

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:11:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068134.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_SRR6068134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:11:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,319
Mapped reads	1,452,891 / 90.28%
Unmapped reads	156,428 / 9.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,304 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	59,813 / 3.72%
Duplication rate	3.49%
Clipped reads	605,249 / 37.61%

2.2. ACGT Content

Number/percentage of A's	27,719,978 / 28.43%
Number/percentage of C's	17,082,142 / 17.52%
Number/percentage of T's	31,930,684 / 32.75%
Number/percentage of G's	20,683,303 / 21.22%
Number/percentage of N's	75,652 / 0.08%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.282
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	48.37
----------------------	-------

2.5. Mismatches and indels

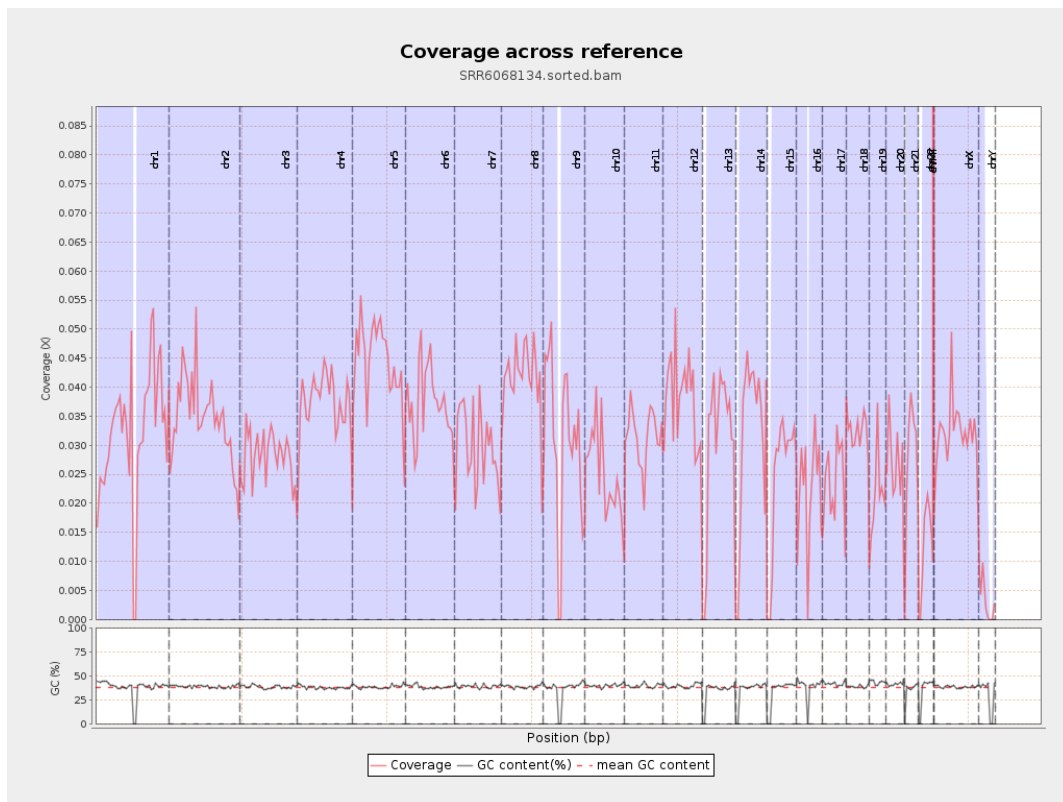
General error rate	0.84%
Mismatches	807,596
Insertions	6,987
Mapped reads with at least one insertion	0.48%
Deletions	21,808
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.15%

2.6. Chromosome stats

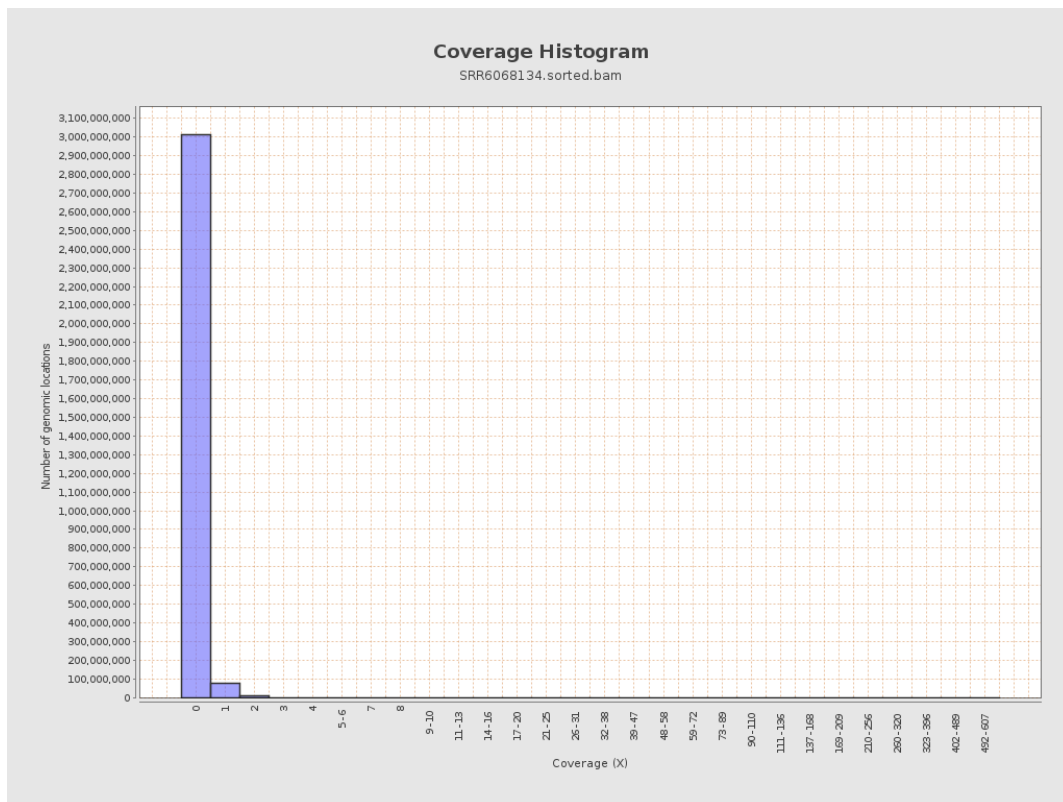
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8053910	0.0323	0.5476
chr2	243199373	8418377	0.0346	0.2822
chr3	198022430	5569074	0.0281	0.1857
chr4	191154276	7193301	0.0376	0.2185
chr5	180915260	8052456	0.0445	0.2351
chr6	171115067	6382671	0.0373	0.2478
chr7	159138663	4778254	0.03	0.2717

chr8	146364022	6098906	0.0417	0.427
chr9	141213431	4397389	0.0311	0.2521
chr10	135534747	3427484	0.0253	0.2351
chr11	135006516	4227473	0.0313	0.2169
chr12	133851895	5035202	0.0376	0.2175
chr13	115169878	3448024	0.0299	0.1926
chr14	107349540	3359478	0.0313	0.2015
chr15	102531392	2517204	0.0246	0.1735
chr16	90354753	2016133	0.0223	0.1736
chr17	81195210	1885738	0.0232	0.1805
chr18	78077248	2549438	0.0327	0.3842
chr19	59128983	1286679	0.0218	0.3481
chr20	63025520	1700554	0.027	0.1873
chr21	48129895	1331283	0.0277	0.1894
chr22	51304566	635351	0.0124	0.1219
chrMT	16571	16232	0.9795	1.0896
chrX	155270560	4960788	0.0319	0.2133
chrY	59373566	185712	0.0031	0.0742

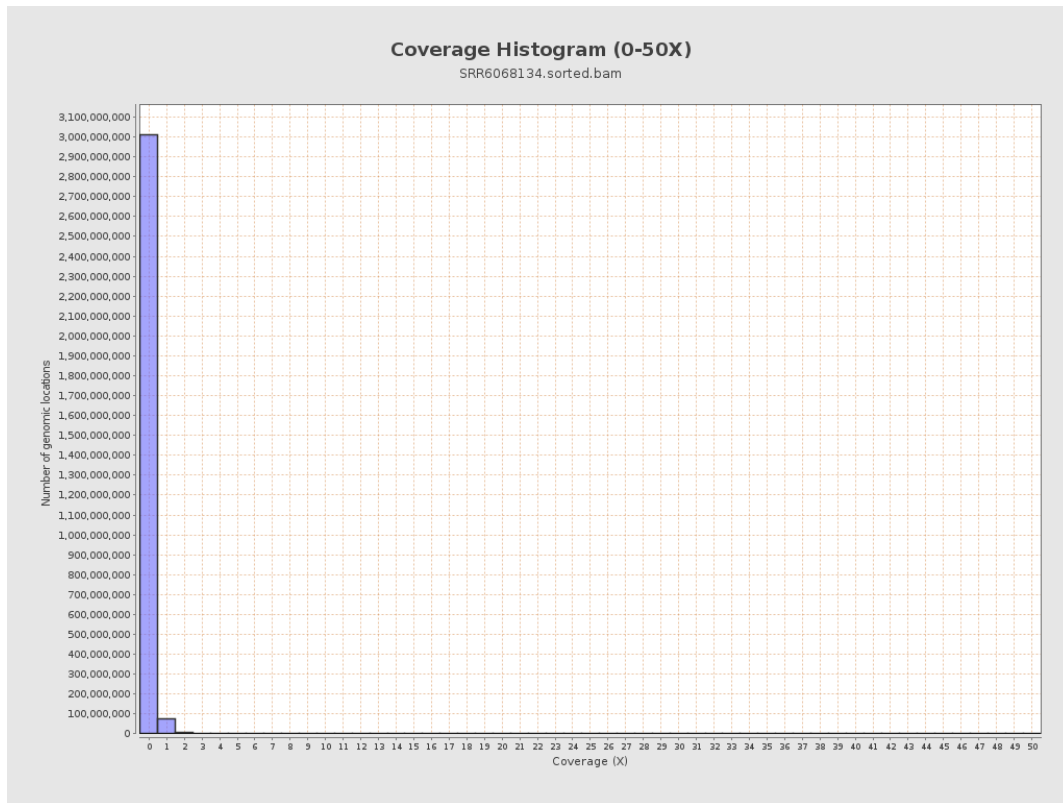
3. Results : Coverage across reference



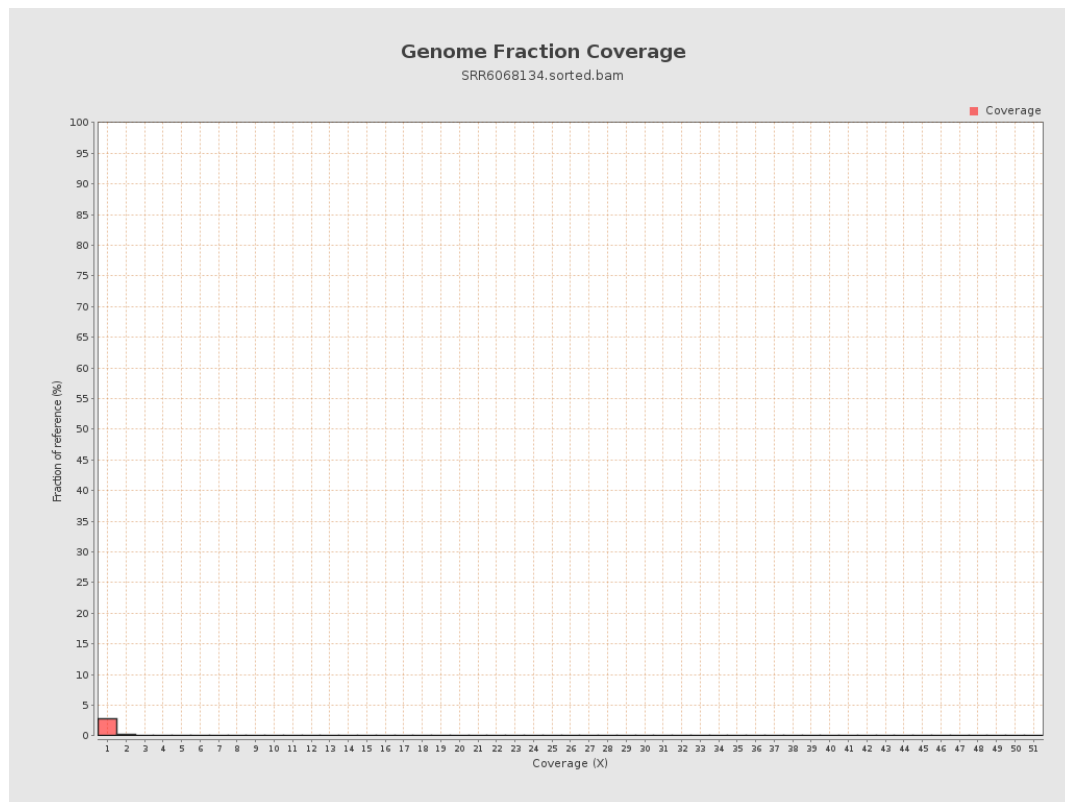
4. Results : Coverage Histogram



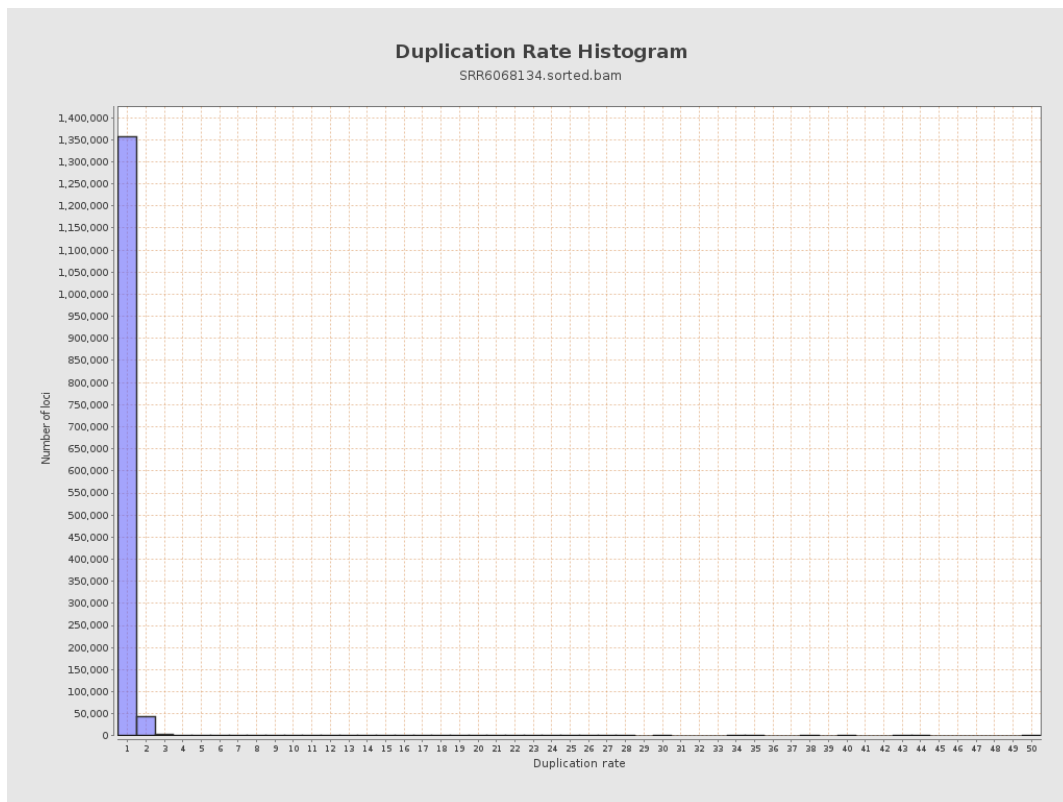
5. Results : Coverage Histogram (0-50X)



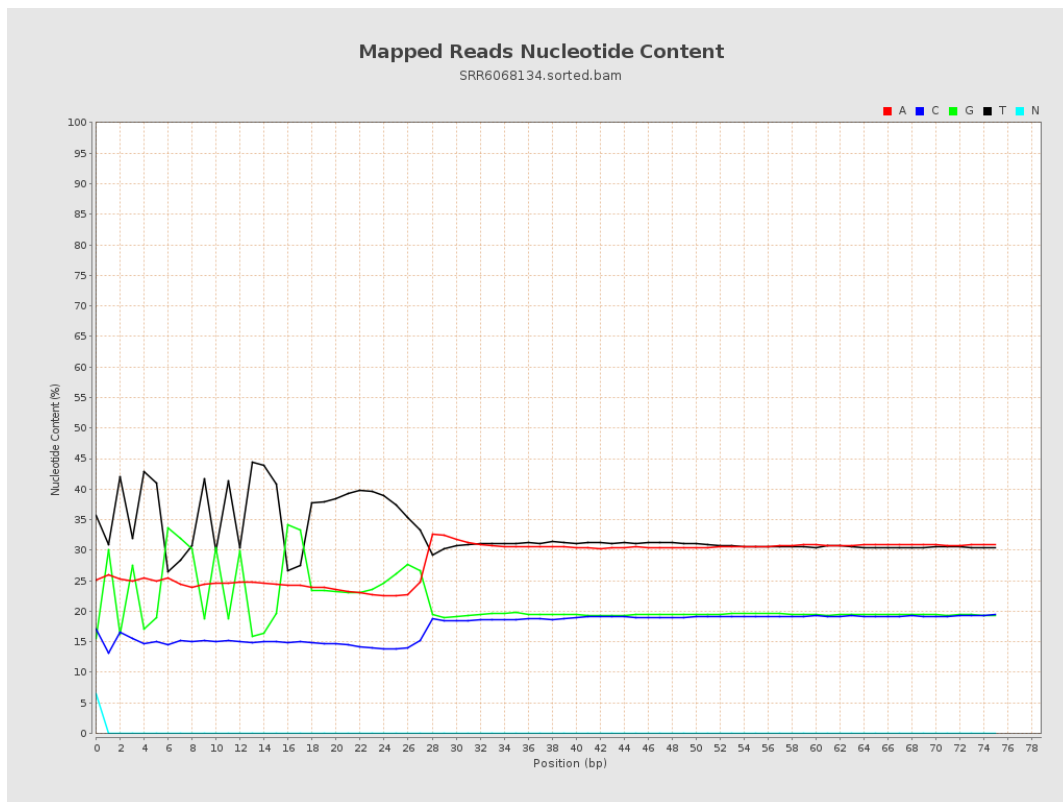
6. Results : Genome Fraction Coverage



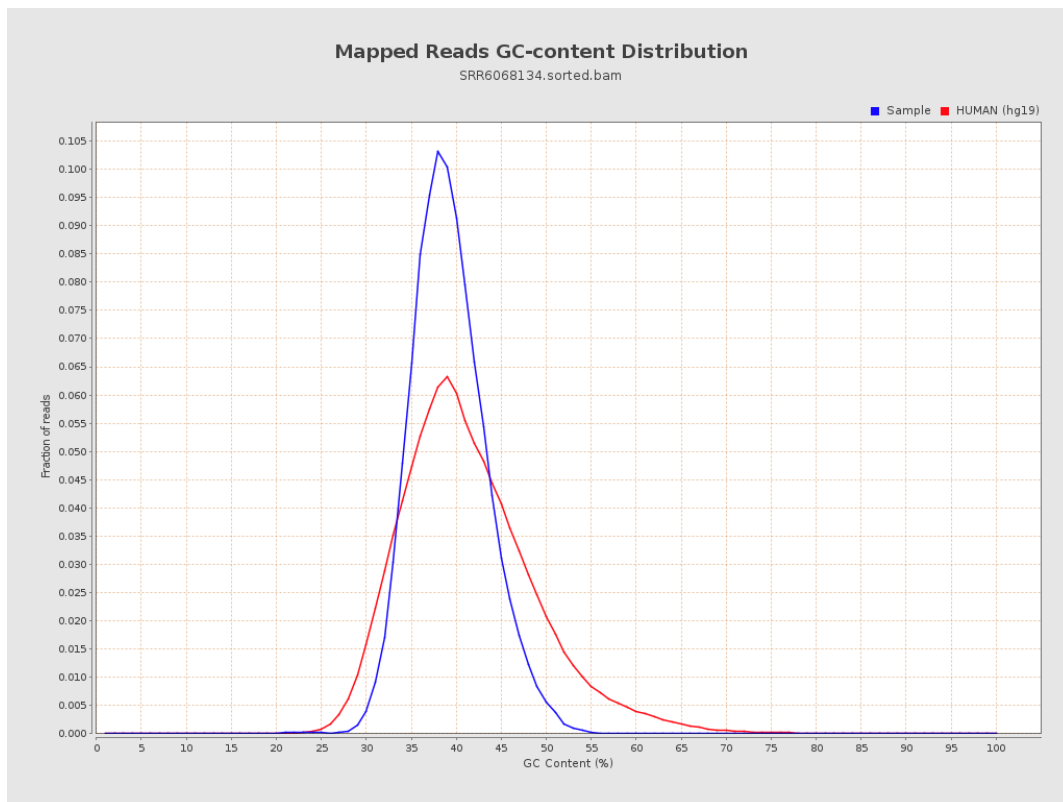
7. Results : Duplication Rate Histogram



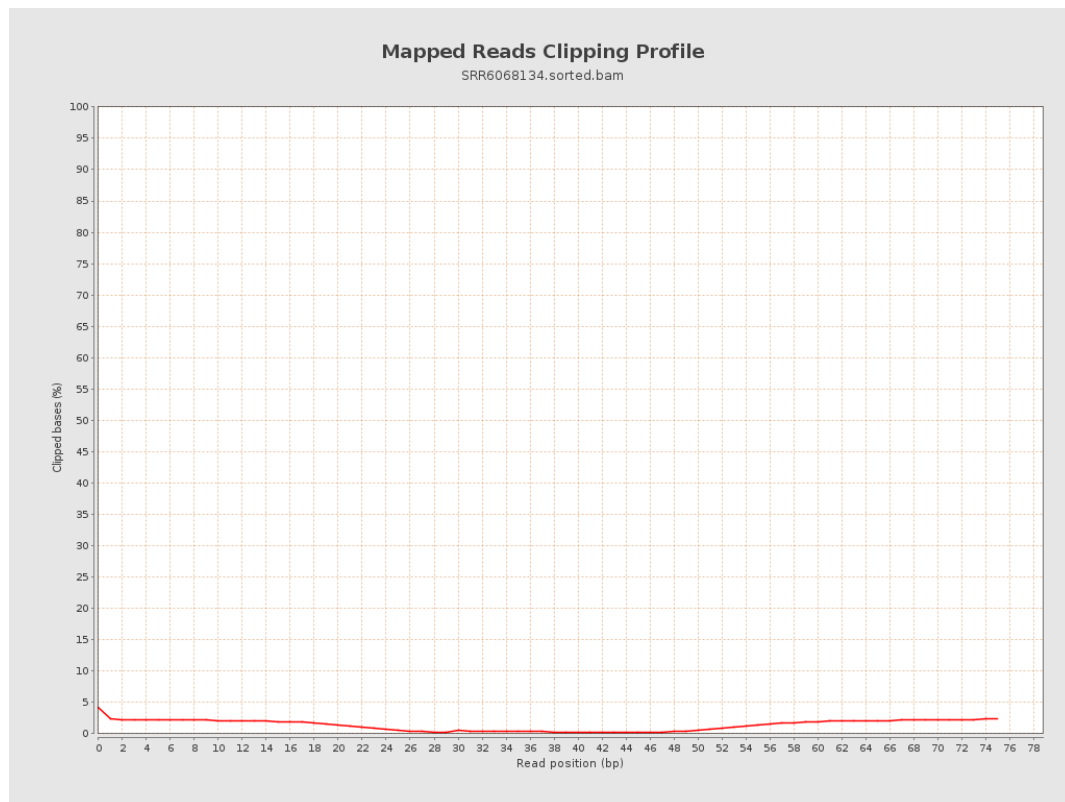
8. Results : Mapped Reads Nucleotide Content



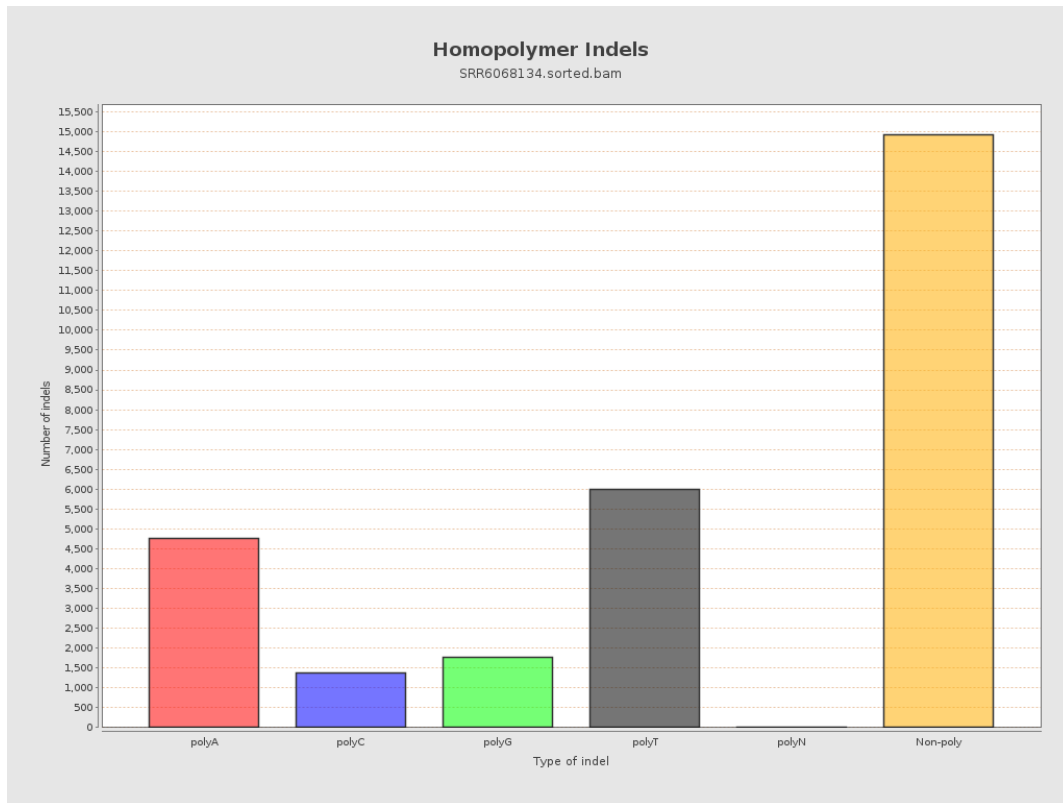
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

