Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:29:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716198.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_SRR9716198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:29:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,016,377
Mapped reads	2,735,469 / 90.69%
Unmapped reads	280,908 / 9.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	73,724 / 2.44%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	111,586 / 3.7%
Duplication rate	2.84%
Clipped reads	2,807,182 / 93.06%

2.2. ACGT Content

Number/percentage of A's	51,750,453 / 25.48%
Number/percentage of C's	42,818,876 / 21.08%
Number/percentage of T's	59,588,485 / 29.33%
Number/percentage of G's	48,955,778 / 24.1%
Number/percentage of N's	23,553 / 0.01%
GC Percentage	45.18%

2.3. Coverage

Mean	0.0656

Standard Deviation	0.488

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

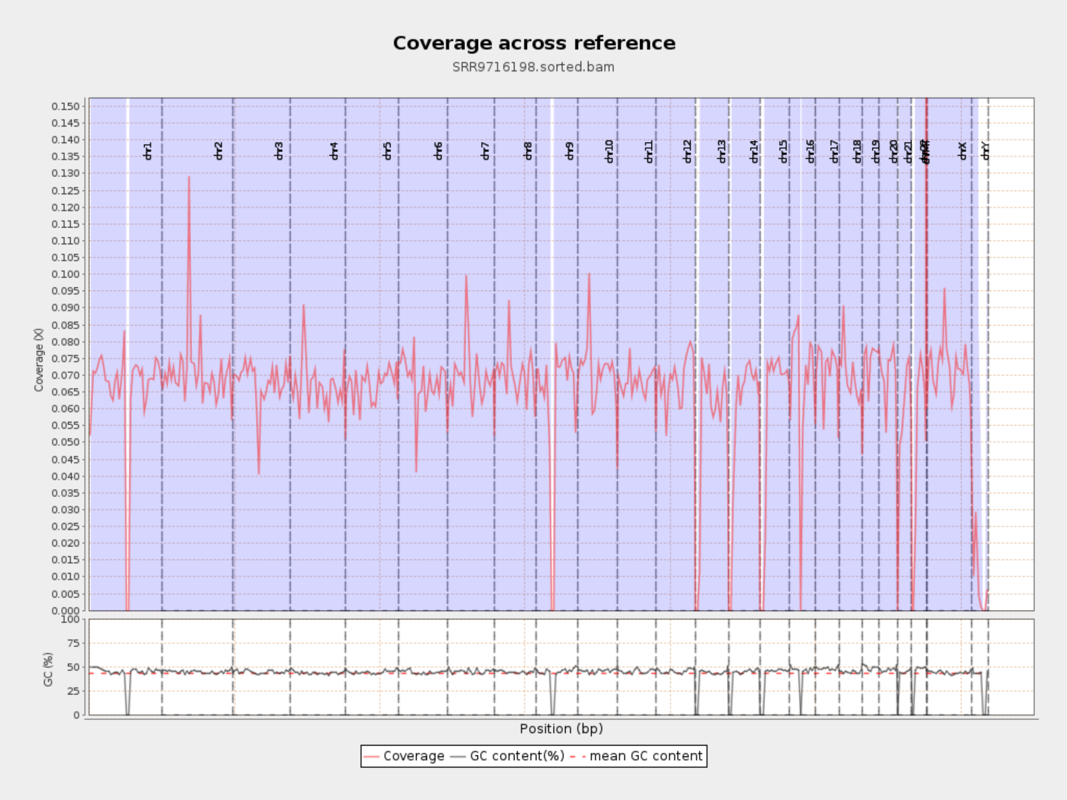
General error rate	0.74%
Mismatches	1,476,611
Insertions	15,853
Mapped reads with at least one insertion	0.57%
Deletions	41,444
Mapped reads with at least one deletion	1.5%
Homopolymer indels	41.12%

2.6. Chromosome stats

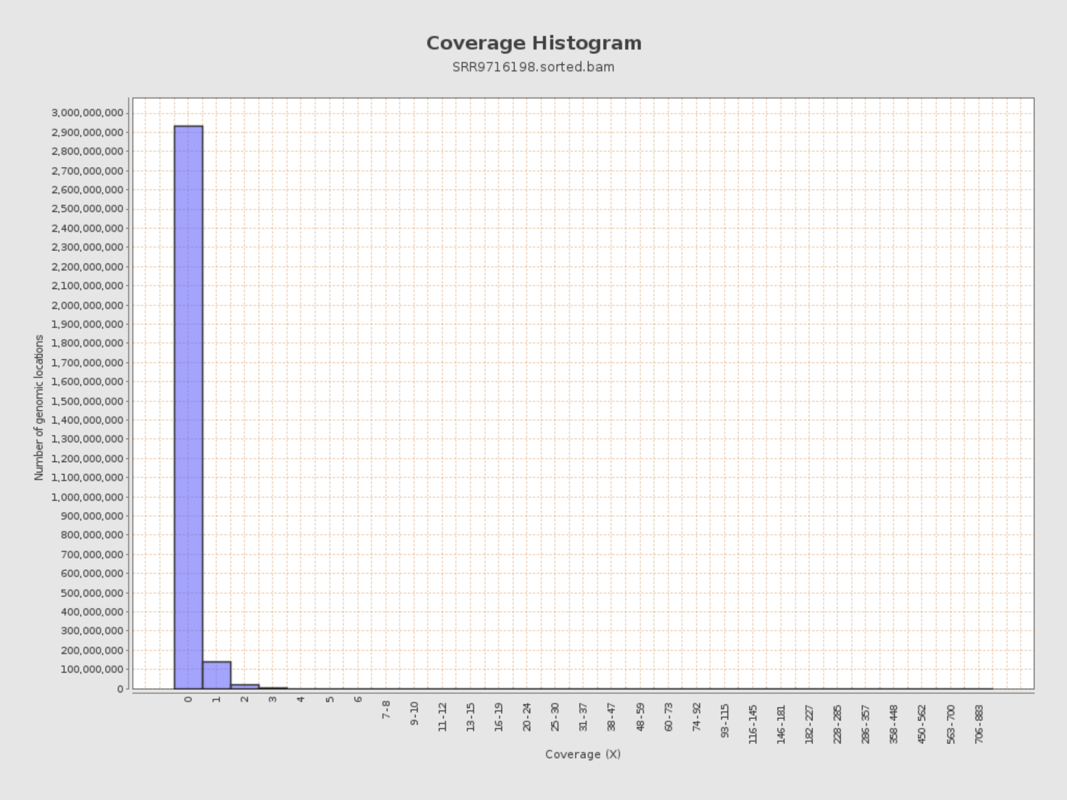
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16219417	0.0651	0.5605
chr2	243199373	17363685	0.0714	0.742
chr3	198022430	13406396	0.0677	0.308
chr4	191154276	12770492	0.0668	0.3464
chr5	180915260	12152744	0.0672	0.3112
chr6	171115067	11663892	0.0682	0.3711
chr7	159138663	11132298	0.07	0.6445

chr8	146364022	10323464	0.0705	0.6285
chr9	141213431	8675524	0.0614	0.5216
chr10	135534747	9753758	0.072	0.5008
chr11	135006516	9146255	0.0677	0.5432
chr12	133851895	9186312	0.0686	0.3164
chr13	115169878	6258954	0.0543	0.2747
chr14	107349540	6124358	0.0571	0.3625
chr15	102531392	5948776	0.058	0.2877
chr16	90354753	6127251	0.0678	0.3599
chr17	81195210	5788004	0.0713	0.355
chr18	78077248	5508557	0.0706	0.9977
chr19	59128983	4351664	0.0736	0.5035
chr20	63025520	4373517	0.0694	0.3355
chr21	48129895	2689585	0.0559	0.3192
chr22	51304566	2444056	0.0476	0.261
chrMT	16571	13437	0.8109	1.0786
chrX	155270560	11255156	0.0725	0.4204
chrY	59373566	531469	0.009	0.2402

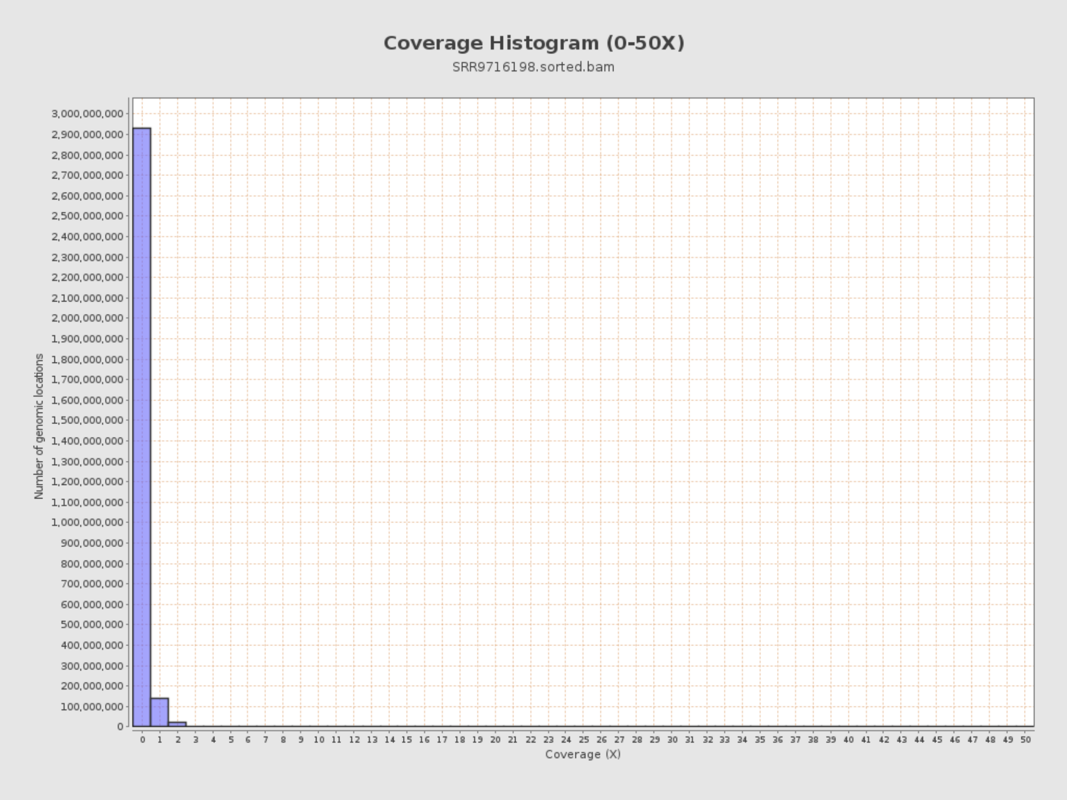
3. Results : Coverage across reference



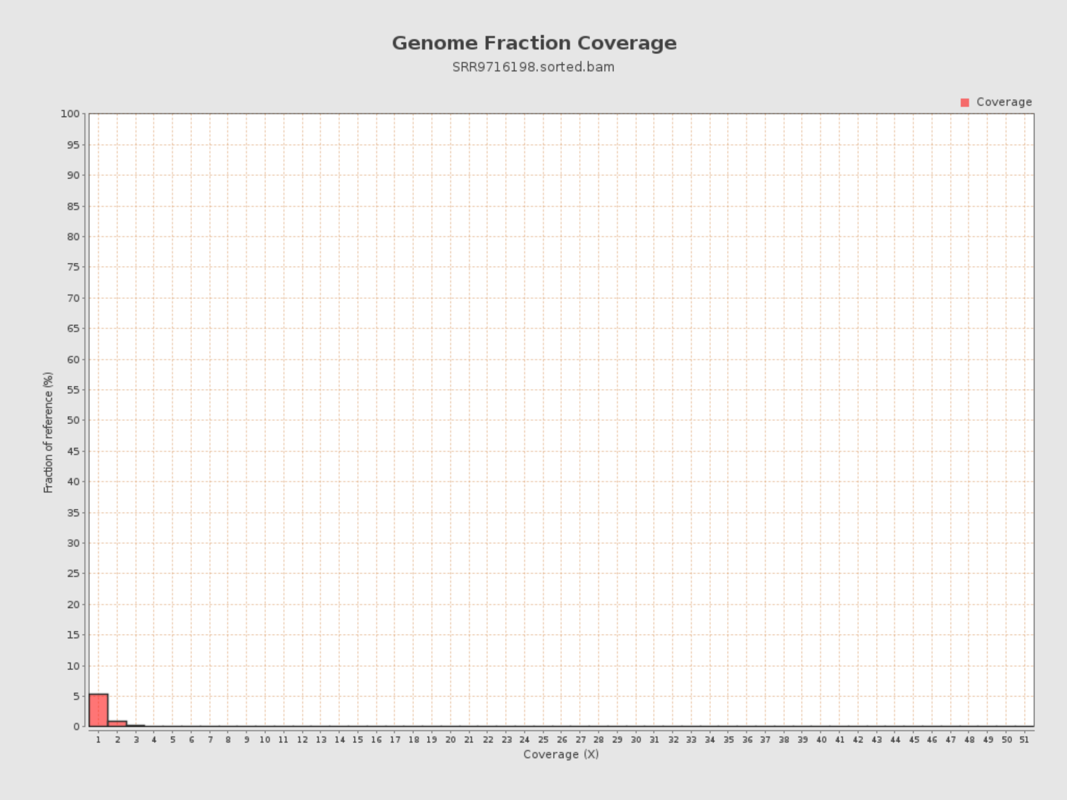
4. Results : Coverage Histogram



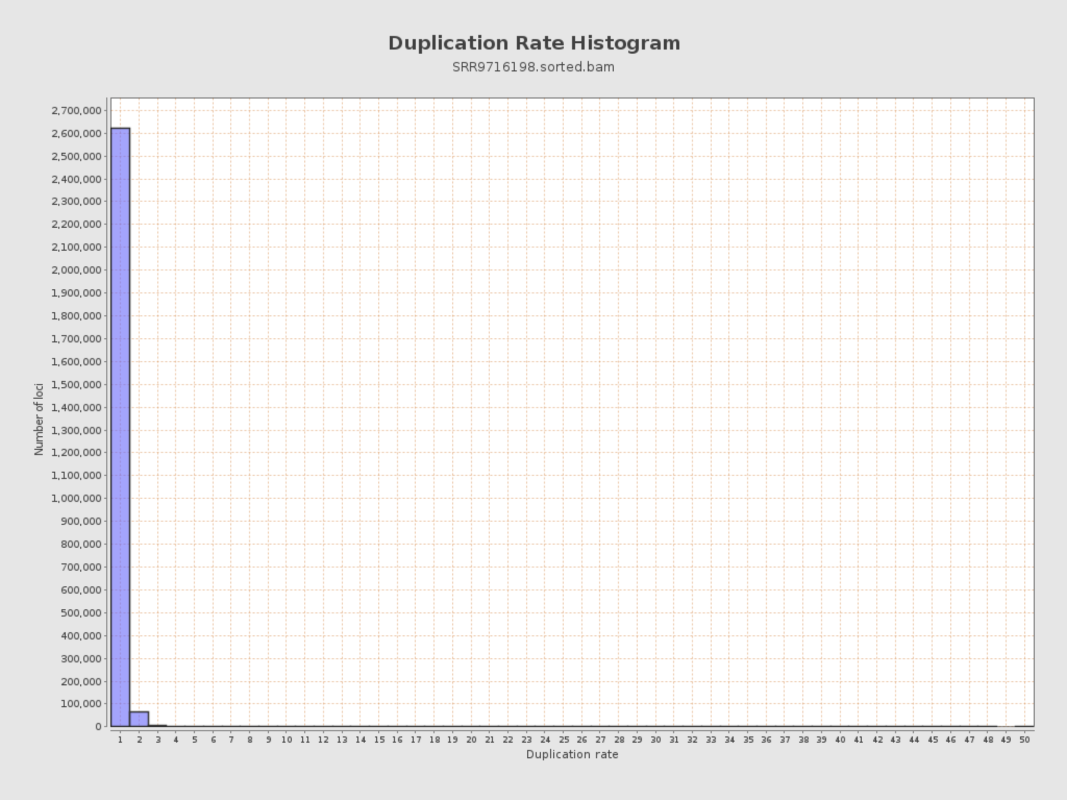
5. Results : Coverage Histogram (0-50X)



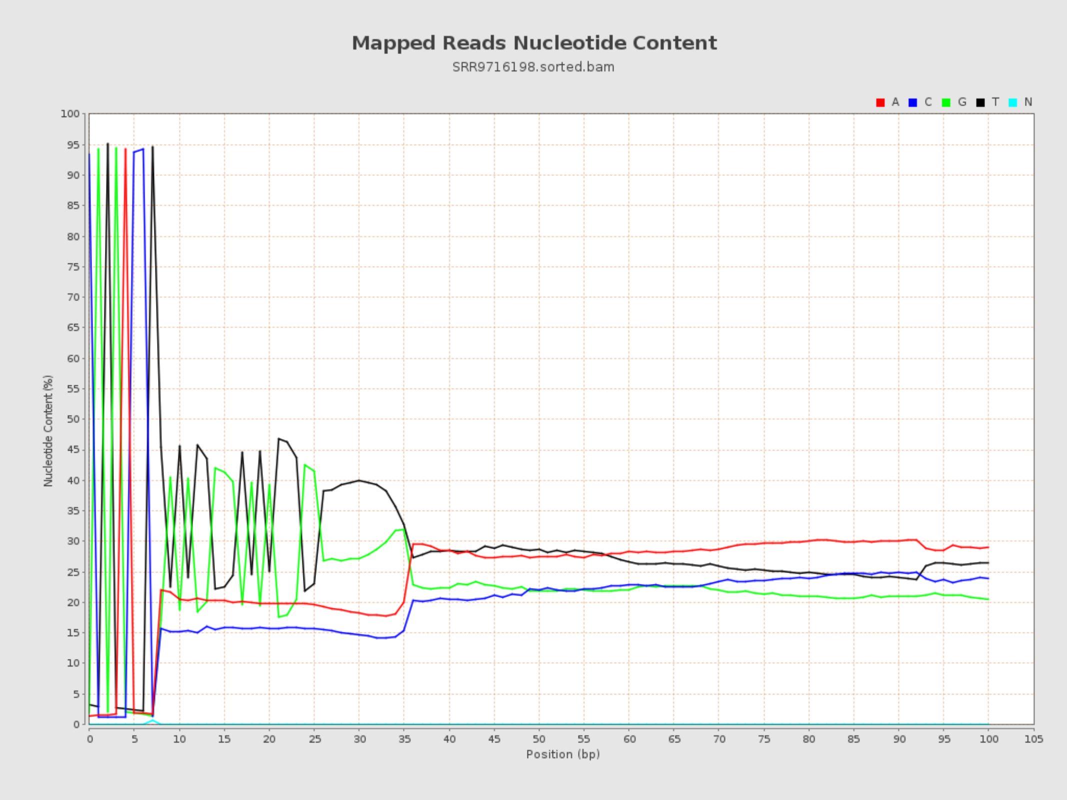
6. Results : Genome Fraction Coverage



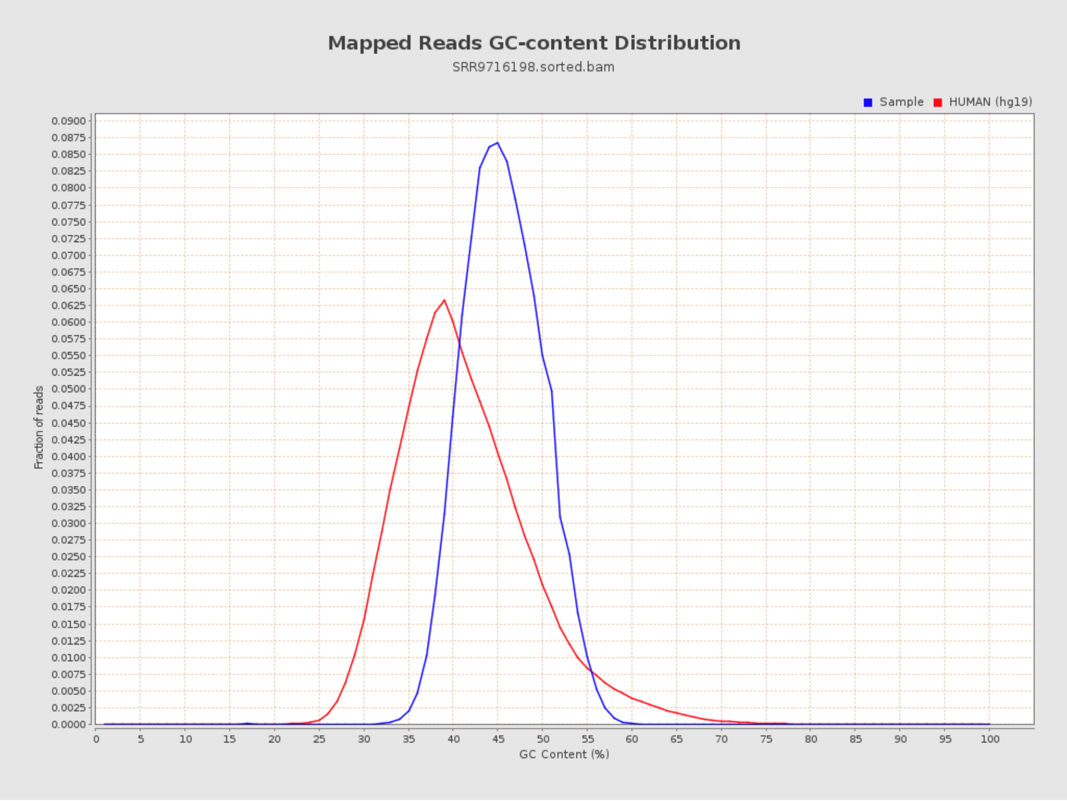
7. Results : Duplication Rate Histogram



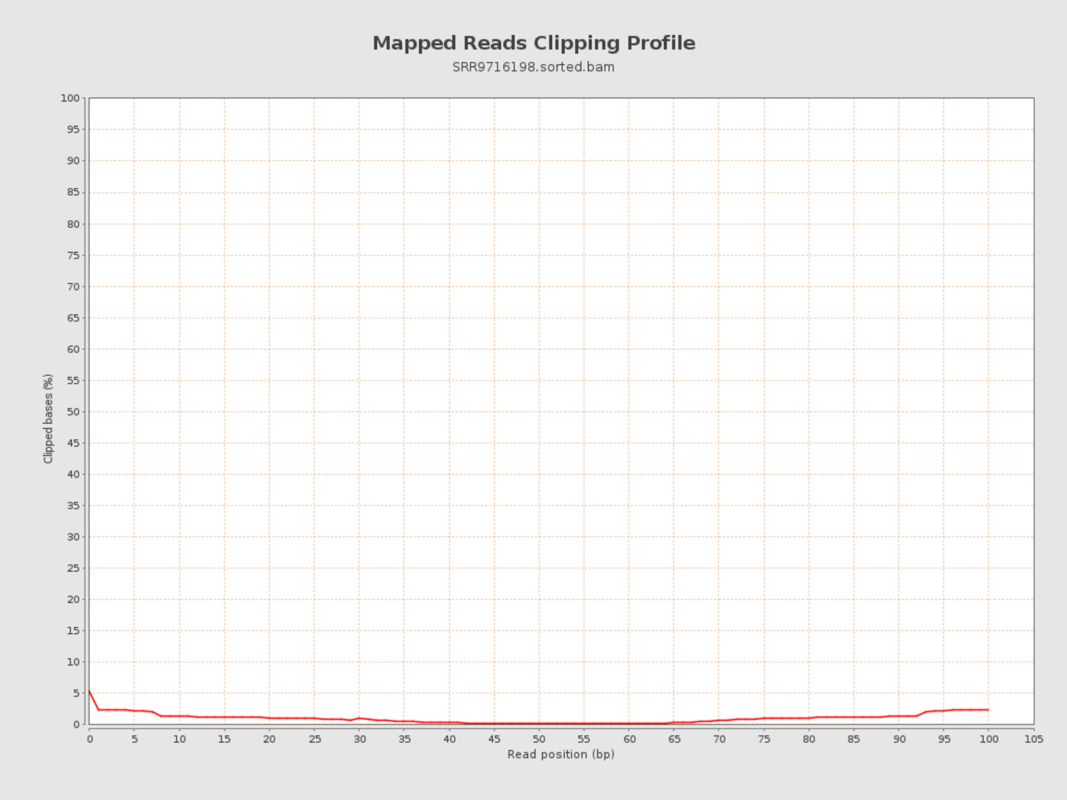
8. Results : Mapped Reads Nucleotide Content



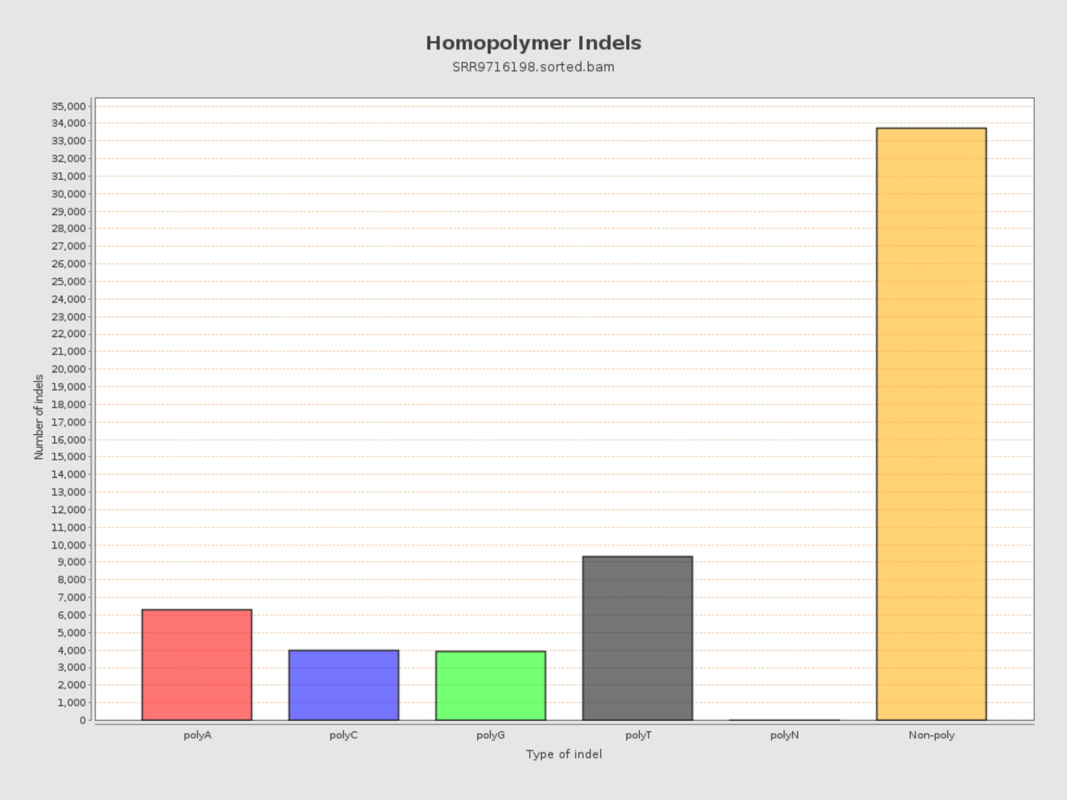
9. Results : Mapped Reads GC-content Distribution



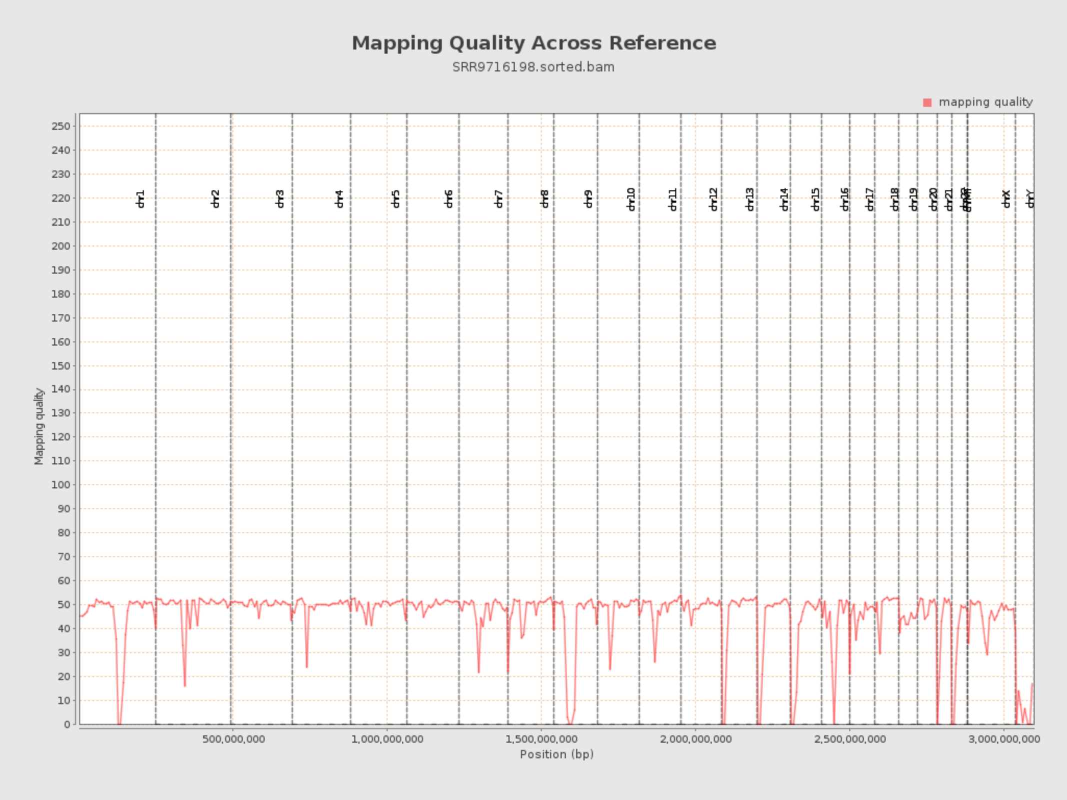
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram