Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:48:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716599.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_SRR9716599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716599.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:48:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,064,993
Mapped reads	979,855 / 92.01%
Unmapped reads	85,138 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,183 / 0.58%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	26,490 / 2.49%
Duplication rate	2.11%
Clipped reads	982,938 / 92.3%

2.2. ACGT Content

Number/percentage of A's	14,812,785 / 25.78%
Number/percentage of C's	11,182,158 / 19.46%
Number/percentage of T's	17,028,315 / 29.64%
Number/percentage of G's	14,427,188 / 25.11%
Number/percentage of N's	711 / 0%
GC Percentage	44.58%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.179

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

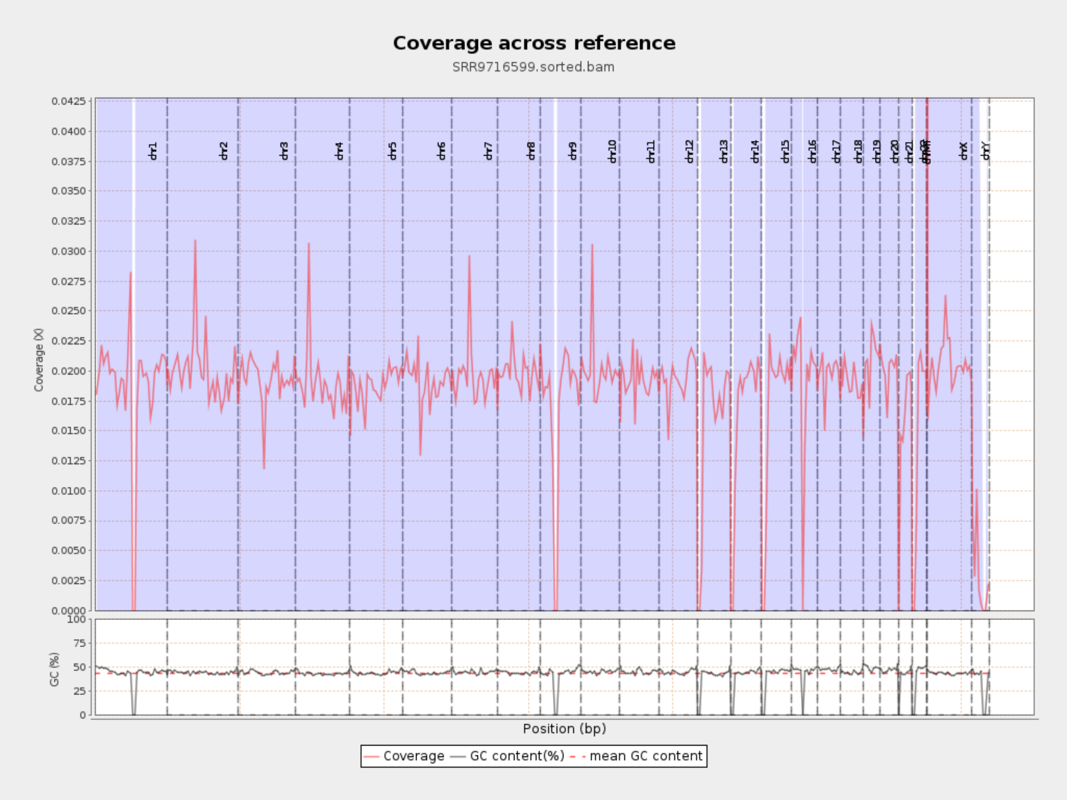
General error rate	0.52%
Mismatches	287,173
Insertions	4,219
Mapped reads with at least one insertion	0.43%
Deletions	10,764
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.15%

2.6. Chromosome stats

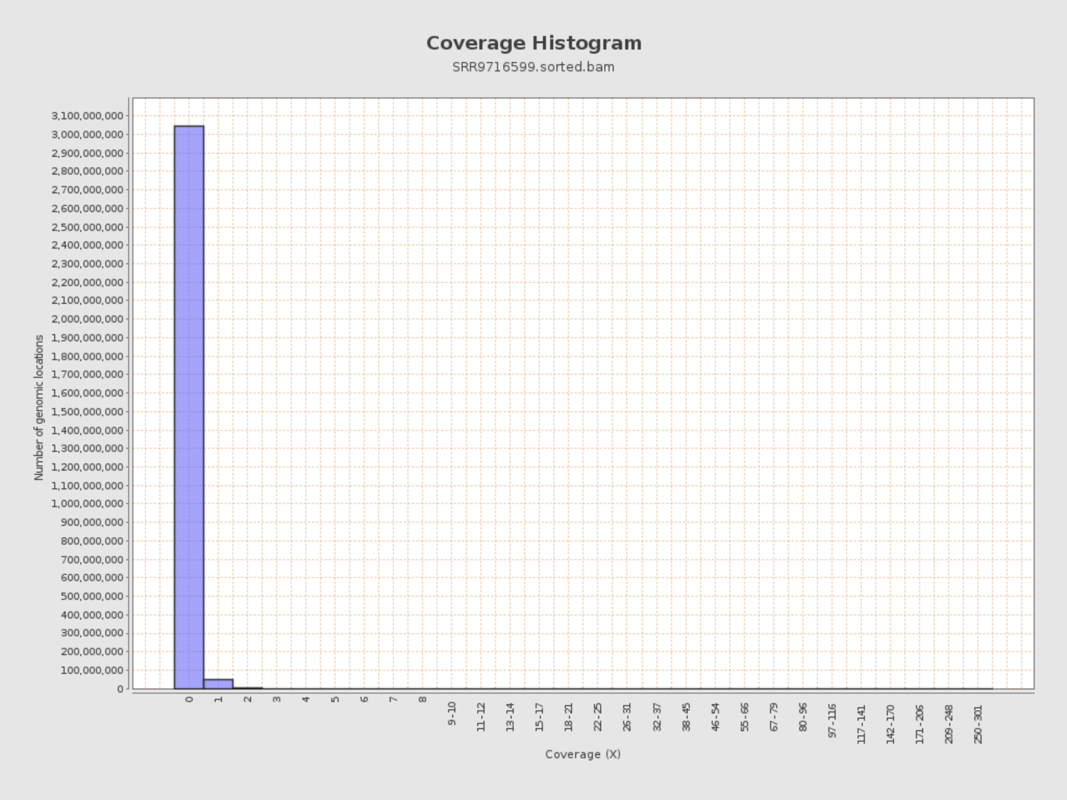
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4652220	0.0187	0.2647
chr2	243199373	4869317	0.02	0.2118
chr3	198022430	3816210	0.0193	0.1476
chr4	191154276	3652495	0.0191	0.1587
chr5	180915260	3428194	0.0189	0.1463
chr6	171115067	3269251	0.0191	0.1549
chr7	159138663	3141227	0.0197	0.2228

chr8	146364022	2919970	0.02	0.1915
chr9	141213431	2395810	0.017	0.1567
chr10	135534747	2737902	0.0202	0.1857
chr11	135006516	2609909	0.0193	0.1692
chr12	133851895	2598924	0.0194	0.1485
chr13	115169878	1800144	0.0156	0.1325
chr14	107349540	1763365	0.0164	0.1397
chr15	102531392	1688703	0.0165	0.1378
chr16	90354753	1698907	0.0188	0.1513
chr17	81195210	1600483	0.0197	0.1568
chr18	78077248	1492915	0.0191	0.2484
chr19	59128983	1237394	0.0209	0.2191
chr20	63025520	1256502	0.0199	0.1521
chr21	48129895	746699	0.0155	0.1439
chr22	51304566	725166	0.0141	0.1262
chrMT	16571	5025	0.3032	0.5945
chrX	155270560	3186988	0.0205	0.159
chrY	59373566	174602	0.0029	0.0912

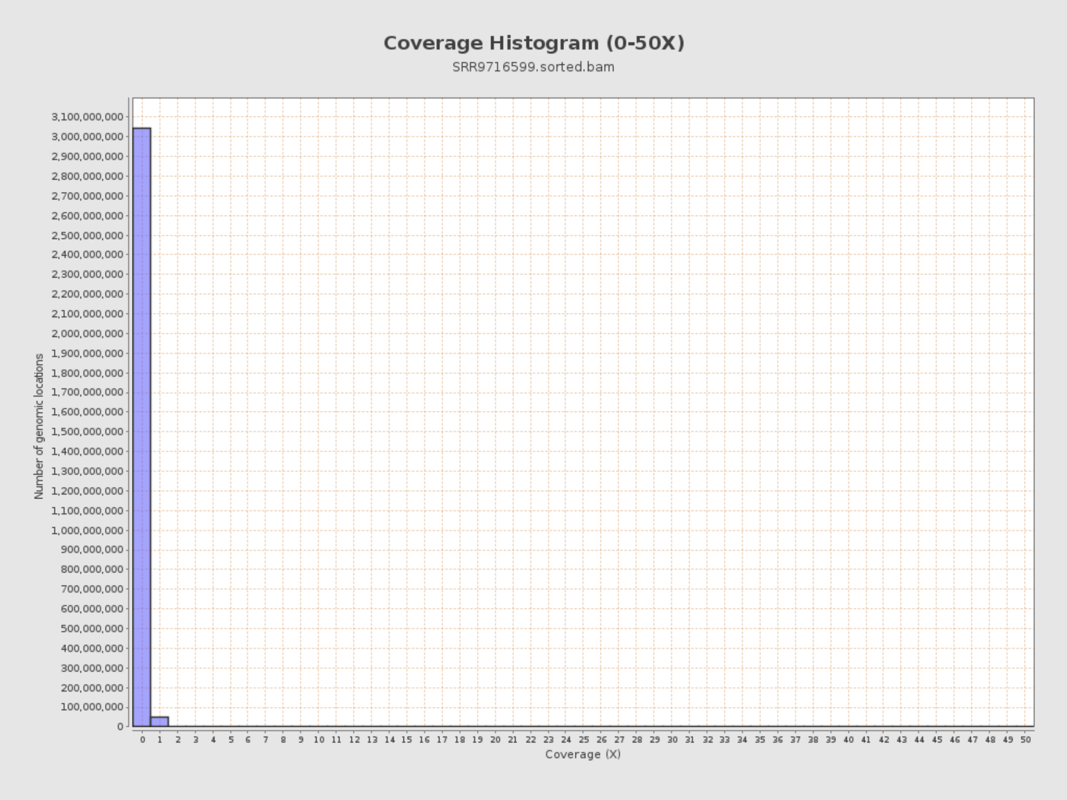
3. Results : Coverage across reference



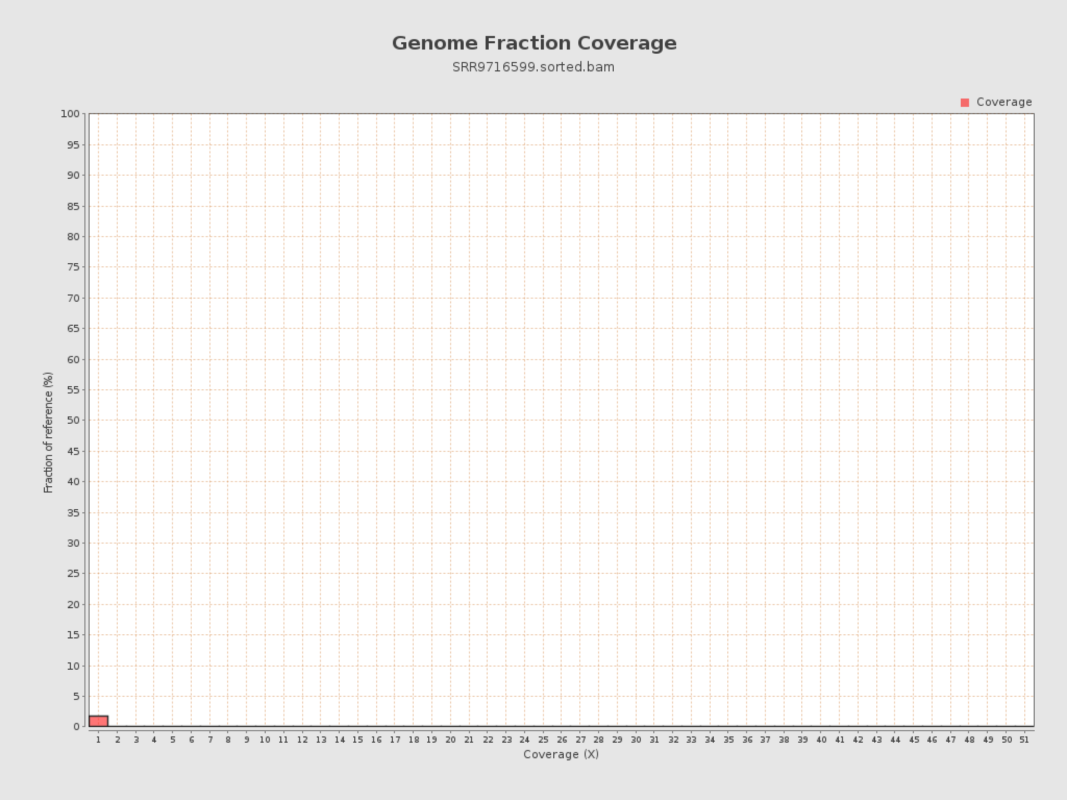
4. Results : Coverage Histogram



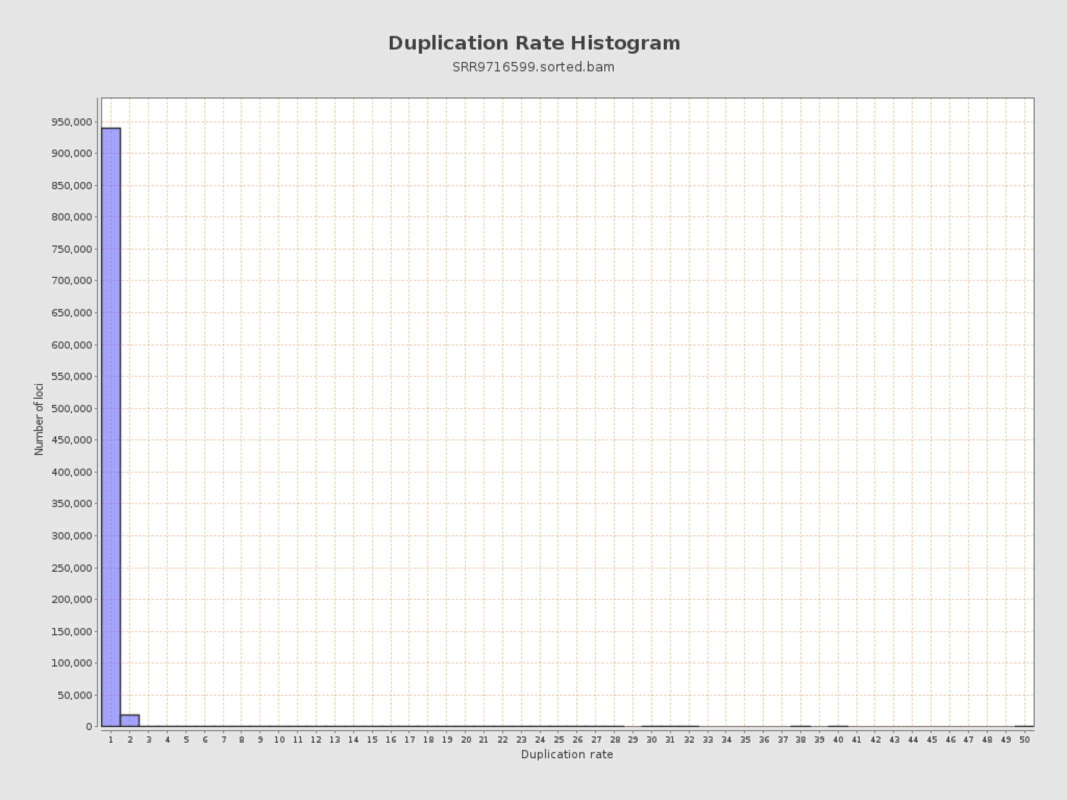
5. Results : Coverage Histogram (0-50X)



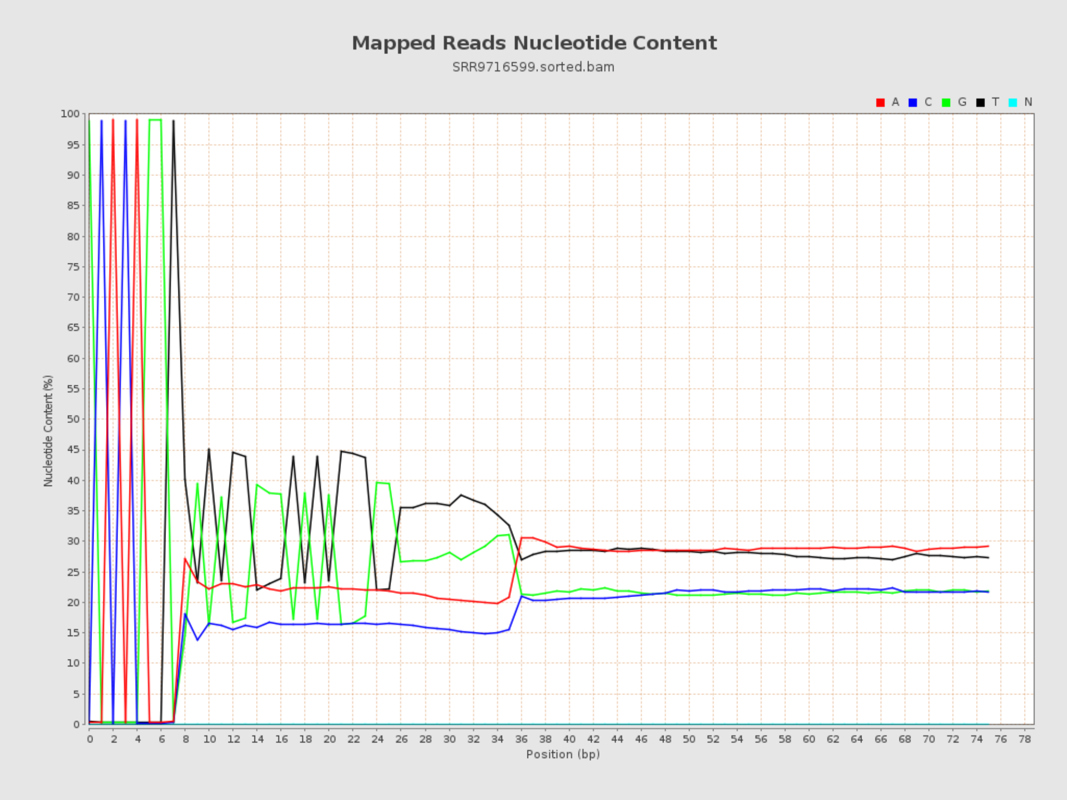
6. Results : Genome Fraction Coverage



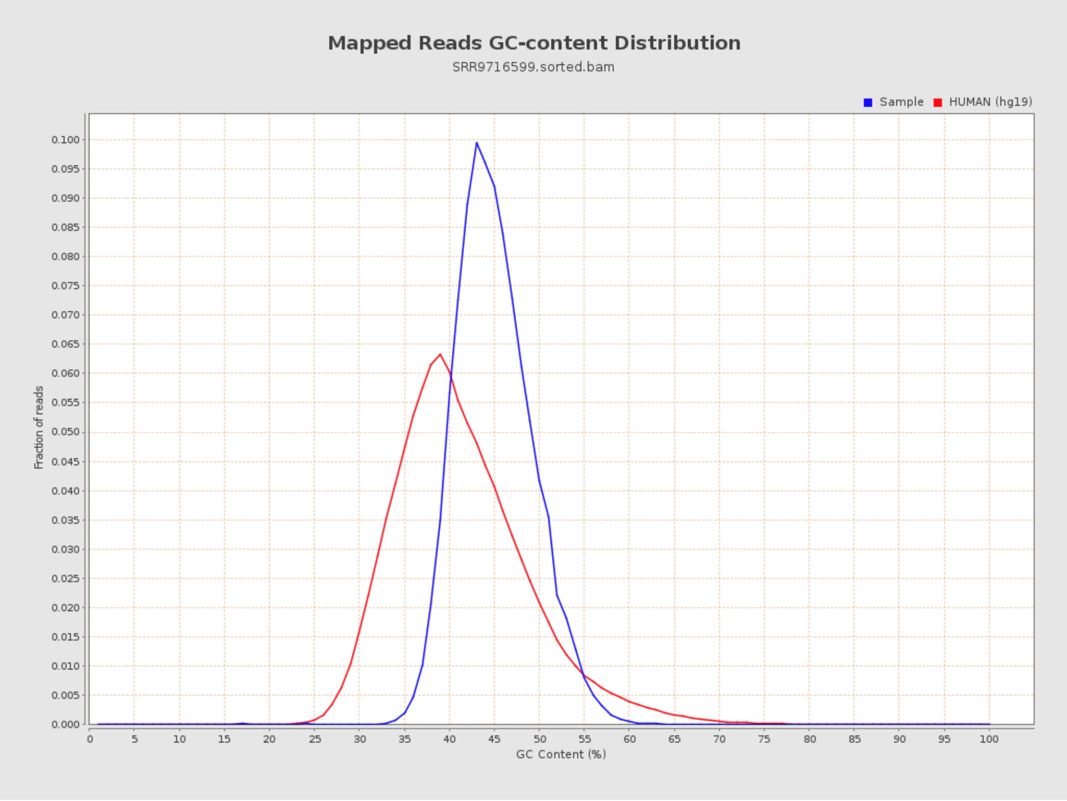
7. Results : Duplication Rate Histogram



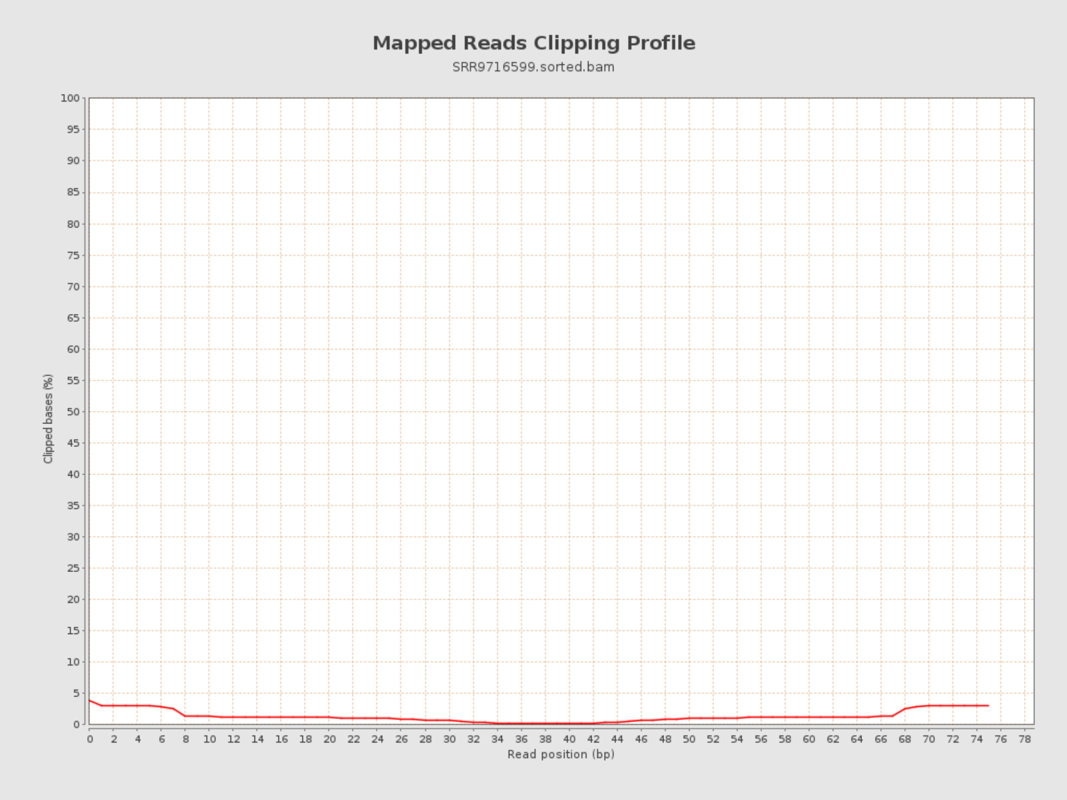
8. Results : Mapped Reads Nucleotide Content



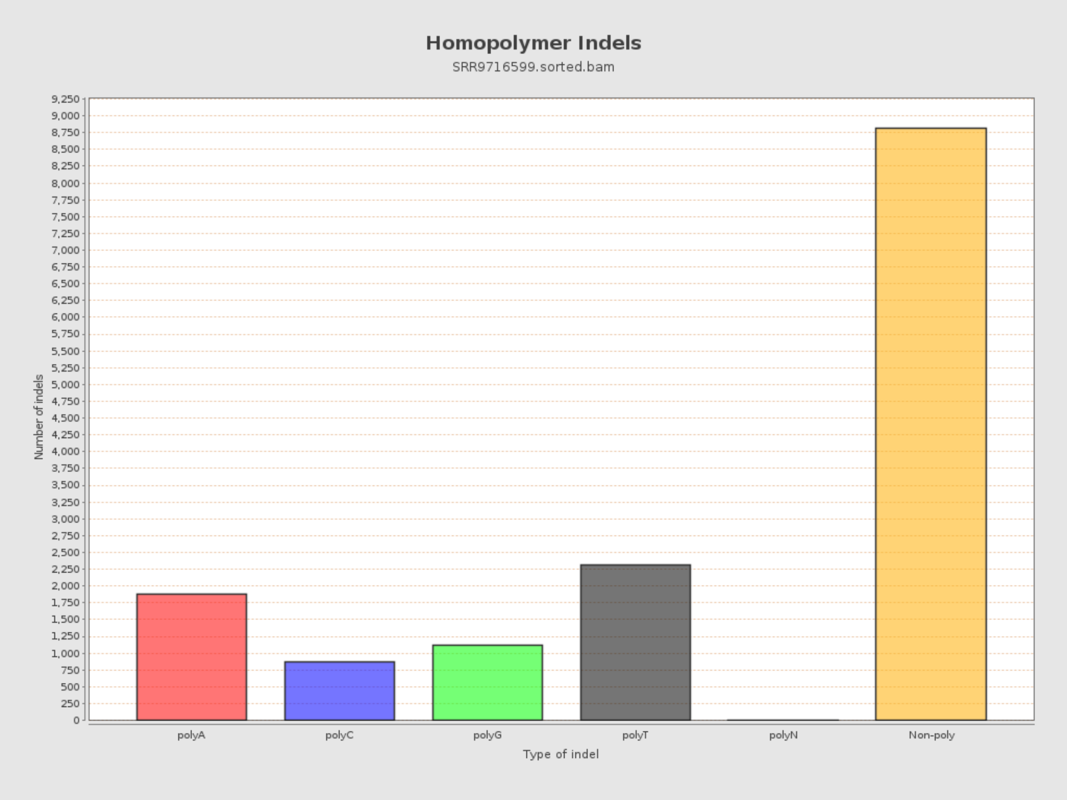
9. Results : Mapped Reads GC-content Distribution



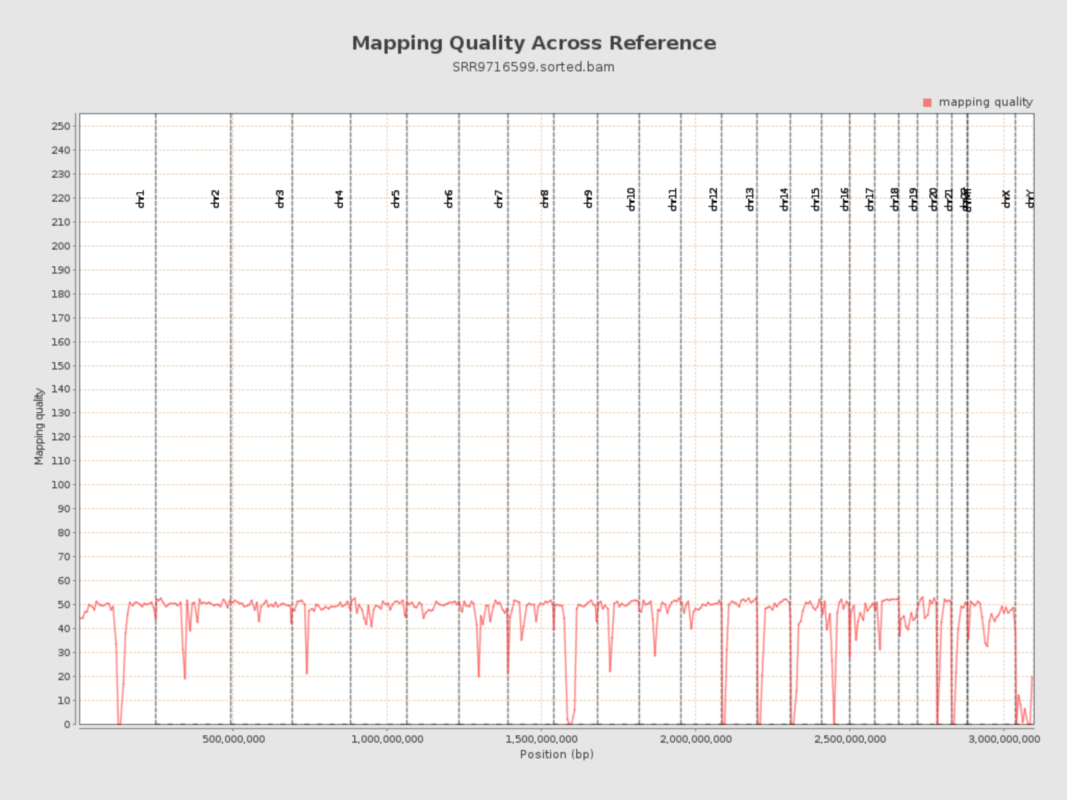
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram