Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:44:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716865.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_SRR9716865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716865.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:44:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,139,272
Mapped reads	694,952 / 61%
Unmapped reads	444,320 / 39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,349 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	13,353 / 1.17%
Duplication rate	1.45%
Clipped reads	695,752 / 61.07%

2.2. ACGT Content

Number/percentage of A's	10,254,301 / 26.07%
Number/percentage of C's	7,210,482 / 18.33%
Number/percentage of T's	12,182,936 / 30.97%
Number/percentage of G's	9,683,313 / 24.62%
Number/percentage of N's	617 / 0%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1367

2.4. Mapping Quality

Mean Mapping Quality	43.29

2.5. Mismatches and indels

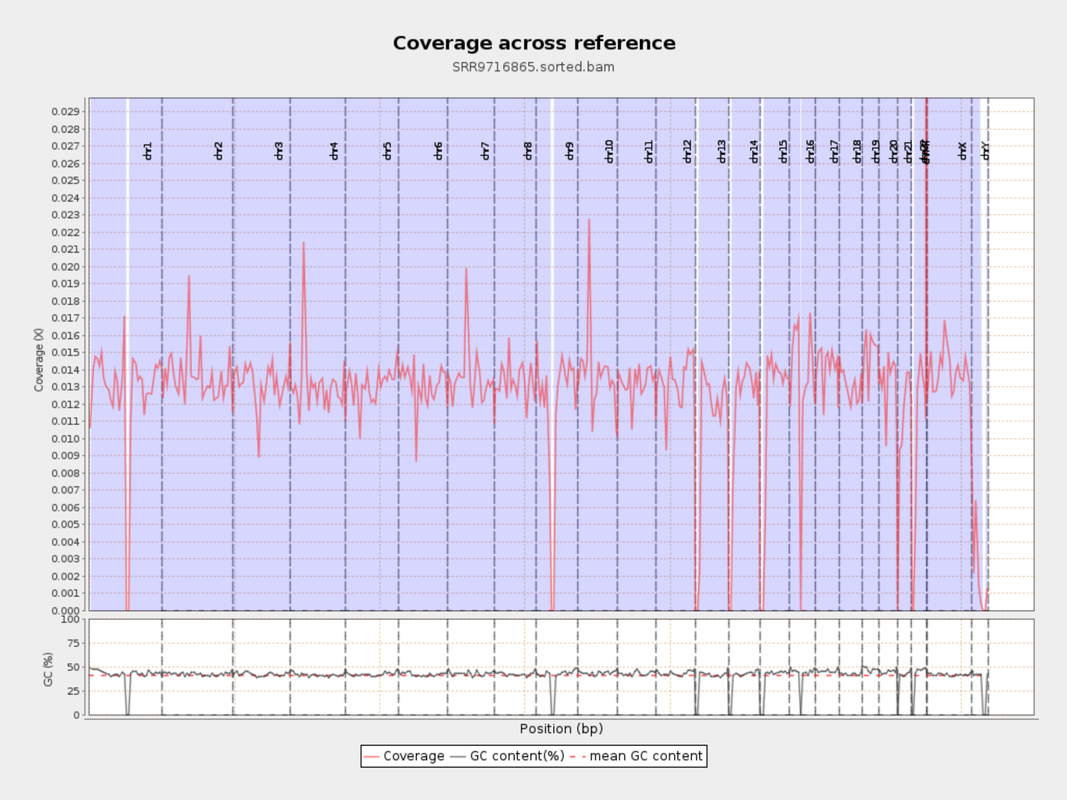
General error rate	0.54%
Mismatches	206,276
Insertions	2,770
Mapped reads with at least one insertion	0.4%
Deletions	7,309
Mapped reads with at least one deletion	1.04%
Homopolymer indels	40.47%

2.6. Chromosome stats

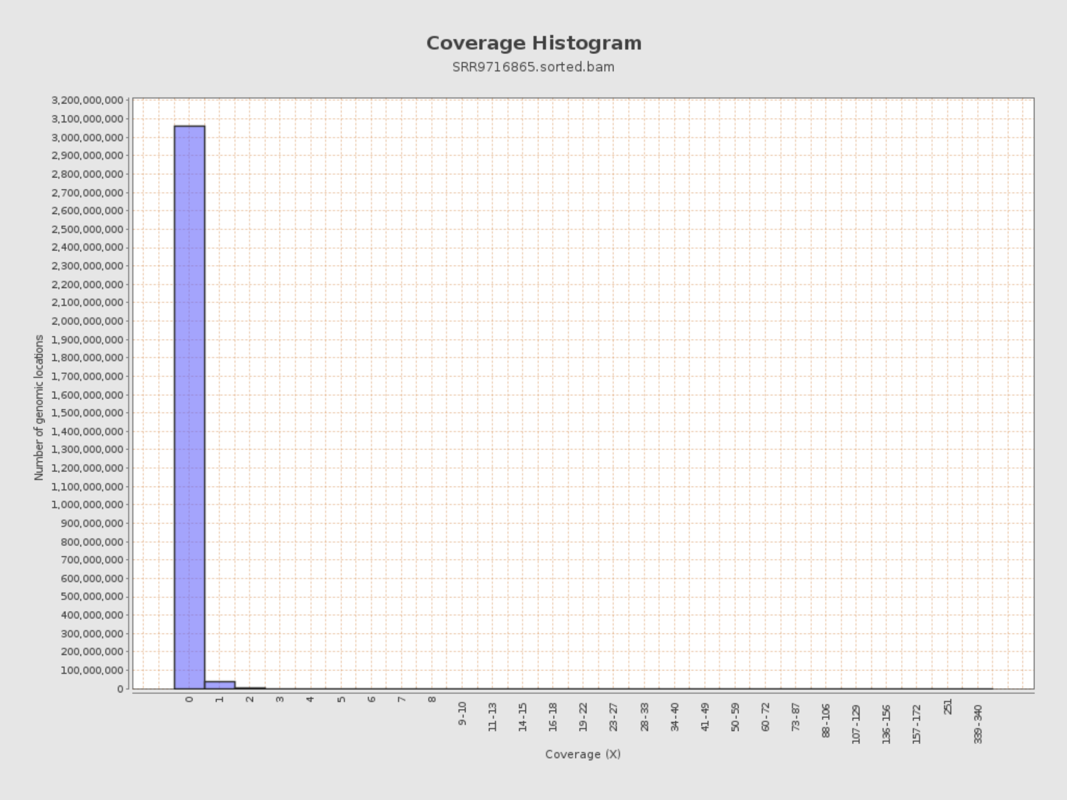
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3136799	0.0126	0.1604
chr2	243199373	3320186	0.0137	0.1897
chr3	198022430	2594484	0.0131	0.1194
chr4	191154276	2506319	0.0131	0.1261
chr5	180915260	2364937	0.0131	0.1192
chr6	171115067	2250434	0.0132	0.1276
chr7	159138663	2172925	0.0137	0.1635

chr8	146364022	1948024	0.0133	0.134
chr9	141213431	1627706	0.0115	0.1225
chr10	135534747	1884207	0.0139	0.1478
chr11	135006516	1785108	0.0132	0.1328
chr12	133851895	1789713	0.0134	0.1213
chr13	115169878	1213115	0.0105	0.1071
chr14	107349540	1203443	0.0112	0.1119
chr15	102531392	1161695	0.0113	0.1124
chr16	90354753	1211514	0.0134	0.1247
chr17	81195210	1149907	0.0142	0.1281
chr18	78077248	1020361	0.0131	0.1636
chr19	59128983	885166	0.015	0.1547
chr20	63025520	840837	0.0133	0.1225
chr21	48129895	513620	0.0107	0.1126
chr22	51304566	478429	0.0093	0.1005
chrMT	16571	2608	0.1574	0.4038
chrX	155270560	2160355	0.0139	0.1296
chrY	59373566	121432	0.002	0.0614

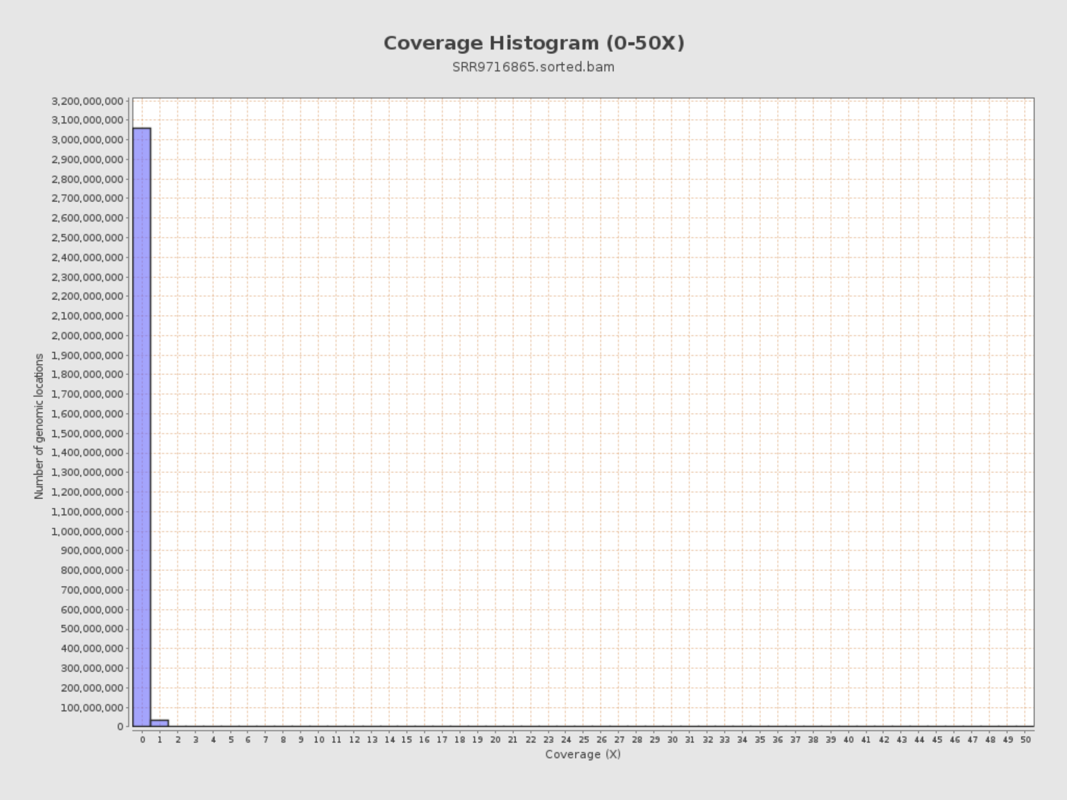
3. Results : Coverage across reference



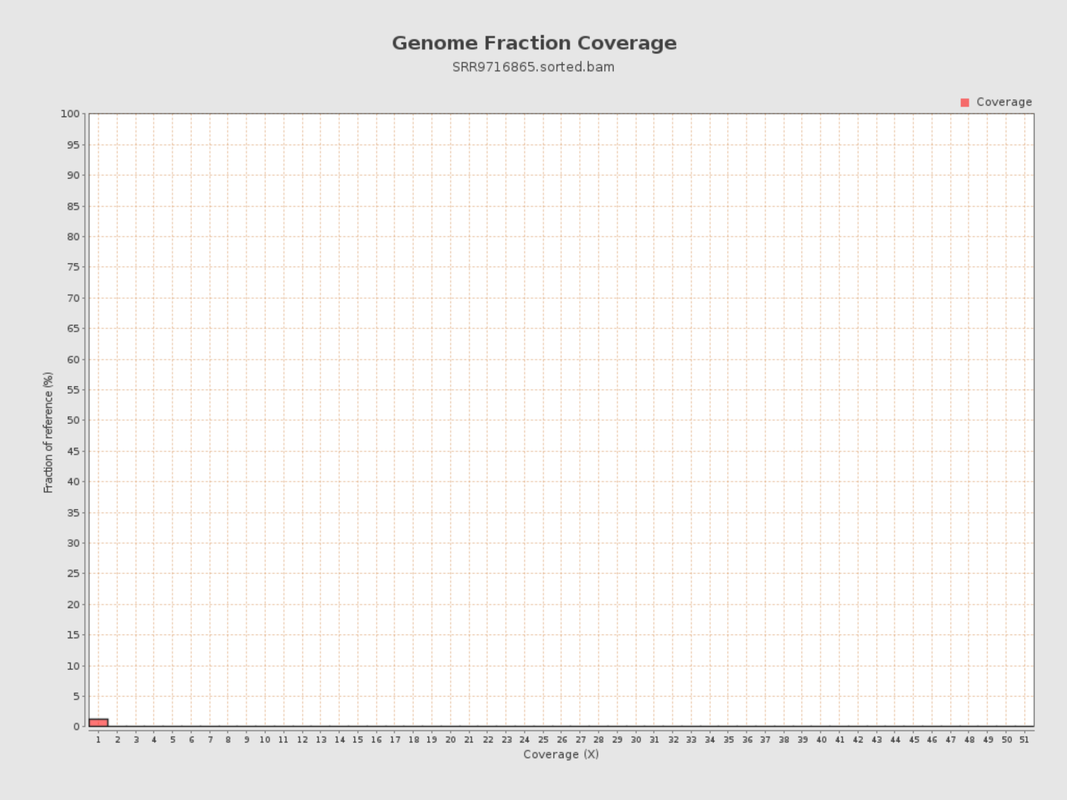
4. Results : Coverage Histogram



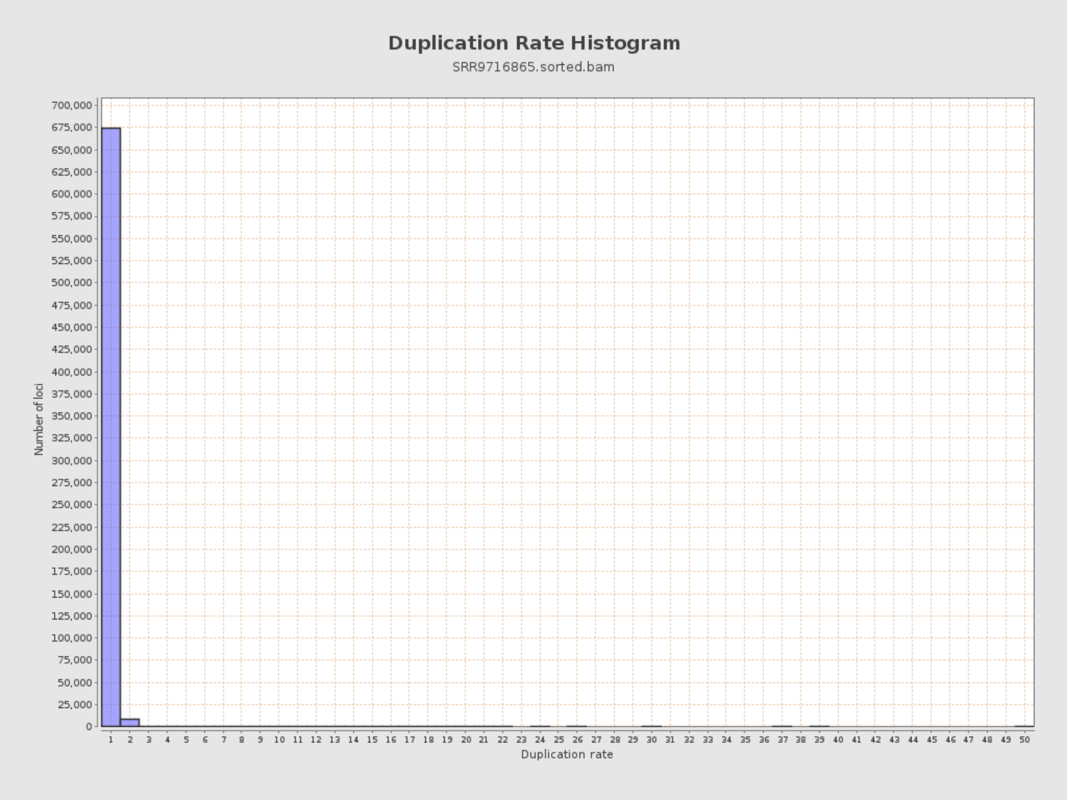
5. Results : Coverage Histogram (0-50X)



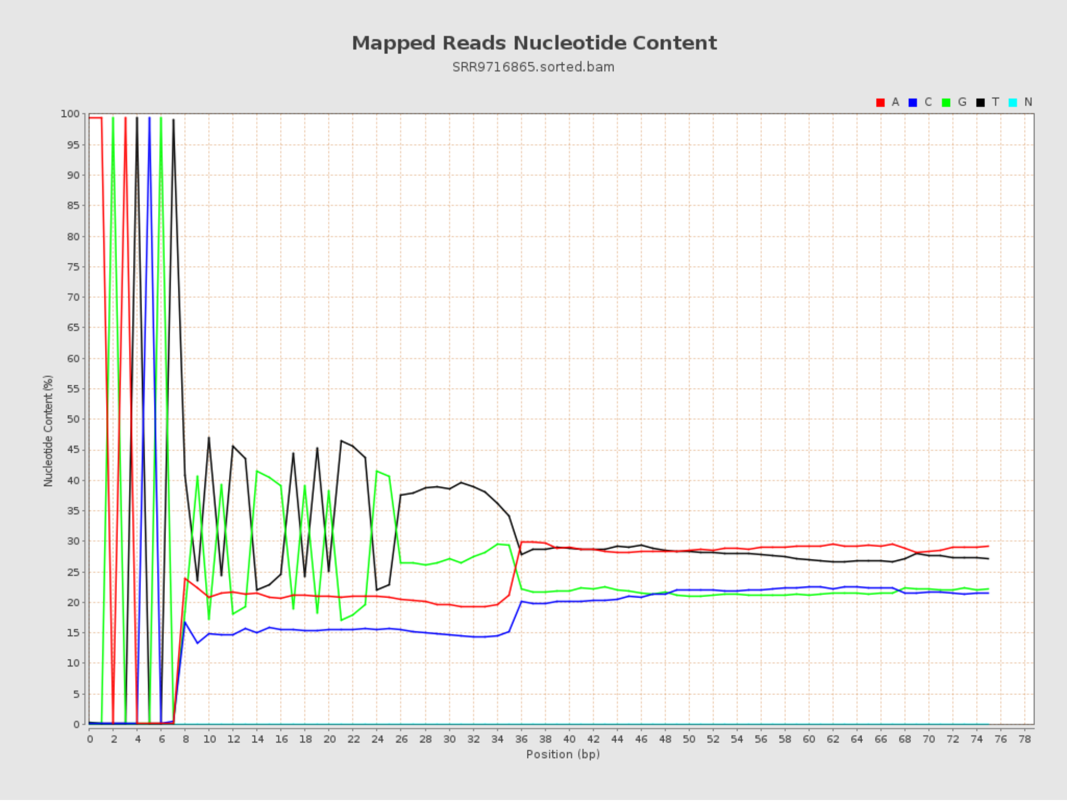
6. Results : Genome Fraction Coverage



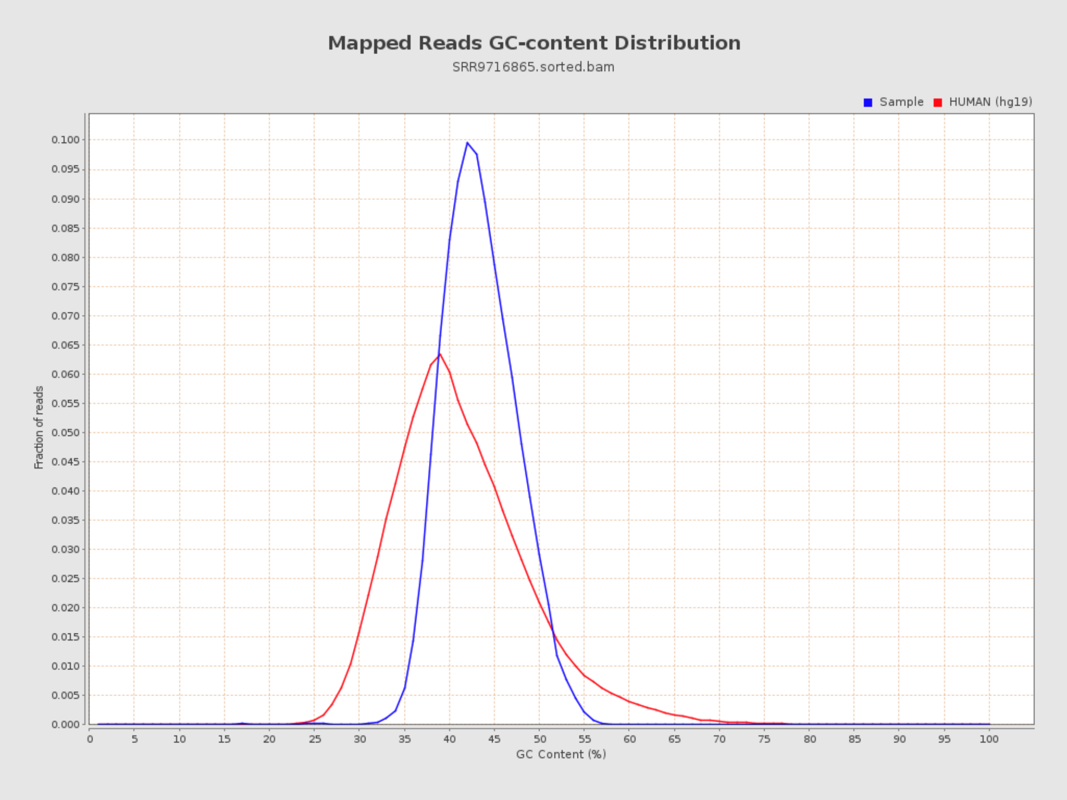
7. Results : Duplication Rate Histogram



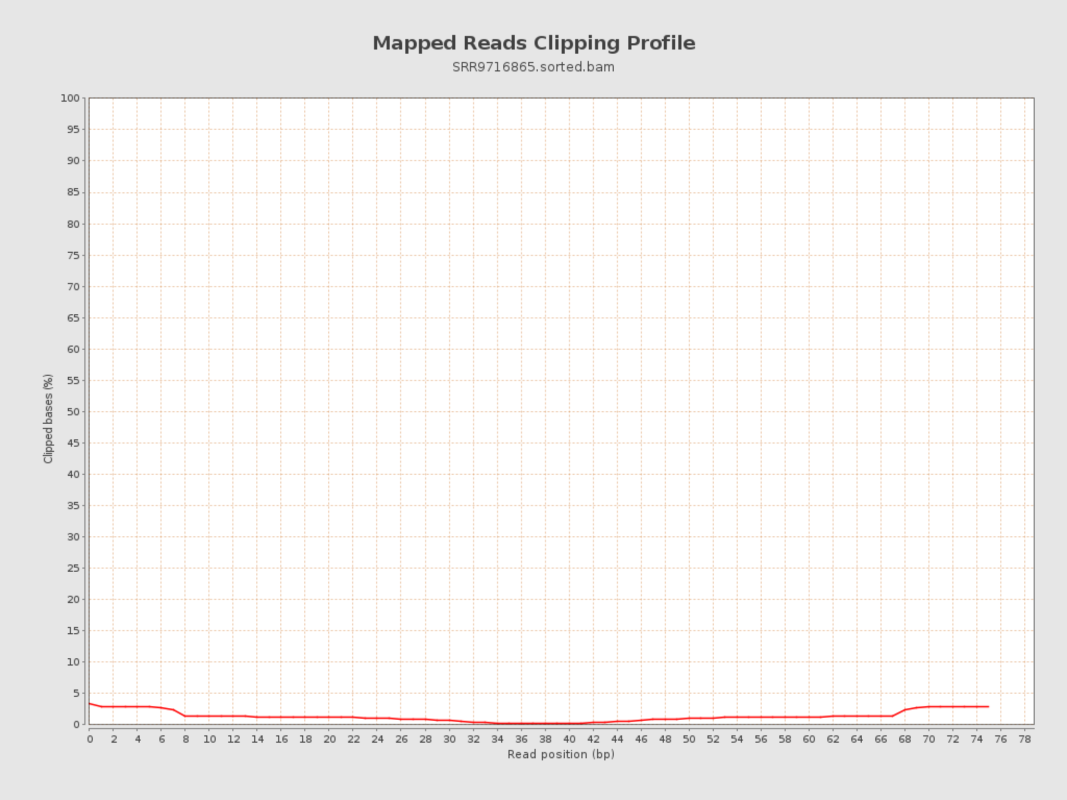
8. Results : Mapped Reads Nucleotide Content



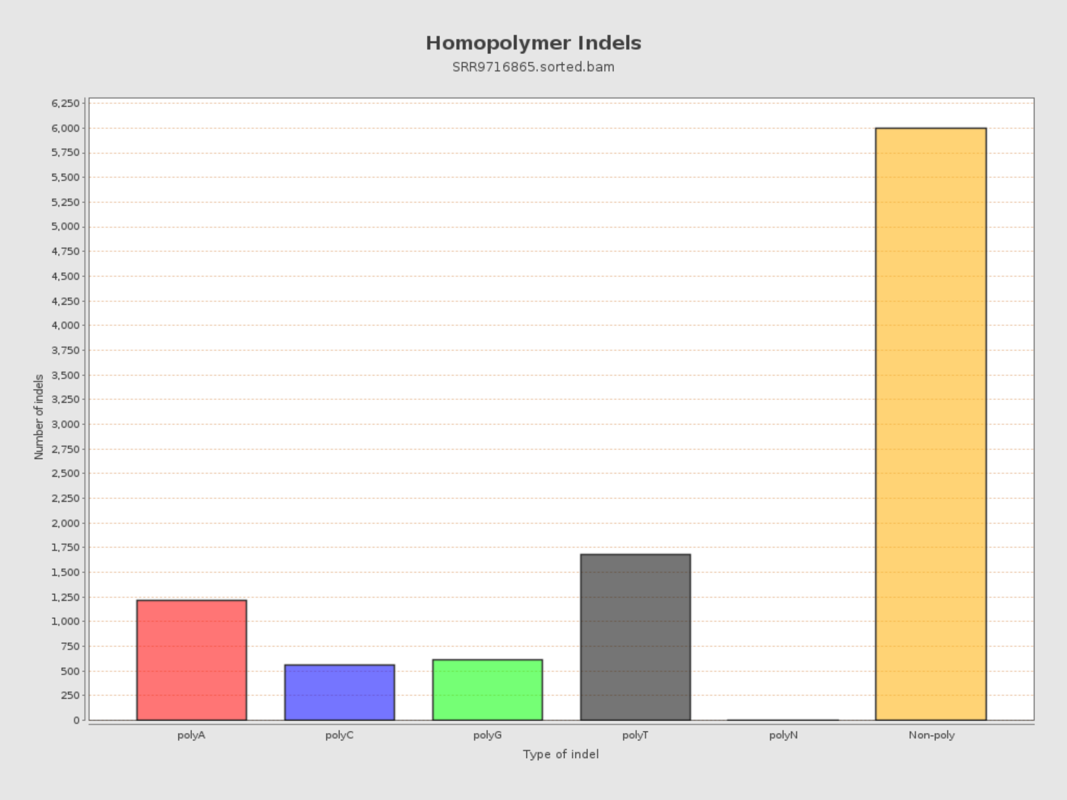
9. Results : Mapped Reads GC-content Distribution



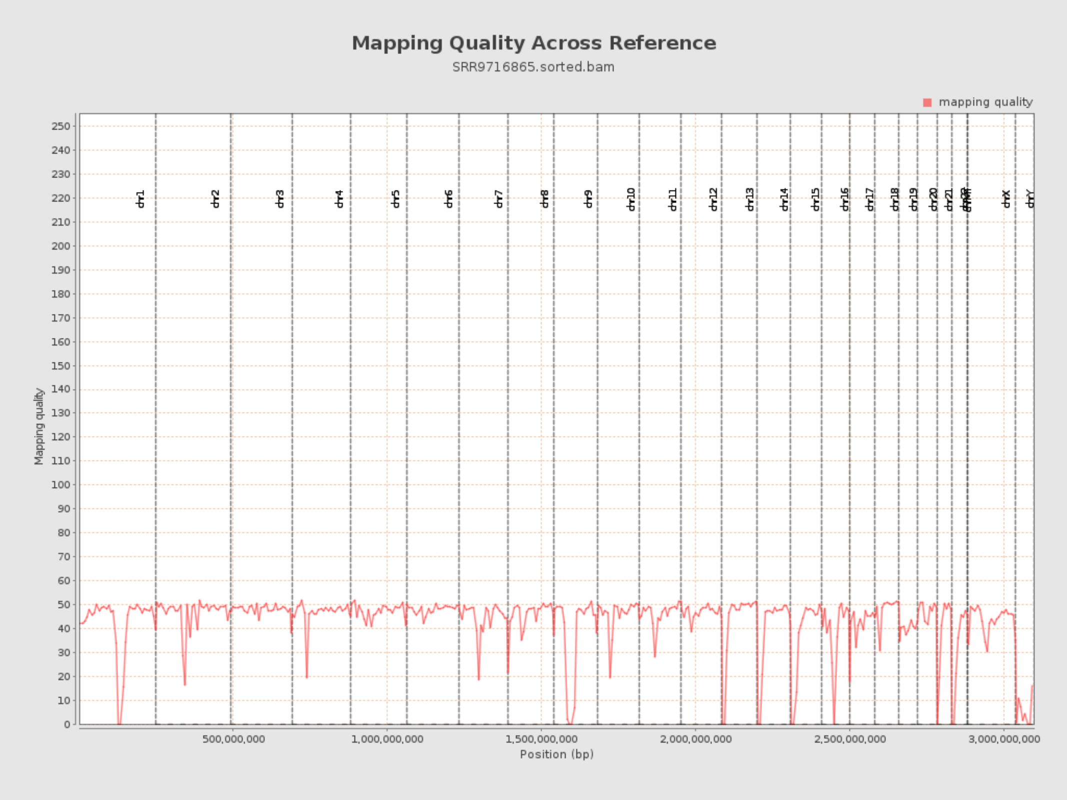
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram