

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:11:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234028.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_SRR6234028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:11:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,133,983
Mapped reads	191,955 / 16.93%
Unmapped reads	942,028 / 83.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,049 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	15,719 / 1.39%
Duplication rate	5.15%
Clipped reads	123,437 / 10.89%

2.2. ACGT Content

Number/percentage of A's	3,056,589 / 26.7%
Number/percentage of C's	1,944,748 / 16.99%
Number/percentage of T's	3,820,449 / 33.37%
Number/percentage of G's	2,626,799 / 22.94%
Number/percentage of N's	994 / 0.01%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0037

Standard Deviation	0.1831
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2.4. Mapping Quality

Mean Mapping Quality	39.17
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2.5. Mismatches and indels

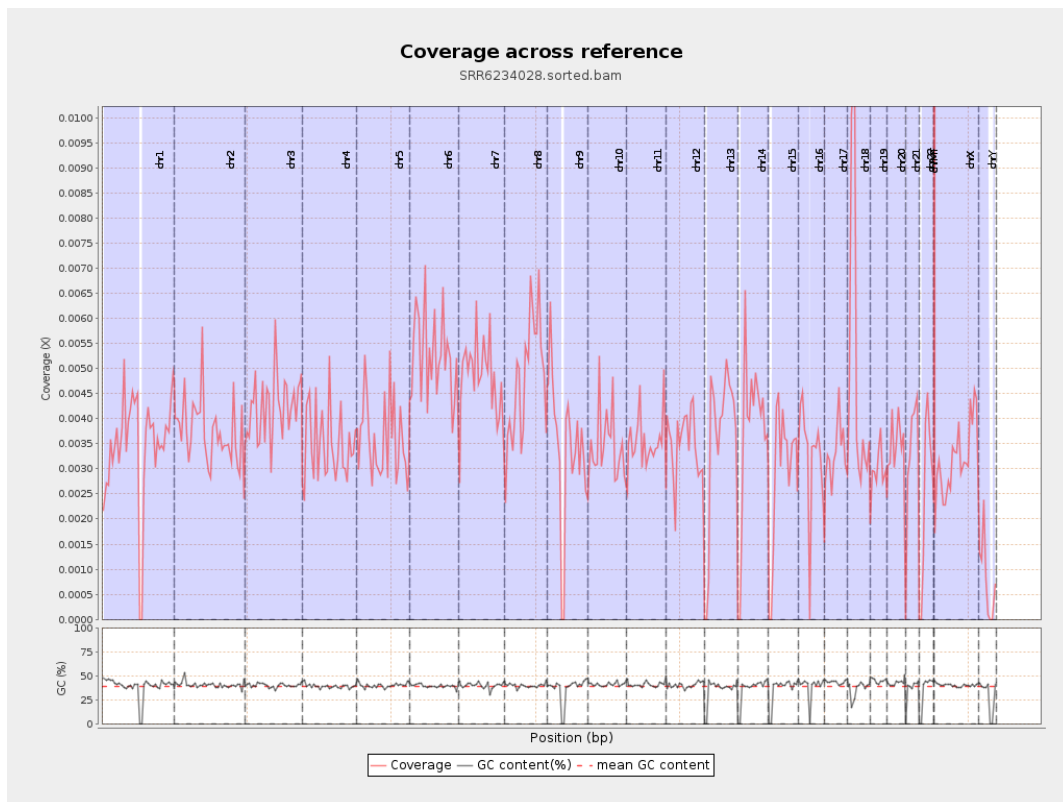
General error rate	1.01%
Mismatches	111,422
Insertions	1,781
Mapped reads with at least one insertion	0.91%
Deletions	3,498
Mapped reads with at least one deletion	1.79%
Homopolymer indels	37.3%

