Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:04:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716977.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_SRR9716977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716977.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:04:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	735,411
Mapped reads	617,851 / 84.01%
Unmapped reads	117,560 / 15.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,295 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	10,516 / 1.43%
Duplication rate	1.22%
Clipped reads	618,744 / 84.14%

2.2. ACGT Content

Number/percentage of A's	8,626,118 / 24.84%
Number/percentage of C's	6,293,763 / 18.12%
Number/percentage of T's	11,392,878 / 32.81%
Number/percentage of G's	8,414,027 / 24.23%
Number/percentage of N's	553 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0112

Standard Deviation	0.1321

2.4. Mapping Quality

Mean Mapping Quality	42.43

2.5. Mismatches and indels

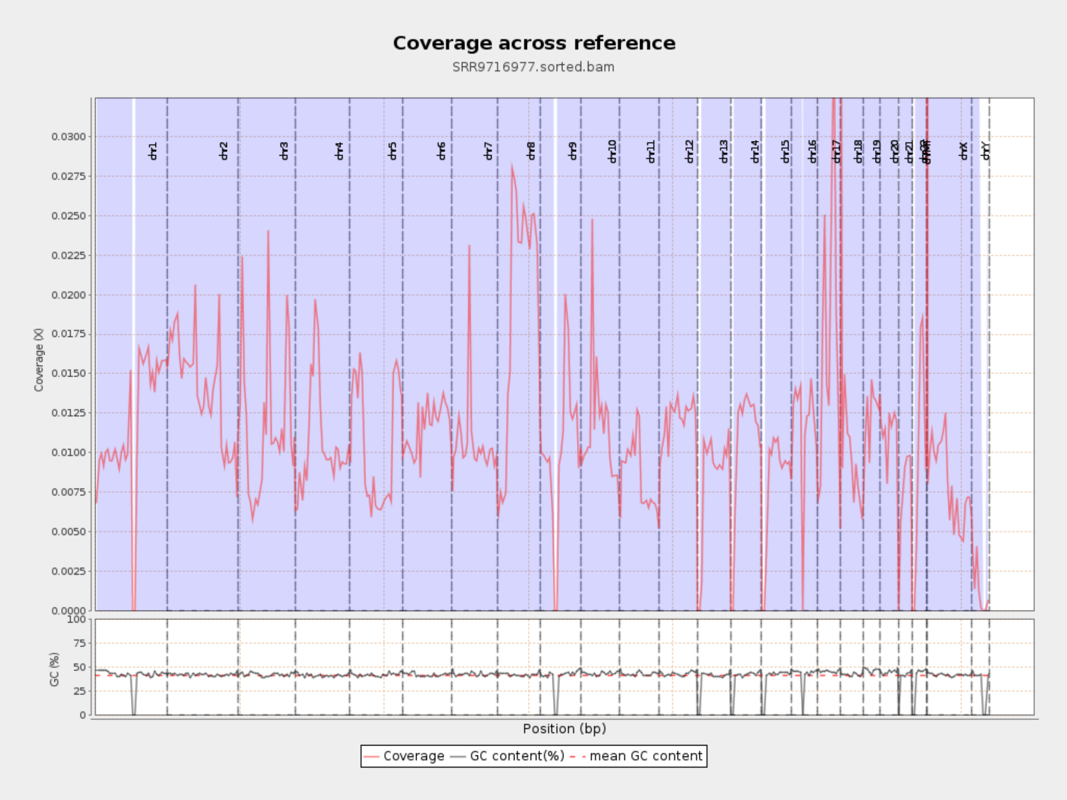
General error rate	0.54%
Mismatches	181,765
Insertions	2,472
Mapped reads with at least one insertion	0.4%
Deletions	6,763
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.89%

2.6. Chromosome stats

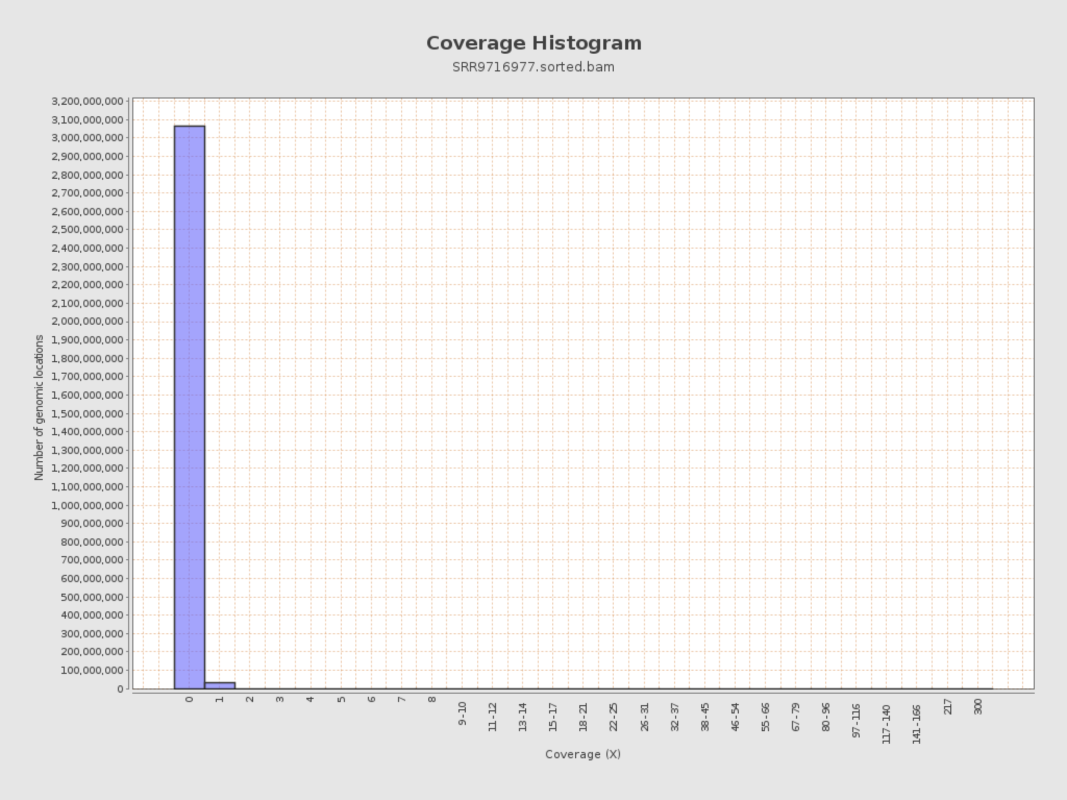
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2897323	0.0116	0.1613
chr2	243199373	3437754	0.0141	0.1771
chr3	198022430	2310997	0.0117	0.1124
chr4	191154276	2020112	0.0106	0.1083
chr5	180915260	1898601	0.0105	0.106
chr6	171115067	1983970	0.0116	0.1172
chr7	159138663	1702696	0.0107	0.2016

chr8	146364022	2868387	0.0196	0.1582
chr9	141213431	1432778	0.0101	0.1132
chr10	135534747	1568003	0.0116	0.1416
chr11	135006516	1167908	0.0087	0.1078
chr12	133851895	1616290	0.0121	0.1152
chr13	115169878	951791	0.0083	0.0951
chr14	107349540	1131863	0.0105	0.1078
chr15	102531392	821480	0.008	0.0946
chr16	90354753	1038720	0.0115	0.115
chr17	81195210	1426704	0.0176	0.1402
chr18	78077248	825149	0.0106	0.1473
chr19	59128983	730368	0.0124	0.1643
chr20	63025520	702104	0.0111	0.11
chr21	48129895	359513	0.0075	0.0904
chr22	51304566	483042	0.0094	0.1006
chrMT	16571	26008	1.5695	1.6448
chrX	155270560	1258816	0.0081	0.1002
chrY	59373566	77585	0.0013	0.0436

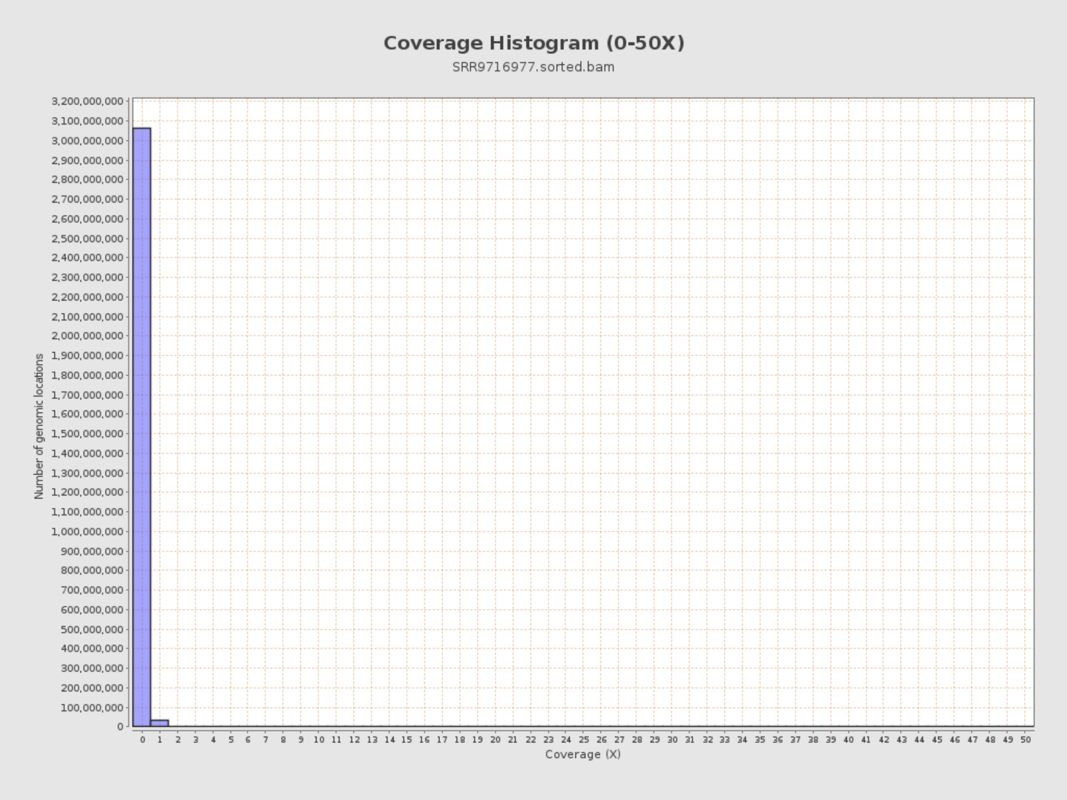
3. Results : Coverage across reference



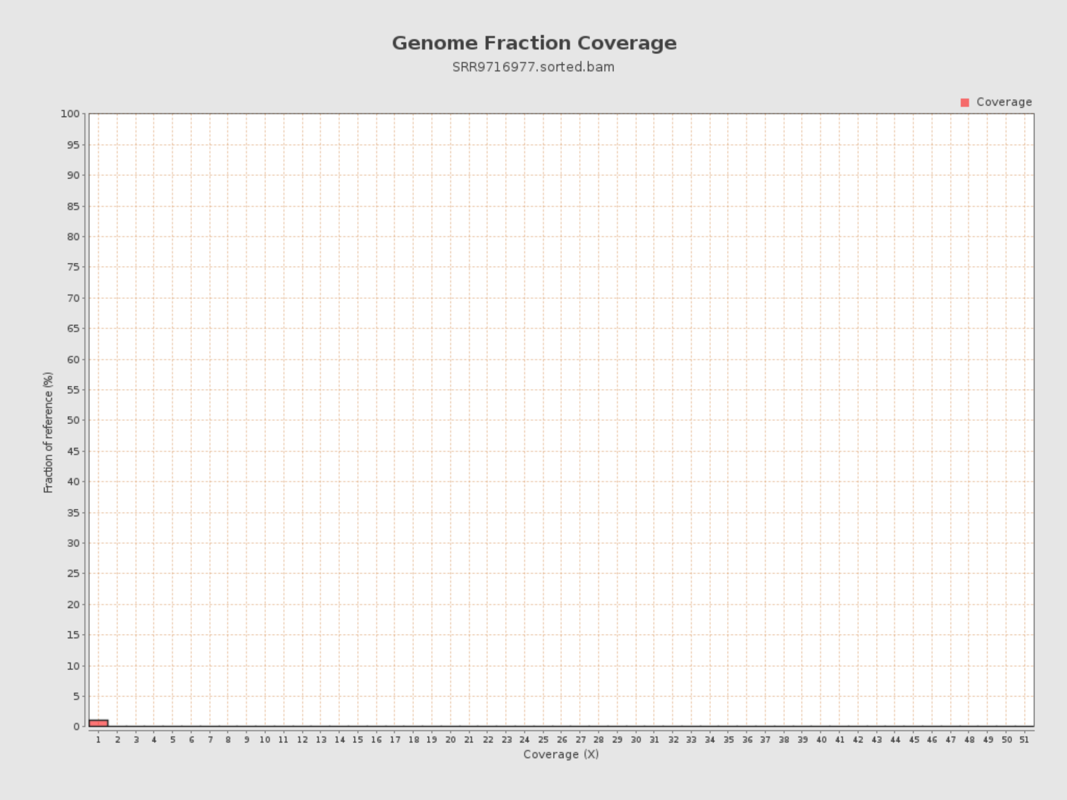
4. Results : Coverage Histogram



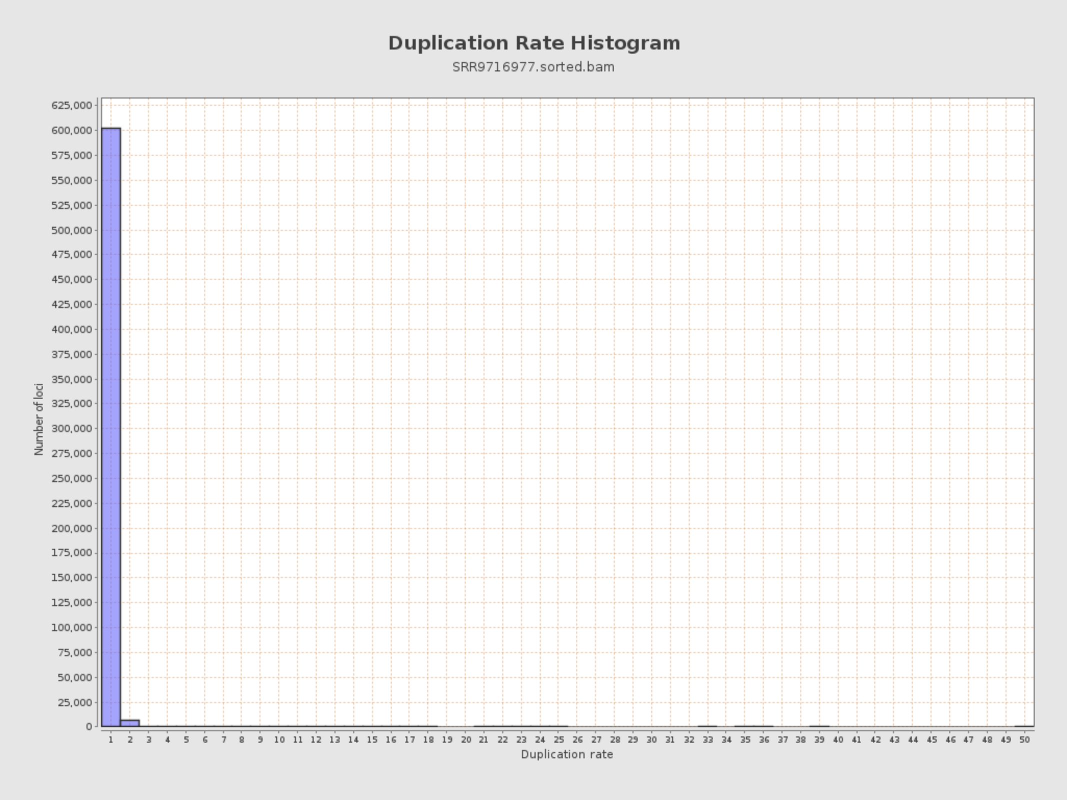
5. Results : Coverage Histogram (0-50X)



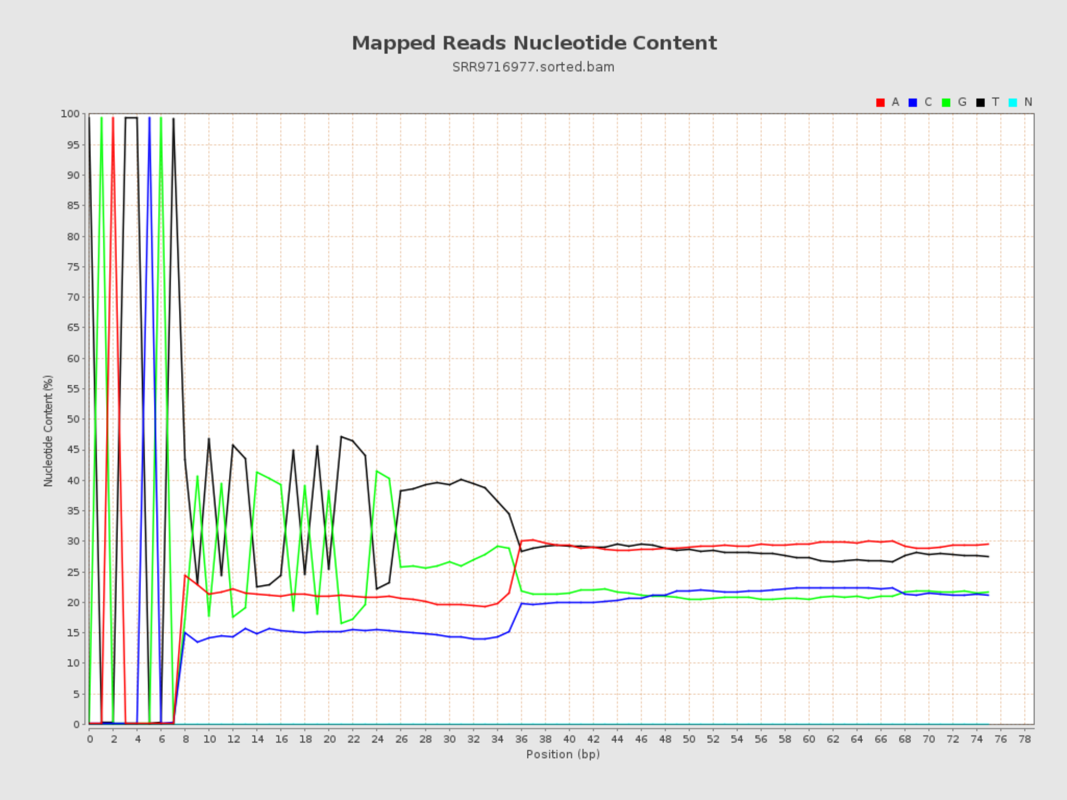
6. Results : Genome Fraction Coverage



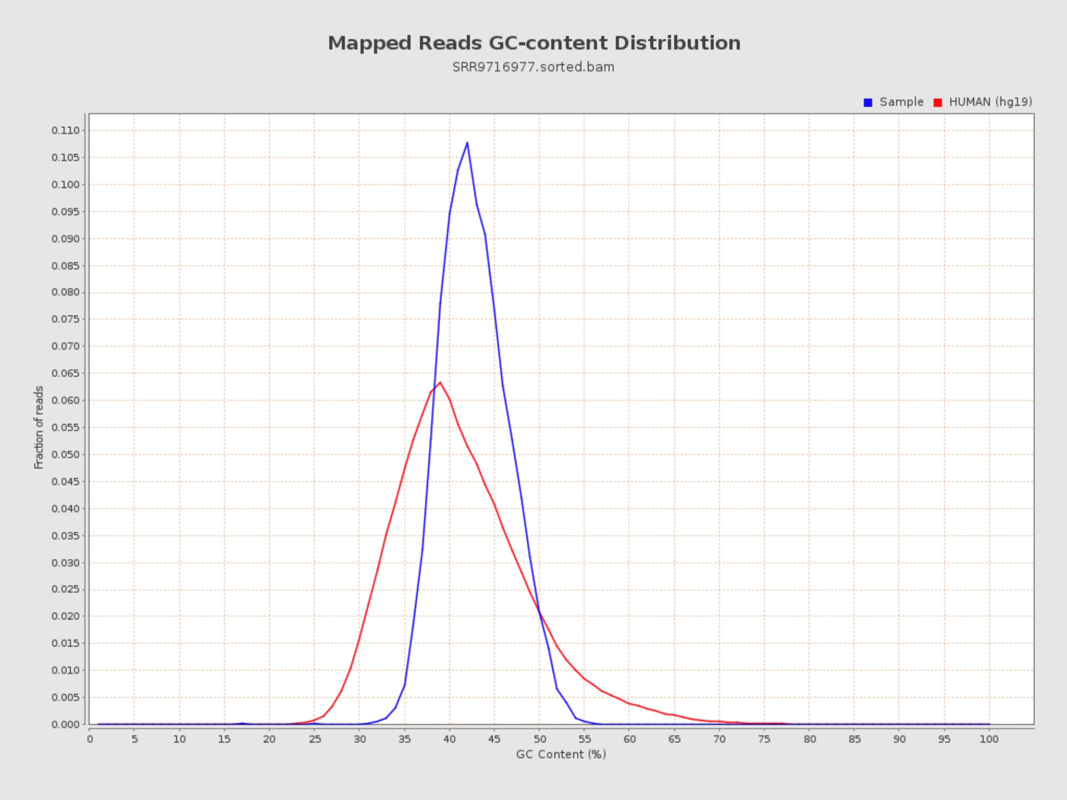
7. Results : Duplication Rate Histogram



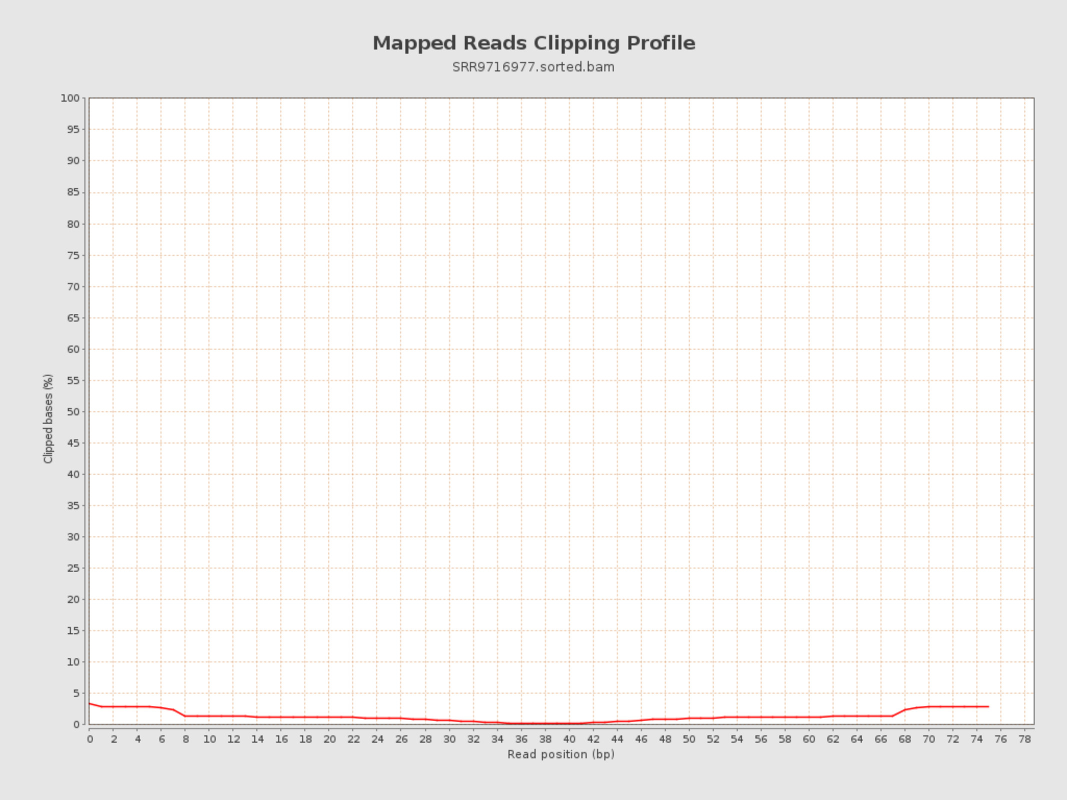
8. Results : Mapped Reads Nucleotide Content



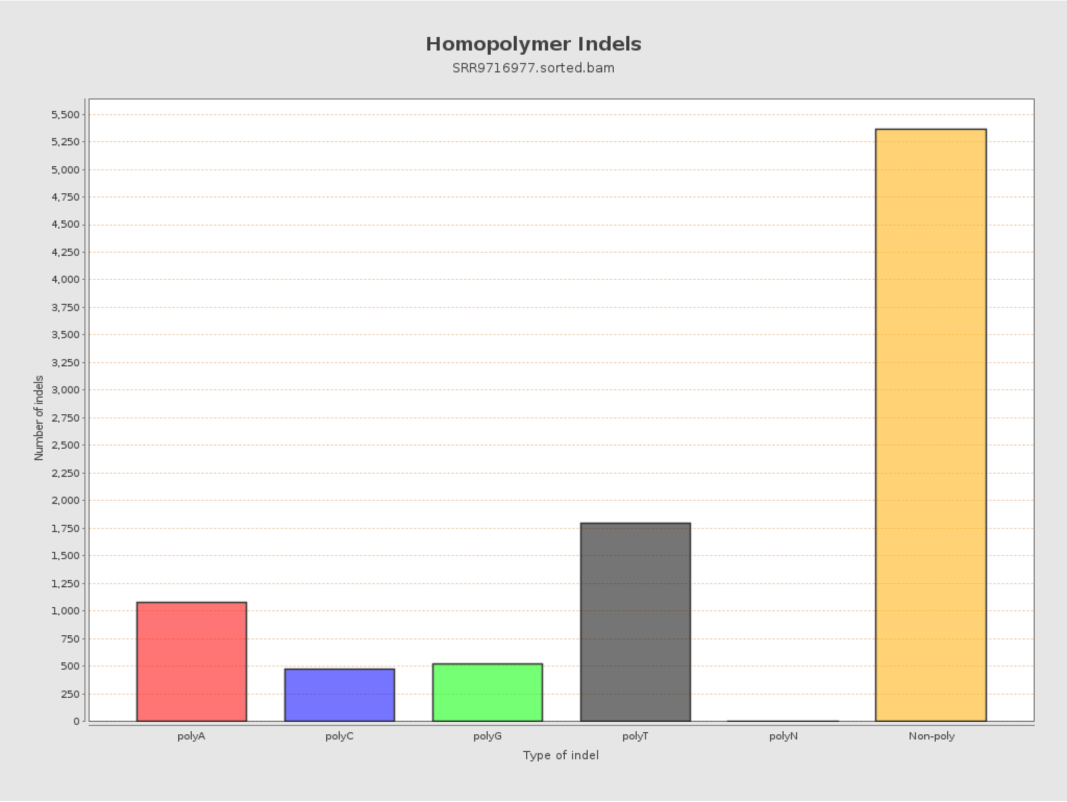
9. Results : Mapped Reads GC-content Distribution



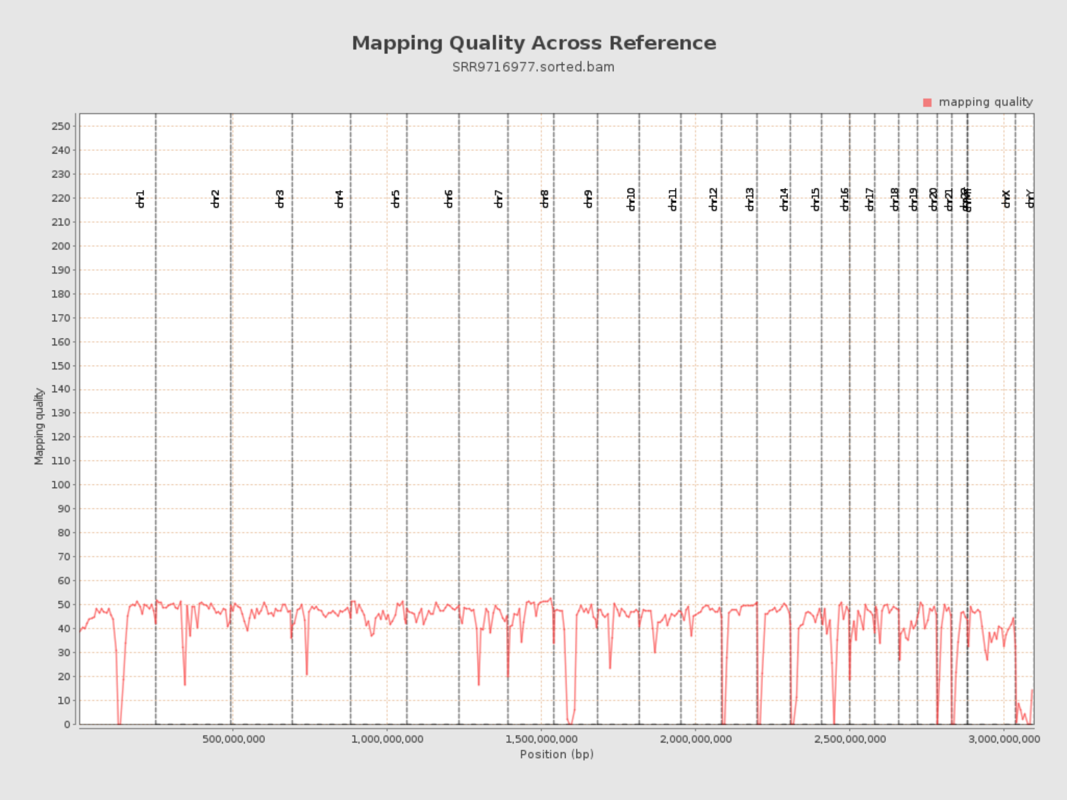
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram