Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 21:04:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716974.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_SRR9716974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716974.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 21:04:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	976,814
Mapped reads	841,273 / 86.12%
Unmapped reads	135,541 / 13.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,438 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	16,457 / 1.68%
Duplication rate	1.36%
Clipped reads	843,761 / 86.38%

2.2. ACGT Content

Number/percentage of A's	11,229,358 / 23.65%
Number/percentage of C's	9,118,927 / 19.21%
Number/percentage of T's	15,017,445 / 31.63%
Number/percentage of G's	12,109,859 / 25.51%
Number/percentage of N's	757 / 0%
GC Percentage	44.71%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1623

2.4. Mapping Quality

Mean Mapping Quality	41.89

2.5. Mismatches and indels

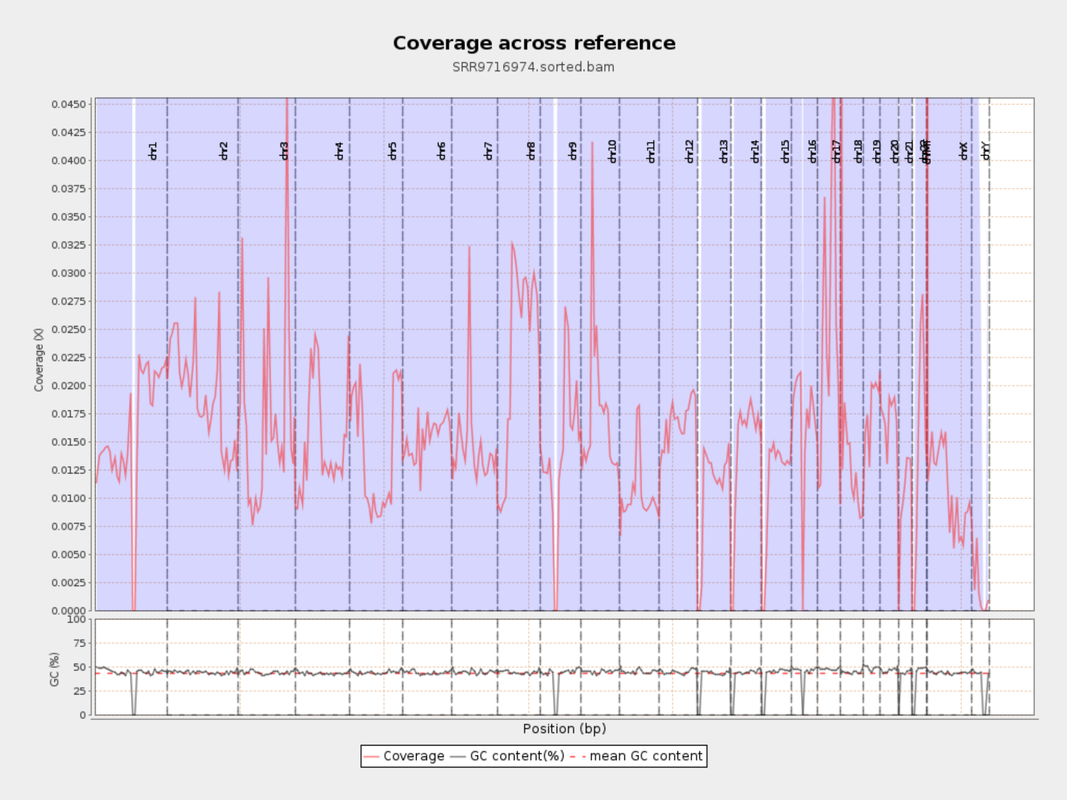
General error rate	0.54%
Mismatches	253,281
Insertions	2,936
Mapped reads with at least one insertion	0.35%
Deletions	9,123
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.5%

2.6. Chromosome stats

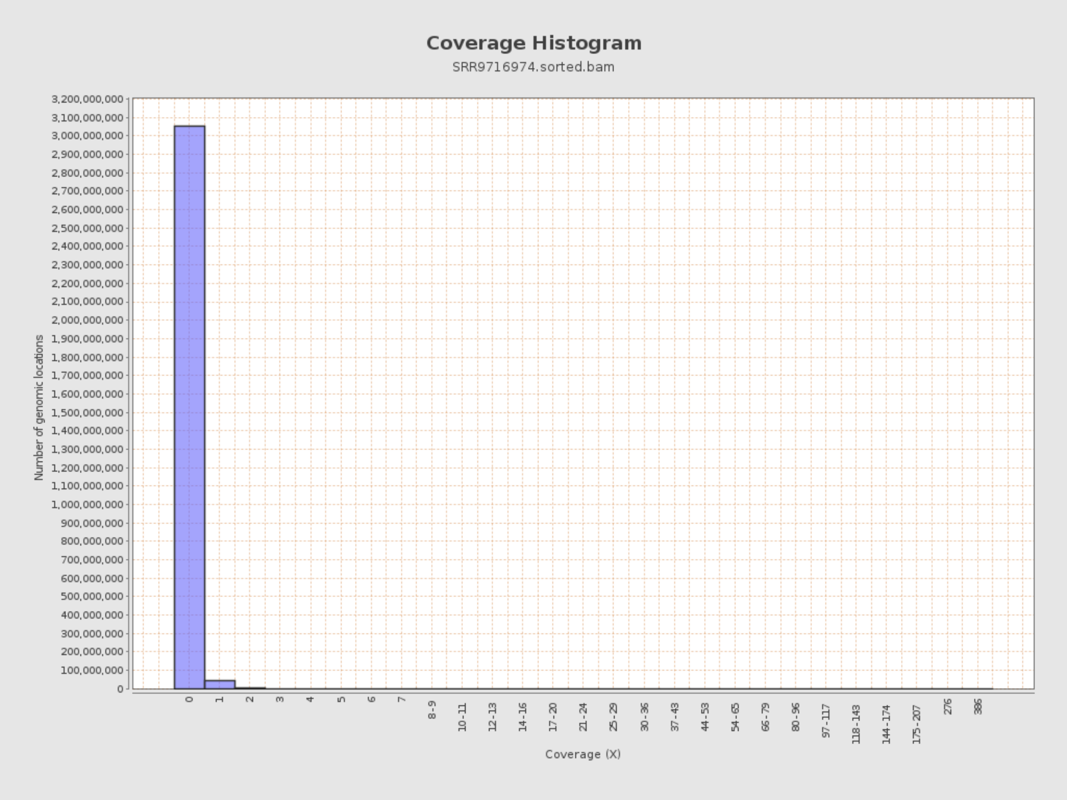
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3948324	0.0158	0.1893
chr2	243199373	4661929	0.0192	0.2247
chr3	198022430	3345695	0.0169	0.1419
chr4	191154276	2859354	0.015	0.1331
chr5	180915260	2541014	0.014	0.1239
chr6	171115067	2628589	0.0154	0.14
chr7	159138663	2346144	0.0147	0.2686

chr8	146364022	3409977	0.0233	0.1751
chr9	141213431	1964172	0.0139	0.1361
chr10	135534747	2373258	0.0175	0.1995
chr11	135006516	1415231	0.0105	0.1181
chr12	133851895	2218772	0.0166	0.1375
chr13	115169878	1222138	0.0106	0.1074
chr14	107349540	1530880	0.0143	0.1264
chr15	102531392	1140271	0.0111	0.1109
chr16	90354753	1496264	0.0166	0.1396
chr17	81195210	2084845	0.0257	0.1731
chr18	78077248	1135663	0.0145	0.1771
chr19	59128983	1045684	0.0177	0.1961
chr20	63025520	1068179	0.0169	0.1381
chr21	48129895	494476	0.0103	0.1086
chr22	51304566	727759	0.0142	0.1257
chrMT	16571	43467	2.6231	2.2555
chrX	155270560	1673896	0.0108	0.1177
chrY	59373566	115074	0.0019	0.0604

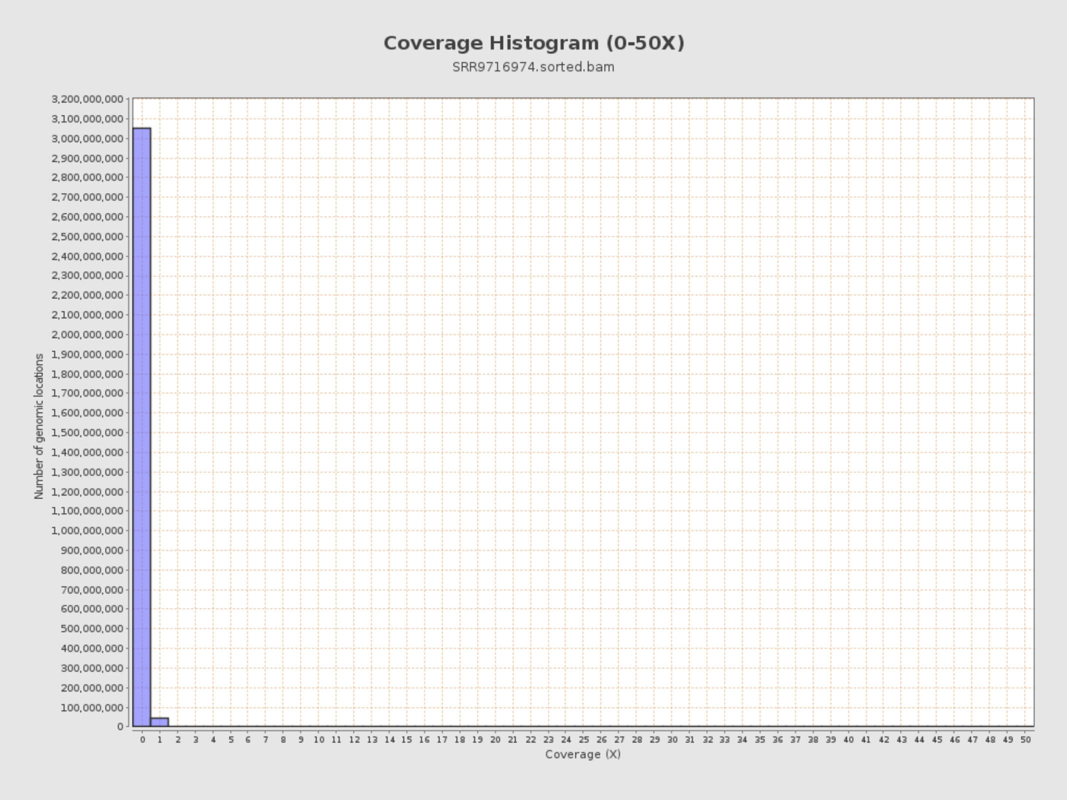
3. Results : Coverage across reference



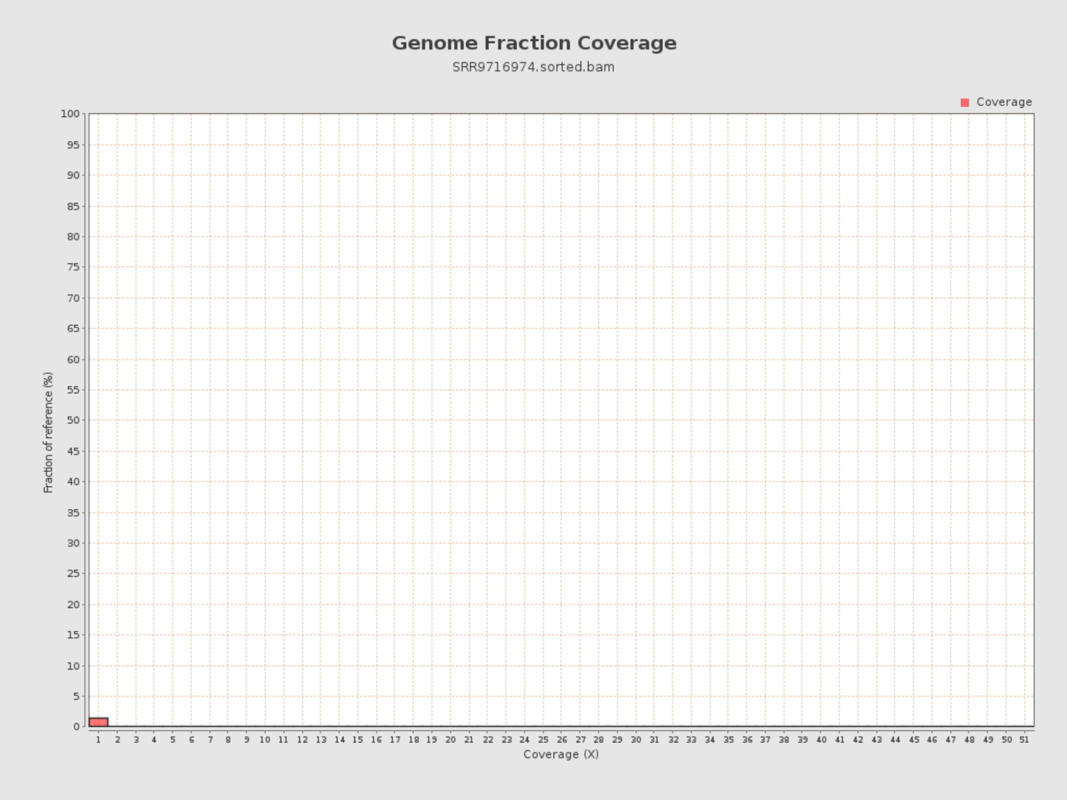
4. Results : Coverage Histogram



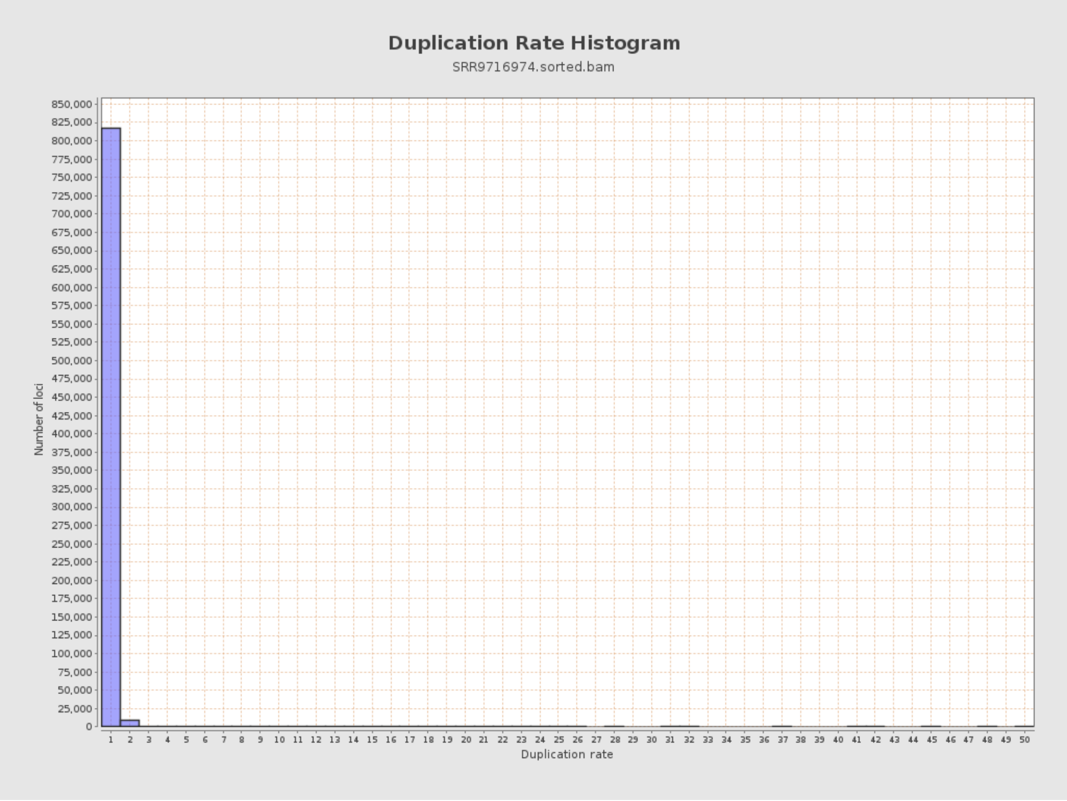
5. Results : Coverage Histogram (0-50X)



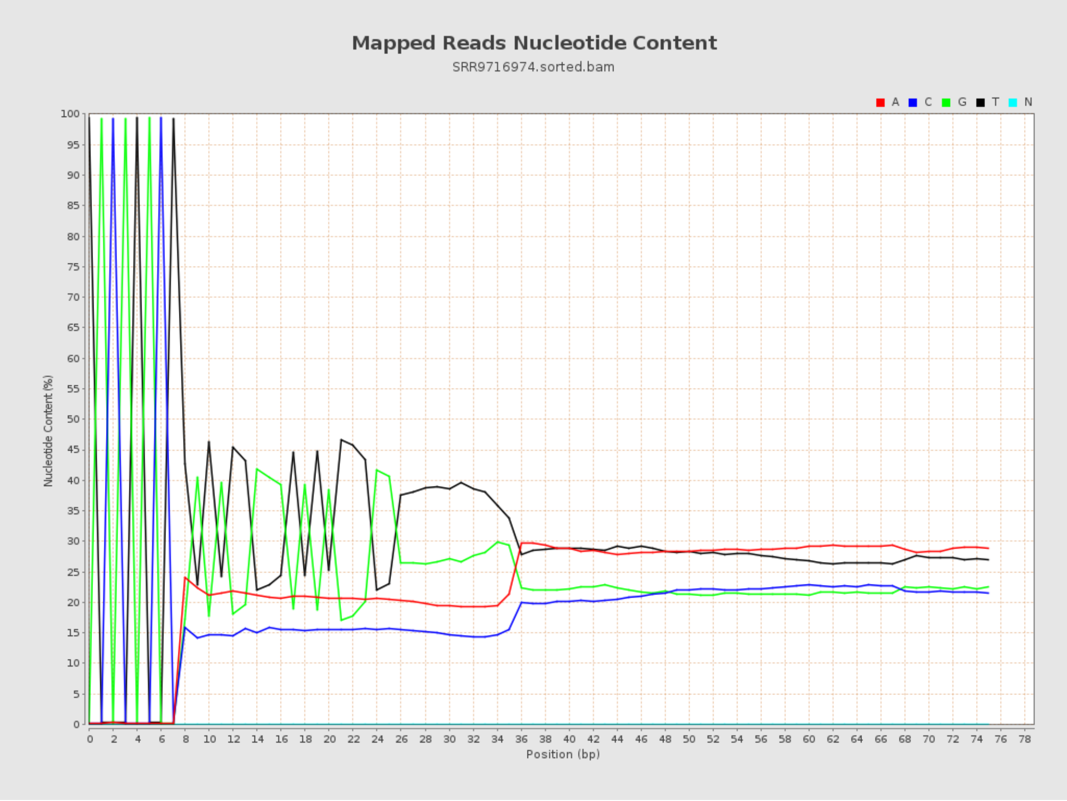
6. Results : Genome Fraction Coverage



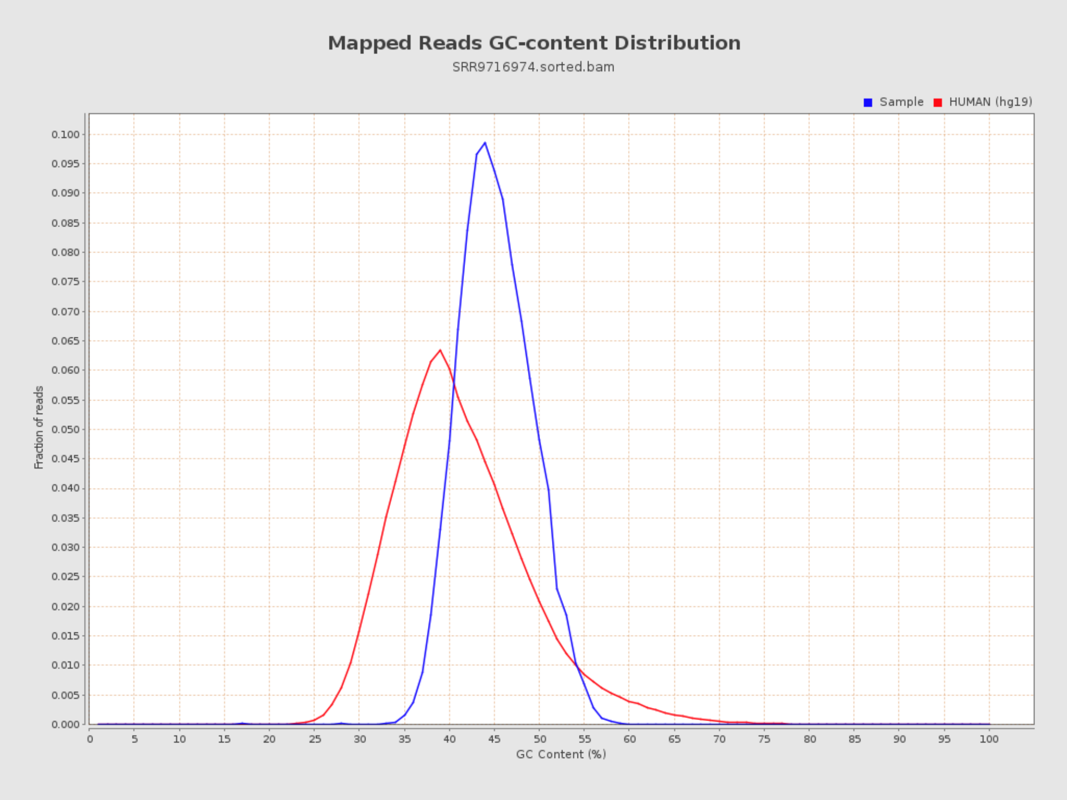
7. Results : Duplication Rate Histogram



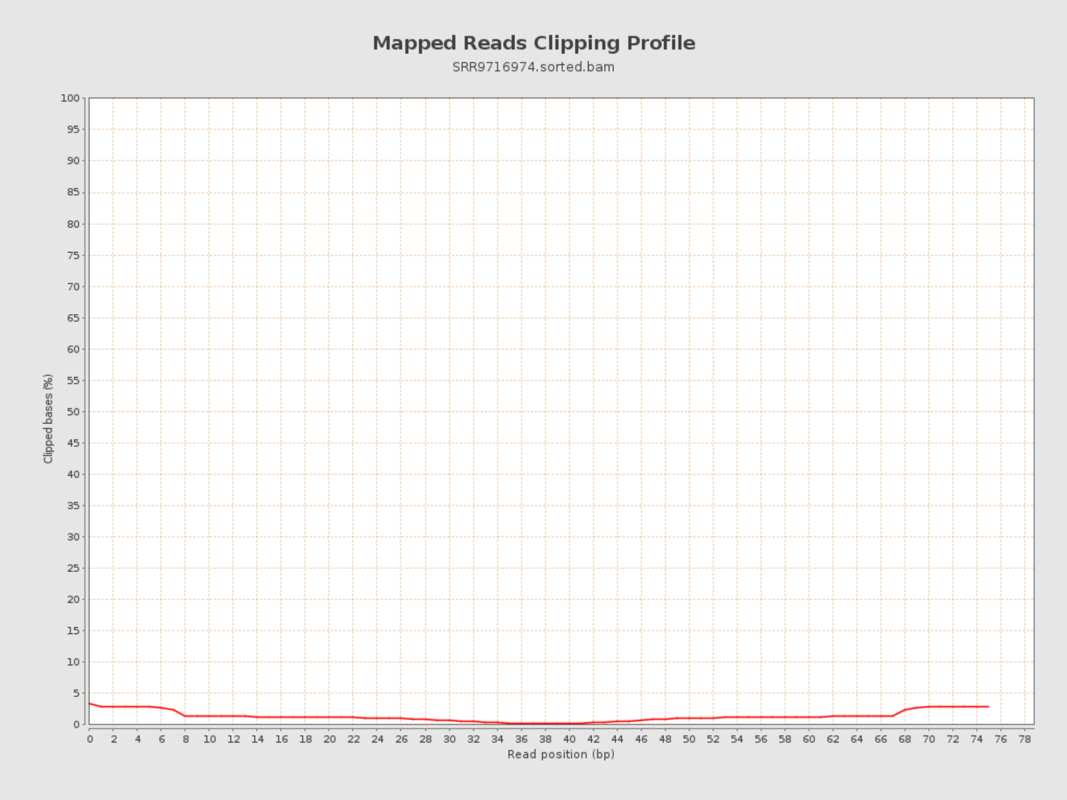
8. Results : Mapped Reads Nucleotide Content



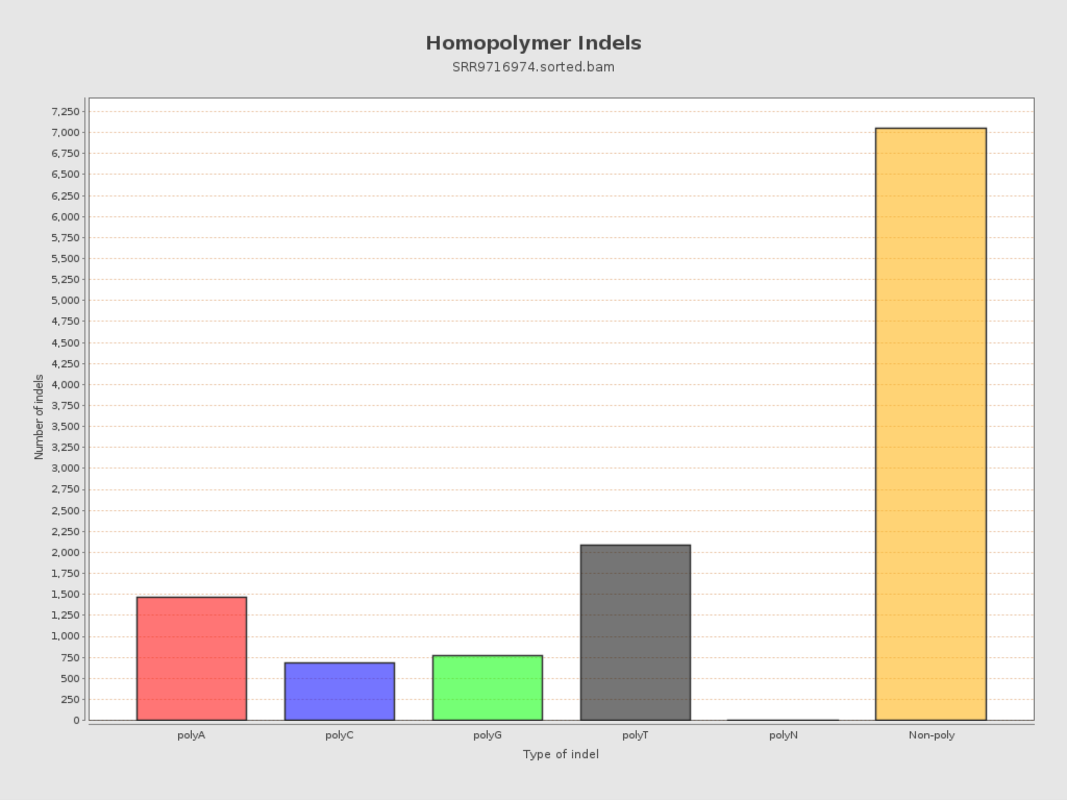
9. Results : Mapped Reads GC-content Distribution



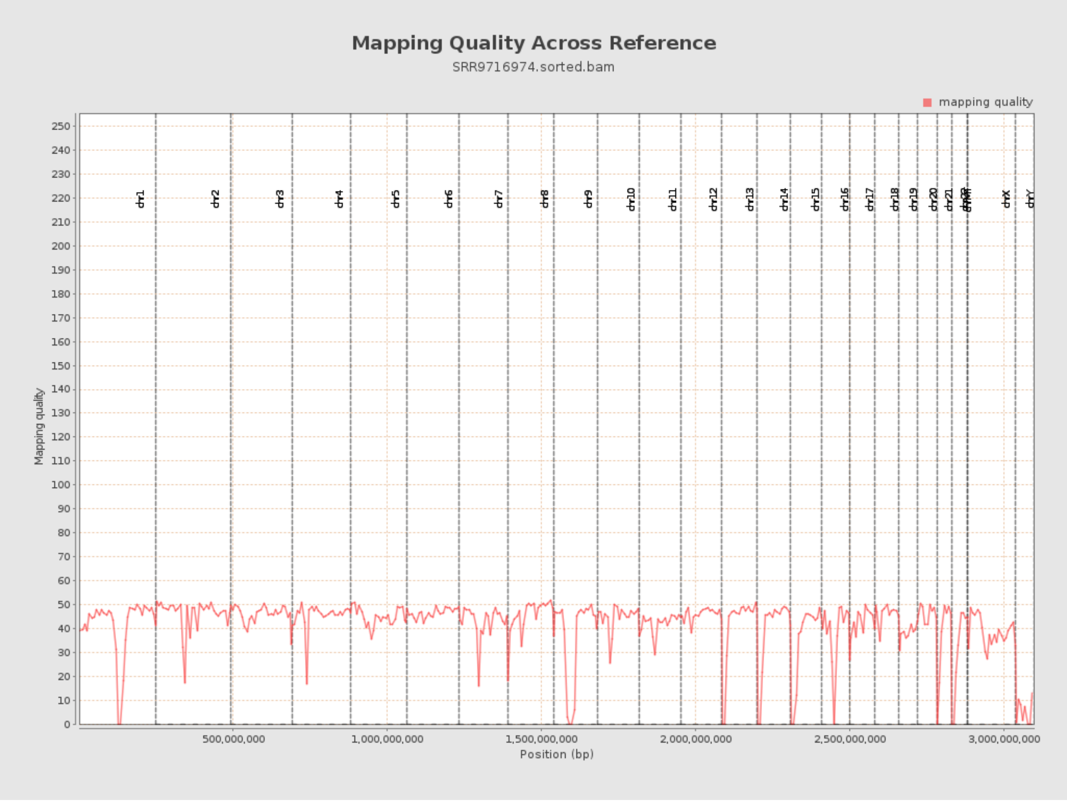
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram