Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:20:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716208.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_SRR9716208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:20:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,769,057
Mapped reads	3,031,555 / 80.43%
Unmapped reads	737,502 / 19.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,130 / 1.89%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	139,761 / 3.71%
Duplication rate	3.24%
Clipped reads	3,097,924 / 82.19%

2.2. ACGT Content

Number/percentage of A's	59,642,618 / 26.32%
Number/percentage of C's	46,777,838 / 20.65%
Number/percentage of T's	65,876,392 / 29.08%
Number/percentage of G's	54,247,244 / 23.94%
Number/percentage of N's	26,871 / 0.01%
GC Percentage	44.59%

2.3. Coverage

Mean	0.0732

Standard Deviation	0.5502

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

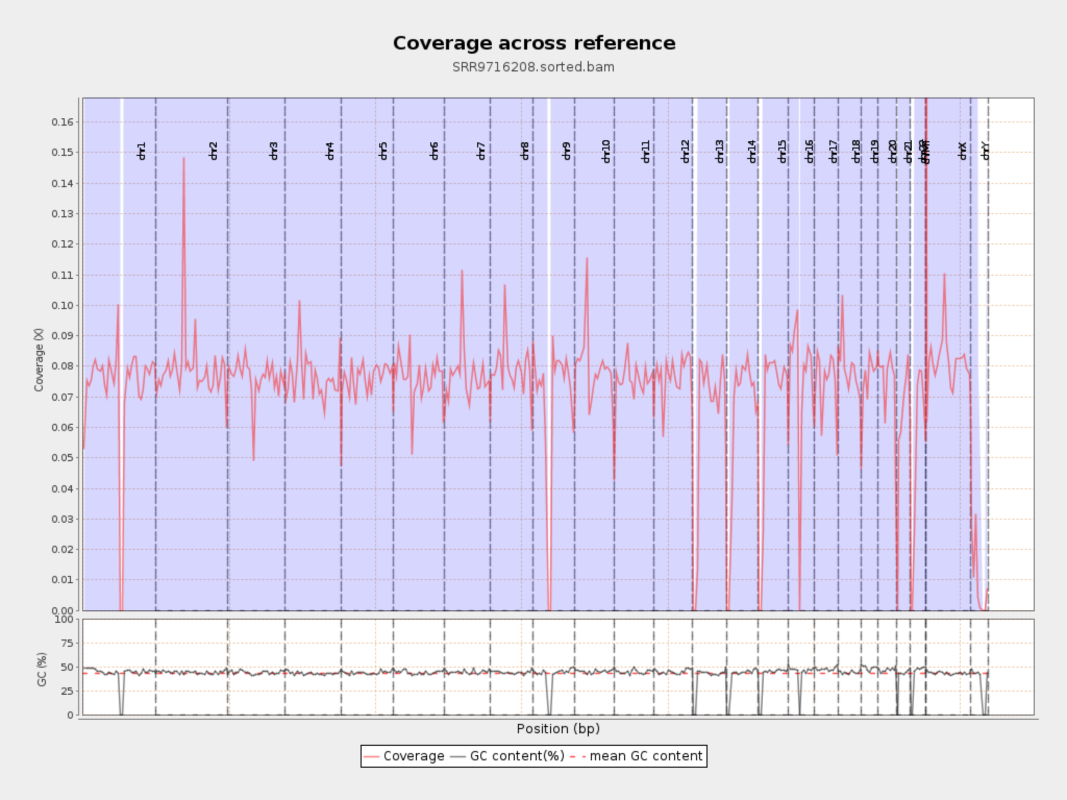
General error rate	0.75%
Mismatches	1,657,940
Insertions	19,731
Mapped reads with at least one insertion	0.64%
Deletions	46,913
Mapped reads with at least one deletion	1.53%
Homopolymer indels	39.57%

2.6. Chromosome stats

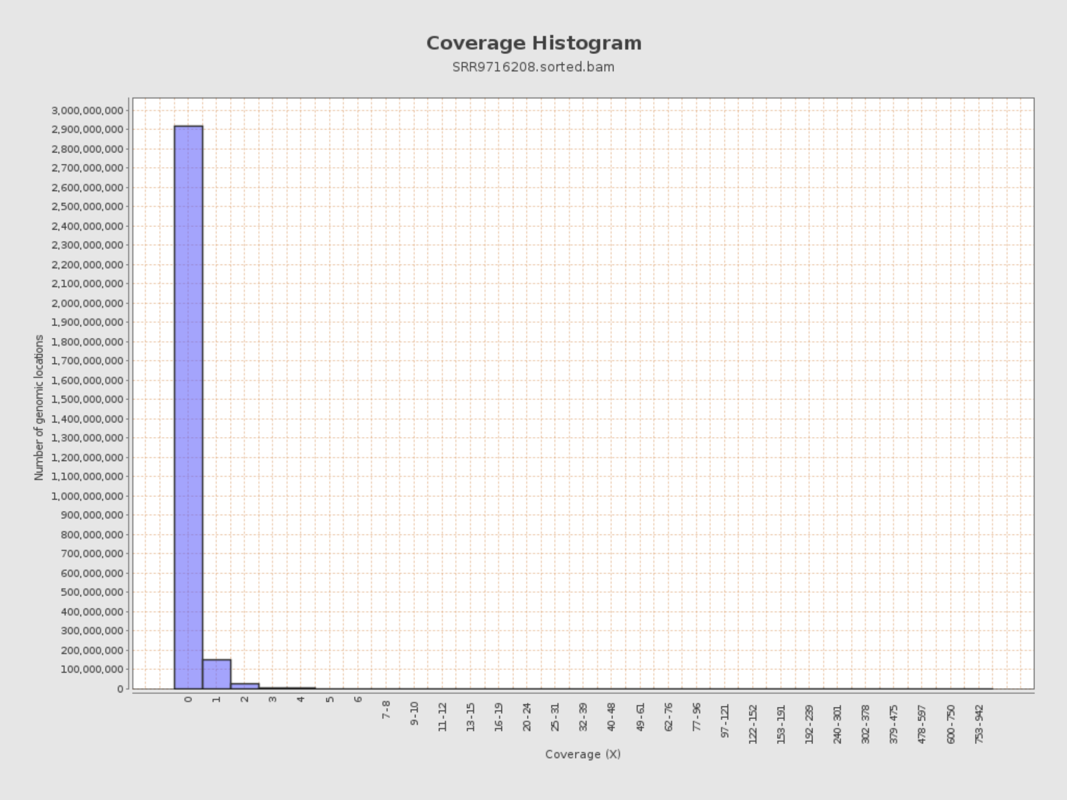
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18098182	0.0726	0.7088
chr2	243199373	19433832	0.0799	0.7921
chr3	198022430	15100148	0.0763	0.3319
chr4	191154276	14663694	0.0767	0.3771
chr5	180915260	13810717	0.0763	0.3407
chr6	171115067	13056020	0.0763	0.3976
chr7	159138663	12286558	0.0772	0.7382

chr8	146364022	11590575	0.0792	0.7109
chr9	141213431	9550217	0.0676	0.6004
chr10	135534747	10802883	0.0797	0.5731
chr11	135006516	10182250	0.0754	0.5977
chr12	133851895	10367803	0.0775	0.3444
chr13	115169878	7190900	0.0624	0.3004
chr14	107349540	6774074	0.0631	0.4068
chr15	102531392	6533805	0.0637	0.3071
chr16	90354753	6643193	0.0735	0.3858
chr17	81195210	6136806	0.0756	0.3841
chr18	78077248	6233025	0.0798	1.1446
chr19	59128983	4534687	0.0767	0.5794
chr20	63025520	4783811	0.0759	0.3572
chr21	48129895	2975307	0.0618	0.3389
chr22	51304566	2616887	0.051	0.2733
chrMT	16571	23681	1.4291	1.7511
chrX	155270560	12695984	0.0818	0.4742
chrY	59373566	565646	0.0095	0.2584

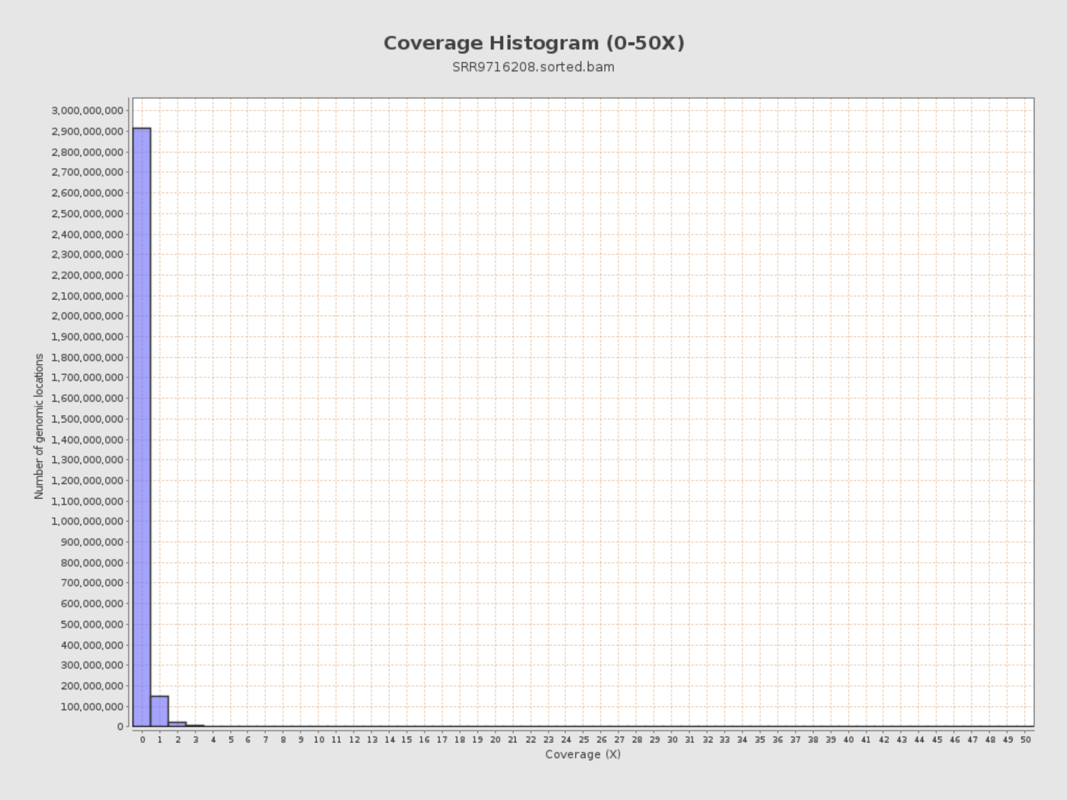
3. Results : Coverage across reference



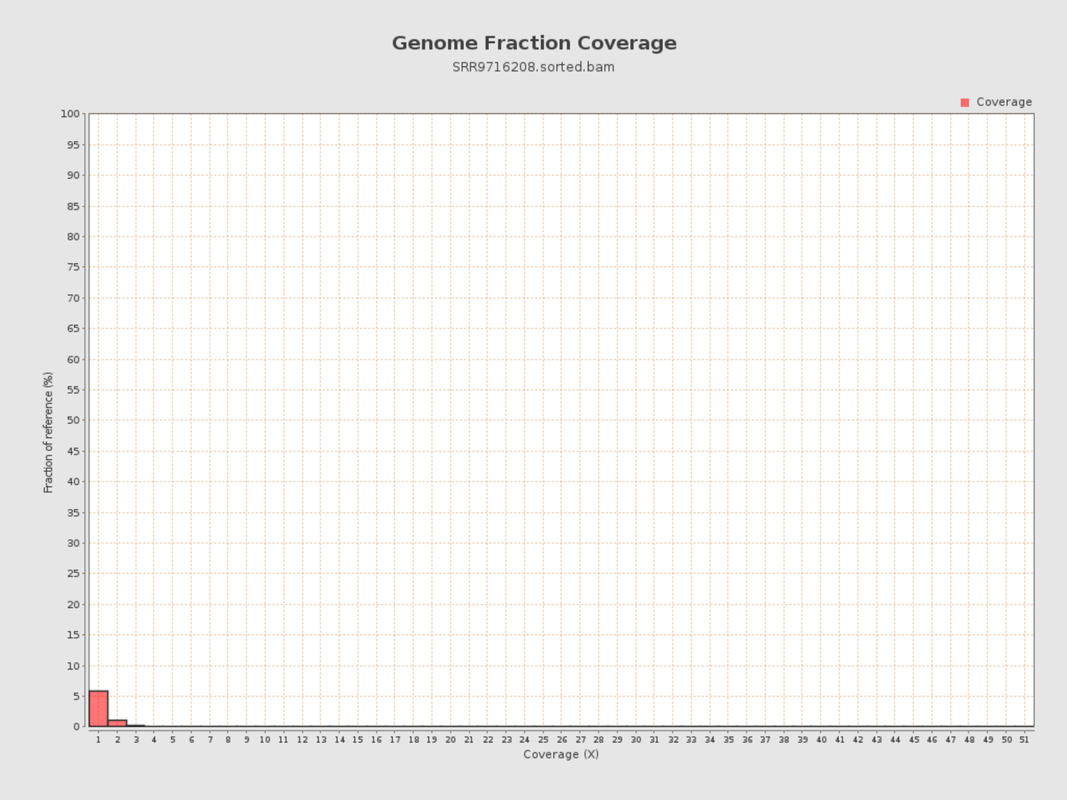
4. Results : Coverage Histogram



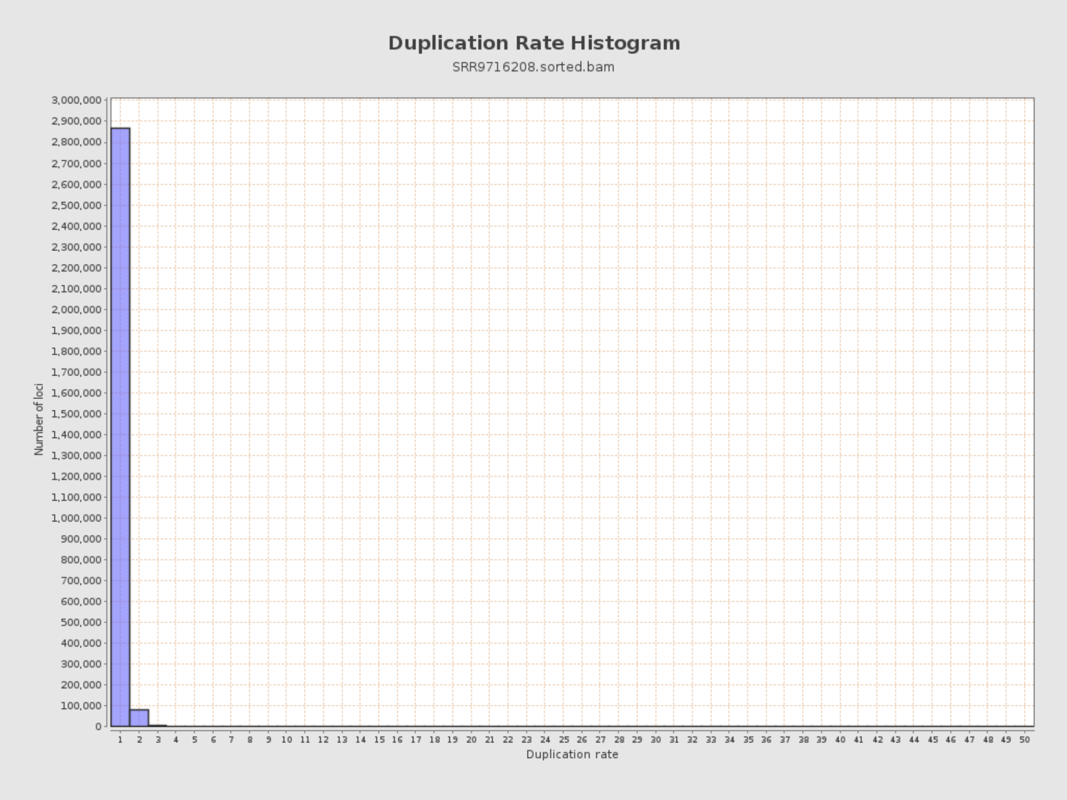
5. Results : Coverage Histogram (0-50X)



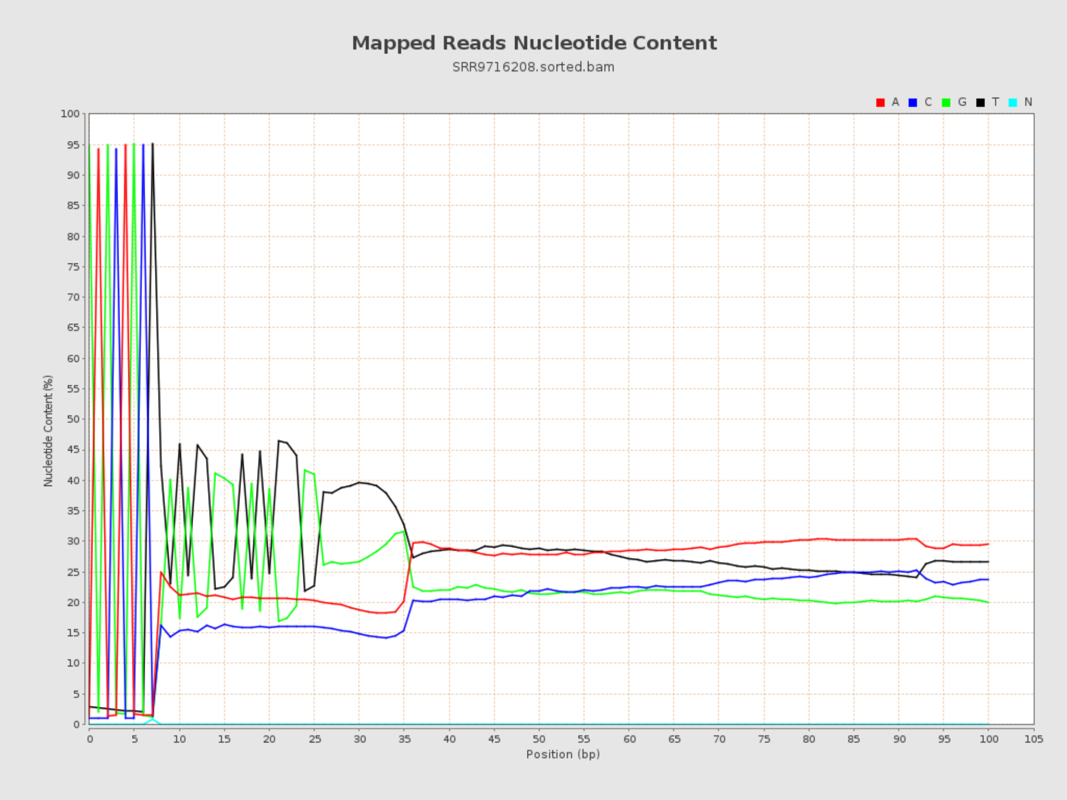
6. Results : Genome Fraction Coverage



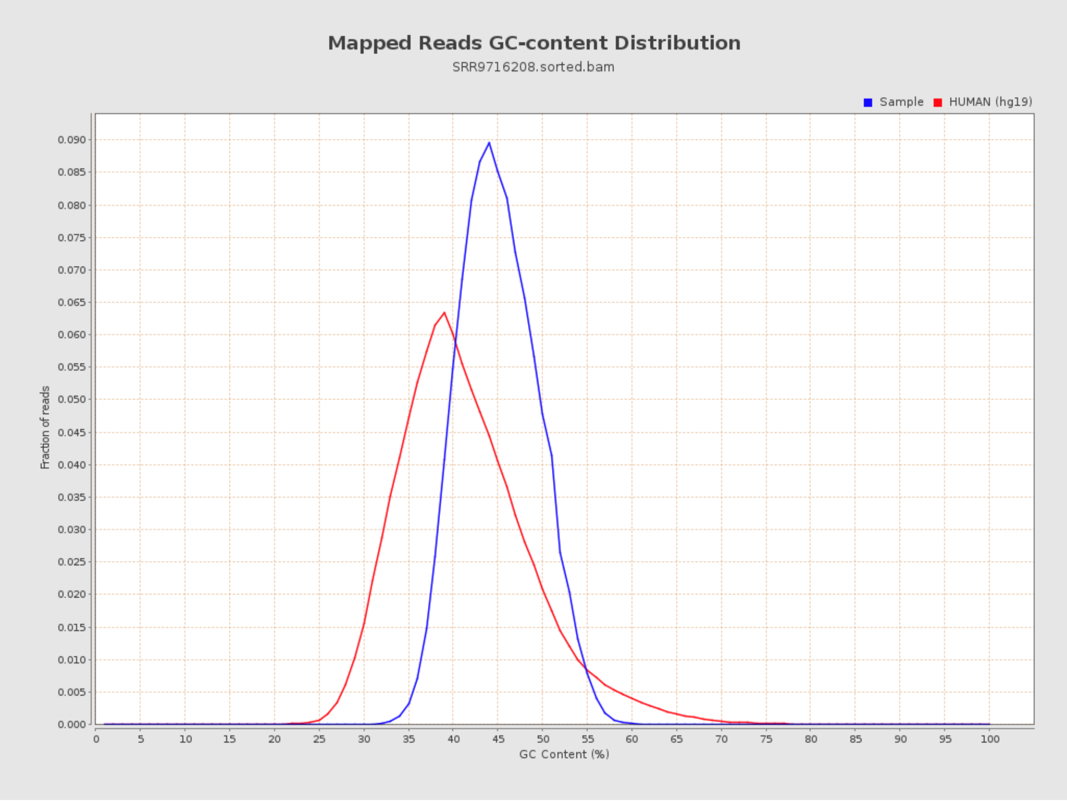
7. Results : Duplication Rate Histogram



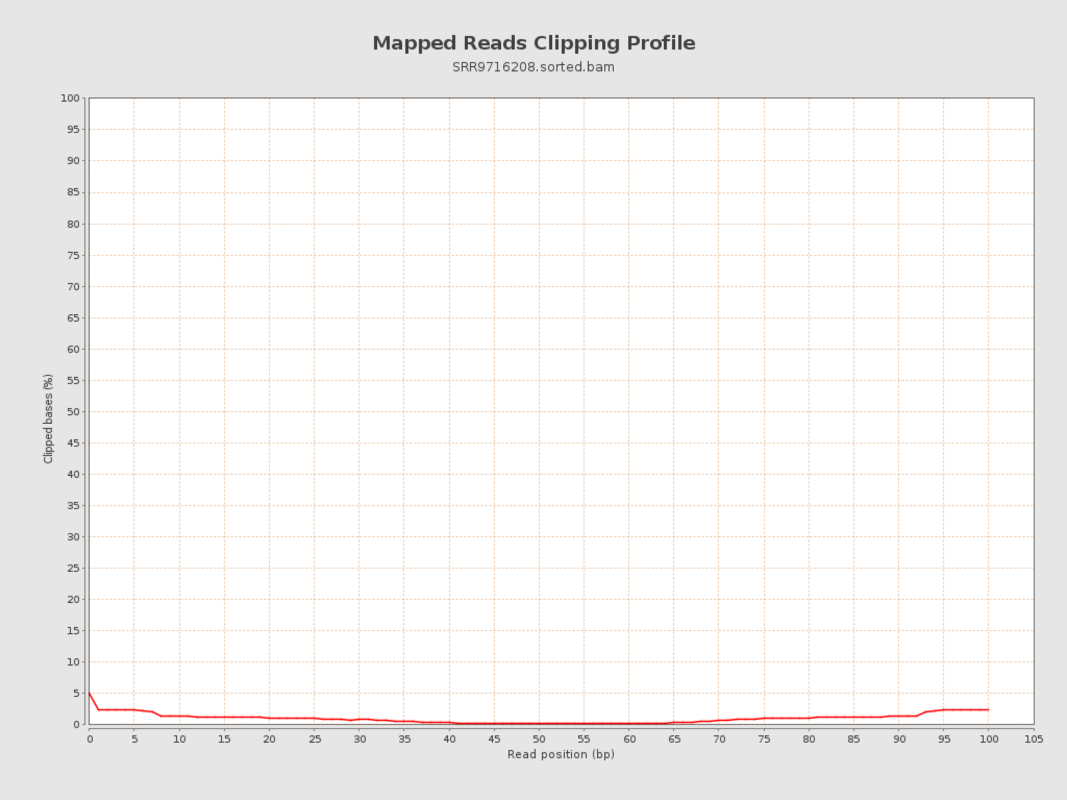
8. Results : Mapped Reads Nucleotide Content



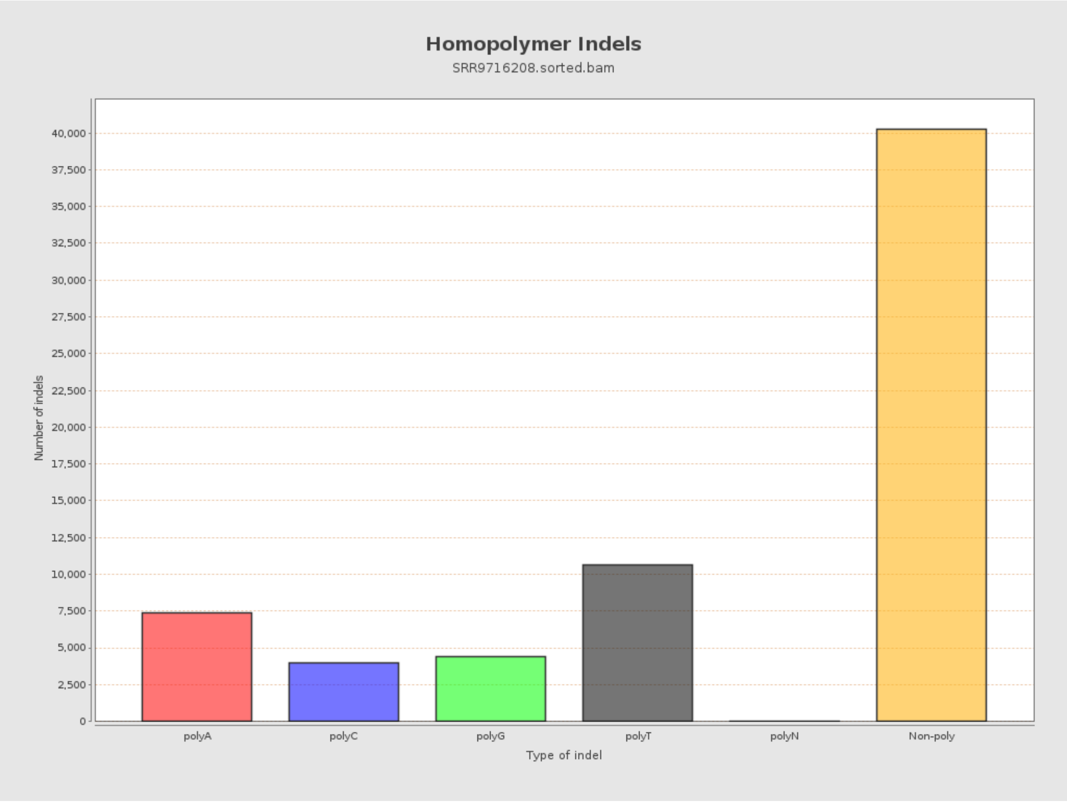
9. Results : Mapped Reads GC-content Distribution



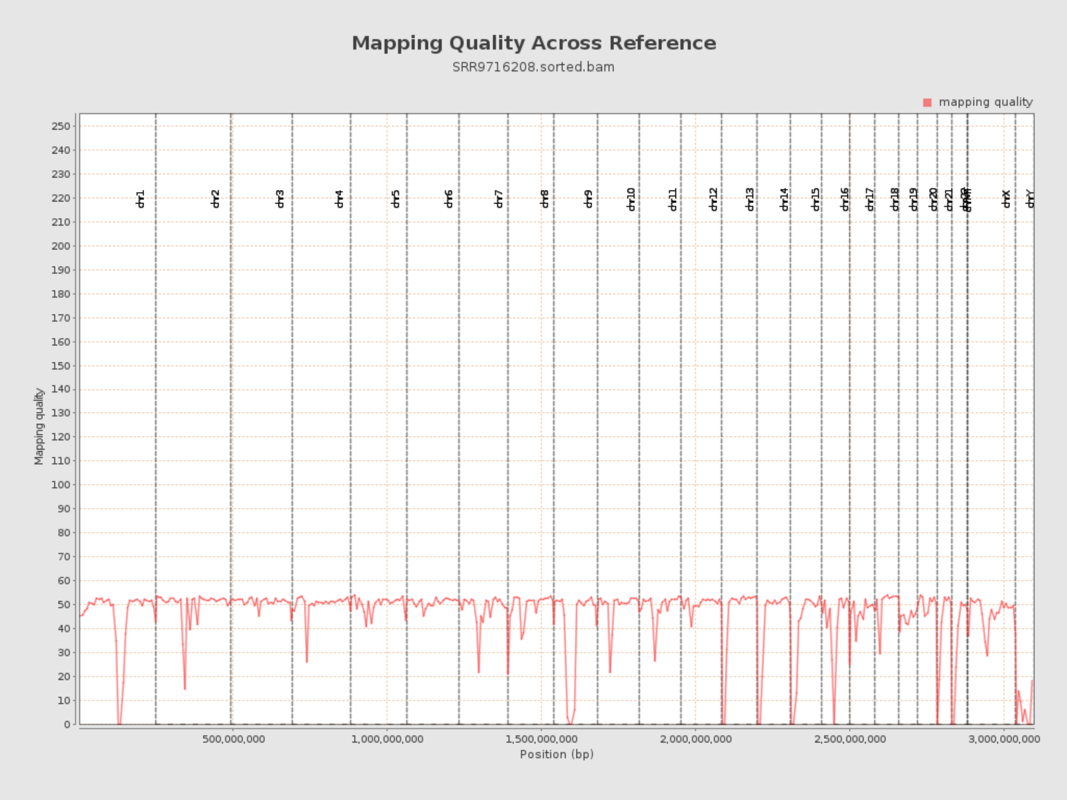
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram