Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:57:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716388.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_SRR9716388 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716388.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:57:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716388.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	928,265
Mapped reads	812,322 / 87.51%
Unmapped reads	115,943 / 12.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,825 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,589 / 1.57%
Duplication rate	1.24%
Clipped reads	813,923 / 87.68%

2.2. ACGT Content

Number/percentage of A's	11,010,539 / 24.06%
Number/percentage of C's	8,729,669 / 19.08%
Number/percentage of T's	14,646,040 / 32.01%
Number/percentage of G's	11,369,406 / 24.85%
Number/percentage of N's	327 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1533

2.4. Mapping Quality

Mean Mapping Quality	41.96

2.5. Mismatches and indels

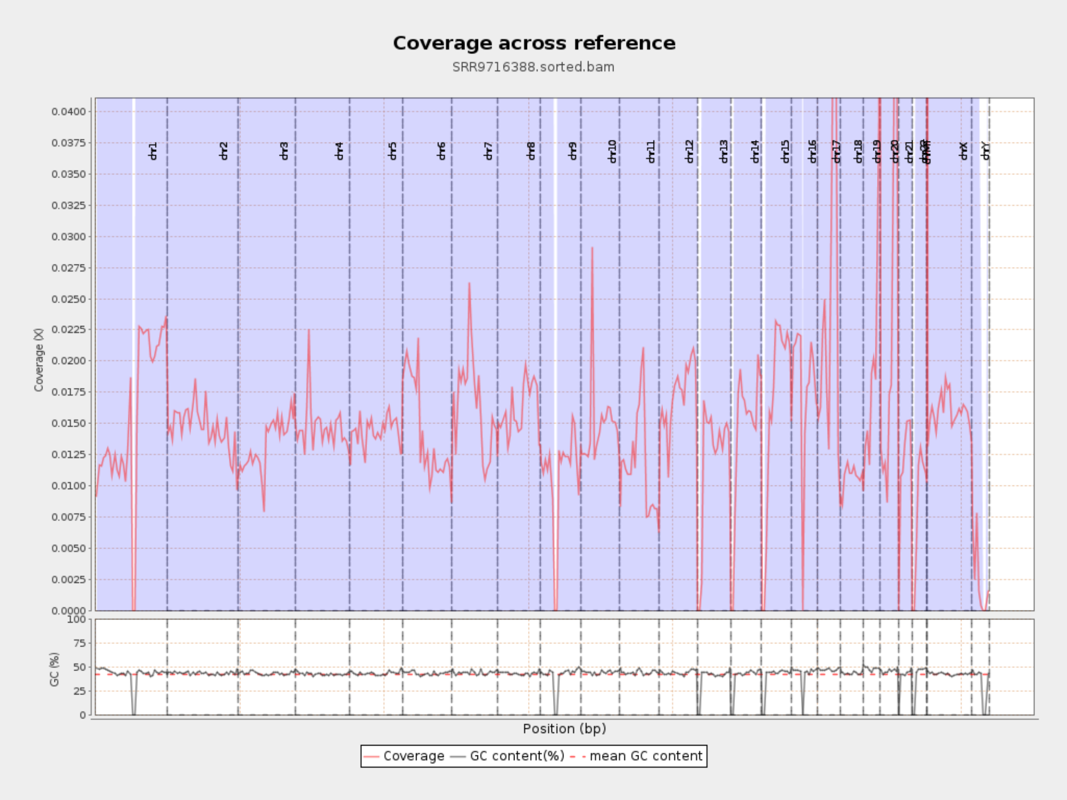
General error rate	0.54%
Mismatches	240,828
Insertions	2,988
Mapped reads with at least one insertion	0.37%
Deletions	8,955
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.12%

2.6. Chromosome stats

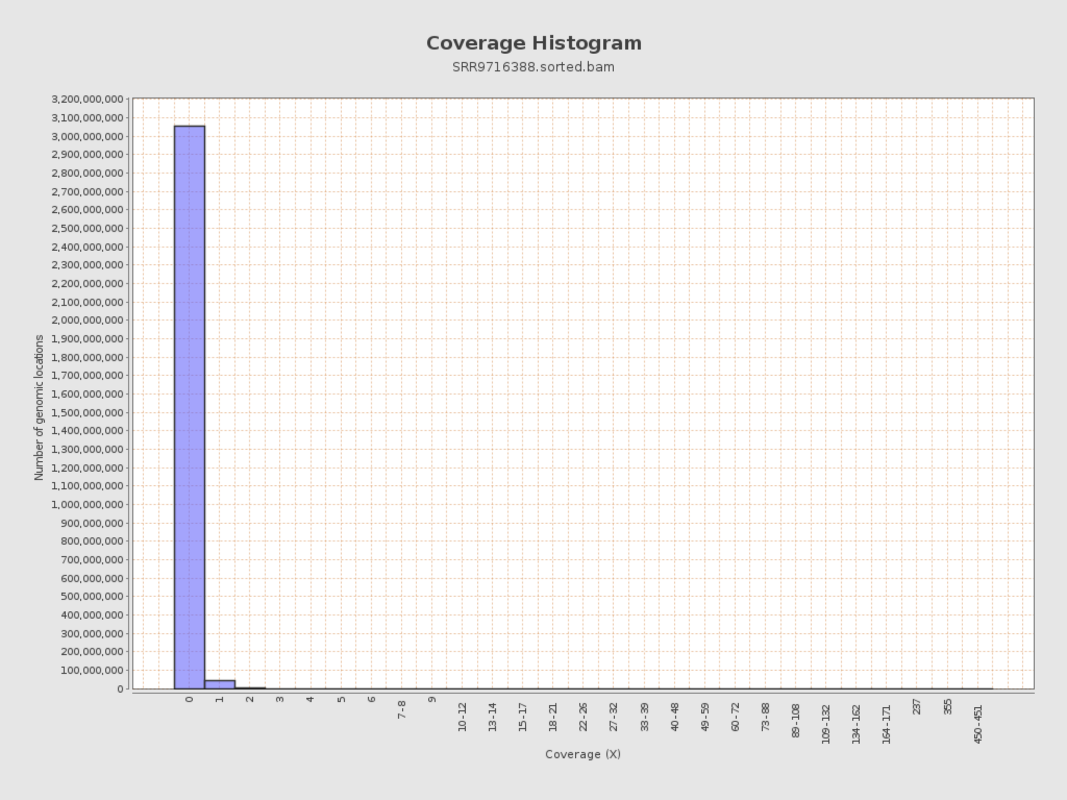
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3851818	0.0155	0.1809
chr2	243199373	3567955	0.0147	0.221
chr3	198022430	2637209	0.0133	0.1219
chr4	191154276	2819377	0.0147	0.1326
chr5	180915260	2614453	0.0145	0.1255
chr6	171115067	2465139	0.0144	0.1386
chr7	159138663	2633907	0.0166	0.2029

chr8	146364022	2368252	0.0162	0.1456
chr9	141213431	1522392	0.0108	0.1212
chr10	135534747	2024199	0.0149	0.178
chr11	135006516	1602802	0.0119	0.1312
chr12	133851895	2304162	0.0172	0.1375
chr13	115169878	1373810	0.0119	0.1139
chr14	107349540	1529918	0.0143	0.1285
chr15	102531392	1680499	0.0164	0.1367
chr16	90354753	1593909	0.0176	0.1447
chr17	81195210	2038294	0.0251	0.1711
chr18	78077248	835676	0.0107	0.153
chr19	59128983	1211405	0.0205	0.1815
chr20	63025520	1453146	0.0231	0.1643
chr21	48129895	567468	0.0118	0.1192
chr22	51304566	428488	0.0084	0.0955
chrMT	16571	17435	1.0521	1.2463
chrX	155270560	2485192	0.016	0.1372
chrY	59373566	143421	0.0024	0.0756

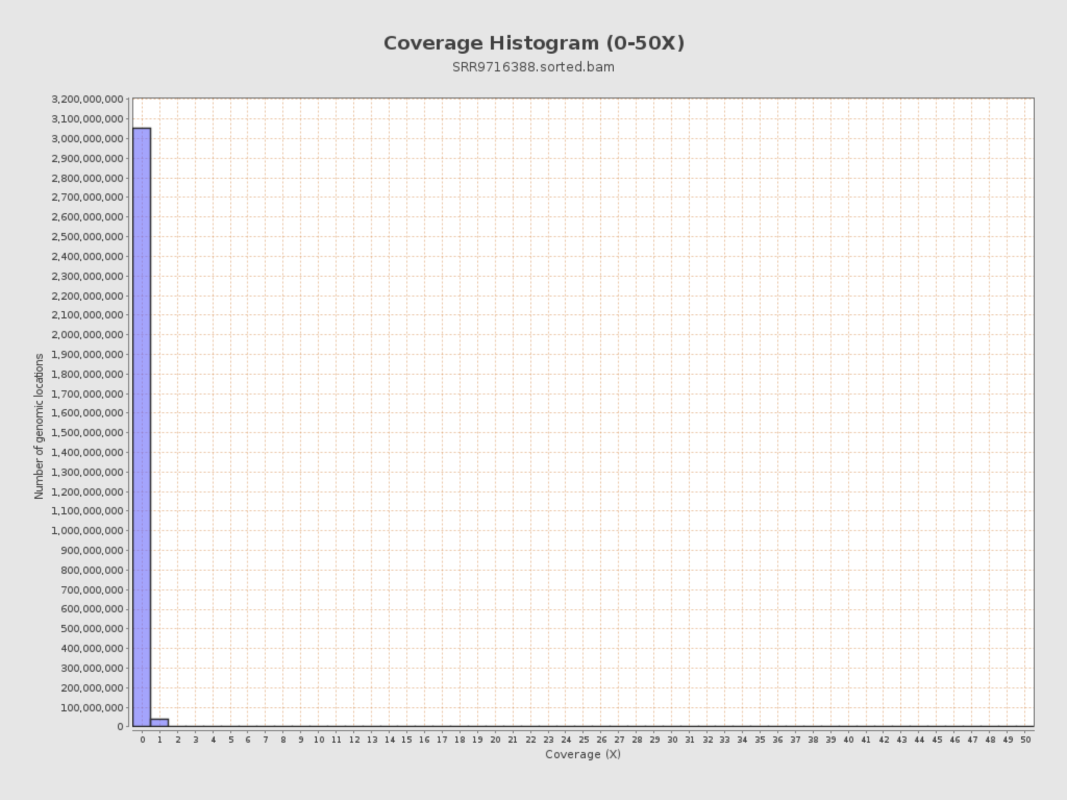
3. Results : Coverage across reference



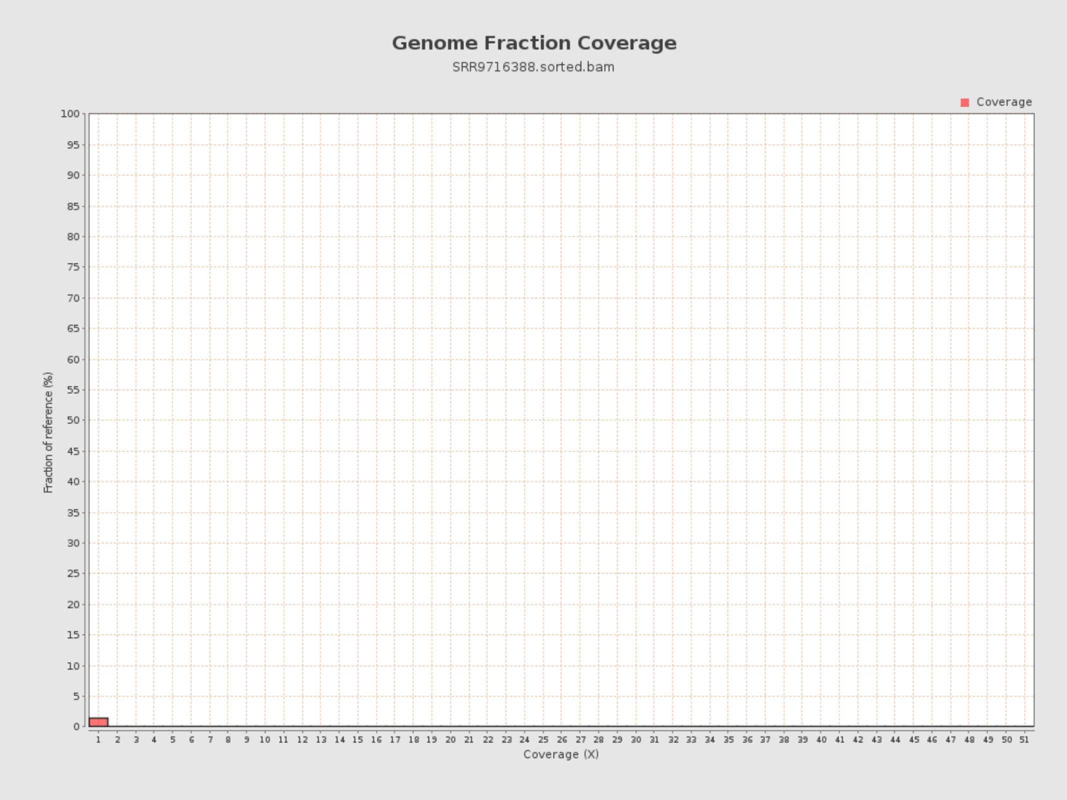
4. Results : Coverage Histogram



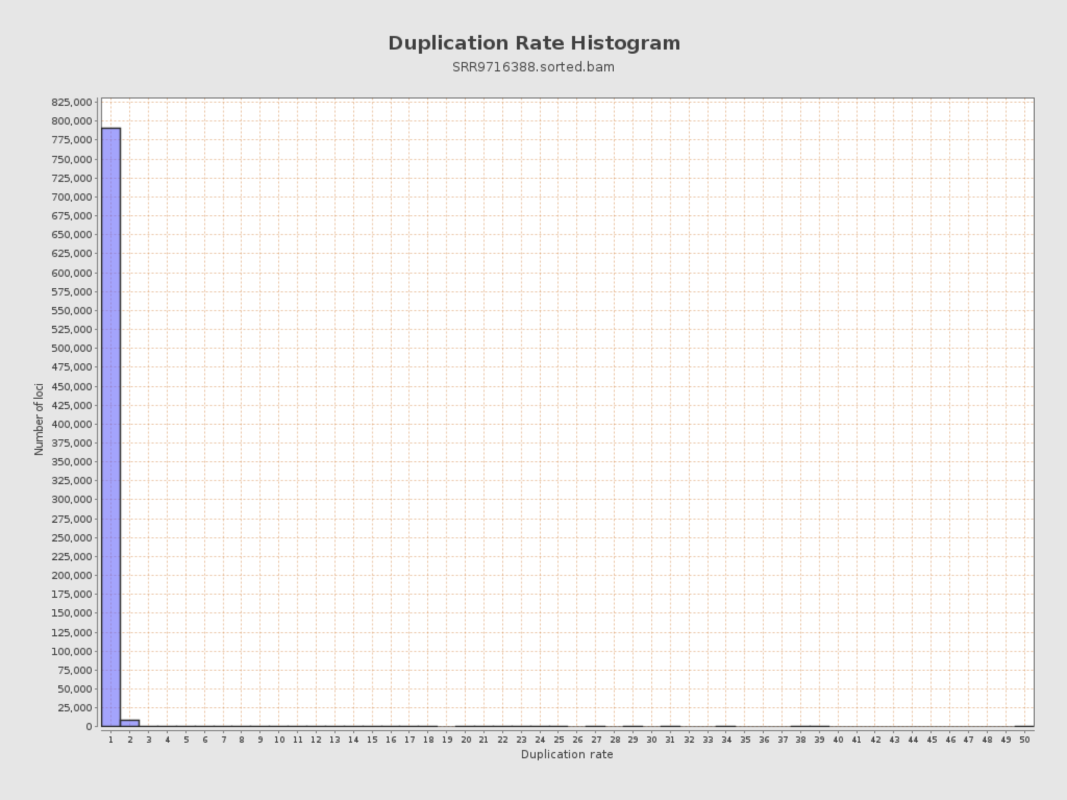
5. Results : Coverage Histogram (0-50X)



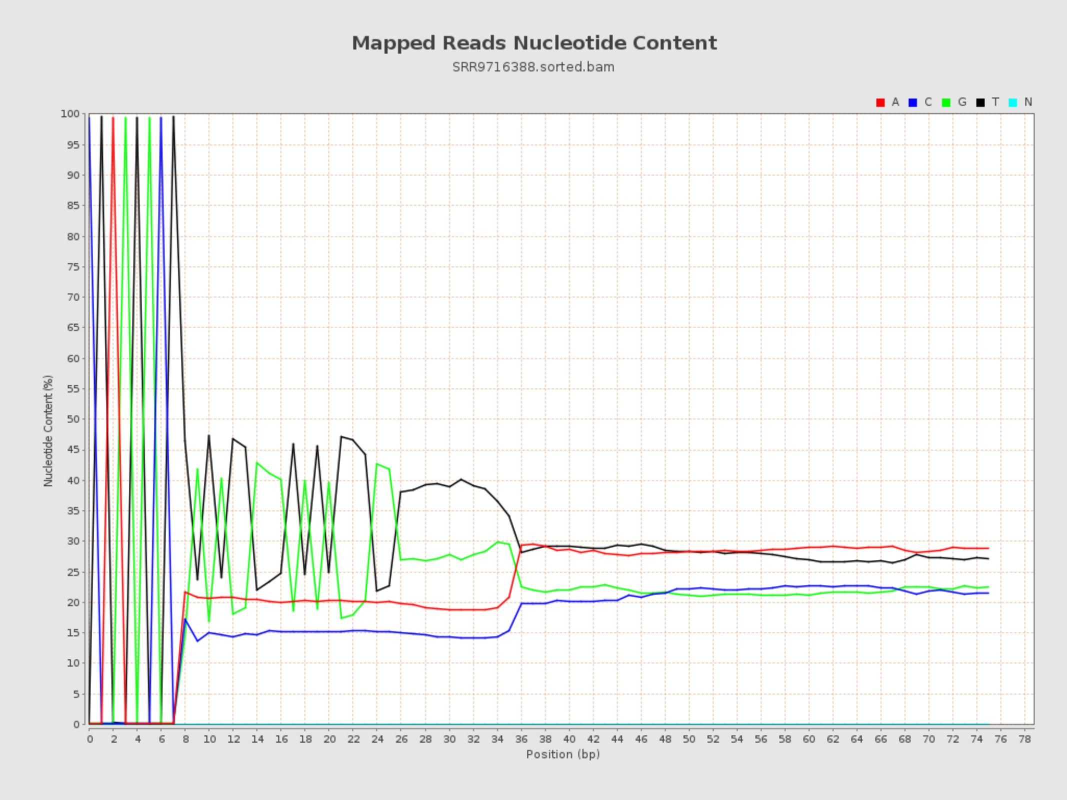
6. Results : Genome Fraction Coverage



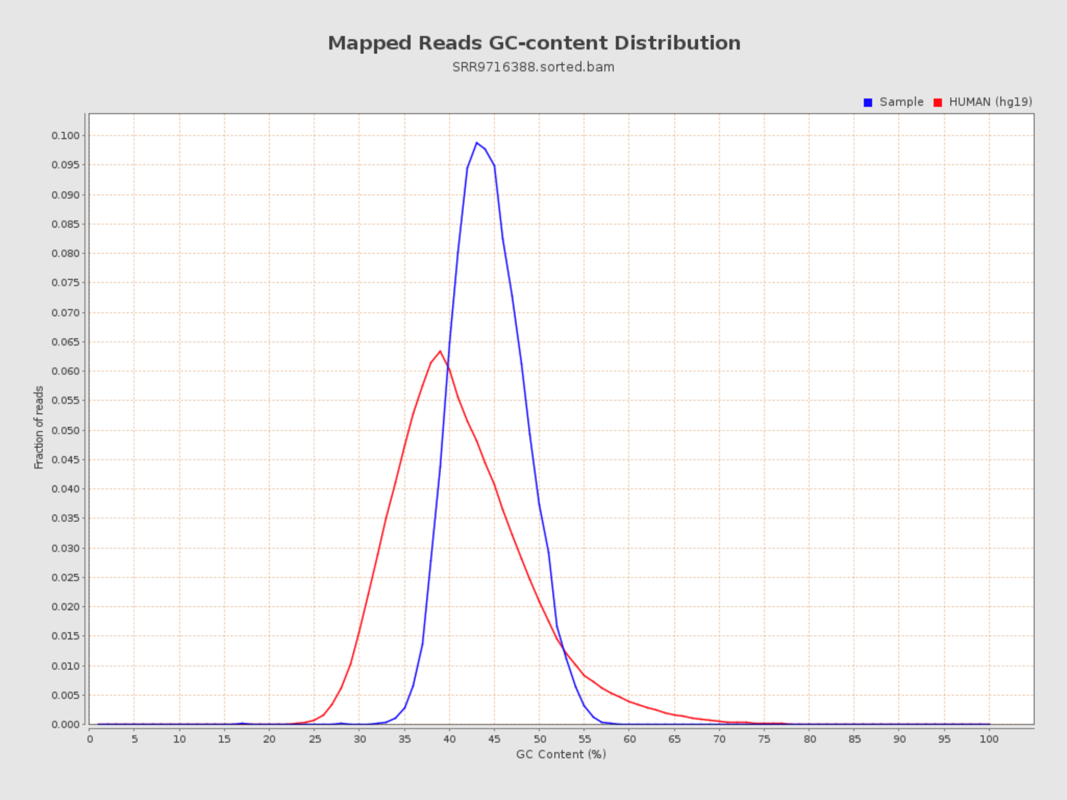
7. Results : Duplication Rate Histogram



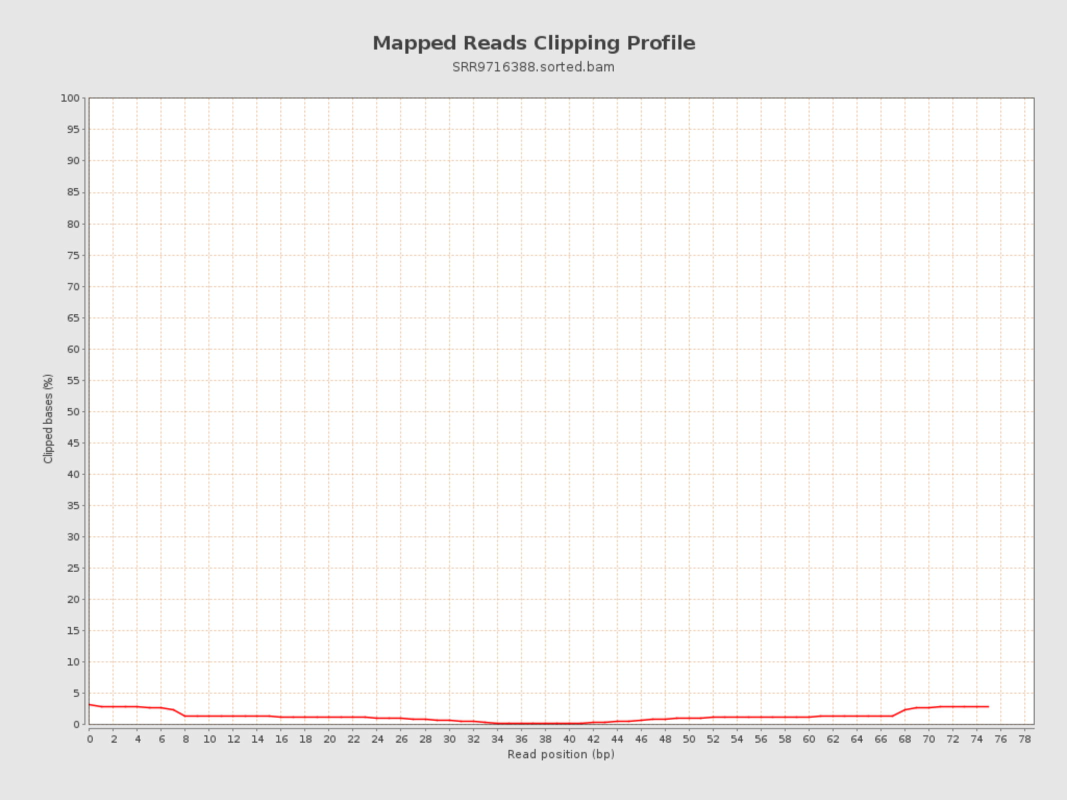
8. Results : Mapped Reads Nucleotide Content



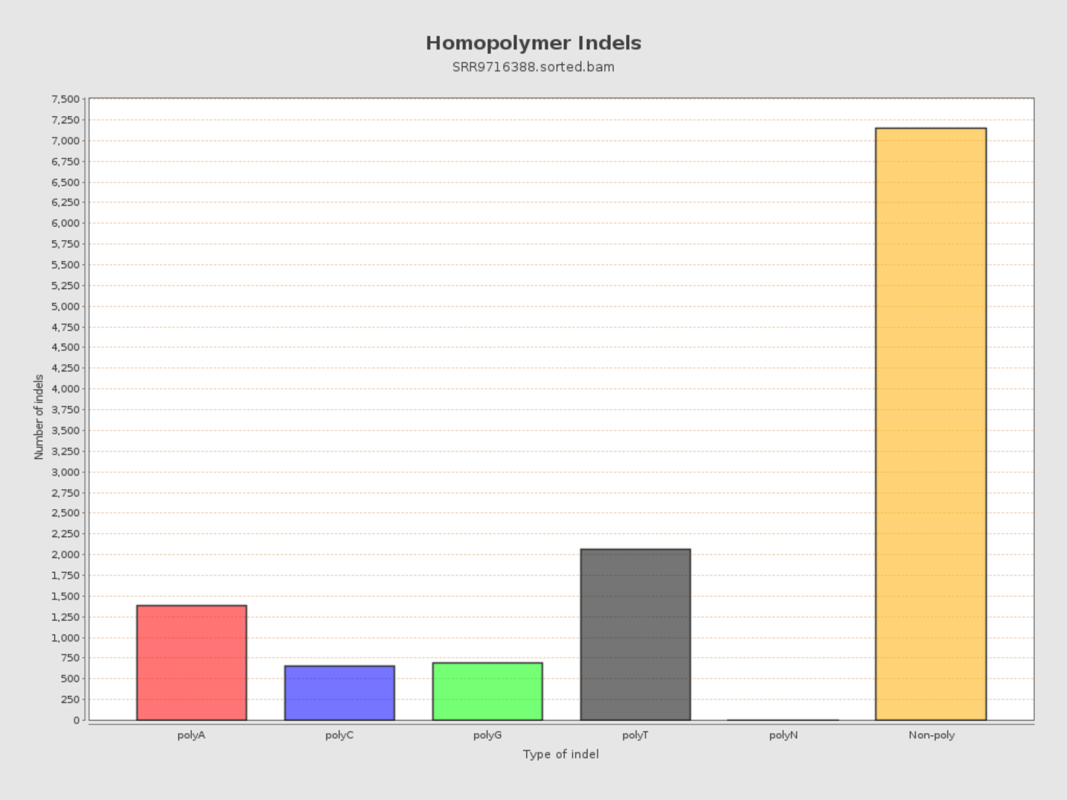
9. Results : Mapped Reads GC-content Distribution



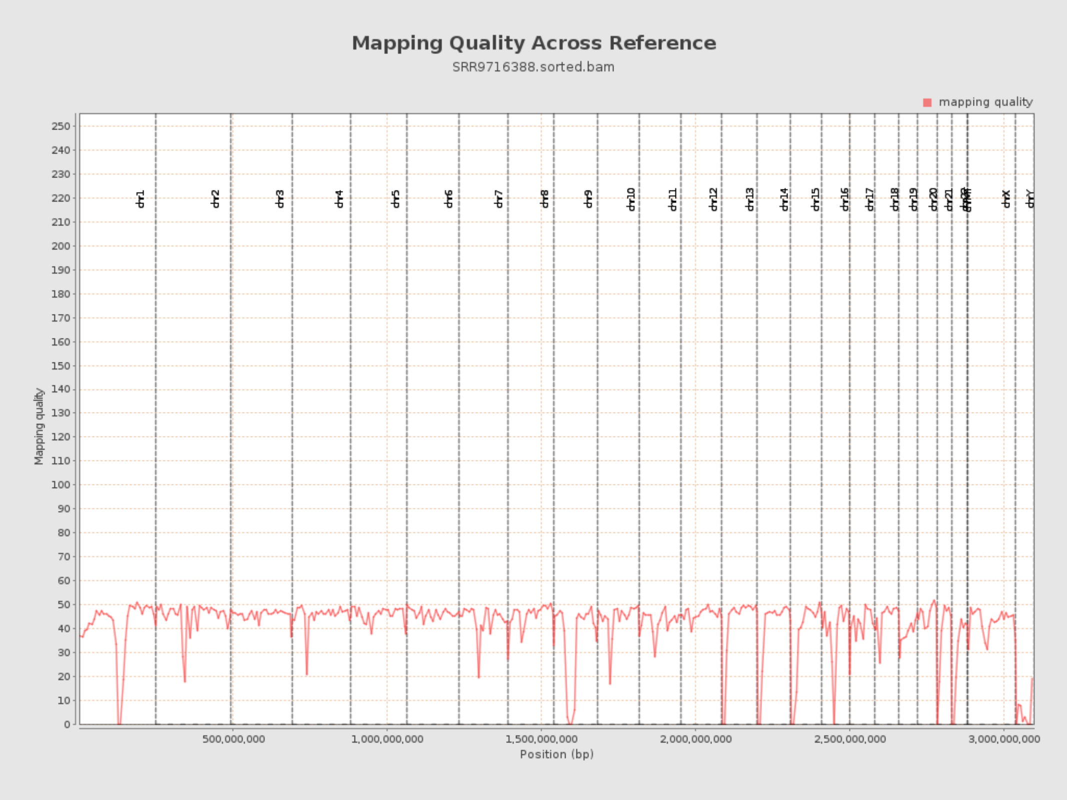
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram