

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:49:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506334.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_SRR1506334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:49:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,764,653
Mapped reads	4,507,537 / 58.05%
Unmapped reads	3,257,116 / 41.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,897 / 0.89%
Read min/max/mean length	30 / 94 / 94.32
Duplicated reads (estimated)	450,035 / 5.8%
Duplication rate	7.48%
Clipped reads	3,068,409 / 39.52%

2.2. ACGT Content

Number/percentage of A's	95,944,500 / 28.09%
Number/percentage of C's	64,662,875 / 18.93%
Number/percentage of T's	97,493,013 / 28.54%
Number/percentage of G's	83,394,125 / 24.41%
Number/percentage of N's	88,476 / 0.03%
GC Percentage	43.34%

2.3. Coverage

Mean	0.1104

Standard Deviation	0.7389
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2.4. Mapping Quality

Mean Mapping Quality	47.23
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2.5. Mismatches and indels

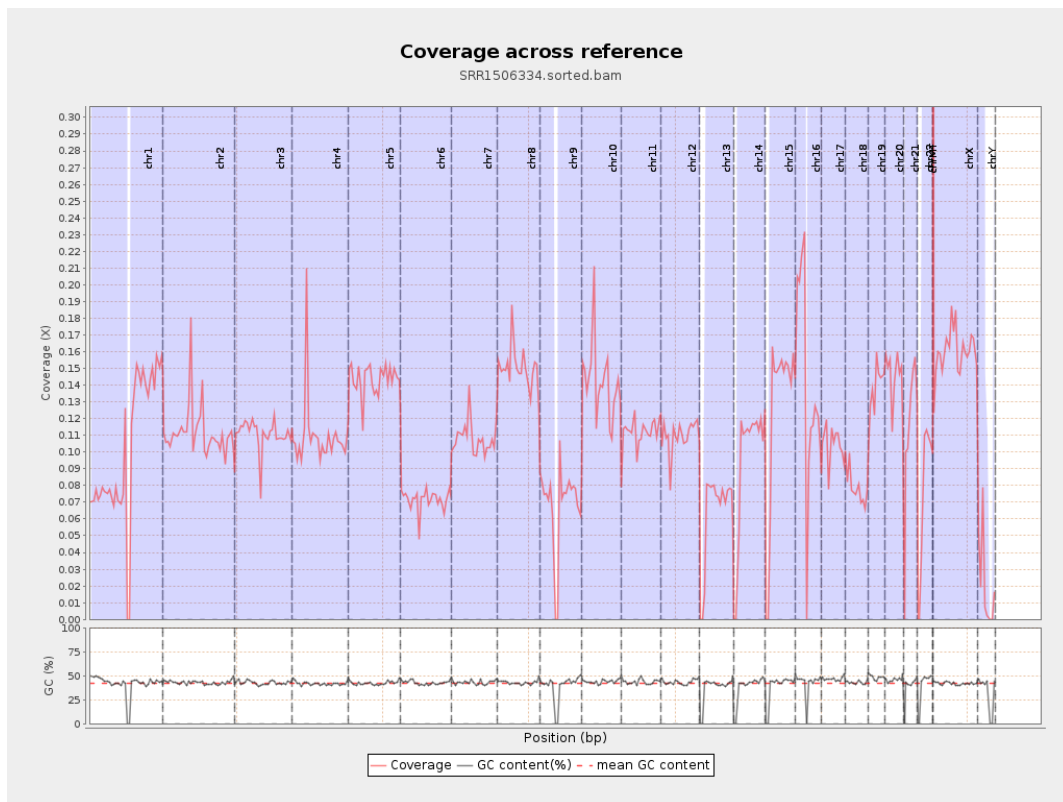
General error rate	0.72%
Mismatches	2,409,040
Insertions	27,189
Mapped reads with at least one insertion	0.59%
Deletions	69,483
Mapped reads with at least one deletion	1.51%
Homopolymer indels	43.6%

2.6. Chromosome stats

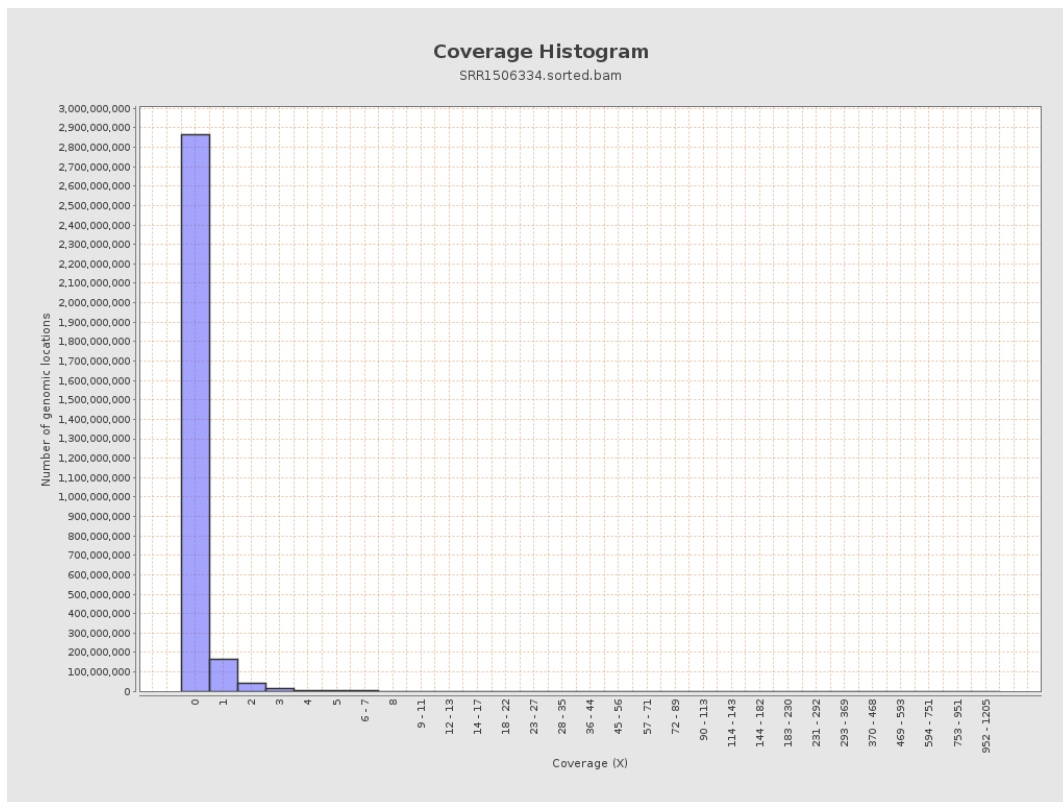
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25396654	0.1019	1.1469
chr2	243199373	27220770	0.1119	0.8223
chr3	198022430	21871817	0.1105	0.4669
chr4	191154276	20936360	0.1095	0.6657
chr5	180915260	25894549	0.1431	0.5357
chr6	171115067	12224408	0.0714	0.391
chr7	159138663	17233825	0.1083	0.9472

chr8	146364022	21932936	0.1499	1.015
chr9	141213431	9626232	0.0682	0.6732
chr10	135534747	19136231	0.1412	0.8839
chr11	135006516	15125469	0.112	0.7204
chr12	133851895	14712703	0.1099	0.5179
chr13	115169878	7336493	0.0637	0.3439
chr14	107349540	10250316	0.0955	0.4986
chr15	102531392	12671363	0.1236	0.5106
chr16	90354753	12586474	0.1393	0.6234
chr17	81195210	8555446	0.1054	0.5454
chr18	78077248	6126566	0.0785	1.1365
chr19	59128983	8216664	0.139	0.9497
chr20	63025520	9142733	0.1451	0.5791
chr21	48129895	5616966	0.1167	0.6002
chr22	51304566	3880087	0.0756	0.3934
chrMT	16571	19239	1.161	1.896
chrX	155270560	24781151	0.1596	0.6466
chrY	59373566	1225595	0.0206	0.6857

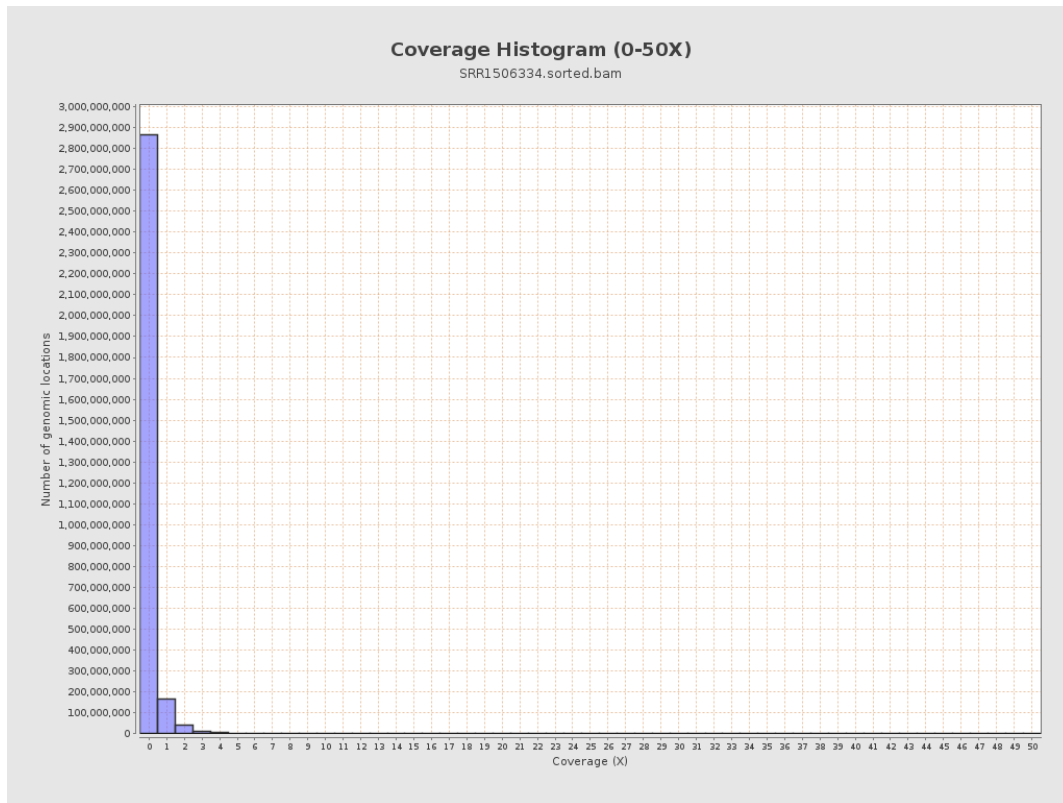
3. Results : Coverage across reference



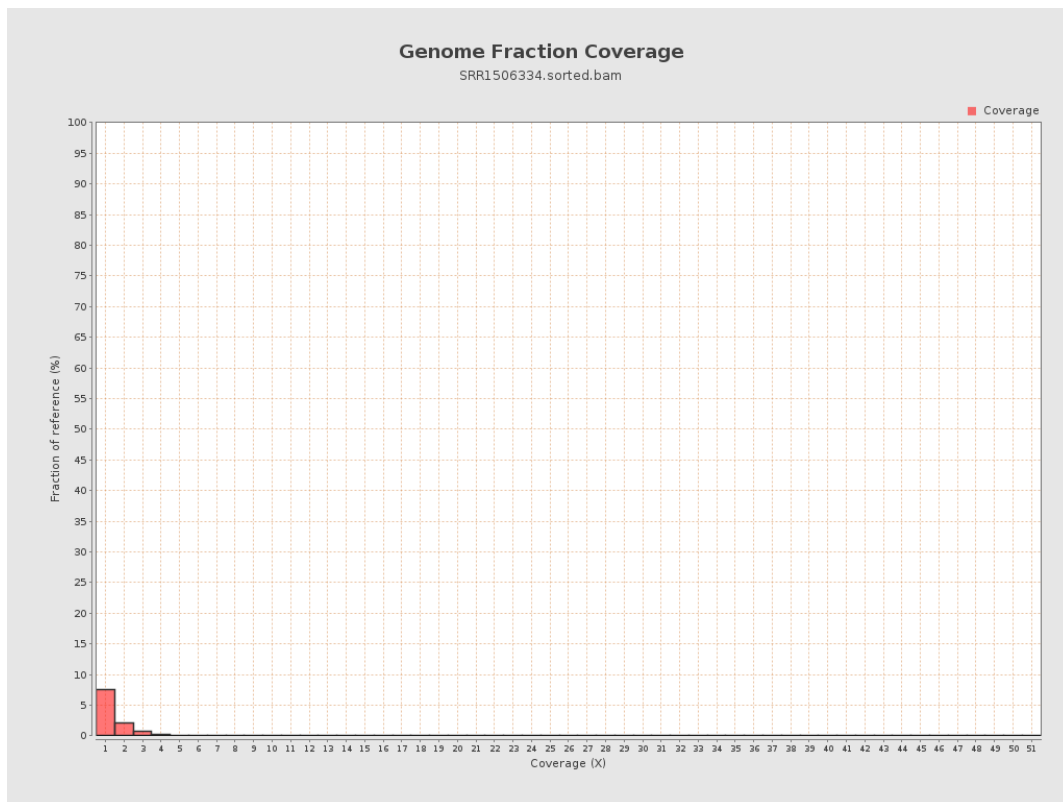
4. Results : Coverage Histogram



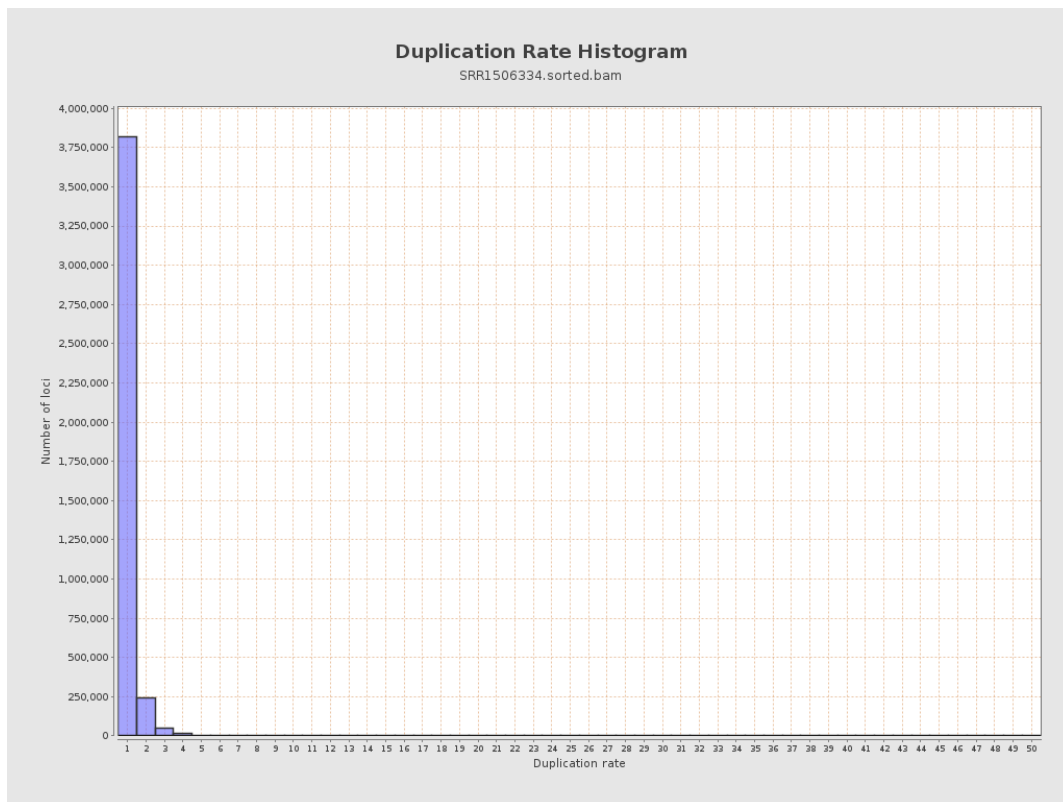
5. Results : Coverage Histogram (0-50X)



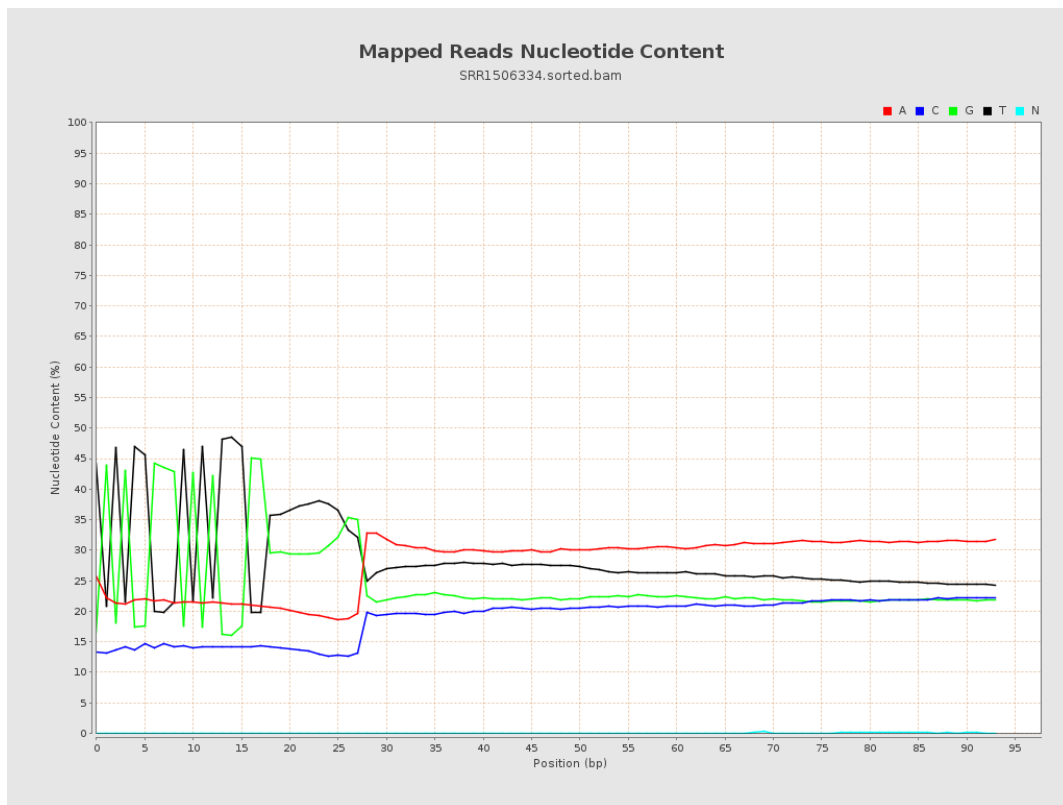
6. Results : Genome Fraction Coverage



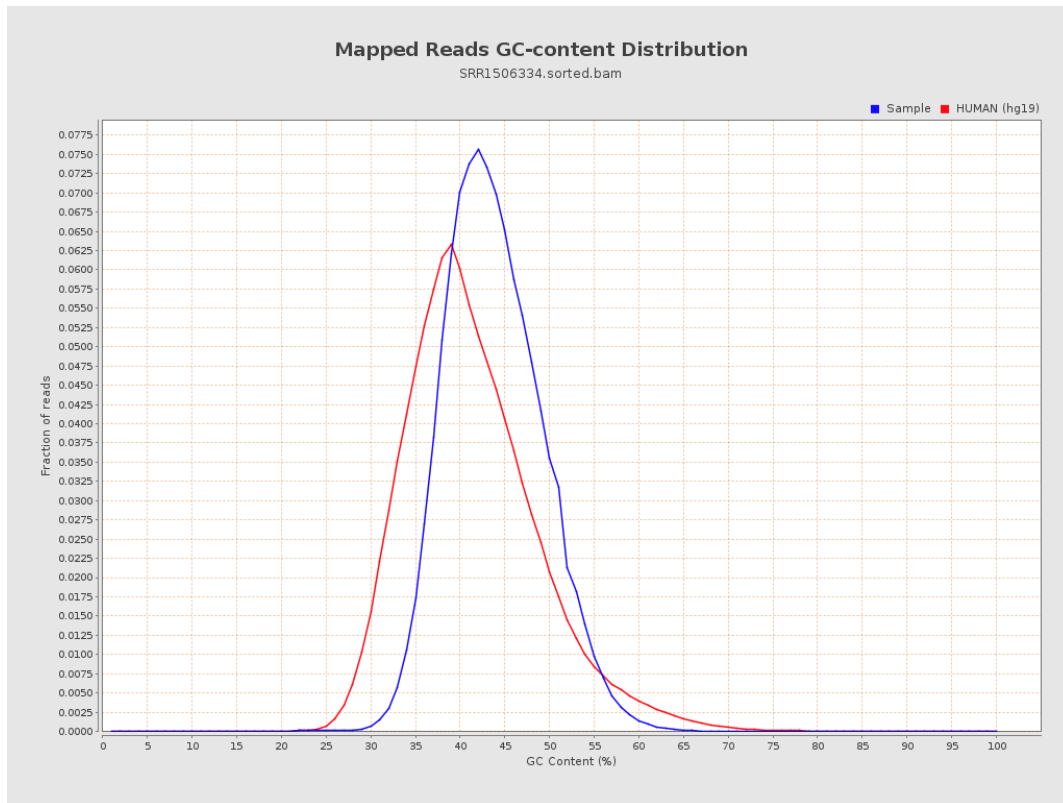
7. Results : Duplication Rate Histogram



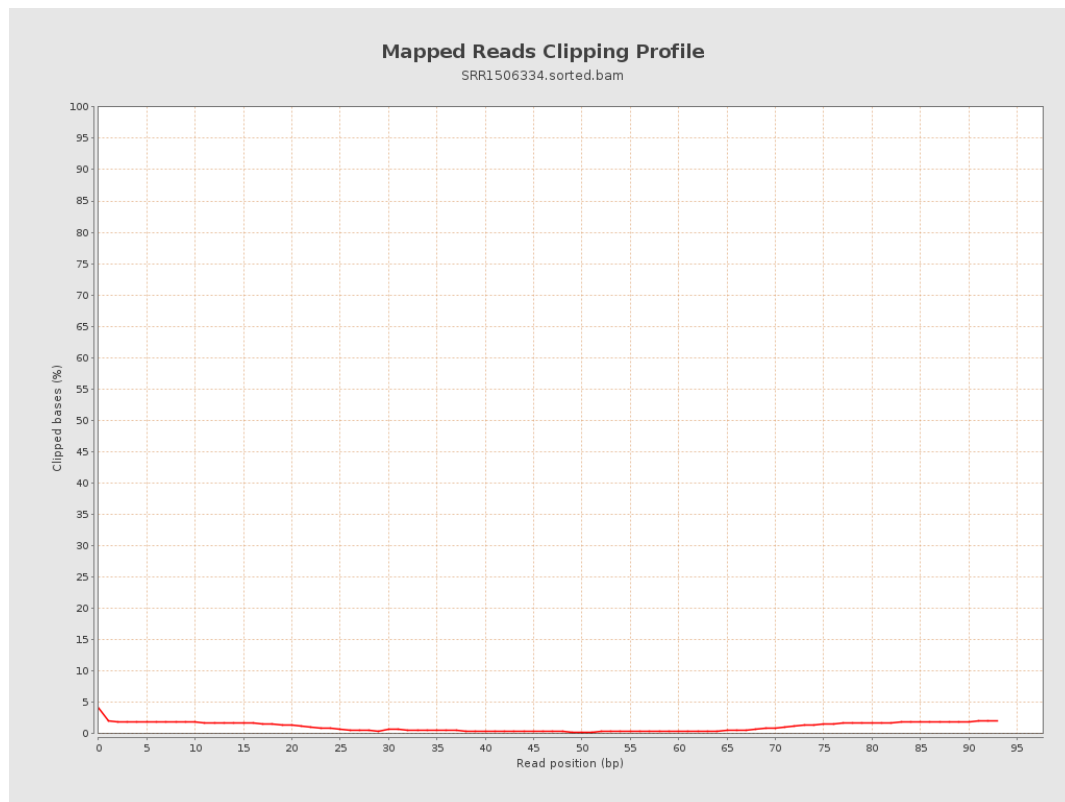
8. Results : Mapped Reads Nucleotide Content



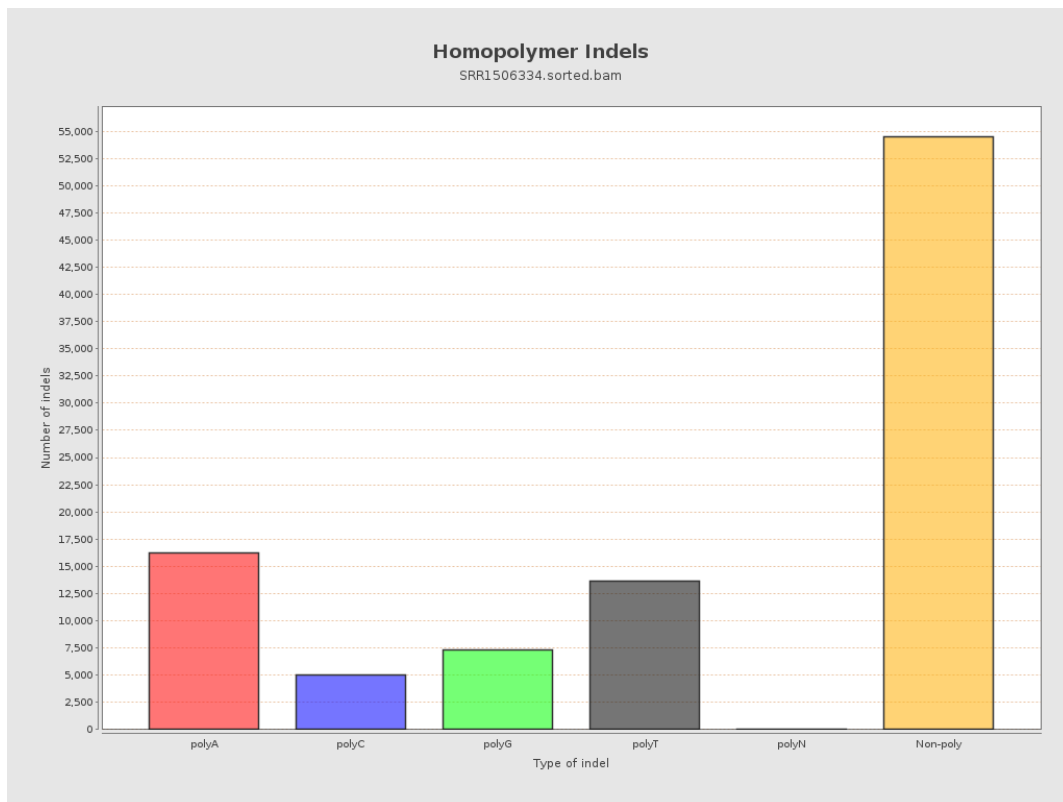
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

