

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:00:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716784.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_SRR9716784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:00:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,047,661
Mapped reads	1,789,641 / 87.4%
Unmapped reads	258,020 / 12.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,451 / 2.17%
Read min/max/mean length	30 / 101 / 101.79
Duplicated reads (estimated)	55,868 / 2.73%
Duplication rate	2.18%
Clipped reads	1,830,533 / 89.4%

2.2. ACGT Content

Number/percentage of A's	34,738,091 / 25.81%
Number/percentage of C's	28,670,013 / 21.3%
Number/percentage of T's	40,419,848 / 30.03%
Number/percentage of G's	30,768,989 / 22.86%
Number/percentage of N's	16,940 / 0.01%
GC Percentage	44.16%

2.3. Coverage

Mean	0.0435

Standard Deviation	0.3361
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2.4. Mapping Quality

Mean Mapping Quality	46.23
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2.5. Mismatches and indels

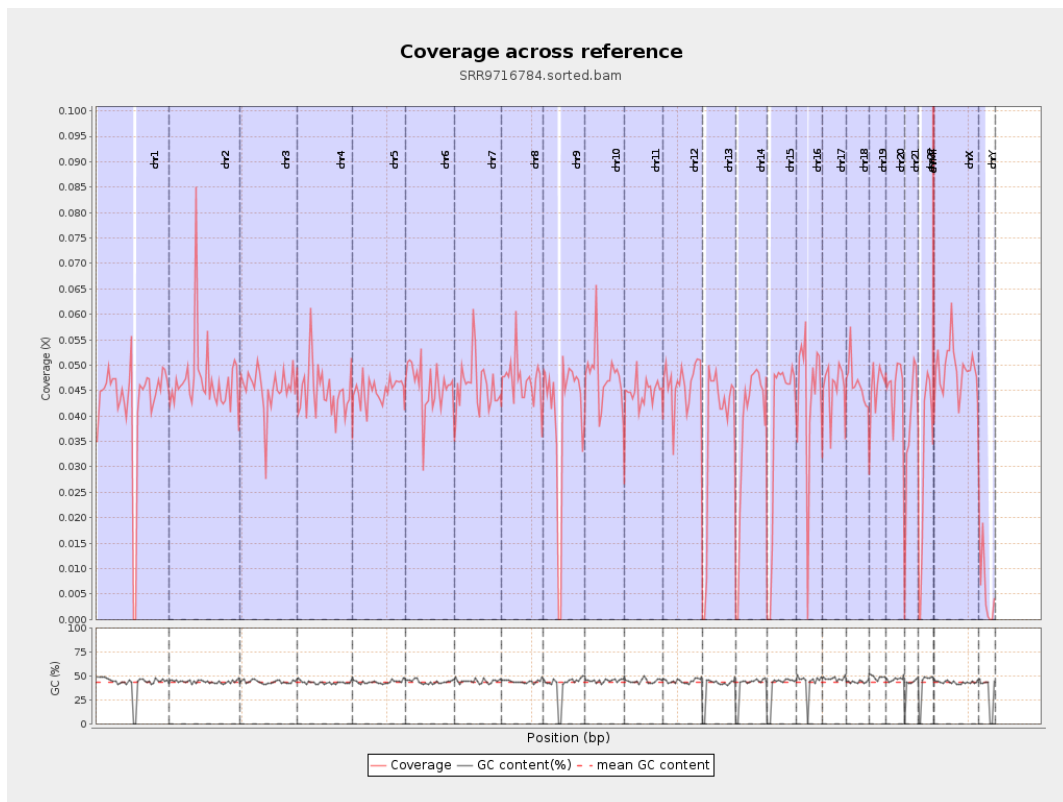
General error rate	0.76%
Mismatches	995,851
Insertions	12,204
Mapped reads with at least one insertion	0.67%
Deletions	27,408
Mapped reads with at least one deletion	1.51%
Homopolymer indels	39.41%

2.6. Chromosome stats

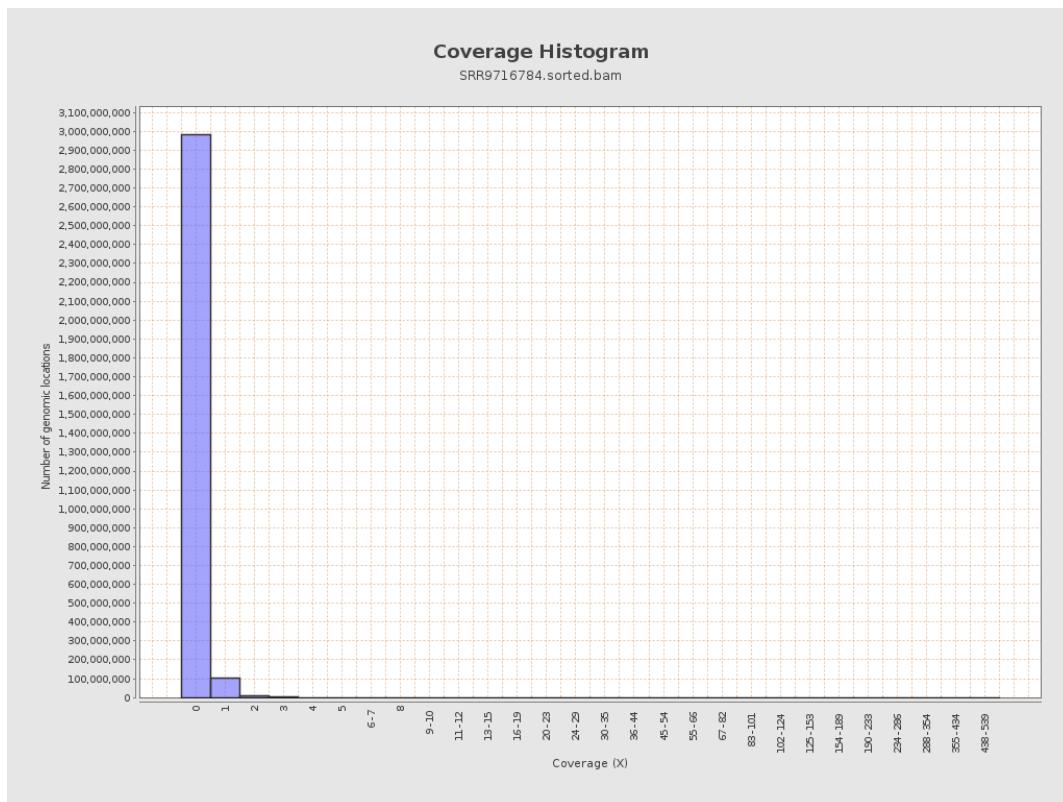
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10595516	0.0425	0.381
chr2	243199373	11440237	0.047	0.4914
chr3	198022430	9006471	0.0455	0.2405
chr4	191154276	8562822	0.0448	0.2601
chr5	180915260	8128665	0.0449	0.2412
chr6	171115067	7835141	0.0458	0.27
chr7	159138663	7359107	0.0462	0.4118

chr8	146364022	6876484	0.047	0.4286
chr9	141213431	5688612	0.0403	0.361
chr10	135534747	6476090	0.0478	0.3442
chr11	135006516	6009557	0.0445	0.3483
chr12	133851895	6176972	0.0461	0.2465
chr13	115169878	4290155	0.0373	0.2175
chr14	107349540	4036777	0.0376	0.2493
chr15	102531392	3923450	0.0383	0.2207
chr16	90354753	3999531	0.0443	0.2667
chr17	81195210	3693190	0.0455	0.2708
chr18	78077248	3629001	0.0465	0.6441
chr19	59128983	2712116	0.0459	0.3595
chr20	63025520	2850012	0.0452	0.2486
chr21	48129895	1805091	0.0375	0.2415
chr22	51304566	1581370	0.0308	0.1991
chrMT	16571	5487	0.3311	0.7205
chrX	155270560	7637641	0.0492	0.3073
chrY	59373566	341694	0.0058	0.1612

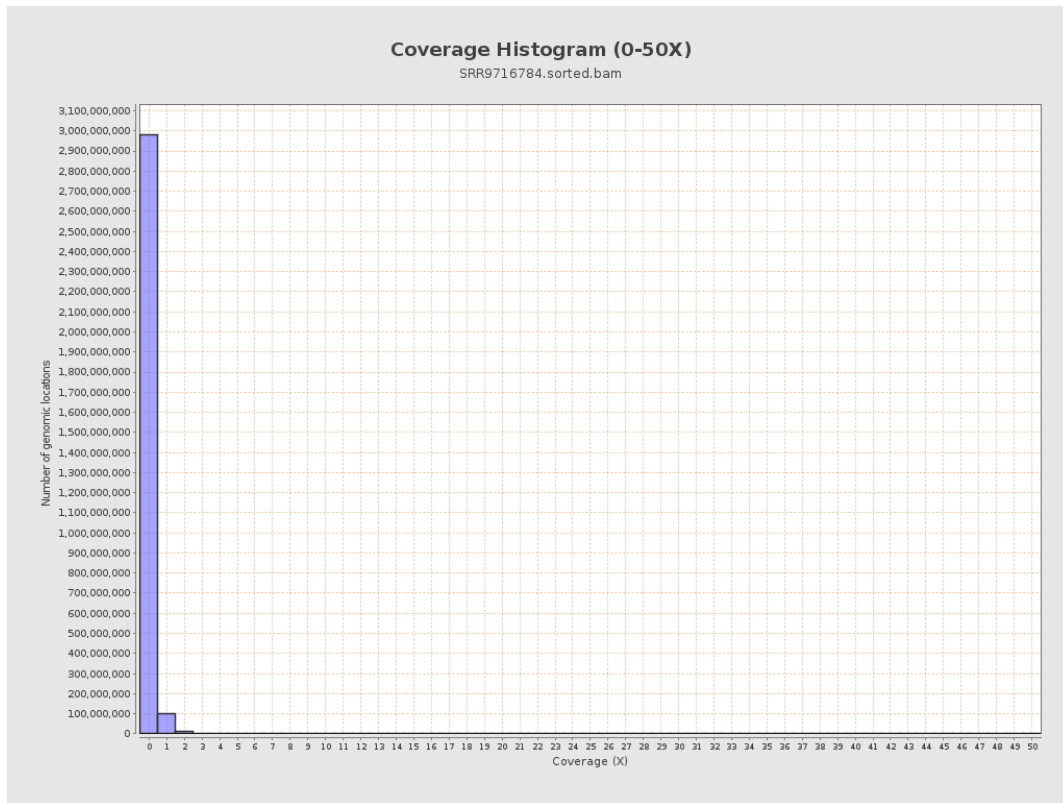
3. Results : Coverage across reference



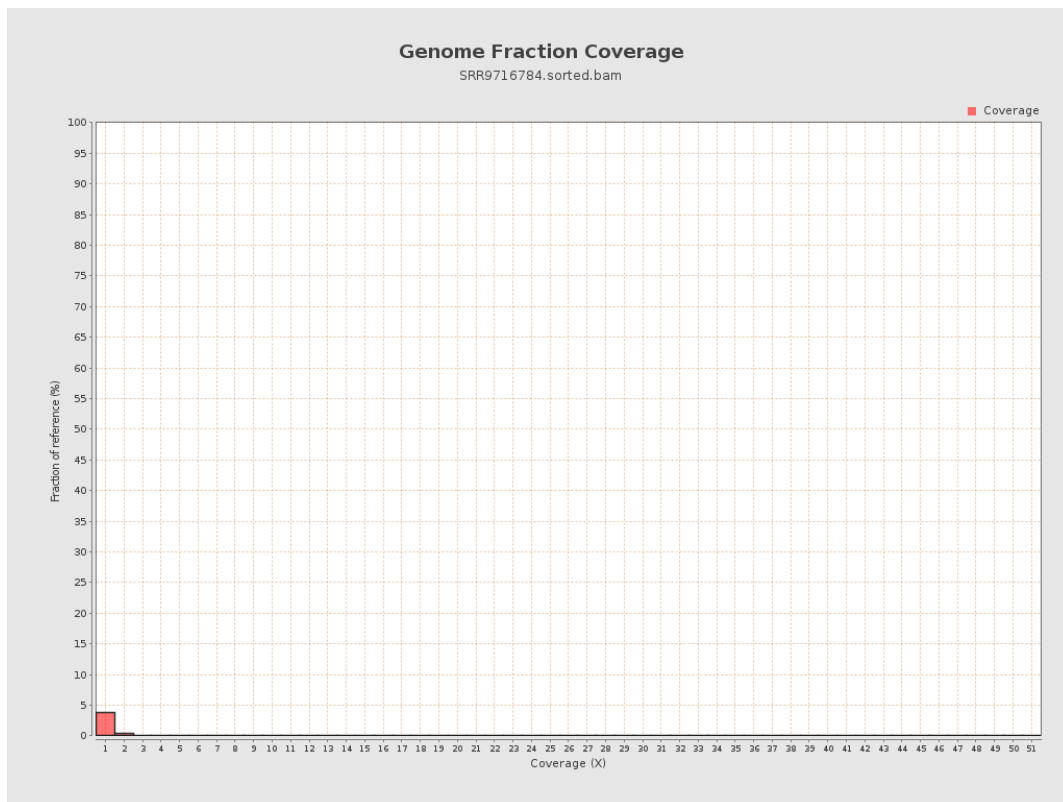
4. Results : Coverage Histogram



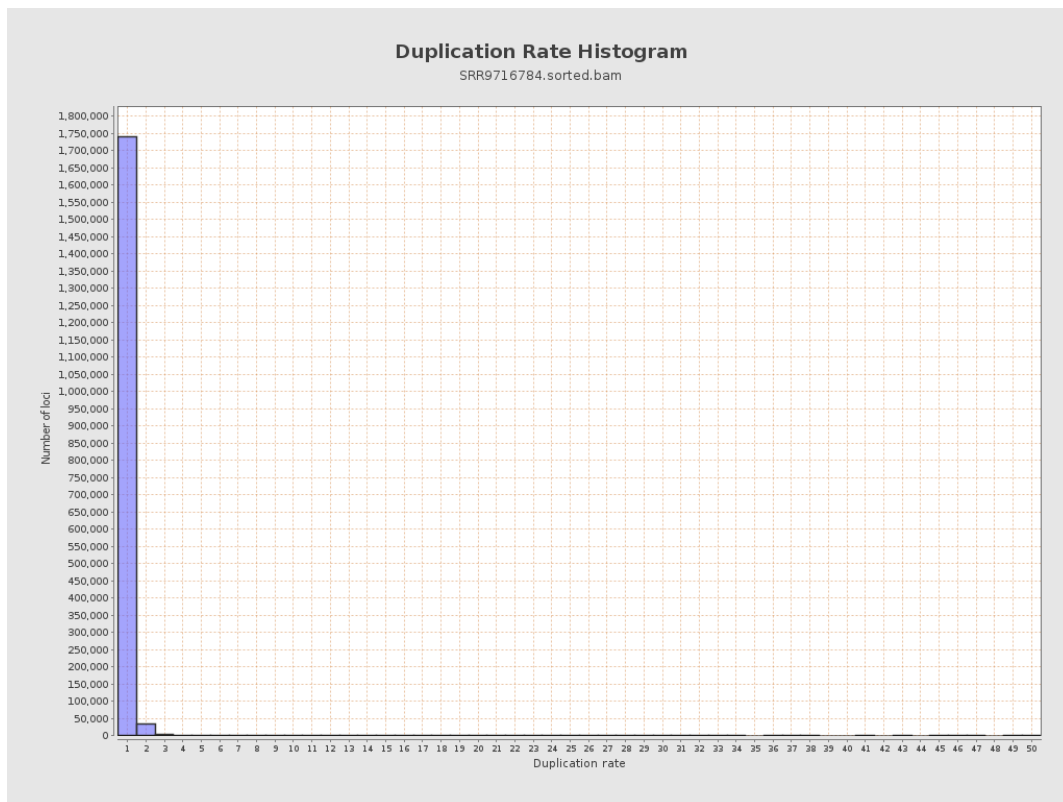
5. Results : Coverage Histogram (0-50X)



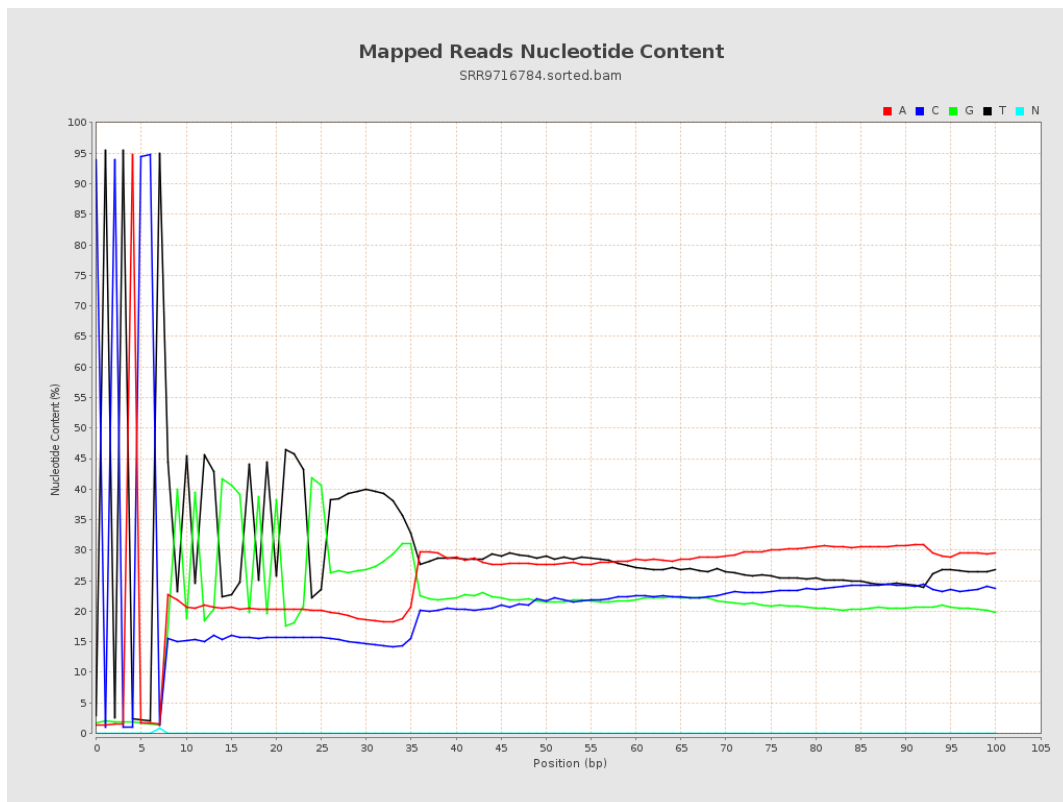
6. Results : Genome Fraction Coverage



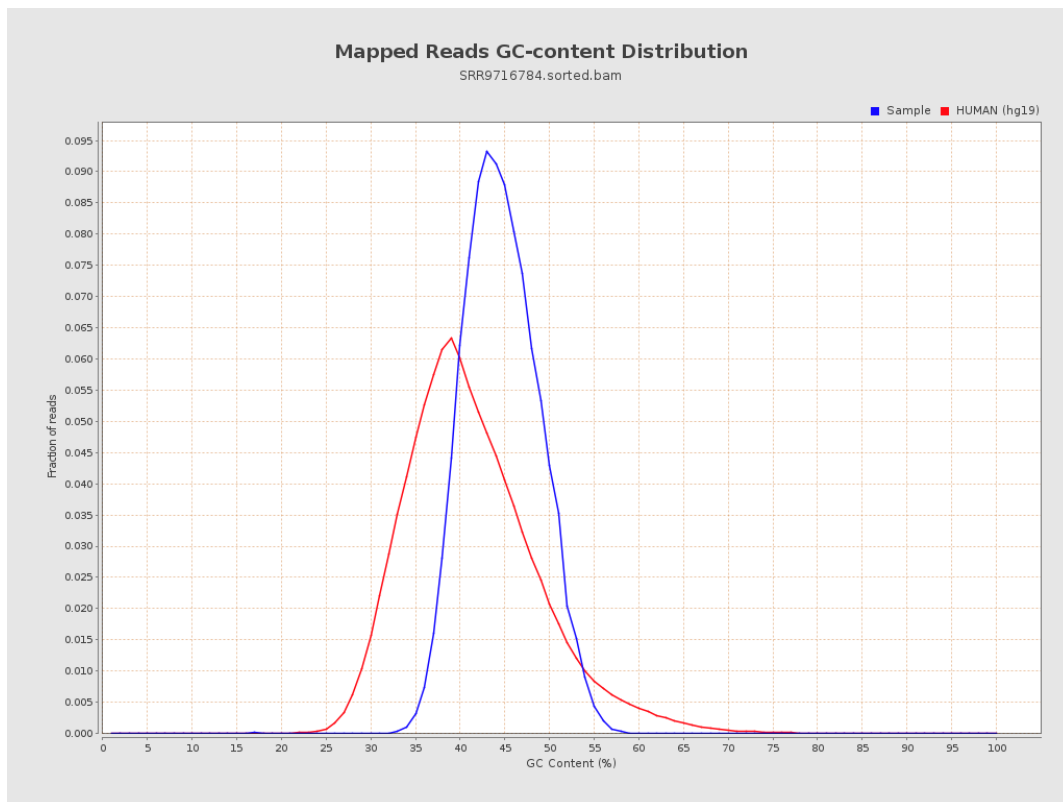
7. Results : Duplication Rate Histogram



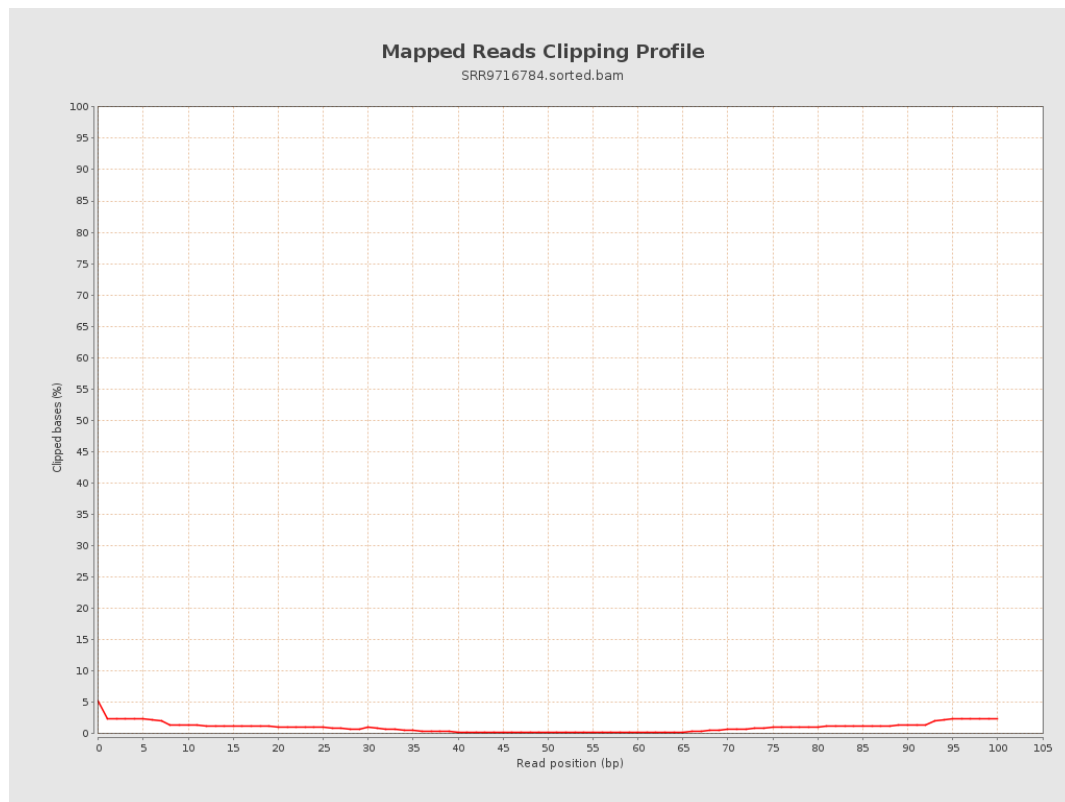
8. Results : Mapped Reads Nucleotide Content



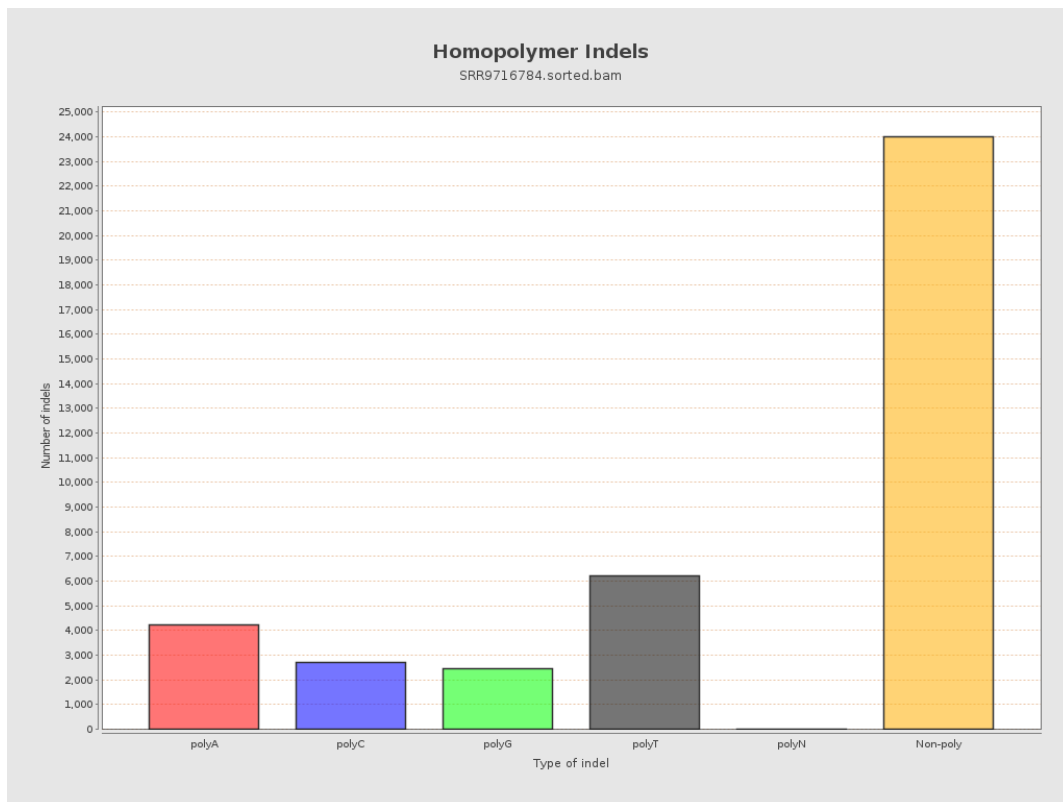
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

