Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 21:02:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716973.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_SRR9716973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716973.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 21:02:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	789,583
Mapped reads	696,409 / 88.2%
Unmapped reads	93,174 / 11.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,484 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	12,603 / 1.6%
Duplication rate	1.29%
Clipped reads	698,568 / 88.47%

2.2. ACGT Content

Number/percentage of A's	10,074,457 / 25.13%
Number/percentage of C's	7,296,703 / 18.2%
Number/percentage of T's	12,437,905 / 31.03%
Number/percentage of G's	10,272,618 / 25.63%
Number/percentage of N's	613 / 0%
GC Percentage	43.83%

2.3. Coverage

Mean	0.013

Standard Deviation	0.1468

2.4. Mapping Quality

Mean Mapping Quality	43.66

2.5. Mismatches and indels

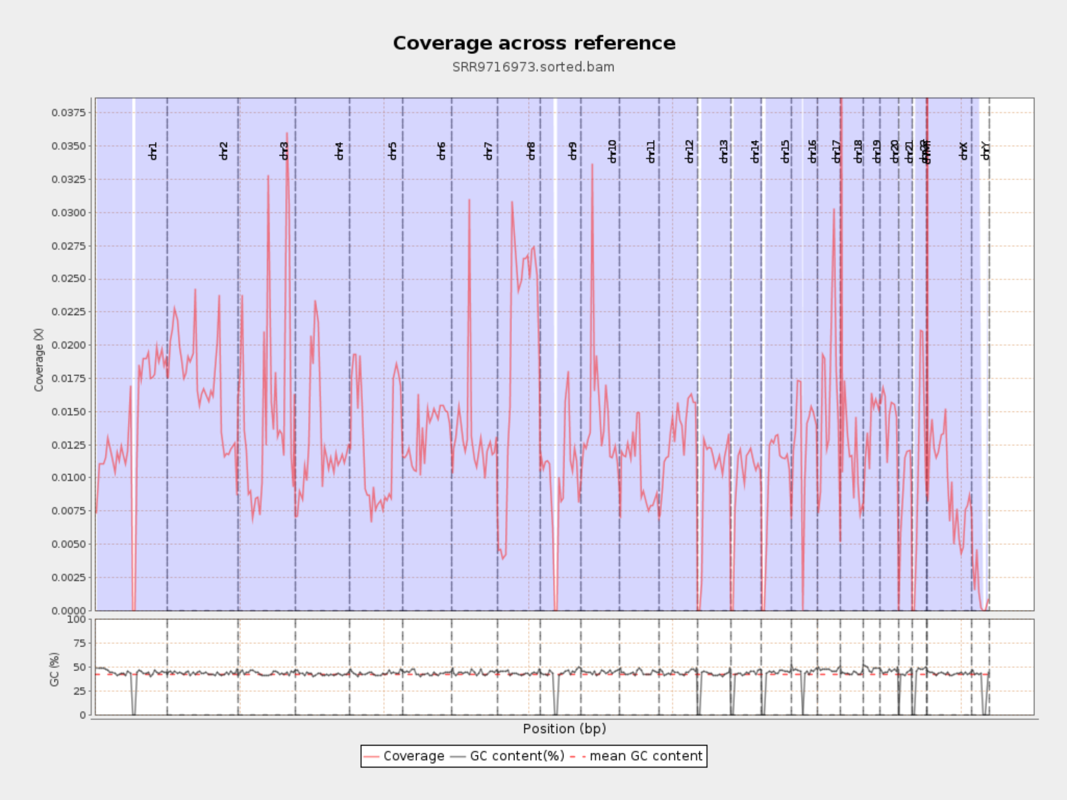
General error rate	0.52%
Mismatches	202,351
Insertions	2,803
Mapped reads with at least one insertion	0.4%
Deletions	7,673
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.31%

2.6. Chromosome stats

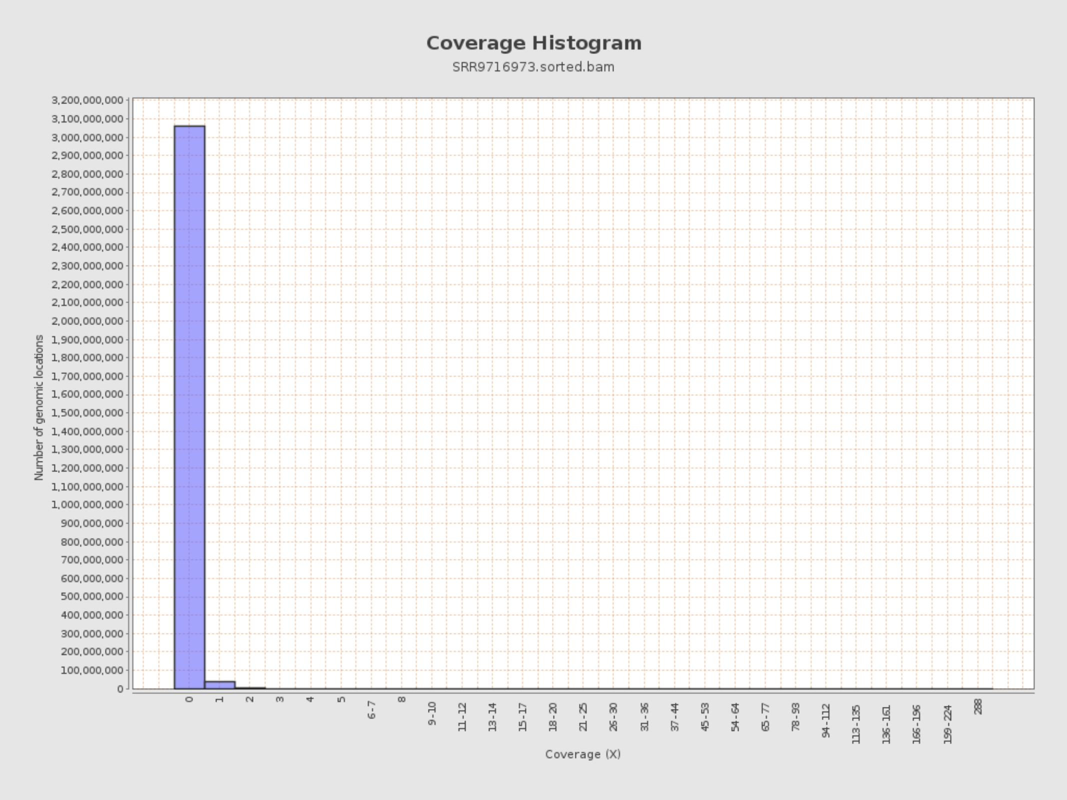
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3435691	0.0138	0.1704
chr2	243199373	4170382	0.0171	0.1882
chr3	198022430	3005574	0.0152	0.1311
chr4	191154276	2396663	0.0125	0.1187
chr5	180915260	2250179	0.0124	0.1161
chr6	171115067	2286592	0.0134	0.1261
chr7	159138663	2108688	0.0133	0.2699

chr8	146364022	2948300	0.0201	0.1635
chr9	141213431	1382927	0.0098	0.1136
chr10	135534747	1982010	0.0146	0.1779
chr11	135006516	1420444	0.0105	0.12
chr12	133851895	1770384	0.0132	0.122
chr13	115169878	1135578	0.0099	0.1034
chr14	107349540	1023771	0.0095	0.1038
chr15	102531392	999639	0.0097	0.1031
chr16	90354753	1145189	0.0127	0.1218
chr17	81195210	1305848	0.0161	0.1332
chr18	78077248	1035800	0.0133	0.1641
chr19	59128983	815785	0.0138	0.1659
chr20	63025520	928402	0.0147	0.1279
chr21	48129895	436597	0.0091	0.1001
chr22	51304566	543203	0.0106	0.1071
chrMT	16571	3734	0.2253	0.5281
chrX	155270560	1477393	0.0095	0.1086
chrY	59373566	85732	0.0014	0.0451

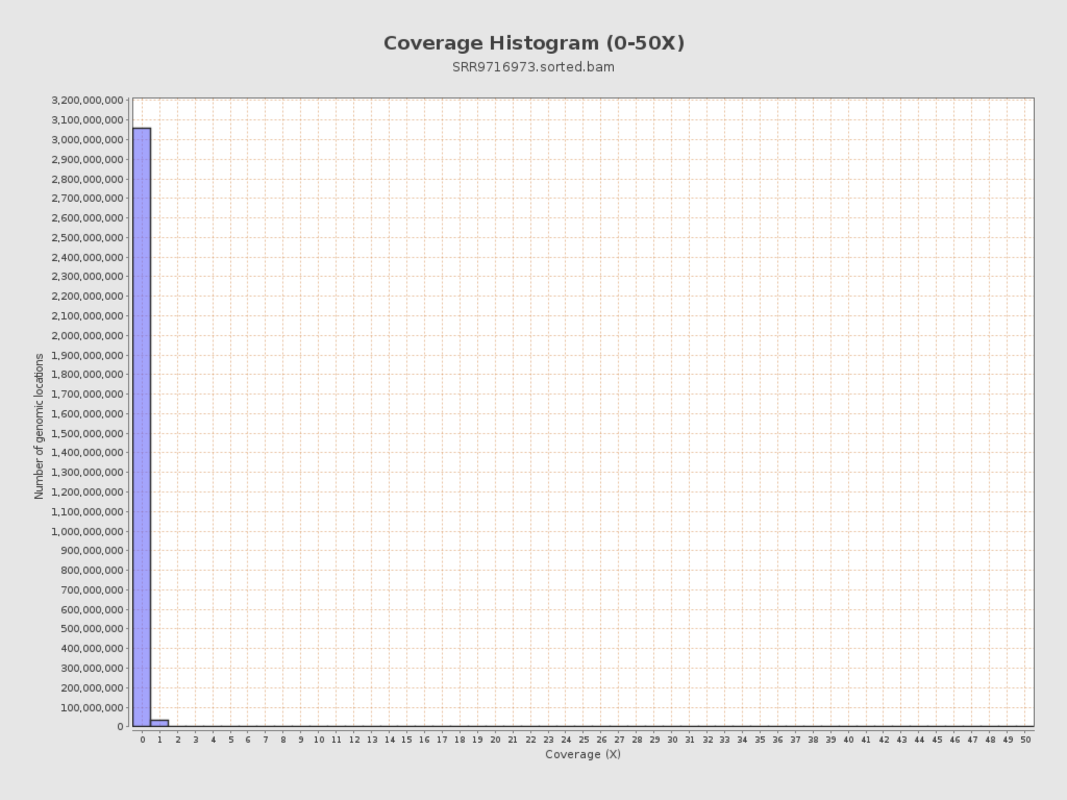
3. Results : Coverage across reference



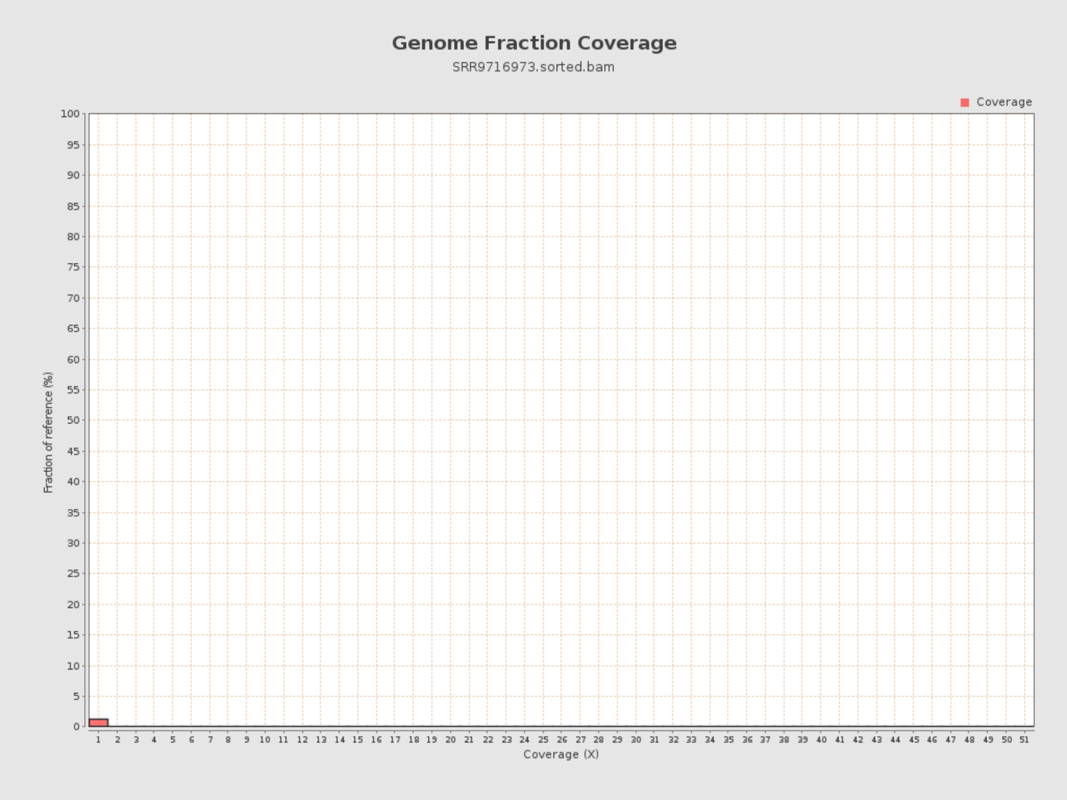
4. Results : Coverage Histogram



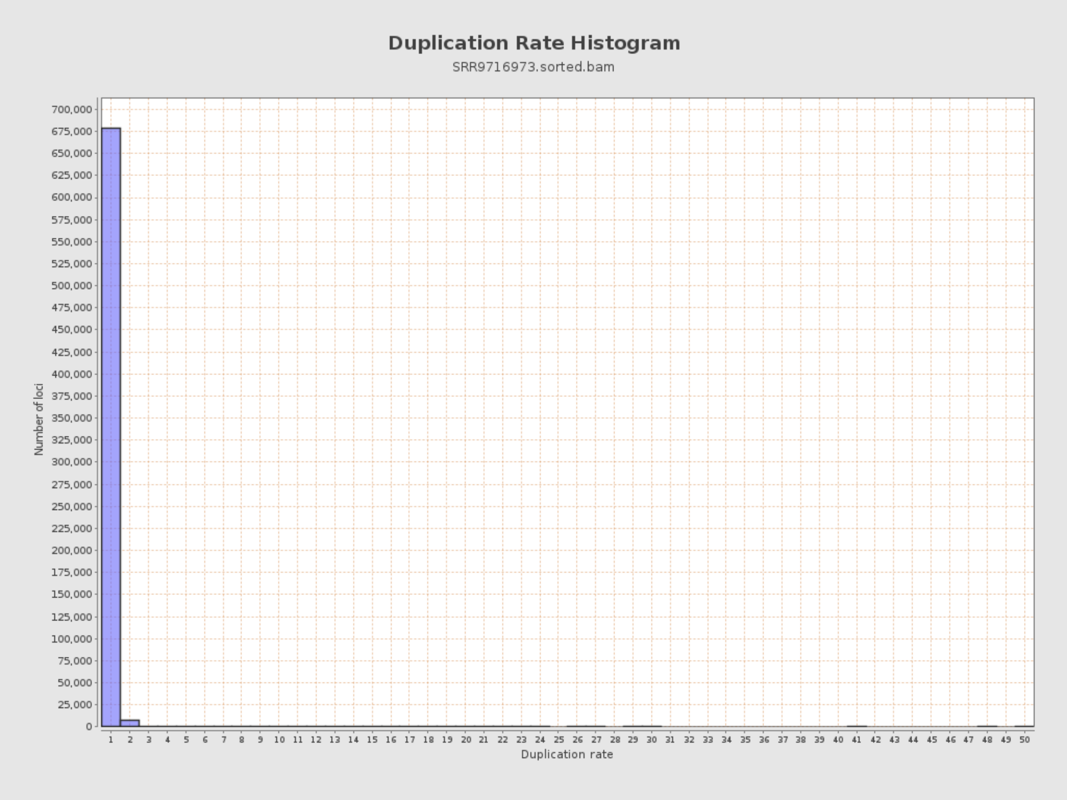
5. Results : Coverage Histogram (0-50X)



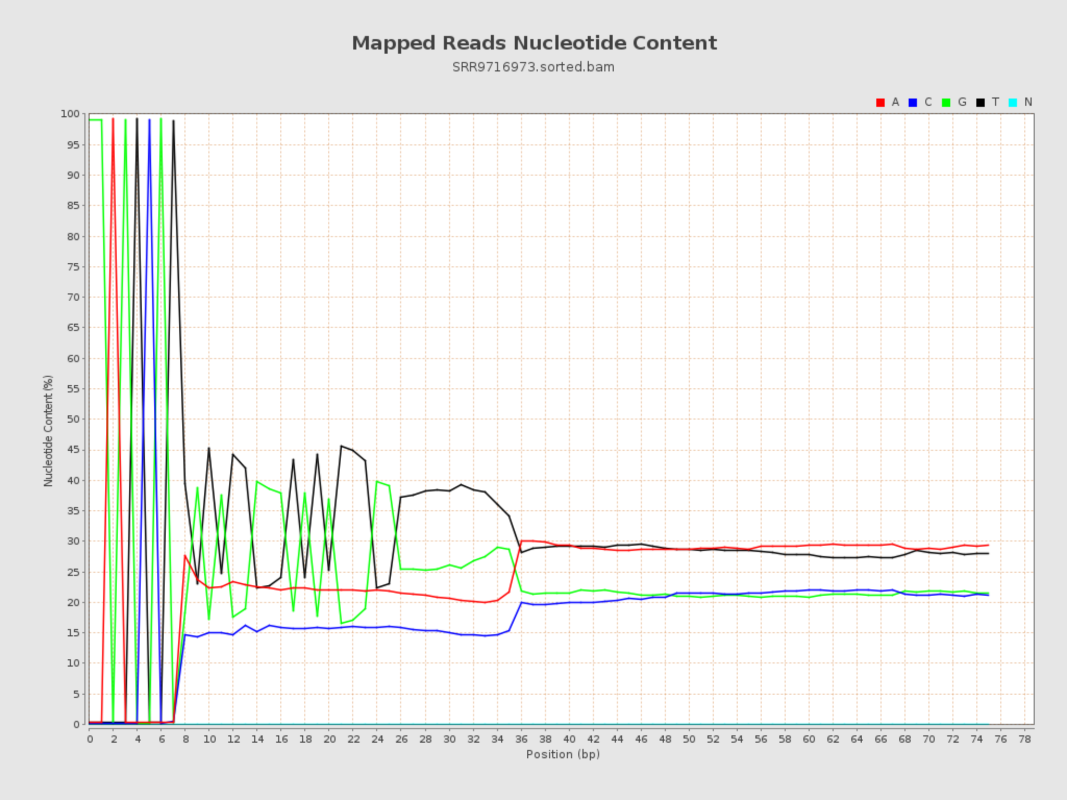
6. Results : Genome Fraction Coverage



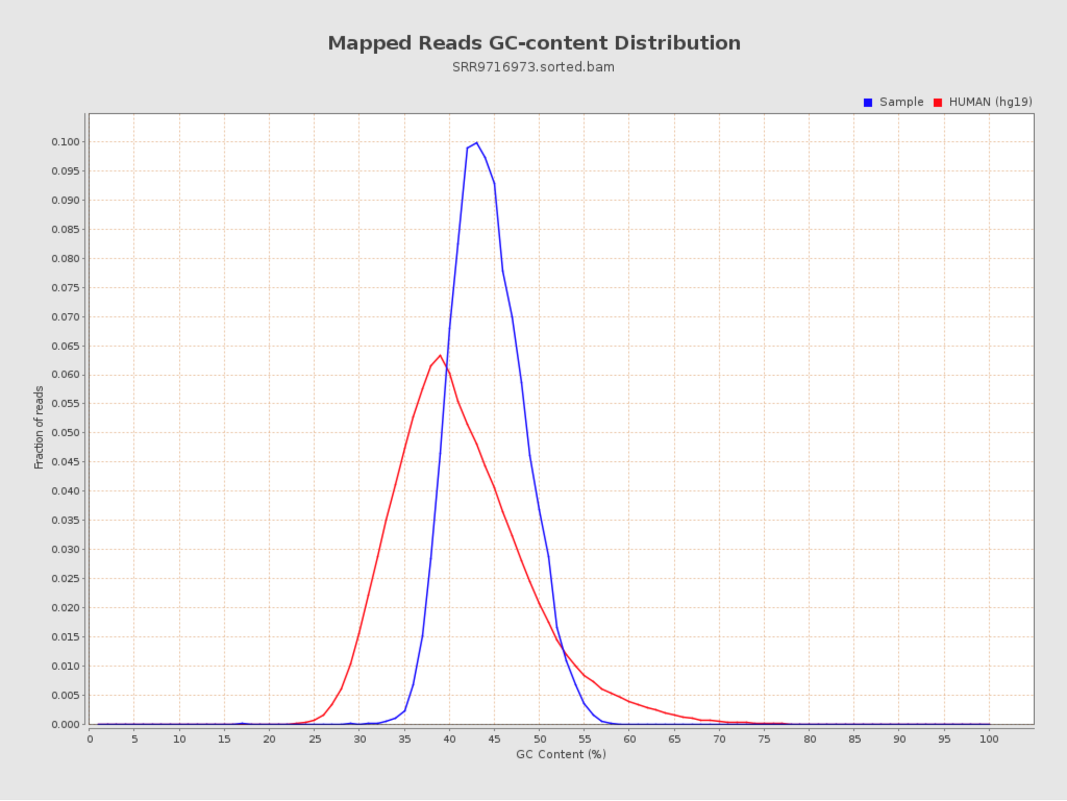
7. Results : Duplication Rate Histogram



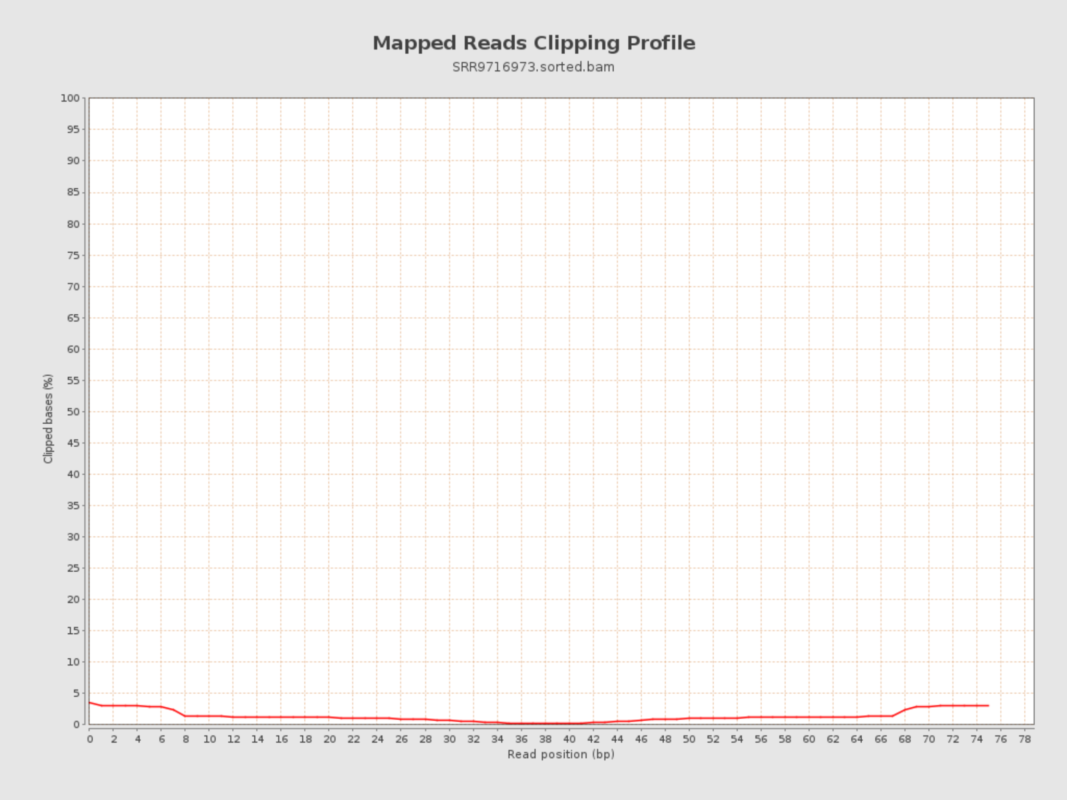
8. Results : Mapped Reads Nucleotide Content



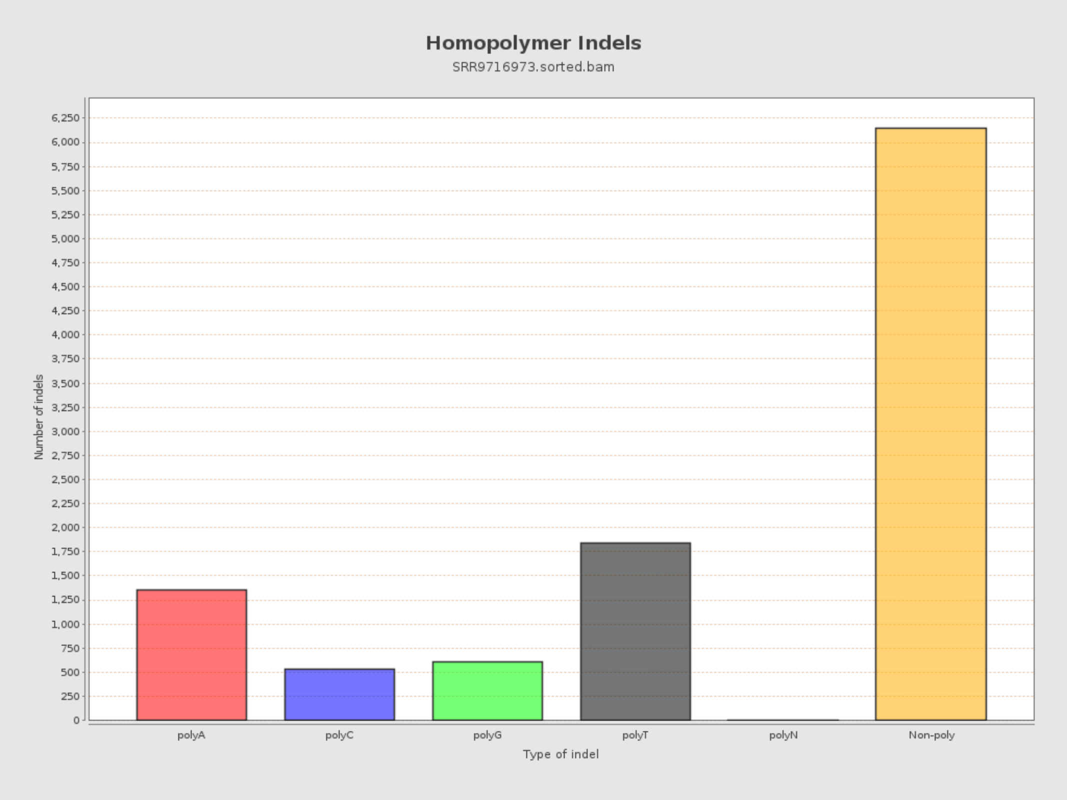
9. Results : Mapped Reads GC-content Distribution



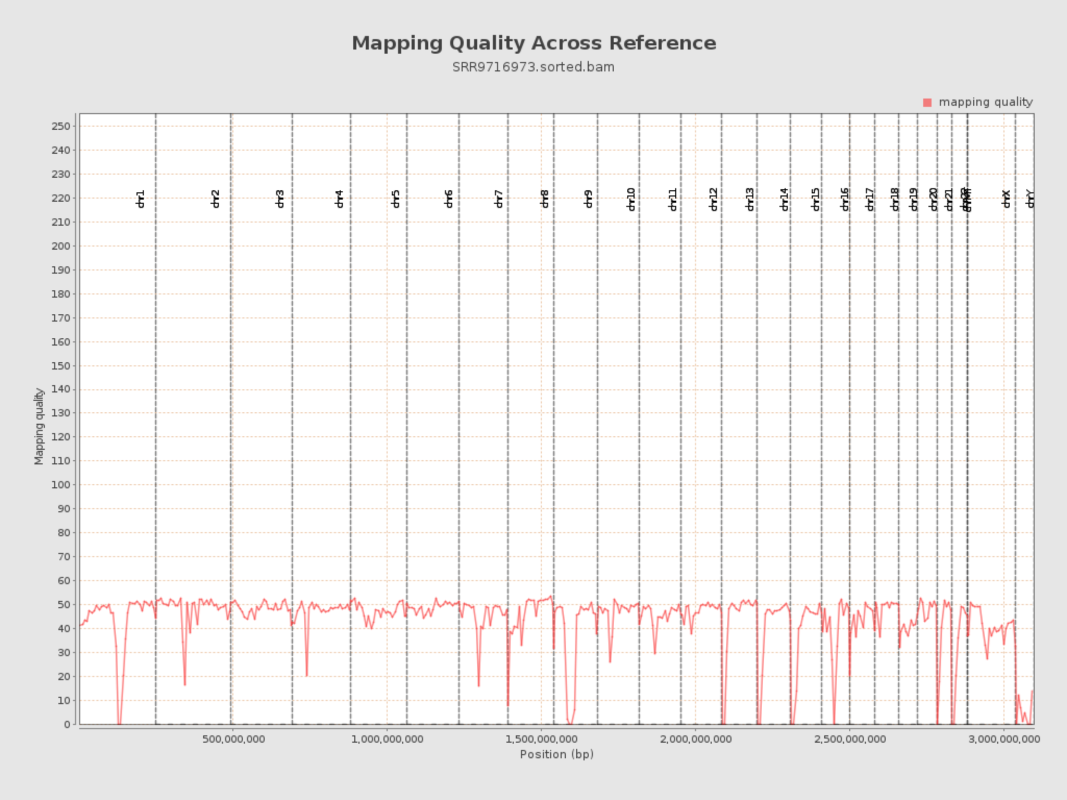
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram