Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:12:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716220.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_SRR9716220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716220.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:12:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,009,525
Mapped reads	2,772,166 / 92.11%
Unmapped reads	237,359 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,589 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	201,845 / 6.71%
Duplication rate	5.69%
Clipped reads	2,782,923 / 92.47%

2.2. ACGT Content

Number/percentage of A's	38,748,856 / 23.95%
Number/percentage of C's	34,190,402 / 21.13%
Number/percentage of T's	50,425,933 / 31.17%
Number/percentage of G's	38,407,073 / 23.74%
Number/percentage of N's	2,118 / 0%
GC Percentage	44.88%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.3982

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

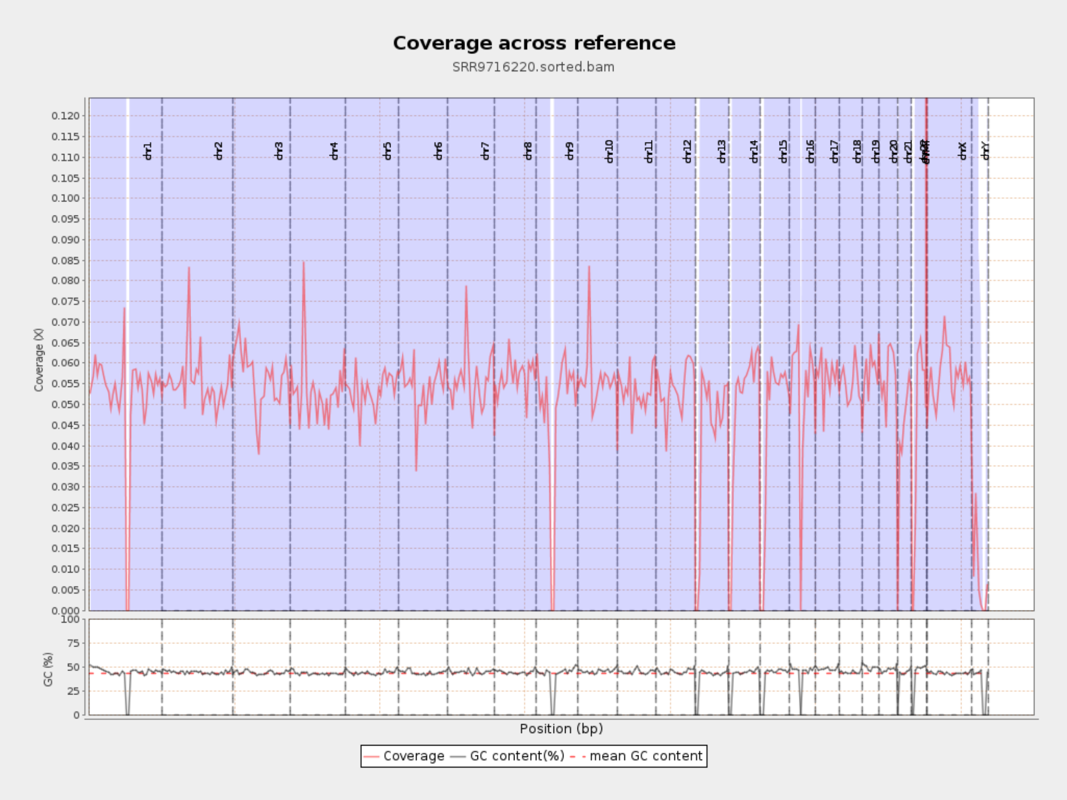
General error rate	0.51%
Mismatches	802,700
Insertions	11,666
Mapped reads with at least one insertion	0.42%
Deletions	28,695
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.44%

2.6. Chromosome stats

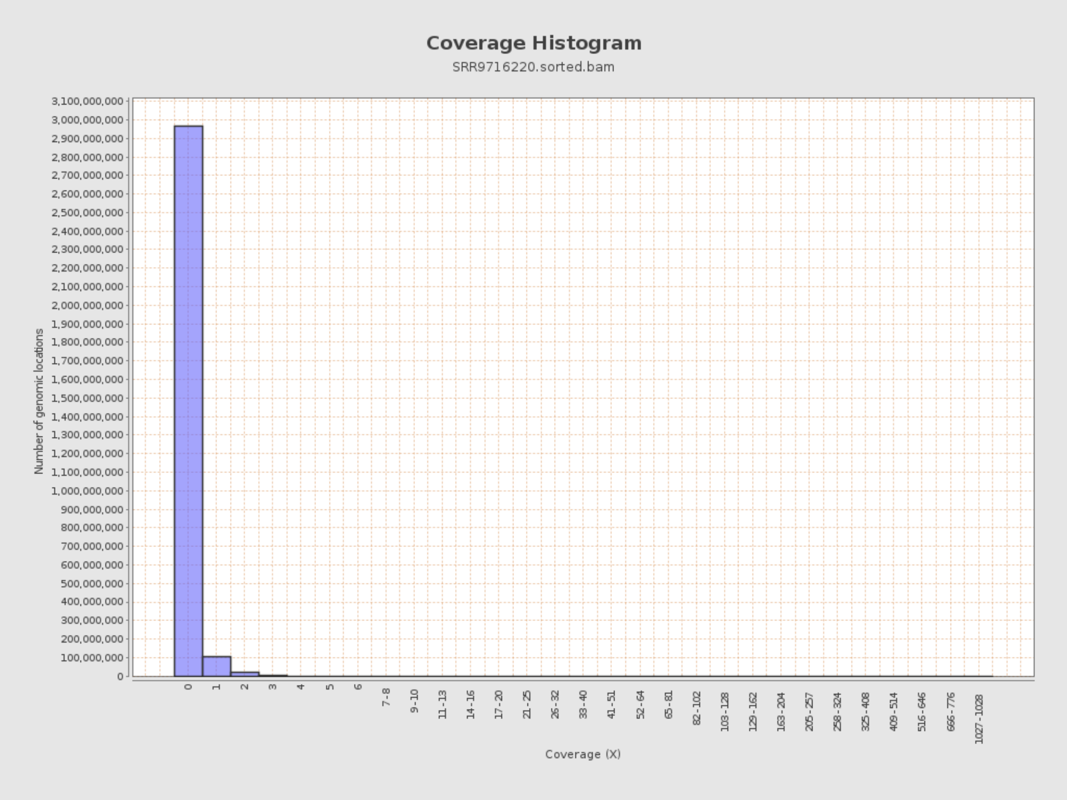
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12917064	0.0518	0.6083
chr2	243199373	13525528	0.0556	0.5547
chr3	198022430	11212056	0.0566	0.2905
chr4	191154276	10159306	0.0531	0.3326
chr5	180915260	9641022	0.0533	0.2826
chr6	171115067	9304751	0.0544	0.318
chr7	159138663	8887776	0.0558	0.5204

chr8	146364022	8314751	0.0568	0.4369
chr9	141213431	6698074	0.0474	0.3328
chr10	135534747	7628223	0.0563	0.4289
chr11	135006516	7180306	0.0532	0.3641
chr12	133851895	7246849	0.0541	0.2892
chr13	115169878	4876977	0.0423	0.2516
chr14	107349540	5204281	0.0485	0.2843
chr15	102531392	4690080	0.0457	0.2655
chr16	90354753	4786278	0.053	0.3011
chr17	81195210	4629233	0.057	0.3174
chr18	78077248	4328166	0.0554	0.5986
chr19	59128983	3412391	0.0577	0.479
chr20	63025520	3579206	0.0568	0.3022
chr21	48129895	2074480	0.0431	0.293
chr22	51304566	2157783	0.0421	0.2527
chrMT	16571	23089	1.3933	1.557
chrX	155270560	8838112	0.0569	0.3192
chrY	59373566	503771	0.0085	0.2259

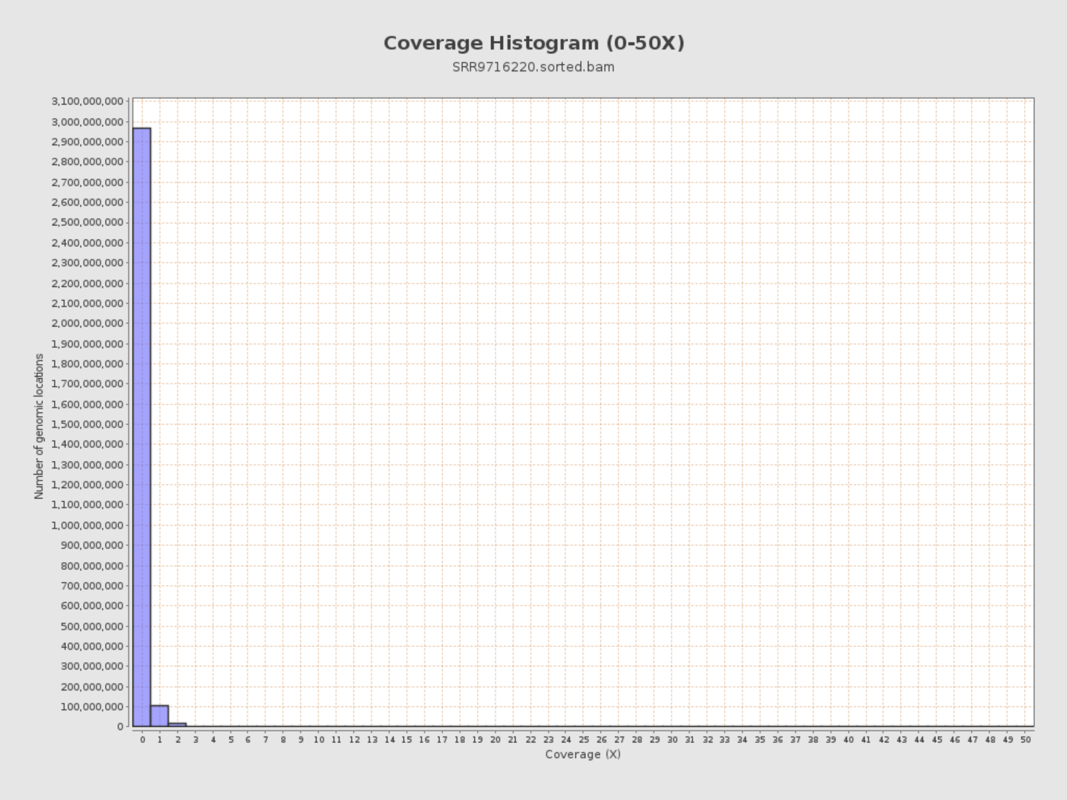
3. Results : Coverage across reference



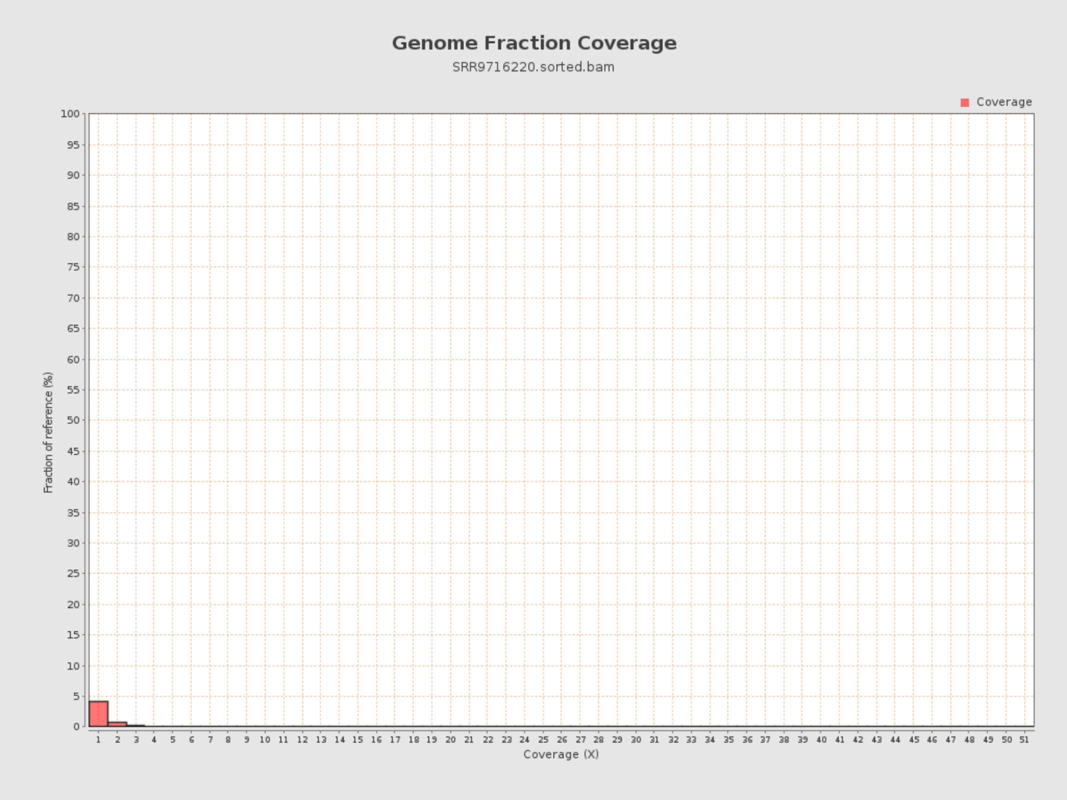
4. Results : Coverage Histogram



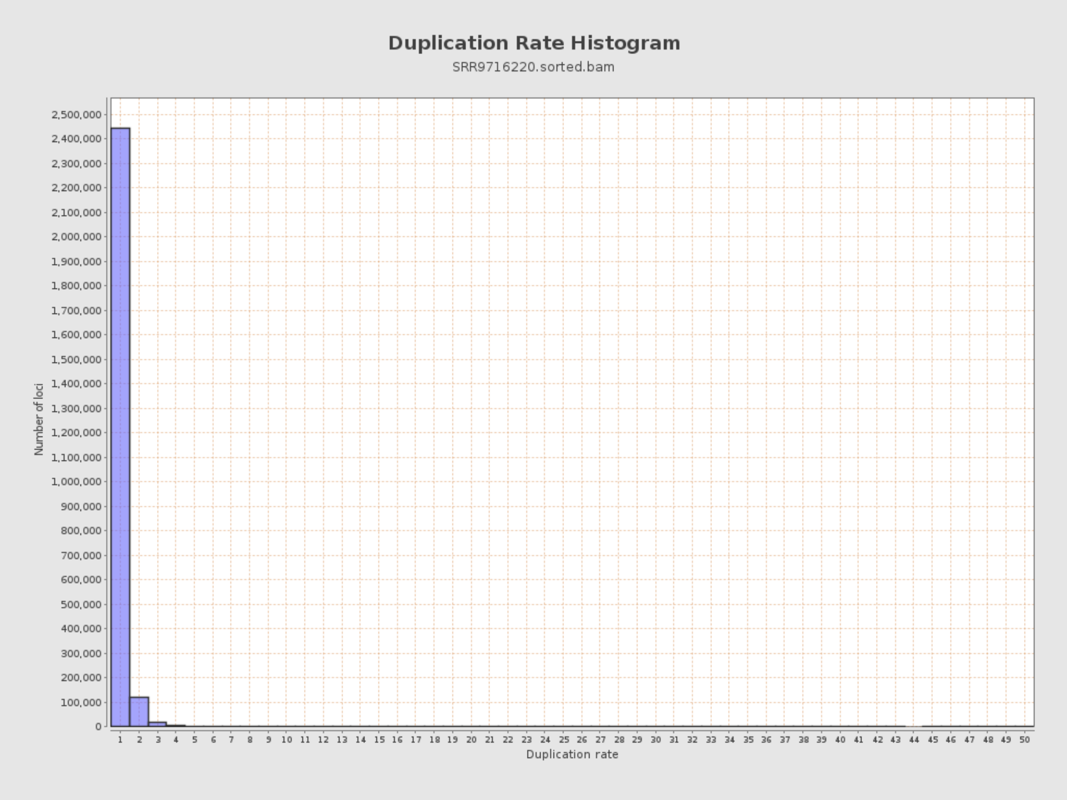
5. Results : Coverage Histogram (0-50X)



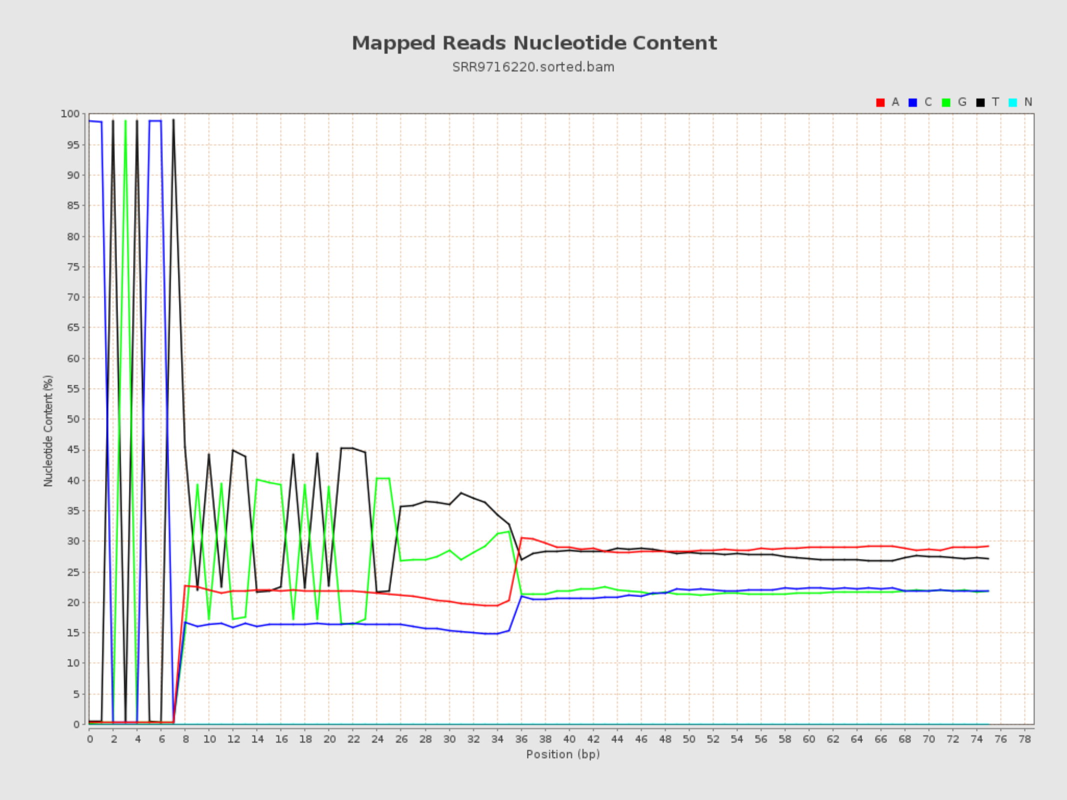
6. Results : Genome Fraction Coverage



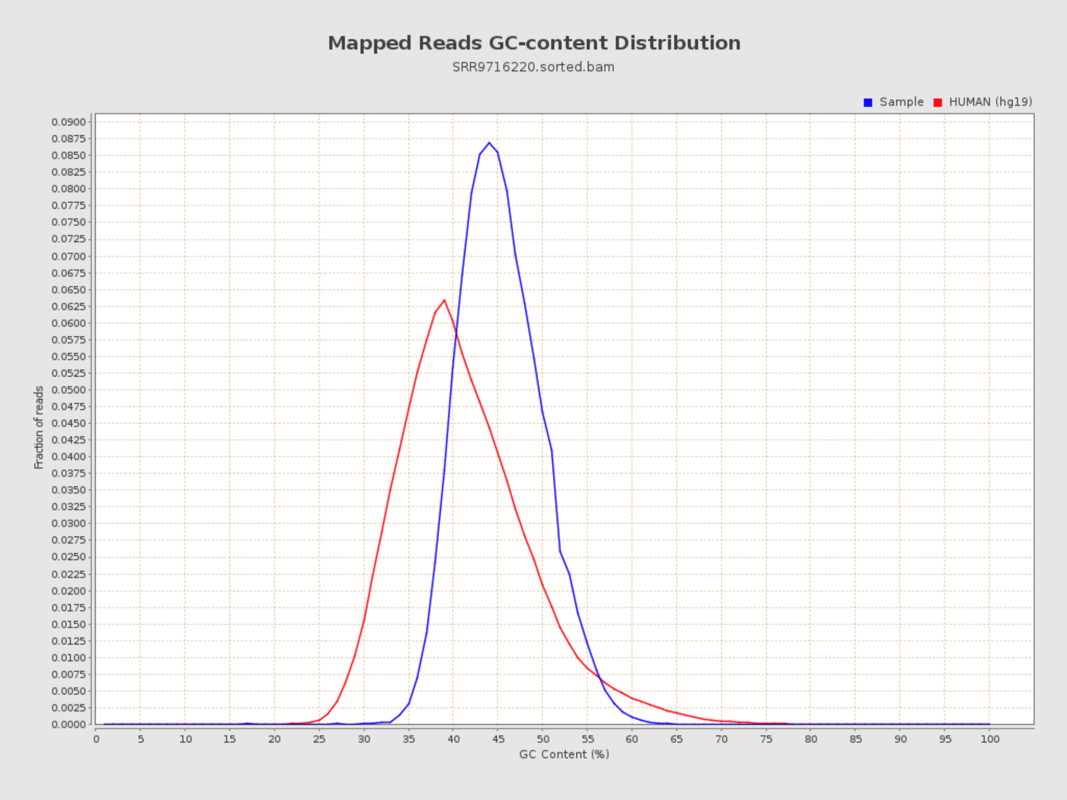
