

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:25:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695980.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695980 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:25:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,349,065
Mapped reads	14,008,186 / 91.26%
Unmapped reads	1,340,879 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	217,713 / 1.42%
Read min/max/mean length	8 / 361 / 128.74
Duplicated reads (estimated)	3,130,253 / 20.39%
Duplication rate	18.31%
Clipped reads	3,576,569 / 23.3%

2.2. ACGT Content

Number/percentage of A's	520,484,820 / 27.89%
Number/percentage of C's	409,613,077 / 21.95%
Number/percentage of T's	515,449,302 / 27.63%
Number/percentage of G's	420,329,314 / 22.53%
Number/percentage of N's	0 / 0%
GC Percentage	44.48%

2.3. Coverage

Mean	0.6073

Standard Deviation	1.5157
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2.4. Mapping Quality

Mean Mapping Quality	51.45
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2.5. Mismatches and indels

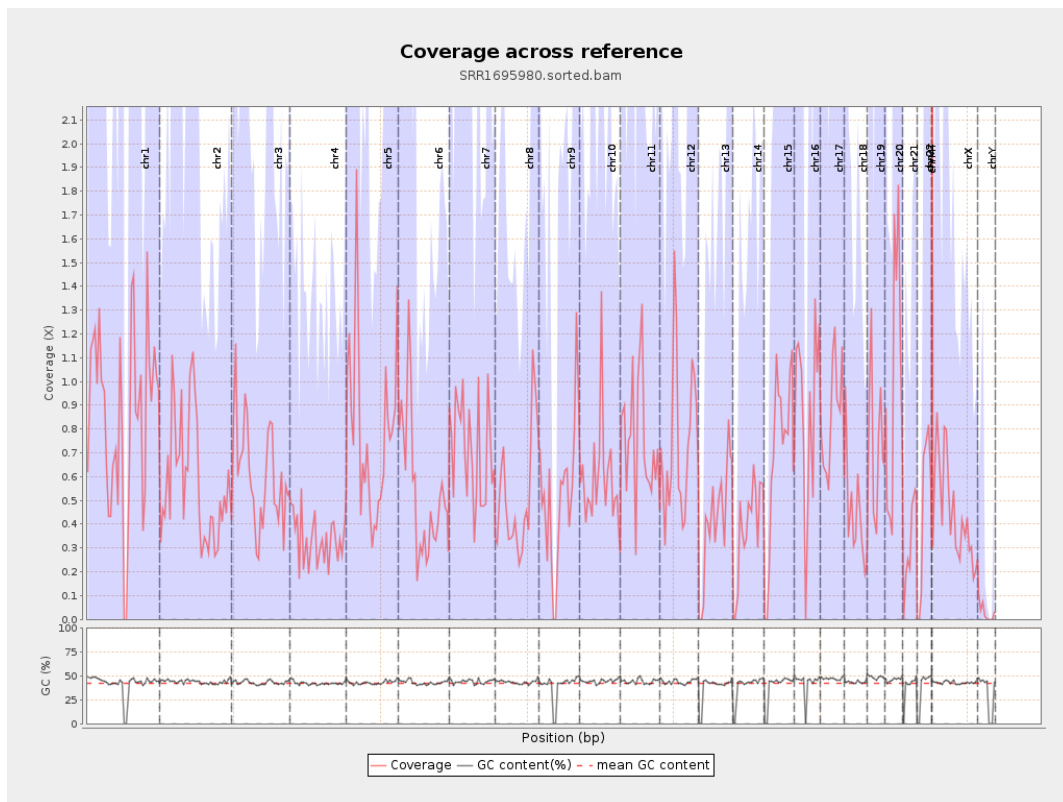
General error rate	1.72%
Mismatches	21,315,240
Insertions	9,994,912
Mapped reads with at least one insertion	44.14%
Deletions	12,809,340
Mapped reads with at least one deletion	53.22%
Homopolymer indels	37.3%

2.6. Chromosome stats

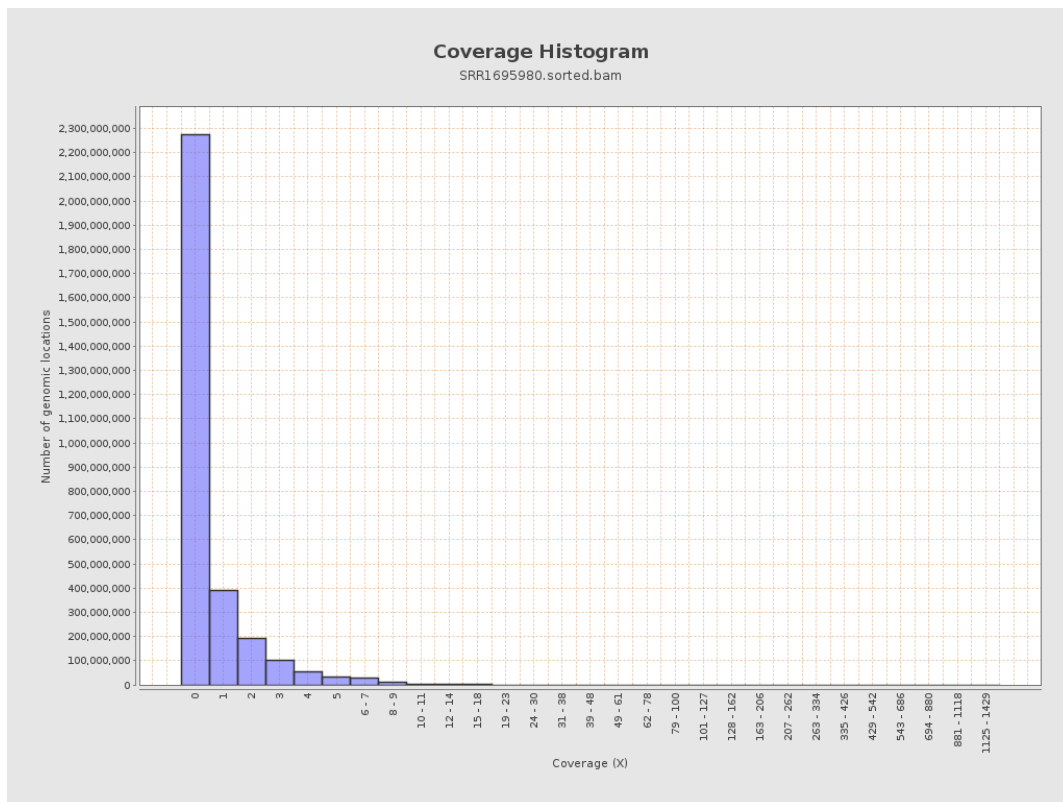
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	214448232	0.8604	2.2345
chr2	243199373	140671029	0.5784	1.39
chr3	198022430	119983725	0.6059	1.3662
chr4	191154276	64394254	0.3369	0.9895
chr5	180915260	143401479	0.7926	1.6451
chr6	171115067	91280549	0.5334	1.38
chr7	159138663	112847173	0.7091	1.518

chr8	146364022	75338625	0.5147	1.2671
chr9	141213431	74771981	0.5295	1.3295
chr10	135534747	80563184	0.5944	1.6105
chr11	135006516	102344221	0.7581	1.5914
chr12	133851895	98908586	0.7389	1.5814
chr13	115169878	48462610	0.4208	1.1304
chr14	107349540	40660600	0.3788	1.08
chr15	102531392	71061409	0.6931	1.5021
chr16	90354753	78304993	0.8666	1.7527
chr17	81195210	69356411	0.8542	1.7921
chr18	78077248	35128921	0.4499	1.4205
chr19	59128983	44752531	0.7569	1.954
chr20	63025520	63696148	1.0106	1.9666
chr21	48129895	15549876	0.3231	1.0873
chr22	51304566	23416821	0.4564	1.2193
chrMT	16571	267927	16.1684	10.1341
chrX	155270560	68757266	0.4428	1.1537
chrY	59373566	1718554	0.0289	0.6086

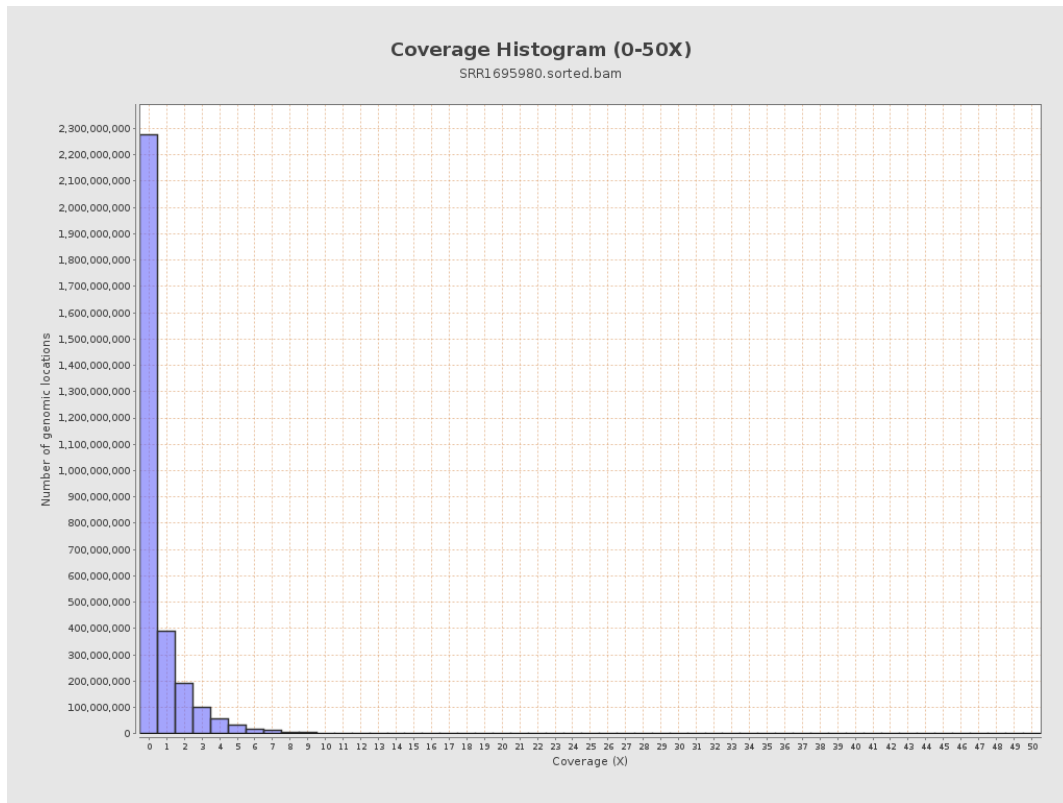
3. Results : Coverage across reference



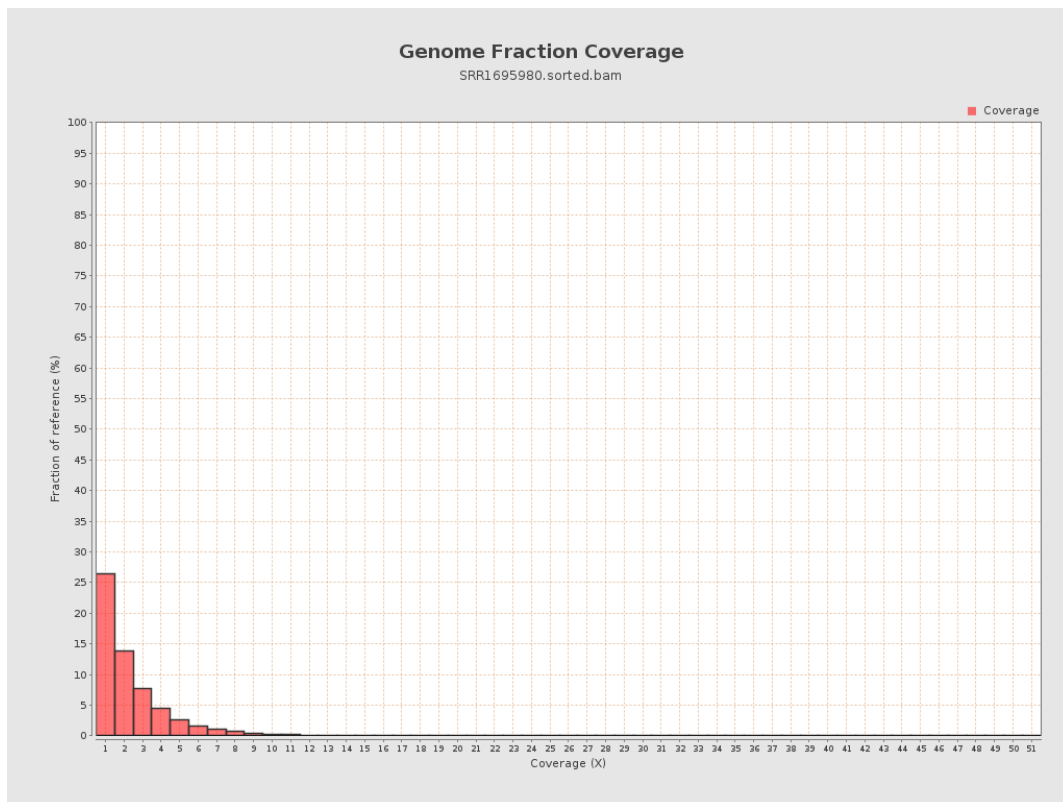
4. Results : Coverage Histogram



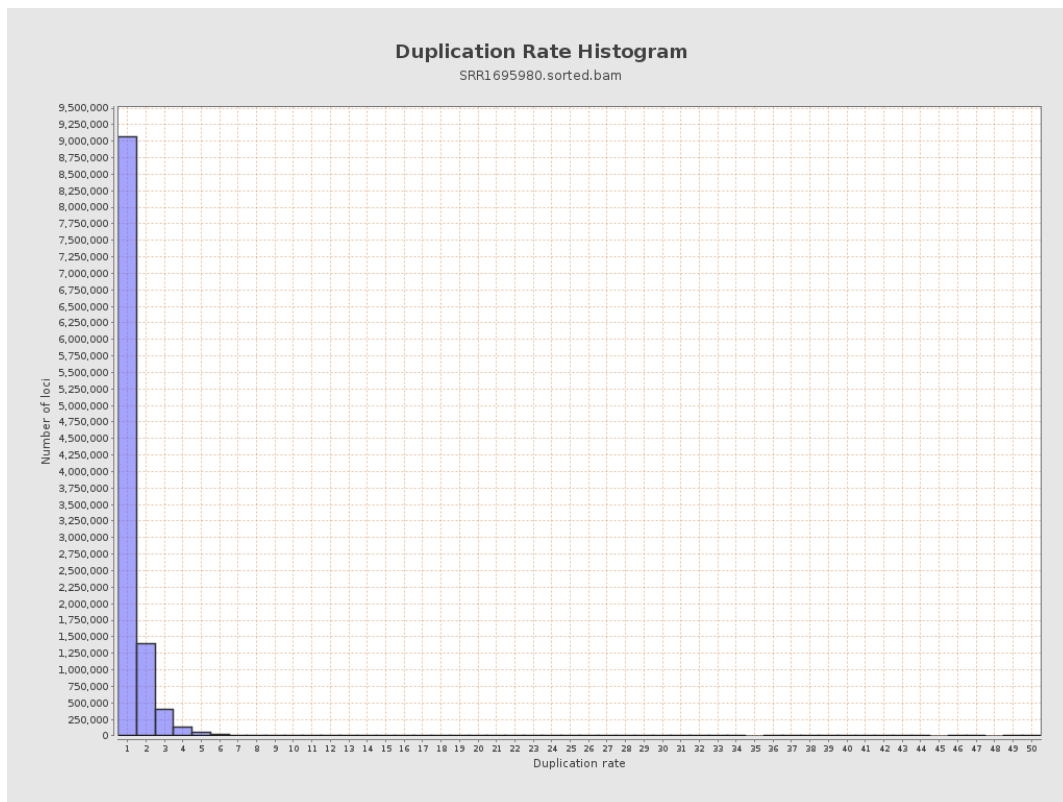
5. Results : Coverage Histogram (0-50X)



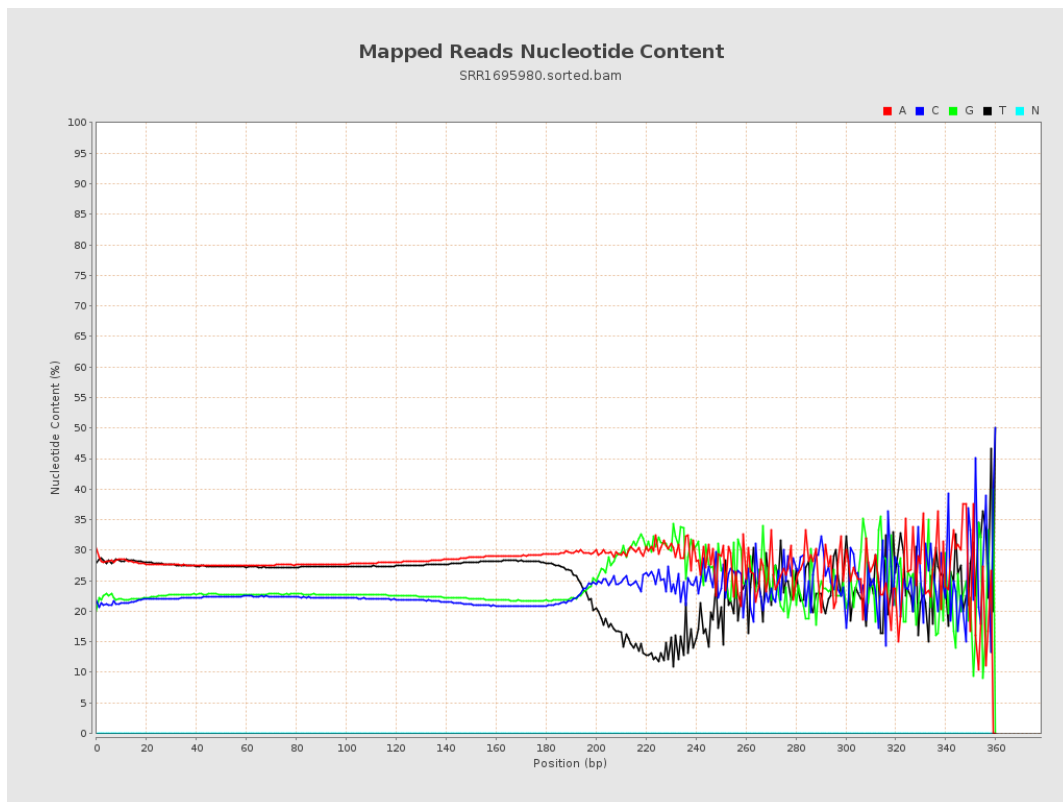
6. Results : Genome Fraction Coverage



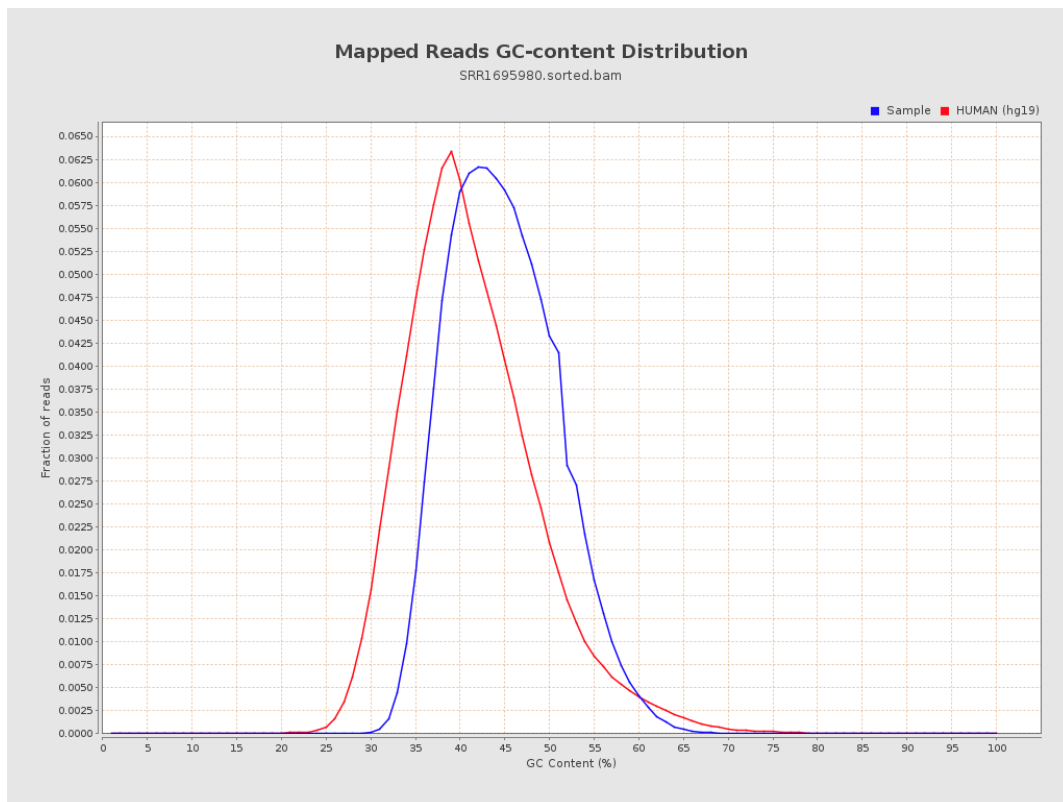
7. Results : Duplication Rate Histogram



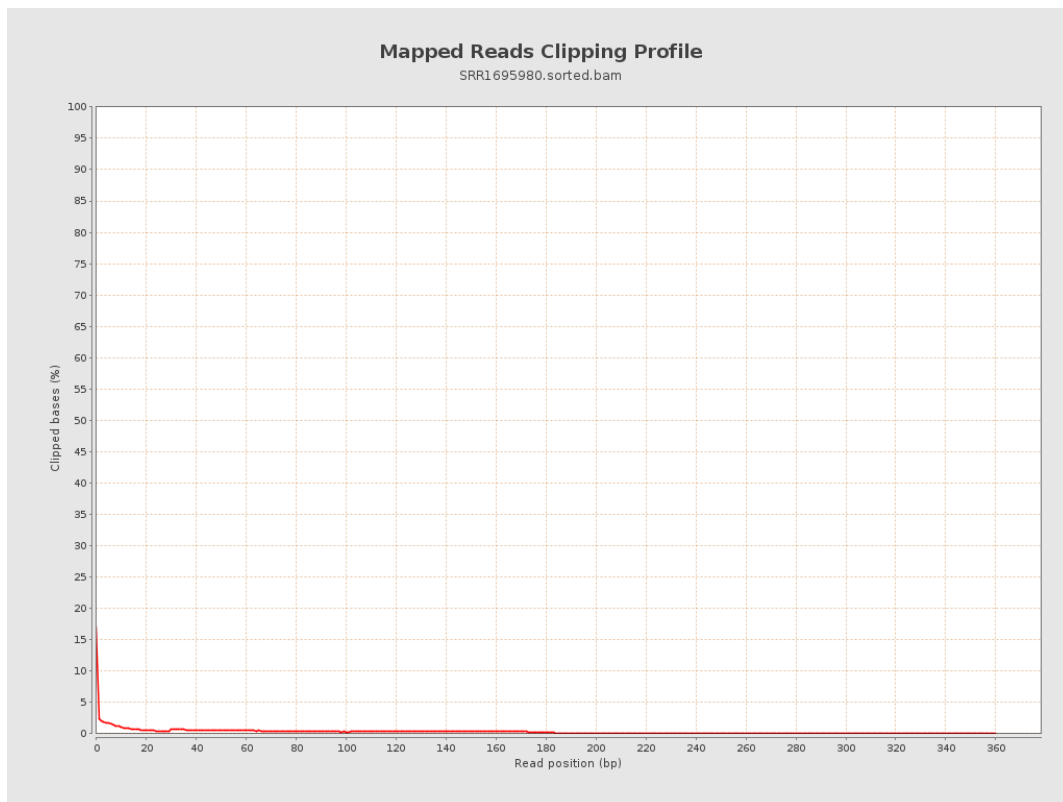
8. Results : Mapped Reads Nucleotide Content



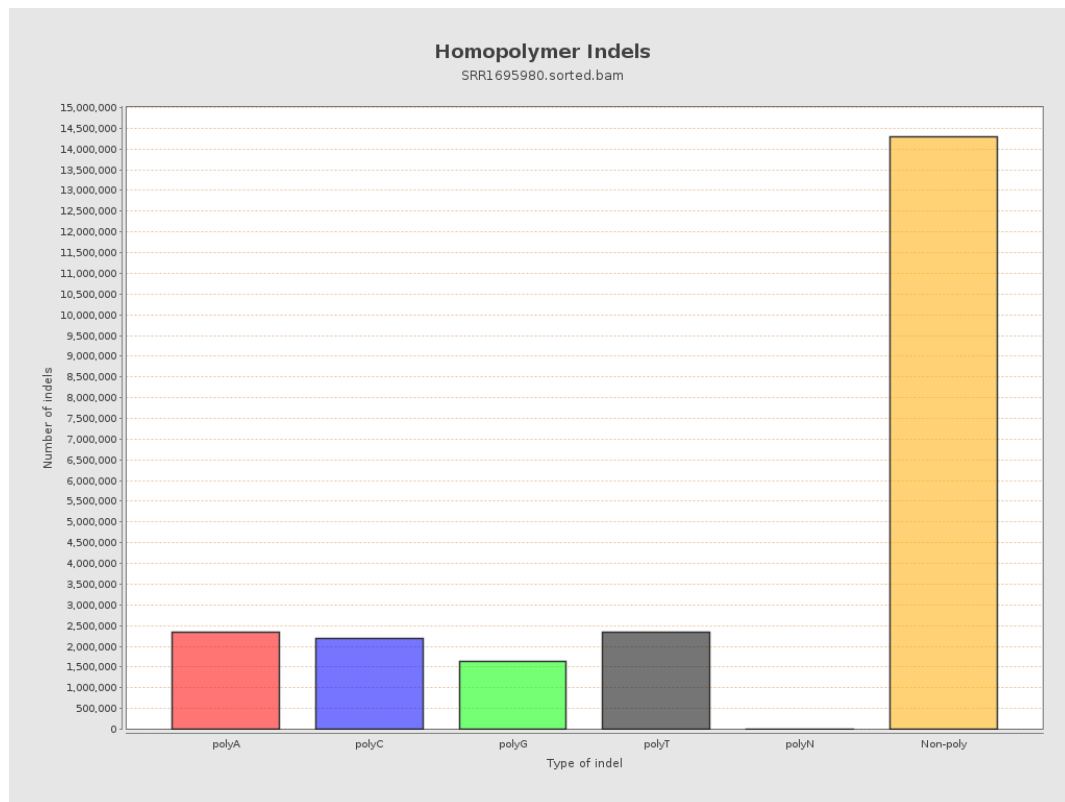
9. Results : Mapped Reads GC-content Distribution



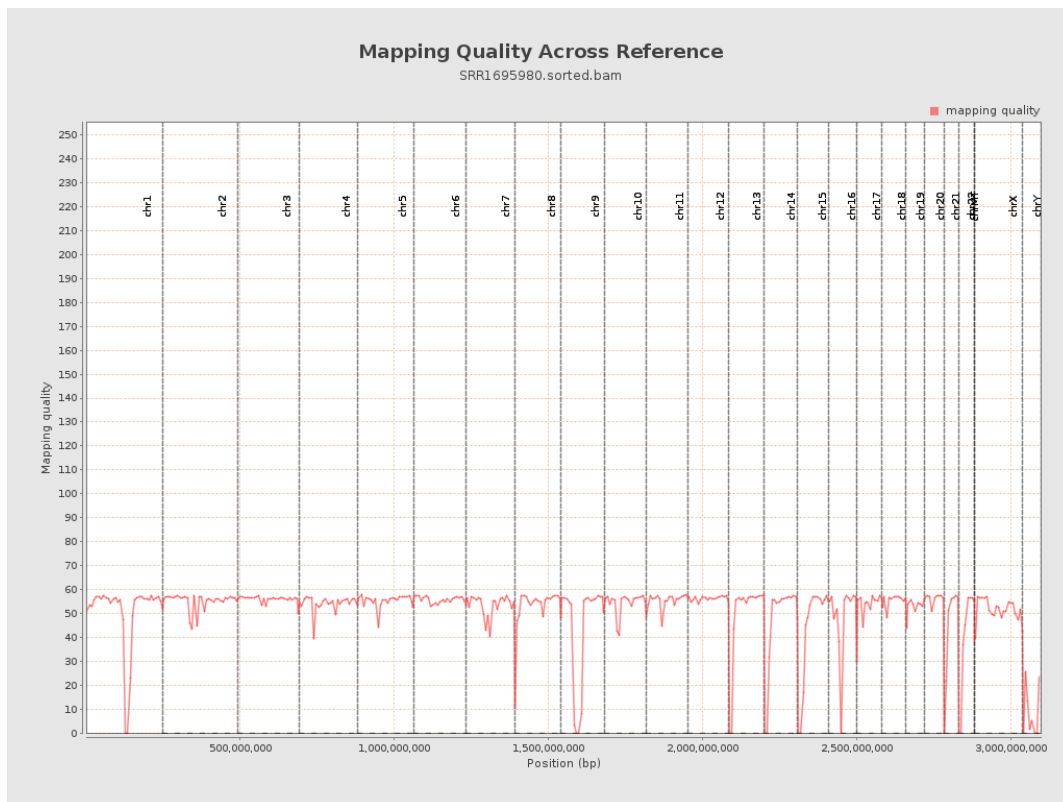
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

