

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 22:02:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153335.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_SRR1153335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 22:02:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	69,873,768
Mapped reads	69,085,529 / 98.87%
Unmapped reads	788,239 / 1.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	486,126 / 0.7%
Read min/max/mean length	30 / 100 / 100.28
Duplicated reads (estimated)	30,547,096 / 43.72%
Duplication rate	35.4%
Clipped reads	3,147,053 / 4.5%

2.2. ACGT Content

Number/percentage of A's	1,774,264,385 / 25.81%
Number/percentage of C's	1,658,392,882 / 24.13%
Number/percentage of T's	1,775,093,741 / 25.83%
Number/percentage of G's	1,665,485,675 / 24.23%
Number/percentage of N's	311,193 / 0%
GC Percentage	48.36%

2.3. Coverage

Mean	2.2207

Standard Deviation	24.2272
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2.4. Mapping Quality

Mean Mapping Quality	48.99
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2.5. Mismatches and indels

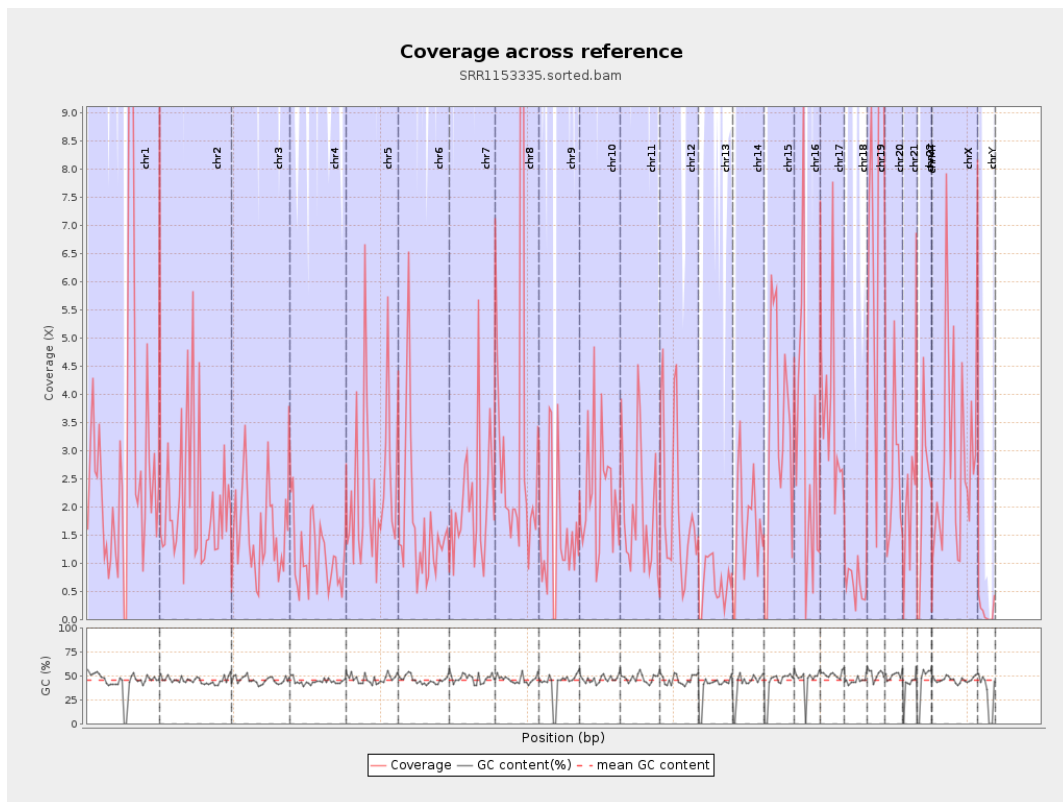
General error rate	0.31%
Mismatches	20,651,643
Insertions	581,293
Mapped reads with at least one insertion	0.83%
Deletions	404,912
Mapped reads with at least one deletion	0.58%
Homopolymer indels	47.86%

2.6. Chromosome stats

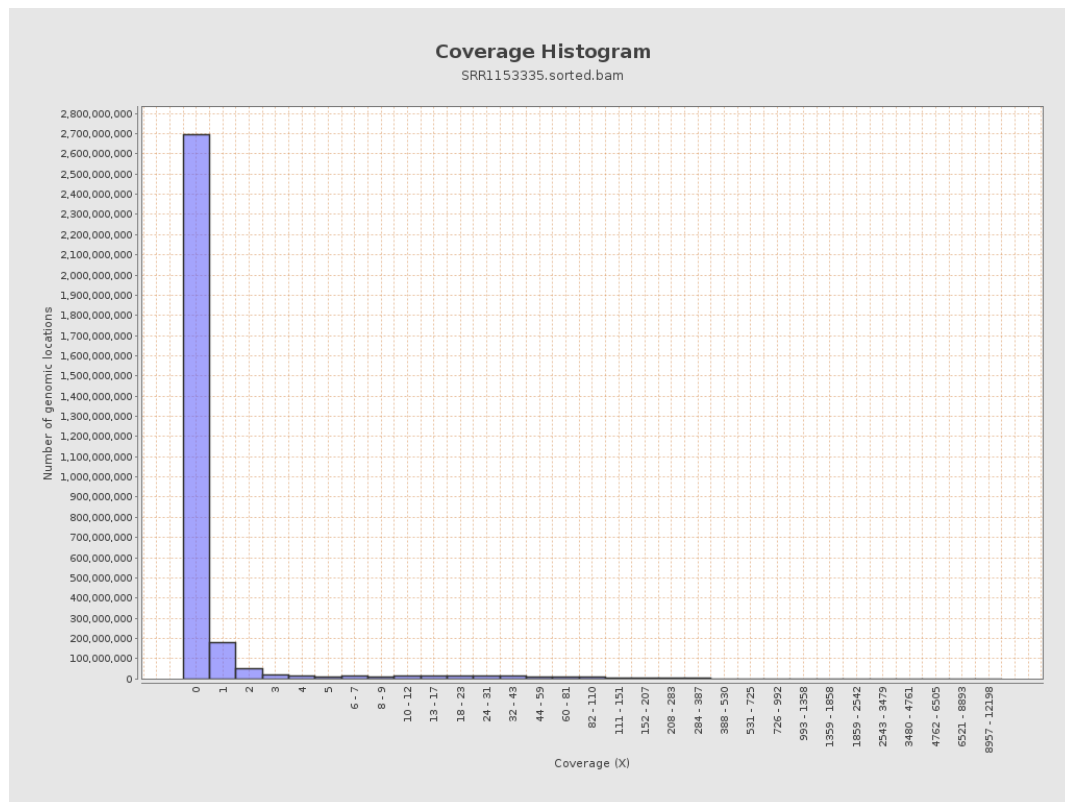
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	736894854	2.9564	24.2346
chr2	243199373	506158148	2.0812	17.749
chr3	198022430	312823000	1.5797	13.8023
chr4	191154276	214505594	1.1222	12.7922
chr5	180915260	432442749	2.3903	29.9272
chr6	171115067	283162400	1.6548	14.8038
chr7	159138663	331820180	2.0851	19.1618

chr8	146364022	489791564	3.3464	65.078
chr9	141213431	207072259	1.4664	14.3216
chr10	135534747	310266995	2.2892	20.3696
chr11	135006516	263496420	1.9517	14.9481
chr12	133851895	263871636	1.9714	16.089
chr13	115169878	73783491	0.6406	7.4675
chr14	107349540	176222958	1.6416	14.386
chr15	102531392	335414718	3.2713	25.2924
chr16	90354753	274463798	3.0376	22.5107
chr17	81195210	291208978	3.5865	22.7558
chr18	78077248	47943072	0.614	7.7846
chr19	59128983	467923399	7.9136	43.3861
chr20	63025520	169143266	2.6837	20.3366
chr21	48129895	116229730	2.4149	31.2632
chr22	51304566	116280251	2.2665	16.84
chrMT	16571	1999	0.1206	0.3513
chrX	155270560	444953512	2.8657	26.0053
chrY	59373566	8603644	0.1449	6.5098

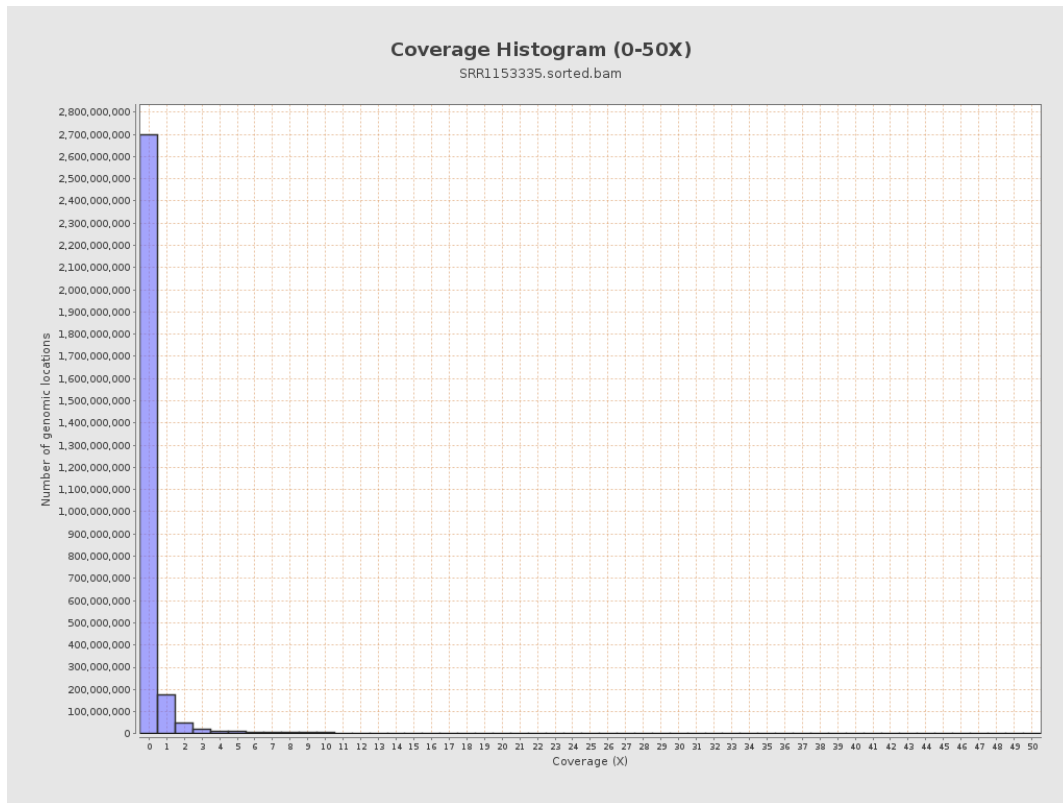
3. Results : Coverage across reference



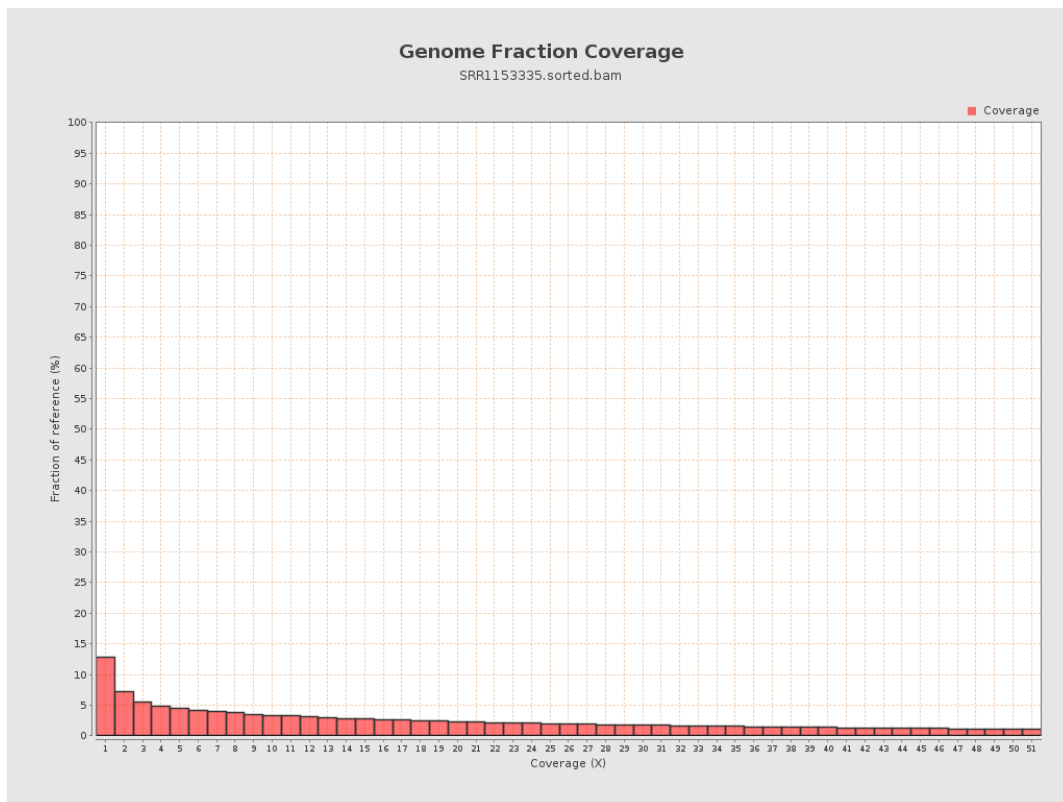
4. Results : Coverage Histogram



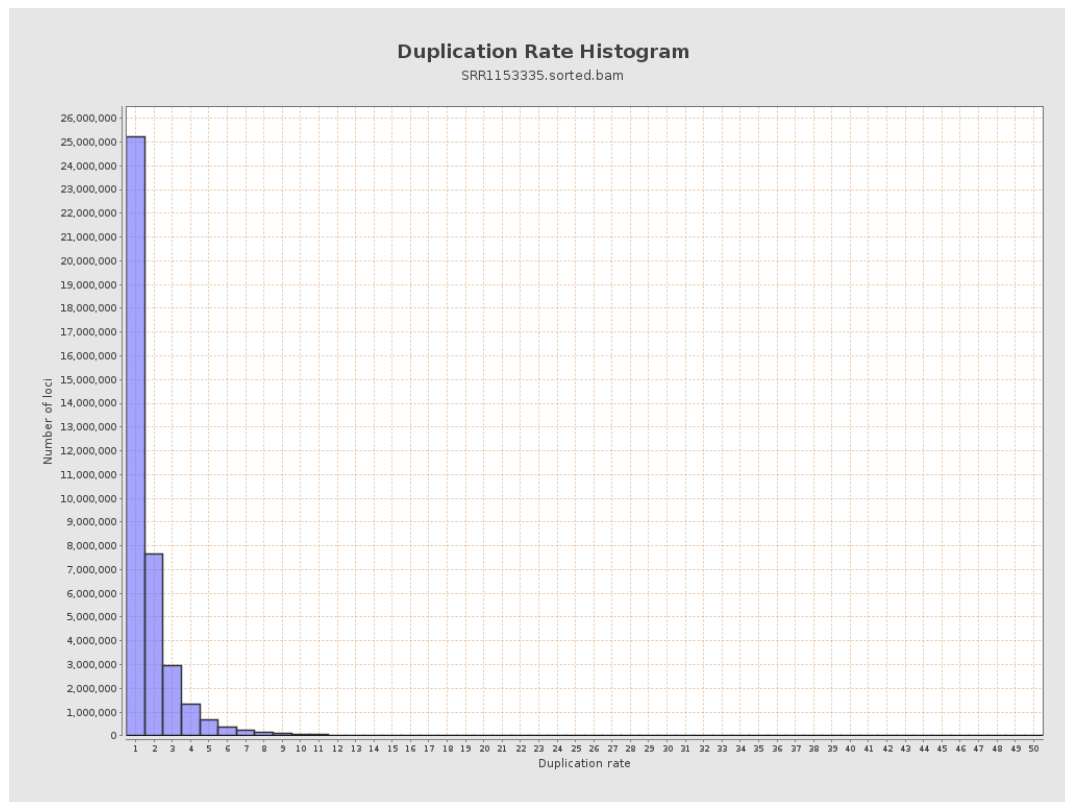
5. Results : Coverage Histogram (0-50X)



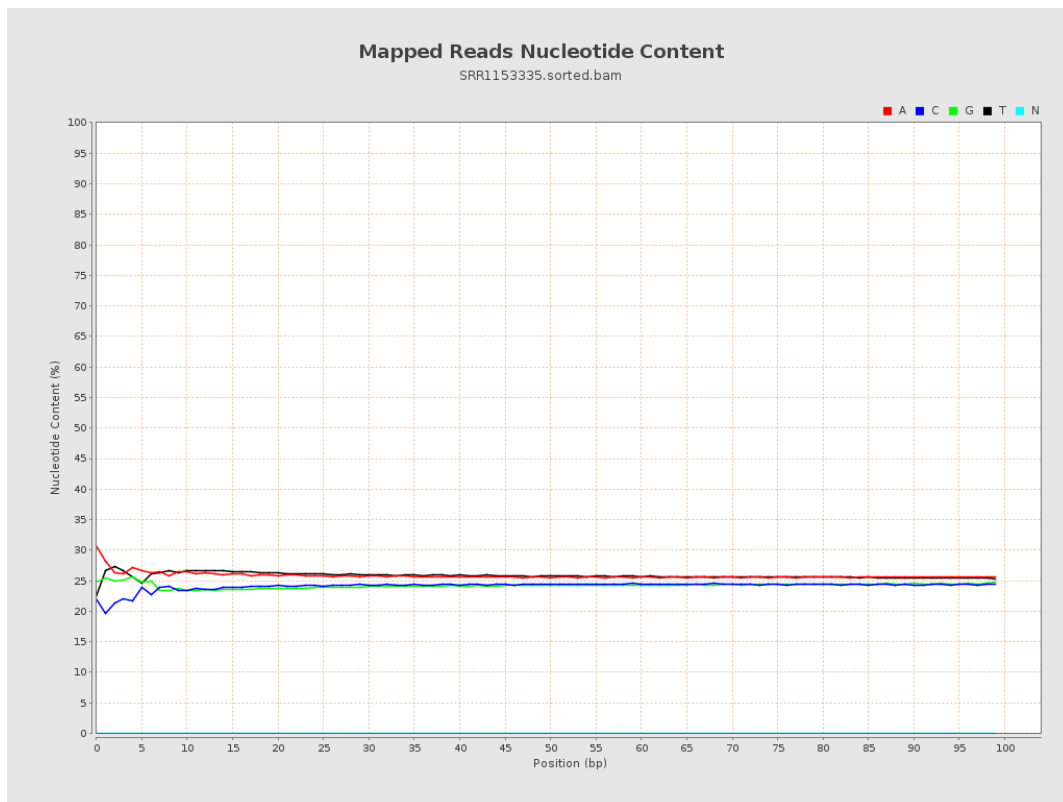
6. Results : Genome Fraction Coverage



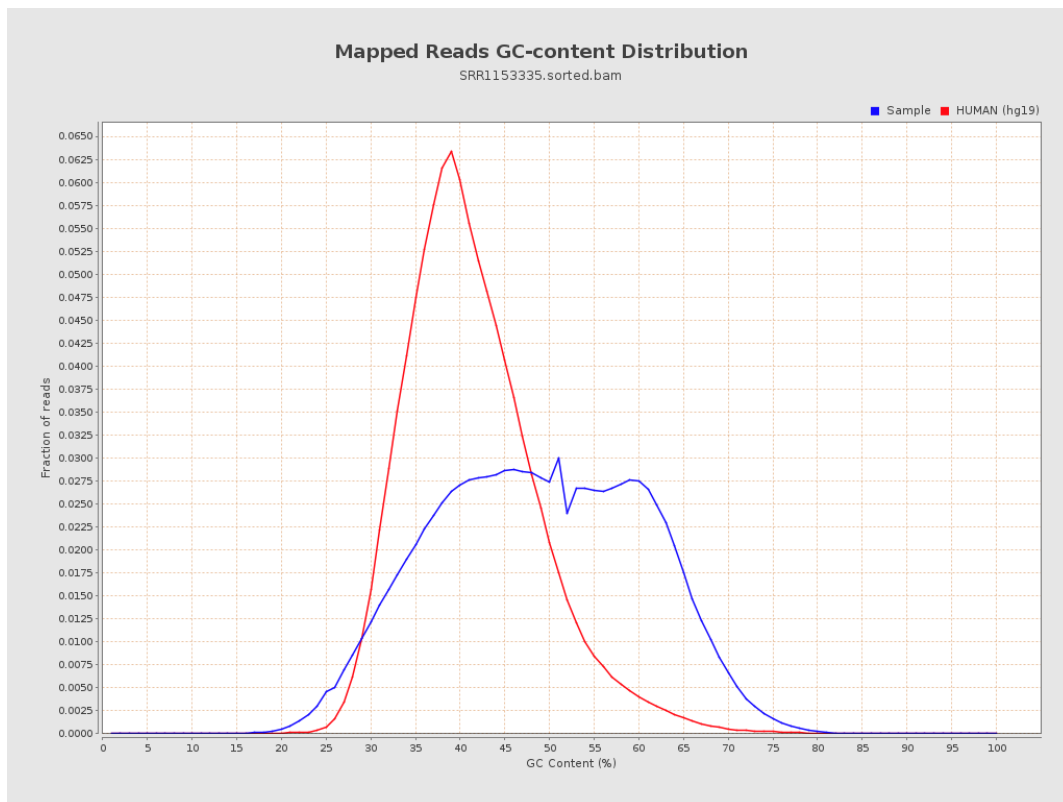
7. Results : Duplication Rate Histogram



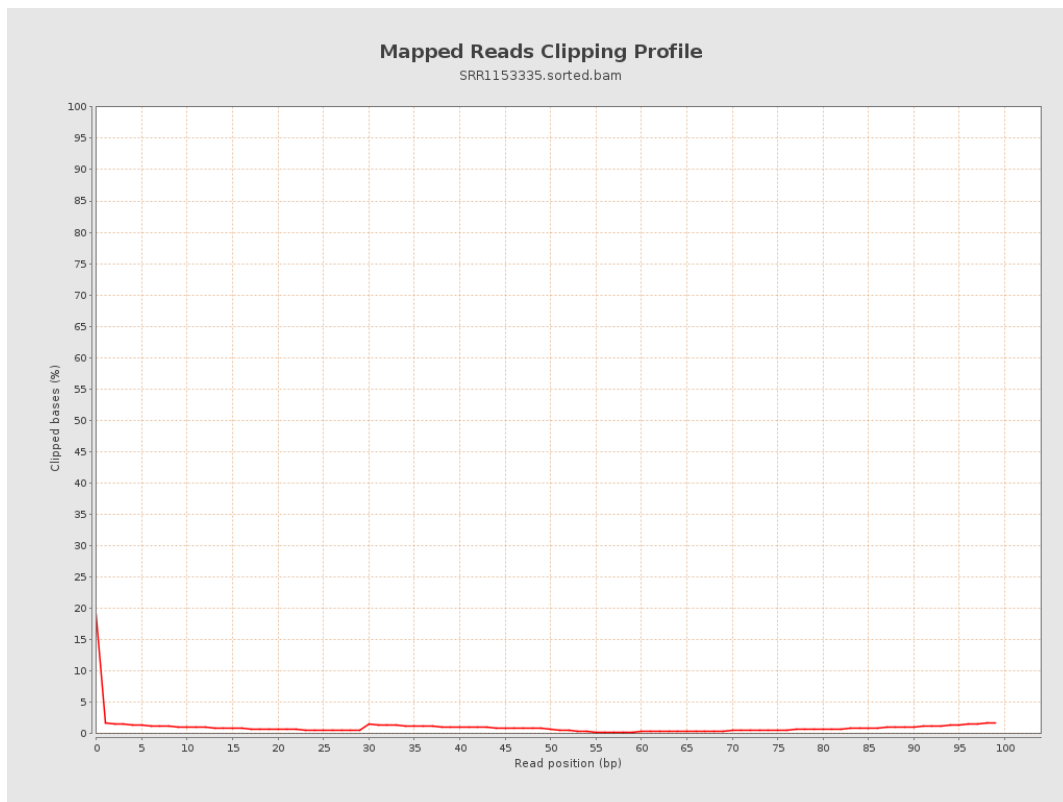
8. Results : Mapped Reads Nucleotide Content



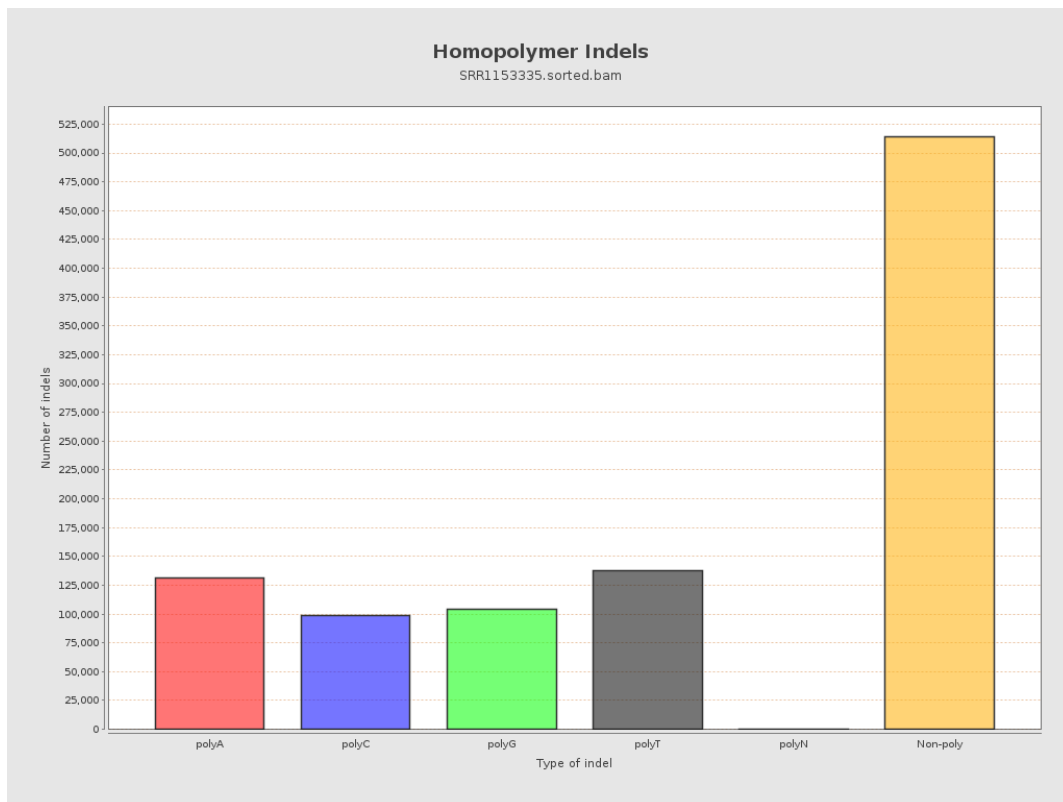
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

