

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 09:47:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153399.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_SRR1153399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153399.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 09:47:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,787,396
Mapped reads	50,176,749 / 98.8%
Unmapped reads	610,647 / 1.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	356,837 / 0.7%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	23,276,932 / 45.83%
Duplication rate	31.01%
Clipped reads	7,084,220 / 13.95%

2.2. ACGT Content

Number/percentage of A's	1,289,164,918 / 26.58%
Number/percentage of C's	1,131,122,176 / 23.32%
Number/percentage of T's	1,313,850,277 / 27.09%
Number/percentage of G's	1,114,035,349 / 22.97%
Number/percentage of N's	1,935,106 / 0.04%
GC Percentage	46.29%

2.3. Coverage

Mean	1.567

Standard Deviation	13.5485
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2.4. Mapping Quality

Mean Mapping Quality	50.24
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2.5. Mismatches and indels

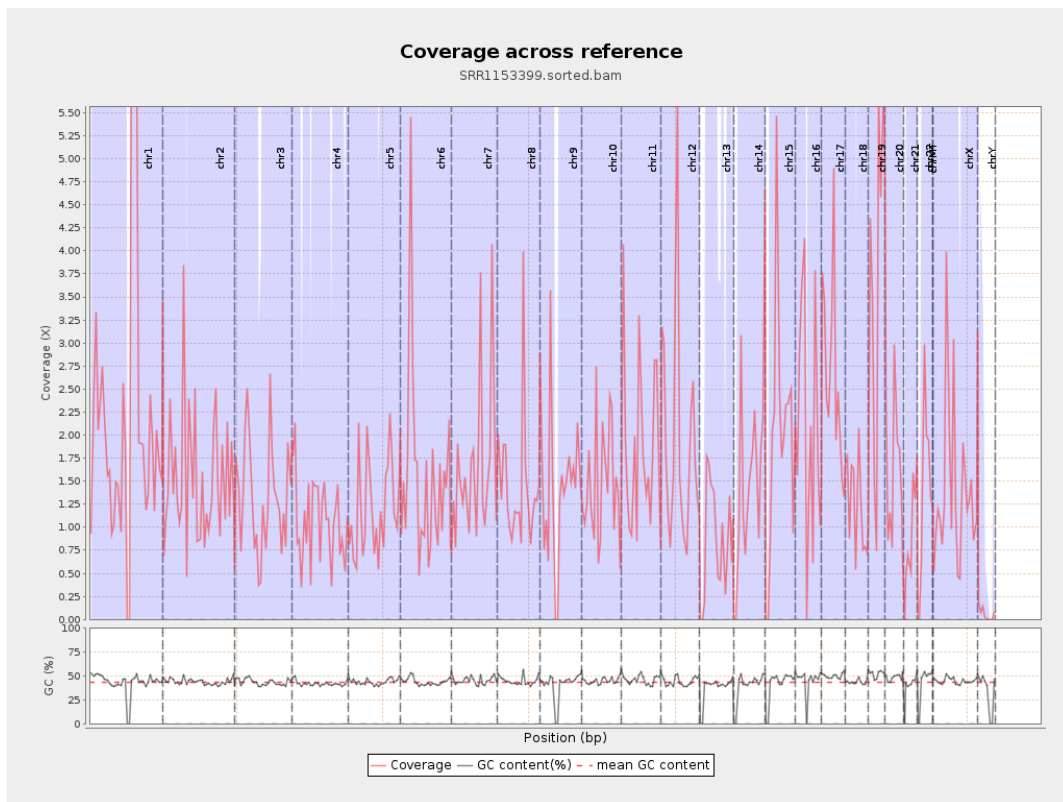
General error rate	0.34%
Mismatches	15,502,832
Insertions	503,113
Mapped reads with at least one insertion	0.99%
Deletions	426,803
Mapped reads with at least one deletion	0.84%
Homopolymer indels	49.12%

2.6. Chromosome stats

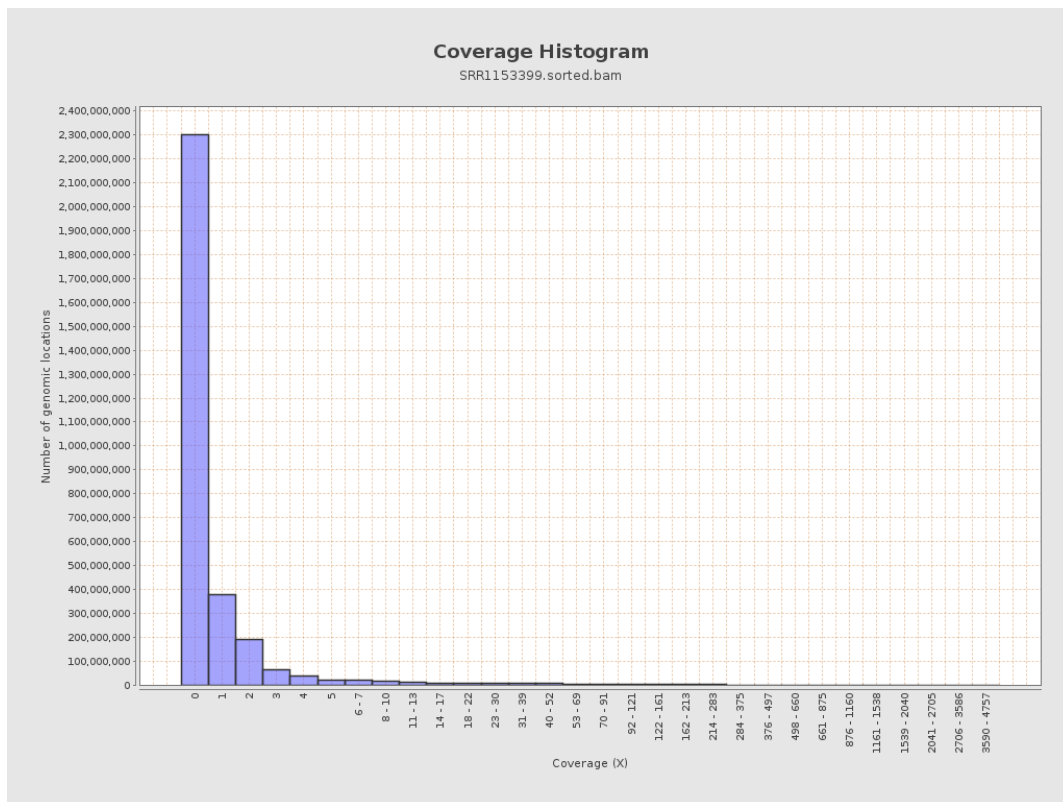
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	535727633	2.1494	17.4904
chr2	243199373	371410442	1.5272	12.5778
chr3	198022430	262514882	1.3257	10.0426
chr4	191154276	205249806	1.0737	8.9693
chr5	180915260	221169687	1.2225	9.6453
chr6	171115067	261496265	1.5282	13.233
chr7	159138663	262670178	1.6506	15.7576

chr8	146364022	210219921	1.4363	15.6429
chr9	141213431	197245625	1.3968	12.1216
chr10	135534747	199367513	1.471	11.346
chr11	135006516	252278456	1.8686	13.6001
chr12	133851895	268296581	2.0044	16.7511
chr13	115169878	97686486	0.8482	7.6917
chr14	107349540	153728184	1.432	11.9161
chr15	102531392	196894357	1.9203	15.6357
chr16	90354753	185072389	2.0483	15.3475
chr17	81195210	219593329	2.7045	19.2624
chr18	78077248	97615784	1.2502	10.4426
chr19	59128983	215742245	3.6487	25.8243
chr20	63025520	100640885	1.5968	11.1564
chr21	48129895	44071103	0.9157	7.4433
chr22	51304566	71034929	1.3846	12.521
chrMT	16571	8522	0.5143	1.4396
chrX	155270560	217763311	1.4025	13.6964
chrY	59373566	3522718	0.0593	2.3488

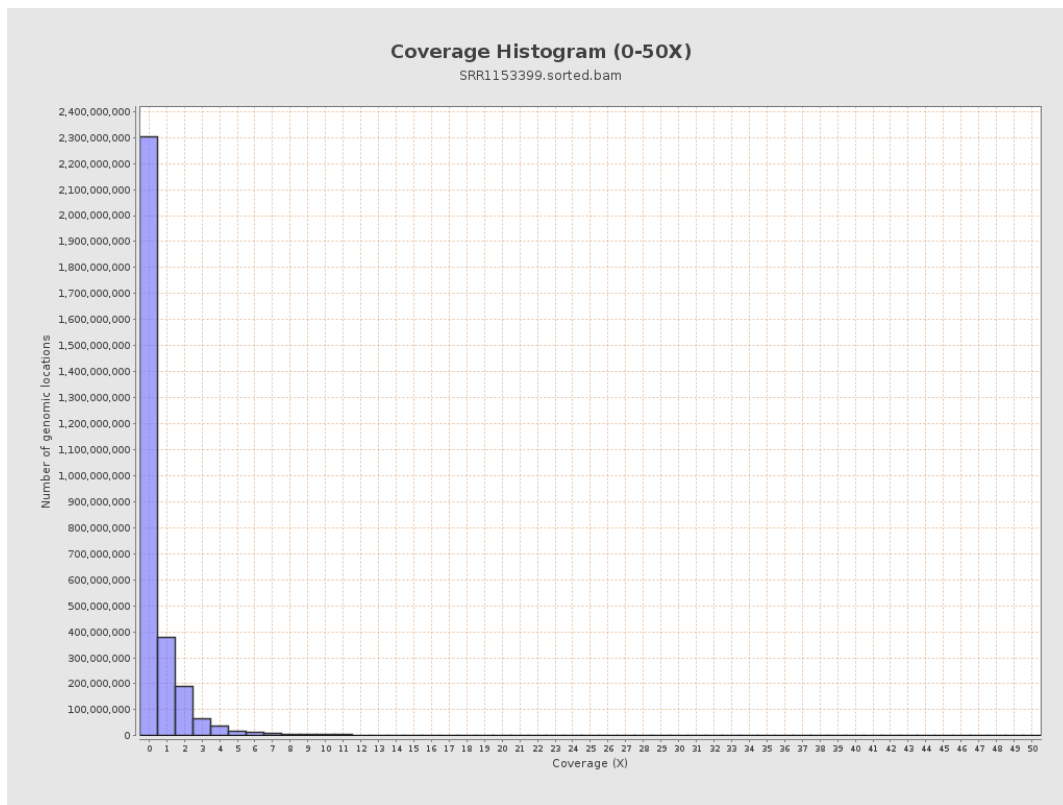
3. Results : Coverage across reference



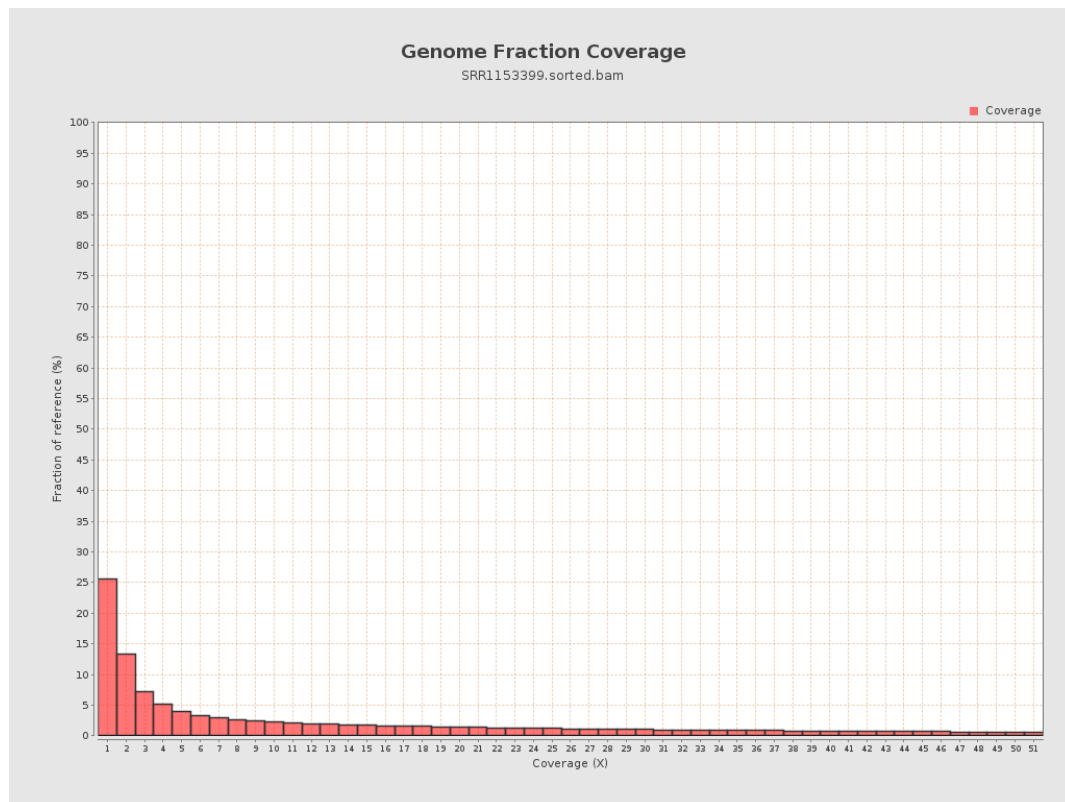
4. Results : Coverage Histogram



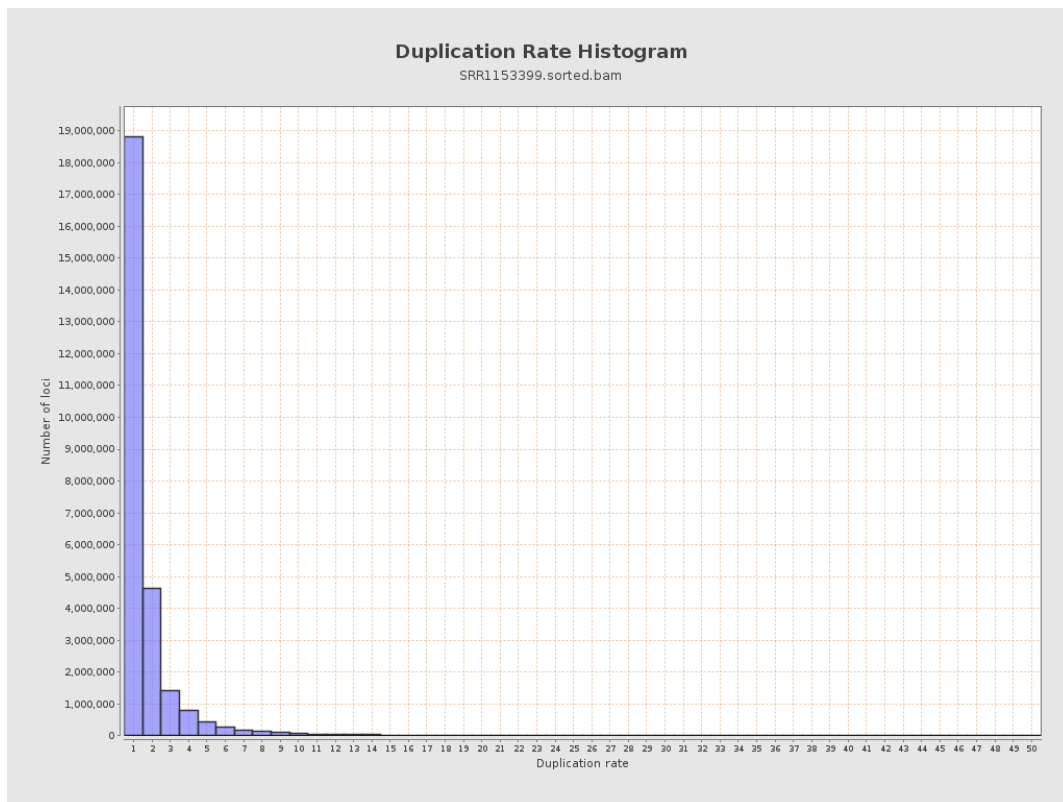
5. Results : Coverage Histogram (0-50X)



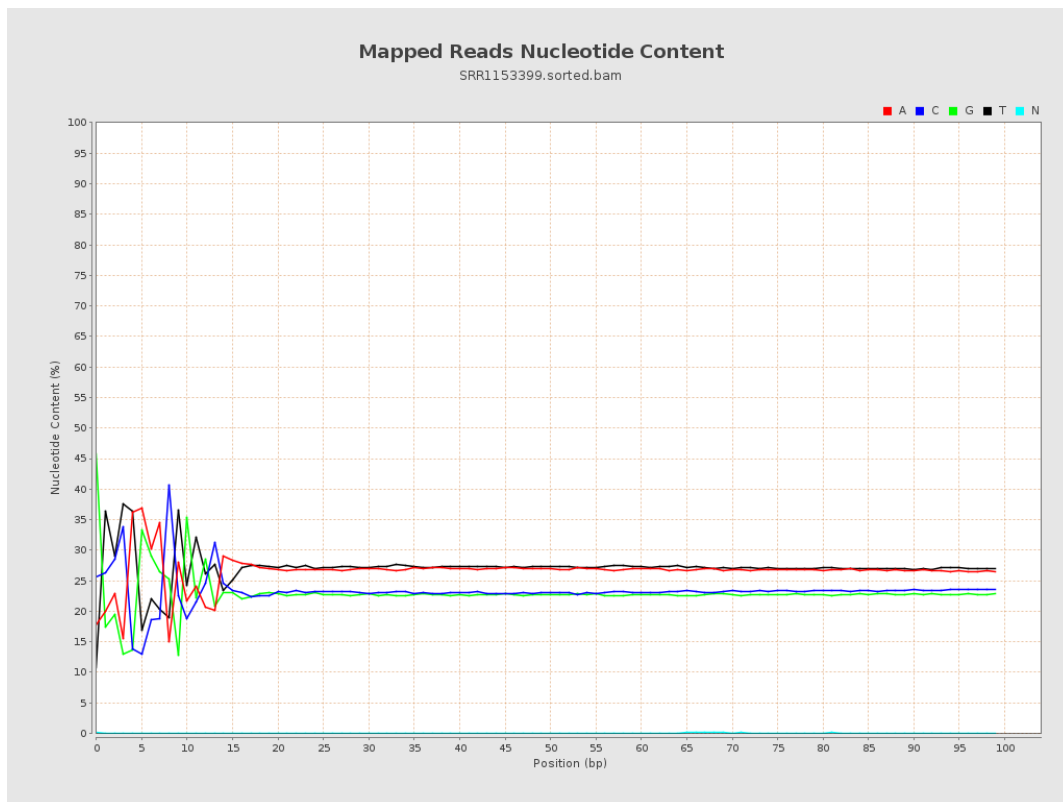
6. Results : Genome Fraction Coverage



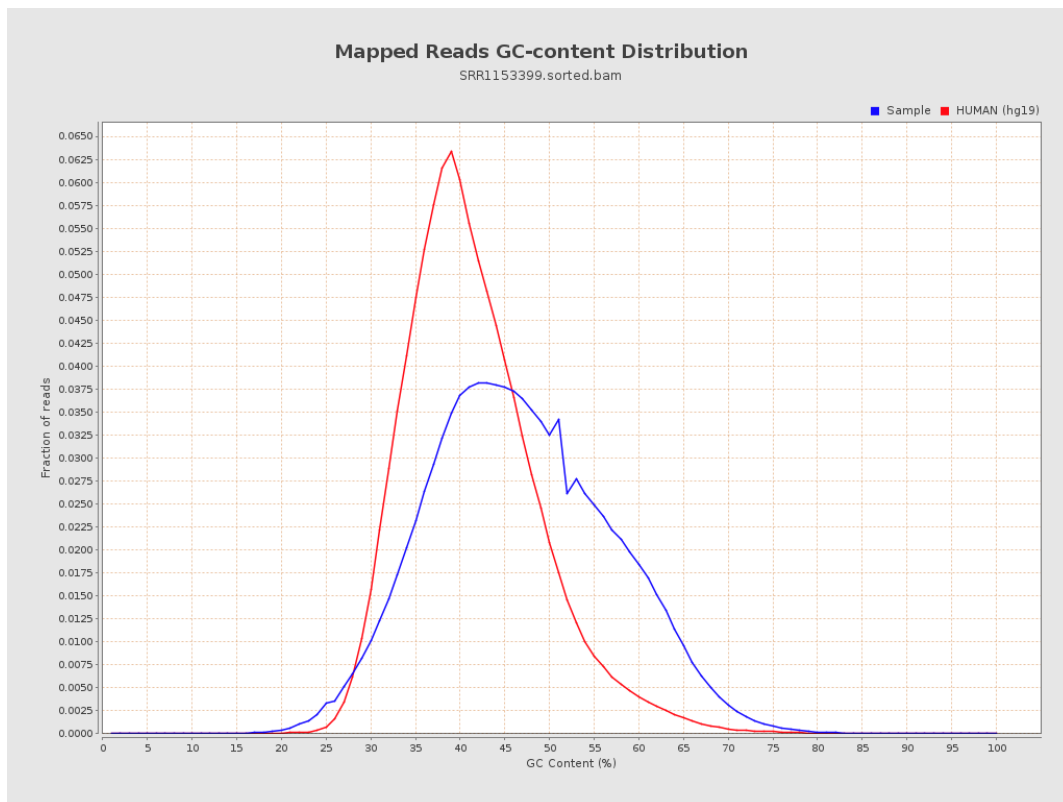
7. Results : Duplication Rate Histogram



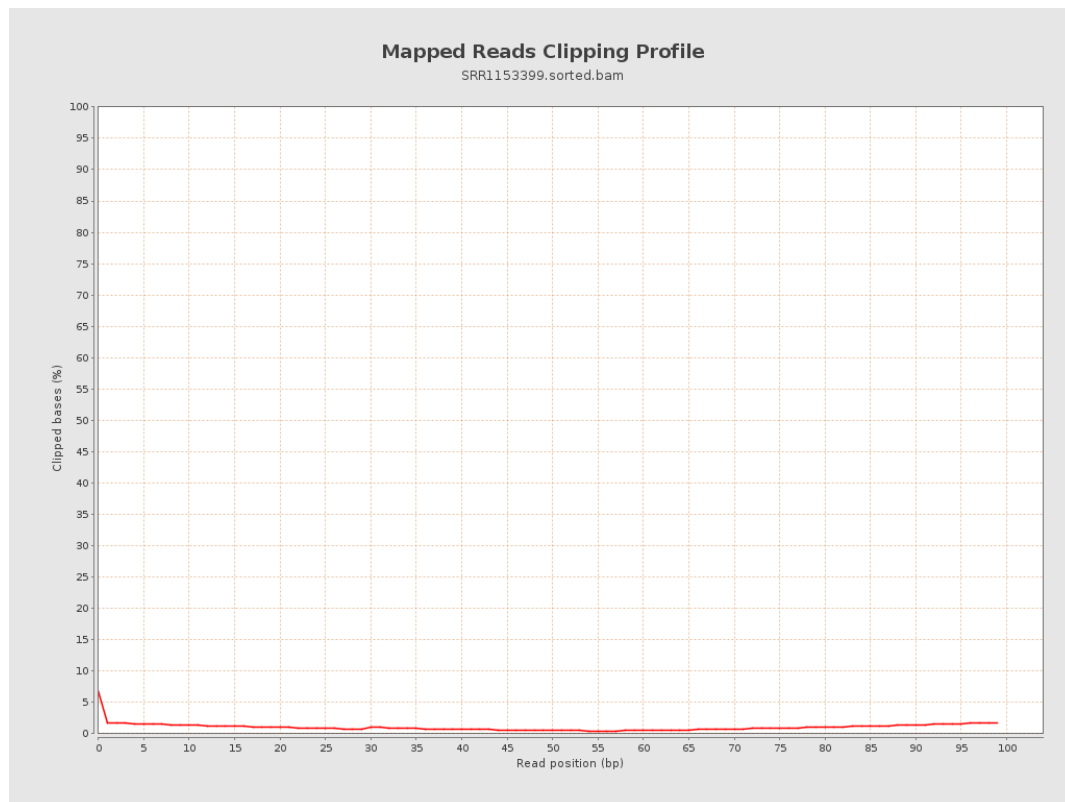
8. Results : Mapped Reads Nucleotide Content



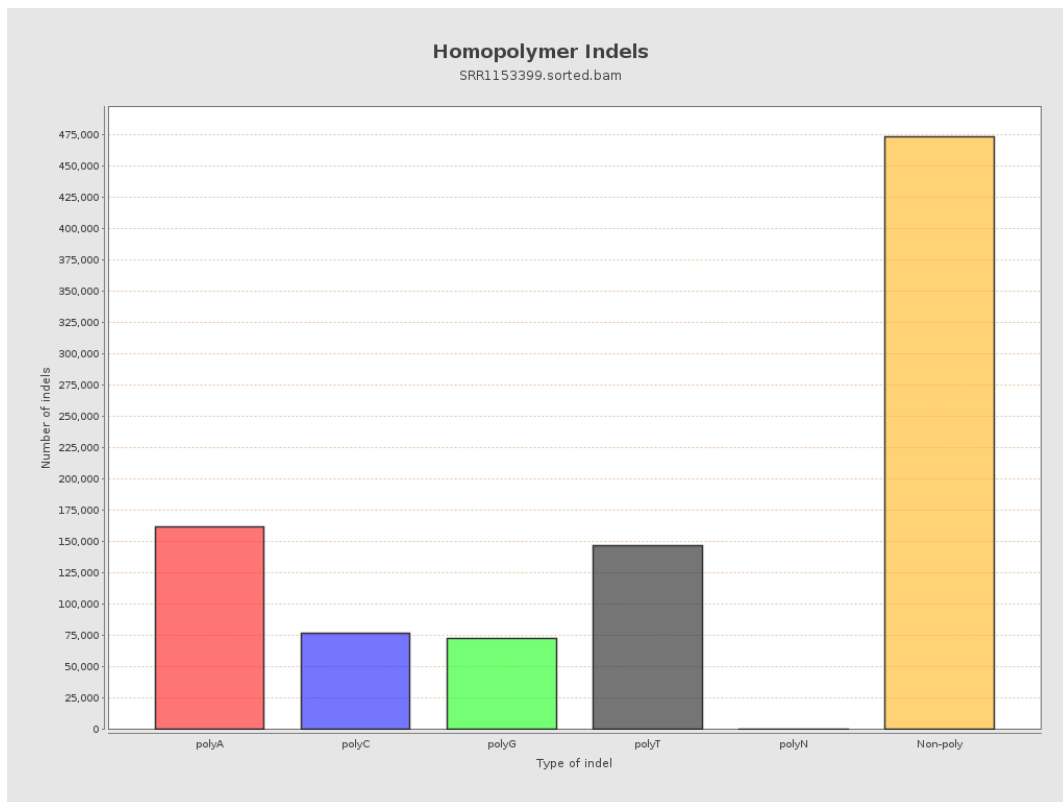
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

