Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:44:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716183.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_SRR9716183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:44:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,370,762
Mapped reads	1,161,535 / 84.74%
Unmapped reads	209,227 / 15.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,515 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,047 / 1.75%
Duplication rate	1.44%
Clipped reads	1,163,134 / 84.85%

2.2. ACGT Content

Number/percentage of A's	15,854,680 / 23.98%
Number/percentage of C's	12,404,874 / 18.76%
Number/percentage of T's	21,182,700 / 32.03%
Number/percentage of G's	16,682,796 / 25.23%
Number/percentage of N's	572 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.1954

2.4. Mapping Quality

Mean Mapping Quality	42.44

2.5. Mismatches and indels

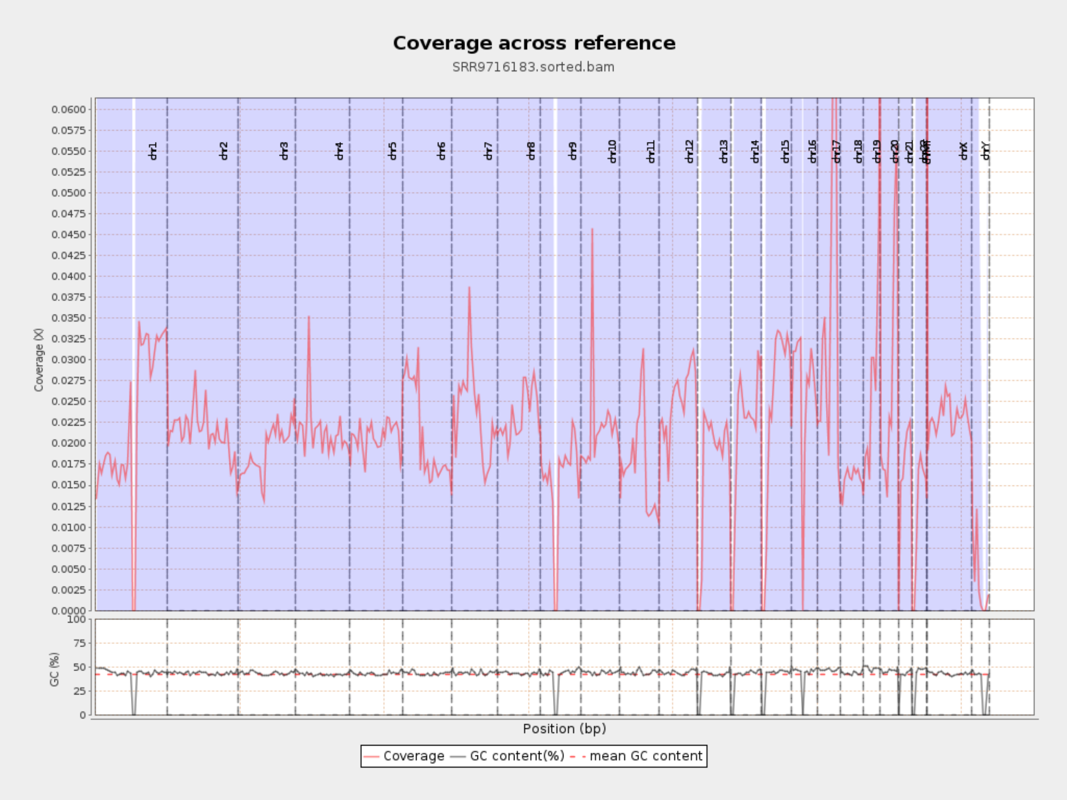
General error rate	0.54%
Mismatches	348,077
Insertions	4,619
Mapped reads with at least one insertion	0.4%
Deletions	12,539
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.95%

2.6. Chromosome stats

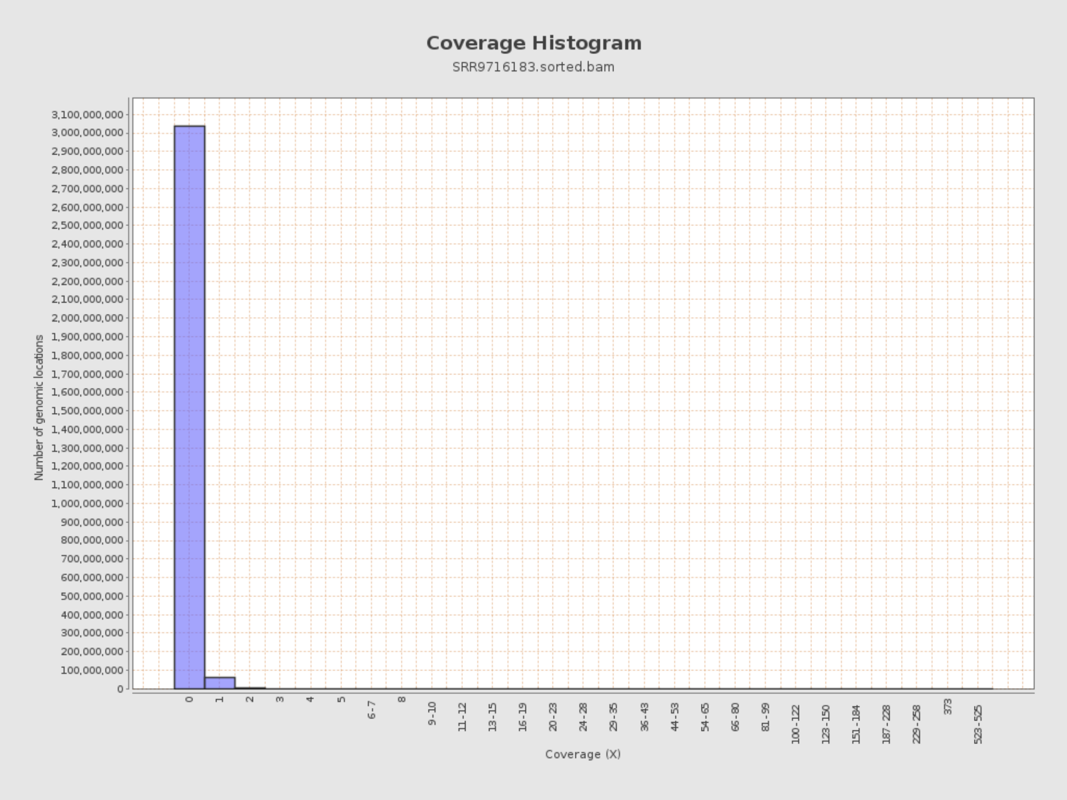
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5644961	0.0226	0.2379
chr2	243199373	5205115	0.0214	0.2679
chr3	198022430	3786824	0.0191	0.1491
chr4	191154276	4113912	0.0215	0.1692
chr5	180915260	3778908	0.0209	0.1532
chr6	171115067	3606478	0.0211	0.1745
chr7	159138663	3775475	0.0237	0.2733

chr8	146364022	3426633	0.0234	0.1895
chr9	141213431	2197577	0.0156	0.1515
chr10	135534747	2991715	0.0221	0.2548
chr11	135006516	2366214	0.0175	0.1662
chr12	133851895	3357743	0.0251	0.1685
chr13	115169878	2020371	0.0175	0.1402
chr14	107349540	2263783	0.0211	0.1591
chr15	102531392	2474991	0.0241	0.1682
chr16	90354753	2338058	0.0259	0.1829
chr17	81195210	2910900	0.0359	0.21
chr18	78077248	1232204	0.0158	0.2166
chr19	59128983	1646486	0.0278	0.2413
chr20	63025520	1753030	0.0278	0.1827
chr21	48129895	822773	0.0171	0.148
chr22	51304566	615093	0.012	0.1157
chrMT	16571	4286	0.2586	0.5612
chrX	155270560	3602081	0.0232	0.1683
chrY	59373566	209889	0.0035	0.102

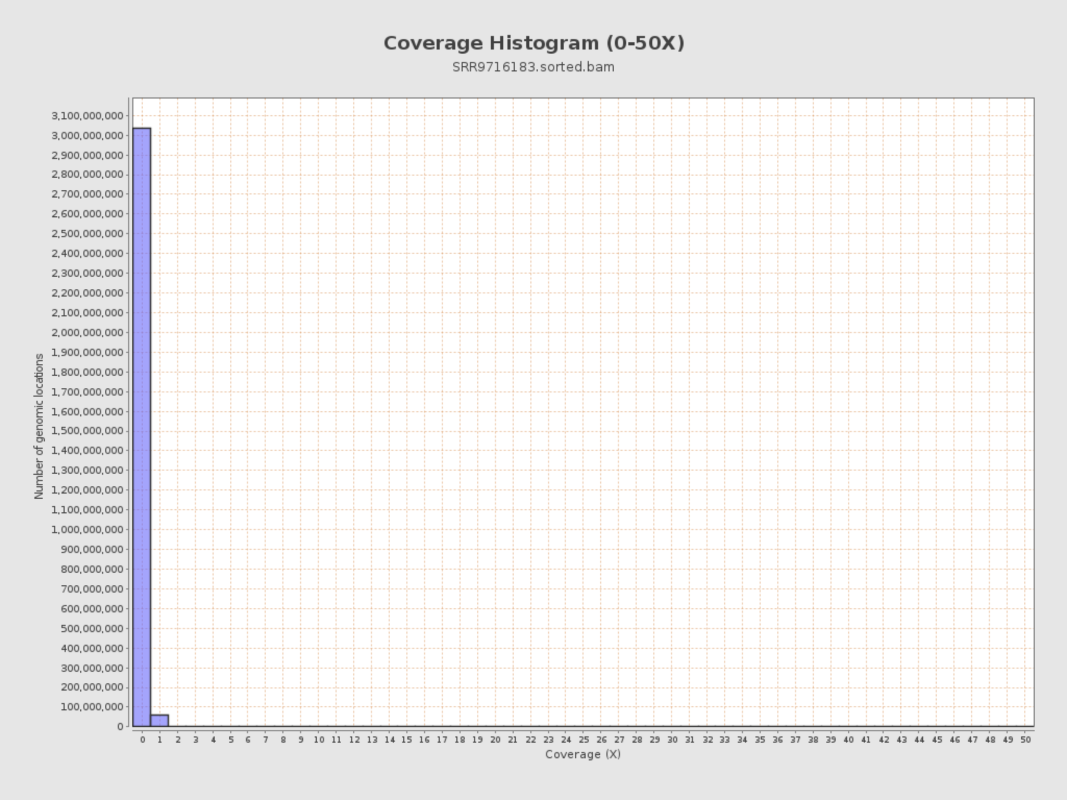
3. Results : Coverage across reference



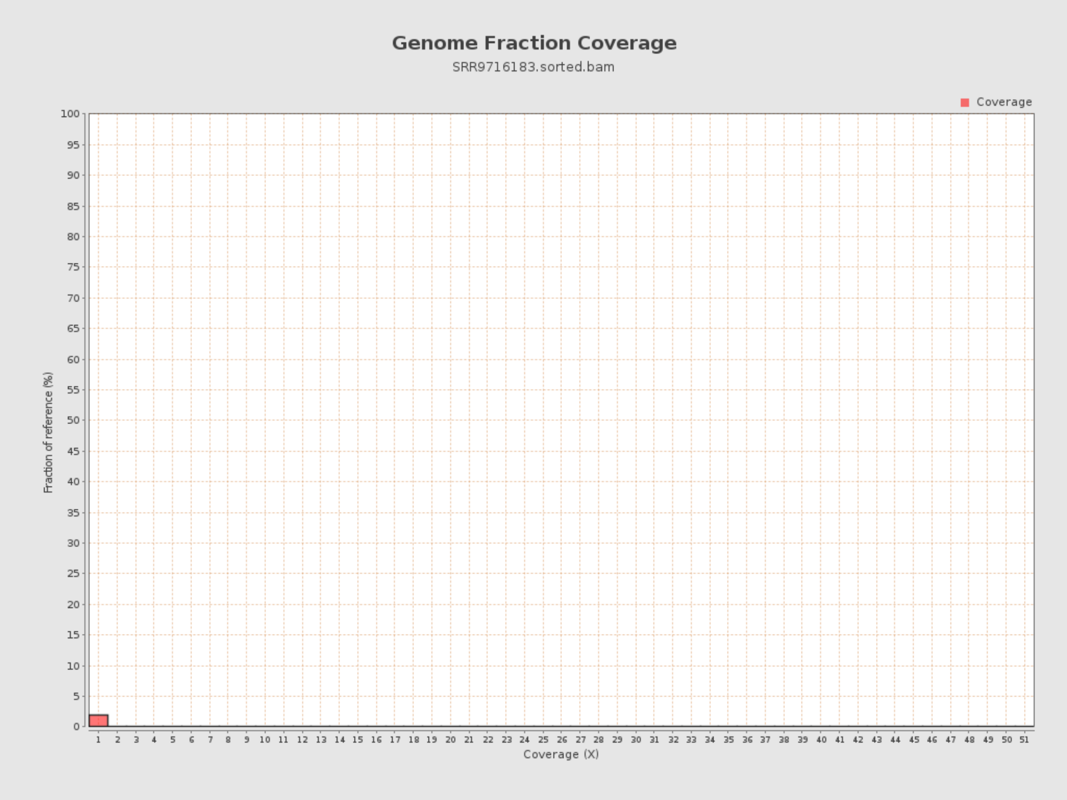
4. Results : Coverage Histogram



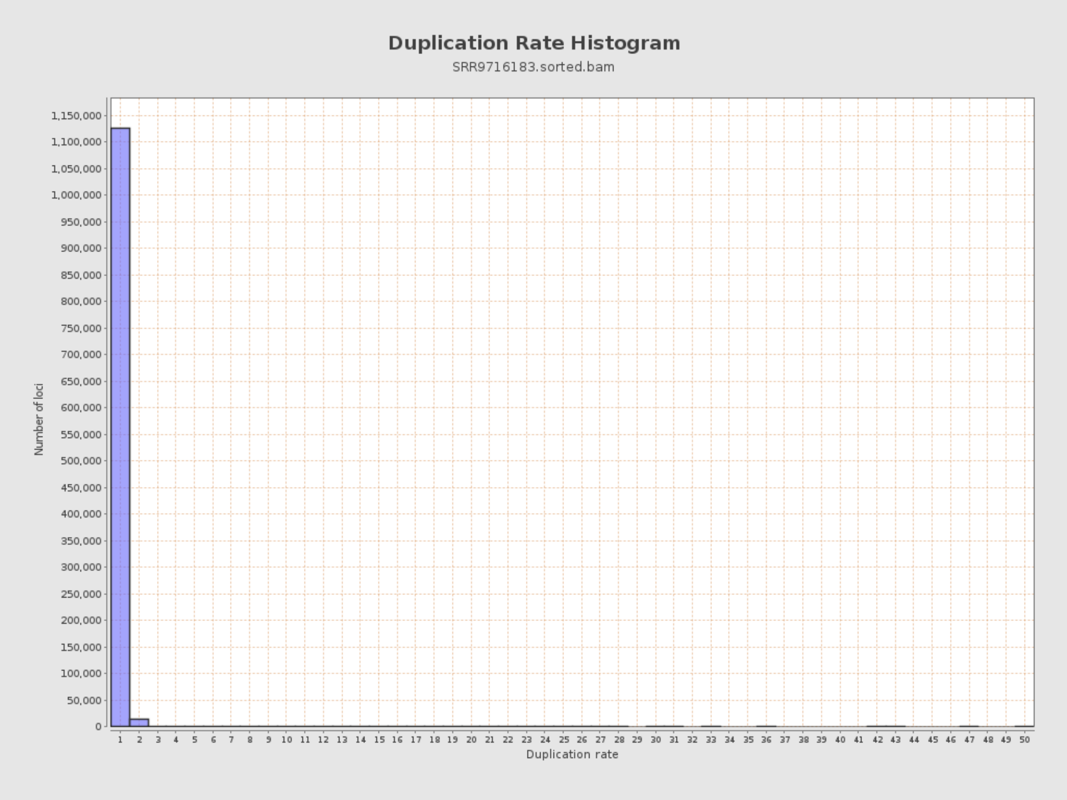
5. Results : Coverage Histogram (0-50X)



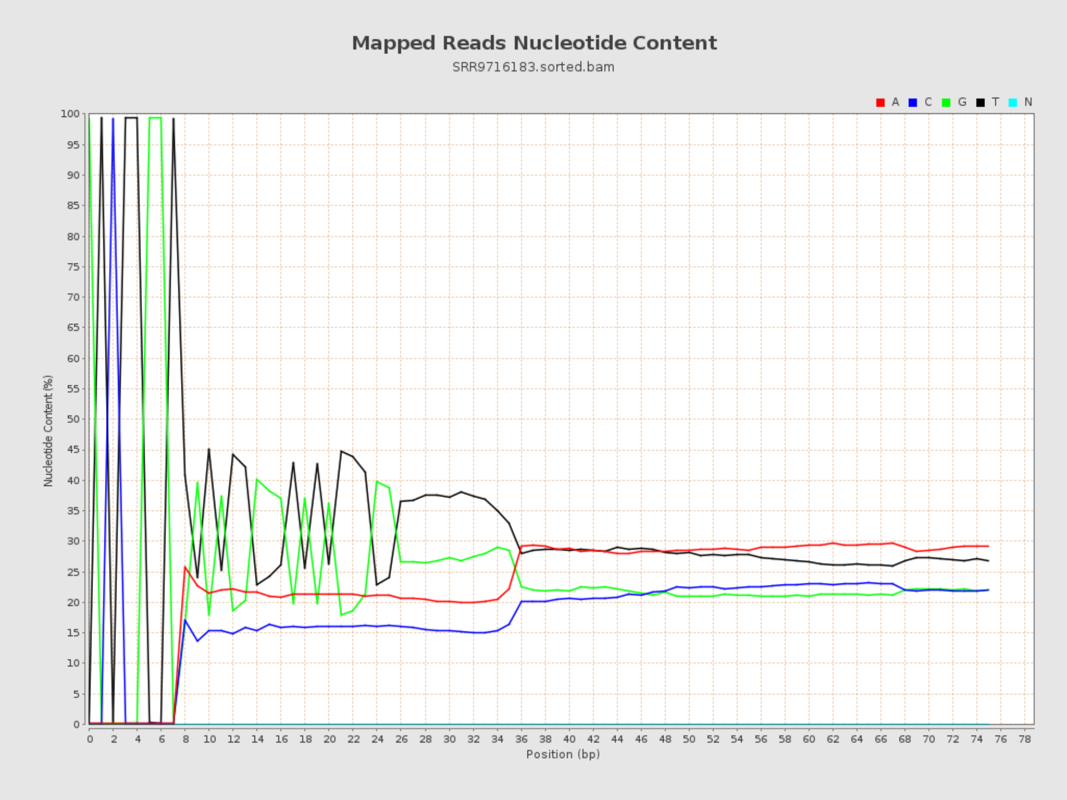
6. Results : Genome Fraction Coverage



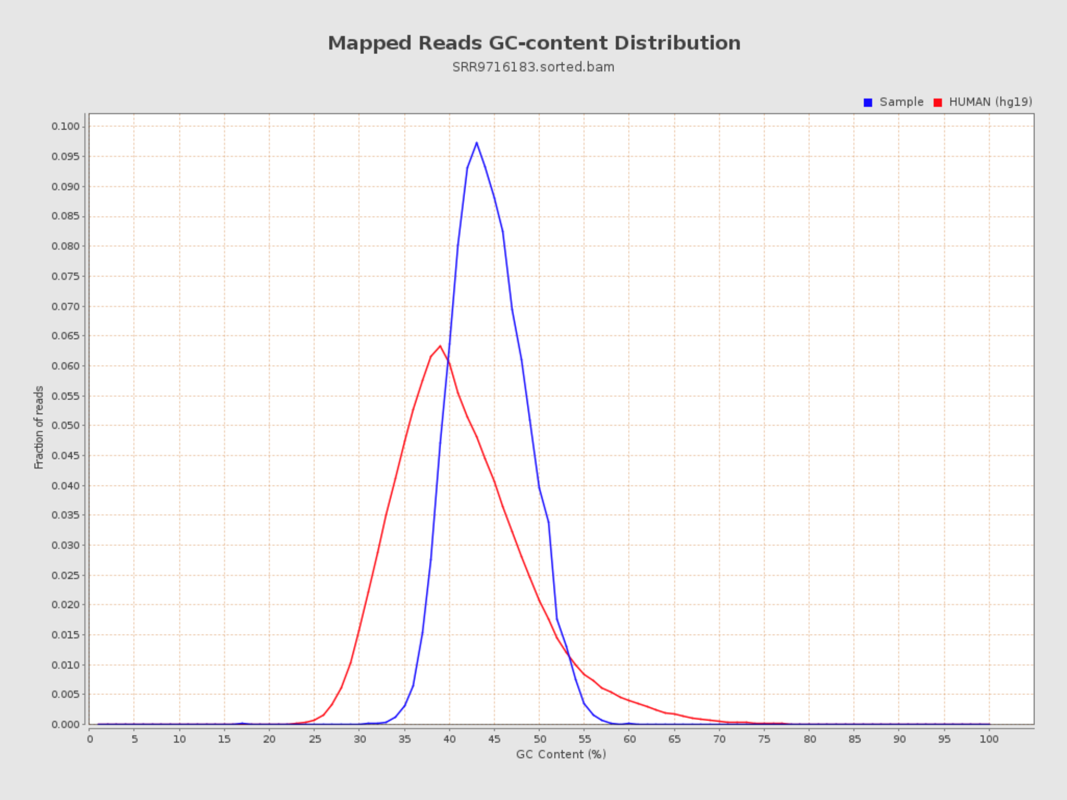
7. Results : Duplication Rate Histogram



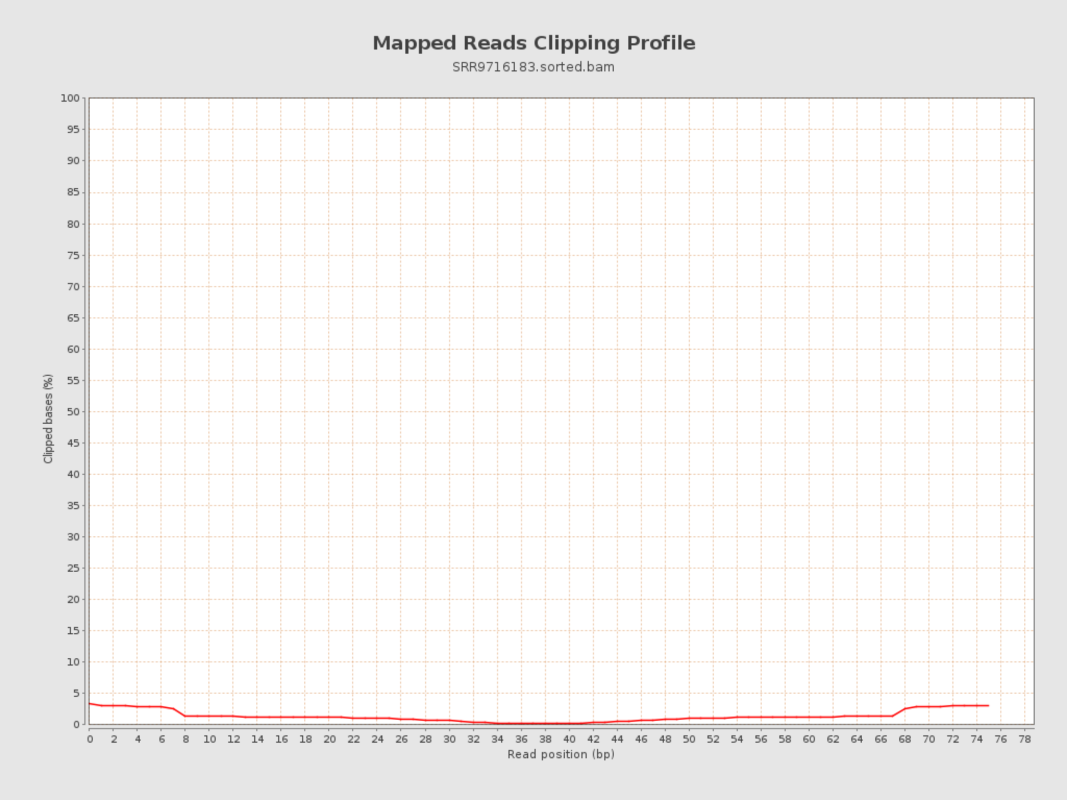
8. Results : Mapped Reads Nucleotide Content



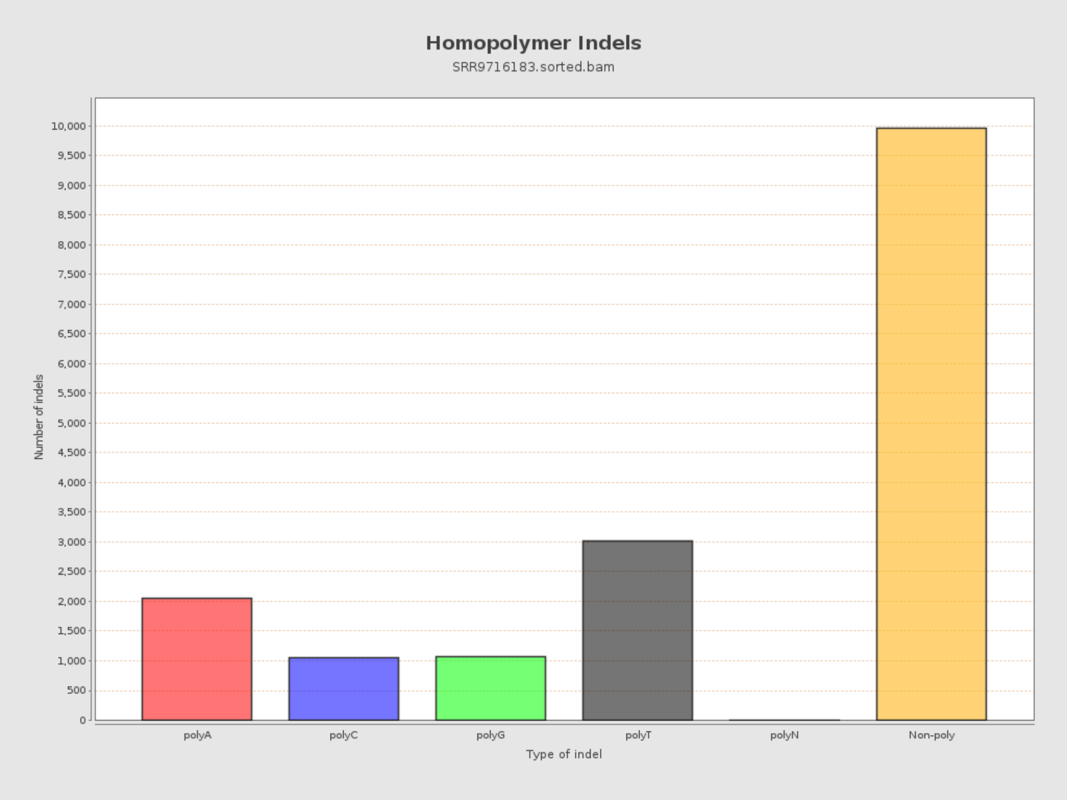
9. Results : Mapped Reads GC-content Distribution



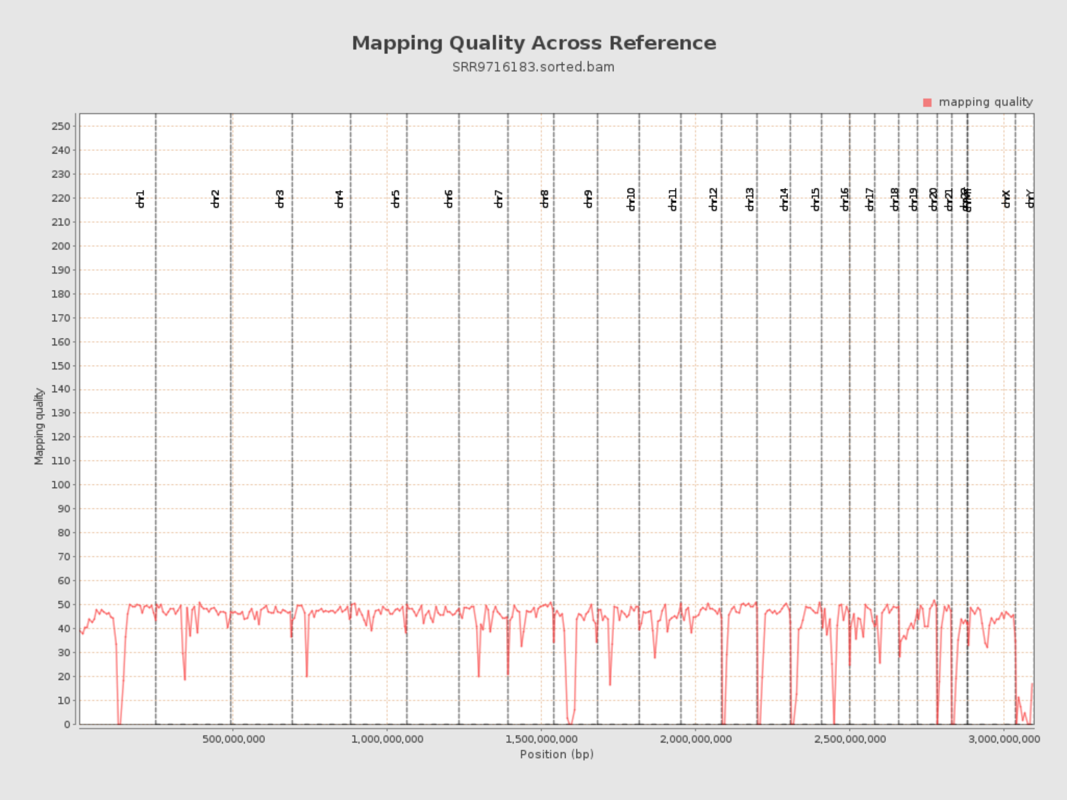
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram