

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:50:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004070.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_SRR6004070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:50:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,046,619
Mapped reads	1,827,123 / 89.28%
Unmapped reads	219,496 / 10.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,617 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	113,041 / 5.52%
Duplication rate	5.42%
Clipped reads	818,849 / 40.01%

2.2. ACGT Content

Number/percentage of A's	34,176,898 / 28.05%
Number/percentage of C's	22,024,509 / 18.07%
Number/percentage of T's	39,349,184 / 32.29%
Number/percentage of G's	26,281,679 / 21.57%
Number/percentage of N's	21,177 / 0.02%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.2877
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2.4. Mapping Quality

Mean Mapping Quality	48.52
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2.5. Mismatches and indels

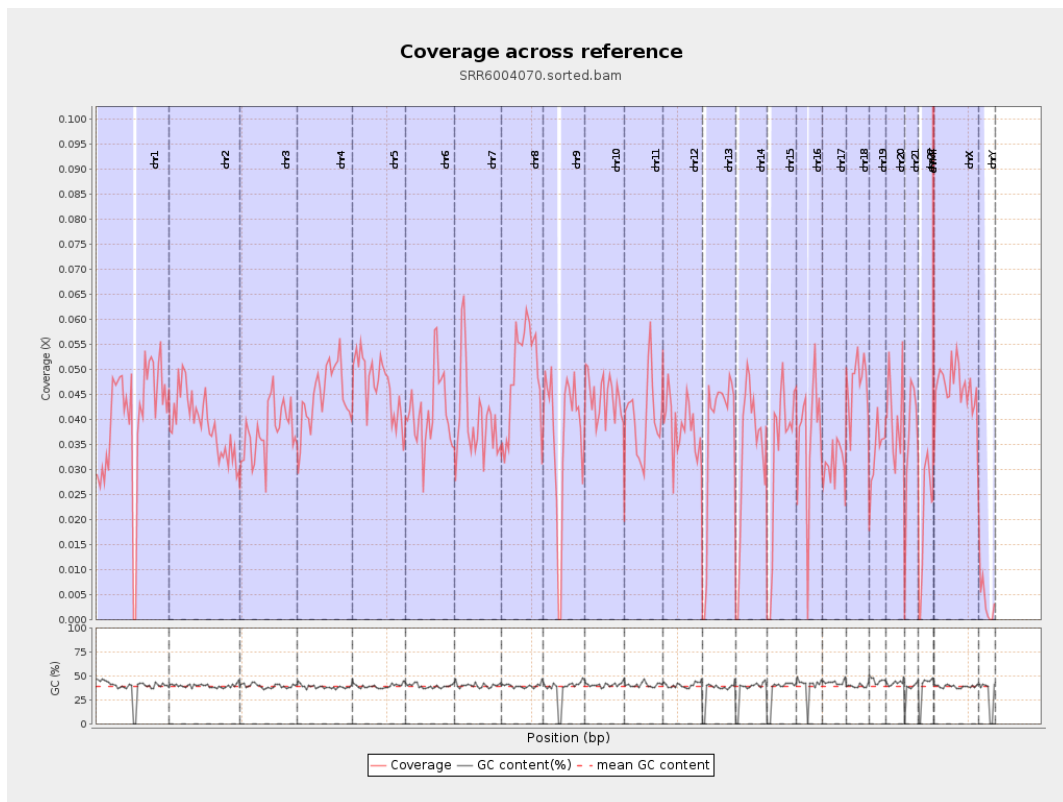
General error rate	0.83%
Mismatches	1,004,625
Insertions	7,558
Mapped reads with at least one insertion	0.41%
Deletions	29,187
Mapped reads with at least one deletion	1.58%
Homopolymer indels	46.78%

2.6. Chromosome stats

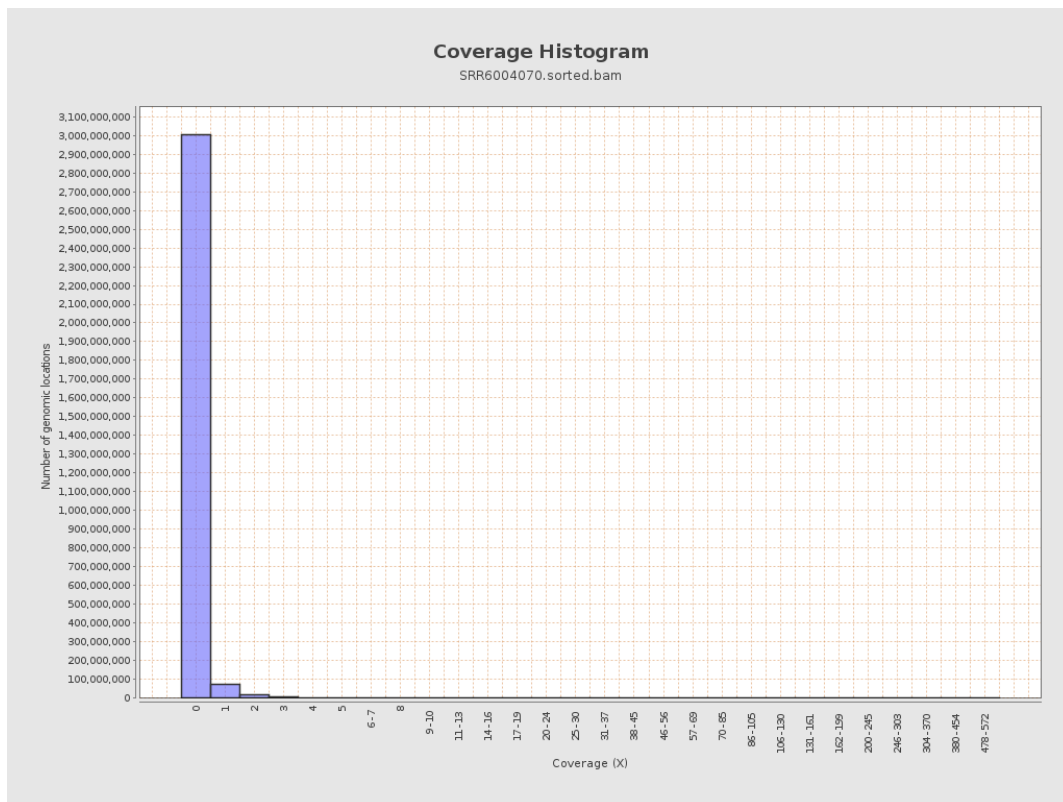
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10007884	0.0402	0.389
chr2	243199373	9472011	0.0389	0.3107
chr3	198022430	7440300	0.0376	0.2424
chr4	191154276	8534077	0.0446	0.2671
chr5	180915260	8438162	0.0466	0.2714
chr6	171115067	7079871	0.0414	0.264
chr7	159138663	6444655	0.0405	0.2933

chr8	146364022	7150038	0.0489	0.4345
chr9	141213431	5221809	0.037	0.2597
chr10	135534747	6040592	0.0446	0.2777
chr11	135006516	5428201	0.0402	0.2802
chr12	133851895	5123659	0.0383	0.2466
chr13	115169878	4272050	0.0371	0.2471
chr14	107349540	3565347	0.0332	0.2318
chr15	102531392	3383259	0.033	0.2268
chr16	90354753	3340010	0.037	0.2433
chr17	81195210	2505164	0.0309	0.2251
chr18	78077248	3688552	0.0472	0.3639
chr19	59128983	1996406	0.0338	0.3036
chr20	63025520	2585980	0.041	0.2558
chr21	48129895	1725722	0.0359	0.2416
chr22	51304566	1029252	0.0201	0.1747
chrMT	16571	36714	2.2156	2.2359
chrX	155270560	7168722	0.0462	0.277
chrY	59373566	224326	0.0038	0.0767

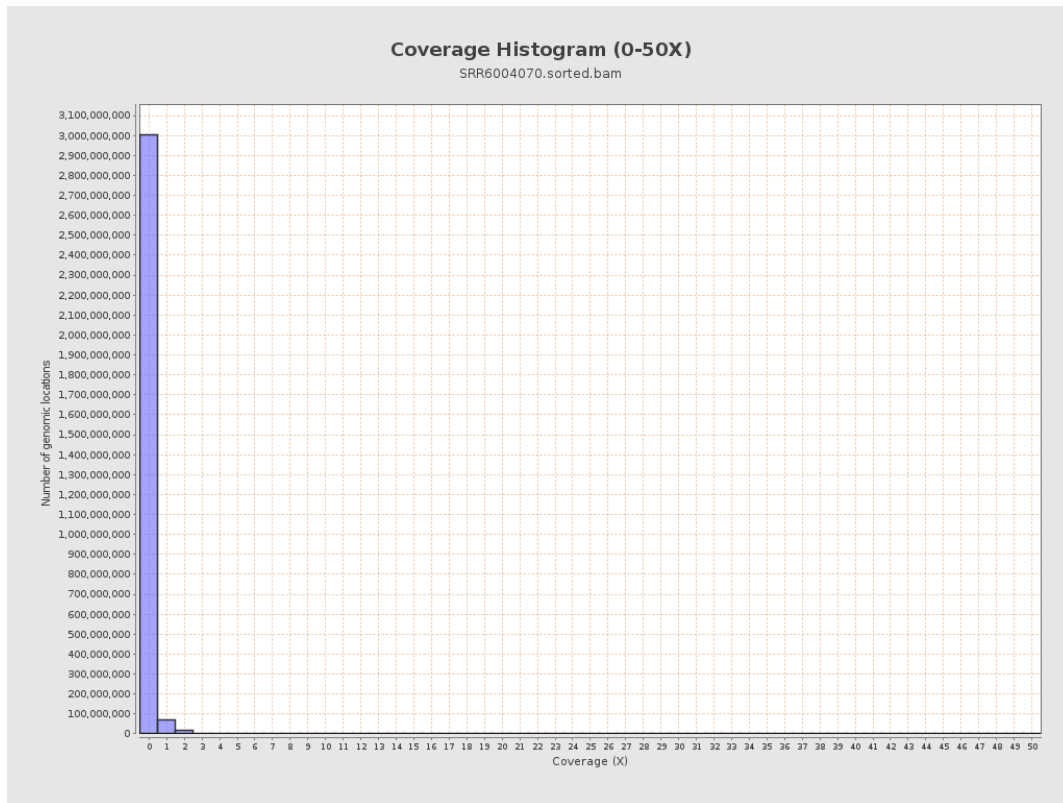
3. Results : Coverage across reference



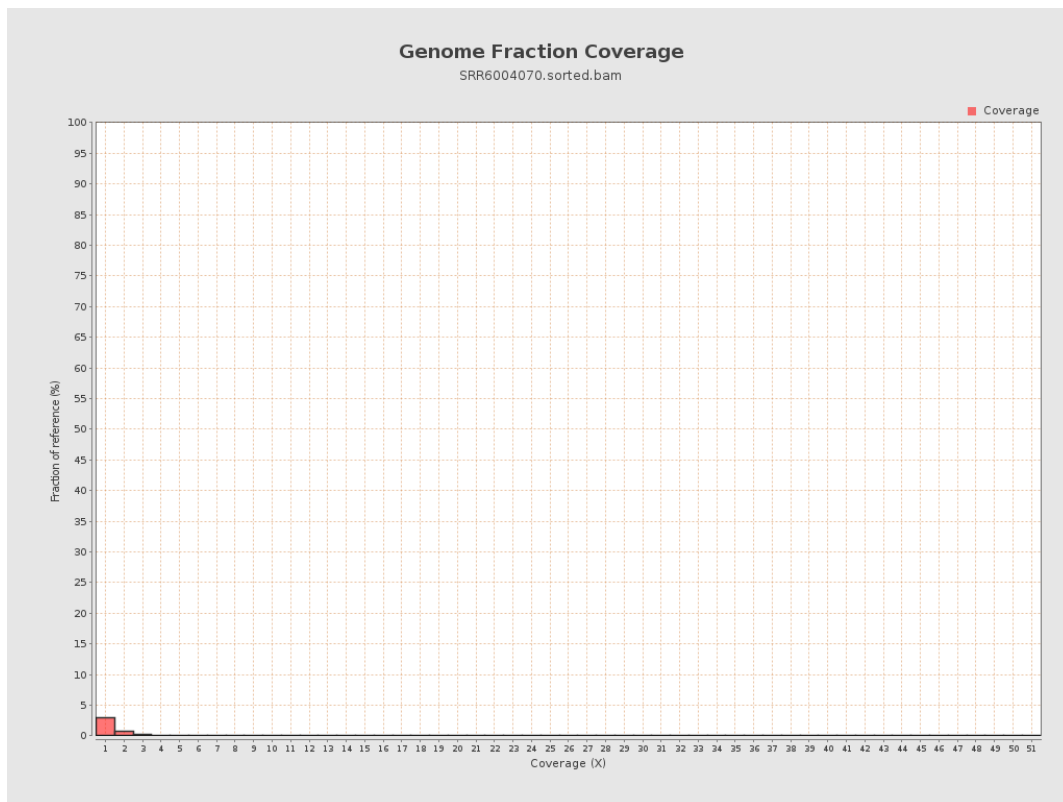
4. Results : Coverage Histogram



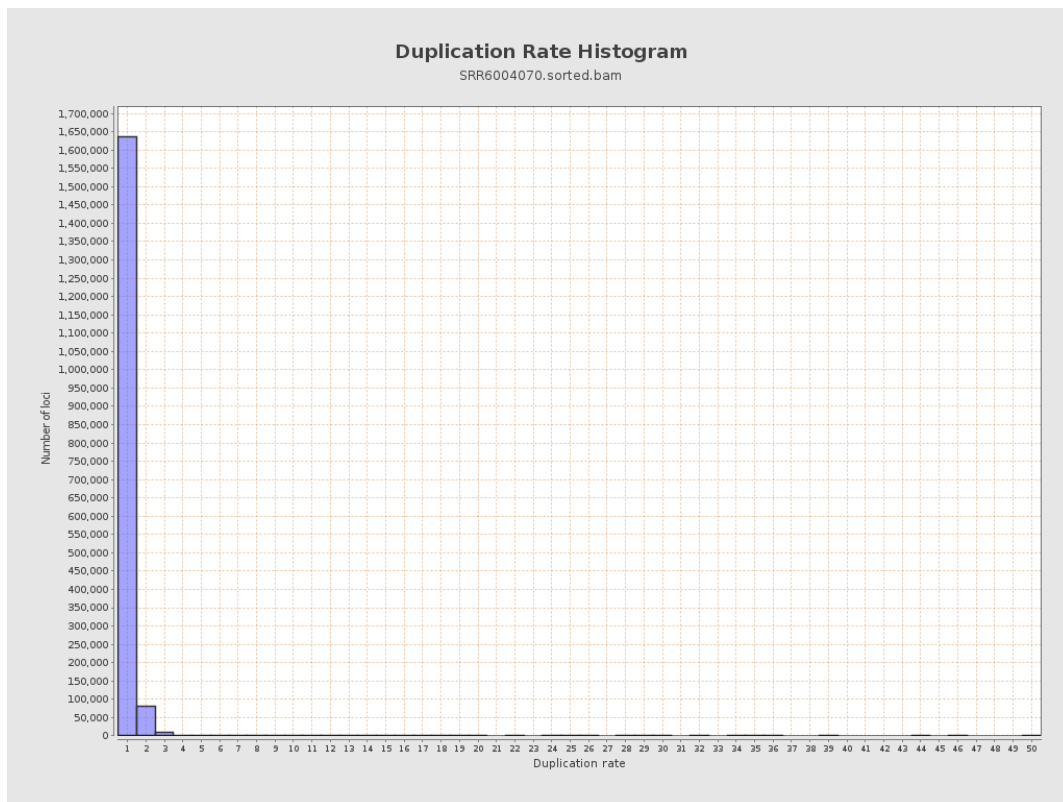
5. Results : Coverage Histogram (0-50X)



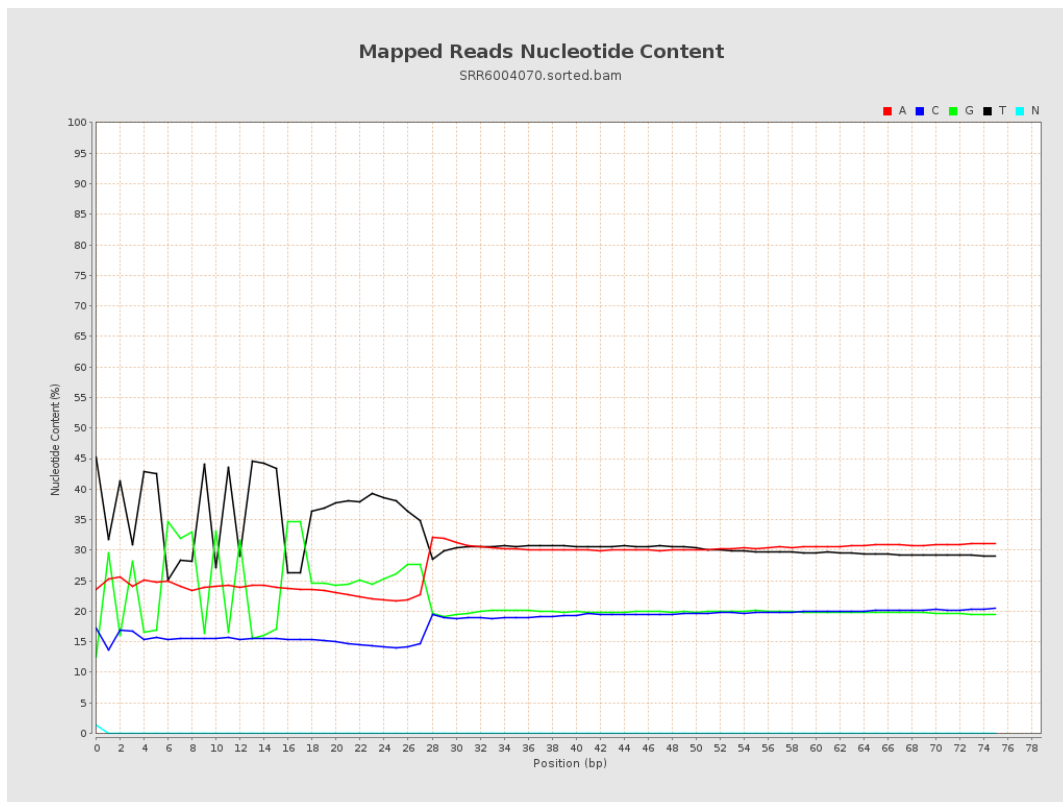
6. Results : Genome Fraction Coverage



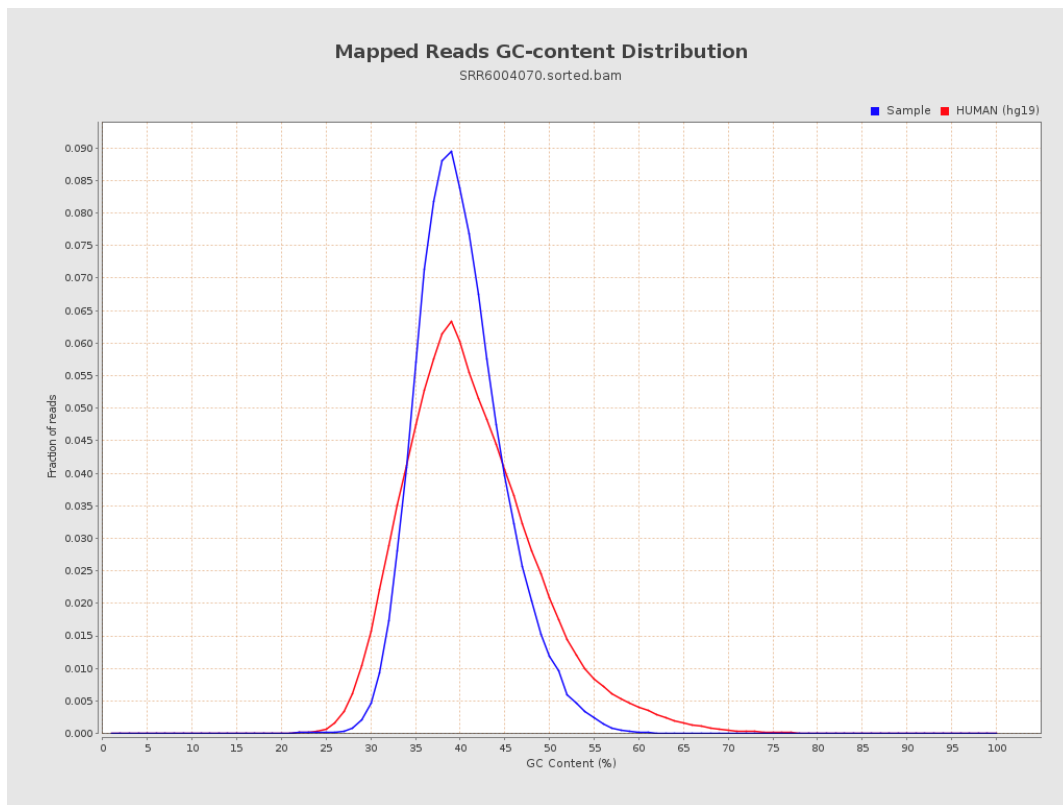
7. Results : Duplication Rate Histogram



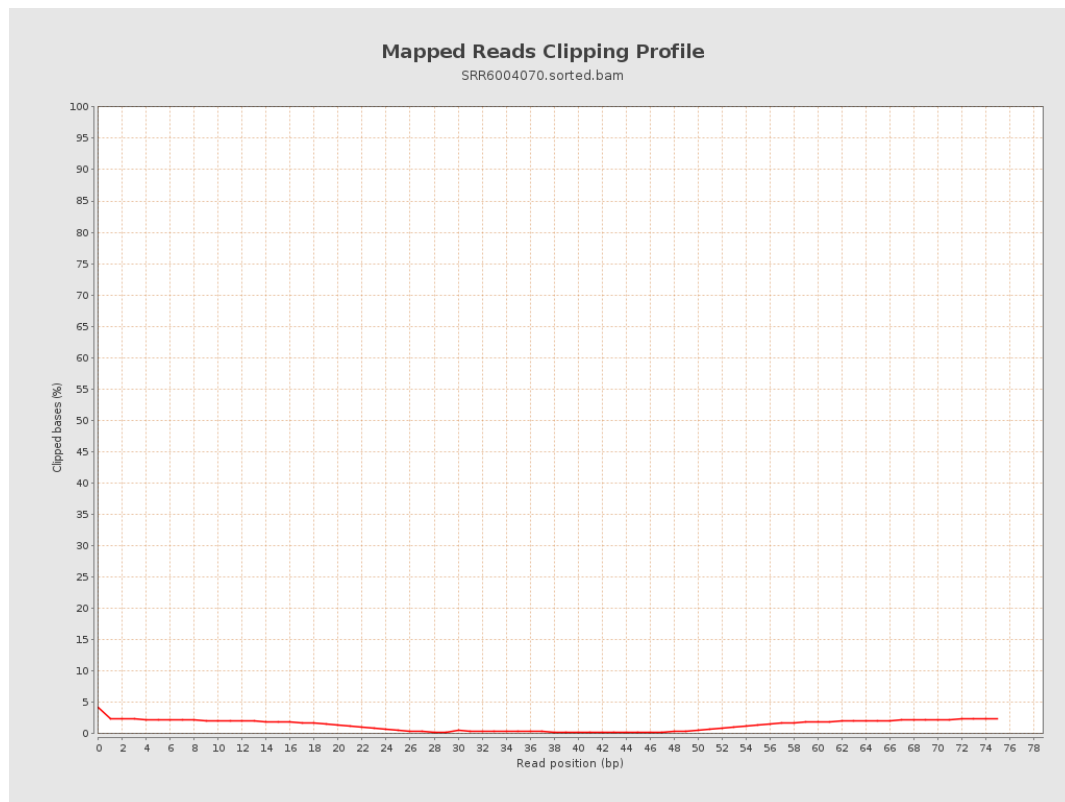
8. Results : Mapped Reads Nucleotide Content



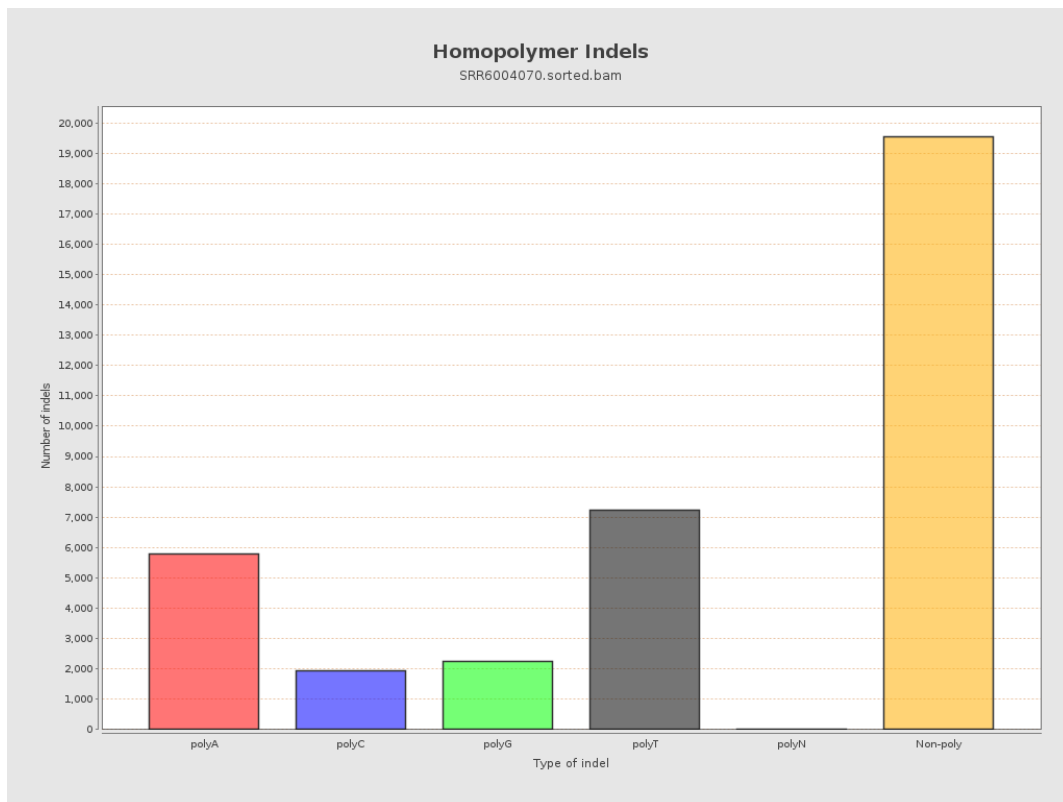
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