2.6. Chromosome stats

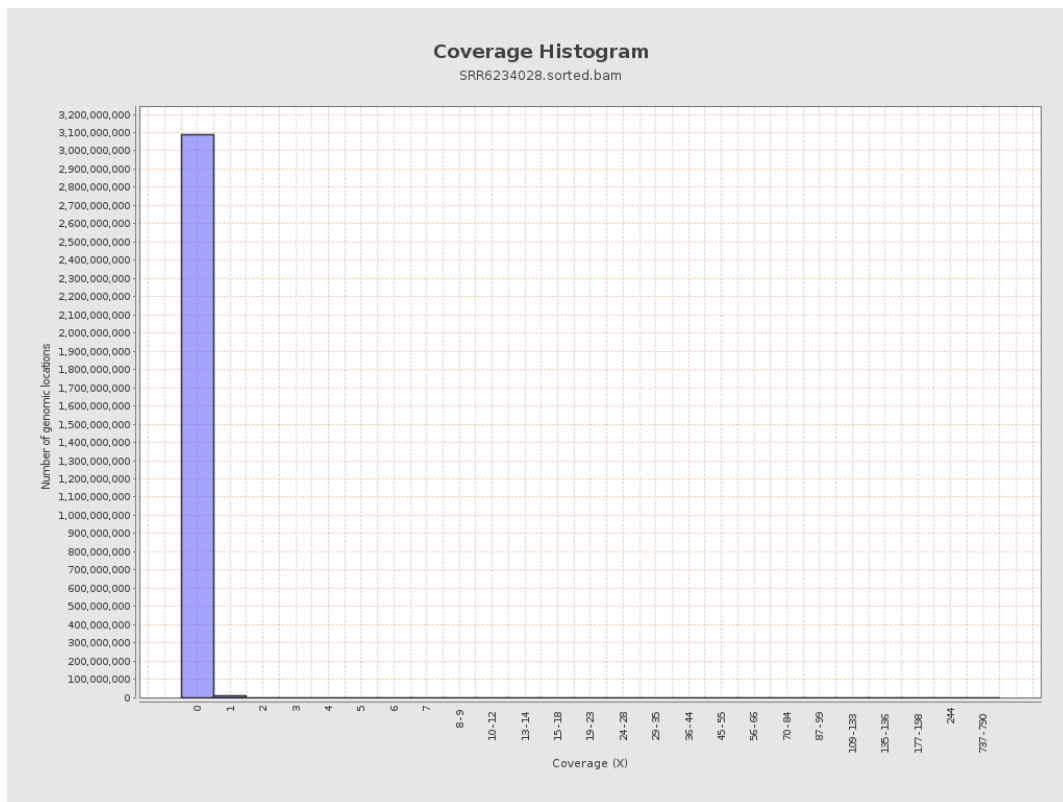
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	866272	0.0035	0.0853
chr2	243199373	905176	0.0037	0.1408
chr3	198022430	836351	0.0042	0.102
chr4	191154276	659250	0.0034	0.0865
chr5	180915260	648656	0.0036	0.0835
chr6	171115067	890505	0.0052	0.1095
chr7	159138663	769268	0.0048	0.1521

chr8	146364022	699689	0.0048	0.1054
chr9	141213431	484564	0.0034	0.0784
chr10	135534747	466451	0.0034	0.0801
chr11	135006516	482529	0.0036	0.0783
chr12	133851895	464395	0.0035	0.1202
chr13	115169878	410042	0.0036	0.0994
chr14	107349540	398231	0.0037	0.0839
chr15	102531392	301095	0.0029	0.0855
chr16	90354753	293415	0.0032	0.0899
chr17	81195210	267942	0.0033	0.0728
chr18	78077248	376898	0.0048	0.9764
chr19	59128983	177319	0.003	0.0764
chr20	63025520	217792	0.0035	0.0785
chr21	48129895	160527	0.0033	0.0722
chr22	51304566	130334	0.0025	0.0632
chrMT	16571	4825	0.2912	0.606
chrX	155270560	497306	0.0032	0.0788
chrY	59373566	46969	0.0008	0.0502

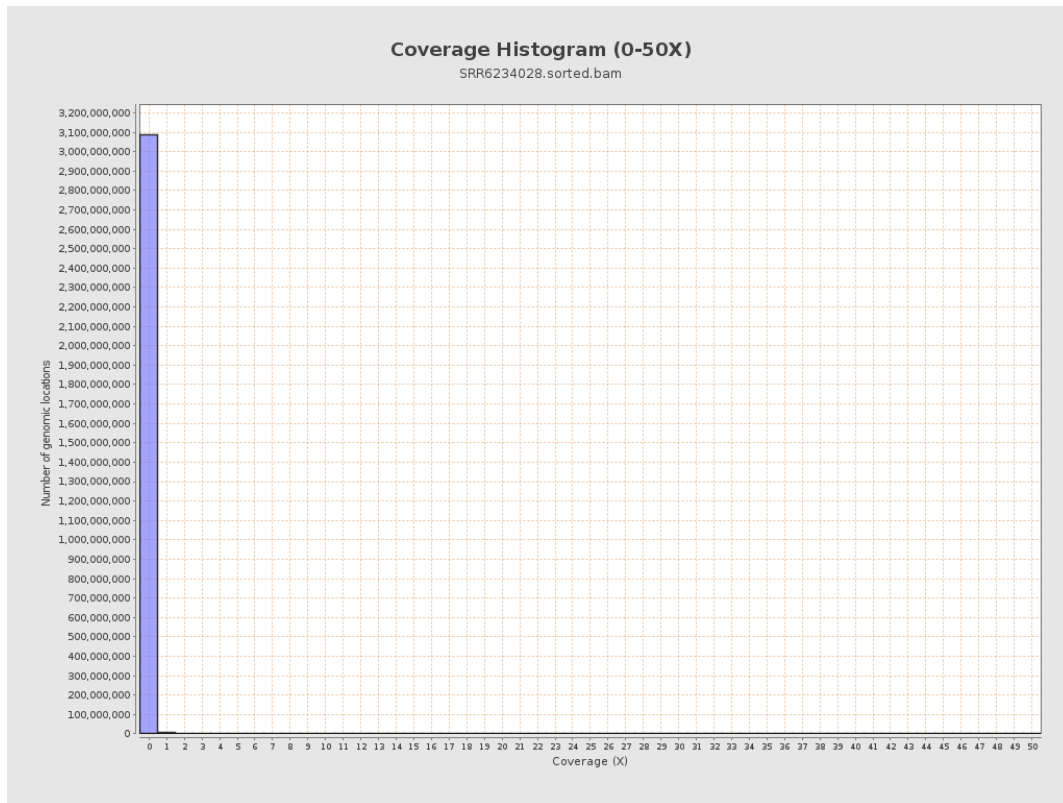
3. Results : Coverage across reference



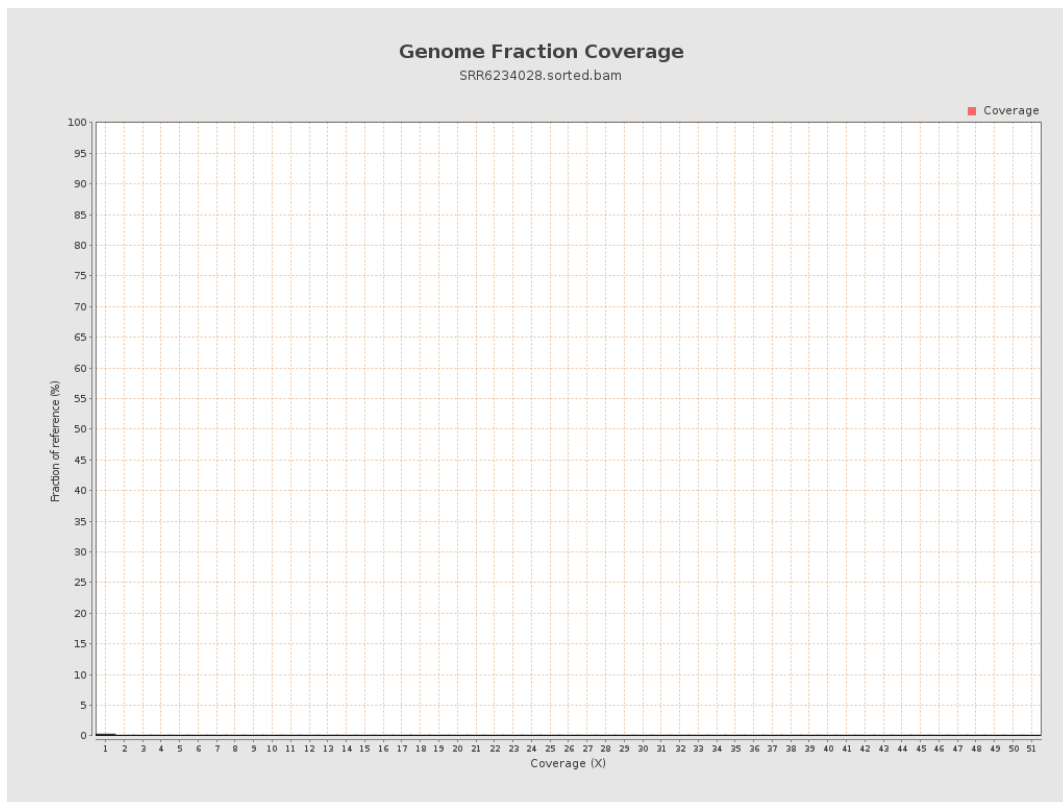
4. Results : Coverage Histogram



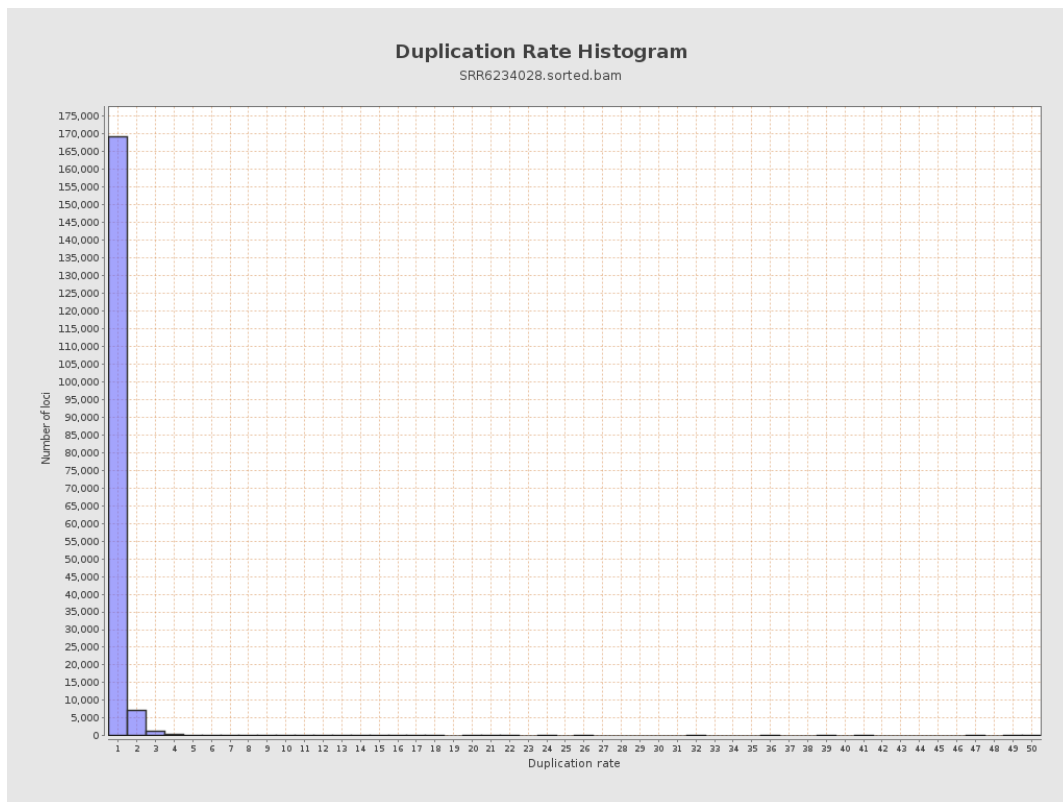
5. Results : Coverage Histogram (0-50X)



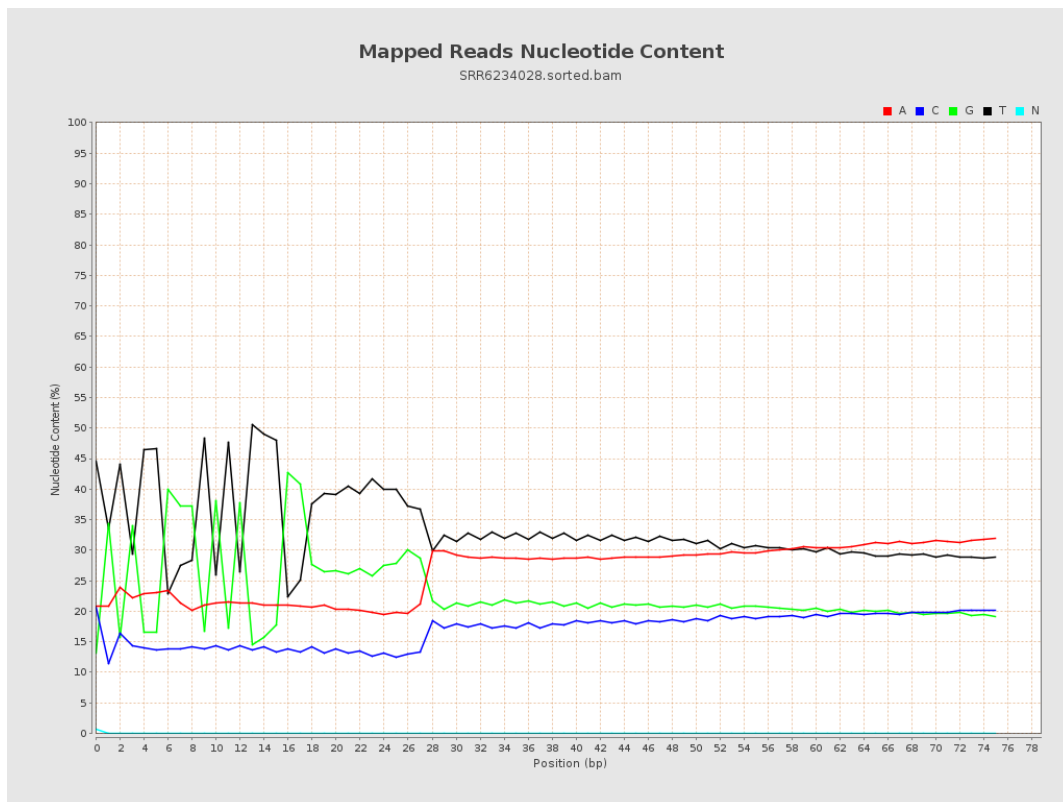
6. Results : Genome Fraction Coverage



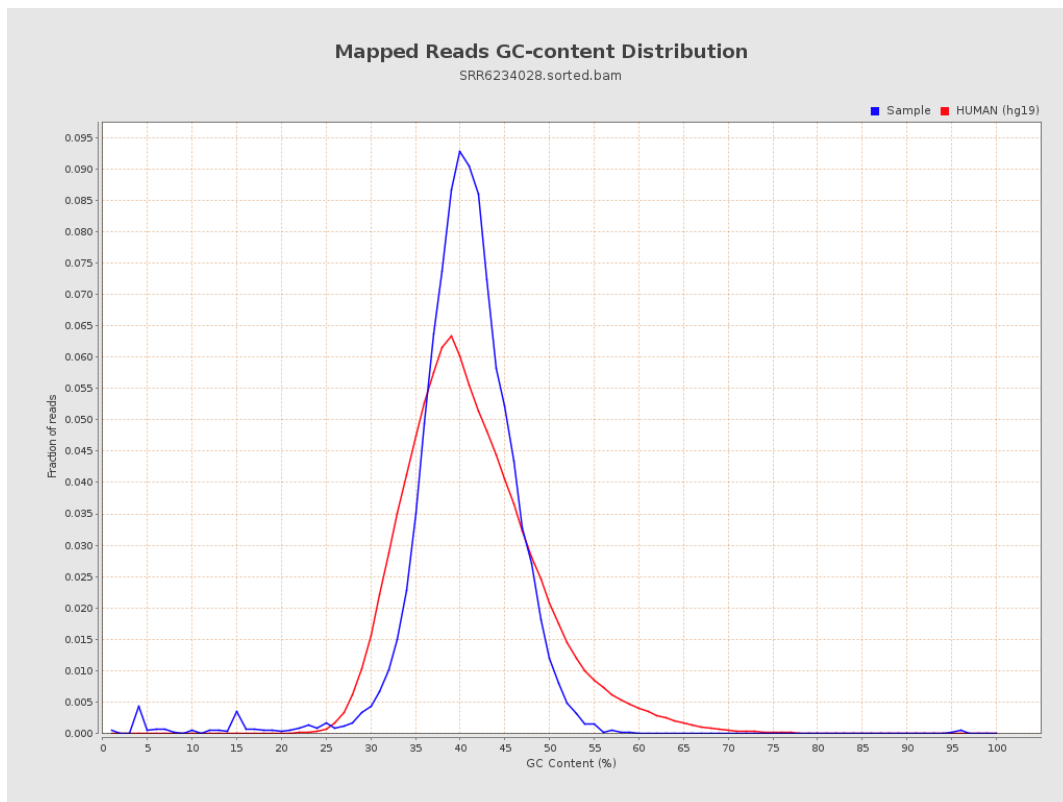
