Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:27:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716913.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_SRR9716913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716913.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:27:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	717,442
Mapped reads	603,219 / 84.08%
Unmapped reads	114,223 / 15.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,269 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,120 / 1.27%
Duplication rate	1.1%
Clipped reads	605,359 / 84.38%

2.2. ACGT Content

Number/percentage of A's	7,362,187 / 21.98%
Number/percentage of C's	7,234,444 / 21.6%
Number/percentage of T's	9,842,901 / 29.39%
Number/percentage of G's	9,051,008 / 27.02%
Number/percentage of N's	856 / 0%
GC Percentage	48.63%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1187

2.4. Mapping Quality

Mean Mapping Quality	39.66

2.5. Mismatches and indels

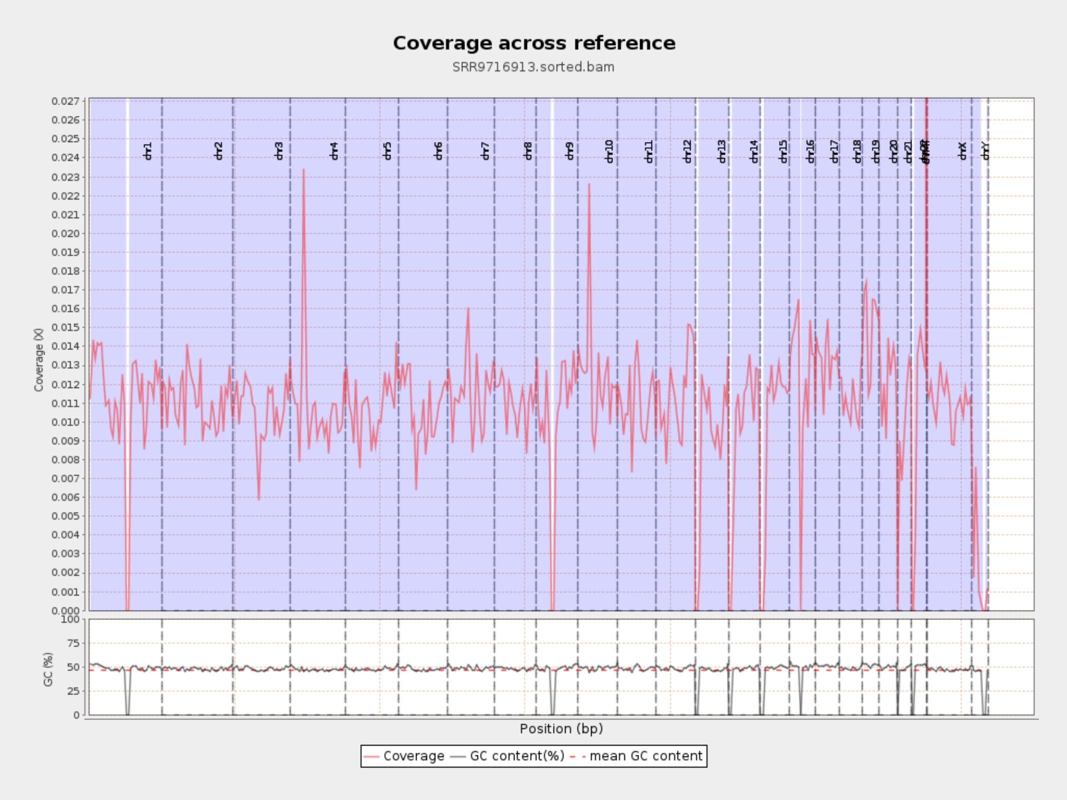
General error rate	0.54%
Mismatches	177,740
Insertions	2,307
Mapped reads with at least one insertion	0.38%
Deletions	5,544
Mapped reads with at least one deletion	0.91%
Homopolymer indels	33.87%

2.6. Chromosome stats

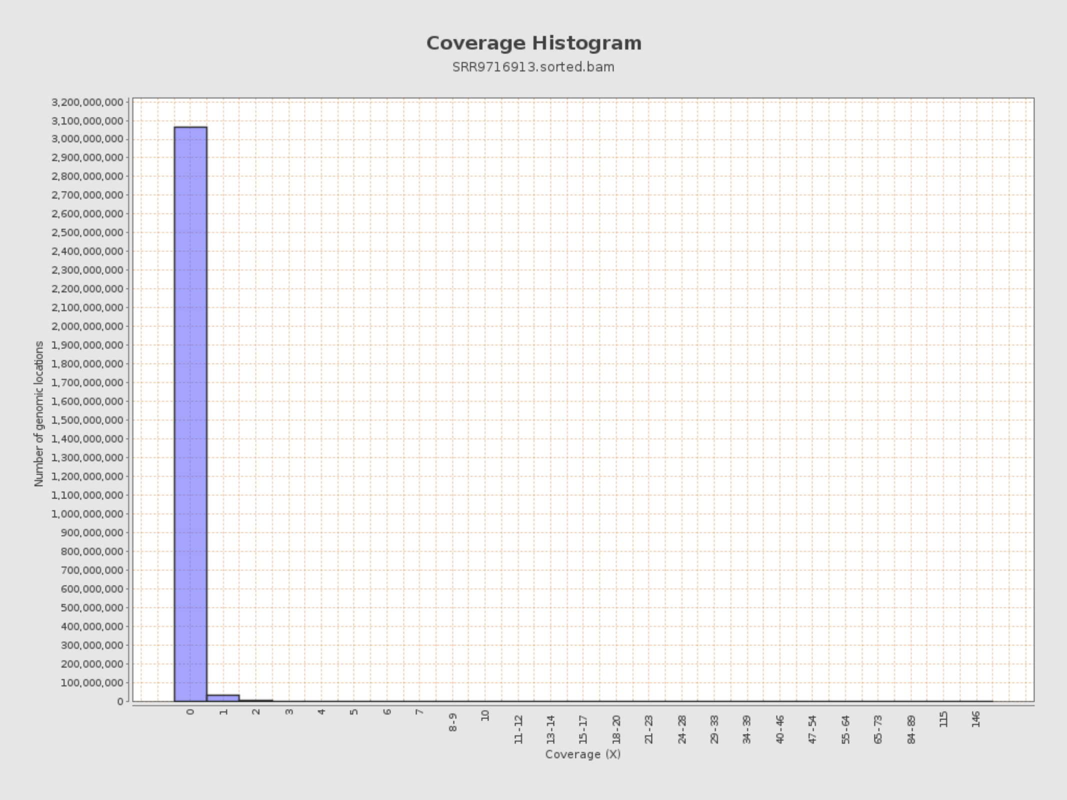
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2746338	0.011	0.1205
chr2	243199373	2710353	0.0111	0.1368
chr3	198022430	2100250	0.0106	0.111
chr4	191154276	2067284	0.0108	0.1228
chr5	180915260	1946472	0.0108	0.1101
chr6	171115067	1843551	0.0108	0.1102
chr7	159138663	1831289	0.0115	0.1265

chr8	146364022	1623881	0.0111	0.1161
chr9	141213431	1402646	0.0099	0.1112
chr10	135534747	1678102	0.0124	0.1483
chr11	135006516	1481239	0.011	0.1197
chr12	133851895	1549306	0.0116	0.1143
chr13	115169878	1005384	0.0087	0.1011
chr14	107349540	1013788	0.0094	0.1043
chr15	102531392	980937	0.0096	0.1036
chr16	90354753	1121754	0.0124	0.1227
chr17	81195210	1084534	0.0134	0.124
chr18	78077248	865551	0.0111	0.1271
chr19	59128983	893972	0.0151	0.1392
chr20	63025520	766838	0.0122	0.1206
chr21	48129895	451102	0.0094	0.1129
chr22	51304566	482782	0.0094	0.1042
chrMT	16571	2741	0.1654	0.4221
chrX	155270560	1726662	0.0111	0.1148
chrY	59373566	124329	0.0021	0.0738

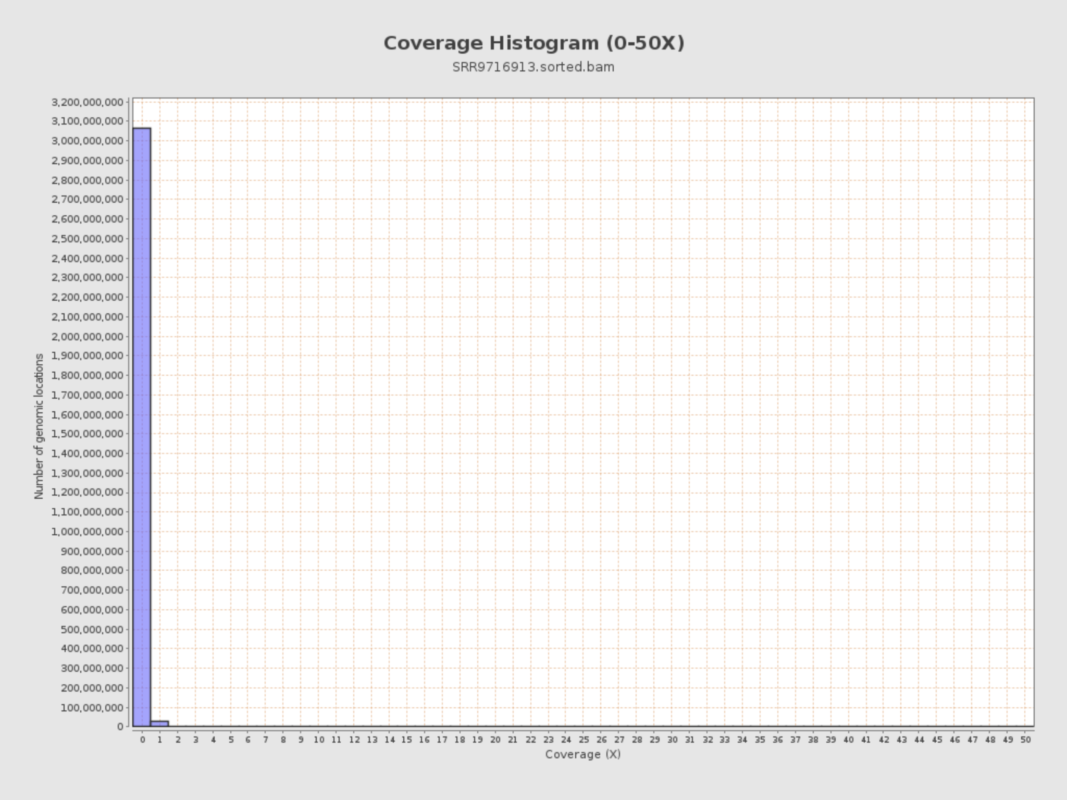
3. Results : Coverage across reference



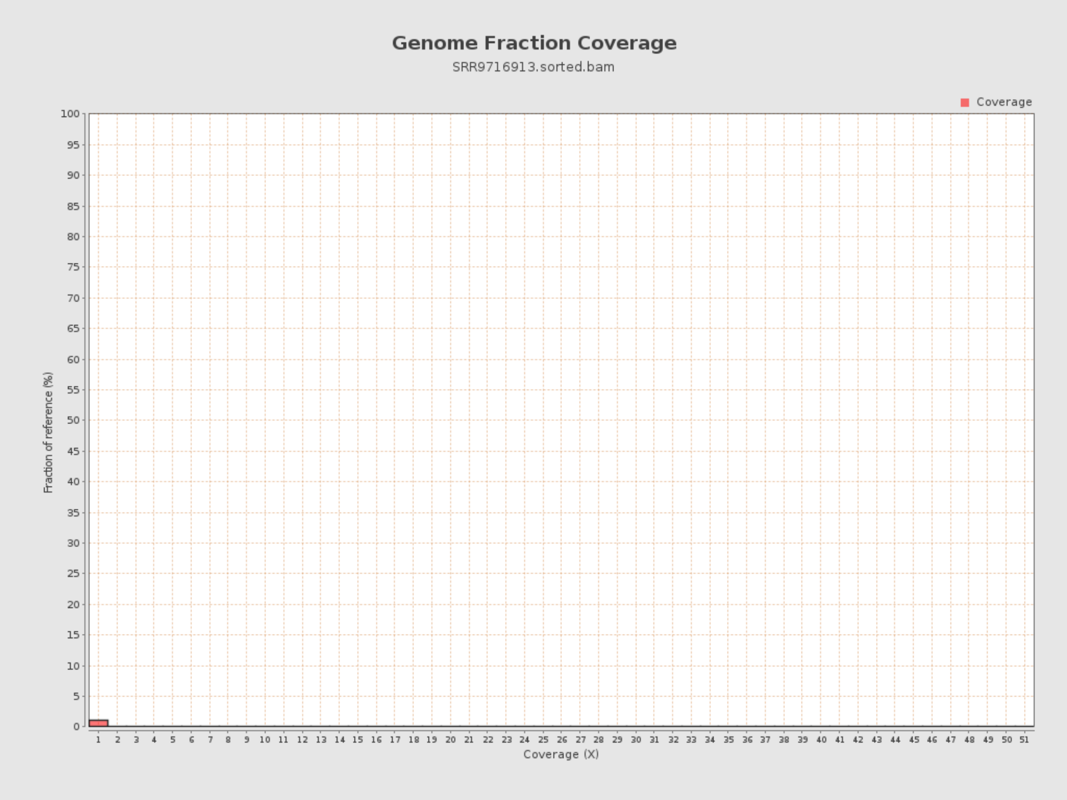
4. Results : Coverage Histogram



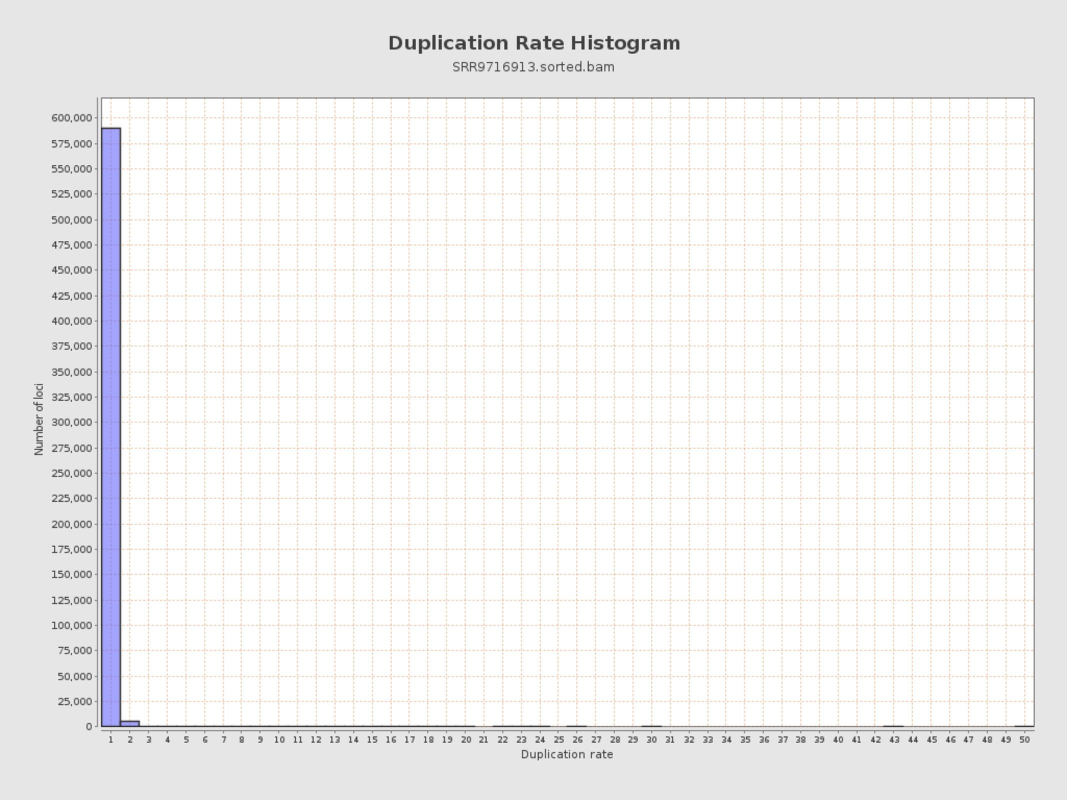
5. Results : Coverage Histogram (0-50X)



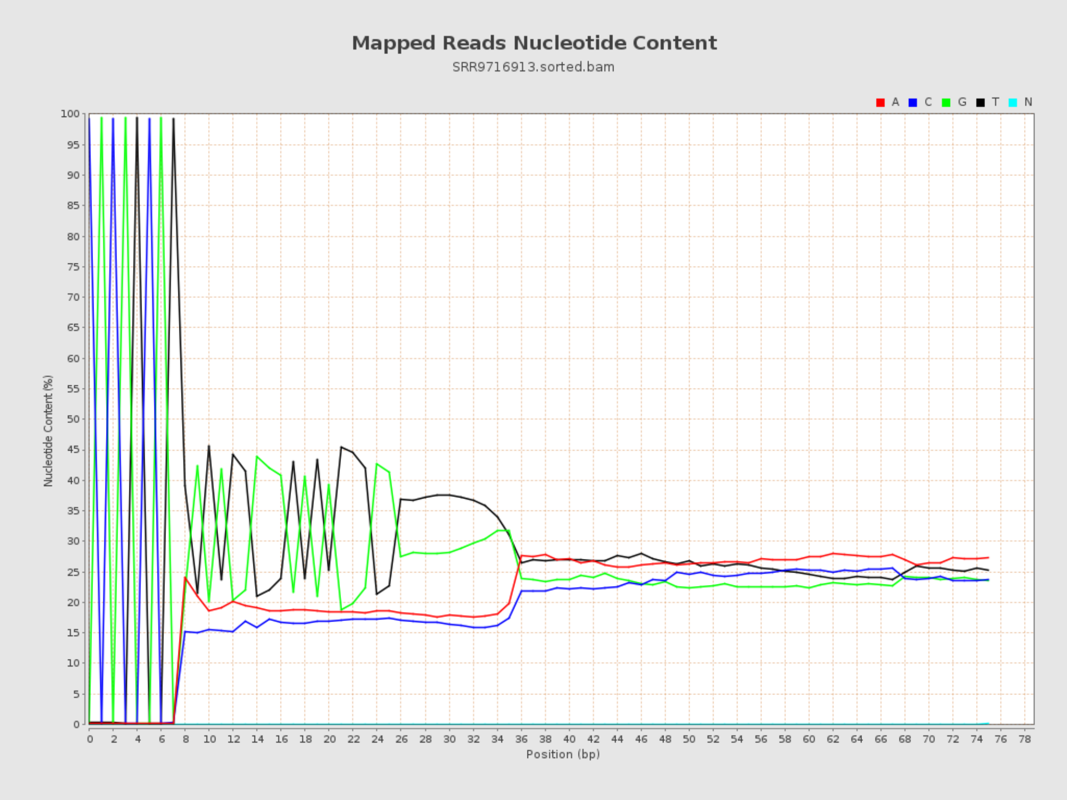
6. Results : Genome Fraction Coverage



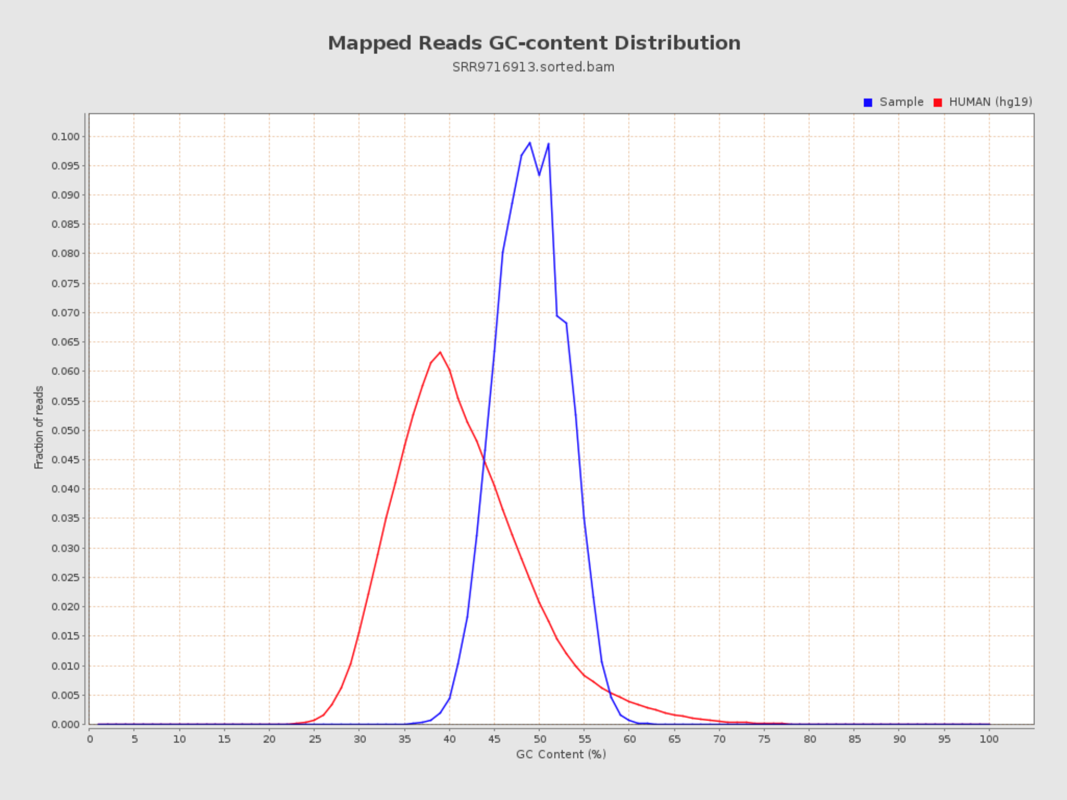
7. Results : Duplication Rate Histogram



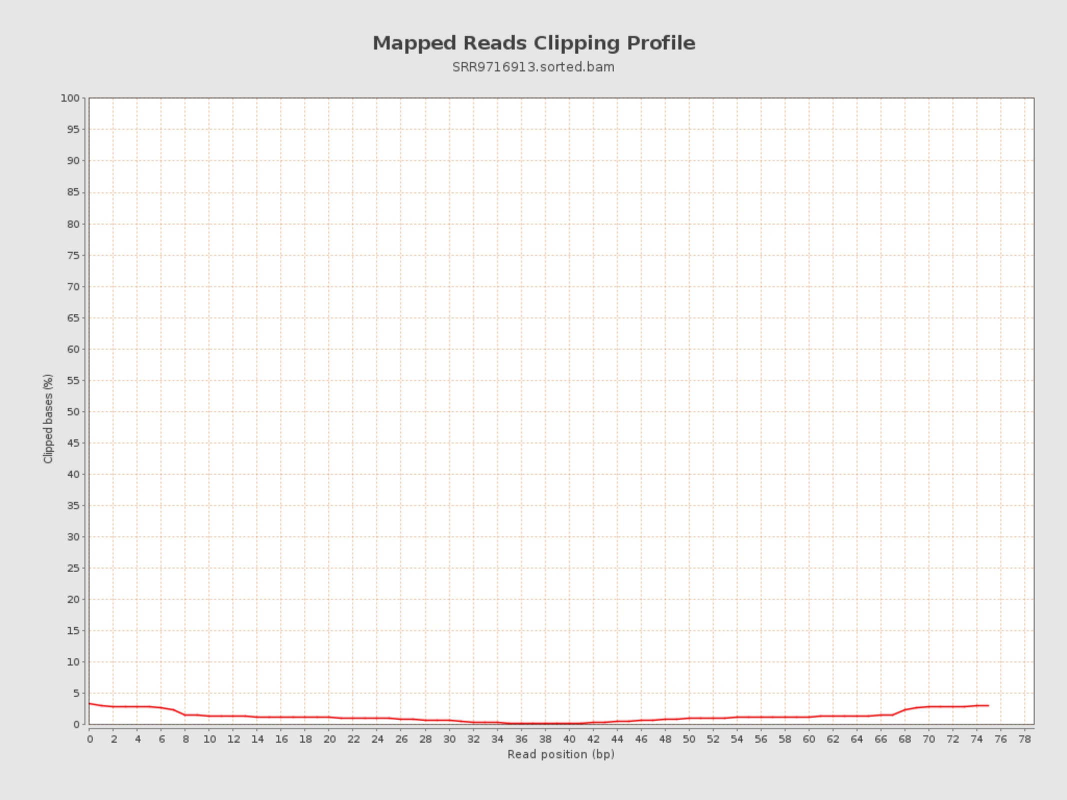
8. Results : Mapped Reads Nucleotide Content



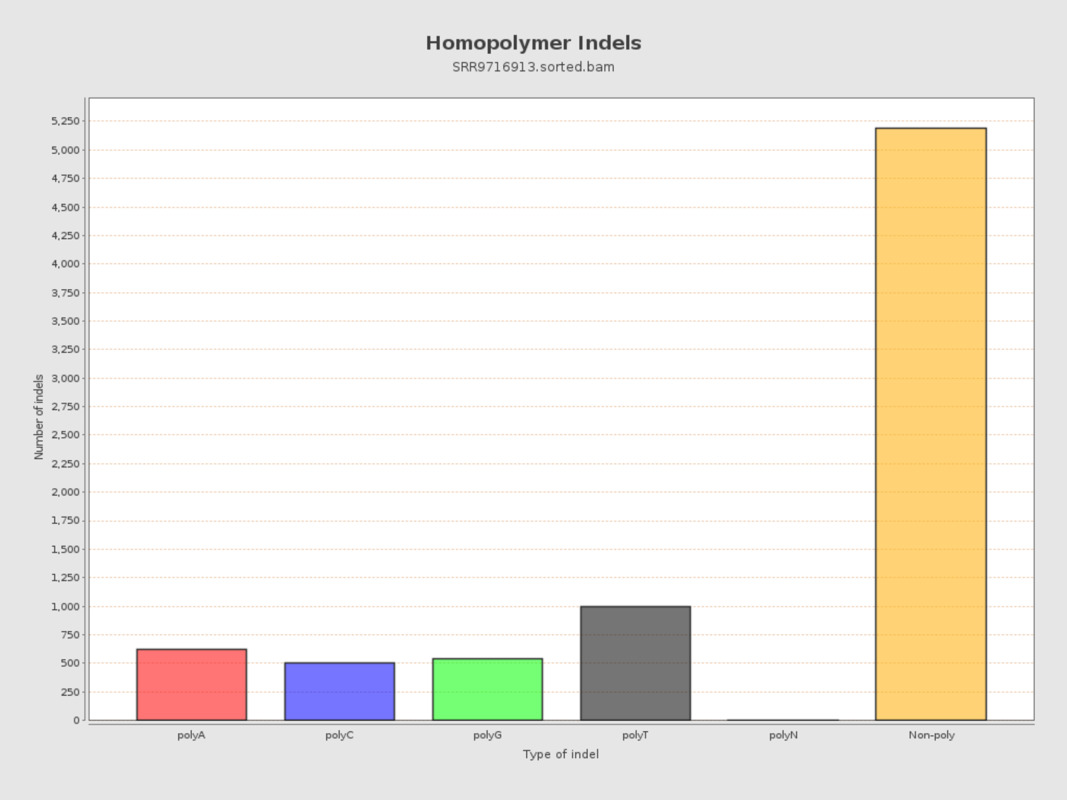
9. Results : Mapped Reads GC-content Distribution



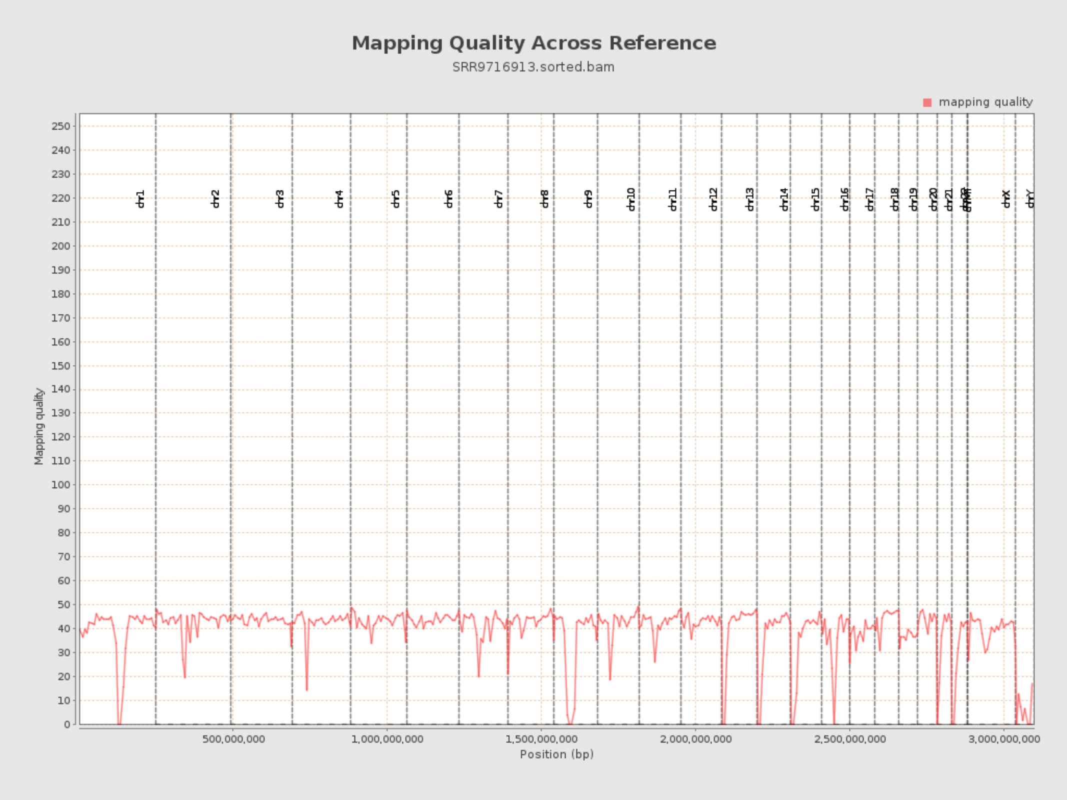
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram