

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:29:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240228.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_SRR6240228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240228.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:29:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,070,526
Mapped reads	767,761 / 71.72%
Unmapped reads	302,765 / 28.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,556 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	46,980 / 4.39%
Duplication rate	5.08%
Clipped reads	472,947 / 44.18%

2.2. ACGT Content

Number/percentage of A's	13,041,558 / 27.3%
Number/percentage of C's	8,384,798 / 17.55%
Number/percentage of T's	15,485,799 / 32.42%
Number/percentage of G's	10,840,714 / 22.7%
Number/percentage of N's	11,744 / 0.02%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1989
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2.4. Mapping Quality

Mean Mapping Quality	45.41
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2.5. Mismatches and indels

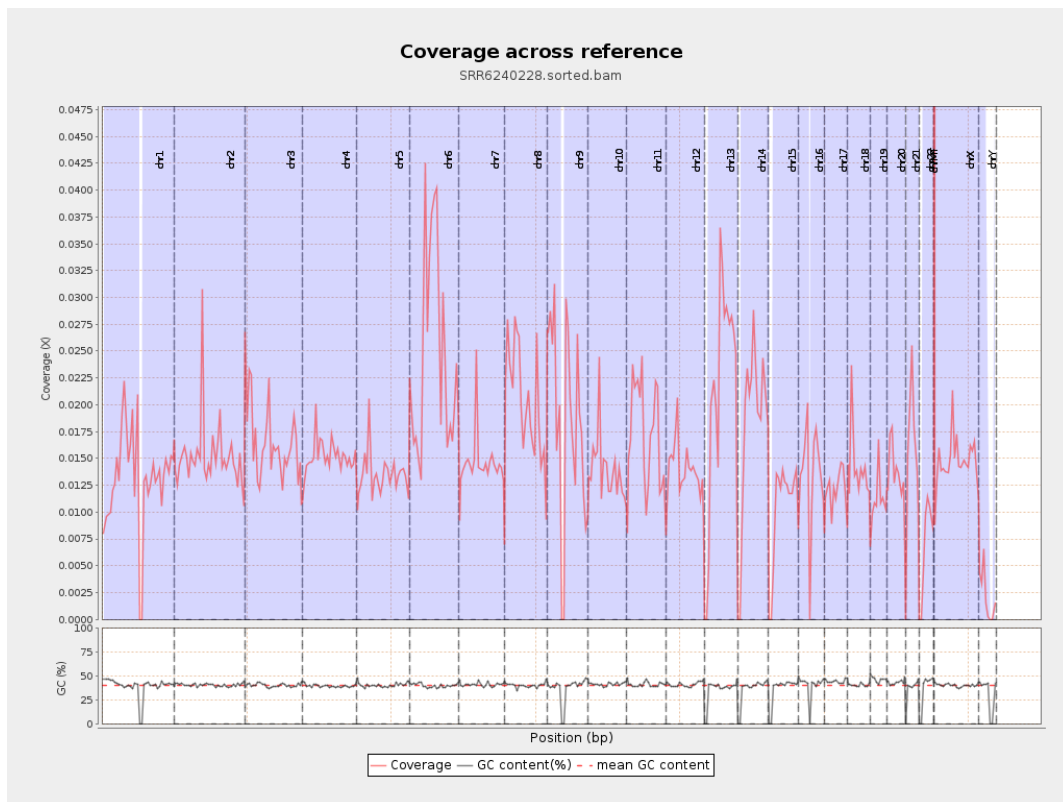
General error rate	0.83%
Mismatches	392,000
Insertions	3,263
Mapped reads with at least one insertion	0.42%
Deletions	11,407
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.42%

2.6. Chromosome stats

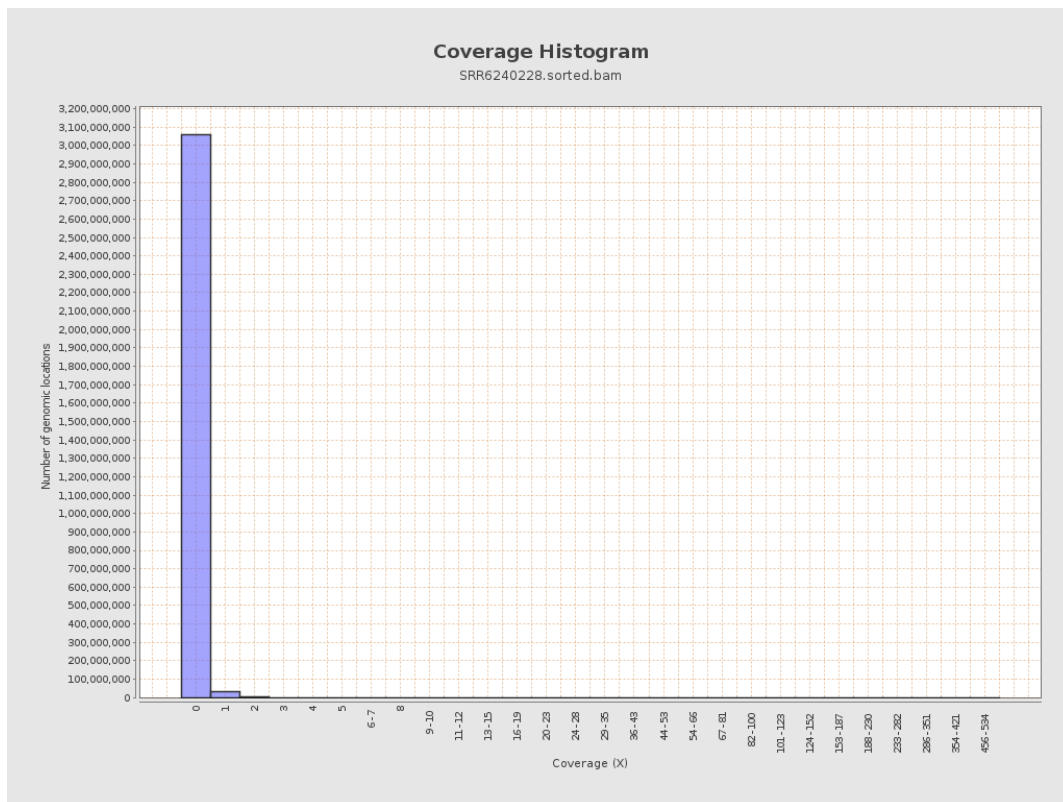
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3282053	0.0132	0.2327
chr2	243199373	3686667	0.0152	0.213
chr3	198022430	3246415	0.0164	0.1506
chr4	191154276	2895274	0.0151	0.148
chr5	180915260	2438759	0.0135	0.1377
chr6	171115067	4254743	0.0249	0.2313
chr7	159138663	2321064	0.0146	0.1884

chr8	146364022	2983770	0.0204	0.3667
chr9	141213431	2654558	0.0188	0.2302
chr10	135534747	1893619	0.014	0.1775
chr11	135006516	2330800	0.0173	0.1842
chr12	133851895	1886373	0.0141	0.1459
chr13	115169878	2463598	0.0214	0.172
chr14	107349540	1971233	0.0184	0.1753
chr15	102531392	1065713	0.0104	0.1236
chr16	90354753	1201704	0.0133	0.1504
chr17	81195210	987433	0.0122	0.1334
chr18	78077248	1104655	0.0141	0.3846
chr19	59128983	668457	0.0113	0.1801
chr20	63025520	870946	0.0138	0.1435
chr21	48129895	766484	0.0159	0.156
chr22	51304566	365559	0.0071	0.0973
chrMT	16571	17515	1.057	1.5452
chrX	155270560	2302314	0.0148	0.1531
chrY	59373566	124234	0.0021	0.0601

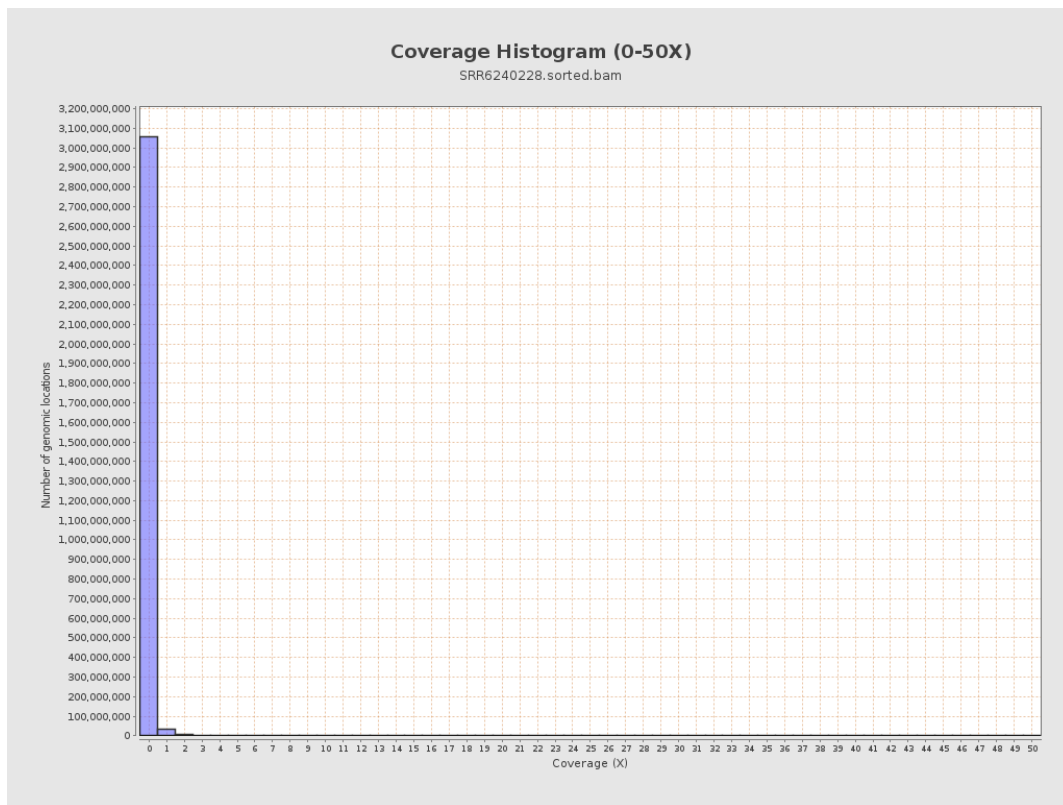
3. Results : Coverage across reference



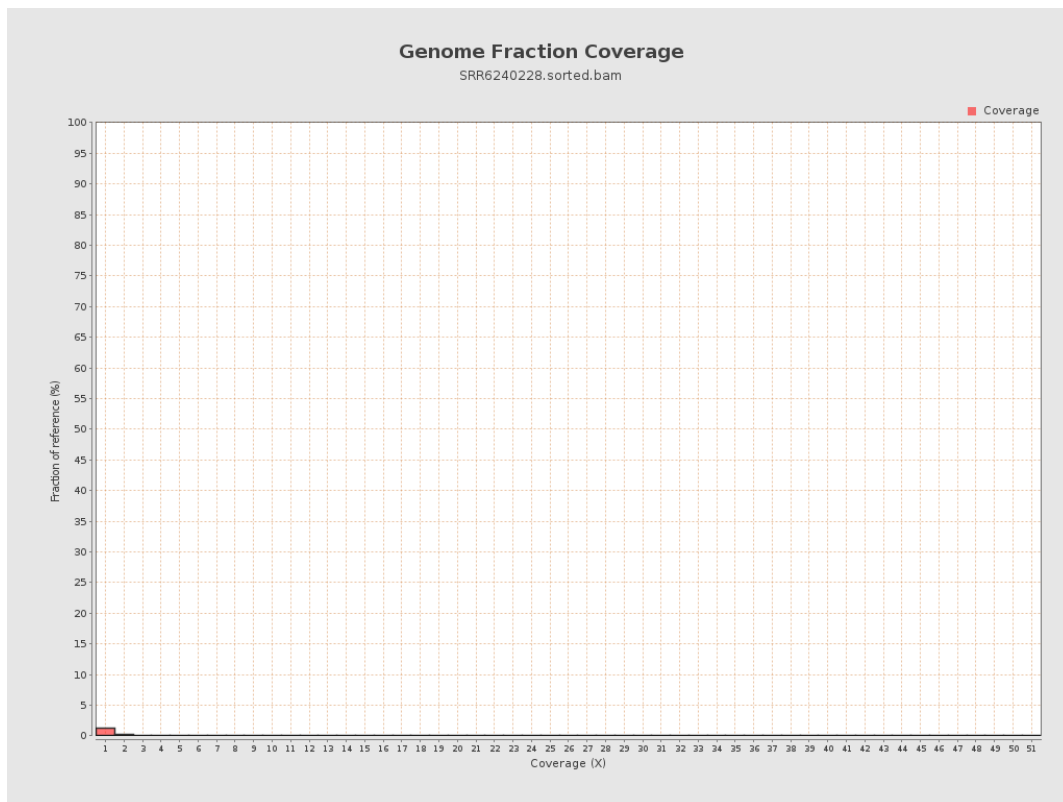
4. Results : Coverage Histogram



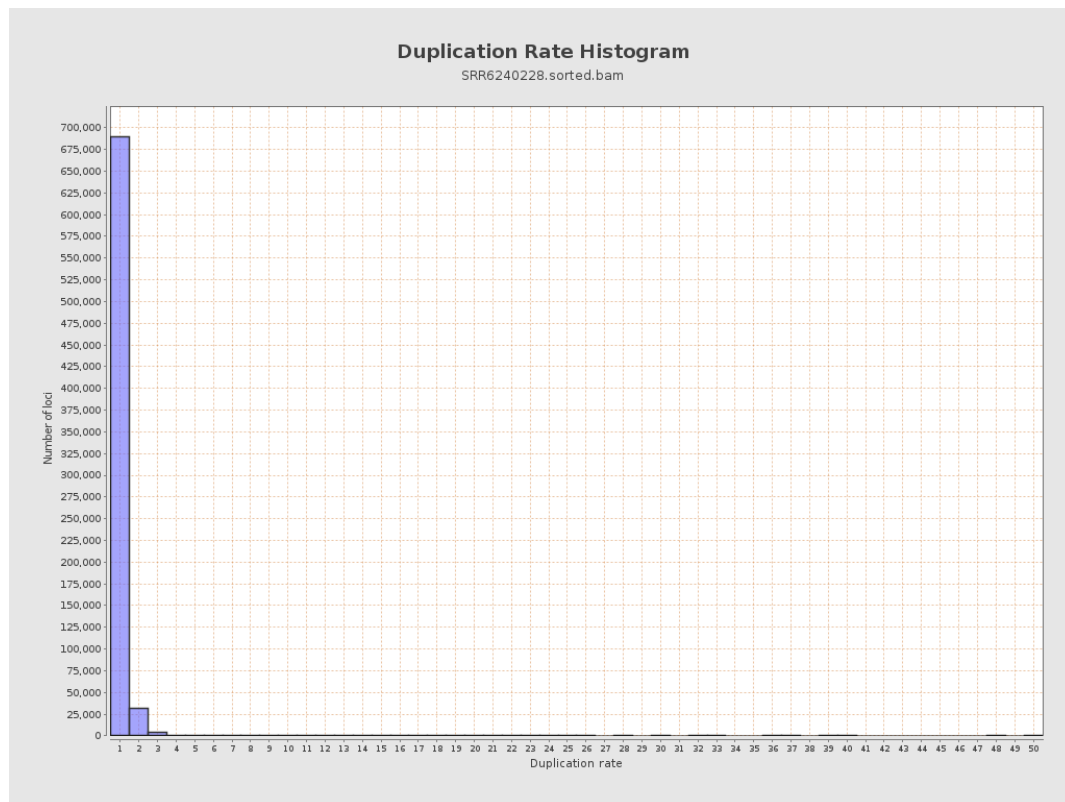
5. Results : Coverage Histogram (0-50X)



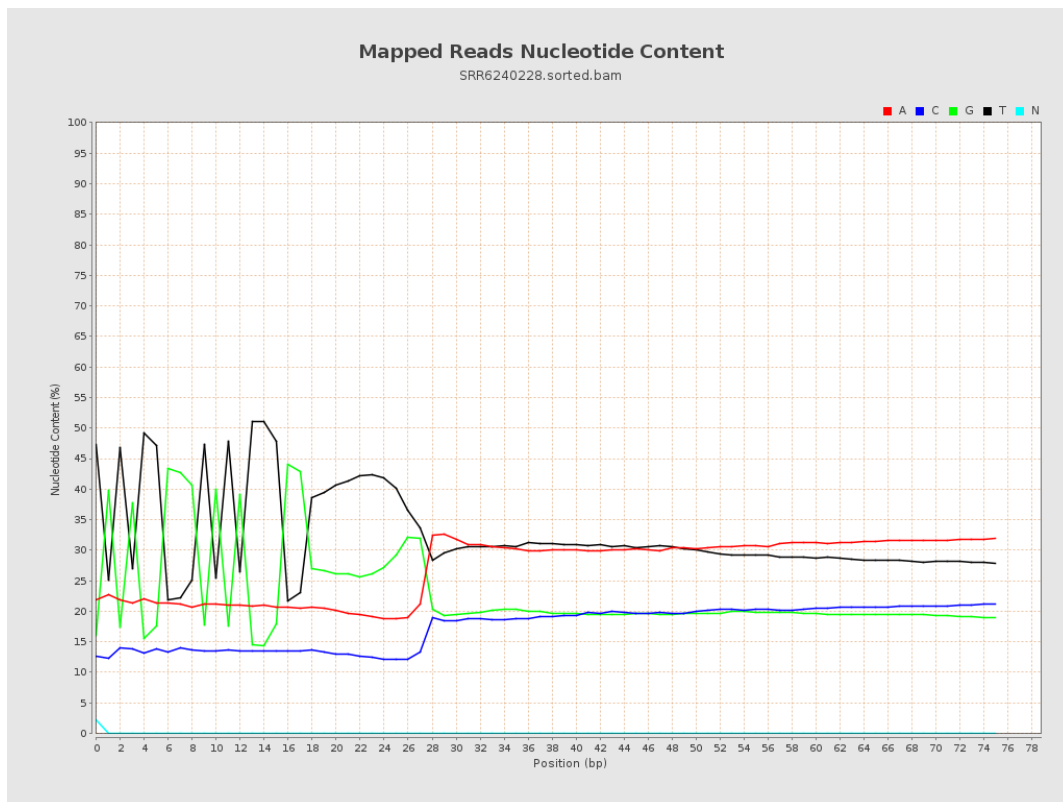
6. Results : Genome Fraction Coverage



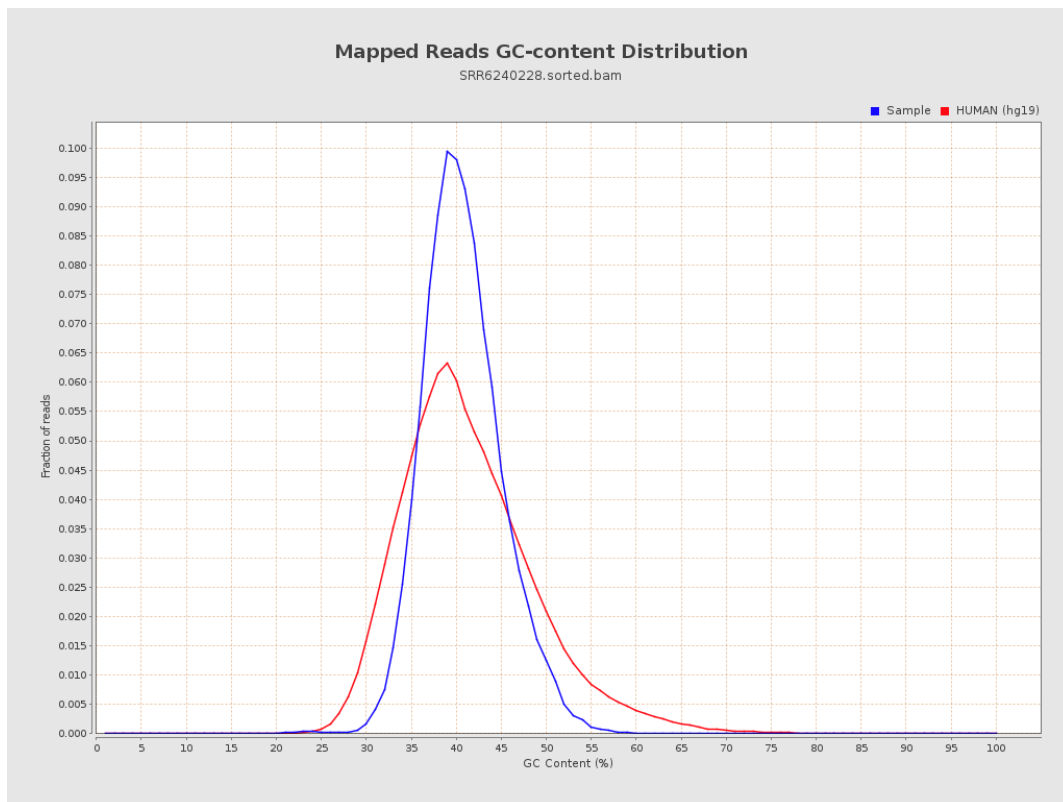
7. Results : Duplication Rate Histogram



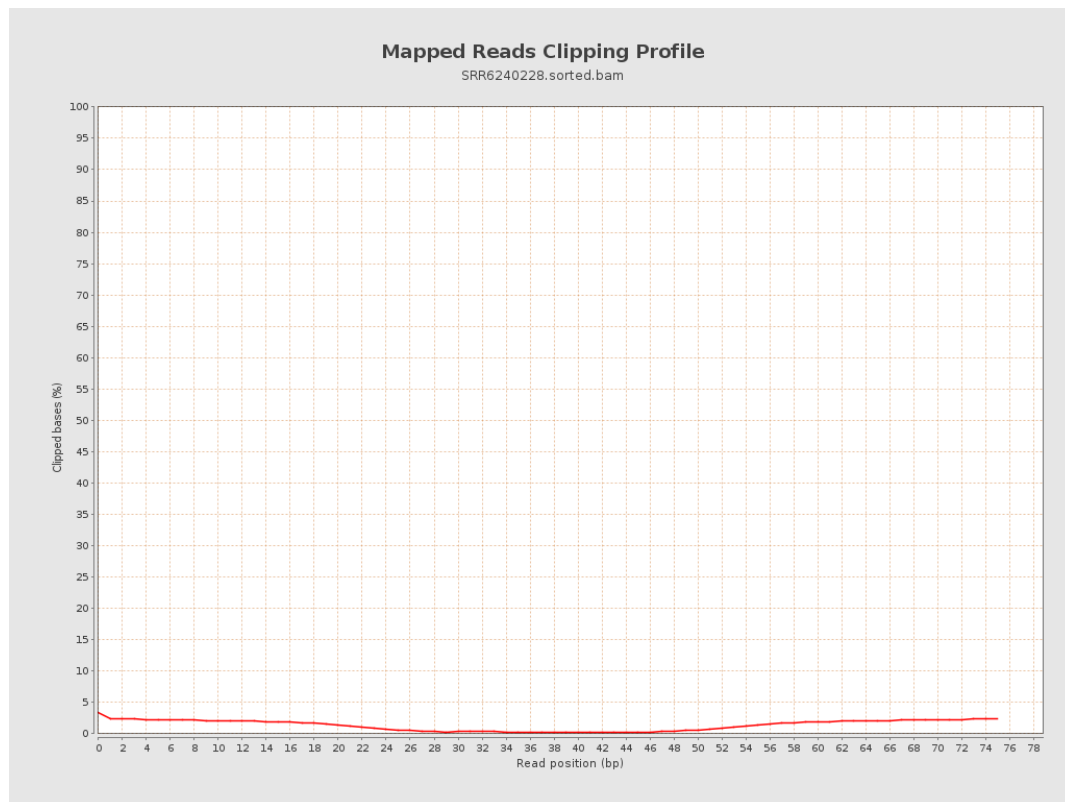
8. Results : Mapped Reads Nucleotide Content



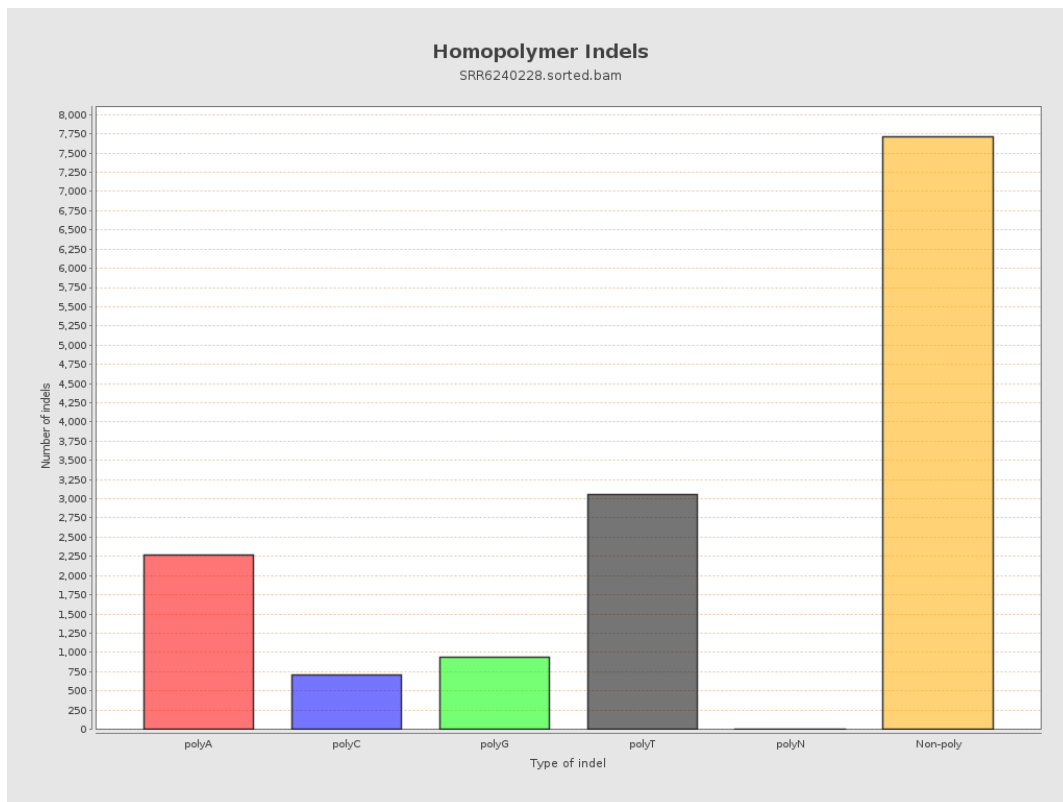
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

