Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:55:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068930.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_SRR6068930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068930.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:55:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,758,841
Mapped reads	1,379,552 / 78.44%
Unmapped reads	379,289 / 21.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,683 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	77,261 / 4.39%
Duplication rate	3.78%
Clipped reads	897,098 / 51.01%

2.2. ACGT Content

Number/percentage of A's	21,791,755 / 25.51%
Number/percentage of C's	14,082,322 / 16.48%
Number/percentage of T's	28,804,151 / 33.71%
Number/percentage of G's	20,568,285 / 24.07%
Number/percentage of N's	194,593 / 0.23%
GC Percentage	40.55%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.4287

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

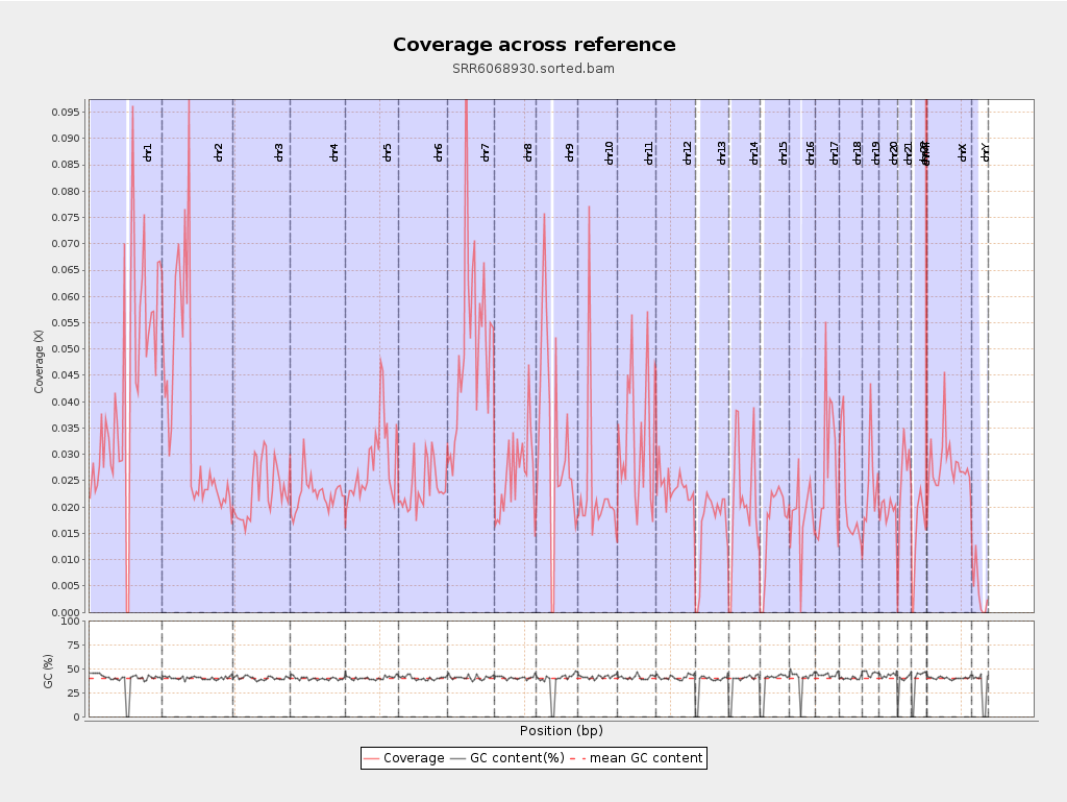
General error rate	1%
Mismatches	839,005
Insertions	7,272
Mapped reads with at least one insertion	0.52%
Deletions	25,808
Mapped reads with at least one deletion	1.85%
Homopolymer indels	48.9%

2.6. Chromosome stats

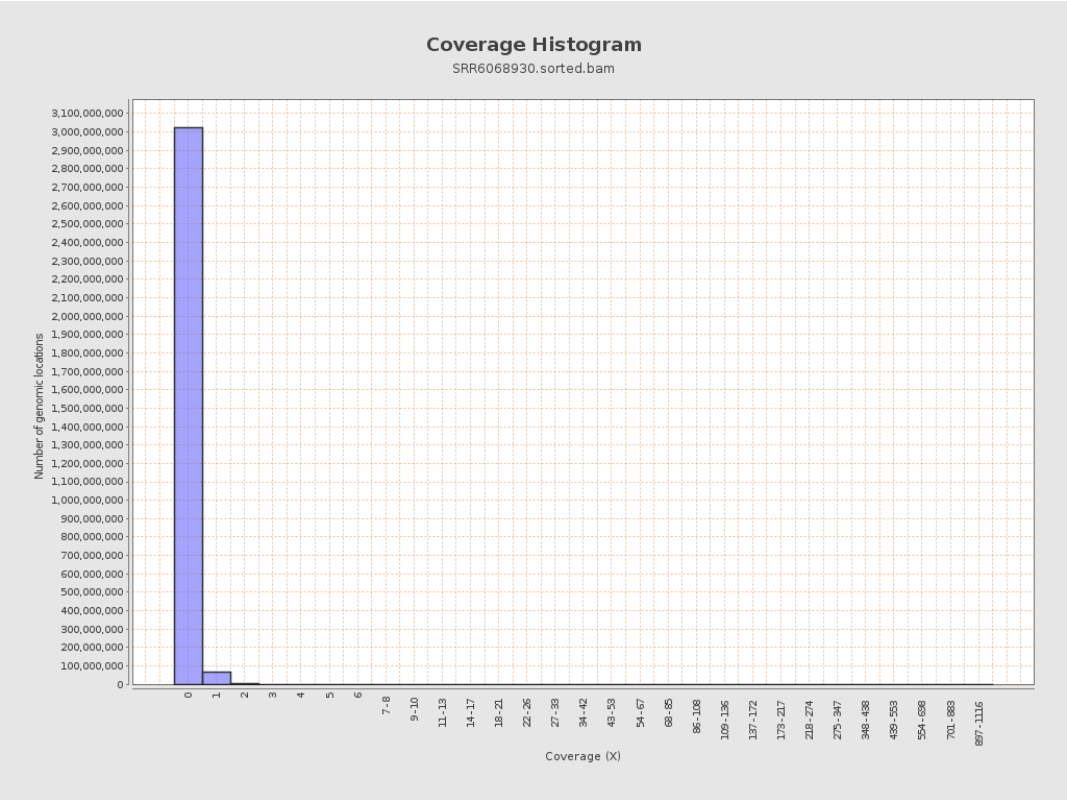
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10575867	0.0424	0.7279
chr2	243199373	8894606	0.0366	0.4305
chr3	198022430	4563464	0.023	0.2084
chr4	191154276	4292864	0.0225	0.184
chr5	180915260	5146694	0.0284	0.1923
chr6	171115067	4086171	0.0239	0.2154
chr7	159138663	8175374	0.0514	1.0817

chr8	146364022	3861907	0.0264	0.2947
chr9	141213431	4572736	0.0324	0.4022
chr10	135534747	3064609	0.0226	0.5497
chr11	135006516	4435445	0.0329	0.4519
chr12	133851895	3166466	0.0237	0.1858
chr13	115169878	1881846	0.0163	0.1426
chr14	107349540	2268572	0.0211	0.2018
chr15	102531392	1729966	0.0169	0.1482
chr16	90354753	1661333	0.0184	0.2042
chr17	81195210	2199243	0.0271	0.2394
chr18	78077248	1669987	0.0214	0.5364
chr19	59128983	1437603	0.0243	0.4236
chr20	63025520	1213032	0.0192	0.1749
chr21	48129895	1195758	0.0248	0.1997
chr22	51304566	749753	0.0146	0.1337
chrMT	16571	84556	5.1026	3.966
chrX	155270560	4328681	0.0279	0.2591
chrY	59373566	224615	0.0038	0.1025

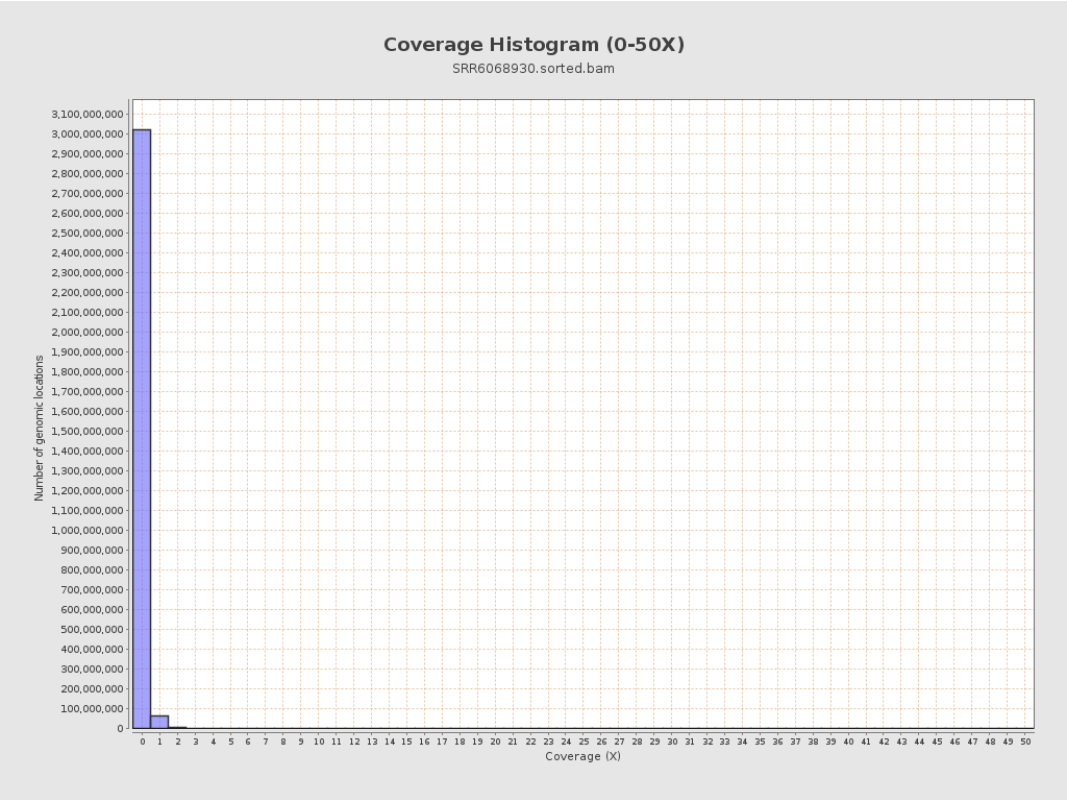
3. Results : Coverage across reference



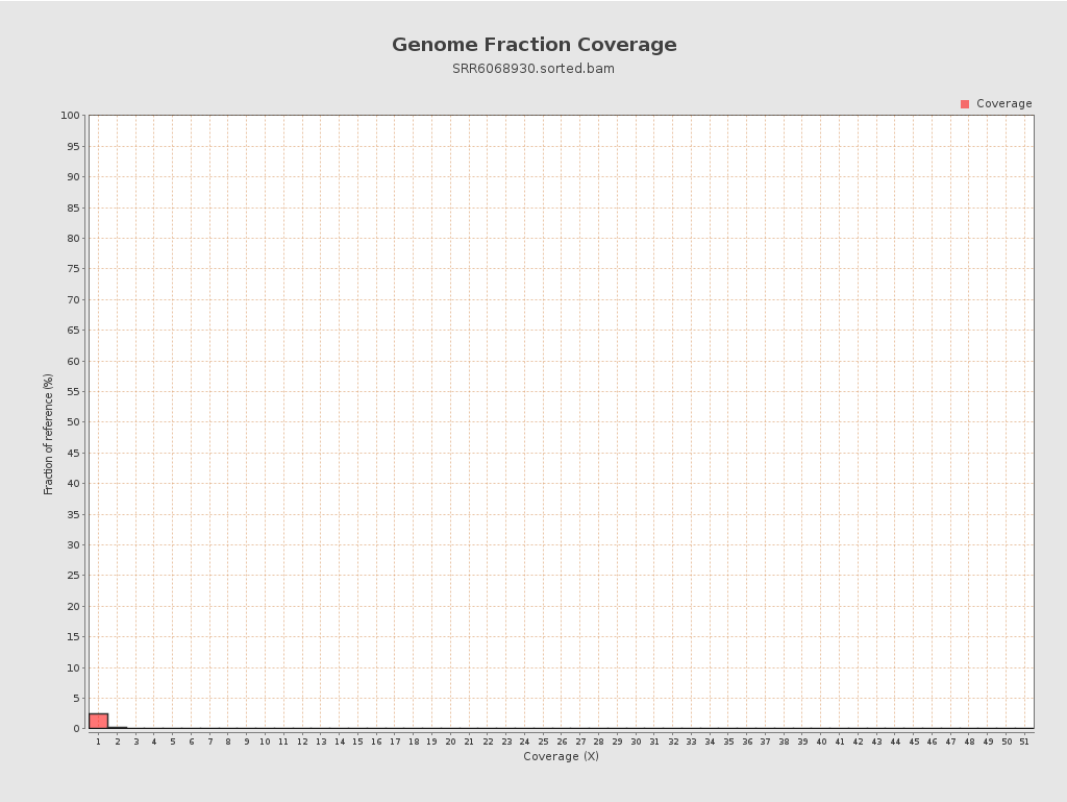
4. Results : Coverage Histogram



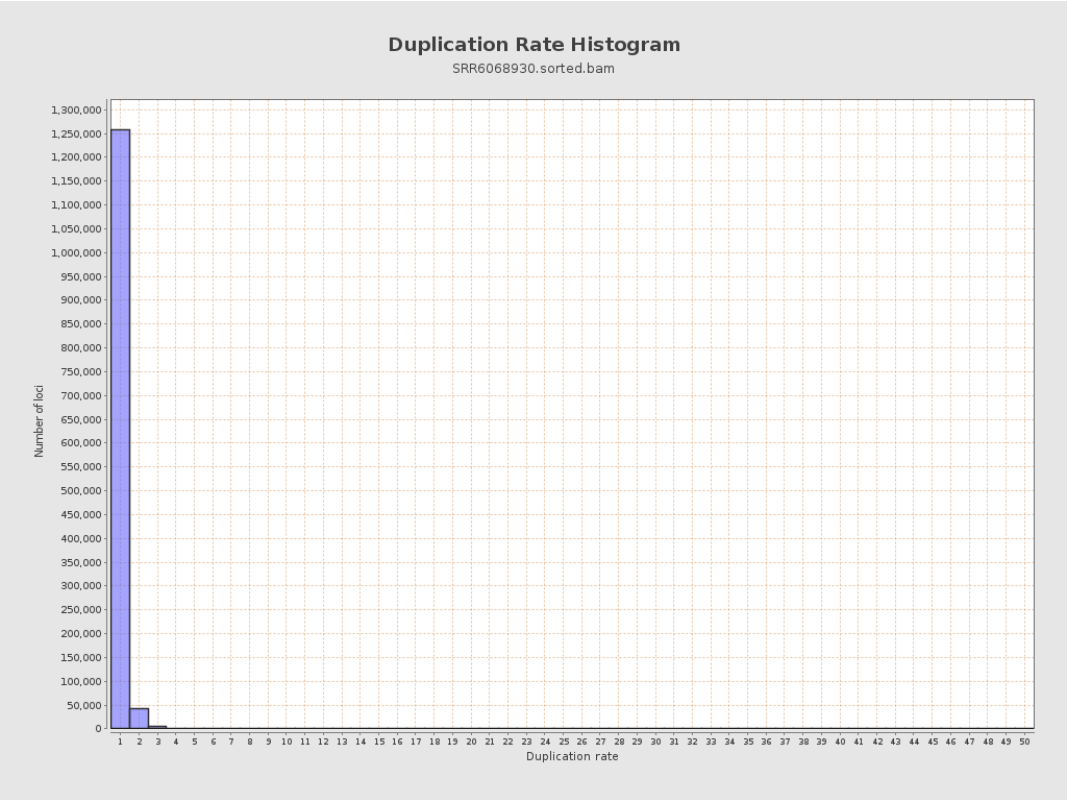
5. Results : Coverage Histogram (0-50X)



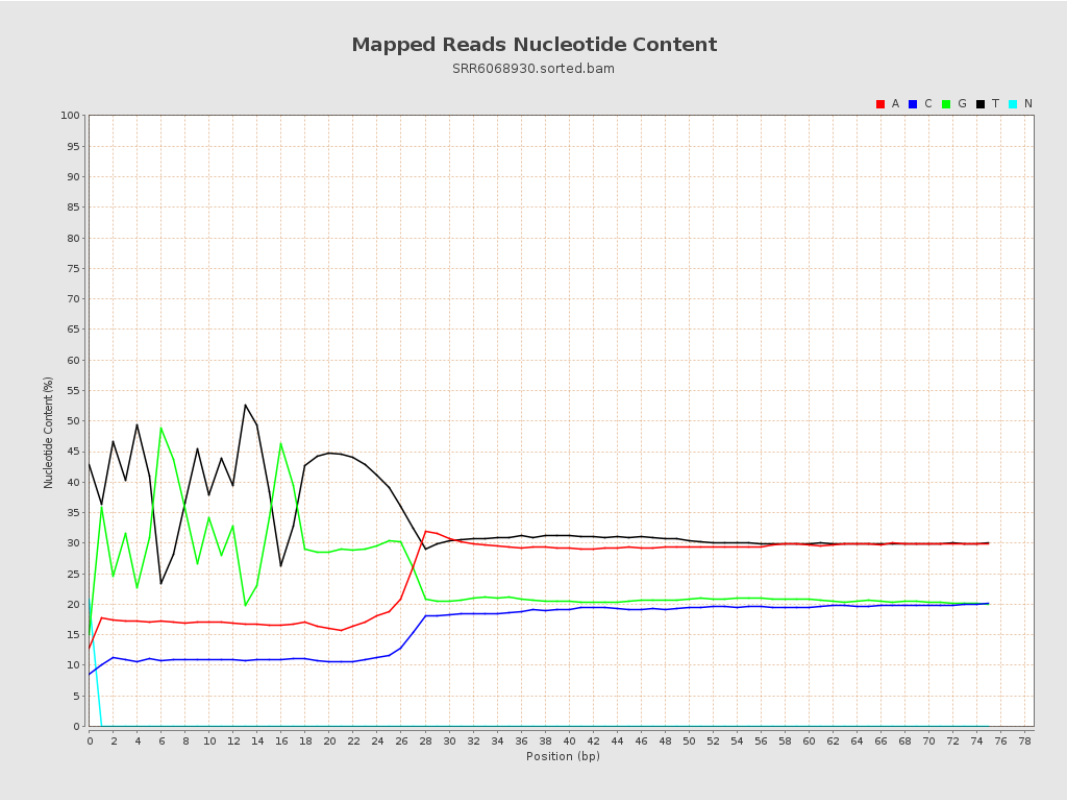
6. Results : Genome Fraction Coverage



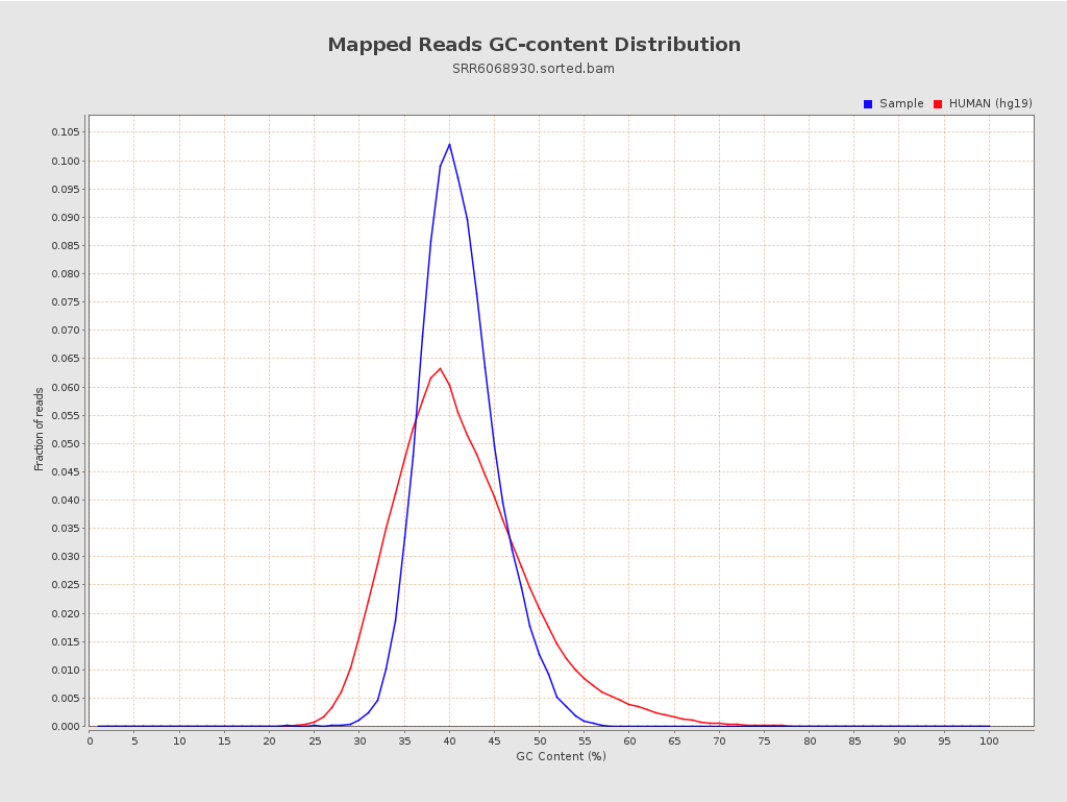
7. Results : Duplication Rate Histogram



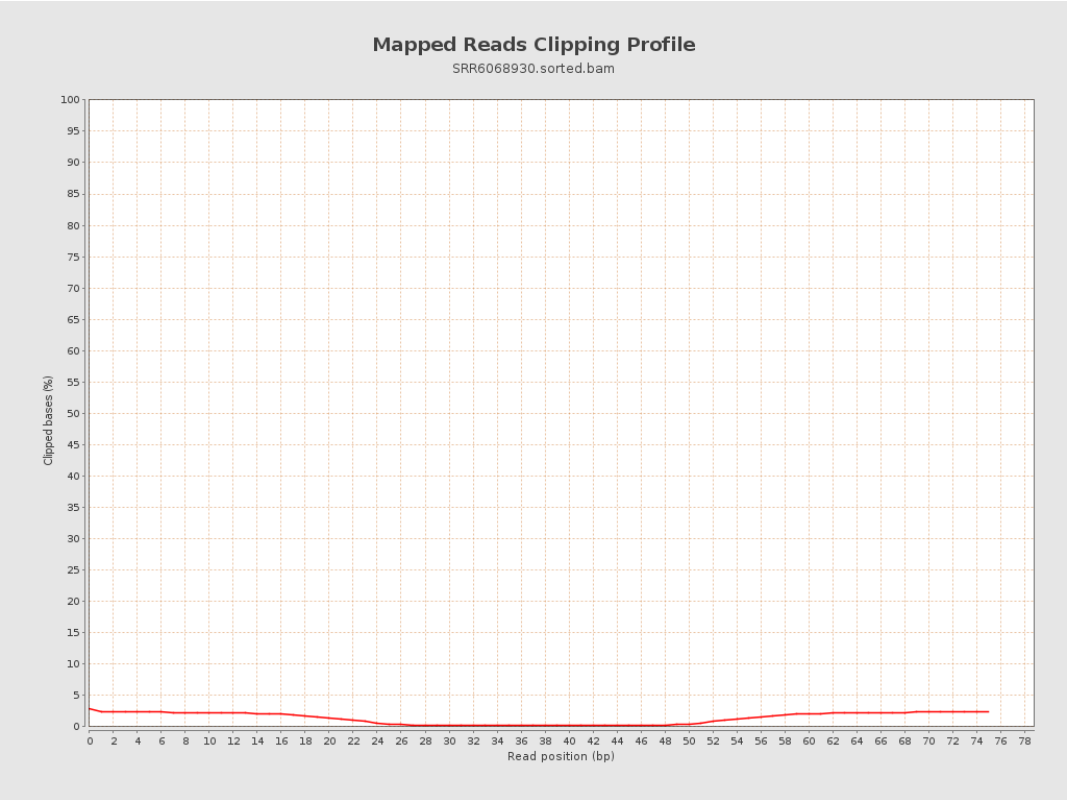
8. Results : Mapped Reads Nucleotide Content



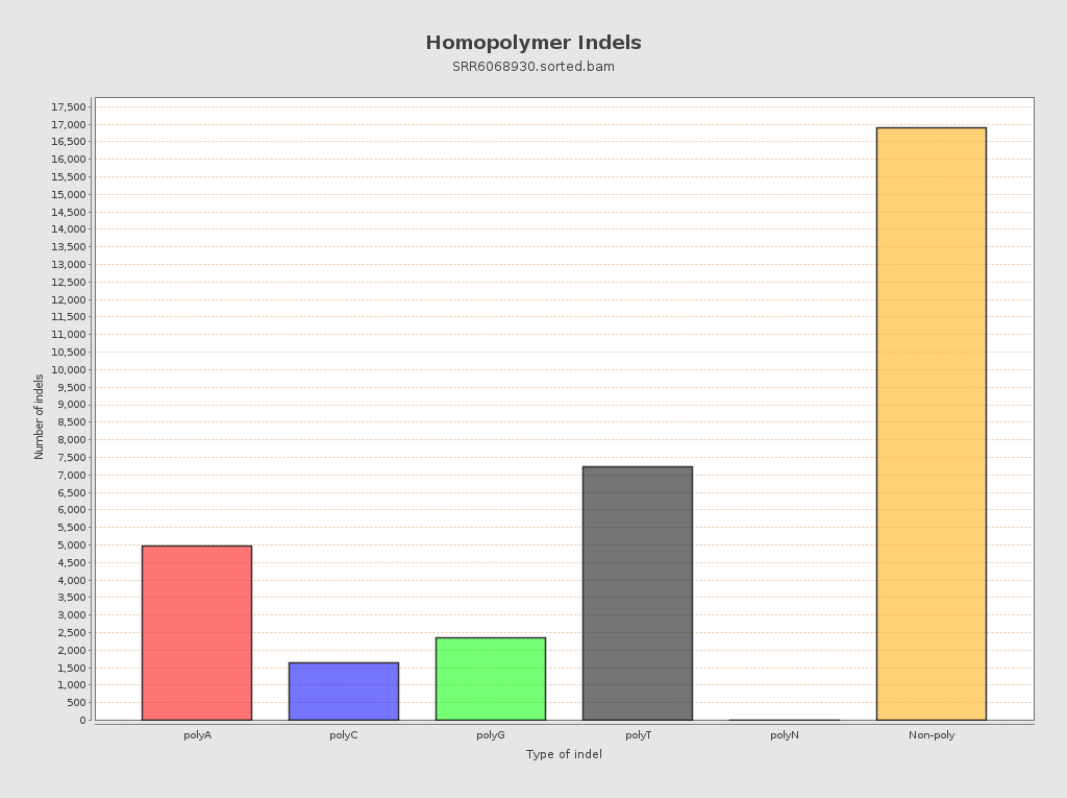
9. Results : Mapped Reads GC-content Distribution



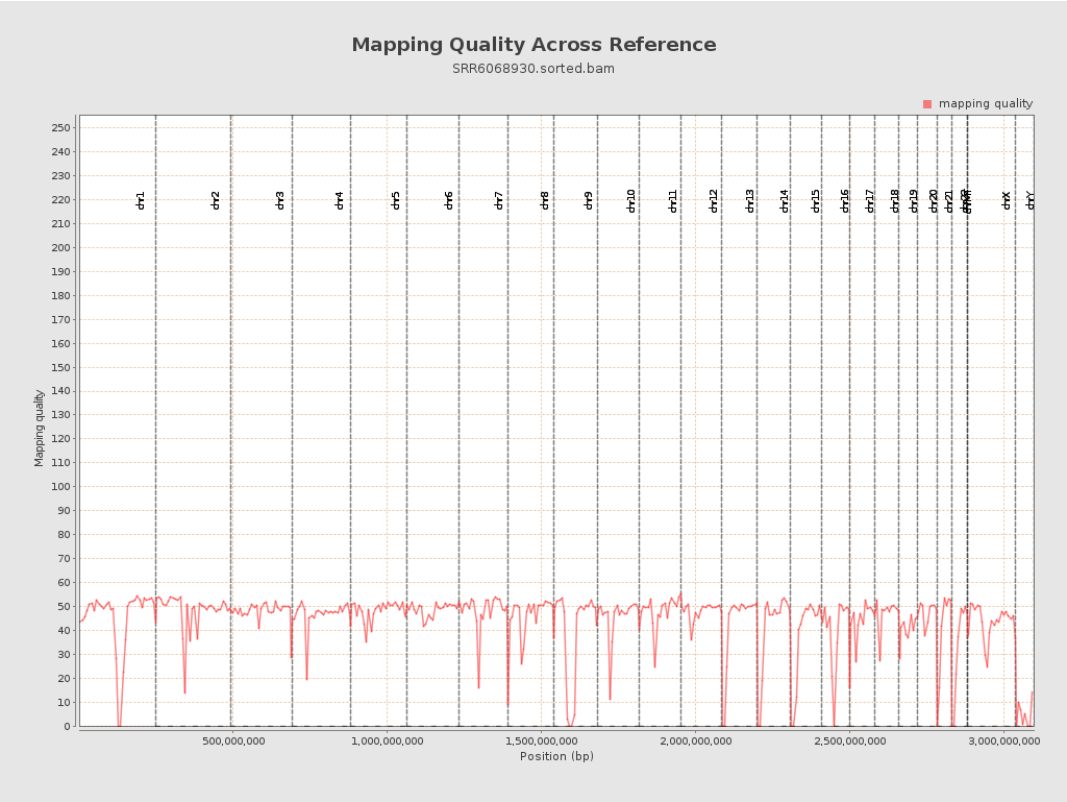
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram