

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 11:46:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163150.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_SRR1163150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 11:46:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,037,010
Mapped reads	50,480,279 / 98.91%
Unmapped reads	556,731 / 1.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	266,300 / 0.52%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	23,376,966 / 45.8%
Duplication rate	37.43%
Clipped reads	5,278,340 / 10.34%

2.2. ACGT Content

Number/percentage of A's	1,202,396,574 / 24.26%
Number/percentage of C's	1,276,163,930 / 25.75%
Number/percentage of T's	1,202,947,146 / 24.27%
Number/percentage of G's	1,274,806,383 / 25.72%
Number/percentage of N's	160,789 / 0%
GC Percentage	51.47%

2.3. Coverage

Mean	1.6013

Standard Deviation	20.461
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2.4. Mapping Quality

Mean Mapping Quality	49.02
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2.5. Mismatches and indels

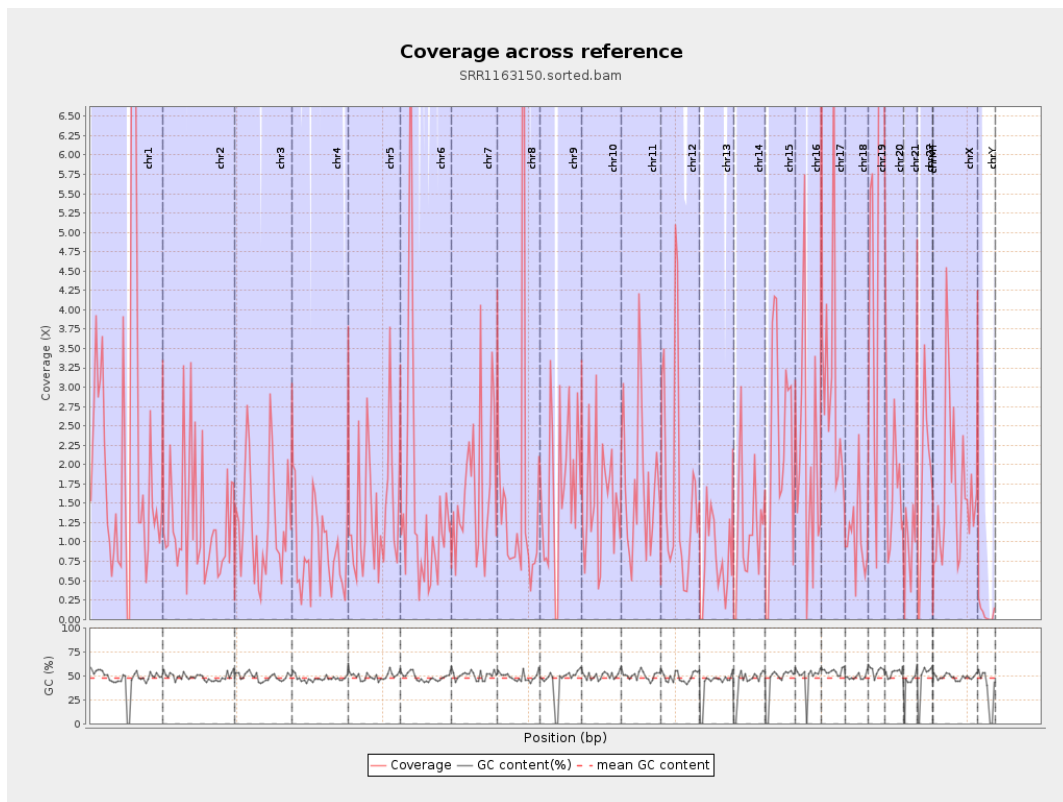
General error rate	0.32%
Mismatches	15,180,703
Insertions	359,316
Mapped reads with at least one insertion	0.7%
Deletions	243,834
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.74%

2.6. Chromosome stats

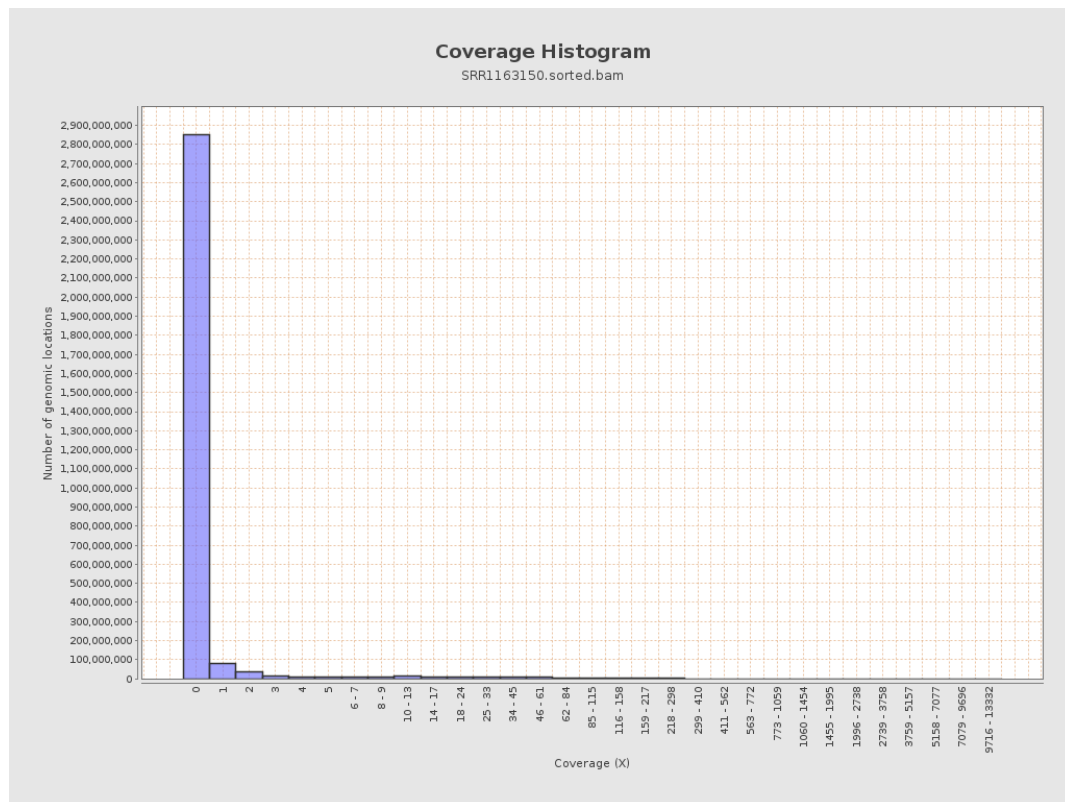
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	535333761	2.1478	20.7623
chr2	243199373	304857219	1.2535	14.7049
chr3	198022430	250709979	1.2661	14.3836
chr4	191154276	168812855	0.8831	13.7844
chr5	180915260	255157306	1.4104	19.9828
chr6	171115067	246965321	1.4433	17.6296
chr7	159138663	263996149	1.6589	20.3827

chr8	146364022	243973435	1.6669	40.4067
chr9	141213431	233858714	1.6561	19.3398
chr10	135534747	208011274	1.5347	24.4374
chr11	135006516	235162407	1.7419	16.6019
chr12	133851895	233344473	1.7433	19.6164
chr13	115169878	91087609	0.7909	10.4579
chr14	107349540	124060640	1.1557	13.7507
chr15	102531392	227389149	2.2178	20.8813
chr16	90354753	182640786	2.0214	18.1003
chr17	81195210	247050682	3.0427	24.552
chr18	78077248	82716530	1.0594	14.0133
chr19	59128983	290574068	4.9142	37.0515
chr20	63025520	108384440	1.7197	19.7615
chr21	48129895	65903951	1.3693	30.0714
chr22	51304566	93123802	1.8151	16.2693
chrMT	16571	753	0.0454	0.2395
chrX	155270560	259101764	1.6687	21.0238
chrY	59373566	4841233	0.0815	4.7415

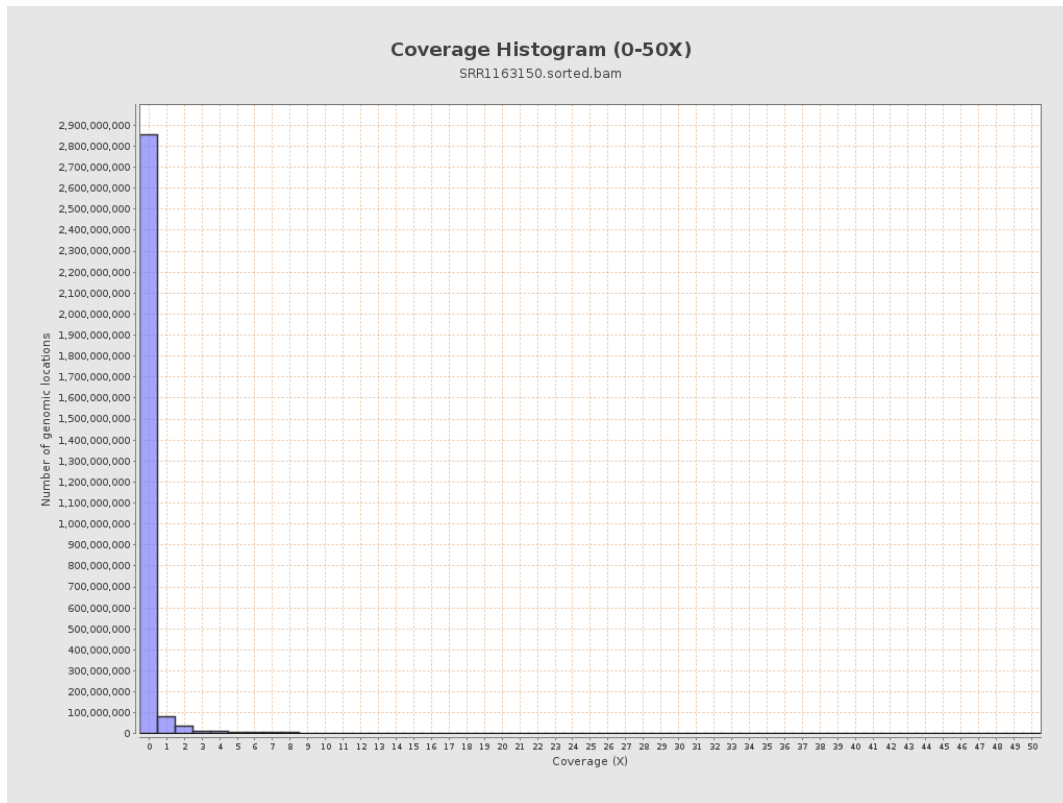
3. Results : Coverage across reference



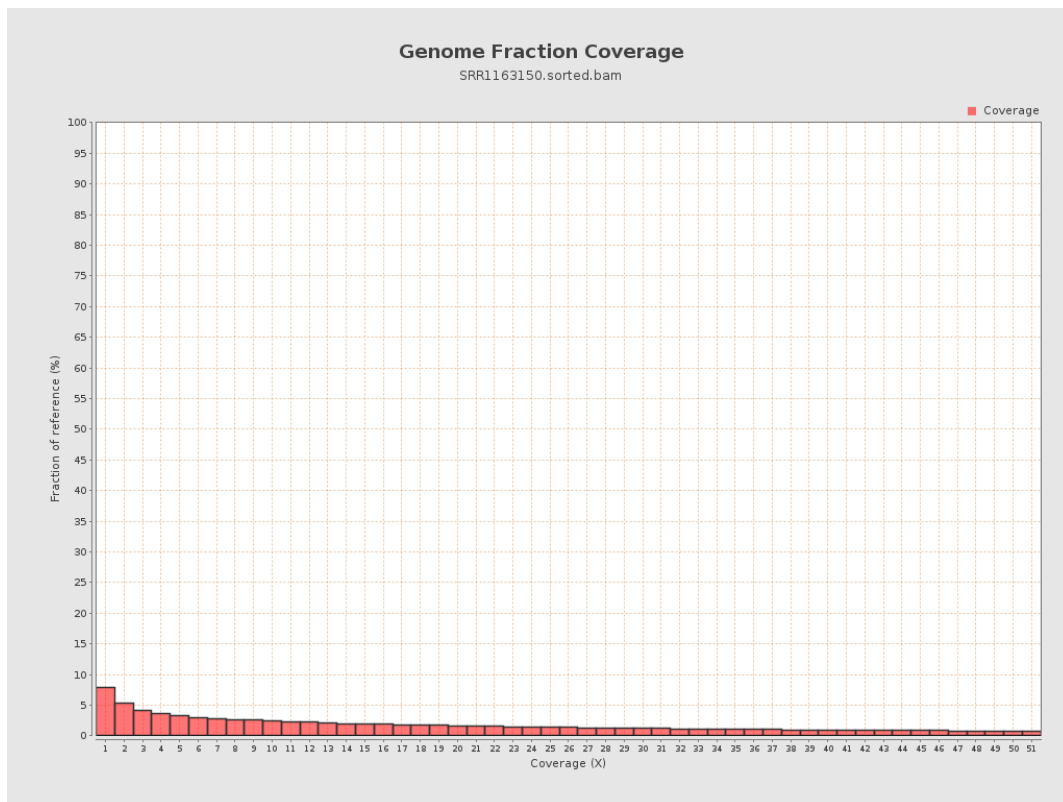
4. Results : Coverage Histogram



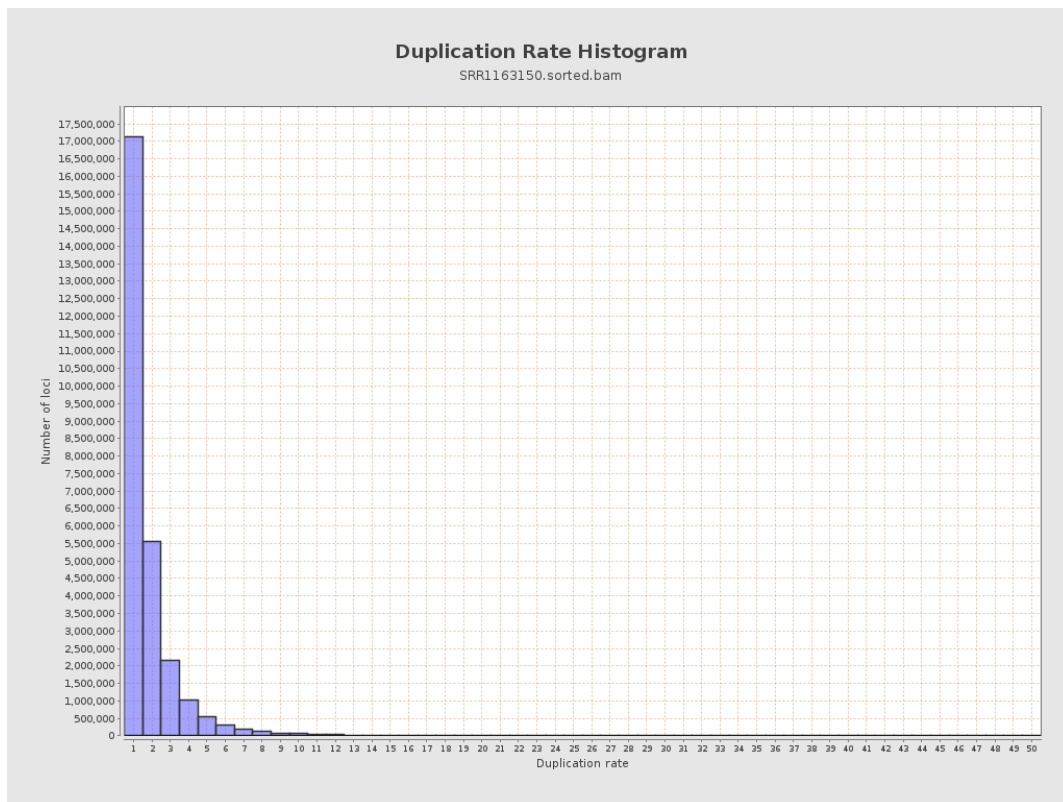
5. Results : Coverage Histogram (0-50X)



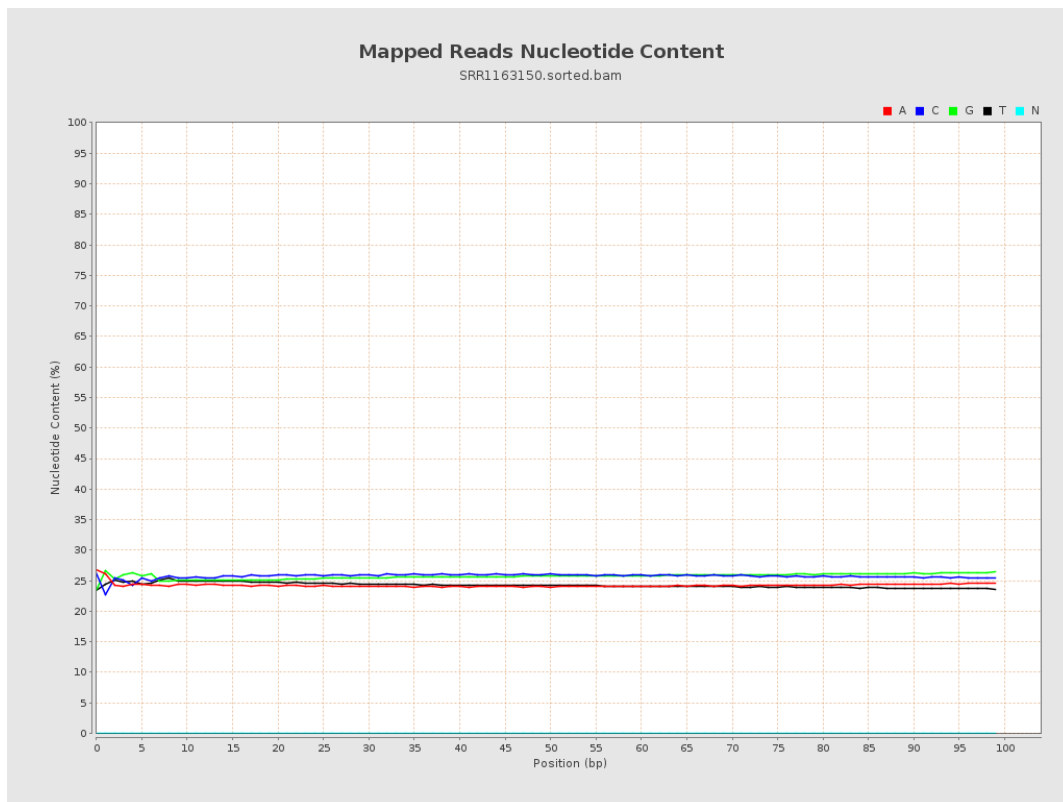
6. Results : Genome Fraction Coverage



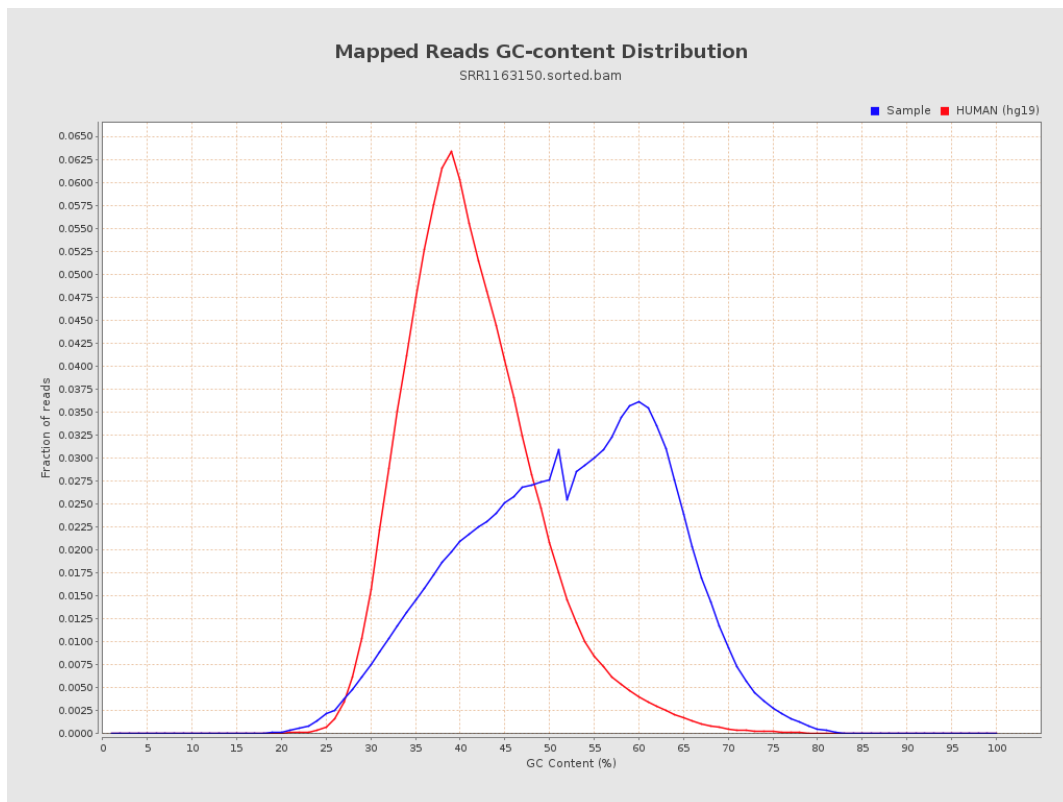
7. Results : Duplication Rate Histogram



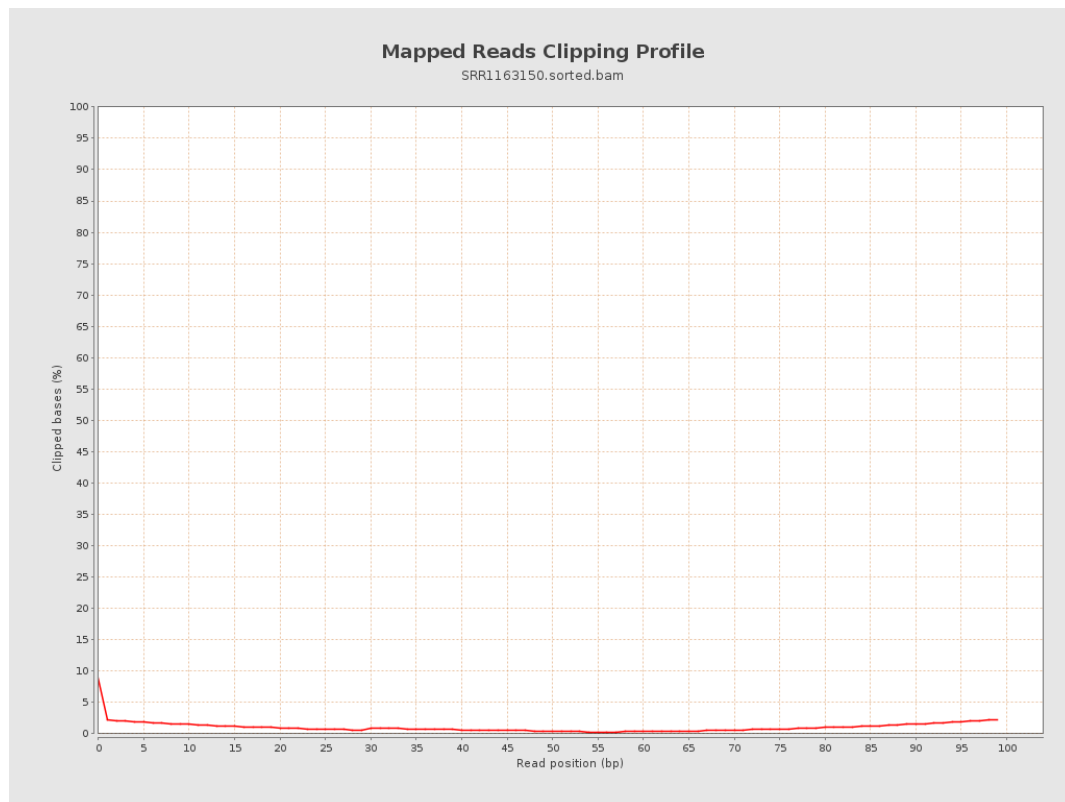
8. Results : Mapped Reads Nucleotide Content



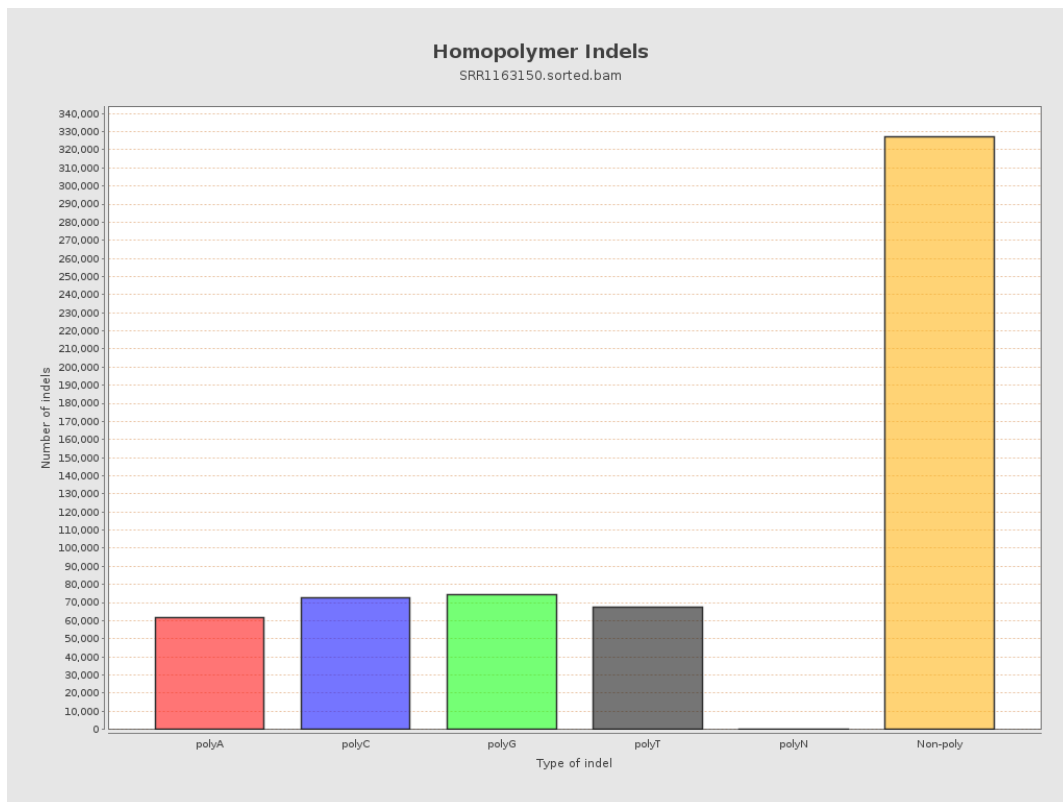
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

