

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 06:27:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153352.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_SRR1153352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153352.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 06:27:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,492,040
Mapped reads	36,250,522 / 99.34%
Unmapped reads	241,518 / 0.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	239,887 / 0.66%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	21,104,103 / 57.83%
Duplication rate	46.32%
Clipped reads	17,248,995 / 47.27%

2.2. ACGT Content

Number/percentage of A's	829,767,322 / 26.49%
Number/percentage of C's	743,029,531 / 23.72%
Number/percentage of T's	855,862,361 / 27.32%
Number/percentage of G's	703,389,341 / 22.45%
Number/percentage of N's	884,792 / 0.03%
GC Percentage	46.17%

2.3. Coverage

Mean	1.0122

Standard Deviation	11.963
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2.4. Mapping Quality

Mean Mapping Quality	49.9
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2.5. Mismatches and indels

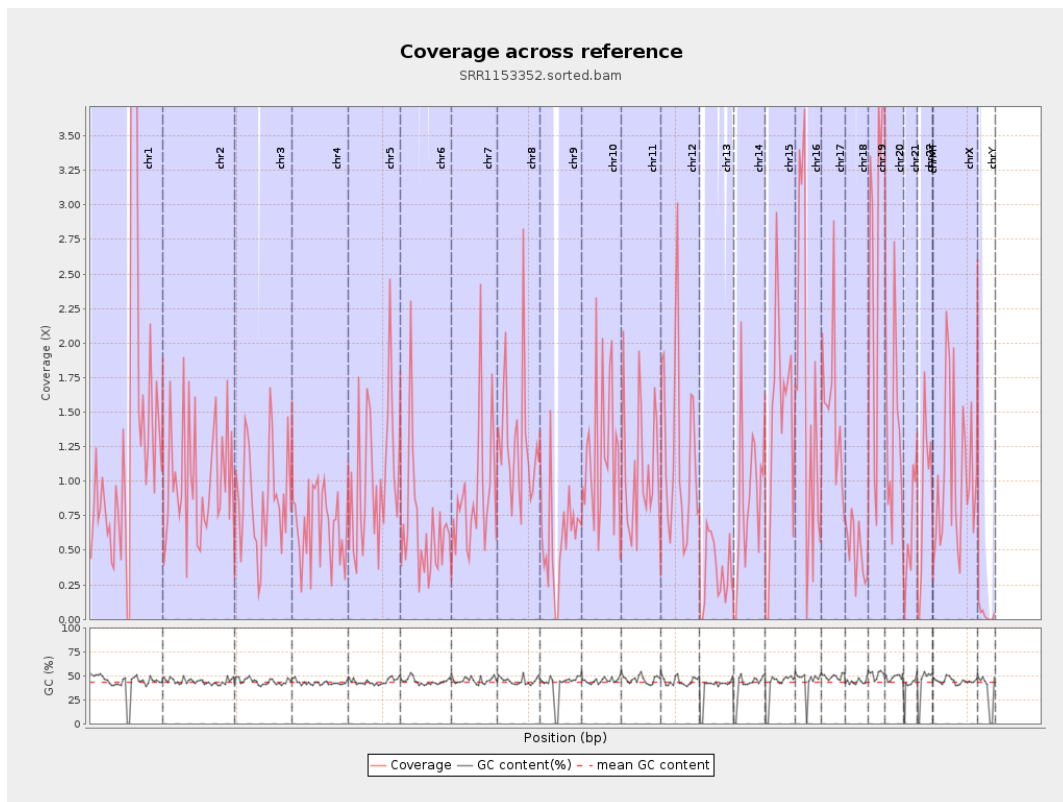
General error rate	0.23%
Mismatches	6,857,446
Insertions	323,773
Mapped reads with at least one insertion	0.88%
Deletions	248,645
Mapped reads with at least one deletion	0.68%
Homopolymer indels	48.95%

2.6. Chromosome stats

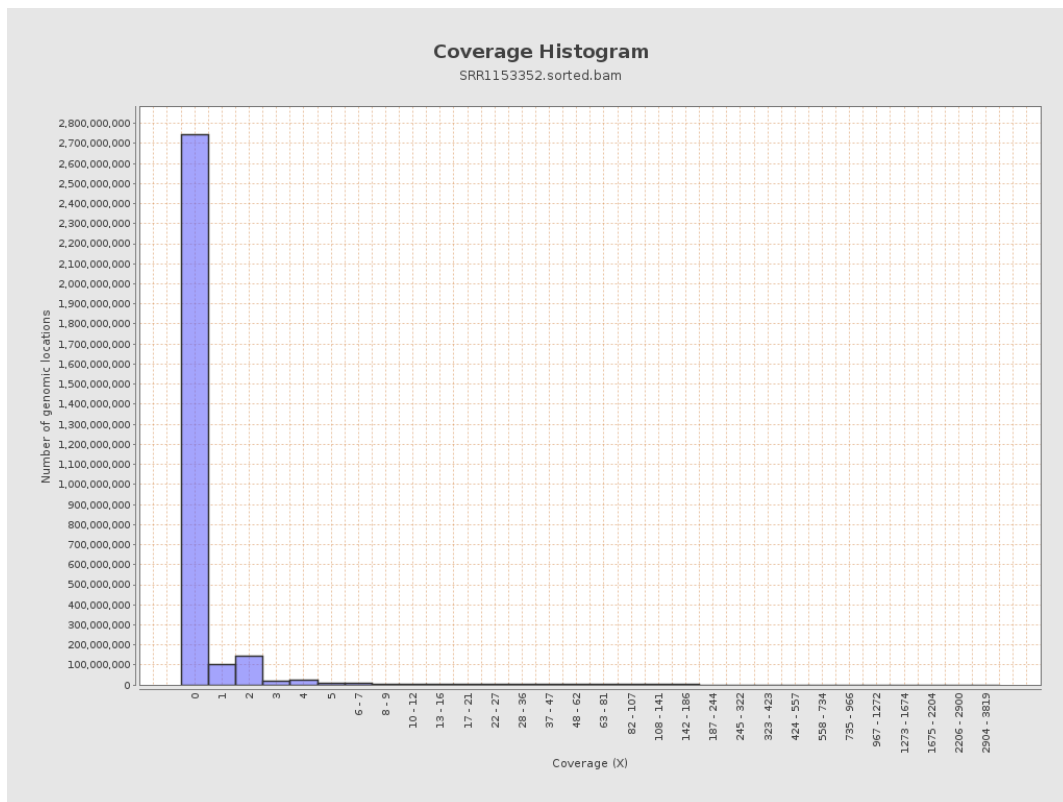
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	331377186	1.3295	15.3695
chr2	243199373	245395405	1.009	11.4262
chr3	198022430	173019007	0.8737	10.0877
chr4	191154276	129673467	0.6784	8.6081
chr5	180915260	188868638	1.044	11.5938
chr6	171115067	111014793	0.6488	8.3298
chr7	159138663	143564289	0.9021	10.8416

chr8	146364022	187699986	1.2824	15.5032
chr9	141213431	81423919	0.5766	7.7467
chr10	135534747	164607693	1.2145	12.9336
chr11	135006516	144212461	1.0682	12.2984
chr12	133851895	165323065	1.2351	12.9579
chr13	115169878	39873171	0.3462	4.7815
chr14	107349540	92658438	0.8631	9.5625
chr15	102531392	141333626	1.3784	13.7856
chr16	90354753	142829090	1.5808	16.8763
chr17	81195210	124977218	1.5392	13.9297
chr18	78077248	39265098	0.5029	6.9687
chr19	59128983	158477747	2.6802	22.8744
chr20	63025520	82817843	1.314	14.3347
chr21	48129895	31895051	0.6627	8.6026
chr22	51304566	46172297	0.9	10.6356
chrMT	16571	4634	0.2796	0.8867
chrX	155270560	164833925	1.0616	12.1199
chrY	59373566	2121589	0.0357	1.8335

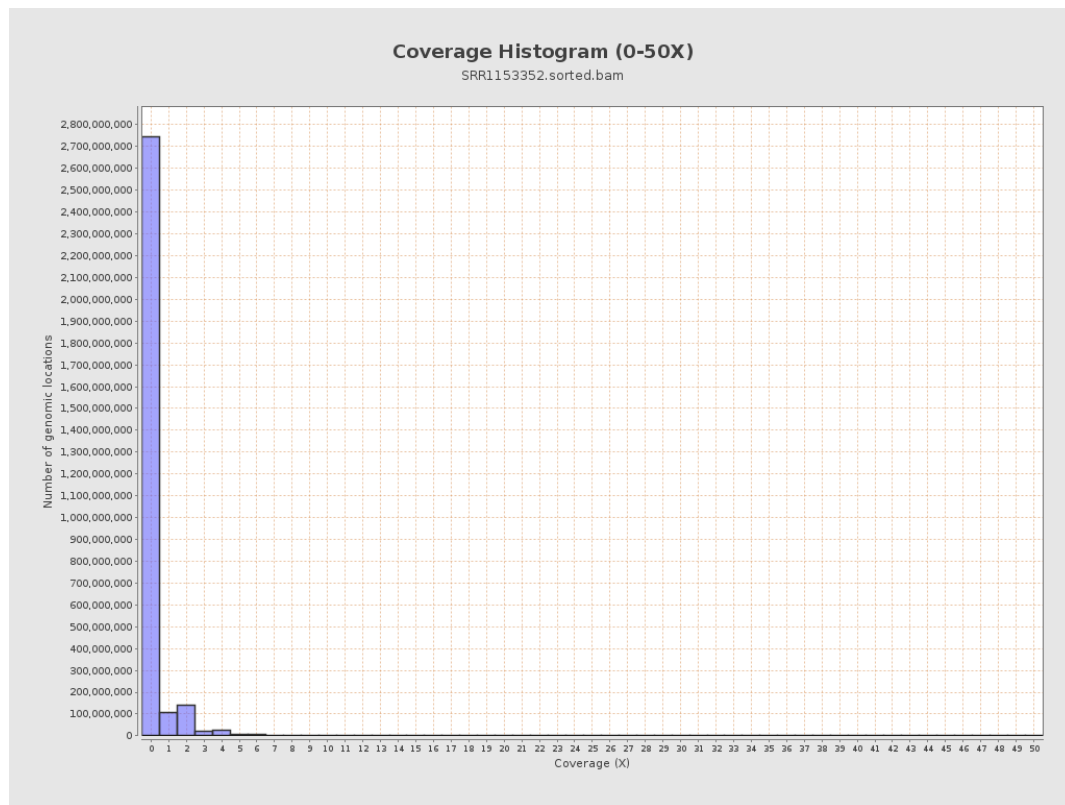
3. Results : Coverage across reference



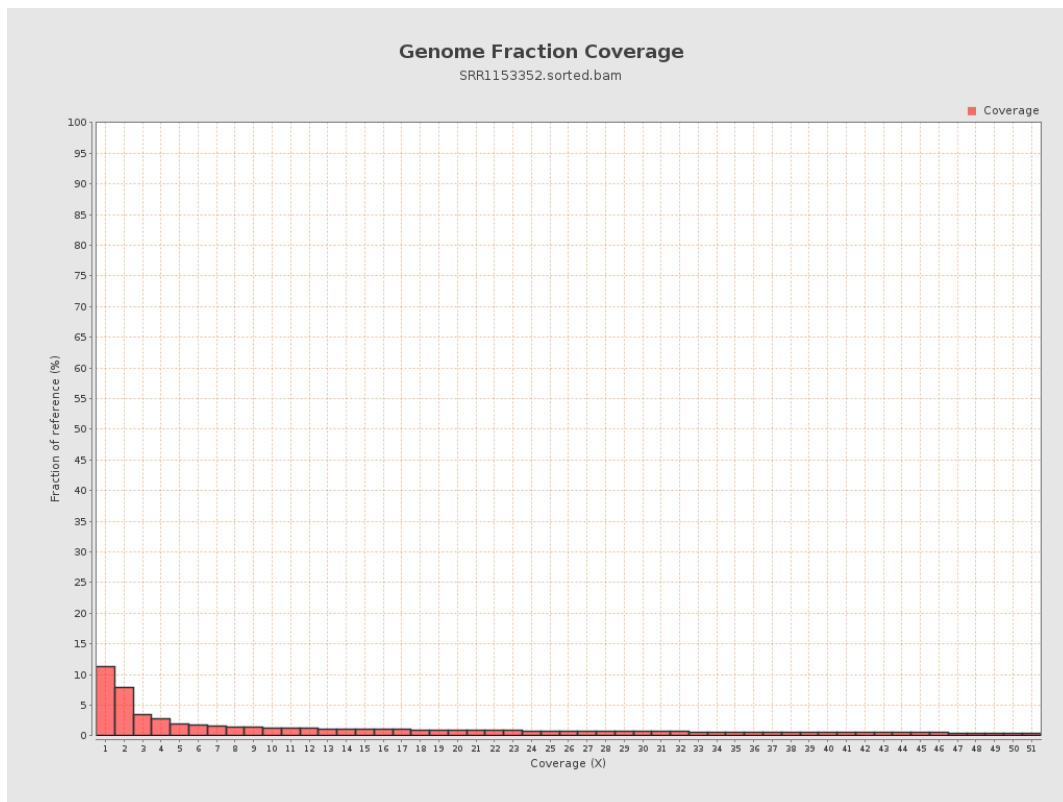
4. Results : Coverage Histogram



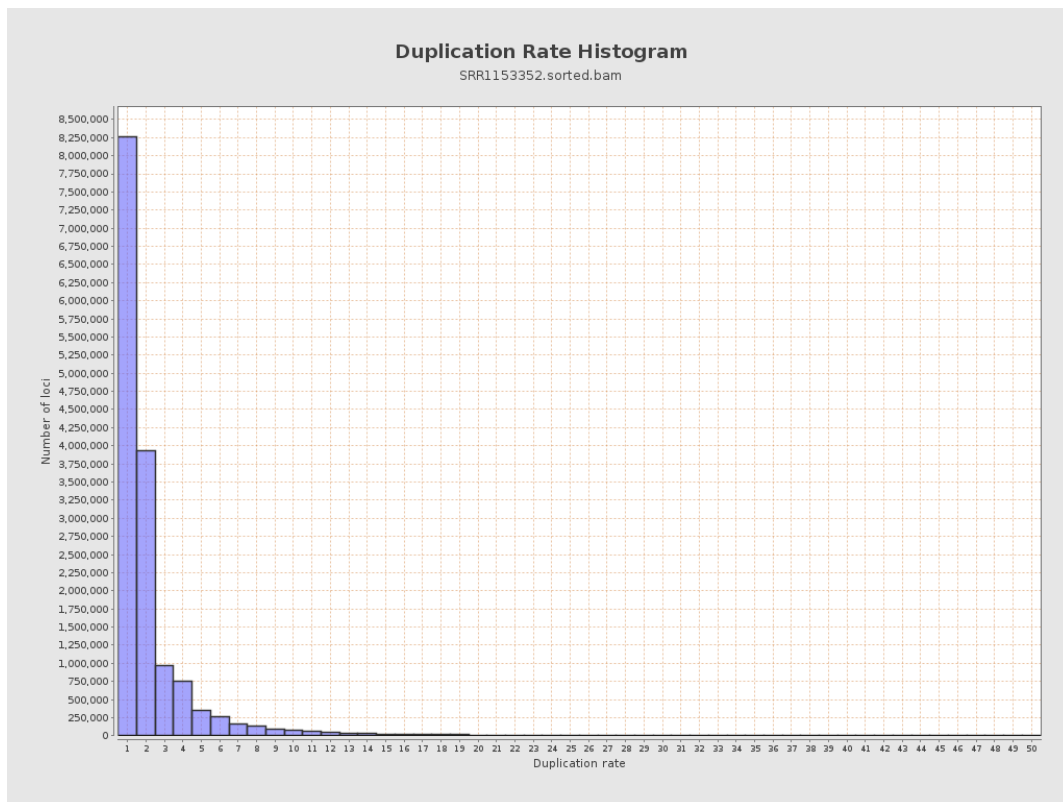
5. Results : Coverage Histogram (0-50X)



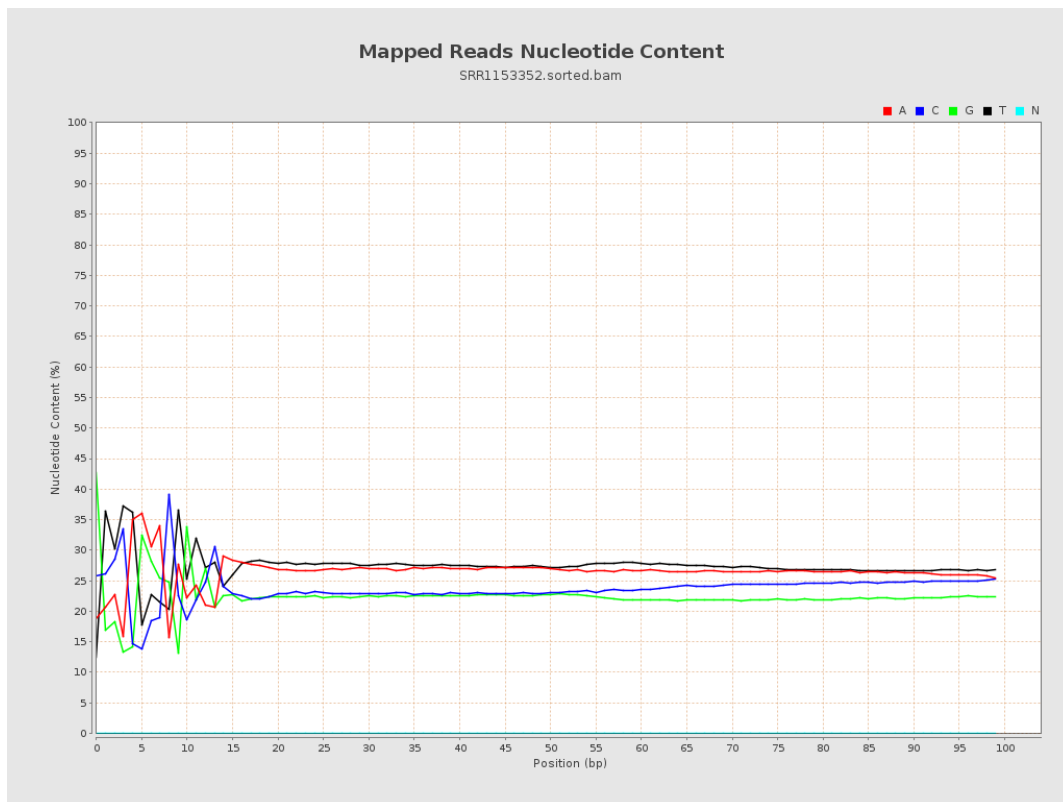
6. Results : Genome Fraction Coverage



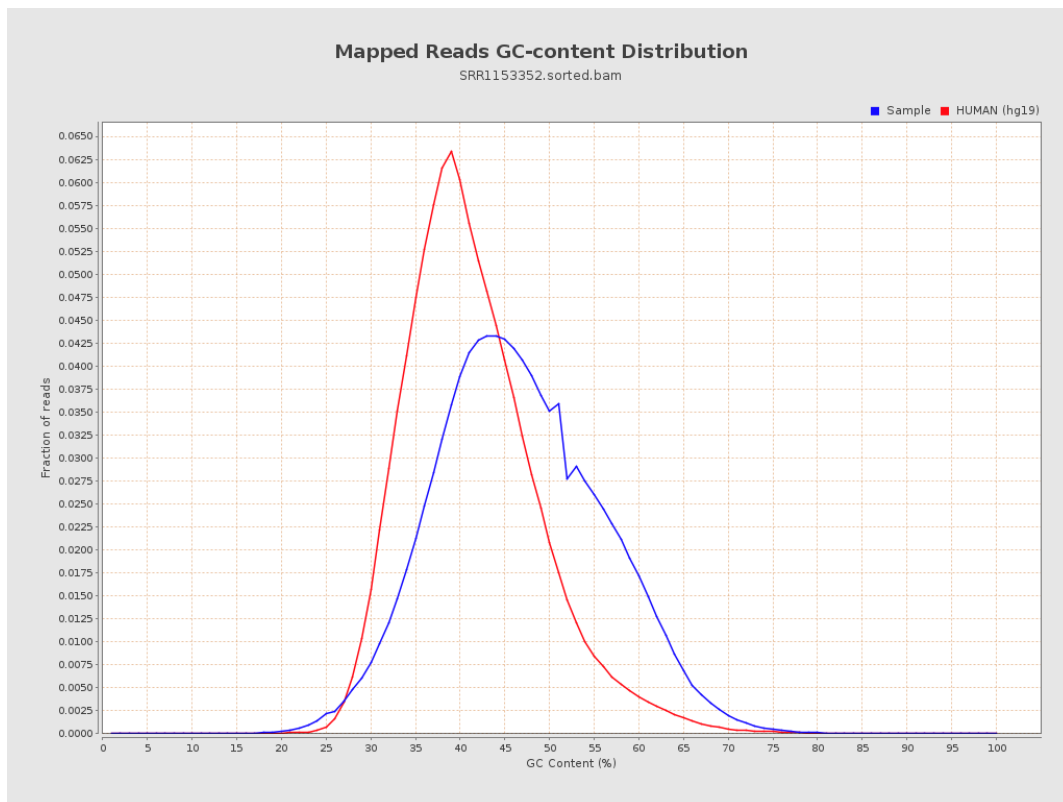
7. Results : Duplication Rate Histogram



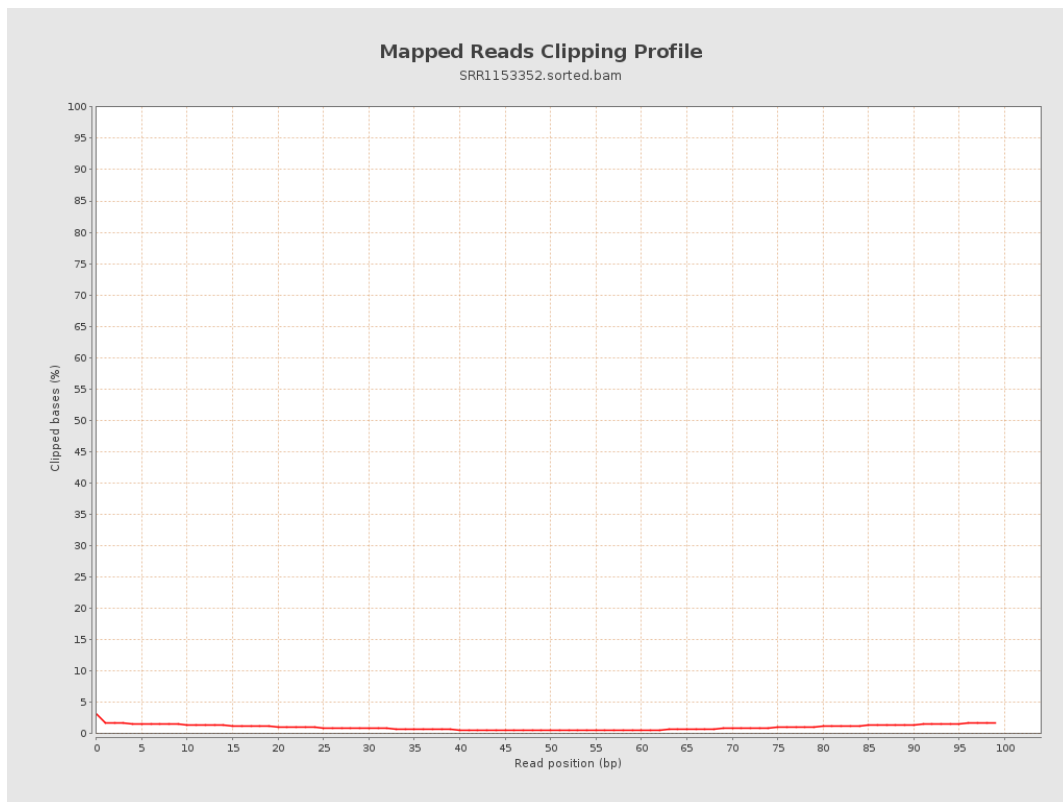
8. Results : Mapped Reads Nucleotide Content



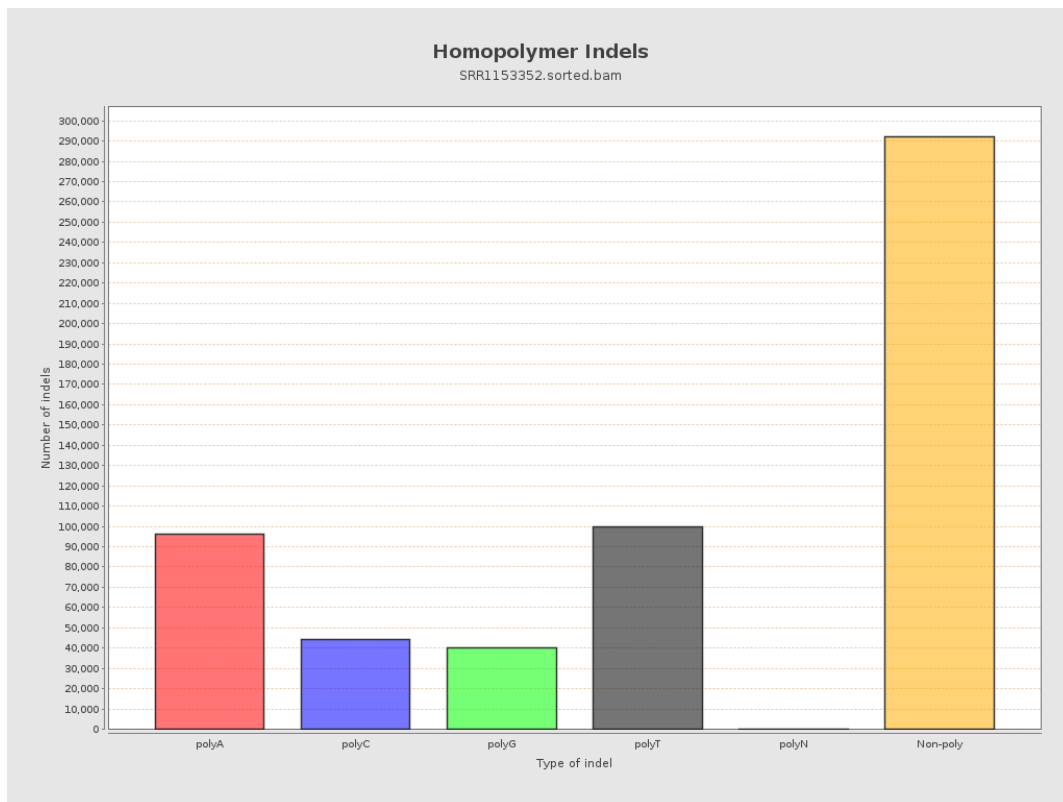
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

