

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:00:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004054.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_SRR6004054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:00:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,504,187
Mapped reads	2,212,224 / 88.34%
Unmapped reads	291,963 / 11.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,577 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	91,768 / 3.66%
Duplication rate	3.31%
Clipped reads	970,034 / 38.74%

2.2. ACGT Content

Number/percentage of A's	40,702,397 / 27.51%
Number/percentage of C's	28,293,482 / 19.12%
Number/percentage of T's	45,657,801 / 30.85%
Number/percentage of G's	33,299,359 / 22.5%
Number/percentage of N's	24,842 / 0.02%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0478

Standard Deviation	0.379
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2.4. Mapping Quality

Mean Mapping Quality	45.87
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2.5. Mismatches and indels

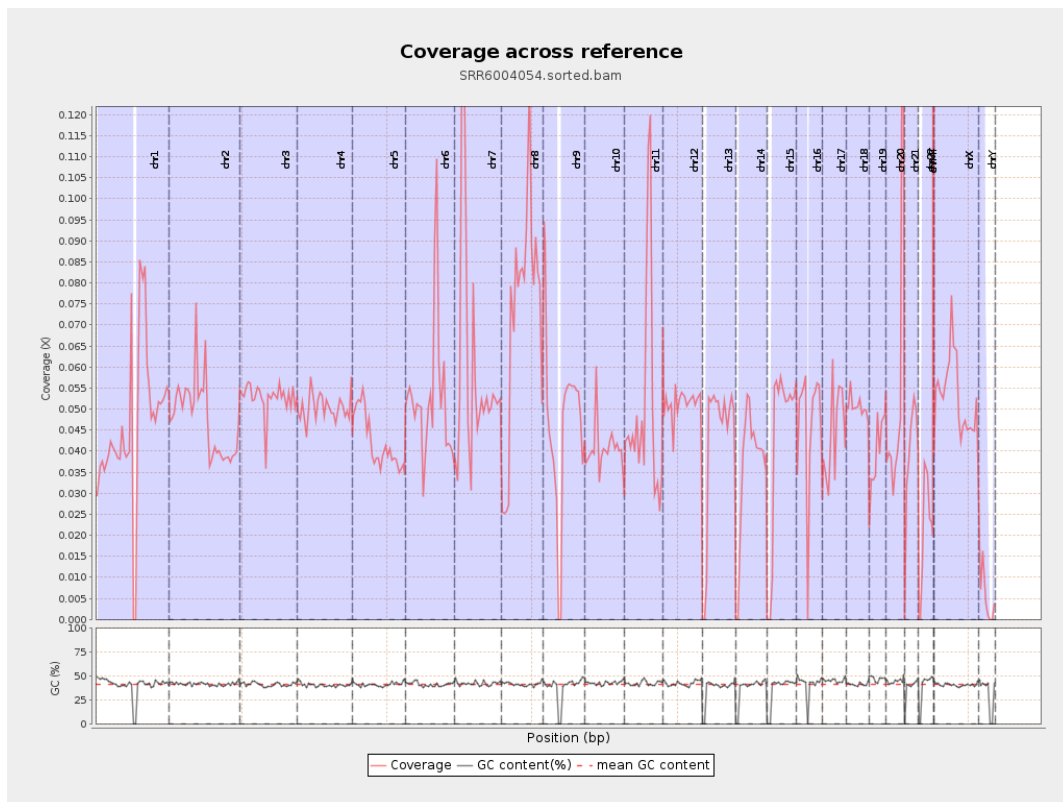
General error rate	0.86%
Mismatches	1,261,278
Insertions	10,231
Mapped reads with at least one insertion	0.46%
Deletions	33,015
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.8%

2.6. Chromosome stats

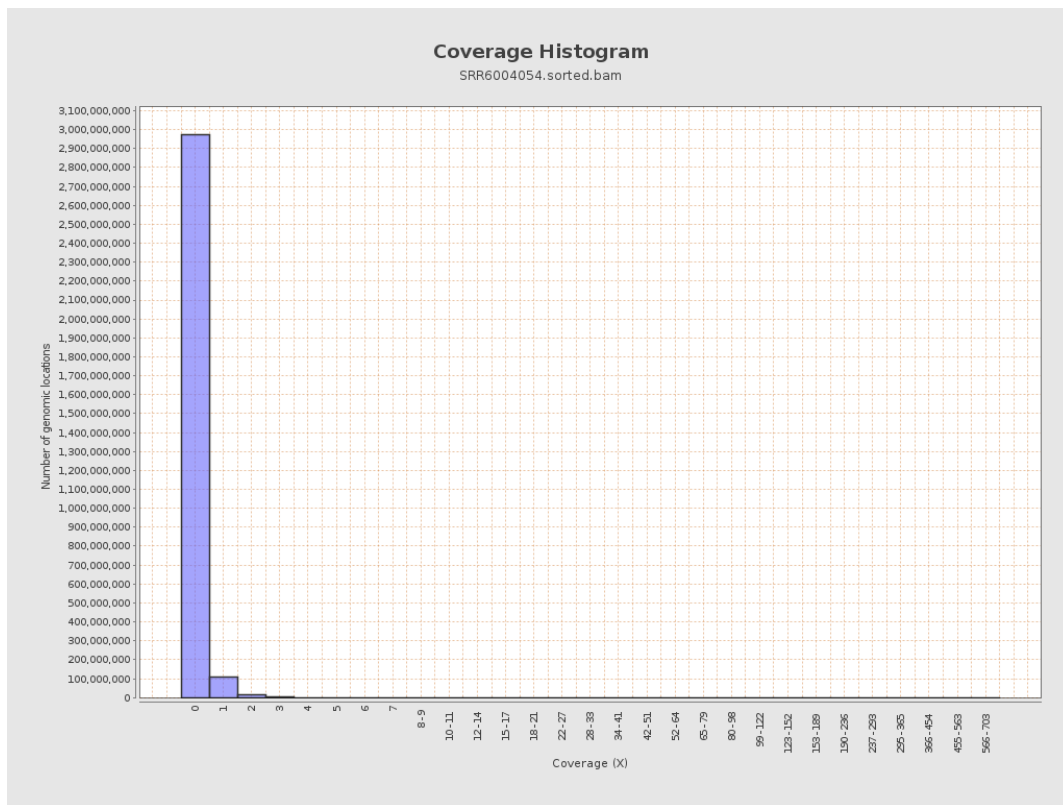
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11538234	0.0463	0.6402
chr2	243199373	11570437	0.0476	0.4132
chr3	198022430	10443785	0.0527	0.2623
chr4	191154276	9612491	0.0503	0.2762
chr5	180915260	7633726	0.0422	0.2366
chr6	171115067	9032564	0.0528	0.294
chr7	159138663	9606079	0.0604	0.6111

chr8	146364022	10482355	0.0716	0.4278
chr9	141213431	6403889	0.0453	0.3786
chr10	135534747	5510160	0.0407	0.3178
chr11	135006516	6823778	0.0505	0.352
chr12	133851895	6829498	0.051	0.2656
chr13	115169878	4836700	0.042	0.2375
chr14	107349540	3892450	0.0363	0.2463
chr15	102531392	4427338	0.0432	0.2474
chr16	90354753	4203463	0.0465	0.2749
chr17	81195210	3618921	0.0446	0.274
chr18	78077248	3957389	0.0507	0.6466
chr19	59128983	2383641	0.0403	0.4479
chr20	63025520	3735683	0.0593	0.2964
chr21	48129895	1886881	0.0392	0.2491
chr22	51304566	1062783	0.0207	0.1616
chrMT	16571	12083	0.7292	0.9614
chrX	155270560	8197171	0.0528	0.2987
chrY	59373566	333967	0.0056	0.1196

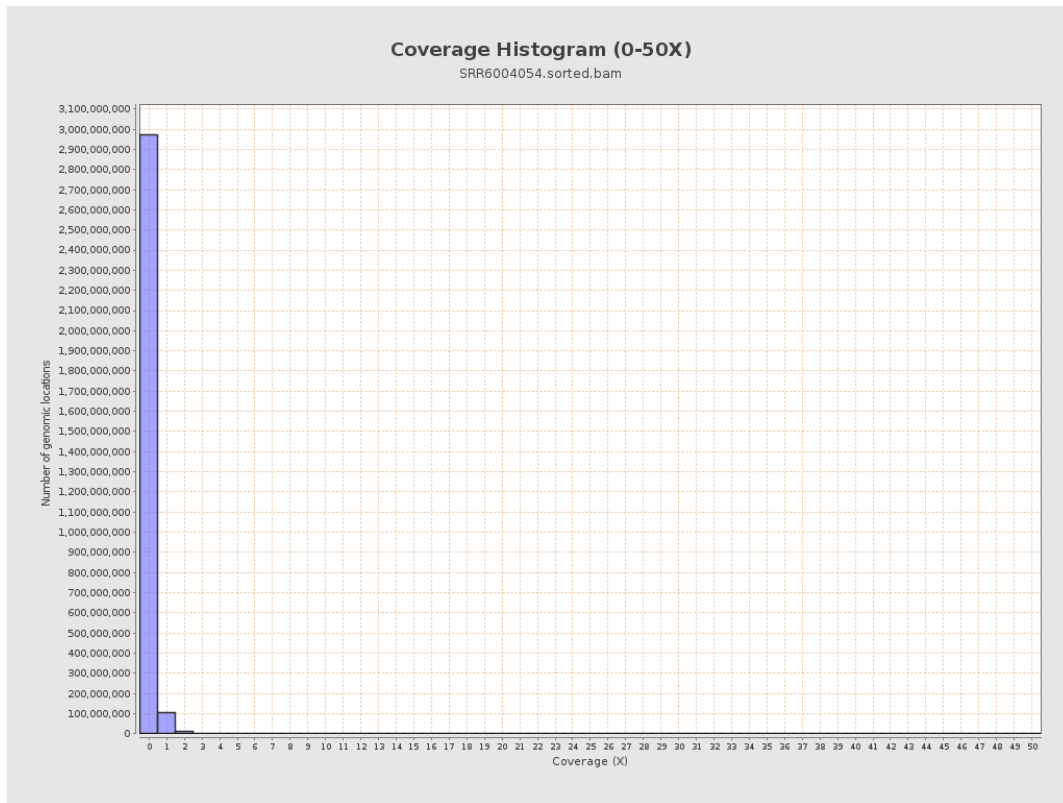
3. Results : Coverage across reference



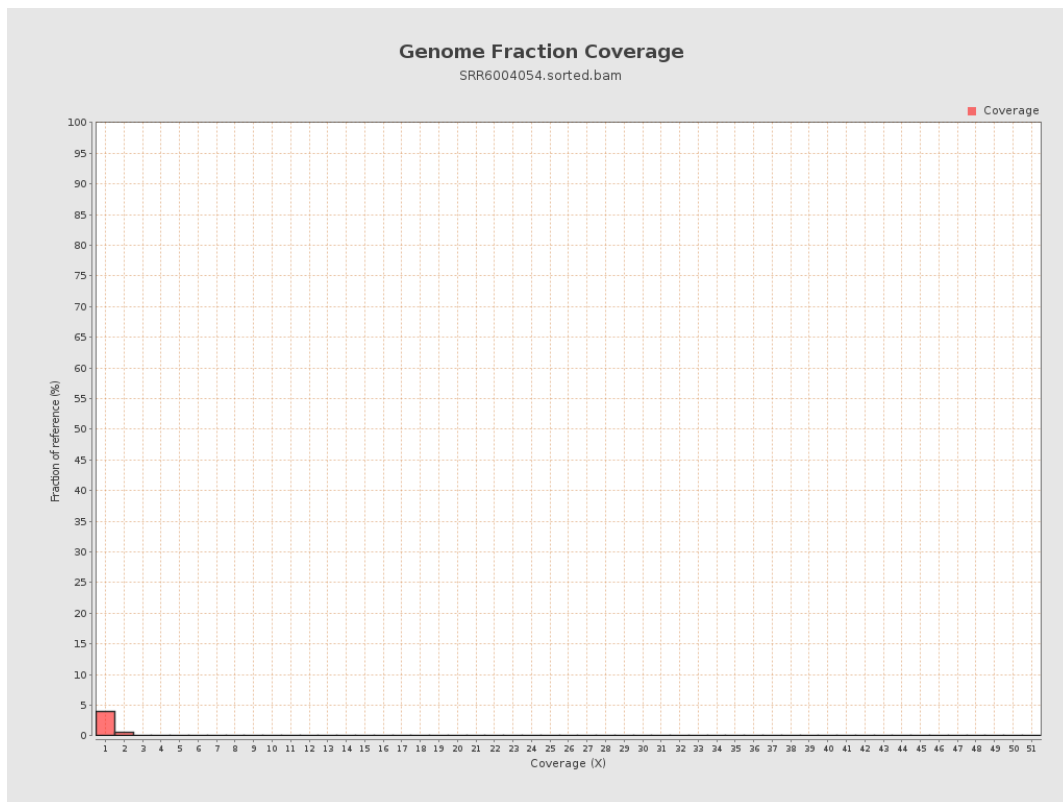
4. Results : Coverage Histogram



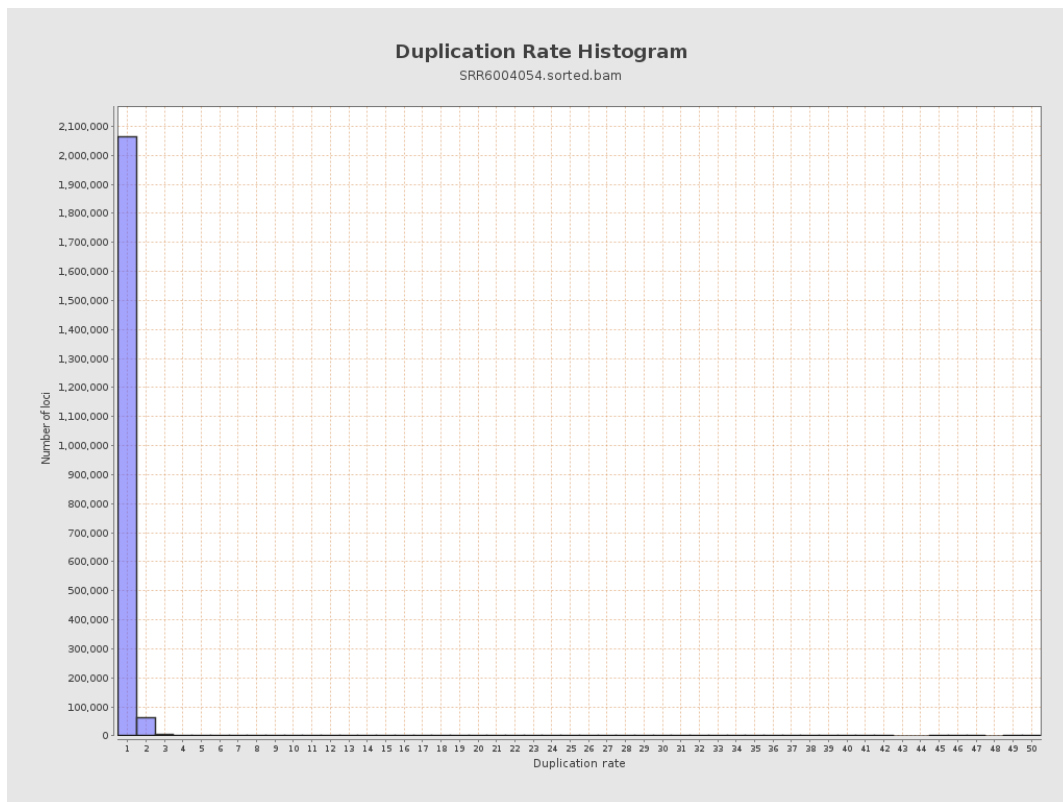
5. Results : Coverage Histogram (0-50X)



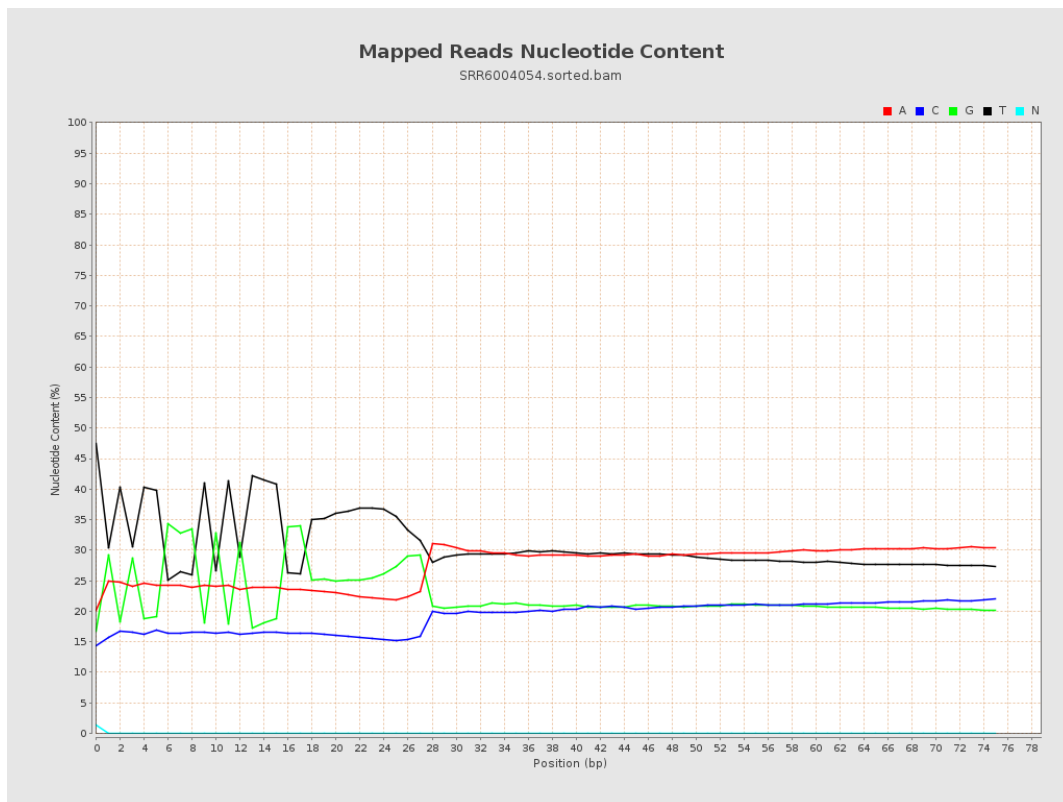
6. Results : Genome Fraction Coverage



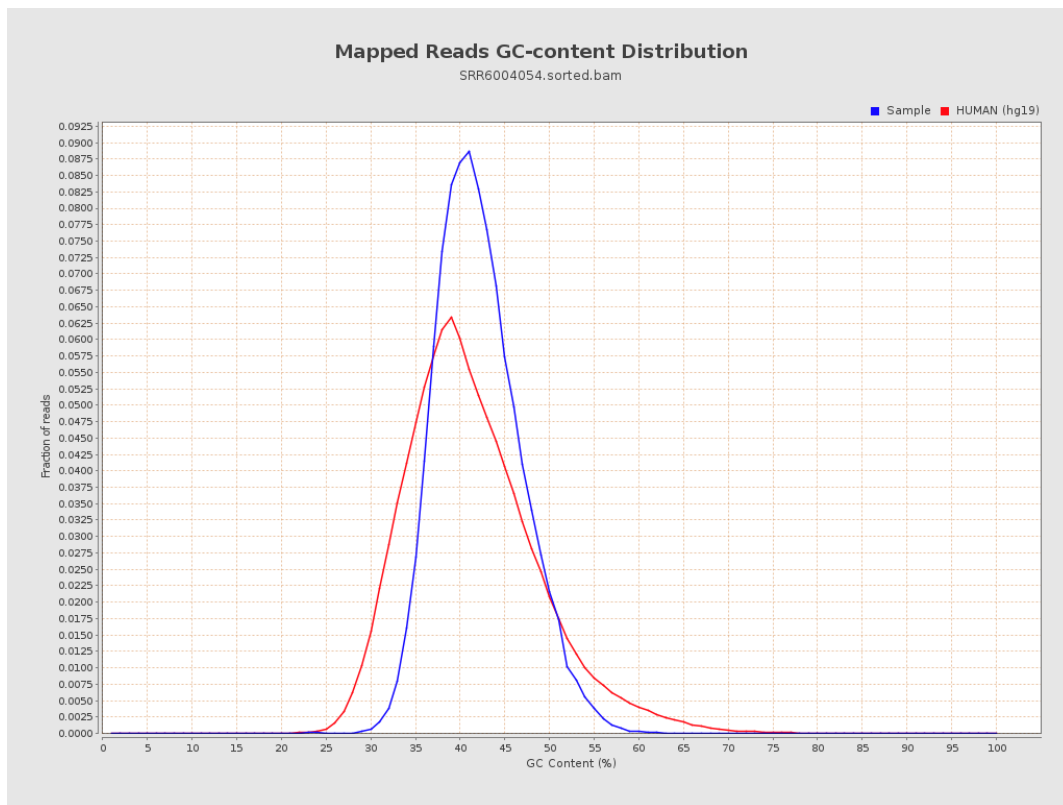
7. Results : Duplication Rate Histogram



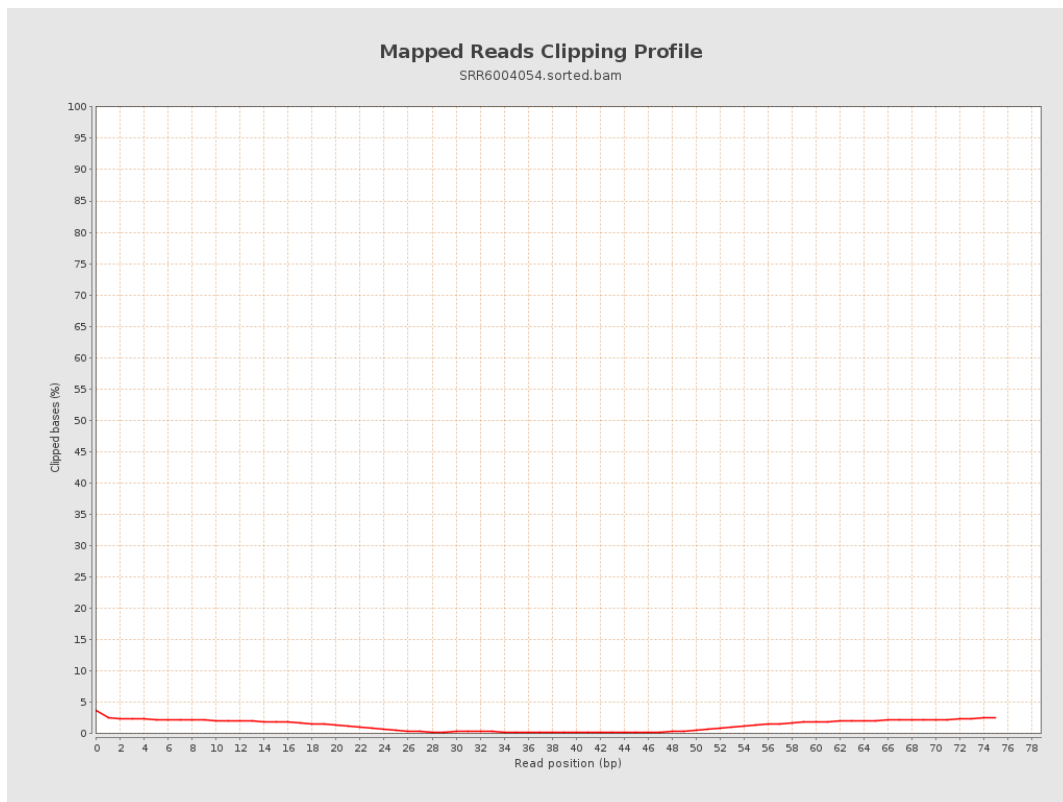
8. Results : Mapped Reads Nucleotide Content



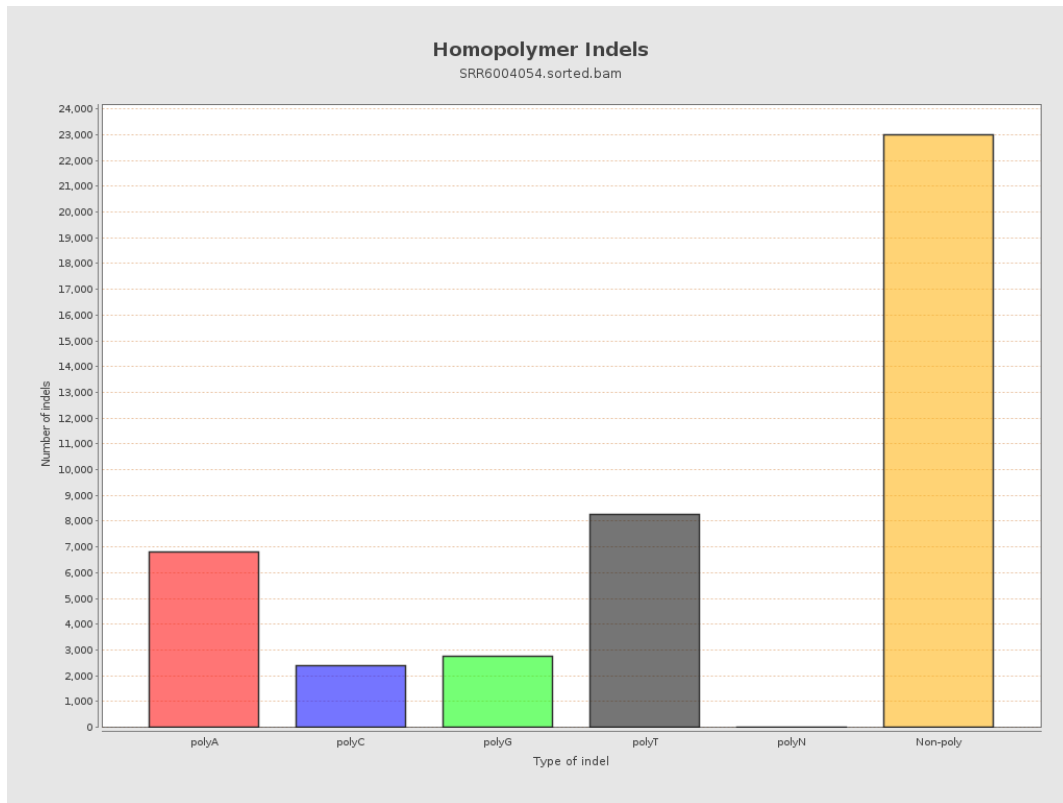
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

