Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:12:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716877.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_SRR9716877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716877.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:12:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	660,595
Mapped reads	584,467 / 88.48%
Unmapped reads	76,128 / 11.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,259 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	12,256 / 1.86%
Duplication rate	1.61%
Clipped reads	584,258 / 88.44%

2.2. ACGT Content

Number/percentage of A's	8,240,701 / 24.76%
Number/percentage of C's	5,815,670 / 17.47%
Number/percentage of T's	10,584,768 / 31.8%
Number/percentage of G's	8,641,586 / 25.96%
Number/percentage of N's	362 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1273

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Mismatches and indels

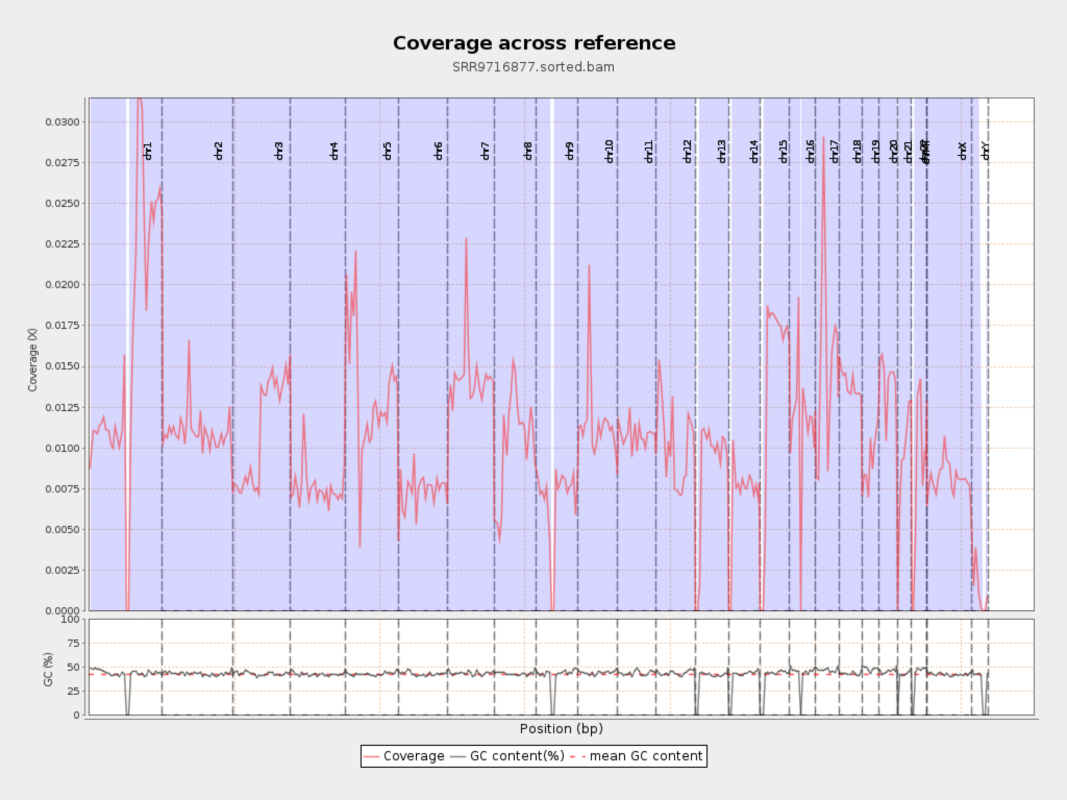
General error rate	0.51%
Mismatches	166,928
Insertions	2,206
Mapped reads with at least one insertion	0.38%
Deletions	6,475
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.84%

2.6. Chromosome stats

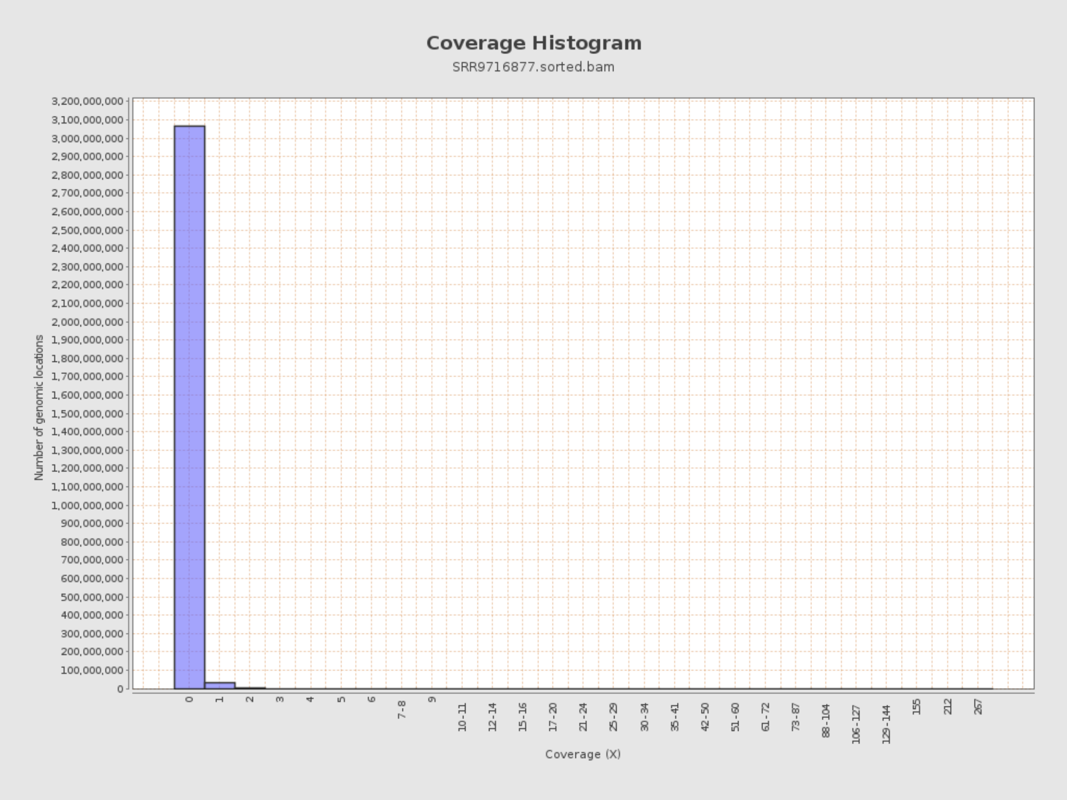
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4000340	0.016	0.1722
chr2	243199373	2677076	0.011	0.1607
chr3	198022430	2166684	0.0109	0.1093
chr4	191154276	1434713	0.0075	0.092
chr5	180915260	2429107	0.0134	0.1204
chr6	171115067	1263723	0.0074	0.0964
chr7	159138663	2296285	0.0144	0.19

chr8	146364022	1527225	0.0104	0.1144
chr9	141213431	934411	0.0066	0.0982
chr10	135534747	1566371	0.0116	0.1433
chr11	135006516	1450525	0.0107	0.1187
chr12	133851895	1361915	0.0102	0.1052
chr13	115169878	988973	0.0086	0.0964
chr14	107349540	738016	0.0069	0.0879
chr15	102531392	1459410	0.0142	0.1249
chr16	90354753	1033365	0.0114	0.1165
chr17	81195210	1261785	0.0155	0.1335
chr18	78077248	1088746	0.0139	0.1693
chr19	59128983	549701	0.0093	0.1376
chr20	63025520	882267	0.014	0.1233
chr21	48129895	443797	0.0092	0.1017
chr22	51304566	397589	0.0077	0.0915
chrMT	16571	214	0.0129	0.1129
chrX	155270560	1265472	0.0082	0.1008
chrY	59373566	75903	0.0013	0.044

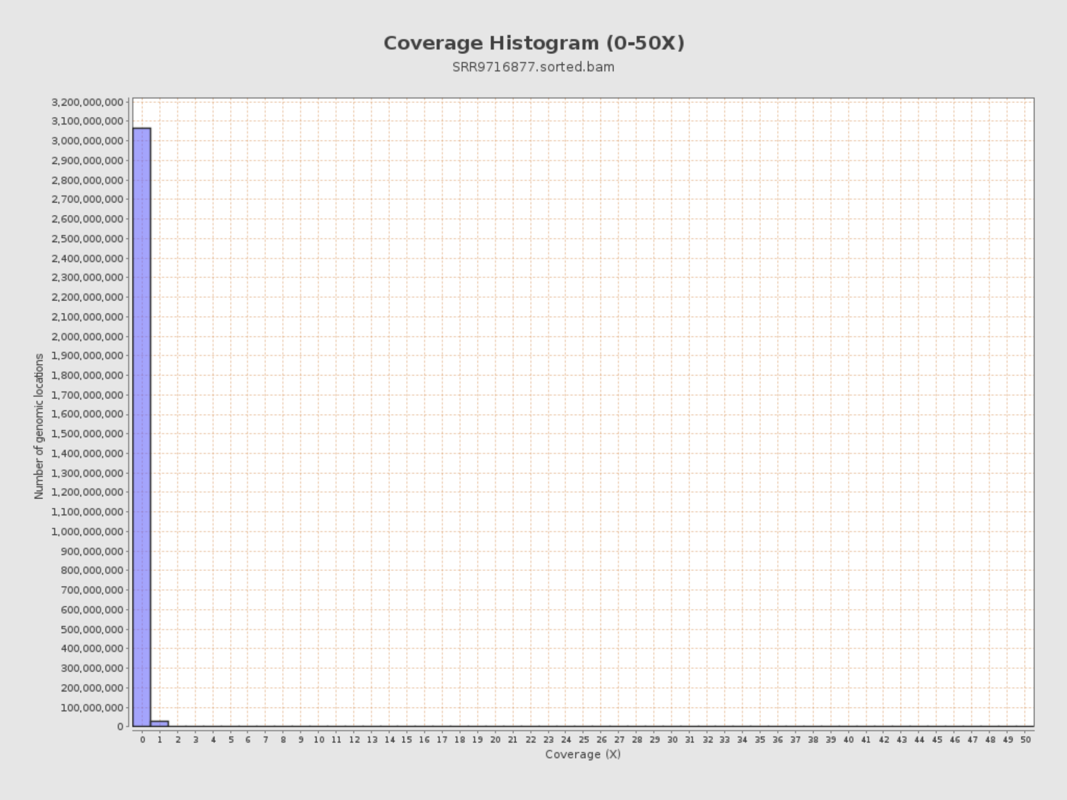
3. Results : Coverage across reference



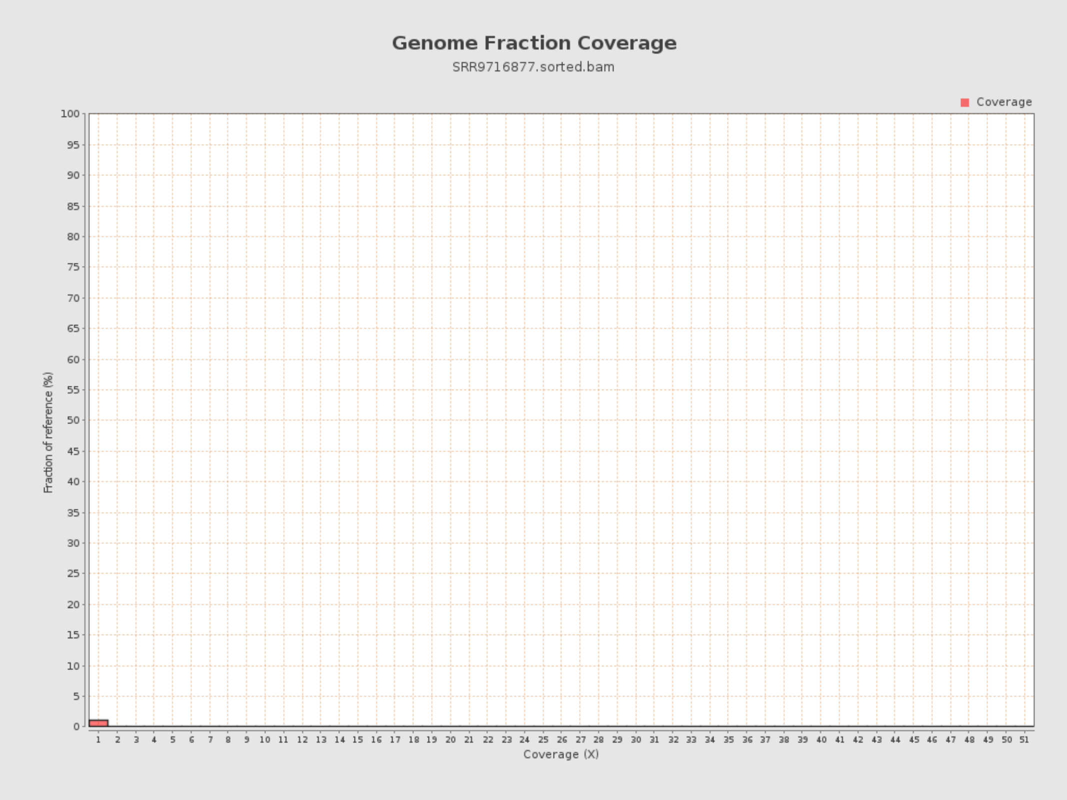
4. Results : Coverage Histogram



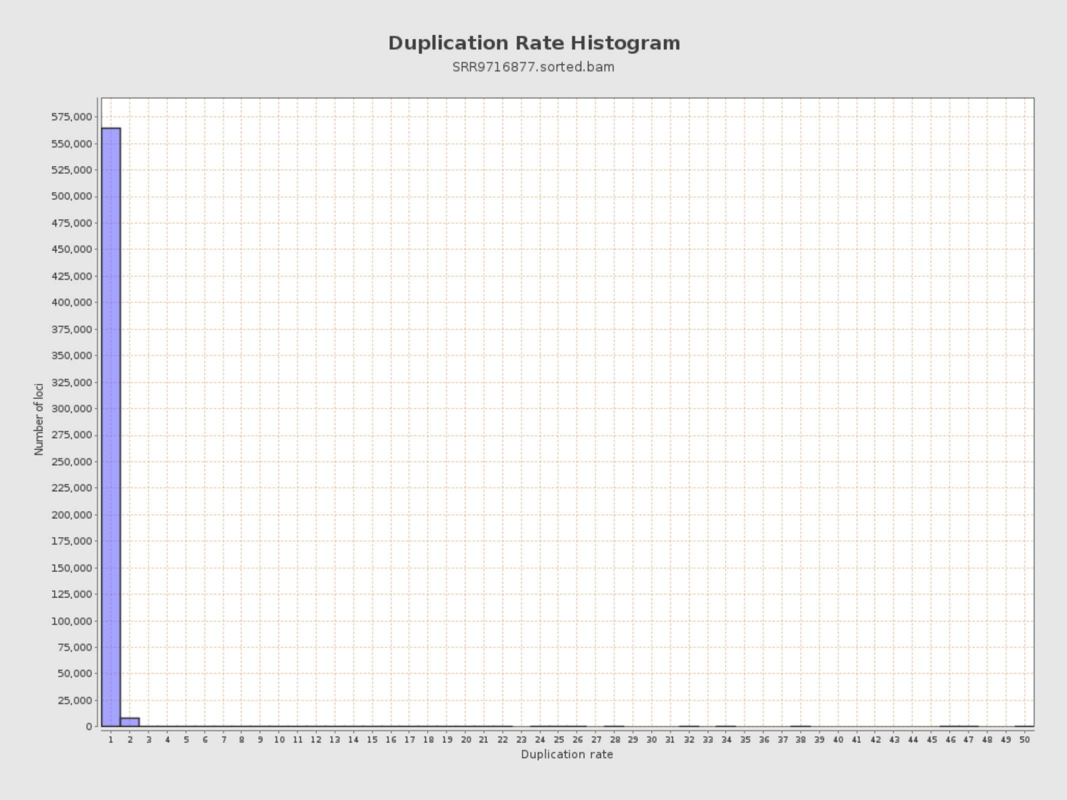
5. Results : Coverage Histogram (0-50X)



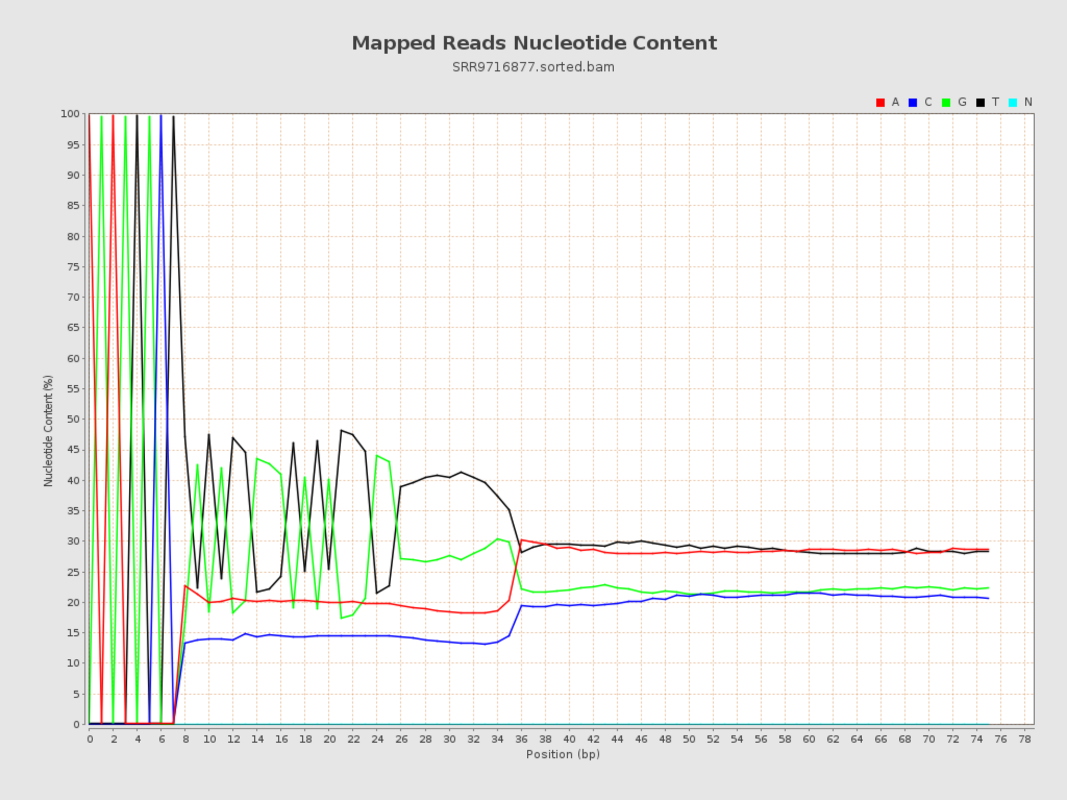
6. Results : Genome Fraction Coverage



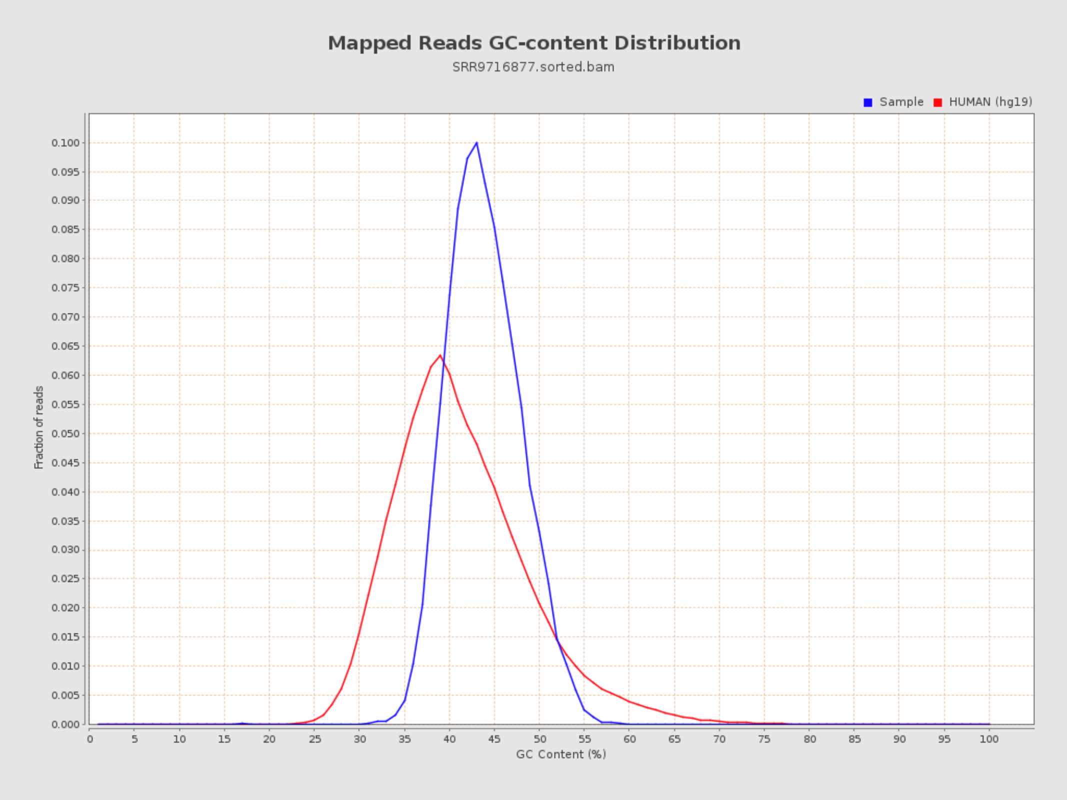
7. Results : Duplication Rate Histogram



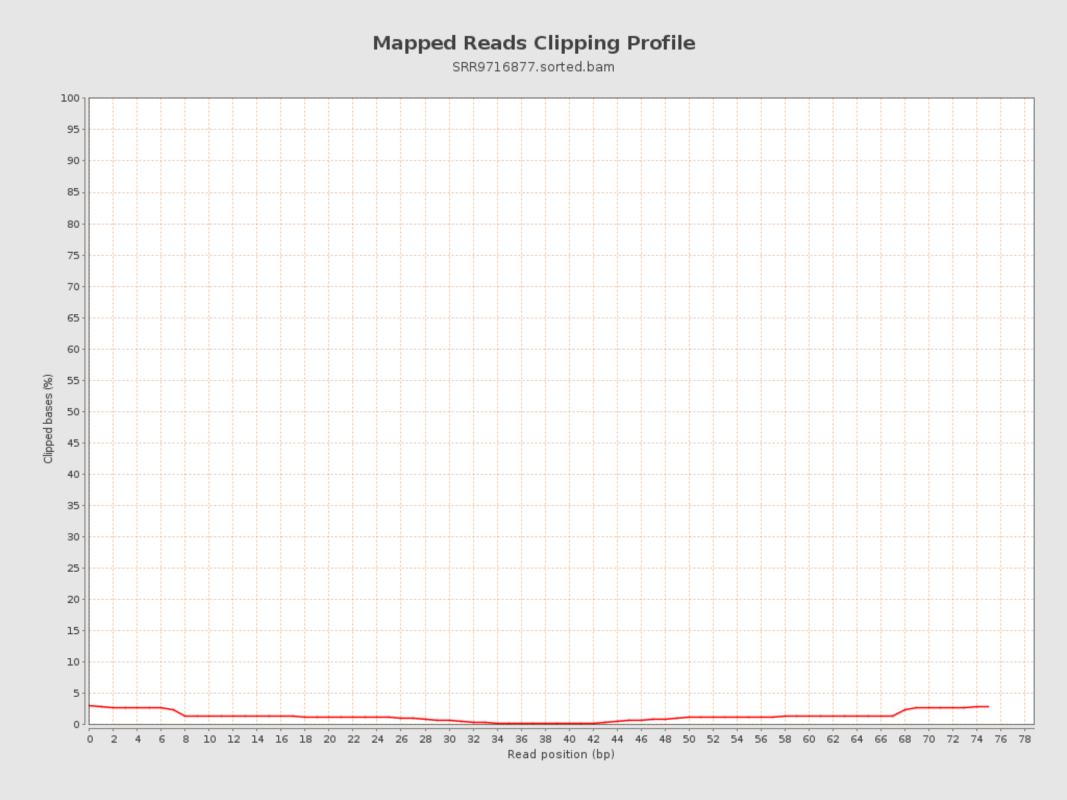
8. Results : Mapped Reads Nucleotide Content



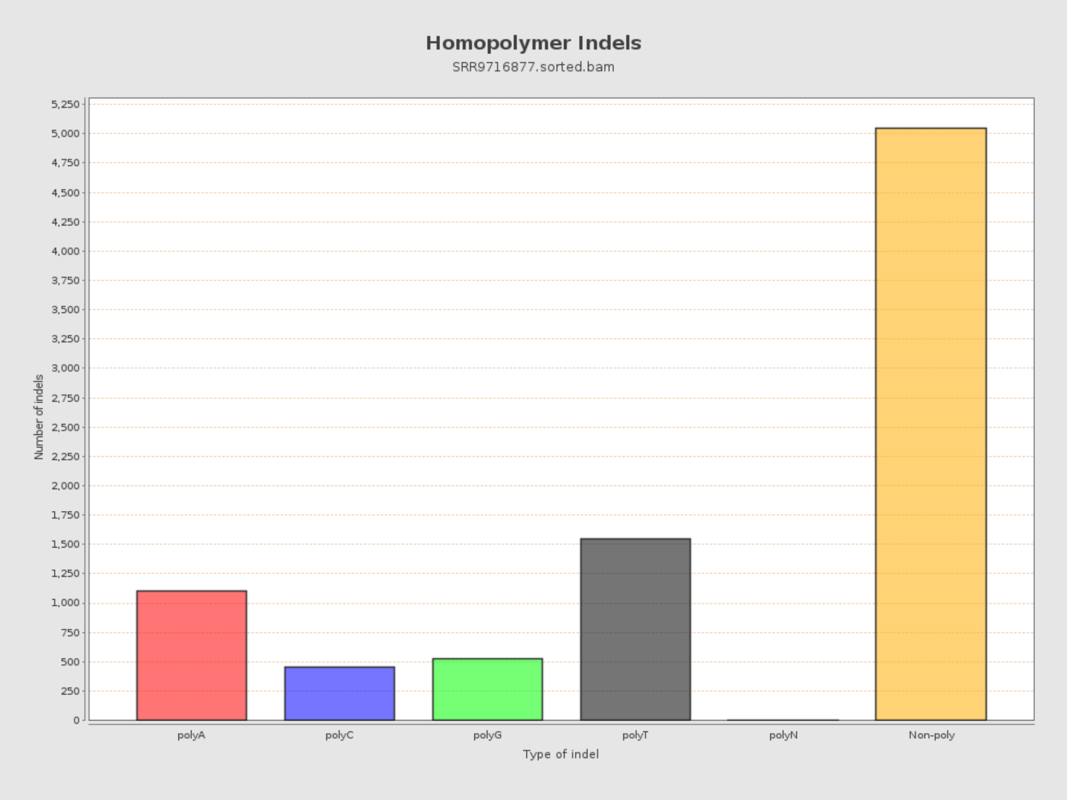
9. Results : Mapped Reads GC-content Distribution



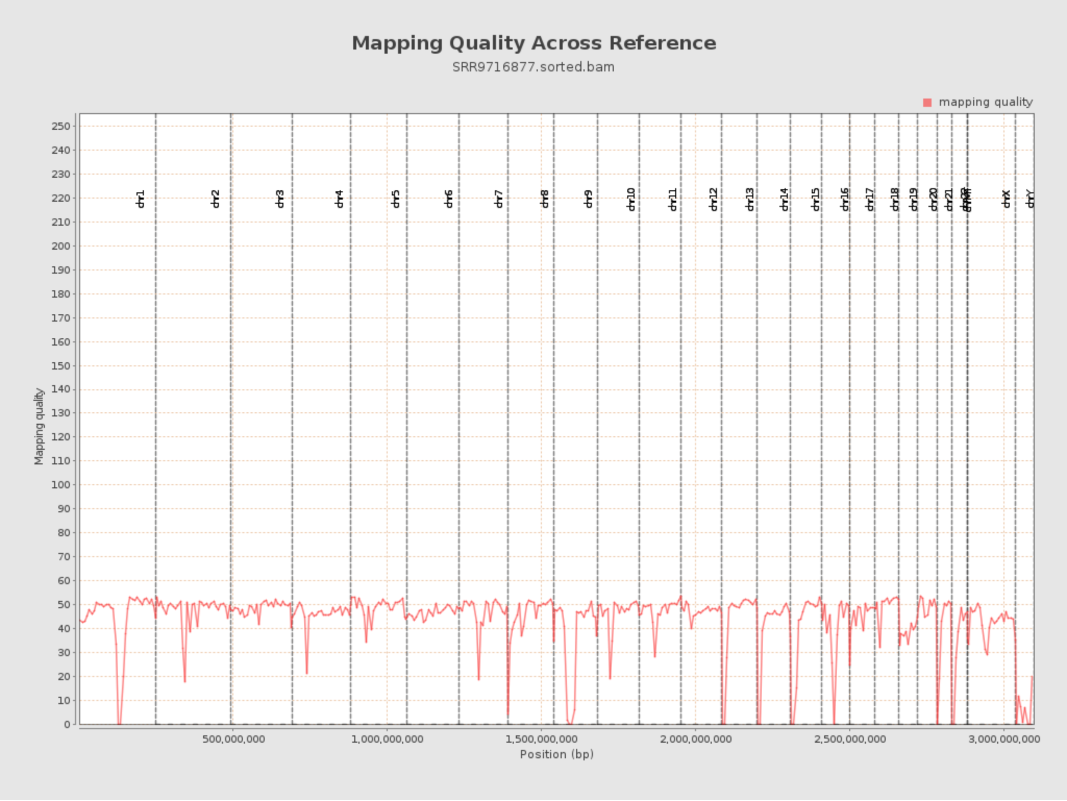
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram