Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:06:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716128.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_SRR9716128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:06:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	453,207
Mapped reads	422,779 / 93.29%
Unmapped reads	30,428 / 6.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,865 / 1.96%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	7,441 / 1.64%
Duplication rate	1.2%
Clipped reads	431,240 / 95.15%

2.2. ACGT Content

Number/percentage of A's	8,630,198 / 25.69%
Number/percentage of C's	6,367,550 / 18.95%
Number/percentage of T's	10,478,797 / 31.19%
Number/percentage of G's	8,117,395 / 24.16%
Number/percentage of N's	2,359 / 0.01%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0109

Standard Deviation	0.1398

2.4. Mapping Quality

Mean Mapping Quality	47.52

2.5. Mismatches and indels

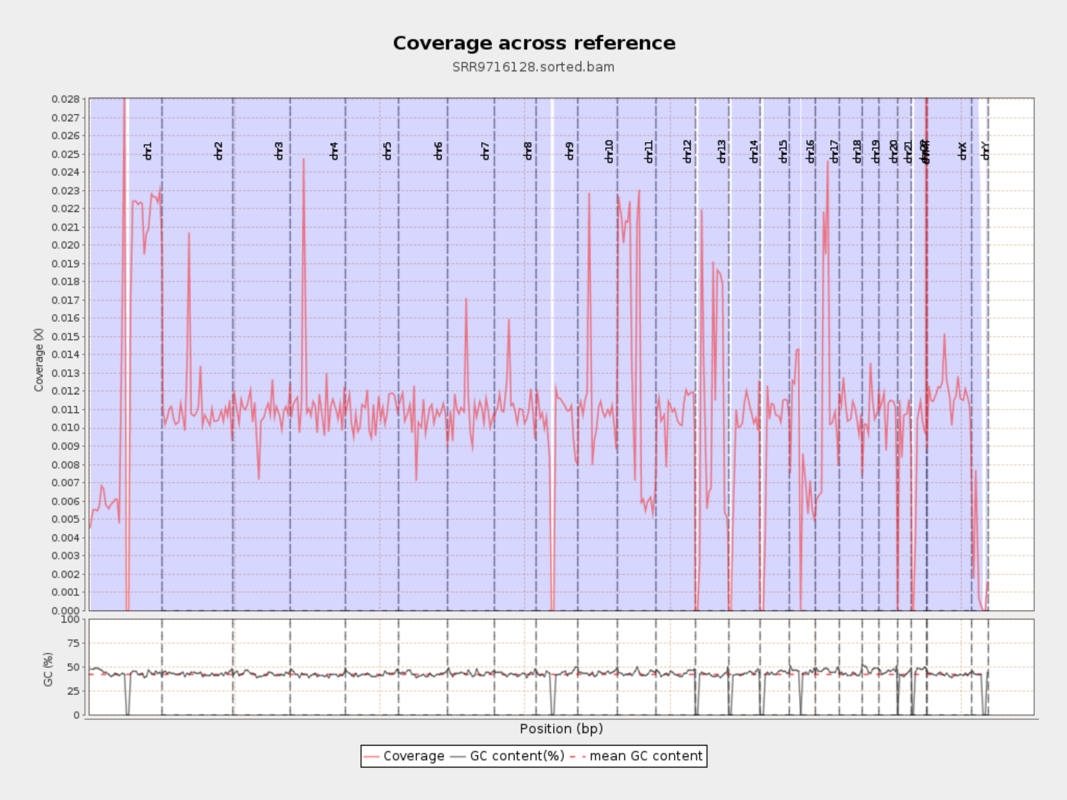
General error rate	0.66%
Mismatches	214,244
Insertions	2,771
Mapped reads with at least one insertion	0.64%
Deletions	8,205
Mapped reads with at least one deletion	1.91%
Homopolymer indels	44.69%

2.6. Chromosome stats

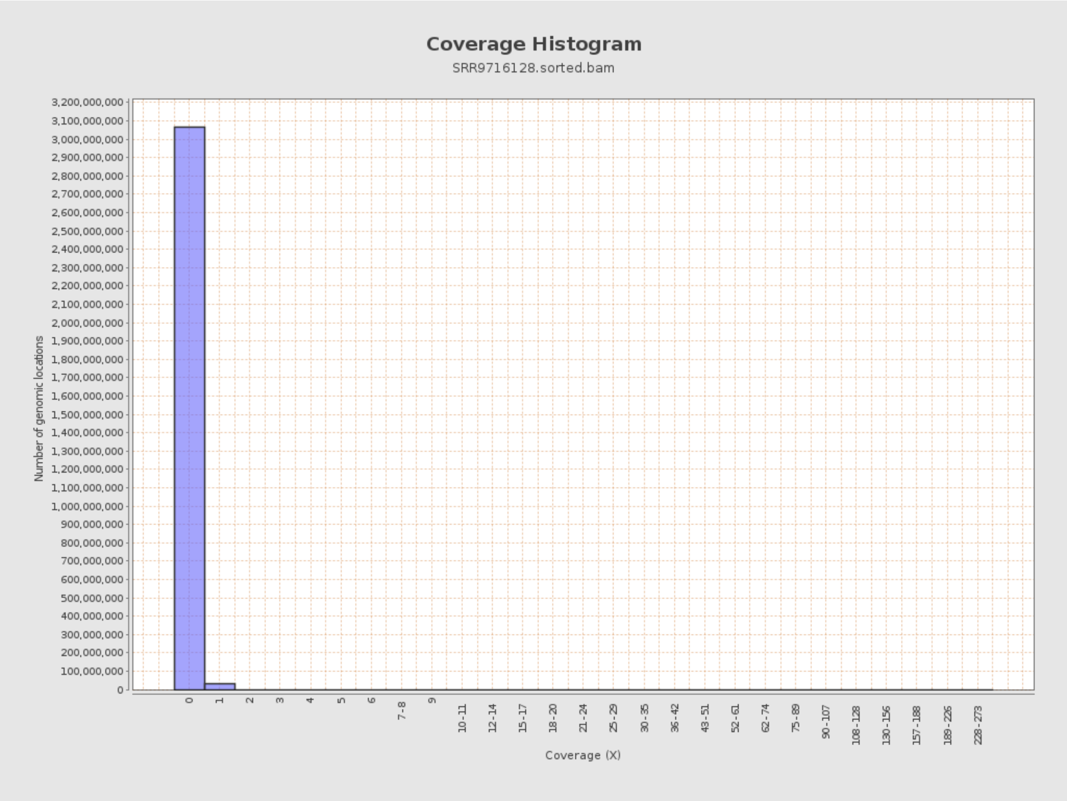
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3358705	0.0135	0.255
chr2	243199373	2706050	0.0111	0.1407
chr3	198022430	2143769	0.0108	0.1073
chr4	191154276	2205706	0.0115	0.1231
chr5	180915260	1958903	0.0108	0.1077
chr6	171115067	1827729	0.0107	0.1093
chr7	159138663	1755272	0.011	0.155

chr8	146364022	1651280	0.0113	0.1488
chr9	141213431	1339780	0.0095	0.1169
chr10	135534747	1534103	0.0113	0.1436
chr11	135006516	1865087	0.0138	0.1497
chr12	133851895	1461883	0.0109	0.1079
chr13	115169878	1190475	0.0103	0.1051
chr14	107349540	958662	0.0089	0.0992
chr15	102531392	927170	0.009	0.0976
chr16	90354753	750987	0.0083	0.0999
chr17	81195210	1002039	0.0123	0.1219
chr18	78077248	859849	0.011	0.1656
chr19	59128983	640002	0.0108	0.1786
chr20	63025520	687334	0.0109	0.11
chr21	48129895	453230	0.0094	0.1096
chr22	51304566	373742	0.0073	0.0882
chrMT	16571	8476	0.5115	0.7399
chrX	155270560	1840417	0.0119	0.119
chrY	59373566	111432	0.0019	0.0798

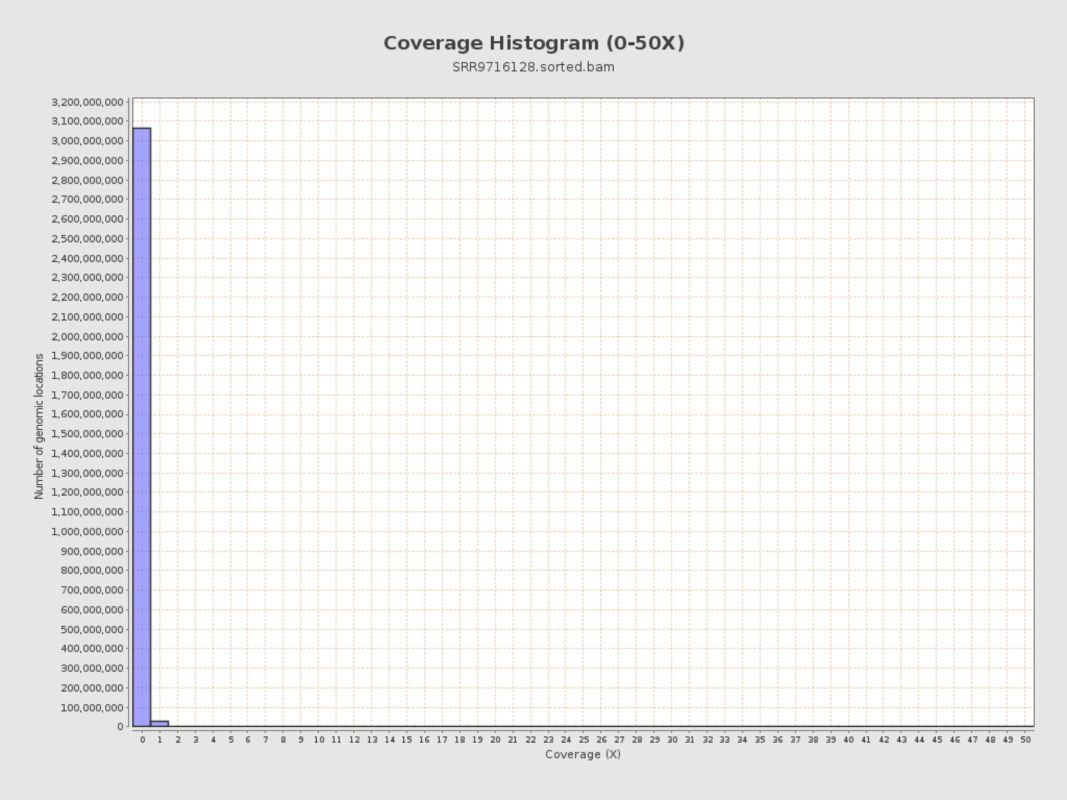
3. Results : Coverage across reference



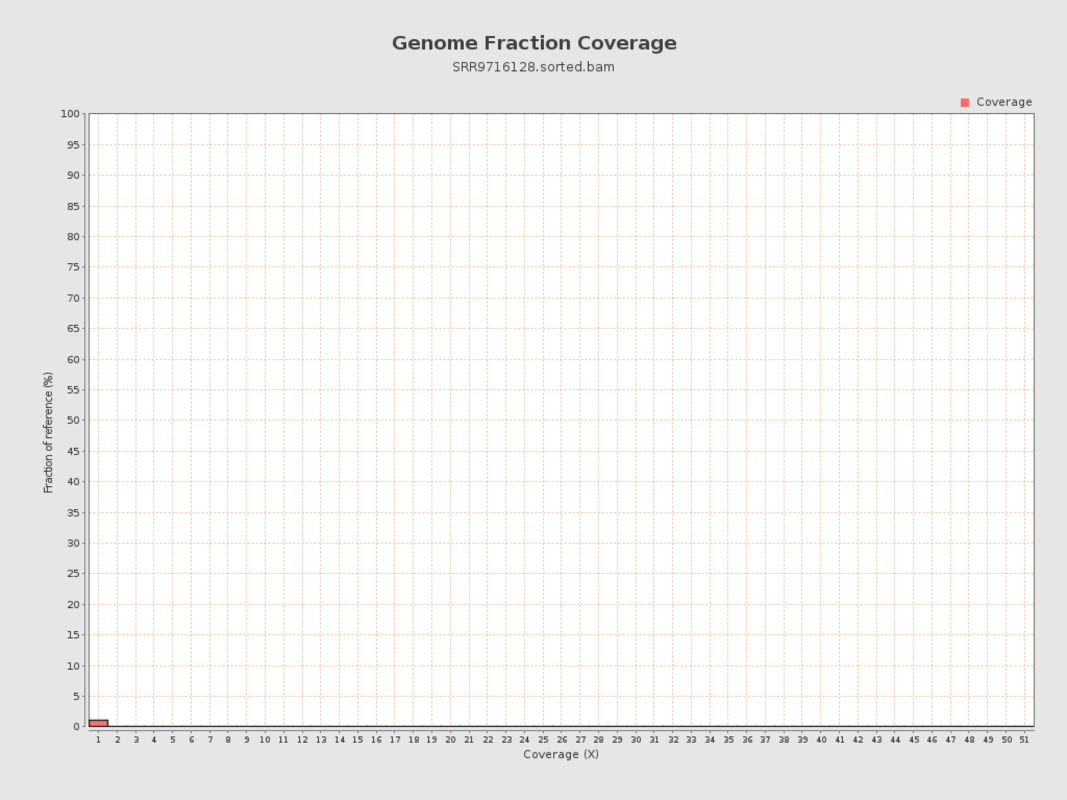
4. Results : Coverage Histogram



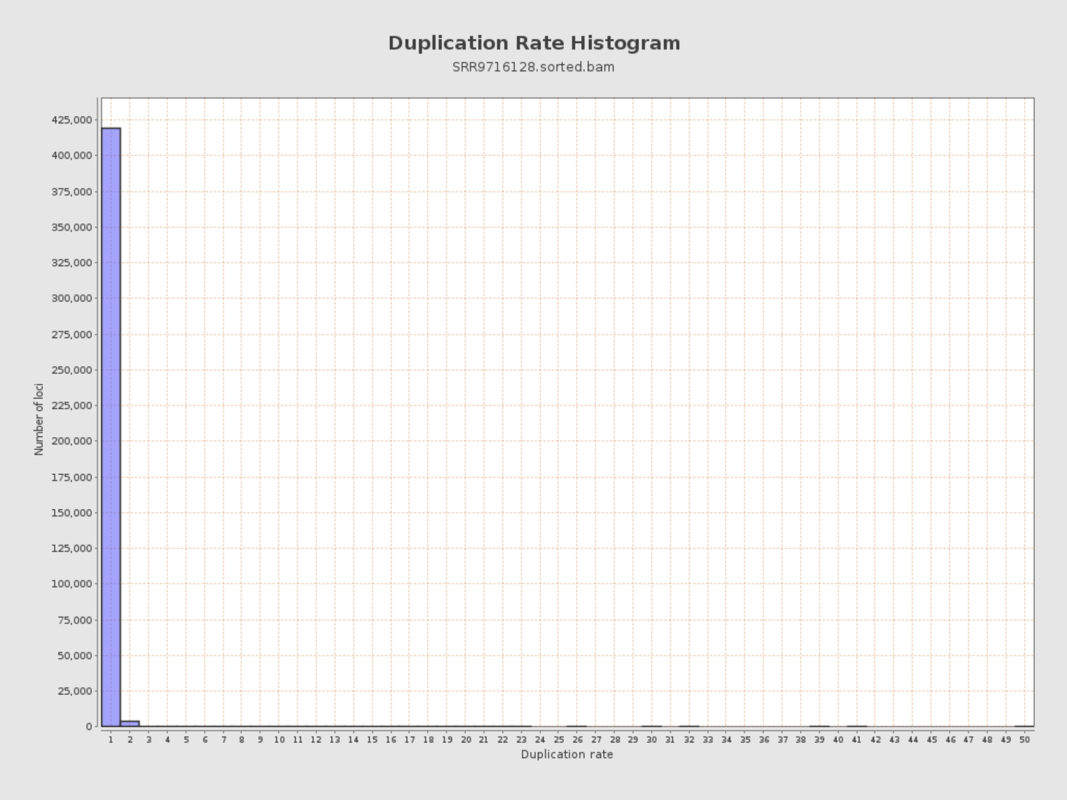
5. Results : Coverage Histogram (0-50X)



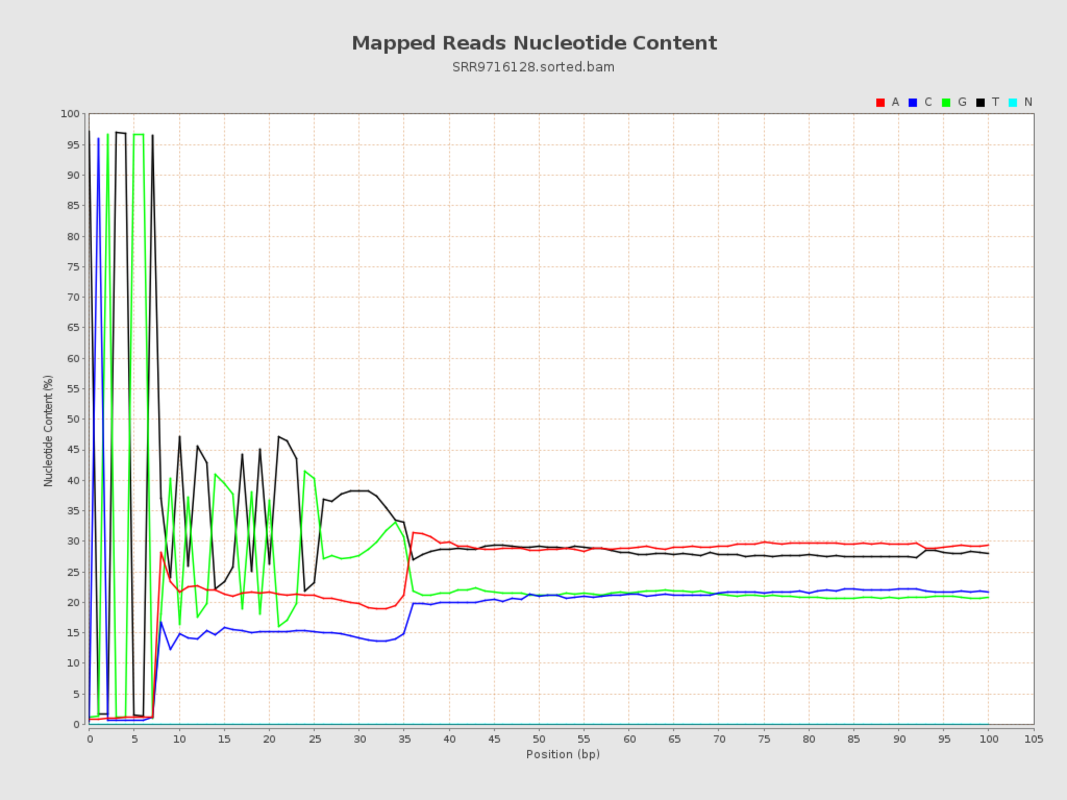
6. Results : Genome Fraction Coverage



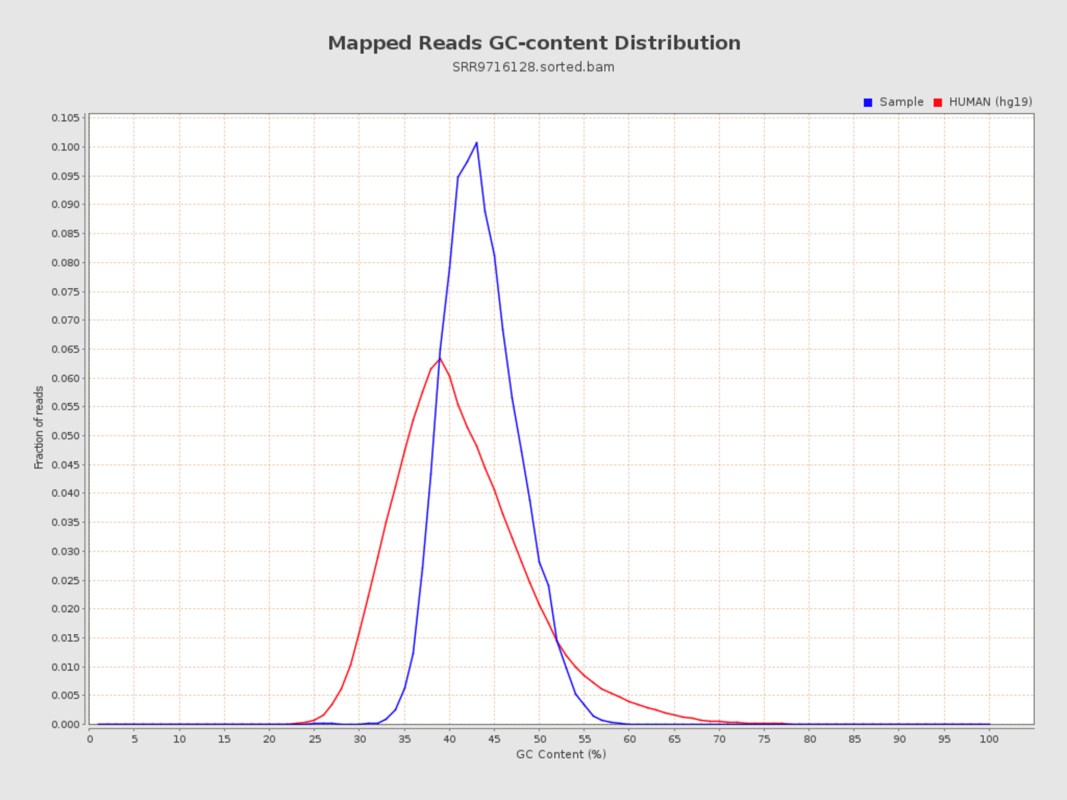
7. Results : Duplication Rate Histogram



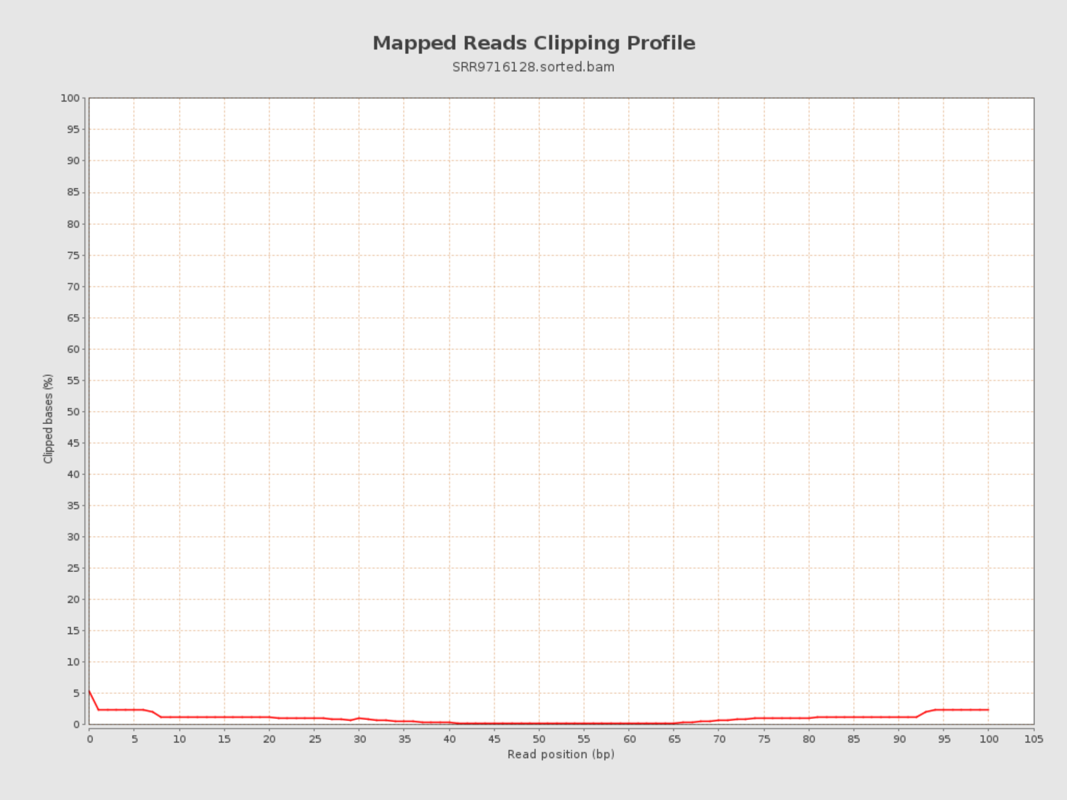
8. Results : Mapped Reads Nucleotide Content



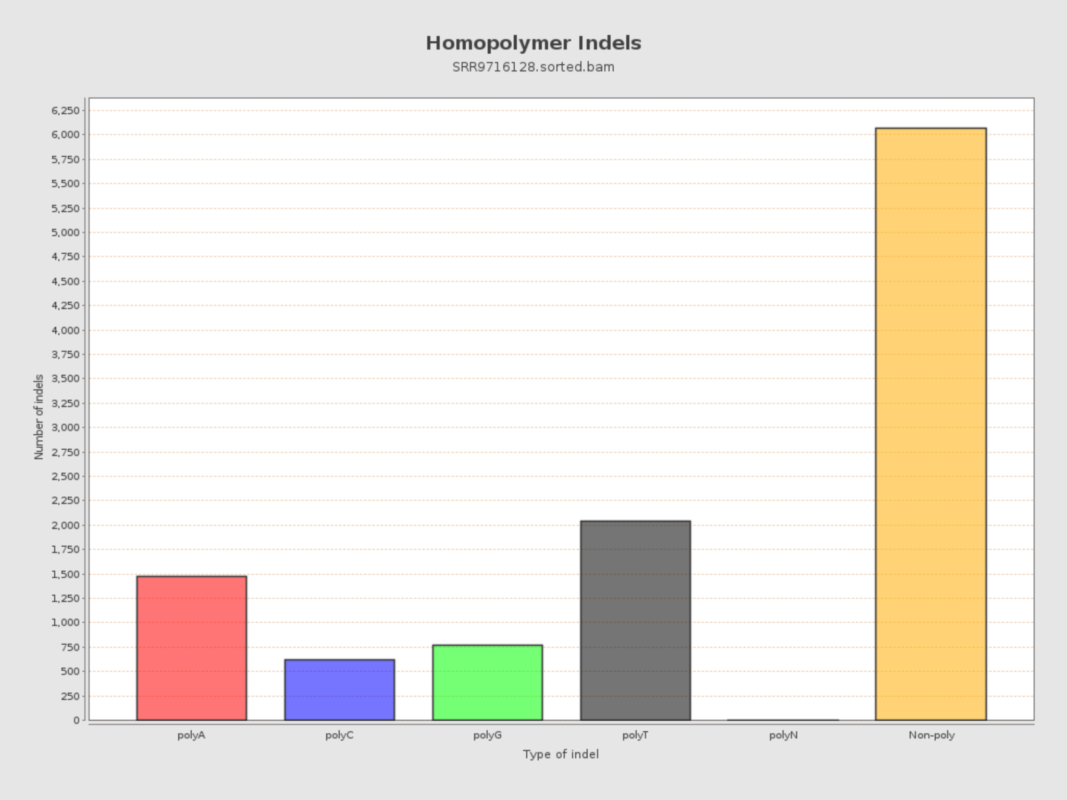
9. Results : Mapped Reads GC-content Distribution



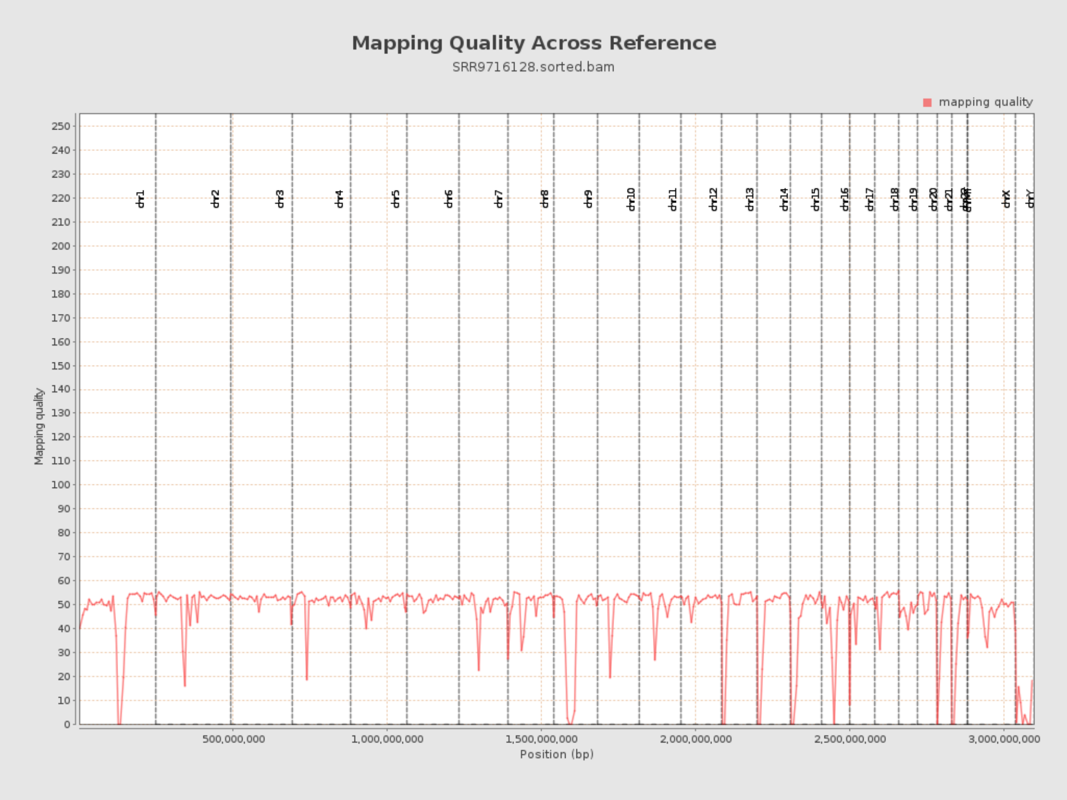
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram