

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:20:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084781.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_SRR3084781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:20:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,192,524
Mapped reads	1,953,282 / 89.09%
Unmapped reads	239,242 / 10.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,226 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	85,998 / 3.92%
Duplication rate	3.56%
Clipped reads	873,745 / 39.85%

2.2. ACGT Content

Number/percentage of A's	36,523,279 / 27.94%
Number/percentage of C's	24,950,104 / 19.08%
Number/percentage of T's	40,327,042 / 30.85%
Number/percentage of G's	28,881,414 / 22.09%
Number/percentage of N's	55,345 / 0.04%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.3375
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.61
----------------------	-------

2.5. Mismatches and indels

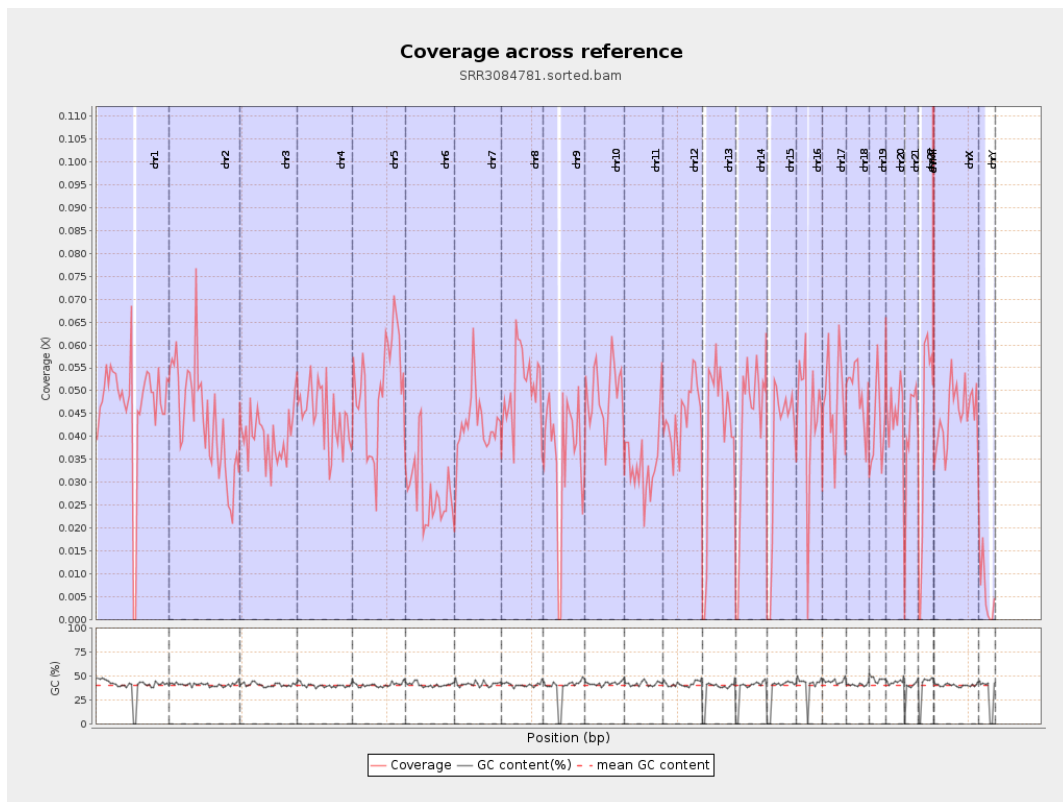
General error rate	0.9%
Mismatches	1,153,497
Insertions	10,386
Mapped reads with at least one insertion	0.53%
Deletions	30,514
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.46%

2.6. Chromosome stats

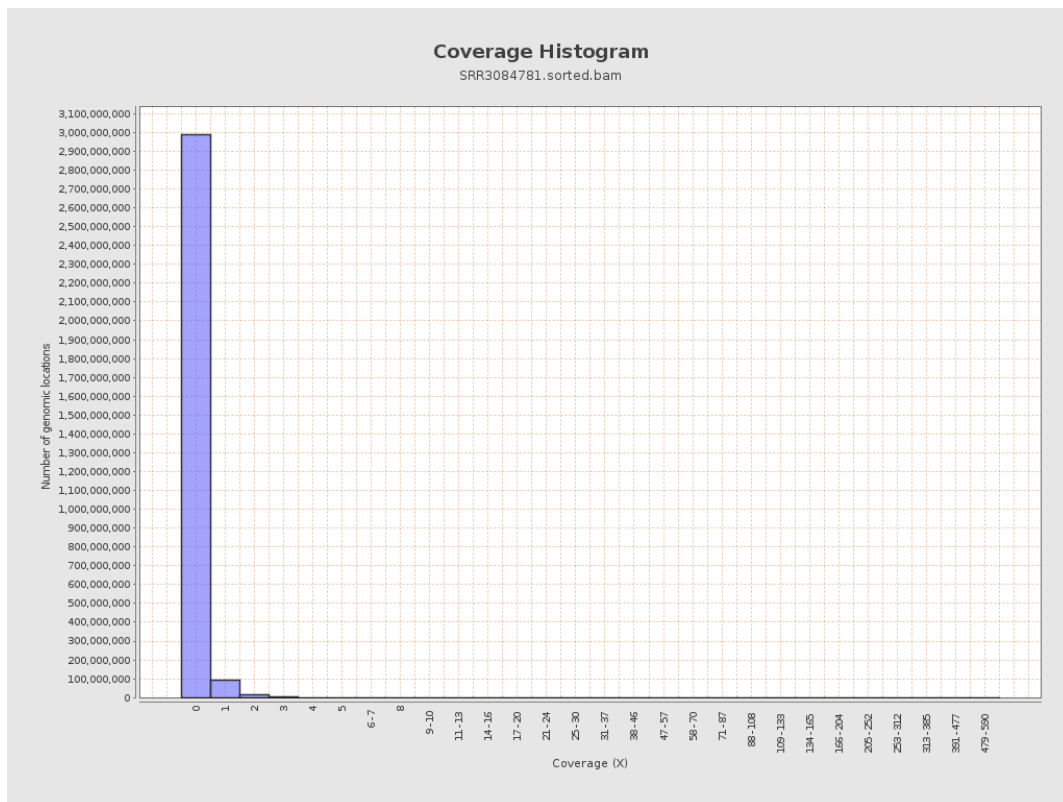
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11694497	0.0469	0.5596
chr2	243199373	10587252	0.0435	0.4046
chr3	198022430	7926264	0.04	0.2307
chr4	191154276	8495426	0.0444	0.2607
chr5	180915260	9157504	0.0506	0.2614
chr6	171115067	4758116	0.0278	0.2146
chr7	159138663	6850660	0.043	0.3571

chr8	146364022	7457172	0.0509	0.383
chr9	141213431	5113669	0.0362	0.3249
chr10	135534747	6650008	0.0491	0.3269
chr11	135006516	4625423	0.0343	0.2875
chr12	133851895	5962927	0.0445	0.2488
chr13	115169878	4672332	0.0406	0.2338
chr14	107349540	4510262	0.042	0.2556
chr15	102531392	3872152	0.0378	0.229
chr16	90354753	4041812	0.0447	0.2724
chr17	81195210	3831005	0.0472	0.2942
chr18	78077248	3864360	0.0495	0.6691
chr19	59128983	2558995	0.0433	0.4255
chr20	63025520	2834340	0.045	0.2541
chr21	48129895	1942667	0.0404	0.2479
chr22	51304566	2071501	0.0404	0.2301
chrMT	16571	9618	0.5804	0.8951
chrX	155270560	6962306	0.0448	0.2712
chrY	59373566	336989	0.0057	0.1304

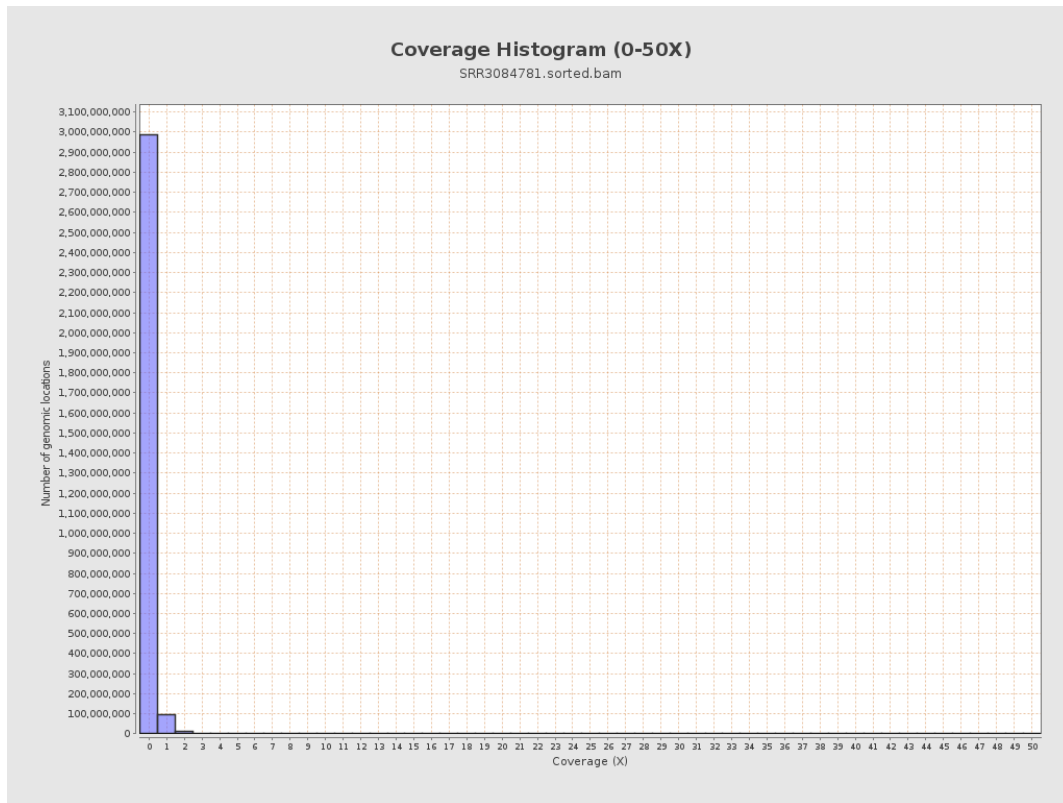
3. Results : Coverage across reference



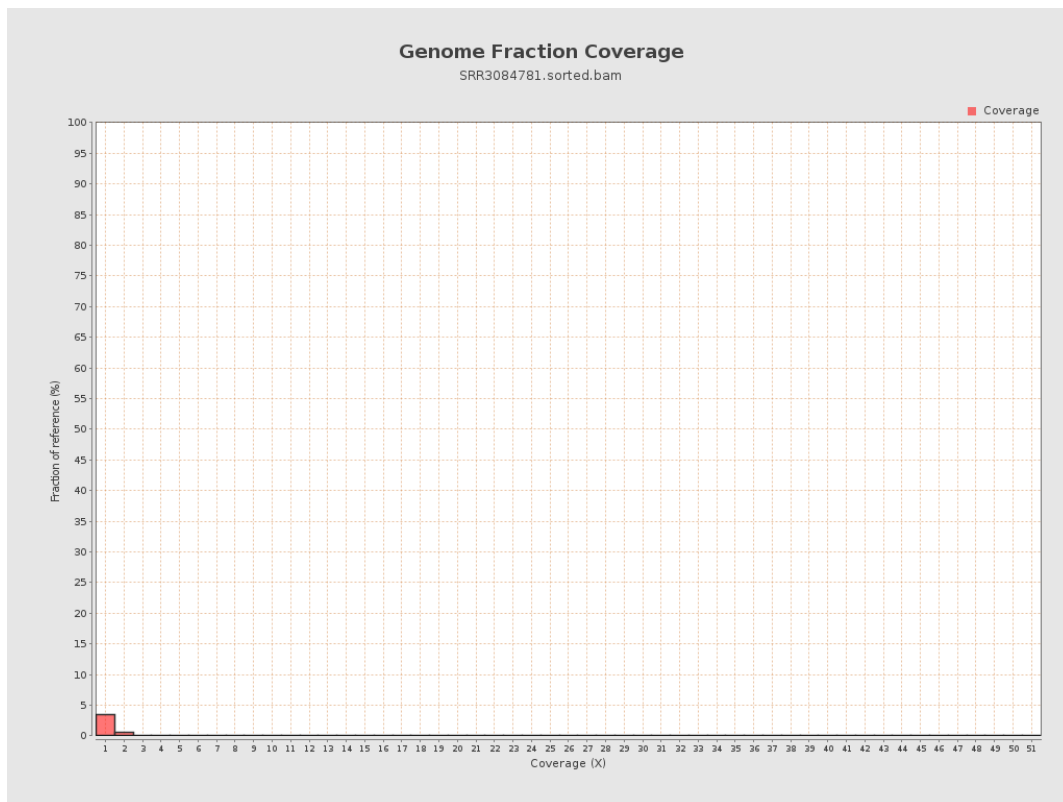
4. Results : Coverage Histogram



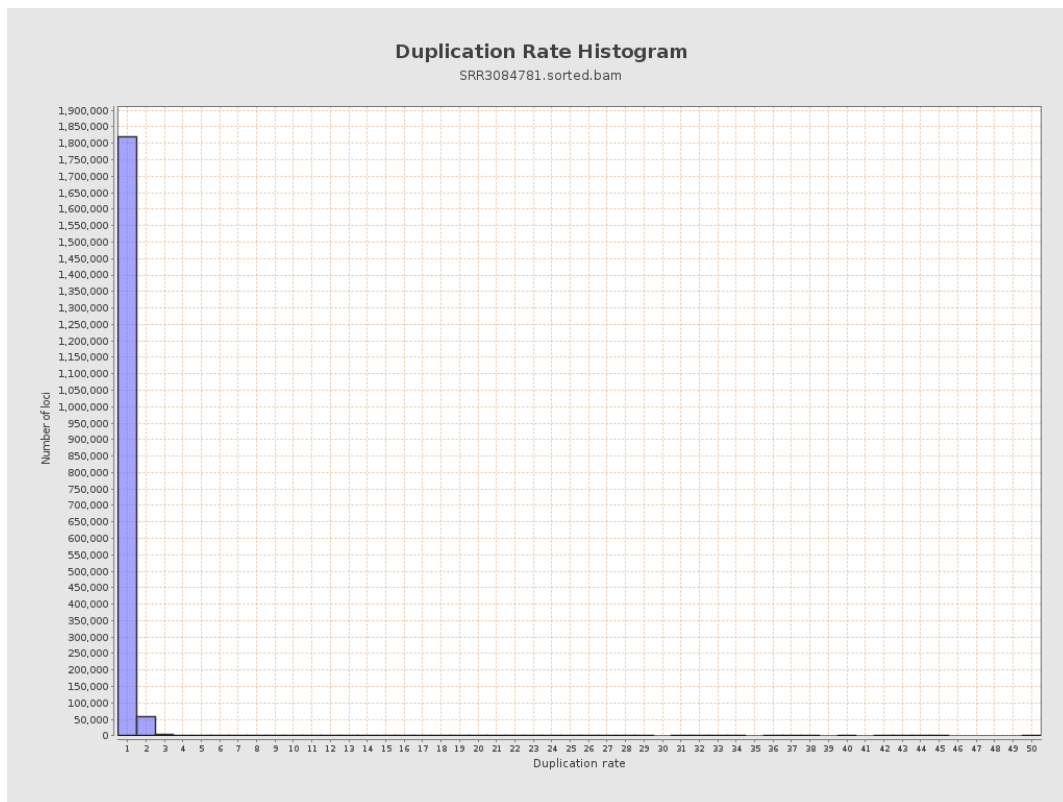
5. Results : Coverage Histogram (0-50X)



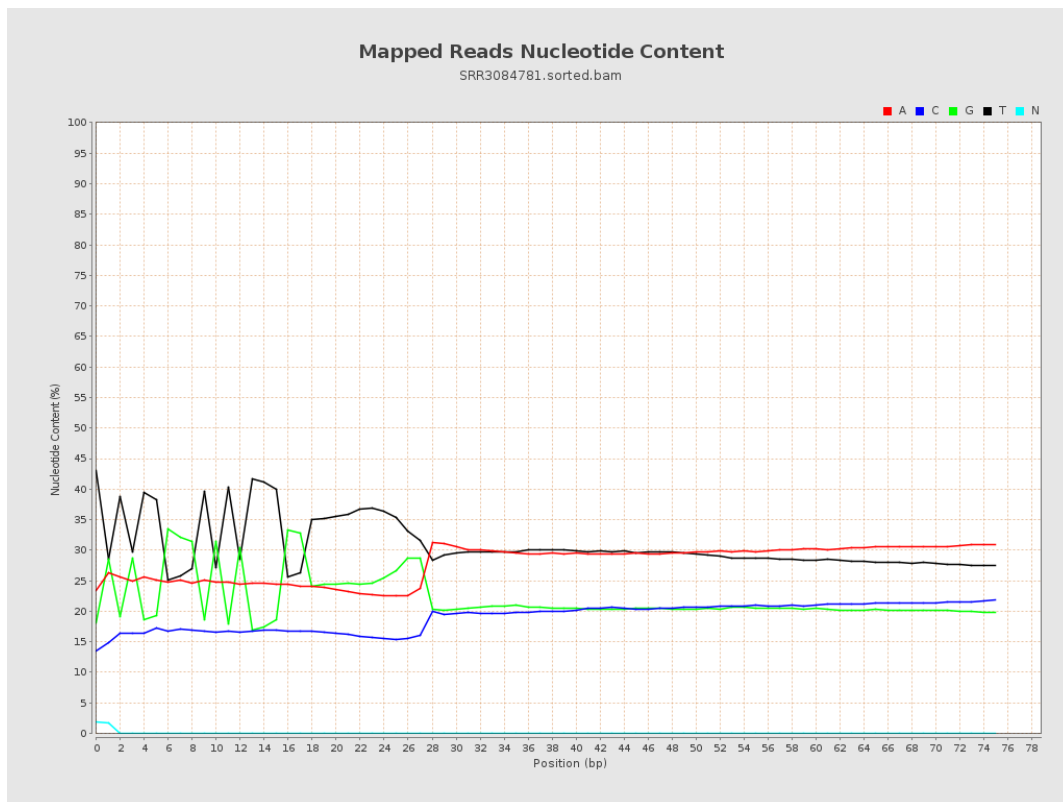
6. Results : Genome Fraction Coverage



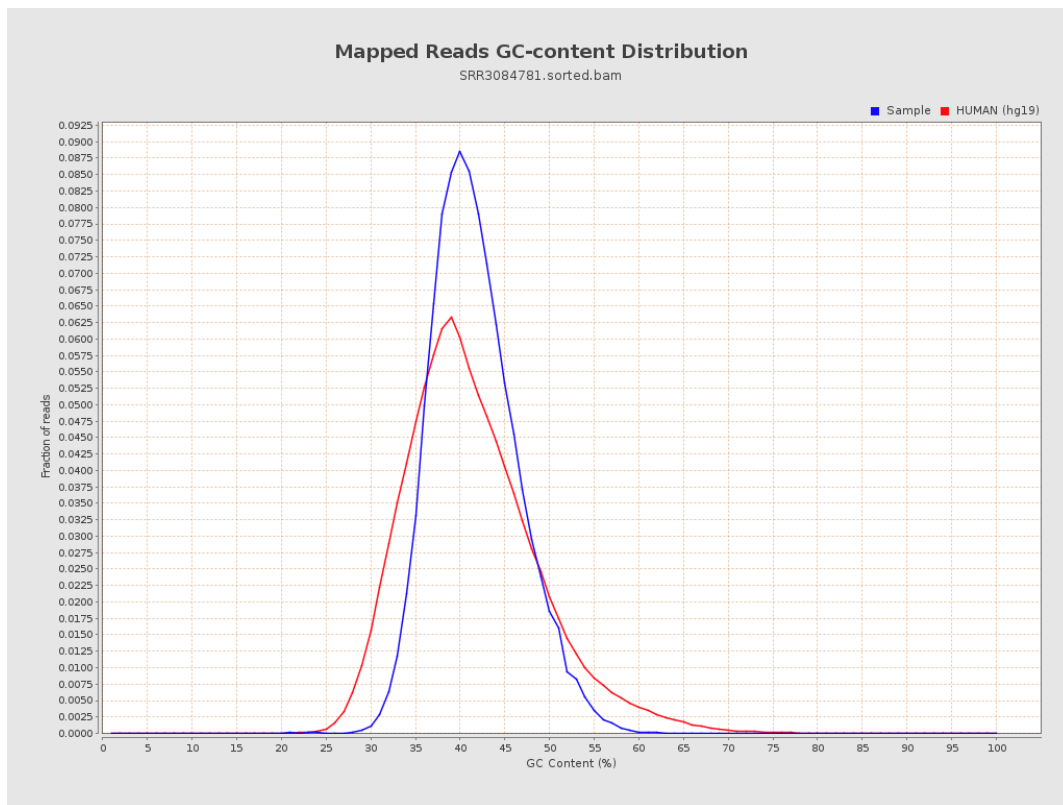
7. Results : Duplication Rate Histogram



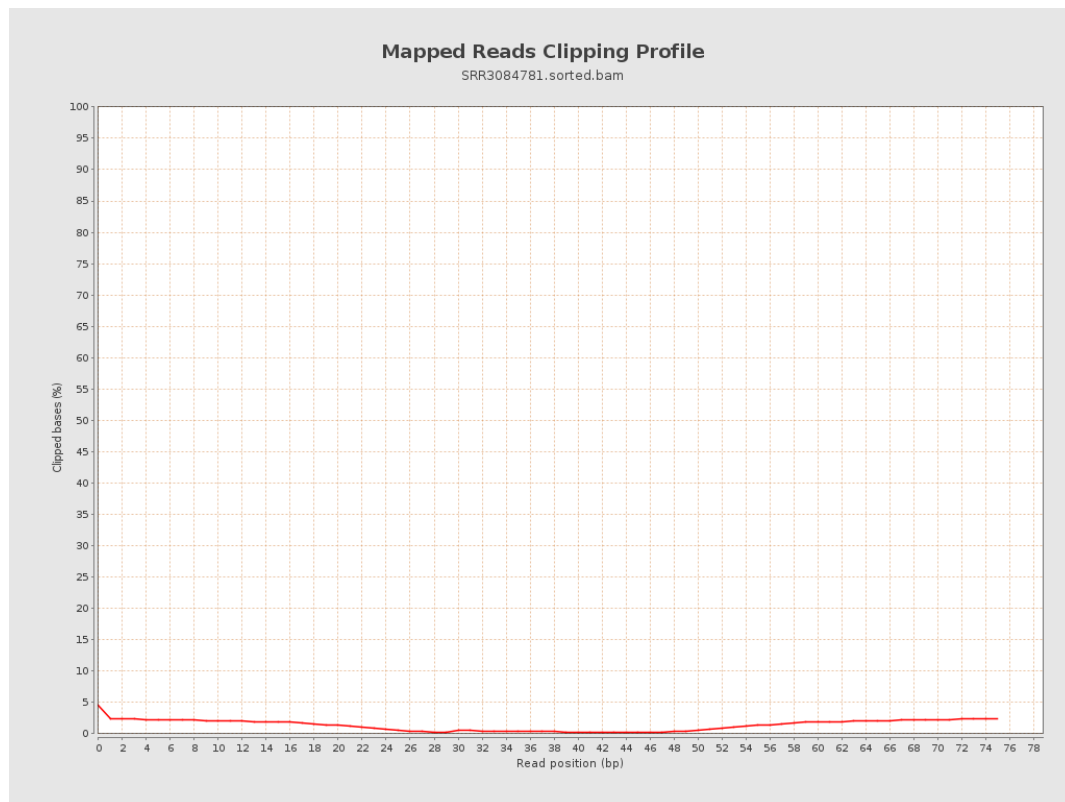
8. Results : Mapped Reads Nucleotide Content



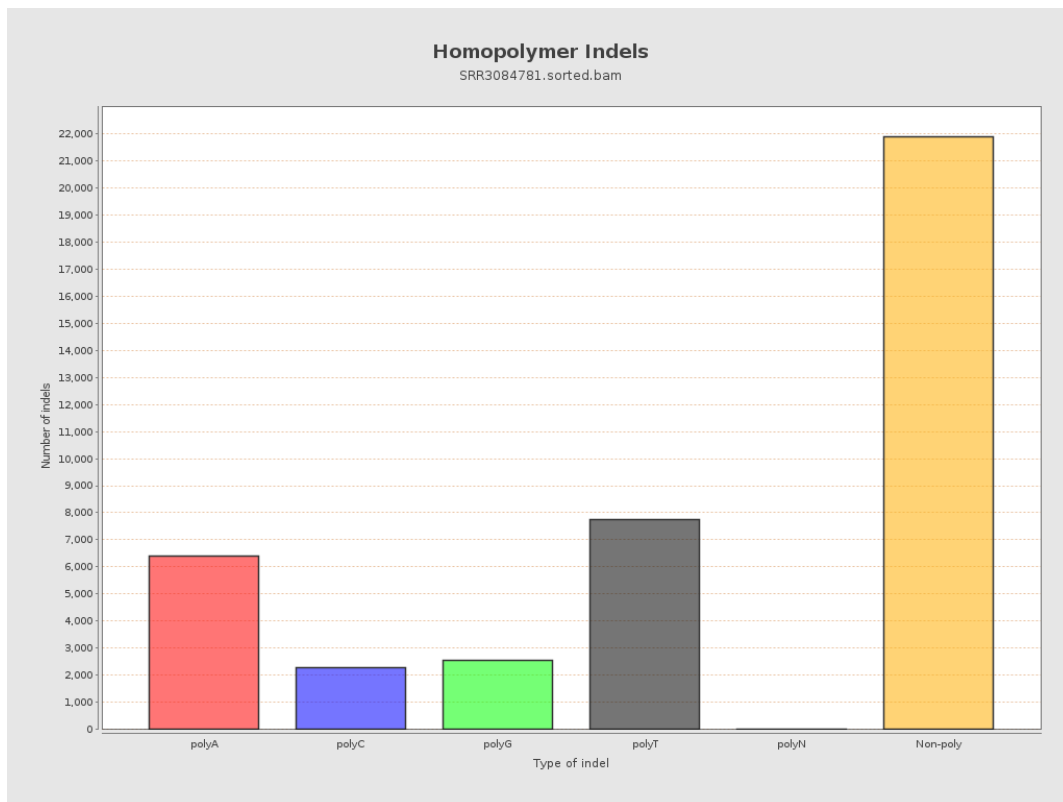
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

