

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 03:51:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153323.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_SRR1153323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 03:51:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	341,589,716
Mapped reads	331,604,824 / 97.08%
Unmapped reads	9,984,892 / 2.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,321,494 / 0.68%
Read min/max/mean length	30 / 100 / 100.28
Duplicated reads (estimated)	286,382,609 / 83.84%
Duplication rate	79.69%
Clipped reads	35,089,935 / 10.27%

2.2. ACGT Content

Number/percentage of A's	6,927,960,505 / 21.27%
Number/percentage of C's	9,375,944,433 / 28.79%
Number/percentage of T's	6,958,366,318 / 21.36%
Number/percentage of G's	9,298,020,283 / 28.55%
Number/percentage of N's	8,973,385 / 0.03%
GC Percentage	57.34%

2.3. Coverage

Mean	10.5223

Standard Deviation	163.9733
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2.4. Mapping Quality

Mean Mapping Quality	48.27
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2.5. Mismatches and indels

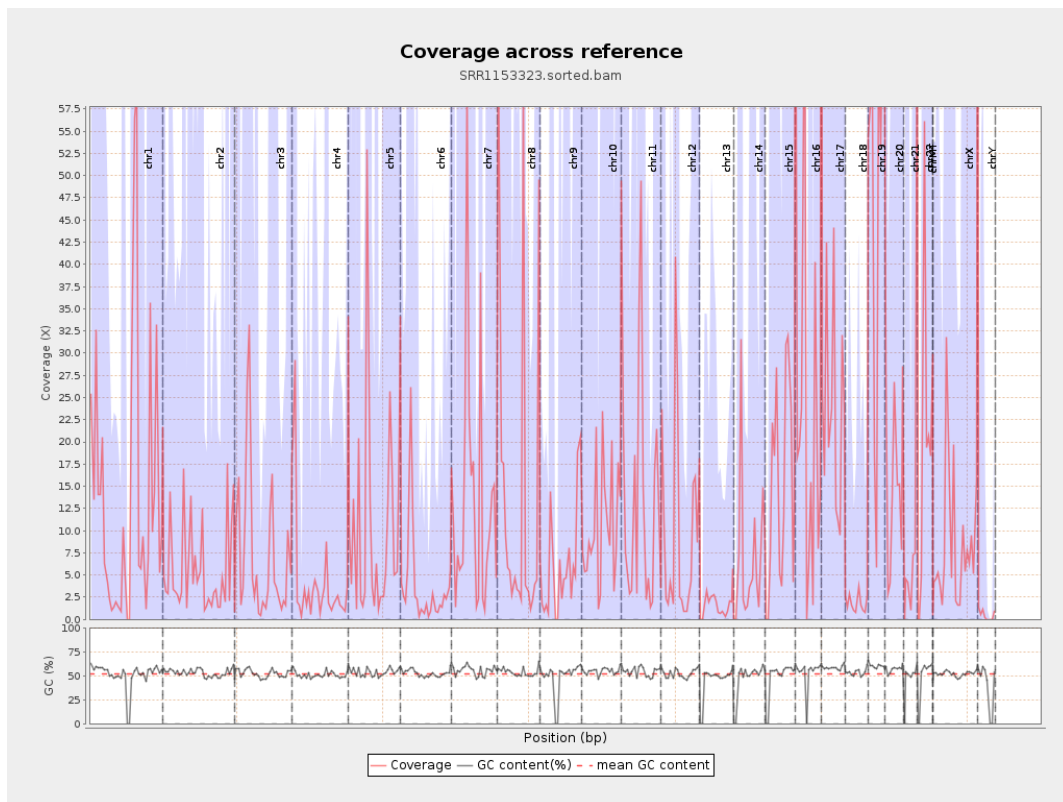
General error rate	0.37%
Mismatches	116,357,231
Insertions	1,439,703
Mapped reads with at least one insertion	0.42%
Deletions	1,582,005
Mapped reads with at least one deletion	0.47%
Homopolymer indels	39.11%

2.6. Chromosome stats

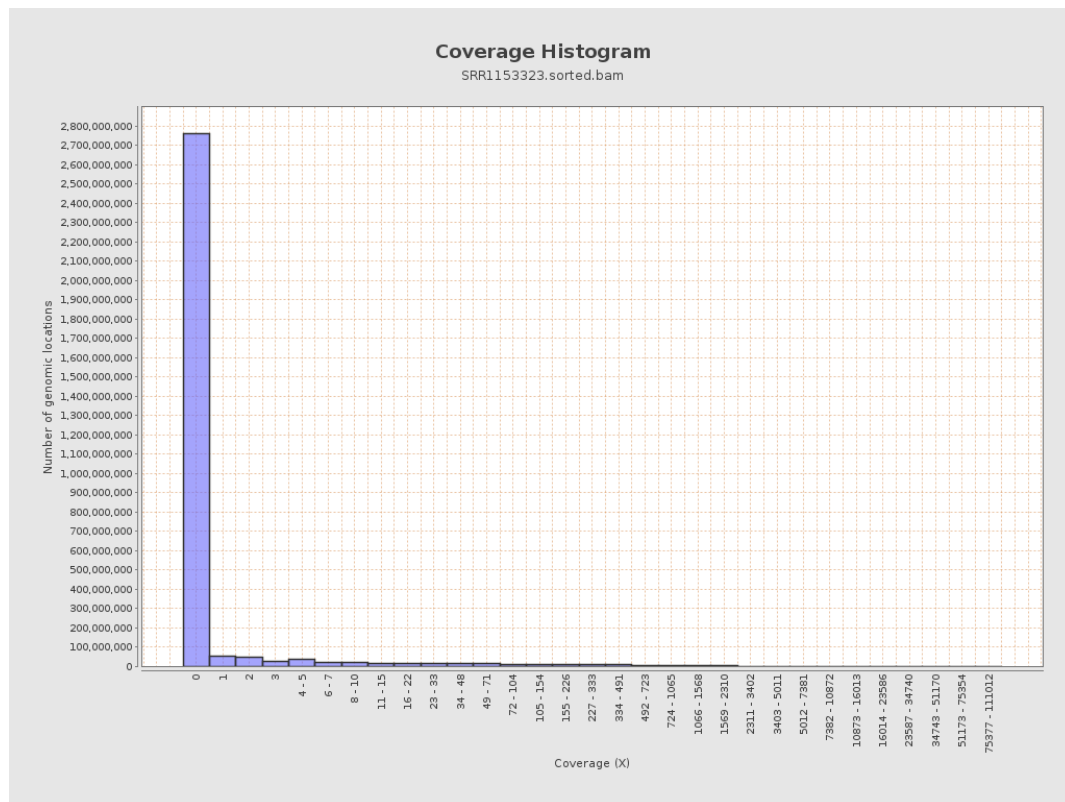
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3398629105	13.6354	167.5731
chr2	243199373	1343687494	5.525	71.552
chr3	198022430	1440676927	7.2753	94.9476
chr4	191154276	775981791	4.0595	91.2423
chr5	180915260	1899133631	10.4974	296.0233
chr6	171115067	618542893	3.6148	52.4221
chr7	159138663	2144601157	13.4763	277.7587

chr8	146364022	2032137118	13.8841	268.3455
chr9	141213431	848451522	6.0083	65.4422
chr10	135534747	1410674939	10.4082	131.1385
chr11	135006516	1824945538	13.5175	142.5214
chr12	133851895	1324203086	9.893	102.3709
chr13	115169878	181595613	1.5768	26.339
chr14	107349540	717839797	6.6869	91.0926
chr15	102531392	1489521064	14.5275	158.5184
chr16	90354753	2211469033	24.4754	221.0806
chr17	81195210	1920077648	23.6477	197.5616
chr18	78077248	137422768	1.7601	24.9011
chr19	59128983	2889433939	48.8666	296.5374
chr20	63025520	913643254	14.4964	139.3365
chr21	48129895	539250251	11.2041	292.9651
chr22	51304566	987020728	19.2385	167.0533
chrMT	16571	6460	0.3898	1.1547
chrX	155270560	1496314559	9.6368	113.1586
chrY	59373566	28536261	0.4806	30.6041

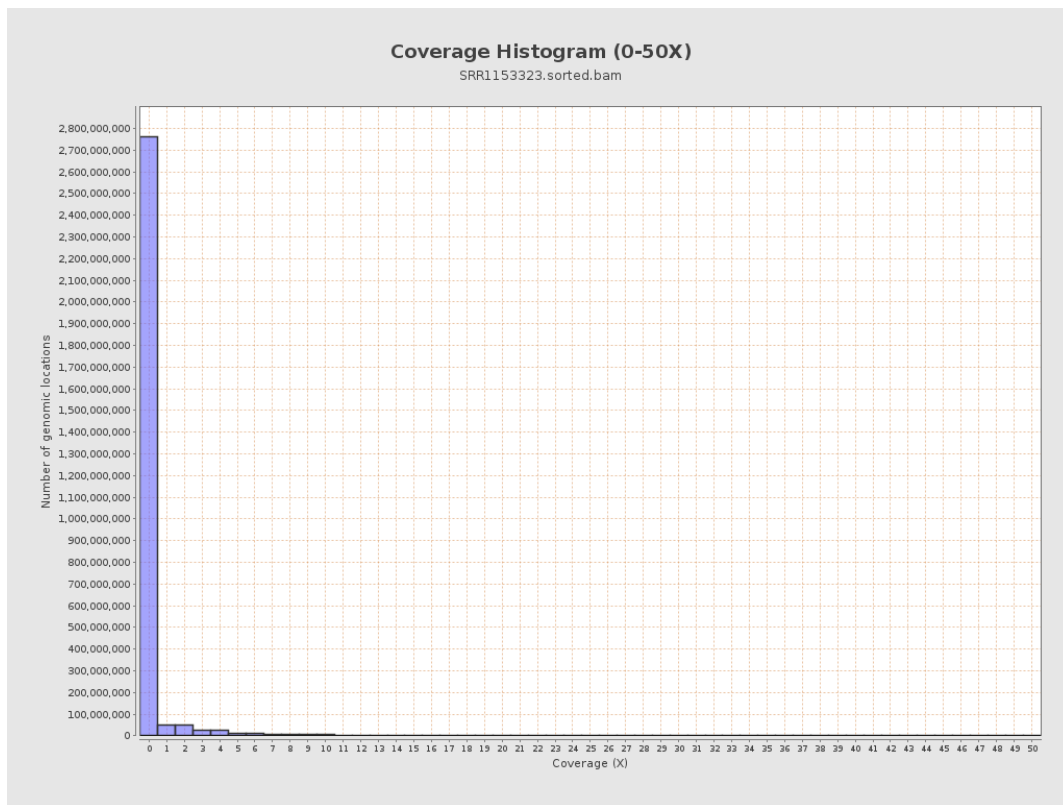
3. Results : Coverage across reference



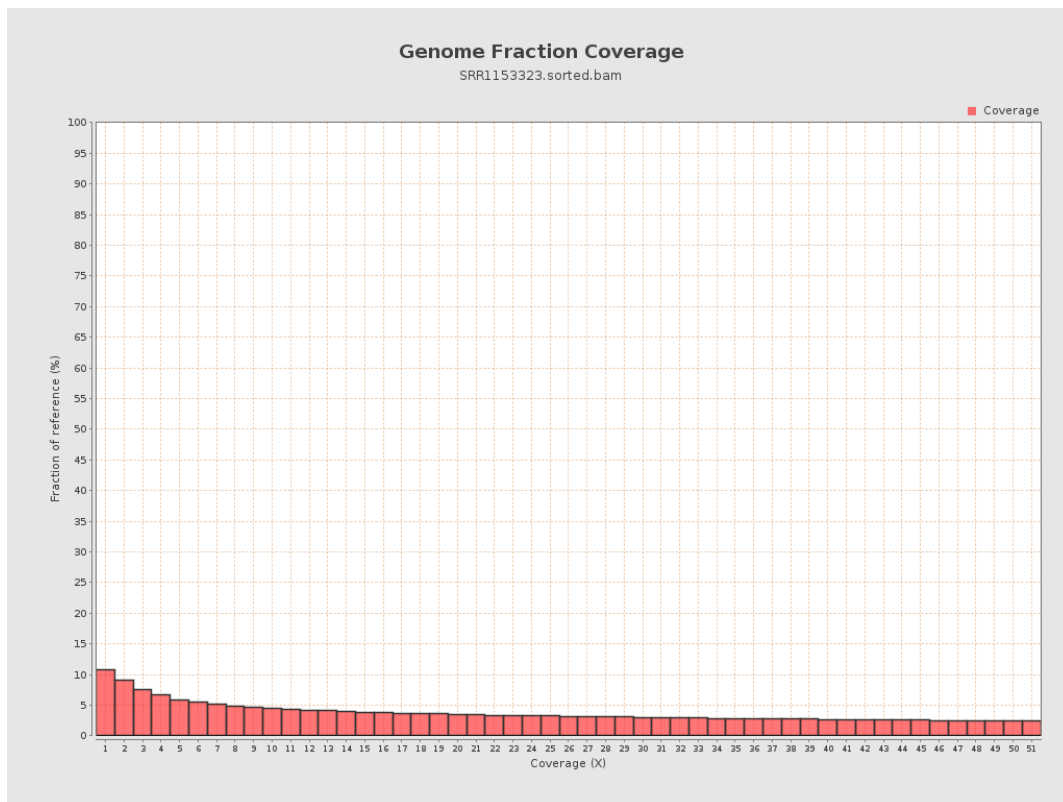
4. Results : Coverage Histogram



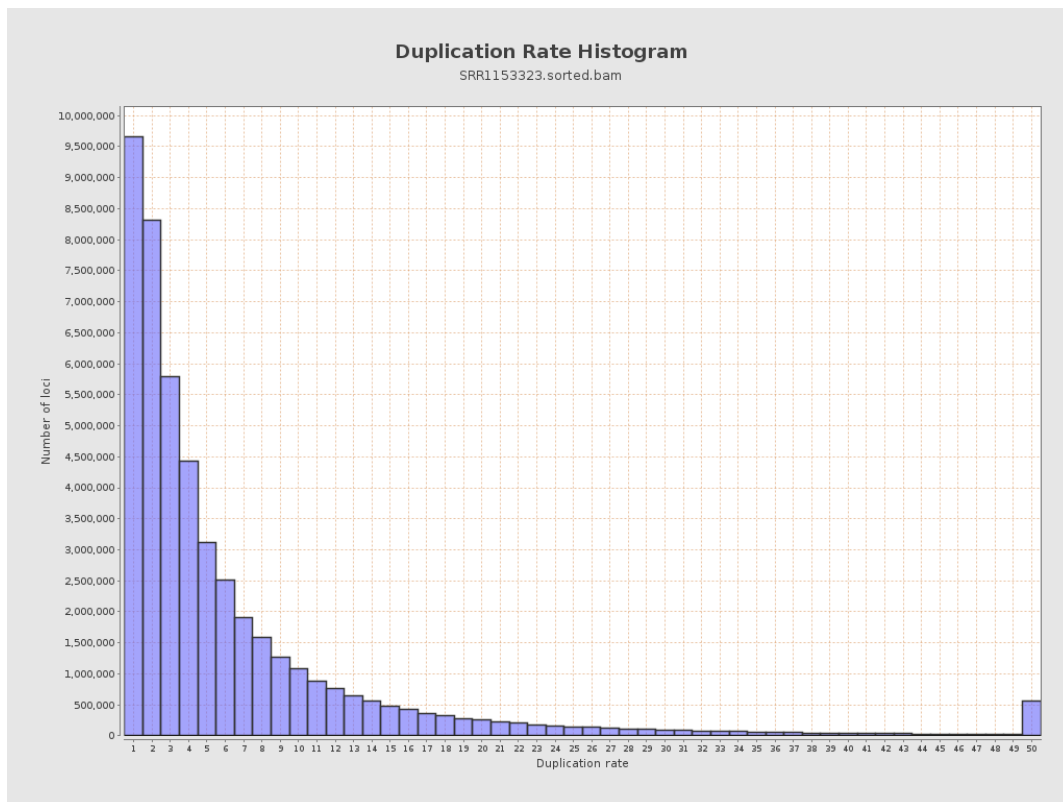
5. Results : Coverage Histogram (0-50X)



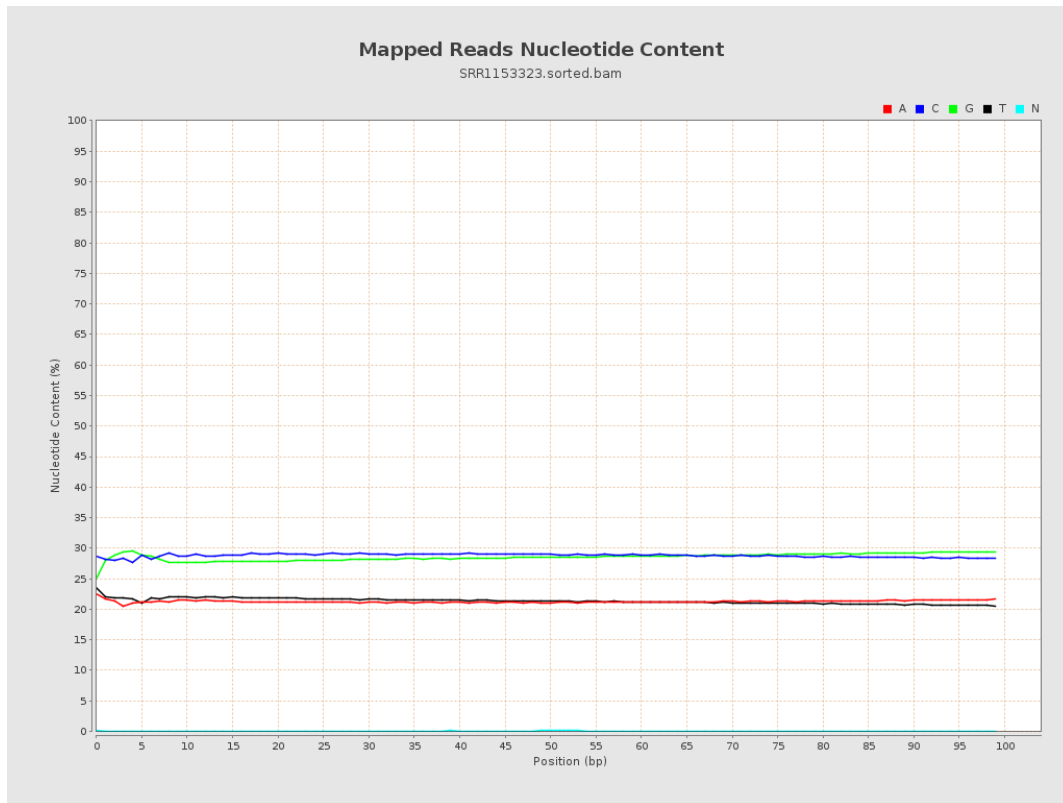
6. Results : Genome Fraction Coverage



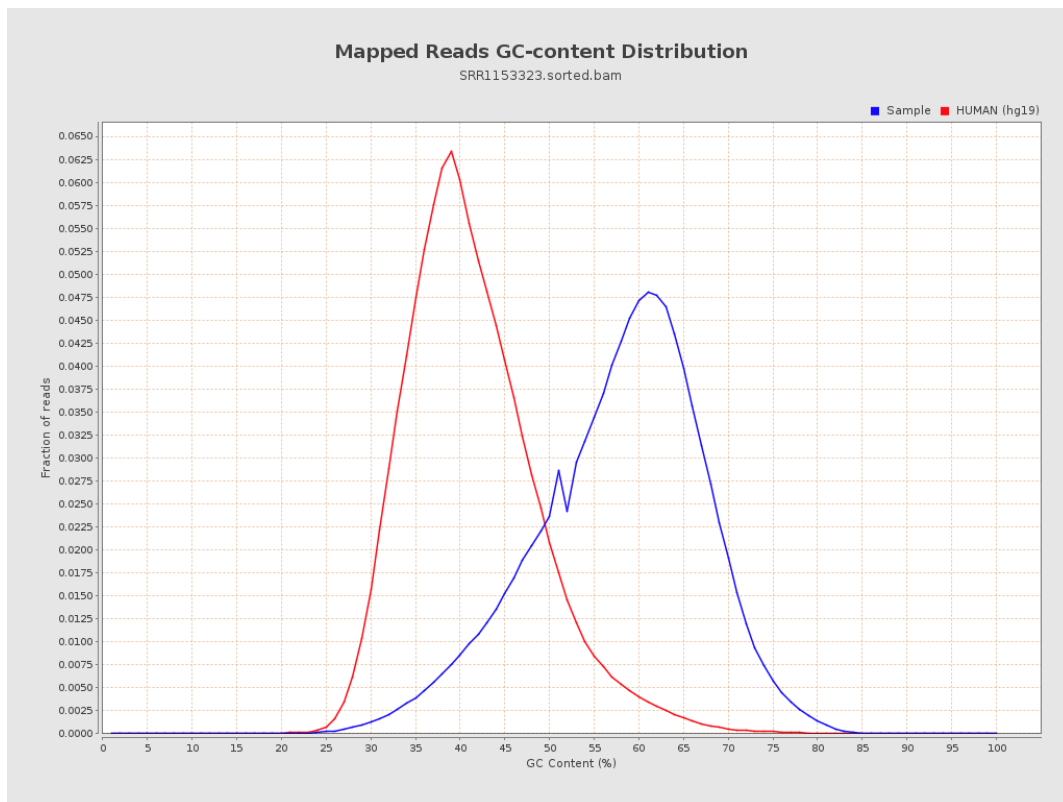
7. Results : Duplication Rate Histogram



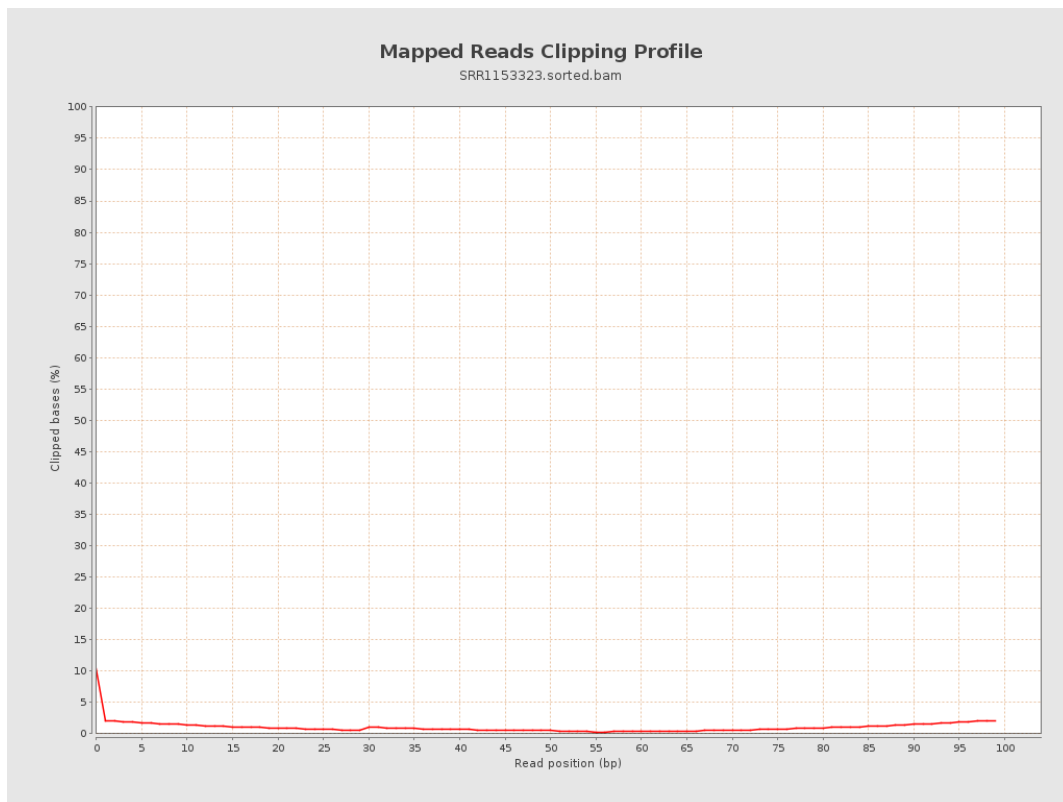
8. Results : Mapped Reads Nucleotide Content



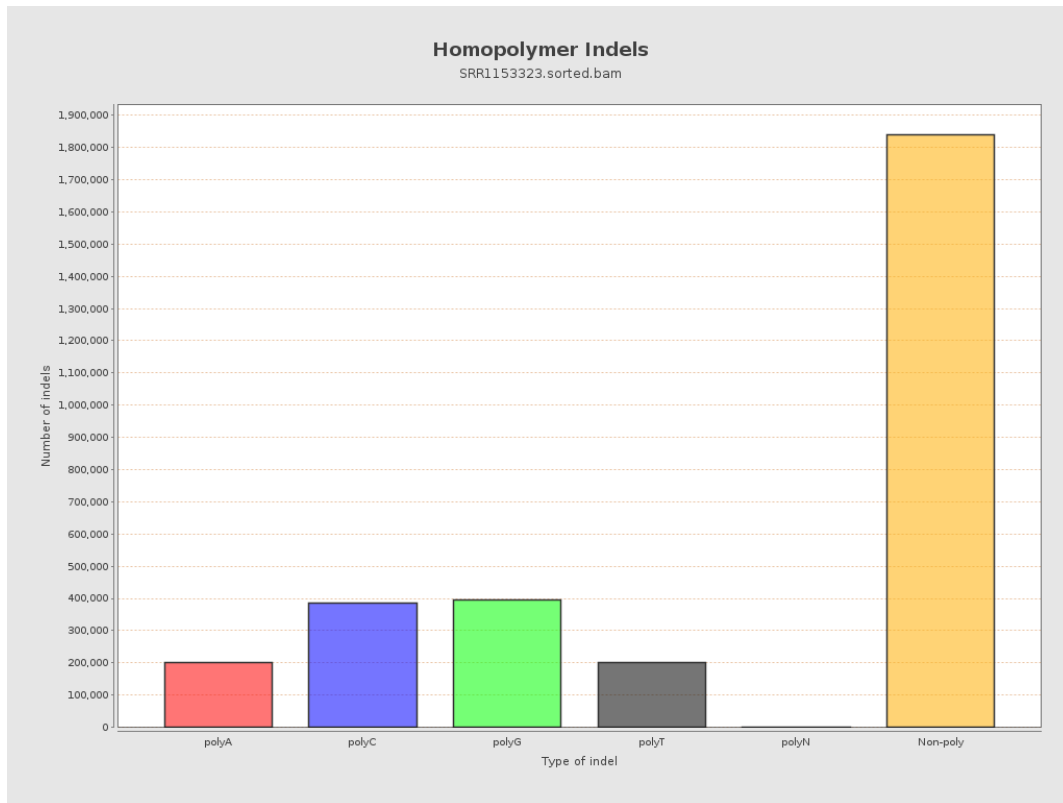
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

