

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230333.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_SRR6230333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:51:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,777,792
Mapped reads	2,294,844 / 82.61%
Unmapped reads	482,948 / 17.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,331 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	95,823 / 3.45%
Duplication rate	3.09%
Clipped reads	1,116,321 / 40.19%

2.2. ACGT Content

Number/percentage of A's	41,161,712 / 27.36%
Number/percentage of C's	26,003,451 / 17.29%
Number/percentage of T's	49,536,133 / 32.93%
Number/percentage of G's	33,442,164 / 22.23%
Number/percentage of N's	284,808 / 0.19%
GC Percentage	39.52%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.4945
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.48
----------------------	-------

2.5. Mismatches and indels

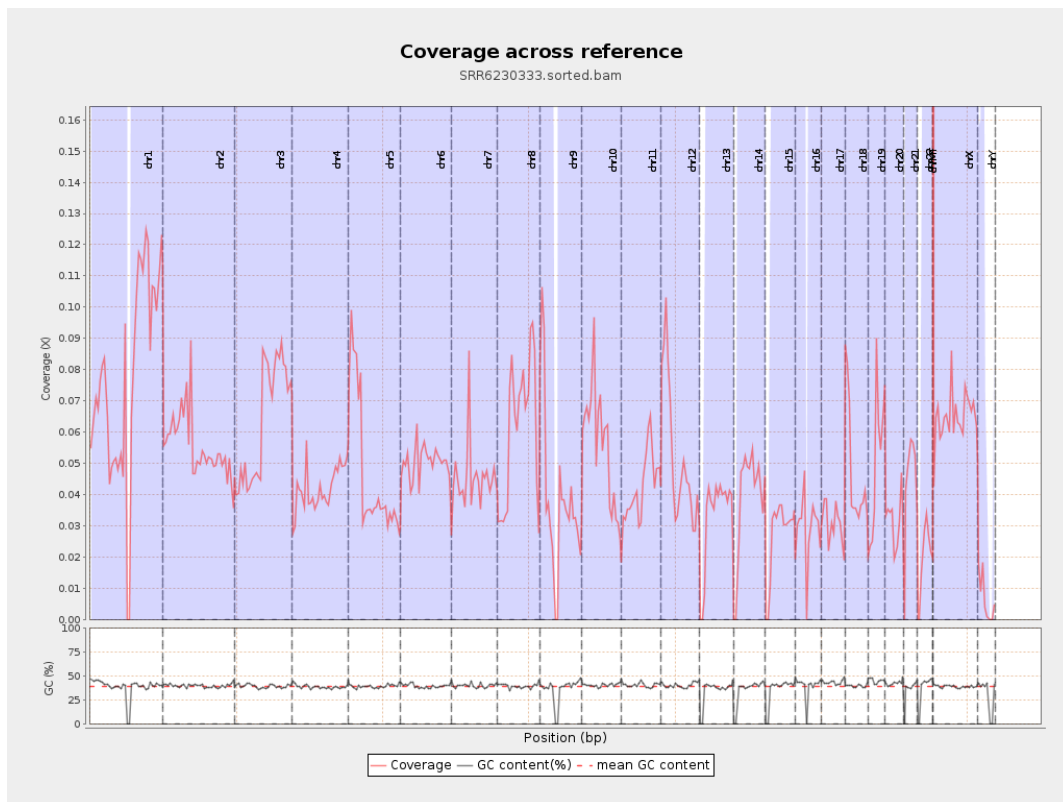
General error rate	0.93%
Mismatches	1,378,190
Insertions	13,179
Mapped reads with at least one insertion	0.57%
Deletions	42,297
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.85%

2.6. Chromosome stats

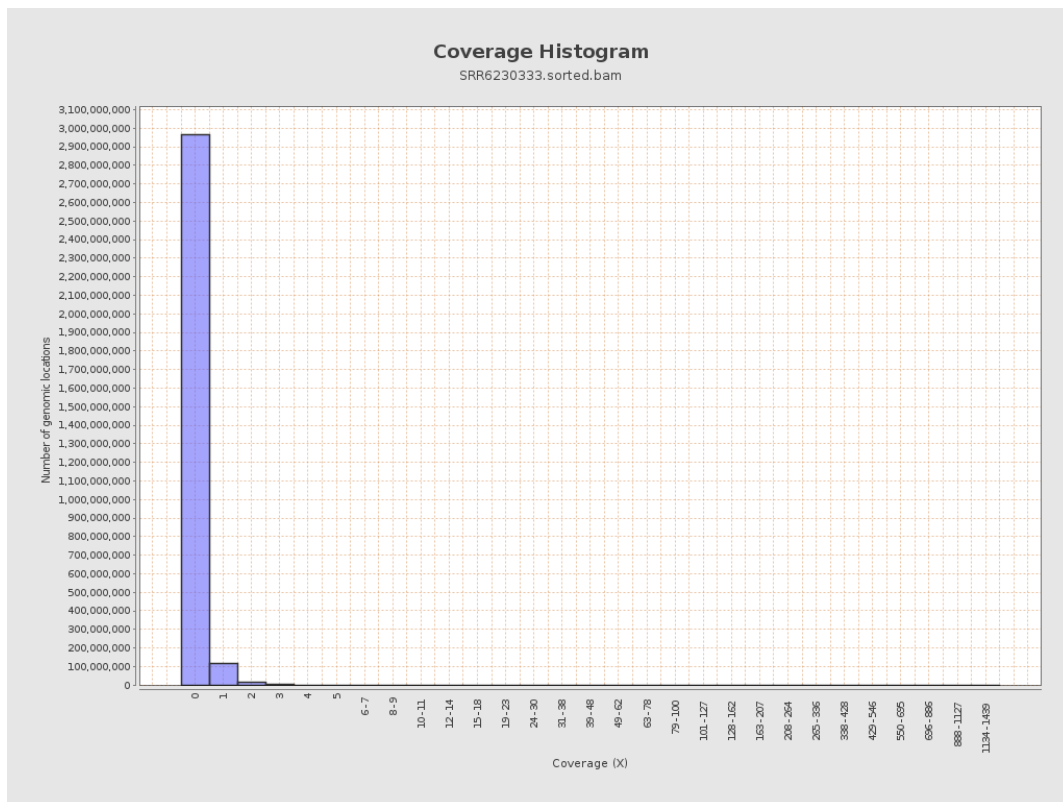
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19406021	0.0779	1.124
chr2	243199373	13523180	0.0556	0.4225
chr3	198022430	12498824	0.0631	0.2843
chr4	191154276	8037618	0.042	0.2471
chr5	180915260	8407232	0.0465	0.2426
chr6	171115067	8624152	0.0504	0.3061
chr7	159138663	7204186	0.0453	0.614

chr8	146364022	8949130	0.0611	0.8647
chr9	141213431	5328537	0.0377	0.3475
chr10	135534747	7506330	0.0554	0.4397
chr11	135006516	5736848	0.0425	0.3262
chr12	133851895	6934308	0.0518	0.259
chr13	115169878	3806531	0.0331	0.2004
chr14	107349540	4204953	0.0392	0.2361
chr15	102531392	2721728	0.0265	0.179
chr16	90354753	2591766	0.0287	0.2273
chr17	81195210	2520854	0.031	0.2196
chr18	78077248	3632839	0.0465	0.6941
chr19	59128983	2996587	0.0507	0.579
chr20	63025520	2048751	0.0325	0.221
chr21	48129895	2158626	0.0449	0.2577
chr22	51304566	1017032	0.0198	0.167
chrMT	16571	180064	10.8662	5.9262
chrX	155270560	10086622	0.065	0.3231
chrY	59373566	375624	0.0063	0.1408

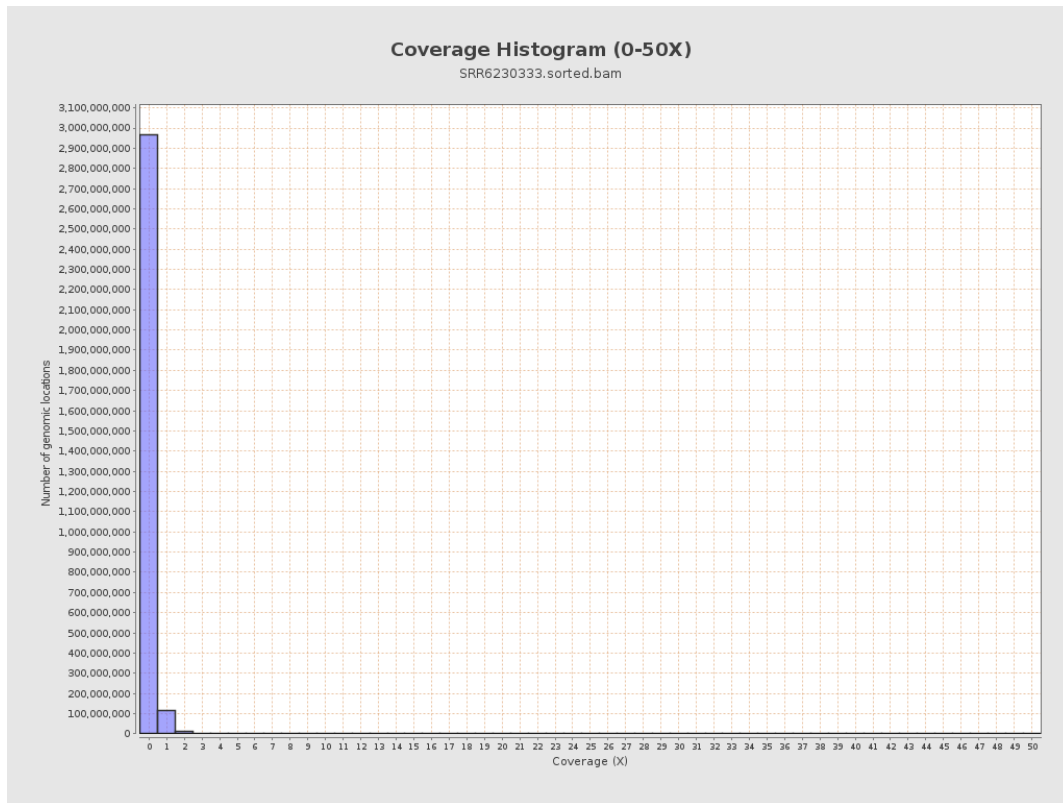
3. Results : Coverage across reference



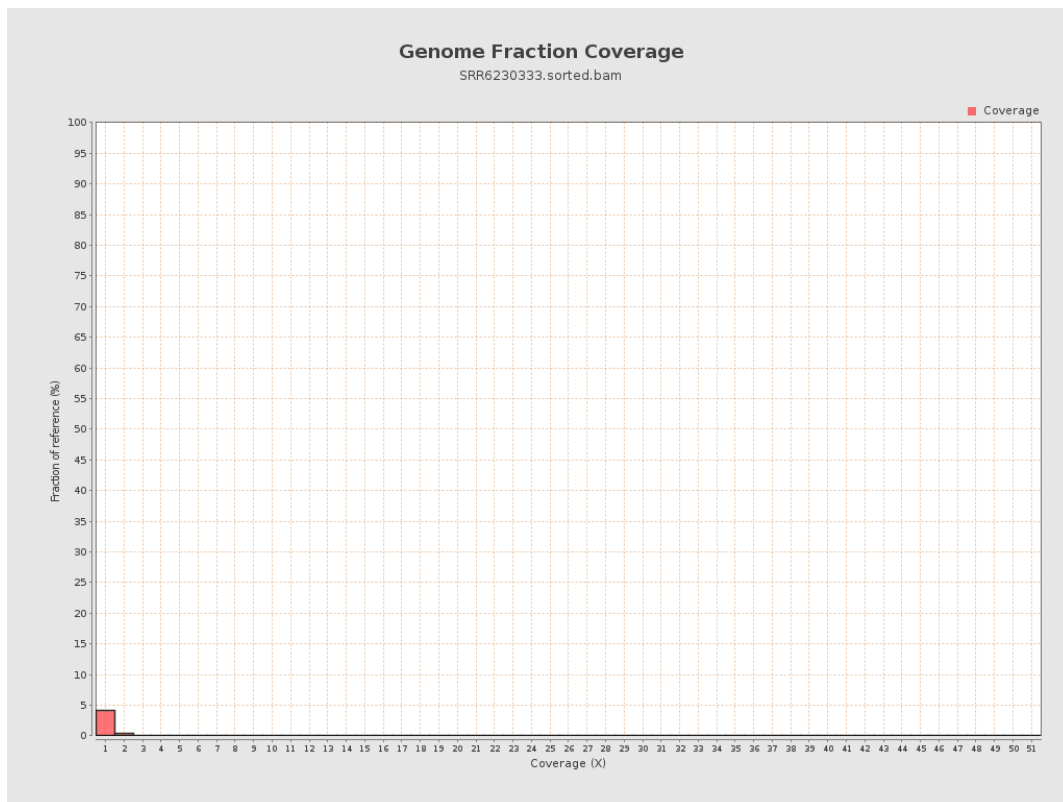
4. Results : Coverage Histogram



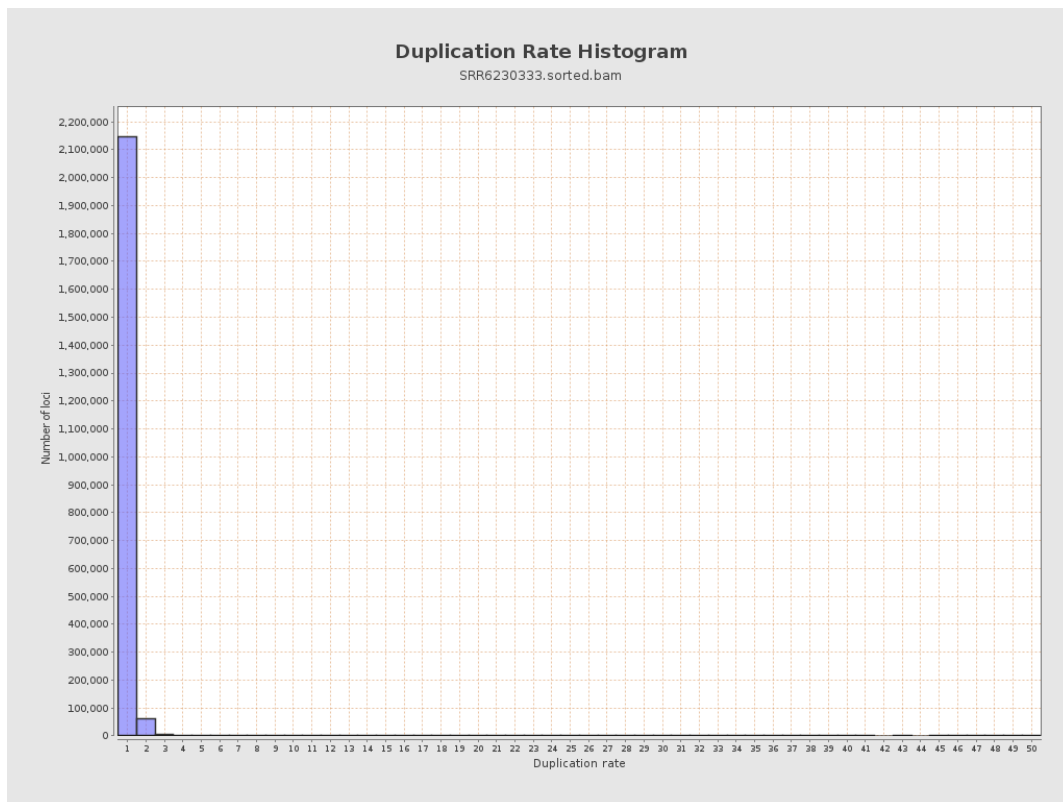
5. Results : Coverage Histogram (0-50X)



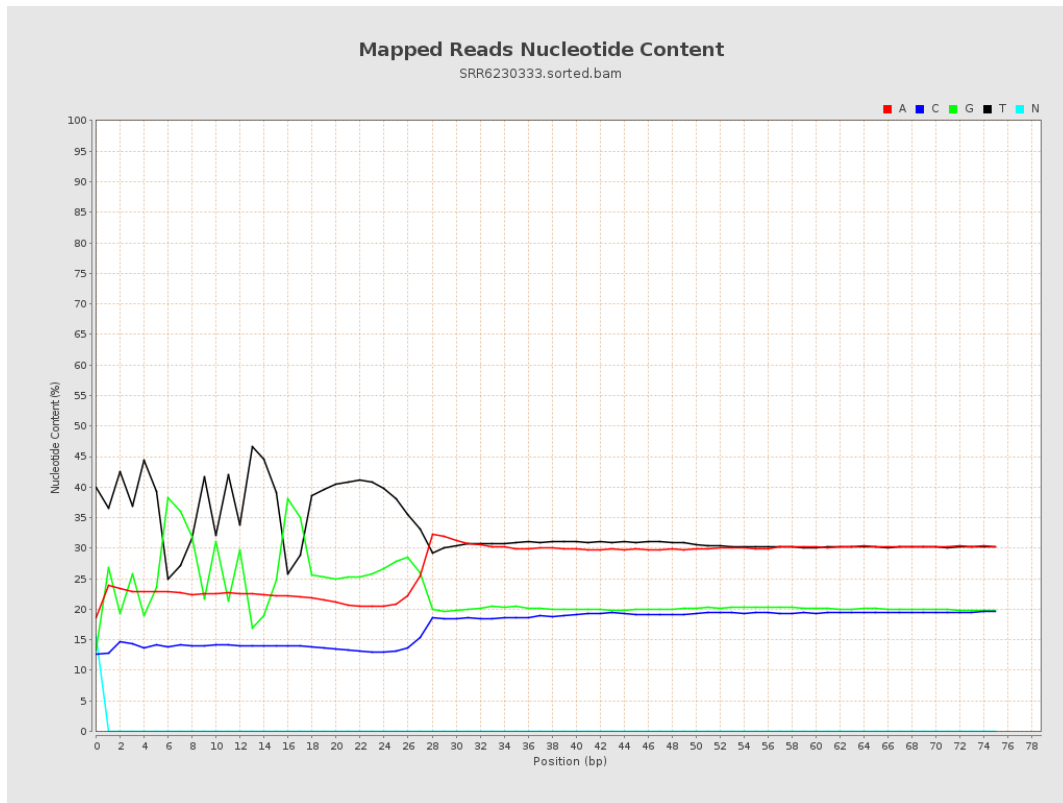
6. Results : Genome Fraction Coverage



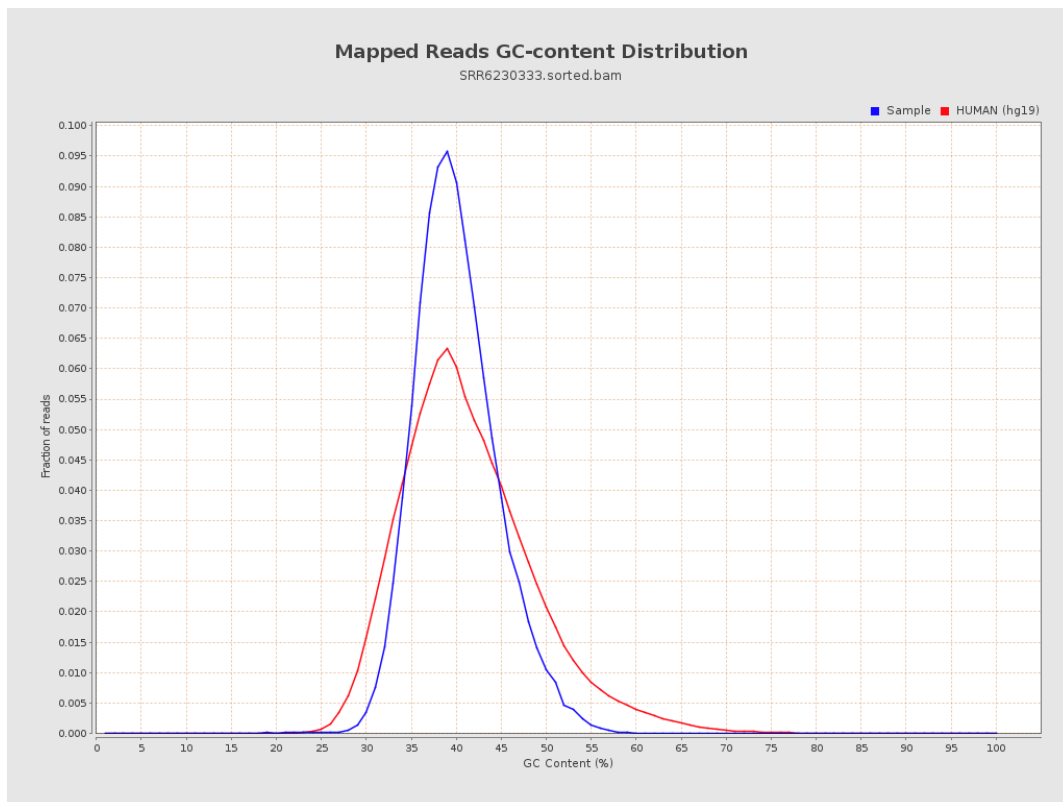
7. Results : Duplication Rate Histogram



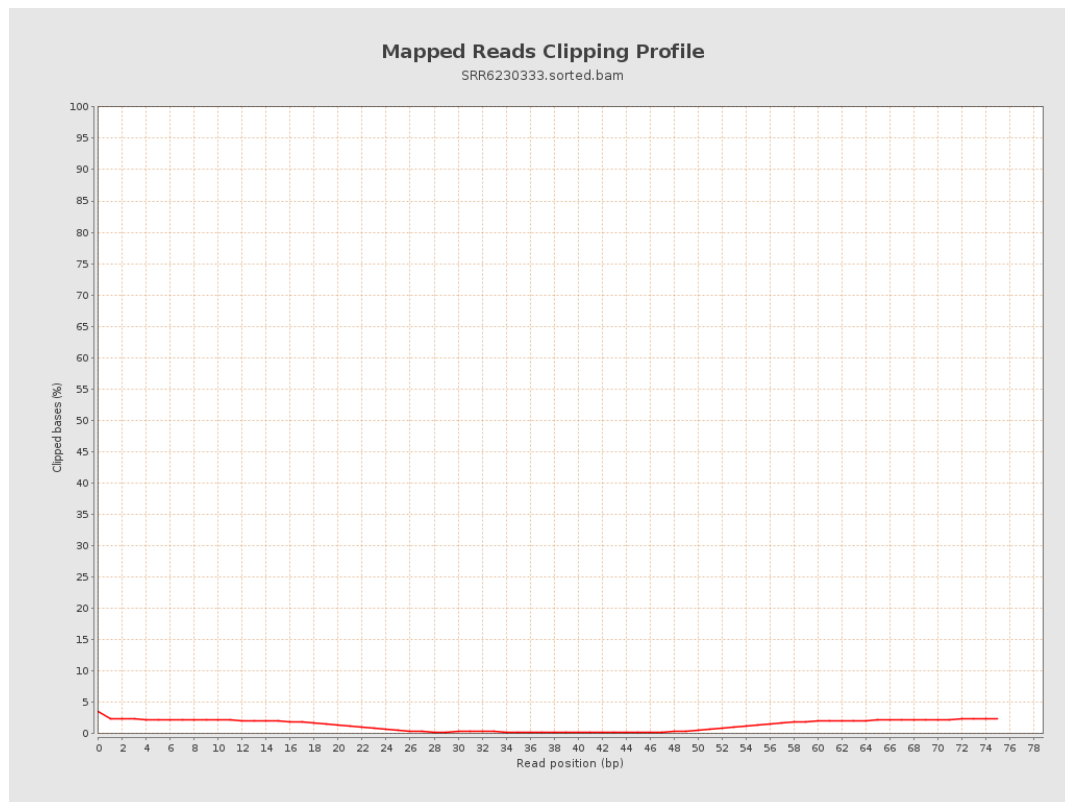
8. Results : Mapped Reads Nucleotide Content



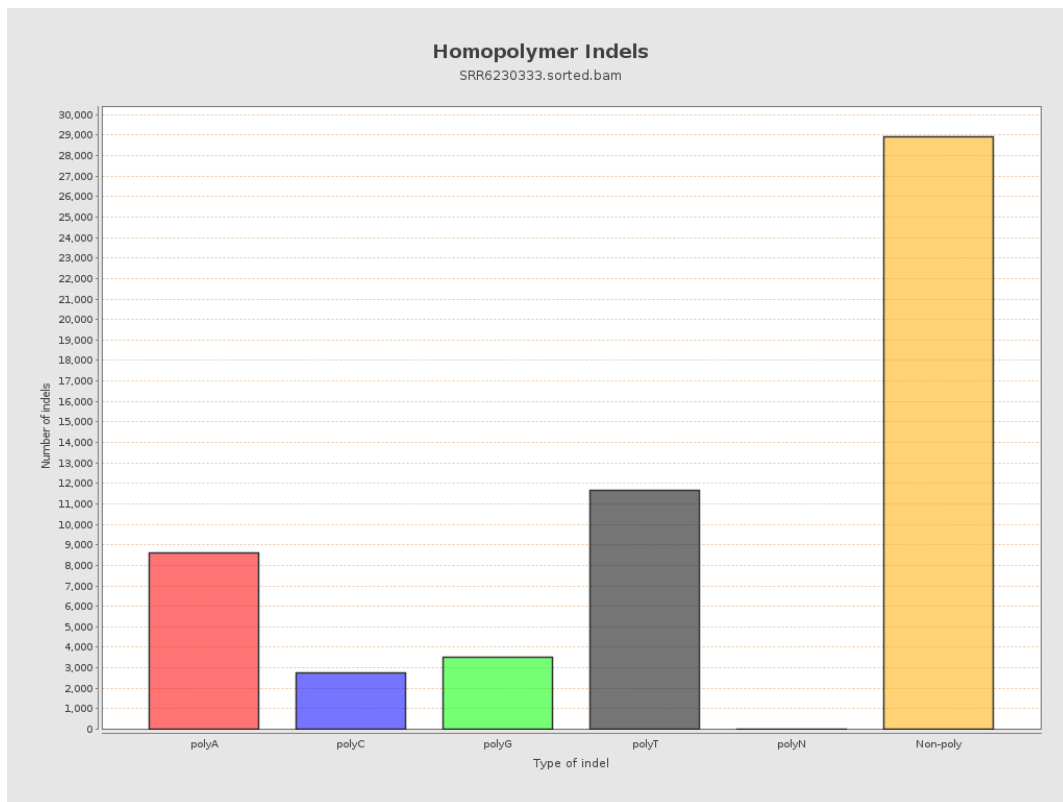
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

