Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:45:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716577.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_SRR9716577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:45:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,571,726
Mapped reads	1,446,732 / 92.05%
Unmapped reads	124,994 / 7.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,153 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	51,499 / 3.28%
Duplication rate	2.57%
Clipped reads	1,452,999 / 92.45%

2.2. ACGT Content

Number/percentage of A's	20,351,372 / 24.04%
Number/percentage of C's	16,328,654 / 19.29%
Number/percentage of T's	26,649,266 / 31.48%
Number/percentage of G's	21,322,423 / 25.19%
Number/percentage of N's	962 / 0%
GC Percentage	44.48%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.271

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

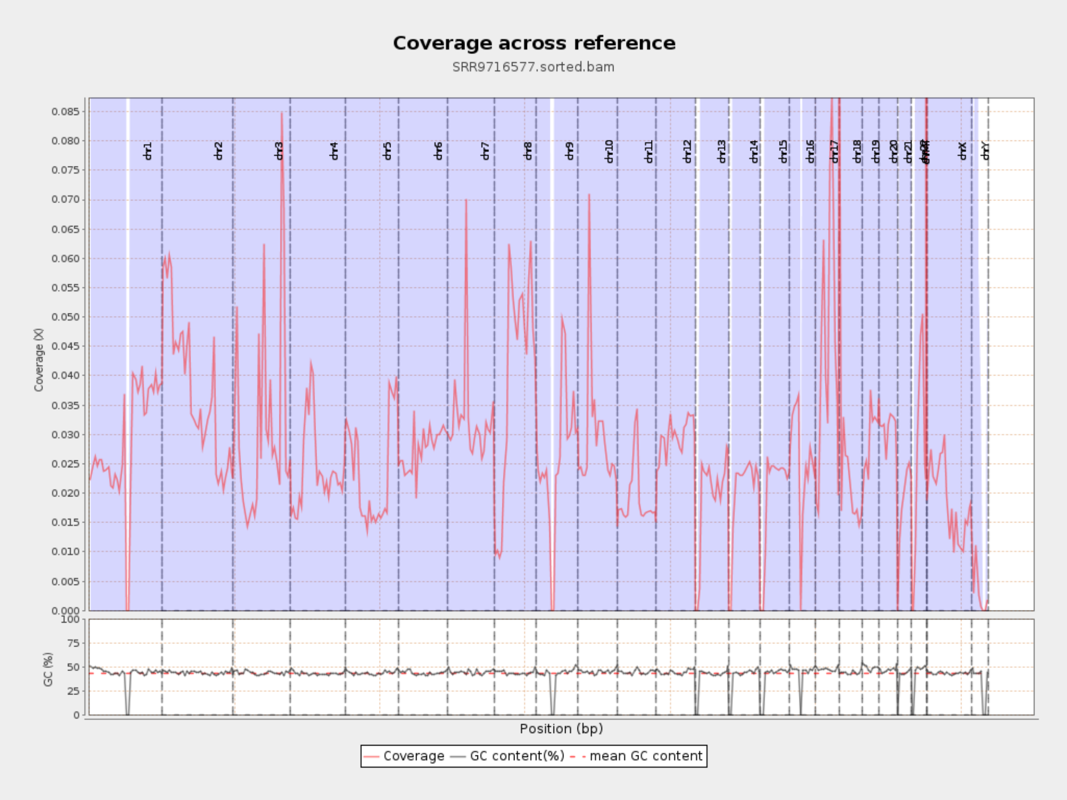
General error rate	0.52%
Mismatches	432,136
Insertions	4,858
Mapped reads with at least one insertion	0.33%
Deletions	15,800
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.98%

2.6. Chromosome stats

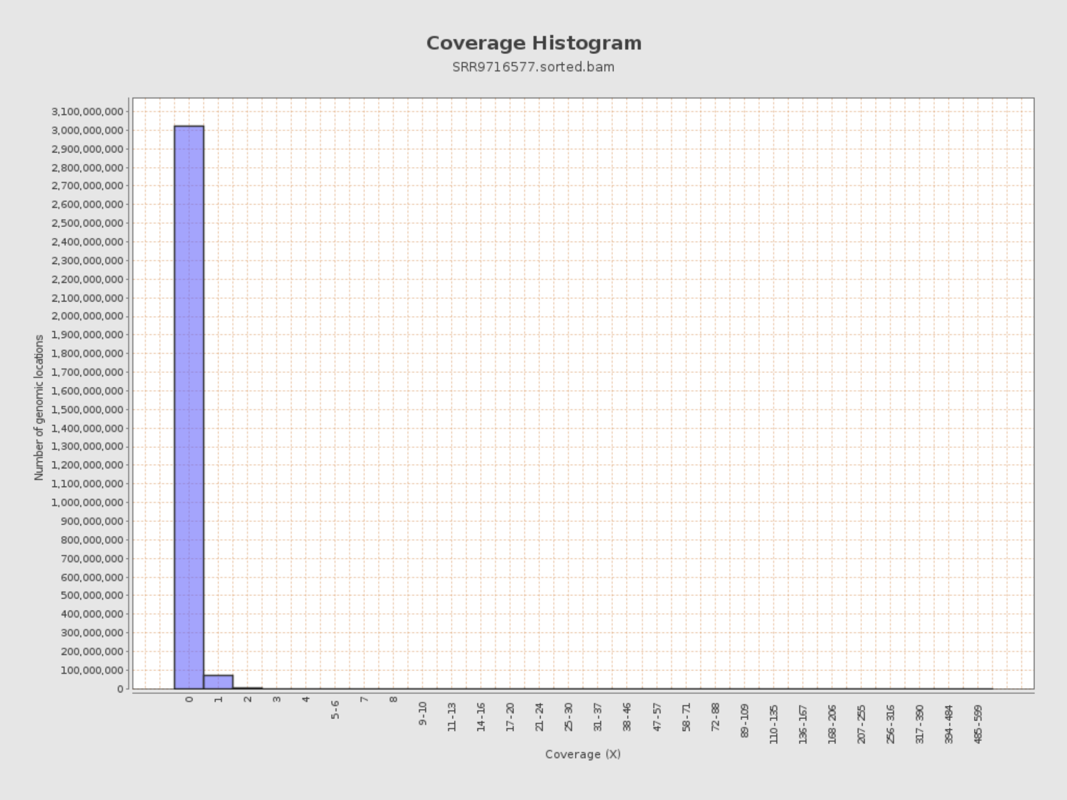
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7082689	0.0284	0.3819
chr2	243199373	9237652	0.038	0.3336
chr3	198022430	6177210	0.0312	0.203
chr4	191154276	4623435	0.0242	0.1871
chr5	180915260	4254133	0.0235	0.1666
chr6	171115067	4722580	0.0276	0.1942
chr7	159138663	5238327	0.0329	0.5773

chr8	146364022	5913109	0.0404	0.2856
chr9	141213431	3602880	0.0255	0.1992
chr10	135534747	4021815	0.0297	0.3642
chr11	135006516	2584970	0.0191	0.1861
chr12	133851895	3965268	0.0296	0.2099
chr13	115169878	2178741	0.0189	0.1495
chr14	107349540	2135928	0.0199	0.157
chr15	102531392	2017887	0.0197	0.1531
chr16	90354753	2318761	0.0257	0.1834
chr17	81195210	3654770	0.045	0.2398
chr18	78077248	1916788	0.0245	0.2823
chr19	59128983	1729474	0.0292	0.3275
chr20	63025520	1955747	0.031	0.2011
chr21	48129895	879346	0.0183	0.1585
chr22	51304566	1301554	0.0254	0.1743
chrMT	16571	38840	2.3439	2.4106
chrX	155270560	2930544	0.0189	0.168
chrY	59373566	195380	0.0033	0.0955

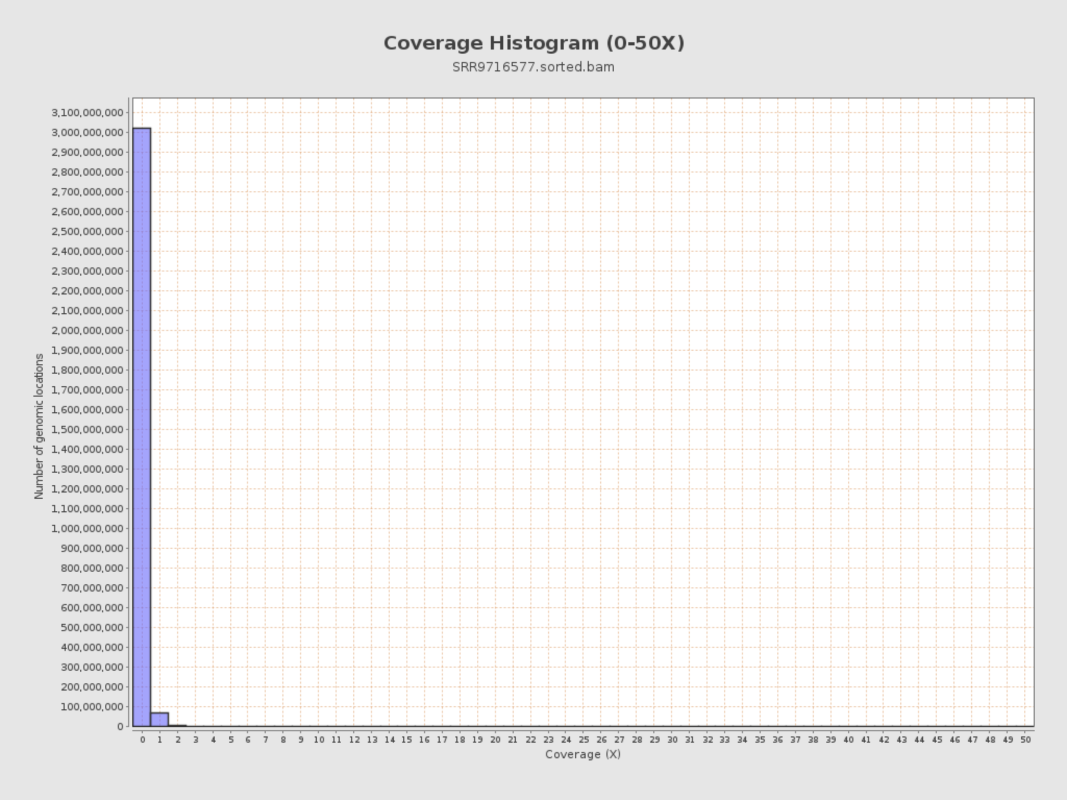
3. Results : Coverage across reference



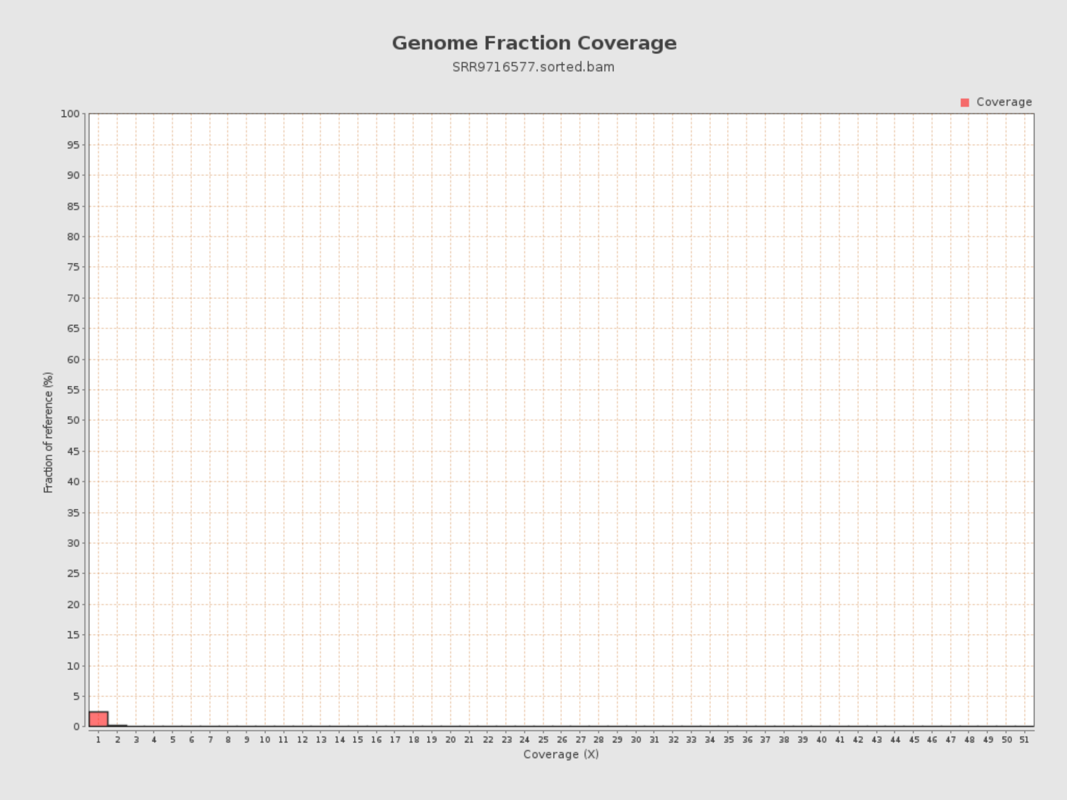
4. Results : Coverage Histogram



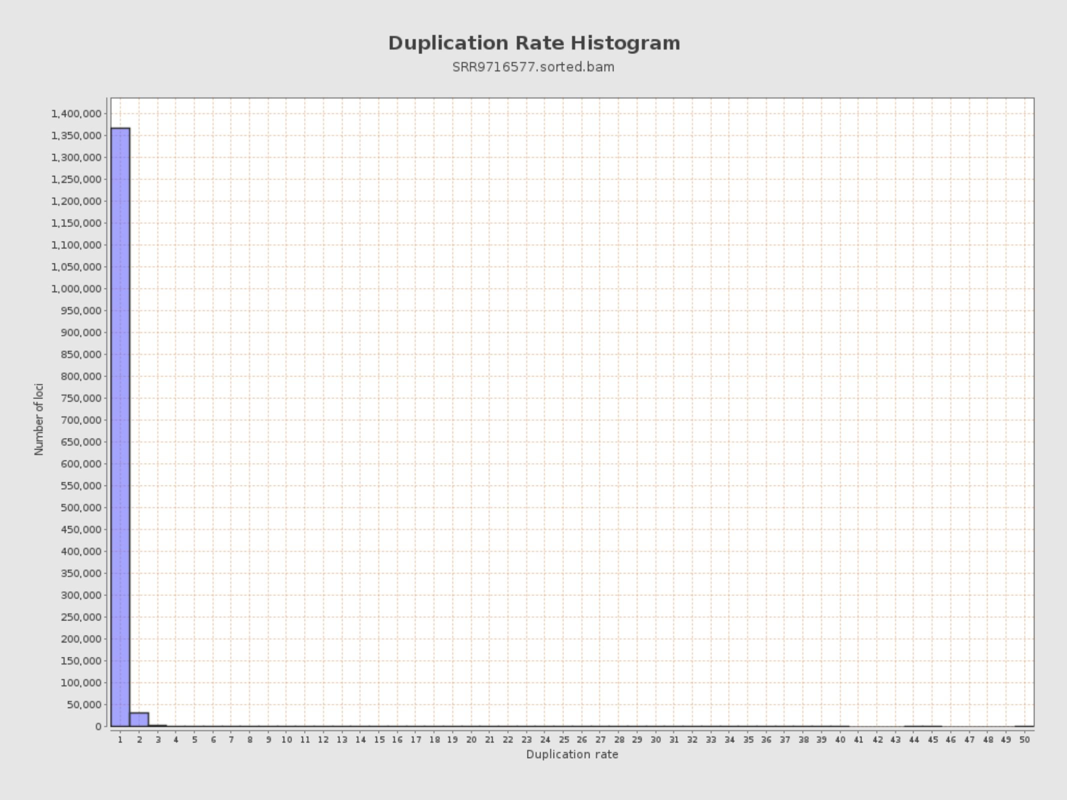
5. Results : Coverage Histogram (0-50X)



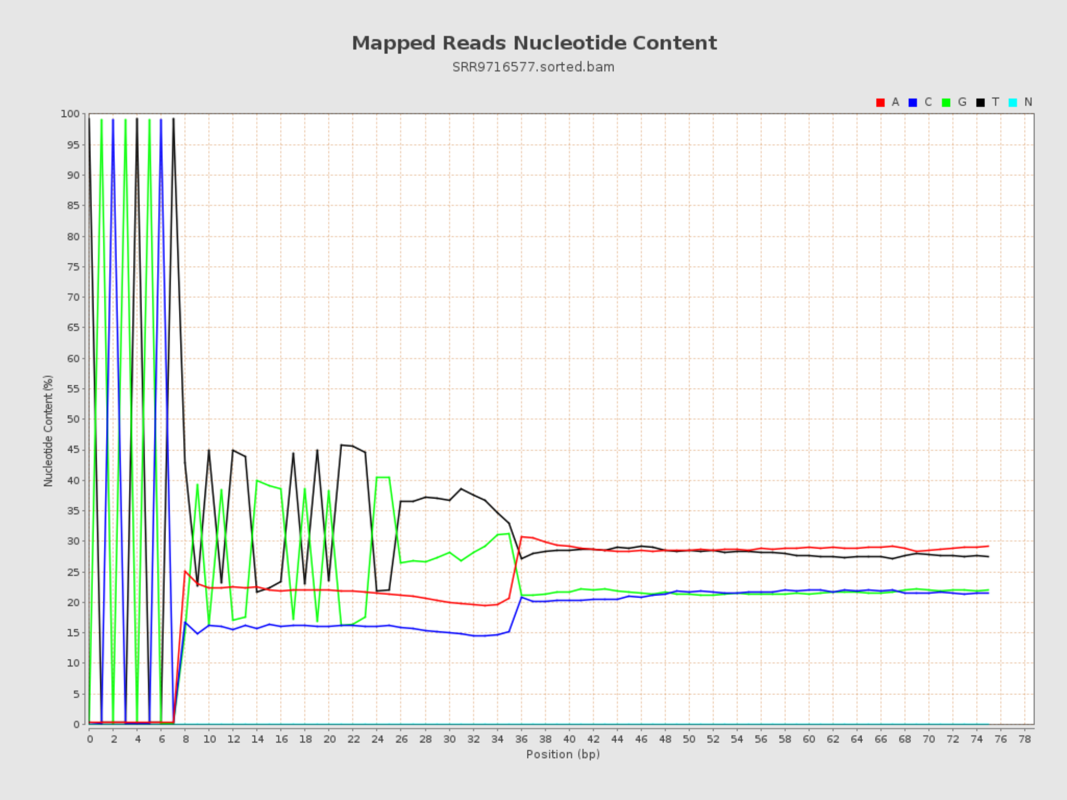
6. Results : Genome Fraction Coverage



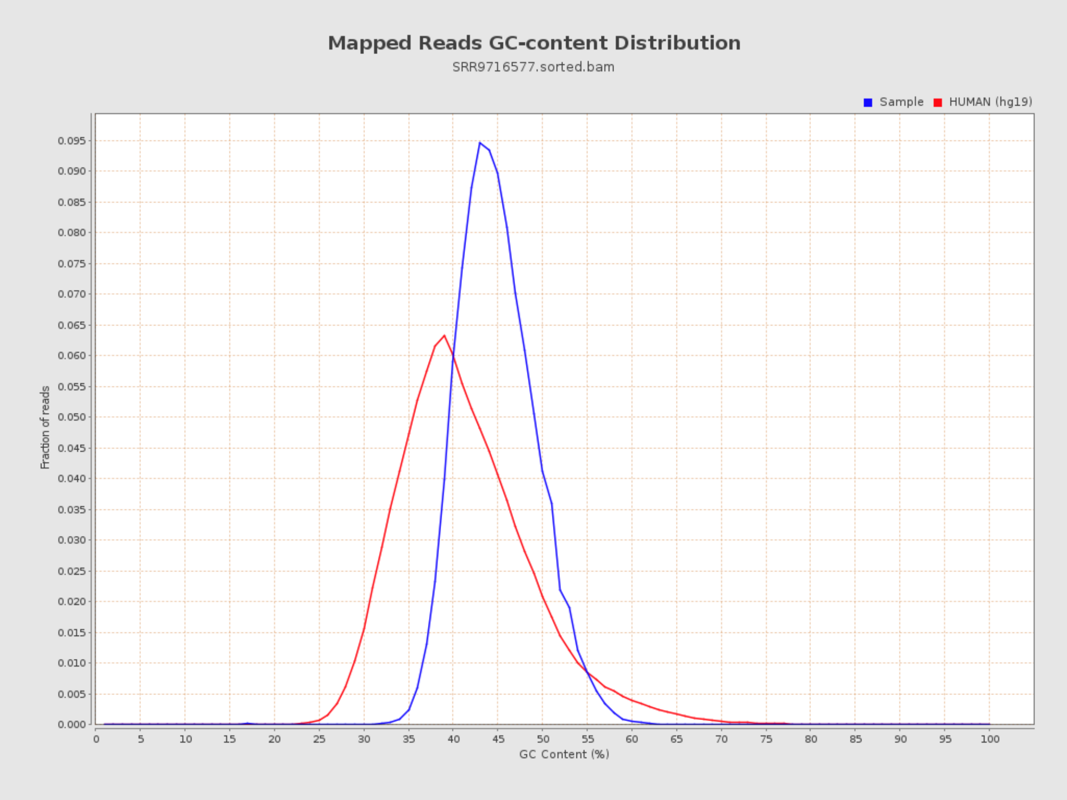
7. Results : Duplication Rate Histogram



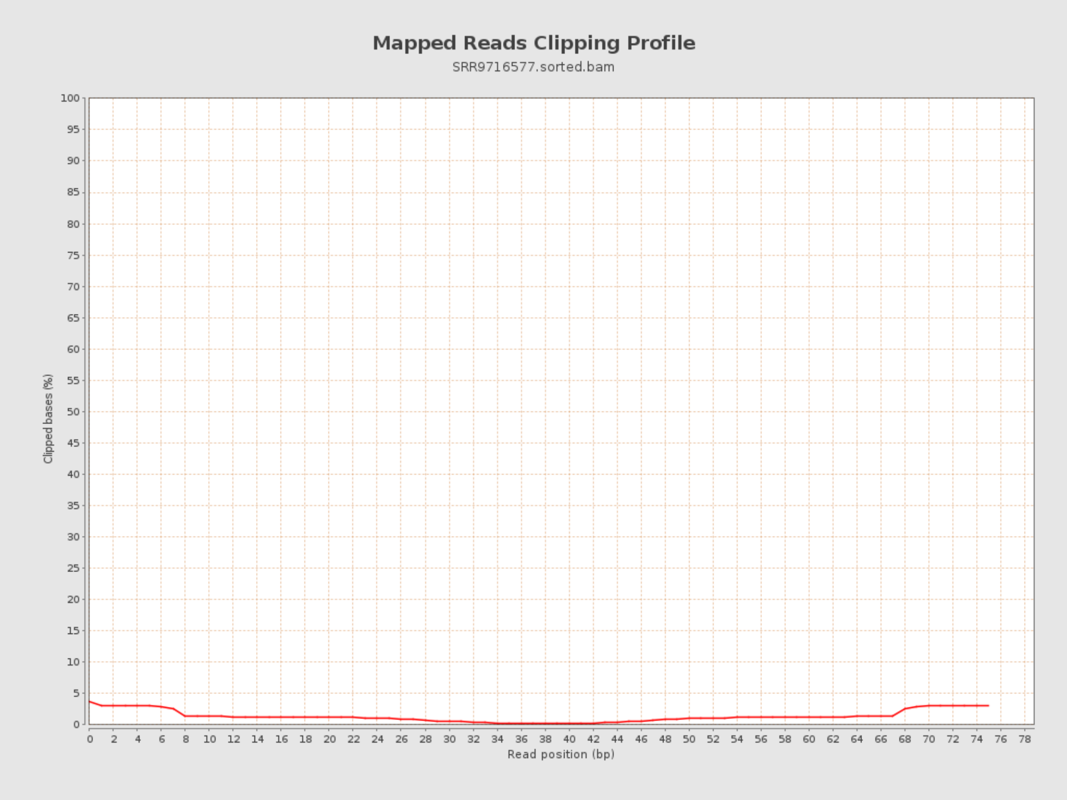
8. Results : Mapped Reads Nucleotide Content



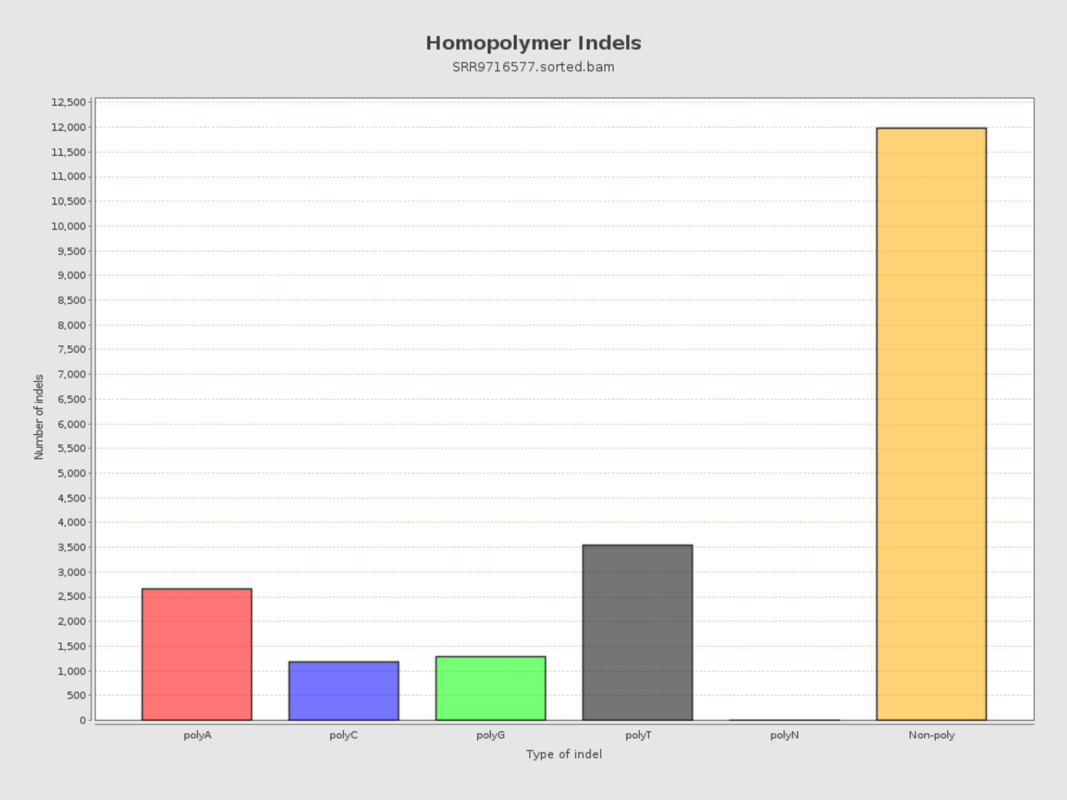
9. Results : Mapped Reads GC-content Distribution



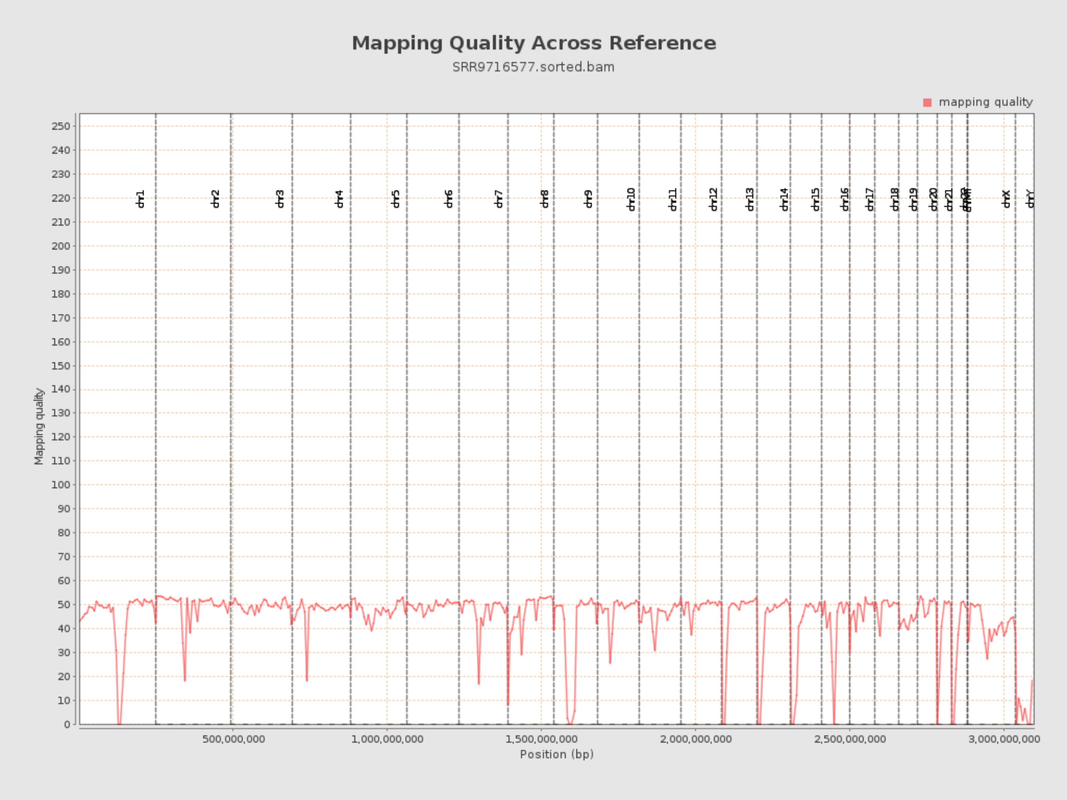
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram