

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:12:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506328.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_SRR1506328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:12:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,355,470
Mapped reads	5,338,437 / 72.58%
Unmapped reads	2,017,033 / 27.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	81,075 / 1.1%
Read min/max/mean length	30 / 94 / 94.4
Duplicated reads (estimated)	932,405 / 12.68%
Duplication rate	11.83%
Clipped reads	3,127,407 / 42.52%

2.2. ACGT Content

Number/percentage of A's	120,462,278 / 28.31%
Number/percentage of C's	79,867,729 / 18.77%
Number/percentage of T's	116,745,635 / 27.44%
Number/percentage of G's	108,281,217 / 25.45%
Number/percentage of N's	102,920 / 0.02%
GC Percentage	44.22%

2.3. Coverage

Mean	0.1375

Standard Deviation	0.9707
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2.4. Mapping Quality

Mean Mapping Quality	47.56
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2.5. Mismatches and indels

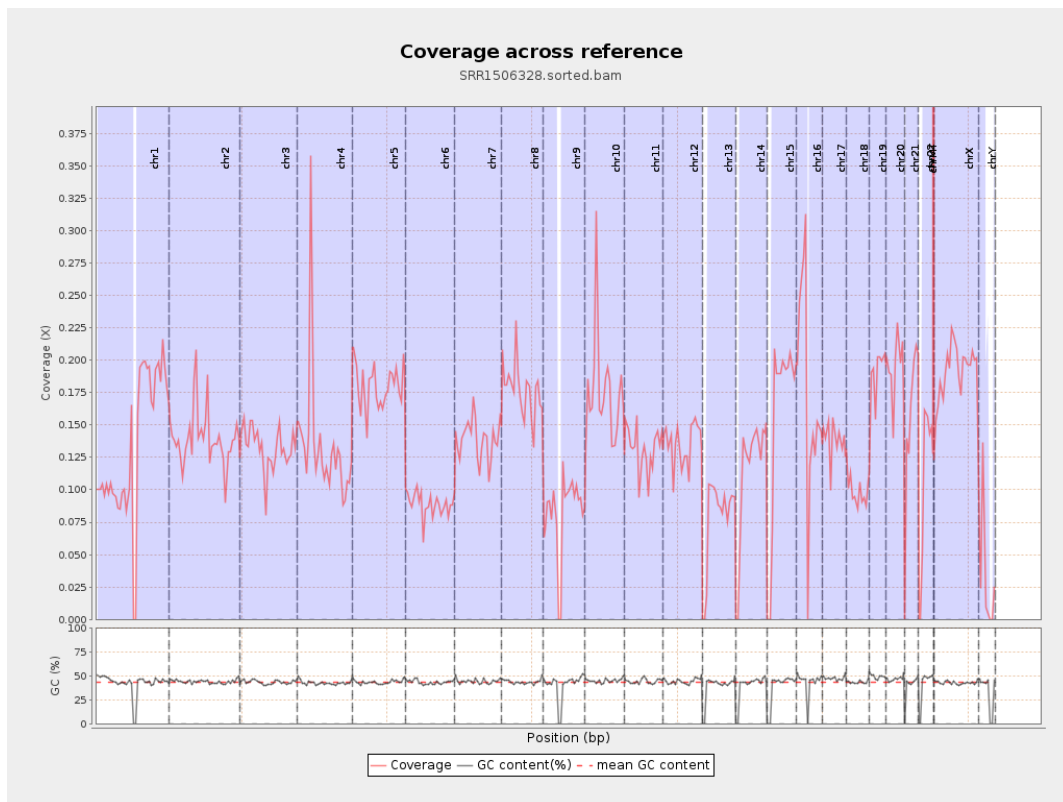
General error rate	0.74%
Mismatches	3,065,253
Insertions	36,874
Mapped reads with at least one insertion	0.67%
Deletions	92,992
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.11%

2.6. Chromosome stats

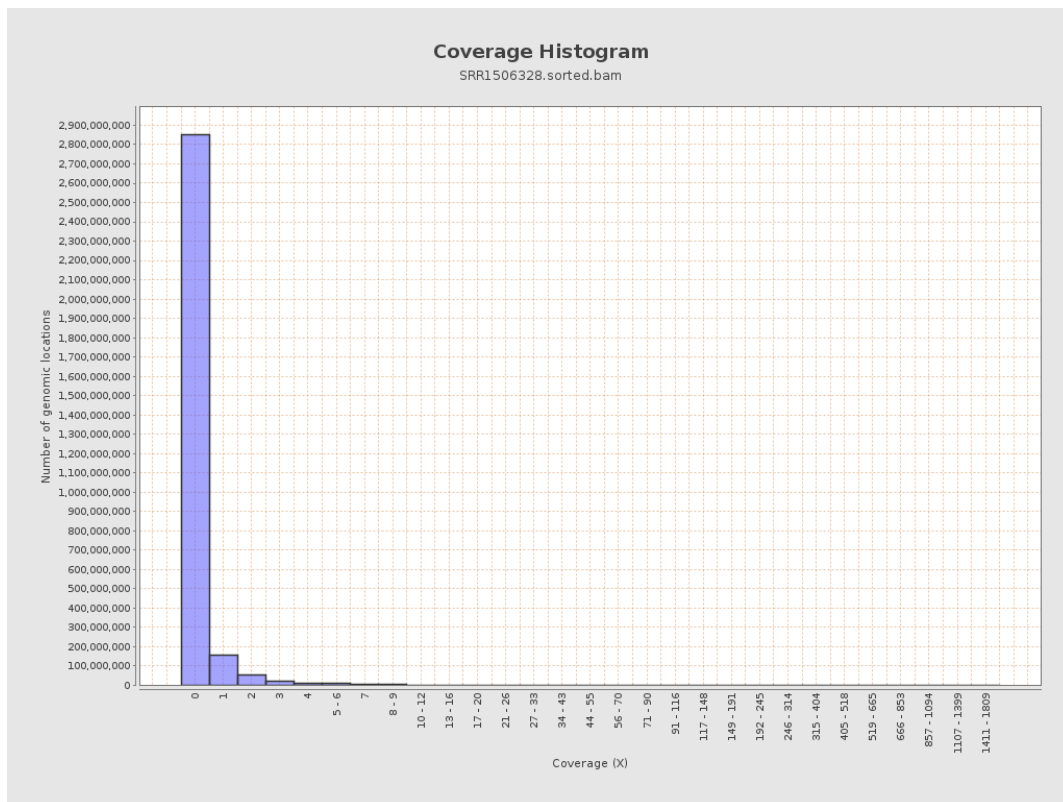
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33174591	0.1331	1.582
chr2	243199373	34099207	0.1402	1.0278
chr3	198022430	26187808	0.1322	0.5841
chr4	191154276	25259825	0.1321	1.0194
chr5	180915260	32501223	0.1796	0.6904
chr6	171115067	15206455	0.0889	0.5035
chr7	159138663	22067404	0.1387	1.1122

chr8	146364022	25886829	0.1769	1.2507
chr9	141213431	11657912	0.0826	0.8252
chr10	135534747	23747178	0.1752	1.2526
chr11	135006516	17723297	0.1313	0.8736
chr12	133851895	18134956	0.1355	0.6278
chr13	115169878	8964378	0.0778	0.4453
chr14	107349540	12145881	0.1131	0.5988
chr15	102531392	16217197	0.1582	0.6695
chr16	90354753	15968575	0.1767	0.9015
chr17	81195210	11238445	0.1384	0.6979
chr18	78077248	7688182	0.0985	1.2637
chr19	59128983	11173244	0.189	1.2941
chr20	63025520	12217869	0.1939	0.8192
chr21	48129895	7566350	0.1572	0.8832
chr22	51304566	5385451	0.105	0.5699
chrMT	16571	51930	3.1338	6.7551
chrX	155270560	29559520	0.1904	0.7897
chrY	59373566	1829425	0.0308	1.3477

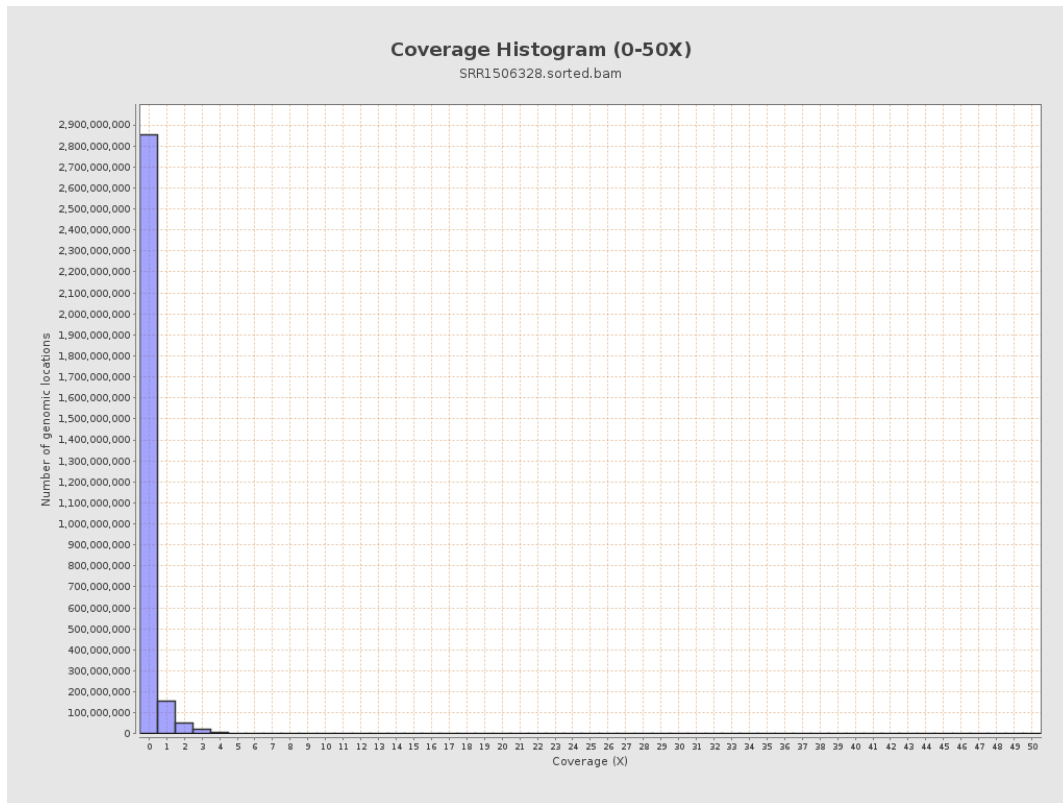
3. Results : Coverage across reference



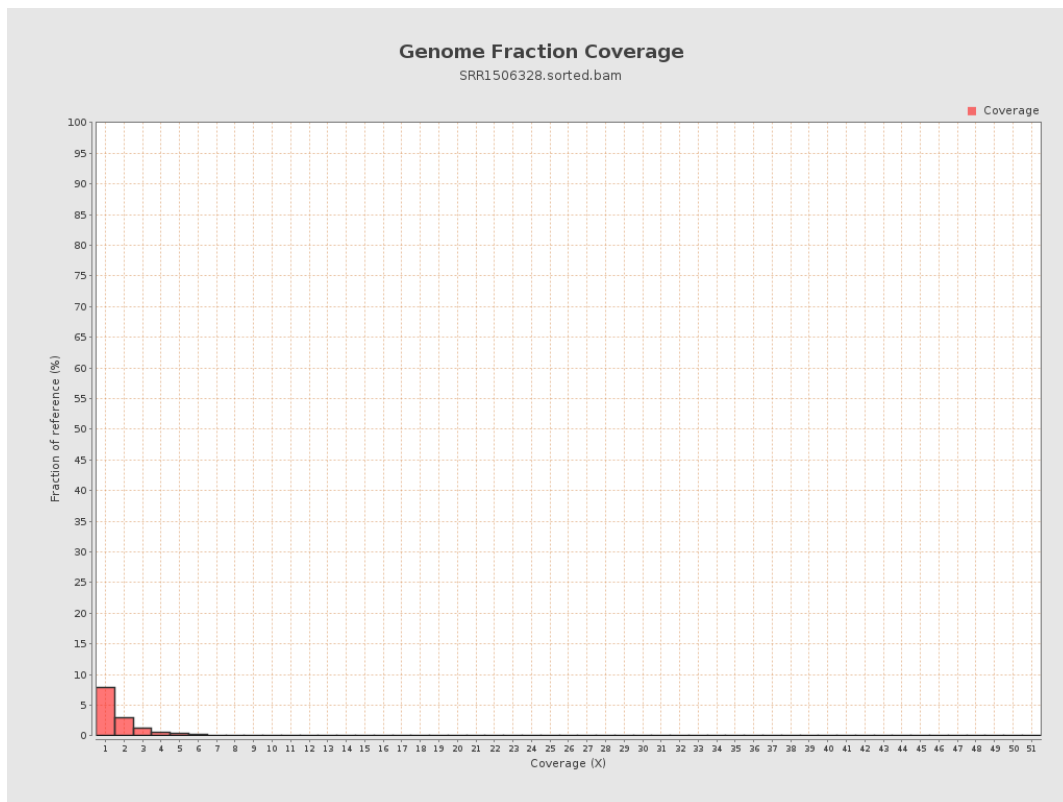
4. Results : Coverage Histogram



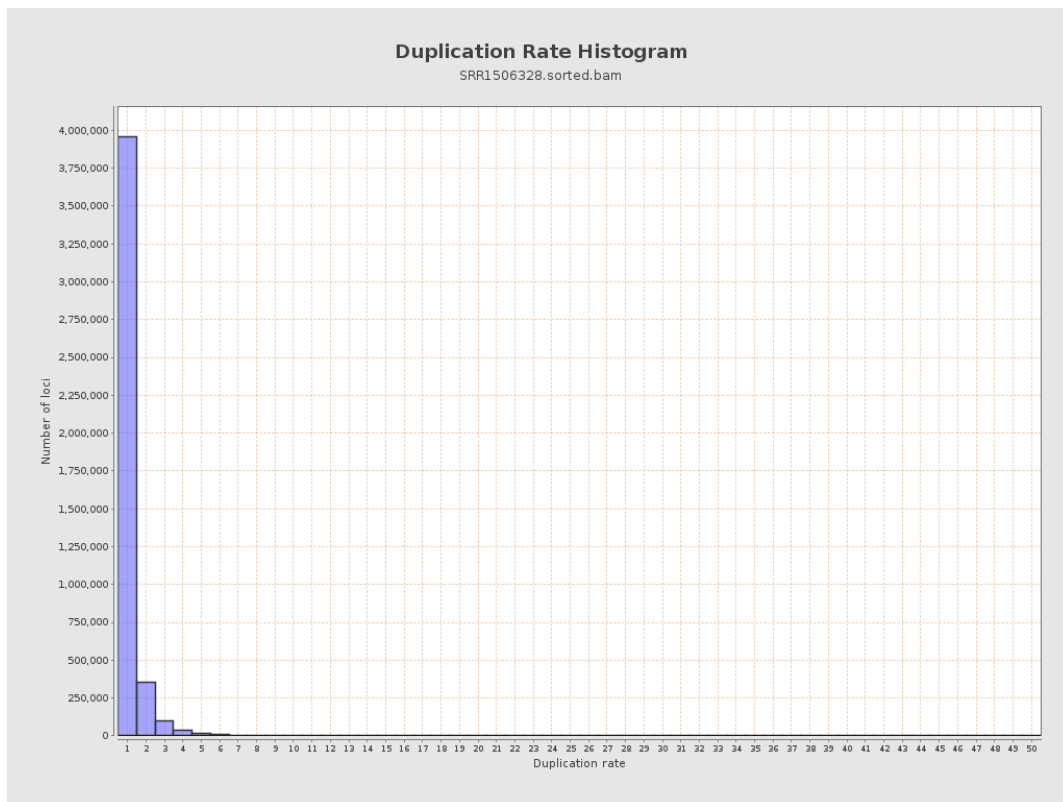
5. Results : Coverage Histogram (0-50X)



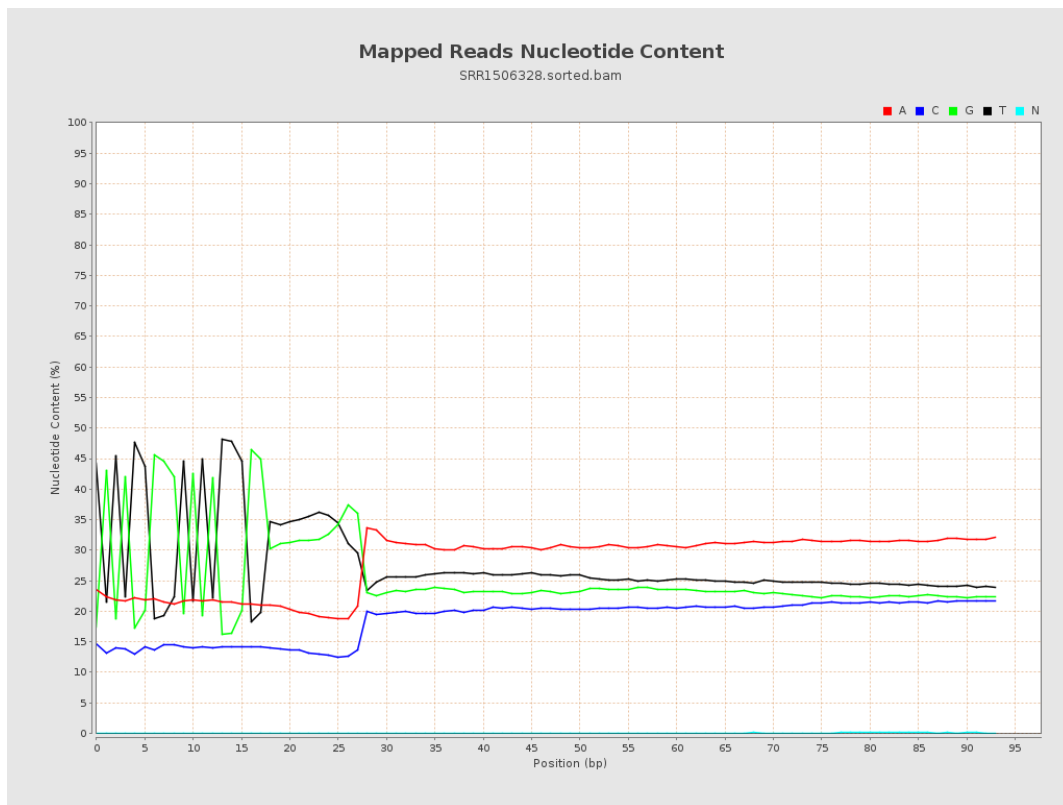
6. Results : Genome Fraction Coverage



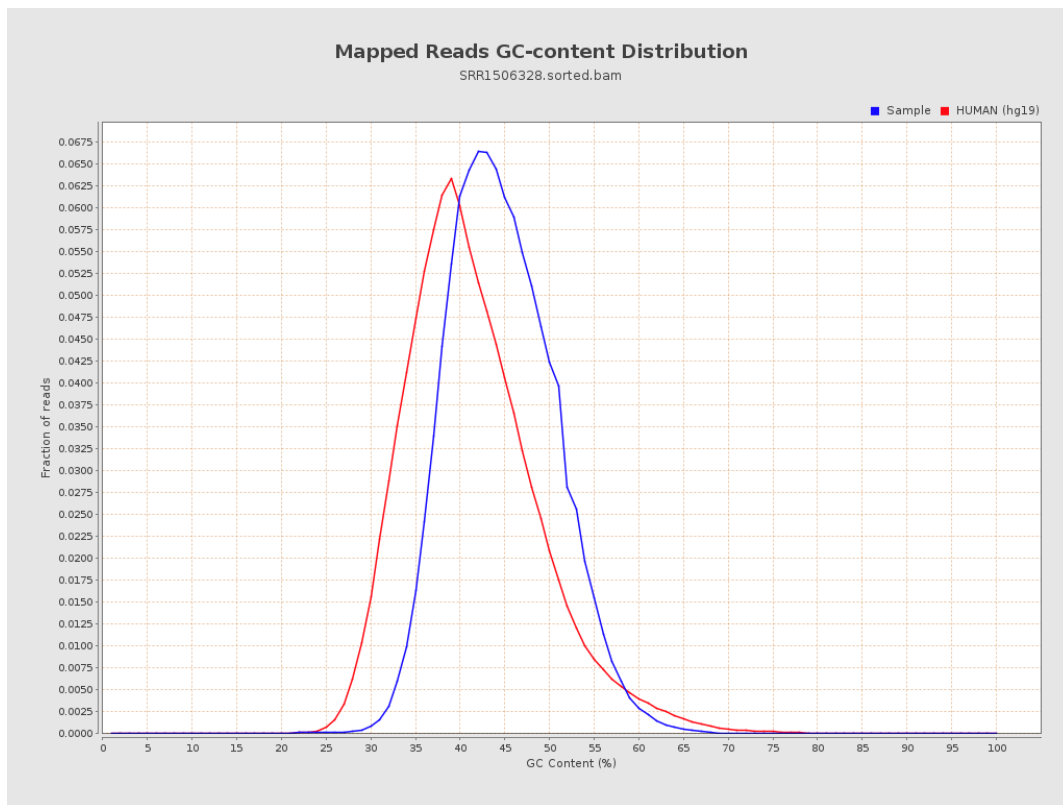
7. Results : Duplication Rate Histogram



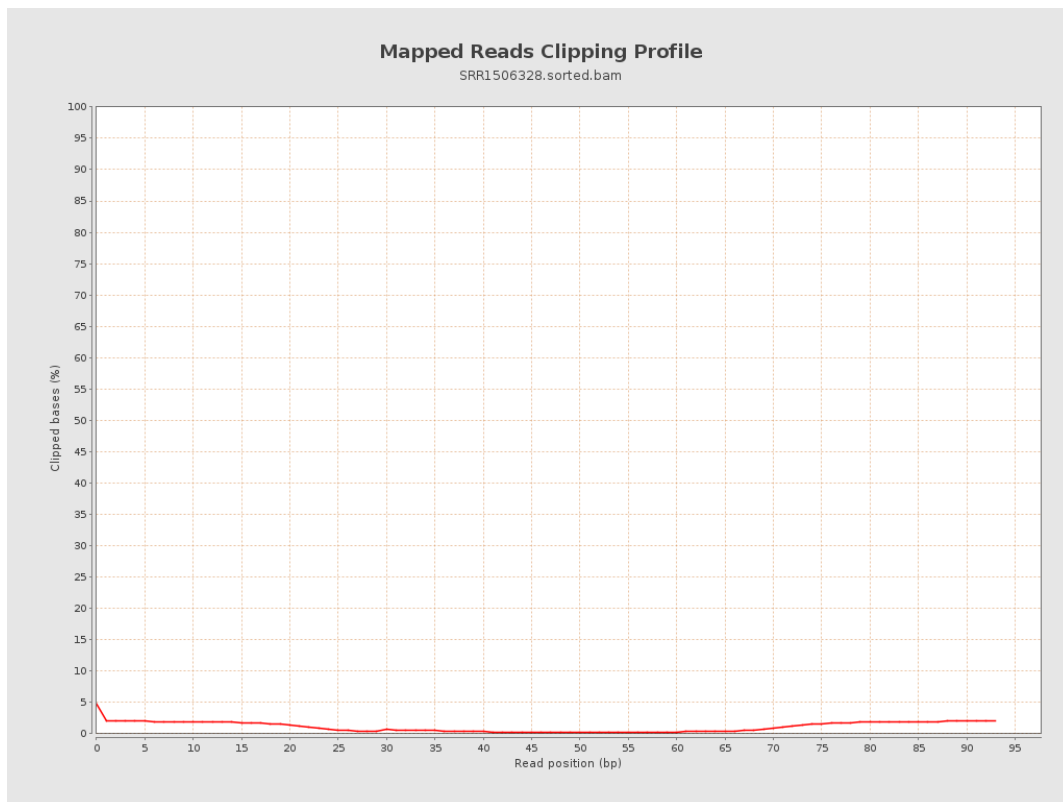
8. Results : Mapped Reads Nucleotide Content



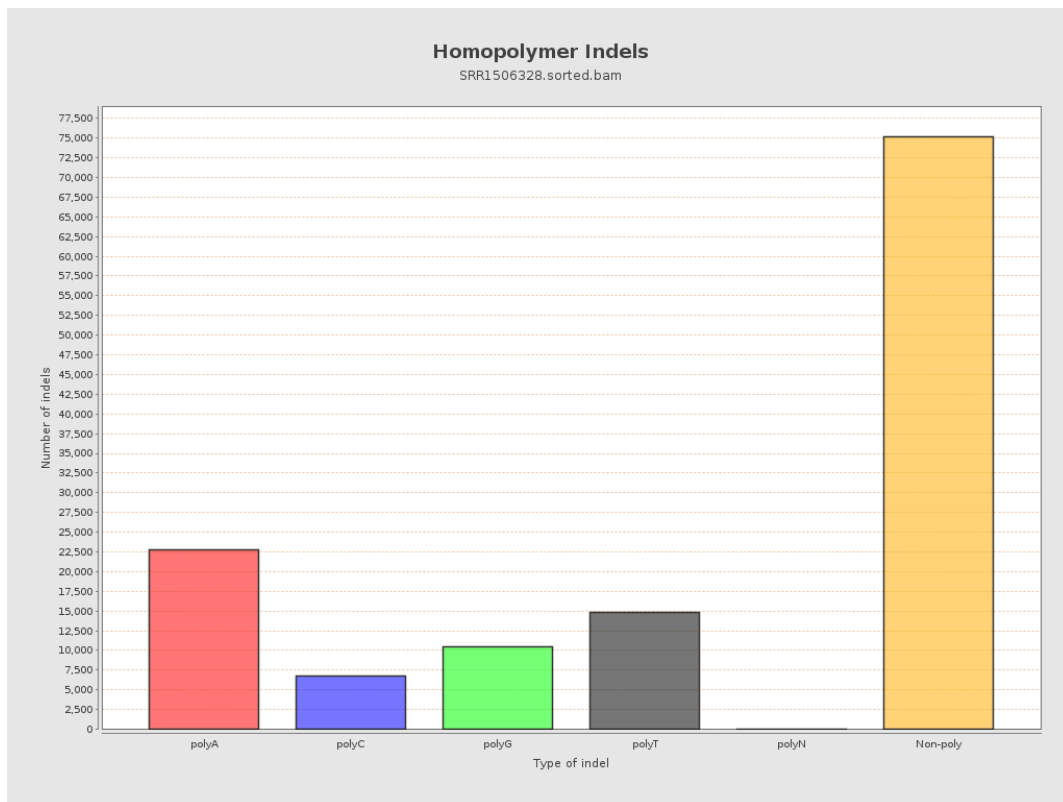
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

