

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:59:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240048.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_SRR6240048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:59:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,916,485
Mapped reads	1,586,350 / 82.77%
Unmapped reads	330,135 / 17.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,316 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	185,176 / 9.66%
Duplication rate	9.47%
Clipped reads	935,947 / 48.84%

2.2. ACGT Content

Number/percentage of A's	27,289,489 / 27.21%
Number/percentage of C's	17,584,367 / 17.53%
Number/percentage of T's	32,819,155 / 32.72%
Number/percentage of G's	22,529,742 / 22.46%
Number/percentage of N's	67,083 / 0.07%
GC Percentage	40%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.3235
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2.4. Mapping Quality

Mean Mapping Quality	45.84
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2.5. Mismatches and indels

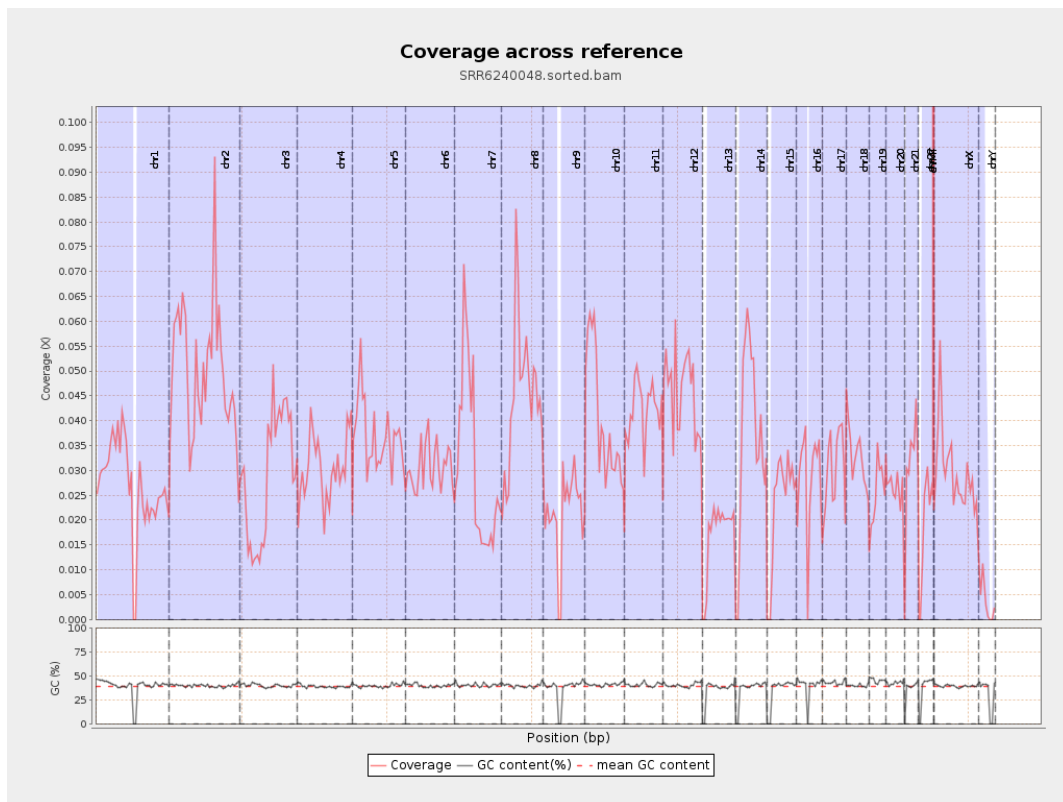
General error rate	0.94%
Mismatches	934,270
Insertions	7,197
Mapped reads with at least one insertion	0.45%
Deletions	31,097
Mapped reads with at least one deletion	1.94%
Homopolymer indels	49.17%

2.6. Chromosome stats

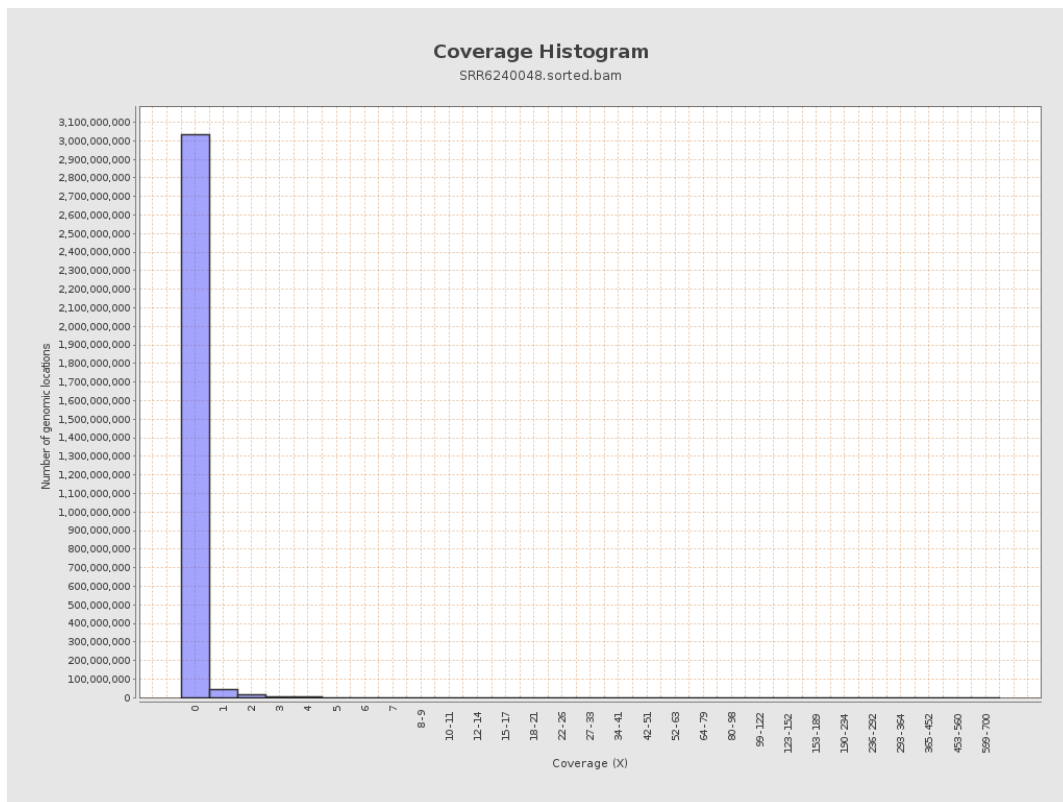
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6696155	0.0269	0.3477
chr2	243199373	12144527	0.0499	0.4184
chr3	198022430	5684081	0.0287	0.2401
chr4	191154276	5823359	0.0305	0.2601
chr5	180915260	6671783	0.0369	0.2755
chr6	171115067	5226679	0.0305	0.285
chr7	159138663	4874405	0.0306	0.4551

chr8	146364022	6590074	0.045	0.5106
chr9	141213431	3003595	0.0213	0.2624
chr10	135534747	5502399	0.0406	0.3298
chr11	135006516	5665128	0.042	0.4049
chr12	133851895	6116751	0.0457	0.3088
chr13	115169878	1945481	0.0169	0.1842
chr14	107349540	4036306	0.0376	0.2831
chr15	102531392	2413544	0.0235	0.225
chr16	90354753	2565873	0.0284	0.2425
chr17	81195210	2438814	0.03	0.2742
chr18	78077248	2566476	0.0329	0.4465
chr19	59128983	1528280	0.0258	0.2833
chr20	63025520	1638065	0.026	0.2295
chr21	48129895	1490362	0.031	0.2572
chr22	51304566	948639	0.0185	0.1894
chrMT	16571	21452	1.2946	1.6636
chrX	155270560	4536238	0.0292	0.2574
chrY	59373566	214205	0.0036	0.0892

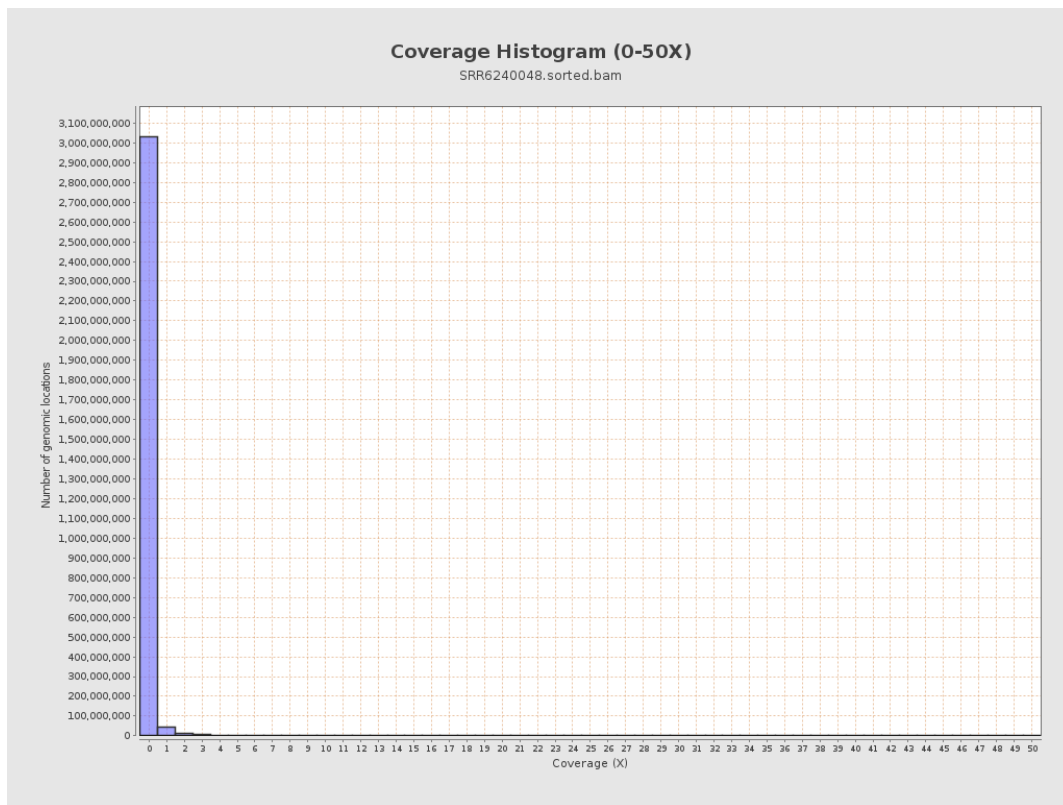
3. Results : Coverage across reference



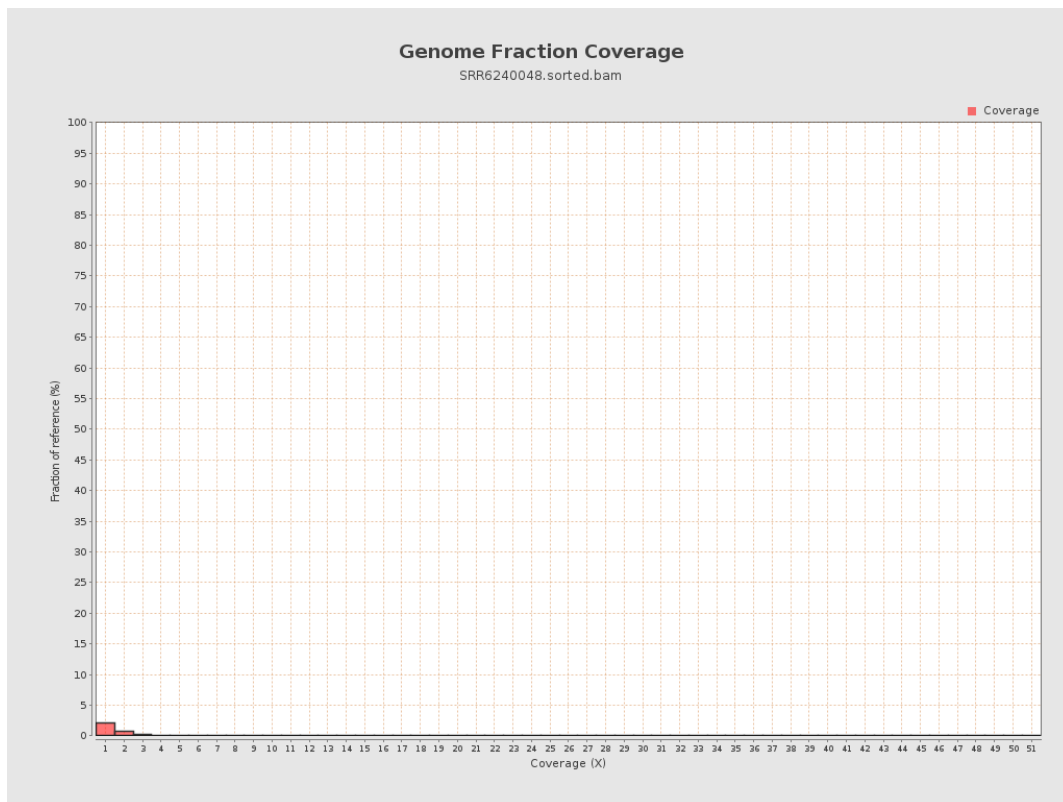
4. Results : Coverage Histogram



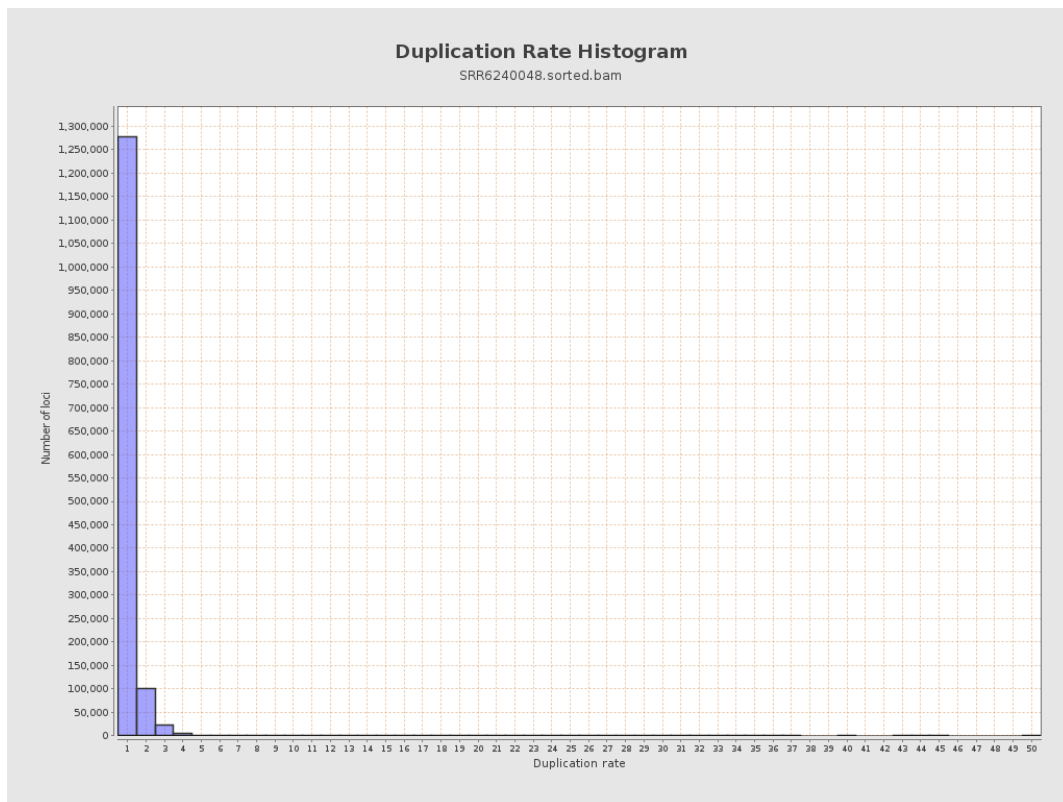
5. Results : Coverage Histogram (0-50X)



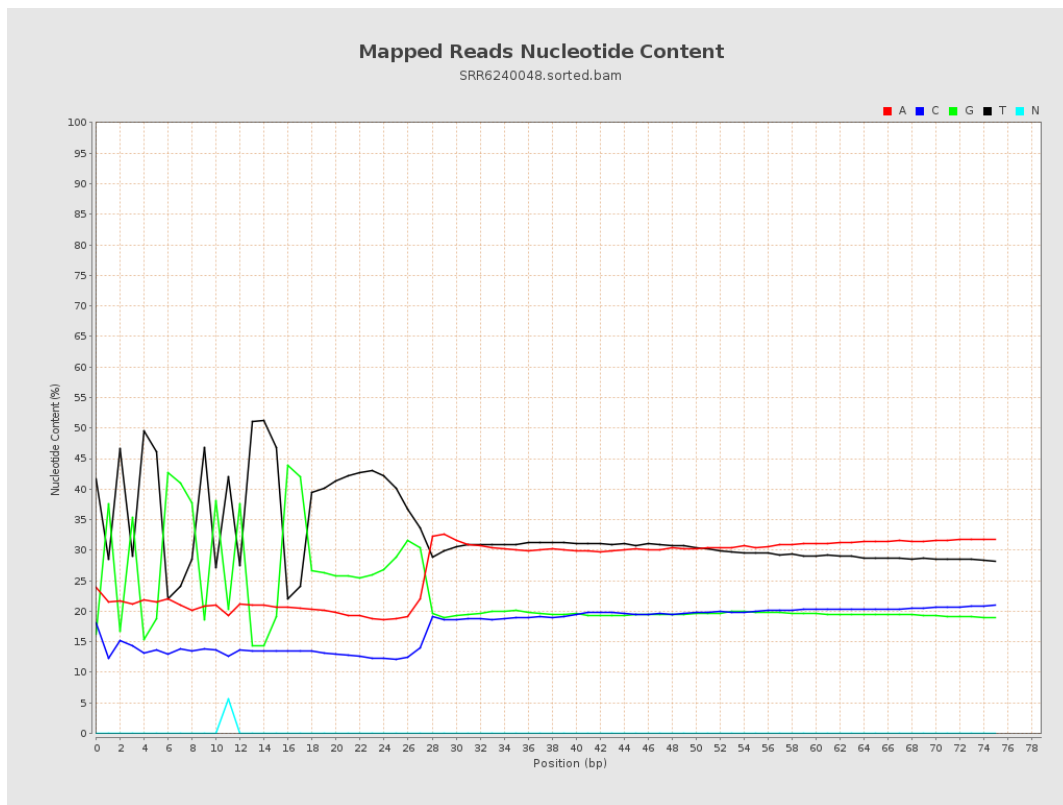
6. Results : Genome Fraction Coverage



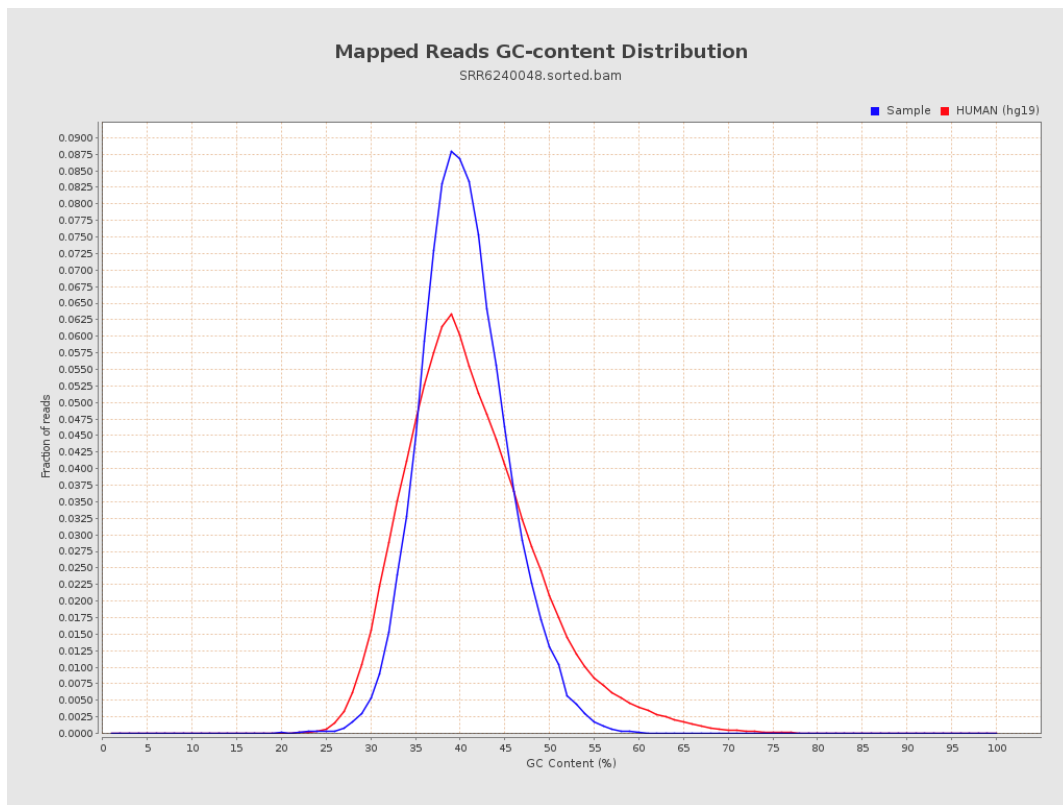
7. Results : Duplication Rate Histogram



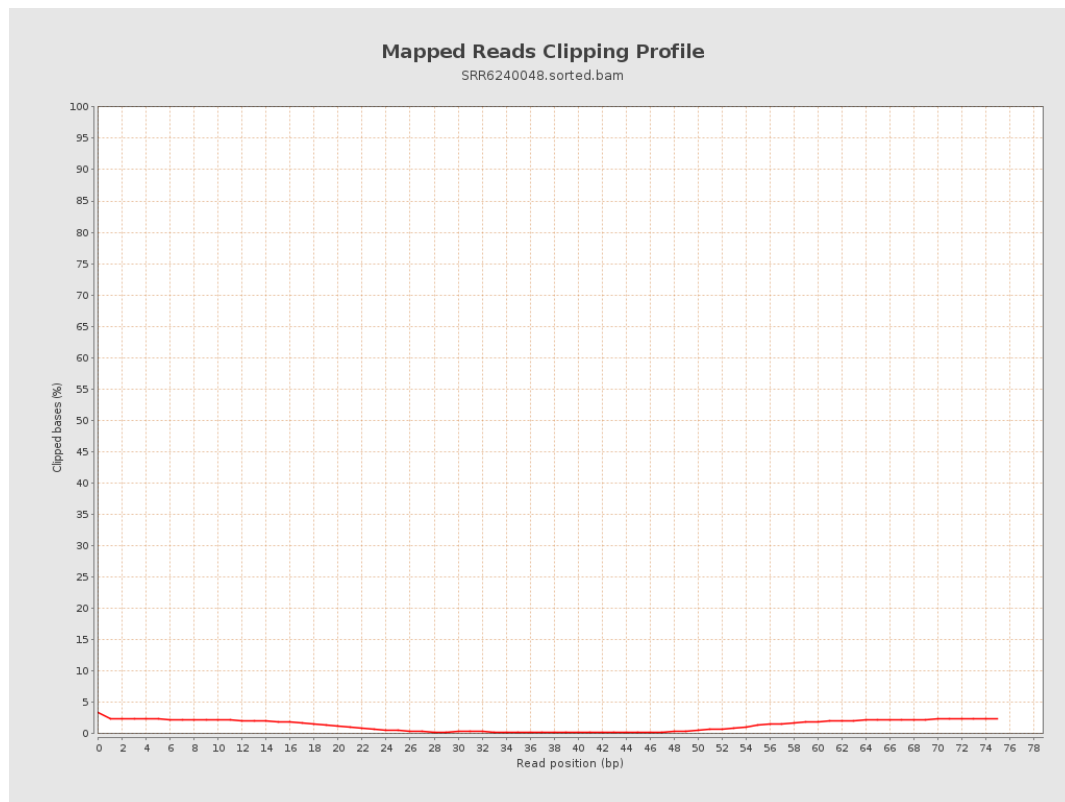
8. Results : Mapped Reads Nucleotide Content



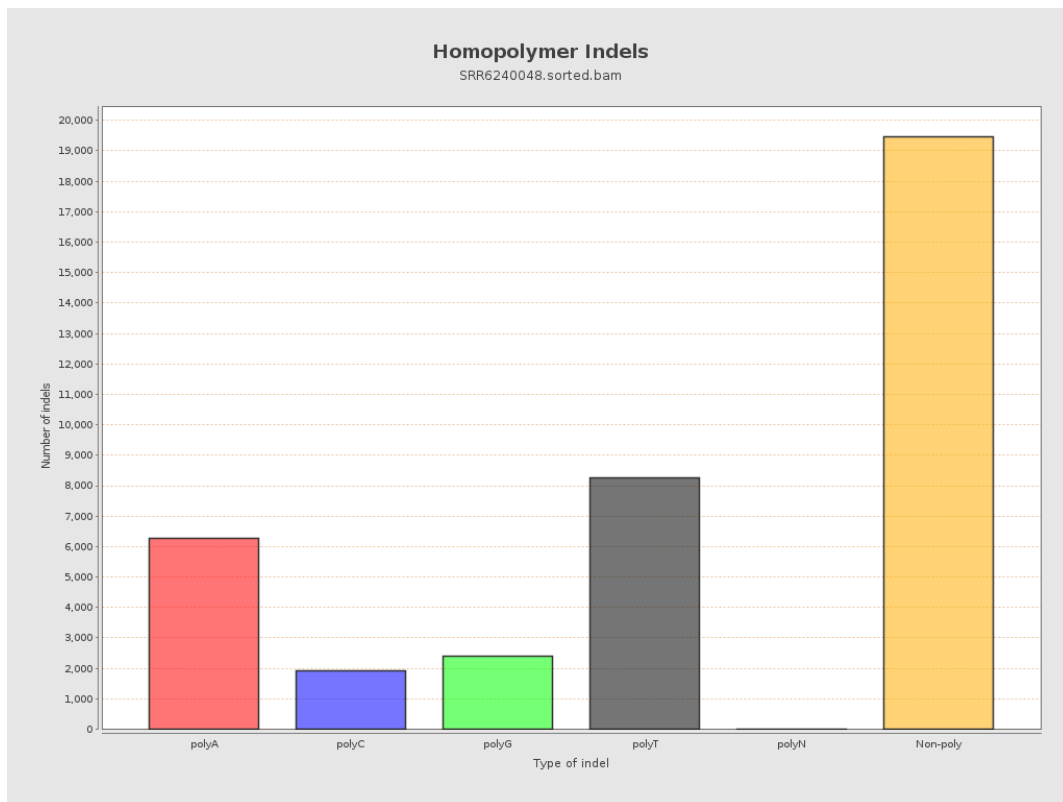
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

