

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:46:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240255.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_SRR6240255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:46:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,362,508
Mapped reads	1,848,012 / 78.22%
Unmapped reads	514,496 / 21.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,348 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	158,901 / 6.73%
Duplication rate	7.17%
Clipped reads	1,257,323 / 53.22%

2.2. ACGT Content

Number/percentage of A's	30,286,613 / 26.93%
Number/percentage of C's	19,413,639 / 17.26%
Number/percentage of T's	36,663,144 / 32.6%
Number/percentage of G's	26,060,673 / 23.18%
Number/percentage of N's	25,739 / 0.02%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.3326
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2.4. Mapping Quality

Mean Mapping Quality	45.24
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2.5. Mismatches and indels

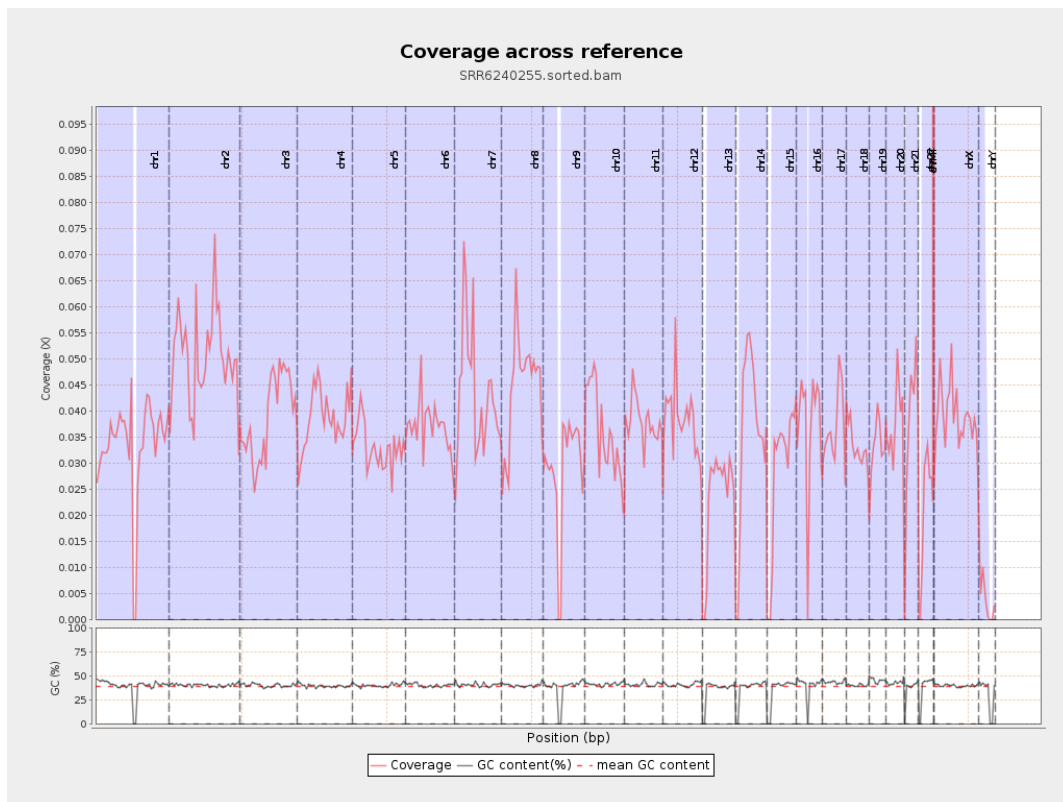
General error rate	0.96%
Mismatches	1,069,619
Insertions	7,712
Mapped reads with at least one insertion	0.41%
Deletions	36,790
Mapped reads with at least one deletion	1.97%
Homopolymer indels	49.64%

2.6. Chromosome stats

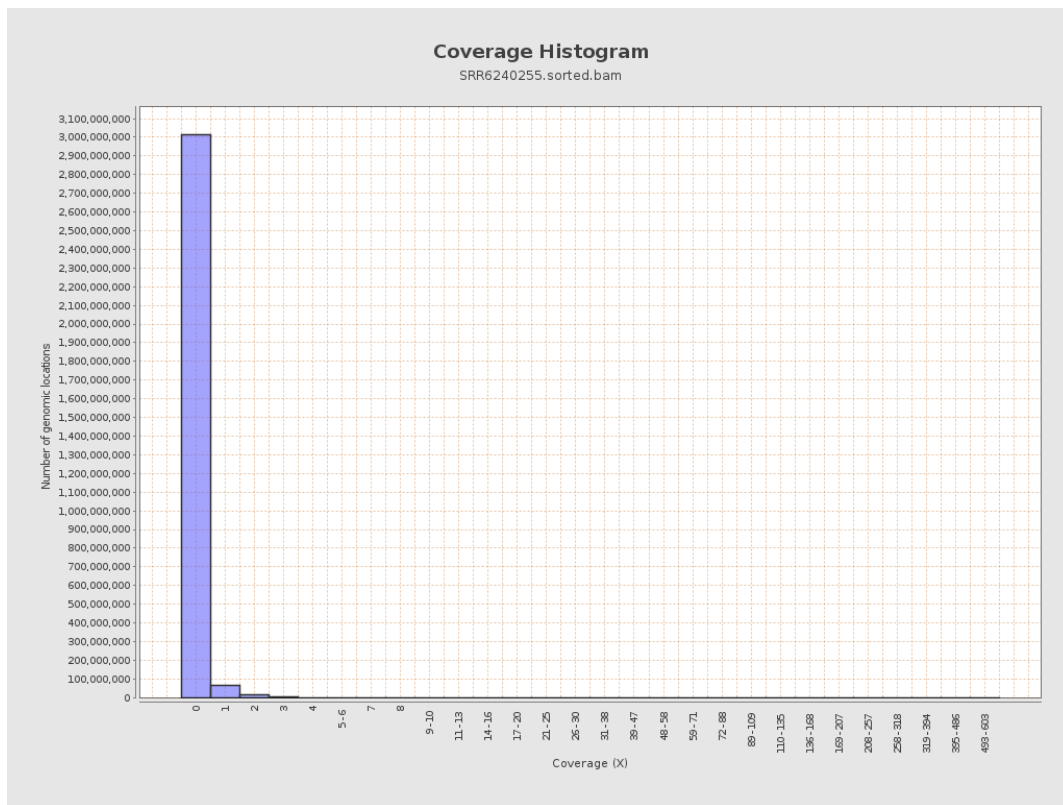
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8340679	0.0335	0.471
chr2	243199373	12278237	0.0505	0.4121
chr3	198022430	7709033	0.0389	0.2554
chr4	191154276	7386976	0.0386	0.2595
chr5	180915260	5999363	0.0332	0.236
chr6	171115067	6306224	0.0369	0.2866
chr7	159138663	6943034	0.0436	0.5828

chr8	146364022	6512584	0.0445	0.4342
chr9	141213431	4042626	0.0286	0.2866
chr10	135534747	4926417	0.0363	0.2765
chr11	135006516	5096443	0.0377	0.3157
chr12	133851895	5132222	0.0383	0.2544
chr13	115169878	2665189	0.0231	0.1962
chr14	107349540	3879301	0.0361	0.2528
chr15	102531392	2914763	0.0284	0.228
chr16	90354753	3342387	0.037	0.2527
chr17	81195210	2956978	0.0364	0.2633
chr18	78077248	2605248	0.0334	0.4257
chr19	59128983	1995719	0.0338	0.3349
chr20	63025520	2337944	0.0371	0.2507
chr21	48129895	1801680	0.0374	0.2555
chr22	51304566	1044192	0.0204	0.1792
chrMT	16571	54689	3.3003	4.1395
chrX	155270560	6012249	0.0387	0.2743
chrY	59373566	228930	0.0039	0.081

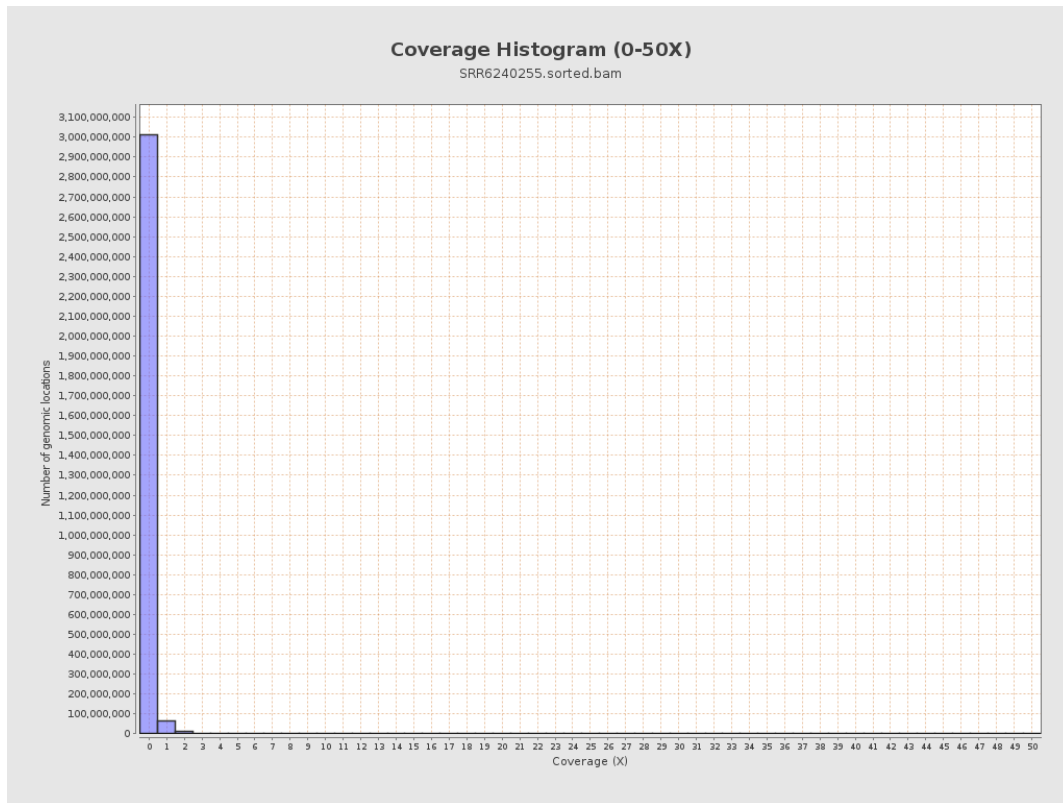
3. Results : Coverage across reference



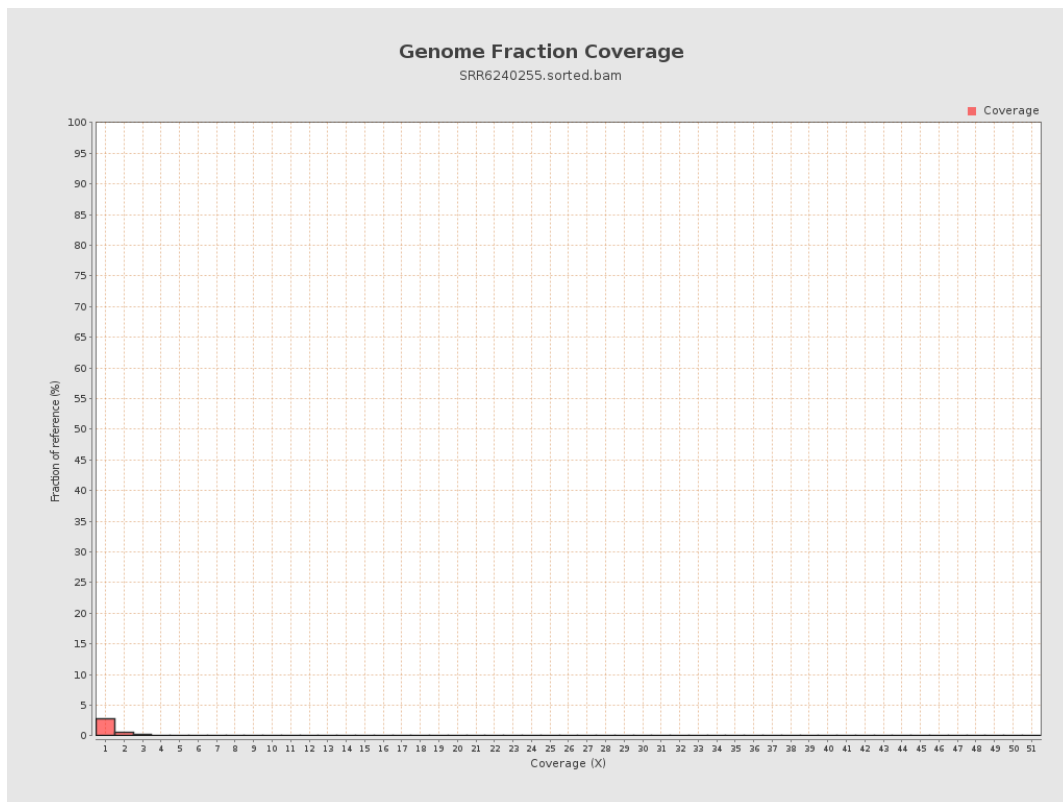
4. Results : Coverage Histogram



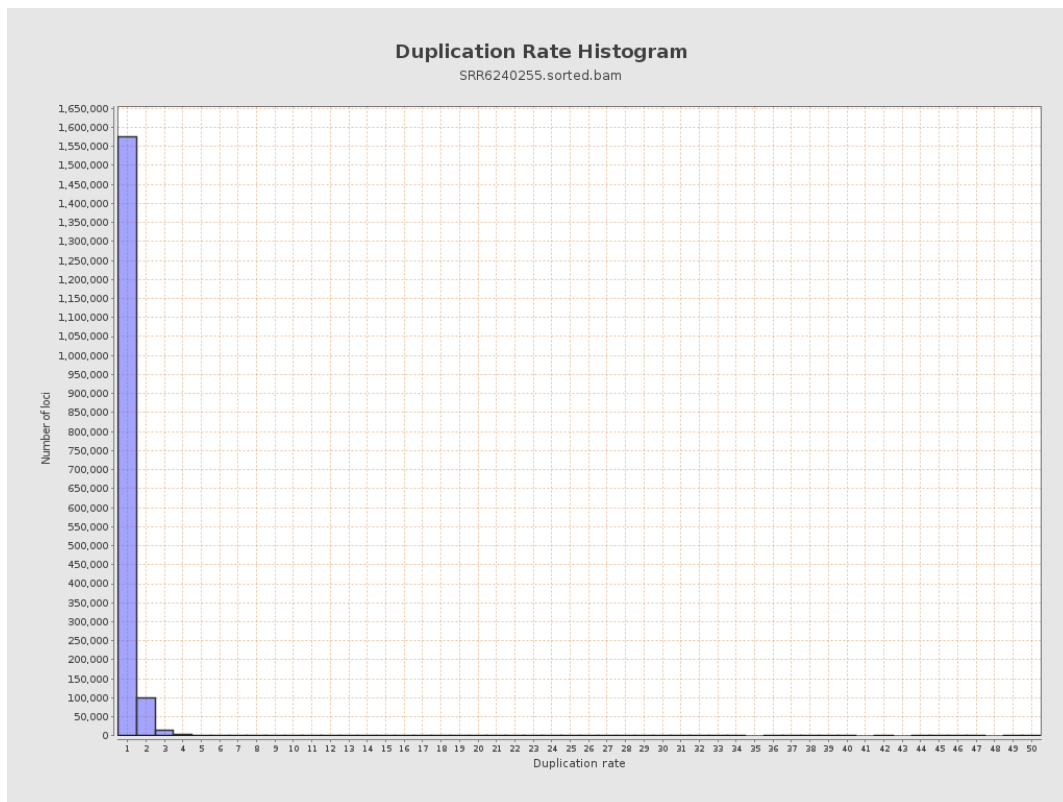
5. Results : Coverage Histogram (0-50X)



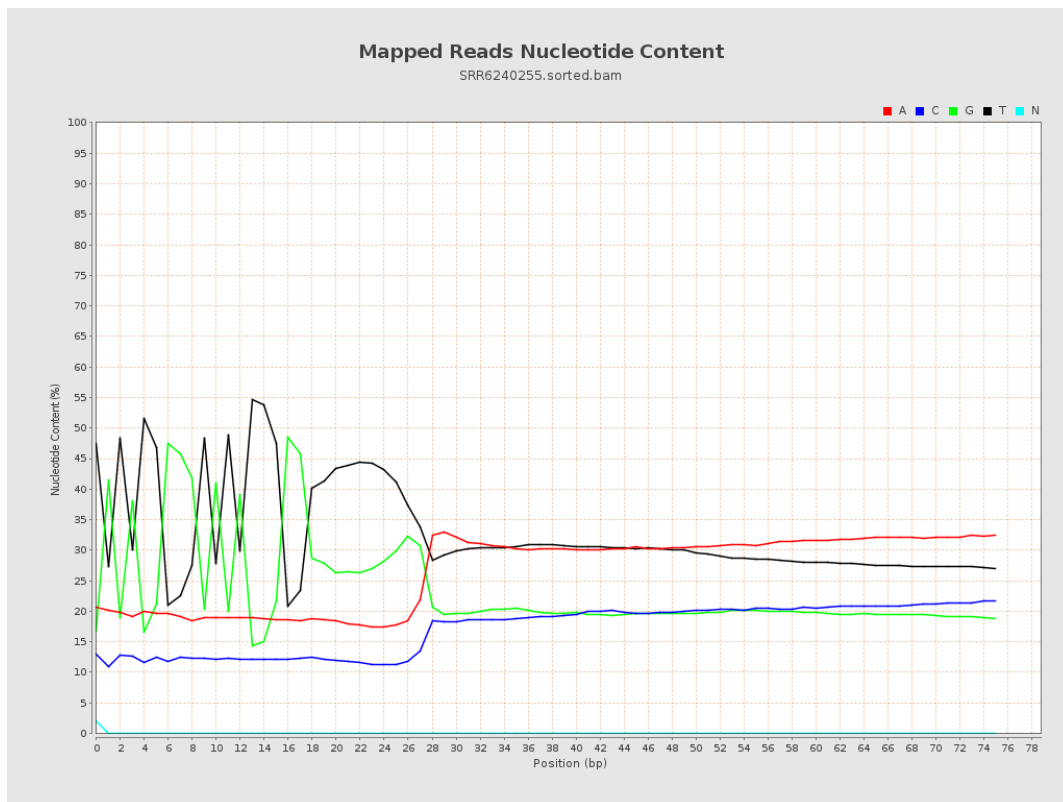
6. Results : Genome Fraction Coverage



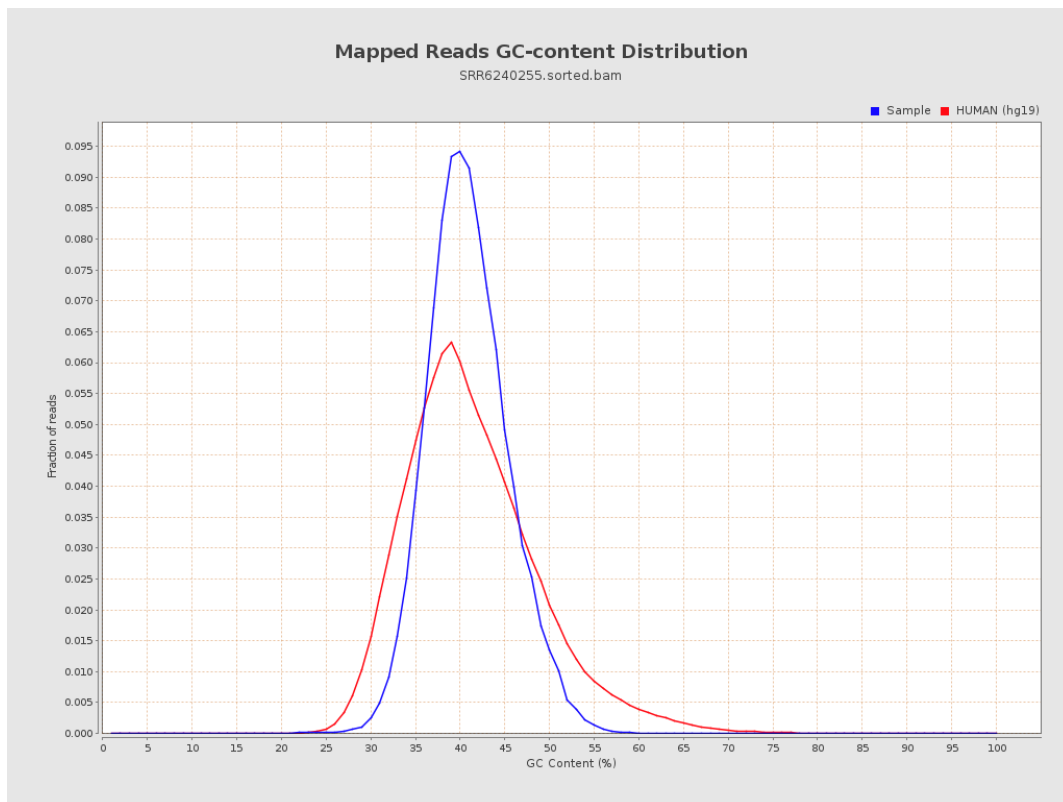
7. Results : Duplication Rate Histogram



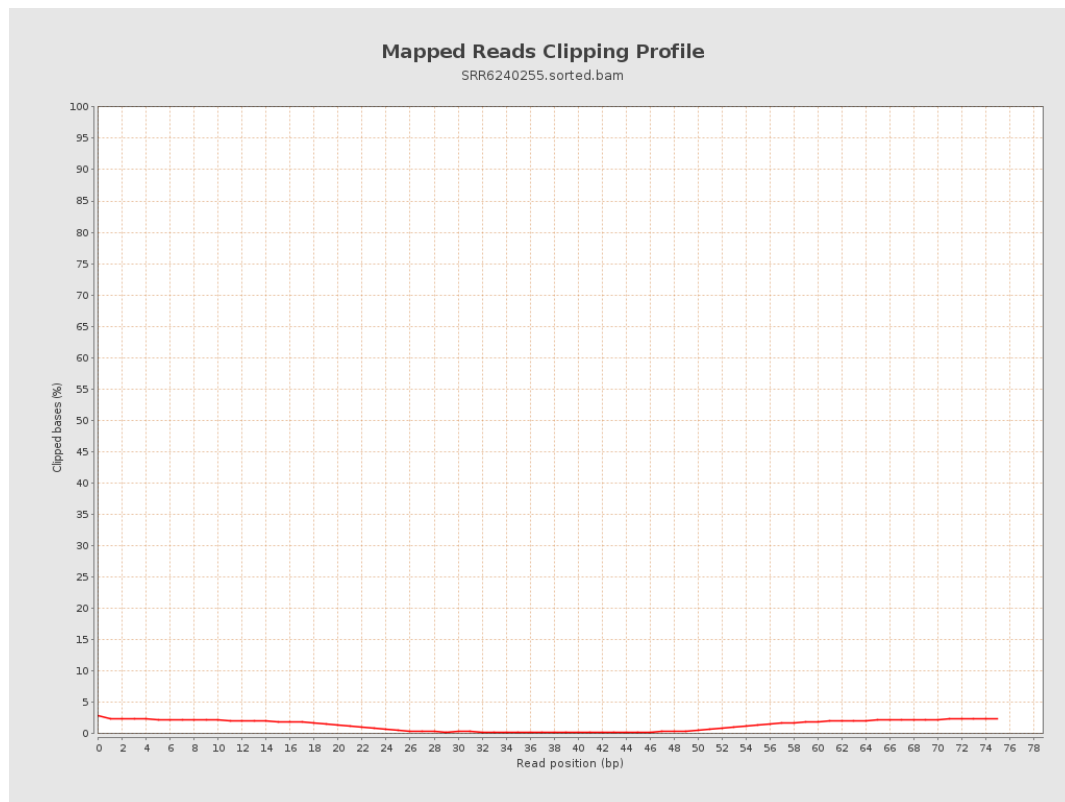
8. Results : Mapped Reads Nucleotide Content



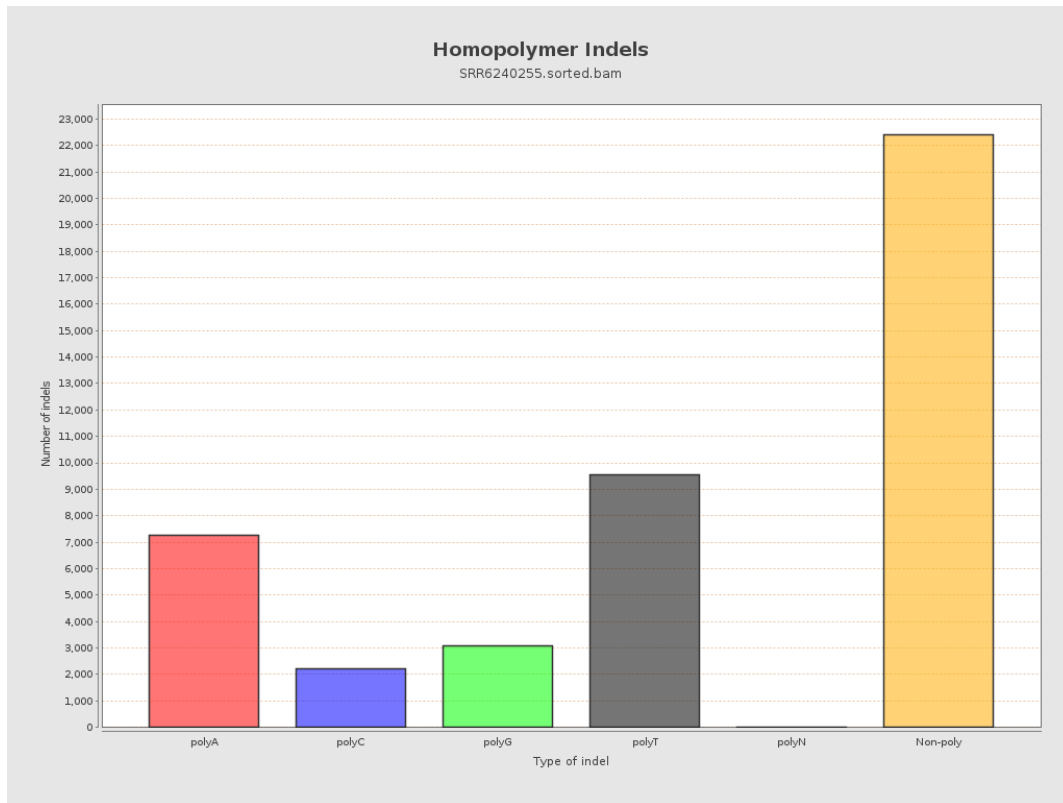
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

