Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:04:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716168.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_SRR9716168 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716168.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,401,143
Mapped reads	1,263,854 / 90.2%
Unmapped reads	137,289 / 9.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,337 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	42,100 / 3%
Duplication rate	2.46%
Clipped reads	1,265,942 / 90.35%

2.2. ACGT Content

Number/percentage of A's	19,199,462 / 26.35%
Number/percentage of C's	13,575,552 / 18.63%
Number/percentage of T's	23,200,239 / 31.84%
Number/percentage of G's	16,879,547 / 23.17%
Number/percentage of N's	1,204 / 0%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2386

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

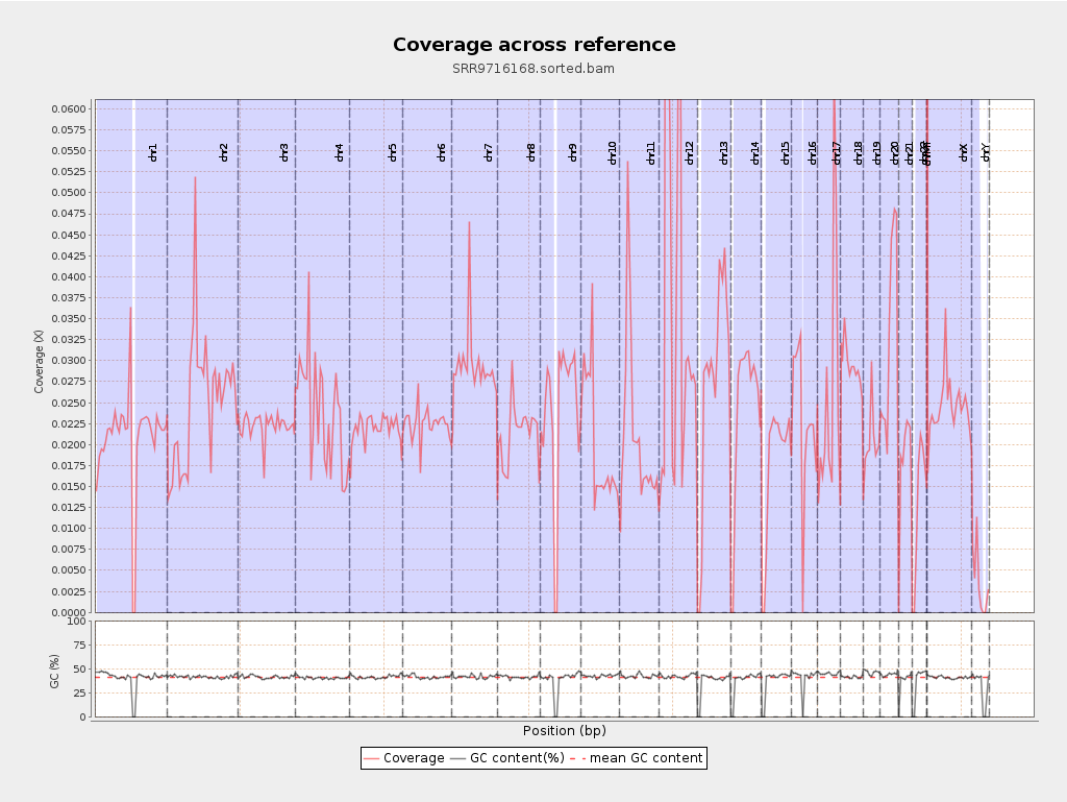
General error rate	0.55%
Mismatches	389,228
Insertions	5,243
Mapped reads with at least one insertion	0.41%
Deletions	12,158
Mapped reads with at least one deletion	0.95%
Homopolymer indels	42.58%

2.6. Chromosome stats

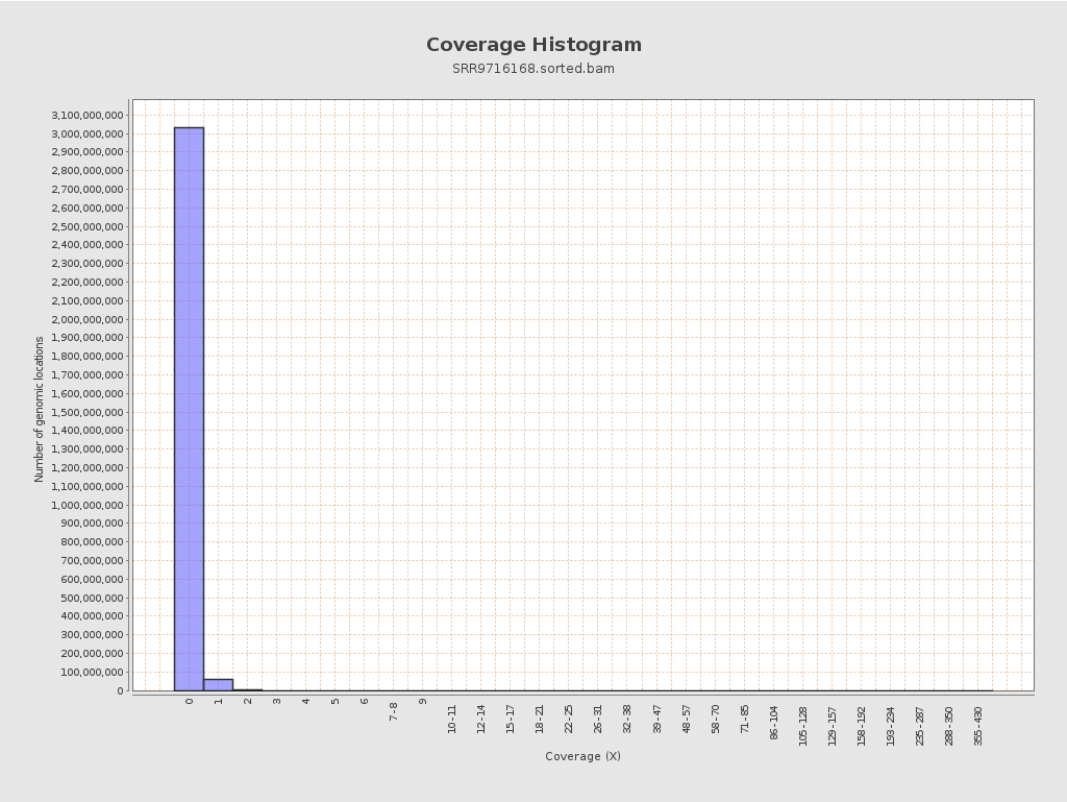
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5149359	0.0207	0.3821
chr2	243199373	6065018	0.0249	0.2662
chr3	198022430	4405763	0.0222	0.1591
chr4	191154276	4520106	0.0236	0.1804
chr5	180915260	3996599	0.0221	0.1612
chr6	171115067	3839496	0.0224	0.1739
chr7	159138663	4675172	0.0294	0.3286

chr8	146364022	3144527	0.0215	0.2315
chr9	141213431	3359837	0.0238	0.2503
chr10	135534747	2701001	0.0199	0.2291
chr11	135006516	2810200	0.0208	0.2006
chr12	133851895	5359132	0.04	0.2352
chr13	115169878	3153348	0.0274	0.1761
chr14	107349540	2579326	0.024	0.1846
chr15	102531392	1805946	0.0176	0.1428
chr16	90354753	2025026	0.0224	0.1788
chr17	81195210	2115499	0.0261	0.1783
chr18	78077248	2303215	0.0295	0.446
chr19	59128983	1218356	0.0206	0.3154
chr20	63025520	2065504	0.0328	0.1987
chr21	48129895	869238	0.0181	0.1636
chr22	51304566	673774	0.0131	0.1211
chrMT	16571	16136	0.9737	1.1858
chrX	155270560	3818567	0.0246	0.2026
chrY	59373566	206136	0.0035	0.0886

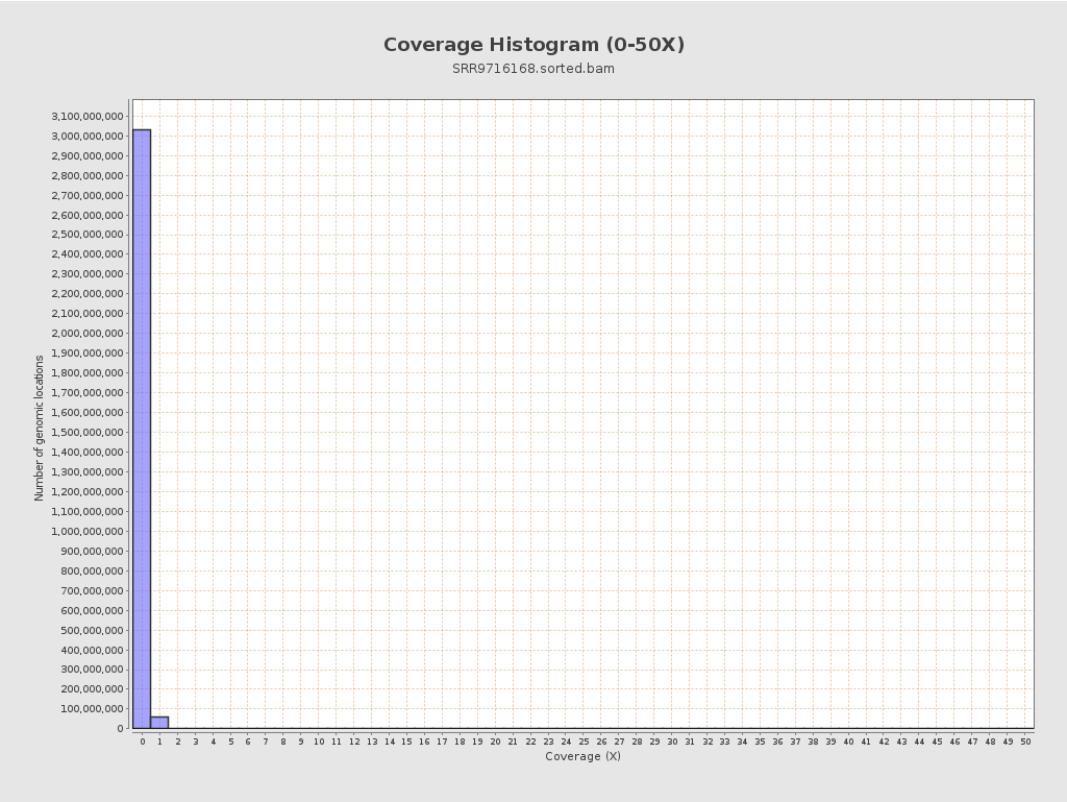
3. Results : Coverage across reference



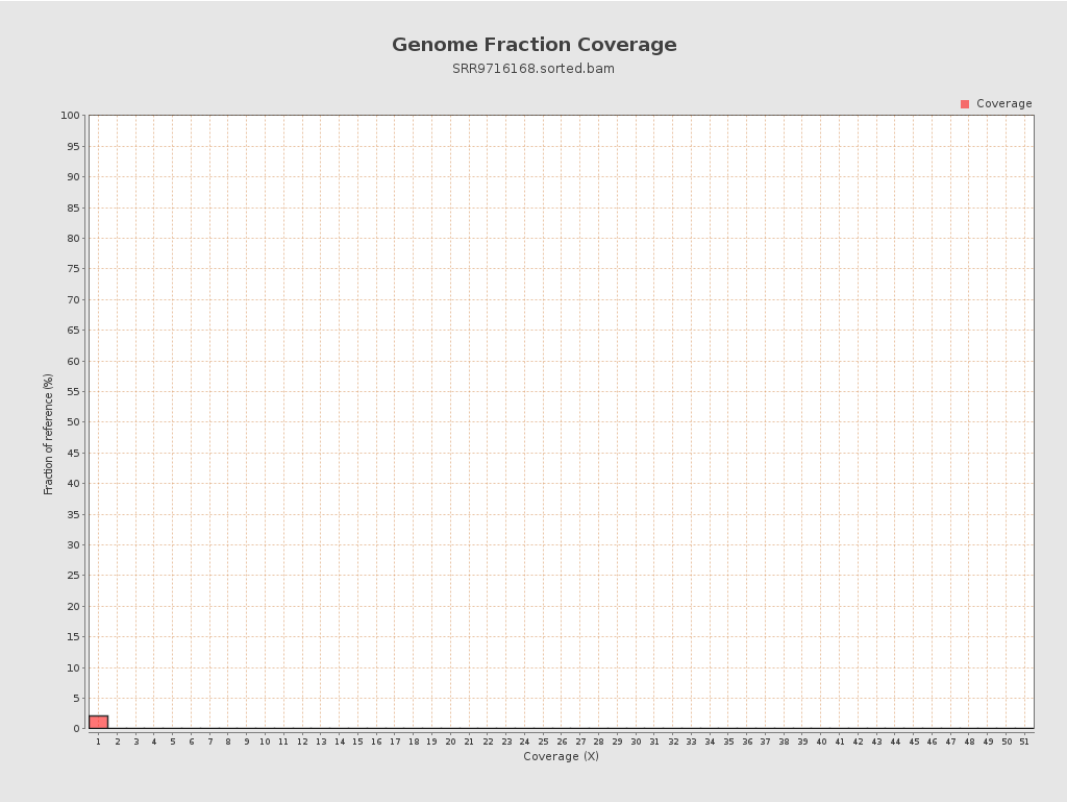
4. Results : Coverage Histogram



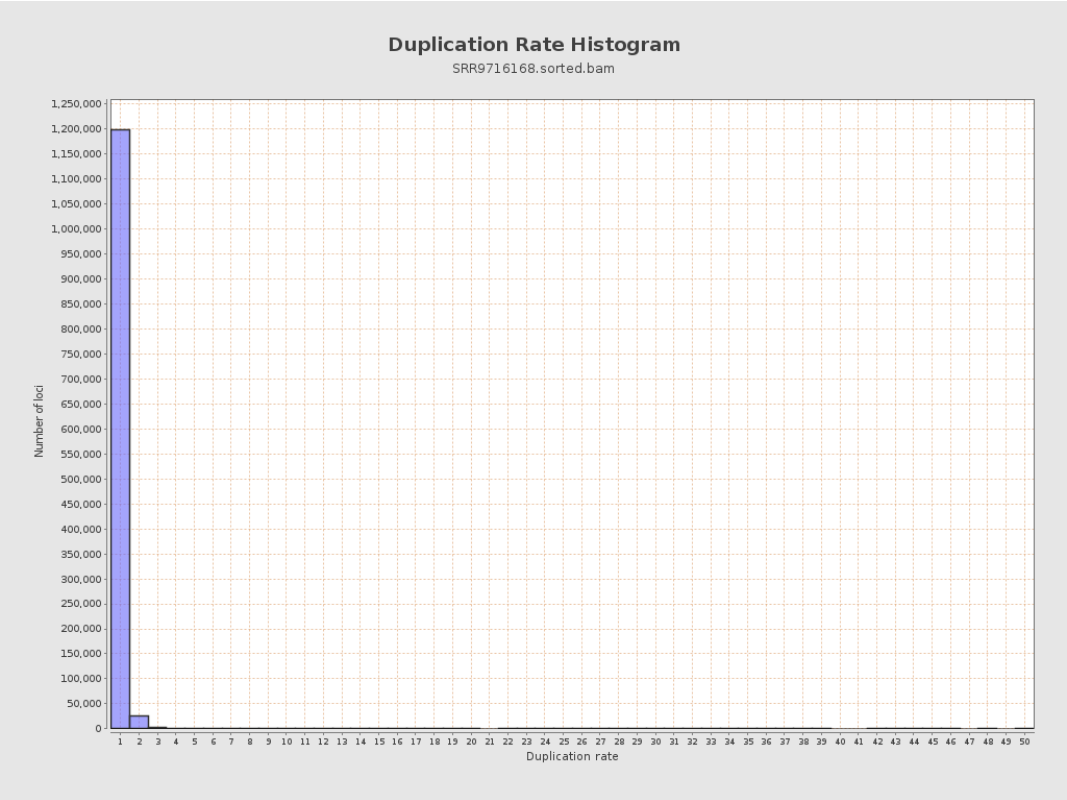
5. Results : Coverage Histogram (0-50X)



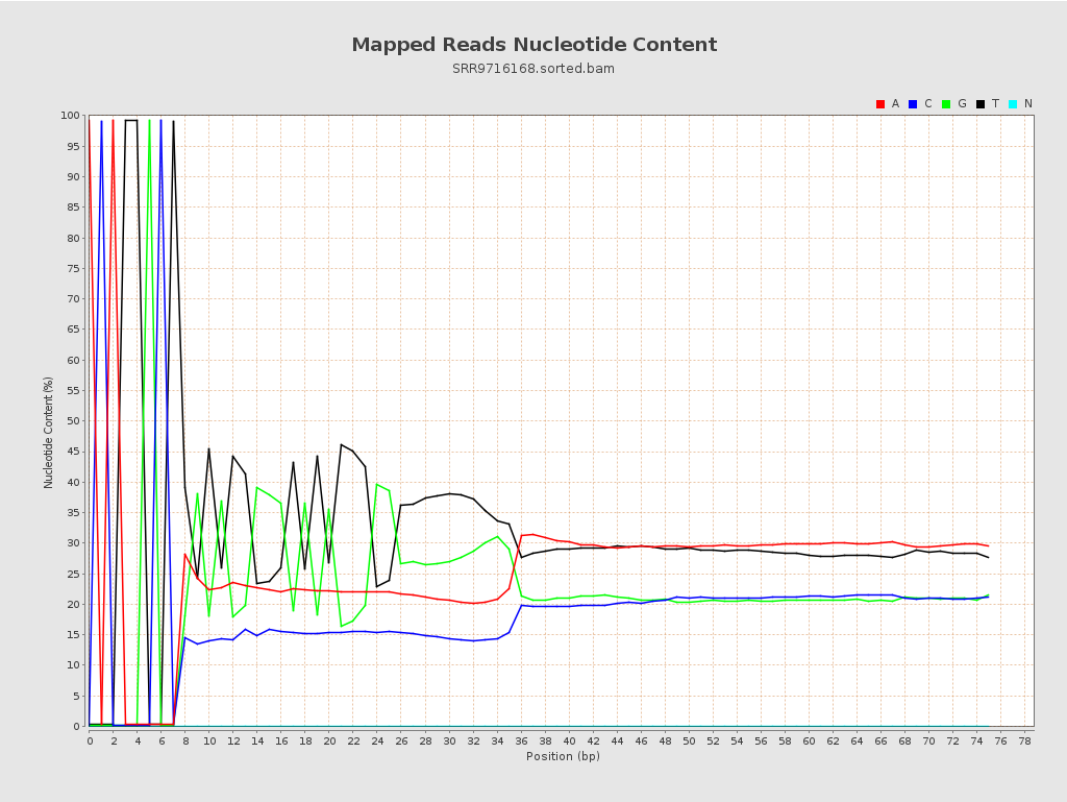
6. Results : Genome Fraction Coverage



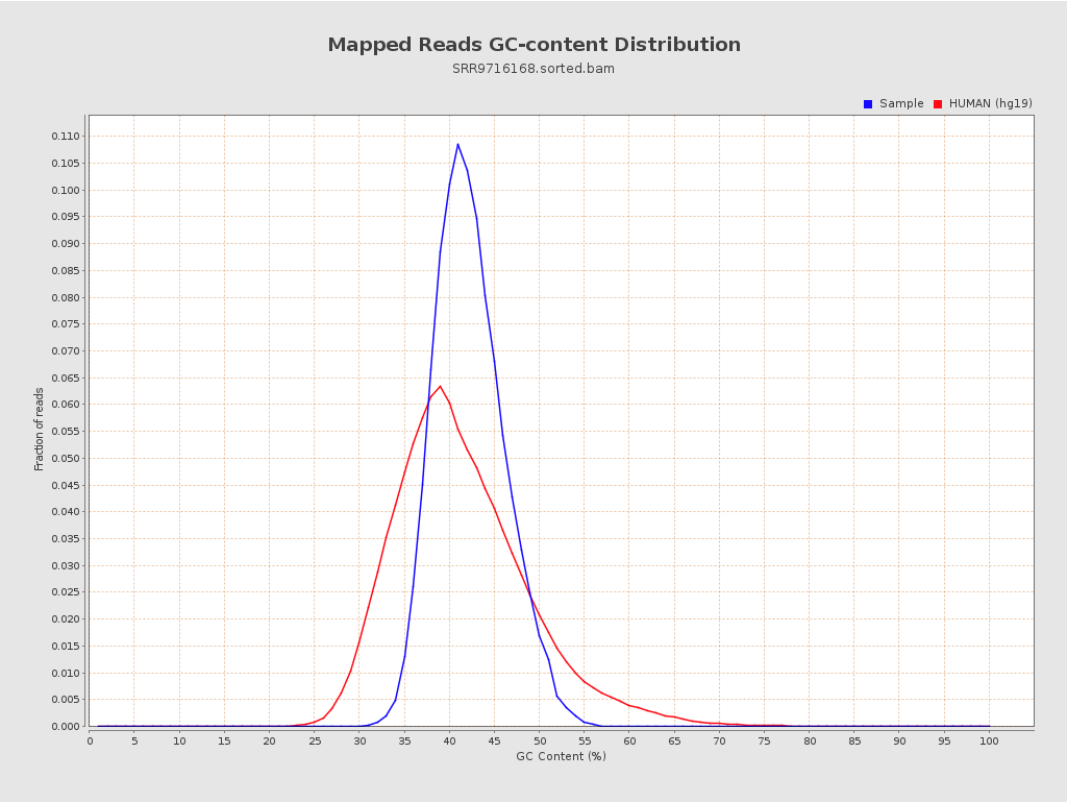
7. Results : Duplication Rate Histogram



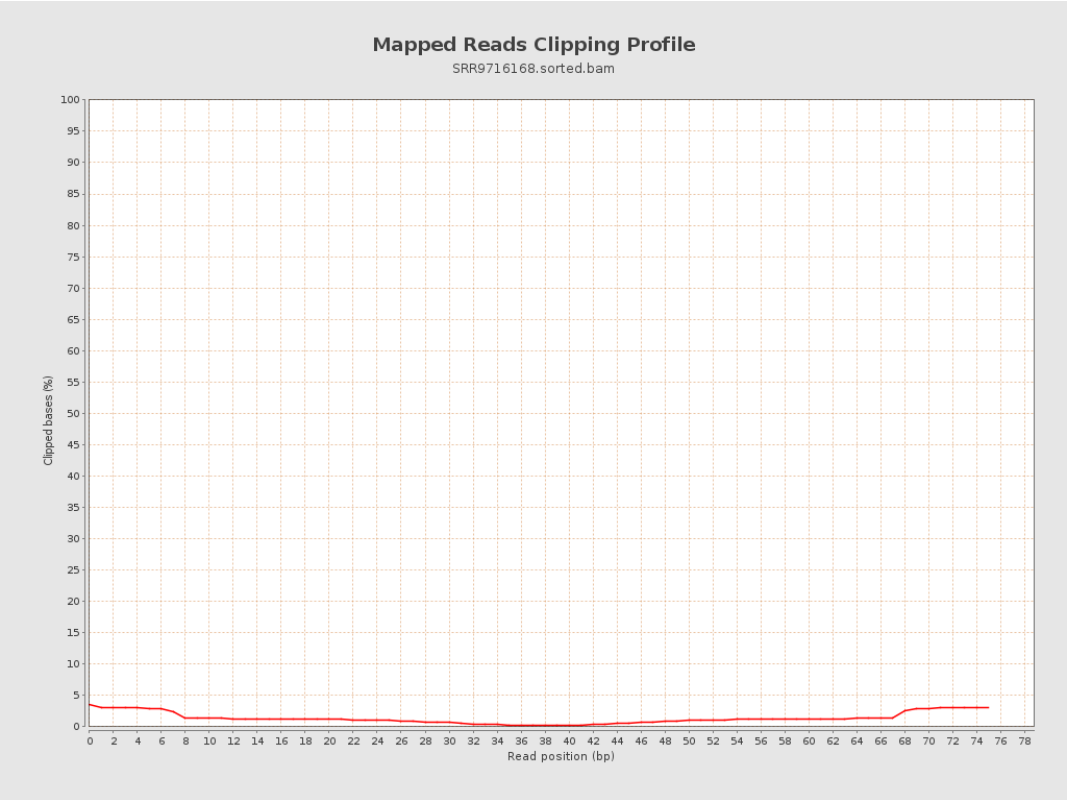
8. Results : Mapped Reads Nucleotide Content



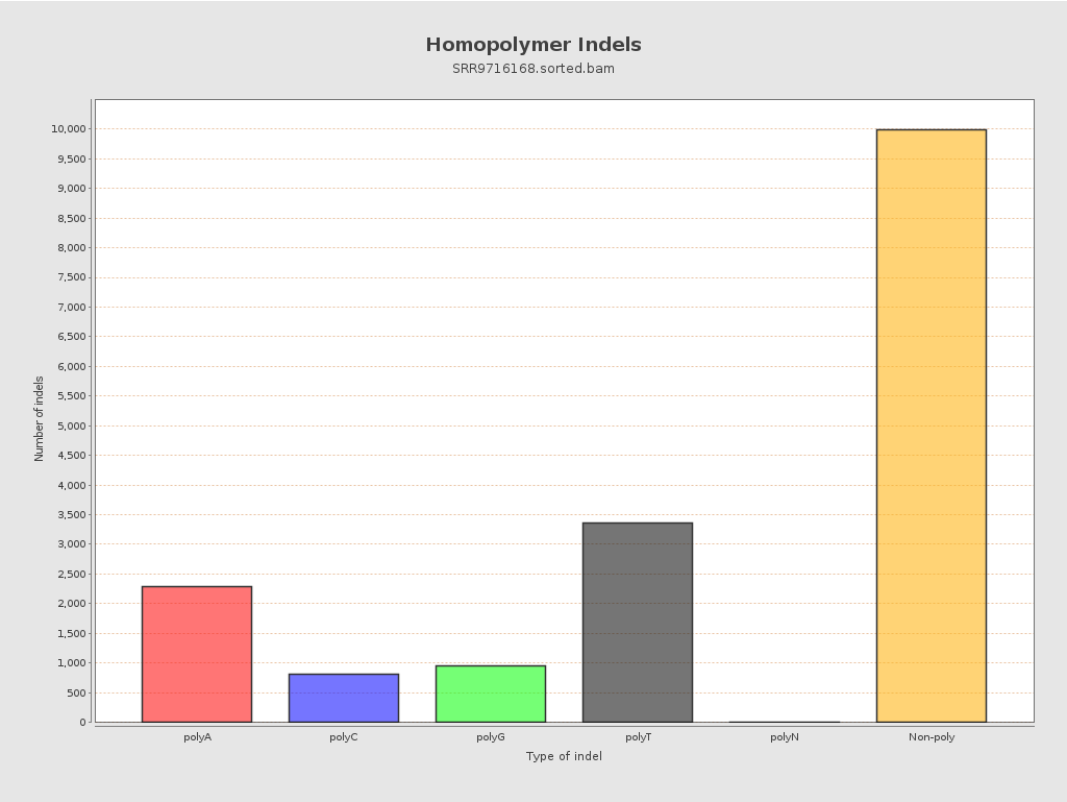
9. Results : Mapped Reads GC-content Distribution



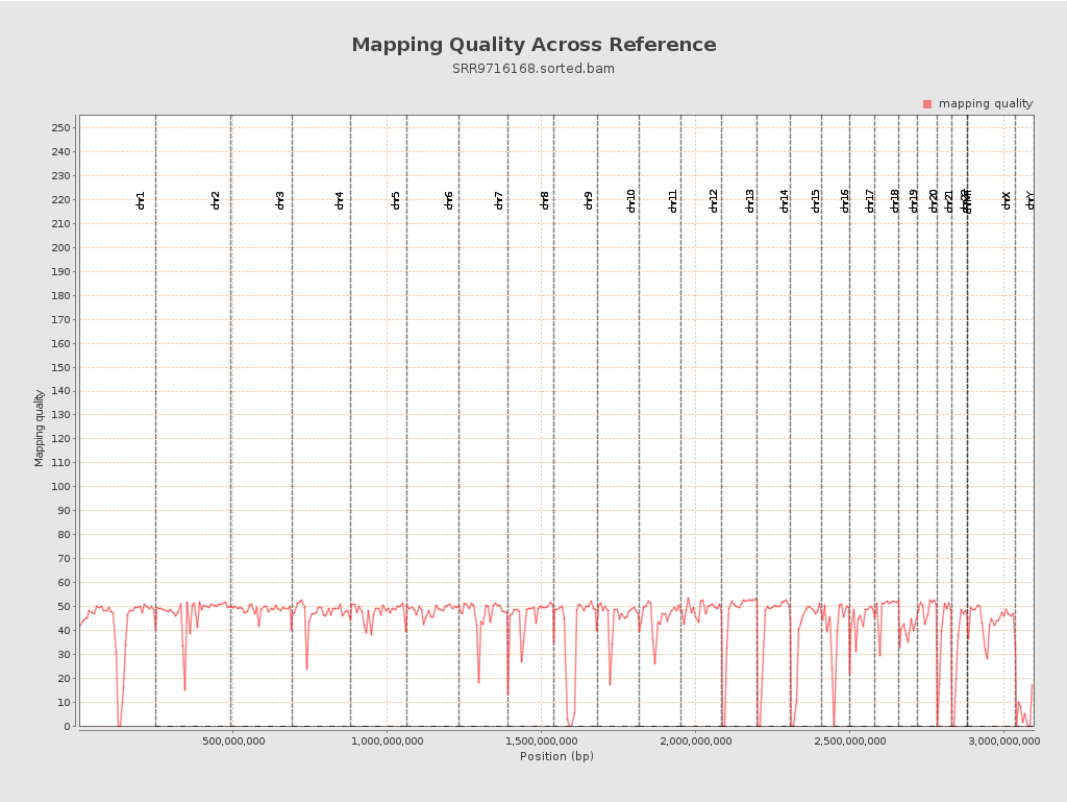
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram