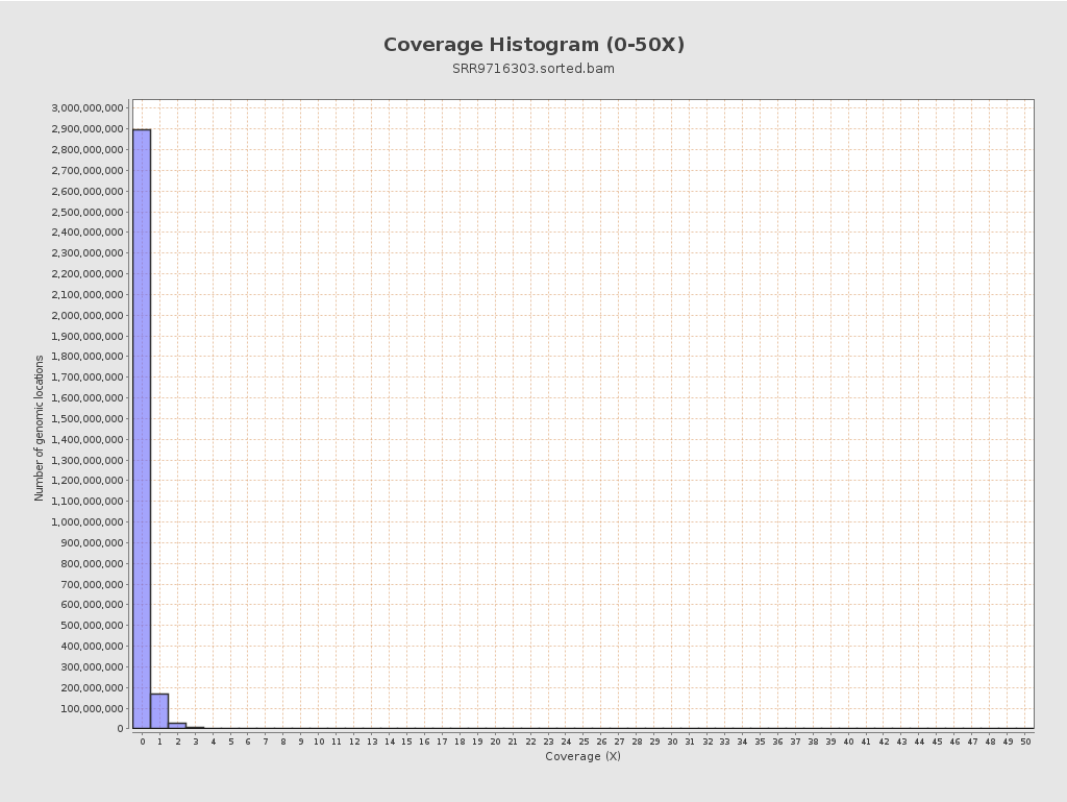
3. Results : Coverage across reference



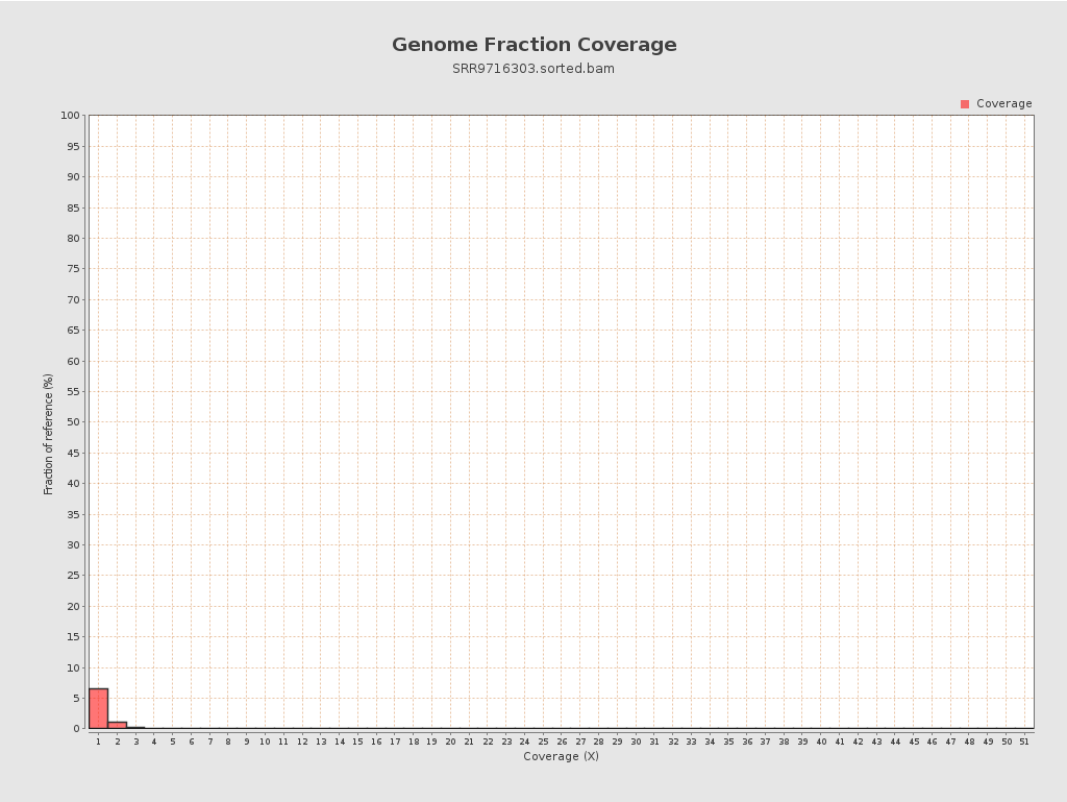
4. Results : Coverage Histogram



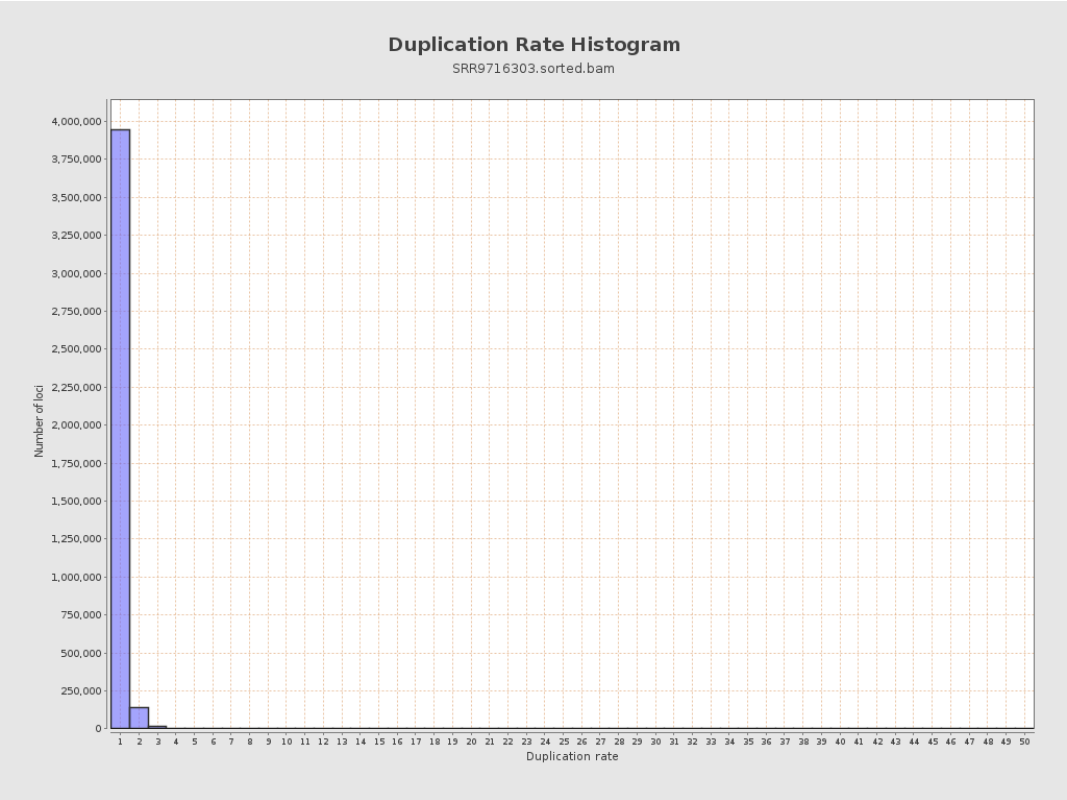
5. Results : Coverage Histogram (0-50X)



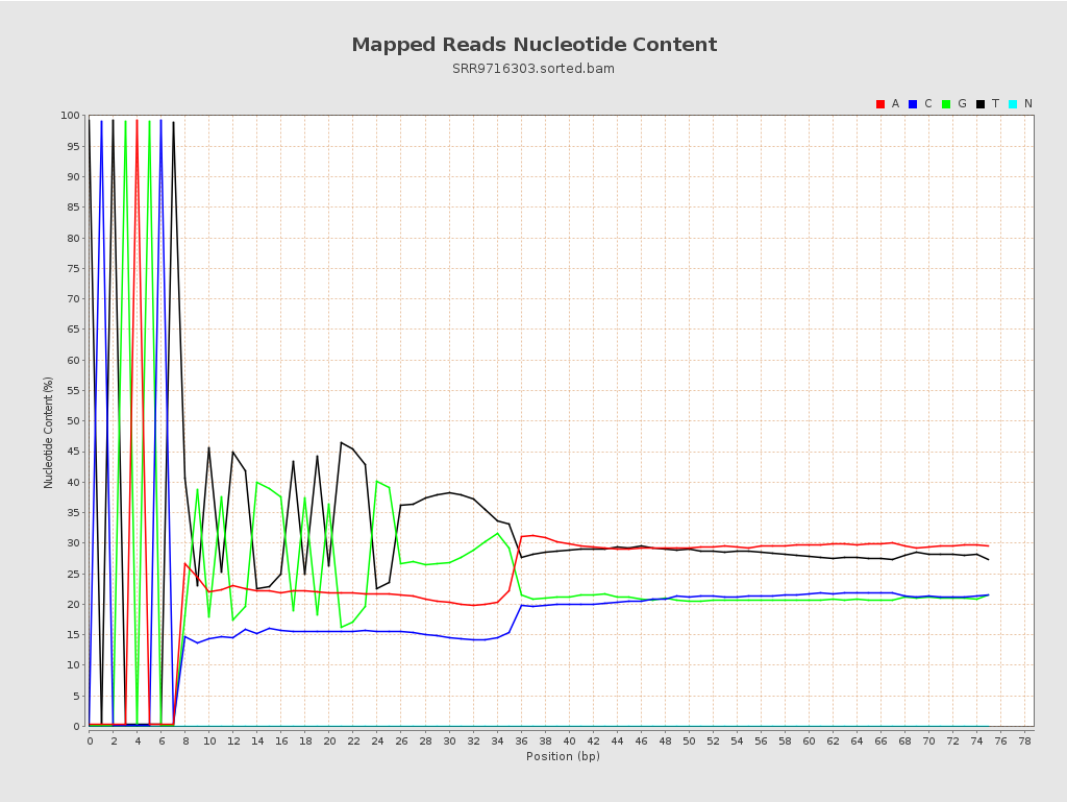
6. Results : Genome Fraction Coverage



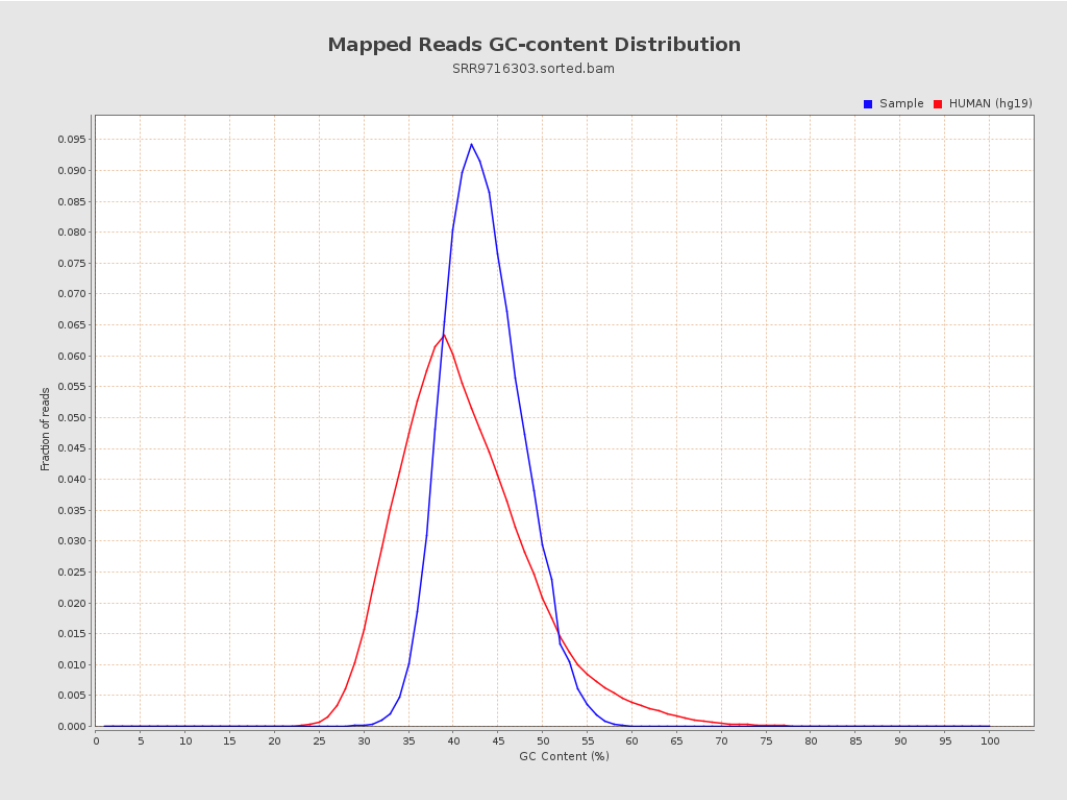
7. Results : Duplication Rate Histogram



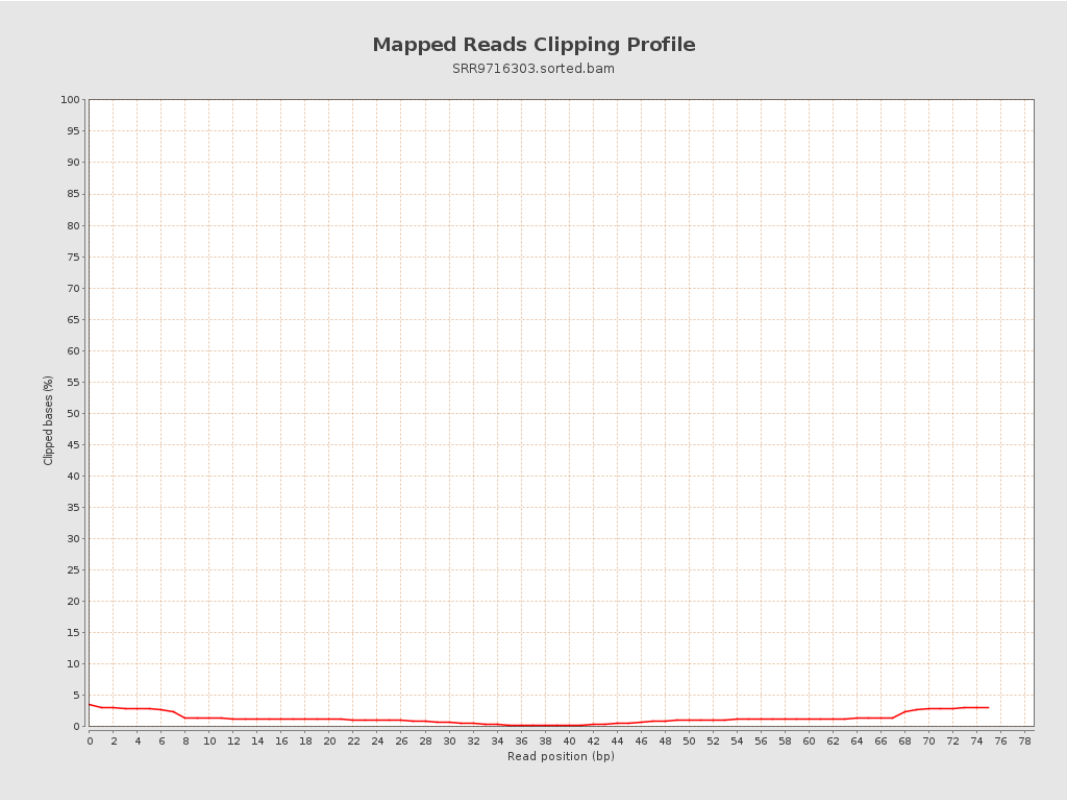
8. Results : Mapped Reads Nucleotide Content



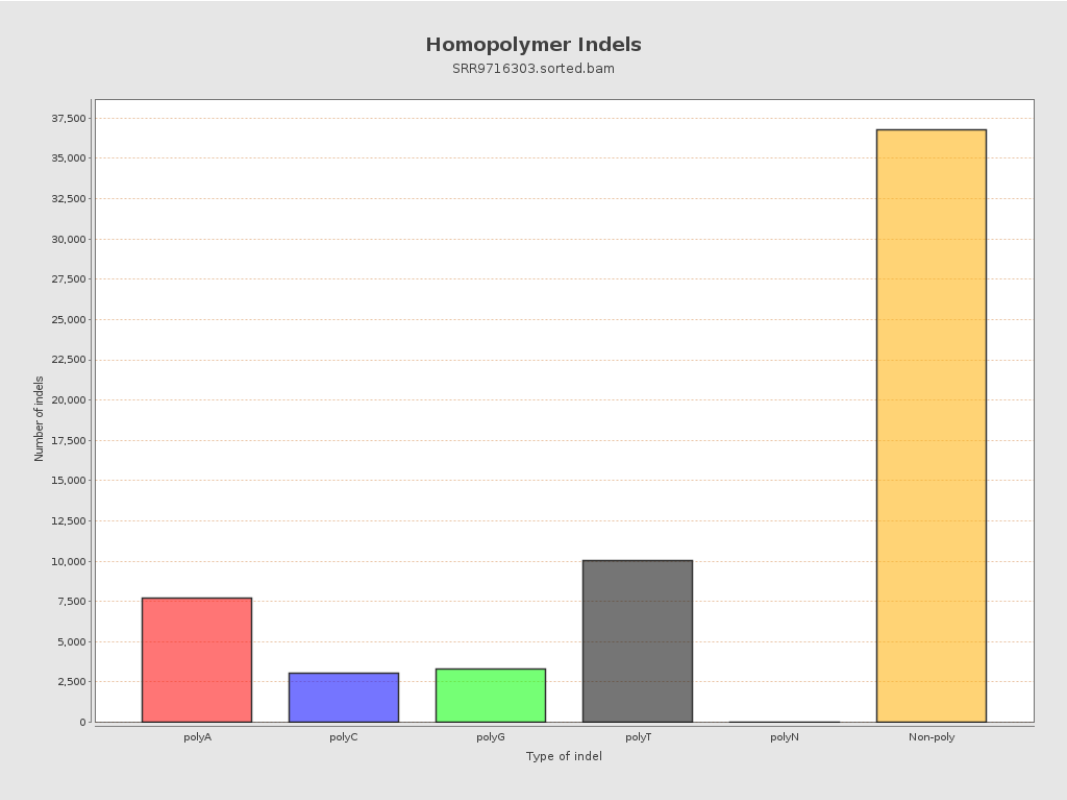
9. Results : Mapped Reads GC-content Distribution



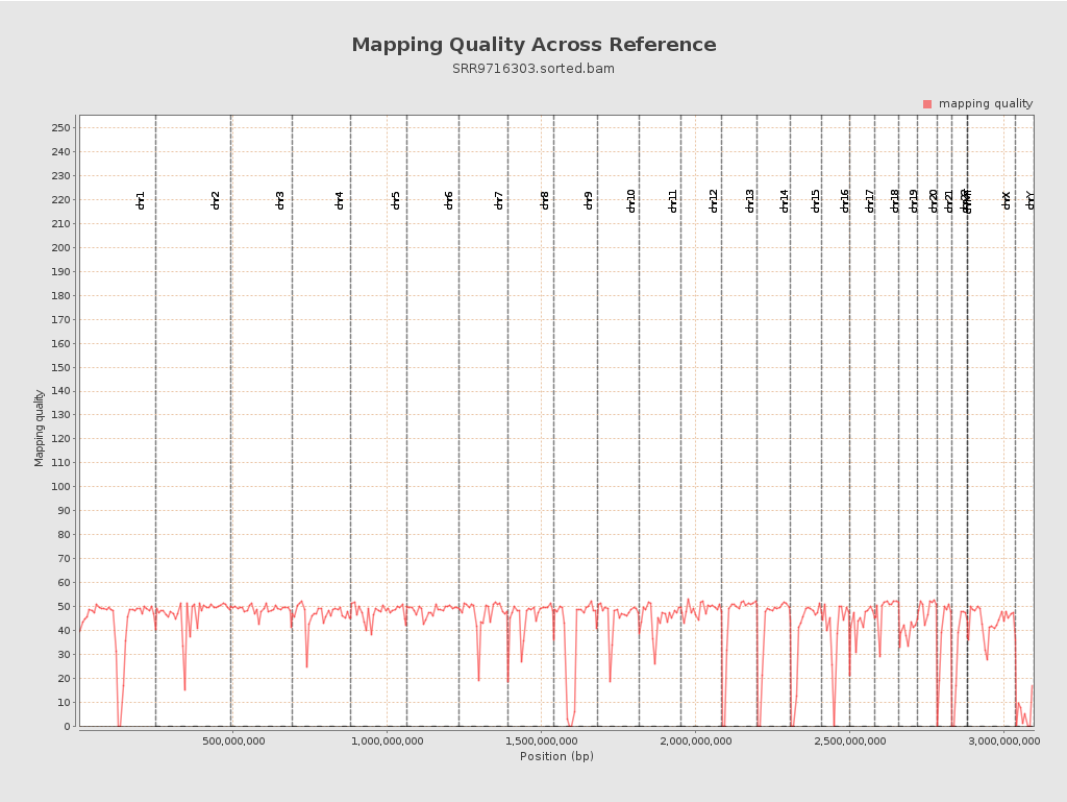
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram