Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:57:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716373.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_SRR9716373 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716373.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:57:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716373.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	462,382
Mapped reads	422,383 / 91.35%
Unmapped reads	39,999 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,178 / 1.98%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	7,546 / 1.63%
Duplication rate	1.22%
Clipped reads	430,772 / 93.16%

2.2. ACGT Content

Number/percentage of A's	8,415,290 / 25.56%
Number/percentage of C's	6,549,395 / 19.89%
Number/percentage of T's	10,033,004 / 30.47%
Number/percentage of G's	7,922,557 / 24.06%
Number/percentage of N's	2,433 / 0.01%
GC Percentage	43.96%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.1419

2.4. Mapping Quality

Mean Mapping Quality	46.63

2.5. Mismatches and indels

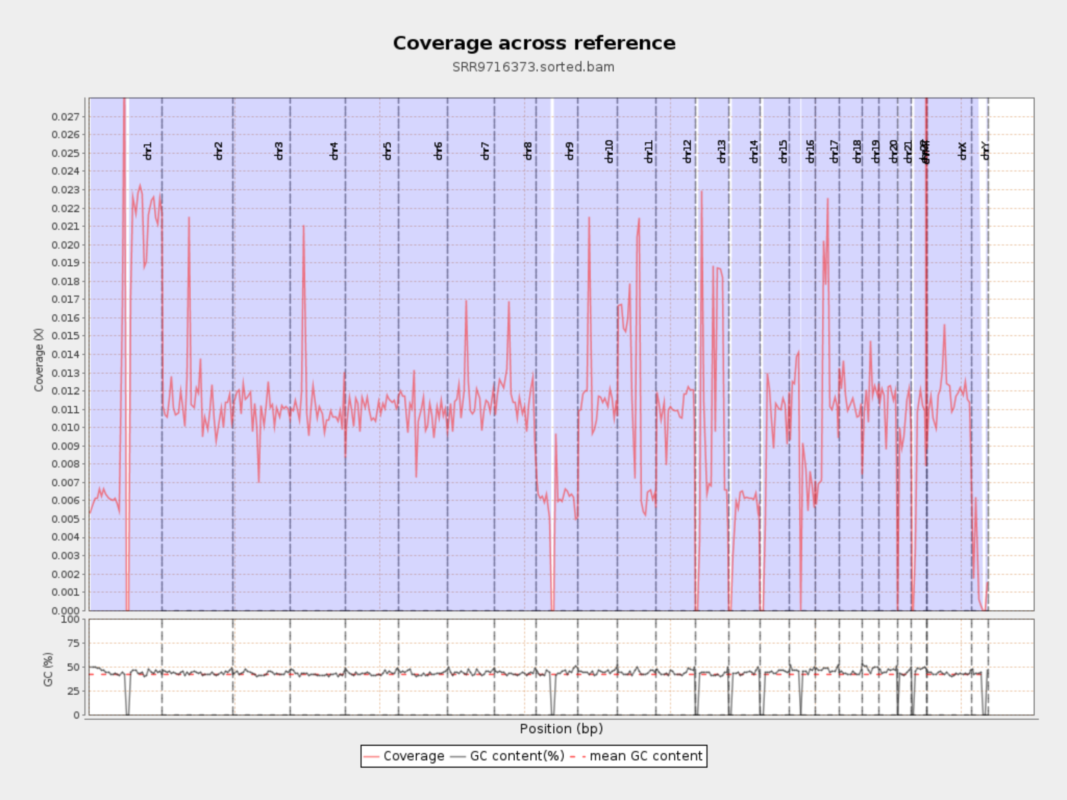
General error rate	0.7%
Mismatches	225,463
Insertions	2,788
Mapped reads with at least one insertion	0.65%
Deletions	8,253
Mapped reads with at least one deletion	1.92%
Homopolymer indels	42.39%

2.6. Chromosome stats

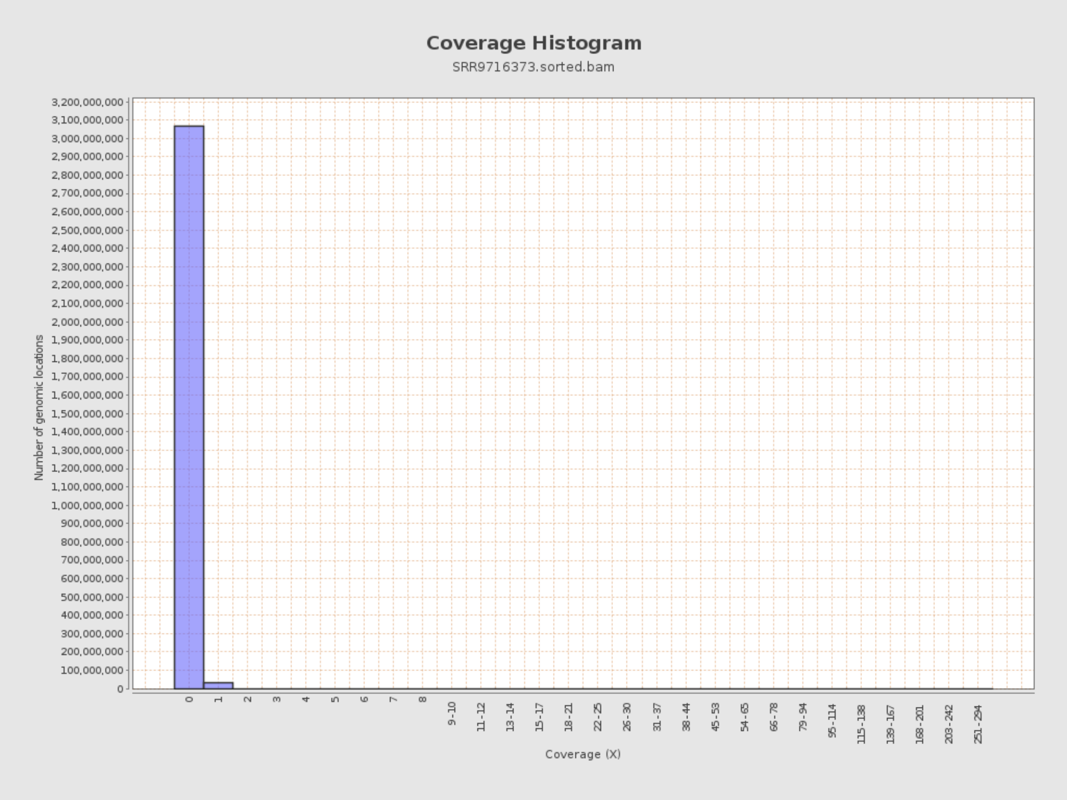
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3386624	0.0136	0.2766
chr2	243199373	2785780	0.0115	0.1485
chr3	198022430	2180170	0.011	0.1075
chr4	191154276	2156124	0.0113	0.1163
chr5	180915260	1995743	0.011	0.1087
chr6	171115067	1854002	0.0108	0.1108
chr7	159138663	1834913	0.0115	0.1524

chr8	146364022	1723705	0.0118	0.1515
chr9	141213431	791270	0.0056	0.0961
chr10	135534747	1601393	0.0118	0.1387
chr11	135006516	1587982	0.0118	0.1336
chr12	133851895	1485866	0.0111	0.1084
chr13	115169878	1212883	0.0105	0.1057
chr14	107349540	548308	0.0051	0.0762
chr15	102531392	919719	0.009	0.0978
chr16	90354753	785289	0.0087	0.0984
chr17	81195210	1007140	0.0124	0.1201
chr18	78077248	905228	0.0116	0.165
chr19	59128983	694847	0.0118	0.2114
chr20	63025520	714522	0.0113	0.1113
chr21	48129895	451492	0.0094	0.1043
chr22	51304566	390632	0.0076	0.0898
chrMT	16571	5739	0.3463	0.6002
chrX	155270560	1818440	0.0117	0.1177
chrY	59373566	100920	0.0017	0.0627

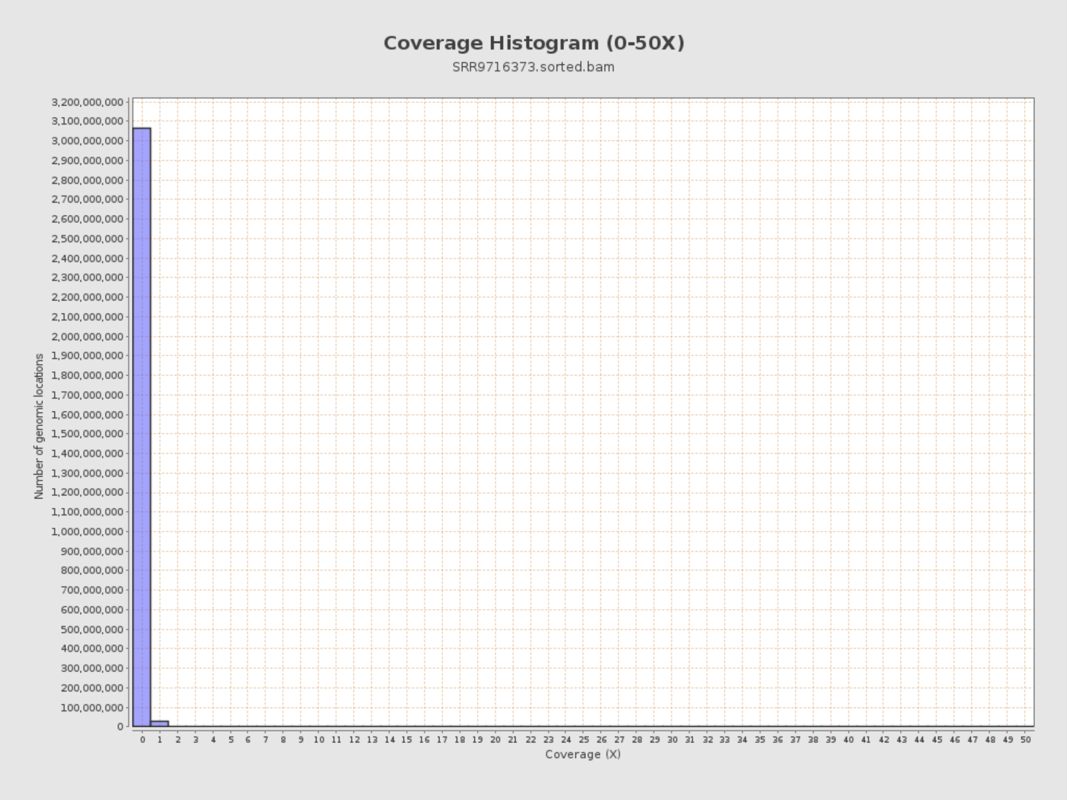
3. Results : Coverage across reference



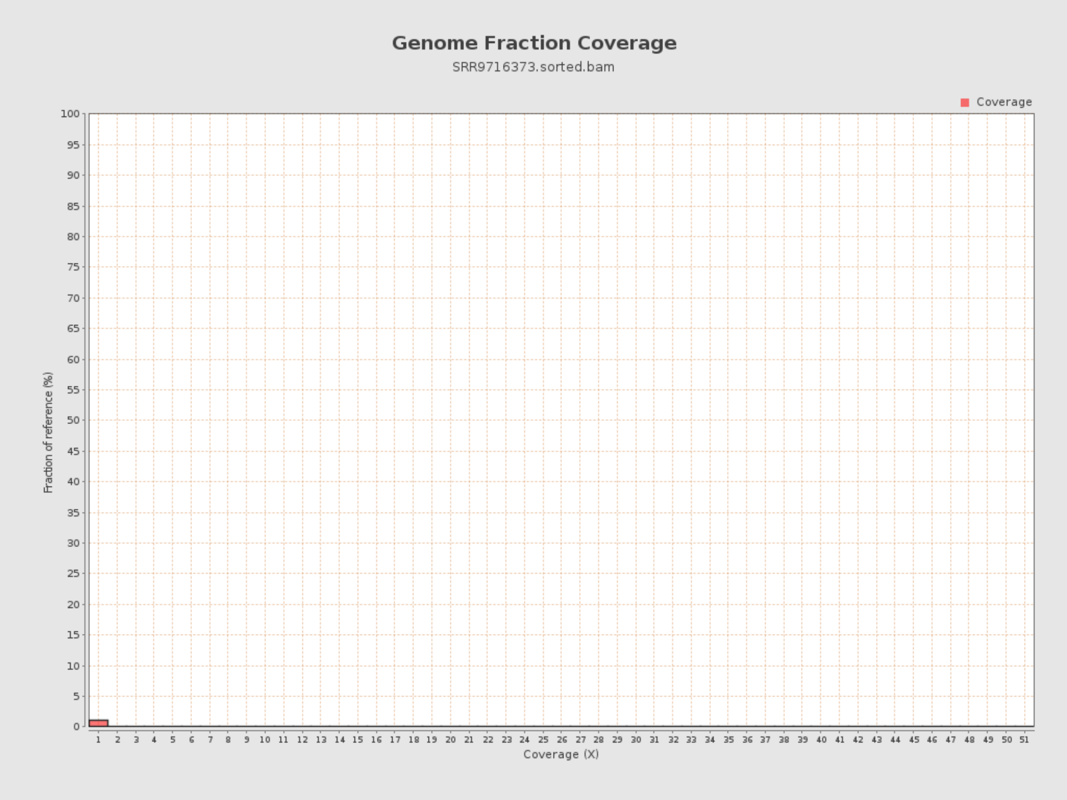
4. Results : Coverage Histogram



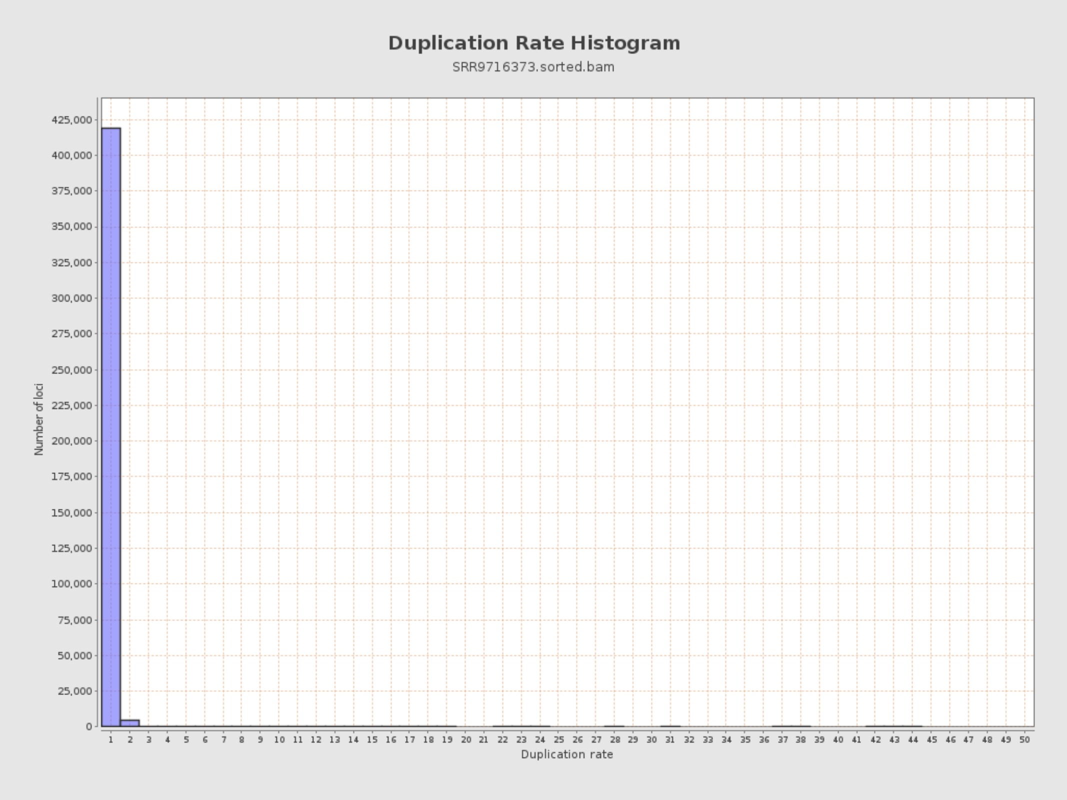
5. Results : Coverage Histogram (0-50X)



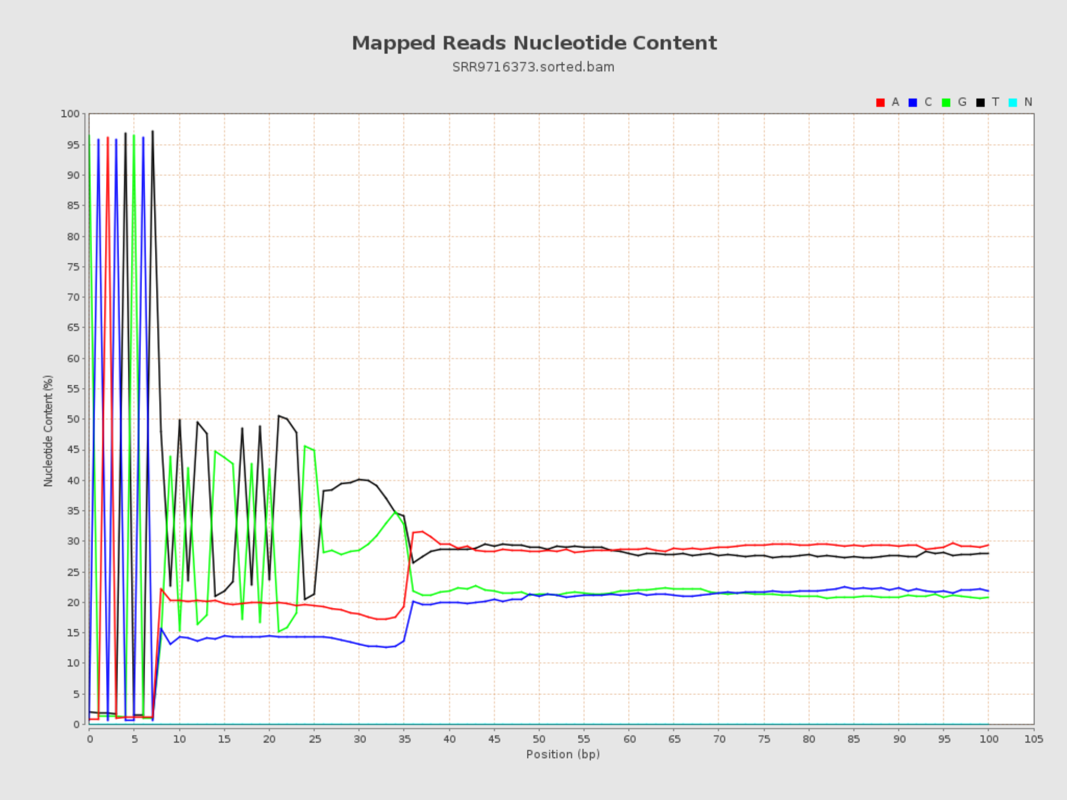
6. Results : Genome Fraction Coverage



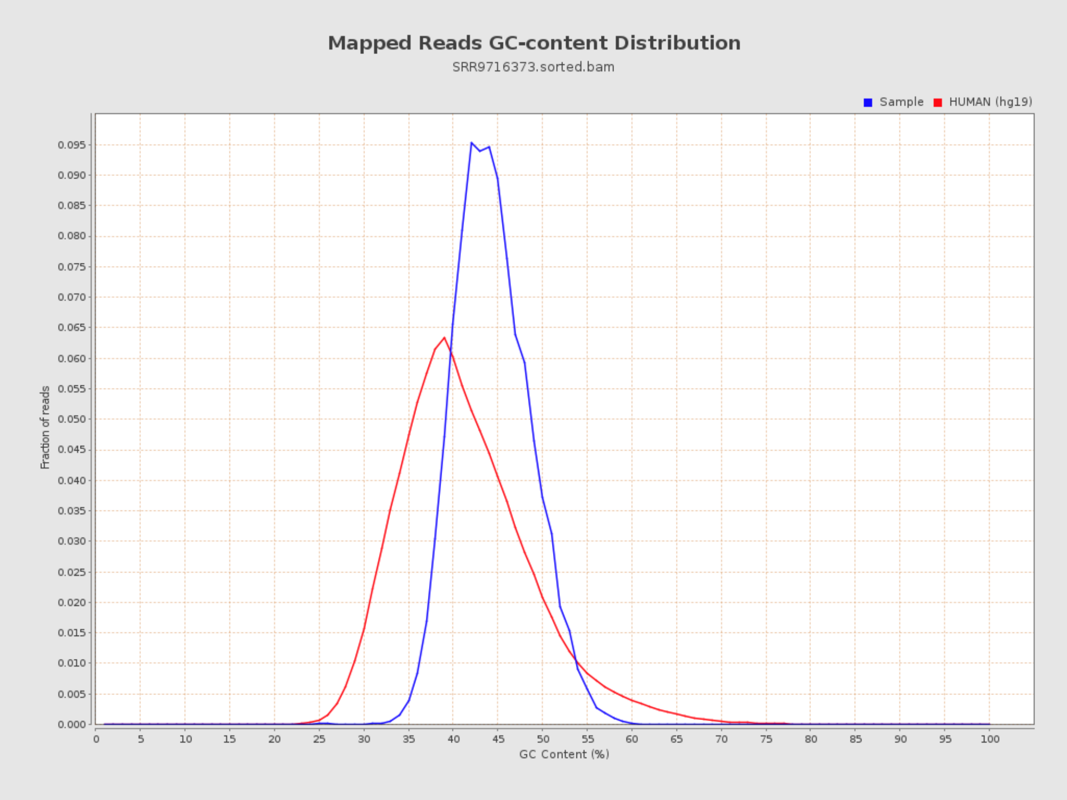
7. Results : Duplication Rate Histogram



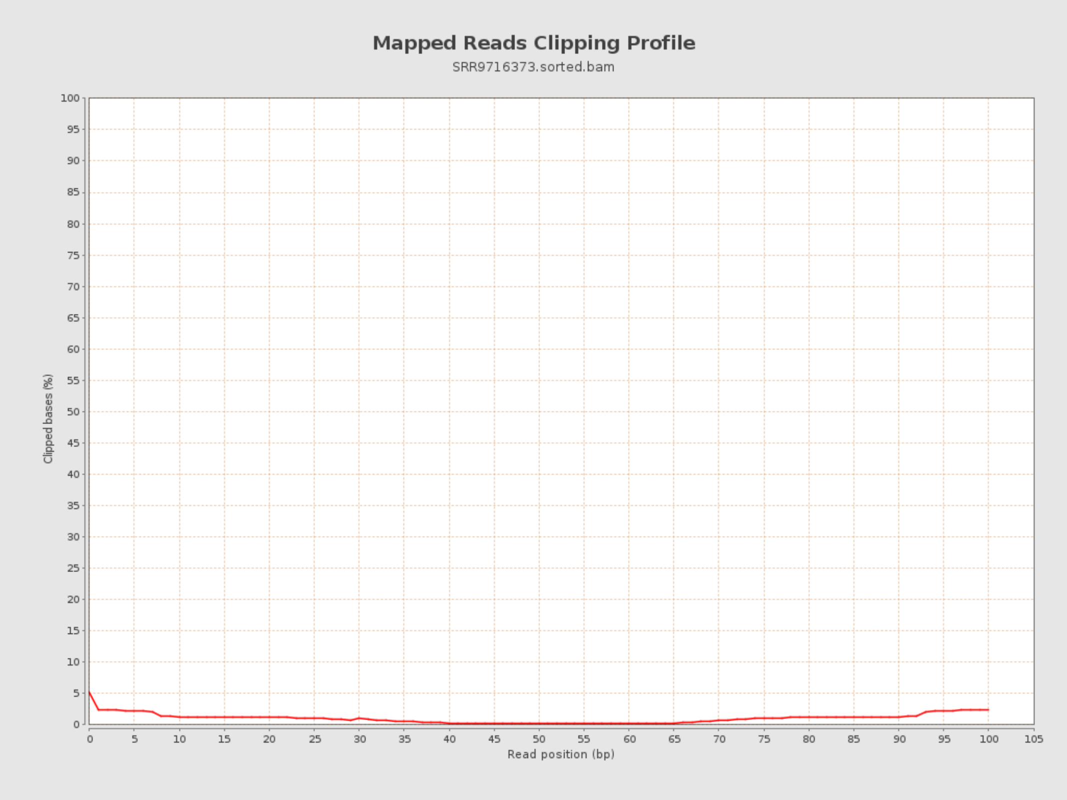
8. Results : Mapped Reads Nucleotide Content



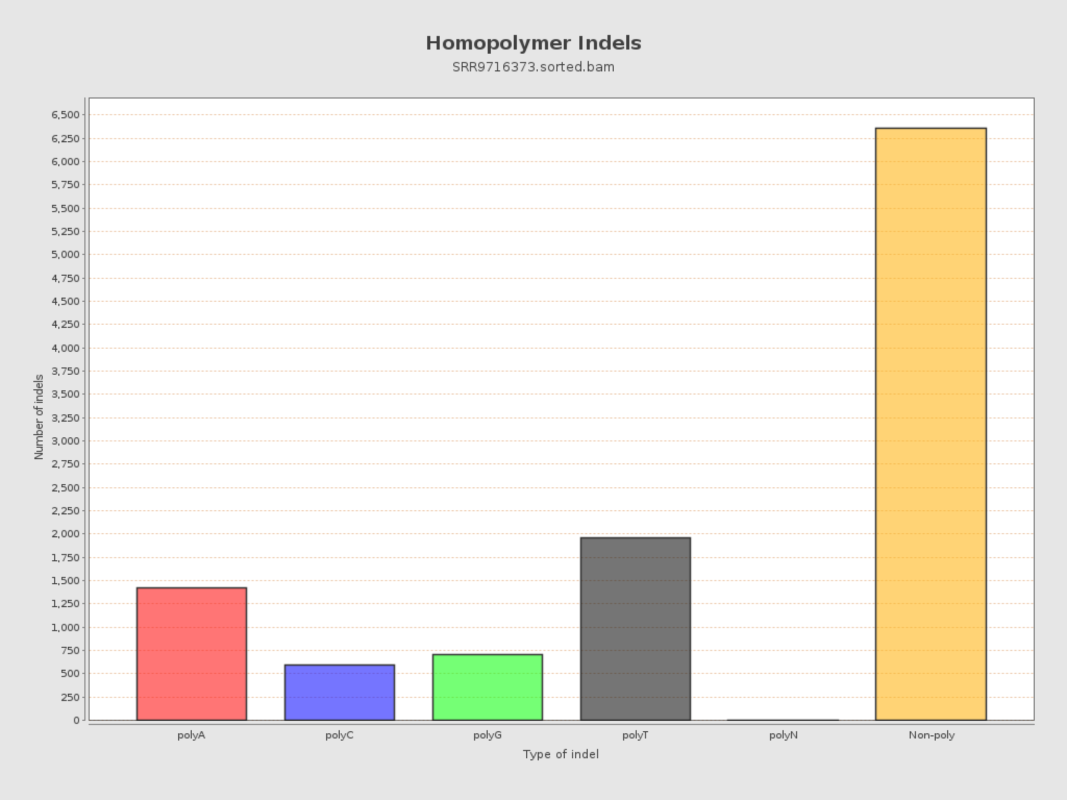
9. Results : Mapped Reads GC-content Distribution



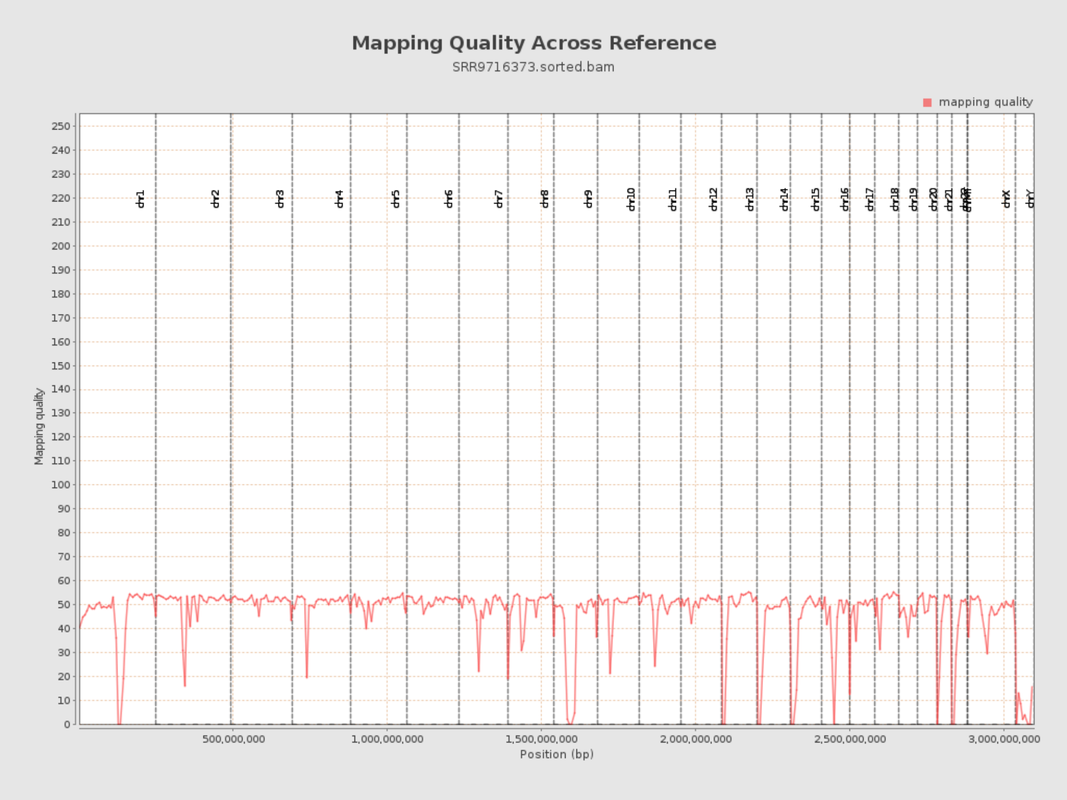
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram