Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:41:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716324.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_SRR9716324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:41:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,572,748
Mapped reads	3,248,058 / 90.91%
Unmapped reads	324,690 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,325 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	138,879 / 3.89%
Duplication rate	3.13%
Clipped reads	3,254,803 / 91.1%

2.2. ACGT Content

Number/percentage of A's	43,302,995 / 23.51%
Number/percentage of C's	35,825,824 / 19.45%
Number/percentage of T's	57,638,589 / 31.29%
Number/percentage of G's	47,408,116 / 25.74%
Number/percentage of N's	3,877 / 0%
GC Percentage	45.19%

2.3. Coverage

Mean	0.0595

Standard Deviation	0.421

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

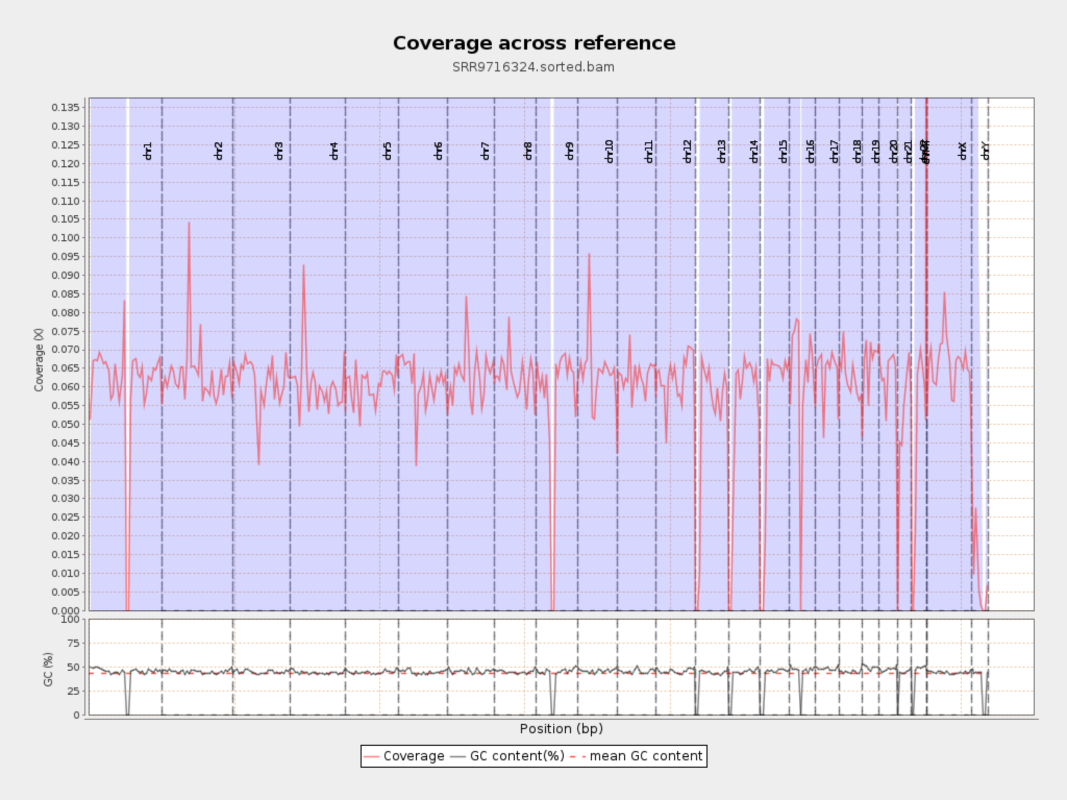
General error rate	0.5%
Mismatches	902,954
Insertions	10,805
Mapped reads with at least one insertion	0.33%
Deletions	28,767
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.37%

2.6. Chromosome stats

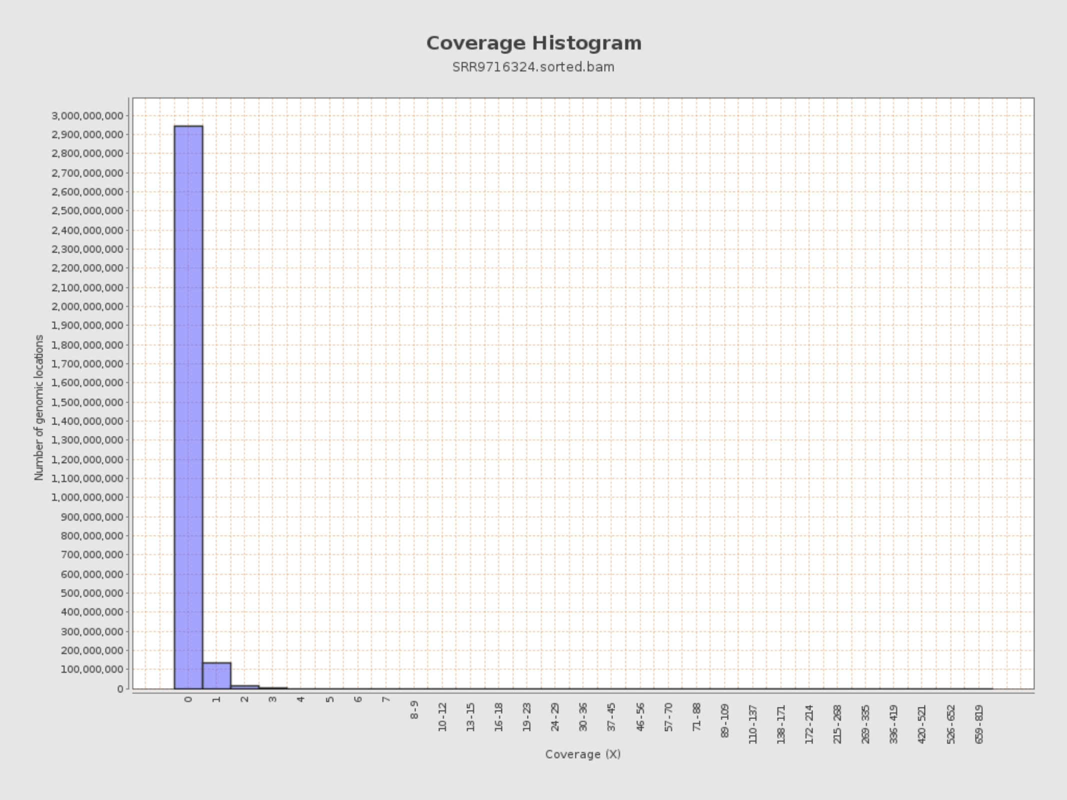
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14922748	0.0599	0.6666
chr2	243199373	15455872	0.0636	0.5155
chr3	198022430	12184240	0.0615	0.2902
chr4	191154276	11591531	0.0606	0.3269
chr5	180915260	10982902	0.0607	0.2939
chr6	171115067	10517432	0.0615	0.3184
chr7	159138663	10098718	0.0635	0.4837

chr8	146364022	9171916	0.0627	0.3664
chr9	141213431	7834660	0.0555	0.4662
chr10	135534747	8722980	0.0644	0.4213
chr11	135006516	8454445	0.0626	0.4384
chr12	133851895	8370977	0.0625	0.3039
chr13	115169878	5734672	0.0498	0.2567
chr14	107349540	5619279	0.0523	0.2965
chr15	102531392	5398363	0.0527	0.2695
chr16	90354753	5637484	0.0624	0.3356
chr17	81195210	5197089	0.064	0.3208
chr18	78077248	4900156	0.0628	0.8588
chr19	59128983	3949077	0.0668	0.4998
chr20	63025520	3947592	0.0626	0.3046
chr21	48129895	2432177	0.0505	0.3134
chr22	51304566	2265099	0.0442	0.2433
chrMT	16571	9334	0.5633	0.8092
chrX	155270560	10301397	0.0663	0.3775
chrY	59373566	527959	0.0089	0.1796

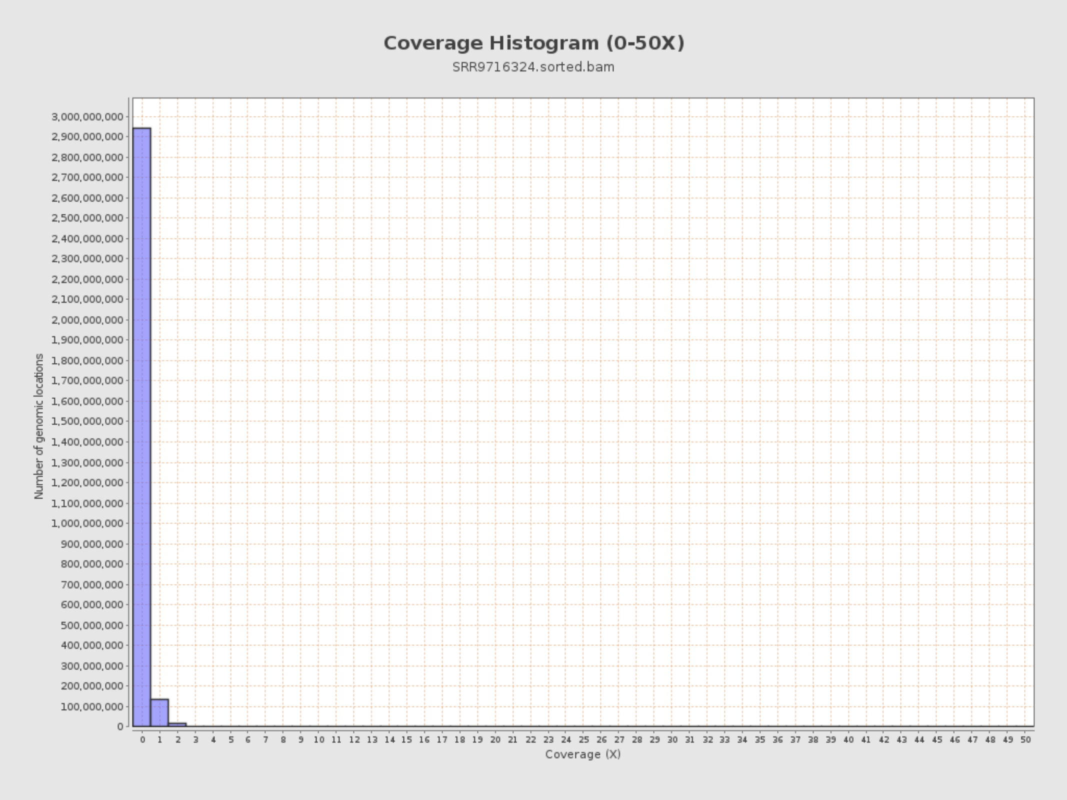
3. Results : Coverage across reference



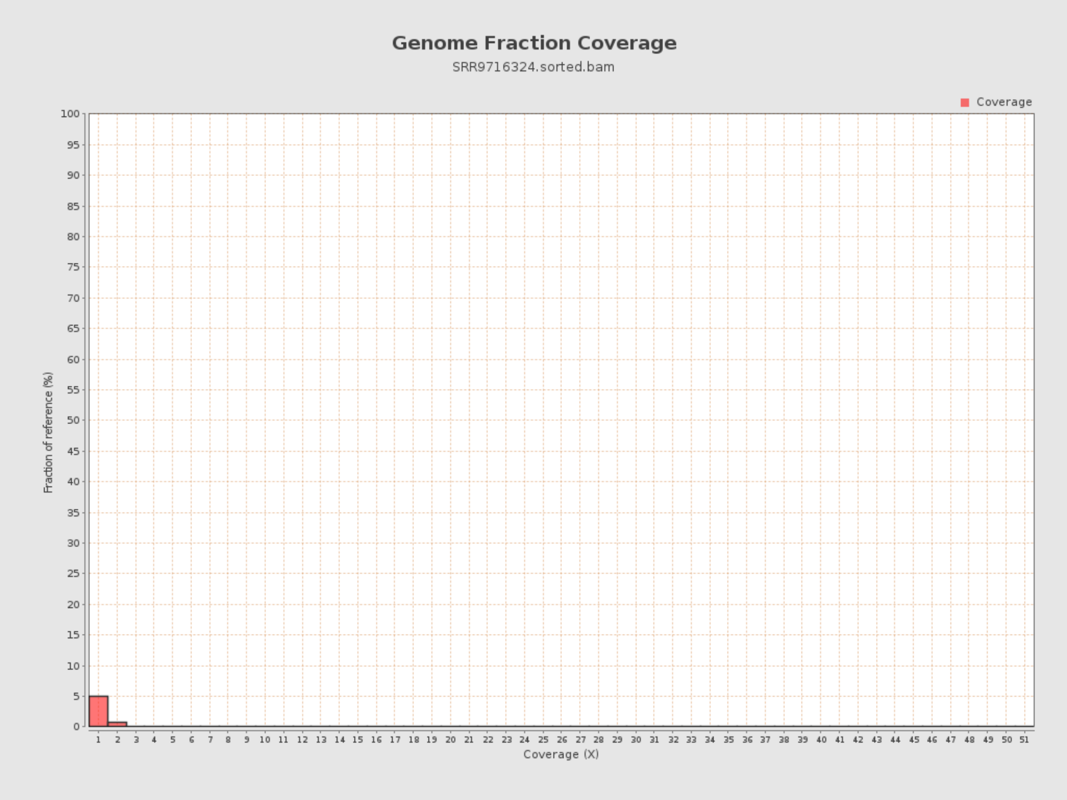
4. Results : Coverage Histogram



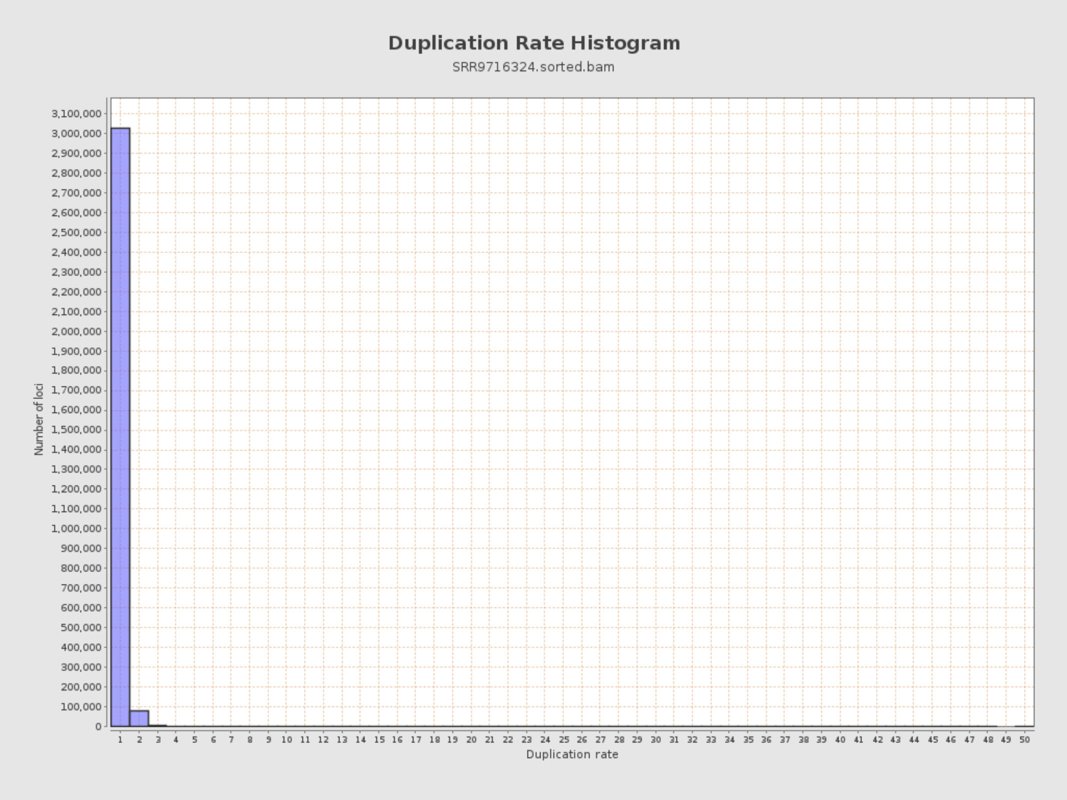
5. Results : Coverage Histogram (0-50X)



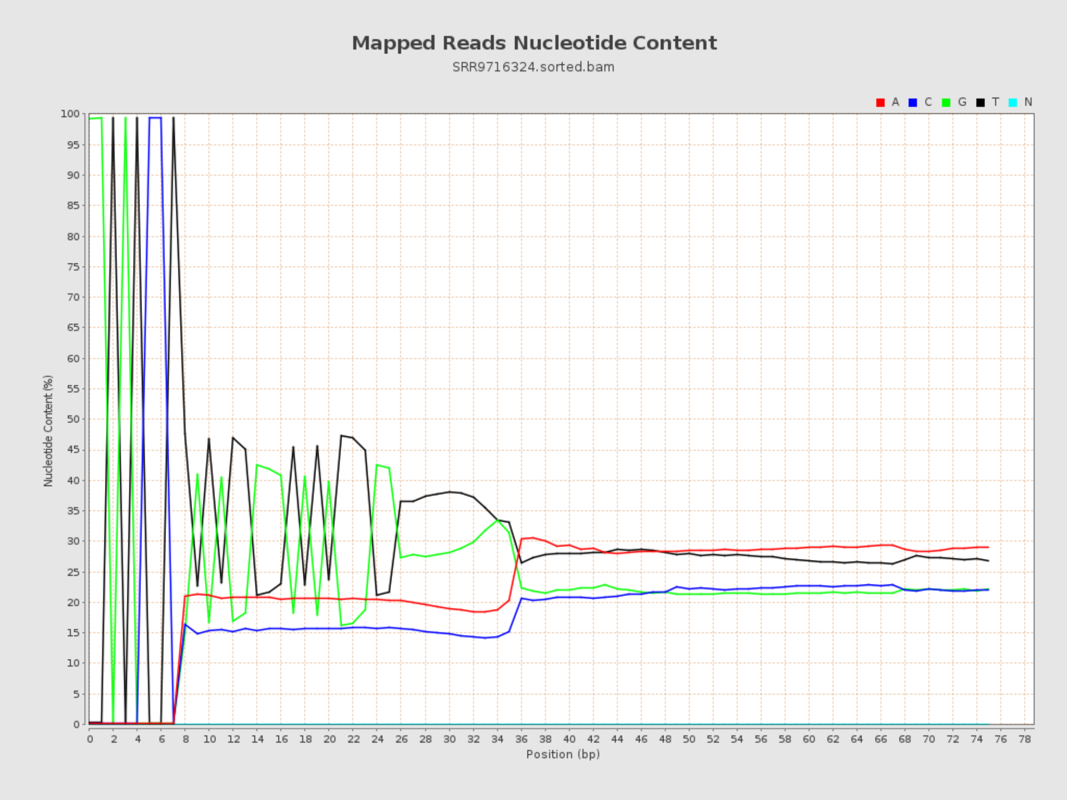
6. Results : Genome Fraction Coverage



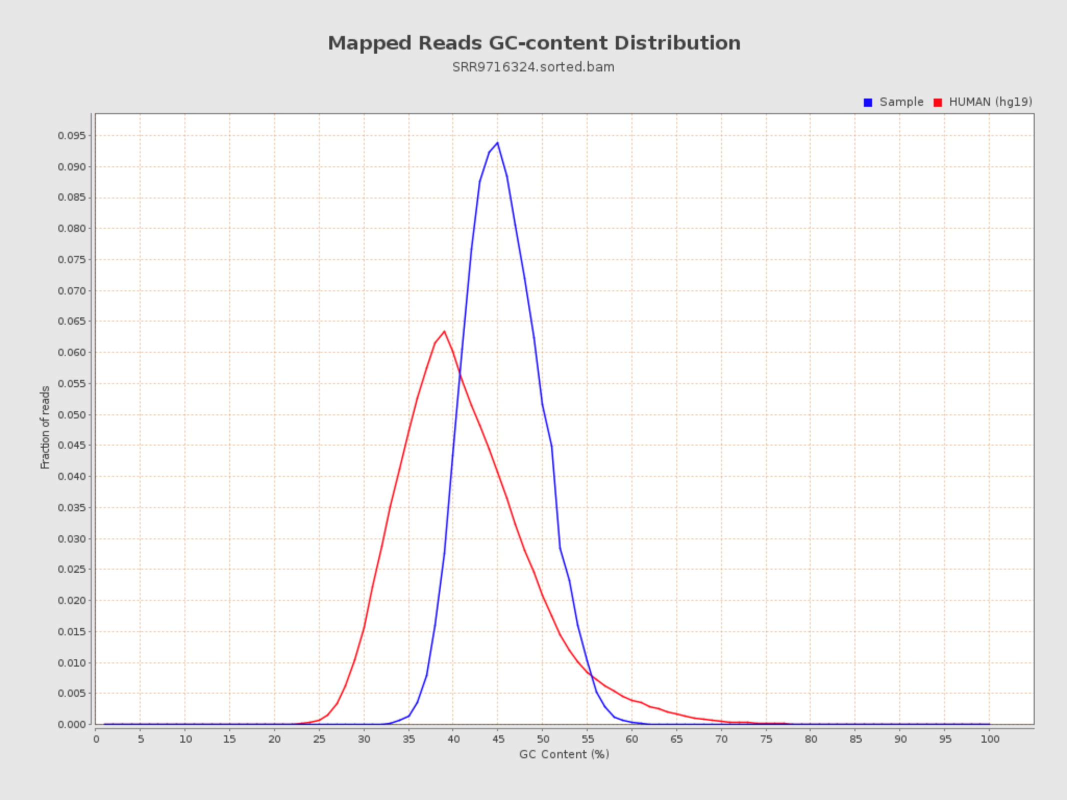
7. Results : Duplication Rate Histogram



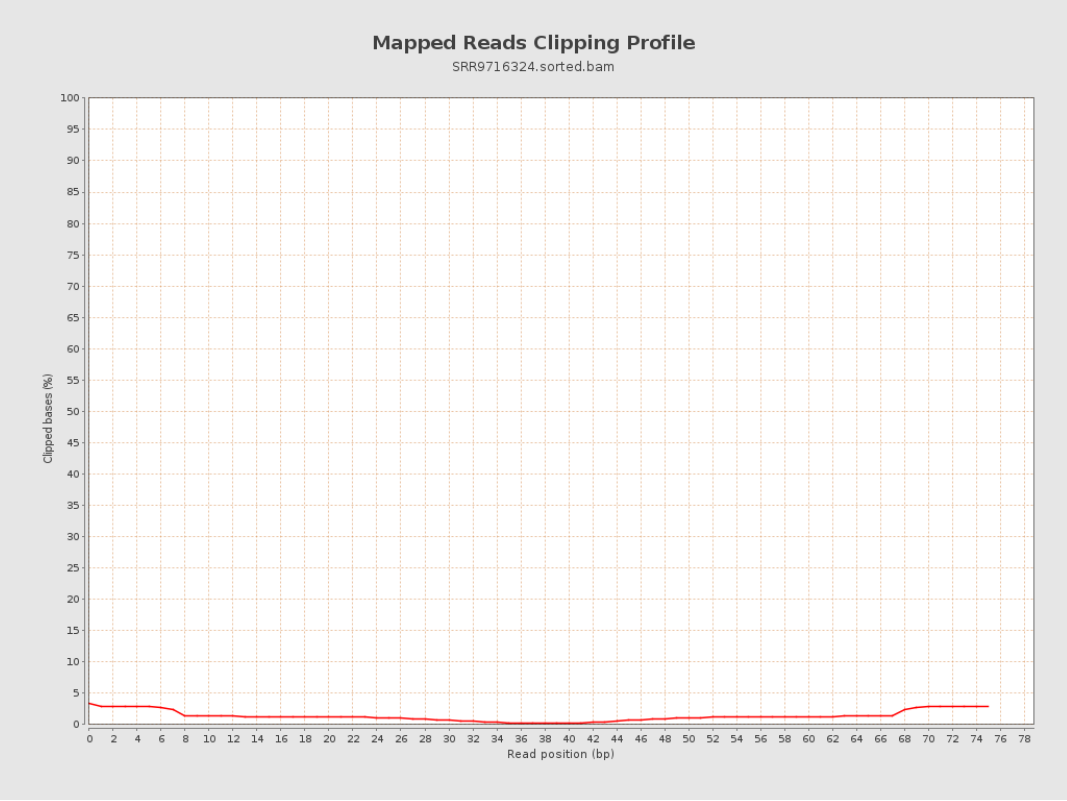
8. Results : Mapped Reads Nucleotide Content



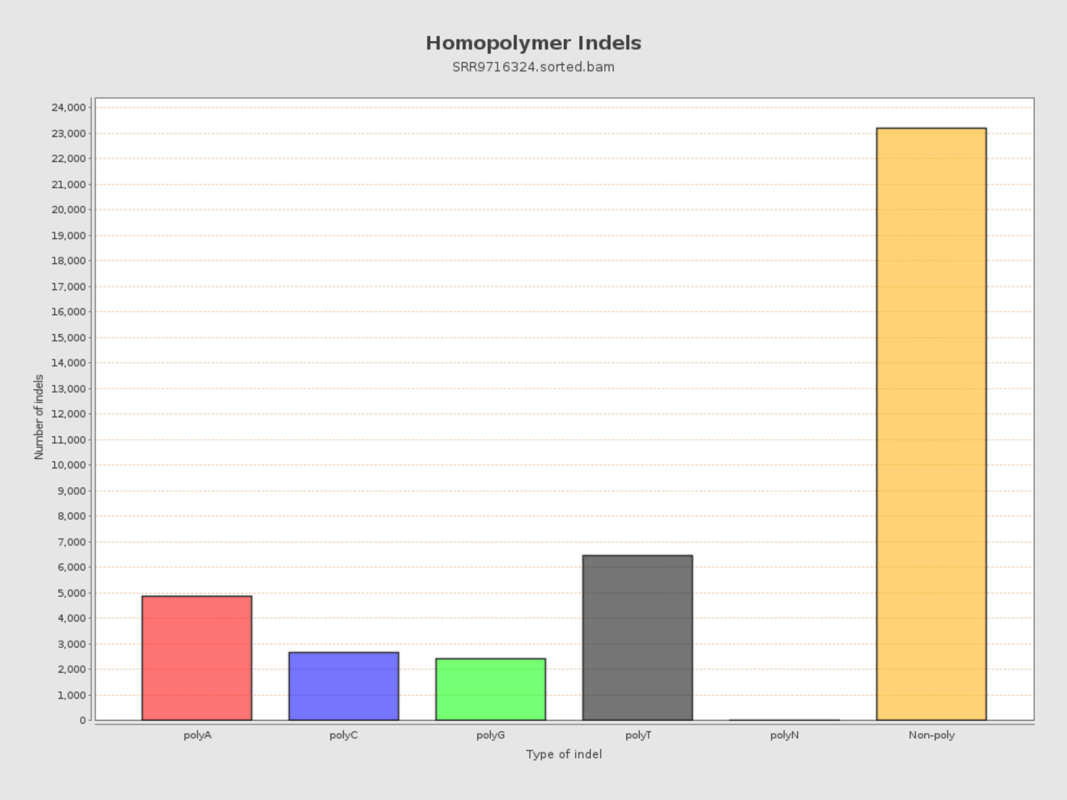
9. Results : Mapped Reads GC-content Distribution



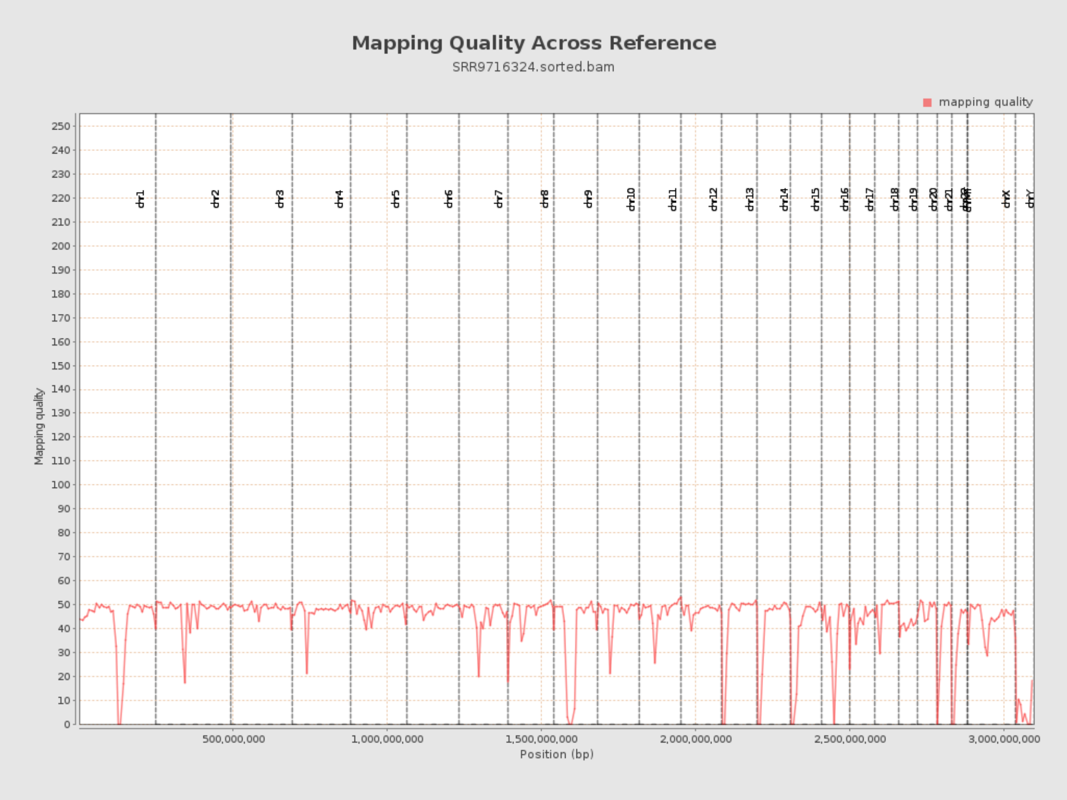
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram