

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716248.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_SRR9716248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716248.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:35:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,848,223
Mapped reads	1,755,943 / 95.01%
Unmapped reads	92,280 / 4.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,982 / 2.06%
Read min/max/mean length	30 / 101 / 101.74
Duplicated reads (estimated)	80,706 / 4.37%
Duplication rate	3.59%
Clipped reads	1,790,951 / 96.9%

2.2. ACGT Content

Number/percentage of A's	33,687,246 / 24.67%
Number/percentage of C's	29,621,322 / 21.7%
Number/percentage of T's	39,256,926 / 28.75%
Number/percentage of G's	33,954,859 / 24.87%
Number/percentage of N's	4,995 / 0%
GC Percentage	46.57%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.3509
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.49
----------------------	-------

2.5. Mismatches and indels

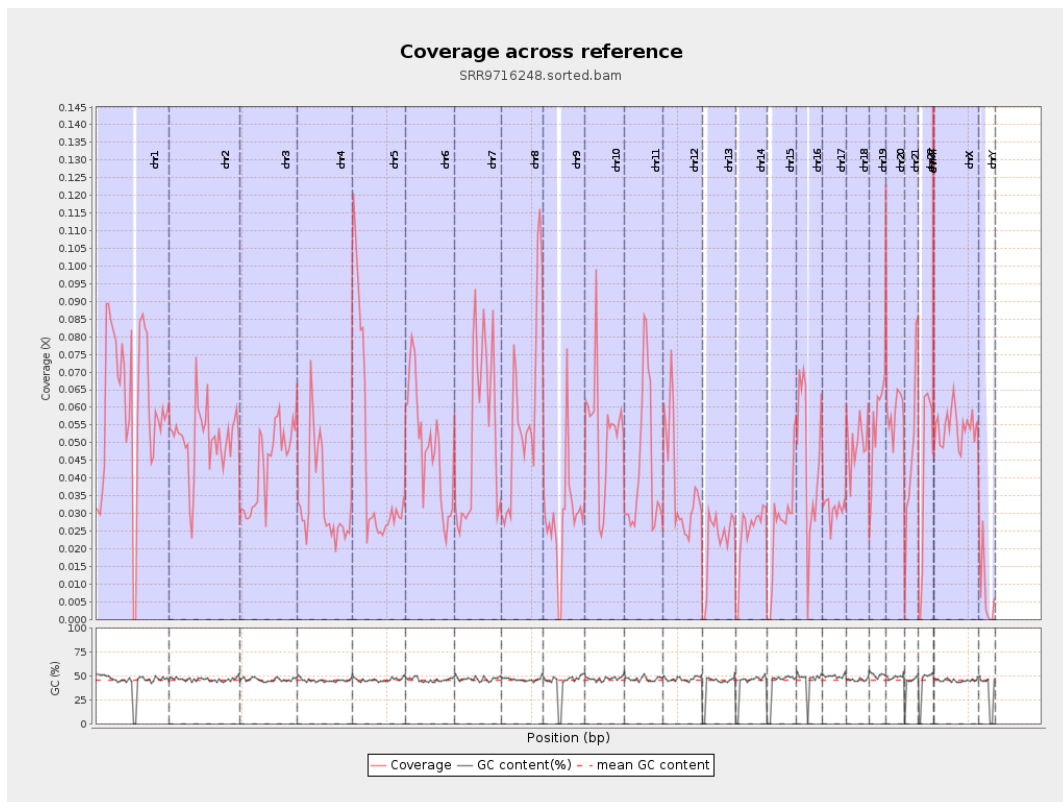
General error rate	0.66%
Mismatches	871,783
Insertions	11,584
Mapped reads with at least one insertion	0.65%
Deletions	25,197
Mapped reads with at least one deletion	1.41%
Homopolymer indels	38.79%

2.6. Chromosome stats

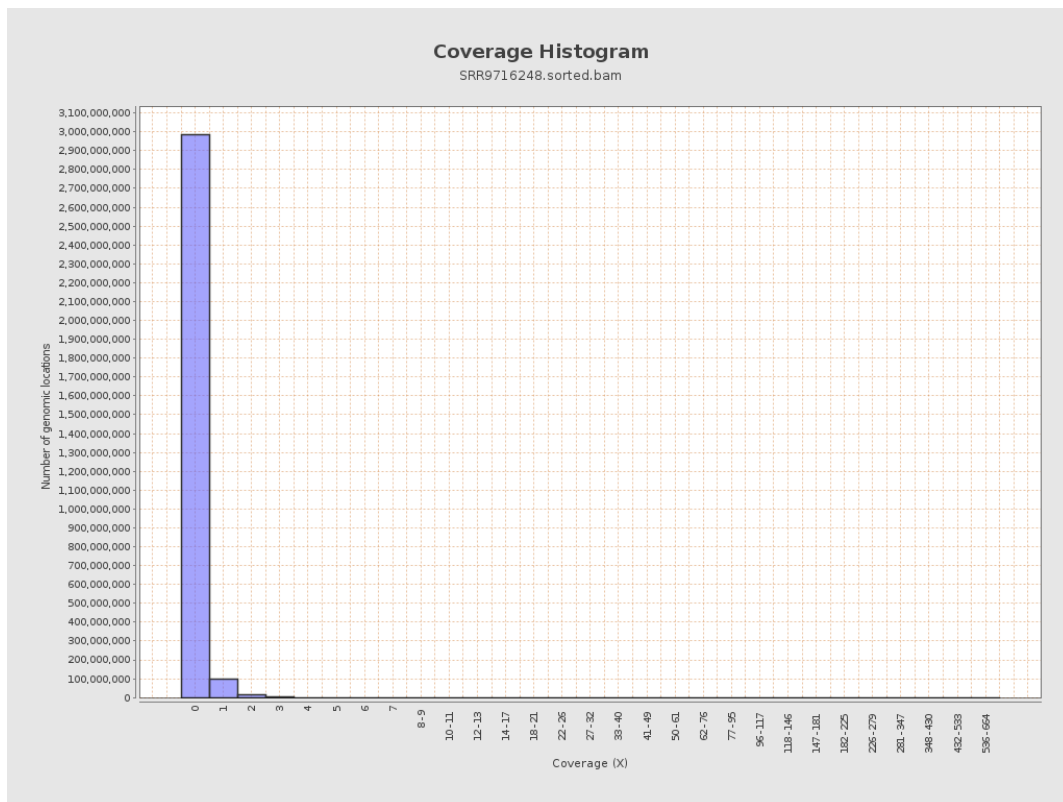
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14972394	0.0601	0.6348
chr2	243199373	12410323	0.051	0.3751
chr3	198022430	8664204	0.0438	0.2482
chr4	191154276	6353969	0.0332	0.2991
chr5	180915260	8040318	0.0444	0.2513
chr6	171115067	8316647	0.0486	0.271
chr7	159138663	8422319	0.0529	0.4684

chr8	146364022	8462783	0.0578	0.374
chr9	141213431	4035603	0.0286	0.2435
chr10	135534747	7179888	0.053	0.4866
chr11	135006516	5762321	0.0427	0.3099
chr12	133851895	5076865	0.0379	0.2275
chr13	115169878	2524136	0.0219	0.1695
chr14	107349540	2580332	0.024	0.1945
chr15	102531392	2722276	0.0266	0.1885
chr16	90354753	4163437	0.0461	0.2688
chr17	81195210	2527215	0.0311	0.2297
chr18	78077248	3924944	0.0503	0.3723
chr19	59128983	3421734	0.0579	0.4925
chr20	63025520	3686192	0.0585	0.2967
chr21	48129895	2312109	0.048	0.3029
chr22	51304566	2121629	0.0414	0.2421
chrMT	16571	22297	1.3455	1.4241
chrX	155270560	8438269	0.0543	0.2858
chrY	59373566	434542	0.0073	0.2676

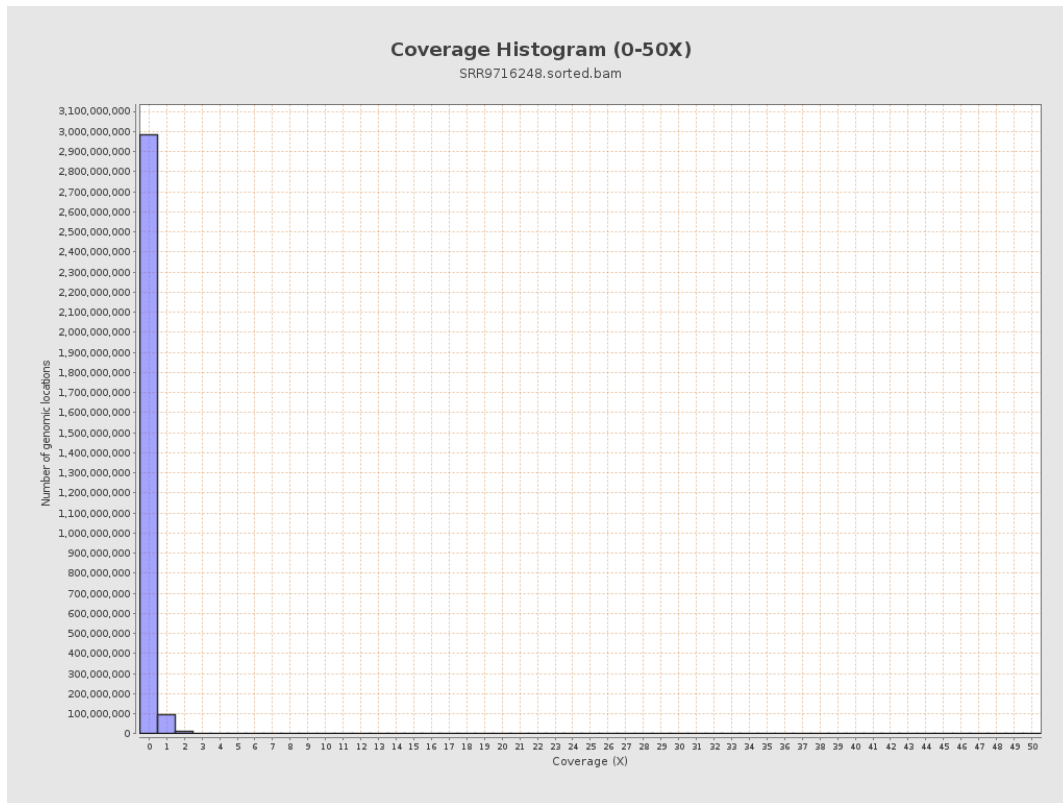
3. Results : Coverage across reference



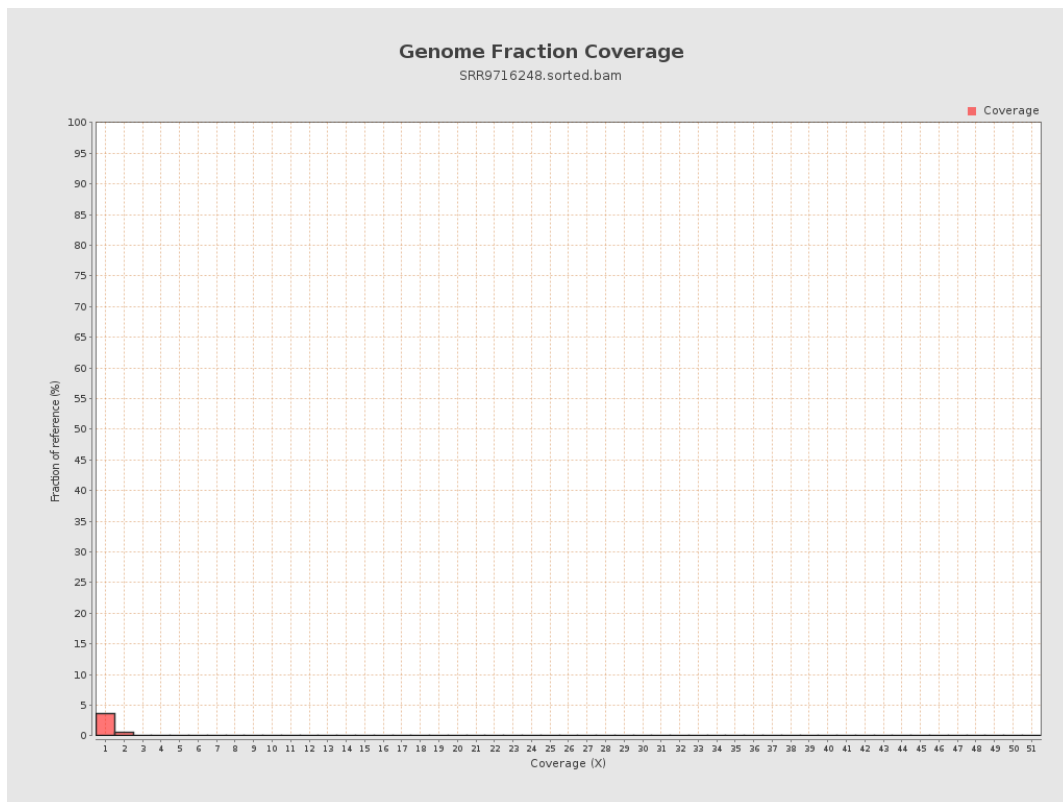
4. Results : Coverage Histogram



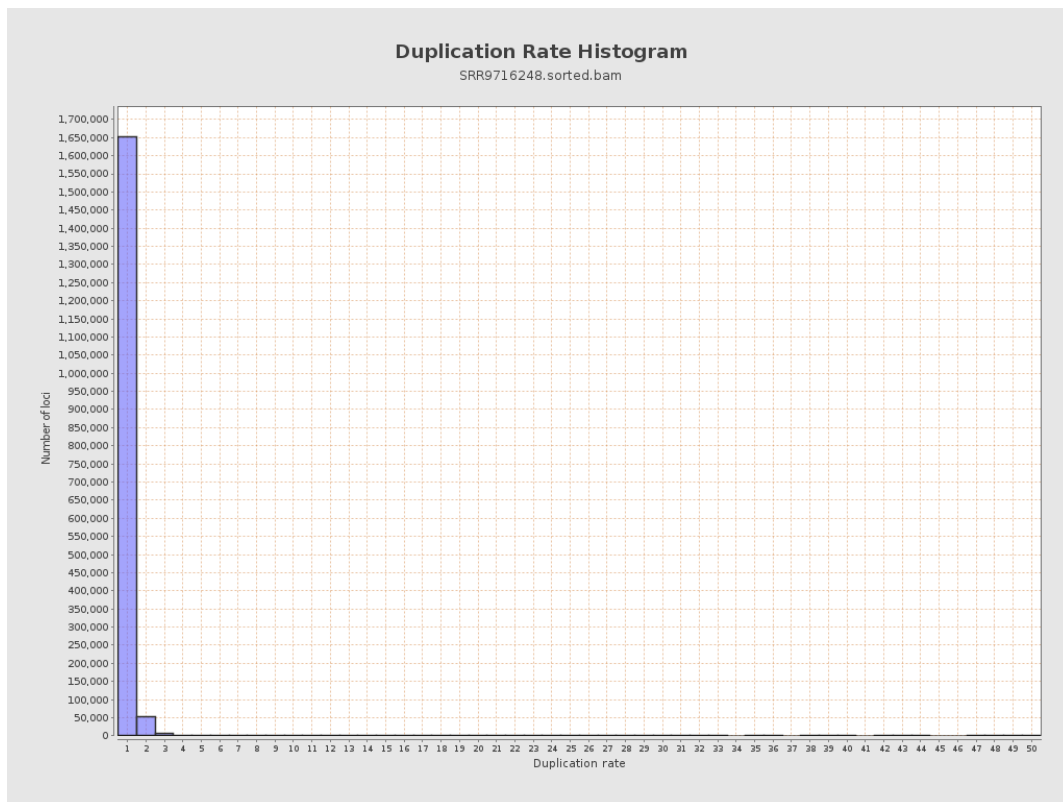
5. Results : Coverage Histogram (0-50X)



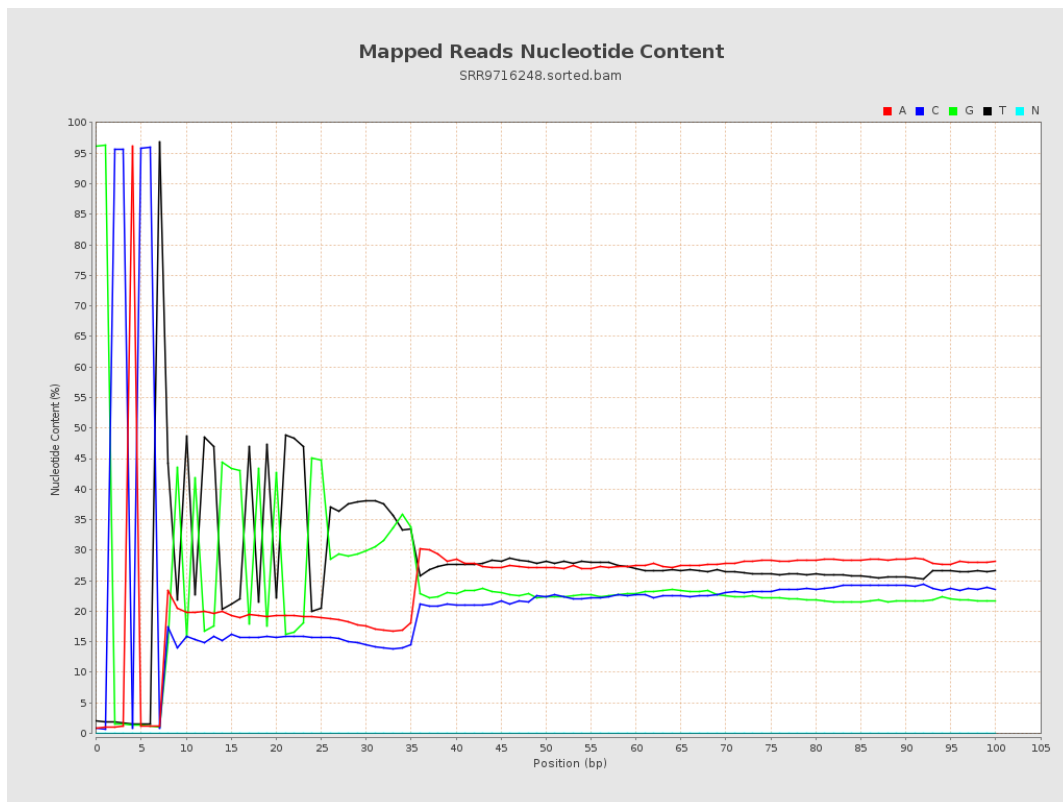
6. Results : Genome Fraction Coverage



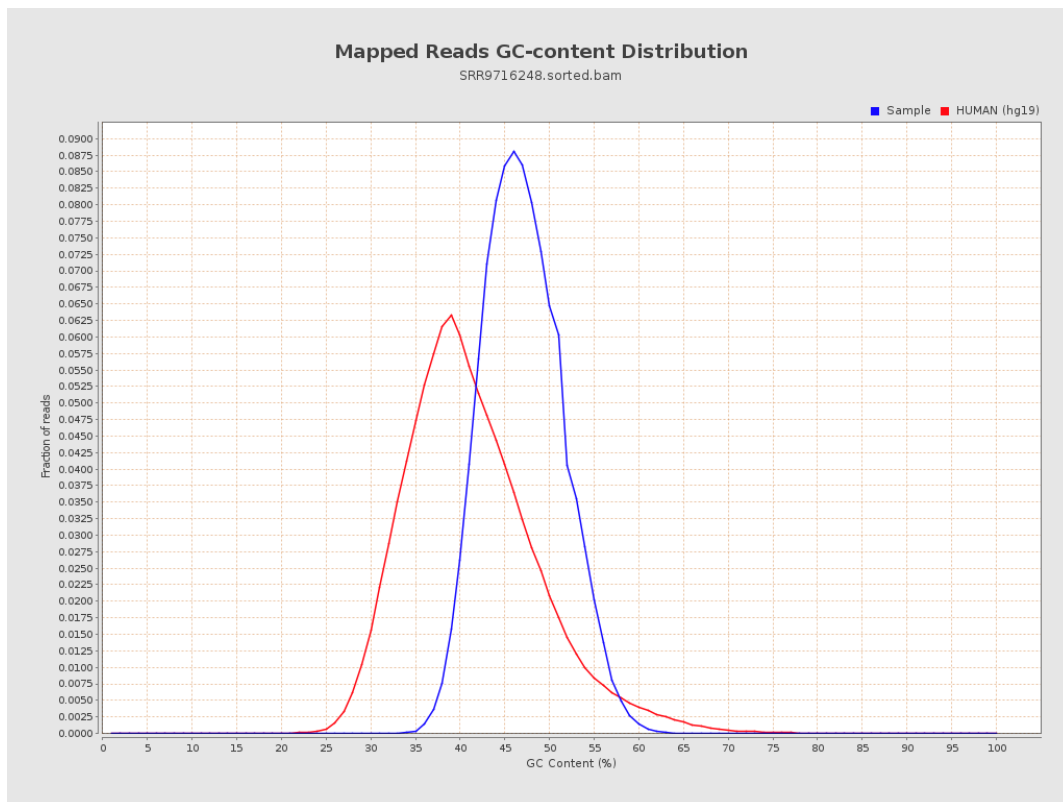
7. Results : Duplication Rate Histogram



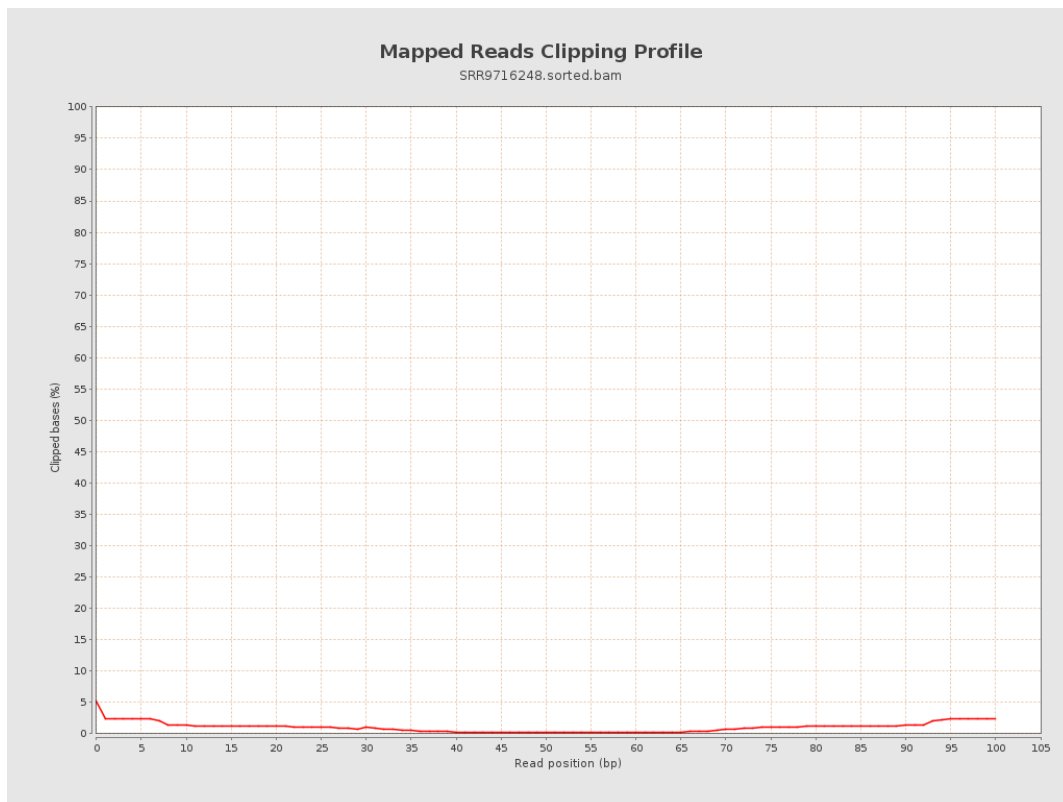
8. Results : Mapped Reads Nucleotide Content



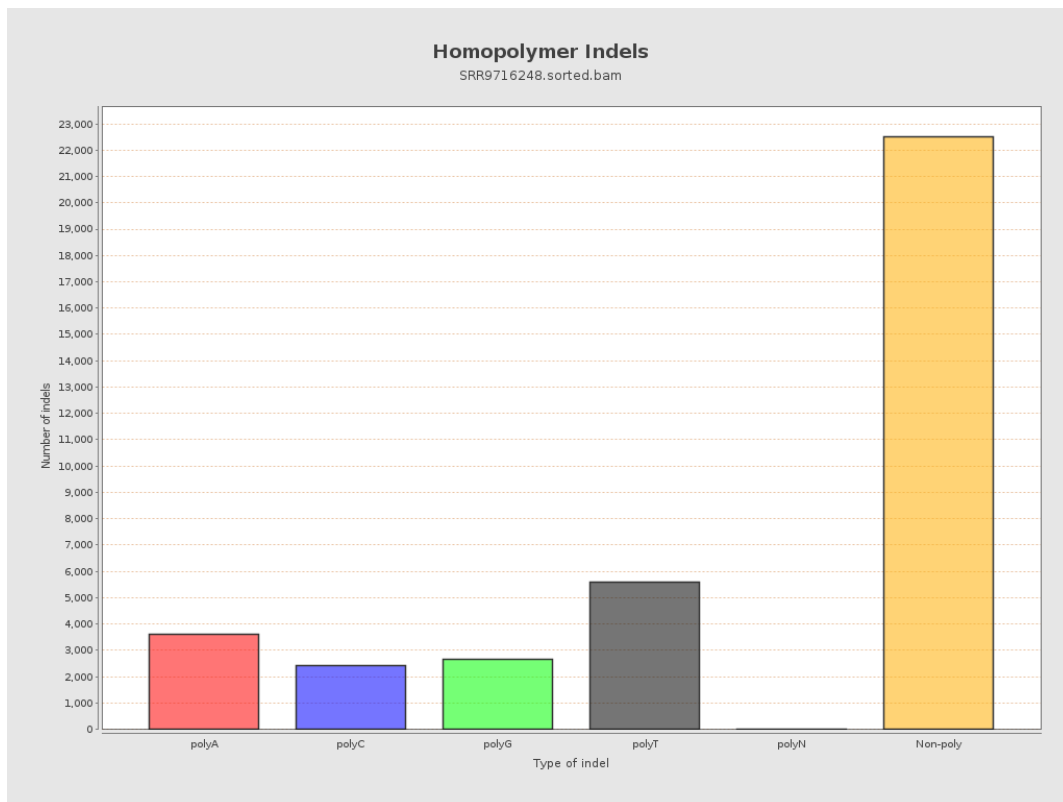
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

