Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716771.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_SRR9716771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716771.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:06:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	619,782
Mapped reads	576,132 / 92.96%
Unmapped reads	43,650 / 7.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,115 / 2.28%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	11,909 / 1.92%
Duplication rate	1.58%
Clipped reads	588,618 / 94.97%

2.2. ACGT Content

Number/percentage of A's	11,497,118 / 26.03%
Number/percentage of C's	8,904,160 / 20.16%
Number/percentage of T's	12,906,357 / 29.22%
Number/percentage of G's	10,854,801 / 24.58%
Number/percentage of N's	1,705 / 0%
GC Percentage	44.74%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.1525

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

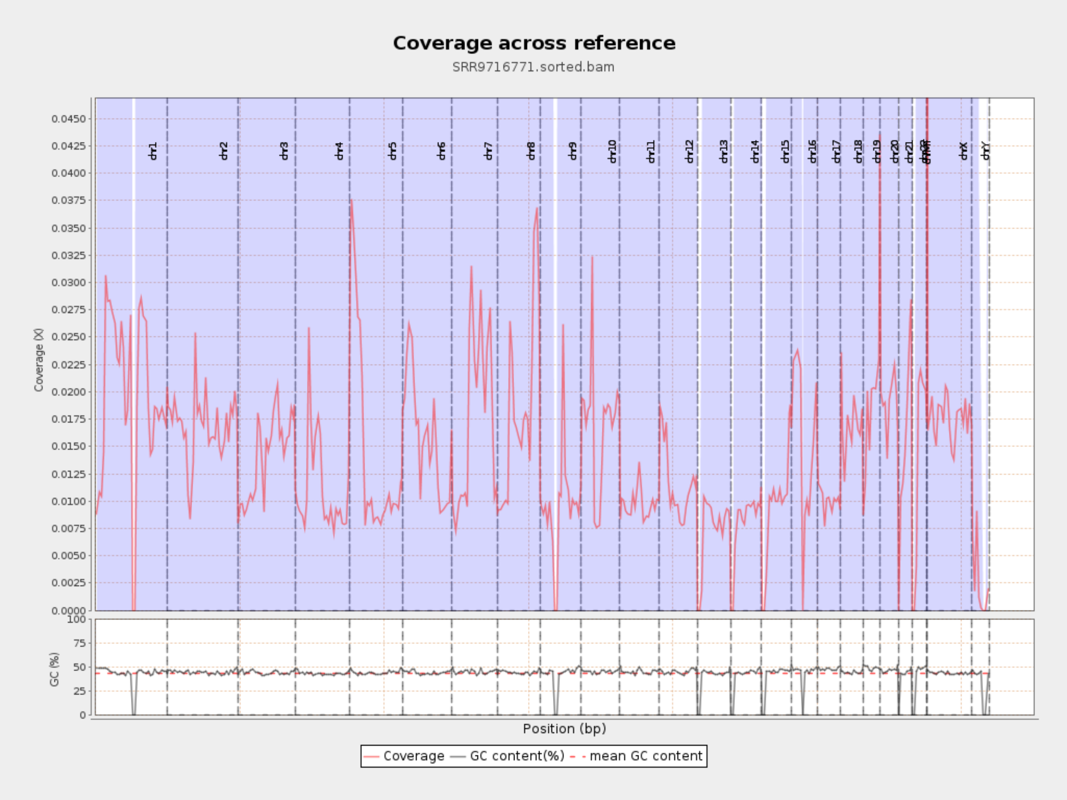
General error rate	0.68%
Mismatches	290,322
Insertions	4,454
Mapped reads with at least one insertion	0.76%
Deletions	8,830
Mapped reads with at least one deletion	1.51%
Homopolymer indels	38.25%

2.6. Chromosome stats

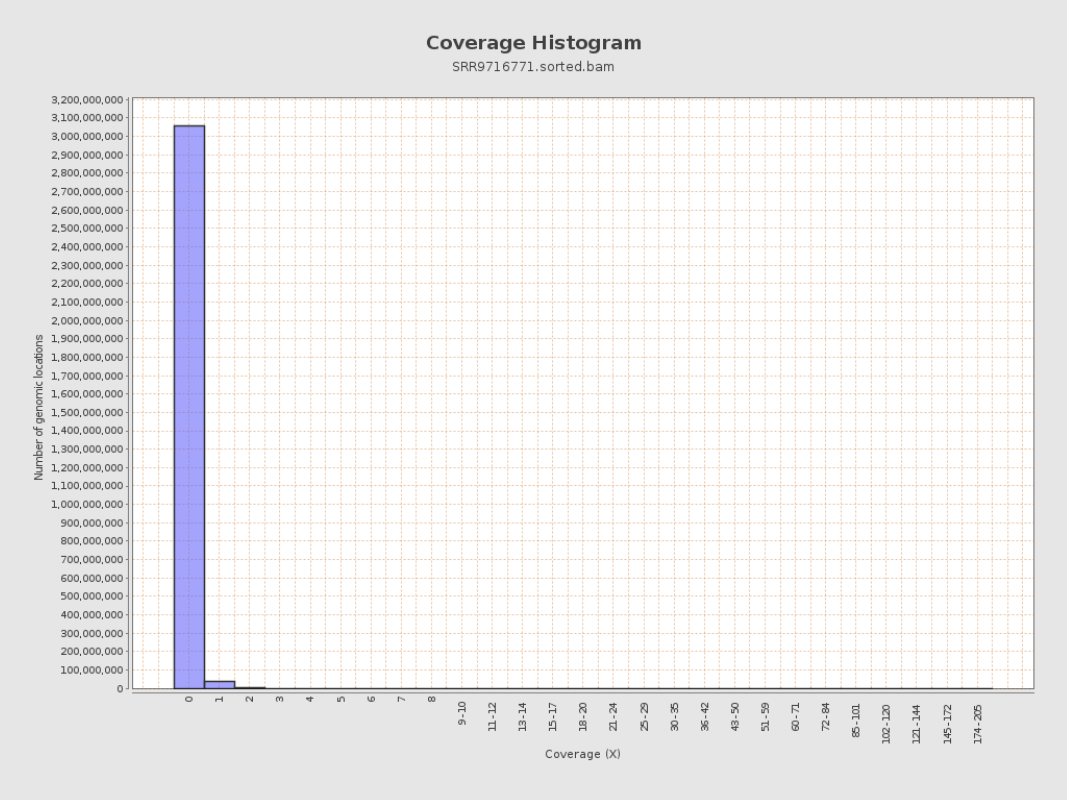
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4892178	0.0196	0.2394
chr2	243199373	4114934	0.0169	0.1672
chr3	198022430	2809956	0.0142	0.1258
chr4	191154276	2122027	0.0111	0.137
chr5	180915260	2649785	0.0146	0.1294
chr6	171115067	2695740	0.0158	0.1373
chr7	159138663	2782787	0.0175	0.1848

chr8	146364022	2697826	0.0184	0.1687
chr9	141213431	1335770	0.0095	0.116
chr10	135534747	2321557	0.0171	0.2007
chr11	135006516	1327488	0.0098	0.1223
chr12	133851895	1566988	0.0117	0.1144
chr13	115169878	840620	0.0073	0.0896
chr14	107349540	843691	0.0079	0.0978
chr15	102531392	944126	0.0092	0.1017
chr16	90354753	1385325	0.0153	0.1343
chr17	81195210	819830	0.0101	0.1112
chr18	78077248	1323745	0.017	0.1686
chr19	59128983	1123800	0.019	0.19
chr20	63025520	1199631	0.019	0.15
chr21	48129895	770210	0.016	0.1482
chr22	51304566	713926	0.0139	0.1254
chrMT	16571	22029	1.3294	1.4323
chrX	155270560	2733499	0.0176	0.1433
chrY	59373566	145191	0.0024	0.1004

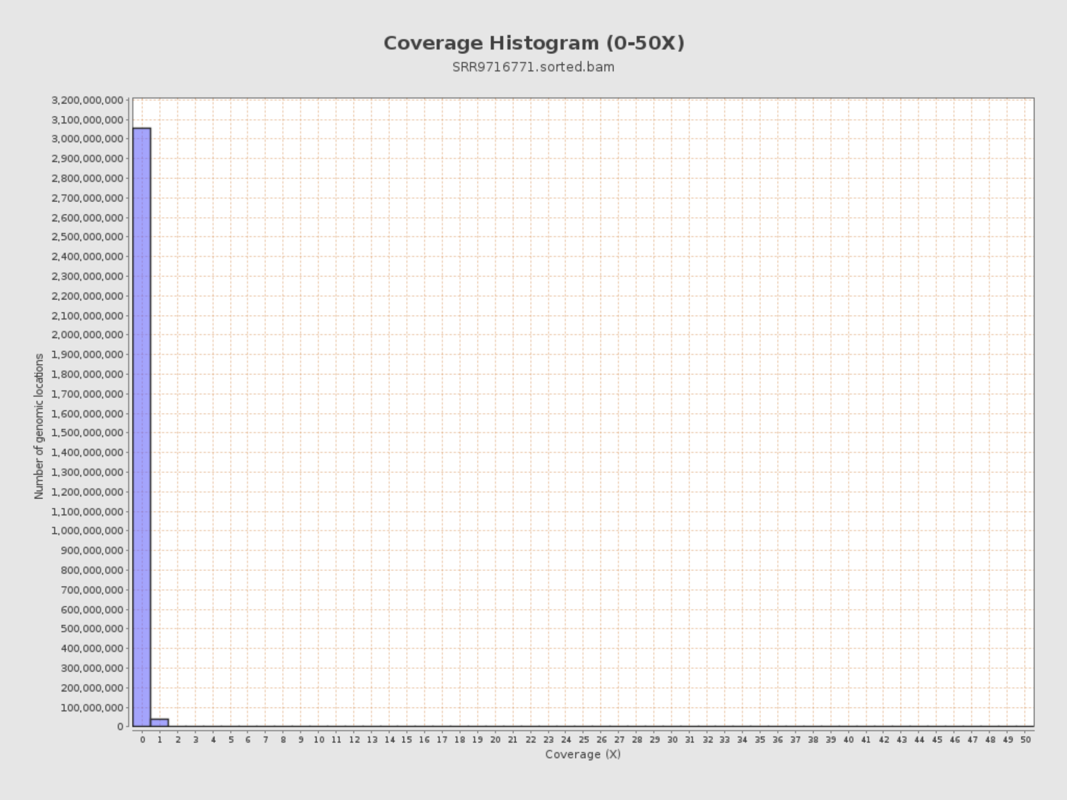
3. Results : Coverage across reference



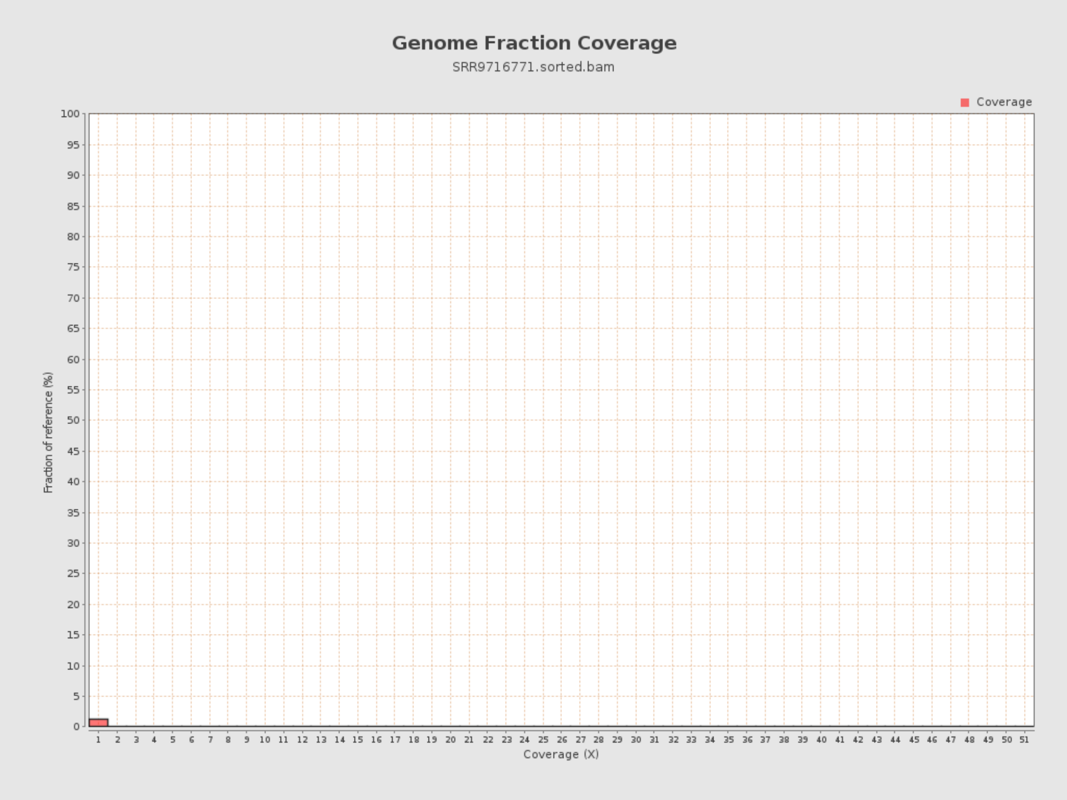
4. Results : Coverage Histogram



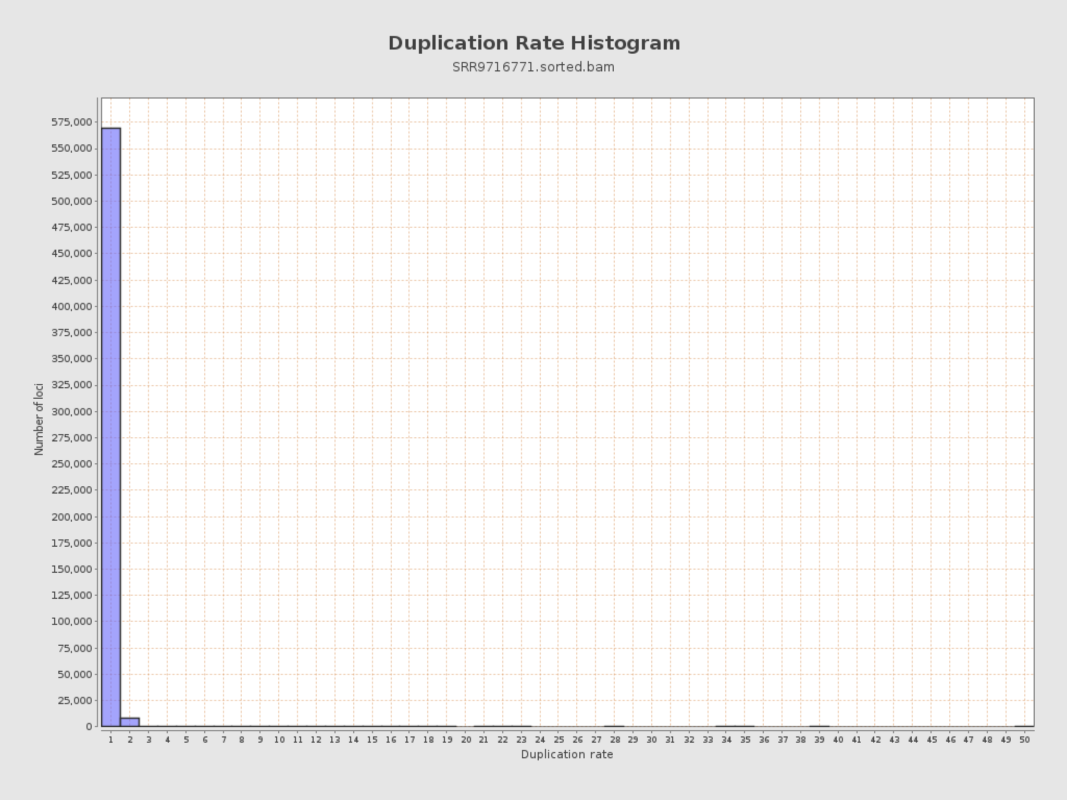
5. Results : Coverage Histogram (0-50X)



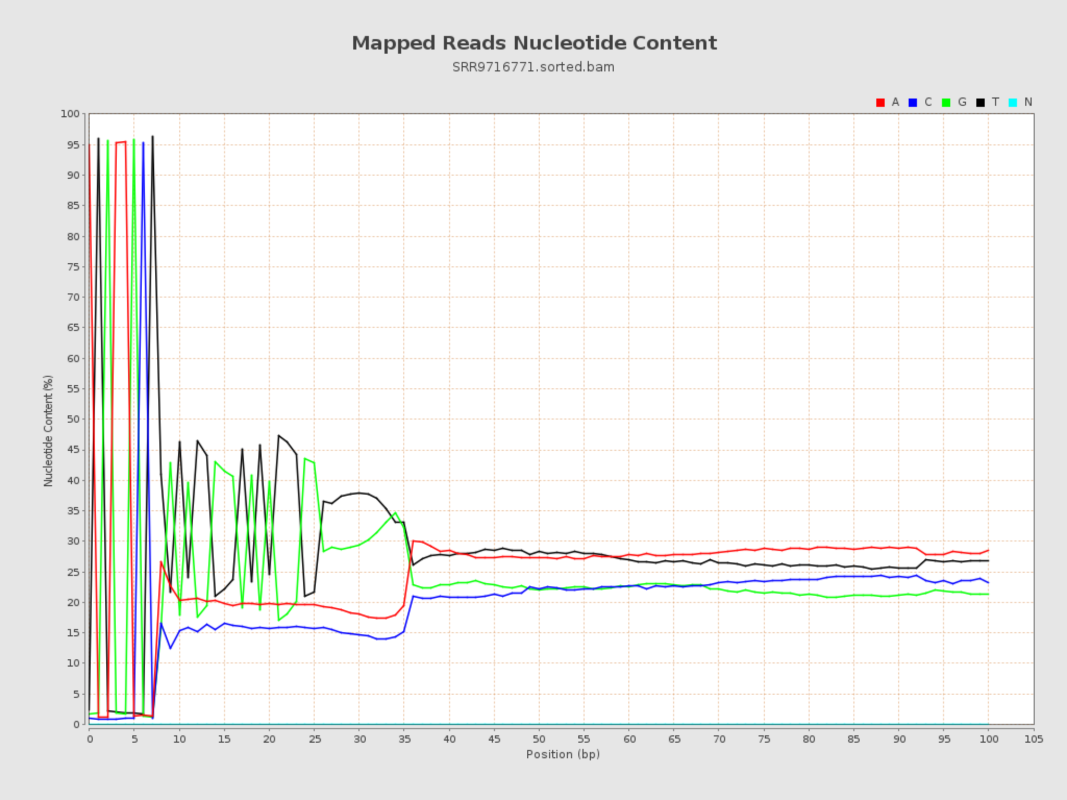
6. Results : Genome Fraction Coverage



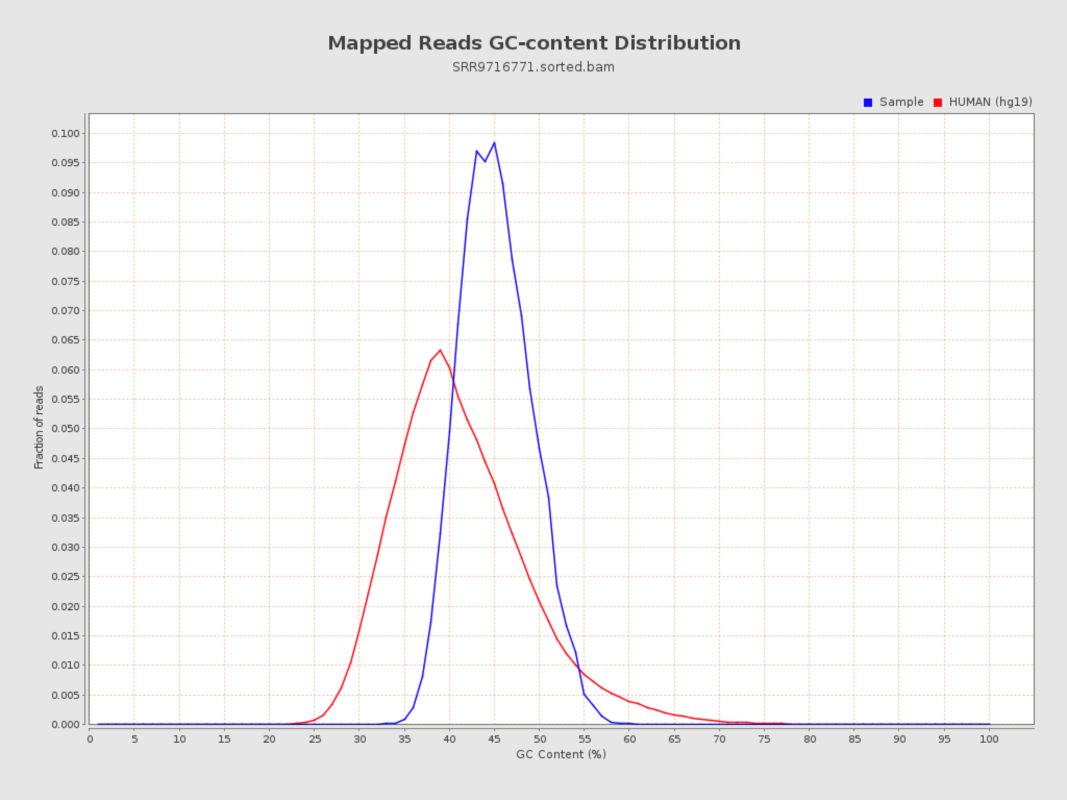
7. Results : Duplication Rate Histogram



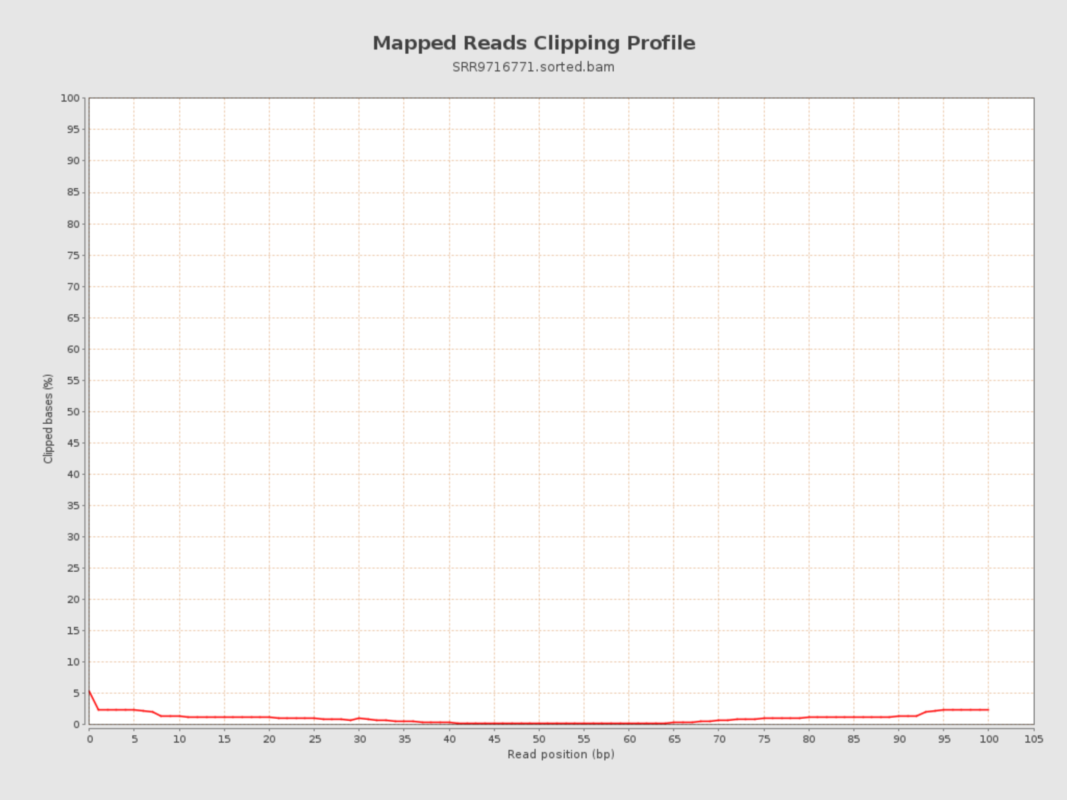
8. Results : Mapped Reads Nucleotide Content



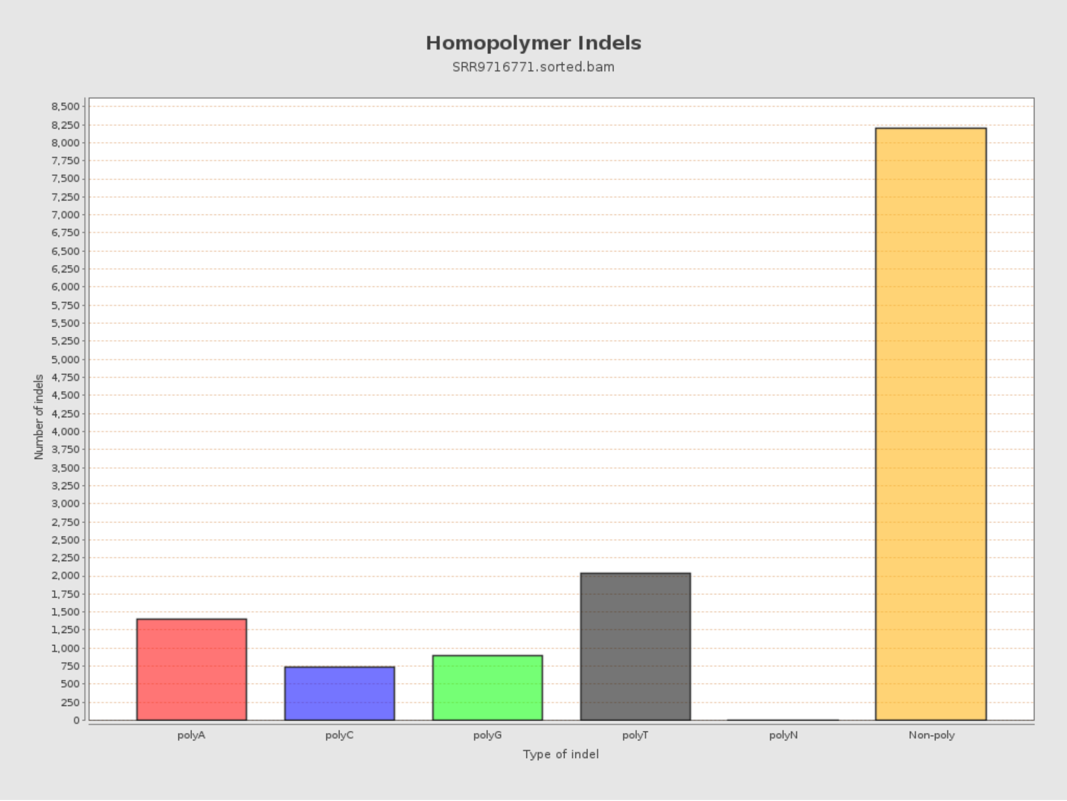
9. Results : Mapped Reads GC-content Distribution



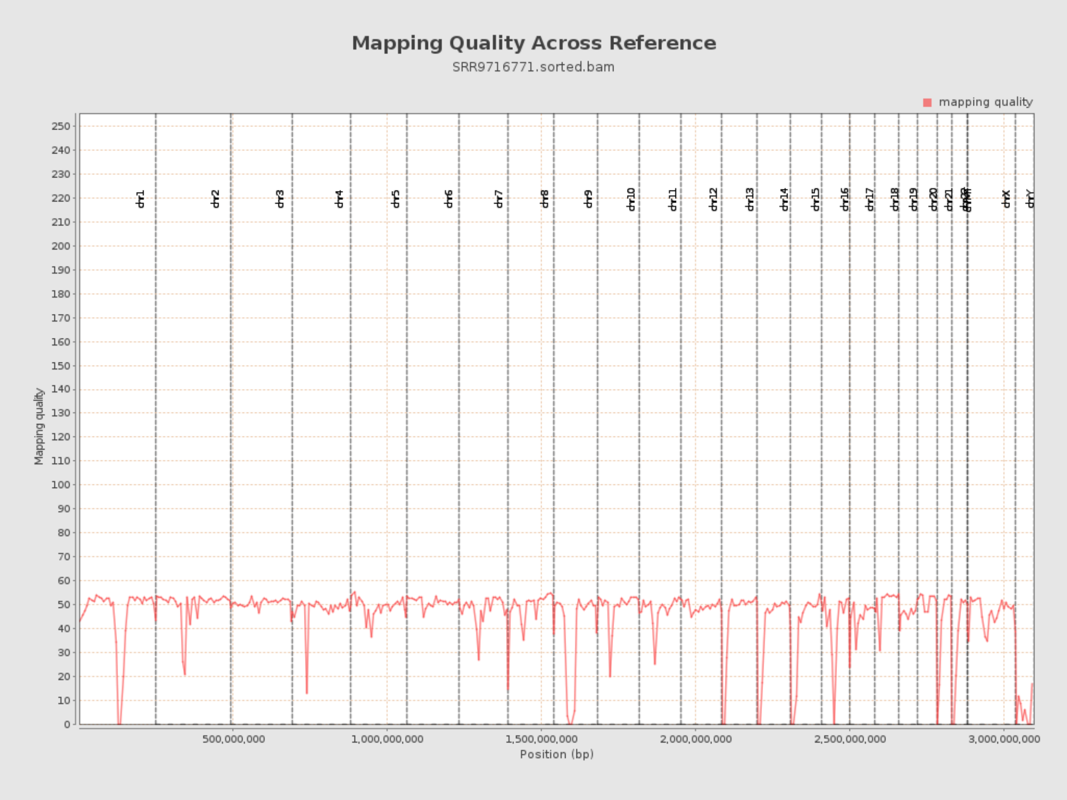
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram