Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:58:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068931.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_SRR6068931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068931.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:58:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,219,600
Mapped reads	631,650 / 51.79%
Unmapped reads	587,950 / 48.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,401 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	39,995 / 3.28%
Duplication rate	5.46%
Clipped reads	415,948 / 34.11%

2.2. ACGT Content

Number/percentage of A's	9,755,515 / 25.15%
Number/percentage of C's	6,502,126 / 16.76%
Number/percentage of T's	13,133,435 / 33.86%
Number/percentage of G's	9,320,017 / 24.03%
Number/percentage of N's	76,067 / 0.2%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.1531

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

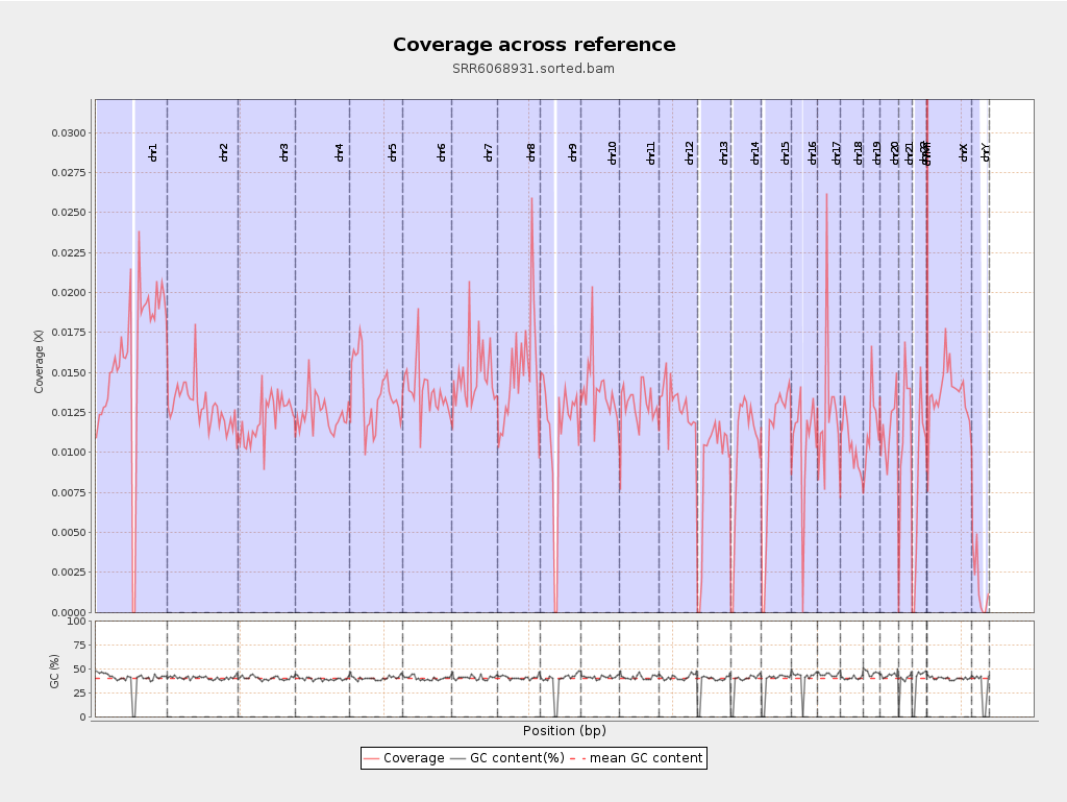
General error rate	1.19%
Mismatches	454,520
Insertions	3,395
Mapped reads with at least one insertion	0.53%
Deletions	13,363
Mapped reads with at least one deletion	2.09%
Homopolymer indels	49.15%

2.6. Chromosome stats

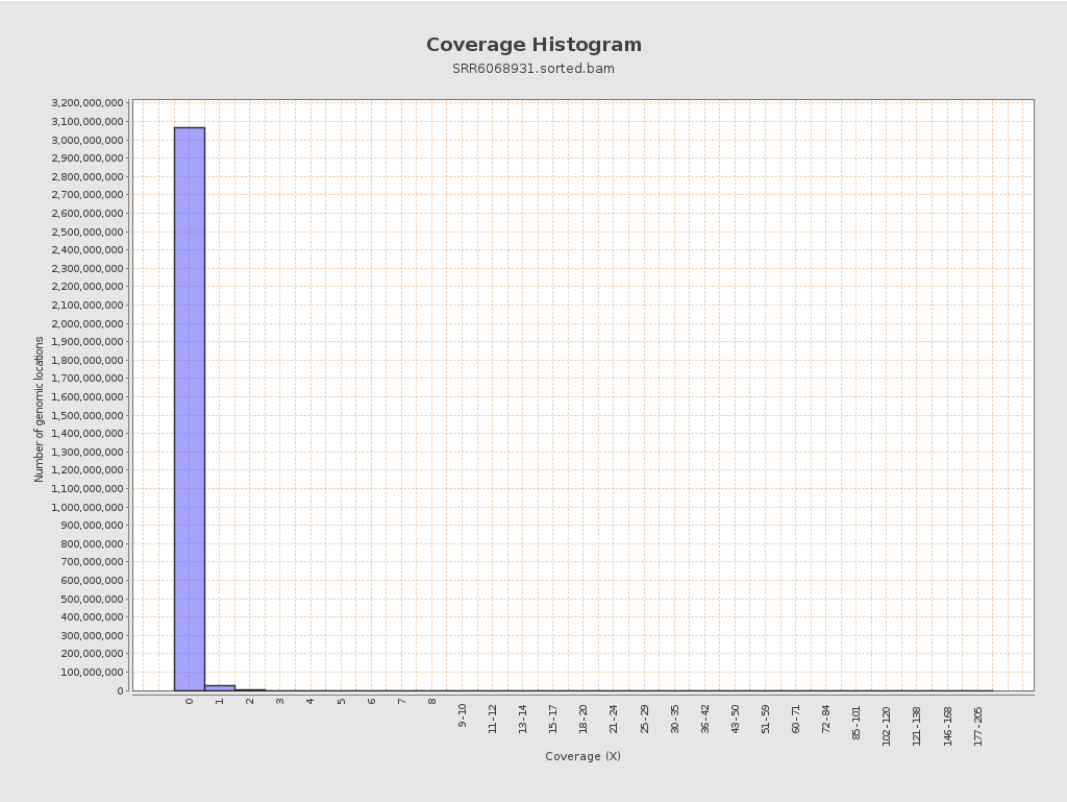
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3948319	0.0158	0.2059
chr2	243199373	3130765	0.0129	0.1626
chr3	198022430	2400666	0.0121	0.1332
chr4	191154276	2368484	0.0124	0.1358
chr5	180915260	2482817	0.0137	0.1412
chr6	171115067	2363582	0.0138	0.1544
chr7	159138663	2350489	0.0148	0.1886

chr8	146364022	2178285	0.0149	0.175
chr9	141213431	1590093	0.0113	0.1435
chr10	135534747	1865491	0.0138	0.1588
chr11	135006516	1756207	0.013	0.1532
chr12	133851895	1728594	0.0129	0.1382
chr13	115169878	1046636	0.0091	0.1167
chr14	107349540	1080932	0.0101	0.1243
chr15	102531392	1074185	0.0105	0.1251
chr16	90354753	947827	0.0105	0.1274
chr17	81195210	1011425	0.0125	0.1398
chr18	78077248	815347	0.0104	0.195
chr19	59128983	693842	0.0117	0.1595
chr20	63025520	719677	0.0114	0.1314
chr21	48129895	549098	0.0114	0.1333
chr22	51304566	421658	0.0082	0.1082
chrMT	16571	58131	3.508	3.1681
chrX	155270560	2125645	0.0137	0.1435
chrY	59373566	99929	0.0017	0.0511

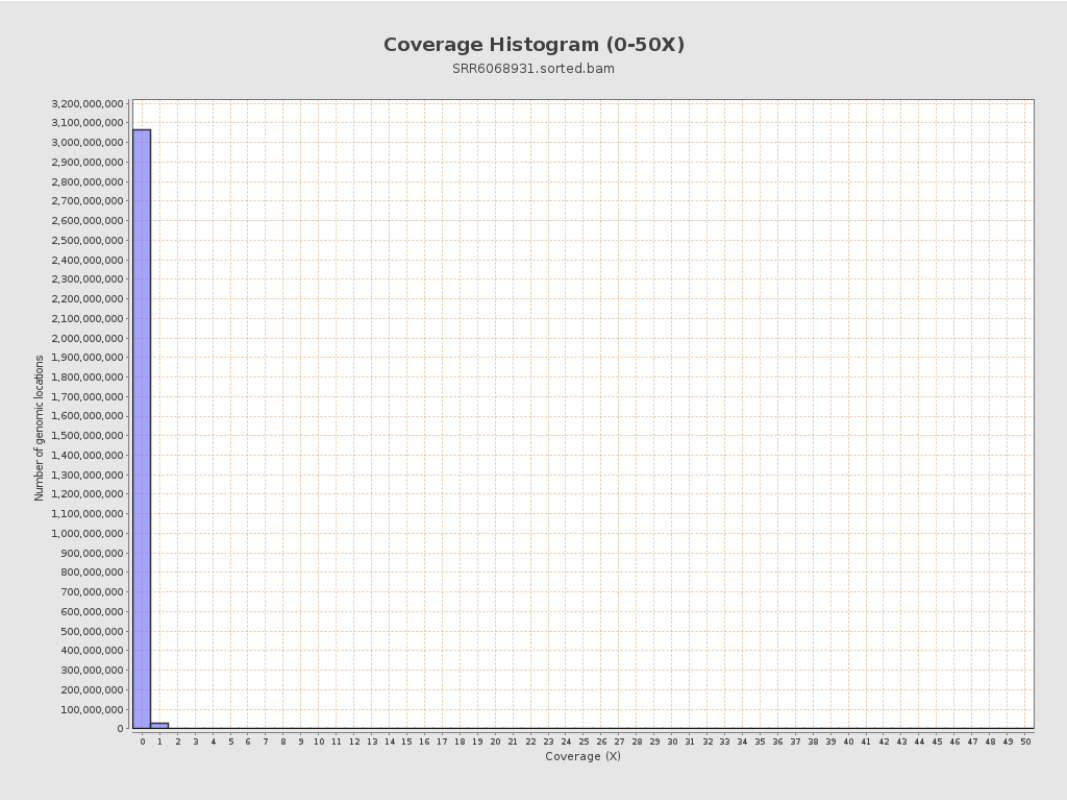
3. Results : Coverage across reference



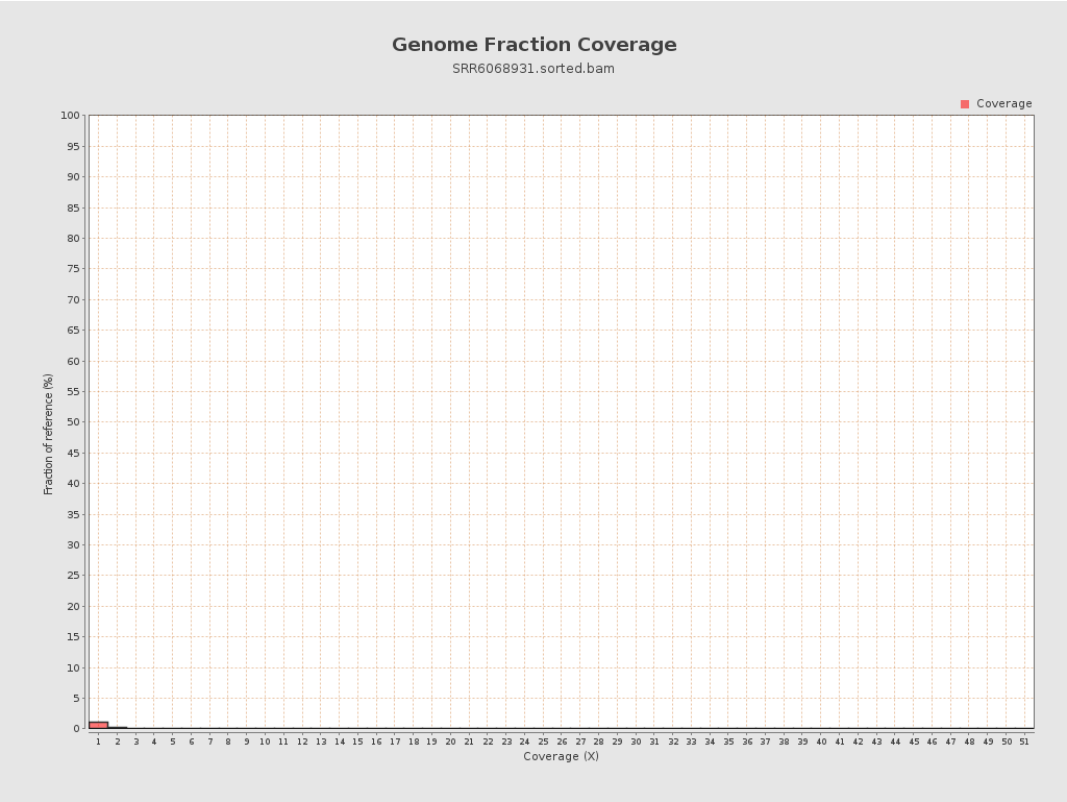
4. Results : Coverage Histogram



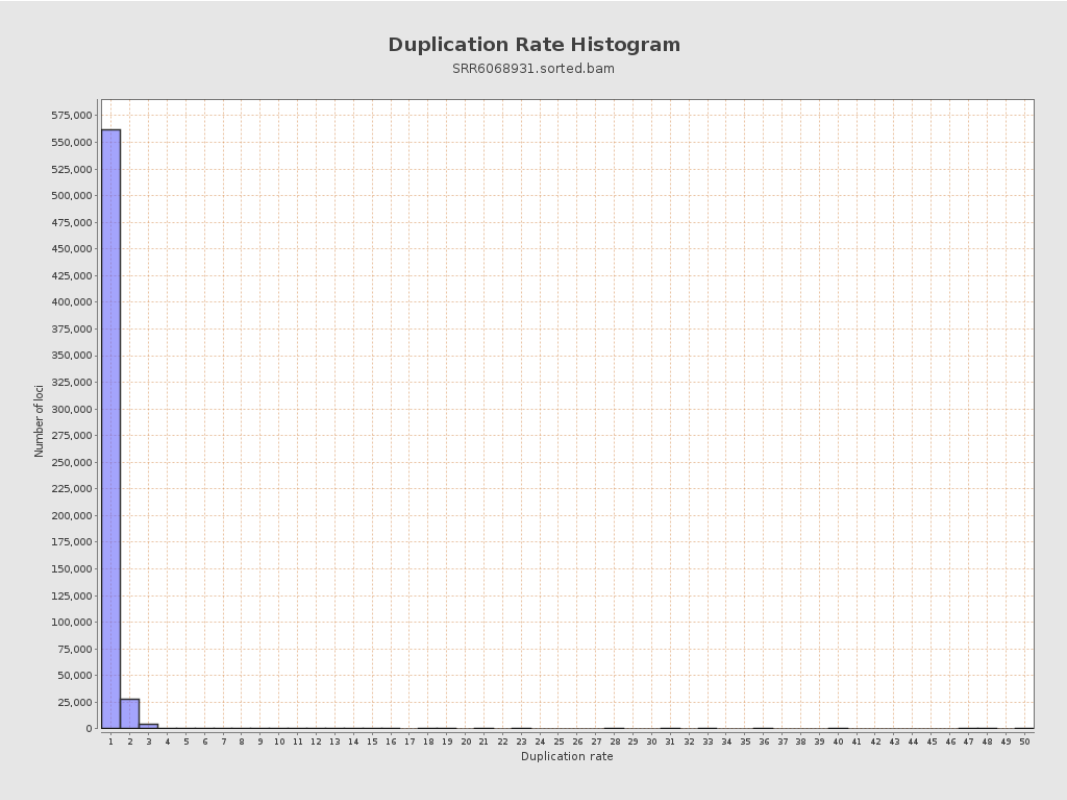
5. Results : Coverage Histogram (0-50X)



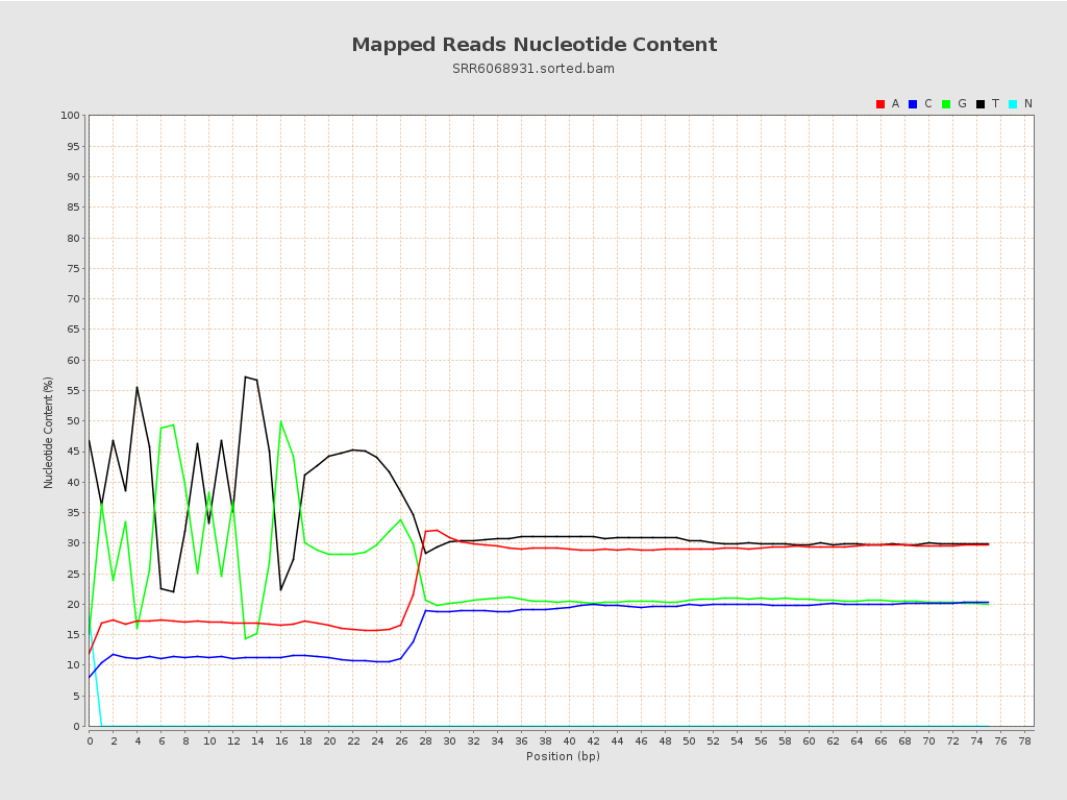
6. Results : Genome Fraction Coverage



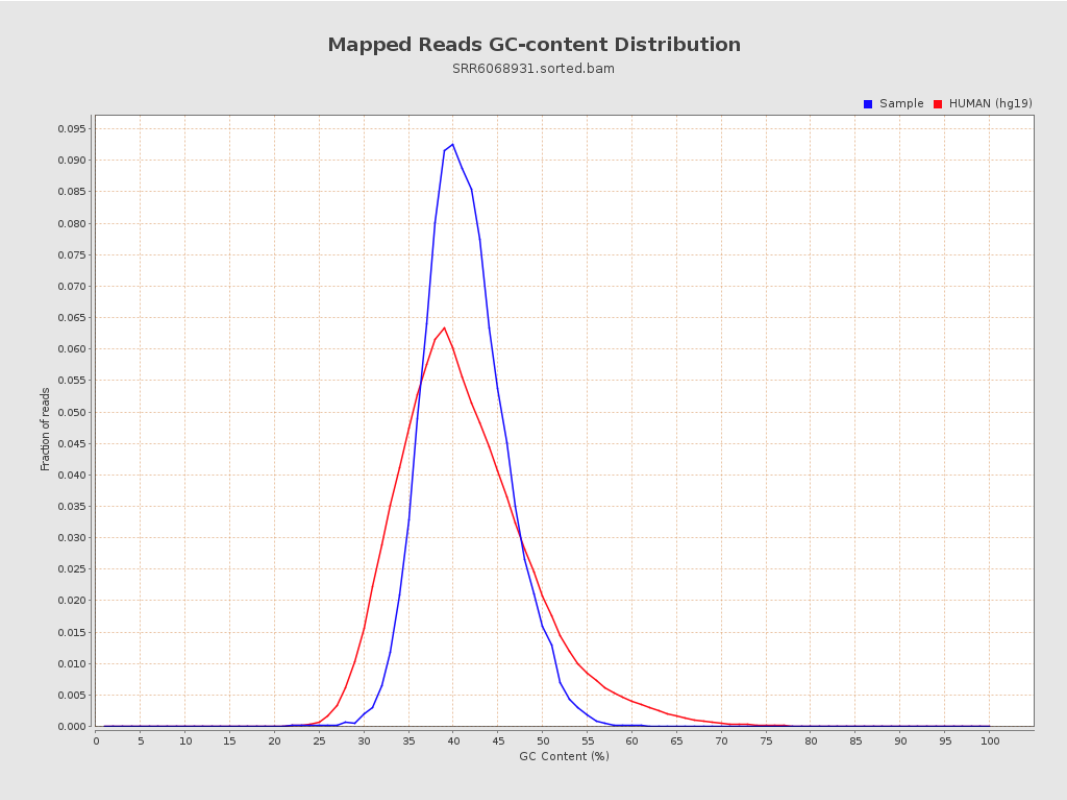
7. Results : Duplication Rate Histogram



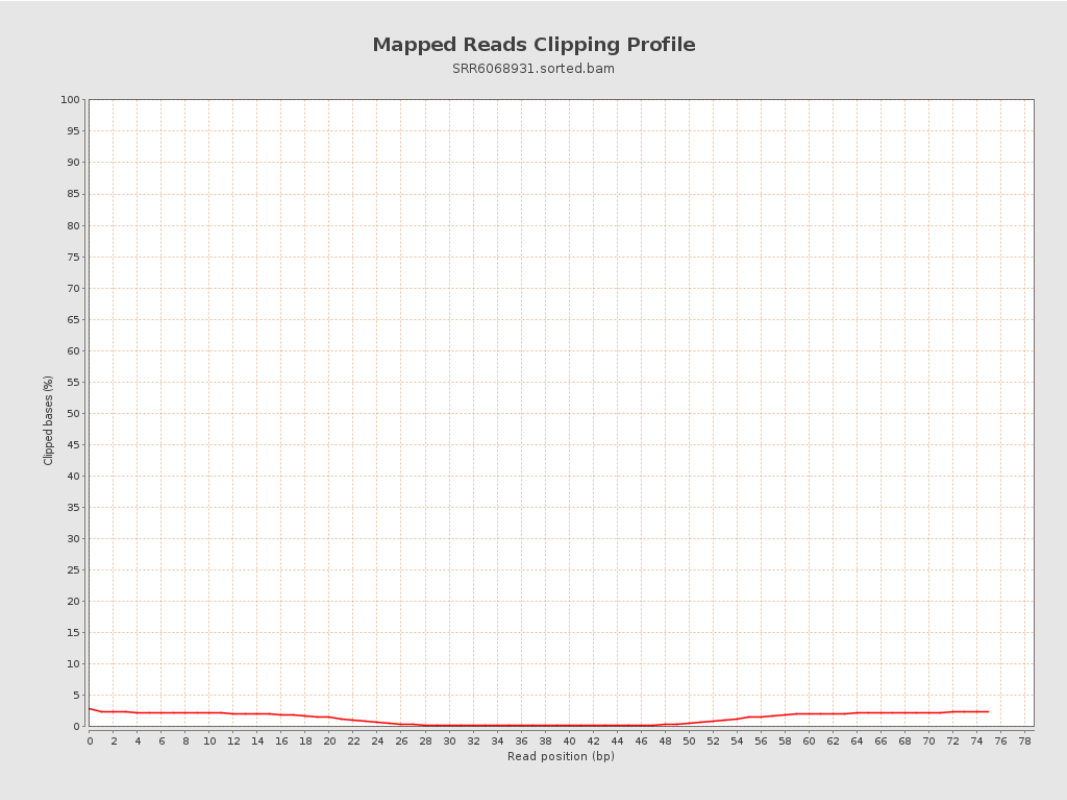
8. Results : Mapped Reads Nucleotide Content



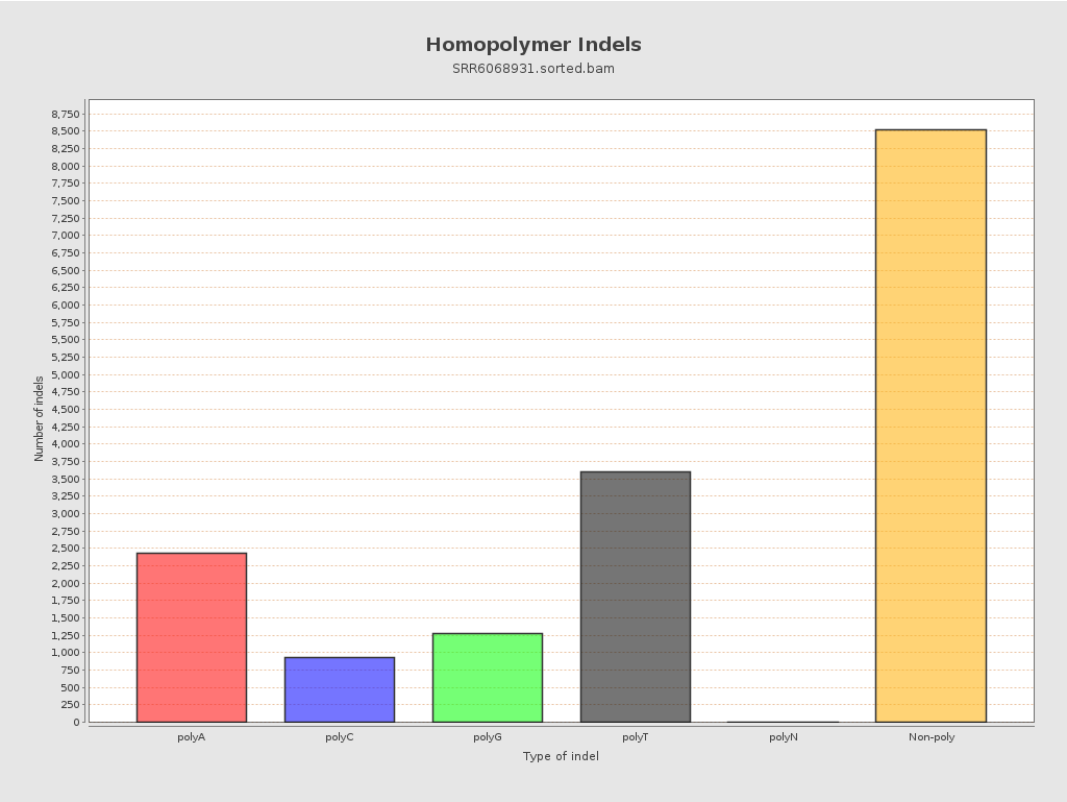
9. Results : Mapped Reads GC-content Distribution



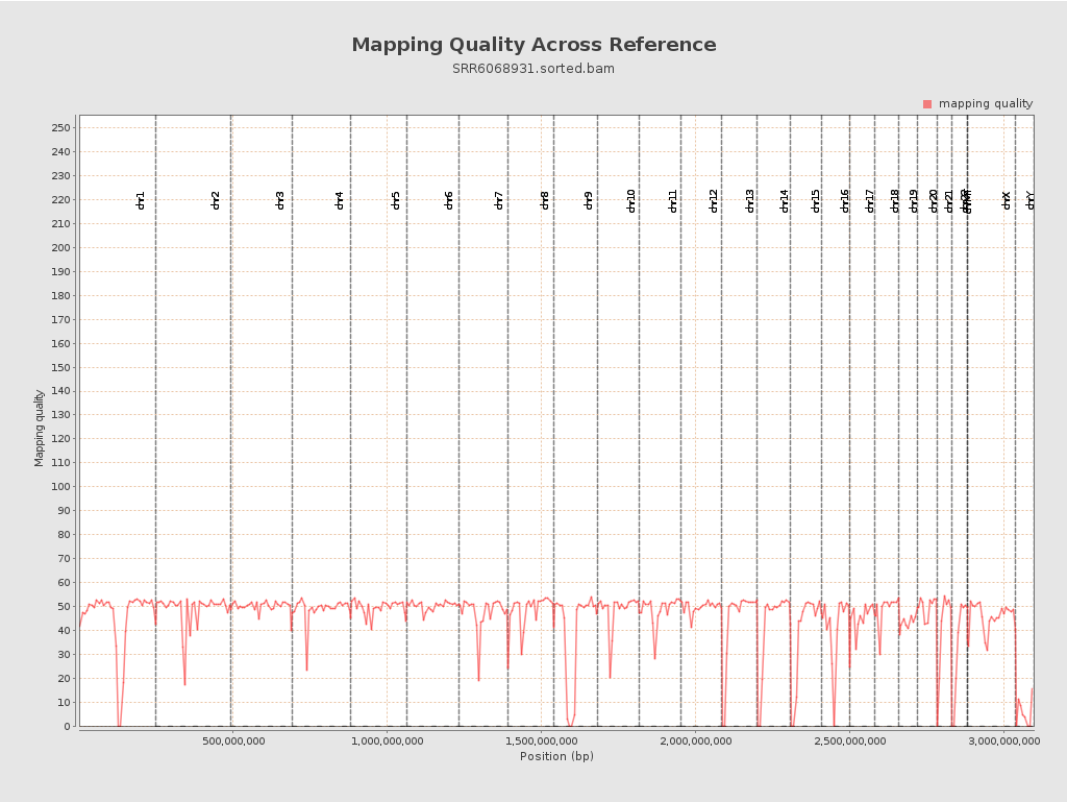
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram