Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:11:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716809.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_SRR9716809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:11:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	765,570
Mapped reads	643,584 / 84.07%
Unmapped reads	121,986 / 15.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,283 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	14,943 / 1.95%
Duplication rate	1.8%
Clipped reads	645,057 / 84.26%

2.2. ACGT Content

Number/percentage of A's	8,988,895 / 23.99%
Number/percentage of C's	6,881,030 / 18.36%
Number/percentage of T's	12,164,260 / 32.46%
Number/percentage of G's	9,434,769 / 25.18%
Number/percentage of N's	530 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0121

Standard Deviation	0.1404

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

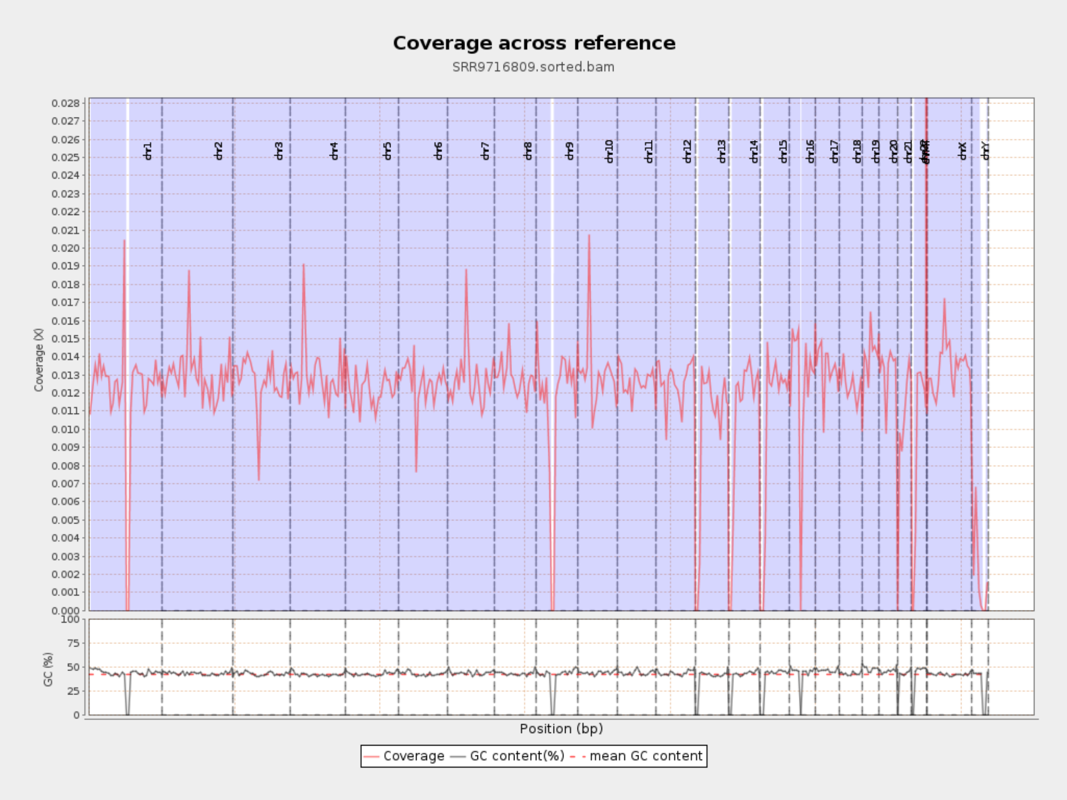
General error rate	0.52%
Mismatches	188,154
Insertions	2,572
Mapped reads with at least one insertion	0.4%
Deletions	6,887
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.12%

2.6. Chromosome stats

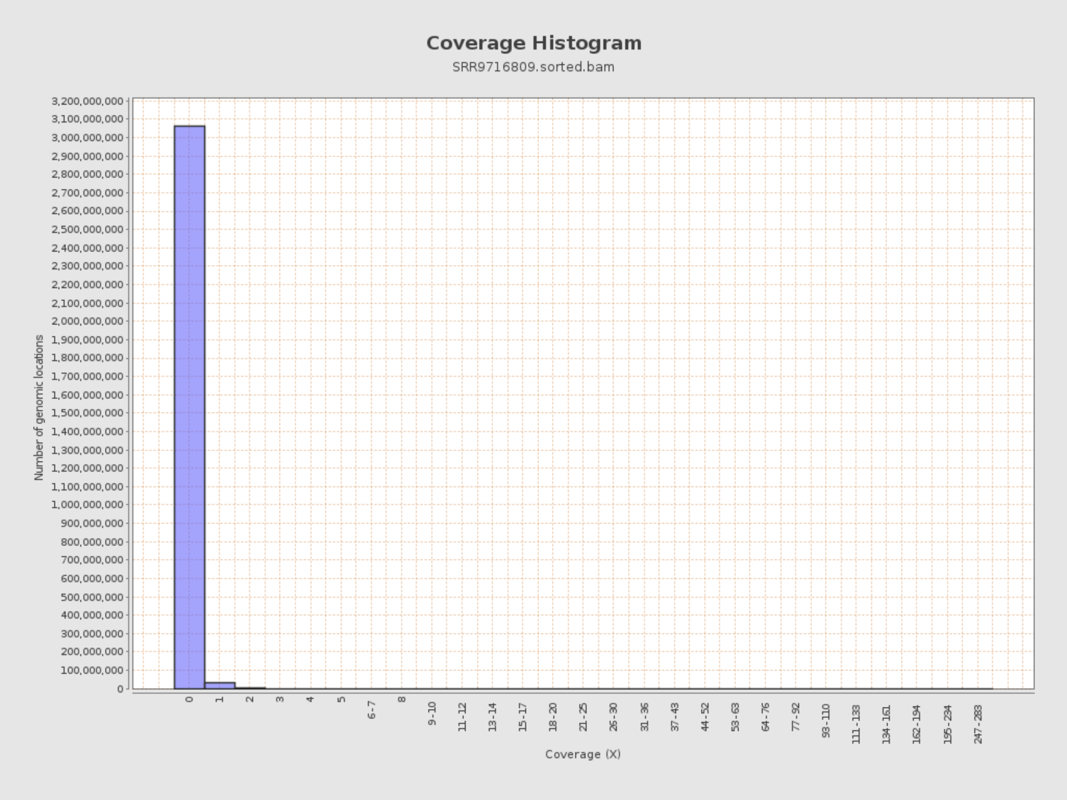
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3000209	0.012	0.2234
chr2	243199373	3163120	0.013	0.1692
chr3	198022430	2508887	0.0127	0.1183
chr4	191154276	2486128	0.013	0.124
chr5	180915260	2213509	0.0122	0.1159
chr6	171115067	2147953	0.0126	0.1249
chr7	159138663	2037238	0.0128	0.1578

chr8	146364022	1877956	0.0128	0.1333
chr9	141213431	1561292	0.0111	0.1227
chr10	135534747	1770128	0.0131	0.1401
chr11	135006516	1706346	0.0126	0.1323
chr12	133851895	1690272	0.0126	0.1178
chr13	115169878	1148178	0.01	0.1044
chr14	107349540	1124873	0.0105	0.1093
chr15	102531392	1070661	0.0104	0.1083
chr16	90354753	1124219	0.0124	0.1207
chr17	81195210	1077626	0.0133	0.124
chr18	78077248	974714	0.0125	0.1845
chr19	59128983	831770	0.0141	0.1605
chr20	63025520	824555	0.0131	0.1221
chr21	48129895	491453	0.0102	0.1103
chr22	51304566	446480	0.0087	0.0975
chrMT	16571	2803	0.1692	0.4537
chrX	155270560	2082777	0.0134	0.1253
chrY	59373566	117225	0.002	0.0652

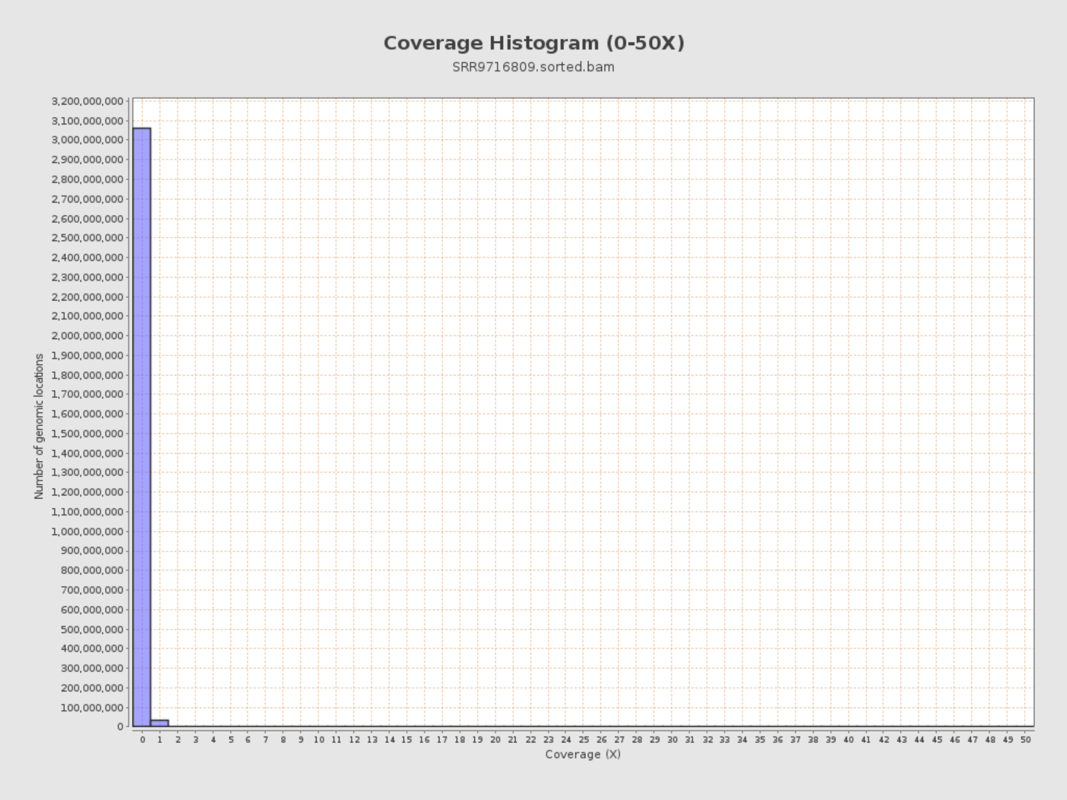
3. Results : Coverage across reference



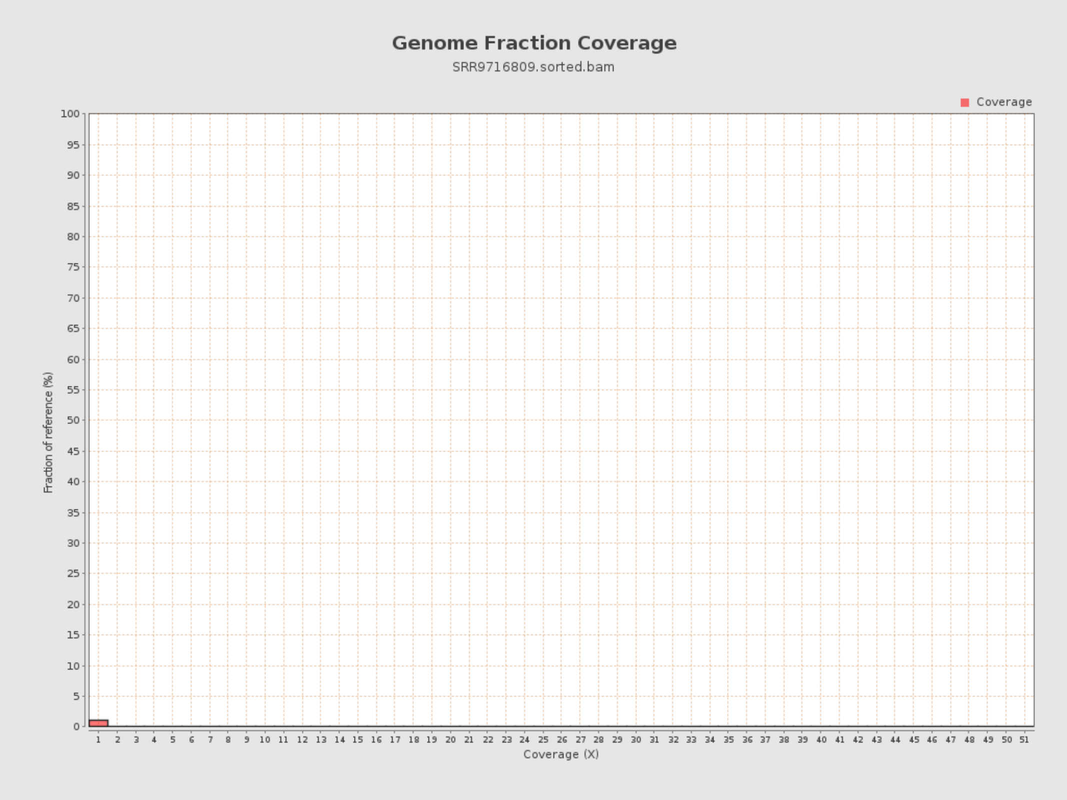
4. Results : Coverage Histogram



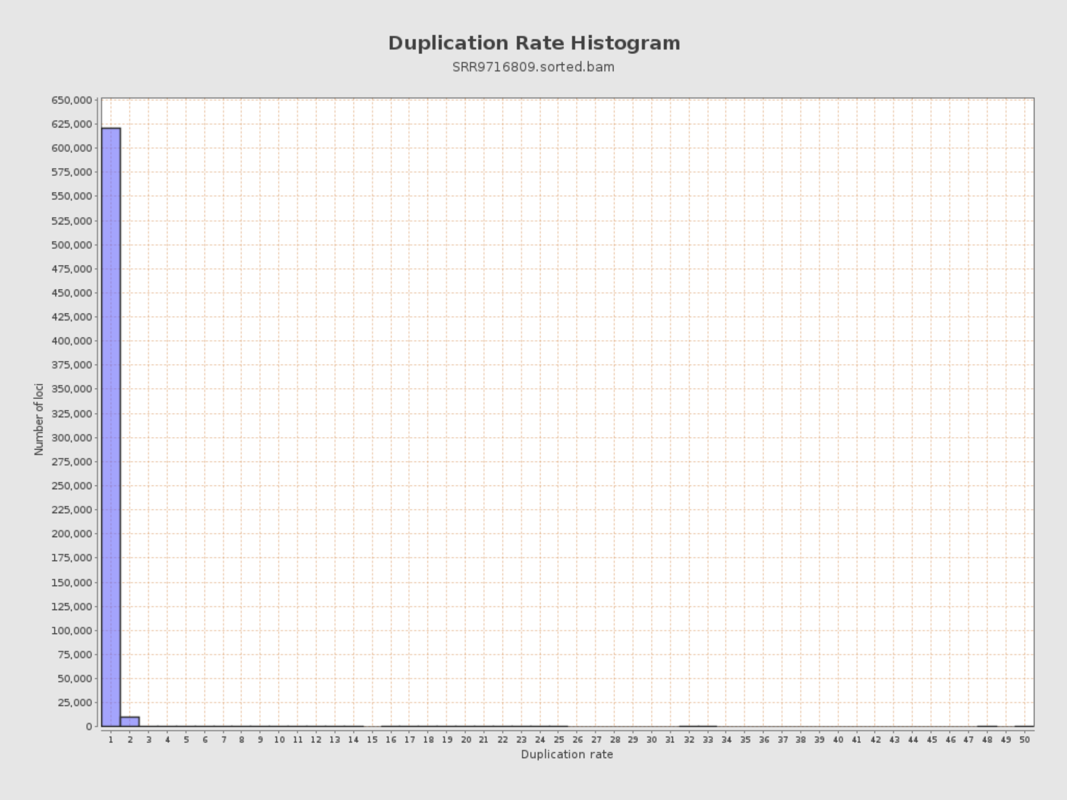
5. Results : Coverage Histogram (0-50X)



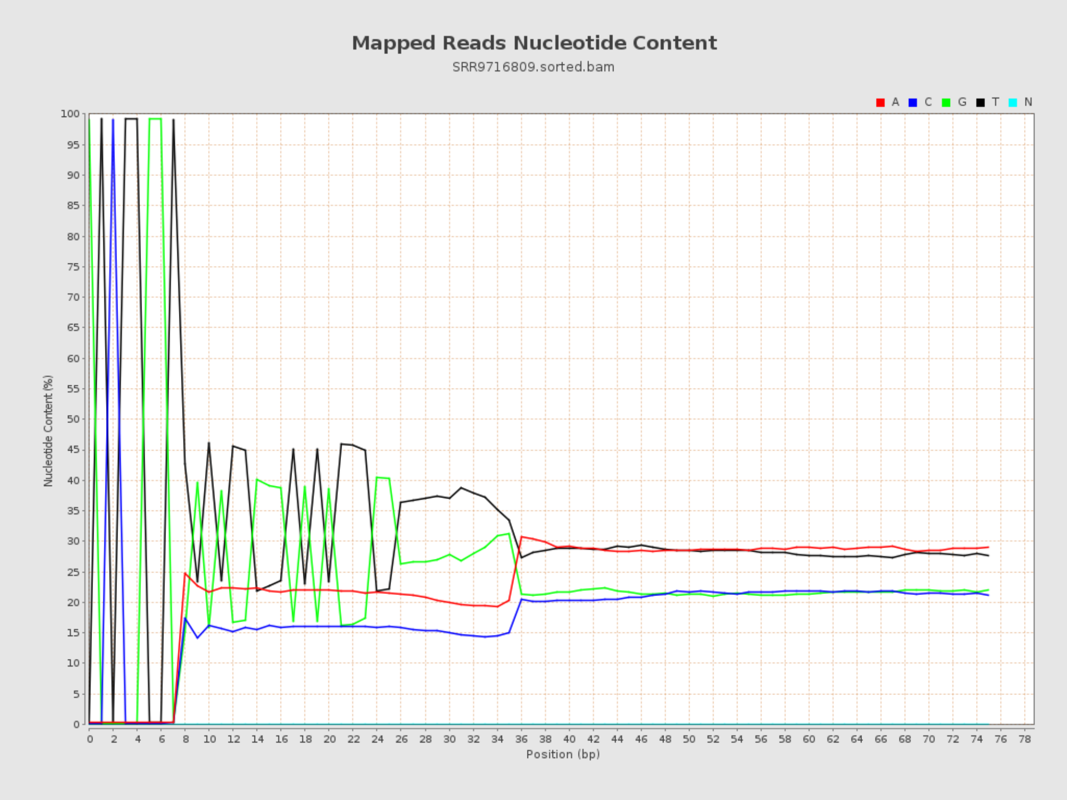
6. Results : Genome Fraction Coverage



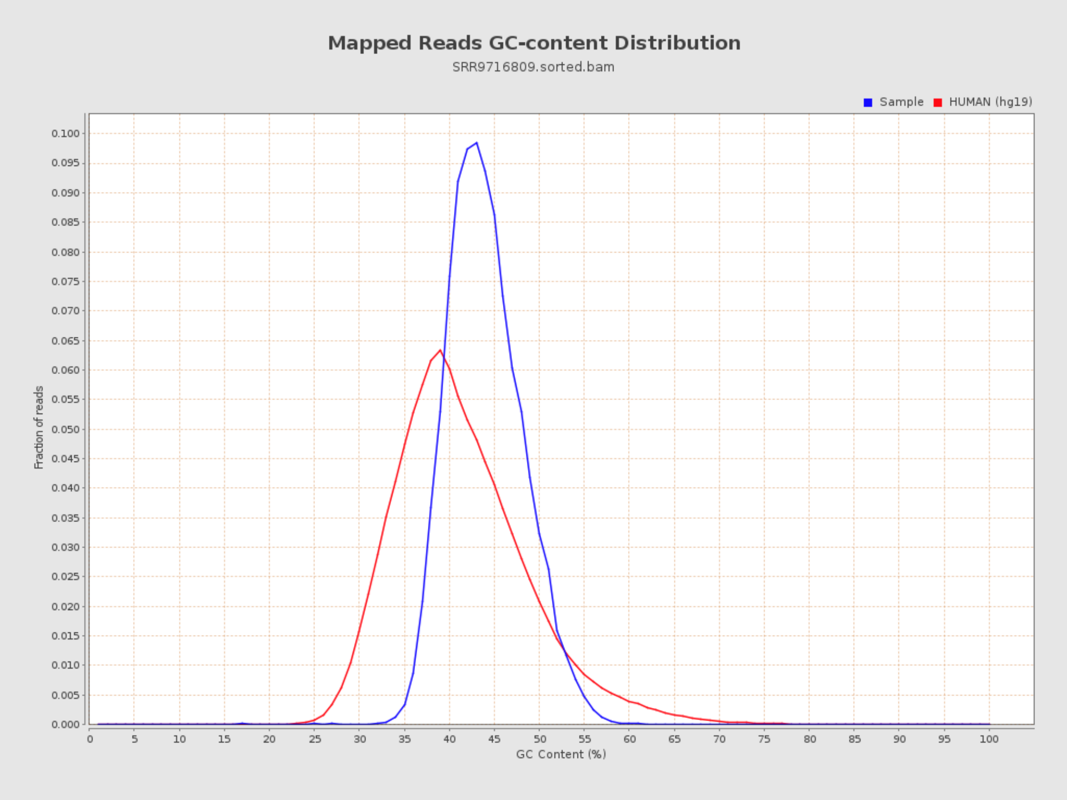
7. Results : Duplication Rate Histogram



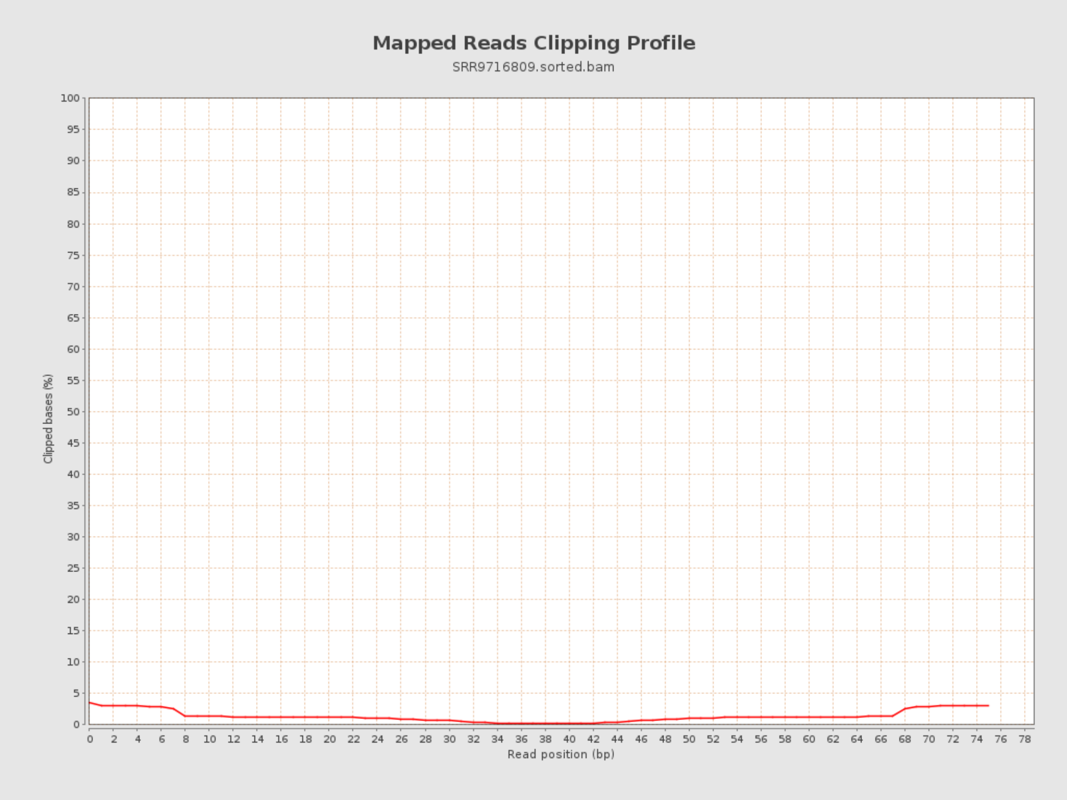
8. Results : Mapped Reads Nucleotide Content



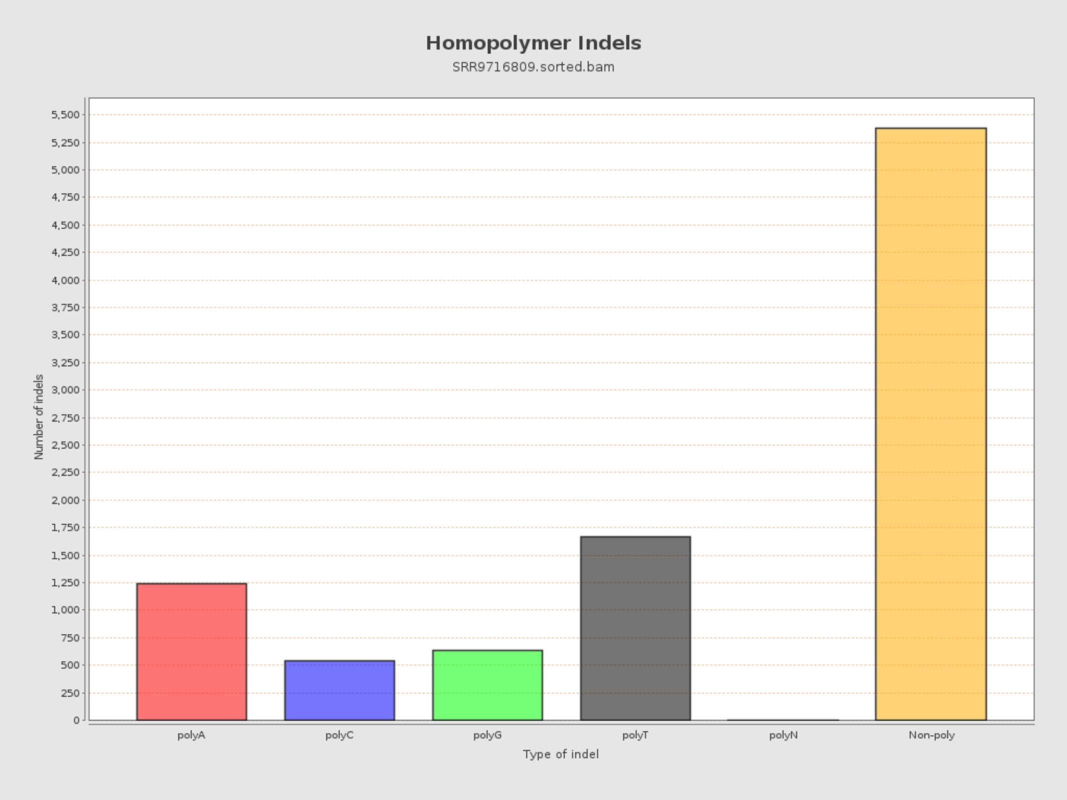
9. Results : Mapped Reads GC-content Distribution



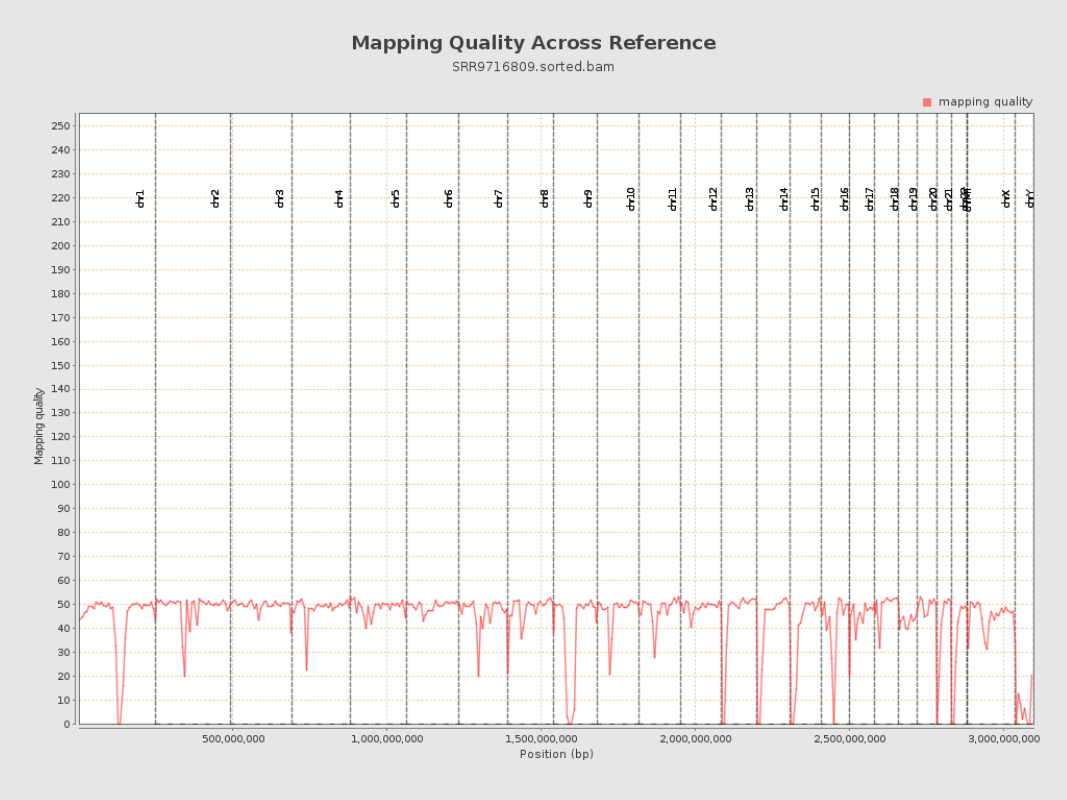
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram