

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 05:18:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506345.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_SRR1506345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506345.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 05:18:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,296,961
Mapped reads	6,890,422 / 66.92%
Unmapped reads	3,406,539 / 33.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	96,109 / 0.93%
Read min/max/mean length	30 / 94 / 94.34
Duplicated reads (estimated)	1,184,552 / 11.5%
Duplication rate	12.51%
Clipped reads	5,032,545 / 48.87%

2.2. ACGT Content

Number/percentage of A's	144,551,182 / 28.22%
Number/percentage of C's	95,647,152 / 18.68%
Number/percentage of T's	140,552,005 / 27.44%
Number/percentage of G's	131,266,514 / 25.63%
Number/percentage of N's	127,737 / 0.02%
GC Percentage	44.31%

2.3. Coverage

Mean	0.1655

Standard Deviation	1.0518
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.39
----------------------	-------

2.5. Mismatches and indels

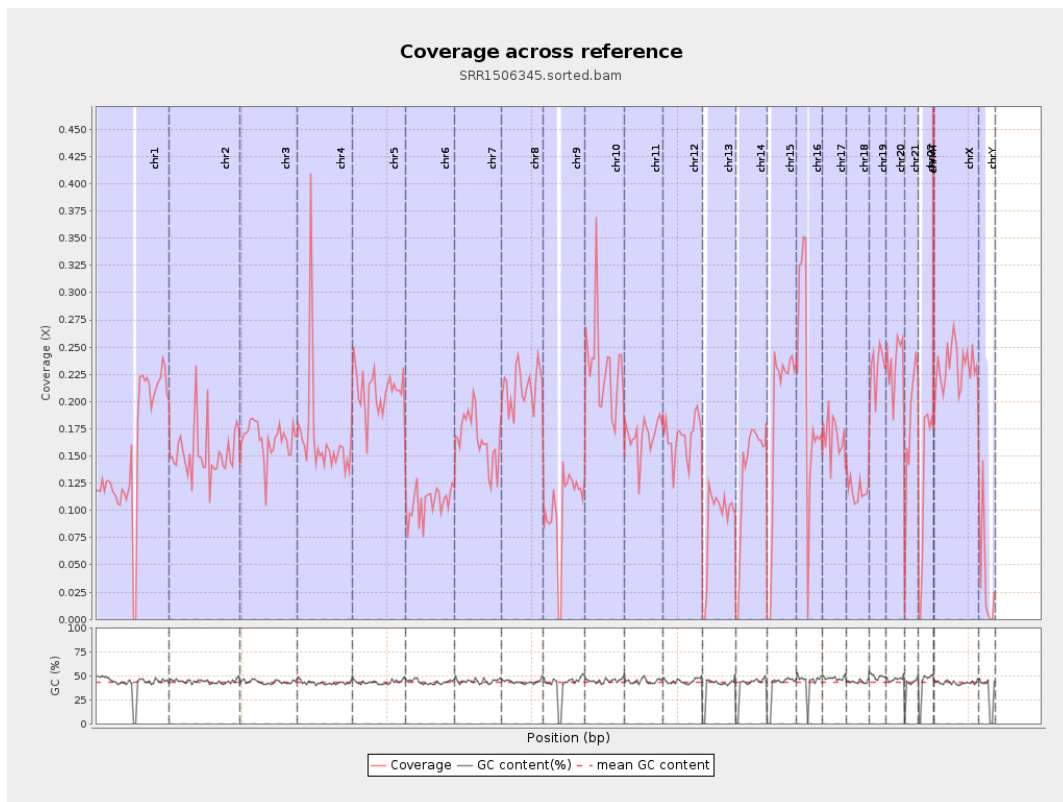
General error rate	0.78%
Mismatches	3,882,557
Insertions	43,831
Mapped reads with at least one insertion	0.62%
Deletions	103,535
Mapped reads with at least one deletion	1.47%
Homopolymer indels	41.67%

2.6. Chromosome stats

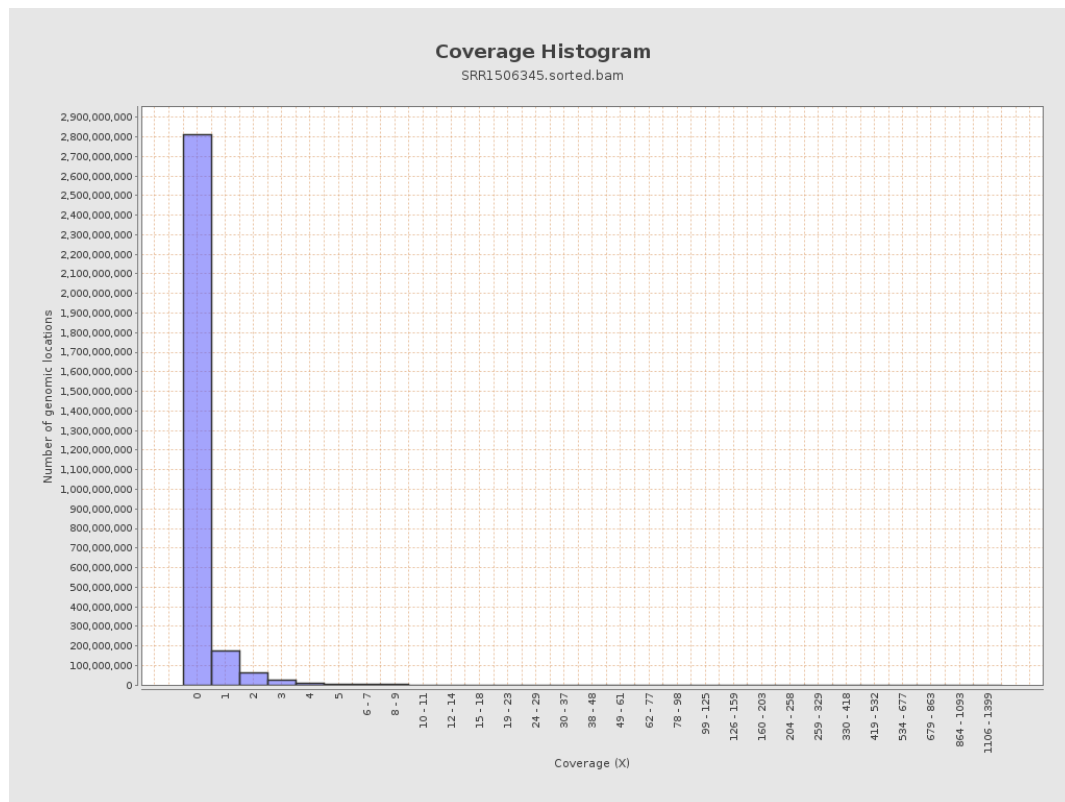
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	38614070	0.1549	1.3845
chr2	243199373	37186339	0.1529	1.1995
chr3	198022430	32668308	0.165	0.6852
chr4	191154276	31603320	0.1653	1.1938
chr5	180915260	37903261	0.2095	0.784
chr6	171115067	18403813	0.1076	0.5869
chr7	159138663	26477859	0.1664	1.3702

chr8	146364022	31298444	0.2138	1.2499
chr9	141213431	14322895	0.1014	0.869
chr10	135534747	31311604	0.231	1.5287
chr11	135006516	22798410	0.1689	0.9637
chr12	133851895	22267867	0.1664	0.7992
chr13	115169878	10295092	0.0894	0.4844
chr14	107349540	14373779	0.1339	0.6936
chr15	102531392	19302114	0.1883	0.8007
chr16	90354753	19125932	0.2117	0.9834
chr17	81195210	13626914	0.1678	0.8241
chr18	78077248	9258322	0.1186	1.3877
chr19	59128983	13648201	0.2308	1.2133
chr20	63025520	14753793	0.2341	0.9236
chr21	48129895	8620811	0.1791	1.0391
chr22	51304566	6473051	0.1262	0.6447
chrMT	16571	66870	4.0354	3.4846
chrX	155270560	35863581	0.231	0.8904
chrY	59373566	2093583	0.0353	1.4156

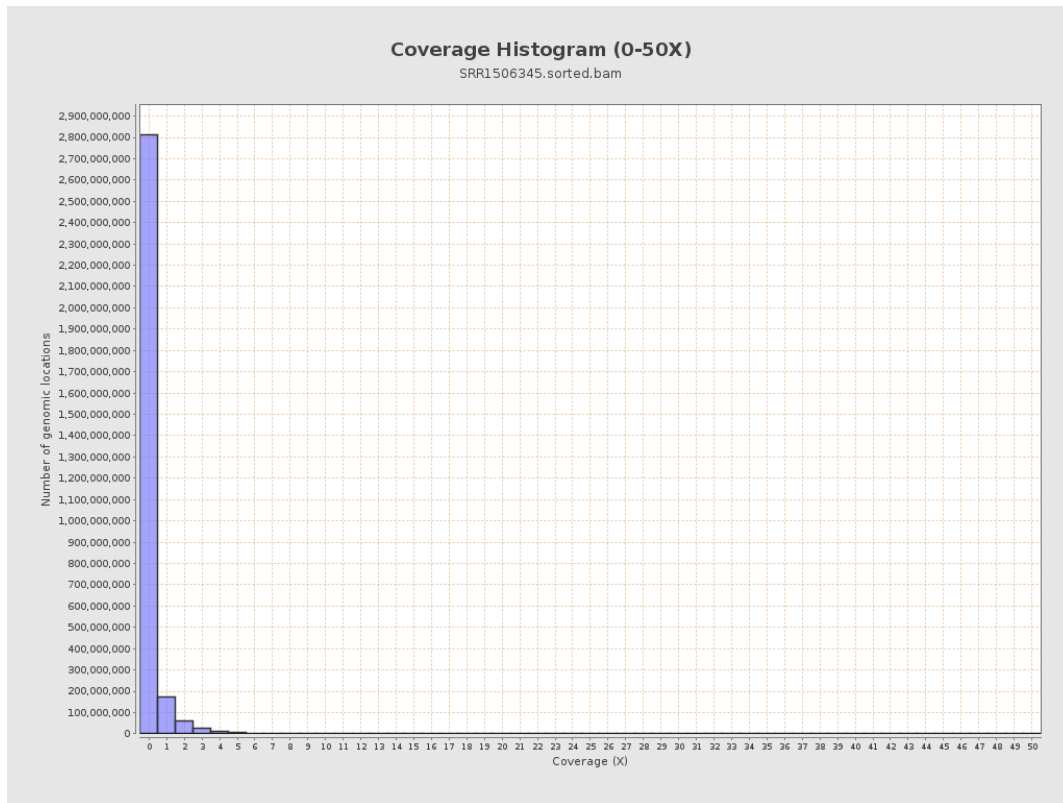
3. Results : Coverage across reference



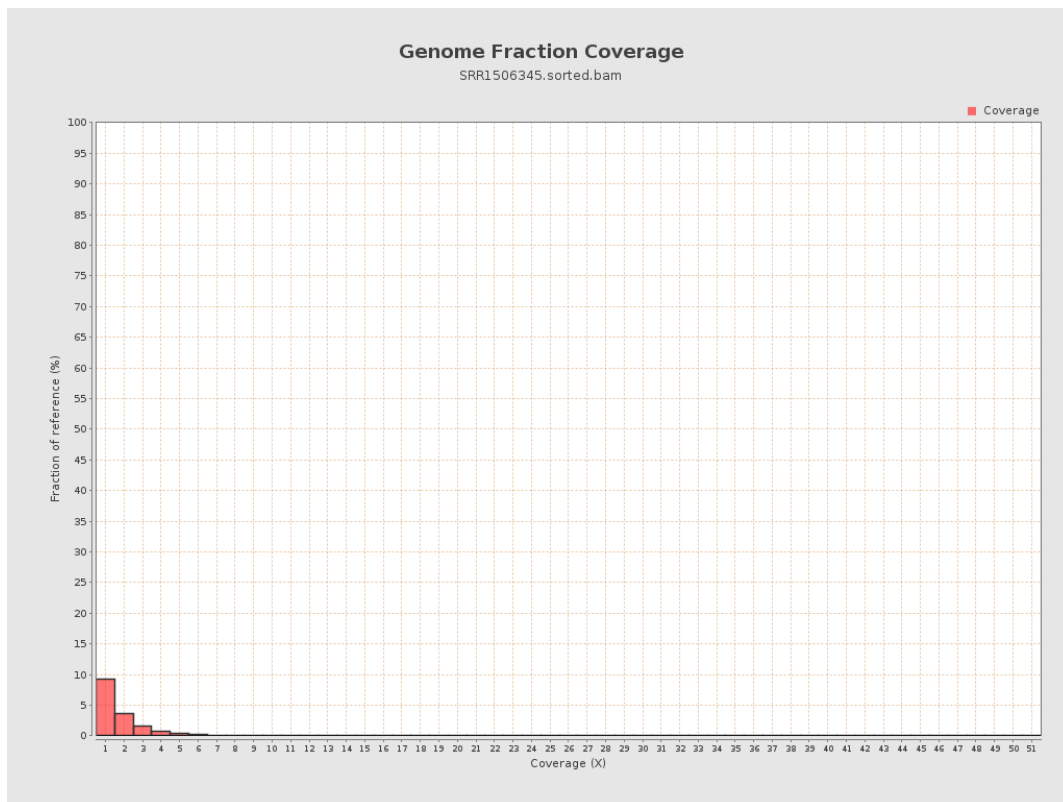
4. Results : Coverage Histogram



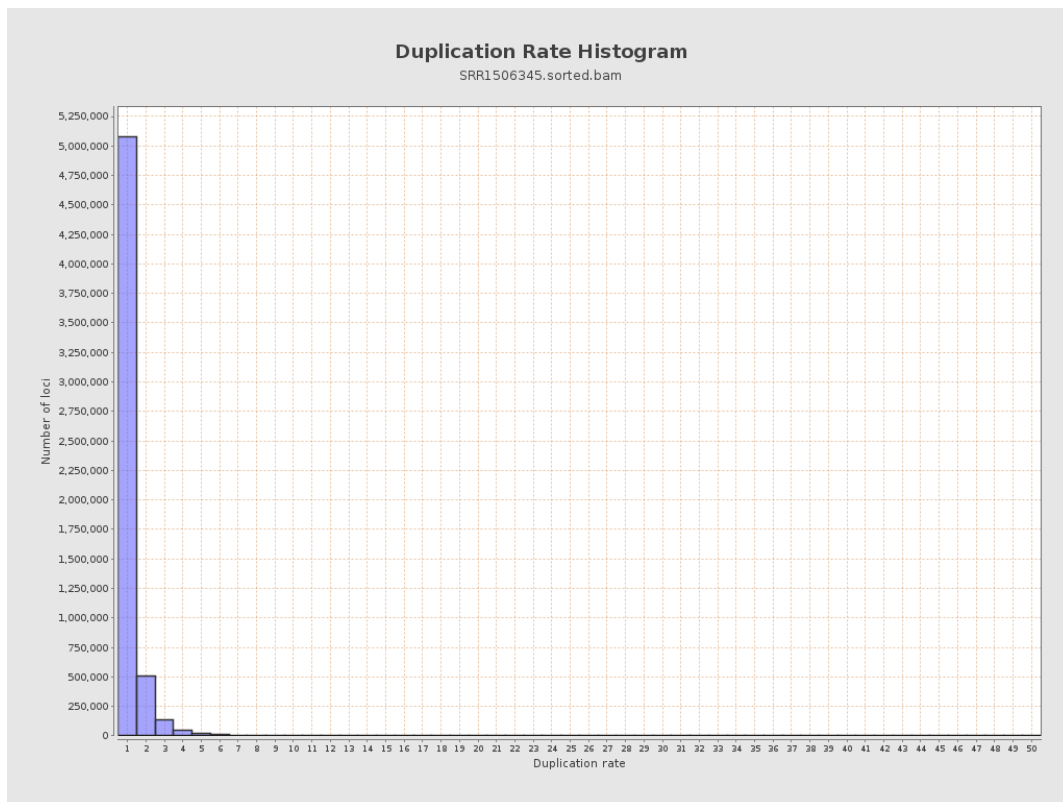
5. Results : Coverage Histogram (0-50X)



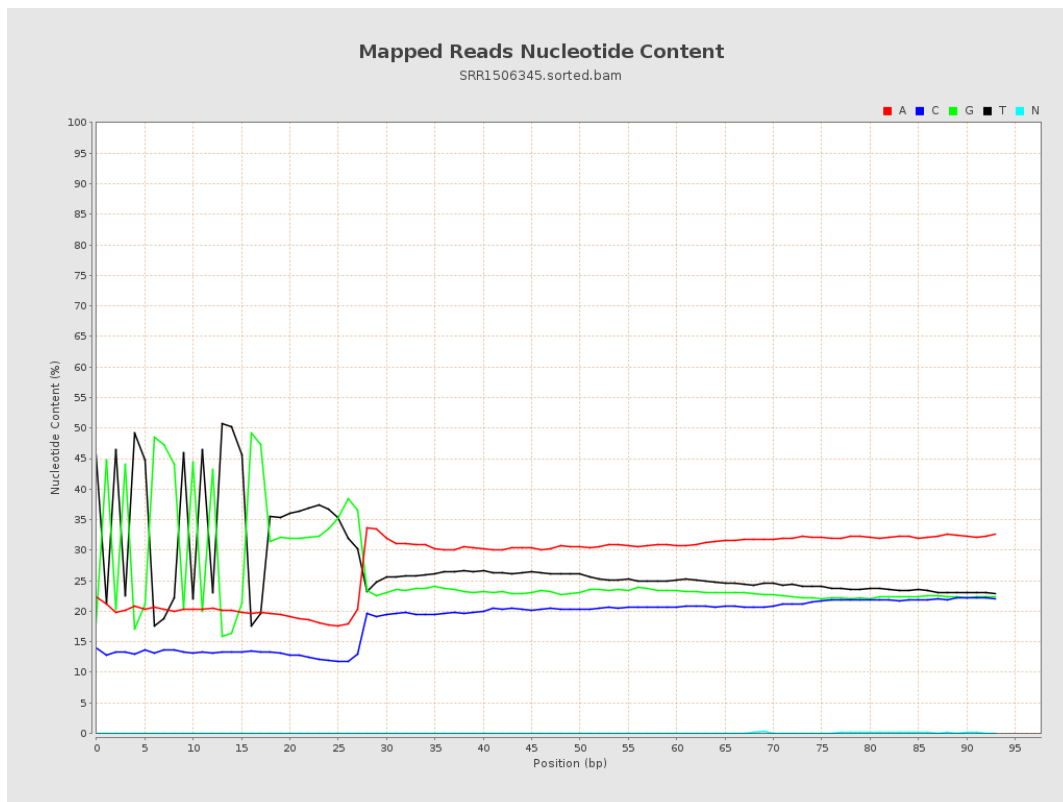
6. Results : Genome Fraction Coverage



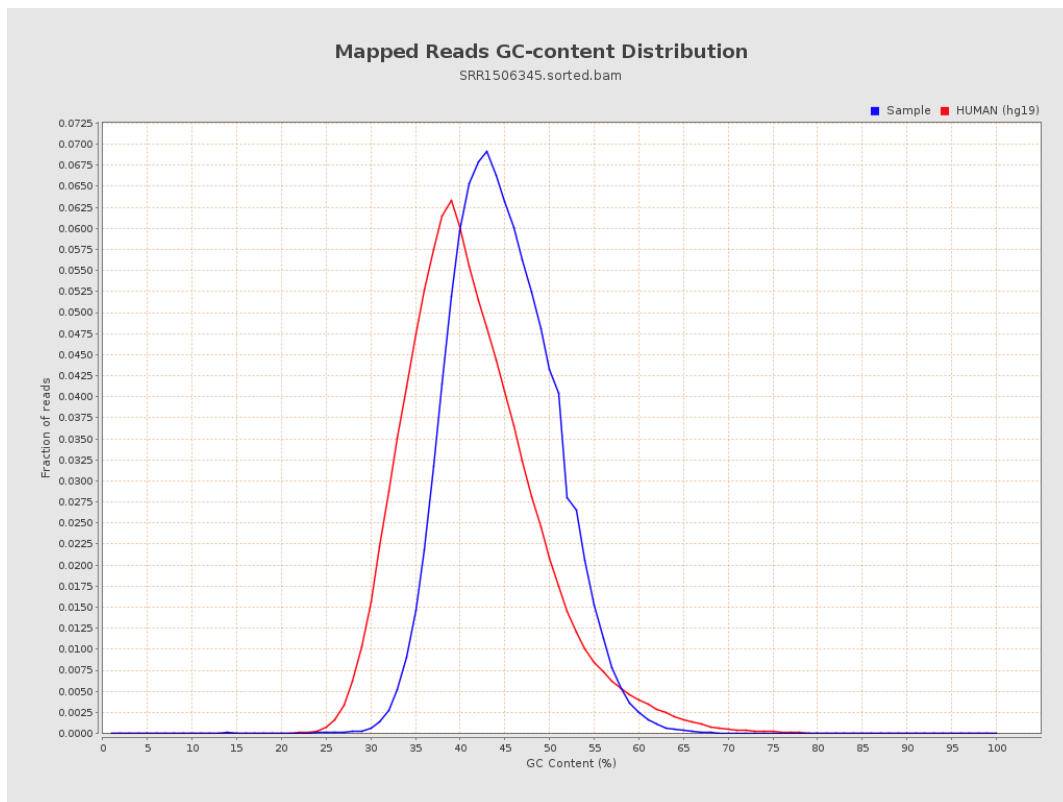
7. Results : Duplication Rate Histogram



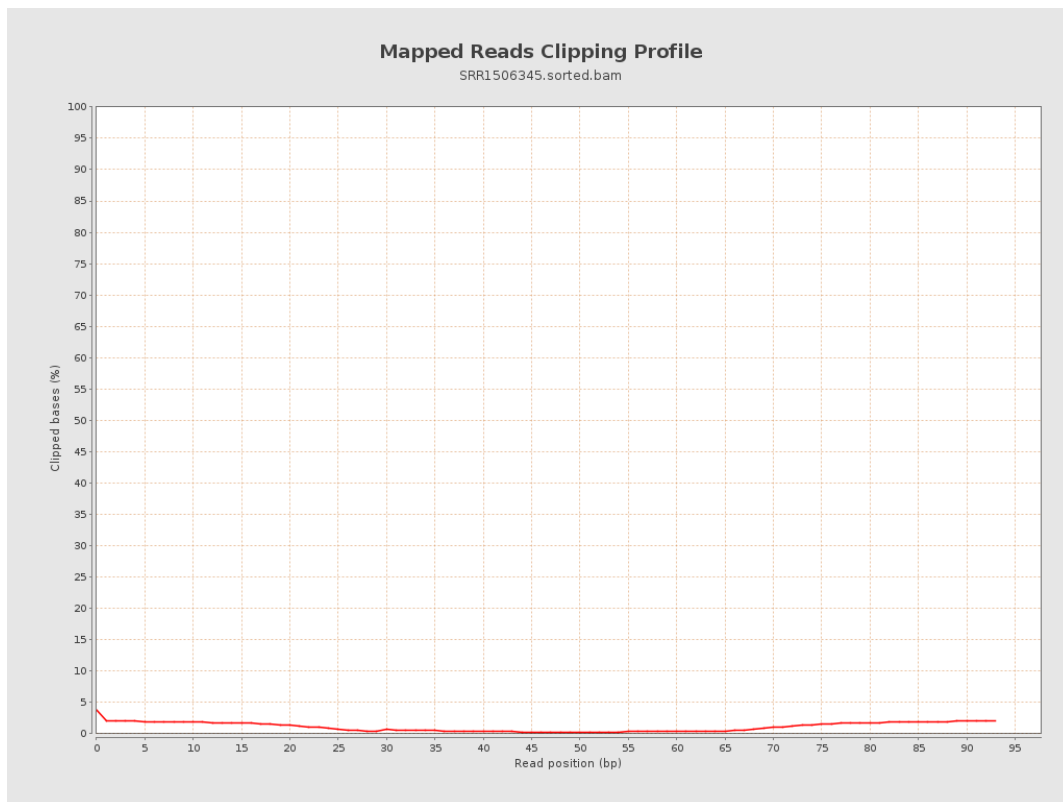
8. Results : Mapped Reads Nucleotide Content



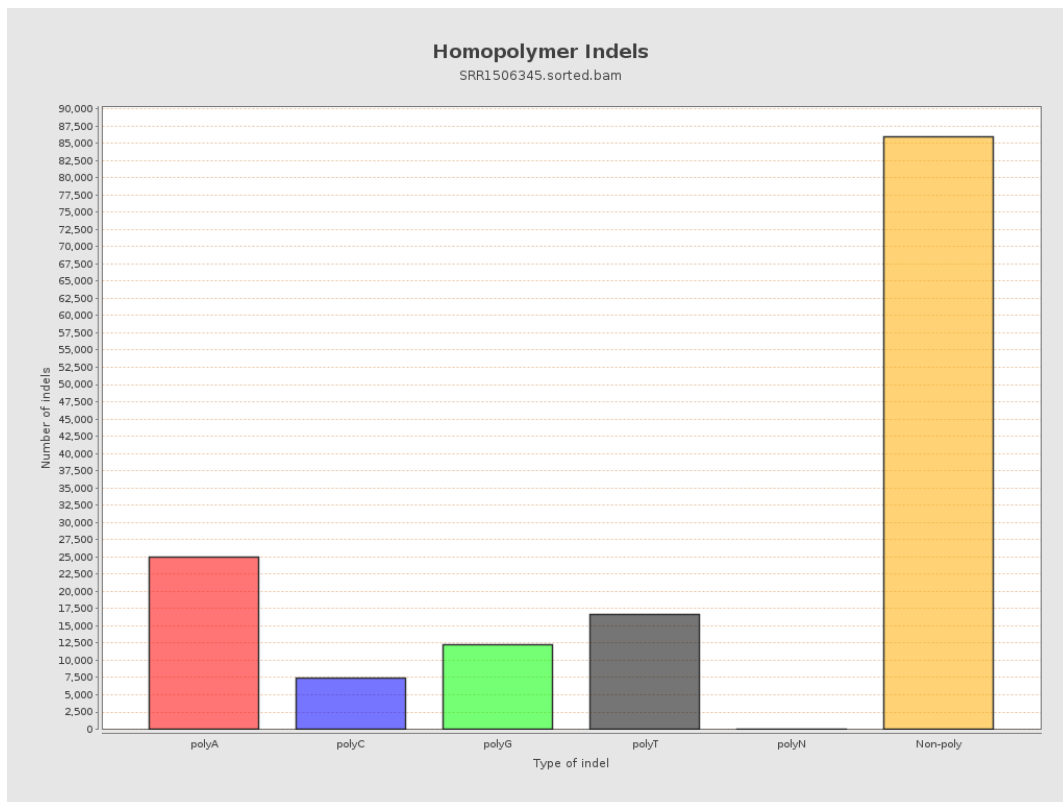
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

