Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:30:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068141.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_SRR6068141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:30:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,830,764
Mapped reads	2,462,083 / 86.98%
Unmapped reads	368,681 / 13.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,039 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	122,670 / 4.33%
Duplication rate	3.6%
Clipped reads	1,049,863 / 37.09%

2.2. ACGT Content

Number/percentage of A's	46,898,680 / 28.34%
Number/percentage of C's	30,122,794 / 18.2%
Number/percentage of T's	52,941,350 / 31.99%
Number/percentage of G's	35,538,787 / 21.47%
Number/percentage of N's	3,638 / 0%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.6139

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

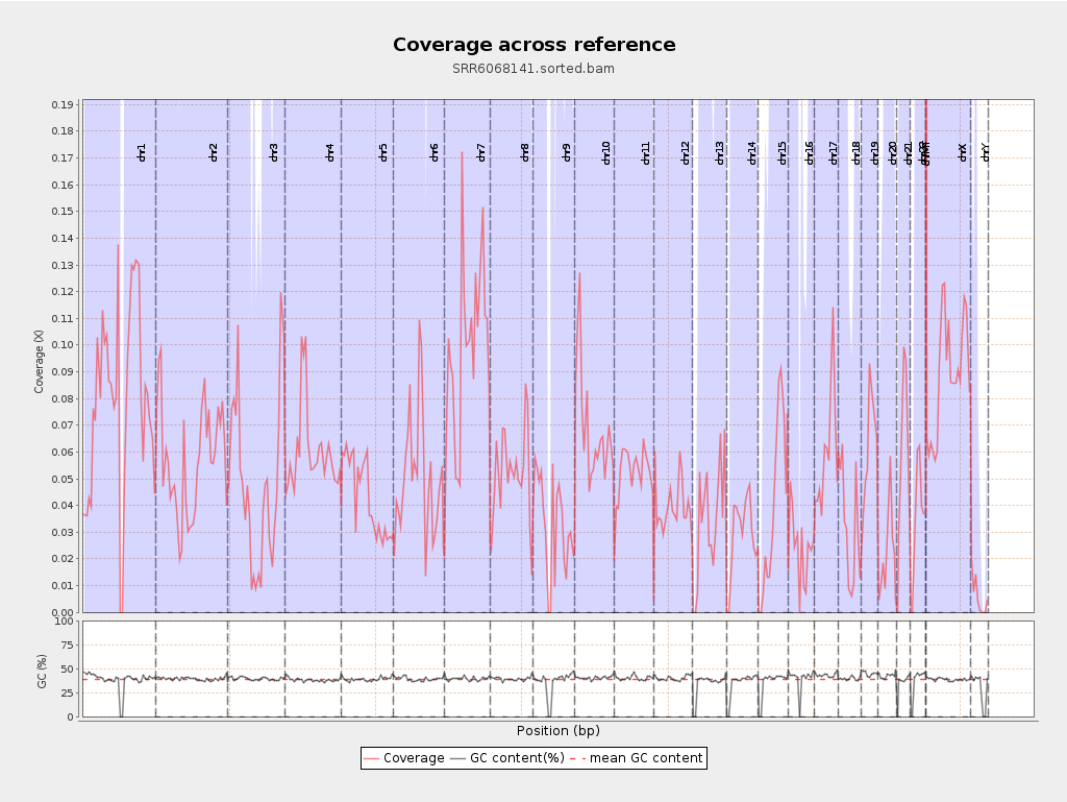
General error rate	0.82%
Mismatches	1,342,475
Insertions	12,902
Mapped reads with at least one insertion	0.52%
Deletions	55,837
Mapped reads with at least one deletion	2.24%
Homopolymer indels	45.75%

2.6. Chromosome stats

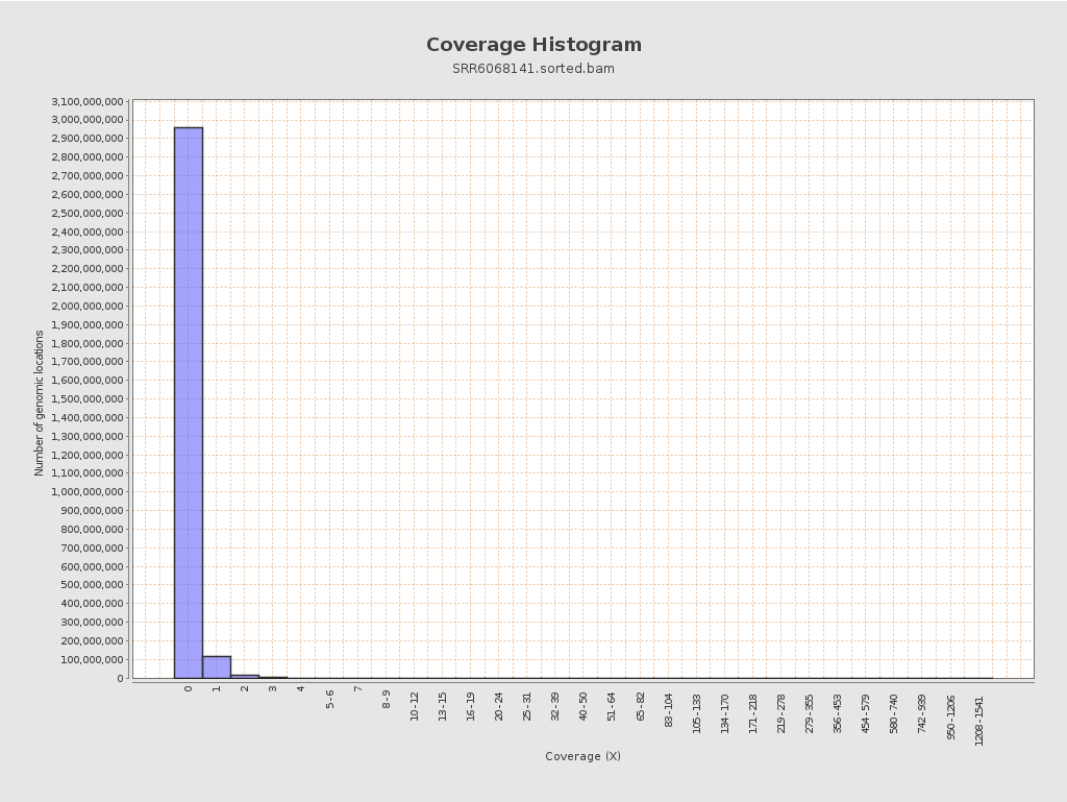
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19697028	0.079	1.3225
chr2	243199373	13868402	0.057	0.538
chr3	198022430	9582604	0.0484	0.2571
chr4	191154276	11603543	0.0607	0.2902
chr5	180915260	7819827	0.0432	0.2439
chr6	171115067	8762481	0.0512	0.3363
chr7	159138663	15562416	0.0978	1.2599

chr8	146364022	7637558	0.0522	0.8161
chr9	141213431	4626028	0.0328	0.453
chr10	135534747	9350835	0.069	0.3965
chr11	135006516	7092608	0.0525	0.4217
chr12	133851895	5352079	0.04	0.2602
chr13	115169878	3970444	0.0345	0.2166
chr14	107349540	3219641	0.03	0.2644
chr15	102531392	4065885	0.0397	0.2348
chr16	90354753	2157273	0.0239	0.2188
chr17	81195210	5032494	0.062	0.3281
chr18	78077248	2541108	0.0325	0.7946
chr19	59128983	3657471	0.0619	0.8995
chr20	63025520	1384026	0.022	0.2119
chr21	48129895	2712741	0.0564	0.2856
chr22	51304566	1804813	0.0352	0.2133
chrMT	16571	18879	1.1393	1.4395
chrX	155270560	13731721	0.0884	0.4209
chrY	59373566	344112	0.0058	0.1174

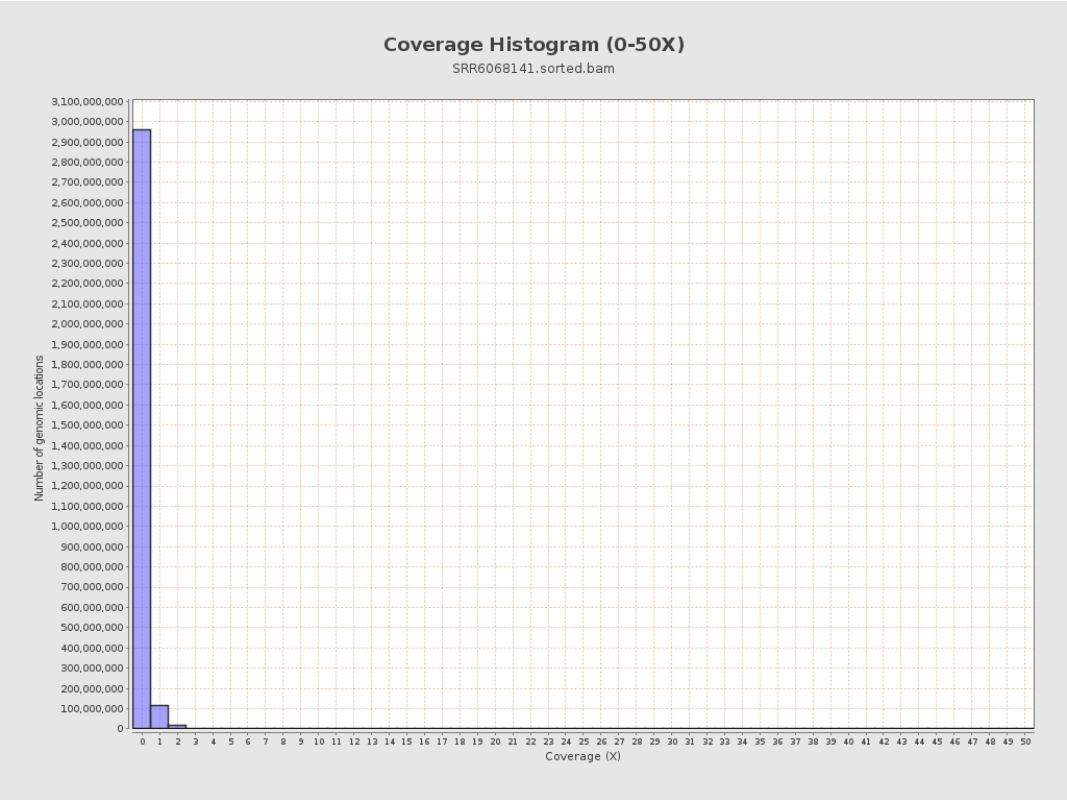
3. Results : Coverage across reference



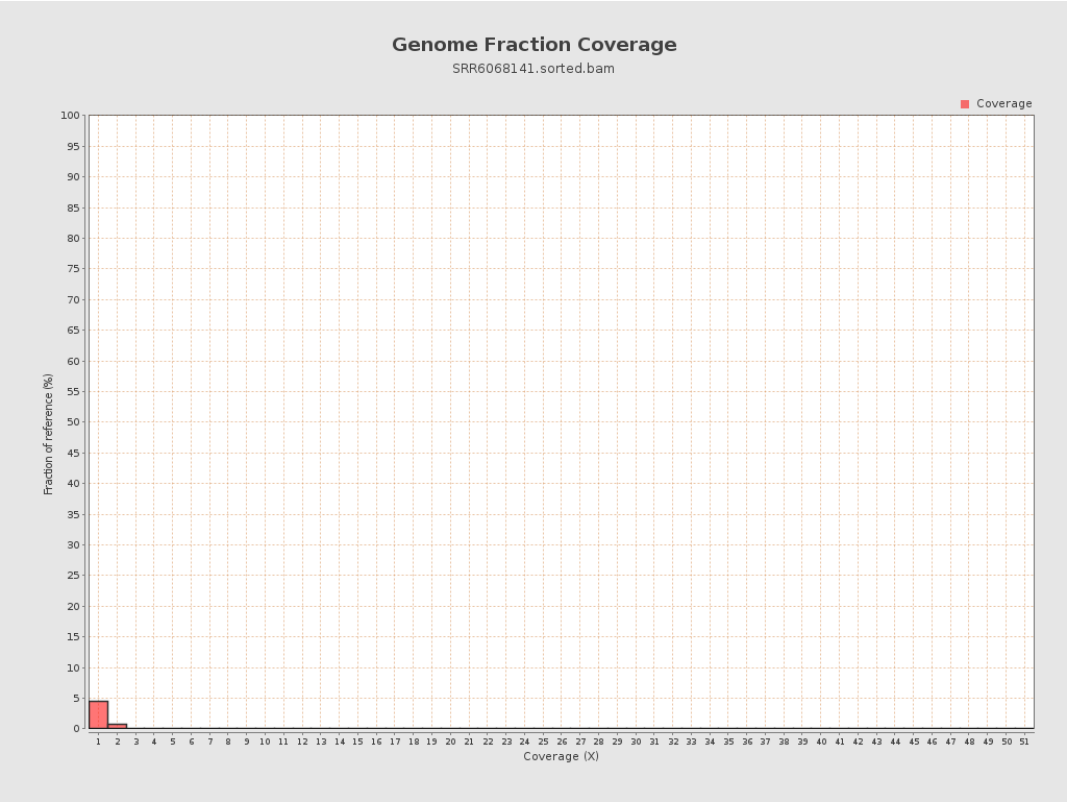
4. Results : Coverage Histogram



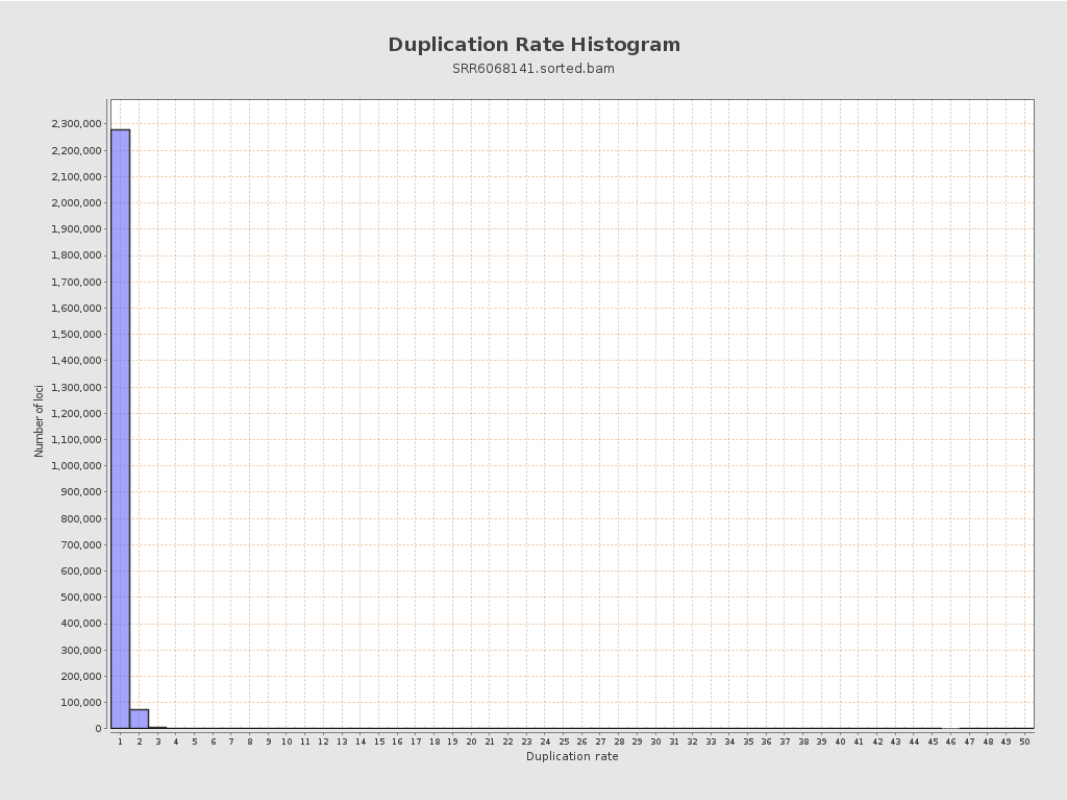
5. Results : Coverage Histogram (0-50X)



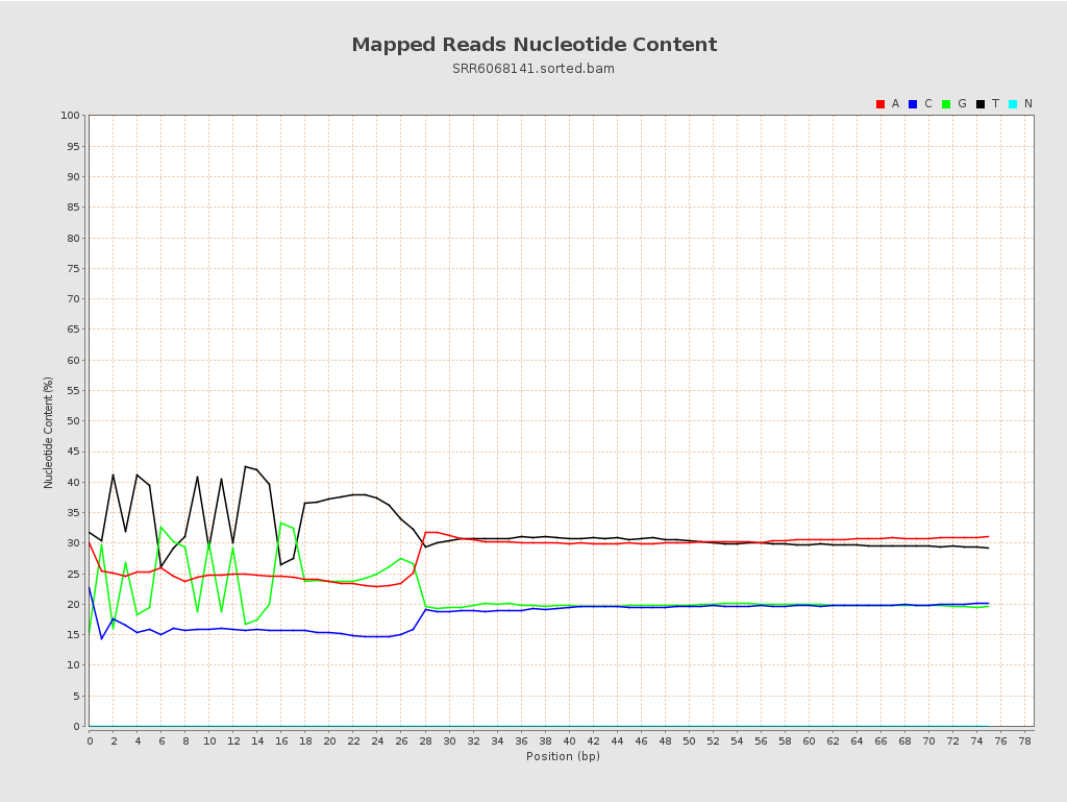
6. Results : Genome Fraction Coverage



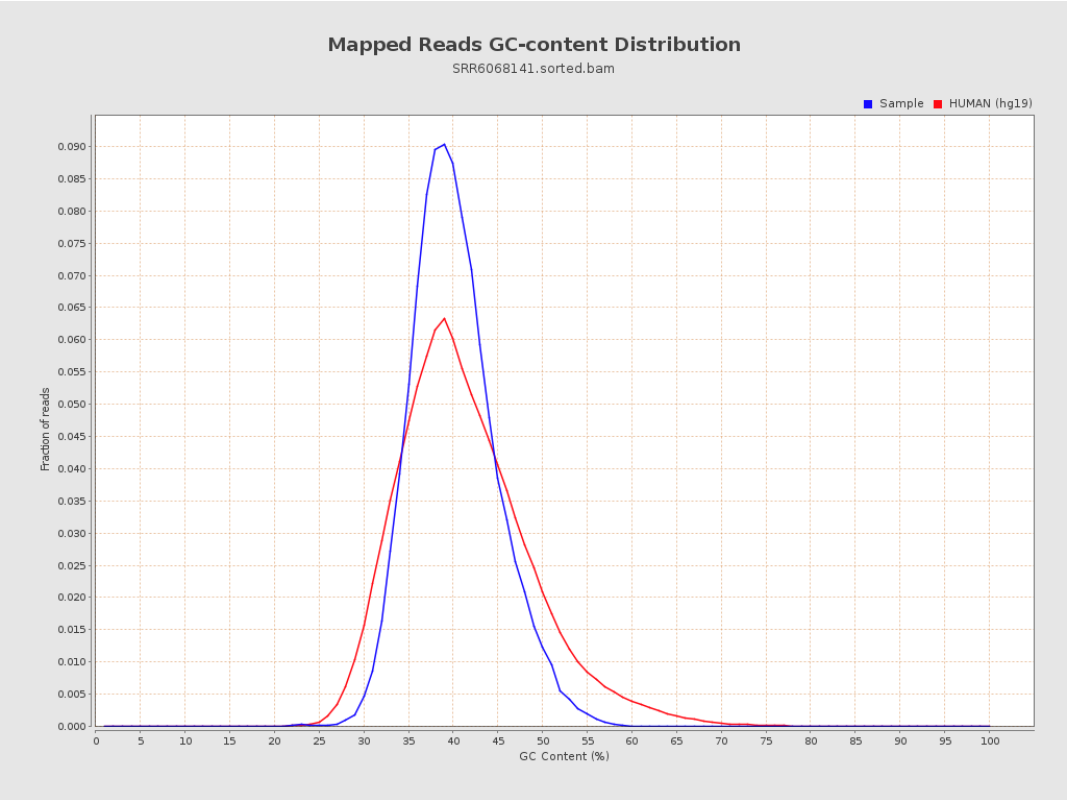
7. Results : Duplication Rate Histogram



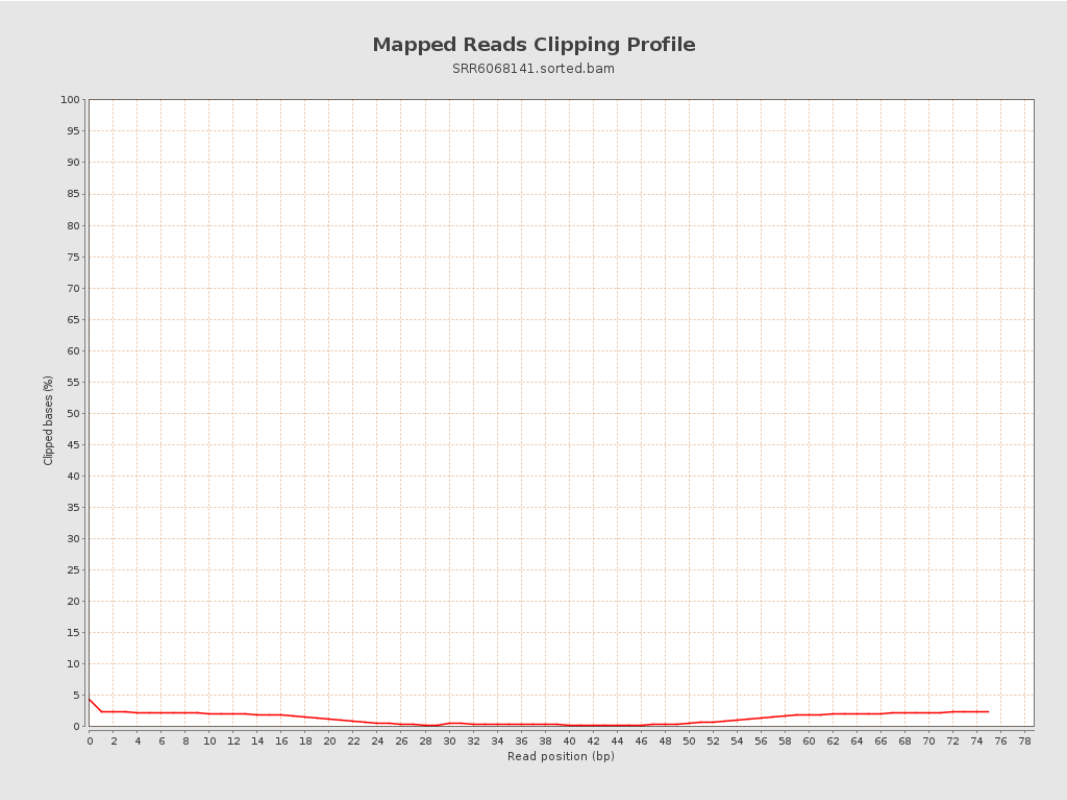
8. Results : Mapped Reads Nucleotide Content



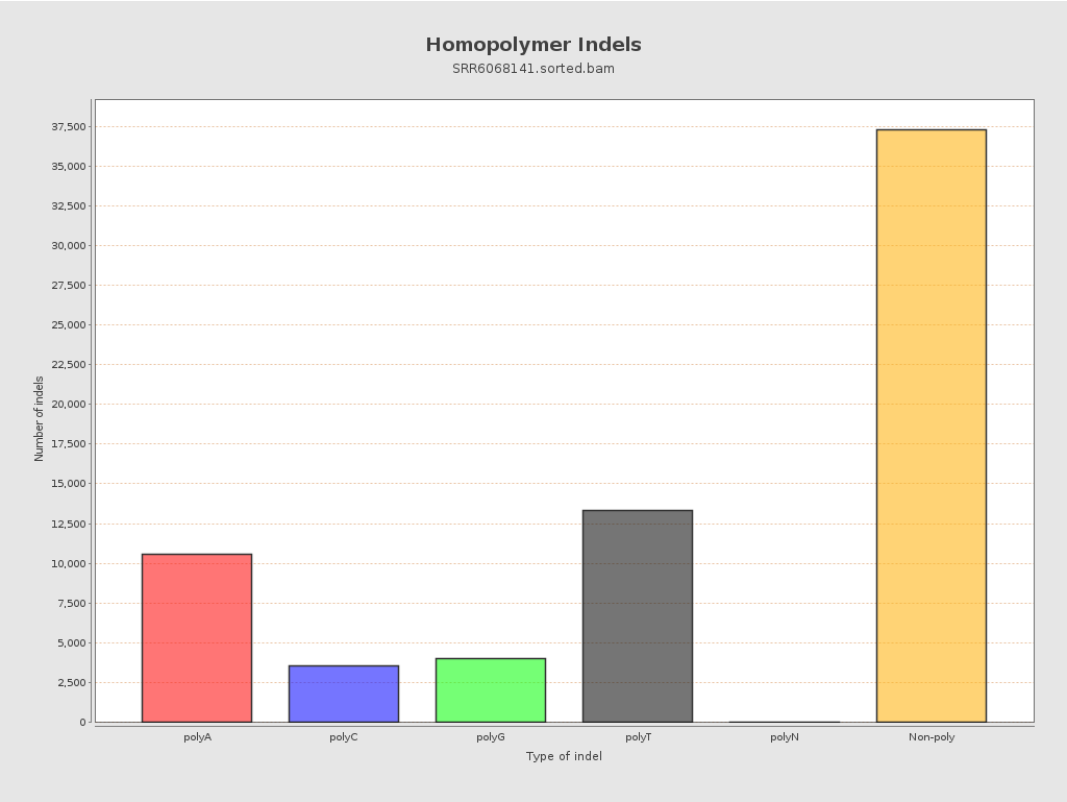
9. Results : Mapped Reads GC-content Distribution



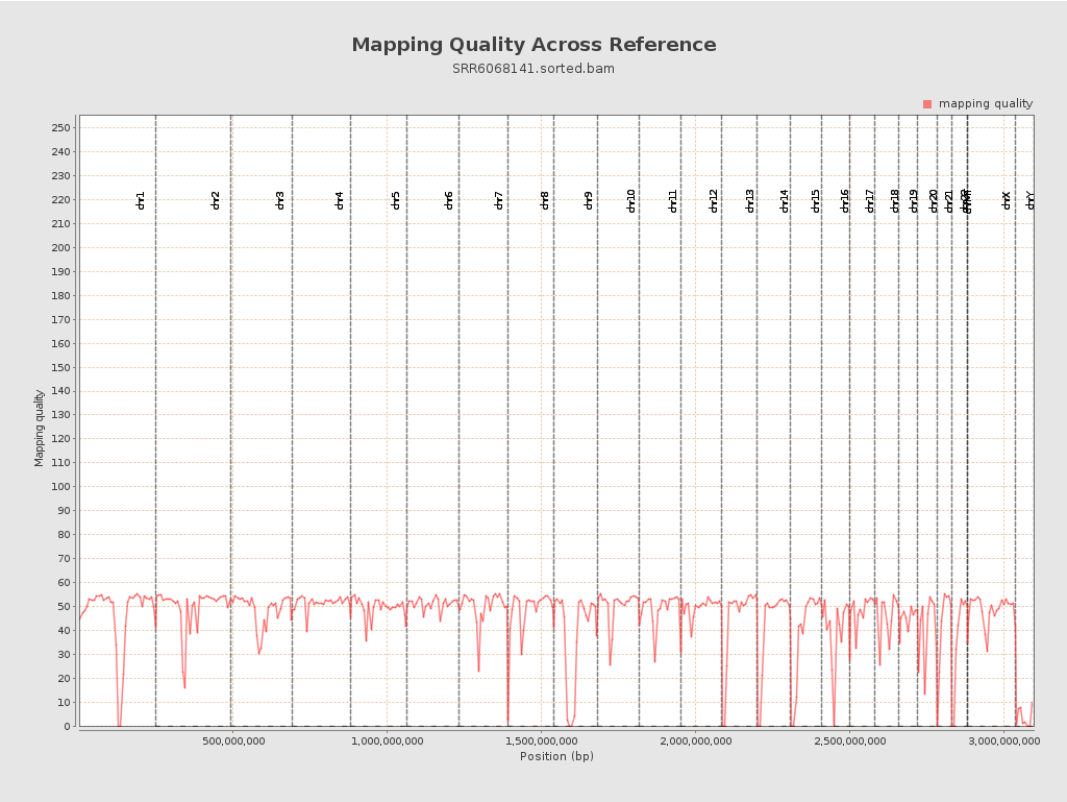
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram