

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 06:49:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153396.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_SRR1153396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153396.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 06:49:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,180,632
Mapped reads	35,874,962 / 99.16%
Unmapped reads	305,670 / 0.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	236,399 / 0.65%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	19,012,018 / 52.55%
Duplication rate	42.92%
Clipped reads	17,456,622 / 48.25%

2.2. ACGT Content

Number/percentage of A's	819,898,567 / 26.72%
Number/percentage of C's	720,671,538 / 23.48%
Number/percentage of T's	848,743,443 / 27.66%
Number/percentage of G's	678,338,554 / 22.1%
Number/percentage of N's	1,236,993 / 0.04%
GC Percentage	45.59%

2.3. Coverage

Mean	0.9915

Standard Deviation	10.8474
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2.4. Mapping Quality

Mean Mapping Quality	49.62
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2.5. Mismatches and indels

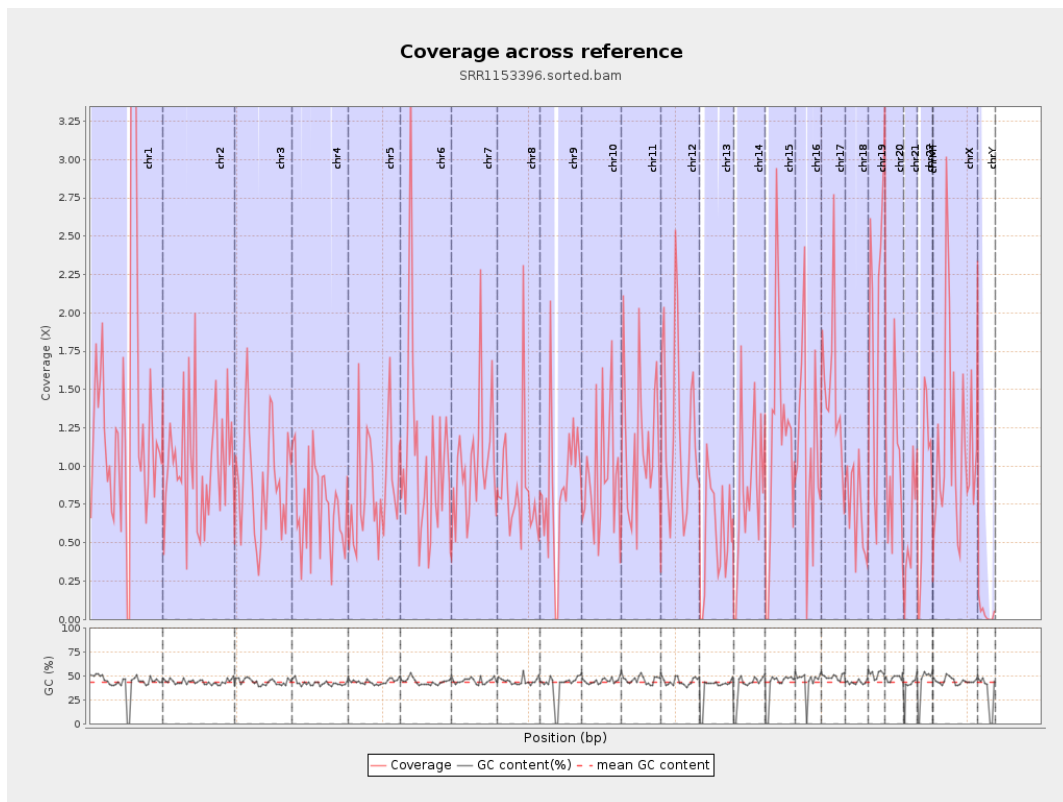
General error rate	0.24%
Mismatches	6,997,836
Insertions	337,172
Mapped reads with at least one insertion	0.93%
Deletions	283,406
Mapped reads with at least one deletion	0.78%
Homopolymer indels	49.62%

2.6. Chromosome stats

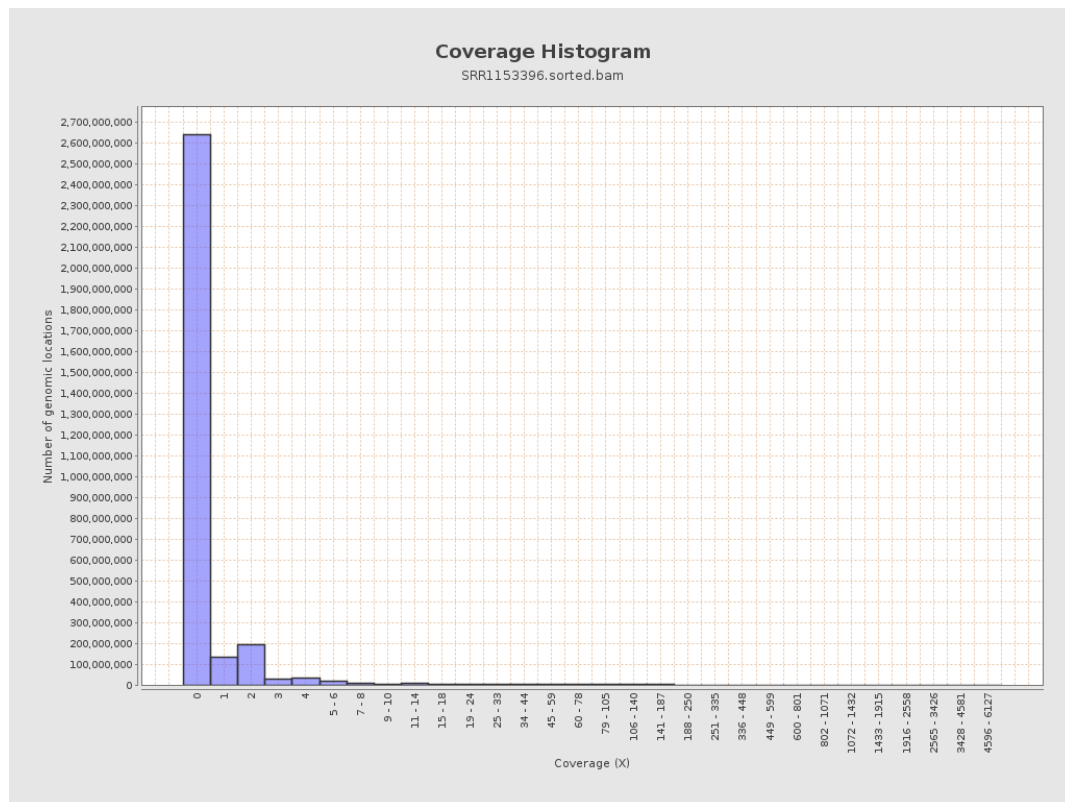
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	334947616	1.3438	14.1007
chr2	243199373	248521669	1.0219	10.535
chr3	198022430	177004449	0.8939	9.2128
chr4	191154276	141161183	0.7385	8.082
chr5	180915260	156673750	0.866	9.081
chr6	171115067	176880170	1.0337	13.3448
chr7	159138663	160406628	1.008	10.553

chr8	146364022	122855541	0.8394	10.3343
chr9	141213431	121378855	0.8595	9.2856
chr10	135534747	129085651	0.9524	9.8071
chr11	135006516	152278095	1.1279	10.7507
chr12	133851895	167841799	1.2539	12.5482
chr13	115169878	64097394	0.5565	6.5736
chr14	107349540	91148200	0.8491	8.887
chr15	102531392	118050502	1.1514	11.665
chr16	90354753	98787832	1.0933	9.9904
chr17	81195210	122086218	1.5036	12.9596
chr18	78077248	56054070	0.7179	7.8822
chr19	59128983	115234877	1.9489	17.0194
chr20	63025520	60353657	0.9576	9.7355
chr21	48129895	28994488	0.6024	7.6252
chr22	51304566	45830702	0.8933	10.3383
chrMT	16571	4004	0.2416	0.6991
chrX	155270560	177331386	1.1421	14.1377
chrY	59373566	2463183	0.0415	1.8817

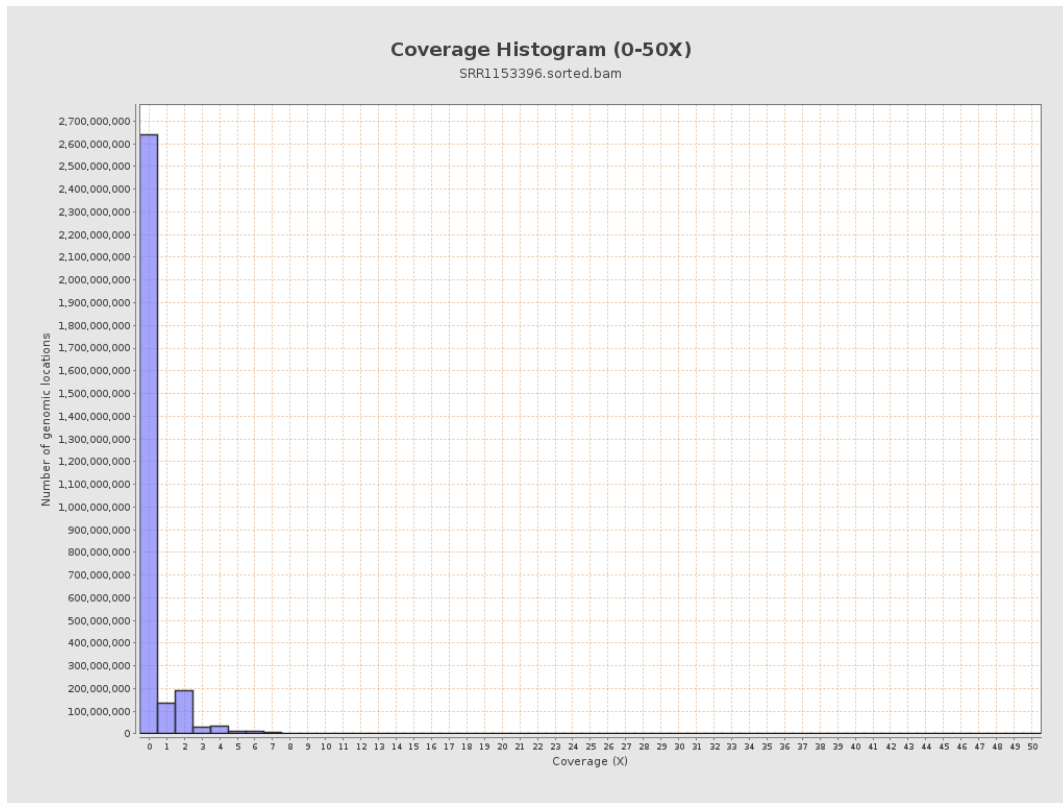
3. Results : Coverage across reference



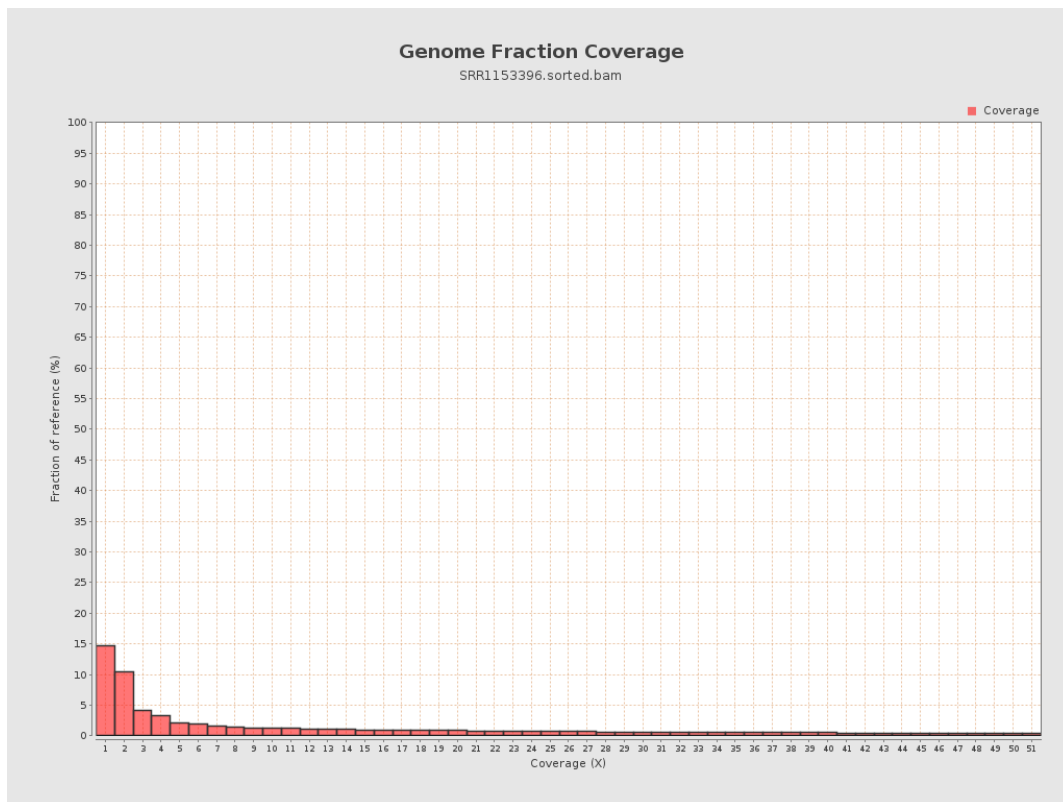
4. Results : Coverage Histogram



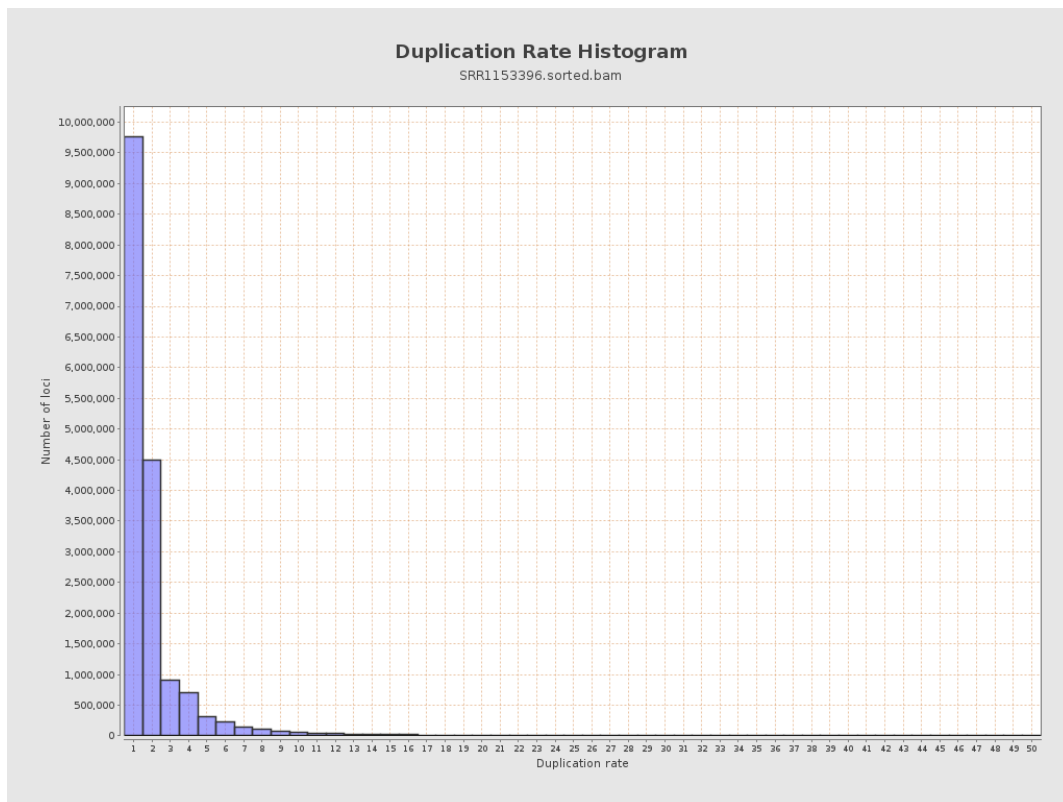
5. Results : Coverage Histogram (0-50X)



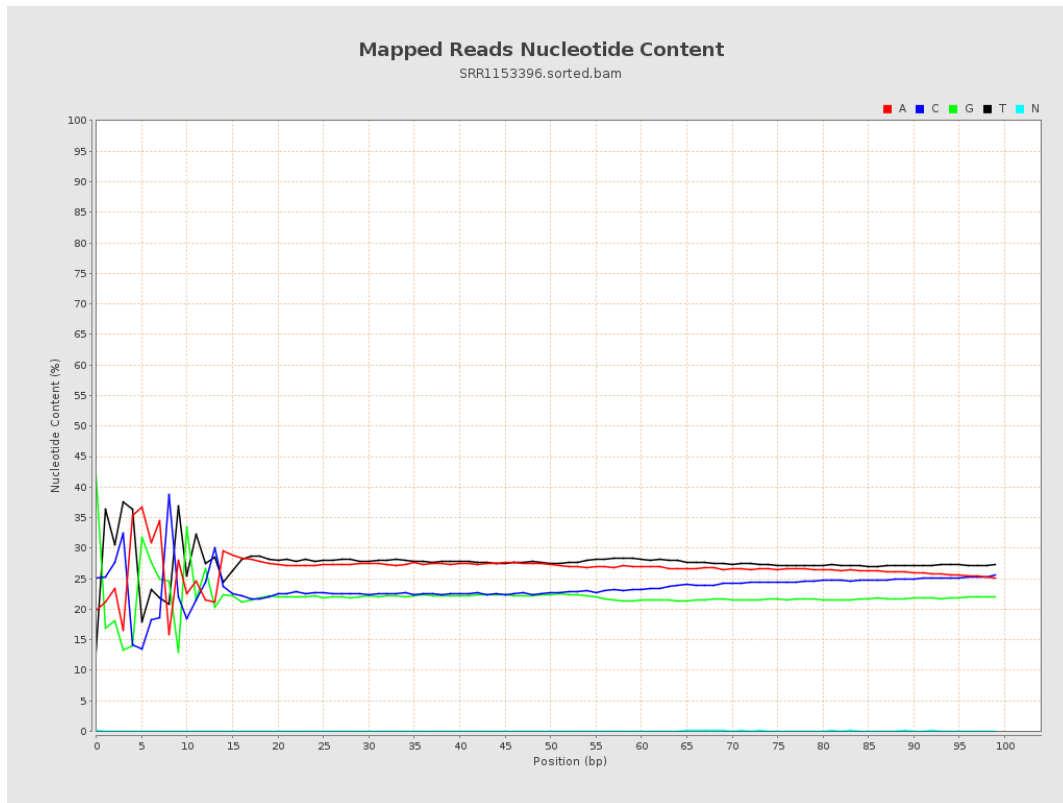
6. Results : Genome Fraction Coverage



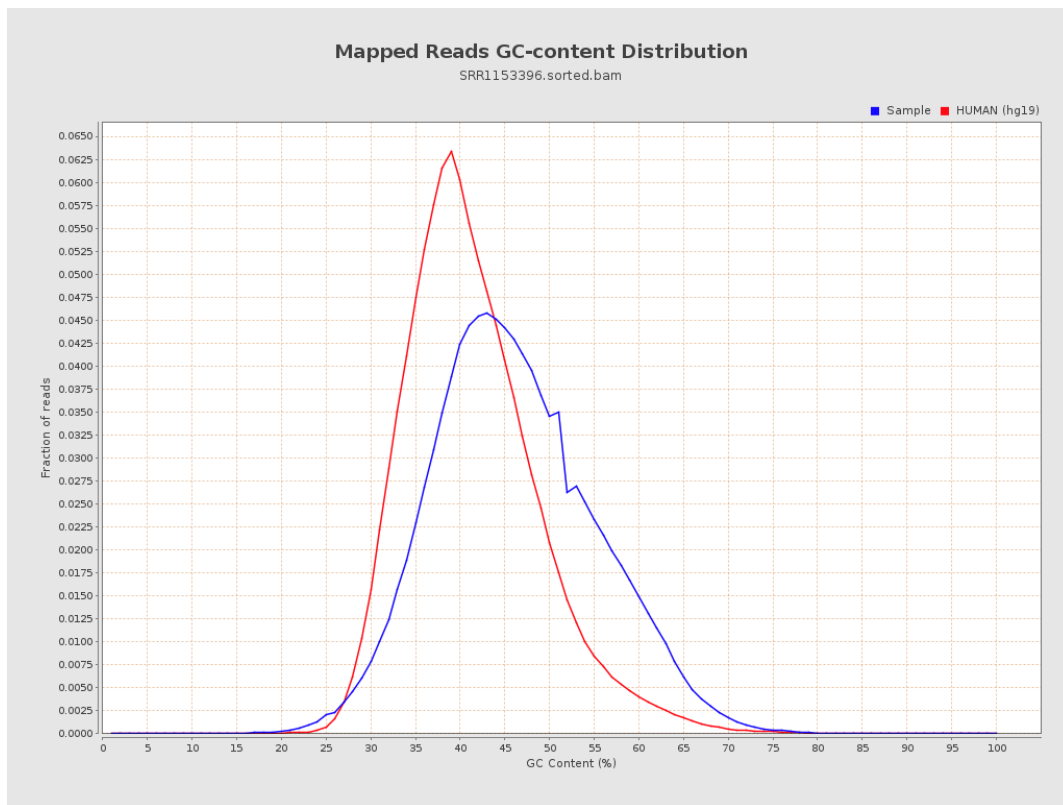
7. Results : Duplication Rate Histogram



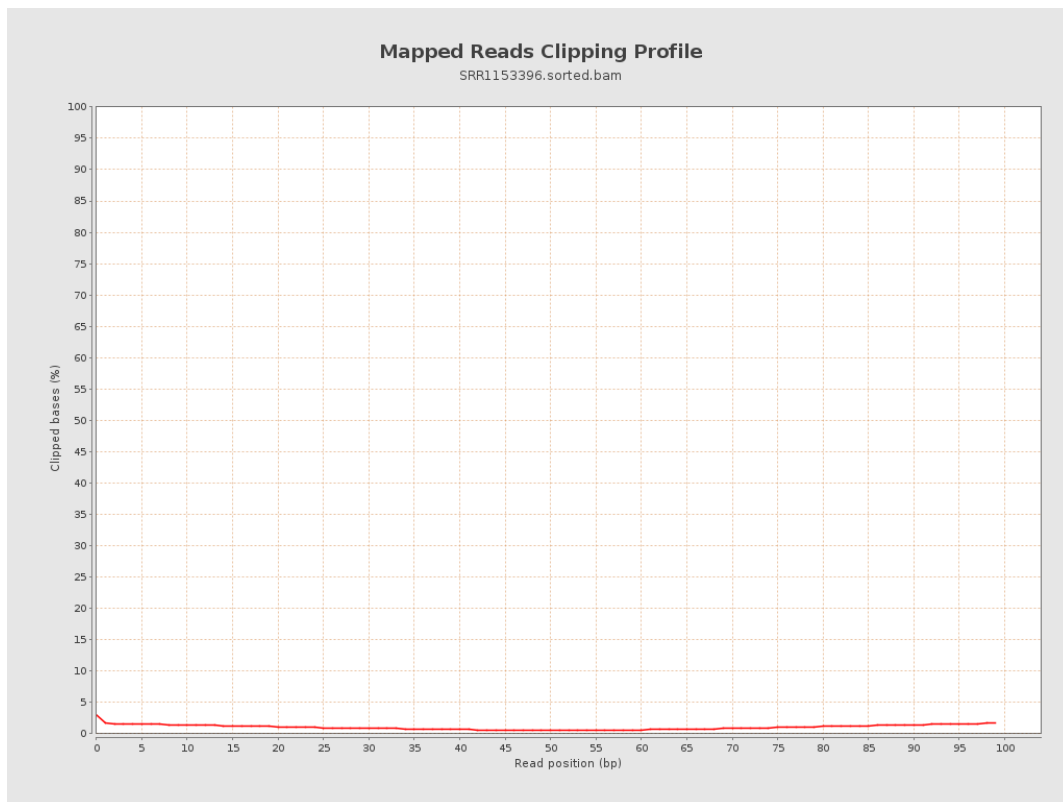
8. Results : Mapped Reads Nucleotide Content



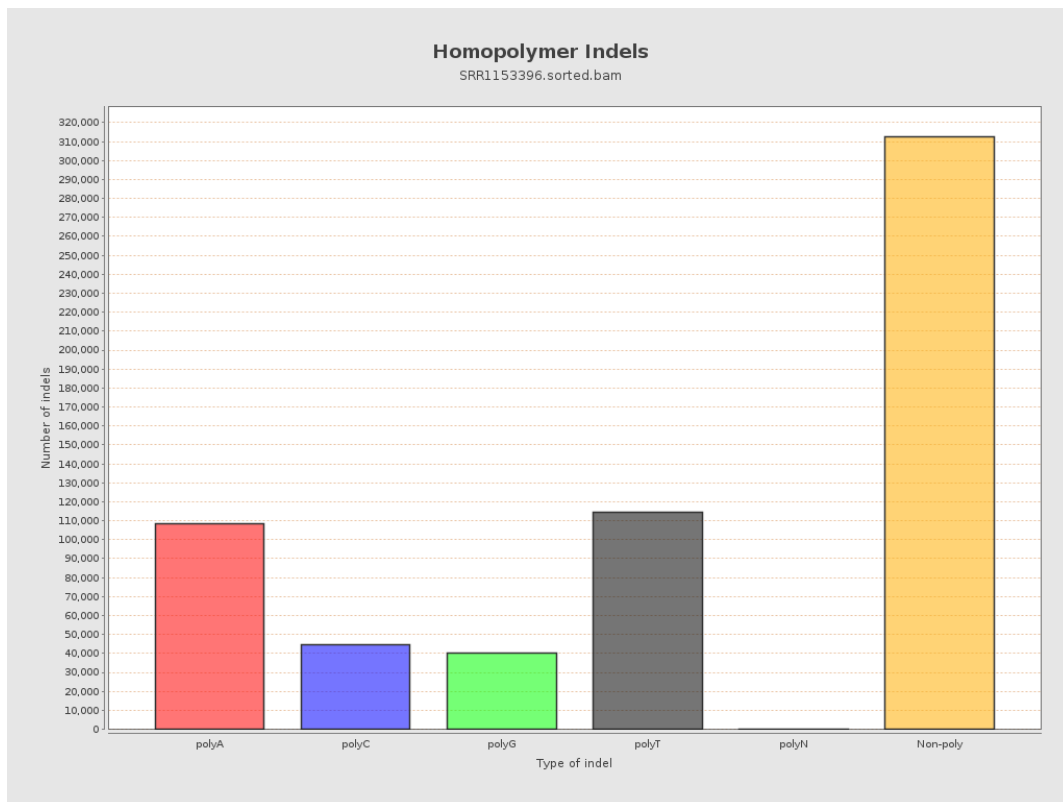
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

