Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:46:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716120.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_SRR9716120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:46:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,650
Mapped reads	608,011 / 79.1%
Unmapped reads	160,639 / 20.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,480 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,312 / 1.47%
Duplication rate	1.31%
Clipped reads	609,709 / 79.32%

2.2. ACGT Content

Number/percentage of A's	8,557,710 / 25.27%
Number/percentage of C's	6,438,858 / 19.01%
Number/percentage of T's	10,748,011 / 31.73%
Number/percentage of G's	8,125,012 / 23.99%
Number/percentage of N's	400 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0109

Standard Deviation	0.1354

2.4. Mapping Quality

Mean Mapping Quality	41.58

2.5. Mismatches and indels

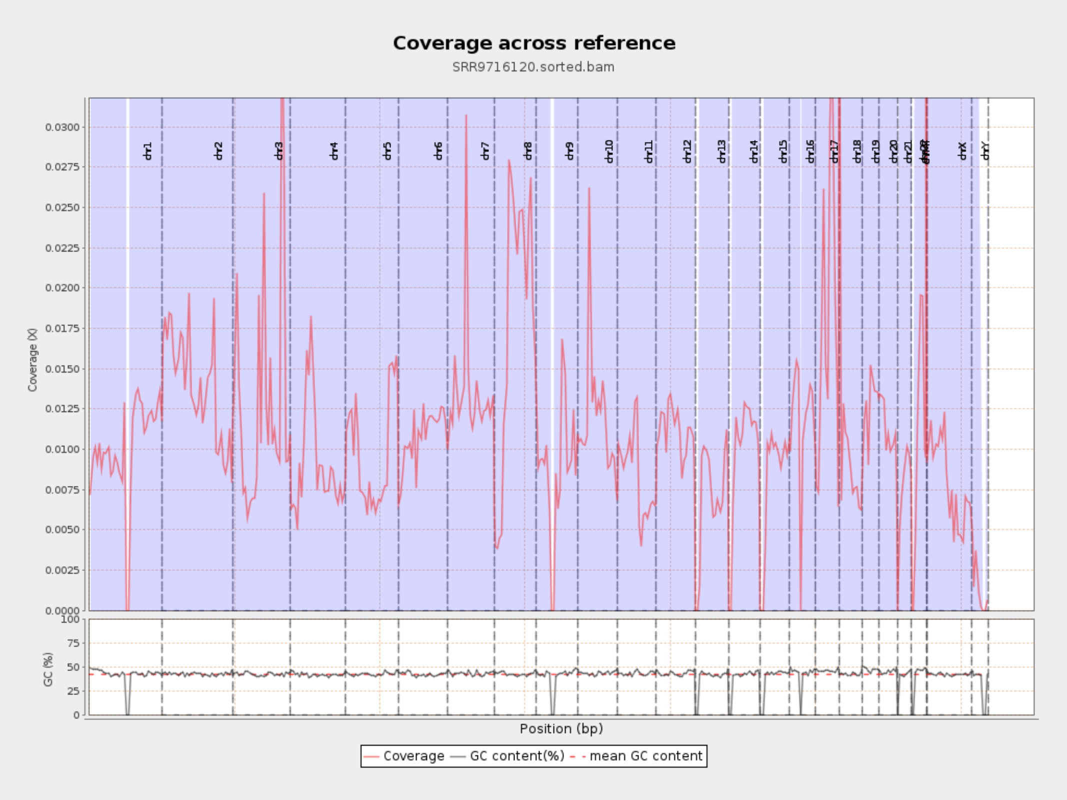
General error rate	0.54%
Mismatches	178,788
Insertions	2,117
Mapped reads with at least one insertion	0.35%
Deletions	6,114
Mapped reads with at least one deletion	1%
Homopolymer indels	40.3%

2.6. Chromosome stats

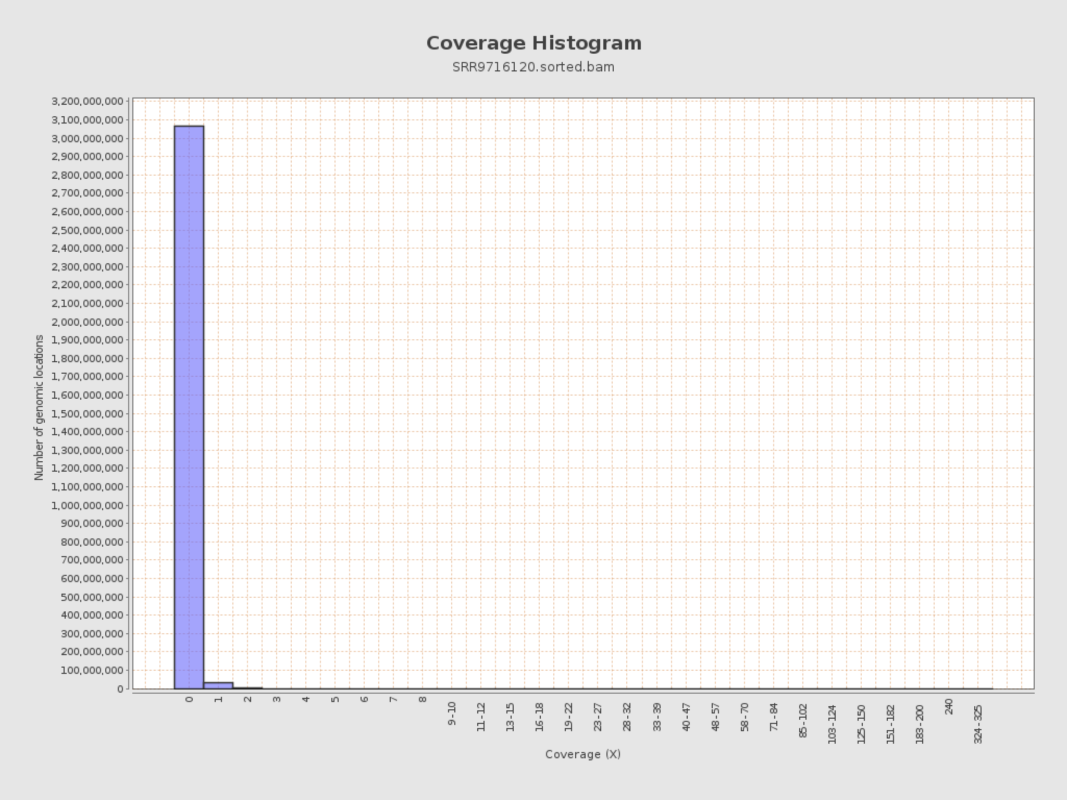
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2494626	0.01	0.1414
chr2	243199373	3417670	0.0141	0.1824
chr3	198022430	2598098	0.0131	0.1232
chr4	191154276	1746714	0.0091	0.1008
chr5	180915260	1762772	0.0097	0.1027
chr6	171115067	1841421	0.0108	0.114
chr7	159138663	2176139	0.0137	0.2678

chr8	146364022	2669619	0.0182	0.1508
chr9	141213431	1219848	0.0086	0.1044
chr10	135534747	1636536	0.0121	0.1534
chr11	135006516	1114519	0.0083	0.1042
chr12	133851895	1488757	0.0111	0.1128
chr13	115169878	797565	0.0069	0.0864
chr14	107349540	1046699	0.0098	0.1031
chr15	102531392	834753	0.0081	0.095
chr16	90354753	1072226	0.0119	0.1163
chr17	81195210	1469993	0.0181	0.1428
chr18	78077248	806740	0.0103	0.1372
chr19	59128983	753875	0.0127	0.1454
chr20	63025520	709434	0.0113	0.1111
chr21	48129895	356332	0.0074	0.0907
chr22	51304566	520893	0.0102	0.1051
chrMT	16571	6096	0.3679	0.6901
chrX	155270560	1259482	0.0081	0.0996
chrY	59373566	79096	0.0013	0.0424

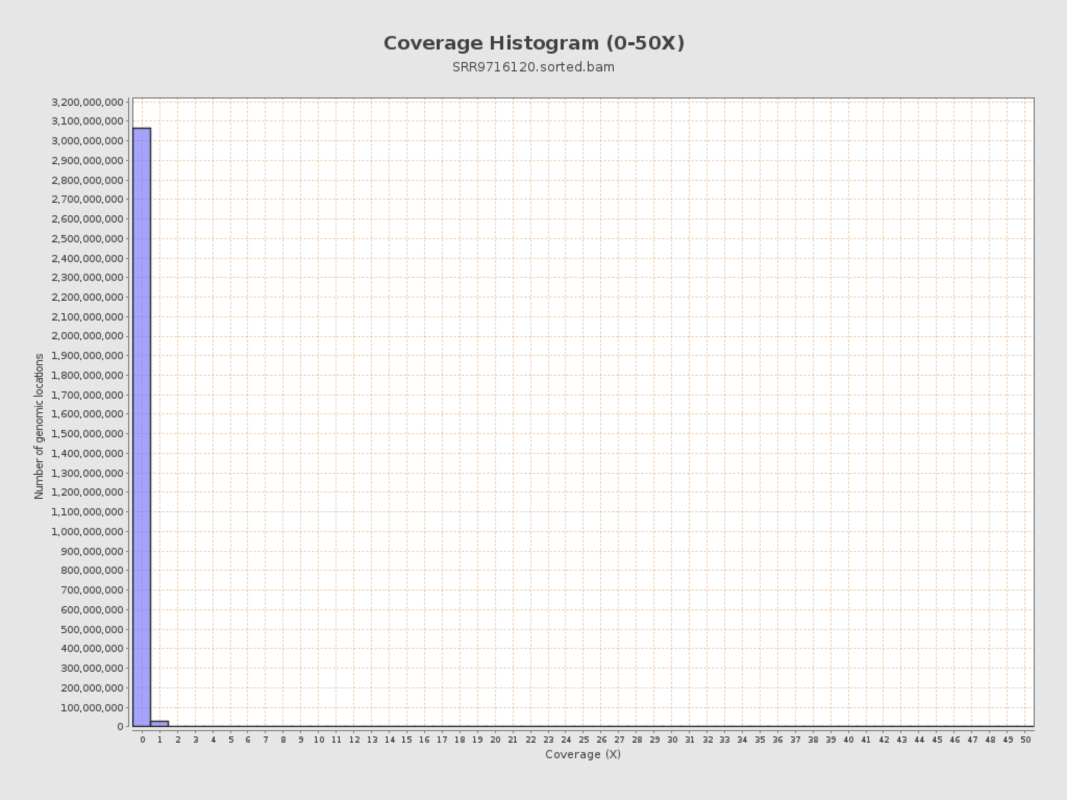
3. Results : Coverage across reference



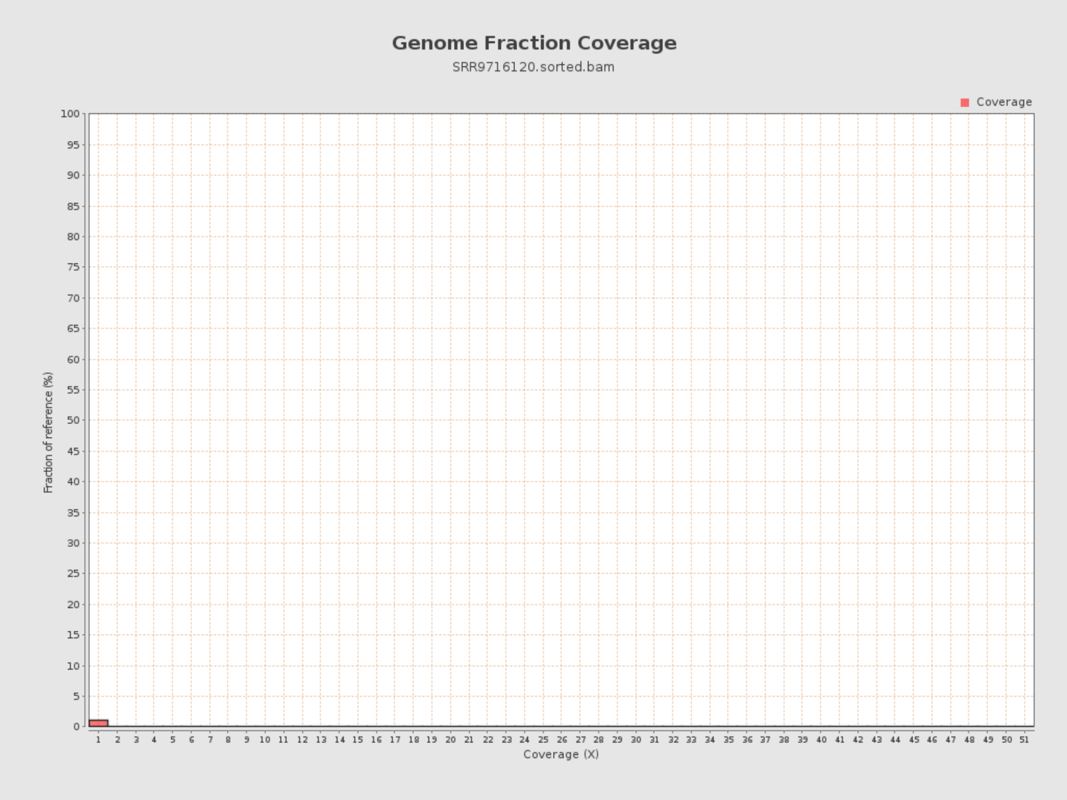
4. Results : Coverage Histogram



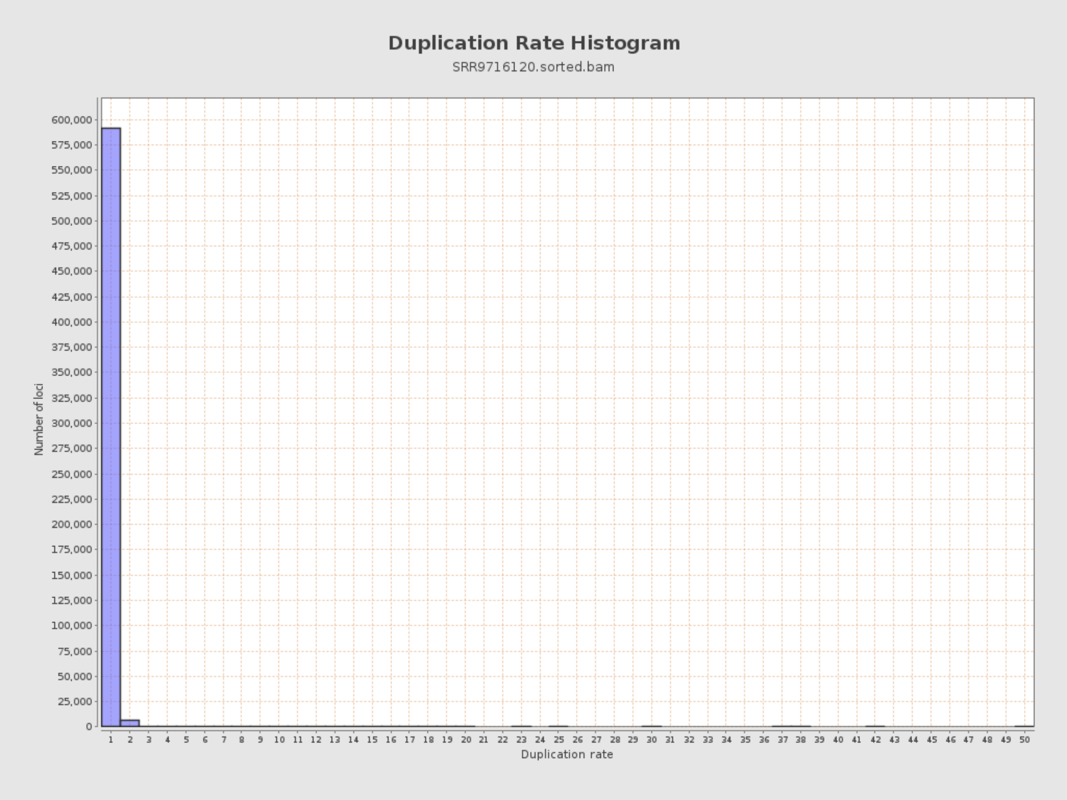
5. Results : Coverage Histogram (0-50X)



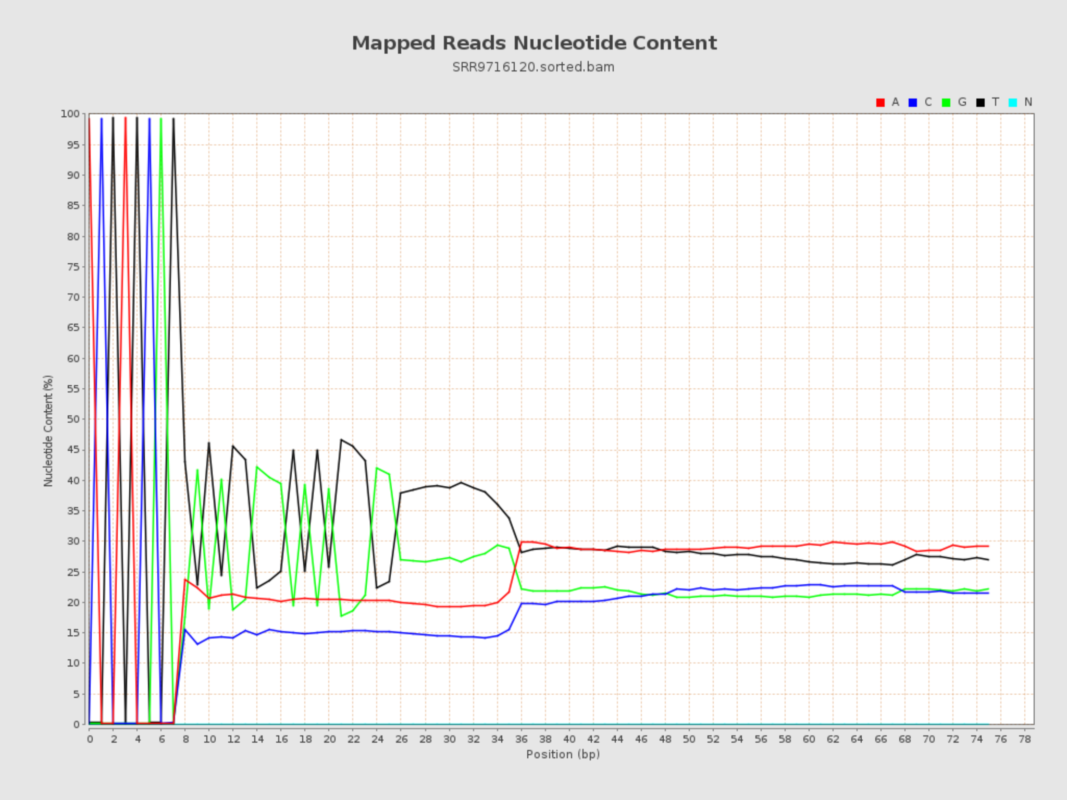
6. Results : Genome Fraction Coverage



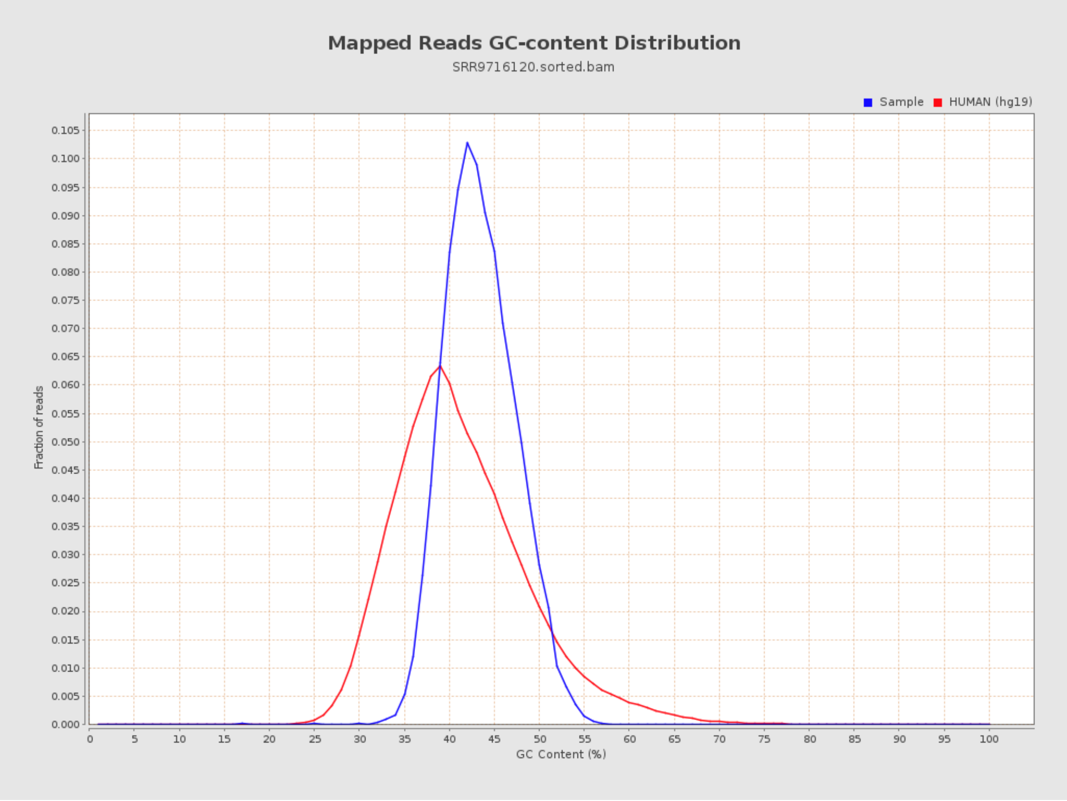
7. Results : Duplication Rate Histogram



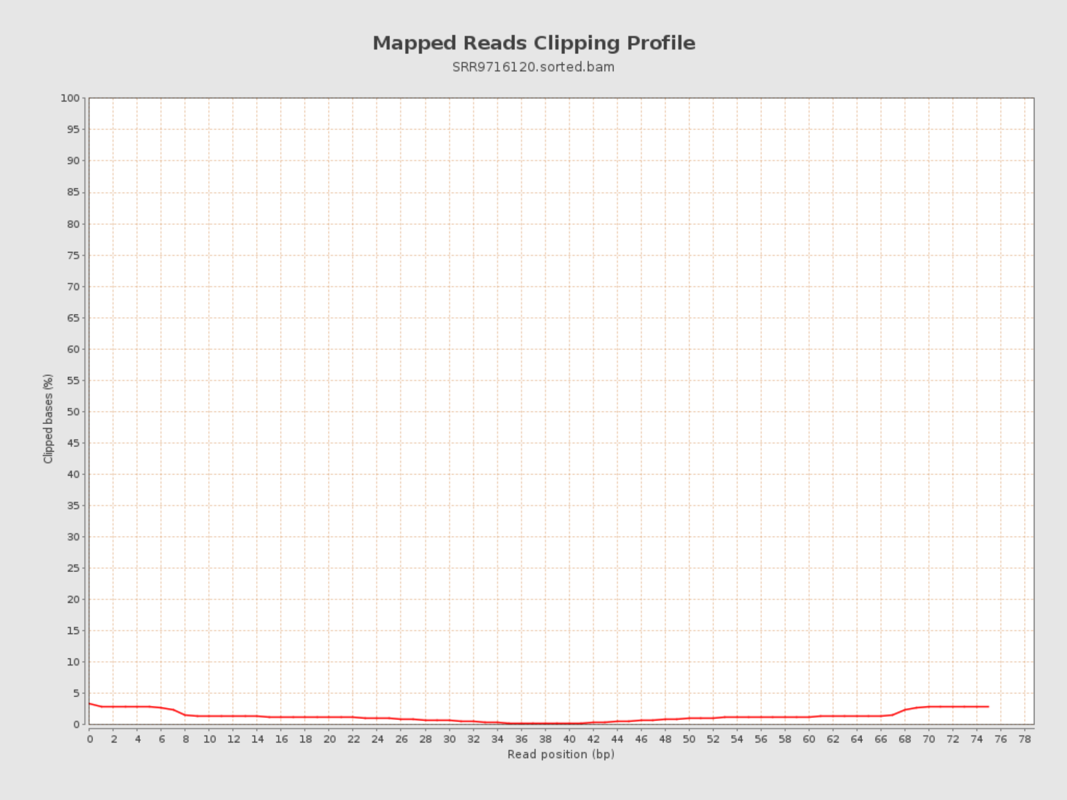
8. Results : Mapped Reads Nucleotide Content



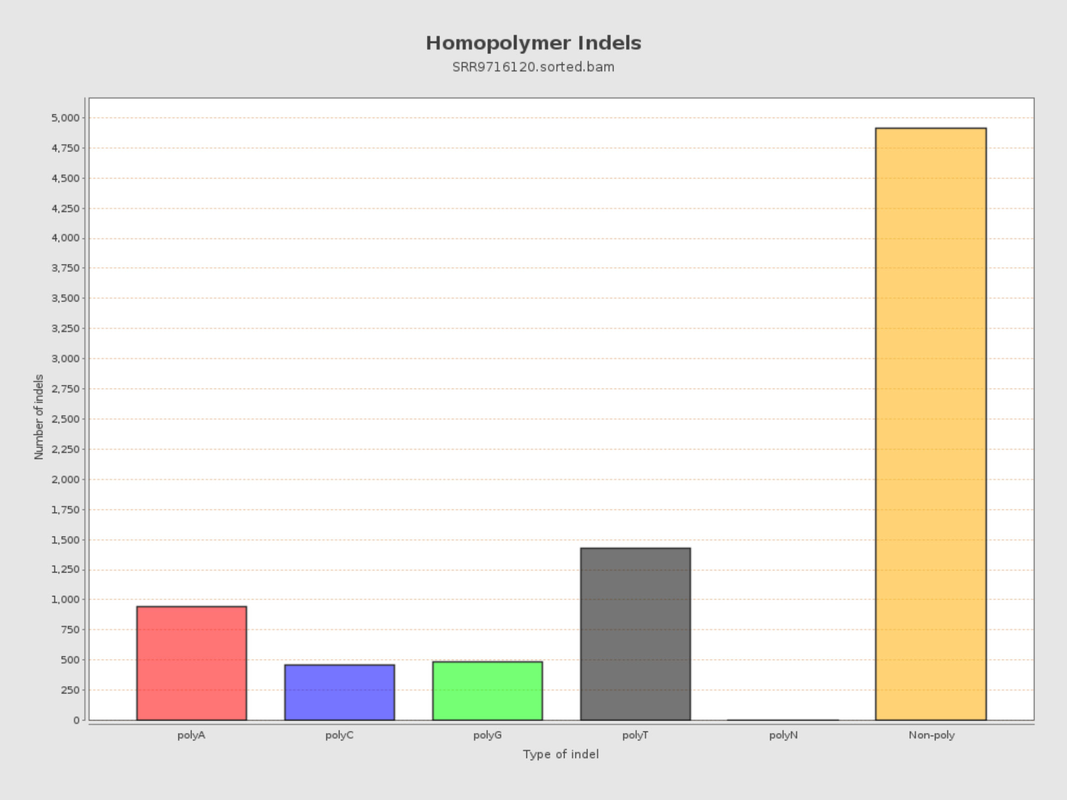
9. Results : Mapped Reads GC-content Distribution



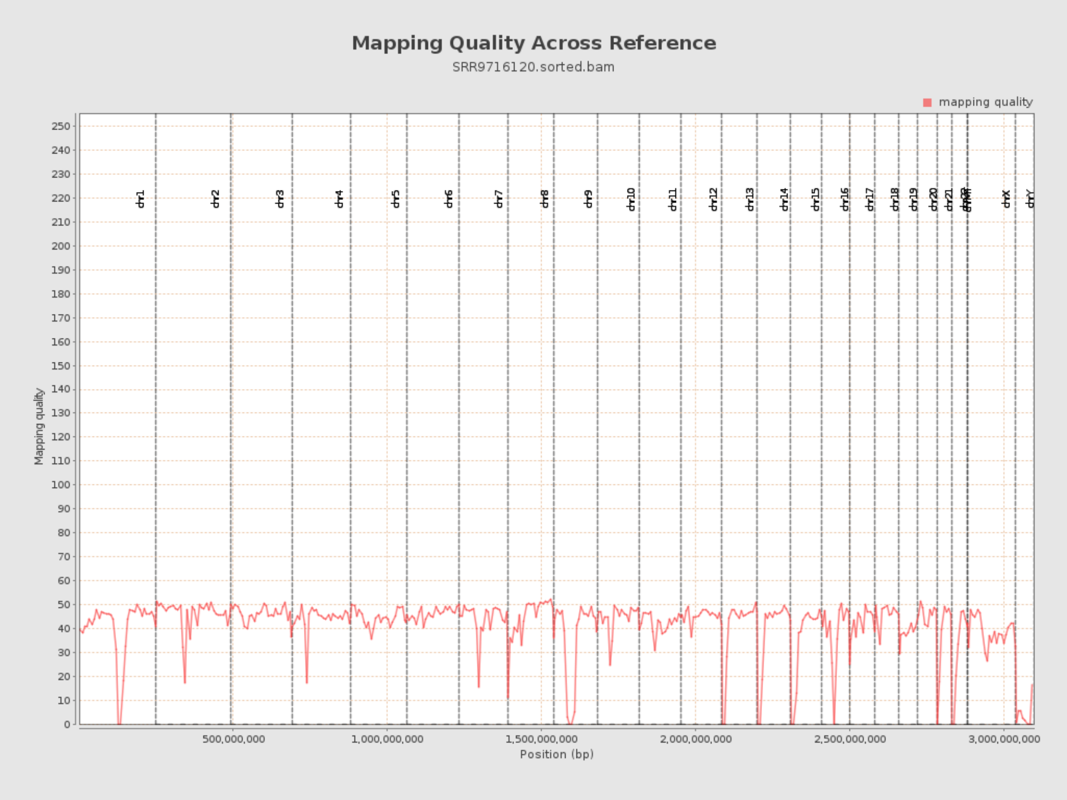
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram