Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:24:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716884.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_SRR9716884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716884.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:24:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	996,245
Mapped reads	876,174 / 87.95%
Unmapped reads	120,071 / 12.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,955 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	21,459 / 2.15%
Duplication rate	1.85%
Clipped reads	877,370 / 88.07%

2.2. ACGT Content

Number/percentage of A's	12,965,535 / 25.62%
Number/percentage of C's	9,822,290 / 19.41%
Number/percentage of T's	15,918,939 / 31.46%
Number/percentage of G's	11,892,810 / 23.5%
Number/percentage of N's	1,479 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.166

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

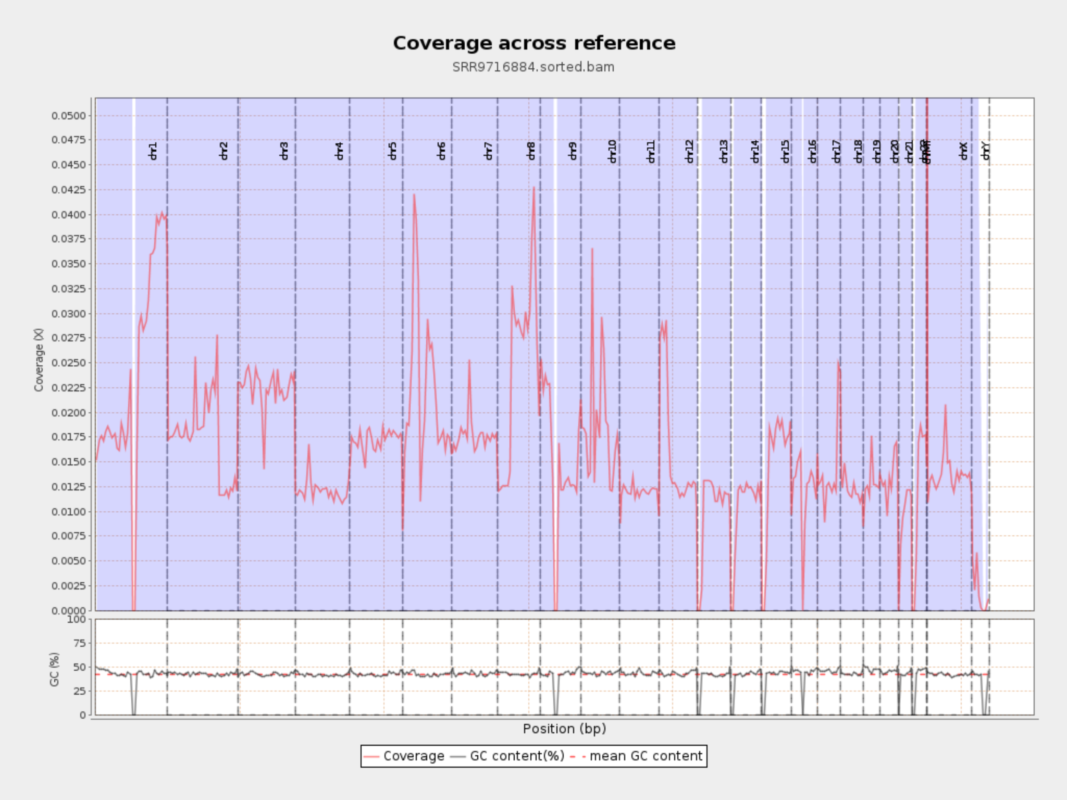
General error rate	0.51%
Mismatches	248,822
Insertions	4,128
Mapped reads with at least one insertion	0.47%
Deletions	9,274
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41%

2.6. Chromosome stats

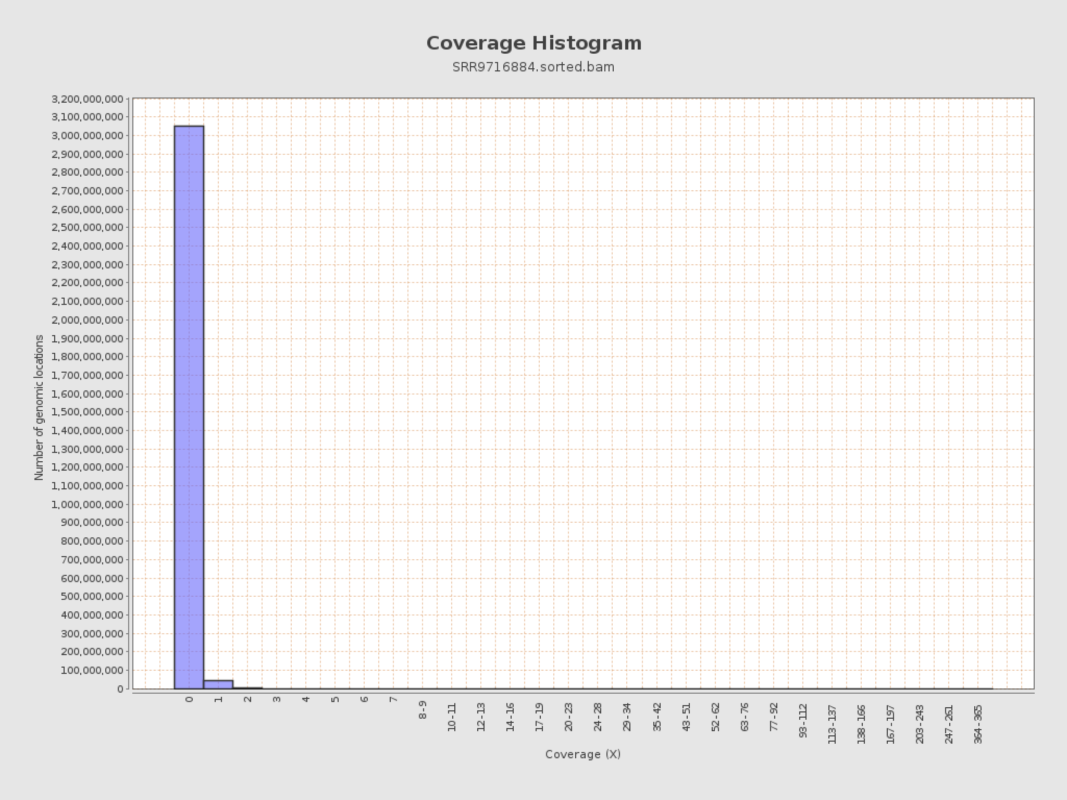
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5911195	0.0237	0.2414
chr2	243199373	4271223	0.0176	0.2087
chr3	198022430	4446743	0.0225	0.1577
chr4	191154276	2318612	0.0121	0.1204
chr5	180915260	3133203	0.0173	0.1392
chr6	171115067	3752450	0.0219	0.1829
chr7	159138663	2832812	0.0178	0.2027

chr8	146364022	3612736	0.0247	0.177
chr9	141213431	2104670	0.0149	0.1634
chr10	135534747	2545670	0.0188	0.1912
chr11	135006516	1623652	0.012	0.1359
chr12	133851895	2199027	0.0164	0.1381
chr13	115169878	1161158	0.0101	0.1063
chr14	107349540	1090729	0.0102	0.1163
chr15	102531392	1484086	0.0145	0.1279
chr16	90354753	1070052	0.0118	0.1237
chr17	81195210	1146440	0.0141	0.1286
chr18	78077248	953765	0.0122	0.2222
chr19	59128983	764294	0.0129	0.1848
chr20	63025520	852079	0.0135	0.1228
chr21	48129895	453781	0.0094	0.1087
chr22	51304566	622449	0.0121	0.116
chrMT	16571	1776	0.1072	0.3235
chrX	155270560	2152743	0.0139	0.1368
chrY	59373566	110266	0.0019	0.0566

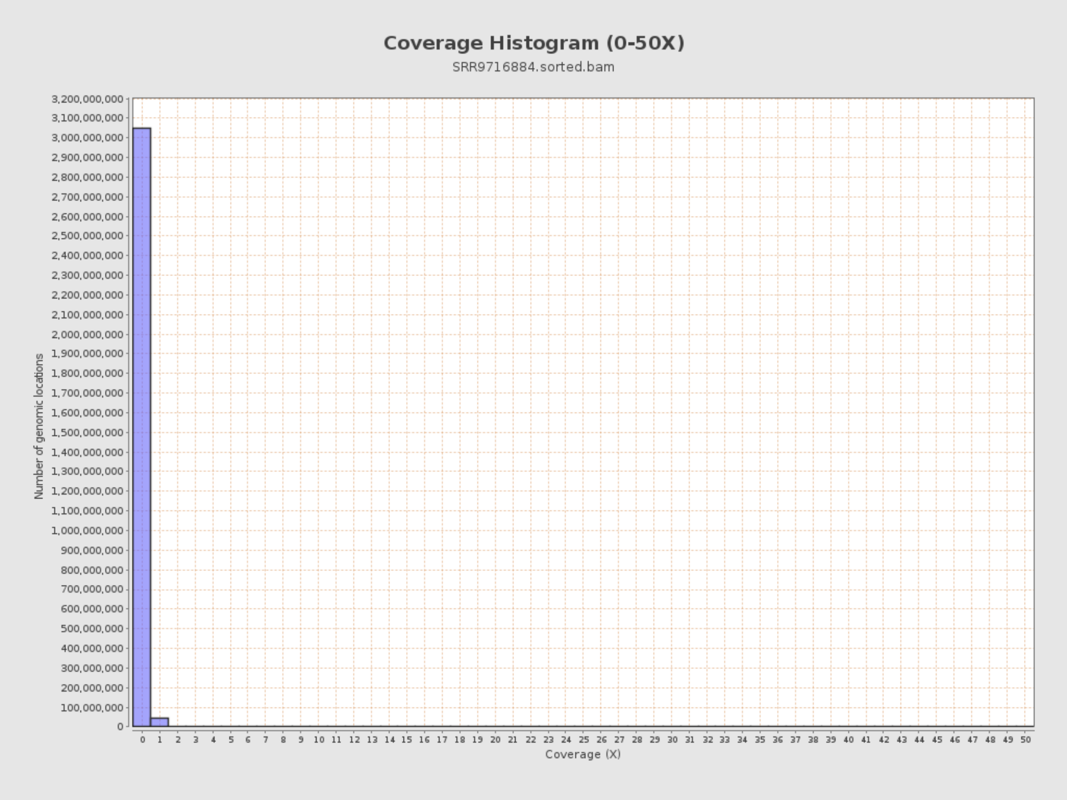
3. Results : Coverage across reference



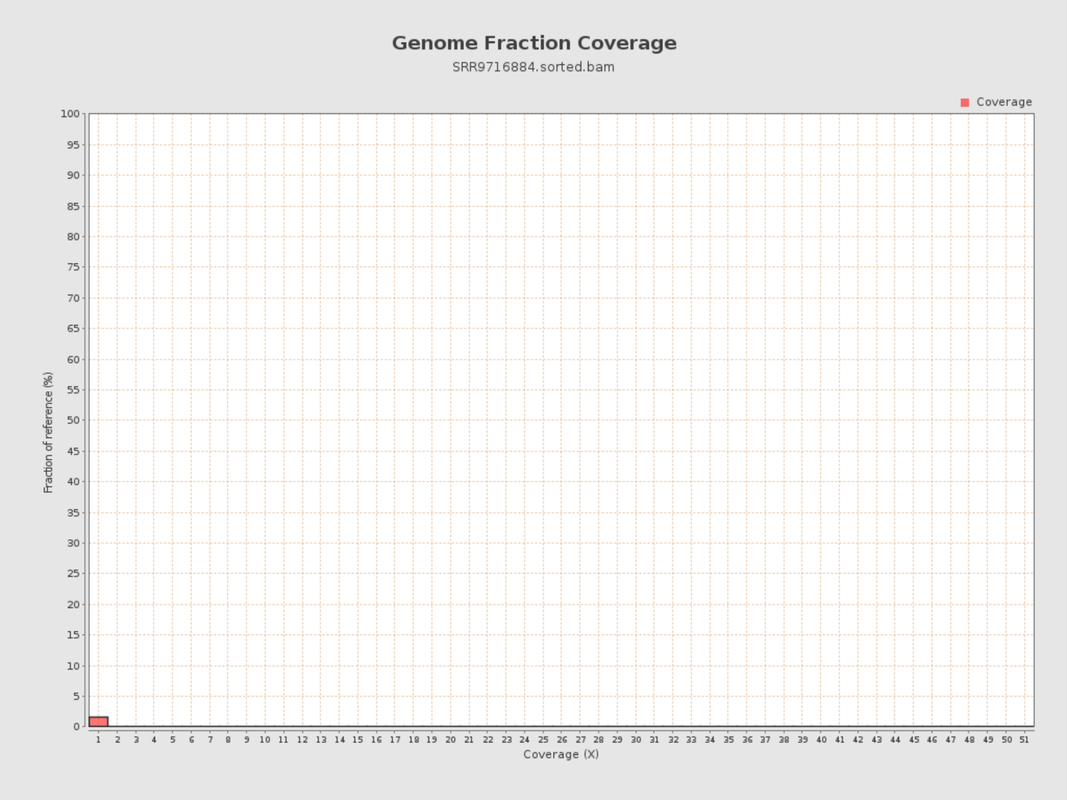
4. Results : Coverage Histogram



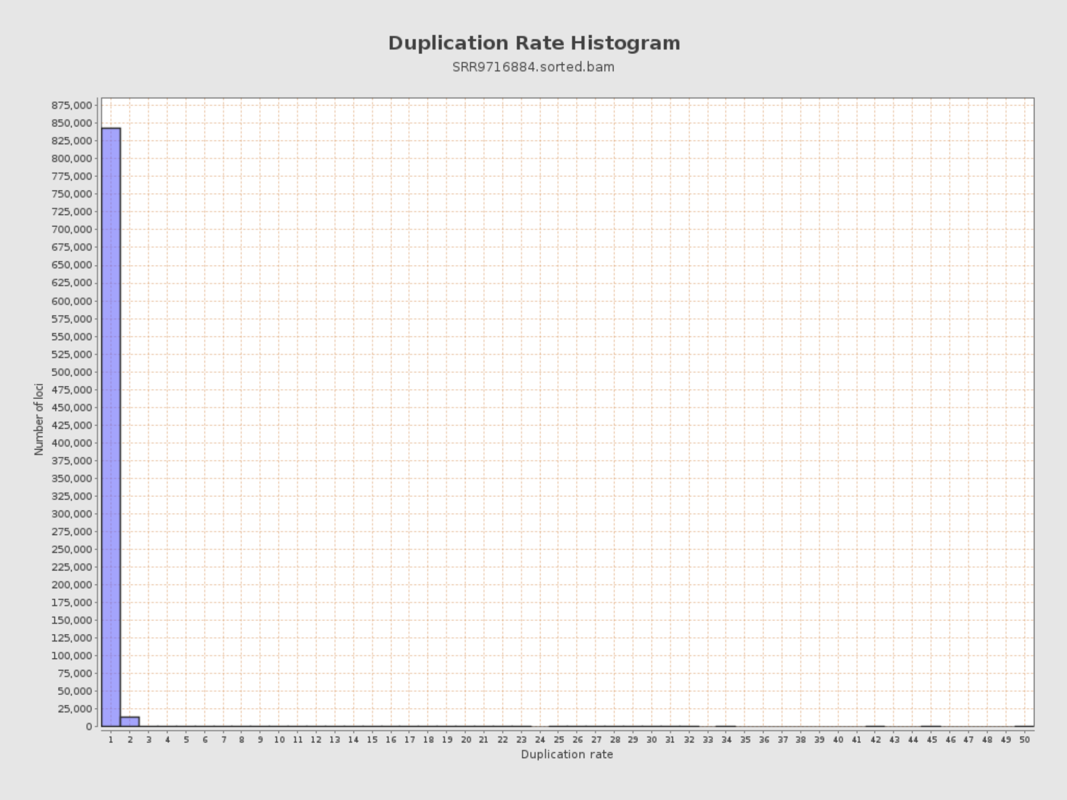
5. Results : Coverage Histogram (0-50X)



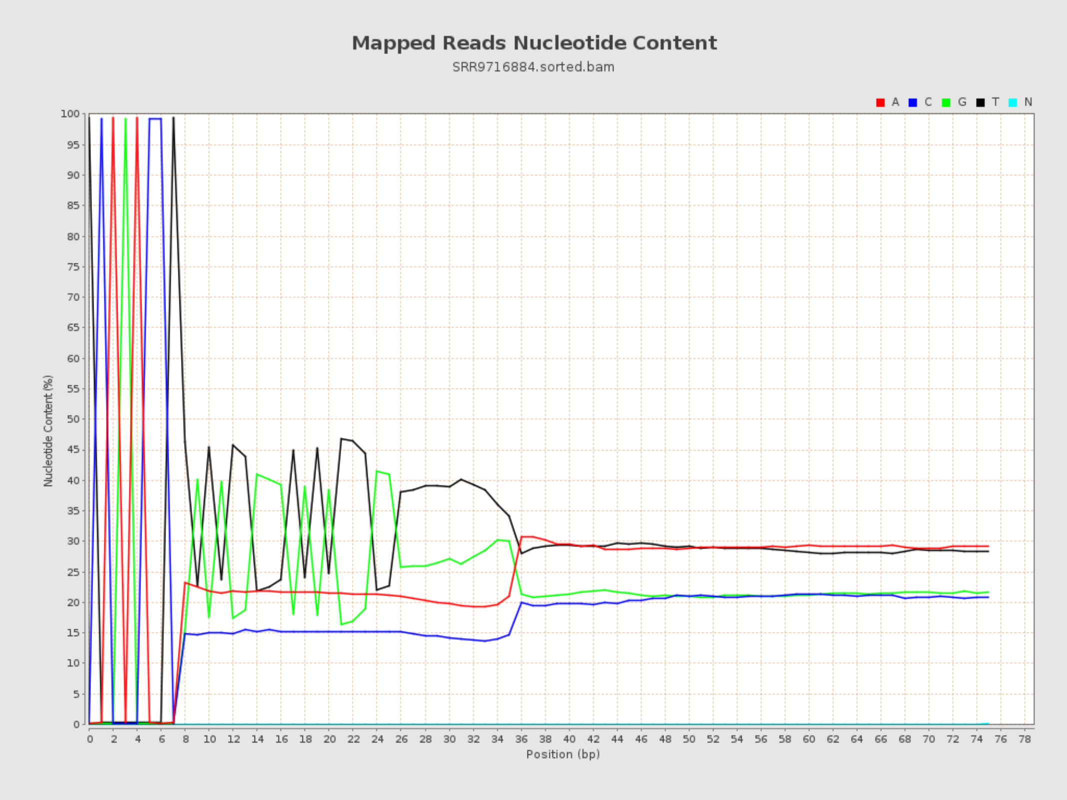
6. Results : Genome Fraction Coverage



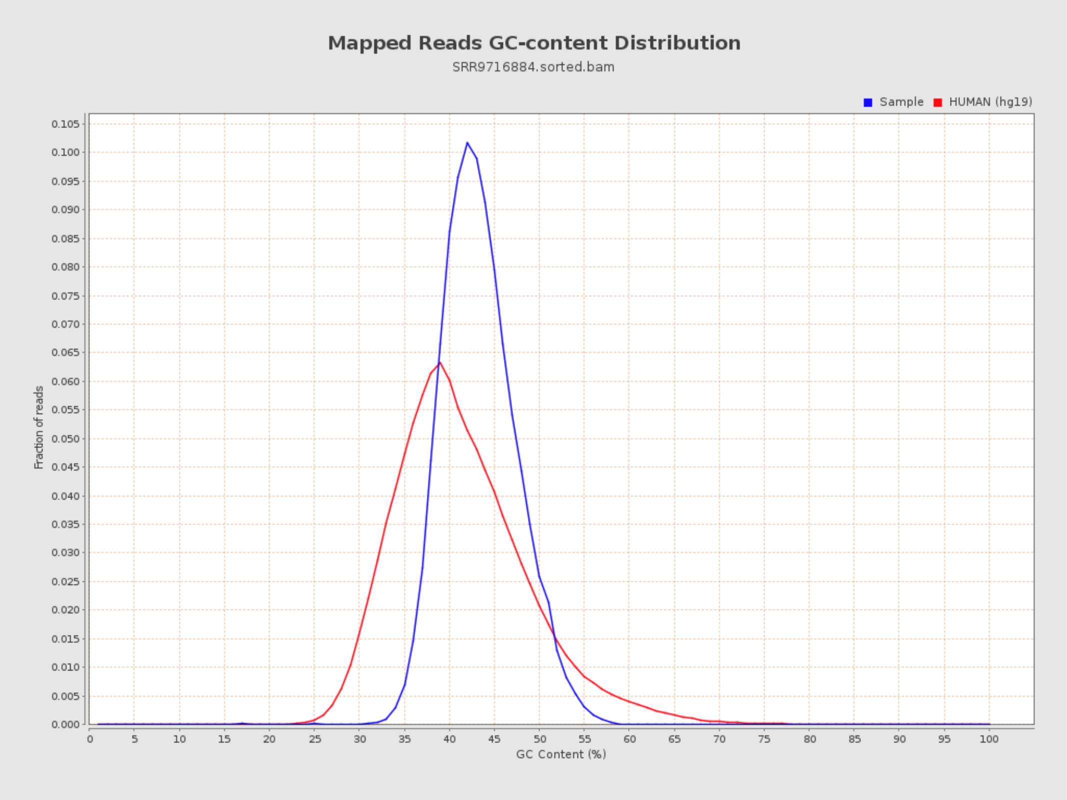
7. Results : Duplication Rate Histogram



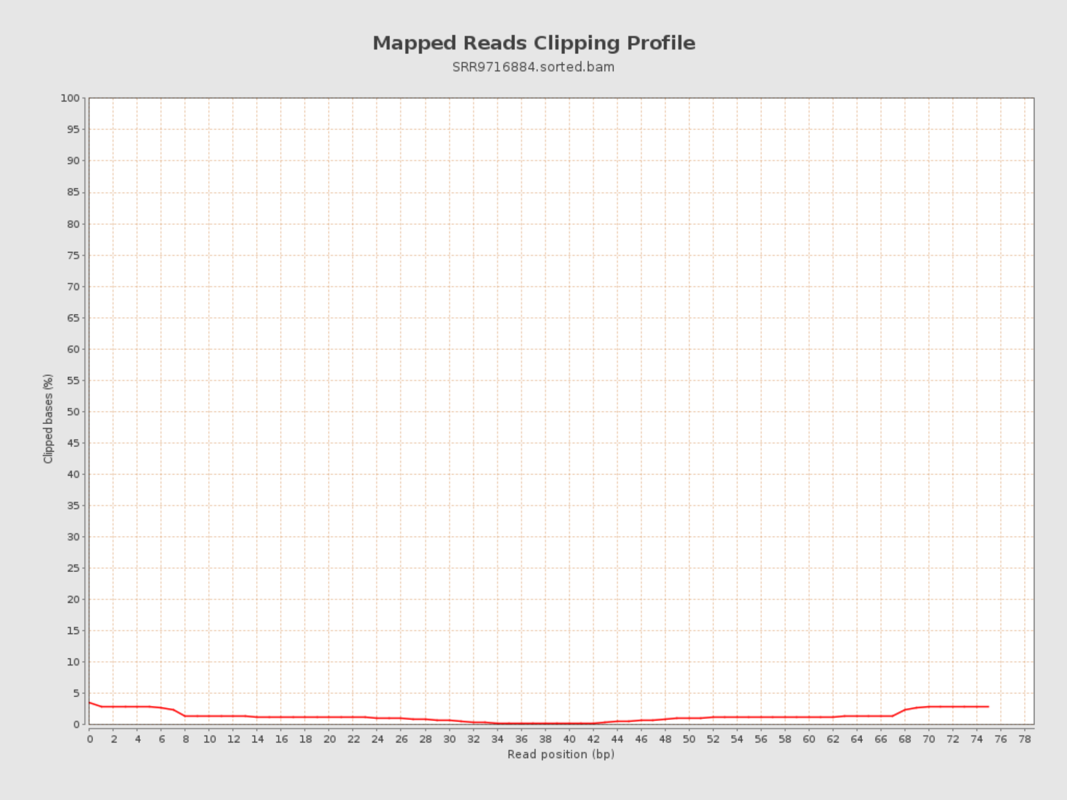
8. Results : Mapped Reads Nucleotide Content



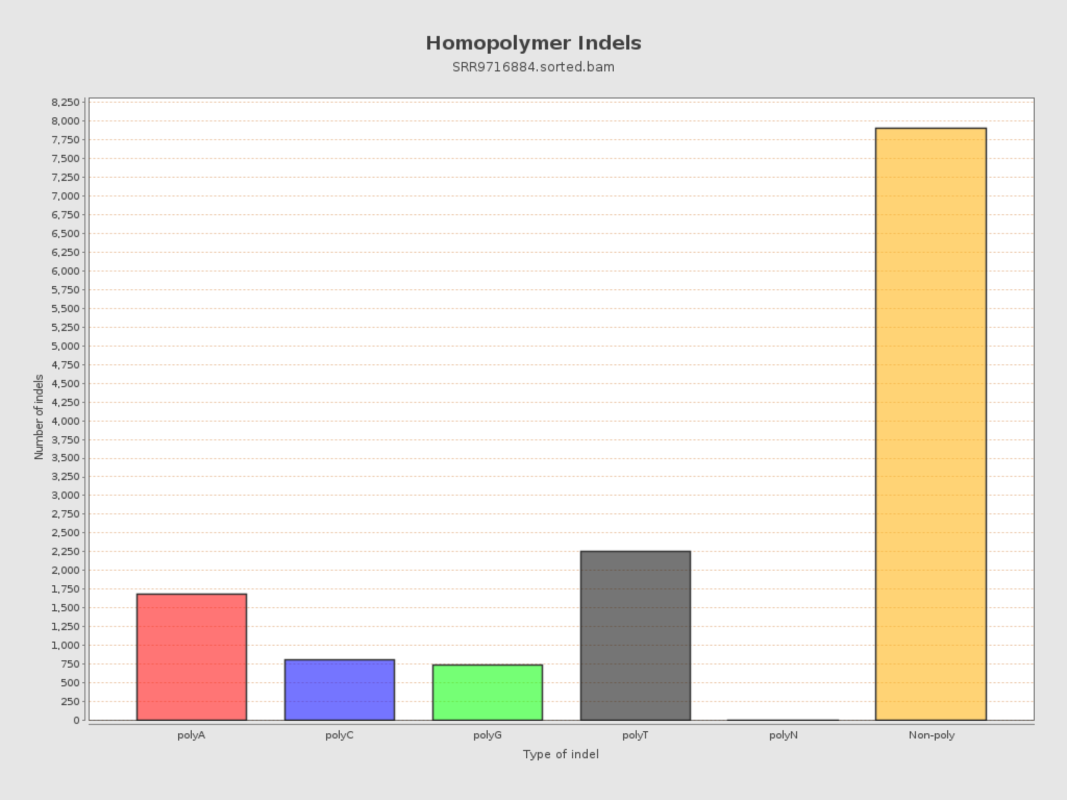
9. Results : Mapped Reads GC-content Distribution



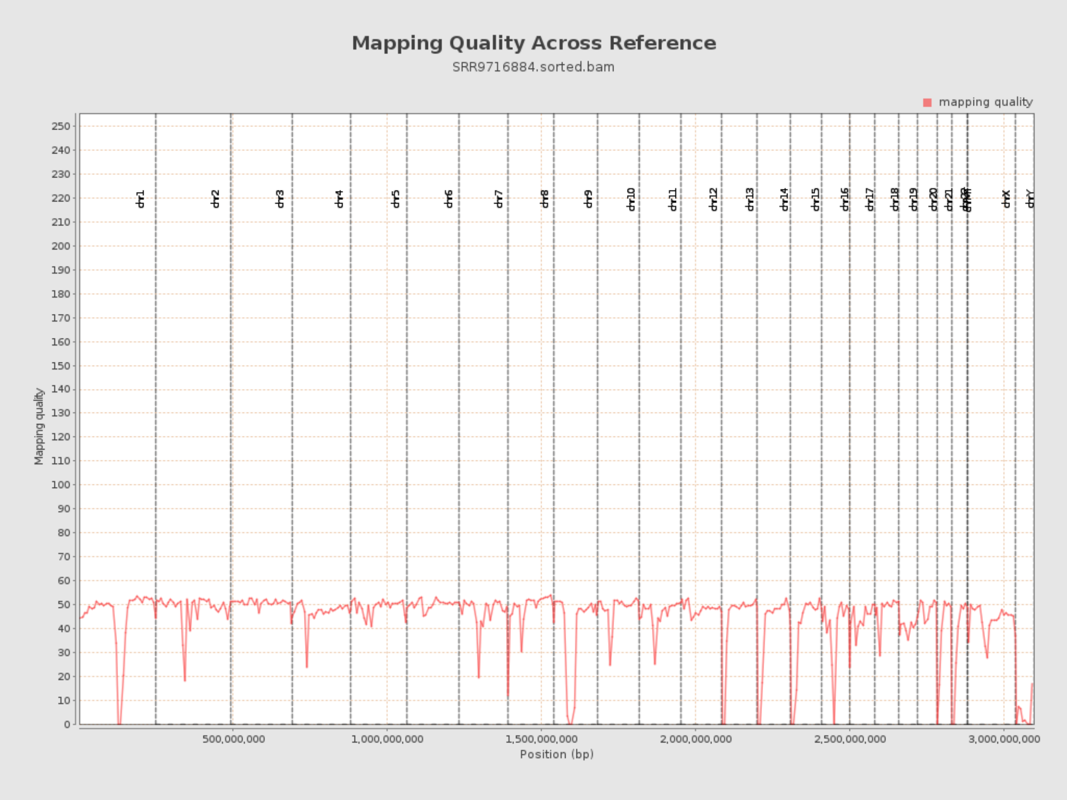
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram