

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:47:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230332.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_SRR6230332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230332.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:47:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,348,137
Mapped reads	2,803,343 / 83.73%
Unmapped reads	544,794 / 16.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,045 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	146,236 / 4.37%
Duplication rate	3.93%
Clipped reads	1,295,966 / 38.71%

2.2. ACGT Content

Number/percentage of A's	51,459,842 / 27.74%
Number/percentage of C's	32,356,112 / 17.44%
Number/percentage of T's	62,121,383 / 33.49%
Number/percentage of G's	39,206,945 / 21.14%
Number/percentage of N's	358,121 / 0.19%
GC Percentage	38.58%

2.3. Coverage

Mean	0.0599

Standard Deviation	0.581
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2.4. Mapping Quality

Mean Mapping Quality	46.86
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2.5. Mismatches and indels

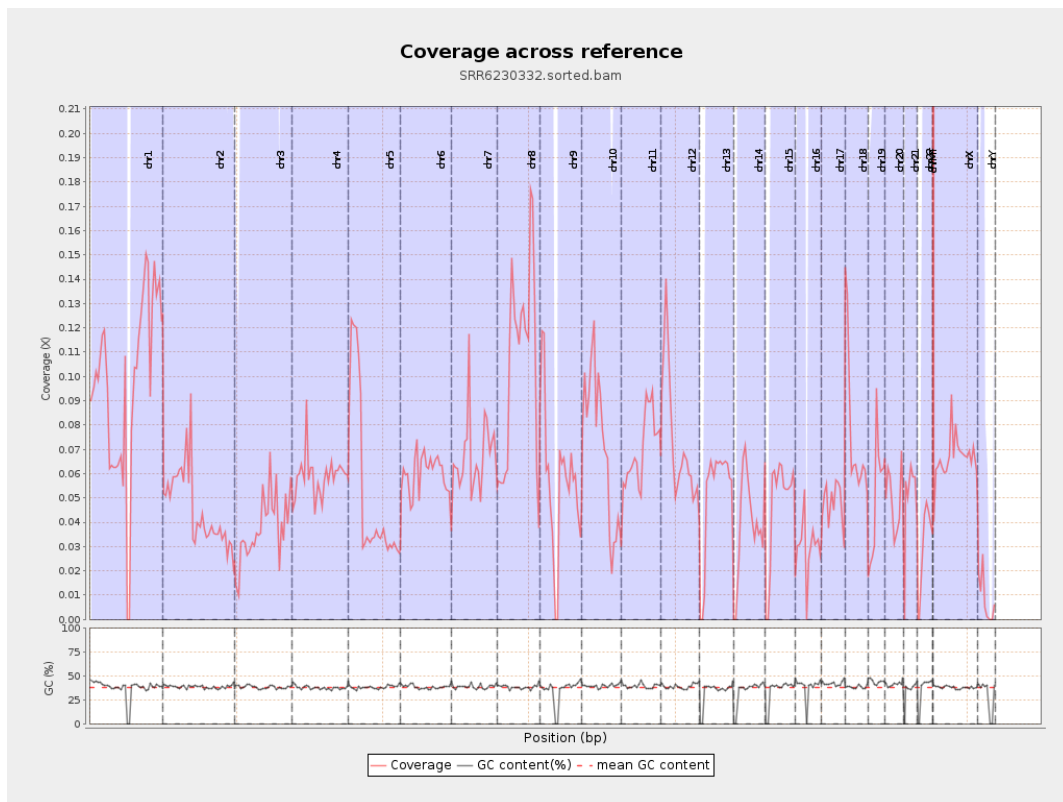
General error rate	1.13%
Mismatches	2,073,166
Insertions	17,112
Mapped reads with at least one insertion	0.61%
Deletions	48,895
Mapped reads with at least one deletion	1.73%
Homopolymer indels	48.05%

2.6. Chromosome stats

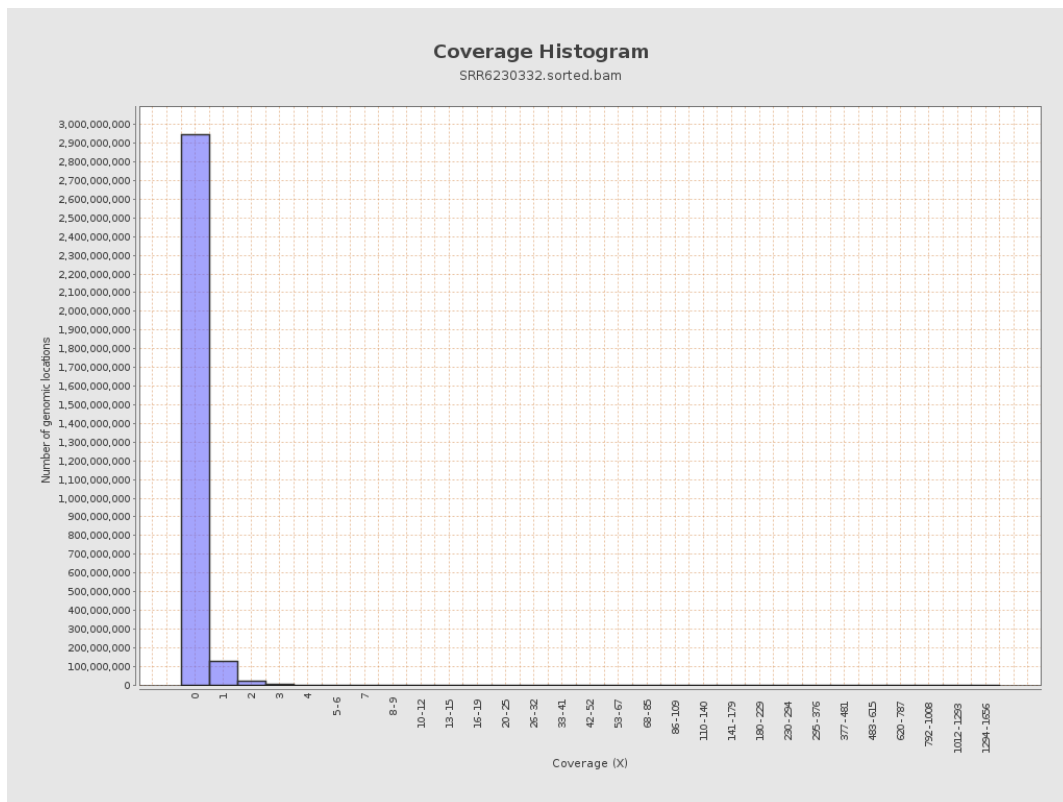
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24149416	0.0969	1.1544
chr2	243199373	11044485	0.0454	0.4611
chr3	198022430	7469382	0.0377	0.234
chr4	191154276	11265980	0.0589	0.3317
chr5	180915260	9375723	0.0518	0.2747
chr6	171115067	10293917	0.0602	0.3462
chr7	159138663	10672392	0.0671	0.824

chr8	146364022	15307590	0.1046	1.1263
chr9	141213431	8030614	0.0569	0.4485
chr10	135534747	9626012	0.071	0.4895
chr11	135006516	9412593	0.0697	0.4733
chr12	133851895	9782612	0.0731	0.3264
chr13	115169878	5904402	0.0513	0.2692
chr14	107349540	4248783	0.0396	0.2663
chr15	102531392	4804607	0.0469	0.2538
chr16	90354753	2646007	0.0293	0.25
chr17	81195210	3938856	0.0485	0.3027
chr18	78077248	5845964	0.0749	0.8462
chr19	59128983	3011602	0.0509	0.6204
chr20	63025520	3144122	0.0499	0.295
chr21	48129895	2426693	0.0504	0.3152
chr22	51304566	1565261	0.0305	0.208
chrMT	16571	796833	48.086	23.6658
chrX	155270560	10328512	0.0665	0.3406
chrY	59373566	490284	0.0083	0.1957

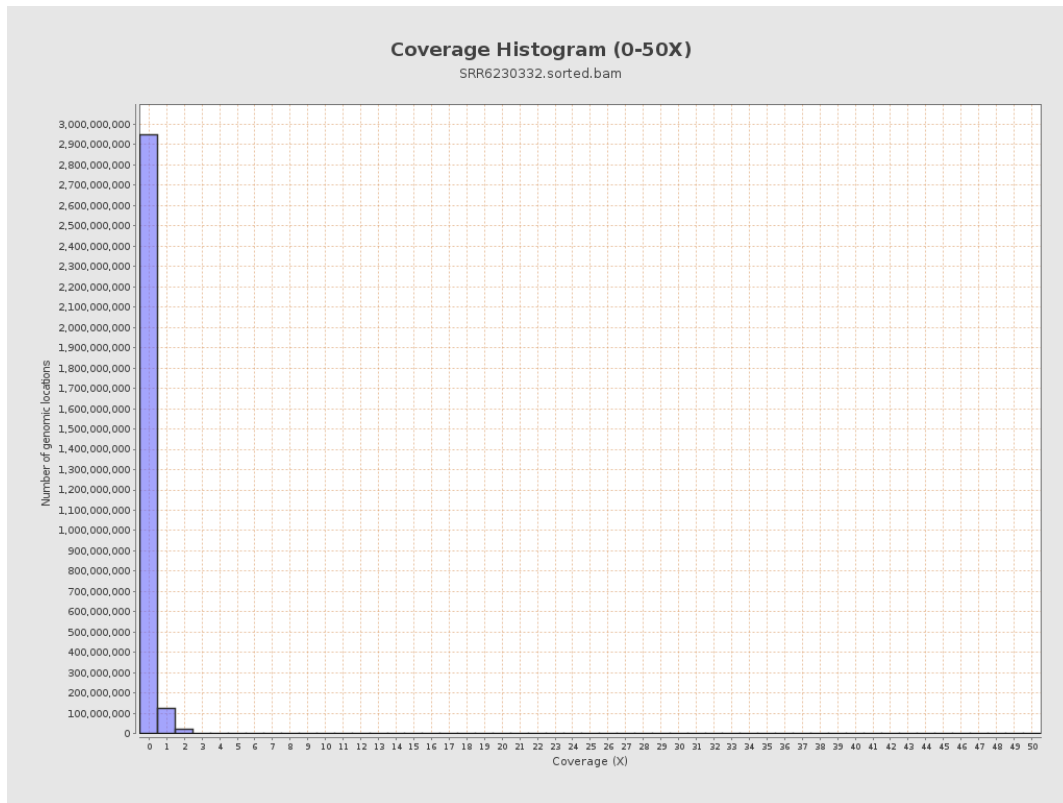
3. Results : Coverage across reference



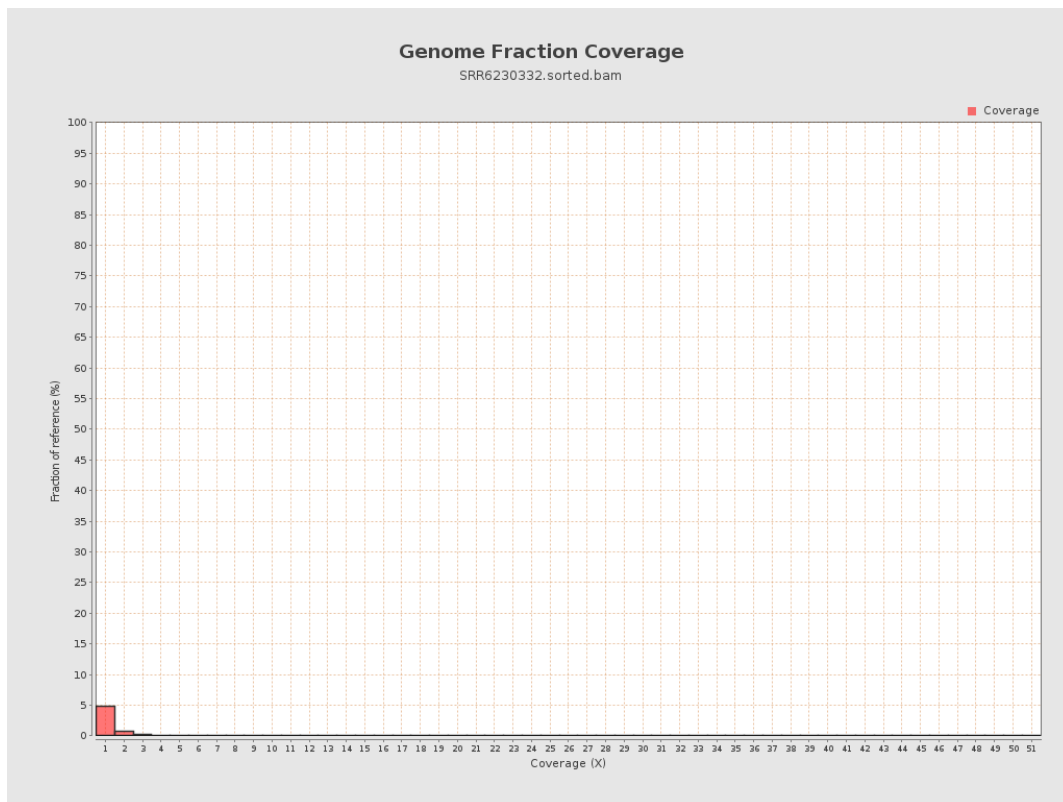
4. Results : Coverage Histogram



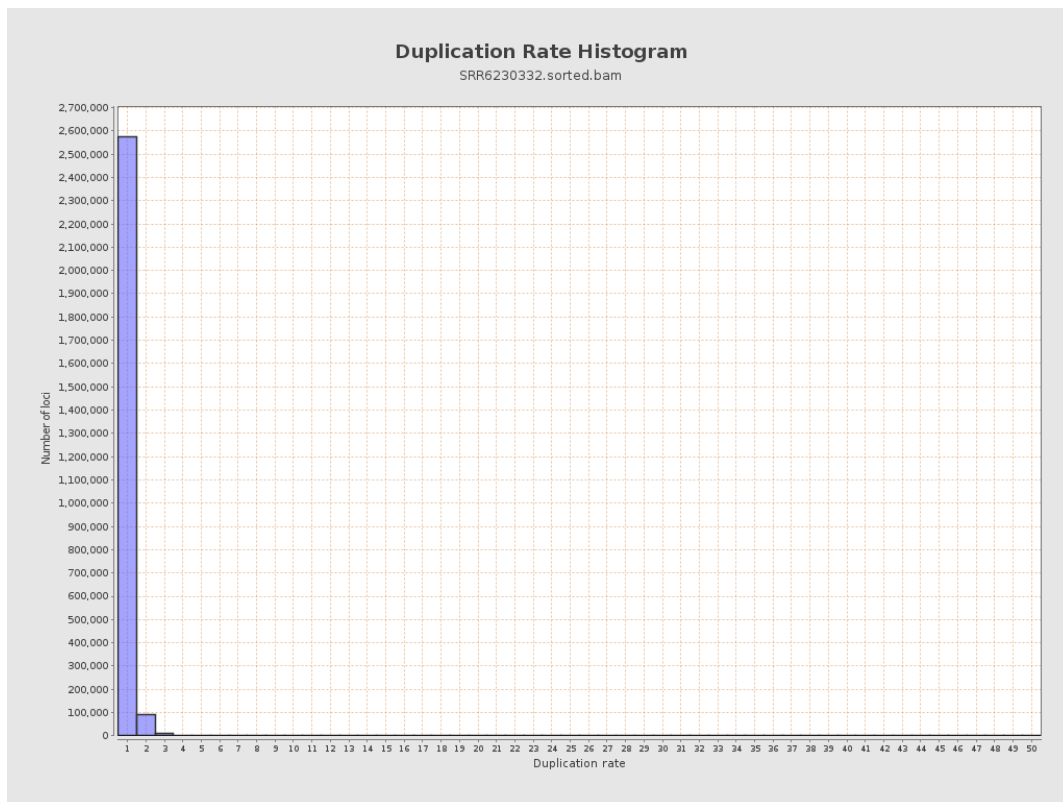
5. Results : Coverage Histogram (0-50X)



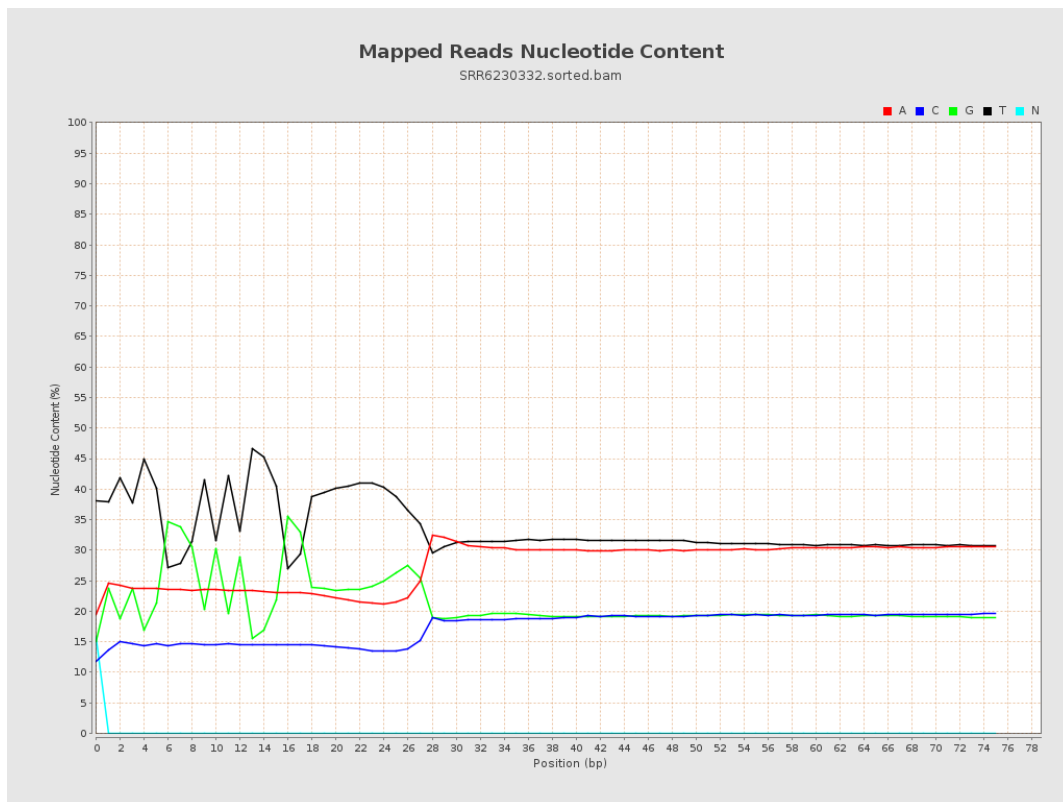
6. Results : Genome Fraction Coverage



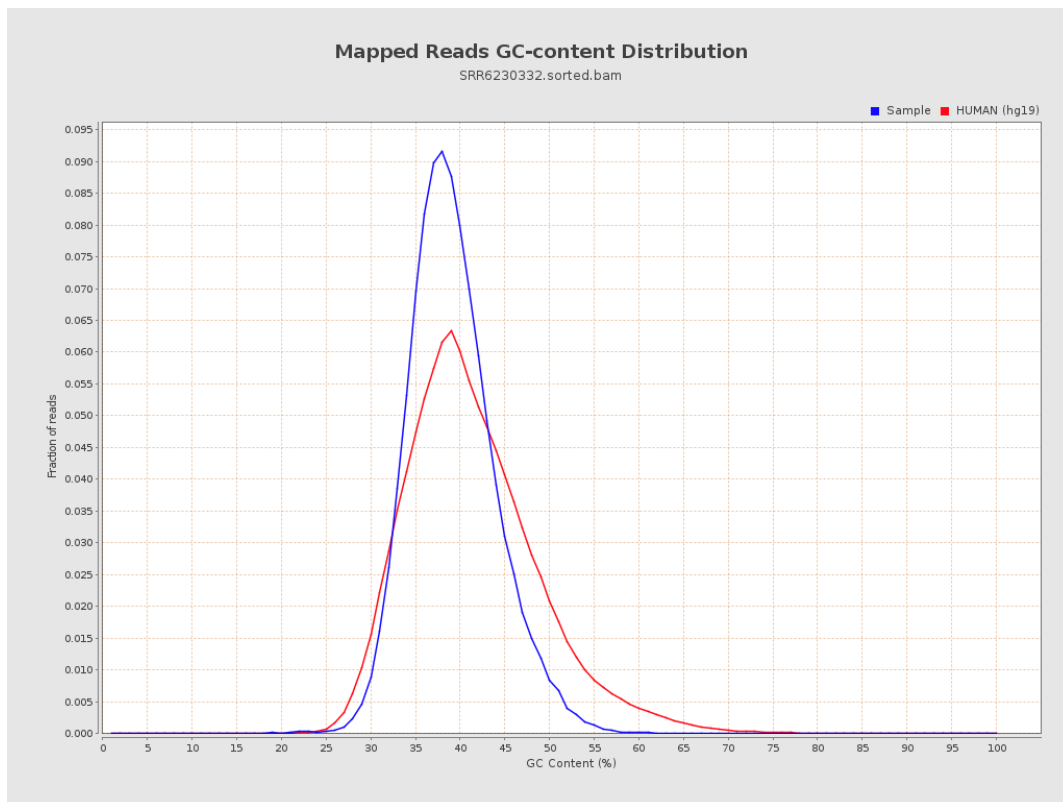
7. Results : Duplication Rate Histogram



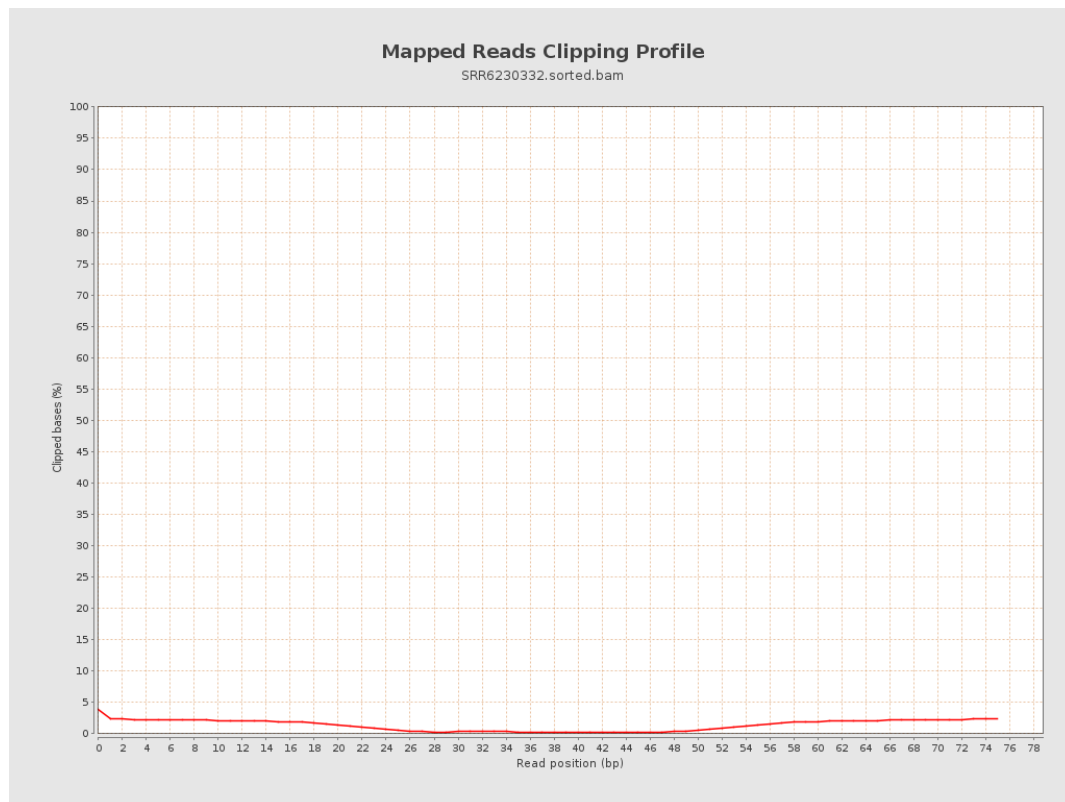
8. Results : Mapped Reads Nucleotide Content



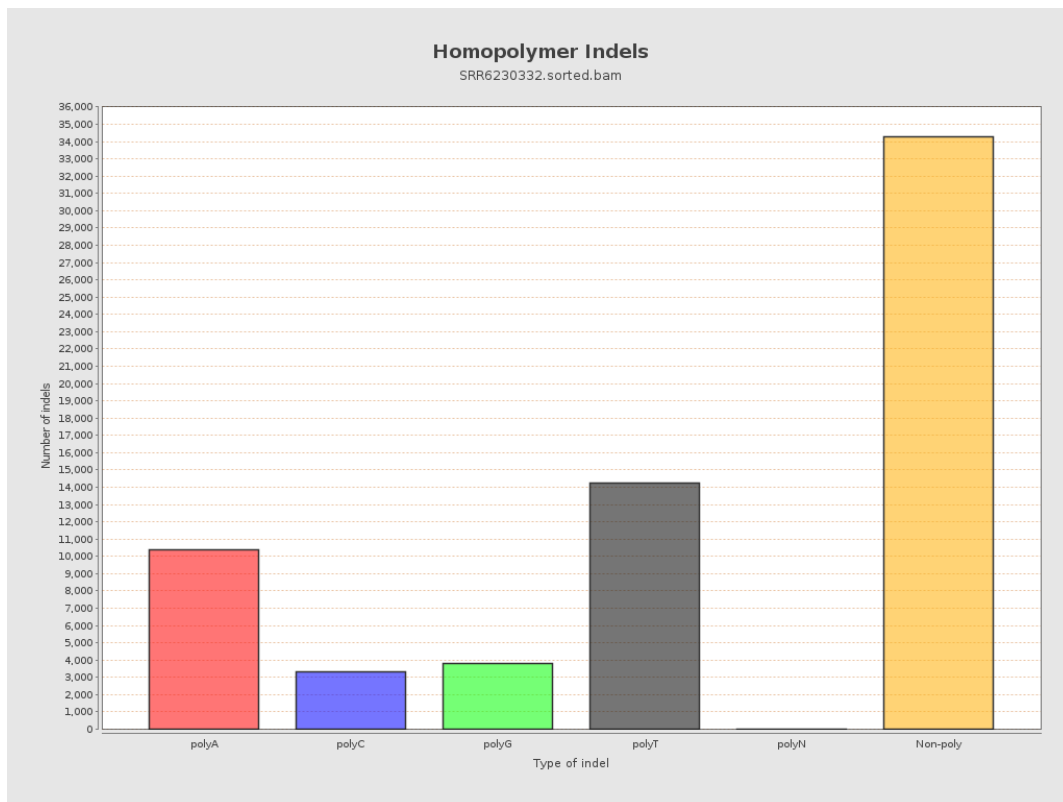
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

