

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240028.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_SRR6240028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:03:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,119,093
Mapped reads	1,670,444 / 78.83%
Unmapped reads	448,649 / 21.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,492 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	213,974 / 10.1%
Duplication rate	9.79%
Clipped reads	781,779 / 36.89%

2.2. ACGT Content

Number/percentage of A's	31,936,739 / 28.77%
Number/percentage of C's	20,720,521 / 18.66%
Number/percentage of T's	35,240,466 / 31.74%
Number/percentage of G's	23,114,097 / 20.82%
Number/percentage of N's	10,200 / 0.01%
GC Percentage	39.48%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.4362
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2.4. Mapping Quality

Mean Mapping Quality	47.04
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2.5. Mismatches and indels

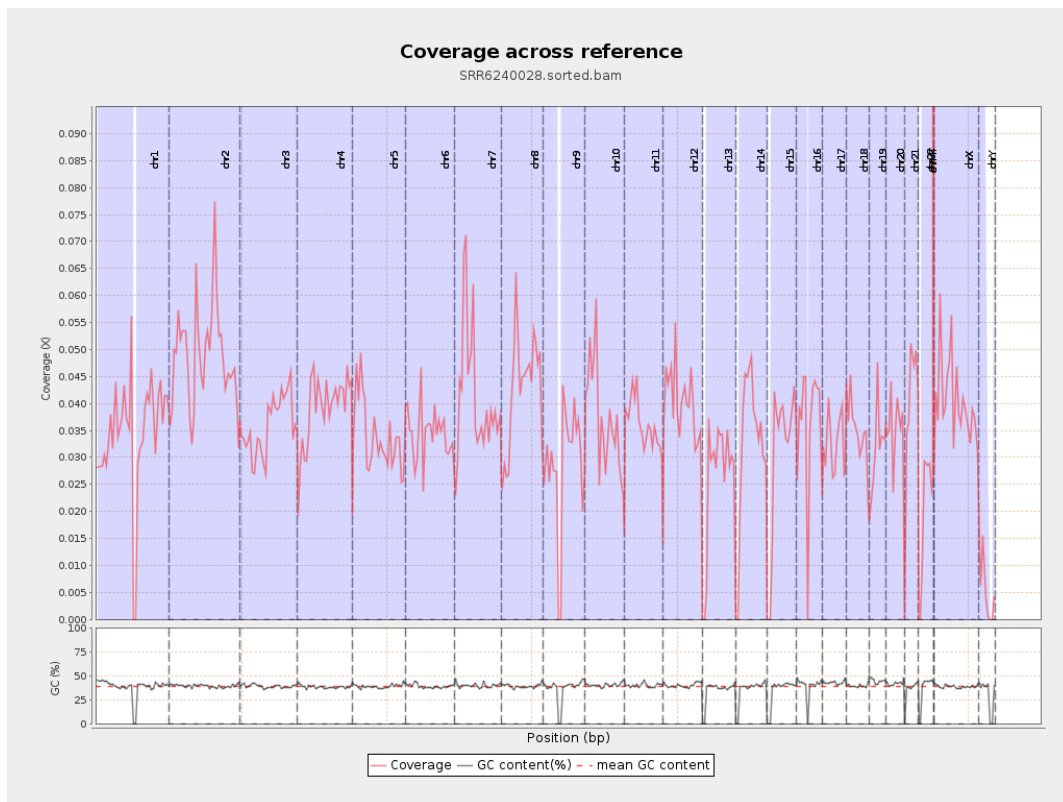
General error rate	0.85%
Mismatches	931,529
Insertions	8,155
Mapped reads with at least one insertion	0.48%
Deletions	30,429
Mapped reads with at least one deletion	1.8%
Homopolymer indels	48.94%

2.6. Chromosome stats

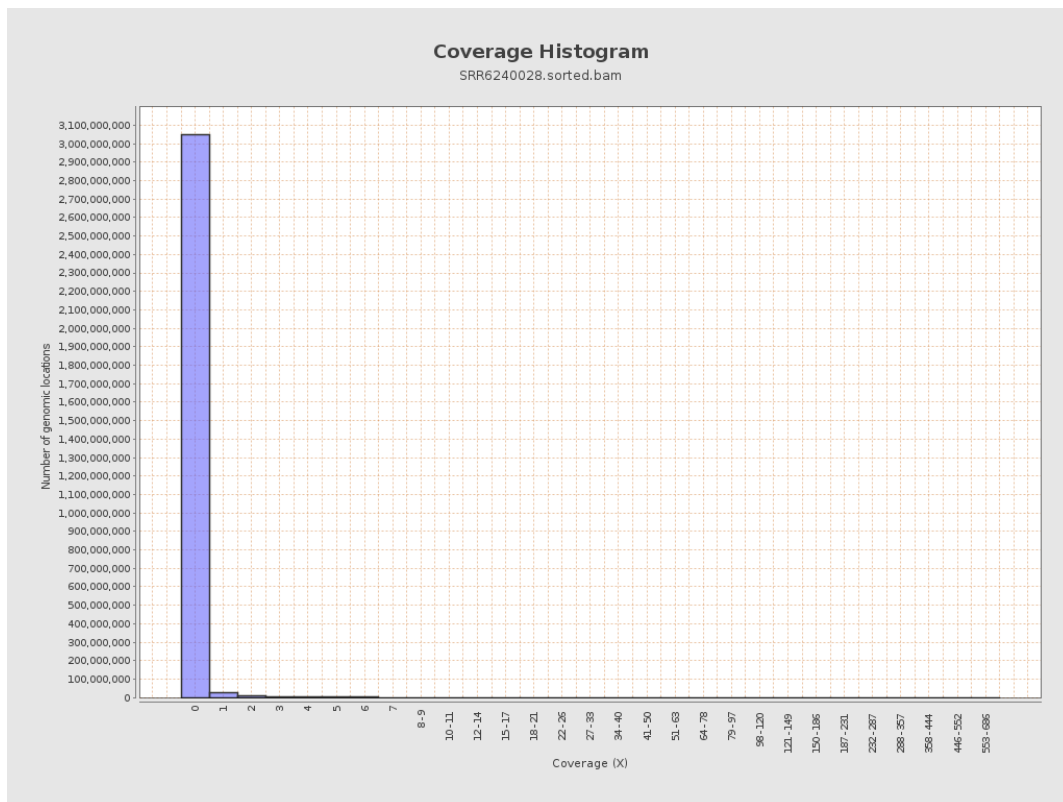
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8623374	0.0346	0.6119
chr2	243199373	11853612	0.0487	0.5009
chr3	198022430	7105263	0.0359	0.3655
chr4	191154276	7463139	0.039	0.382
chr5	180915260	6120201	0.0338	0.3541
chr6	171115067	5897424	0.0345	0.3787
chr7	159138663	6602606	0.0415	0.5666

chr8	146364022	6266318	0.0428	0.581
chr9	141213431	4083281	0.0289	0.3773
chr10	135534747	5065512	0.0374	0.4265
chr11	135006516	4827490	0.0358	0.4162
chr12	133851895	5346371	0.0399	0.3808
chr13	115169878	2995838	0.026	0.3149
chr14	107349540	3510197	0.0327	0.3503
chr15	102531392	3135509	0.0306	0.3343
chr16	90354753	3258101	0.0361	0.3661
chr17	81195210	2617745	0.0322	0.3479
chr18	78077248	2748085	0.0352	0.6355
chr19	59128983	1876523	0.0317	0.4434
chr20	63025520	2216720	0.0352	0.3577
chr21	48129895	1900056	0.0395	0.385
chr22	51304566	990191	0.0193	0.2508
chrMT	16571	15968	0.9636	1.8553
chrX	155270560	6249706	0.0403	0.3952
chrY	59373566	306093	0.0052	0.1285

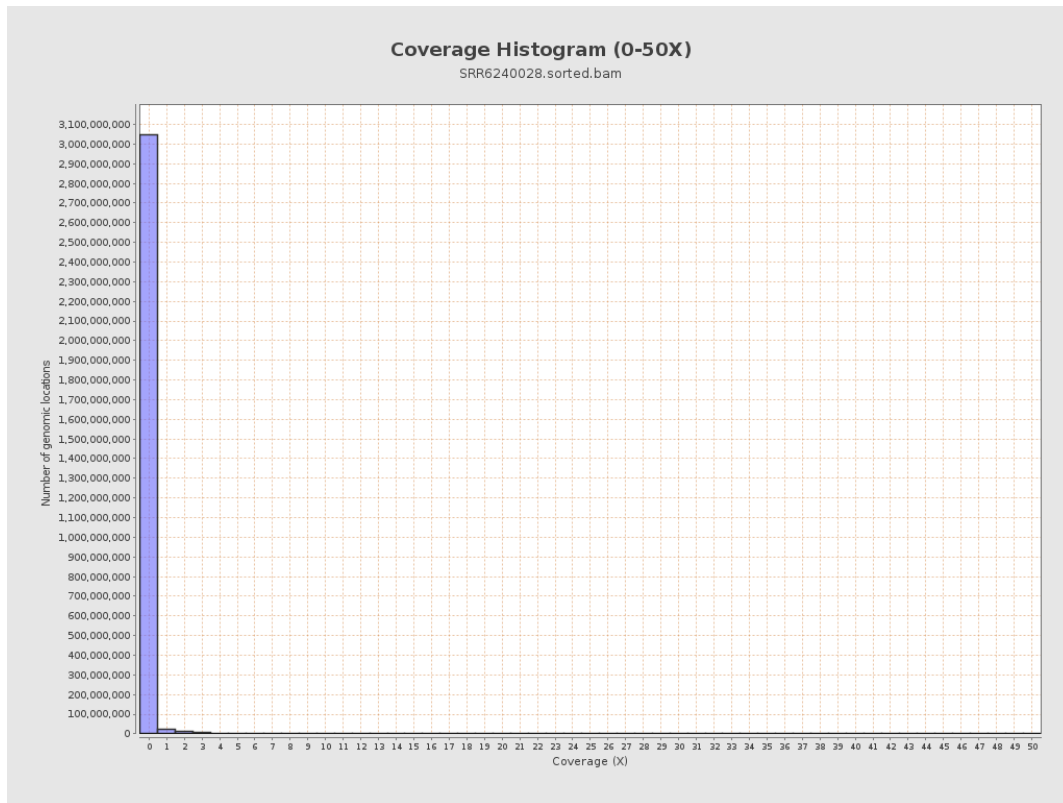
3. Results : Coverage across reference



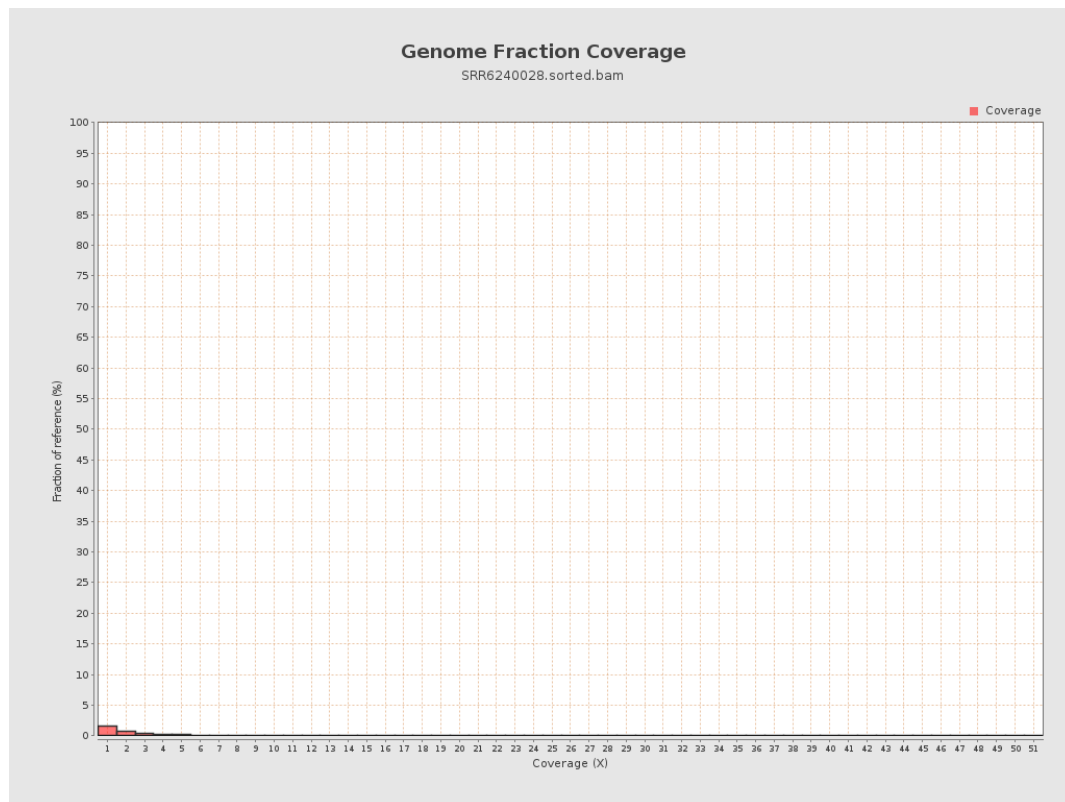
4. Results : Coverage Histogram



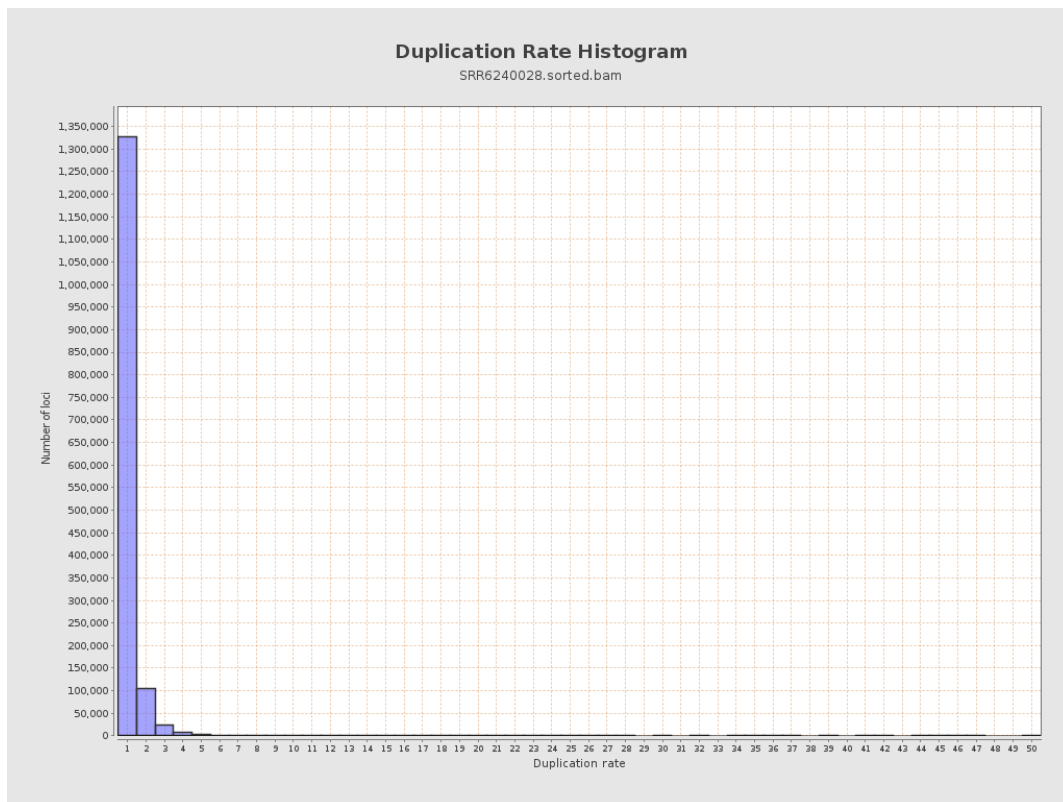
5. Results : Coverage Histogram (0-50X)



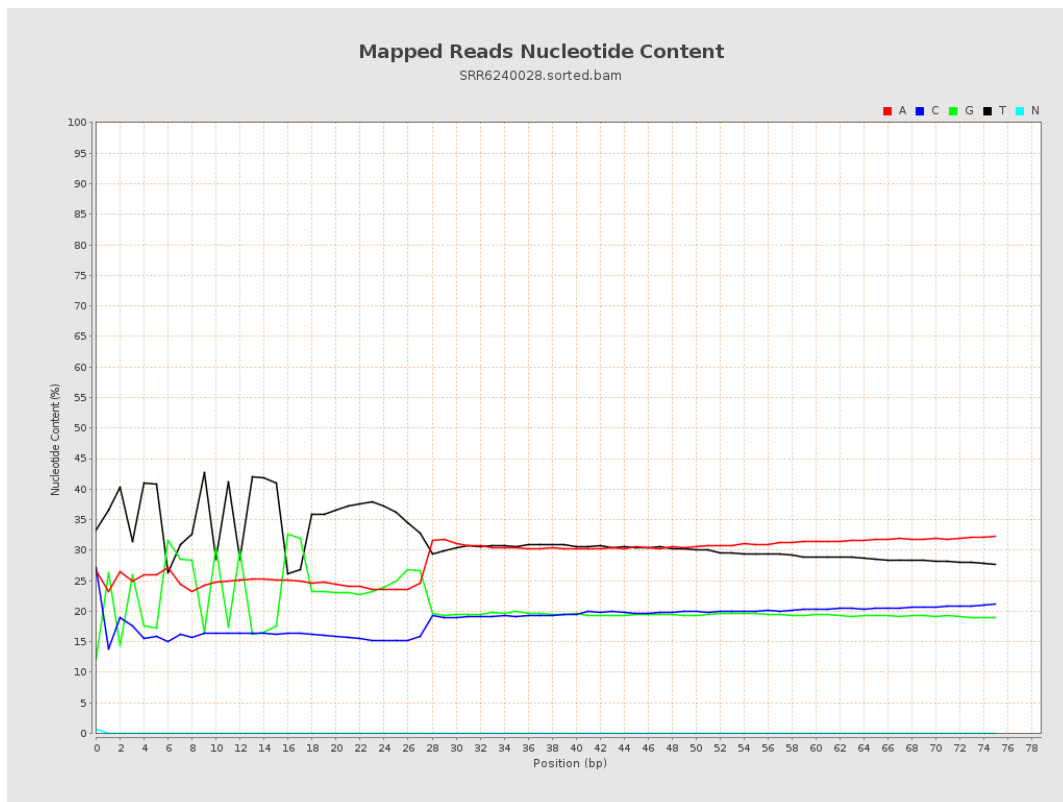
6. Results : Genome Fraction Coverage



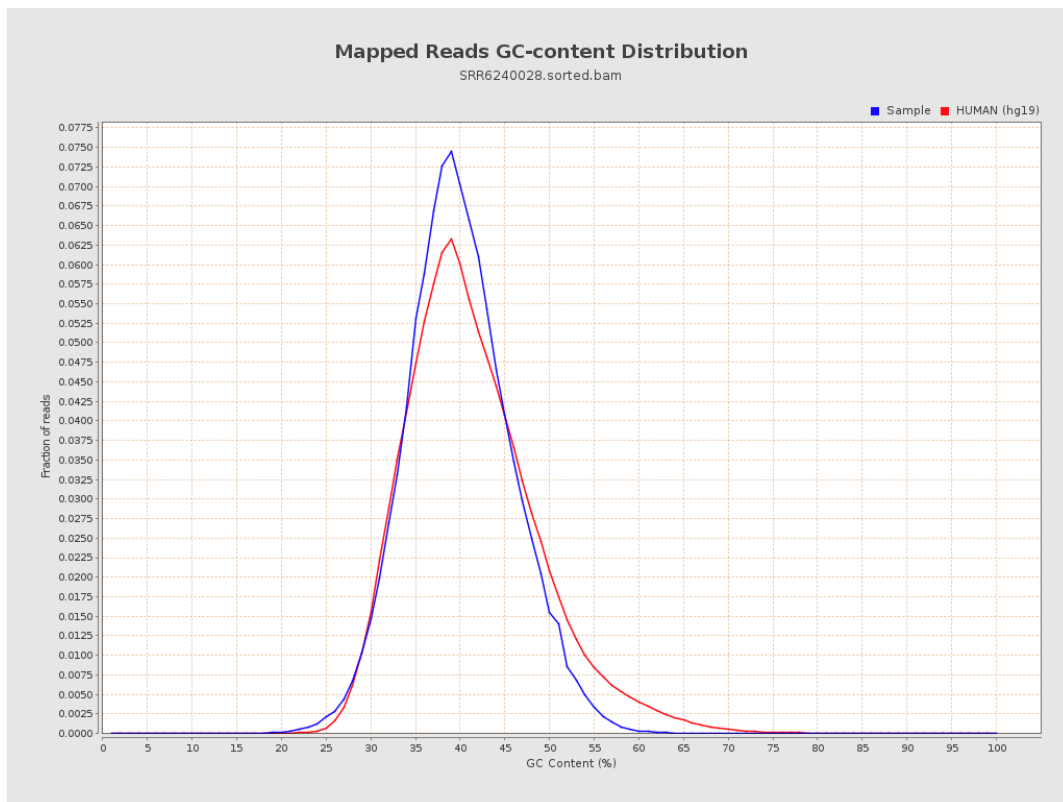
7. Results : Duplication Rate Histogram



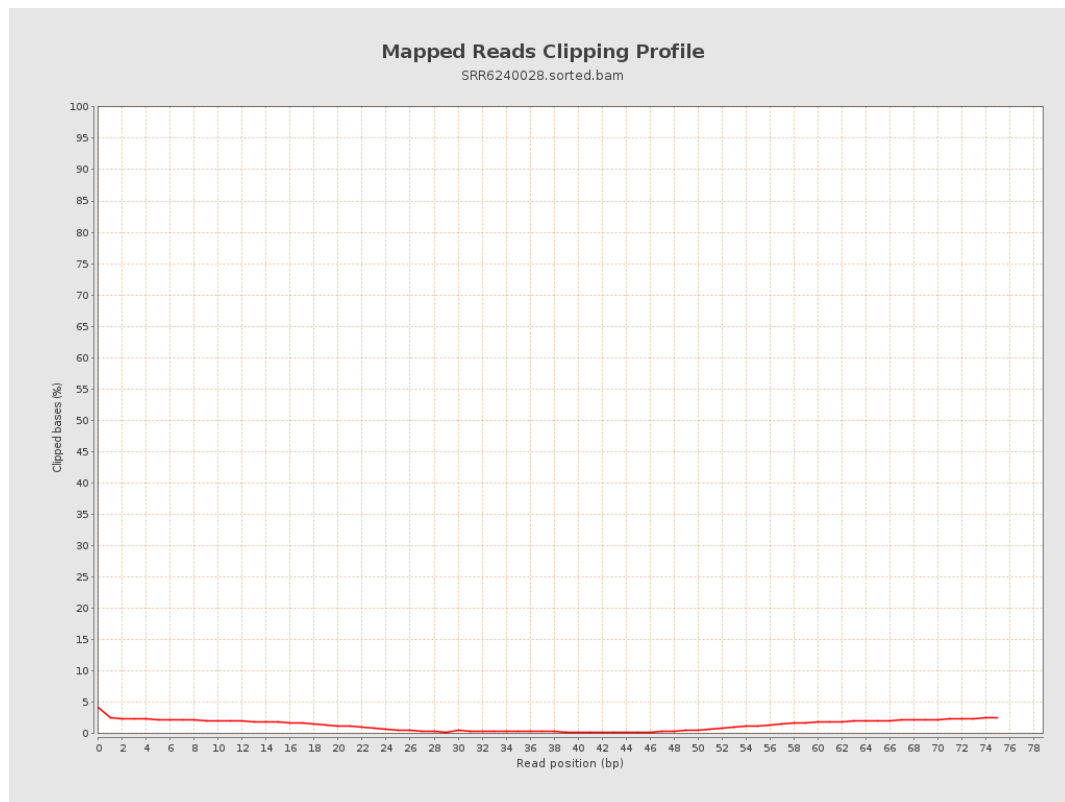
8. Results : Mapped Reads Nucleotide Content



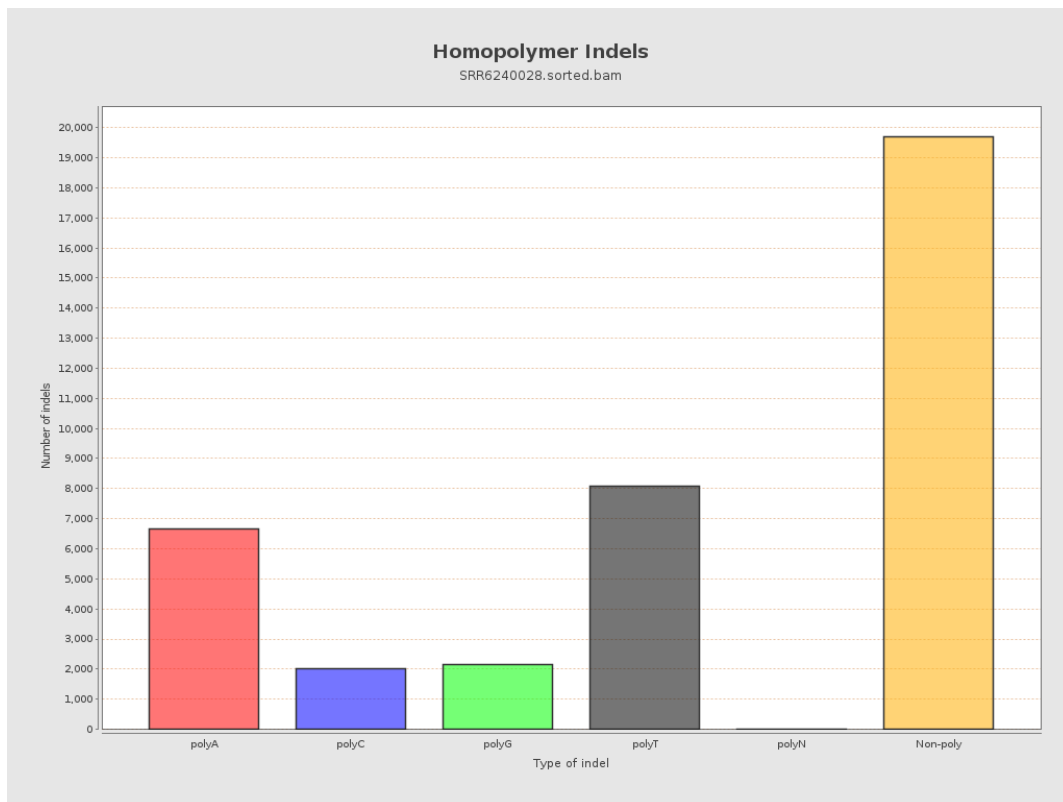
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

