

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:03:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068131.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_SRR6068131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:03:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,583,262
Mapped reads	3,394,430 / 94.73%
Unmapped reads	188,832 / 5.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,778 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	1,338,952 / 37.37%
Duplication rate	18.6%
Clipped reads	1,792,876 / 50.03%

2.2. ACGT Content

Number/percentage of A's	58,627,280 / 26.67%
Number/percentage of C's	39,150,885 / 17.81%
Number/percentage of T's	72,044,397 / 32.78%
Number/percentage of G's	49,944,130 / 22.72%
Number/percentage of N's	24,819 / 0.01%
GC Percentage	40.54%

2.3. Coverage

Mean	0.071

Standard Deviation	0.9255
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2.4. Mapping Quality

Mean Mapping Quality	45.98
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2.5. Mismatches and indels

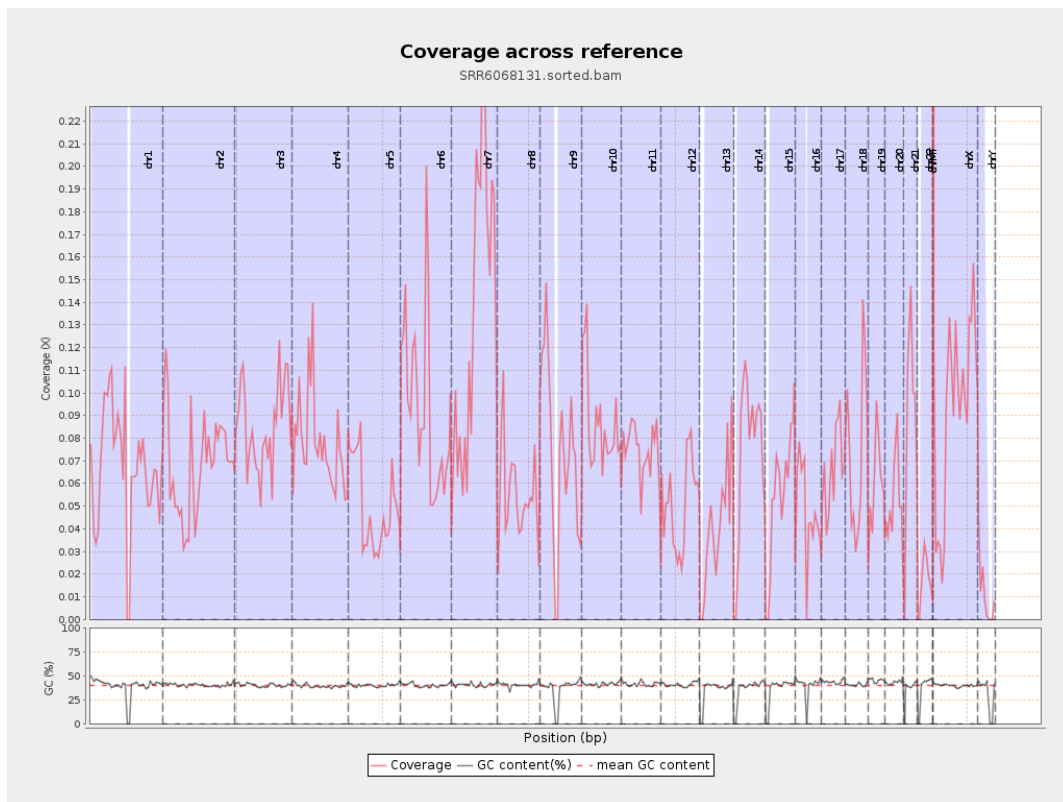
General error rate	0.52%
Mismatches	1,109,320
Insertions	14,273
Mapped reads with at least one insertion	0.42%
Deletions	47,497
Mapped reads with at least one deletion	1.38%
Homopolymer indels	44.52%

2.6. Chromosome stats

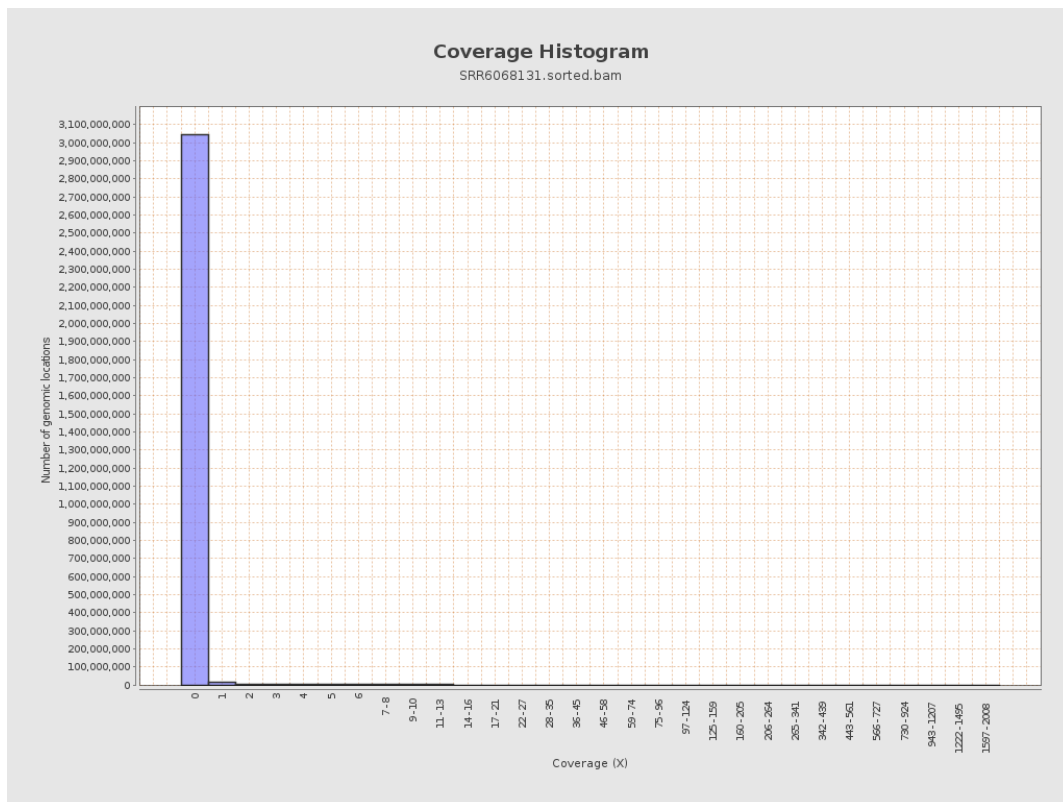
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16660621	0.0668	1.2111
chr2	243199373	16629239	0.0684	0.992
chr3	198022430	16760909	0.0846	0.8474
chr4	191154276	14978765	0.0784	0.845
chr5	180915260	8926498	0.0493	0.6596
chr6	171115067	15987373	0.0934	0.9066
chr7	159138663	21612961	0.1358	1.2203

chr8	146364022	7944275	0.0543	1.3103
chr9	141213431	10513327	0.0744	0.8254
chr10	135534747	11883795	0.0877	1.1282
chr11	135006516	10028969	0.0743	0.8561
chr12	133851895	6823848	0.051	0.67
chr13	115169878	4720969	0.041	0.6075
chr14	107349540	8146471	0.0759	0.806
chr15	102531392	5454308	0.0532	0.6597
chr16	90354753	4197480	0.0465	0.6459
chr17	81195210	5426470	0.0668	0.7845
chr18	78077248	5804994	0.0743	1.0666
chr19	59128983	3623722	0.0613	0.9091
chr20	63025520	3294976	0.0523	0.6748
chr21	48129895	4170733	0.0867	0.8654
chr22	51304566	869711	0.017	0.3968
chrMT	16571	465689	28.1026	31.422
chrX	155270560	14303127	0.0921	0.9565
chrY	59373566	646419	0.0109	0.2671

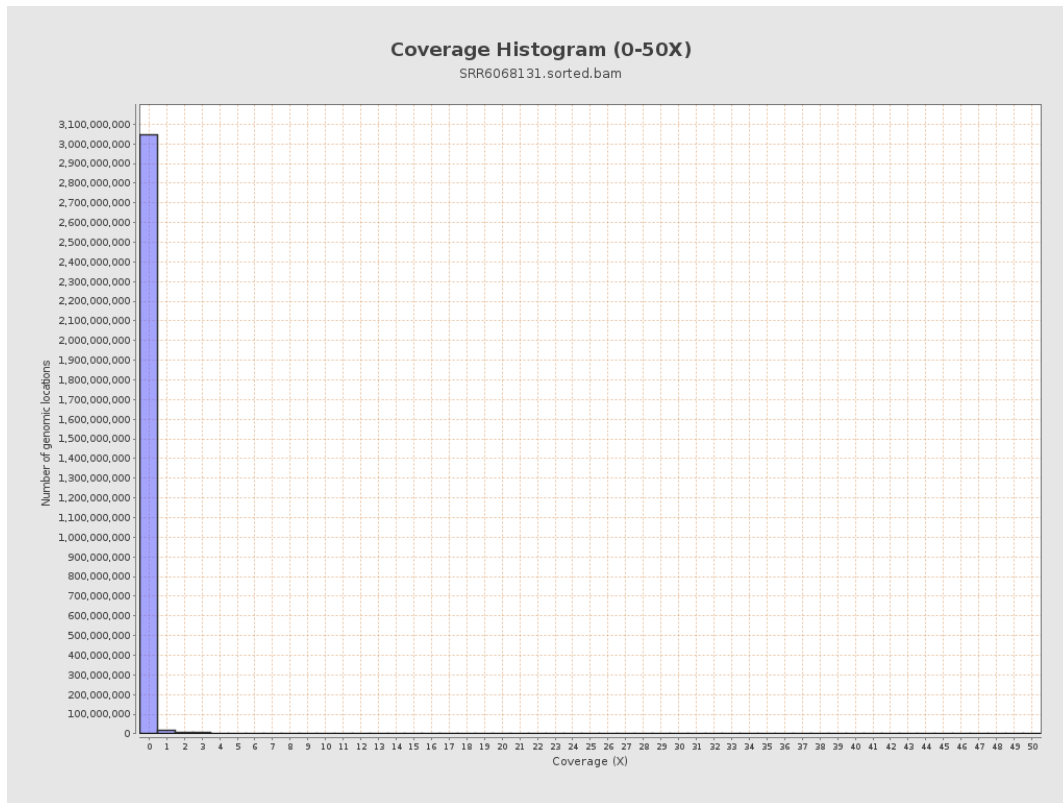
3. Results : Coverage across reference



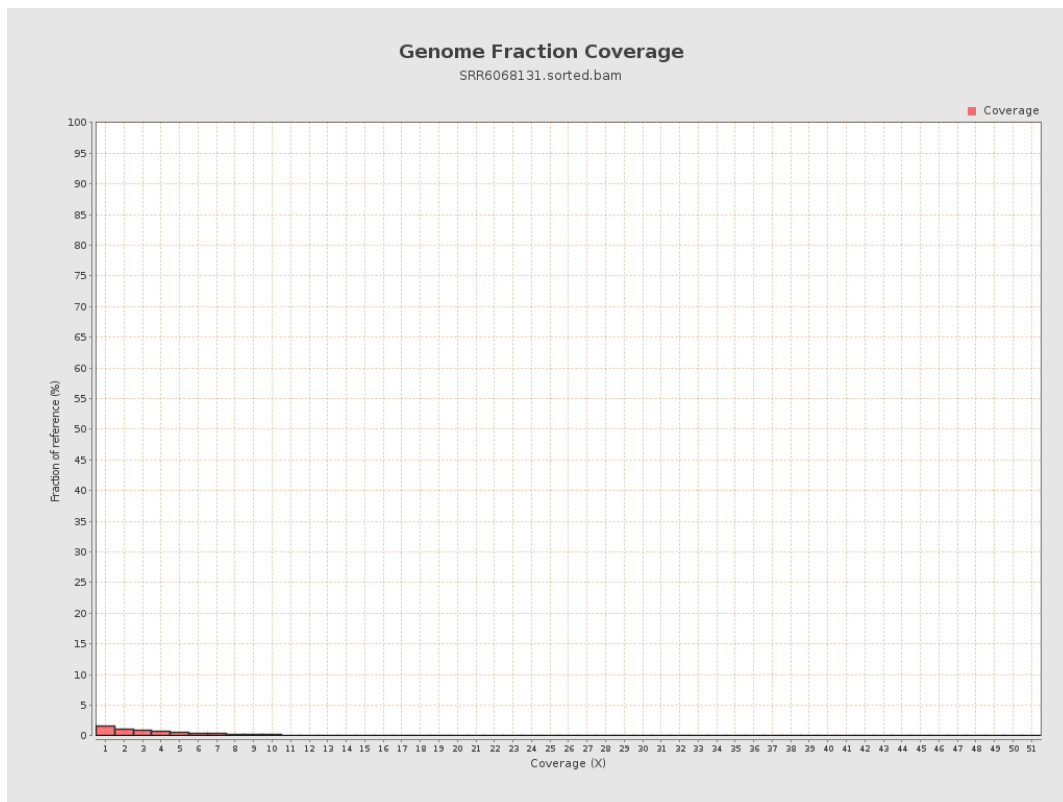
4. Results : Coverage Histogram



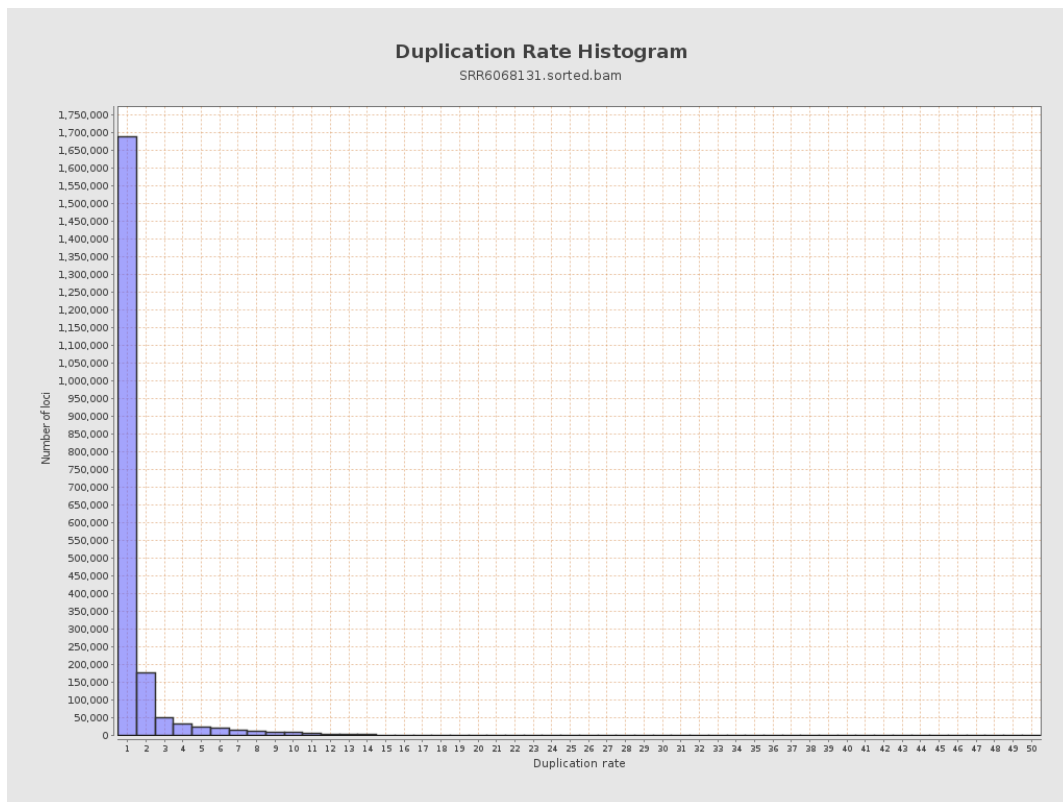
5. Results : Coverage Histogram (0-50X)



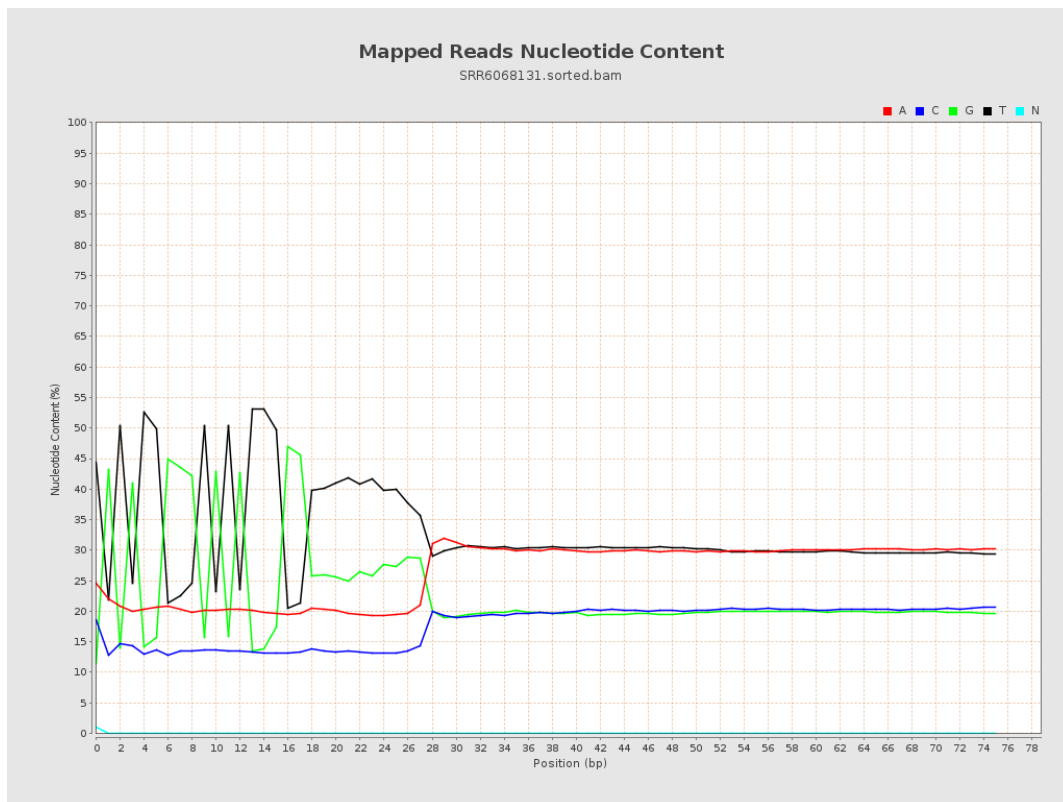
6. Results : Genome Fraction Coverage



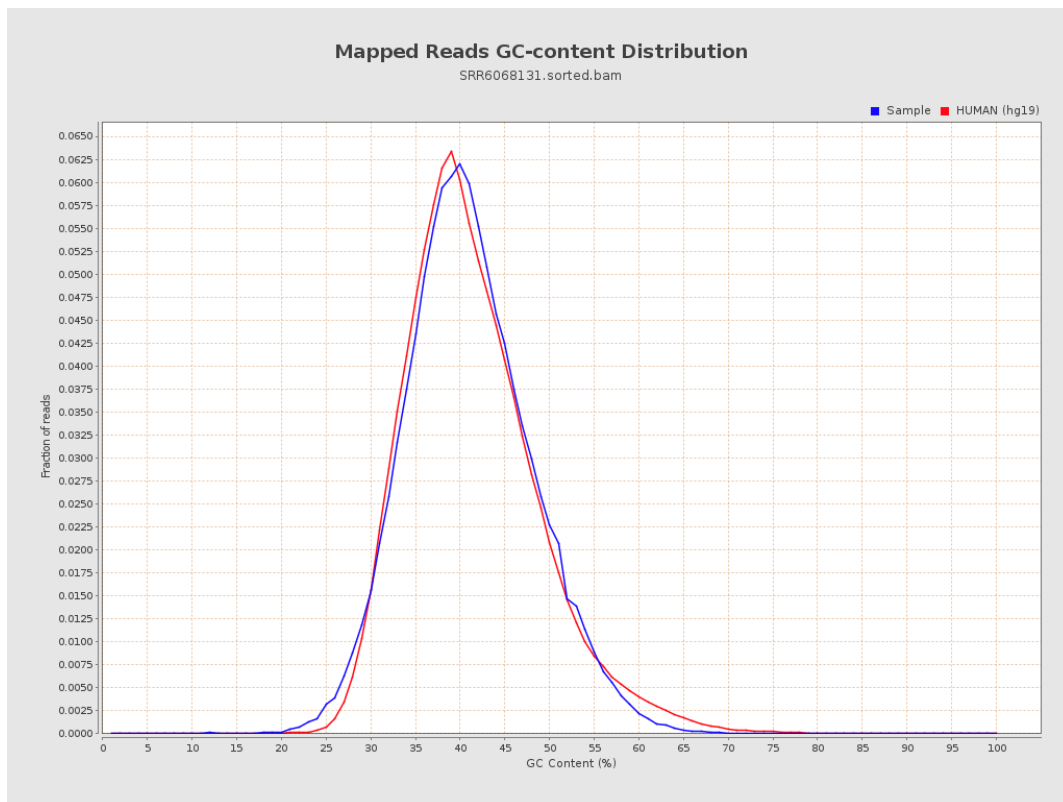
7. Results : Duplication Rate Histogram



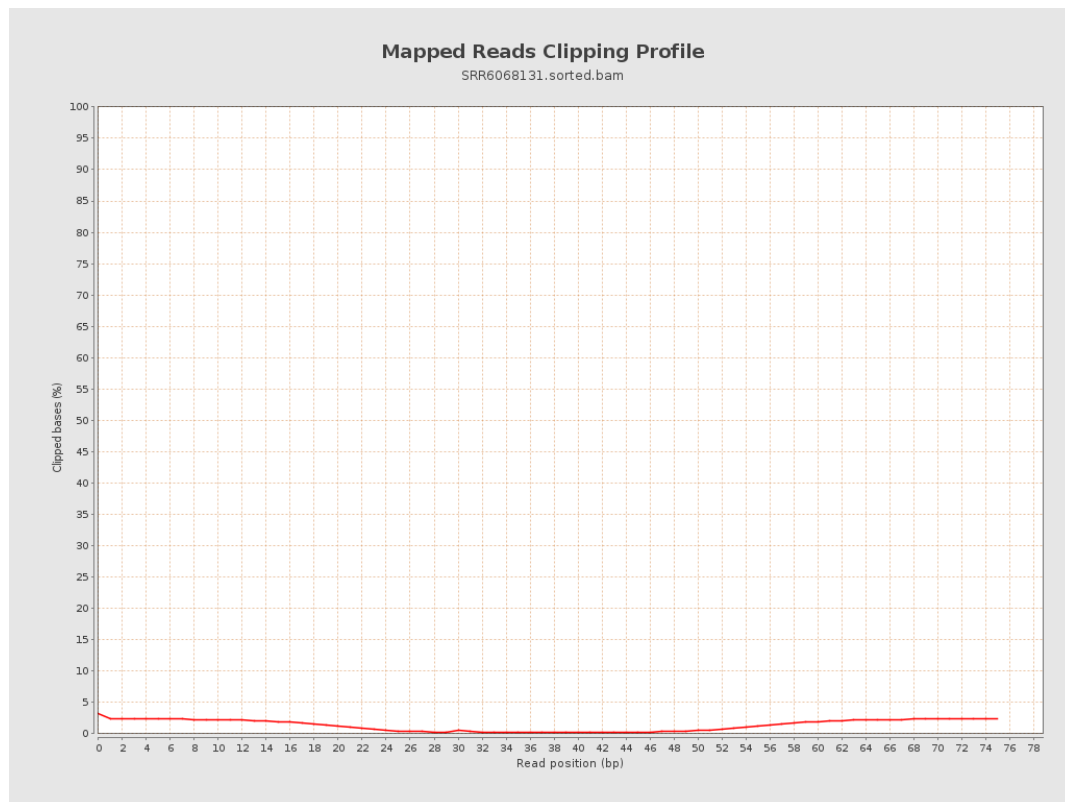
8. Results : Mapped Reads Nucleotide Content



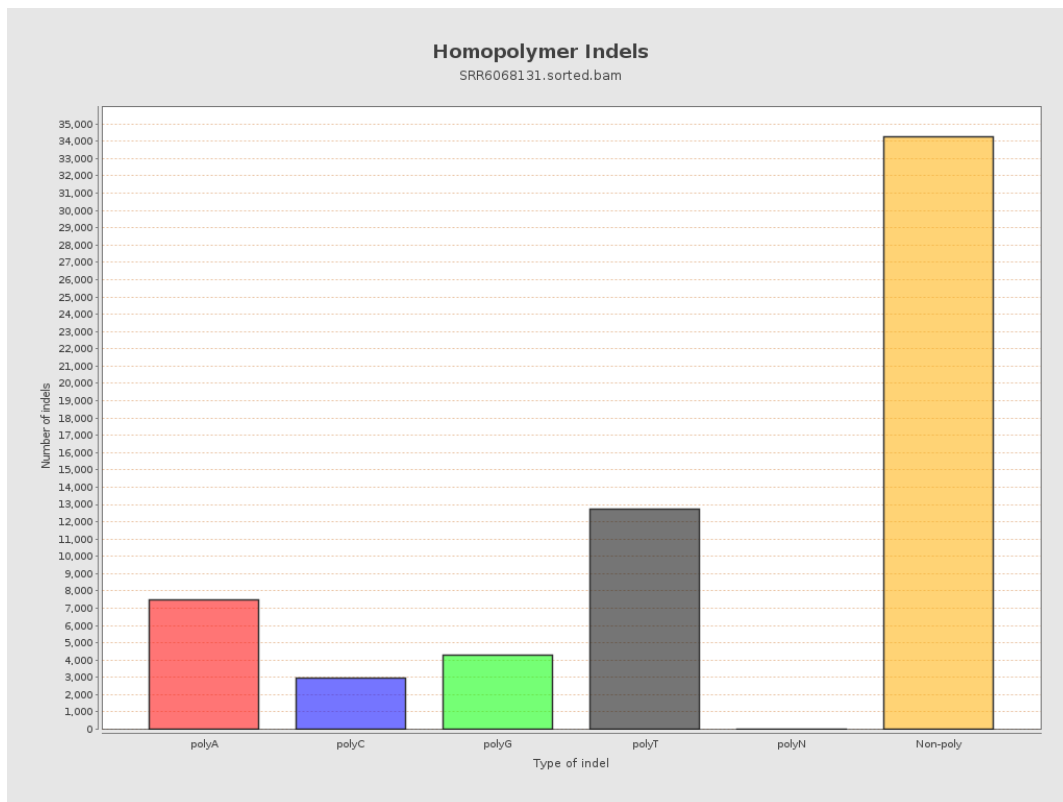
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

