Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:46:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716544.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_SRR9716544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716544.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:46:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	723,696
Mapped reads	630,561 / 87.13%
Unmapped reads	93,135 / 12.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,763 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	17,037 / 2.35%
Duplication rate	2.14%
Clipped reads	631,721 / 87.29%

2.2. ACGT Content

Number/percentage of A's	9,281,978 / 25.42%
Number/percentage of C's	7,127,596 / 19.52%
Number/percentage of T's	11,476,926 / 31.44%
Number/percentage of G's	8,621,765 / 23.62%
Number/percentage of N's	1,068 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.1412

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

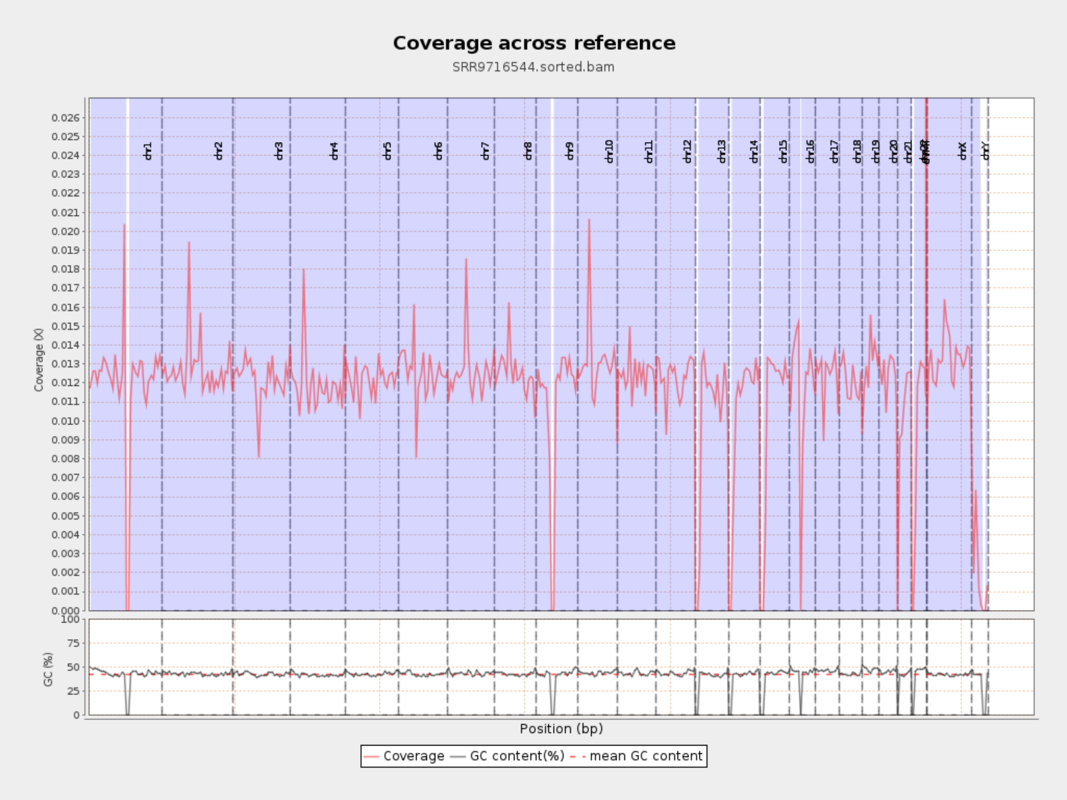
General error rate	0.52%
Mismatches	184,116
Insertions	2,419
Mapped reads with at least one insertion	0.38%
Deletions	6,922
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.84%

2.6. Chromosome stats

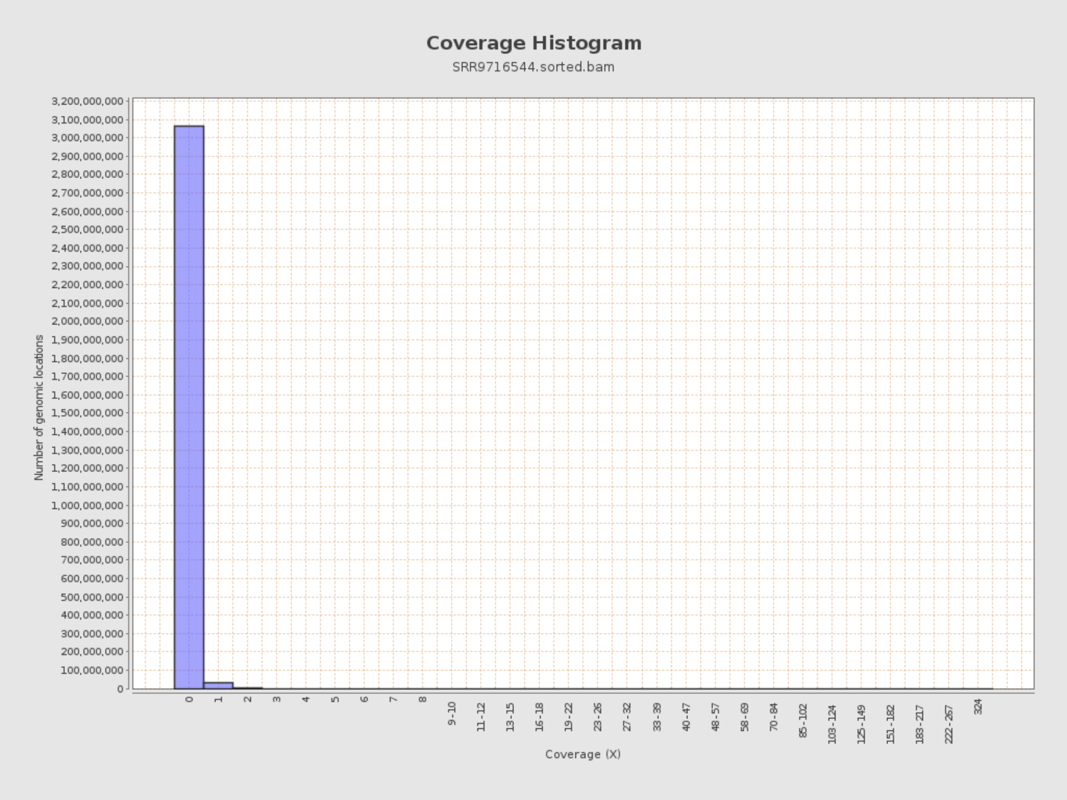
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2967816	0.0119	0.2279
chr2	243199373	3104677	0.0128	0.1807
chr3	198022430	2407416	0.0122	0.1161
chr4	191154276	2276566	0.0119	0.1185
chr5	180915260	2199079	0.0122	0.1166
chr6	171115067	2150839	0.0126	0.1286
chr7	159138663	2004997	0.0126	0.1574

chr8	146364022	1831857	0.0125	0.1351
chr9	141213431	1522021	0.0108	0.1219
chr10	135534747	1780576	0.0131	0.1393
chr11	135006516	1673441	0.0124	0.1301
chr12	133851895	1647616	0.0123	0.1179
chr13	115169878	1144507	0.0099	0.1048
chr14	107349540	1084635	0.0101	0.1065
chr15	102531392	1054567	0.0103	0.1064
chr16	90354753	1059317	0.0117	0.1166
chr17	81195210	1001307	0.0123	0.1189
chr18	78077248	950599	0.0122	0.1779
chr19	59128983	769989	0.013	0.1641
chr20	63025520	781901	0.0124	0.1175
chr21	48129895	481480	0.01	0.1094
chr22	51304566	448270	0.0087	0.0982
chrMT	16571	7771	0.469	0.7365
chrX	155270560	2055703	0.0132	0.1262
chrY	59373566	113213	0.0019	0.0617

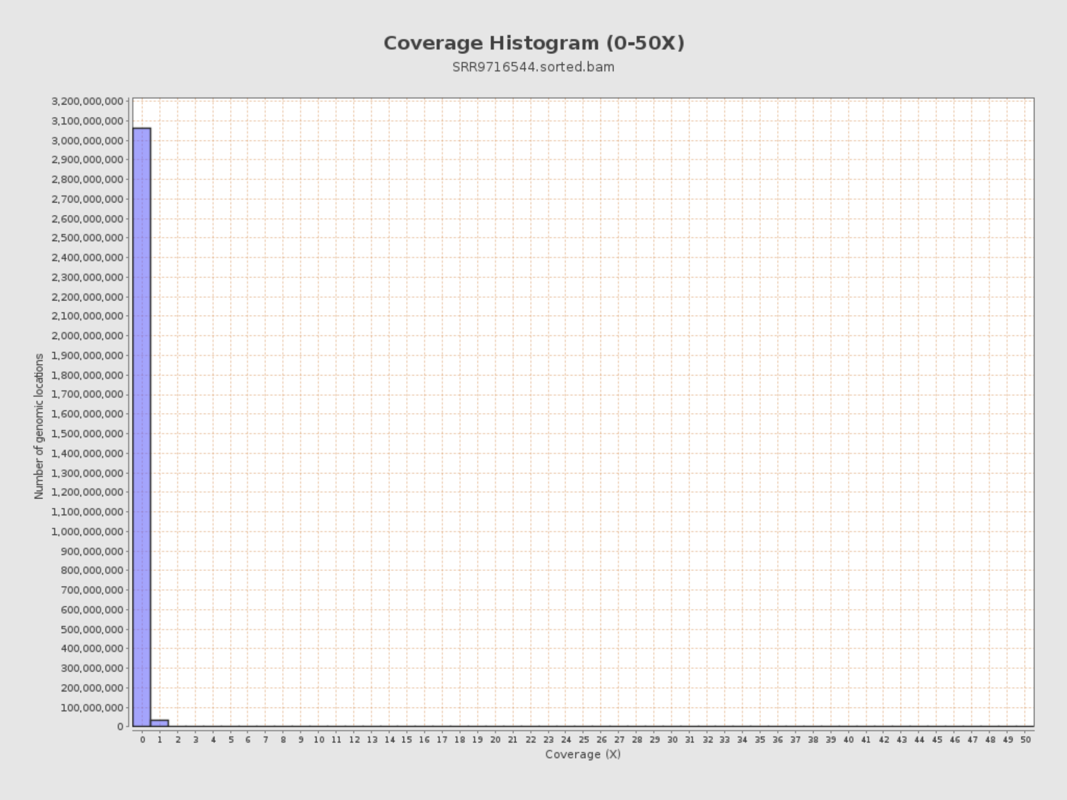
3. Results : Coverage across reference



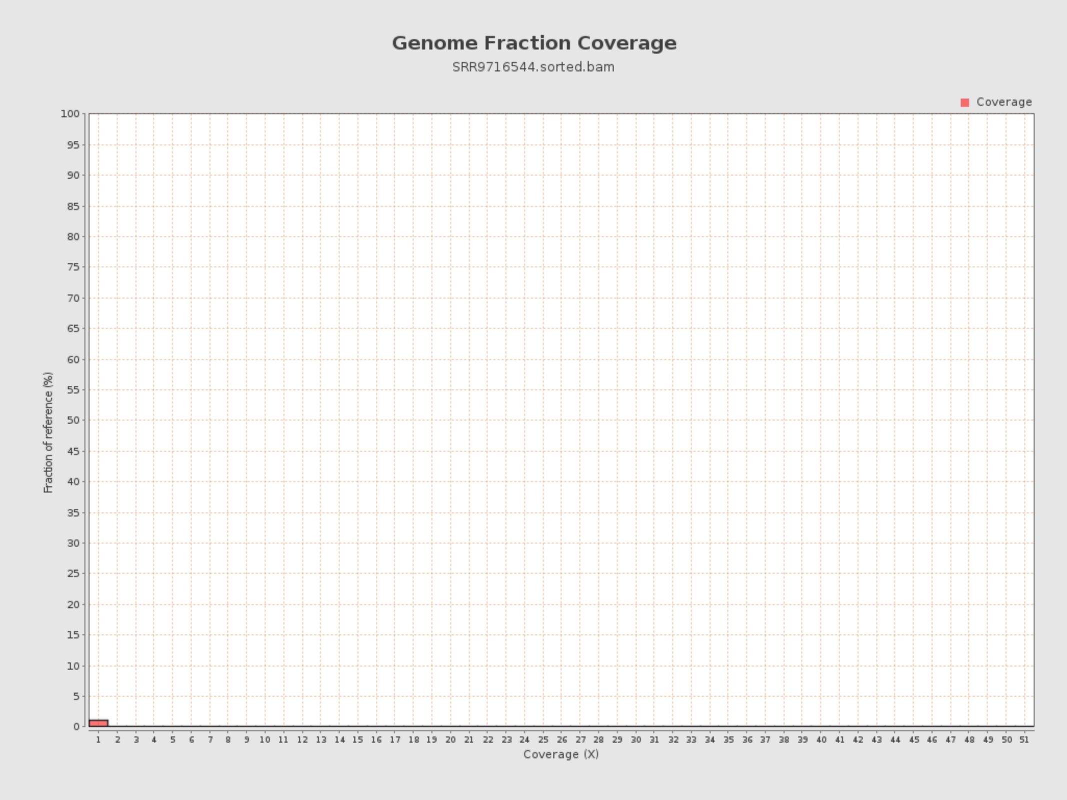
4. Results : Coverage Histogram



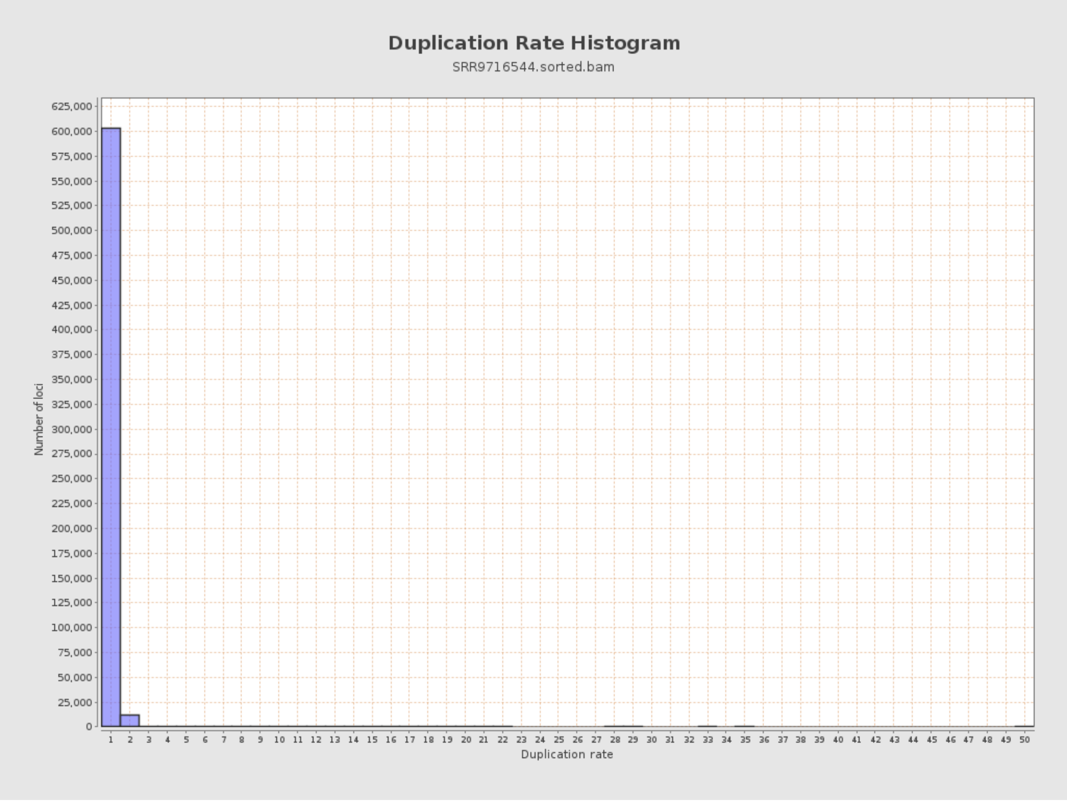
5. Results : Coverage Histogram (0-50X)



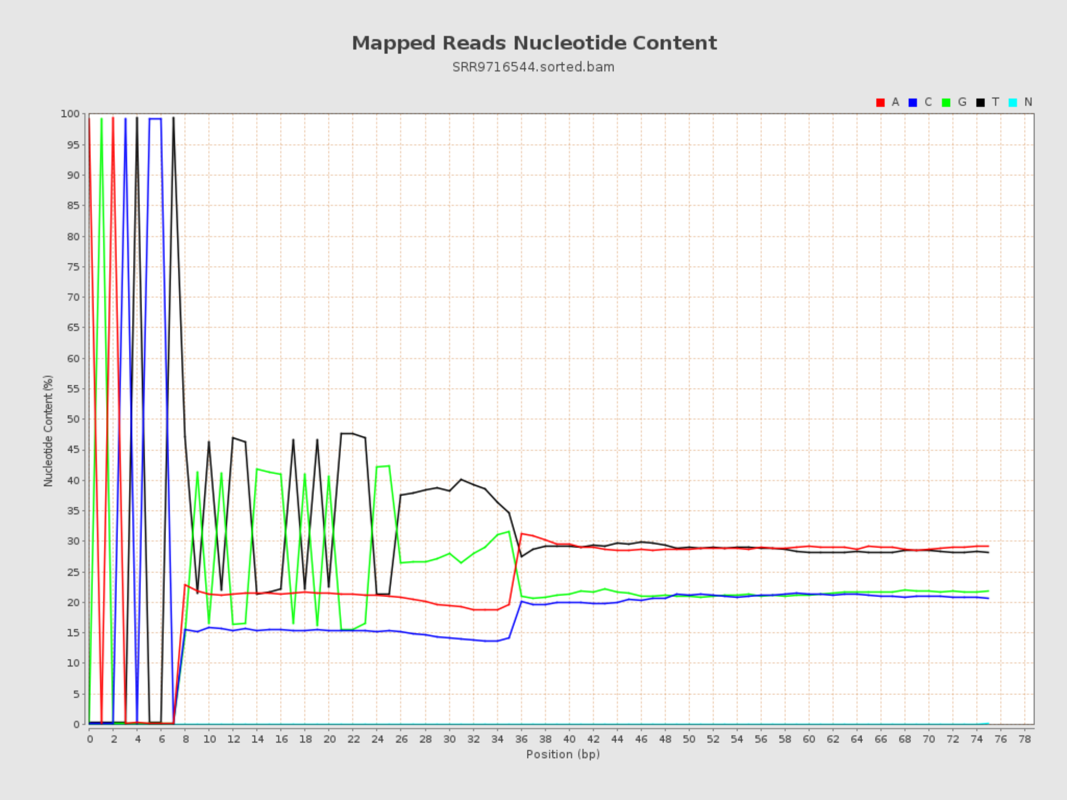
6. Results : Genome Fraction Coverage



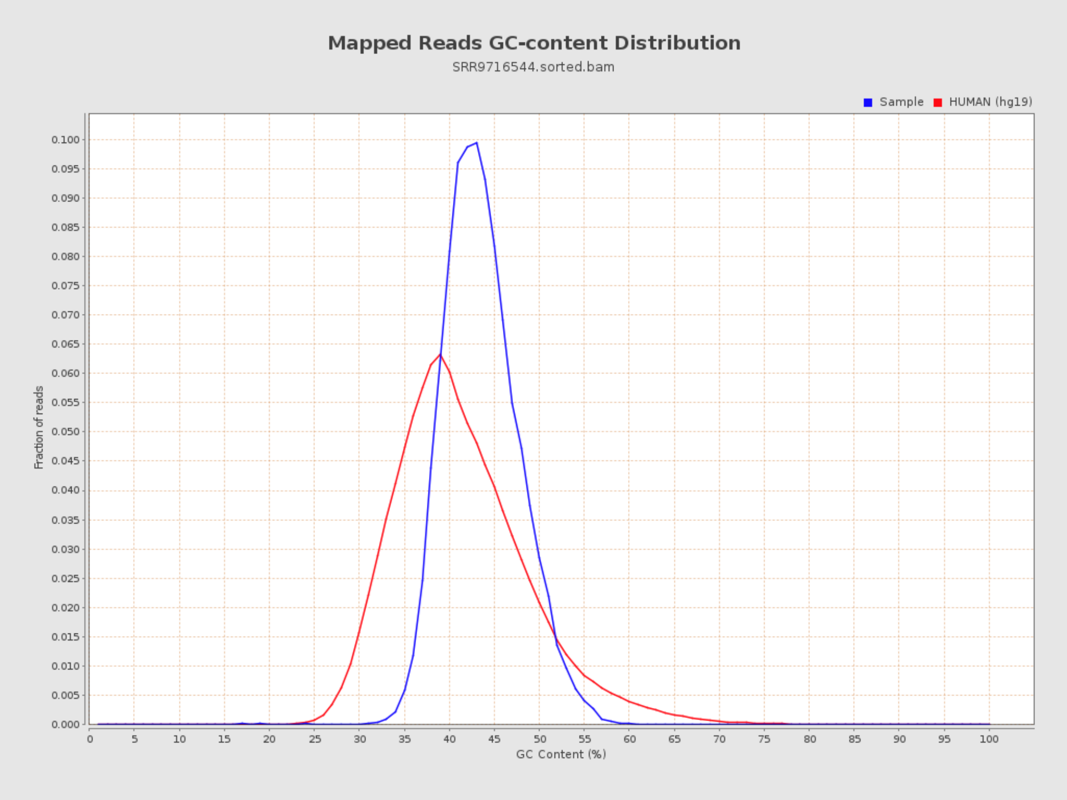
7. Results : Duplication Rate Histogram



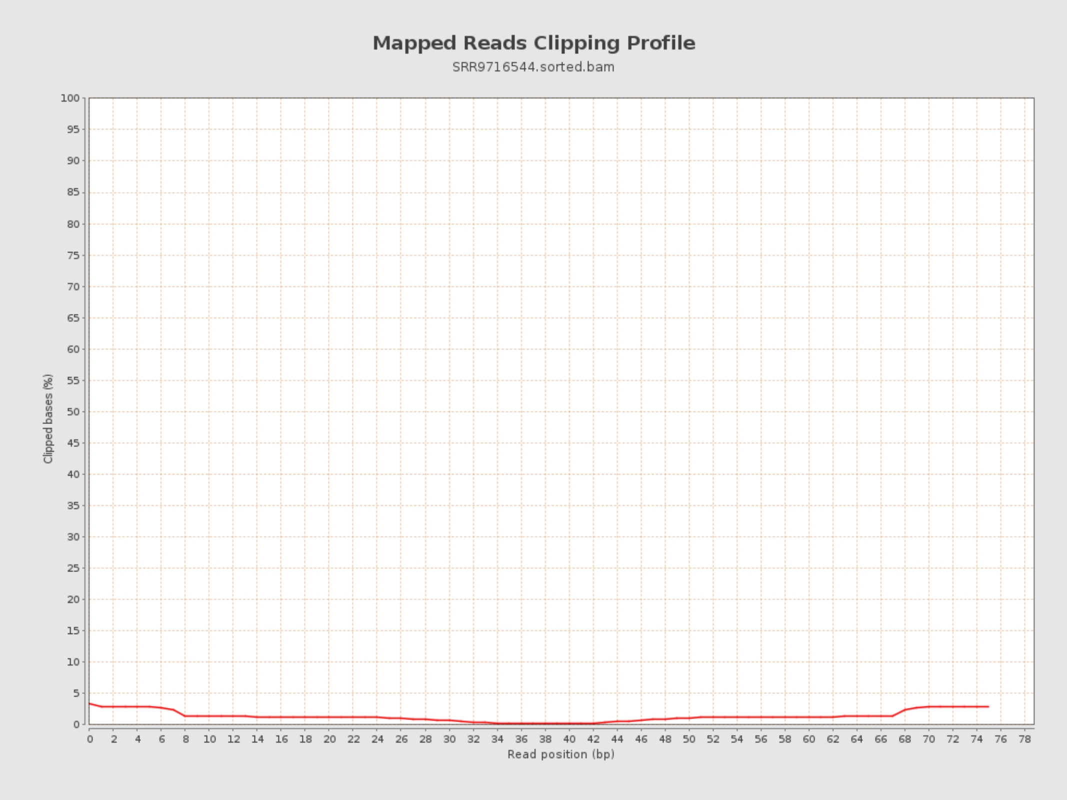
8. Results : Mapped Reads Nucleotide Content



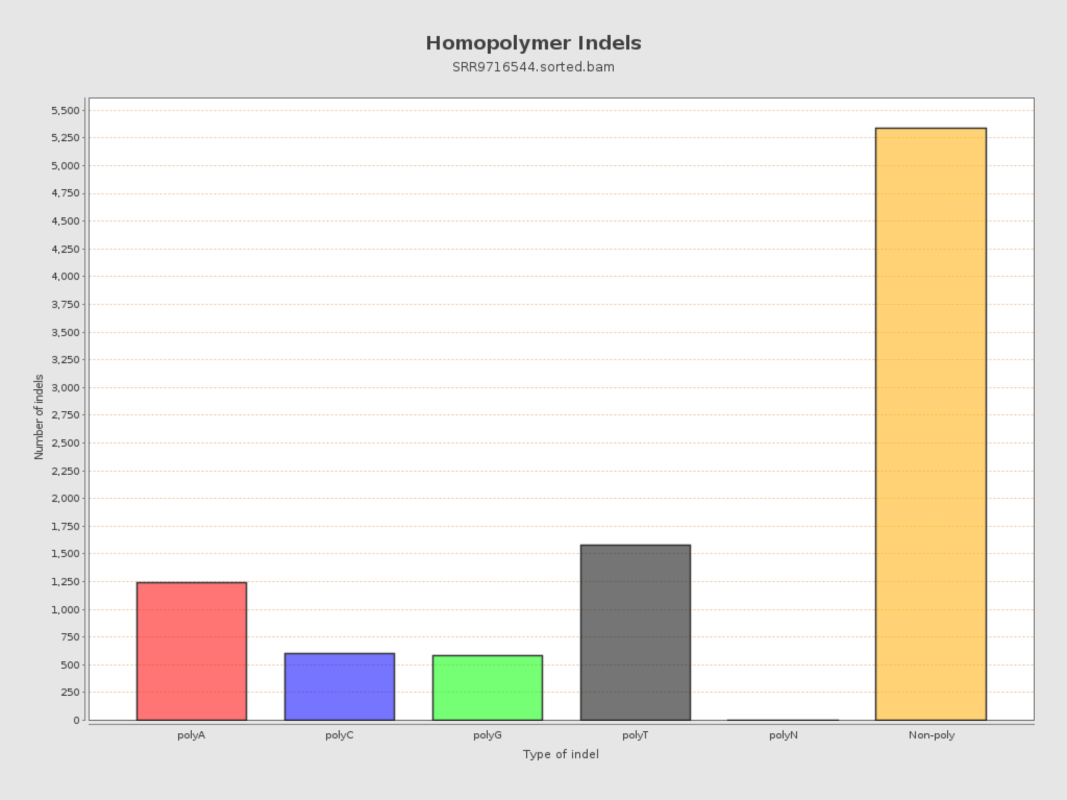
9. Results : Mapped Reads GC-content Distribution



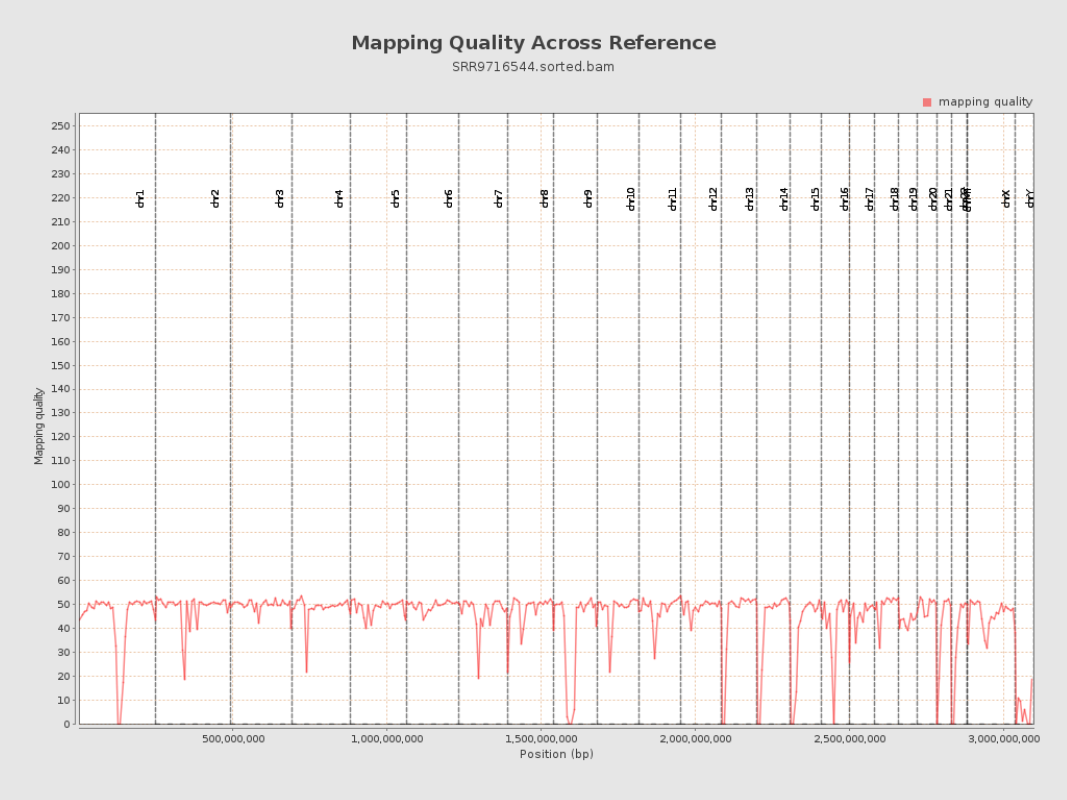
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram