Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/09/03 15:03:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716853.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_SRR9716853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716853.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:03:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,808,688
Mapped reads	3,467,962 / 91.05%
Unmapped reads	340,726 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,533 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	199,300 / 5.23%
Duplication rate	4.31%
Clipped reads	3,483,306 / 91.46%

2.2. ACGT Content

Number/percentage of A's	48,815,693 / 24.13%
Number/percentage of C's	38,971,740 / 19.27%
Number/percentage of T's	63,732,848 / 31.51%
Number/percentage of G's	50,766,867 / 25.1%
Number/percentage of N's	2,775 / 0%
GC Percentage	44.36%

2.3. Coverage

Mean	0.0654

Standard Deviation	0.5213

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

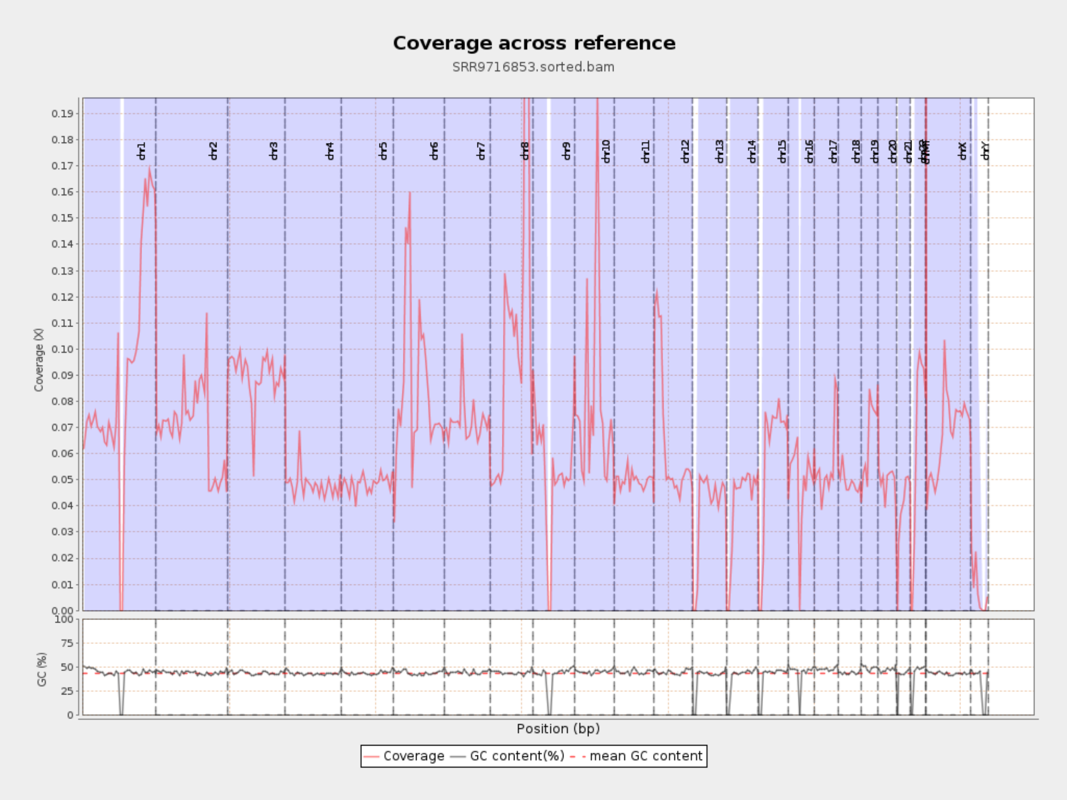
General error rate	0.49%
Mismatches	974,767
Insertions	10,645
Mapped reads with at least one insertion	0.31%
Deletions	34,604
Mapped reads with at least one deletion	0.99%
Homopolymer indels	44.54%

2.6. Chromosome stats

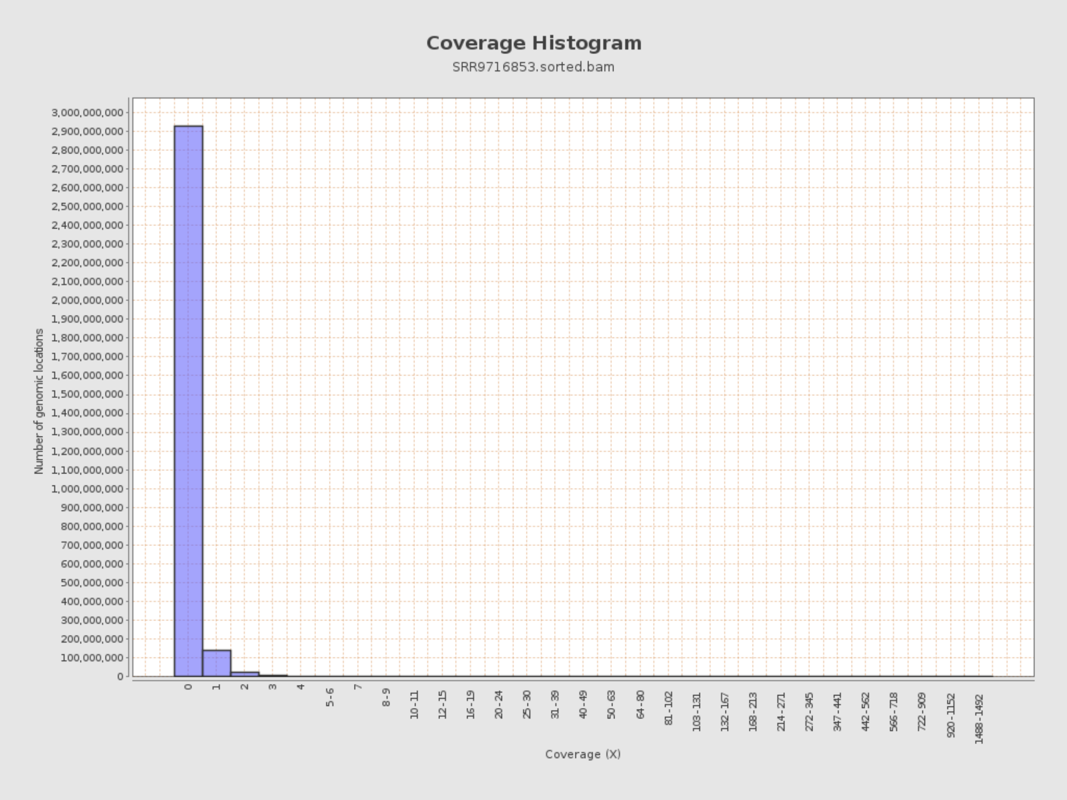
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22669781	0.091	0.9468
chr2	243199373	16966558	0.0698	0.688
chr3	198022430	17806663	0.0899	0.3596
chr4	191154276	9211840	0.0482	0.2842
chr5	180915260	8798083	0.0486	0.2643
chr6	171115067	14716083	0.086	0.7399
chr7	159138663	11583738	0.0728	0.6787

chr8	146364022	16071104	0.1098	0.4676
chr9	141213431	7370327	0.0522	0.4071
chr10	135534747	10861683	0.0801	0.5073
chr11	135006516	6698730	0.0496	0.4165
chr12	133851895	8883332	0.0664	0.3185
chr13	115169878	4479273	0.0389	0.2347
chr14	107349540	4375202	0.0408	0.2858
chr15	102531392	6004969	0.0586	0.2964
chr16	90354753	4362035	0.0483	0.302
chr17	81195210	4477573	0.0551	0.299
chr18	78077248	3861148	0.0495	0.8209
chr19	59128983	3942250	0.0667	0.6469
chr20	63025520	3124812	0.0496	0.2714
chr21	48129895	1845550	0.0383	0.2675
chr22	51304566	3276497	0.0639	0.3024
chrMT	16571	5007	0.3022	0.6012
chrX	155270560	10489596	0.0676	0.3775
chrY	59373566	462551	0.0078	0.1575

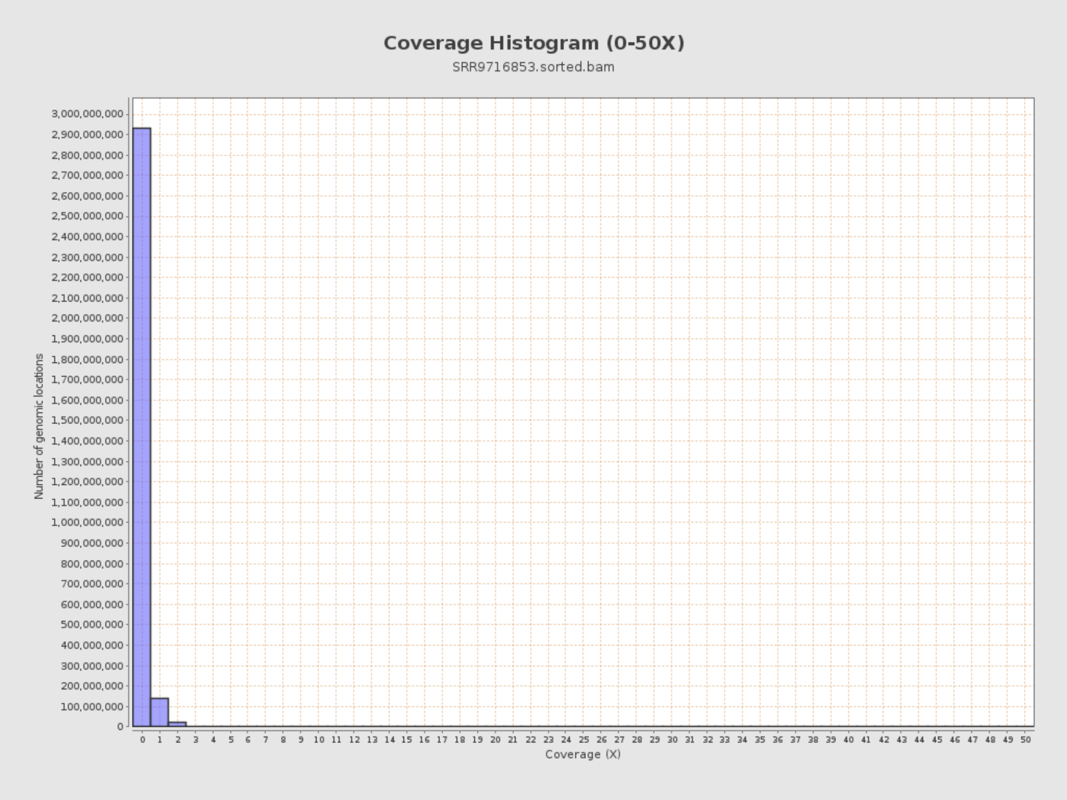
3. Results : Coverage across reference



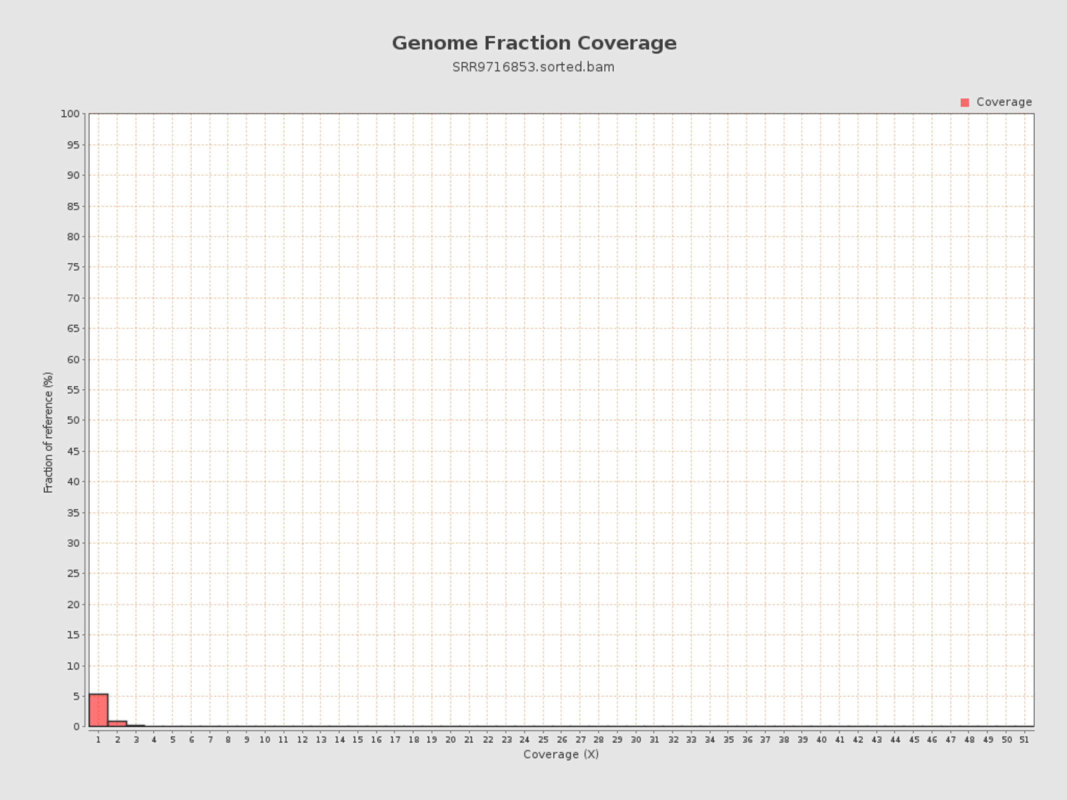
4. Results : Coverage Histogram



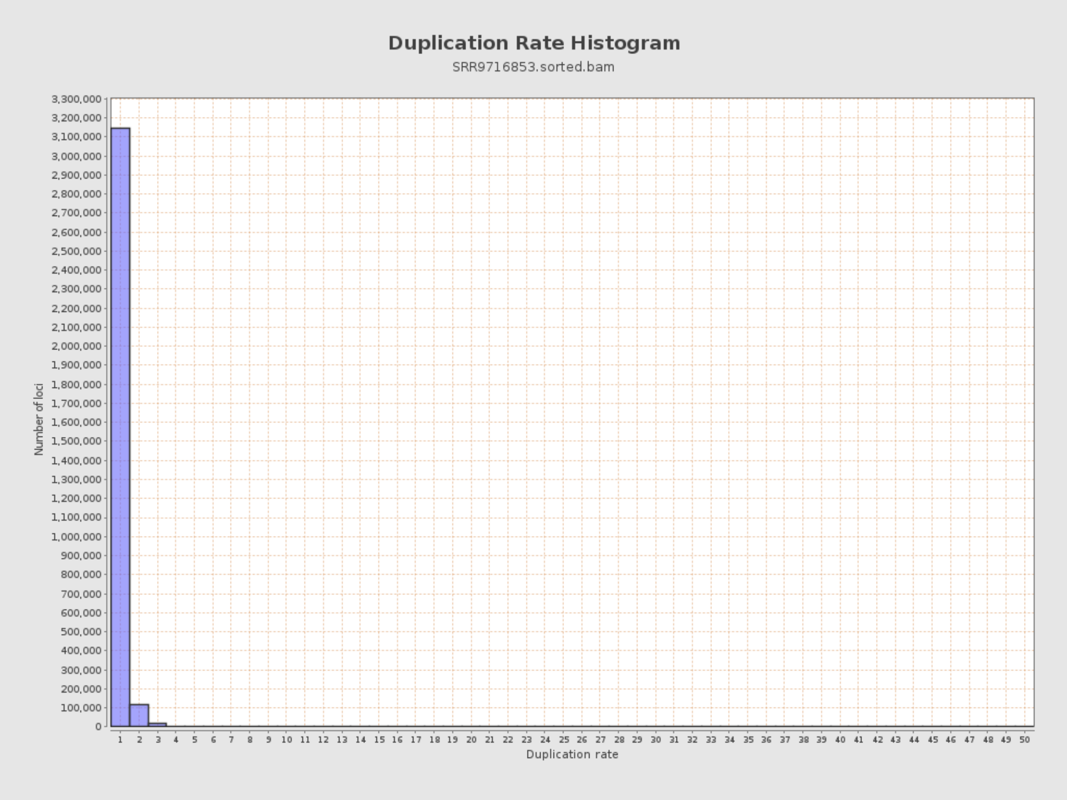
5. Results : Coverage Histogram (0-50X)



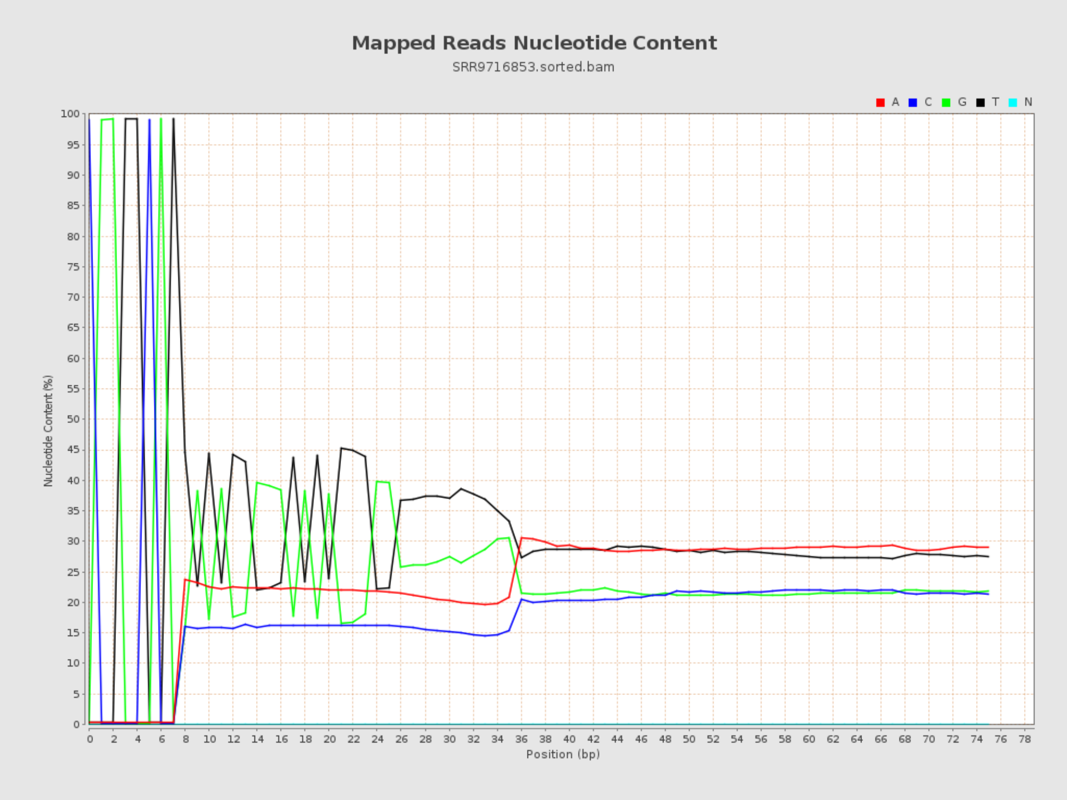
6. Results : Genome Fraction Coverage



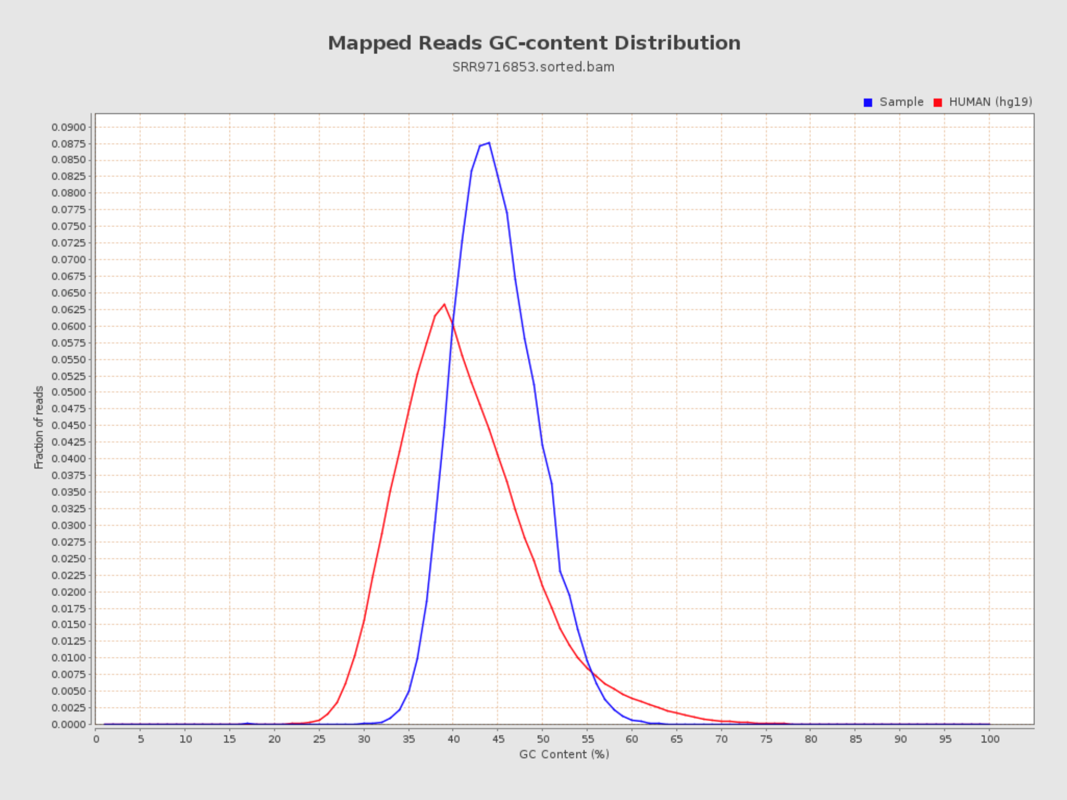
7. Results : Duplication Rate Histogram



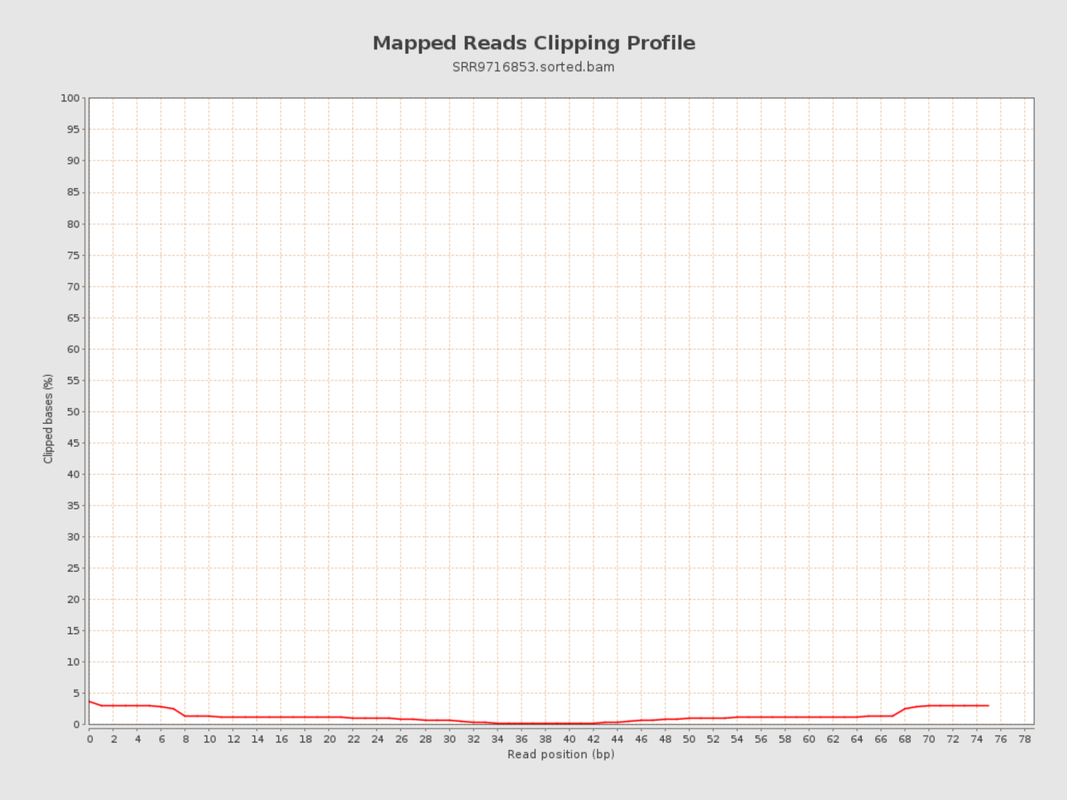
8. Results : Mapped Reads Nucleotide Content



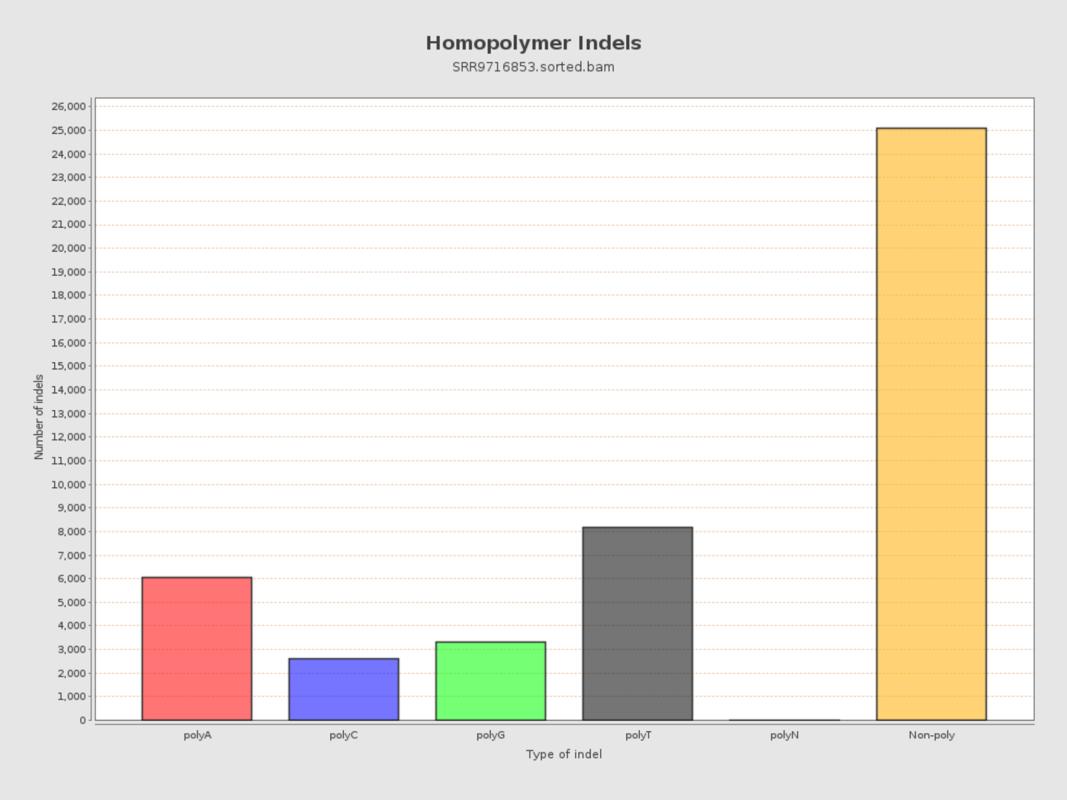
9. Results : Mapped Reads GC-content Distribution



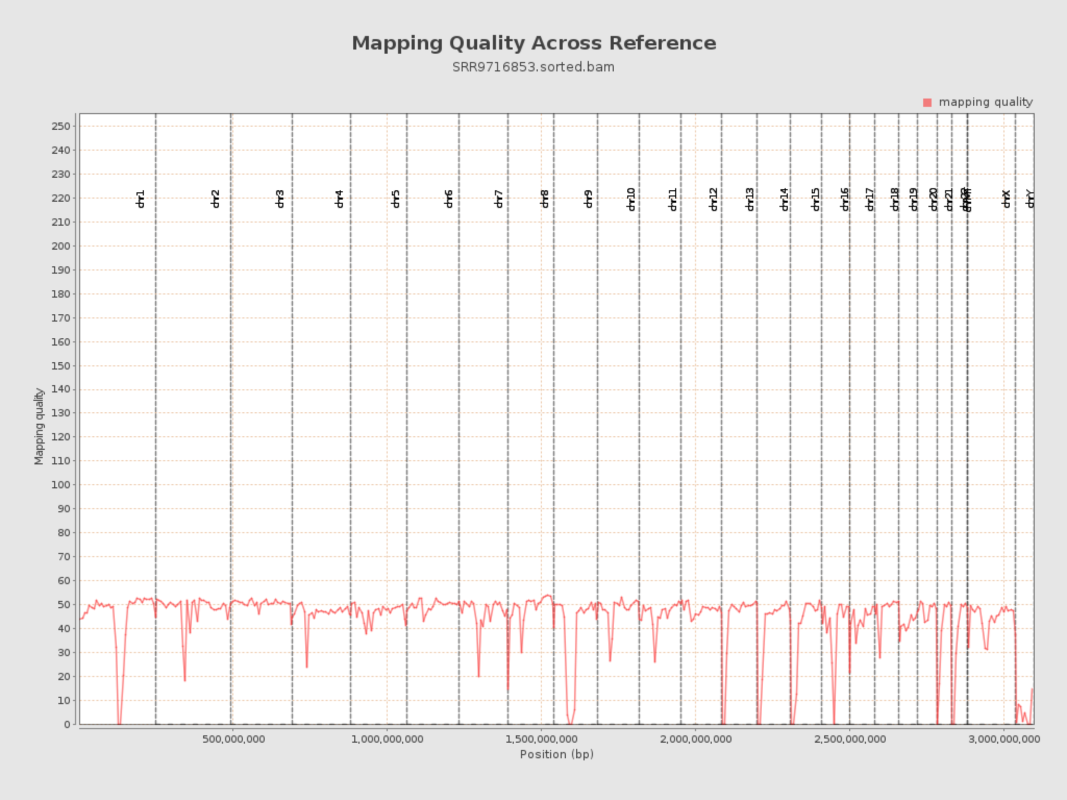
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram