

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 21:08:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163159.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_SRR1163159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 21:08:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	118,969,444
Mapped reads	117,204,910 / 98.52%
Unmapped reads	1,764,534 / 1.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,132,208 / 0.95%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	73,306,718 / 61.62%
Duplication rate	53.85%
Clipped reads	5,833,264 / 4.9%

2.2. ACGT Content

Number/percentage of A's	3,034,869,861 / 26.02%
Number/percentage of C's	2,788,878,168 / 23.91%
Number/percentage of T's	3,063,441,172 / 26.26%
Number/percentage of G's	2,769,749,557 / 23.74%
Number/percentage of N's	8,879,714 / 0.08%
GC Percentage	47.65%

2.3. Coverage

Mean	3.7689

Standard Deviation	39.8672
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2.4. Mapping Quality

Mean Mapping Quality	49.17
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2.5. Mismatches and indels

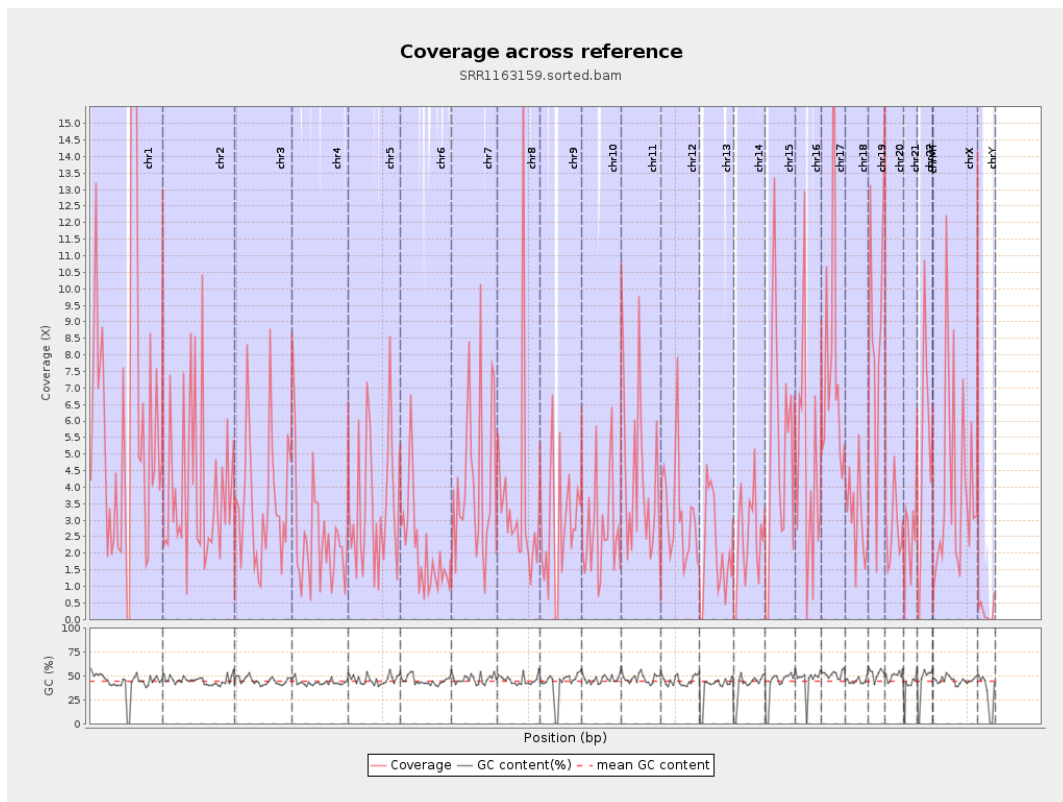
General error rate	0.59%
Mismatches	67,298,581
Insertions	841,945
Mapped reads with at least one insertion	0.71%
Deletions	793,425
Mapped reads with at least one deletion	0.67%
Homopolymer indels	46.92%

2.6. Chromosome stats

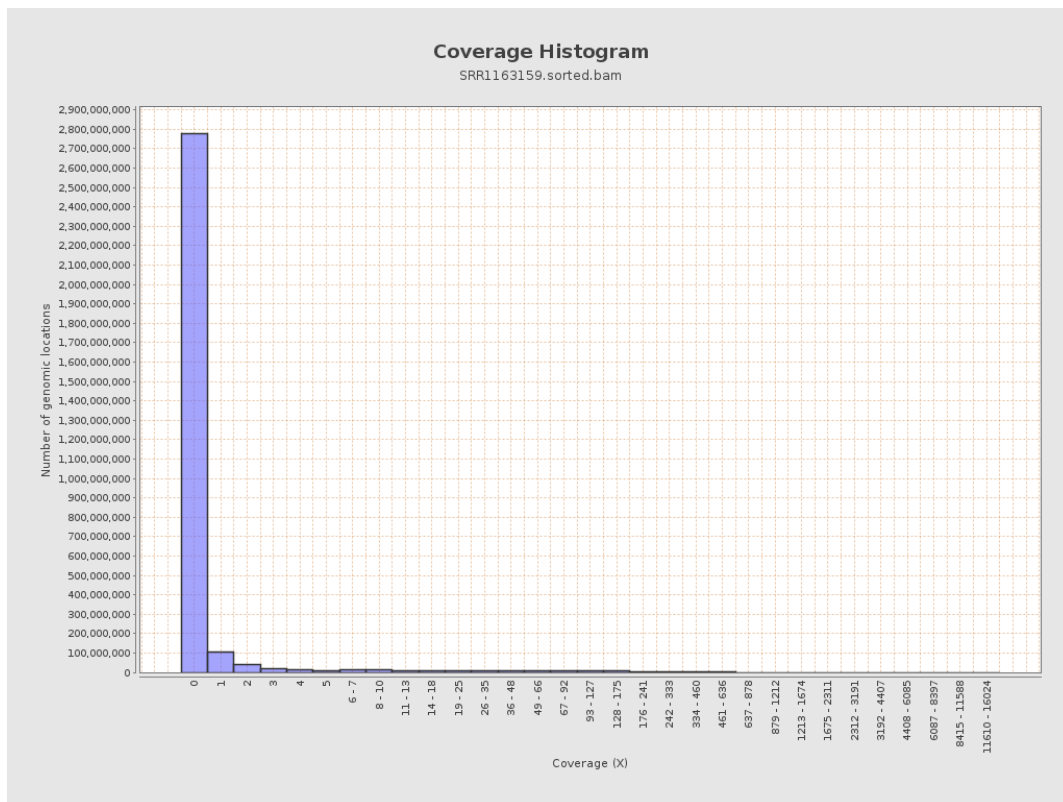
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1572699092	6.3097	55.5485
chr2	243199373	955503326	3.9289	38.7913
chr3	198022430	705184923	3.5611	32.8096
chr4	191154276	471166142	2.4648	29.2222
chr5	180915260	633496477	3.5016	46.0484
chr6	171115067	354524912	2.0719	24.5873
chr7	159138663	651974871	4.0969	48.2567

chr8	146364022	520297737	3.5548	50.1794
chr9	141213431	390565038	2.7658	31.0537
chr10	135534747	370509771	2.7337	27.0677
chr11	135006516	566633355	4.1971	34.8169
chr12	133851895	438459396	3.2757	30.6501
chr13	115169878	239108997	2.0761	22.8534
chr14	107349540	257687842	2.4005	24.8341
chr15	102531392	537951815	5.2467	49.0618
chr16	90354753	403429174	4.4649	38.5706
chr17	81195210	635664389	7.8288	65.0351
chr18	78077248	246072794	3.1517	30.8863
chr19	59128983	515350026	8.7157	59.6755
chr20	63025520	168479600	2.6732	31.2404
chr21	48129895	132420713	2.7513	36.0167
chr22	51304566	261380343	5.0947	44.386
chrMT	16571	2018	0.1218	0.5509
chrX	155270560	623943696	4.0184	40.8409
chrY	59373566	14988792	0.2524	22.5887

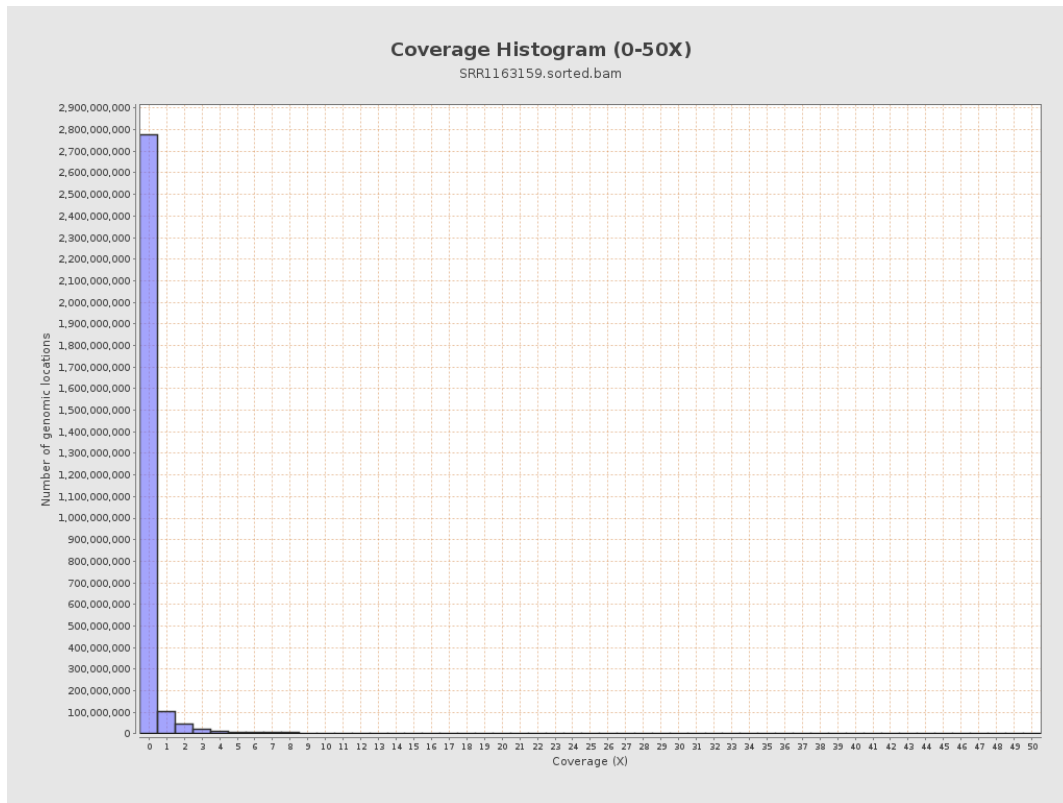
3. Results : Coverage across reference



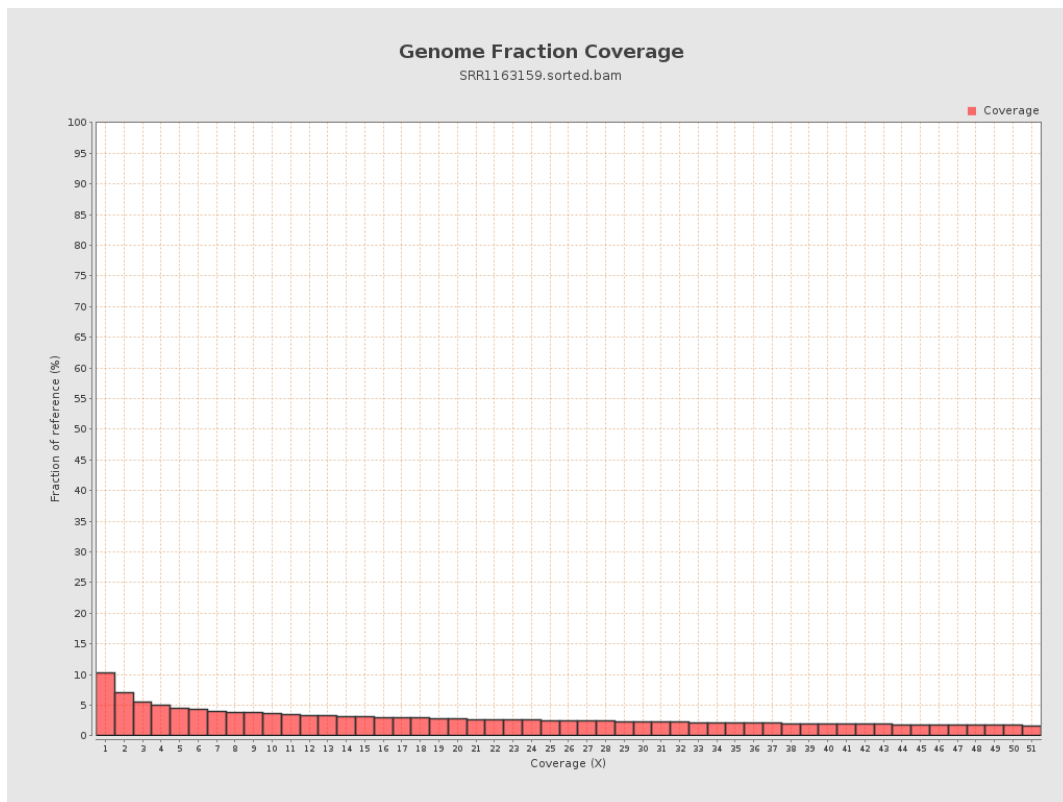
4. Results : Coverage Histogram



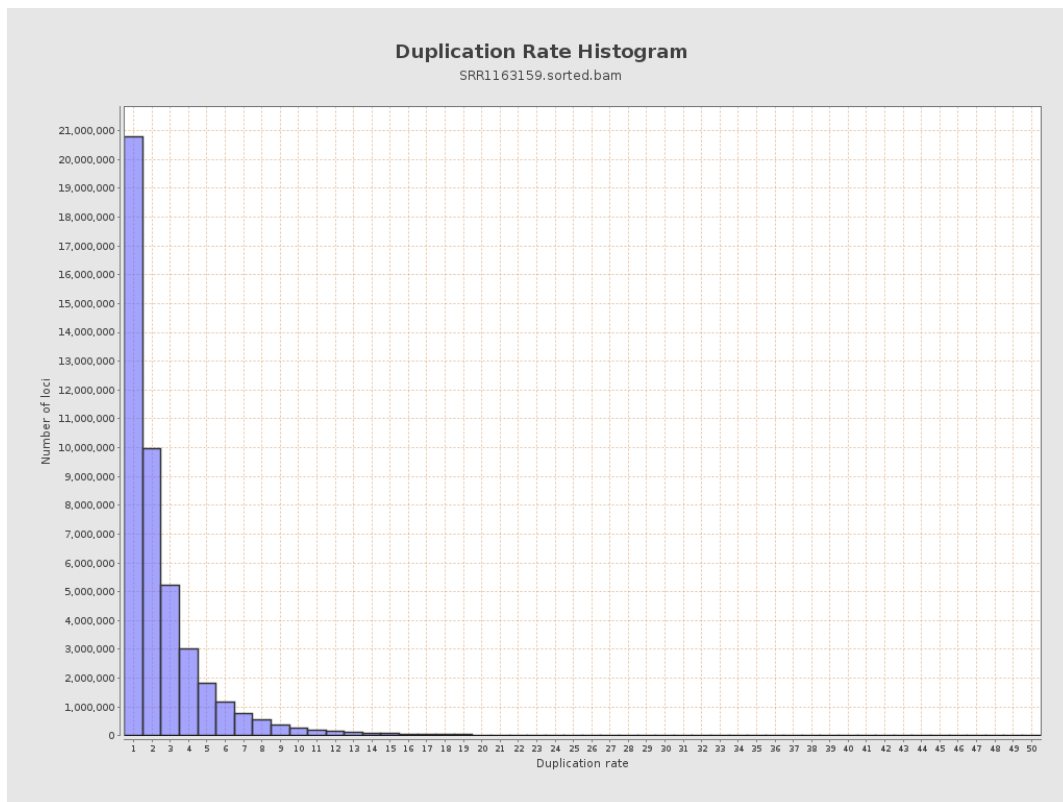
5. Results : Coverage Histogram (0-50X)



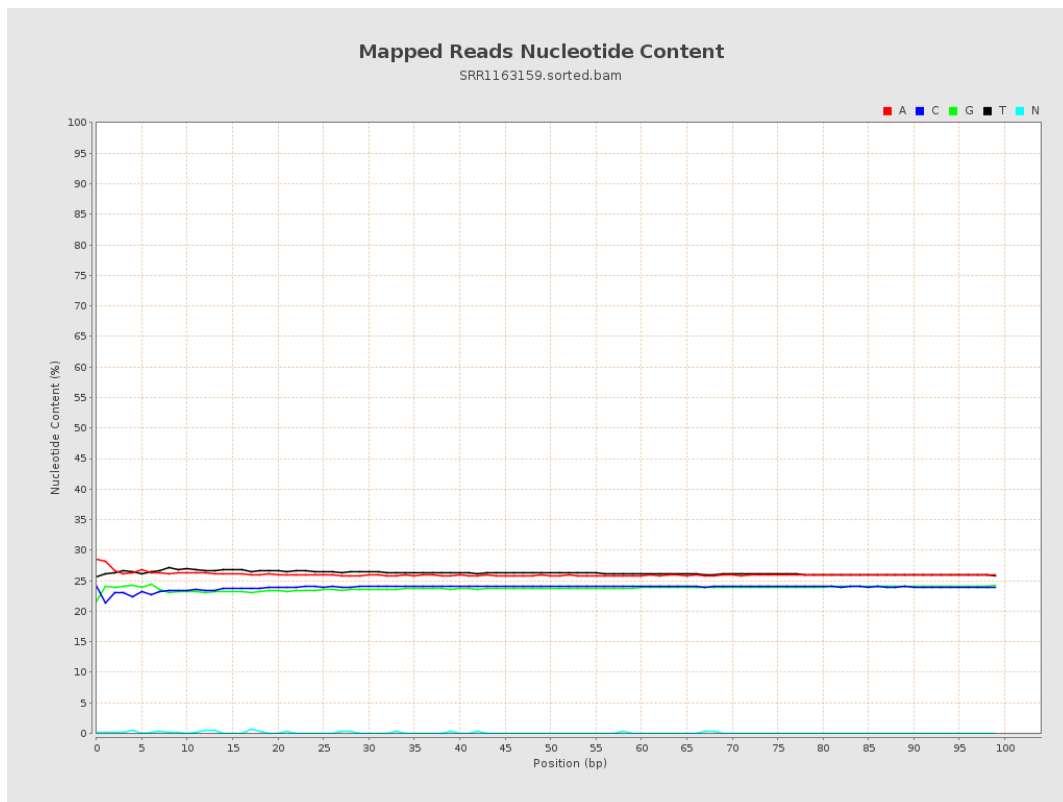
6. Results : Genome Fraction Coverage



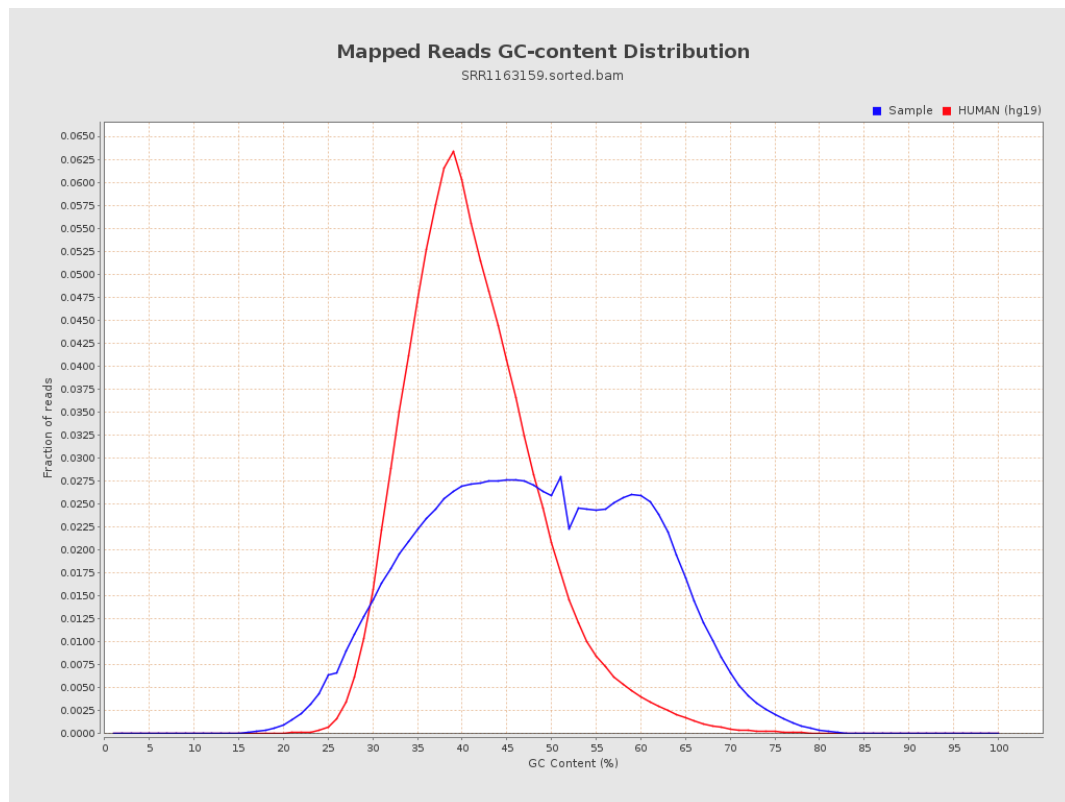
7. Results : Duplication Rate Histogram



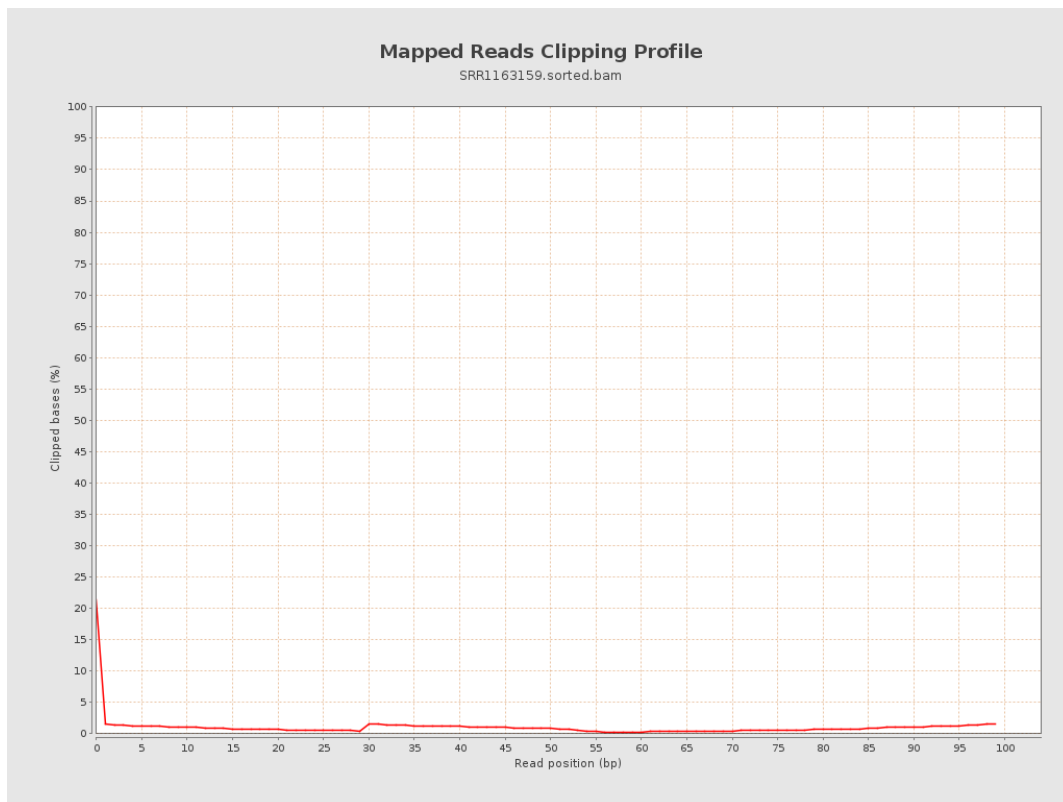
8. Results : Mapped Reads Nucleotide Content



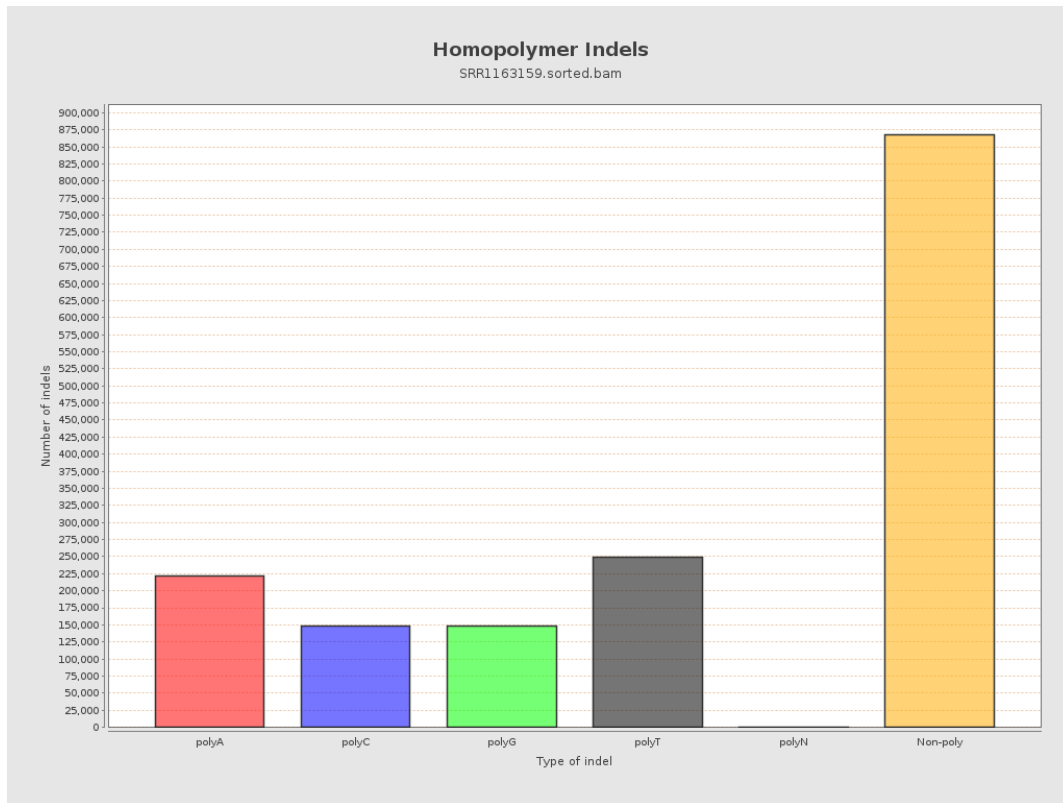
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