7. Results : Duplication Rate Histogram



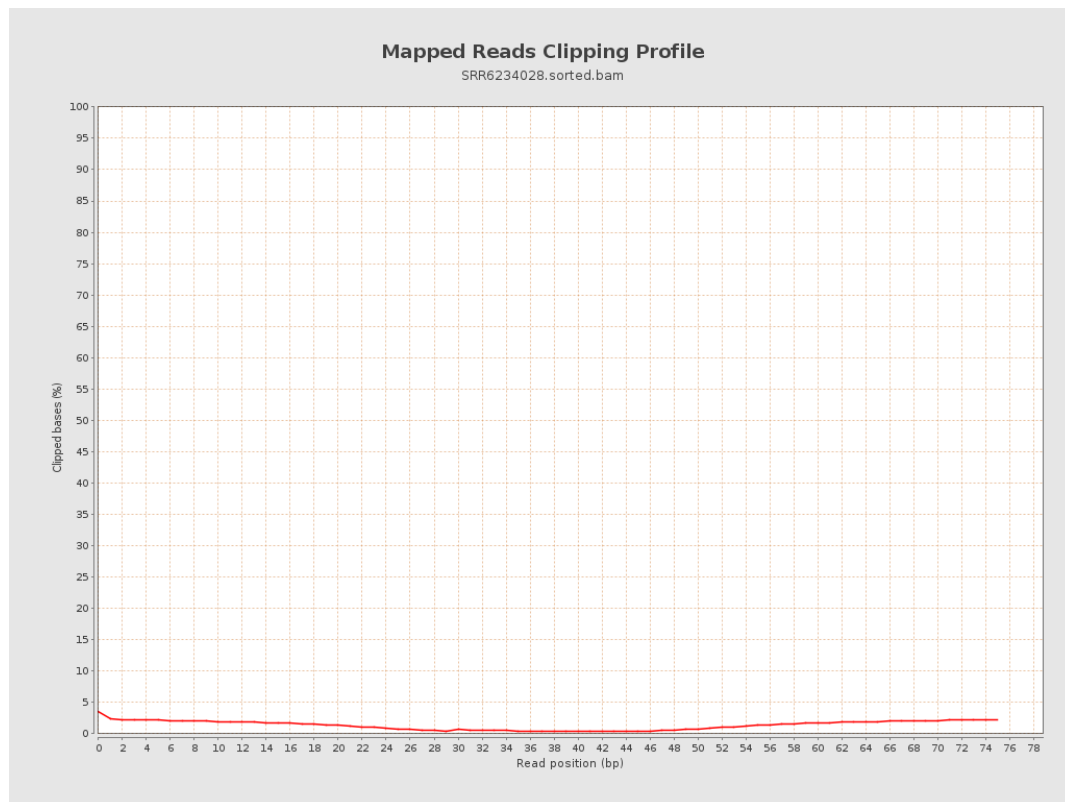
8. Results : Mapped Reads Nucleotide Content



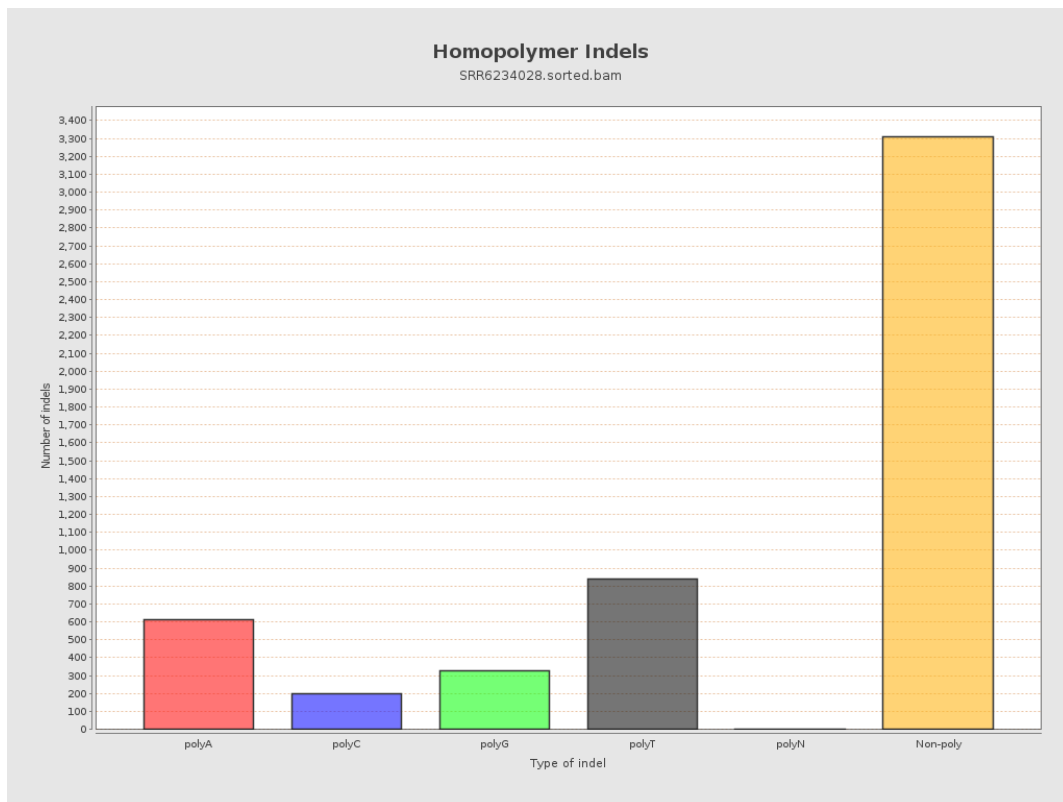
9. Results : Mapped Reads GC-content Distribution



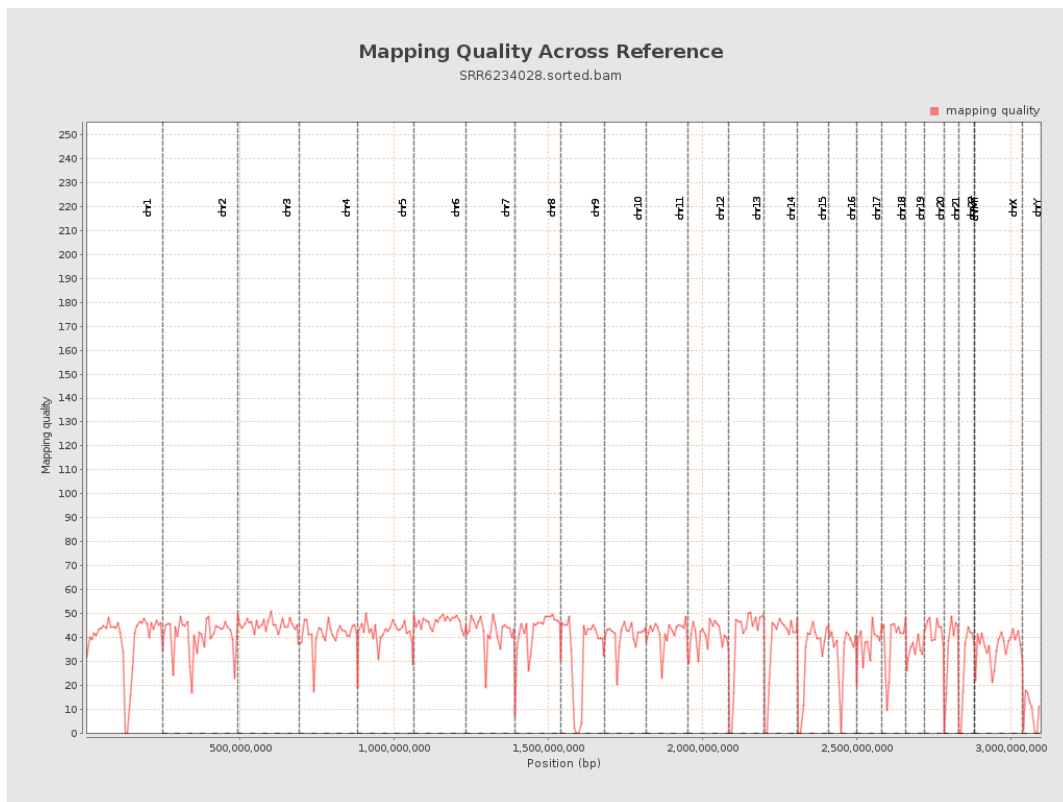
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

