

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:16:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230340.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_SRR6230340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:16:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,191,067
Mapped reads	2,701,795 / 84.67%
Unmapped reads	489,272 / 15.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,261 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	115,813 / 3.63%
Duplication rate	2.98%
Clipped reads	1,372,253 / 43%

2.2. ACGT Content

Number/percentage of A's	47,737,036 / 27.06%
Number/percentage of C's	30,503,555 / 17.29%
Number/percentage of T's	58,020,792 / 32.89%
Number/percentage of G's	39,822,010 / 22.57%
Number/percentage of N's	335,947 / 0.19%
GC Percentage	39.86%

2.3. Coverage

Mean	0.057

Standard Deviation	0.5745
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2.4. Mapping Quality

Mean Mapping Quality	46
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2.5. Mismatches and indels

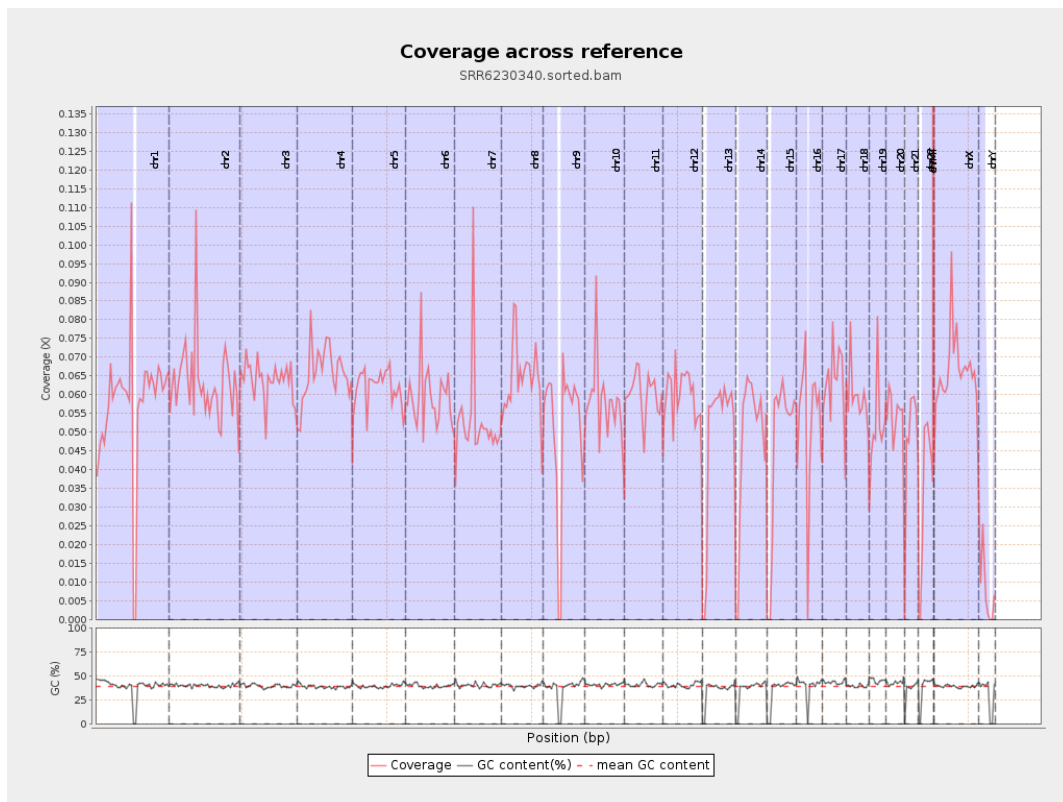
General error rate	0.95%
Mismatches	1,654,616
Insertions	15,980
Mapped reads with at least one insertion	0.59%
Deletions	51,337
Mapped reads with at least one deletion	1.88%
Homopolymer indels	48.28%

2.6. Chromosome stats

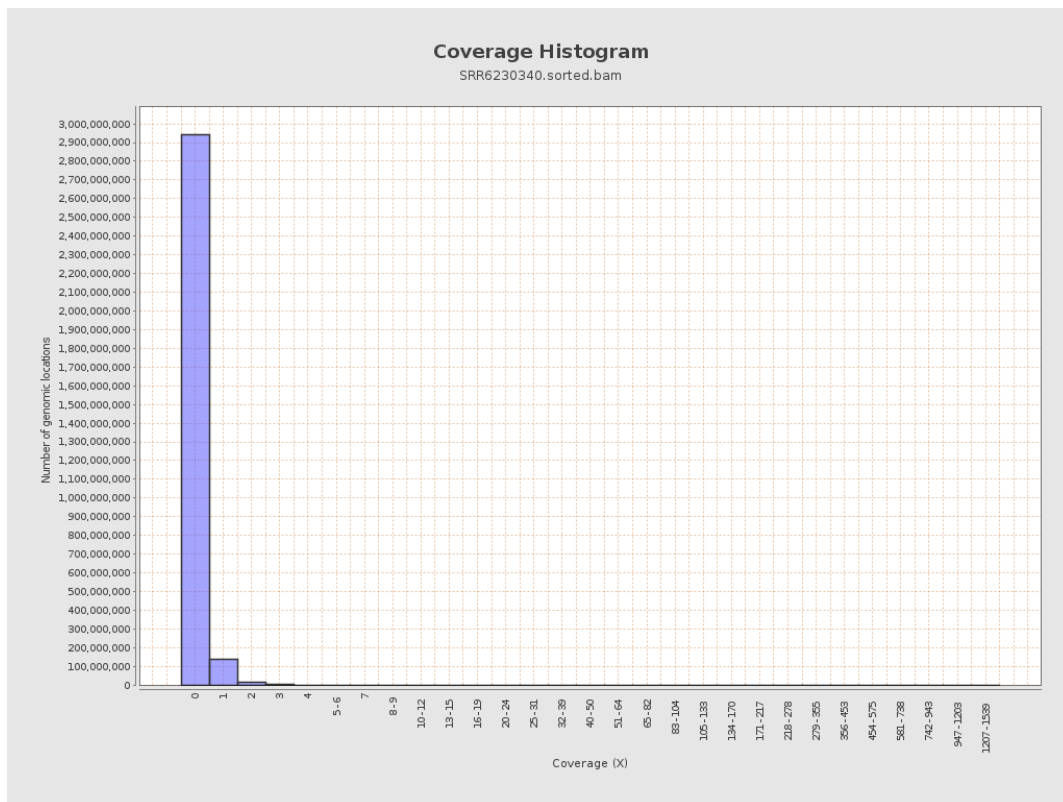
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14348747	0.0576	1.1801
chr2	243199373	15312026	0.063	0.547
chr3	198022430	12641278	0.0638	0.2801
chr4	191154276	12555638	0.0657	0.3192
chr5	180915260	11217044	0.062	0.2806
chr6	171115067	10111171	0.0591	0.3864
chr7	159138663	8412735	0.0529	0.7649

chr8	146364022	9388018	0.0641	0.9832
chr9	141213431	7211194	0.0511	0.5089
chr10	135534747	7866349	0.058	0.4377
chr11	135006516	8056698	0.0597	0.5377
chr12	133851895	7995911	0.0597	0.2817
chr13	115169878	5570937	0.0484	0.2427
chr14	107349540	5146636	0.0479	0.2723
chr15	102531392	4807421	0.0469	0.2427
chr16	90354753	4788228	0.053	0.3141
chr17	81195210	5087598	0.0627	0.3379
chr18	78077248	4657659	0.0597	1.0096
chr19	59128983	3095861	0.0524	0.6944
chr20	63025520	3404771	0.054	0.2816
chr21	48129895	2300597	0.0478	0.2798
chr22	51304566	1728671	0.0337	0.2017
chrMT	16571	86488	5.2192	3.8981
chrX	155270560	10238822	0.0659	0.3515
chrY	59373566	473425	0.008	0.1856

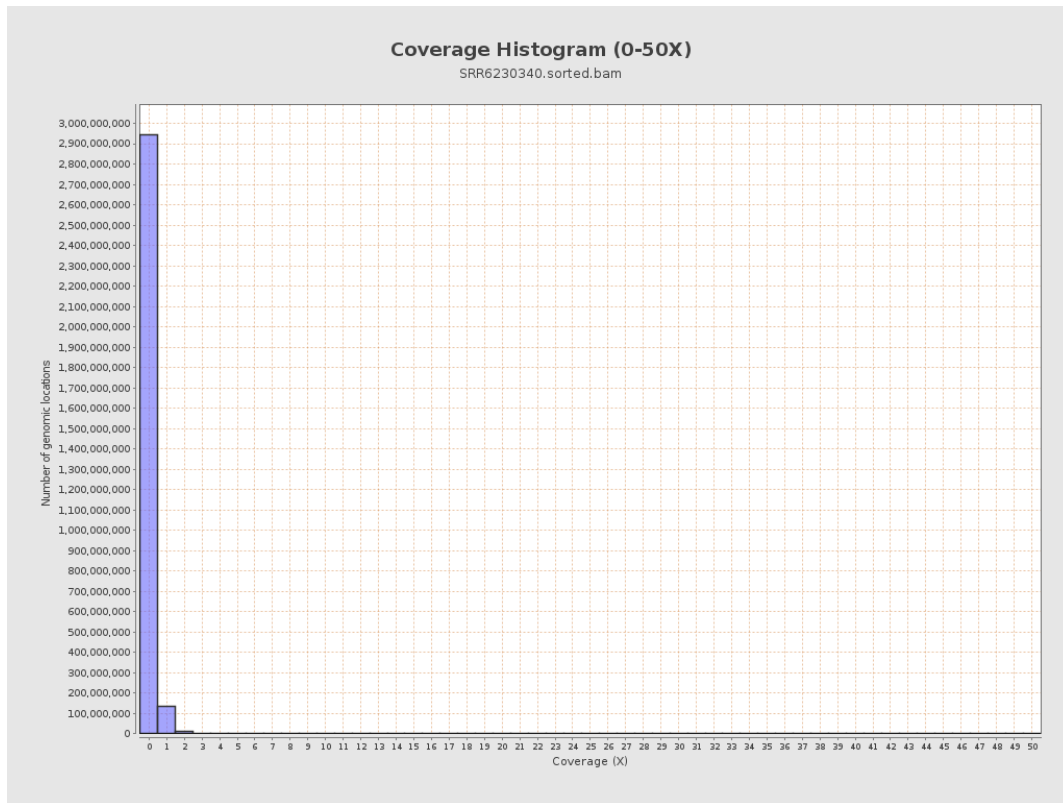
3. Results : Coverage across reference



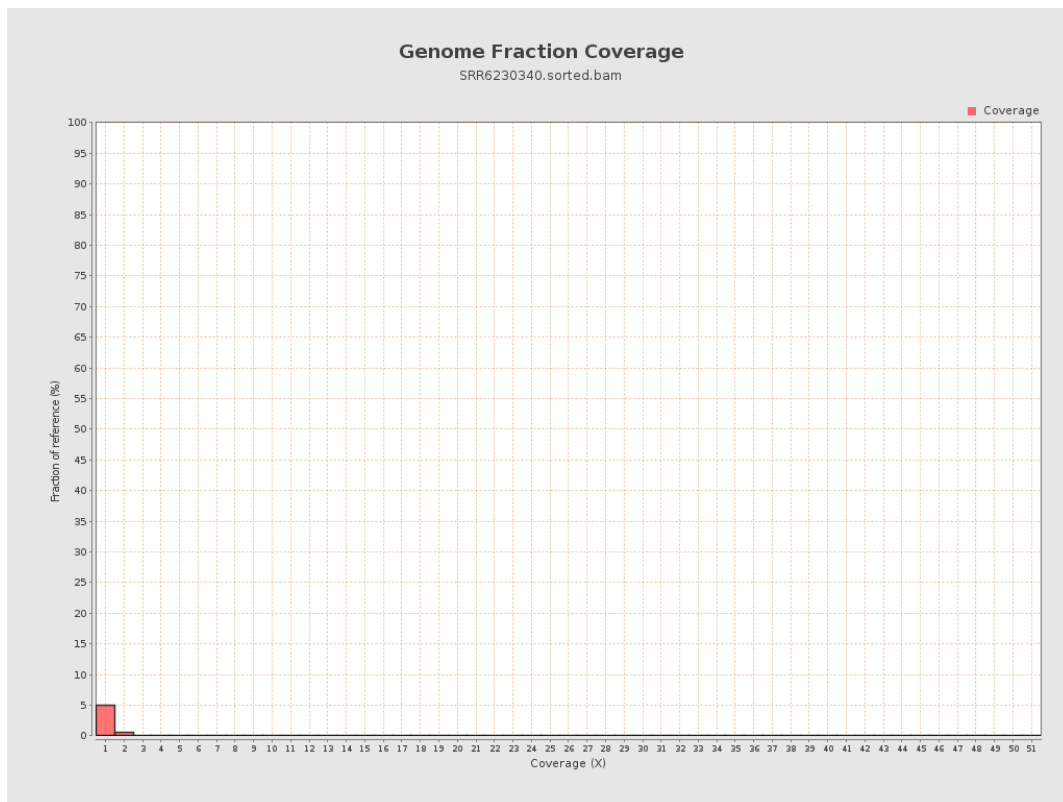
4. Results : Coverage Histogram



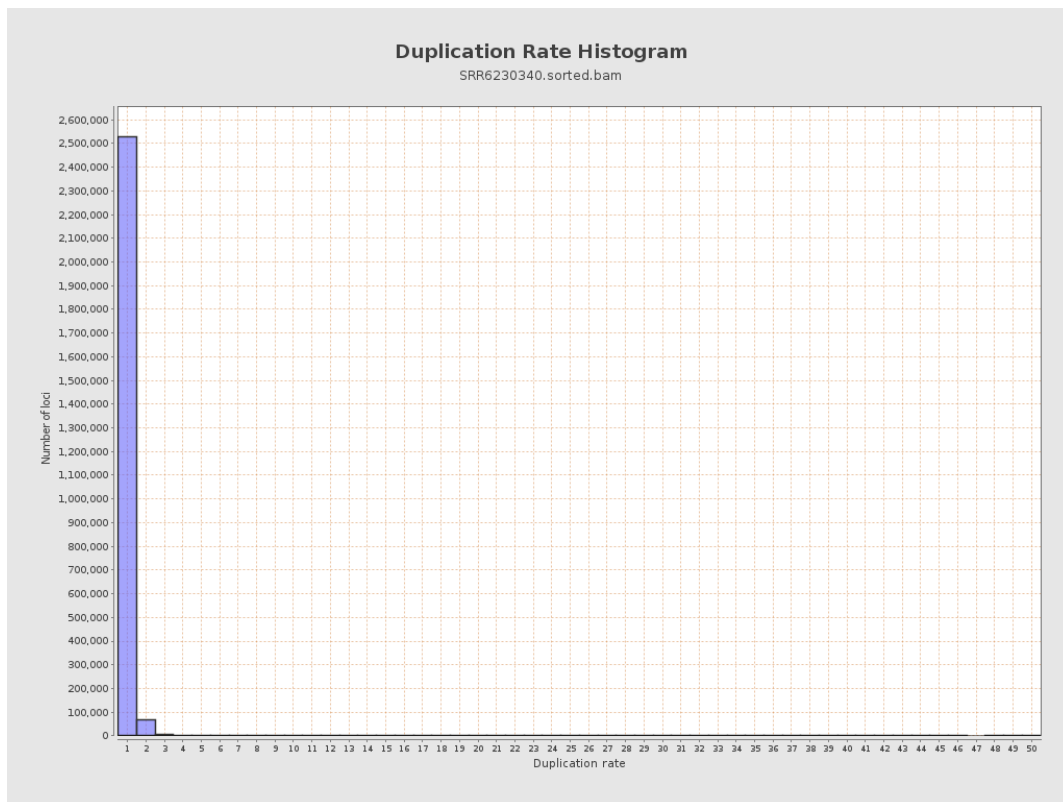
5. Results : Coverage Histogram (0-50X)



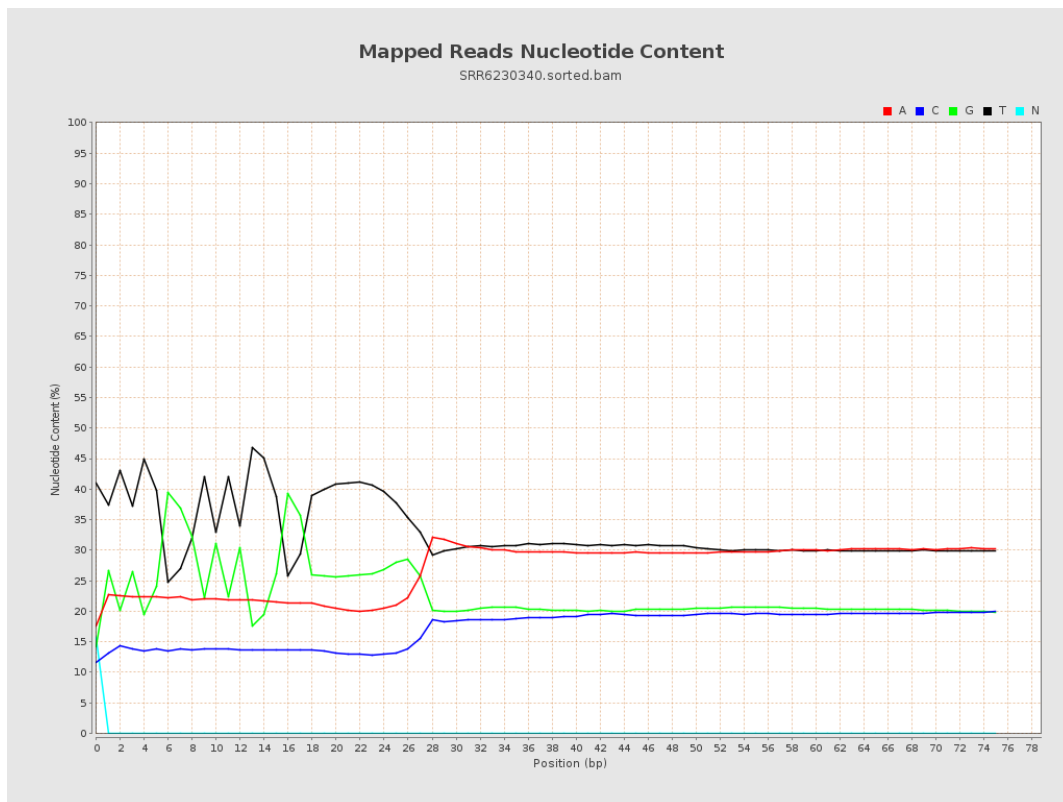
6. Results : Genome Fraction Coverage



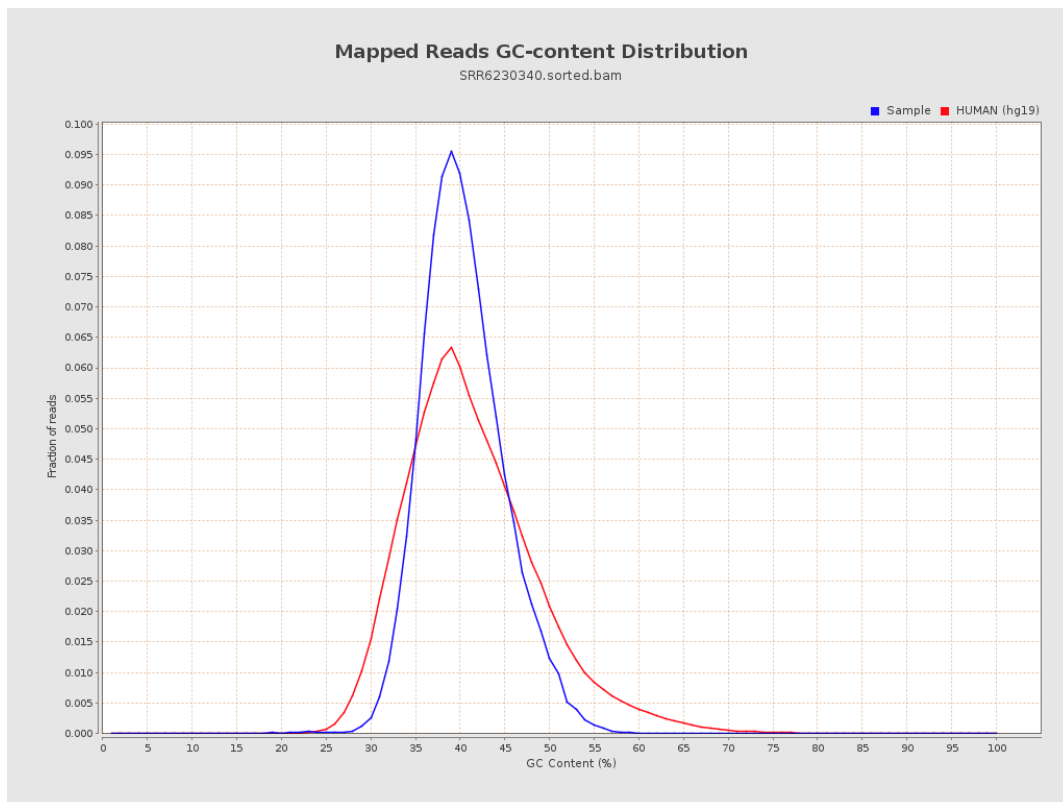
7. Results : Duplication Rate Histogram



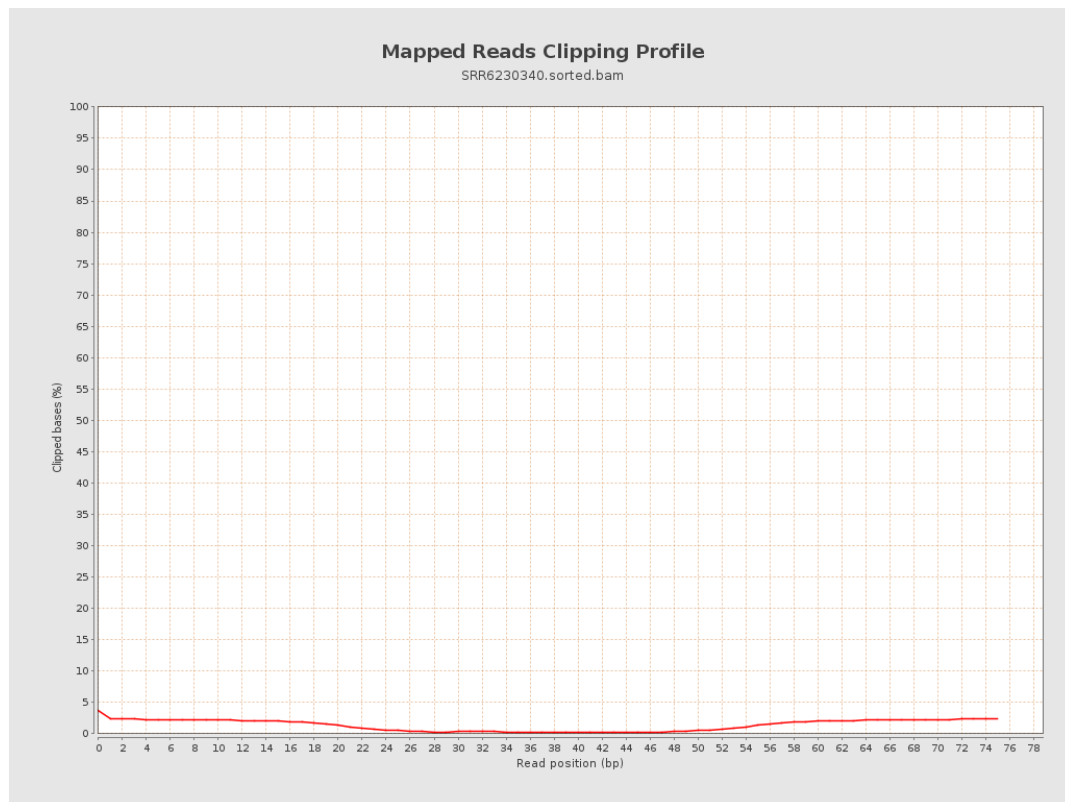
8. Results : Mapped Reads Nucleotide Content



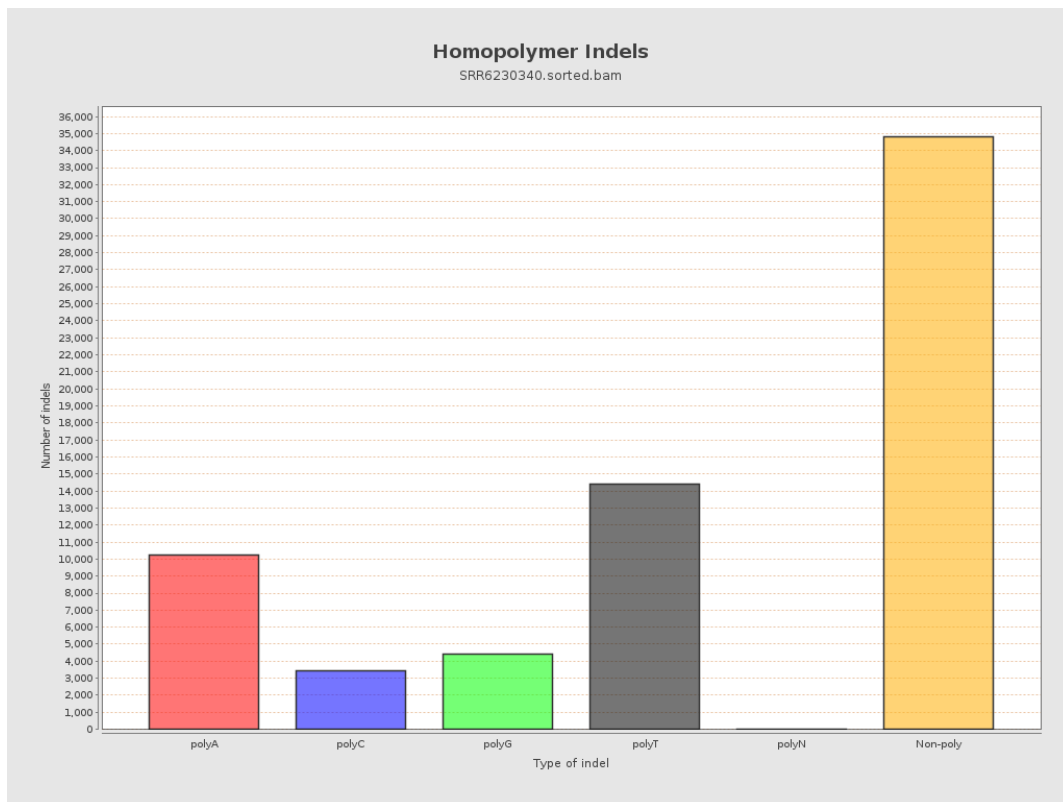
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

