

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:49:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240044.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_SRR6240044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:49:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,961,429
Mapped reads	1,684,541 / 85.88%
Unmapped reads	276,888 / 14.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,303 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	114,038 / 5.81%
Duplication rate	4.95%
Clipped reads	856,248 / 43.65%

2.2. ACGT Content

Number/percentage of A's	30,883,630 / 28.23%
Number/percentage of C's	19,849,583 / 18.14%
Number/percentage of T's	34,839,062 / 31.84%
Number/percentage of G's	23,756,224 / 21.71%
Number/percentage of N's	73,870 / 0.07%
GC Percentage	39.86%

2.3. Coverage

Mean	0.0354

Standard Deviation	0.6201
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.81
----------------------	-------

2.5. Mismatches and indels

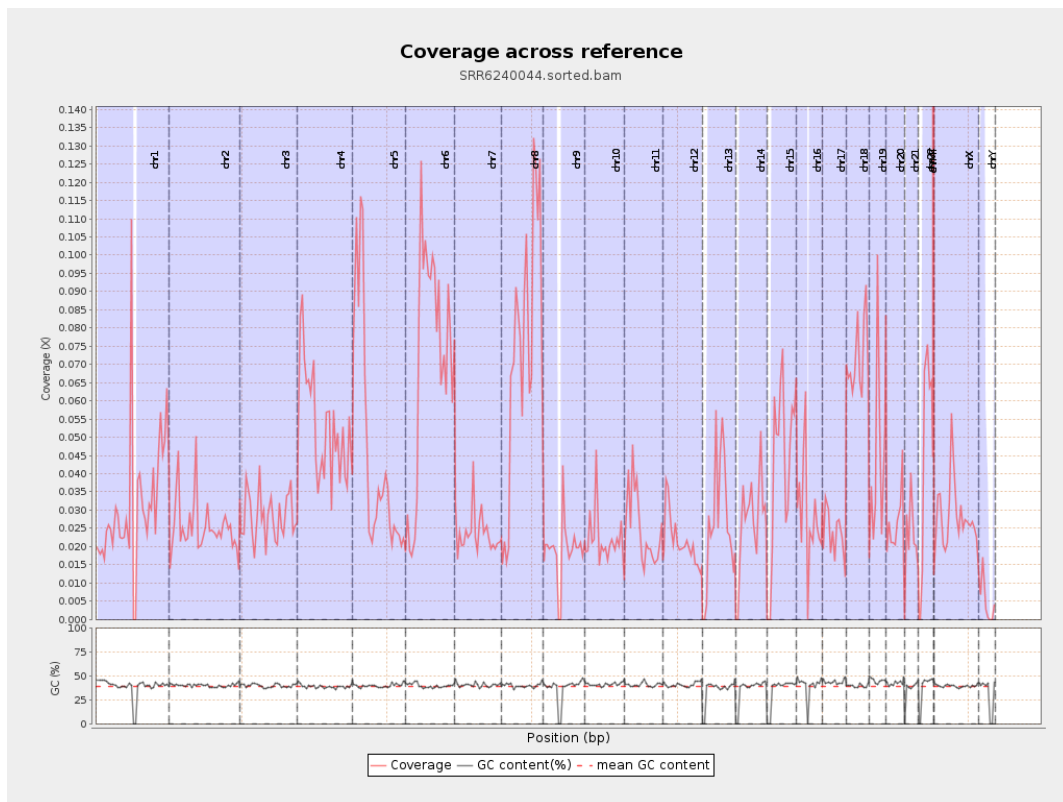
General error rate	0.9%
Mismatches	972,777
Insertions	7,552
Mapped reads with at least one insertion	0.44%
Deletions	25,467
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.9%

2.6. Chromosome stats

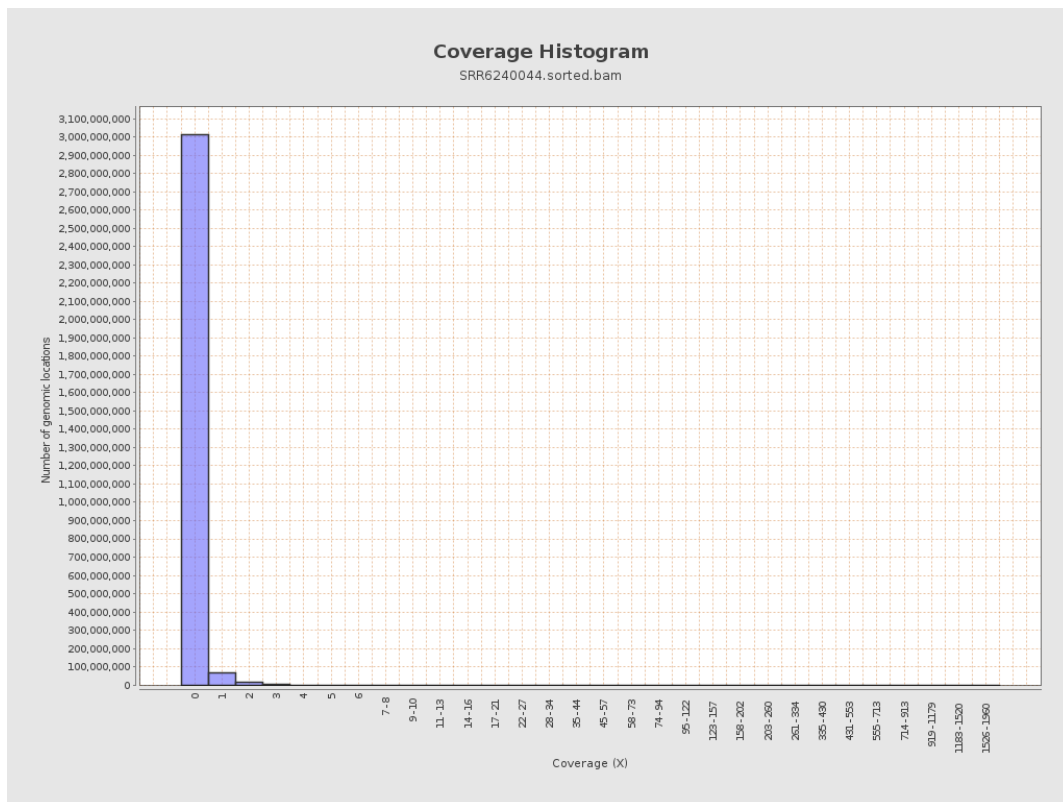
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7795000	0.0313	1.6732
chr2	243199373	6222391	0.0256	0.316
chr3	198022430	5633072	0.0284	0.2098
chr4	191154276	10133229	0.053	0.2926
chr5	180915260	8248073	0.0456	0.2716
chr6	171115067	12088641	0.0706	0.5719
chr7	159138663	3770159	0.0237	0.3186

chr8	146364022	10808585	0.0738	0.8028
chr9	141213431	2695940	0.0191	0.3416
chr10	135534747	2981493	0.022	0.2778
chr11	135006516	3336071	0.0247	0.2841
chr12	133851895	2873007	0.0215	0.1926
chr13	115169878	3056383	0.0265	0.2023
chr14	107349540	2911439	0.0271	0.2247
chr15	102531392	4389449	0.0428	0.2579
chr16	90354753	2606690	0.0288	0.2469
chr17	81195210	1855973	0.0229	0.207
chr18	78077248	5600651	0.0717	0.7436
chr19	59128983	2705248	0.0458	1.4932
chr20	63025520	1664275	0.0264	0.2088
chr21	48129895	1070593	0.0222	0.1951
chr22	51304566	2305194	0.0449	0.2602
chrMT	16571	57529	3.4717	2.816
chrX	155270560	4351483	0.028	0.2438
chrY	59373566	286454	0.0048	0.1303

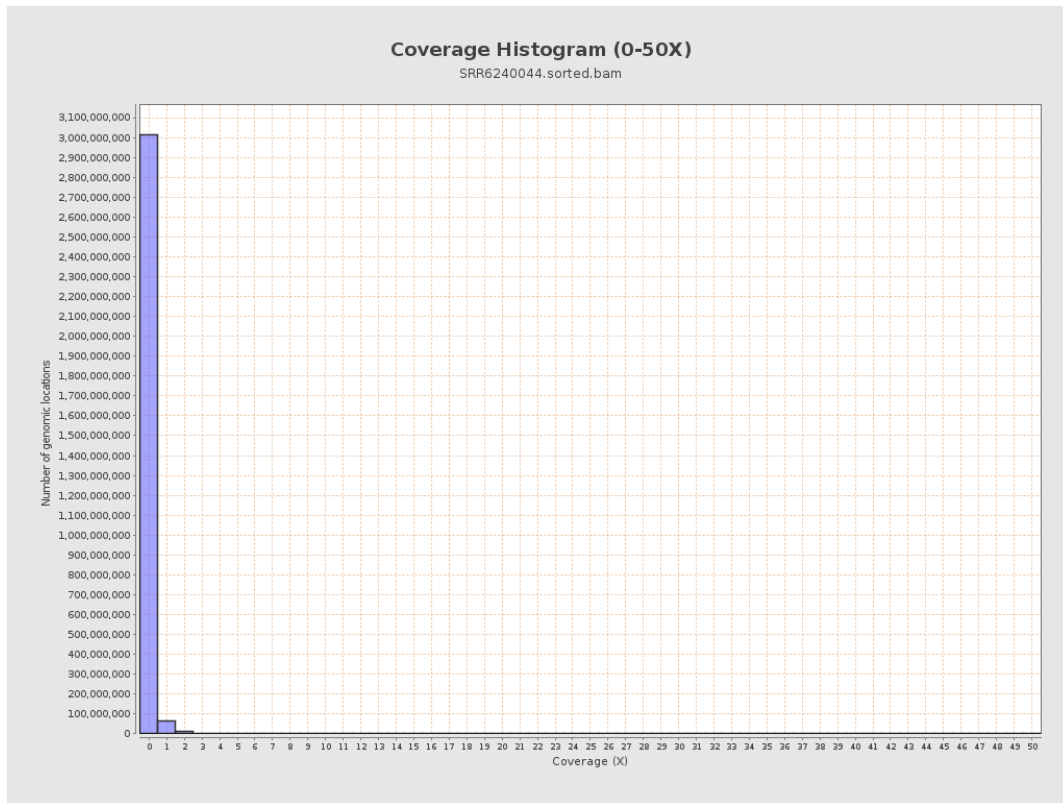
3. Results : Coverage across reference



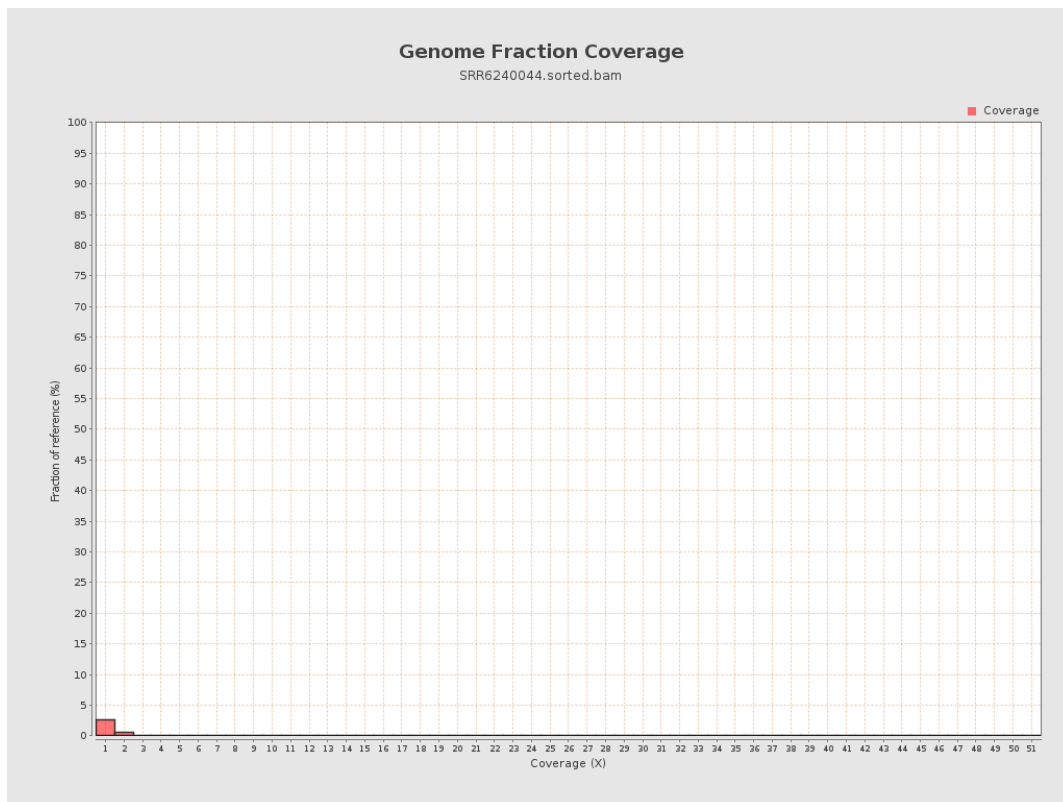
4. Results : Coverage Histogram



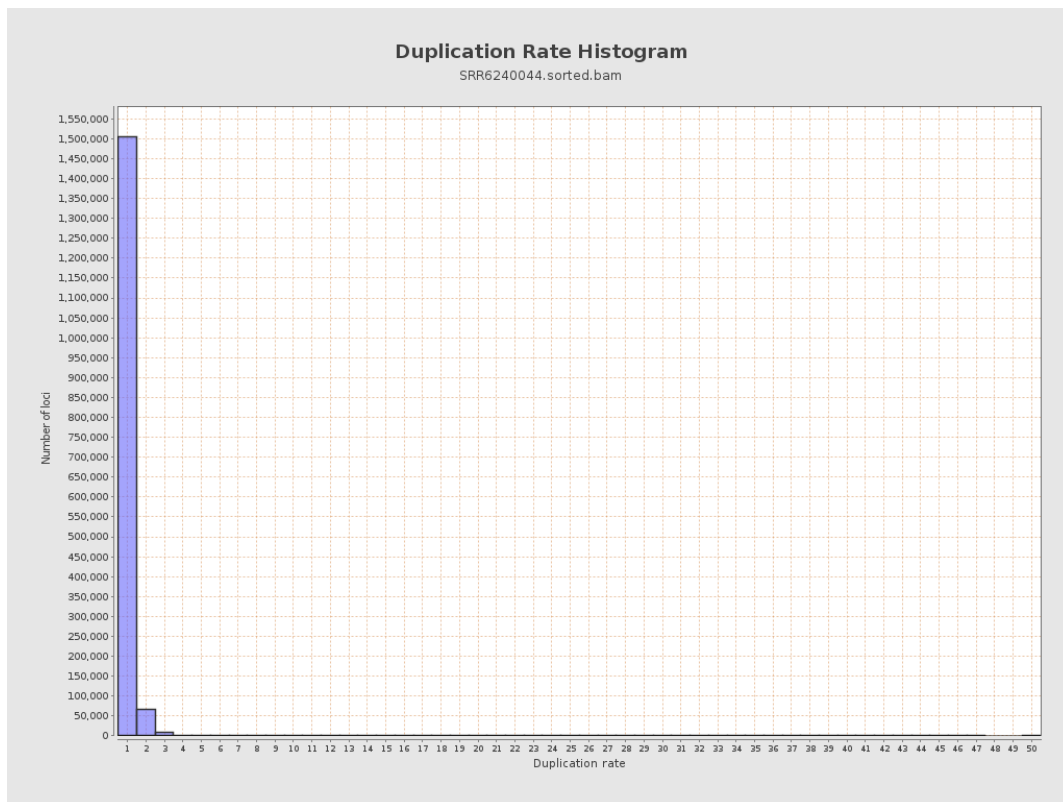
5. Results : Coverage Histogram (0-50X)



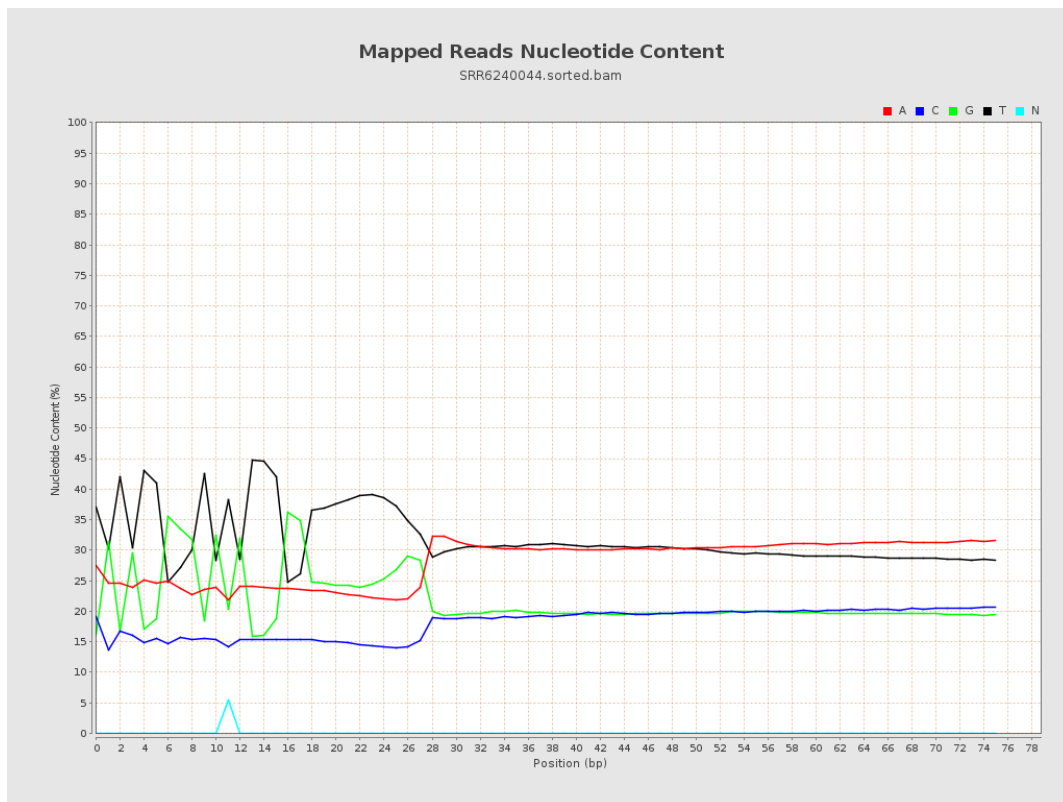
6. Results : Genome Fraction Coverage



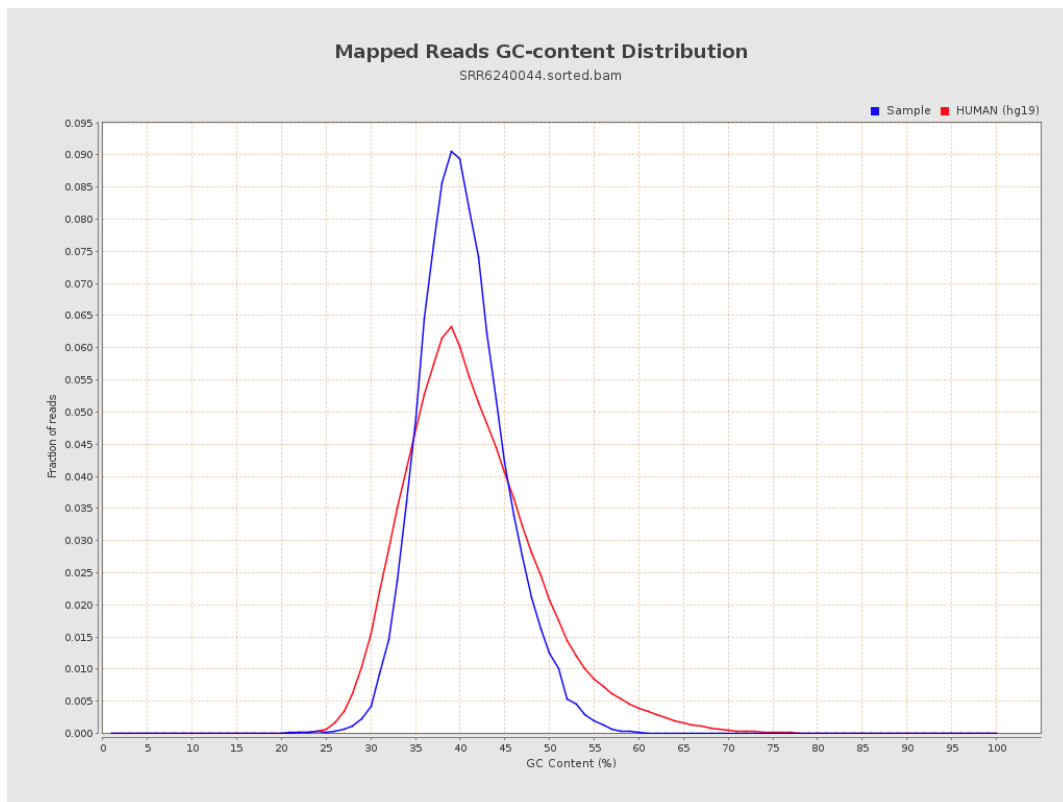
7. Results : Duplication Rate Histogram



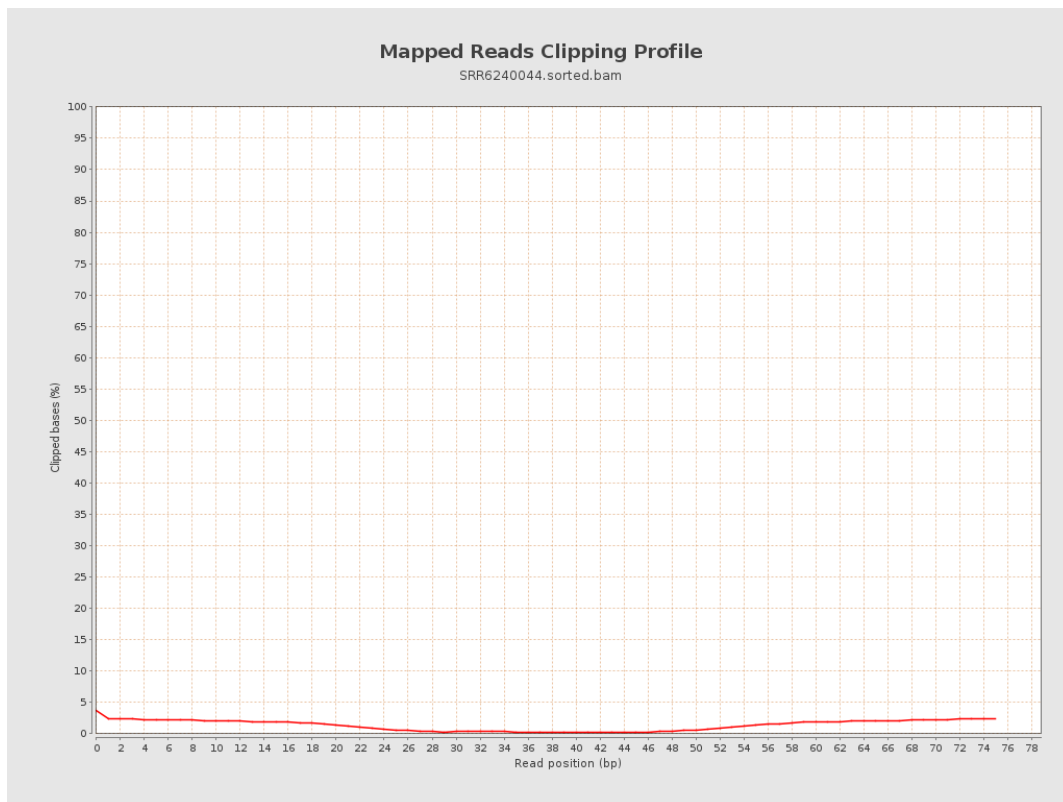
8. Results : Mapped Reads Nucleotide Content



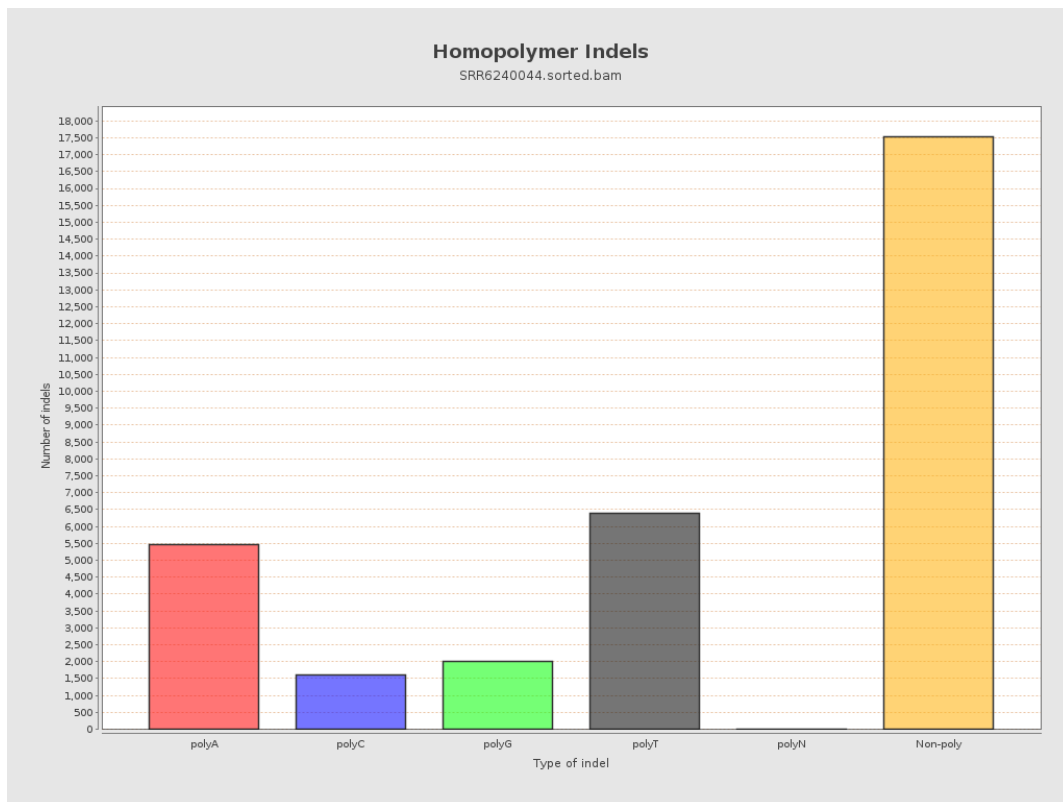
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

