

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 12:53:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153370.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_SRR1153370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153370.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 12:52:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,394,422
Mapped reads	36,149,299 / 99.33%
Unmapped reads	245,123 / 0.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237,406 / 0.65%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	20,955,528 / 57.58%
Duplication rate	45.39%
Clipped reads	16,350,934 / 44.93%

2.2. ACGT Content

Number/percentage of A's	835,188,305 / 26.49%
Number/percentage of C's	746,815,201 / 23.68%
Number/percentage of T's	860,201,002 / 27.28%
Number/percentage of G's	710,345,712 / 22.53%
Number/percentage of N's	885,777 / 0.03%
GC Percentage	46.21%

2.3. Coverage

Mean	1.0188

Standard Deviation	12.7216
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2.4. Mapping Quality

Mean Mapping Quality	49.59
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2.5. Mismatches and indels

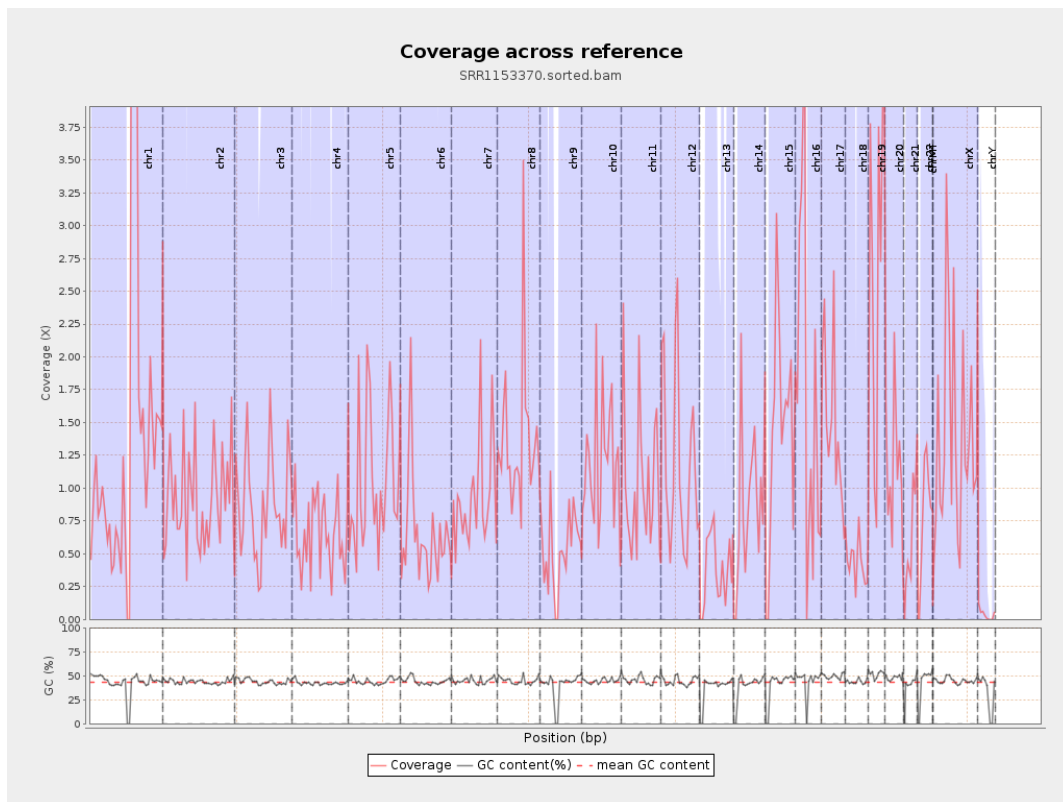
General error rate	0.23%
Mismatches	6,890,009
Insertions	328,810
Mapped reads with at least one insertion	0.9%
Deletions	248,900
Mapped reads with at least one deletion	0.68%
Homopolymer indels	49.12%

2.6. Chromosome stats

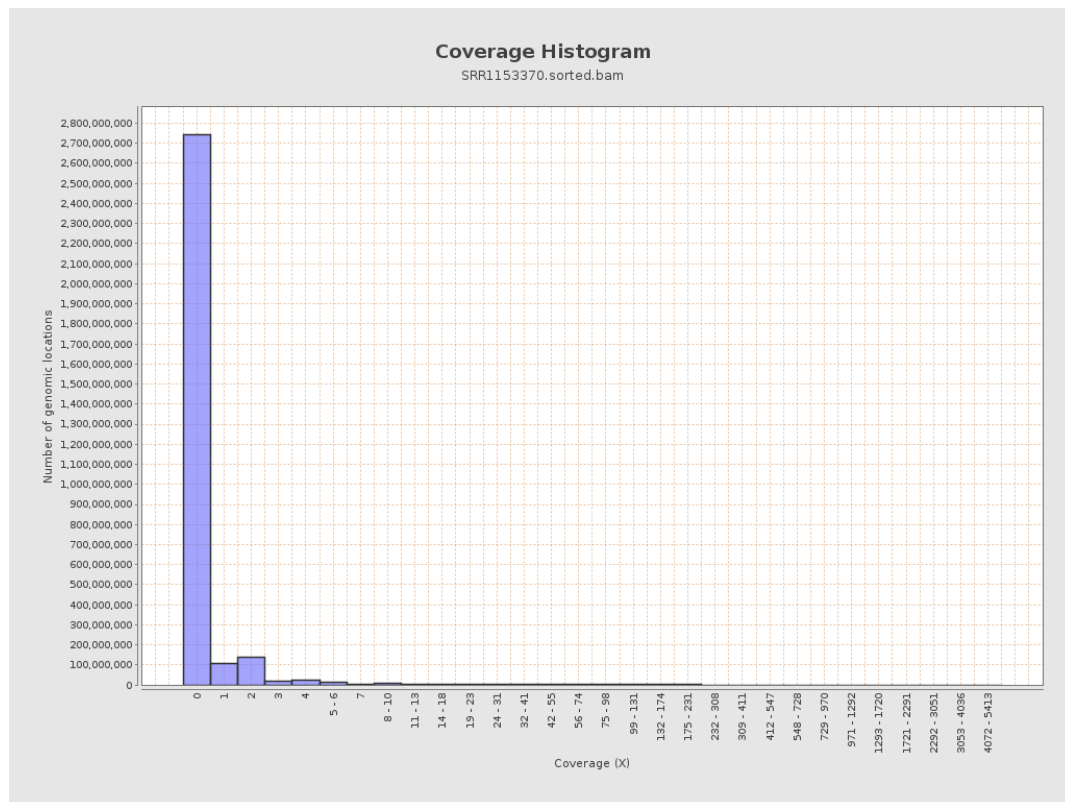
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	340663906	1.3668	16.5524
chr2	243199373	225245252	0.9262	10.2773
chr3	198022430	173260681	0.875	10.3435
chr4	191154276	125385187	0.6559	8.2534
chr5	180915260	191104488	1.0563	12.7735
chr6	171115067	107790880	0.6299	8.4283
chr7	159138663	147029368	0.9239	11.1657

chr8	146364022	199677595	1.3643	17.2324
chr9	141213431	74500711	0.5276	8.6325
chr10	135534747	163195585	1.2041	13.9435
chr11	135006516	141280485	1.0465	11.7307
chr12	133851895	162225665	1.212	13.4571
chr13	115169878	42682098	0.3706	5.9638
chr14	107349540	91410005	0.8515	10.039
chr15	102531392	142370888	1.3886	15.7187
chr16	90354753	149101470	1.6502	18.1931
chr17	81195210	124019822	1.5274	14.328
chr18	78077248	34187409	0.4379	6.1698
chr19	59128983	158056078	2.6731	24.7287
chr20	63025520	72655933	1.1528	11.794
chr21	48129895	30700036	0.6379	8.3324
chr22	51304566	39848250	0.7767	9.985
chrMT	16571	1685	0.1017	0.5491
chrX	155270560	215347810	1.3869	16.8739
chrY	59373566	2197764	0.037	1.8952

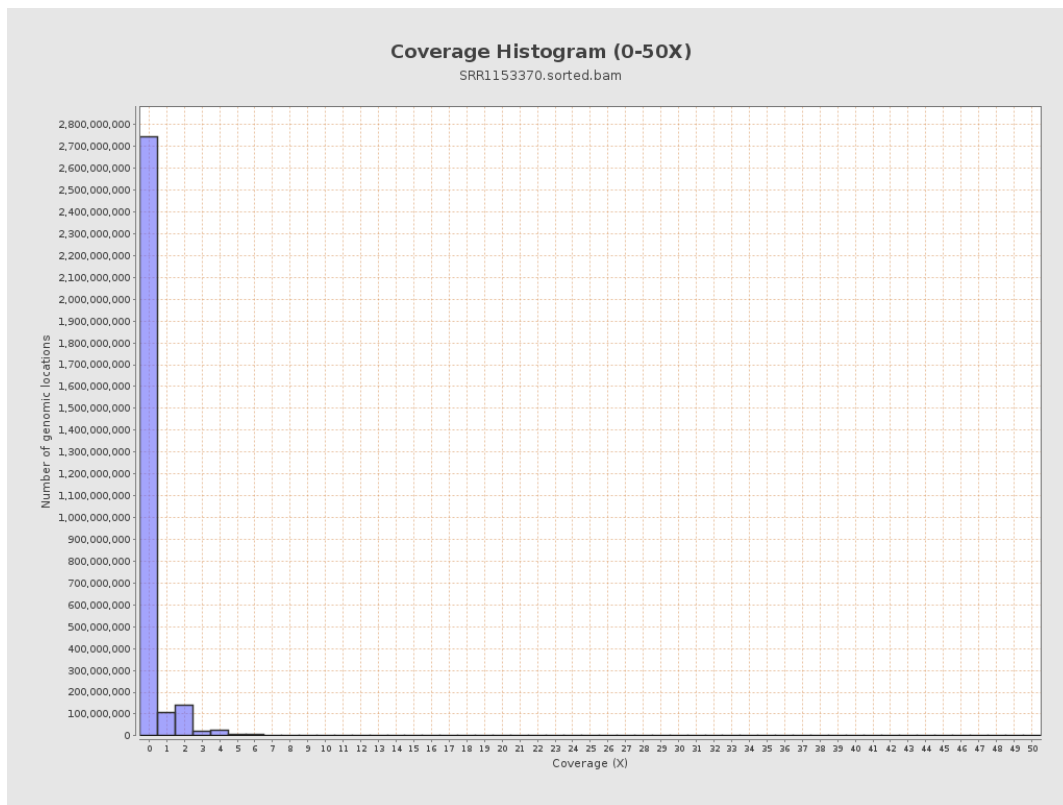
3. Results : Coverage across reference



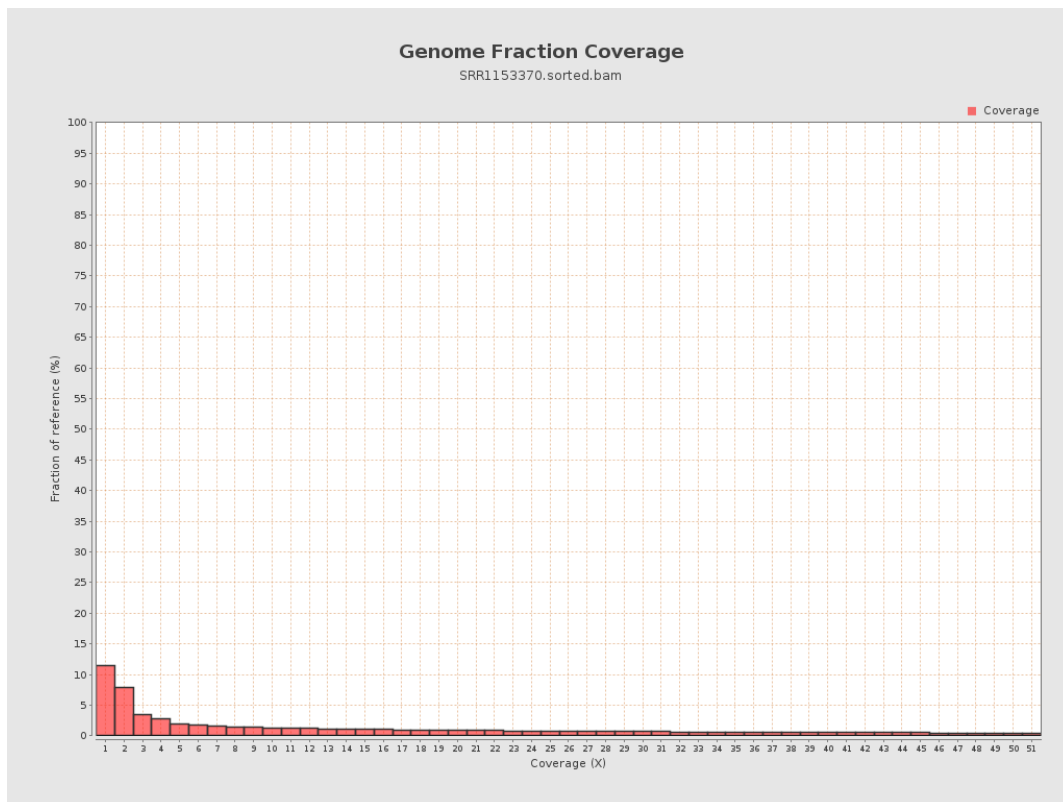
4. Results : Coverage Histogram



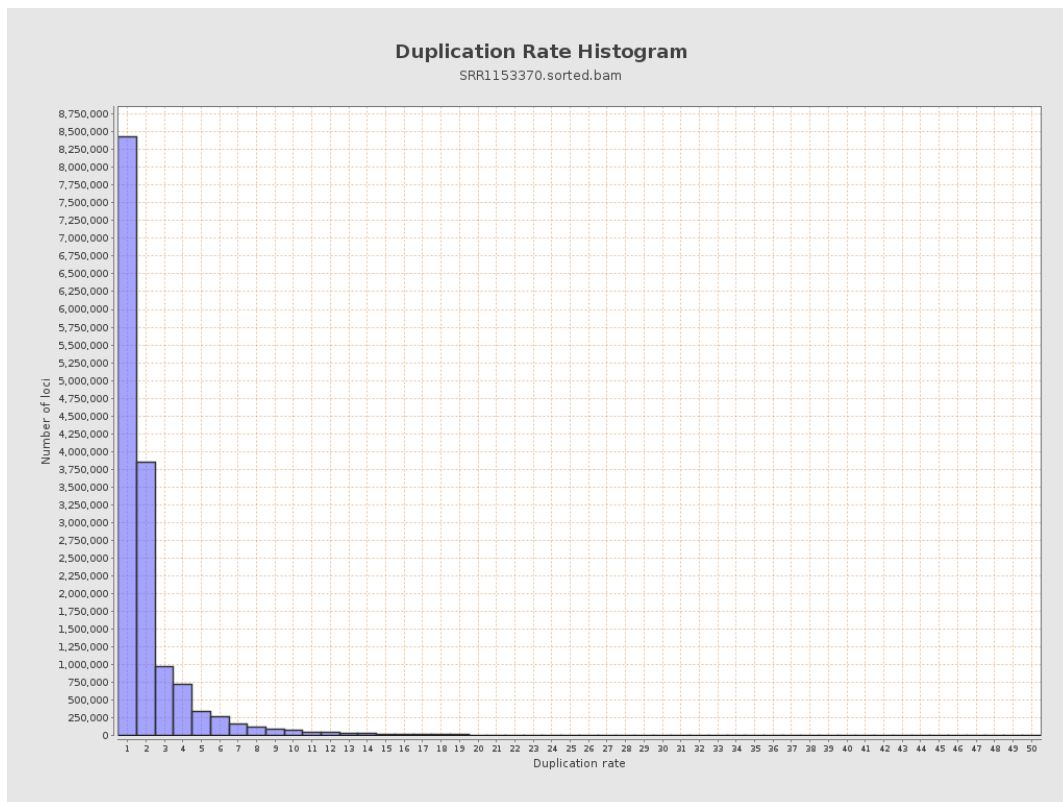
5. Results : Coverage Histogram (0-50X)



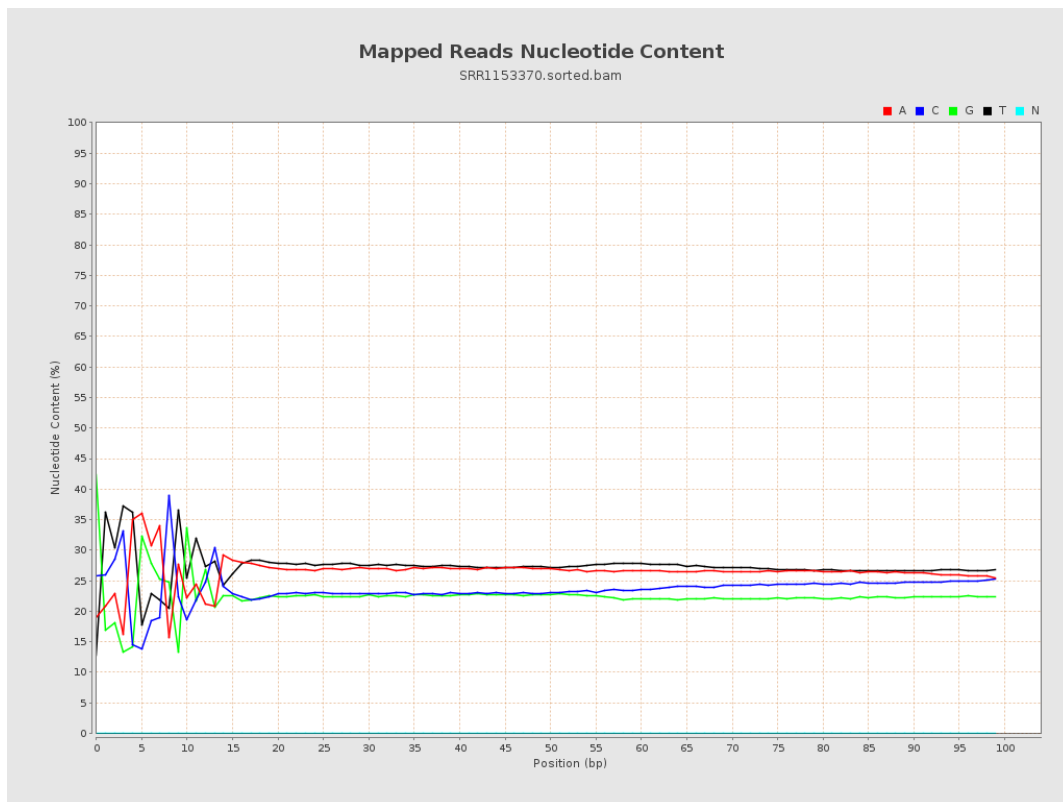
6. Results : Genome Fraction Coverage



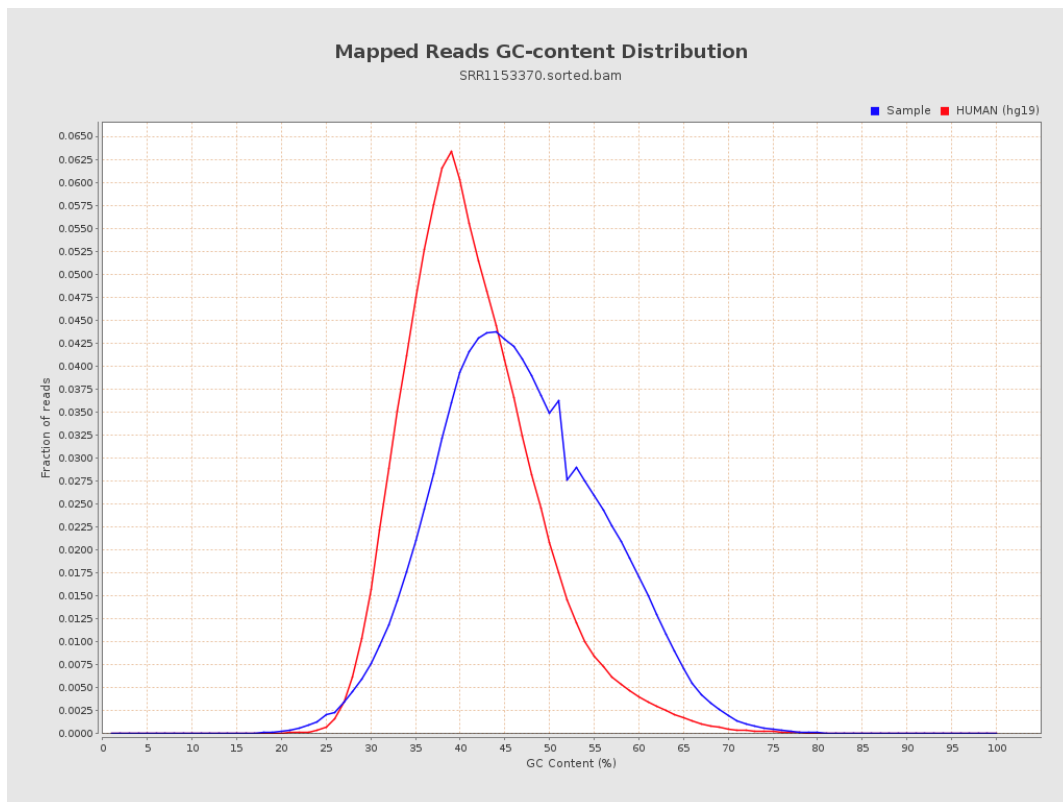
7. Results : Duplication Rate Histogram



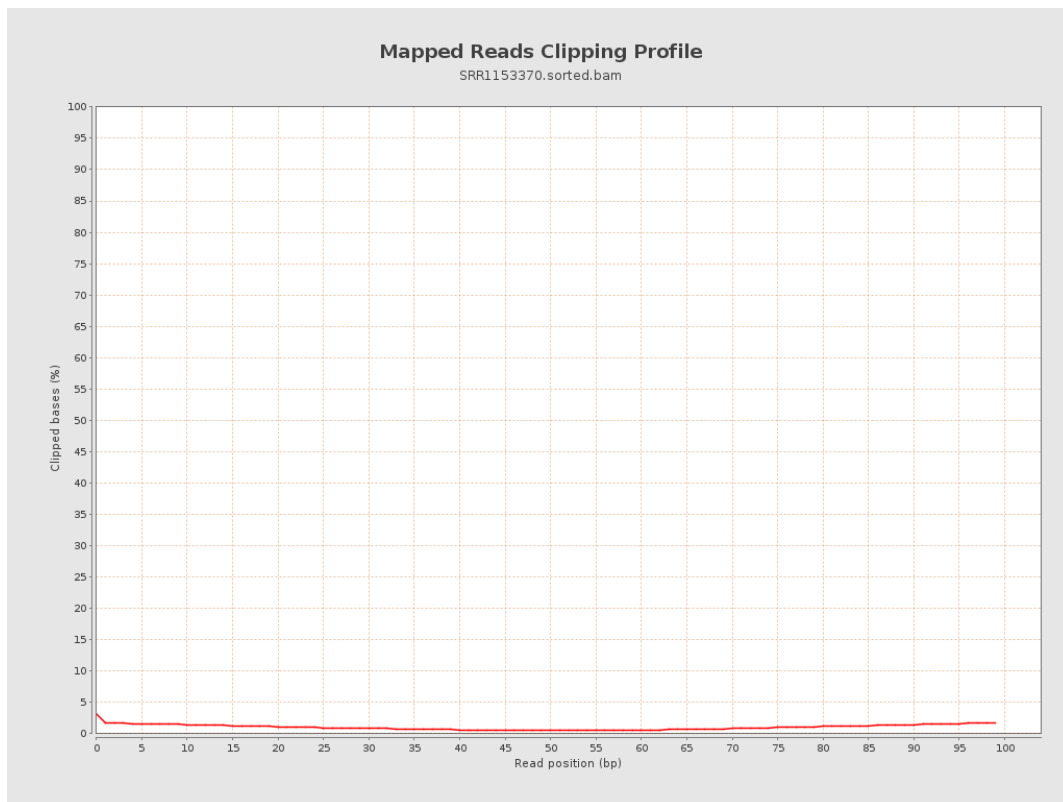
8. Results : Mapped Reads Nucleotide Content



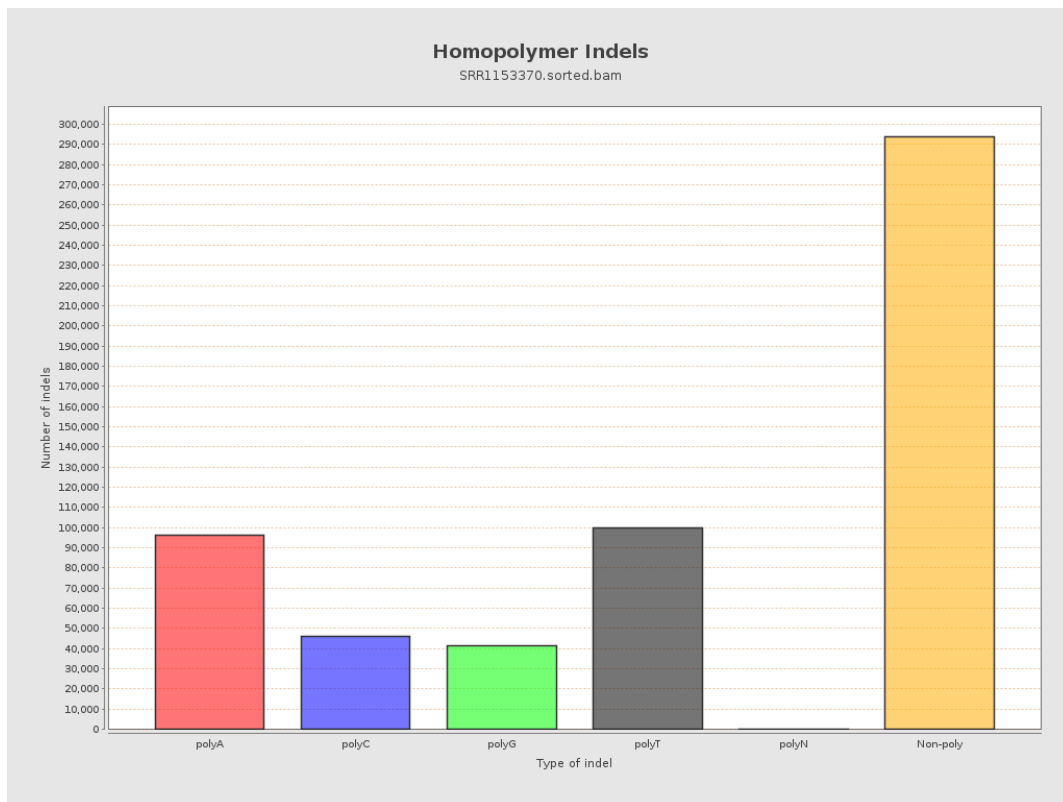
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

