

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:04:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818984.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_SRR1818984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:04:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,840,396
Mapped reads	1,817,568 / 98.76%
Unmapped reads	22,828 / 1.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,565 / 1.23%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	754,118 / 40.98%
Duplication rate	35.32%
Clipped reads	1,831,034 / 99.49%

2.2. ACGT Content

Number/percentage of A's	48,138,335 / 28.54%
Number/percentage of C's	35,384,309 / 20.98%
Number/percentage of T's	46,302,233 / 27.45%
Number/percentage of G's	38,847,411 / 23.03%
Number/percentage of N's	8,258 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0545

Standard Deviation	0.6345
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2.4. Mapping Quality

Mean Mapping Quality	49.37
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2.5. Mismatches and indels

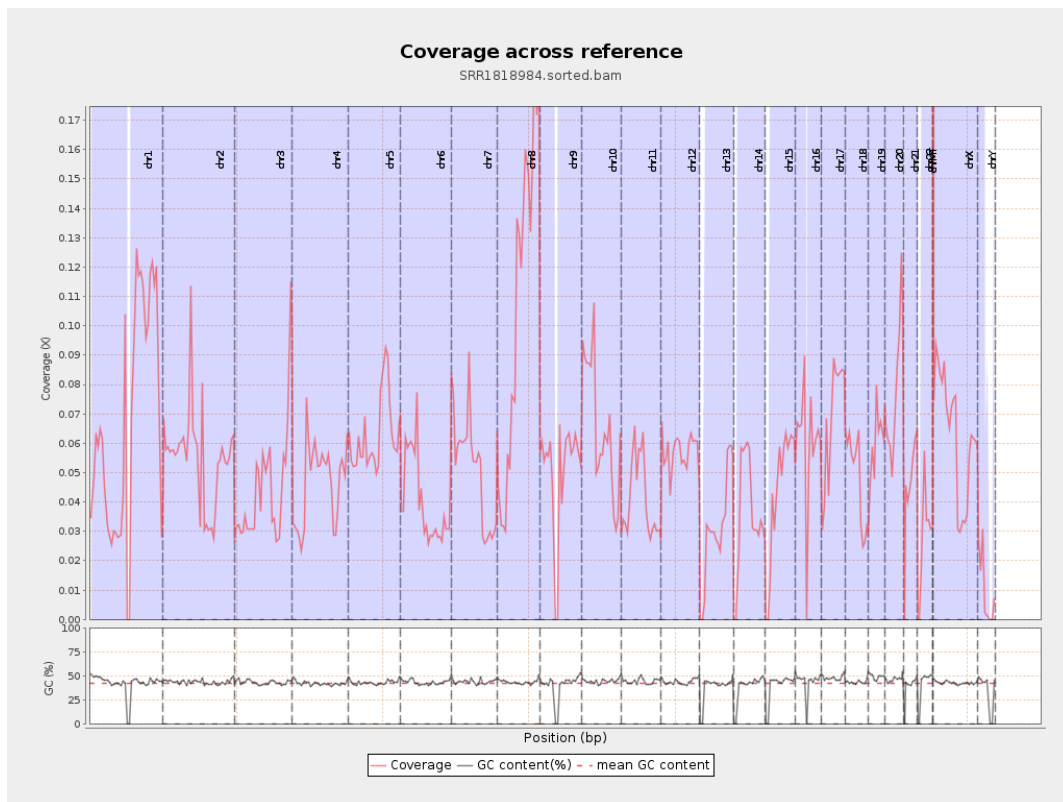
General error rate	0.64%
Mismatches	1,030,986
Insertions	22,727
Mapped reads with at least one insertion	1.22%
Deletions	53,459
Mapped reads with at least one deletion	2.88%
Homopolymer indels	42.79%

2.6. Chromosome stats

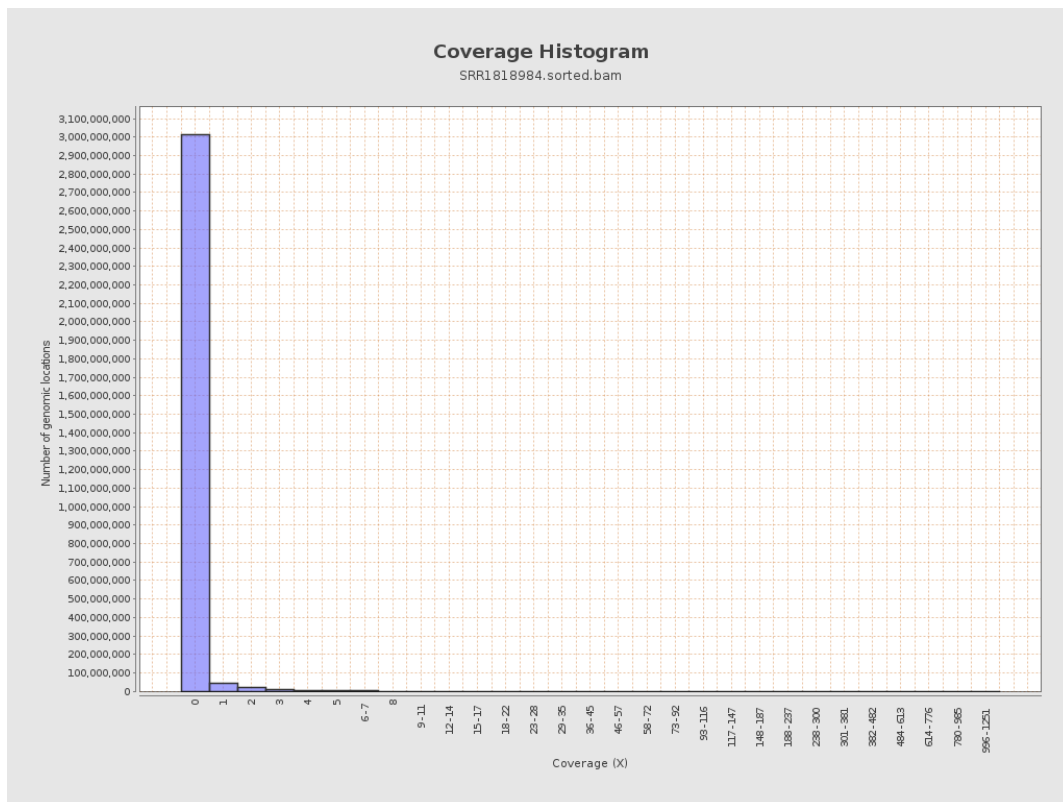
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16554690	0.0664	1.1399
chr2	243199373	13425445	0.0552	0.8395
chr3	198022430	8763870	0.0443	0.3663
chr4	191154276	8903766	0.0466	0.4193
chr5	180915260	11434181	0.0632	0.4491
chr6	171115067	6902440	0.0403	0.4269
chr7	159138663	8144650	0.0512	0.7367

chr8	146364022	15978953	0.1092	0.6438
chr9	141213431	7119538	0.0504	0.5822
chr10	135534747	8804984	0.065	0.7467
chr11	135006516	5517982	0.0409	0.4276
chr12	133851895	7699598	0.0575	0.4294
chr13	115169878	3591282	0.0312	0.3078
chr14	107349540	3915756	0.0365	0.3518
chr15	102531392	4375388	0.0427	0.3643
chr16	90354753	5363540	0.0594	0.6537
chr17	81195210	5573903	0.0686	0.5284
chr18	78077248	3773600	0.0483	0.6678
chr19	59128983	3530318	0.0597	1.056
chr20	63025520	4918048	0.078	0.5308
chr21	48129895	2246599	0.0467	0.4131
chr22	51304566	1405562	0.0274	0.3132
chrMT	16571	375238	22.6443	14.8314
chrX	155270560	9870536	0.0636	0.5079
chrY	59373566	589341	0.0099	0.5749

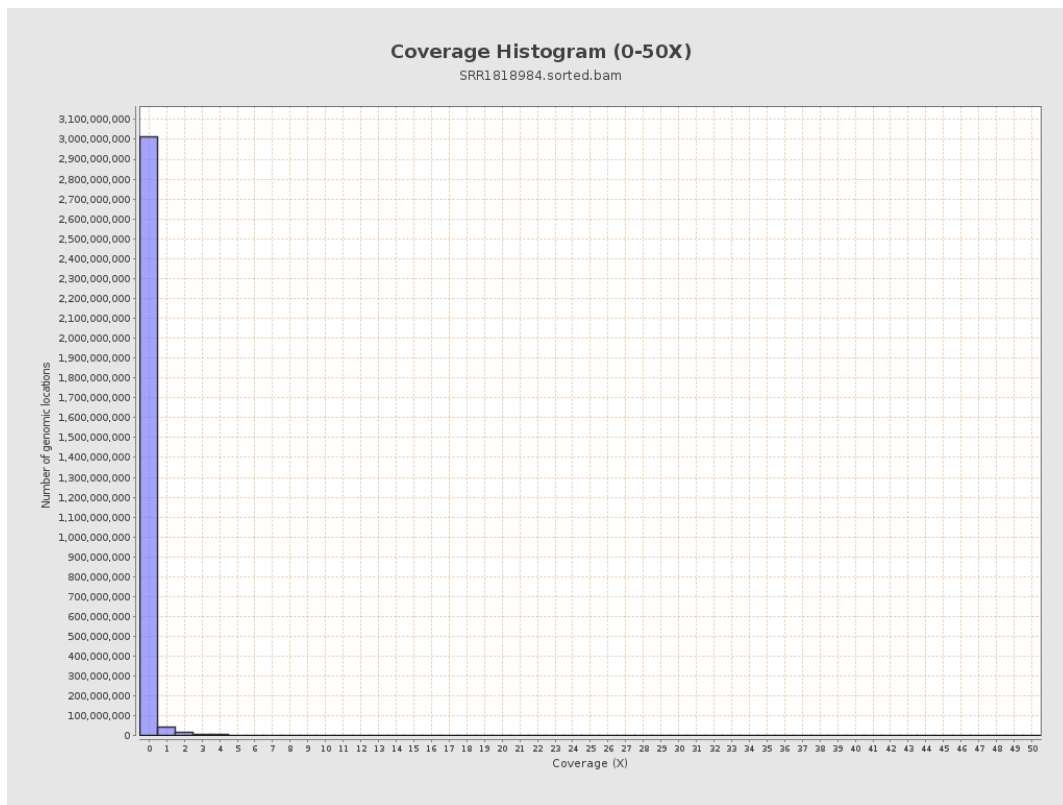
3. Results : Coverage across reference



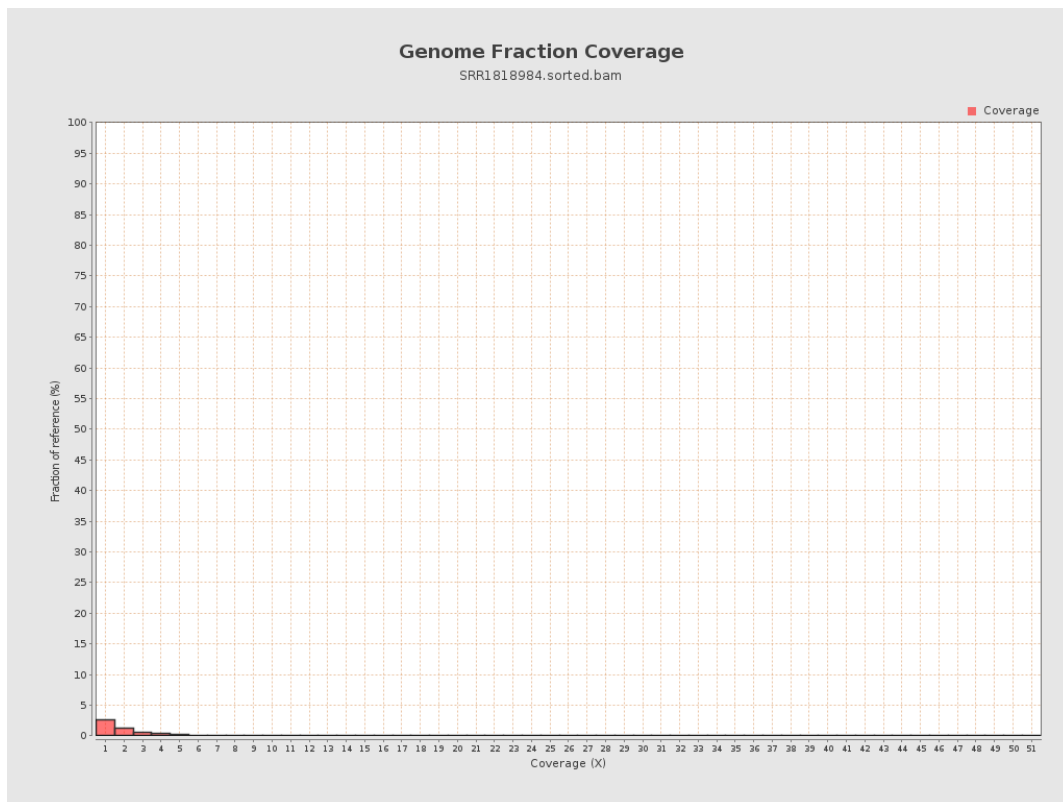
4. Results : Coverage Histogram



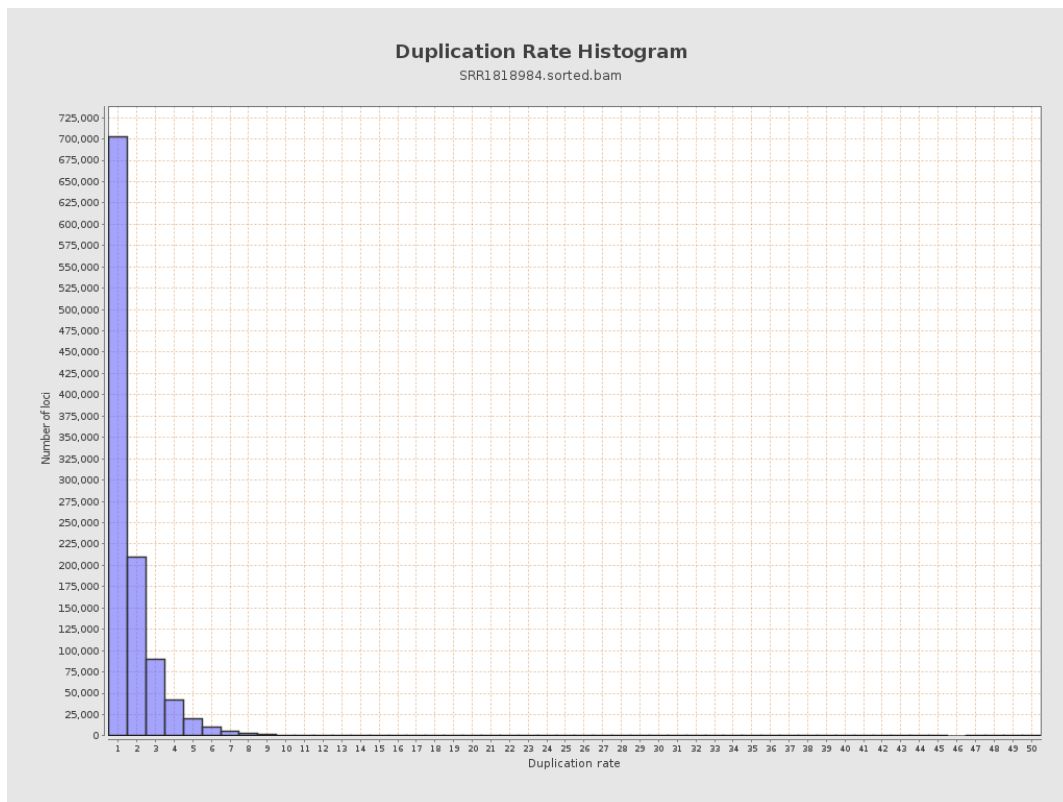
5. Results : Coverage Histogram (0-50X)



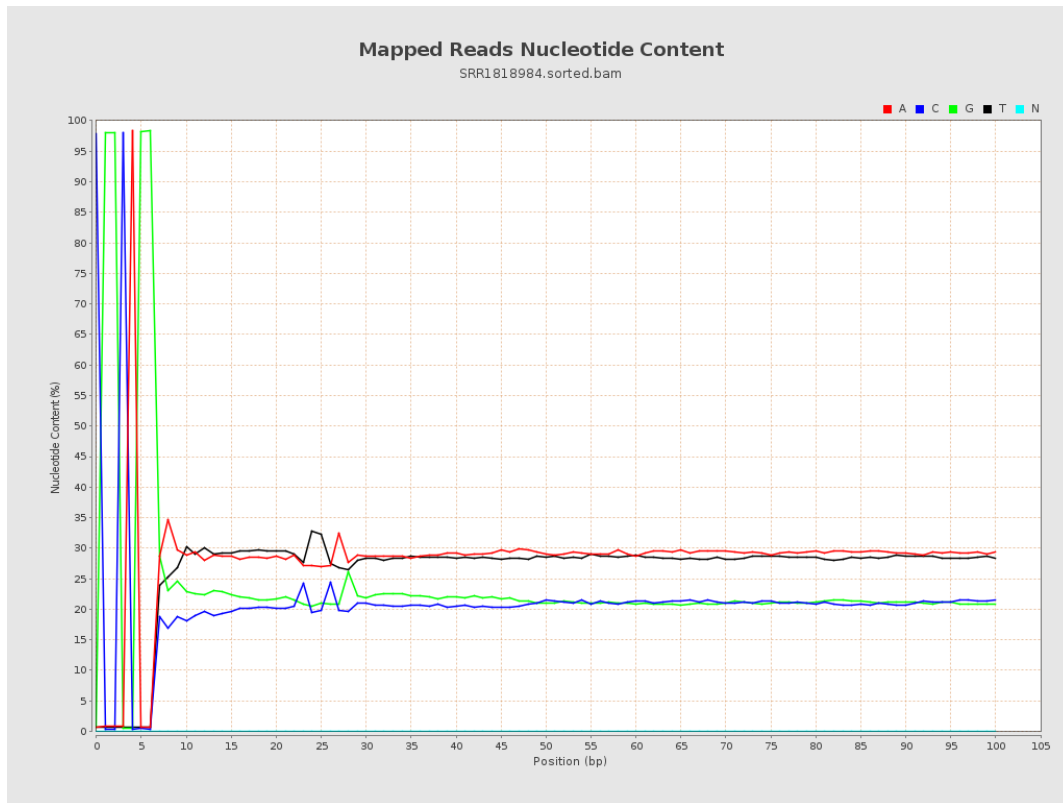
6. Results : Genome Fraction Coverage



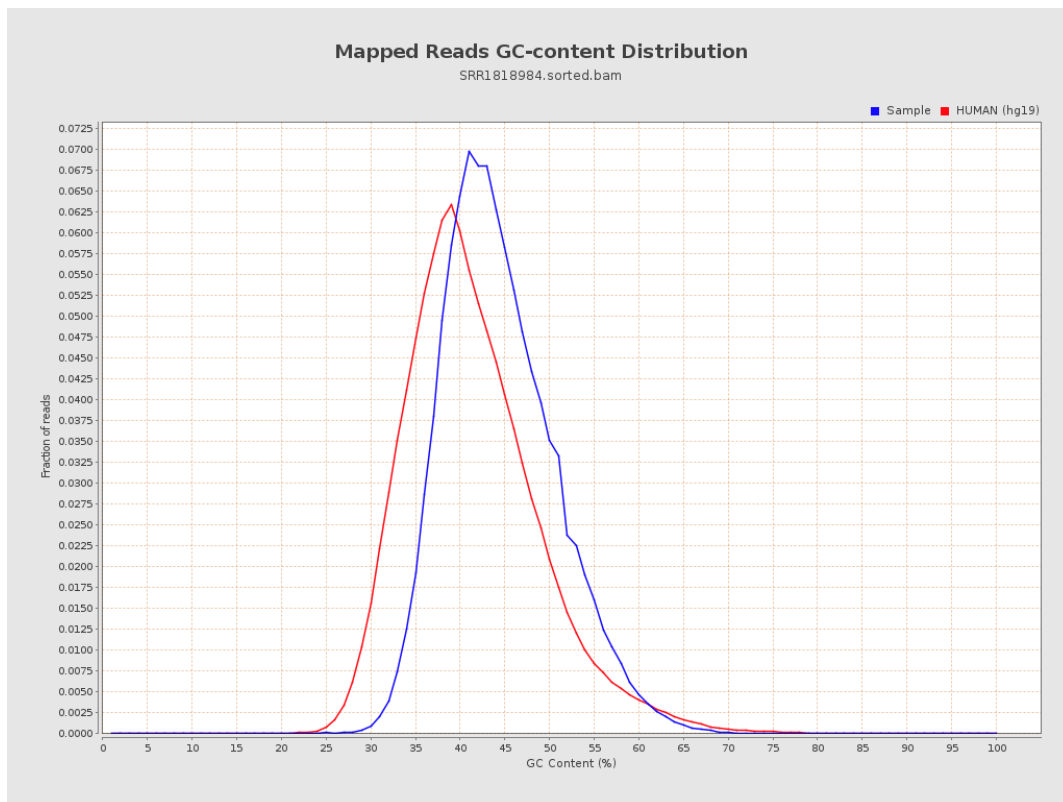
7. Results : Duplication Rate Histogram



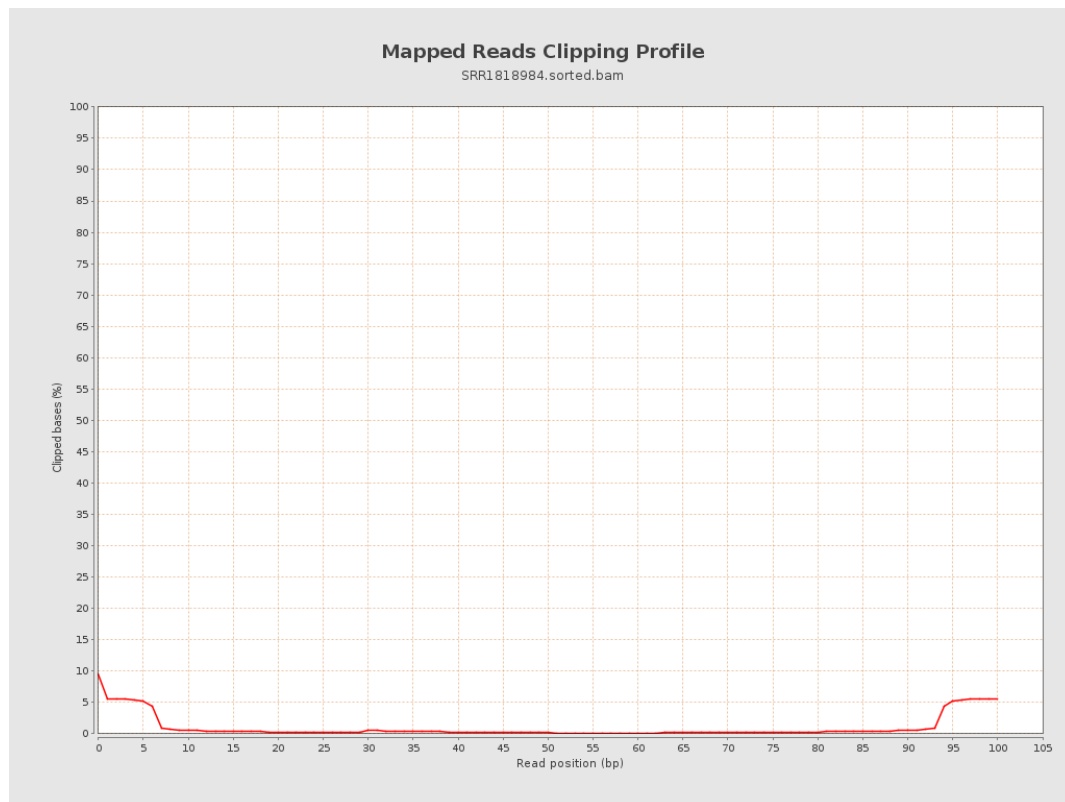
8. Results : Mapped Reads Nucleotide Content



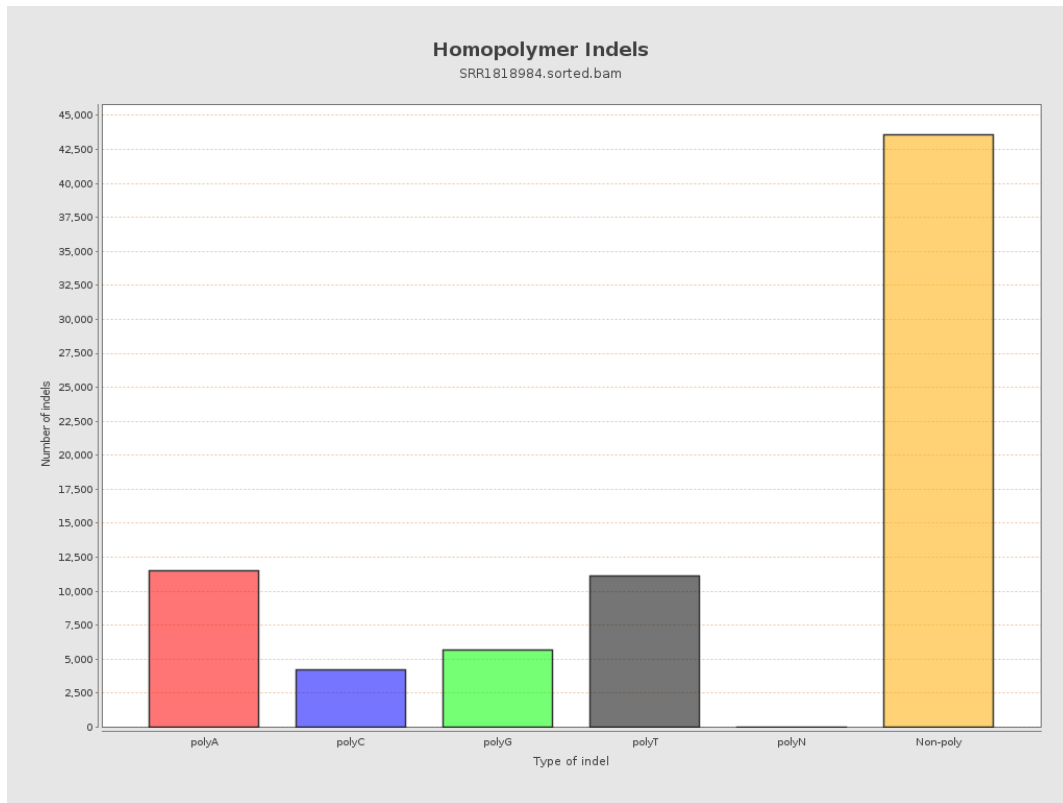
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

