

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:39:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240252.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_SRR6240252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240252.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:39:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,190,973
Mapped reads	901,376 / 75.68%
Unmapped reads	289,597 / 24.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,859 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	71,365 / 5.99%
Duplication rate	6.52%
Clipped reads	442,177 / 37.13%

2.2. ACGT Content

Number/percentage of A's	17,393,543 / 29.17%
Number/percentage of C's	11,208,025 / 18.8%
Number/percentage of T's	18,636,776 / 31.26%
Number/percentage of G's	12,348,680 / 20.71%
Number/percentage of N's	34,185 / 0.06%
GC Percentage	39.51%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.2522
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2.4. Mapping Quality

Mean Mapping Quality	47.08
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2.5. Mismatches and indels

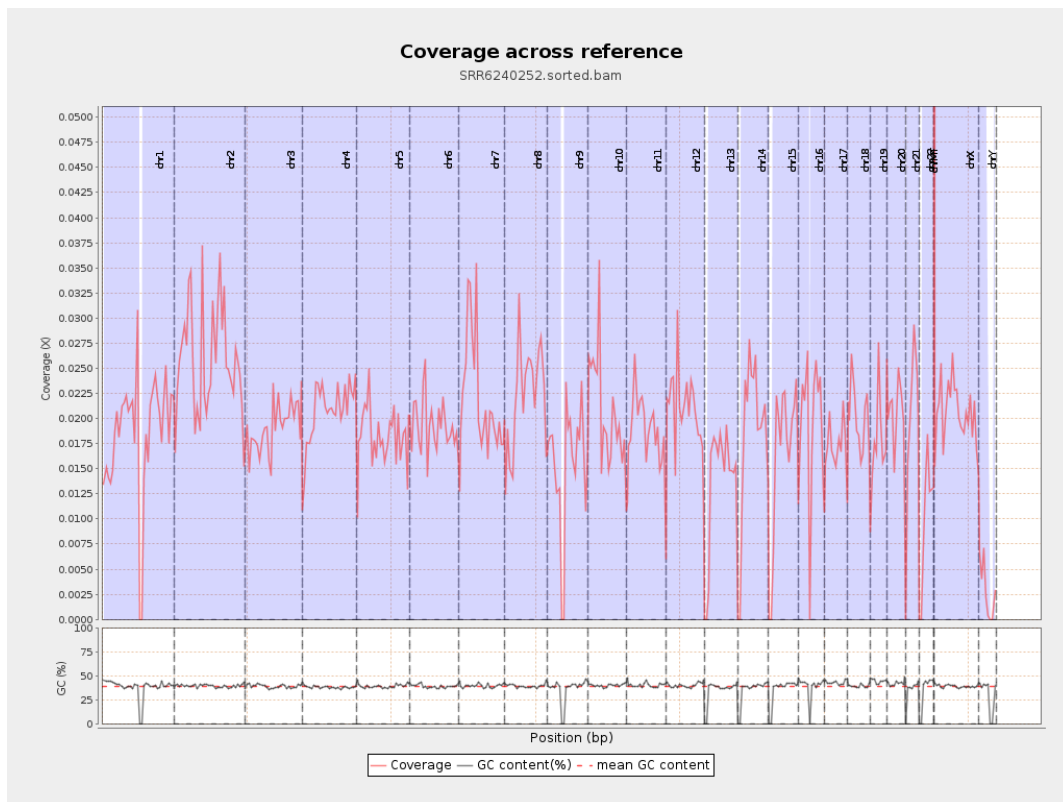
General error rate	0.9%
Mismatches	528,656
Insertions	4,210
Mapped reads with at least one insertion	0.46%
Deletions	15,682
Mapped reads with at least one deletion	1.72%
Homopolymer indels	47.78%

2.6. Chromosome stats

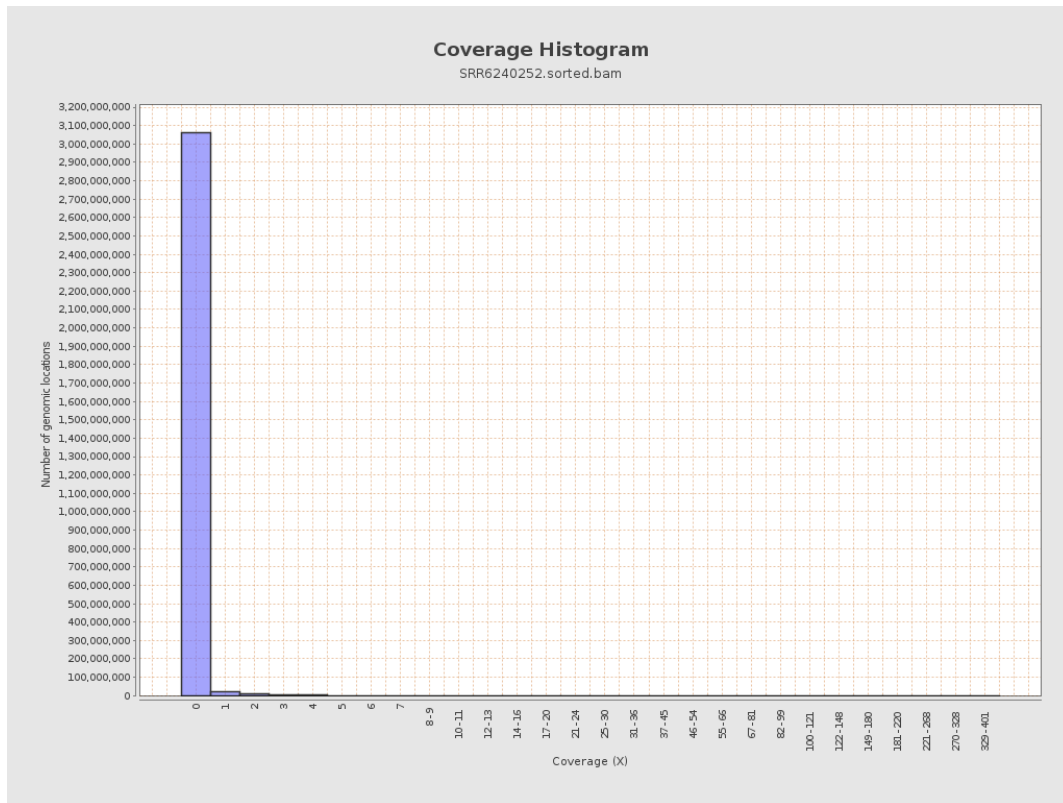
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4618581	0.0185	0.3532
chr2	243199373	6312944	0.026	0.2864
chr3	198022430	3767696	0.019	0.2074
chr4	191154276	3962562	0.0207	0.2233
chr5	180915260	3328264	0.0184	0.2108
chr6	171115067	3303033	0.0193	0.2279
chr7	159138663	3522318	0.0221	0.3063

chr8	146364022	3273121	0.0224	0.3279
chr9	141213431	2177931	0.0154	0.2256
chr10	135534747	2804040	0.0207	0.2552
chr11	135006516	2566202	0.019	0.2454
chr12	133851895	2839374	0.0212	0.221
chr13	115169878	1570009	0.0136	0.1773
chr14	107349540	1988703	0.0185	0.2141
chr15	102531392	1681689	0.0164	0.2178
chr16	90354753	1728197	0.0191	0.217
chr17	81195210	1407843	0.0173	0.2022
chr18	78077248	1563832	0.02	0.349
chr19	59128983	1074382	0.0182	0.2758
chr20	63025520	1269915	0.0201	0.2202
chr21	48129895	970551	0.0202	0.216
chr22	51304566	531384	0.0104	0.1457
chrMT	16571	10199	0.6155	1.228
chrX	155270560	3212640	0.0207	0.2225
chrY	59373566	163625	0.0028	0.0759

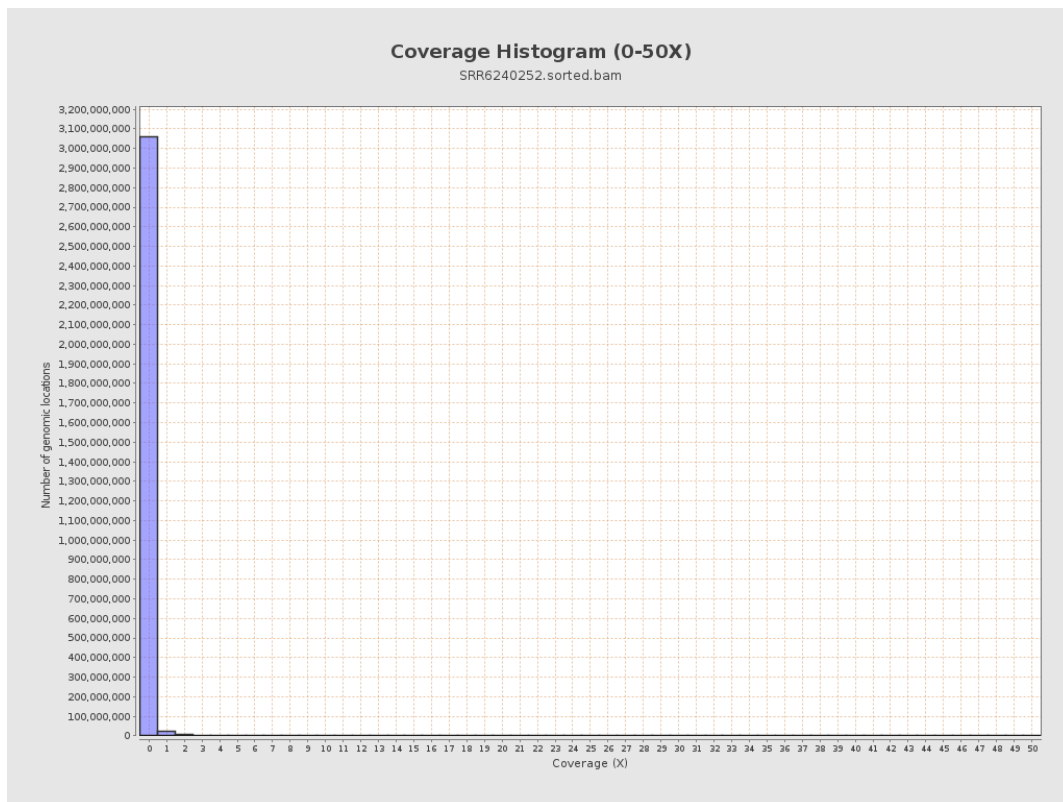
3. Results : Coverage across reference



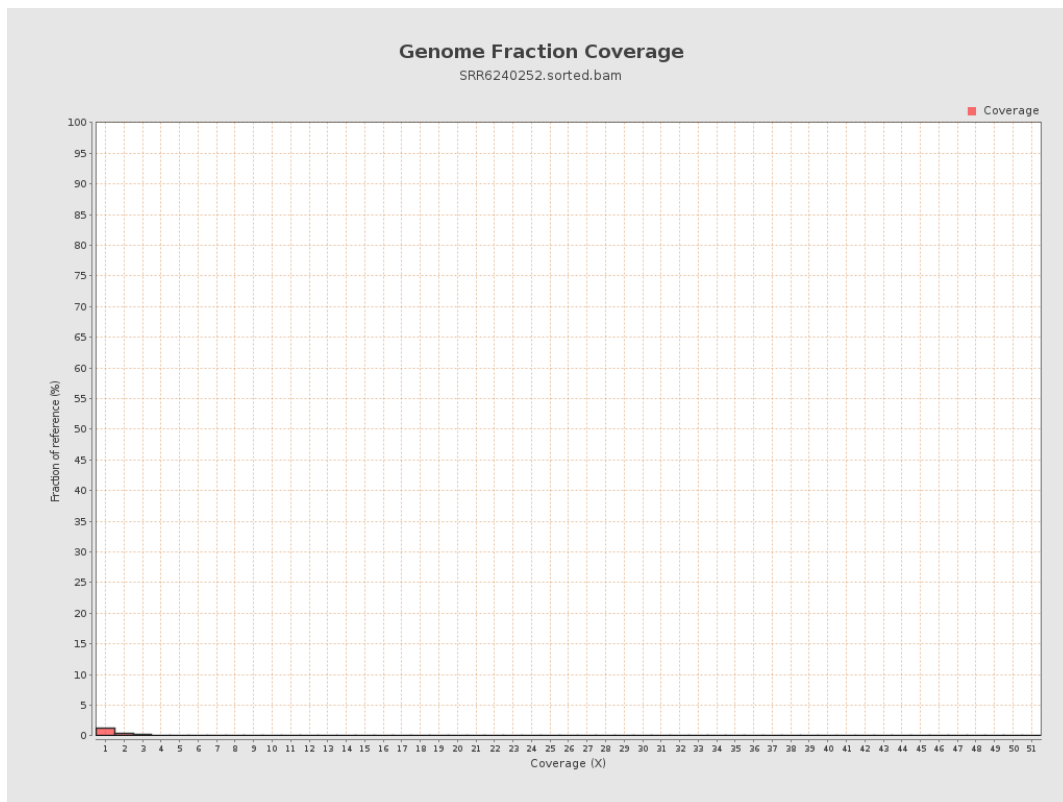
4. Results : Coverage Histogram



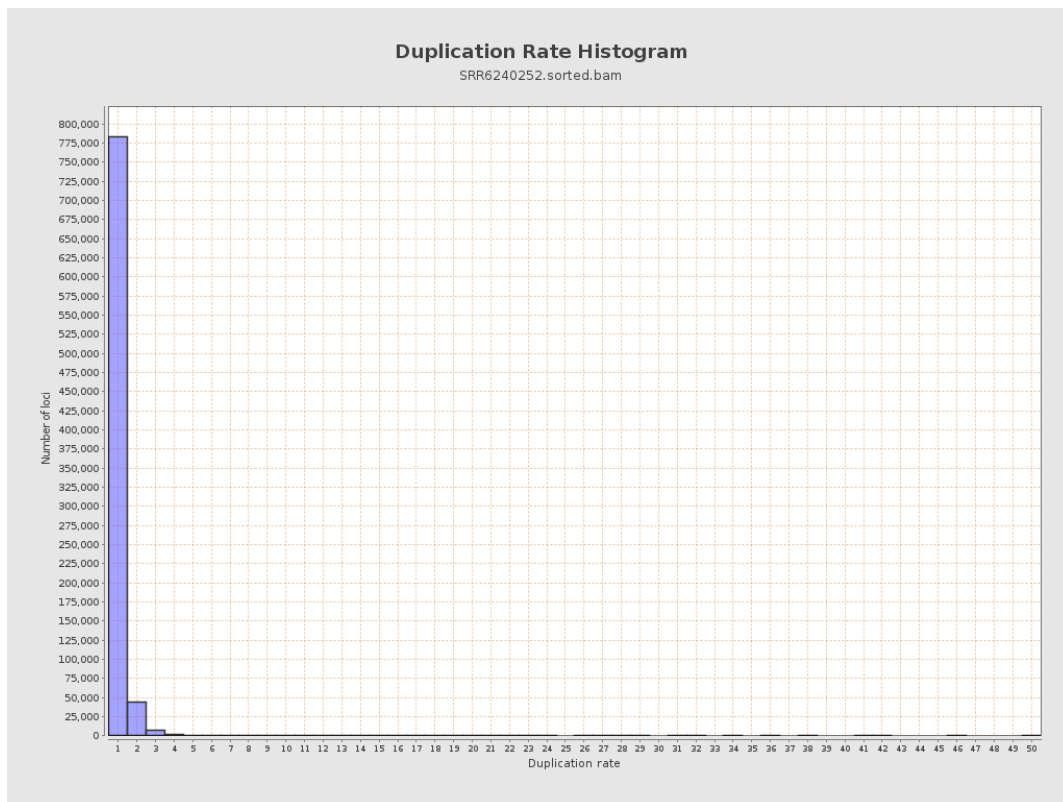
5. Results : Coverage Histogram (0-50X)



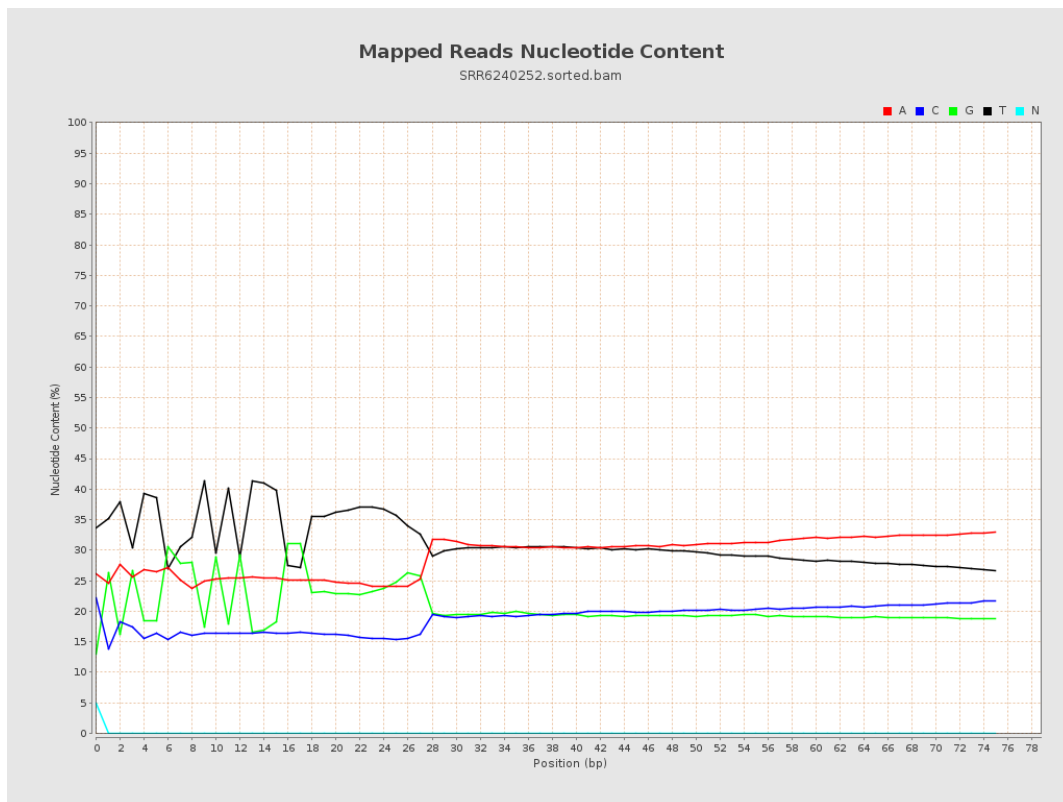
6. Results : Genome Fraction Coverage



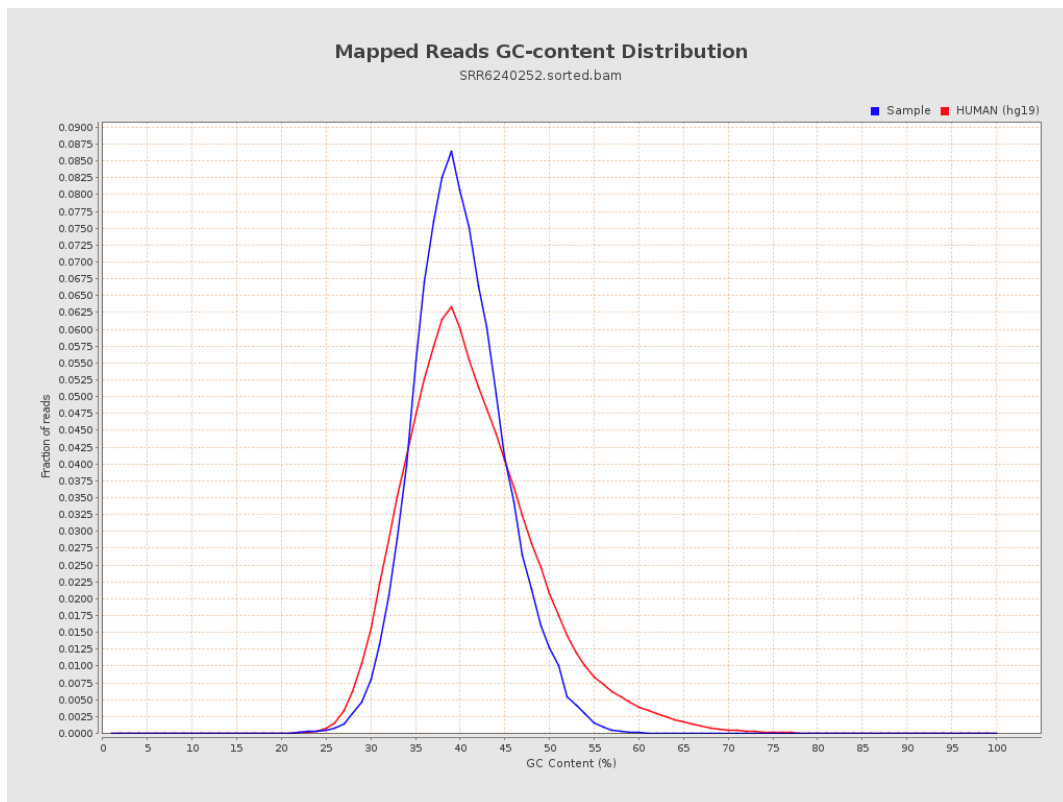
7. Results : Duplication Rate Histogram



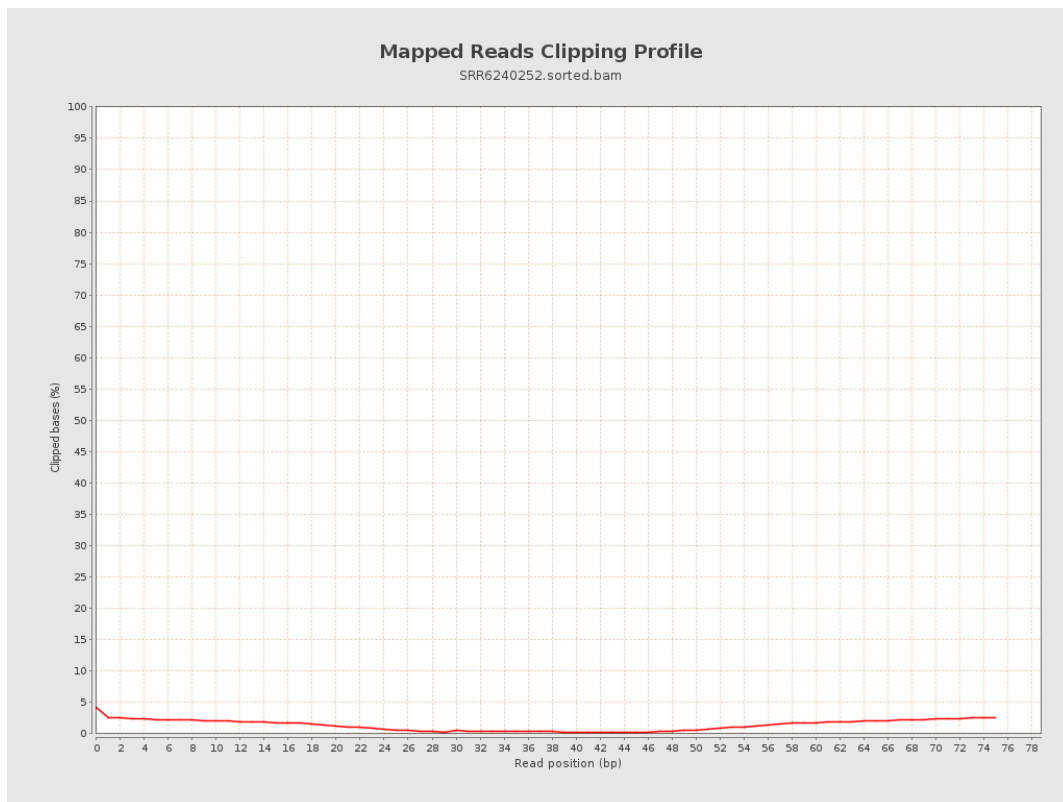
8. Results : Mapped Reads Nucleotide Content



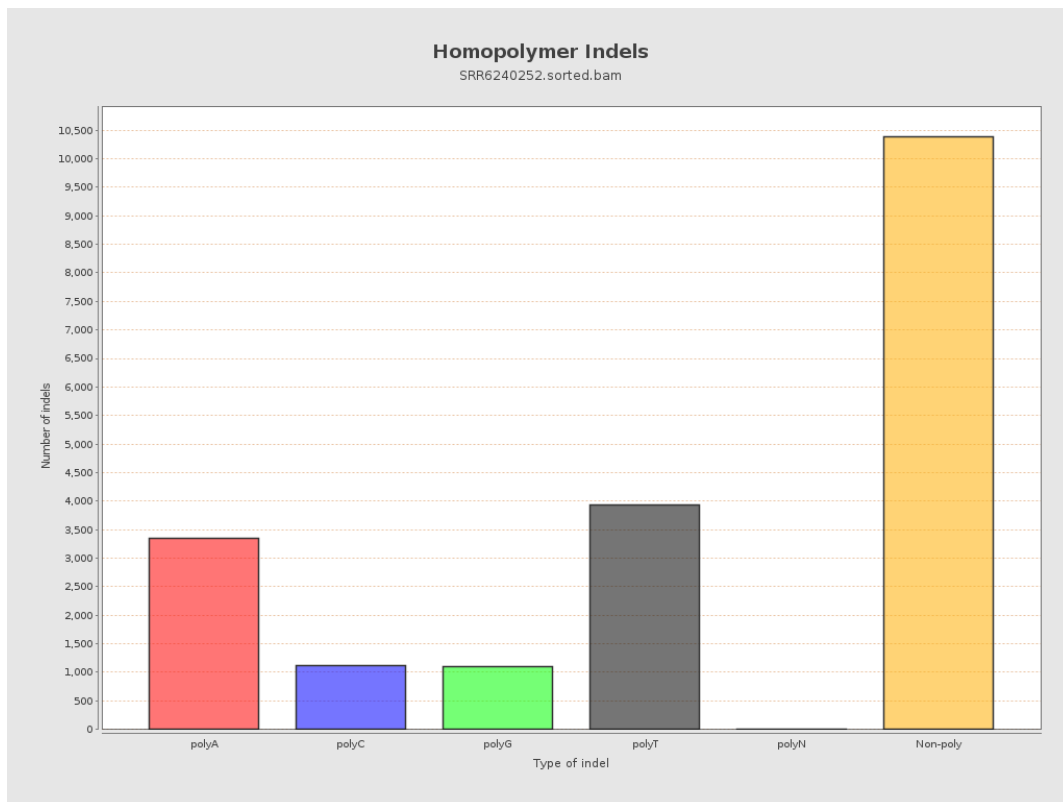
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