7. Results : Duplication Rate Histogram



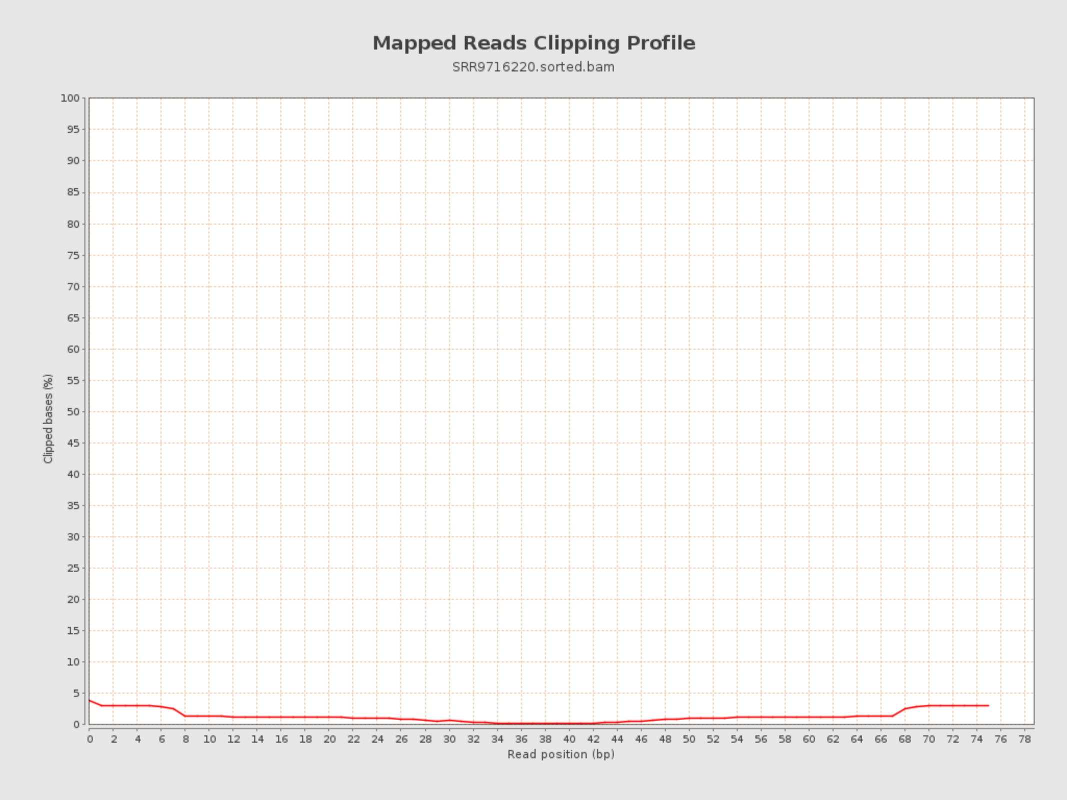
8. Results : Mapped Reads Nucleotide Content



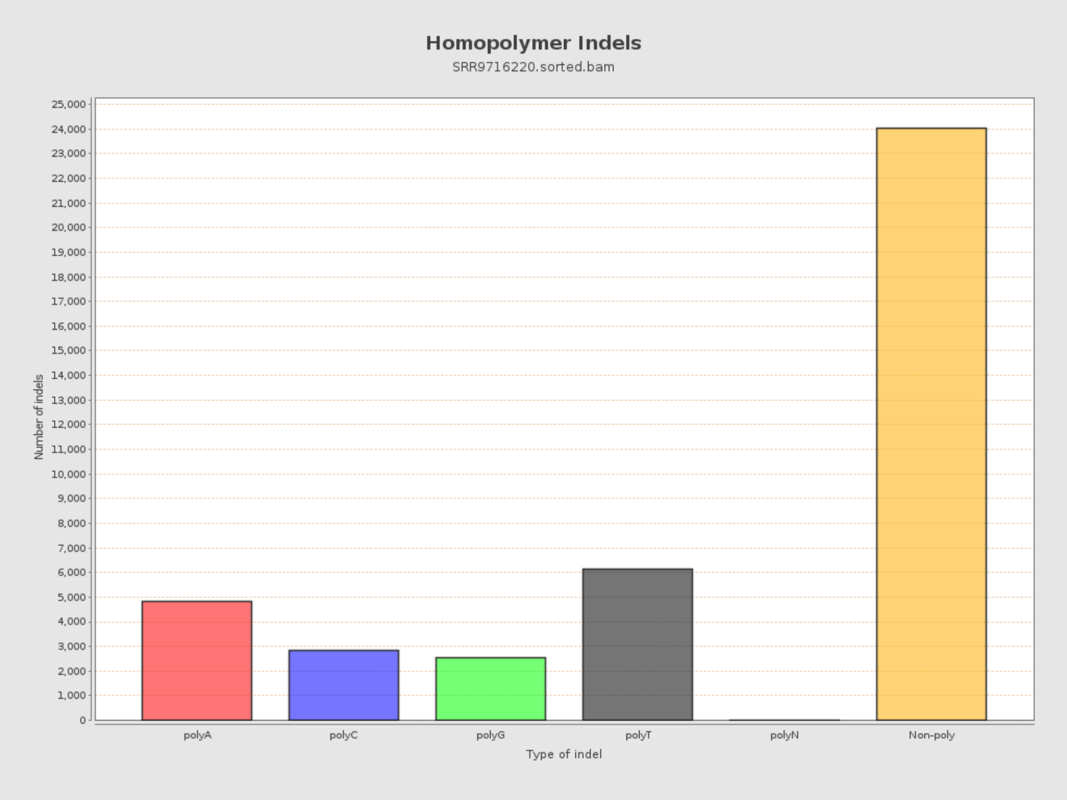
9. Results : Mapped Reads GC-content Distribution



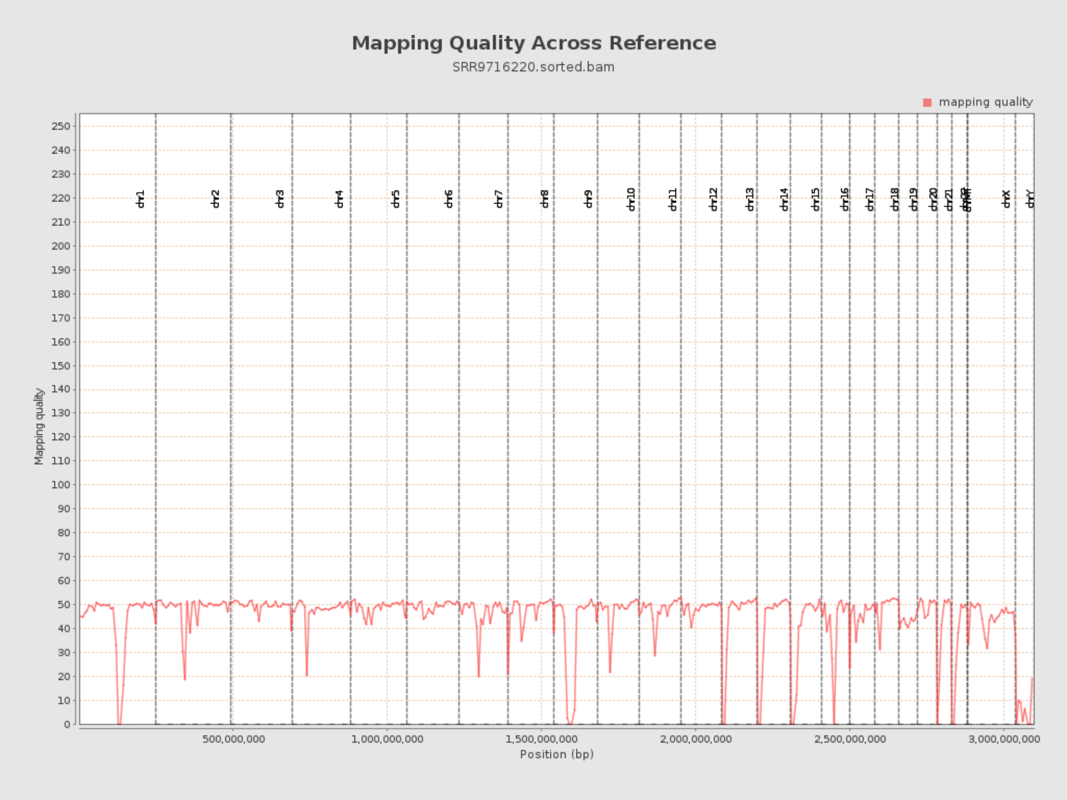
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram