

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 05:09:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506344.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_SRR1506344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506344.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 05:09:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,982,145
Mapped reads	4,092,356 / 68.41%
Unmapped reads	1,889,789 / 31.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	65,106 / 1.09%
Read min/max/mean length	30 / 94 / 94.39
Duplicated reads (estimated)	595,121 / 9.95%
Duplication rate	10.48%
Clipped reads	2,659,602 / 44.46%

2.2. ACGT Content

Number/percentage of A's	91,168,765 / 28.81%
Number/percentage of C's	58,855,136 / 18.6%
Number/percentage of T's	86,954,345 / 27.48%
Number/percentage of G's	79,411,254 / 25.09%
Number/percentage of N's	79,449 / 0.03%
GC Percentage	43.69%

2.3. Coverage

Mean	0.1023

Standard Deviation	0.7128
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2.4. Mapping Quality

Mean Mapping Quality	47.37
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2.5. Mismatches and indels

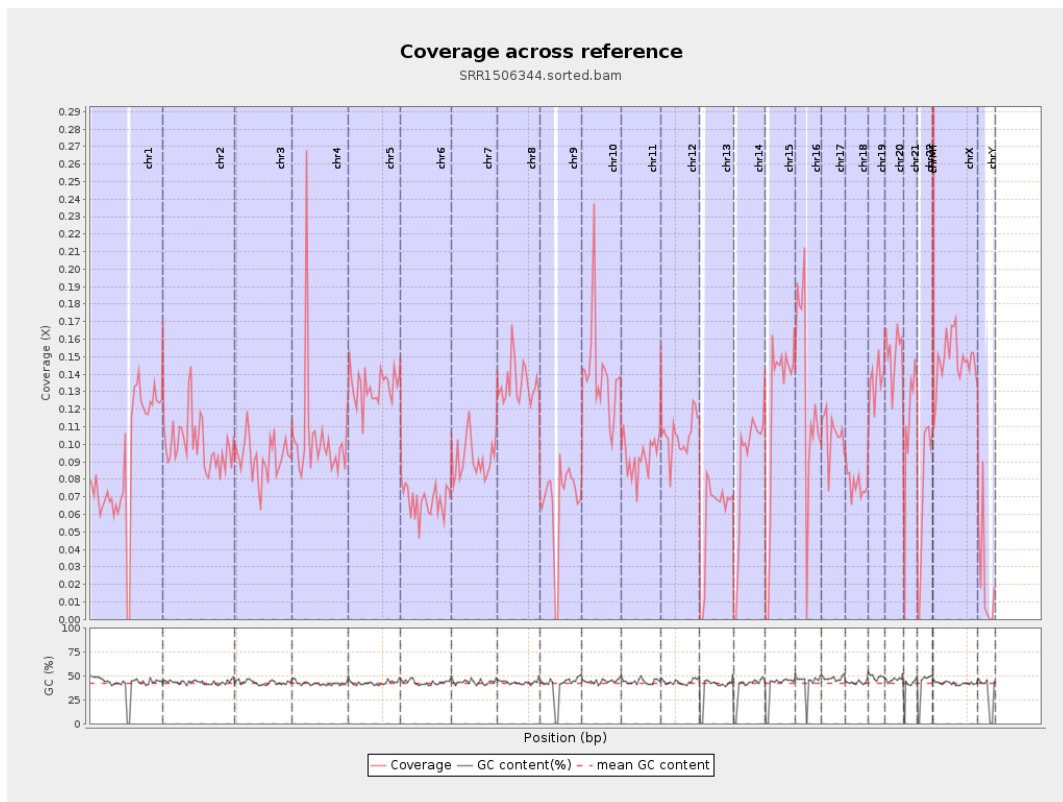
General error rate	0.74%
Mismatches	2,273,015
Insertions	28,563
Mapped reads with at least one insertion	0.68%
Deletions	65,673
Mapped reads with at least one deletion	1.57%
Homopolymer indels	42.88%

2.6. Chromosome stats

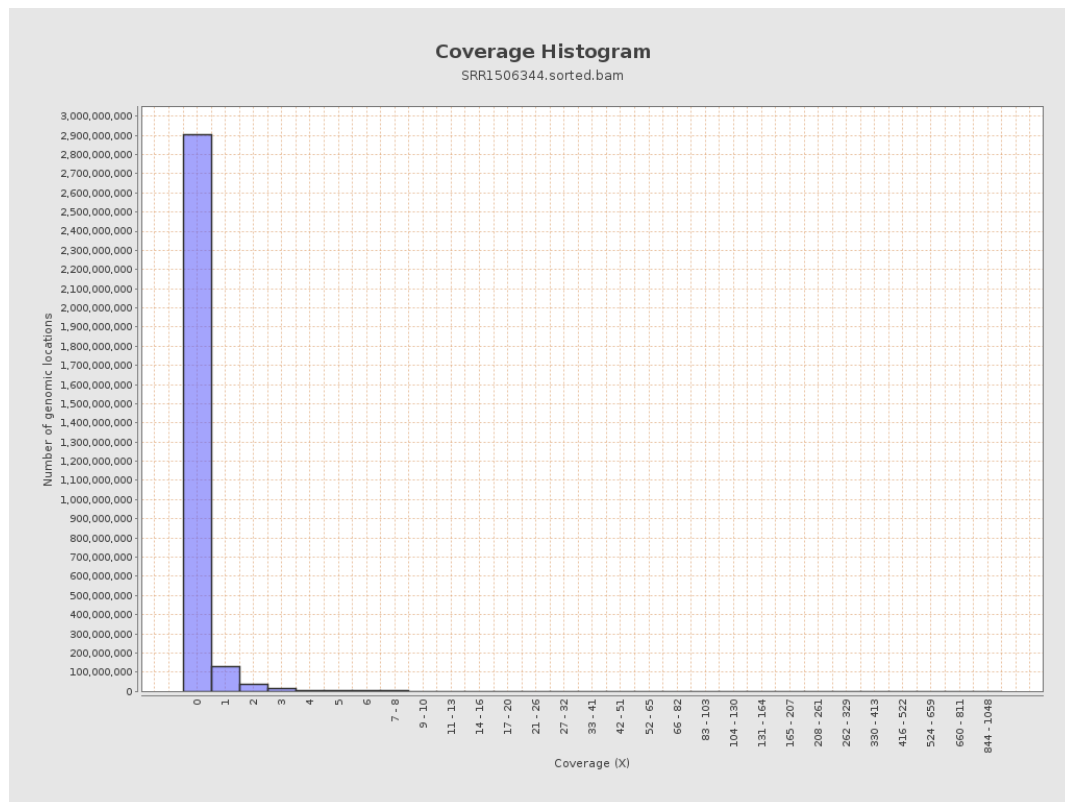
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22672843	0.091	0.9616
chr2	243199373	24279354	0.0998	0.7964
chr3	198022430	18369758	0.0928	0.4648
chr4	191154276	19857710	0.1039	0.8161
chr5	180915260	24081827	0.1331	0.5699
chr6	171115067	11525536	0.0674	0.4092
chr7	159138663	14766199	0.0928	0.7828

chr8	146364022	19672955	0.1344	0.9631
chr9	141213431	9548701	0.0676	0.5759
chr10	135534747	18818265	0.1388	0.979
chr11	135006516	12595297	0.0933	0.5997
chr12	133851895	14070086	0.1051	0.5256
chr13	115169878	6826646	0.0593	0.3663
chr14	107349540	9443508	0.088	0.4895
chr15	102531392	12233782	0.1193	0.5427
chr16	90354753	11520980	0.1275	0.7124
chr17	81195210	8675376	0.1068	0.5698
chr18	78077248	6009661	0.077	0.8284
chr19	59128983	8093123	0.1369	0.8143
chr20	63025520	9536463	0.1513	0.6834
chr21	48129895	5466482	0.1136	0.7997
chr22	51304566	3822661	0.0745	0.4906
chrMT	16571	461211	27.8324	15.6393
chrX	155270560	22936736	0.1477	0.635
chrY	59373566	1320508	0.0222	0.8645

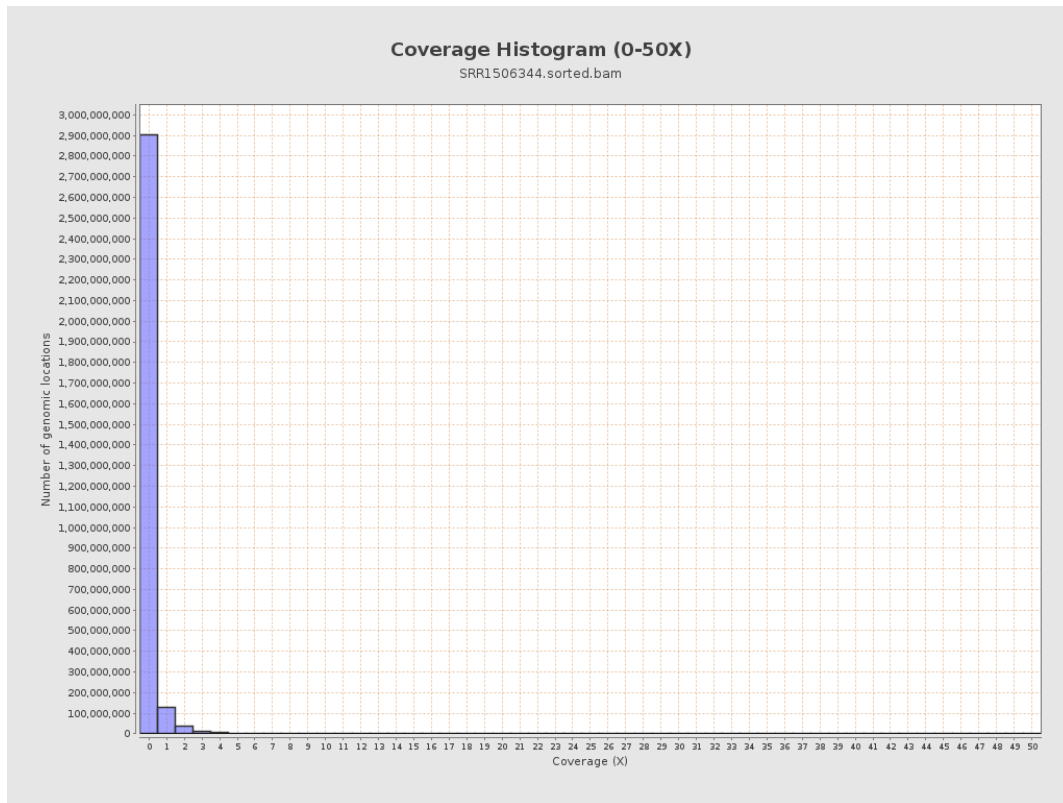
3. Results : Coverage across reference



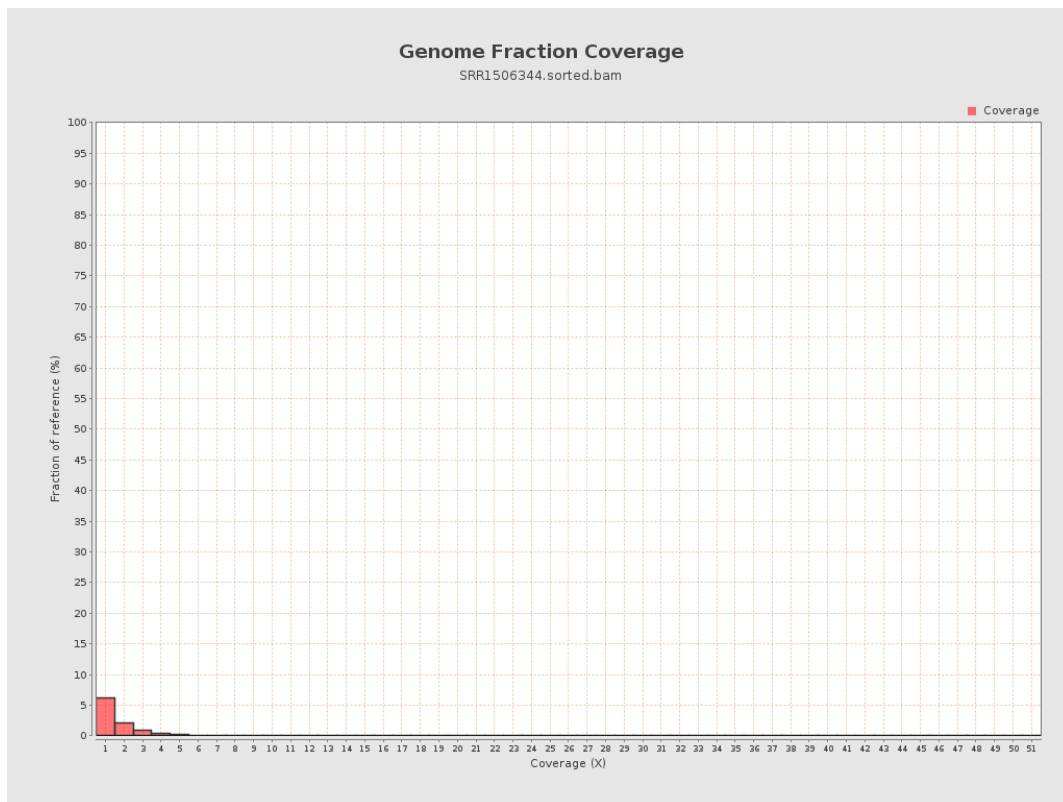
4. Results : Coverage Histogram



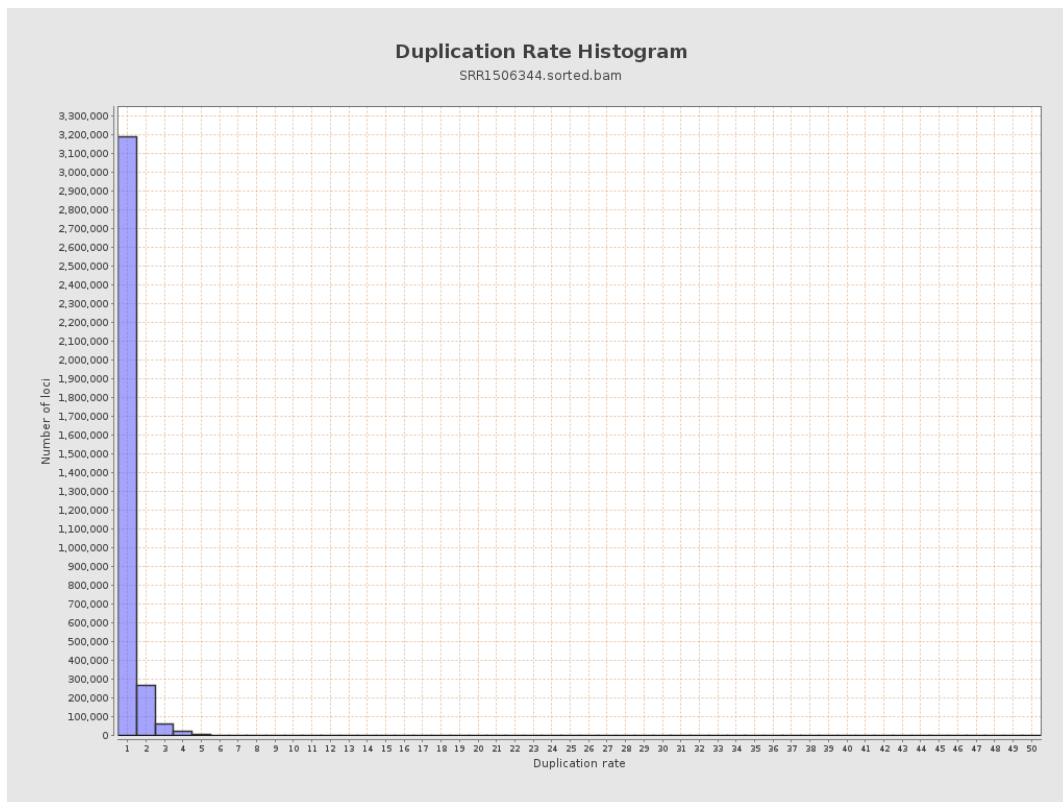
5. Results : Coverage Histogram (0-50X)



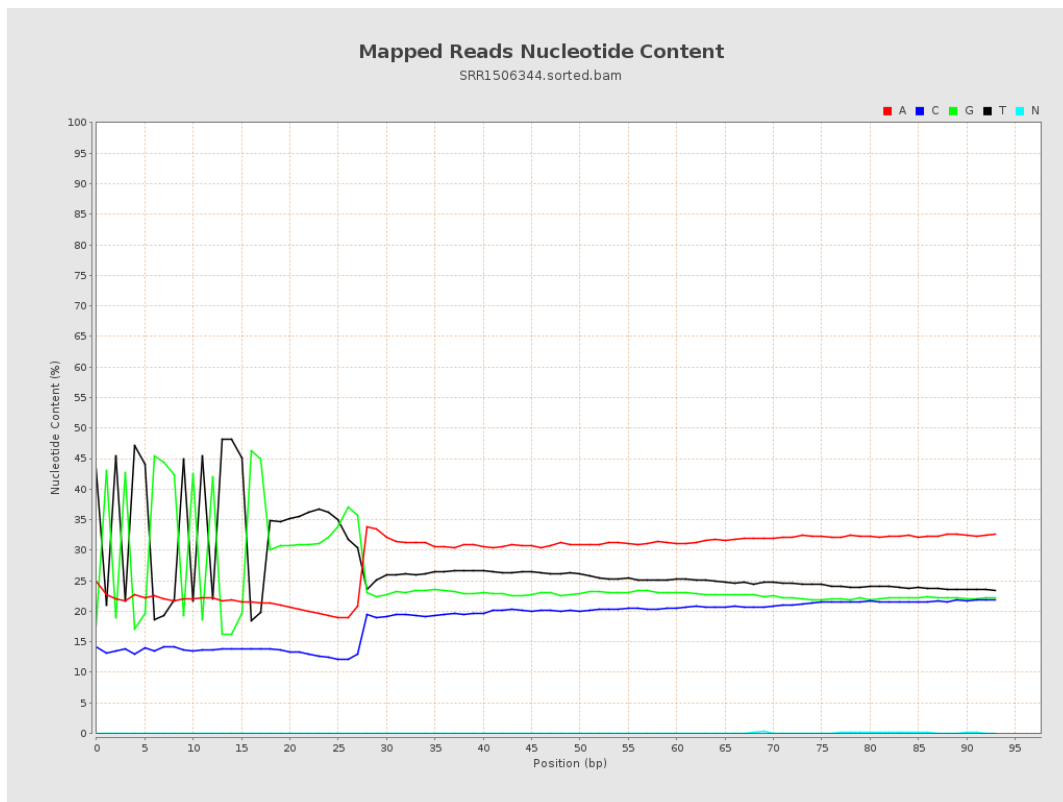
6. Results : Genome Fraction Coverage



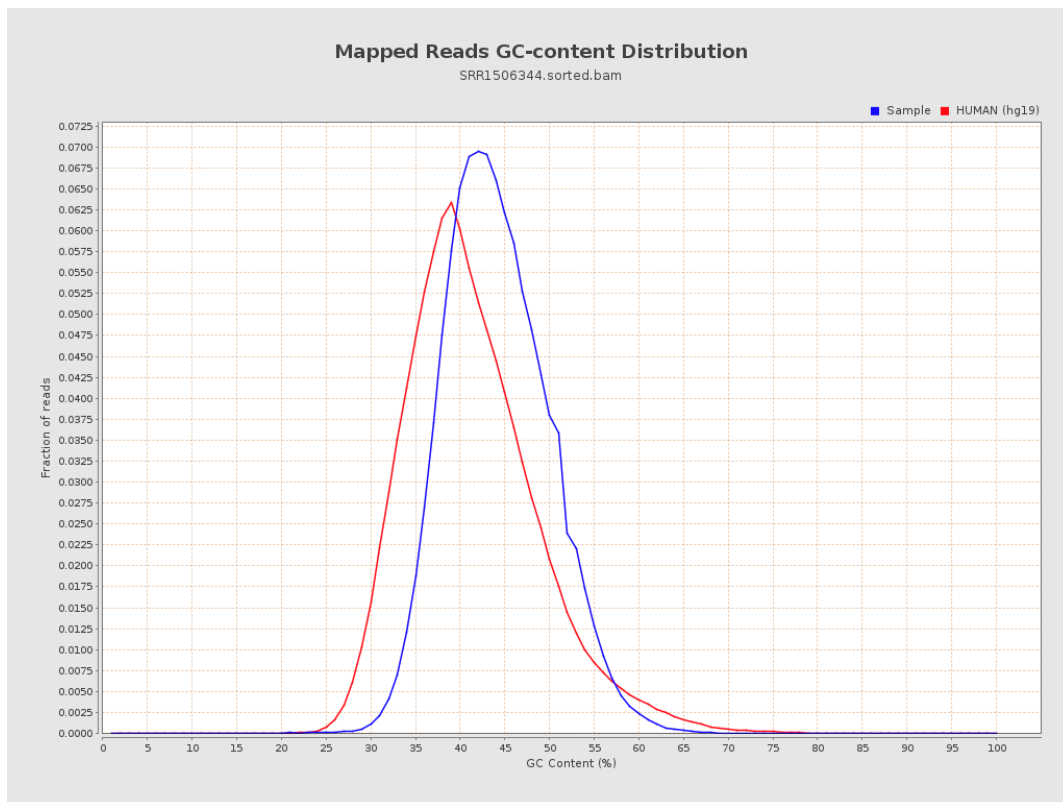
7. Results : Duplication Rate Histogram



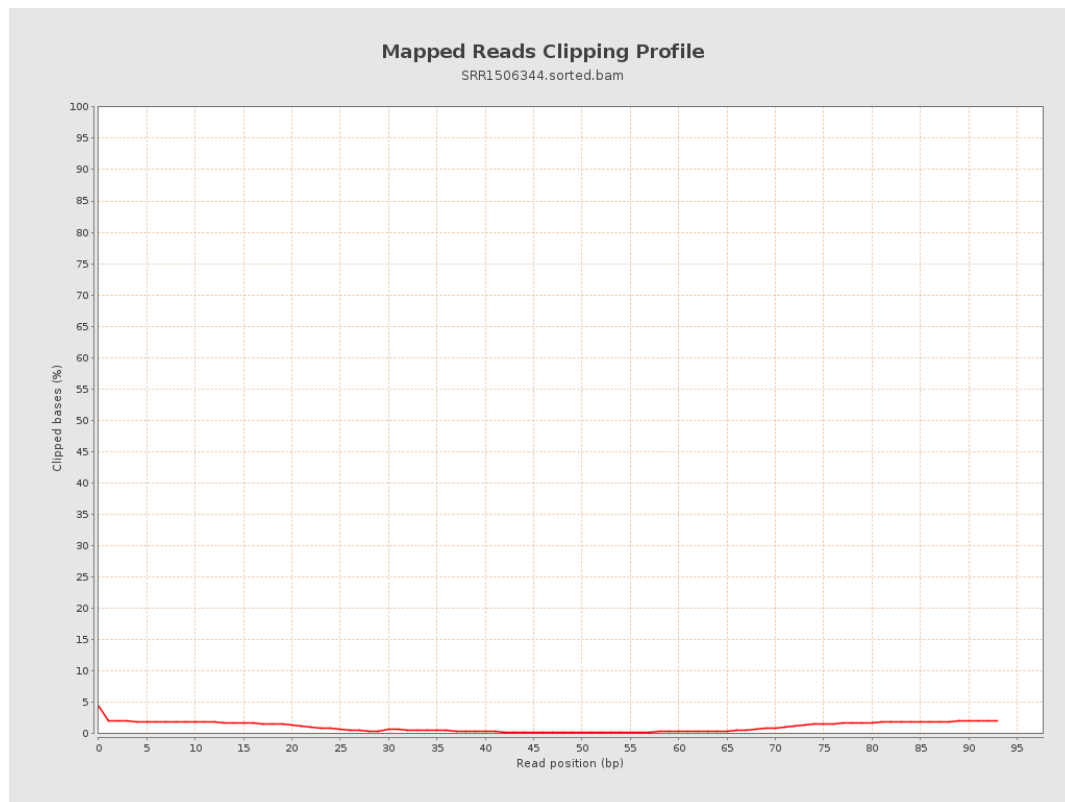
8. Results : Mapped Reads Nucleotide Content



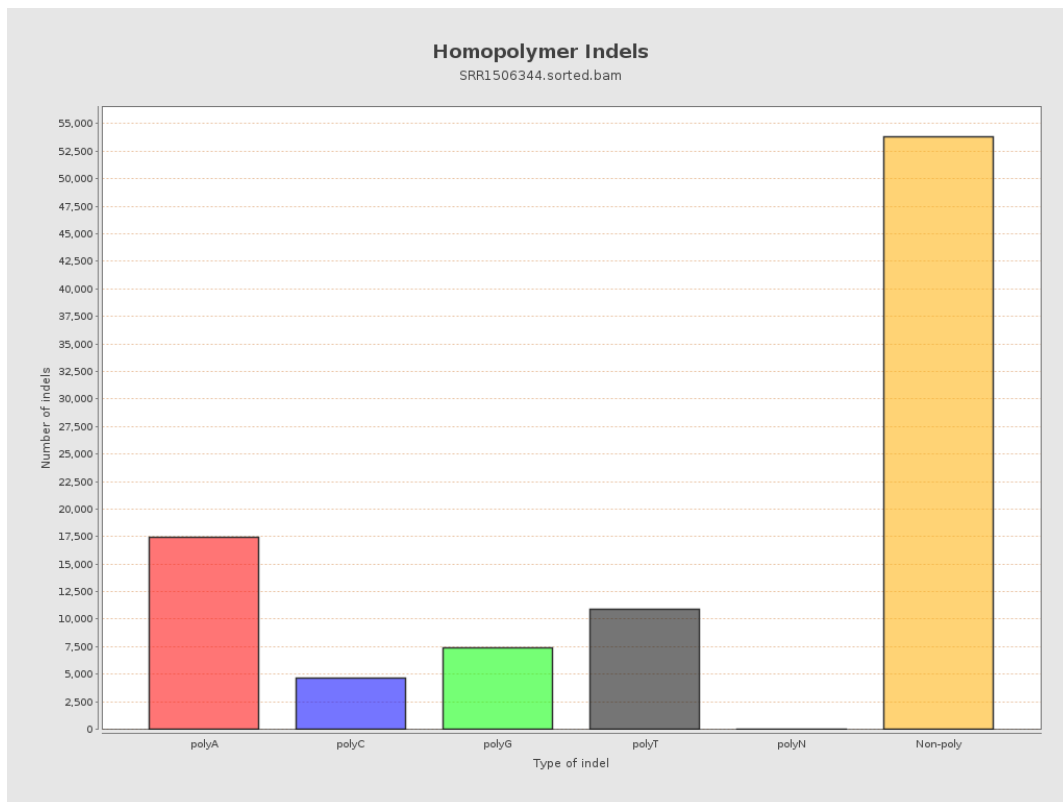
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

