

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:54:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716619.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_SRR9716619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716619.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:53:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	804,322
Mapped reads	745,494 / 92.69%
Unmapped reads	58,828 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,585 / 1.56%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	22,550 / 2.8%
Duplication rate	1.64%
Clipped reads	757,042 / 94.12%

2.2. ACGT Content

Number/percentage of A's	14,584,445 / 24.88%
Number/percentage of C's	10,804,041 / 18.43%
Number/percentage of T's	18,117,294 / 30.91%
Number/percentage of G's	15,101,266 / 25.77%
Number/percentage of N's	2,925 / 0%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.2697
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2.4. Mapping Quality

Mean Mapping Quality	43.7
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2.5. Mismatches and indels

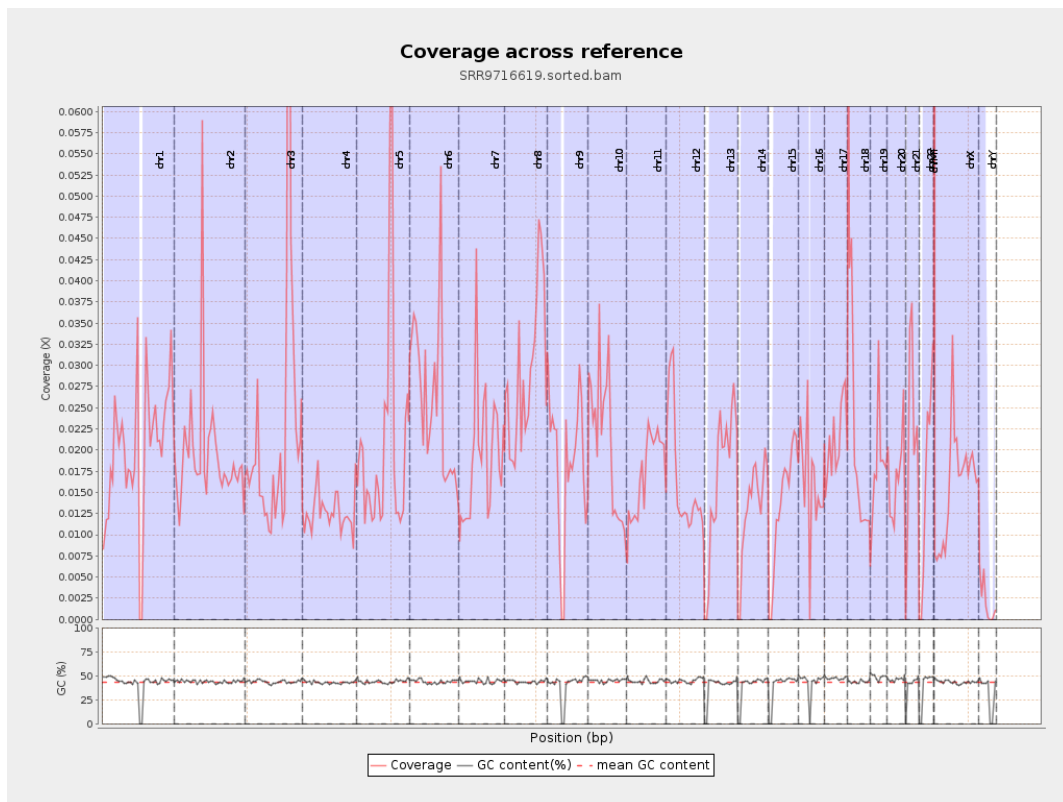
General error rate	0.84%
Mismatches	483,247
Insertions	5,378
Mapped reads with at least one insertion	0.71%
Deletions	14,767
Mapped reads with at least one deletion	1.95%
Homopolymer indels	43.5%

2.6. Chromosome stats

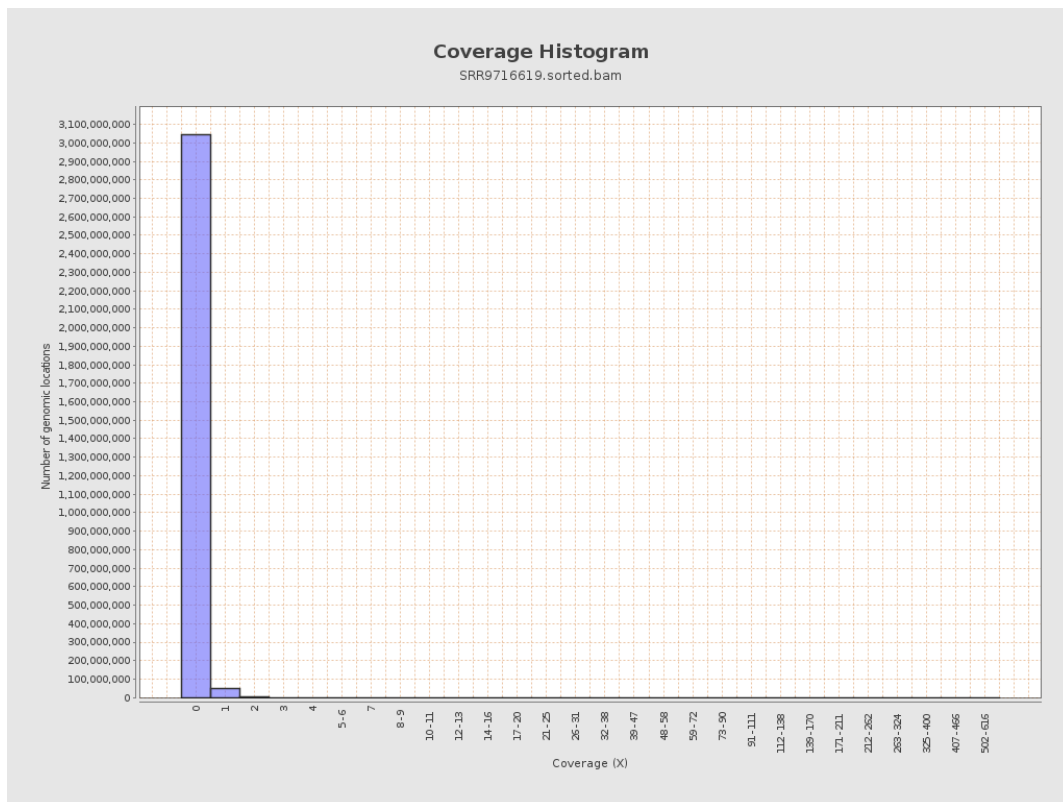
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5005375	0.0201	0.4064
chr2	243199373	4732798	0.0195	0.4446
chr3	198022430	4553761	0.023	0.1636
chr4	191154276	2426902	0.0127	0.1267
chr5	180915260	3774436	0.0209	0.1553
chr6	171115067	4418175	0.0258	0.2024
chr7	159138663	3039434	0.0191	0.4006

chr8	146364022	4274522	0.0292	0.3591
chr9	141213431	2617175	0.0185	0.2526
chr10	135534747	2819528	0.0208	0.2185
chr11	135006516	2357539	0.0175	0.2073
chr12	133851895	2231838	0.0167	0.1387
chr13	115169878	1945614	0.0169	0.1362
chr14	107349540	1423154	0.0133	0.1404
chr15	102531392	1397401	0.0136	0.127
chr16	90354753	1447002	0.016	0.1467
chr17	81195210	1722466	0.0212	0.1778
chr18	78077248	1763156	0.0226	0.5442
chr19	59128983	1094013	0.0185	0.3104
chr20	63025520	1062198	0.0169	0.1506
chr21	48129895	1052551	0.0219	0.1588
chr22	51304566	846362	0.0165	0.1369
chrMT	16571	25947	1.5658	1.6261
chrX	155270560	2481644	0.016	0.1751
chrY	59373566	122657	0.0021	0.0649

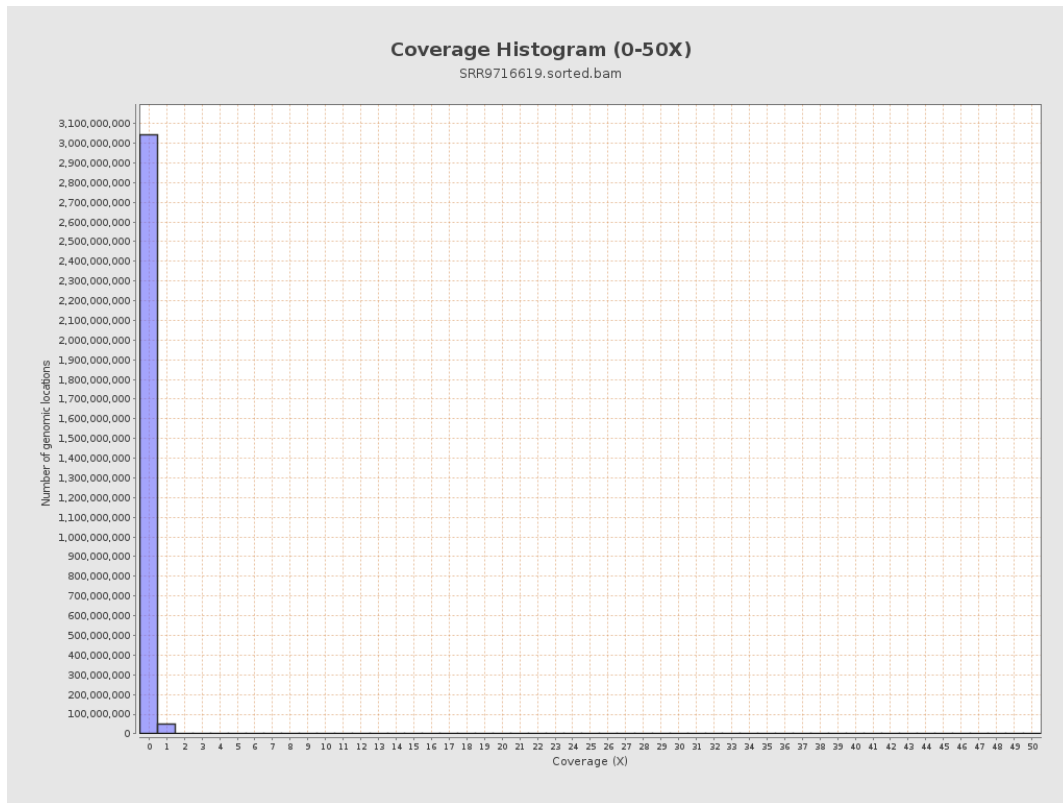
3. Results : Coverage across reference



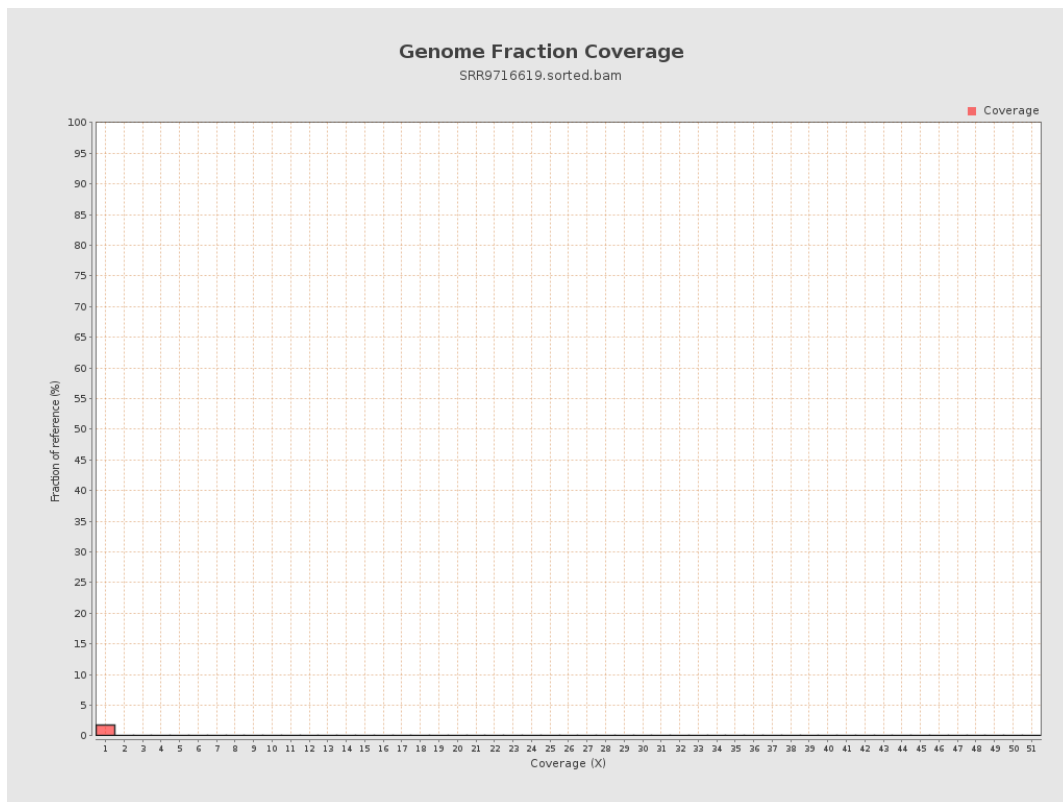
4. Results : Coverage Histogram



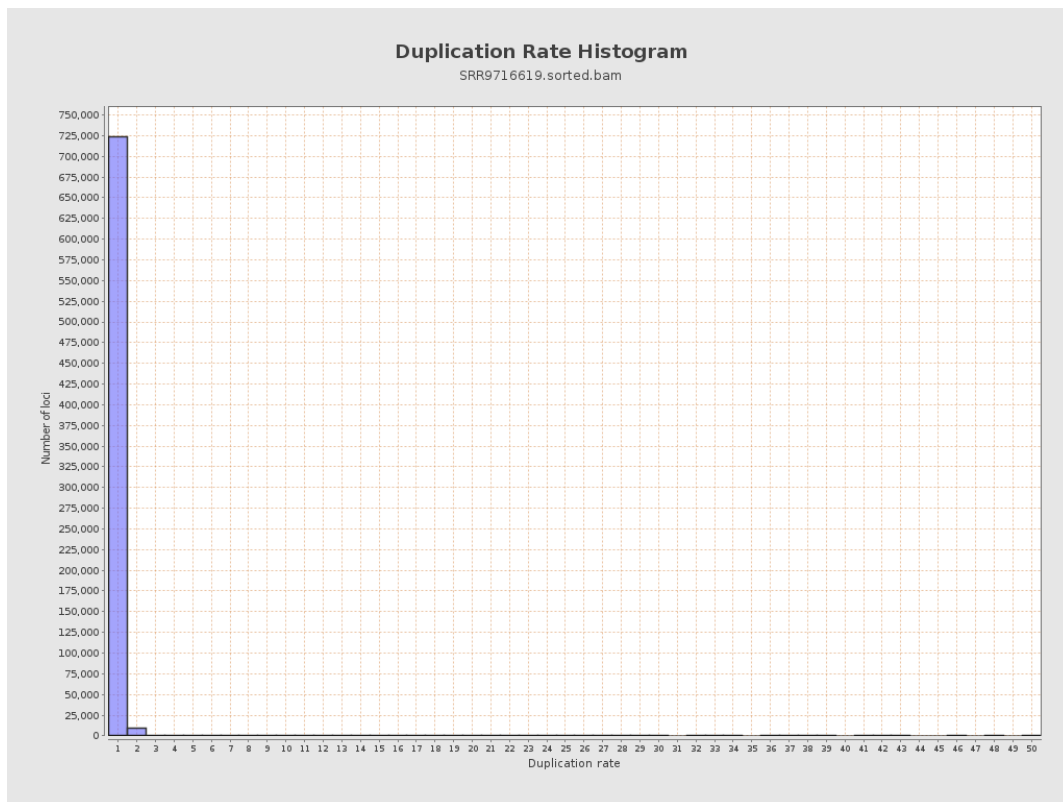
5. Results : Coverage Histogram (0-50X)



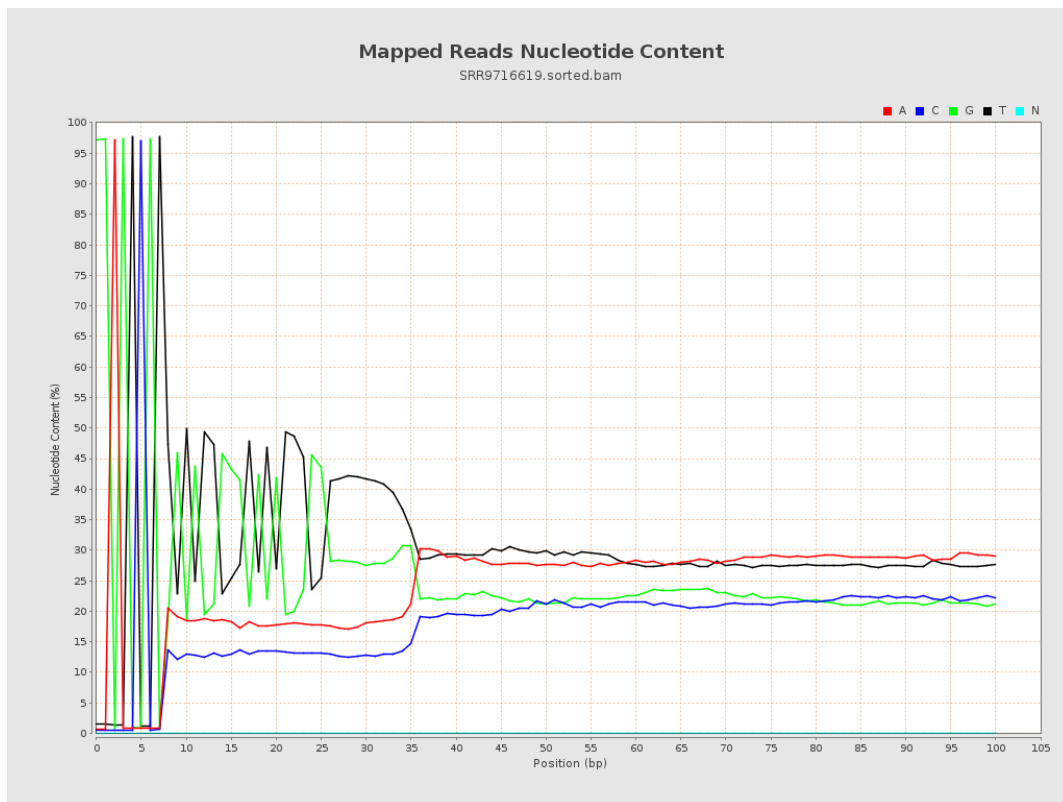
6. Results : Genome Fraction Coverage



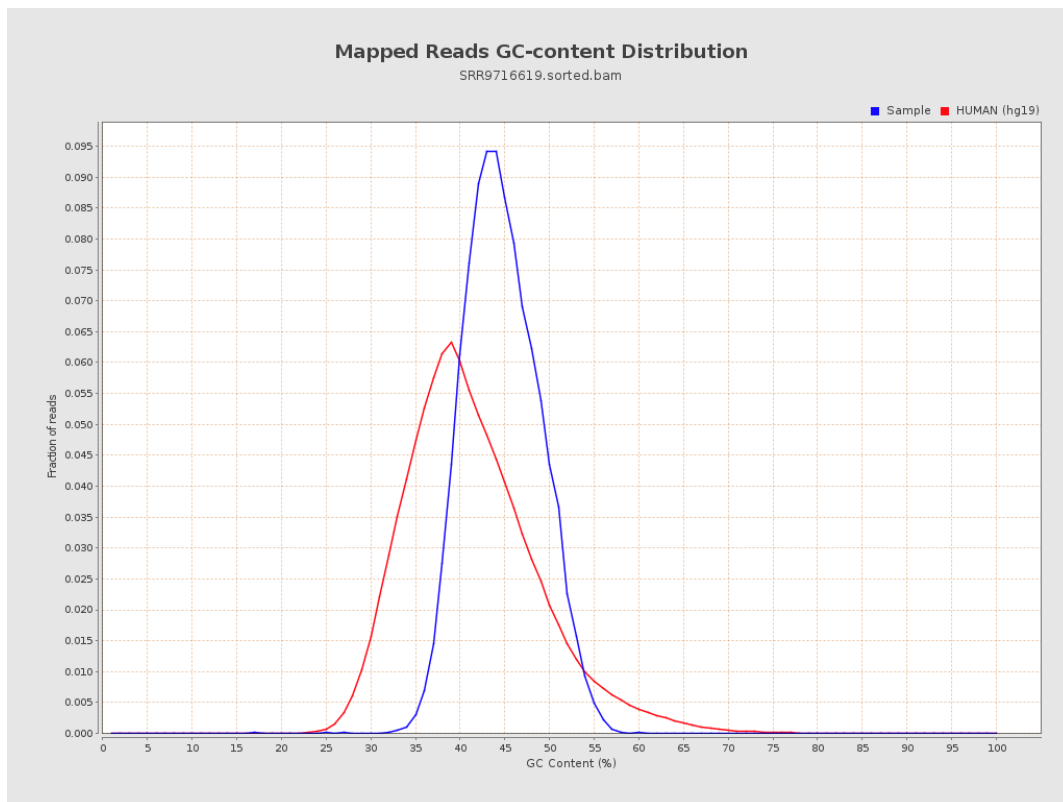
7. Results : Duplication Rate Histogram



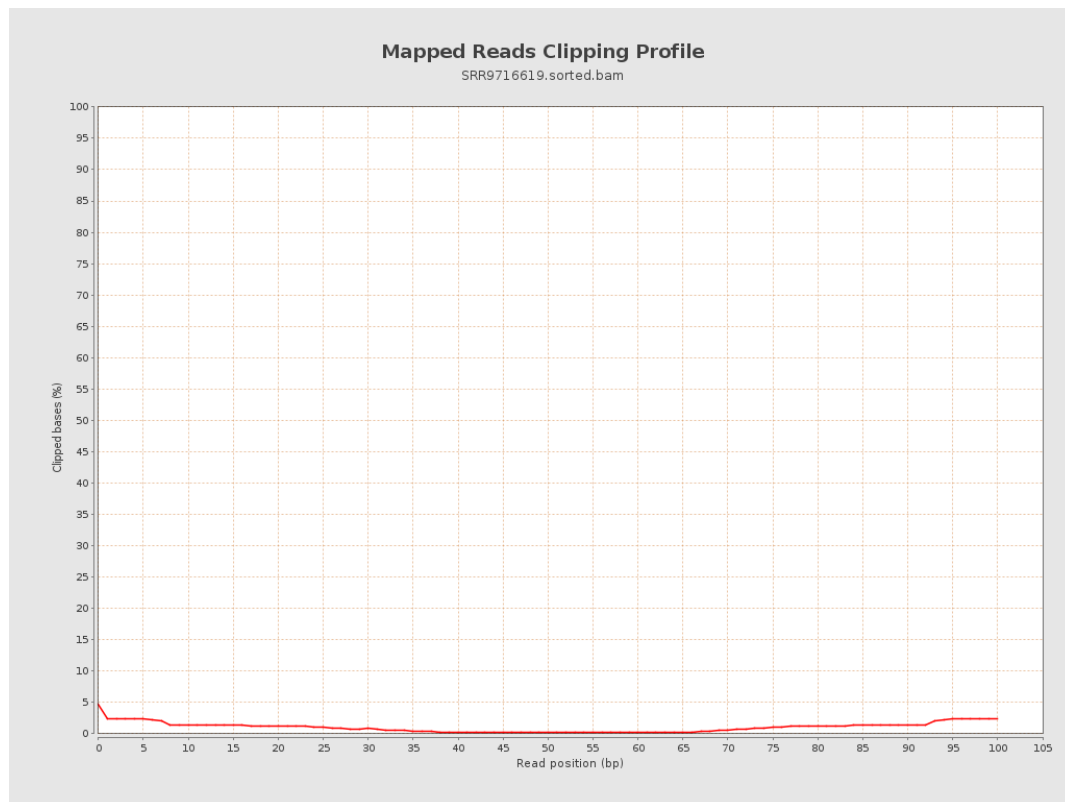
8. Results : Mapped Reads Nucleotide Content



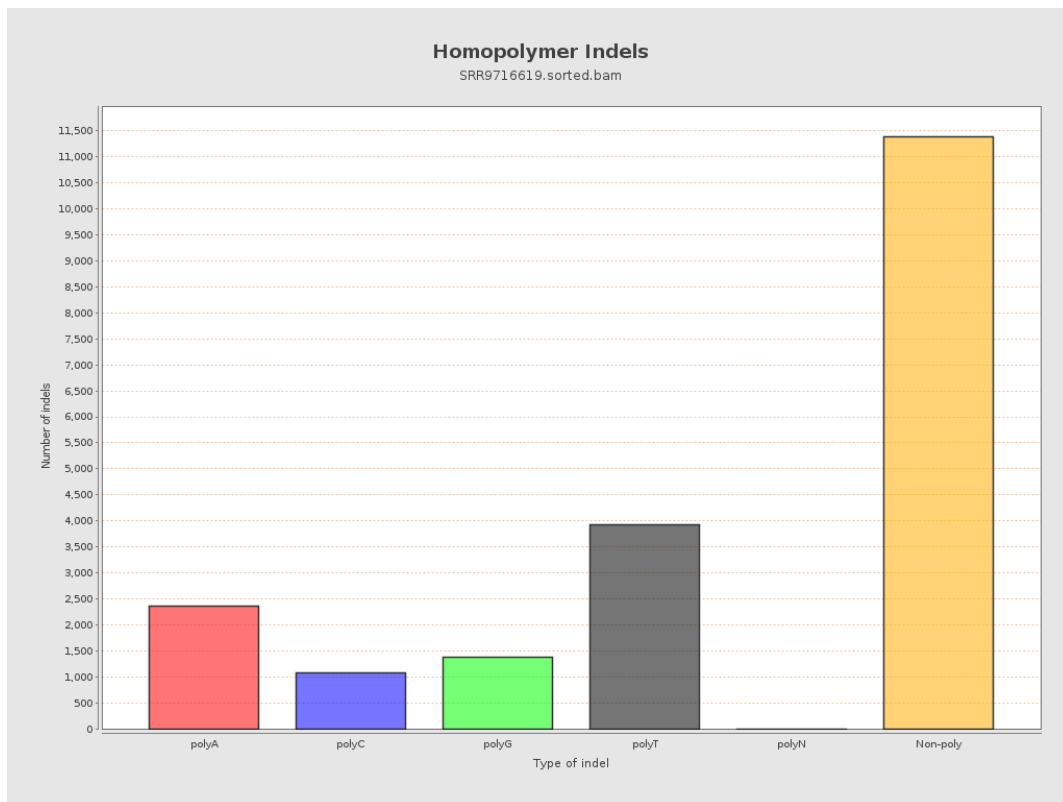
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

