

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004132.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_SRR6004132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:43:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,615,844
Mapped reads	2,336,324 / 89.31%
Unmapped reads	279,520 / 10.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,651 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	98,728 / 3.77%
Duplication rate	3.18%
Clipped reads	1,141,857 / 43.65%

2.2. ACGT Content

Number/percentage of A's	43,075,186 / 27.88%
Number/percentage of C's	28,758,807 / 18.61%
Number/percentage of T's	48,380,430 / 31.32%
Number/percentage of G's	34,268,965 / 22.18%
Number/percentage of N's	11,033 / 0.01%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4561
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2.4. Mapping Quality

Mean Mapping Quality	44.96
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2.5. Mismatches and indels

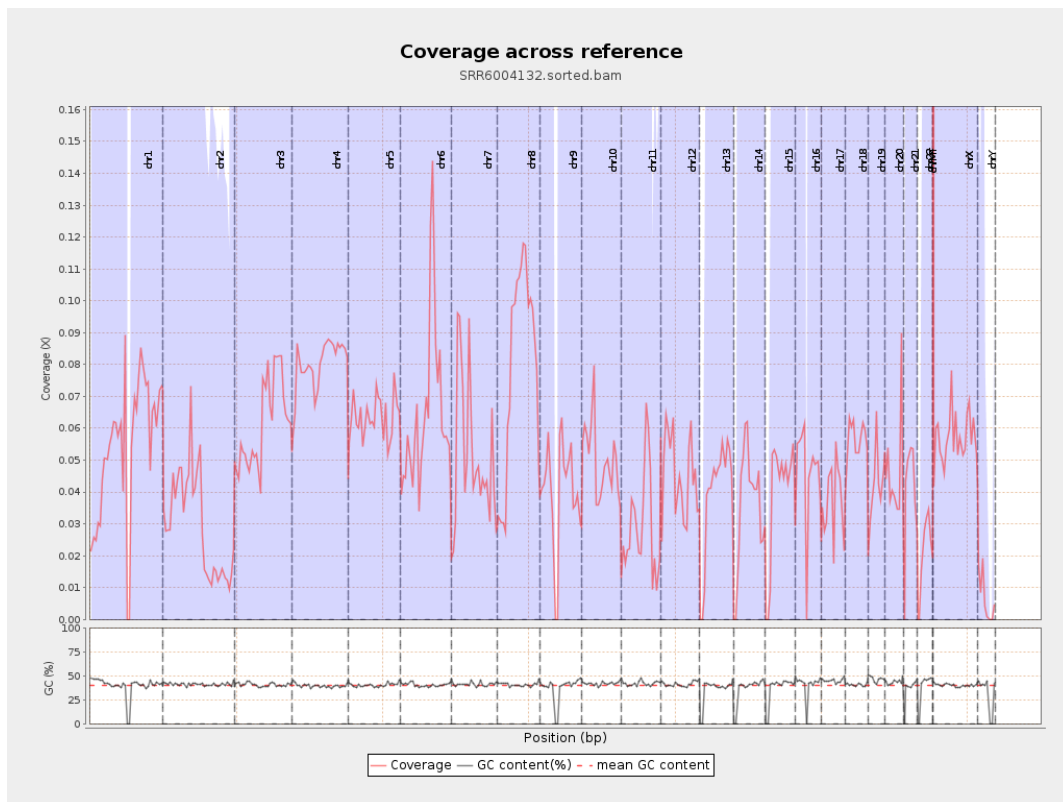
General error rate	0.9%
Mismatches	1,370,507
Insertions	11,676
Mapped reads with at least one insertion	0.5%
Deletions	38,449
Mapped reads with at least one deletion	1.63%
Homopolymer indels	46.17%

2.6. Chromosome stats

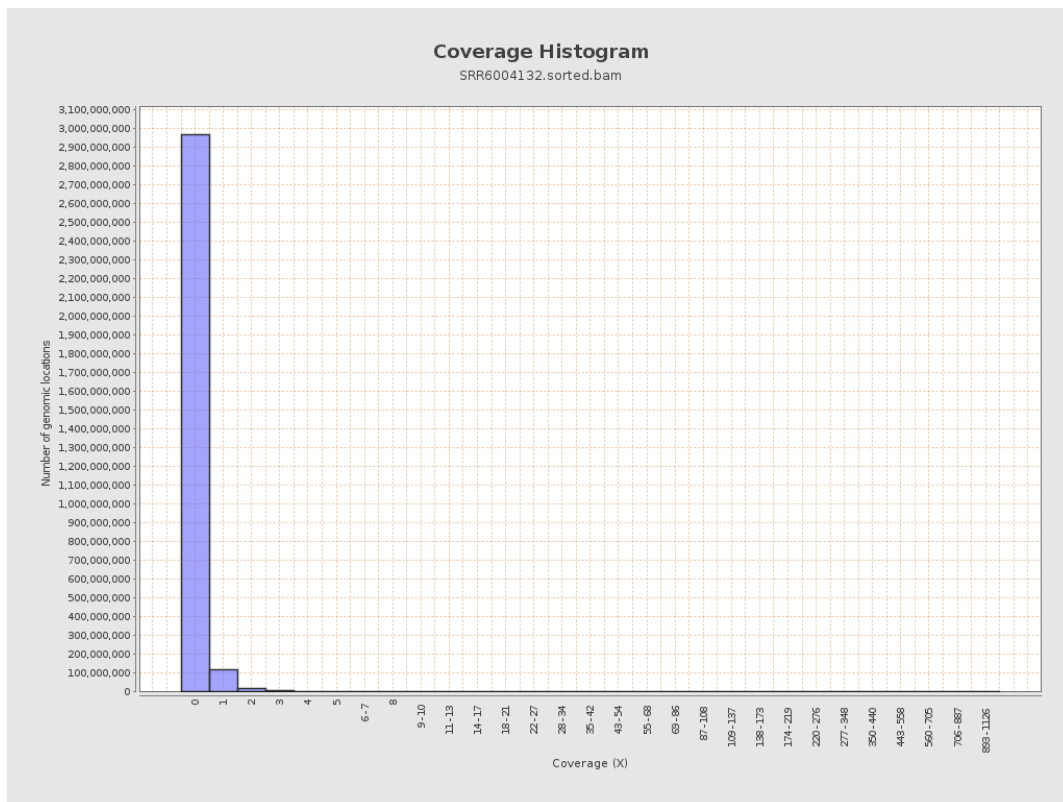
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13483098	0.0541	0.9377
chr2	243199373	7173577	0.0295	0.4372
chr3	198022430	12119045	0.0612	0.2806
chr4	191154276	15375858	0.0804	0.3339
chr5	180915260	11412883	0.0631	0.2906
chr6	171115067	11042602	0.0645	0.3558
chr7	159138663	8062284	0.0507	0.6538

chr8	146364022	11678431	0.0798	0.6244
chr9	141213431	5699691	0.0404	0.3902
chr10	135534747	6722497	0.0496	0.4053
chr11	135006516	3898778	0.0289	0.2503
chr12	133851895	6060881	0.0453	0.2569
chr13	115169878	4539414	0.0394	0.2284
chr14	107349540	3936171	0.0367	0.2622
chr15	102531392	3999607	0.039	0.228
chr16	90354753	4087081	0.0452	0.2774
chr17	81195210	3049111	0.0376	0.2393
chr18	78077248	4434742	0.0568	0.7186
chr19	59128983	2530189	0.0428	0.6156
chr20	63025520	2942436	0.0467	0.2598
chr21	48129895	1968796	0.0409	0.2505
chr22	51304566	1081722	0.0211	0.1618
chrMT	16571	37166	2.2428	1.9712
chrX	155270560	8842342	0.0569	0.3083
chrY	59373566	378192	0.0064	0.127

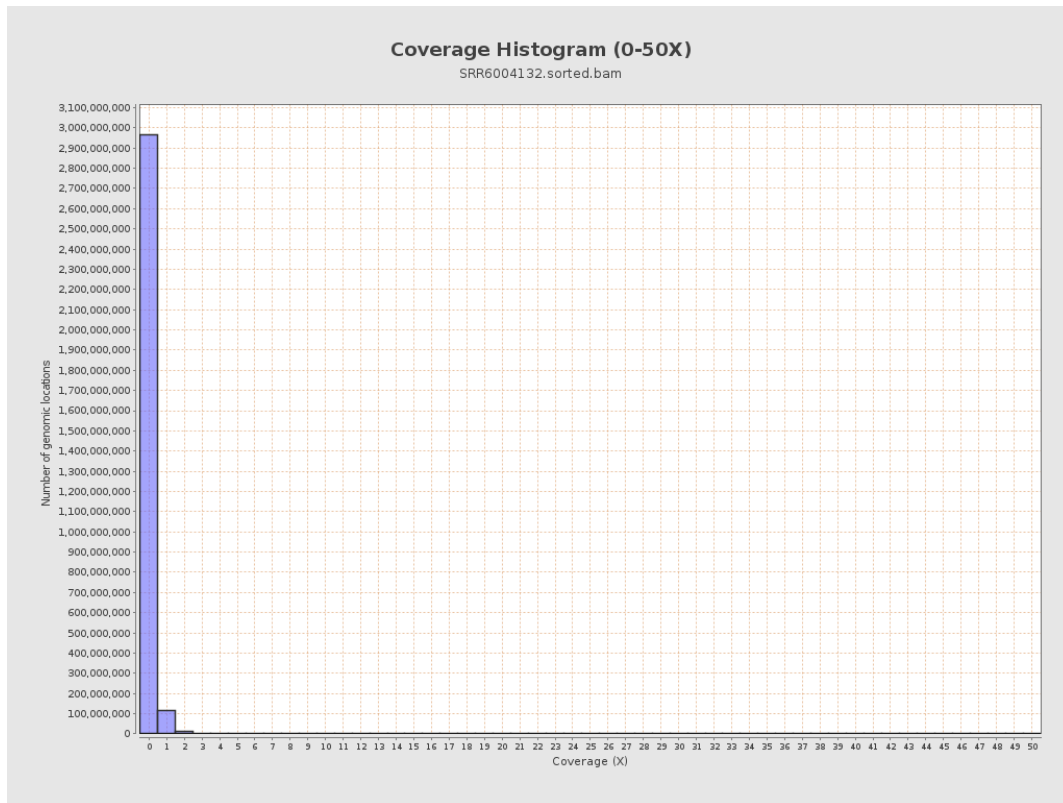
3. Results : Coverage across reference



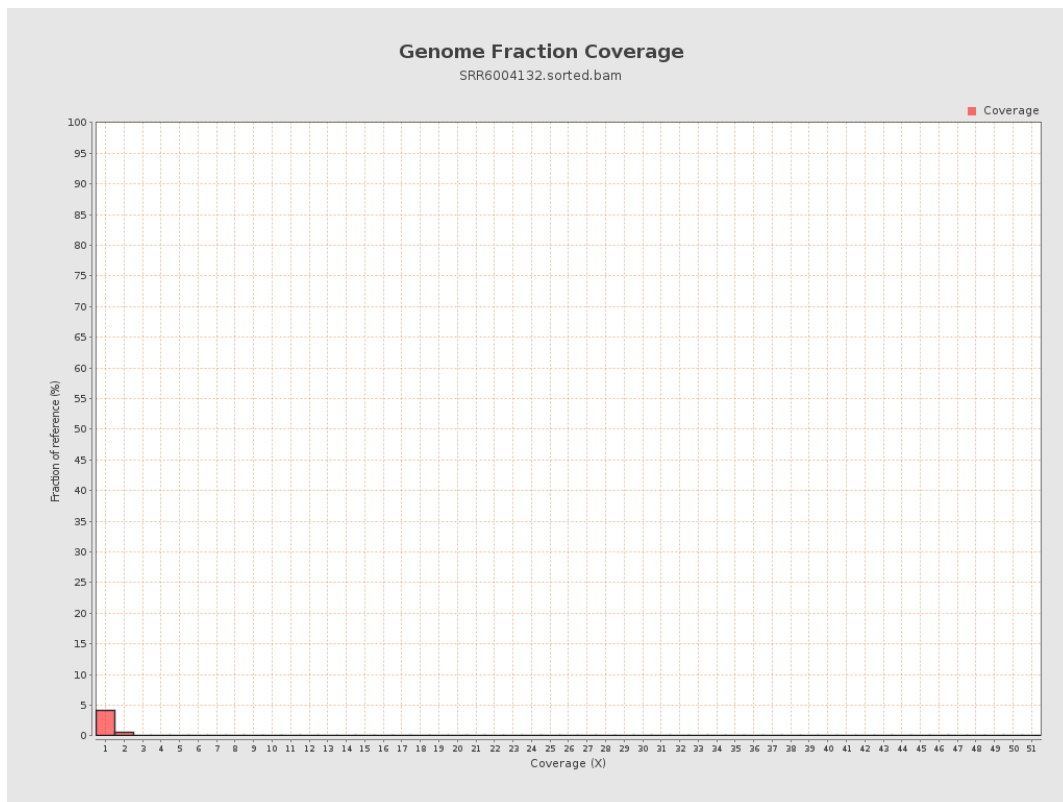
4. Results : Coverage Histogram



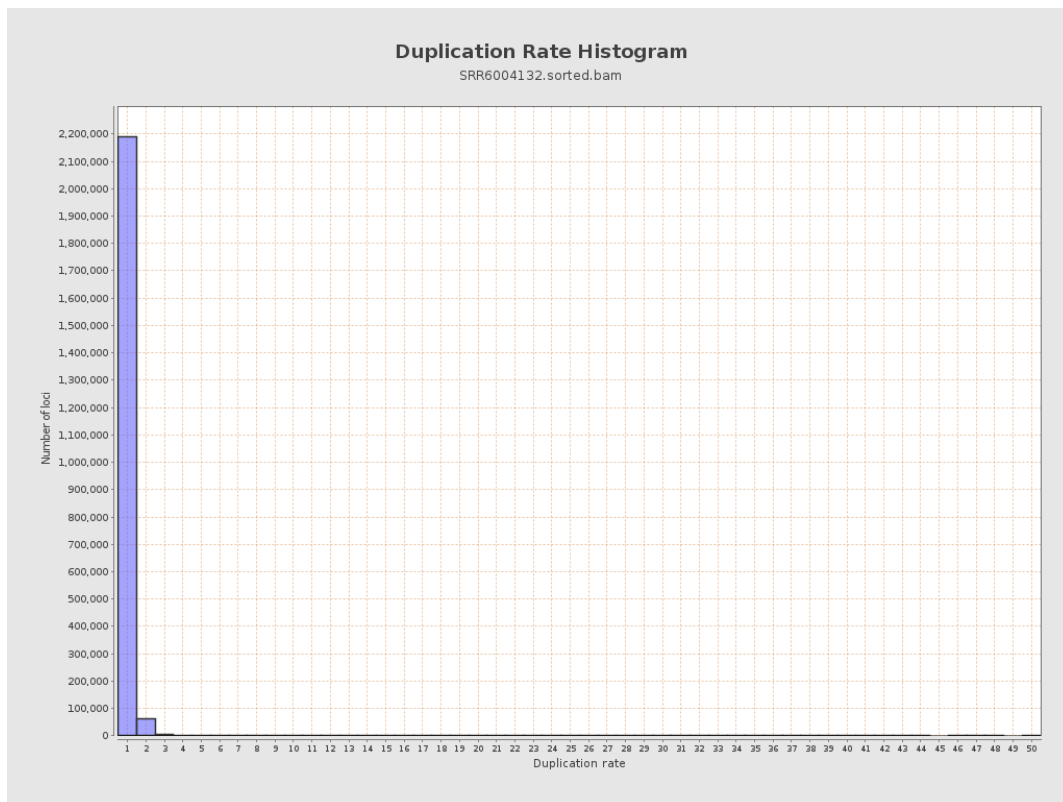
5. Results : Coverage Histogram (0-50X)



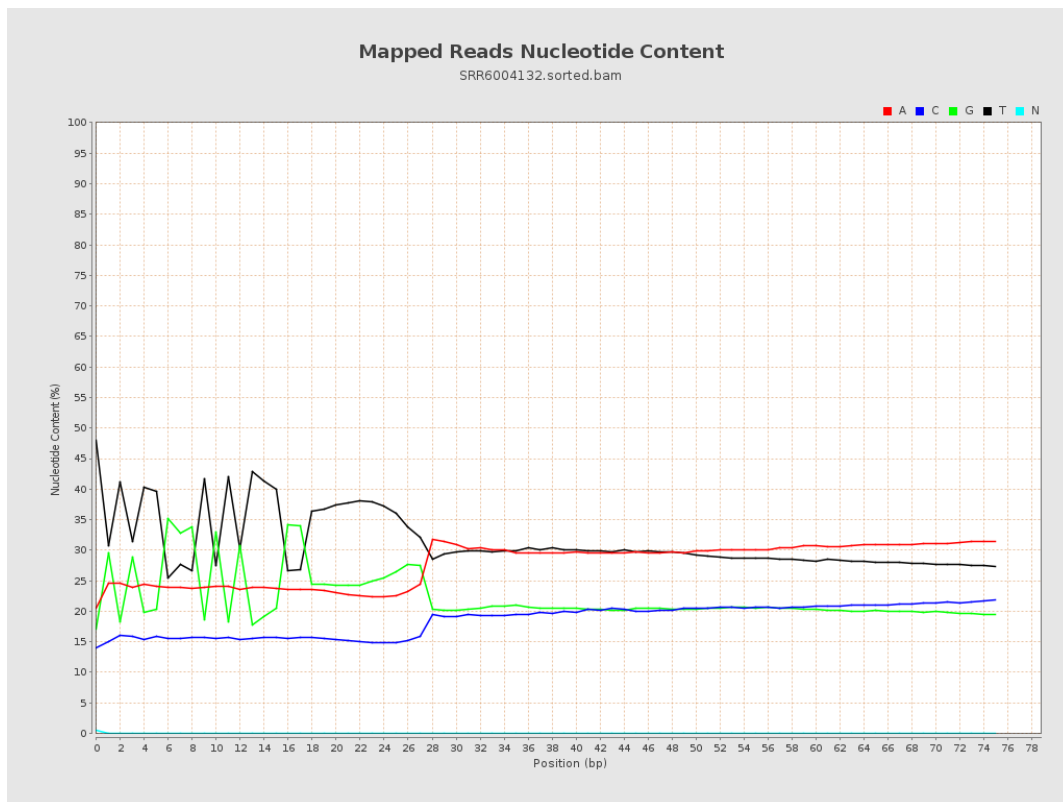
6. Results : Genome Fraction Coverage



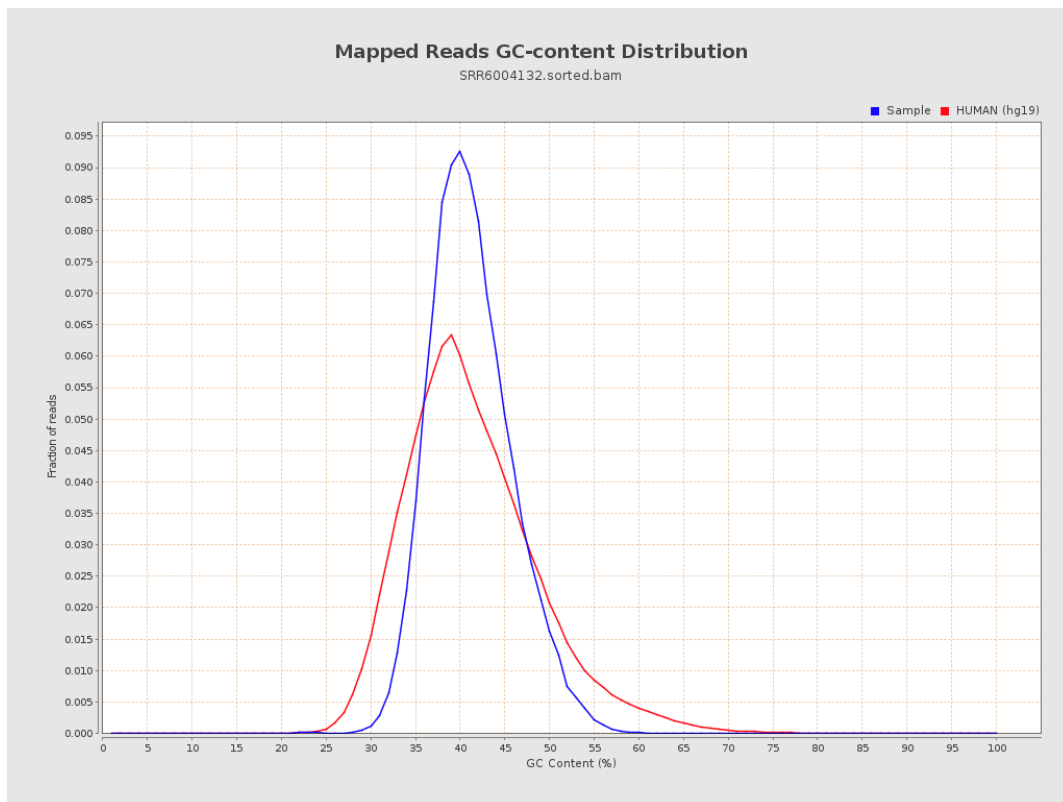
7. Results : Duplication Rate Histogram



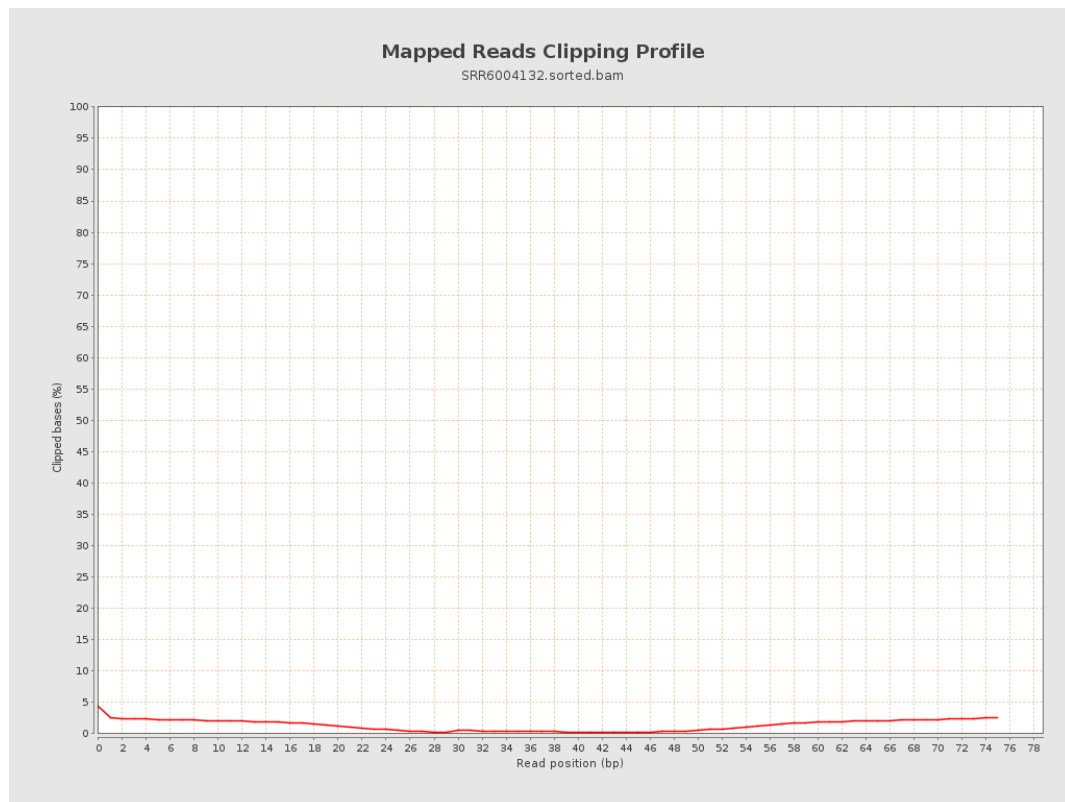
8. Results : Mapped Reads Nucleotide Content



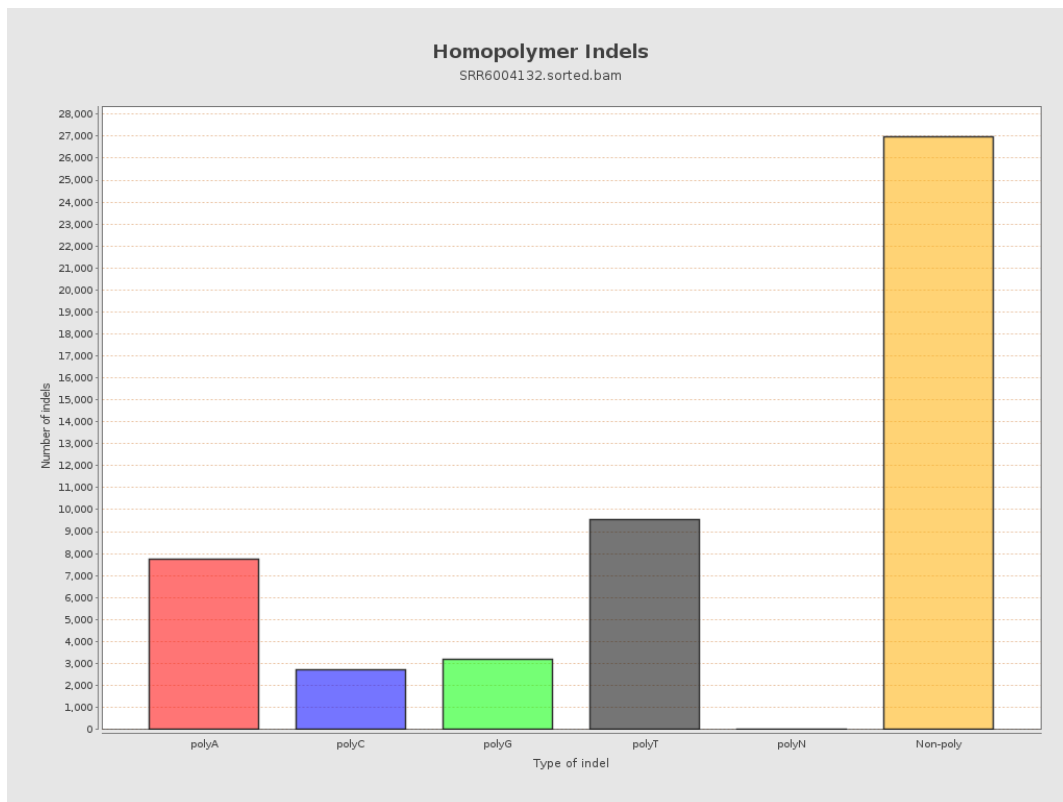
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

