

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:04:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716217.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_SRR9716217 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716217.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,182,994
Mapped reads	1,085,003 / 91.72%
Unmapped reads	97,991 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,225 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	26,839 / 2.27%
Duplication rate	1.66%
Clipped reads	1,087,970 / 91.97%

2.2. ACGT Content

Number/percentage of A's	16,865,736 / 26.34%
Number/percentage of C's	12,481,306 / 19.49%
Number/percentage of T's	20,021,390 / 31.27%
Number/percentage of G's	14,654,503 / 22.89%
Number/percentage of N's	895 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2225
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2.4. Mapping Quality

Mean Mapping Quality	44.64
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2.5. Mismatches and indels

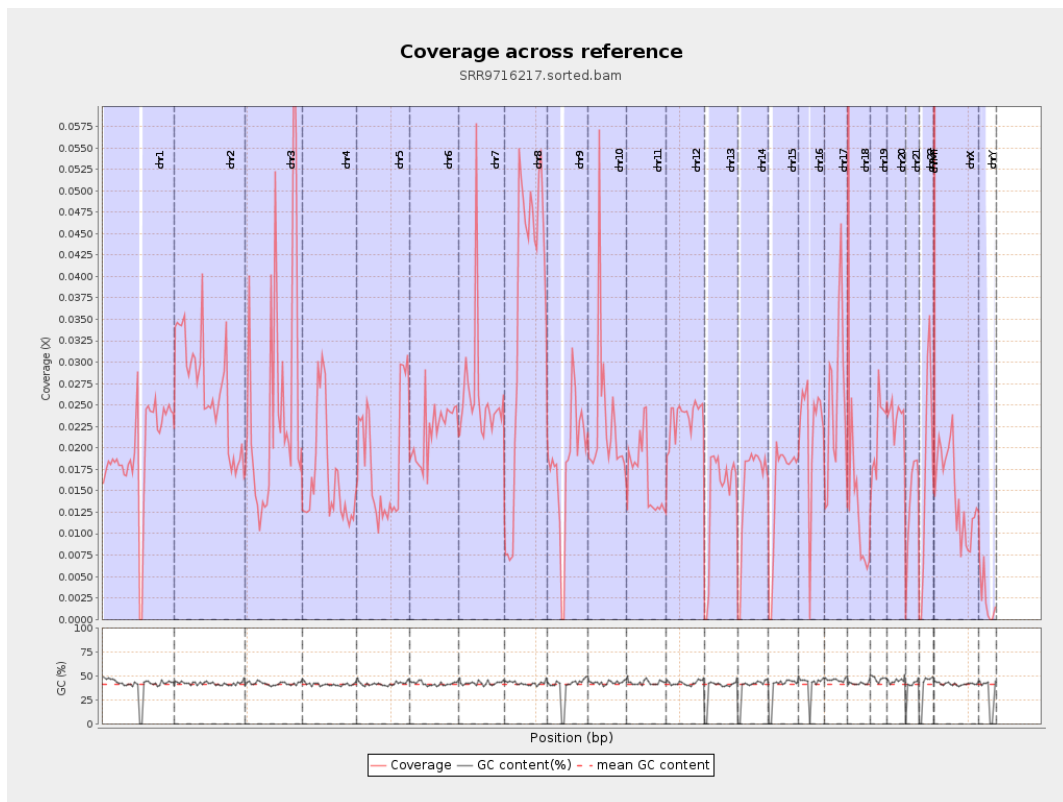
General error rate	0.51%
Mismatches	315,843
Insertions	4,288
Mapped reads with at least one insertion	0.39%
Deletions	12,342
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.19%

2.6. Chromosome stats

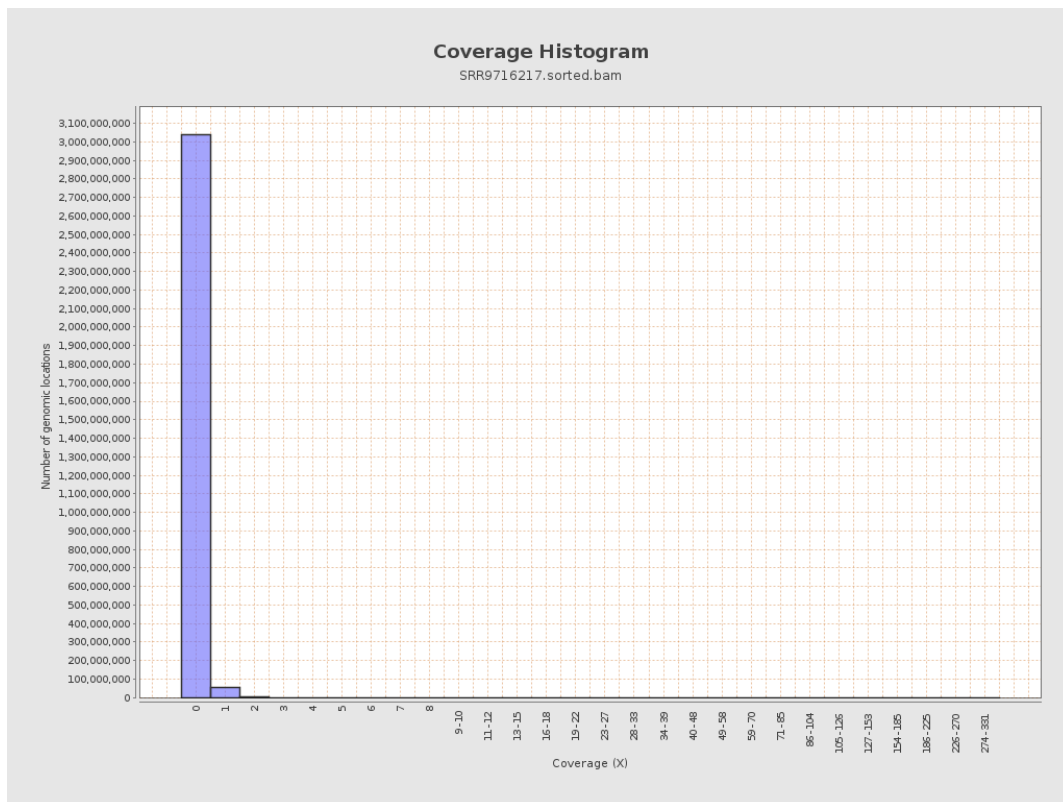
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4870496	0.0195	0.3048
chr2	243199373	6519355	0.0268	0.2365
chr3	198022430	4914189	0.0248	0.1743
chr4	191154276	3133662	0.0164	0.1459
chr5	180915260	3346840	0.0185	0.1441
chr6	171115067	3738685	0.0218	0.1661
chr7	159138663	4165842	0.0262	0.489

chr8	146364022	5340370	0.0365	0.2452
chr9	141213431	2567857	0.0182	0.1599
chr10	135534747	3089639	0.0228	0.304
chr11	135006516	2273409	0.0168	0.165
chr12	133851895	3150840	0.0235	0.1799
chr13	115169878	1656917	0.0144	0.126
chr14	107349540	1666661	0.0155	0.1341
chr15	102531392	1570977	0.0153	0.1344
chr16	90354753	1996121	0.0221	0.1645
chr17	81195210	2061657	0.0254	0.1718
chr18	78077248	1201568	0.0154	0.2354
chr19	59128983	1289313	0.0218	0.2935
chr20	63025520	1485289	0.0236	0.1687
chr21	48129895	675202	0.014	0.1281
chr22	51304566	869775	0.017	0.1376
chrMT	16571	21278	1.2841	1.3264
chrX	155270560	2297700	0.0148	0.1417
chrY	59373566	139865	0.0024	0.0677

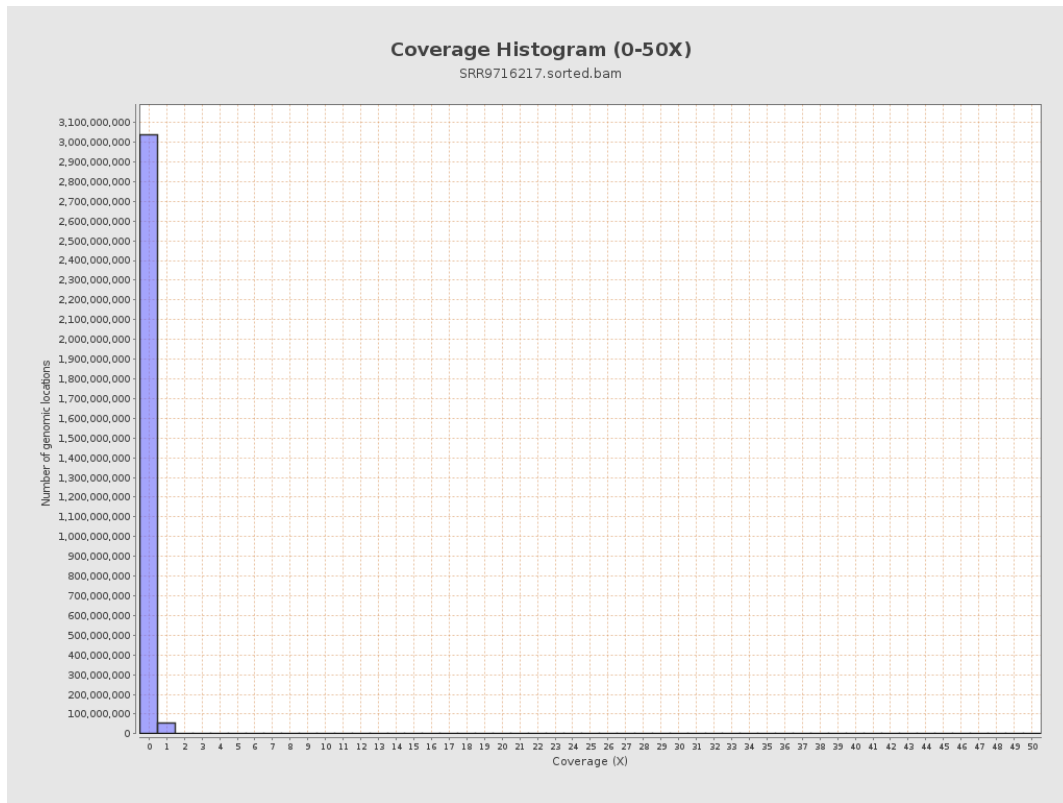
3. Results : Coverage across reference



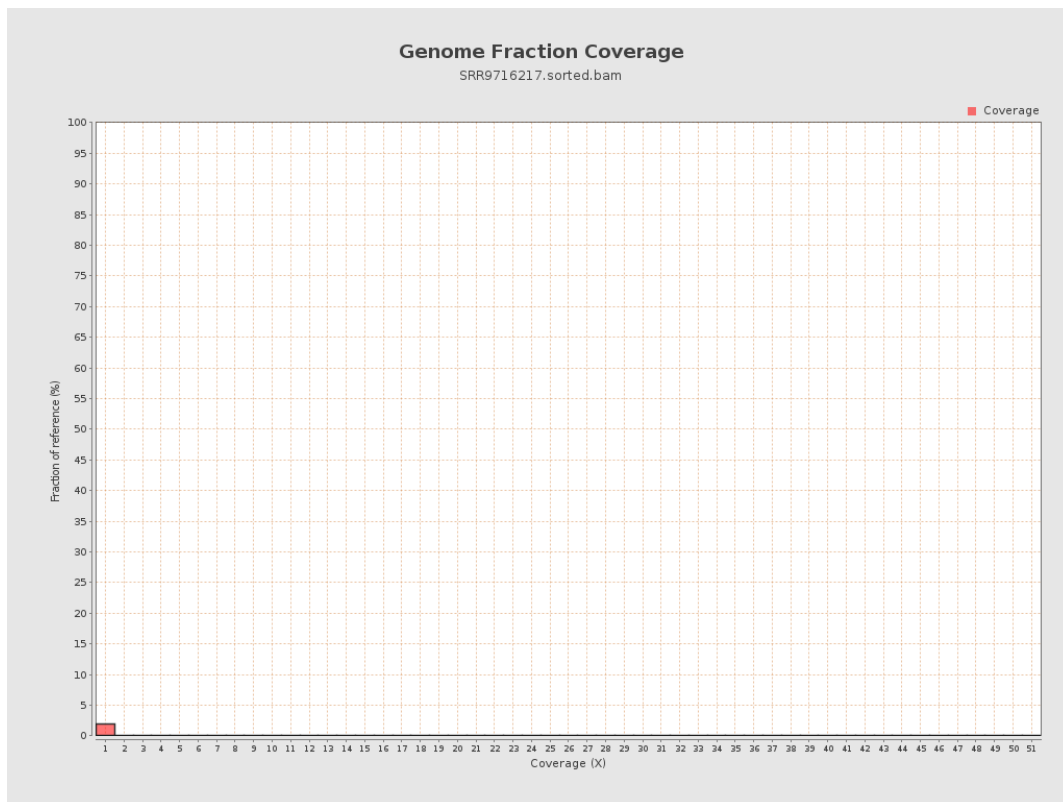
4. Results : Coverage Histogram



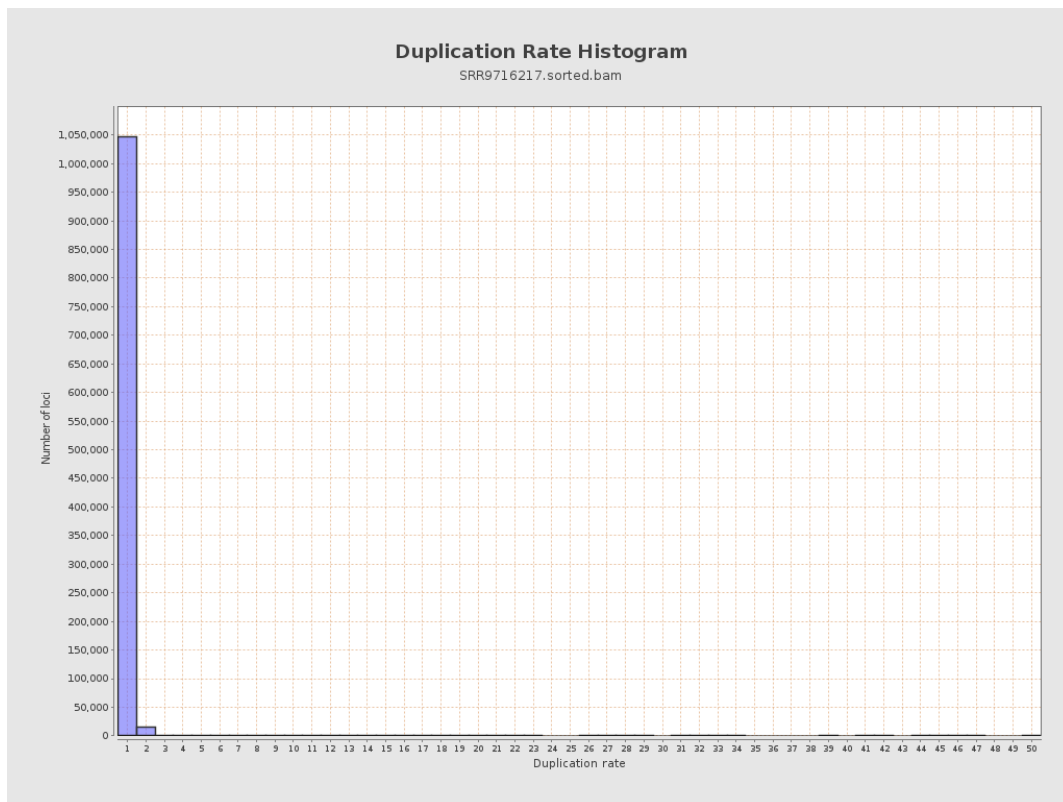
5. Results : Coverage Histogram (0-50X)



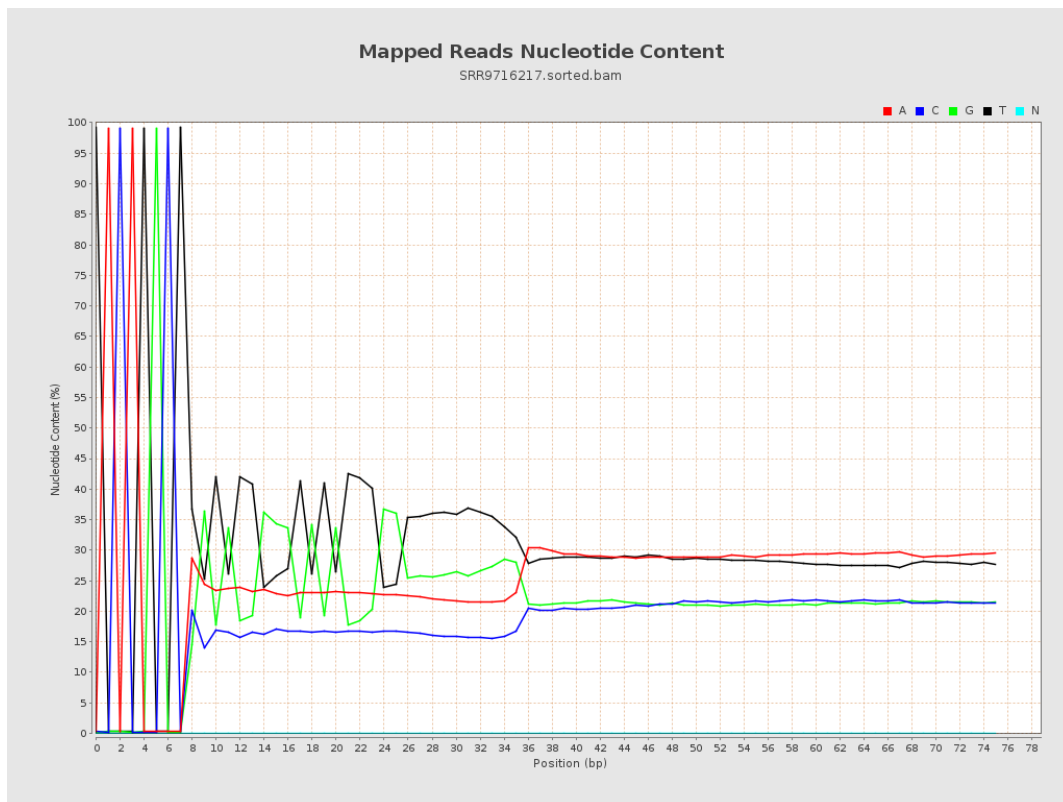
6. Results : Genome Fraction Coverage



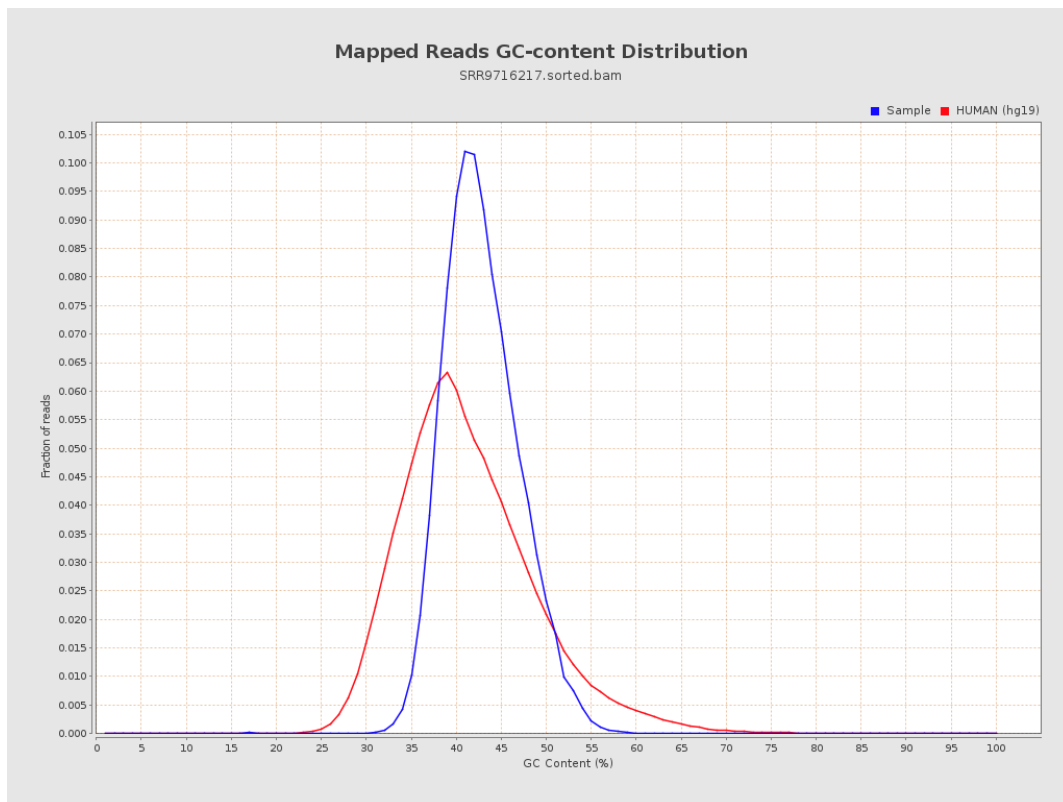
7. Results : Duplication Rate Histogram



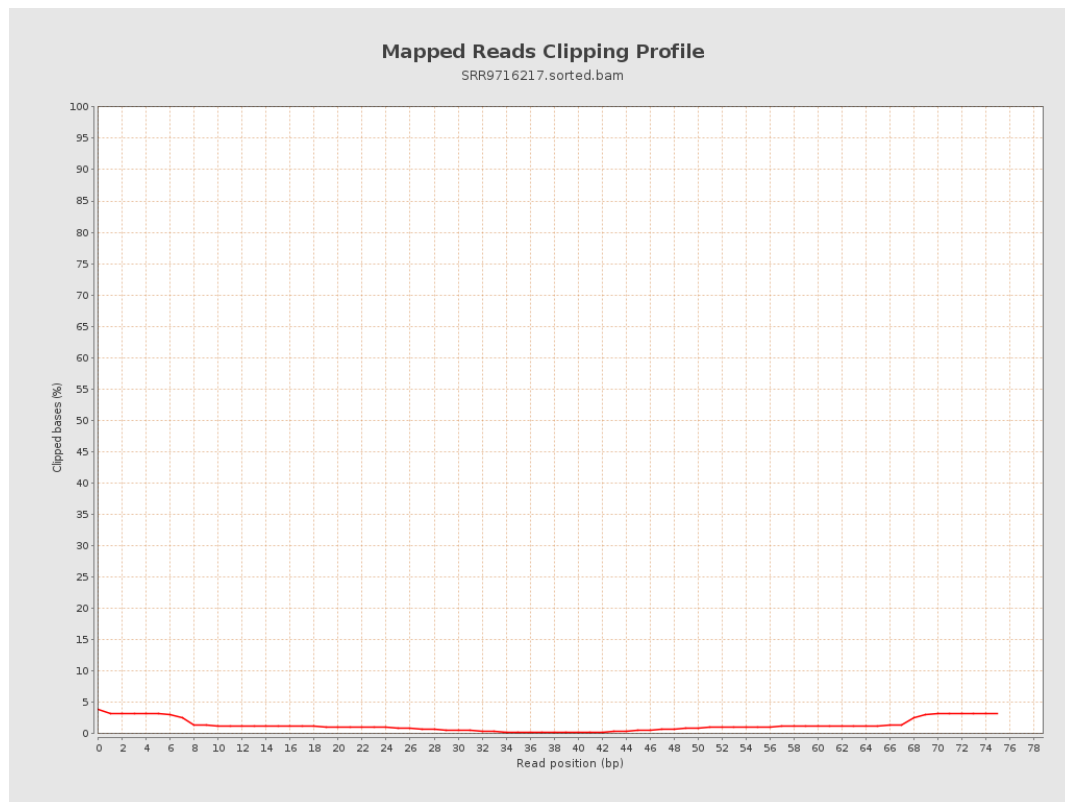
8. Results : Mapped Reads Nucleotide Content



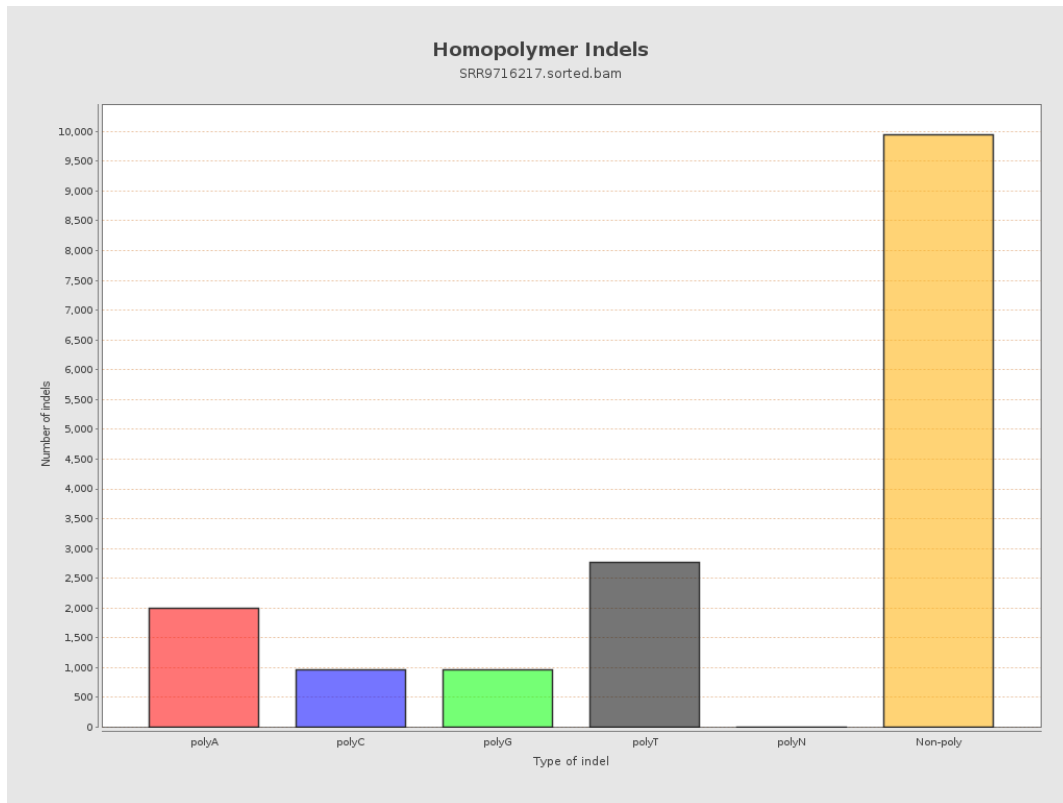
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

