Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:39:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716249.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_SRR9716249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716249.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:39:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,240,636
Mapped reads	3,039,954 / 93.81%
Unmapped reads	200,682 / 6.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	76,914 / 2.37%
Read min/max/mean length	30 / 101 / 101.85
Duplicated reads (estimated)	190,012 / 5.86%
Duplication rate	4.78%
Clipped reads	3,112,660 / 96.05%

2.2. ACGT Content

Number/percentage of A's	55,720,250 / 23.96%
Number/percentage of C's	48,025,004 / 20.65%
Number/percentage of T's	69,034,334 / 29.69%
Number/percentage of G's	59,762,017 / 25.7%
Number/percentage of N's	9,210 / 0%
GC Percentage	46.35%

2.3. Coverage

Mean	0.0752

Standard Deviation	0.5436

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

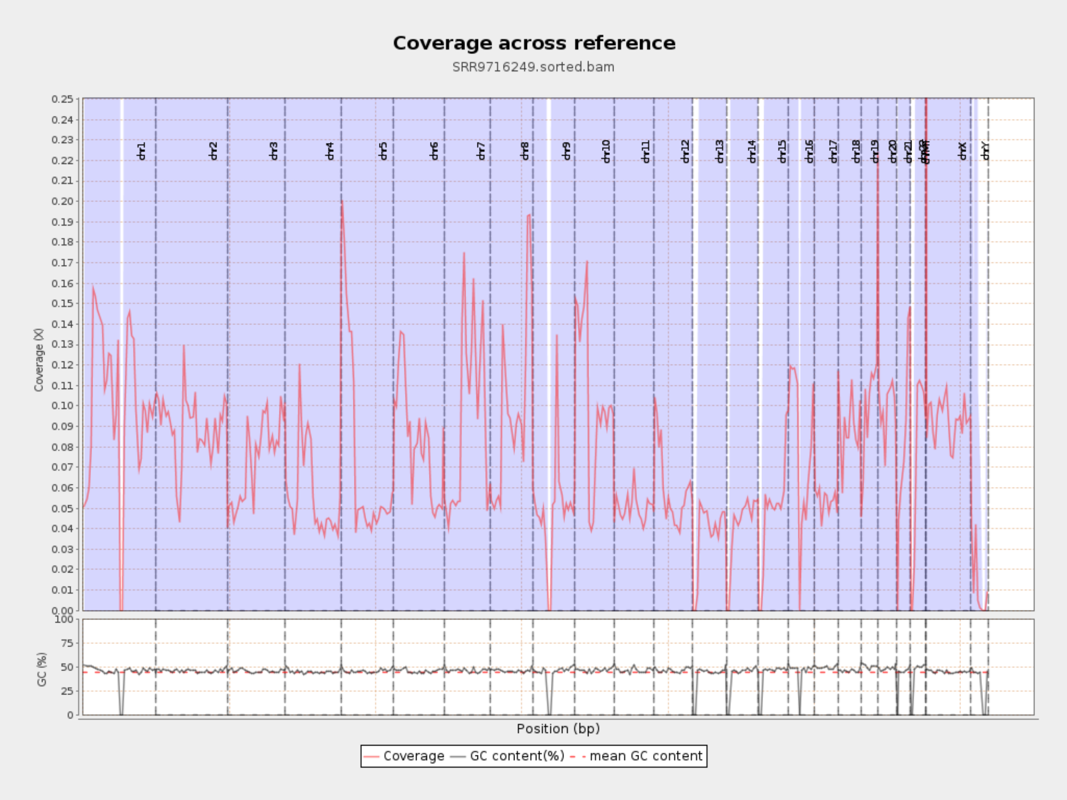
General error rate	0.67%
Mismatches	1,503,807
Insertions	18,621
Mapped reads with at least one insertion	0.6%
Deletions	45,792
Mapped reads with at least one deletion	1.48%
Homopolymer indels	38.66%

2.6. Chromosome stats

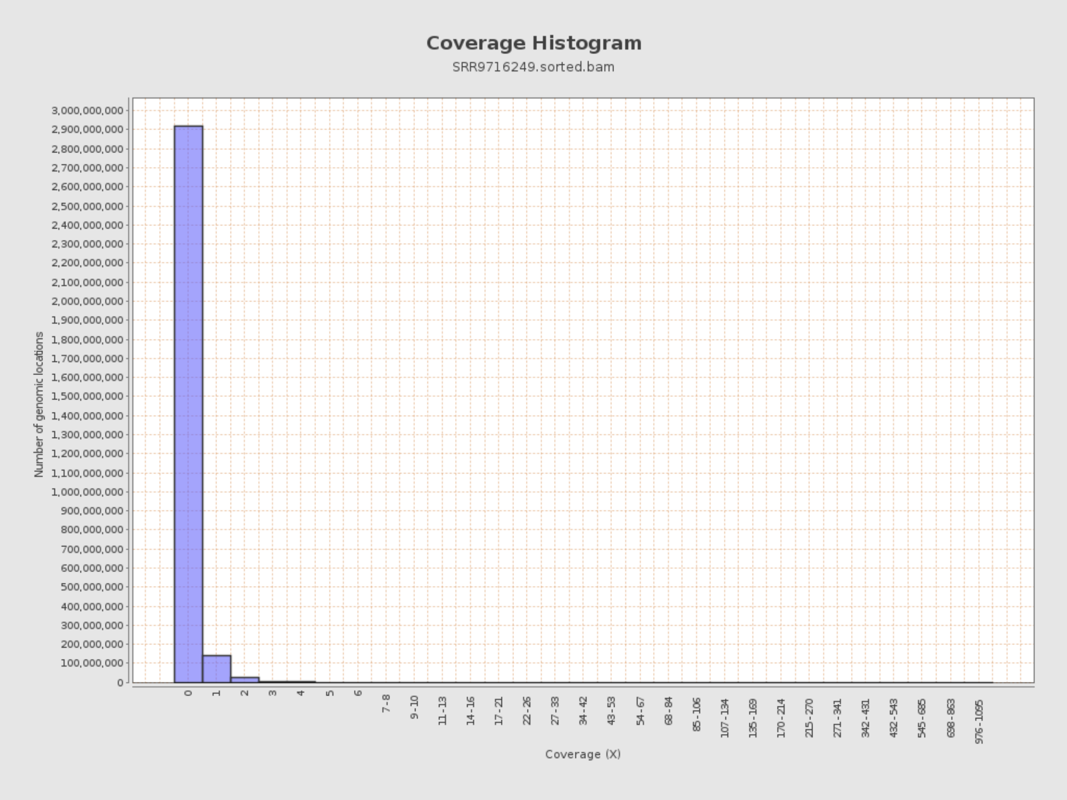
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25250532	0.1013	1.011
chr2	243199373	21806270	0.0897	0.6
chr3	198022430	14555098	0.0735	0.3425
chr4	191154276	10859137	0.0568	0.4638
chr5	180915260	13544317	0.0749	0.3563
chr6	171115067	14097657	0.0824	0.3958
chr7	159138663	14831450	0.0932	0.7671

chr8	146364022	14544884	0.0994	0.5872
chr9	141213431	6937130	0.0491	0.3753
chr10	135534747	14011977	0.1034	0.8017
chr11	135006516	6812660	0.0505	0.4207
chr12	133851895	8080504	0.0604	0.309
chr13	115169878	4282769	0.0372	0.2363
chr14	107349540	4423614	0.0412	0.2801
chr15	102531392	4816678	0.047	0.2711
chr16	90354753	7143931	0.0791	0.386
chr17	81195210	4373232	0.0539	0.3352
chr18	78077248	6932836	0.0888	0.5872
chr19	59128983	6119546	0.1035	0.7421
chr20	63025520	6251284	0.0992	0.4262
chr21	48129895	3913119	0.0813	0.4446
chr22	51304566	3754936	0.0732	0.3617
chrMT	16571	61018	3.6822	3.3762
chrX	155270560	14514430	0.0935	0.4175
chrY	59373566	724327	0.0122	0.4007

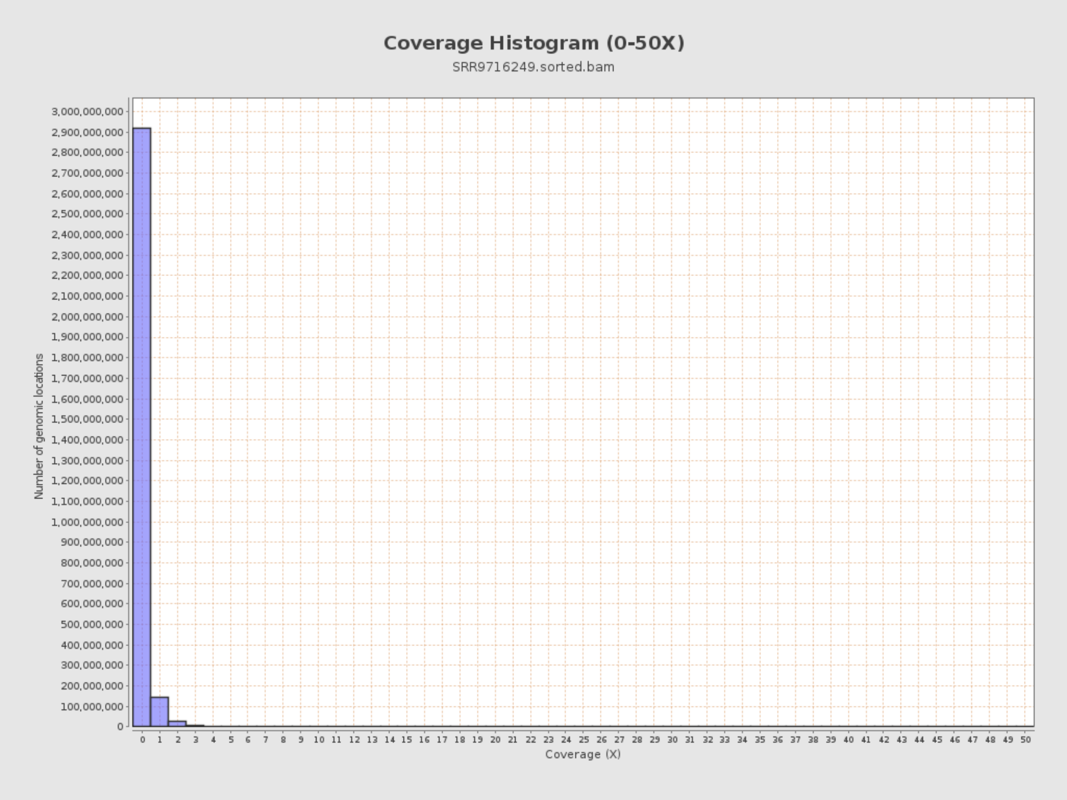
3. Results : Coverage across reference



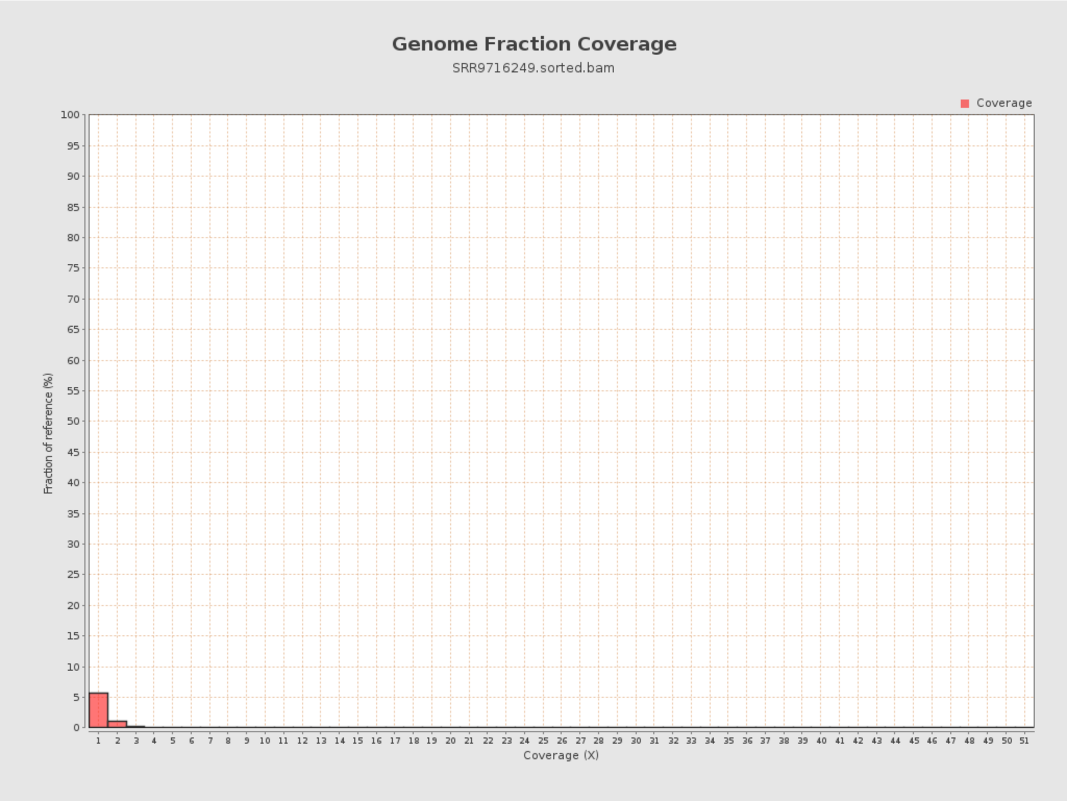
4. Results : Coverage Histogram



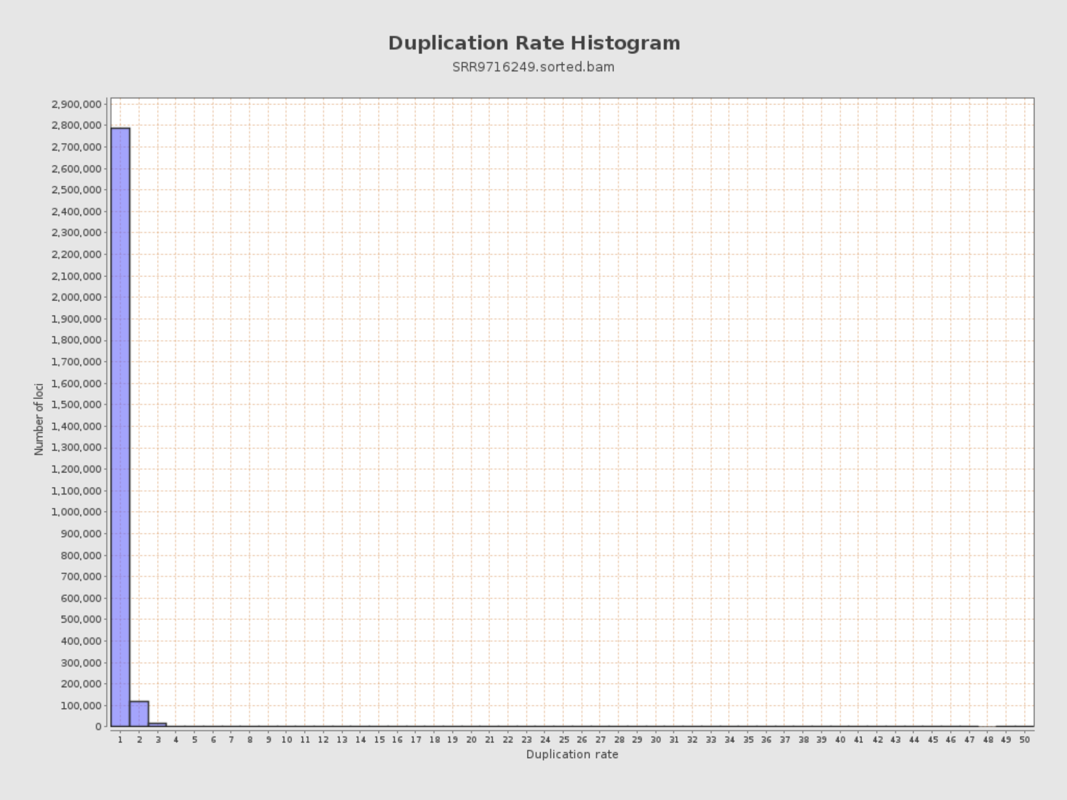
5. Results : Coverage Histogram (0-50X)



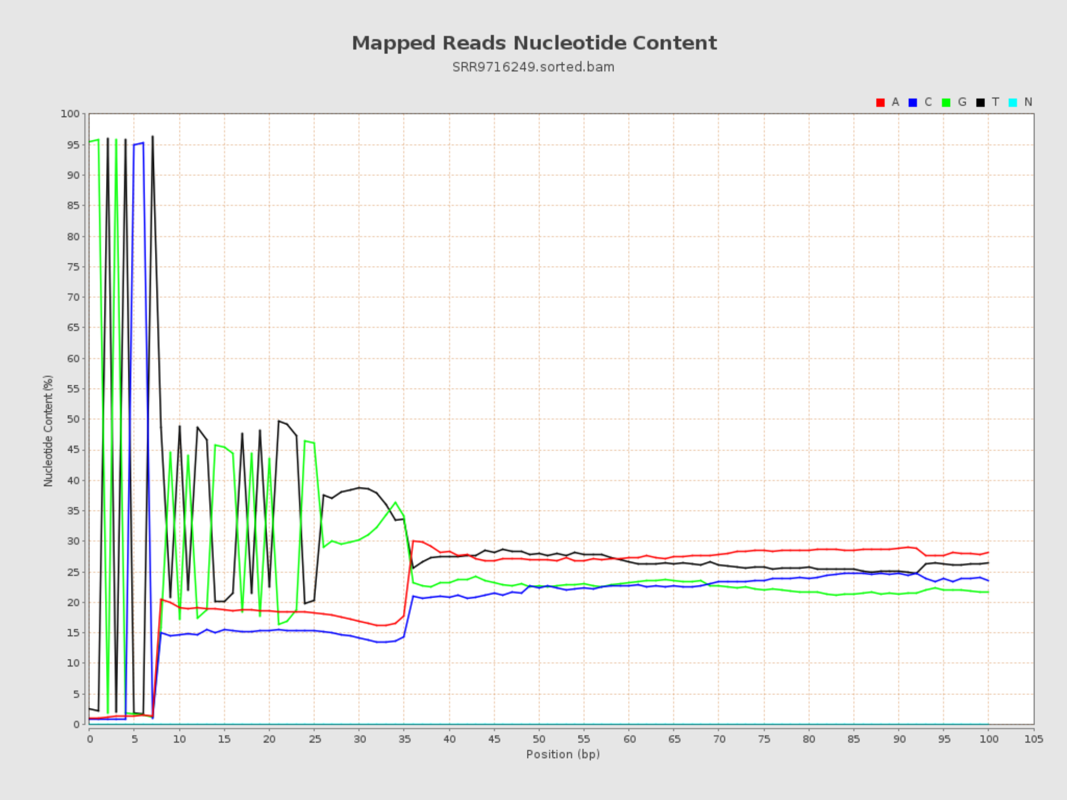
6. Results : Genome Fraction Coverage



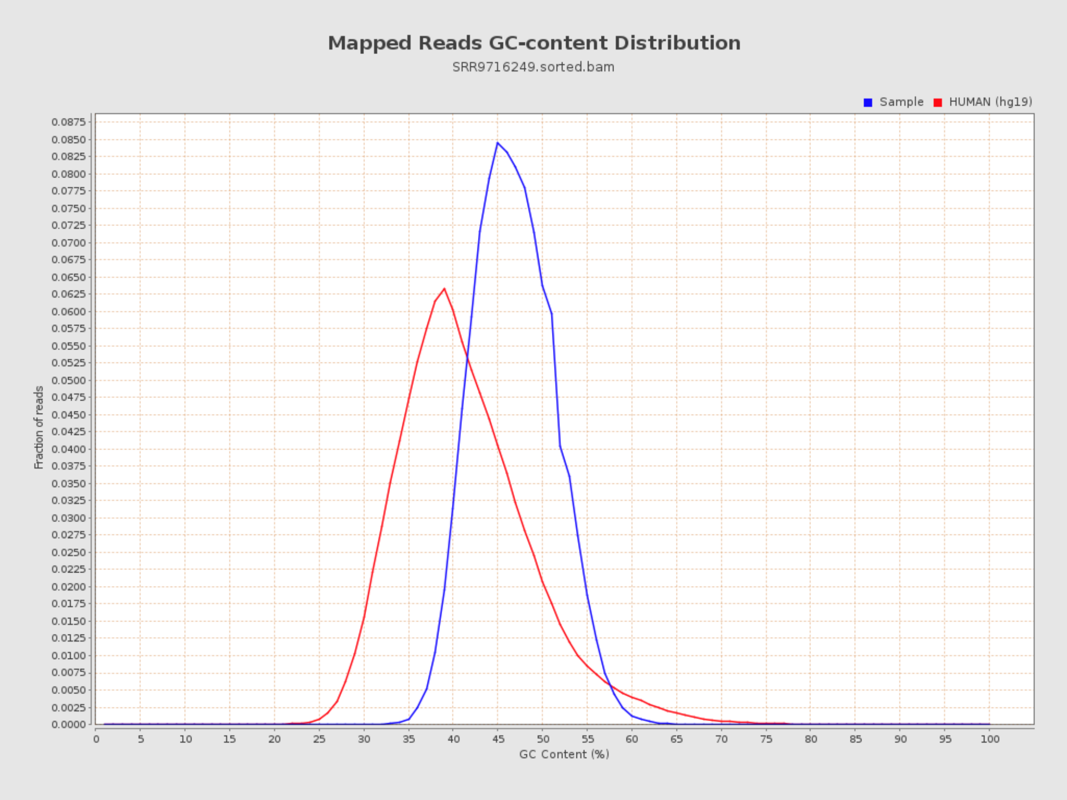
7. Results : Duplication Rate Histogram



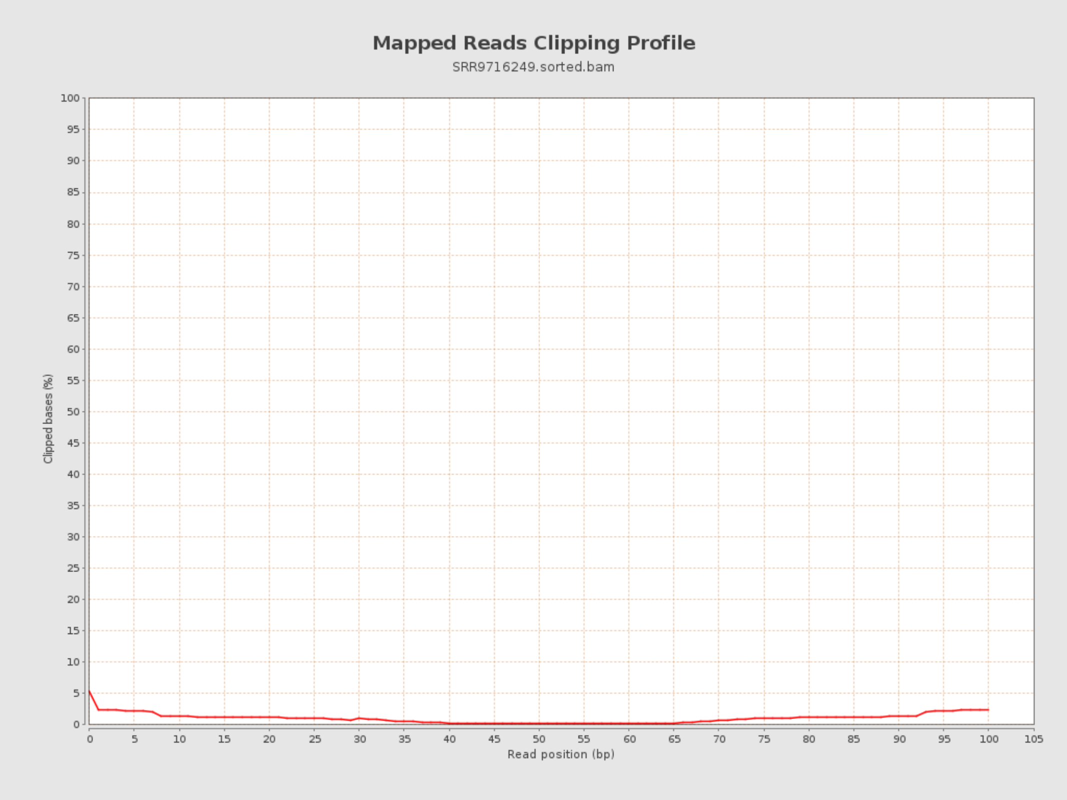
8. Results : Mapped Reads Nucleotide Content



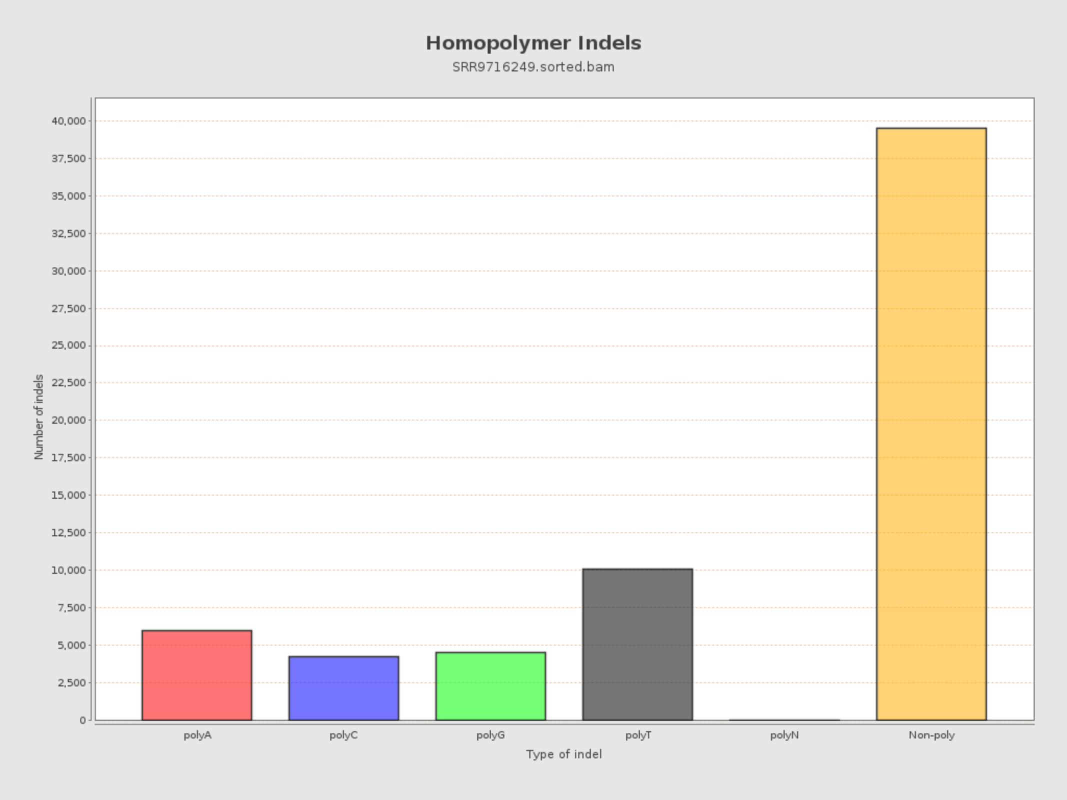
9. Results : Mapped Reads GC-content Distribution



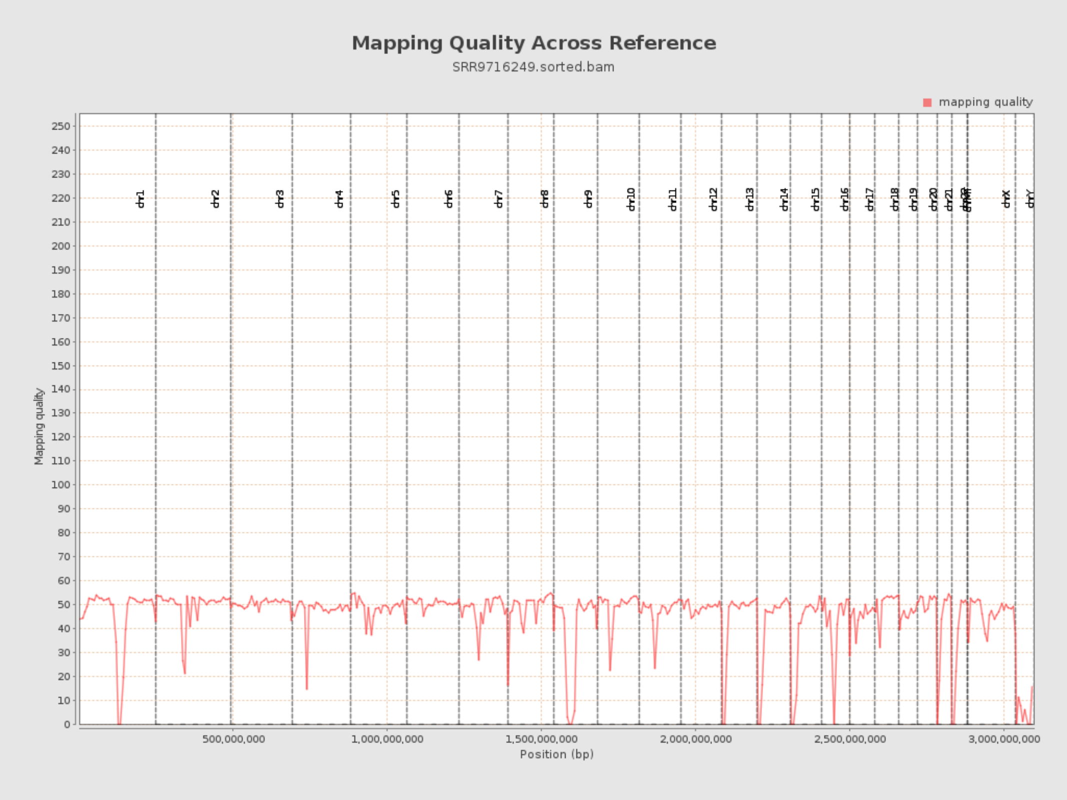
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram