Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:27:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716138.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_SRR9716138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:27:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,944,410
Mapped reads	1,747,469 / 89.87%
Unmapped reads	196,941 / 10.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,551 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	65,657 / 3.38%
Duplication rate	2.56%
Clipped reads	1,754,245 / 90.22%

2.2. ACGT Content

Number/percentage of A's	25,264,627 / 25.15%
Number/percentage of C's	17,238,573 / 17.16%
Number/percentage of T's	31,820,581 / 31.67%
Number/percentage of G's	26,145,382 / 26.02%
Number/percentage of N's	1,400 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.3243

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

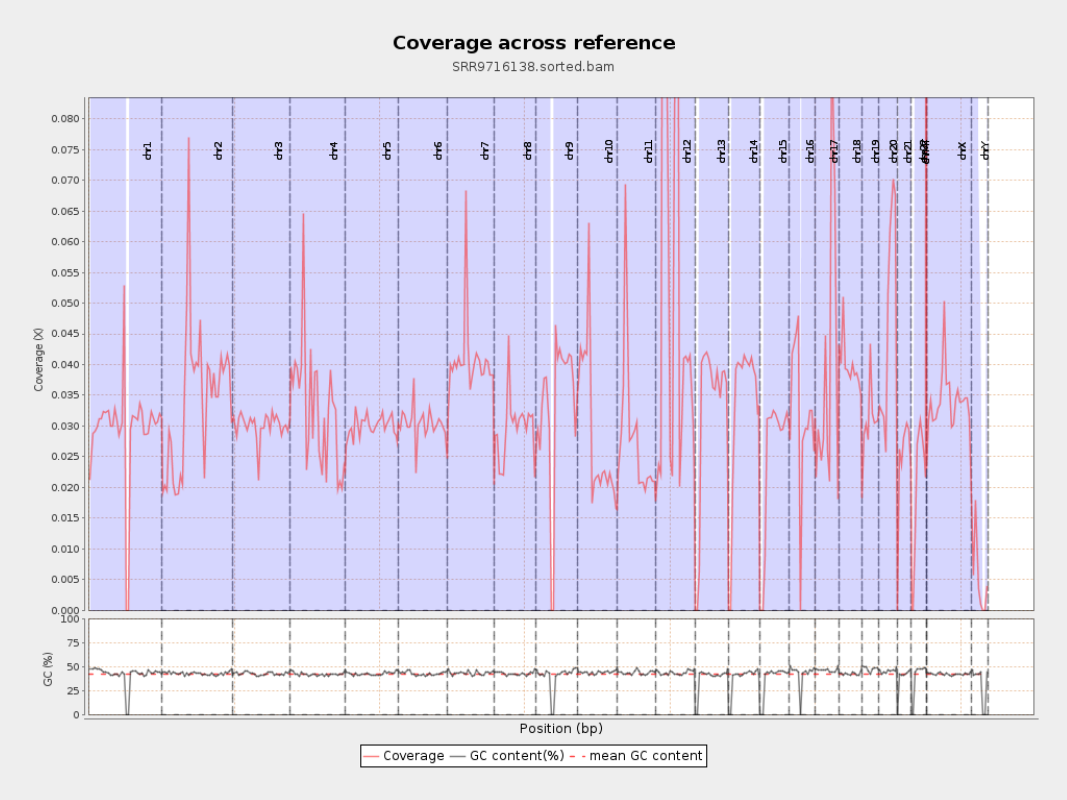
General error rate	0.57%
Mismatches	557,877
Insertions	7,097
Mapped reads with at least one insertion	0.4%
Deletions	16,962
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.05%

2.6. Chromosome stats

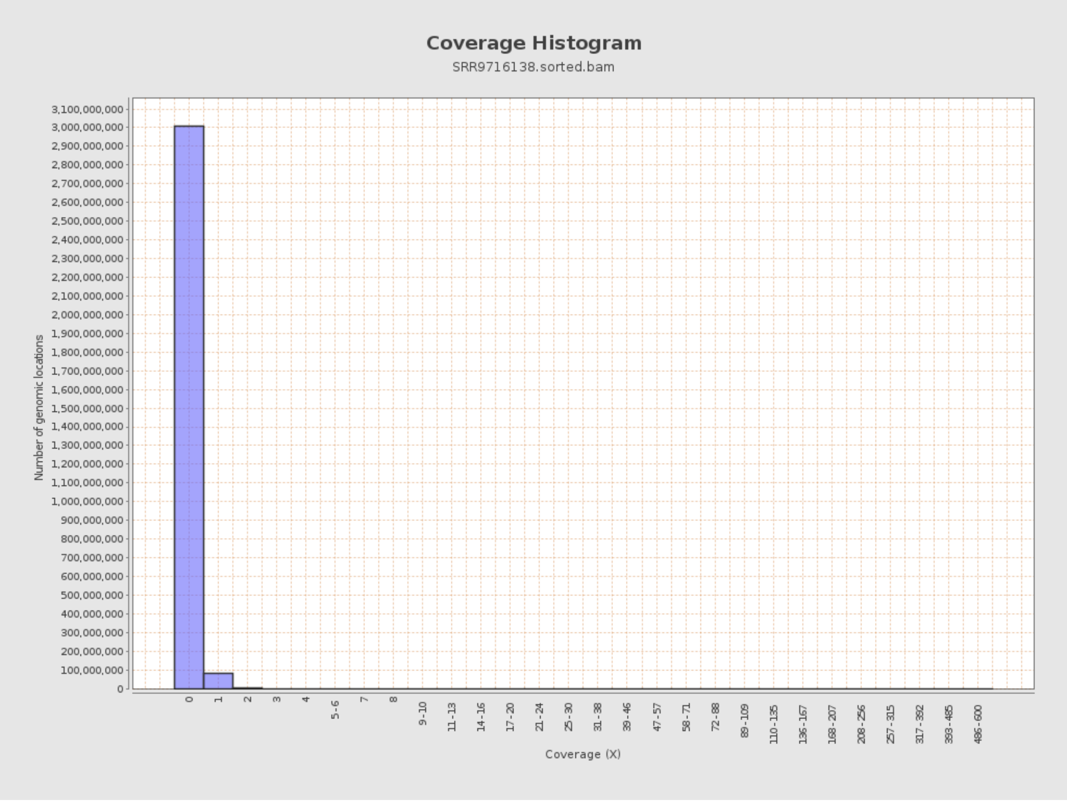
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7301217	0.0293	0.535
chr2	243199373	8370462	0.0344	0.3807
chr3	198022430	5957200	0.0301	0.1879
chr4	191154276	6246552	0.0327	0.2336
chr5	180915260	5431689	0.03	0.1928
chr6	171115067	5195259	0.0304	0.2159
chr7	159138663	6504471	0.0409	0.4434

chr8	146364022	4349026	0.0297	0.288
chr9	141213431	4663368	0.033	0.3715
chr10	135534747	3905680	0.0288	0.3311
chr11	135006516	3828336	0.0284	0.2745
chr12	133851895	7286787	0.0544	0.2871
chr13	115169878	3694154	0.0321	0.1924
chr14	107349540	3533901	0.0329	0.2349
chr15	102531392	2561983	0.025	0.1733
chr16	90354753	2901189	0.0321	0.2282
chr17	81195210	3081445	0.038	0.2225
chr18	78077248	3123704	0.04	0.6725
chr19	59128983	1848287	0.0313	0.4438
chr20	63025520	2953907	0.0469	0.2493
chr21	48129895	1180066	0.0245	0.2126
chr22	51304566	991738	0.0193	0.1491
chrMT	16571	6042	0.3646	0.7219
chrX	155270560	5273375	0.034	0.2597
chrY	59373566	309294	0.0052	0.1355

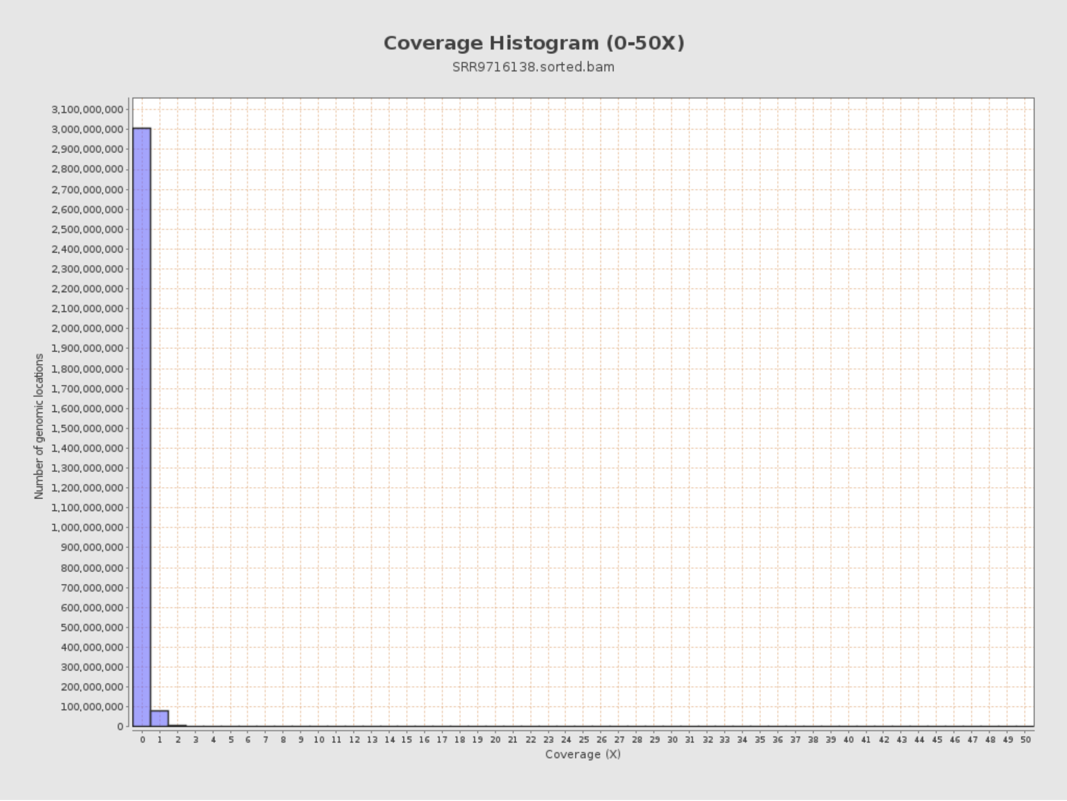
3. Results : Coverage across reference



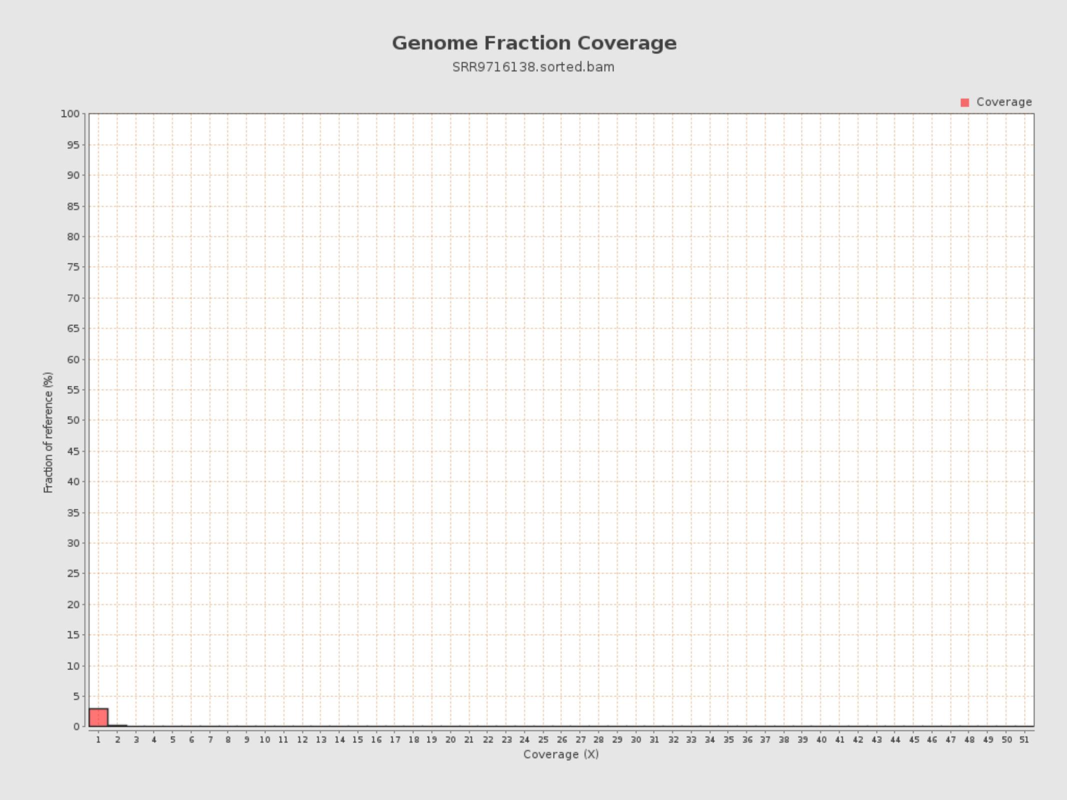
4. Results : Coverage Histogram



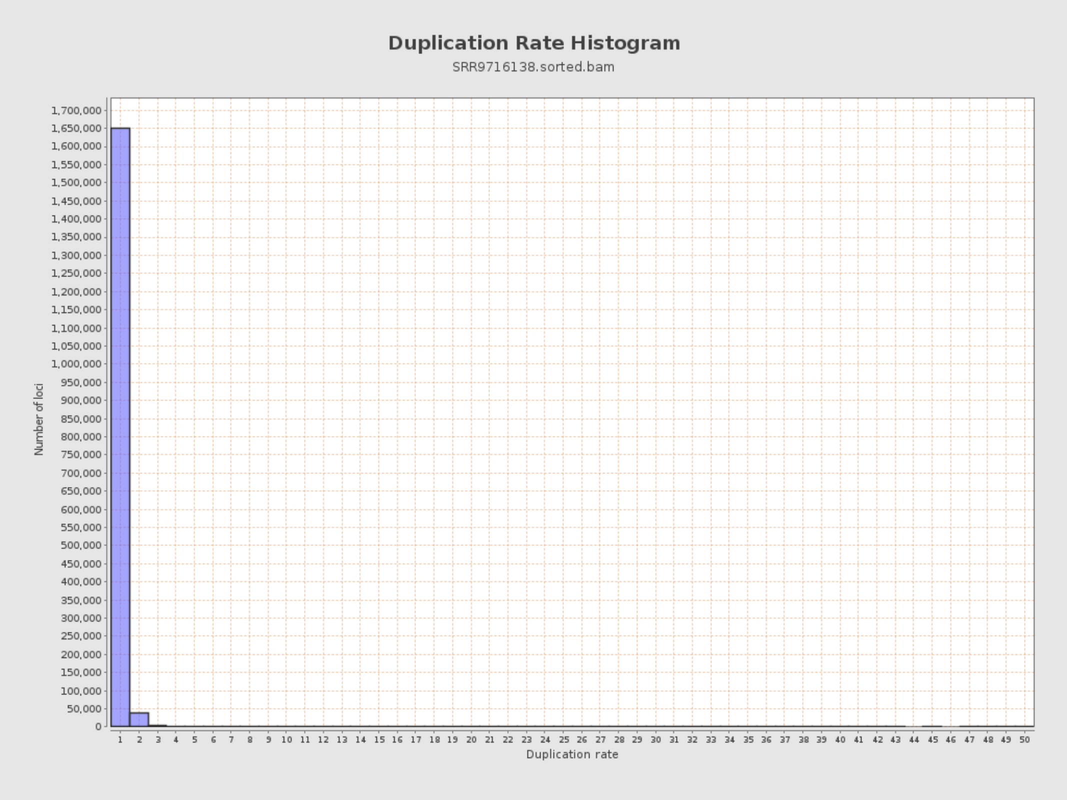
5. Results : Coverage Histogram (0-50X)



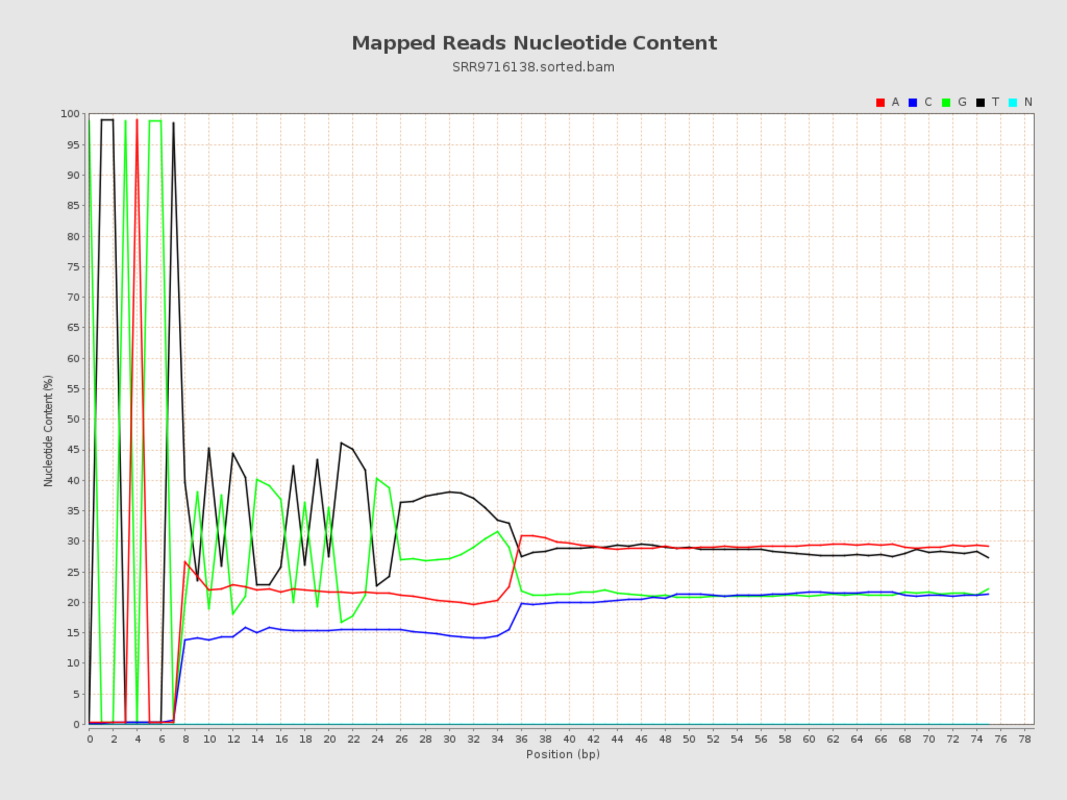
6. Results : Genome Fraction Coverage



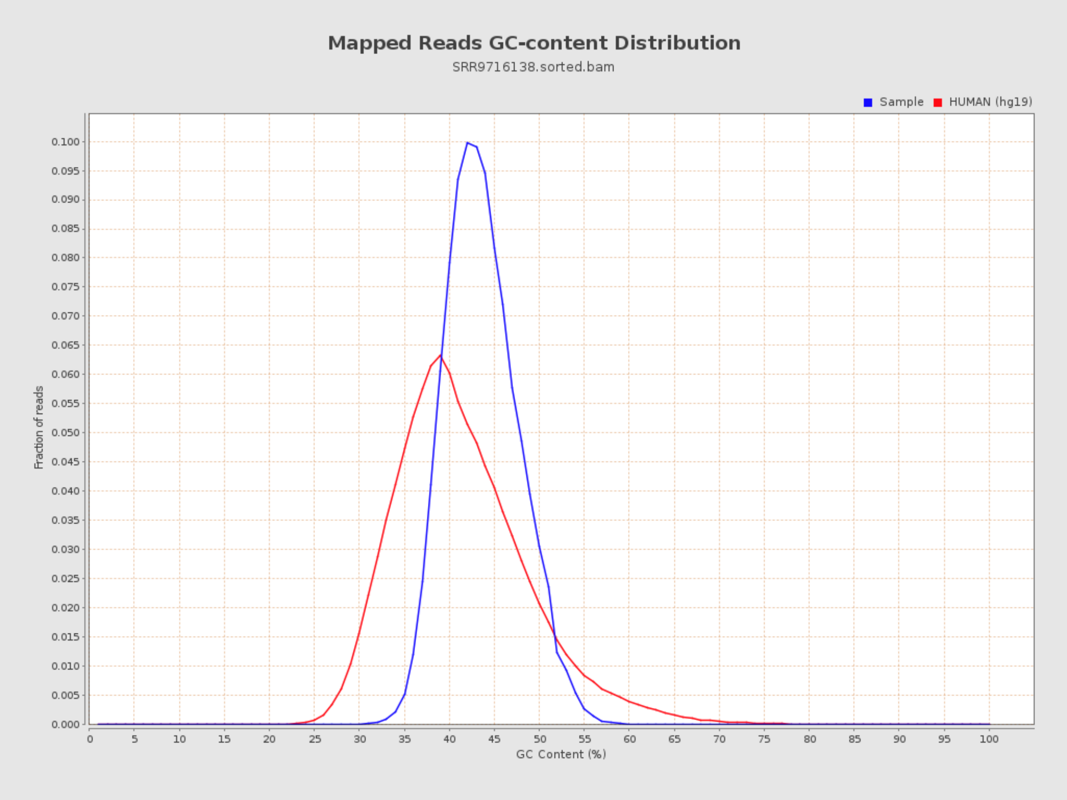
7. Results : Duplication Rate Histogram



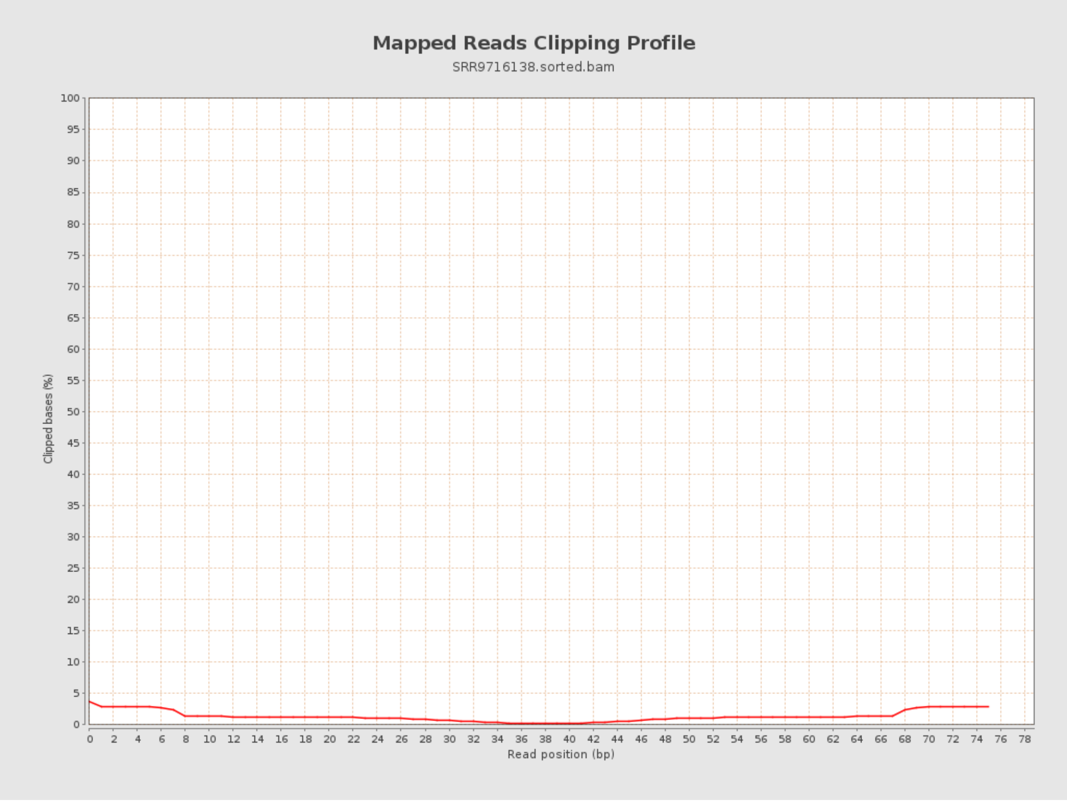
8. Results : Mapped Reads Nucleotide Content



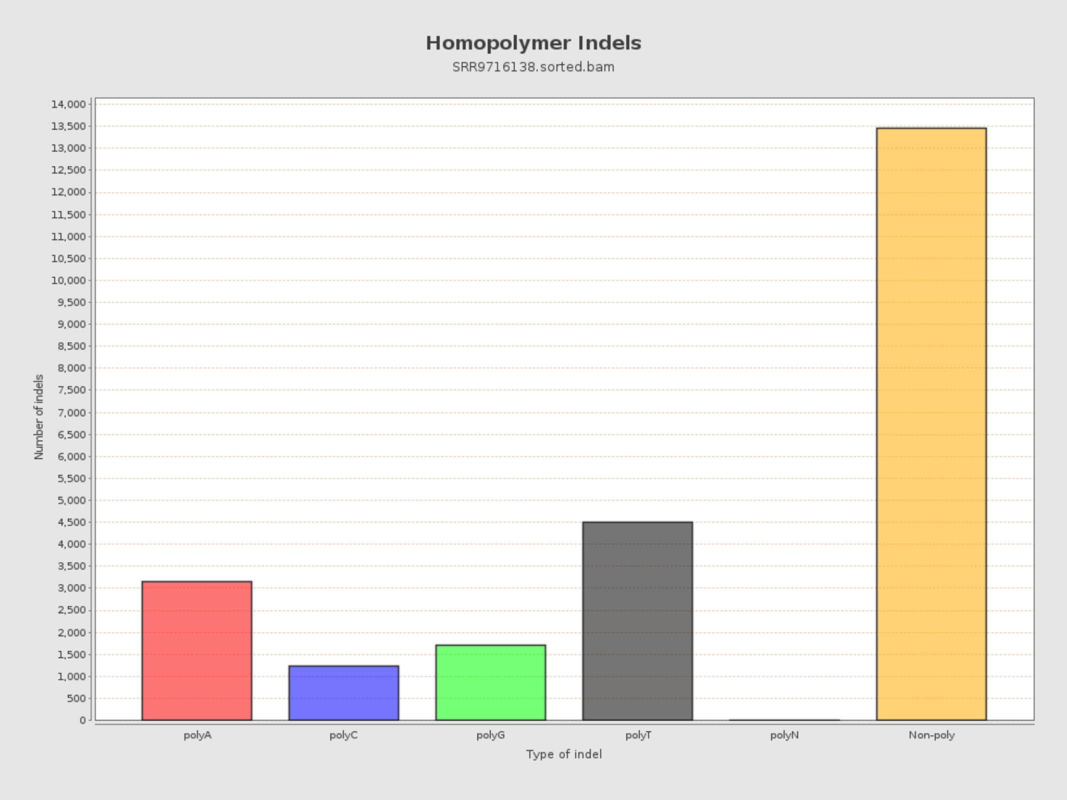
9. Results : Mapped Reads GC-content Distribution



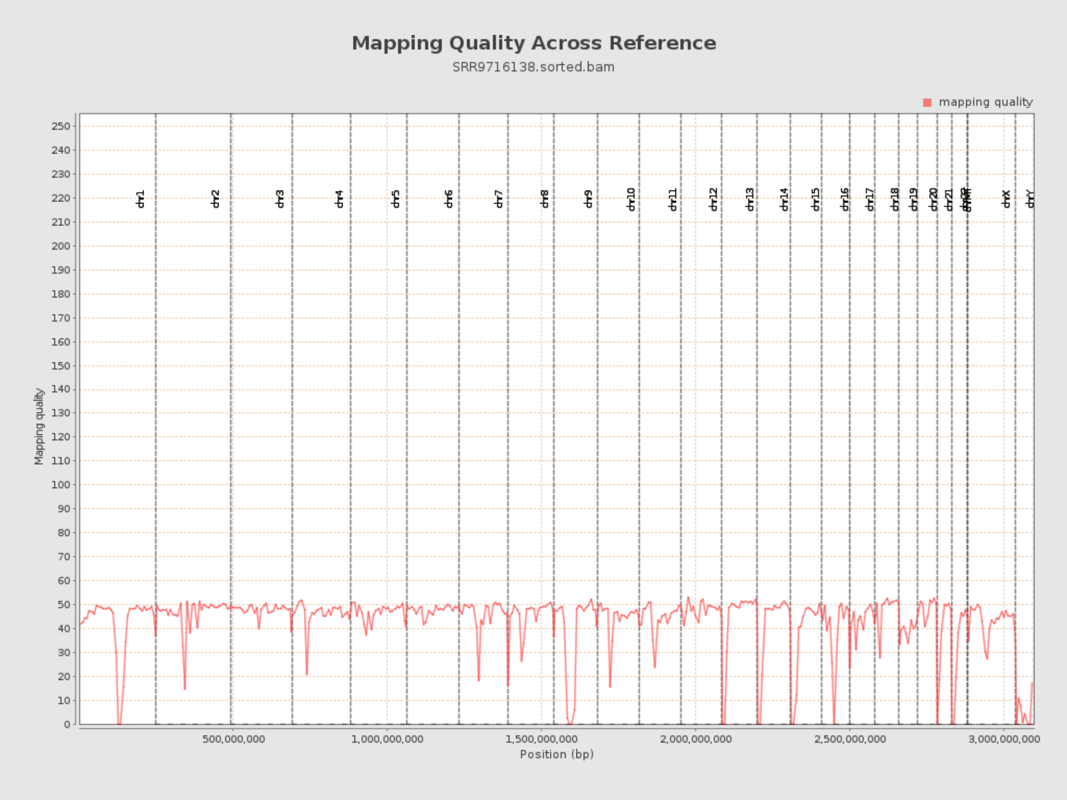
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram