

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:35:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506106.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_SRR1506106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:35:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,784,728
Mapped reads	4,321,687 / 74.71%
Unmapped reads	1,463,041 / 25.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	76,406 / 1.32%
Read min/max/mean length	30 / 94 / 94.47
Duplicated reads (estimated)	718,278 / 12.42%
Duplication rate	11.78%
Clipped reads	2,714,818 / 46.93%

2.2. ACGT Content

Number/percentage of A's	90,162,557 / 26.68%
Number/percentage of C's	65,445,452 / 19.36%
Number/percentage of T's	98,512,635 / 29.15%
Number/percentage of G's	83,818,780 / 24.8%
Number/percentage of N's	57,552 / 0.02%
GC Percentage	44.16%

2.3. Coverage

Mean	0.1092

Standard Deviation	0.7571
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2.4. Mapping Quality

Mean Mapping Quality	47.54
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2.5. Mismatches and indels

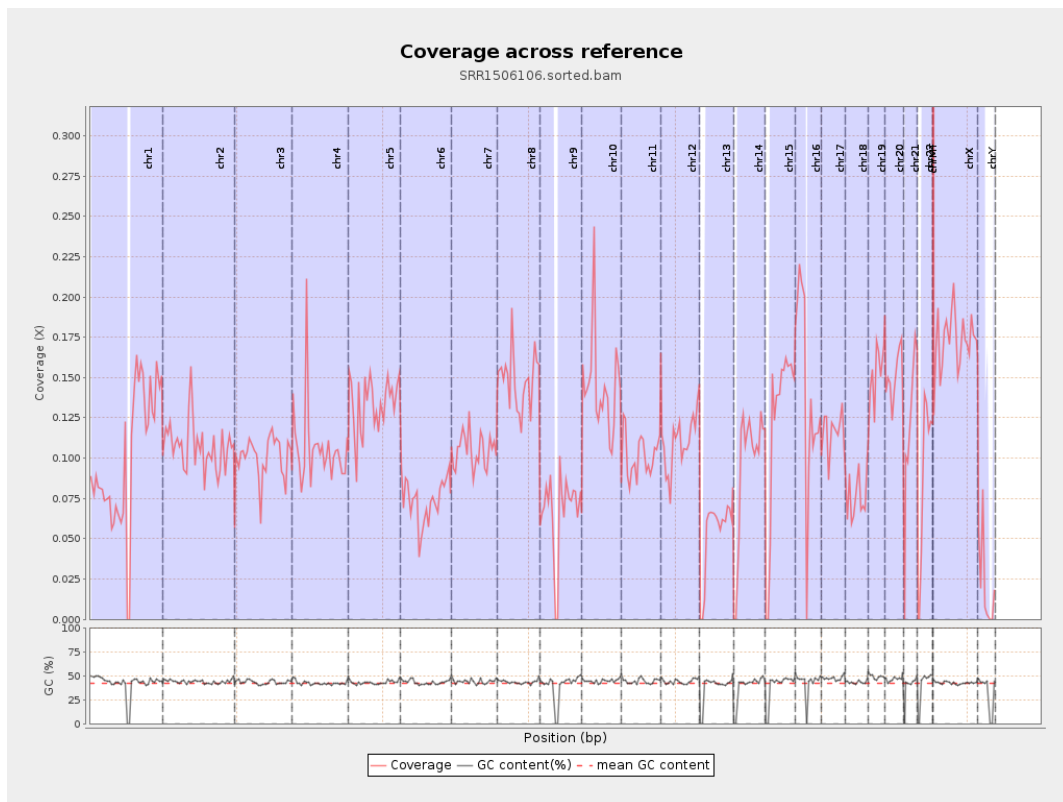
General error rate	0.79%
Mismatches	2,604,834
Insertions	26,707
Mapped reads with at least one insertion	0.6%
Deletions	66,542
Mapped reads with at least one deletion	1.51%
Homopolymer indels	42.09%

2.6. Chromosome stats

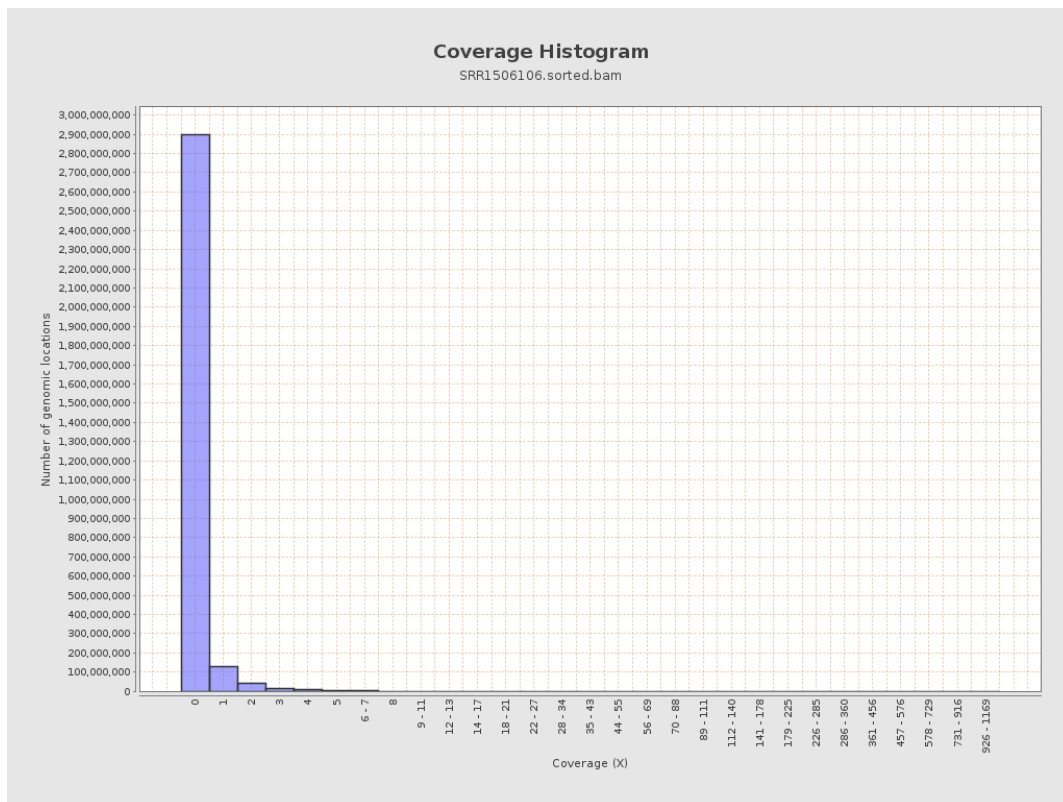
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24954672	0.1001	1.1815
chr2	243199373	26148865	0.1075	0.7828
chr3	198022430	19835002	0.1002	0.4951
chr4	191154276	20371639	0.1066	0.712
chr5	180915260	24290704	0.1343	0.5859
chr6	171115067	12622821	0.0738	0.4536
chr7	159138663	16675709	0.1048	0.894

chr8	146364022	21626240	0.1478	0.8476
chr9	141213431	9584323	0.0679	0.6555
chr10	135534747	19439330	0.1434	1.0031
chr11	135006516	13735012	0.1017	0.6759
chr12	133851895	14736793	0.1101	0.571
chr13	115169878	6155509	0.0534	0.3628
chr14	107349540	10269915	0.0957	0.5441
chr15	102531392	12356975	0.1205	0.565
chr16	90354753	12699519	0.1406	0.7228
chr17	81195210	9519376	0.1172	0.6549
chr18	78077248	5880533	0.0753	1.1035
chr19	59128983	9066131	0.1533	1.0012
chr20	63025520	9520064	0.1511	0.6956
chr21	48129895	5921115	0.123	0.7602
chr22	51304566	4550853	0.0887	0.5259
chrMT	16571	23315	1.407	2.0365
chrX	155270560	26867487	0.173	0.7147
chrY	59373566	1282357	0.0216	0.6985

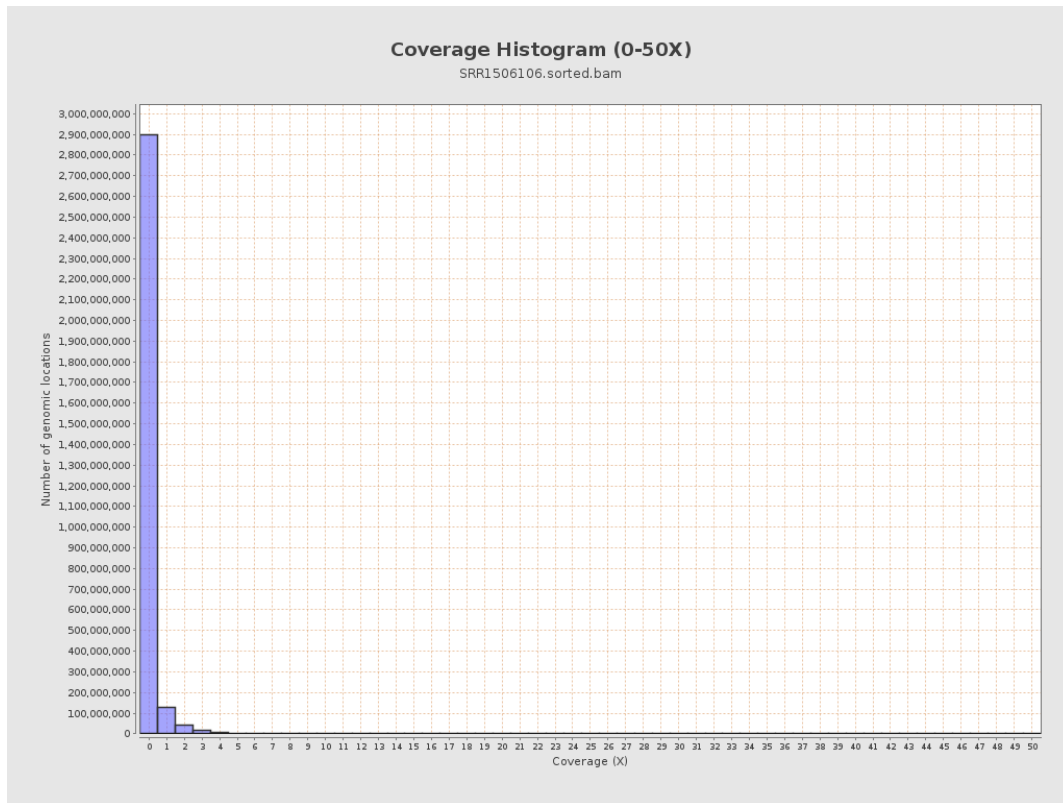
3. Results : Coverage across reference



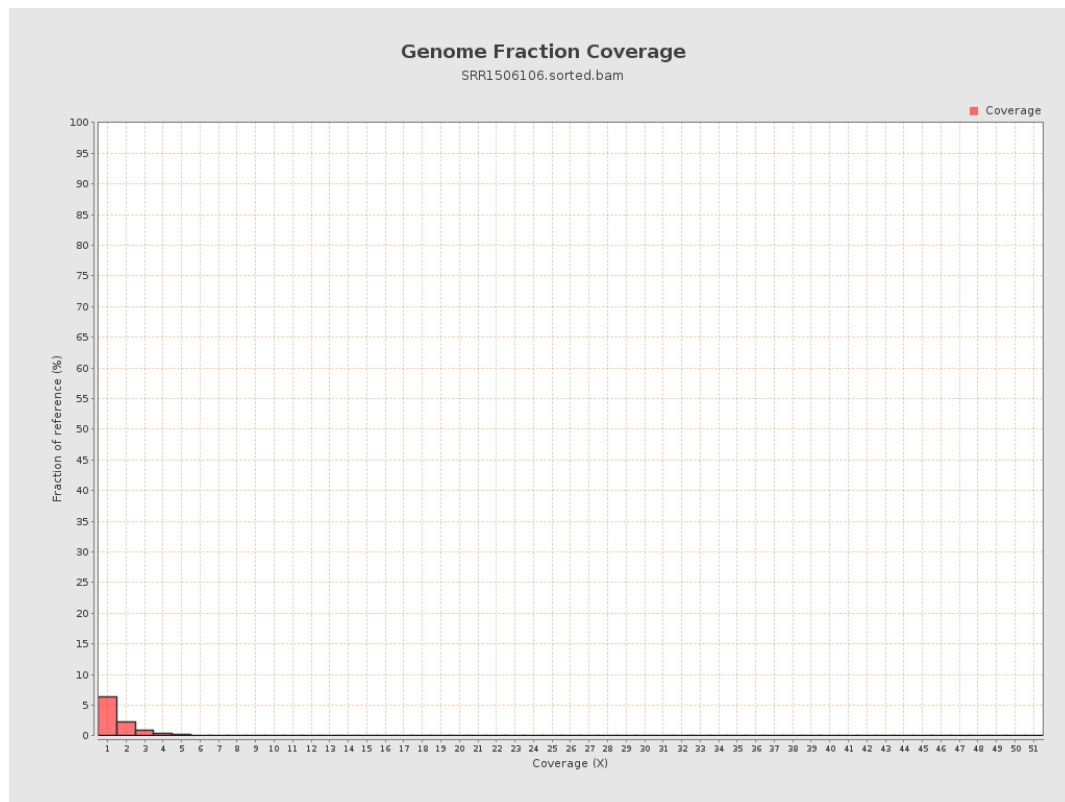
4. Results : Coverage Histogram



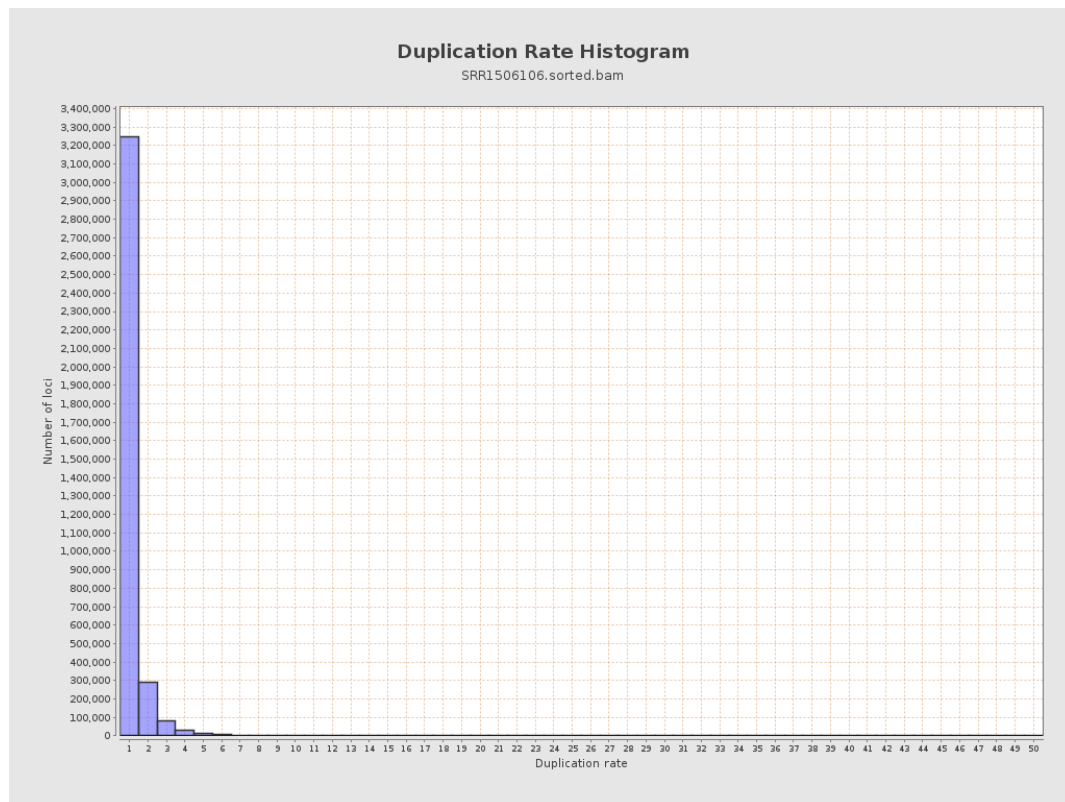
5. Results : Coverage Histogram (0-50X)



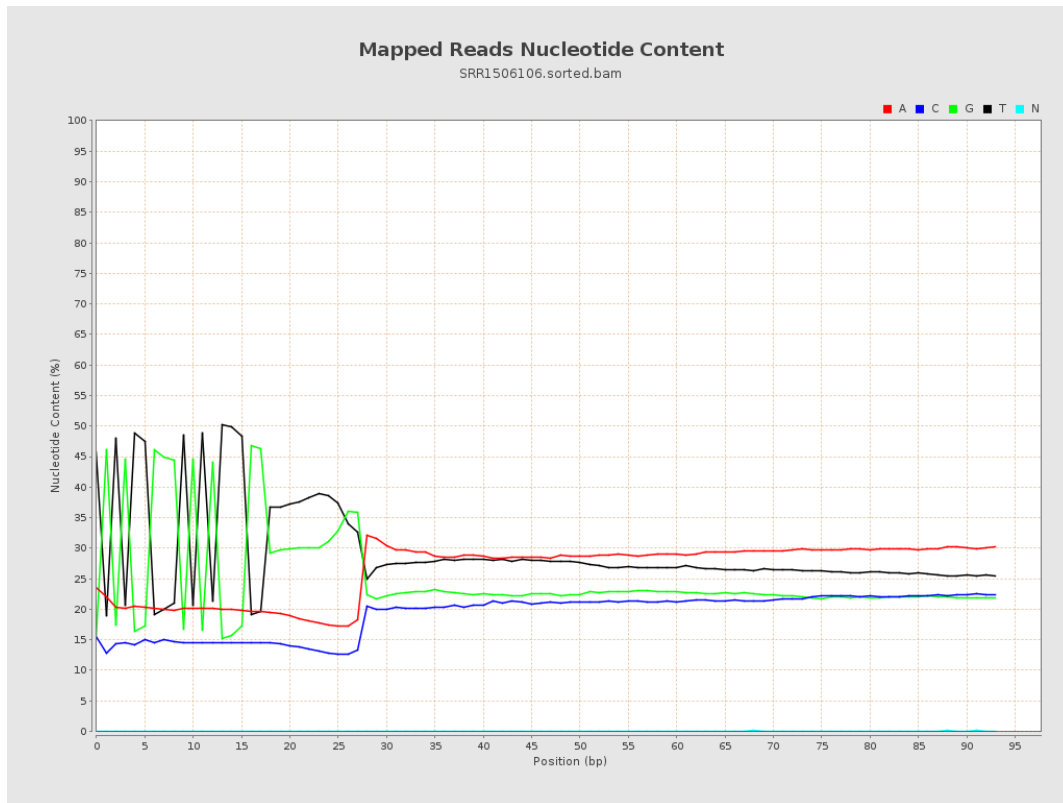
6. Results : Genome Fraction Coverage



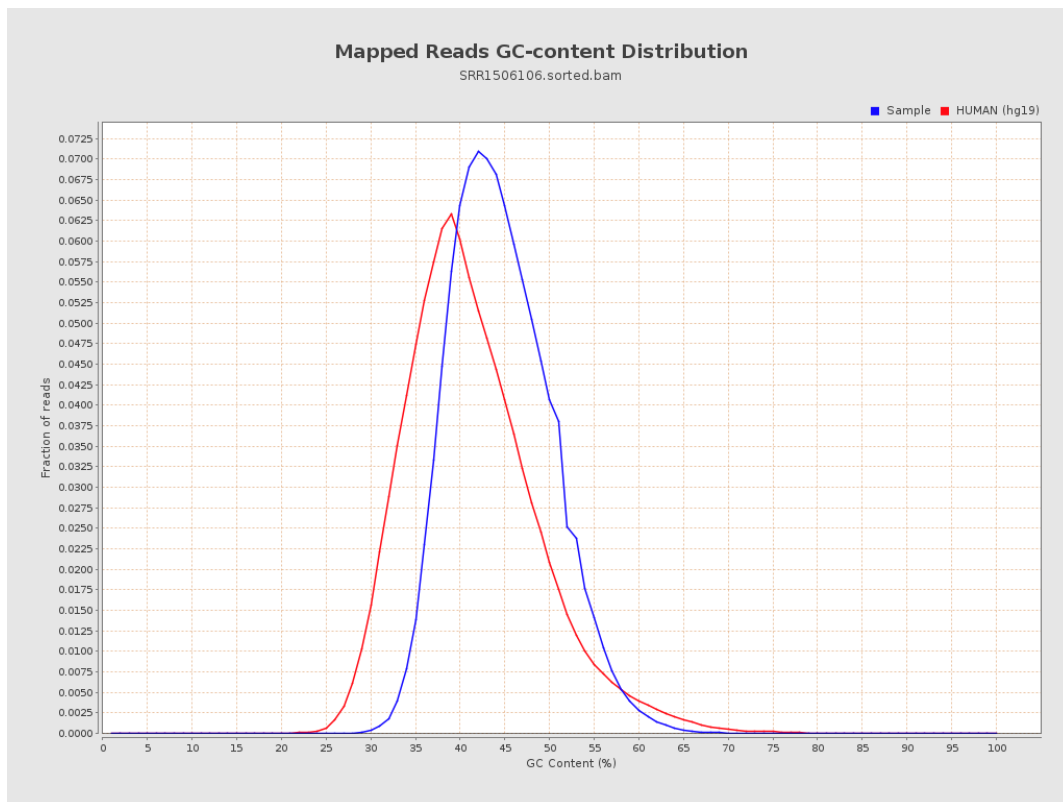
7. Results : Duplication Rate Histogram



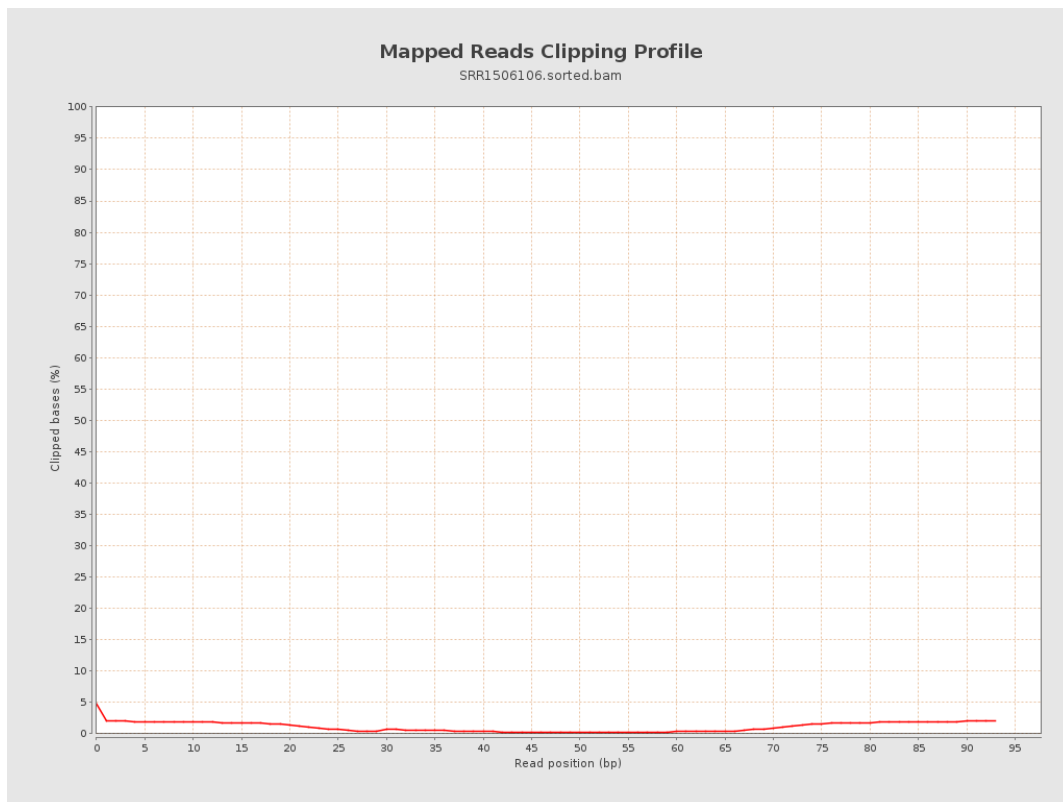
8. Results : Mapped Reads Nucleotide Content



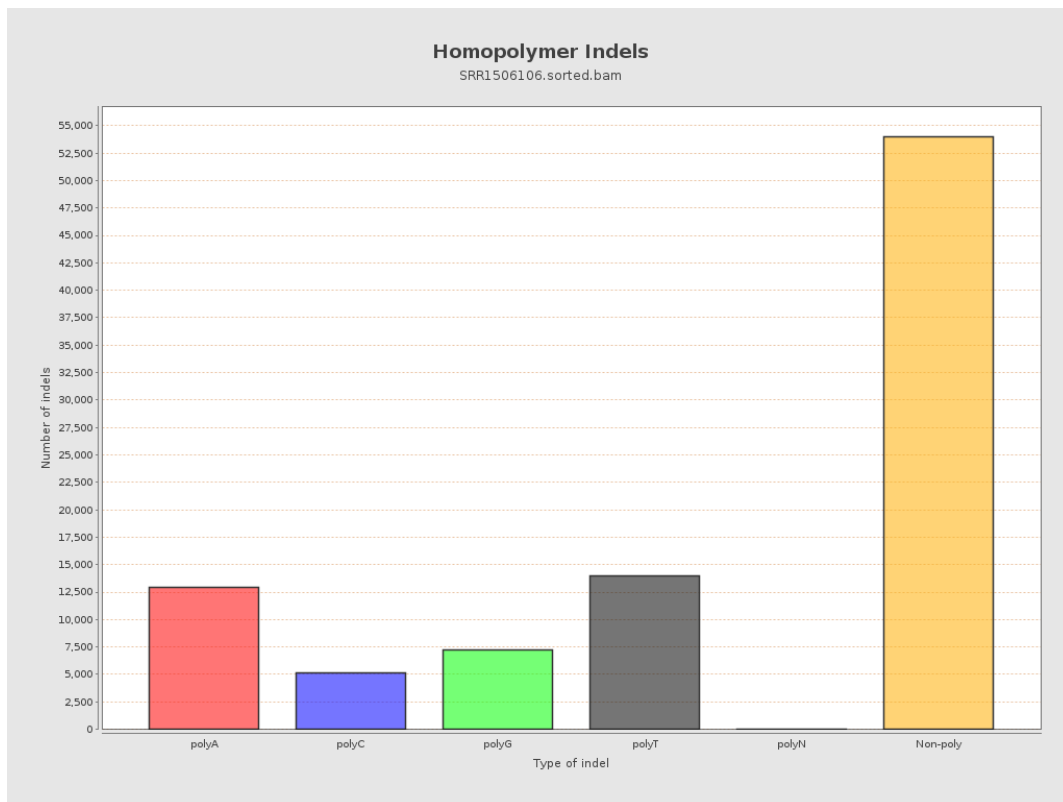
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

