

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:27:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231785.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_SRR6231785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:27:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,584,079
Mapped reads	1,311,219 / 82.77%
Unmapped reads	272,860 / 17.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,995 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	84,366 / 5.33%
Duplication rate	2.52%
Clipped reads	881,211 / 55.63%

2.2. ACGT Content

Number/percentage of A's	22,988,069 / 28.78%
Number/percentage of C's	15,911,915 / 19.92%
Number/percentage of T's	21,284,596 / 26.64%
Number/percentage of G's	19,694,103 / 24.65%
Number/percentage of N's	6,745 / 0.01%
GC Percentage	44.57%

2.3. Coverage

Mean	0.0258

Standard Deviation	6.0662
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2.4. Mapping Quality

Mean Mapping Quality	42.61
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2.5. Mismatches and indels

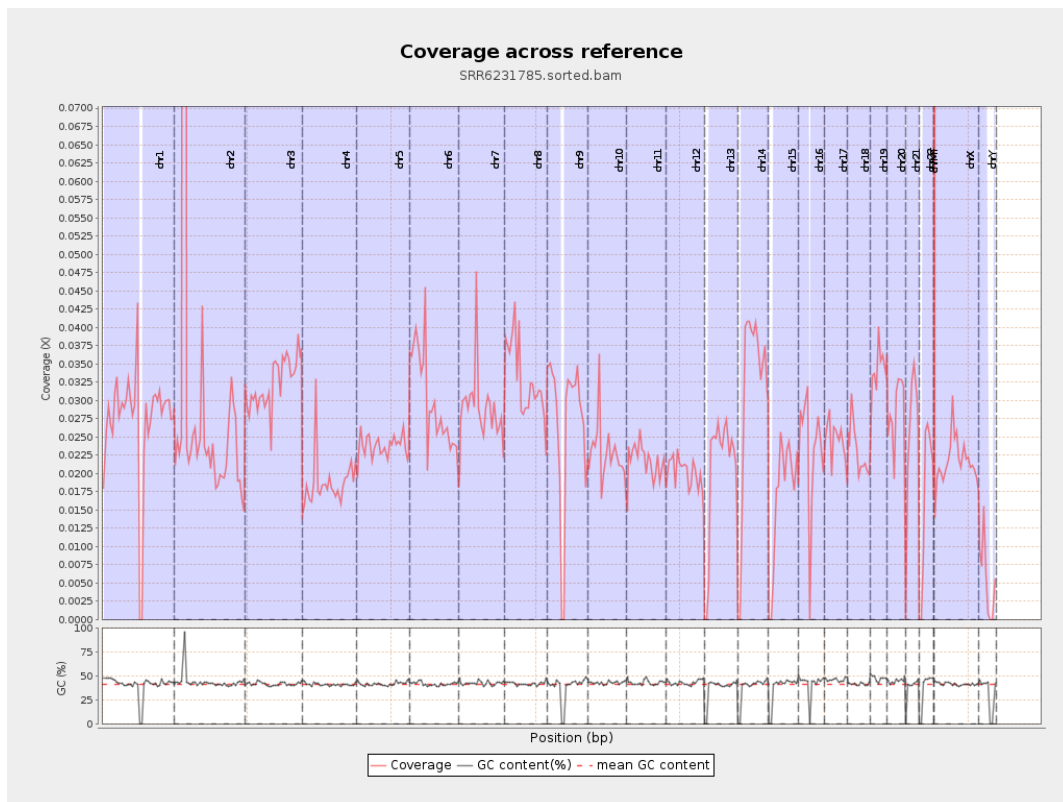
General error rate	0.68%
Mismatches	529,918
Insertions	5,877
Mapped reads with at least one insertion	0.44%
Deletions	17,935
Mapped reads with at least one deletion	1.35%
Homopolymer indels	43.25%

2.6. Chromosome stats

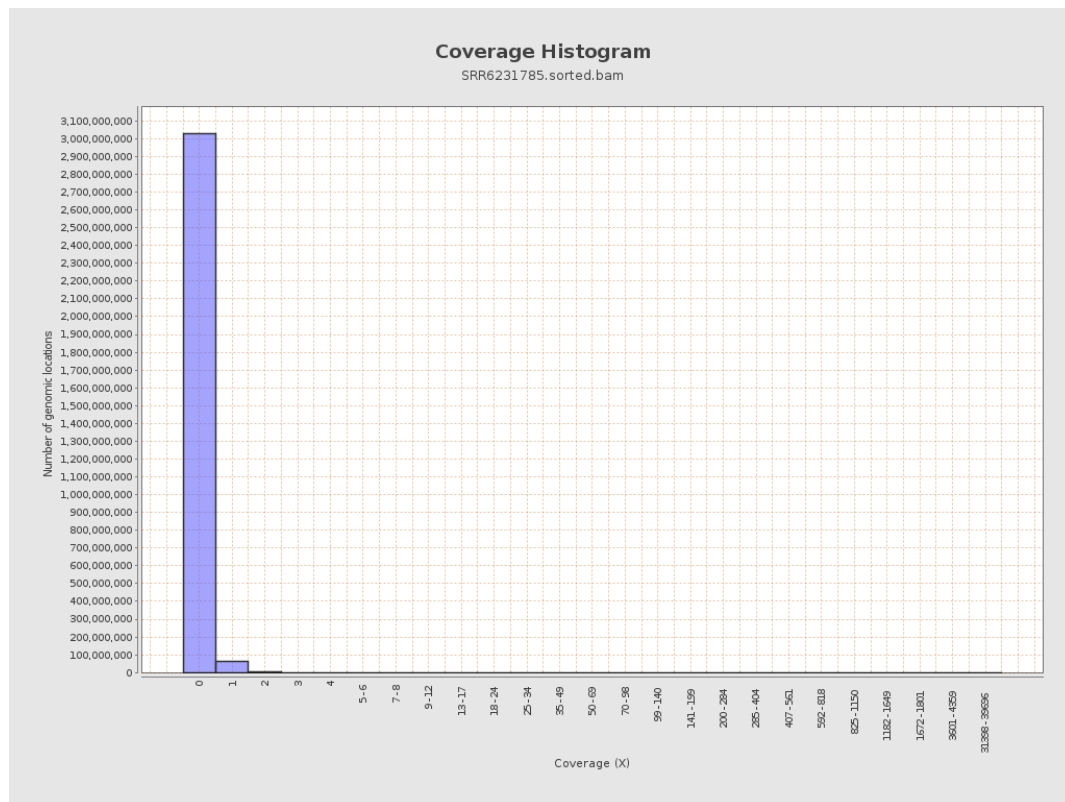
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6768785	0.0272	0.465
chr2	243199373	8874080	0.0365	21.6255
chr3	198022430	6402651	0.0323	0.1949
chr4	191154276	3577801	0.0187	0.1635
chr5	180915260	4306459	0.0238	0.1694
chr6	171115067	5083014	0.0297	0.2148
chr7	159138663	4597057	0.0289	0.3509

chr8	146364022	4803885	0.0328	0.2892
chr9	141213431	3790488	0.0268	0.2334
chr10	135534747	3084847	0.0228	0.2254
chr11	135006516	2944490	0.0218	0.2266
chr12	133851895	2695486	0.0201	0.1574
chr13	115169878	2347083	0.0204	0.1547
chr14	107349540	3359102	0.0313	0.2376
chr15	102531392	1742573	0.017	0.1451
chr16	90354753	2068475	0.0229	0.1782
chr17	81195210	1993909	0.0246	0.1855
chr18	78077248	1790918	0.0229	0.407
chr19	59128983	2028827	0.0343	0.3046
chr20	63025520	1773269	0.0281	0.185
chr21	48129895	1251151	0.026	0.1857
chr22	51304566	871951	0.017	0.1416
chrMT	16571	66865	4.0351	2.9424
chrX	155270560	3366540	0.0217	0.1782
chrY	59373566	325528	0.0055	0.0996

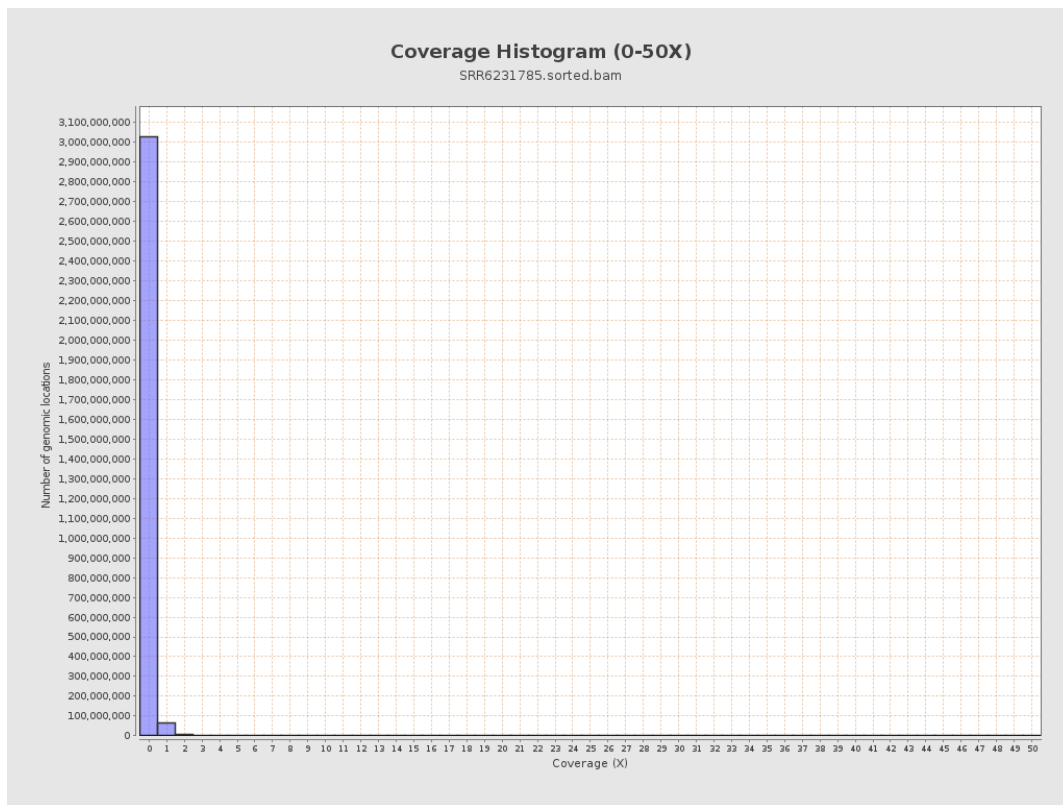
3. Results : Coverage across reference



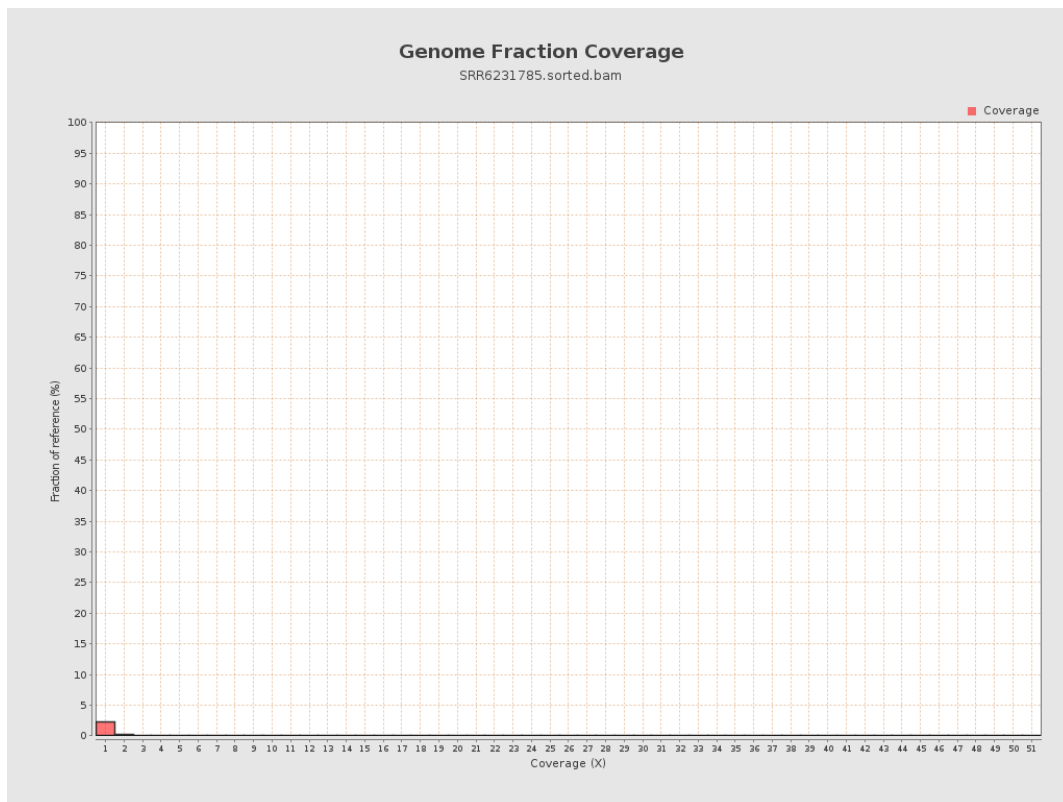
4. Results : Coverage Histogram



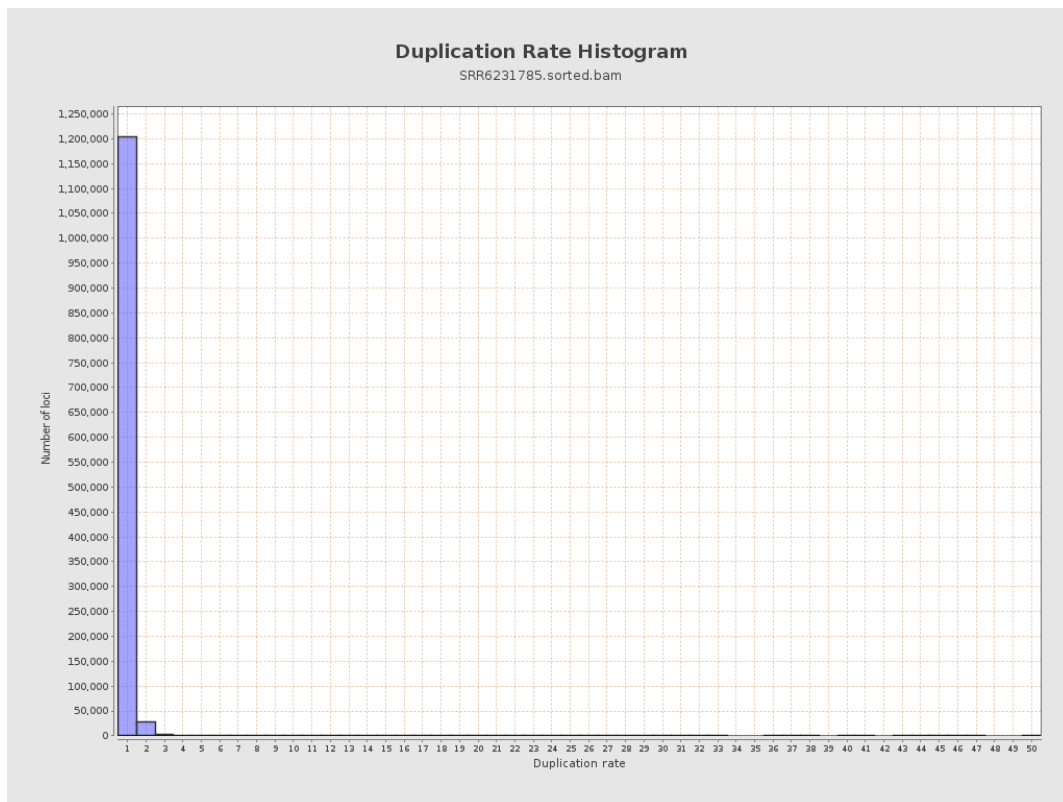
5. Results : Coverage Histogram (0-50X)



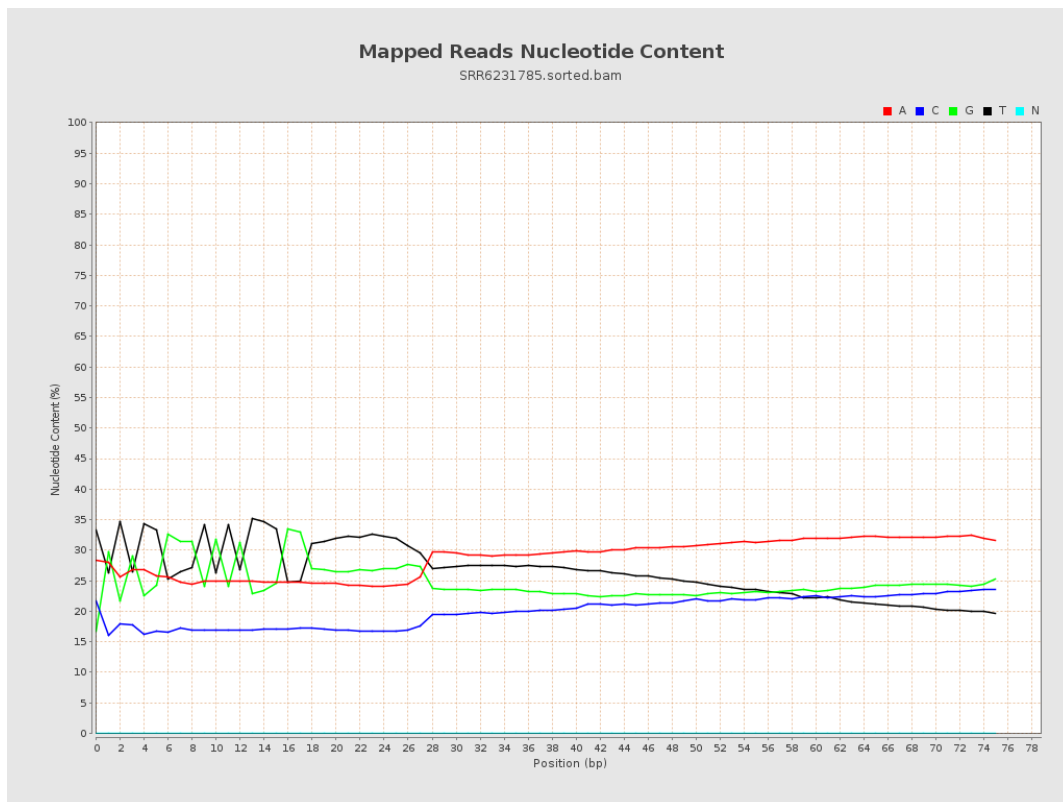
6. Results : Genome Fraction Coverage



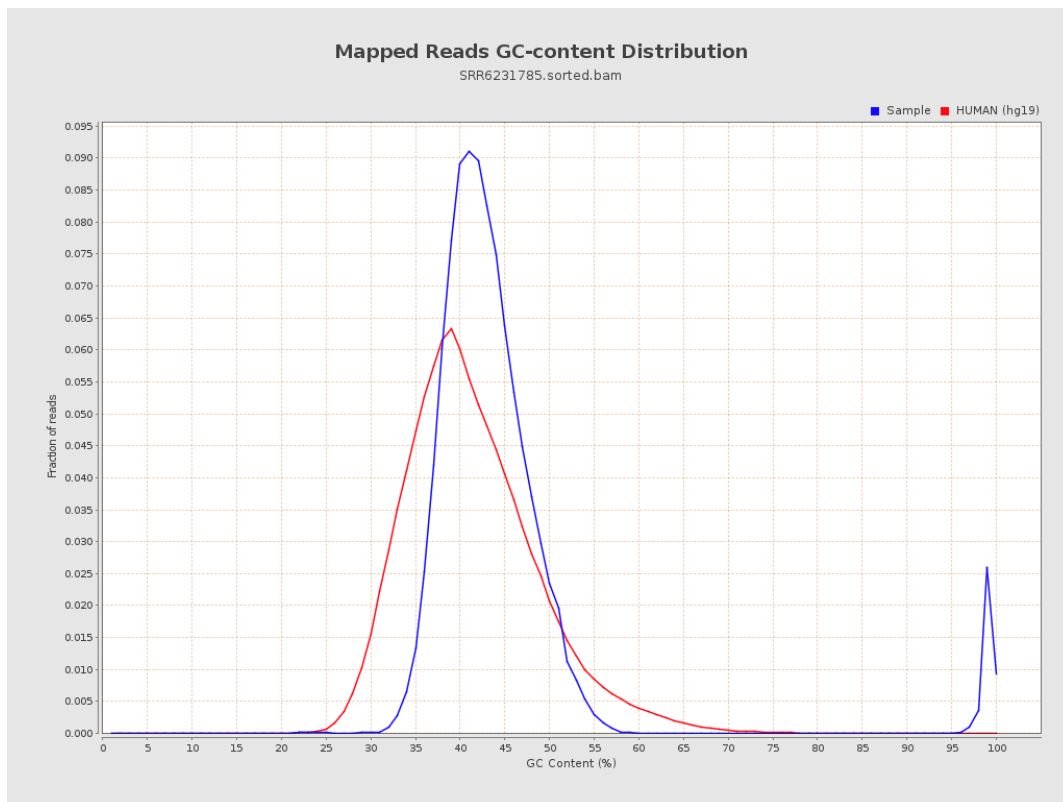
7. Results : Duplication Rate Histogram



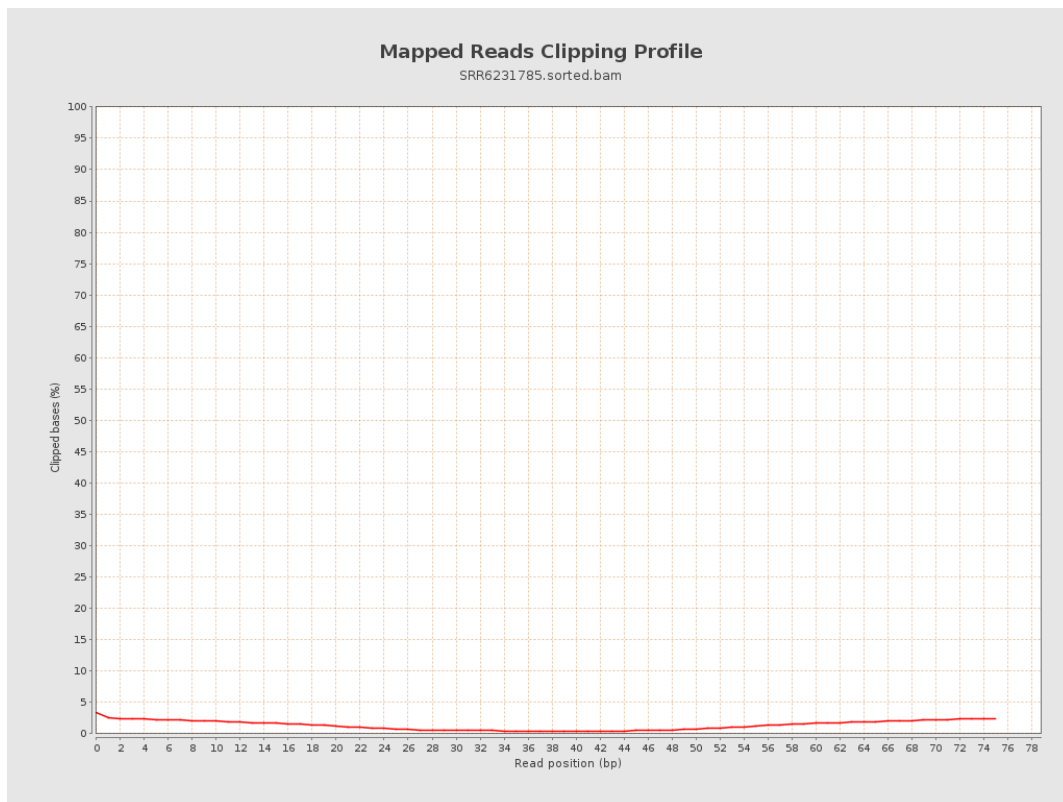
8. Results : Mapped Reads Nucleotide Content



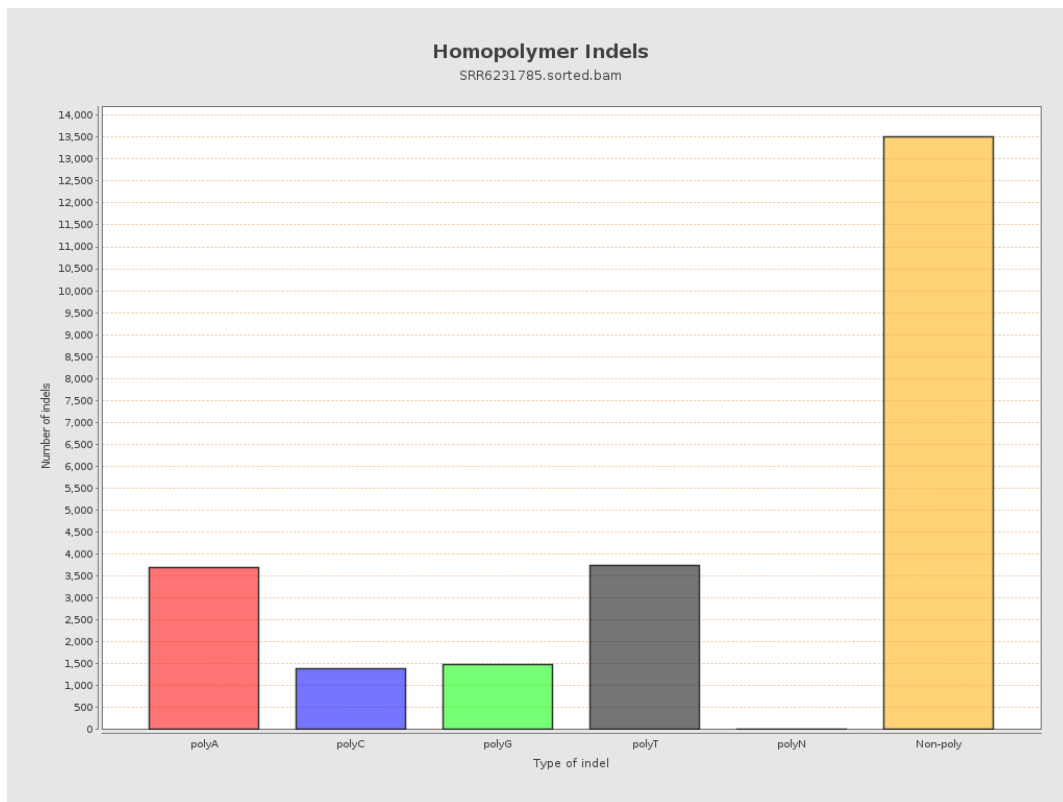
9. Results : Mapped Reads GC-content Distribution



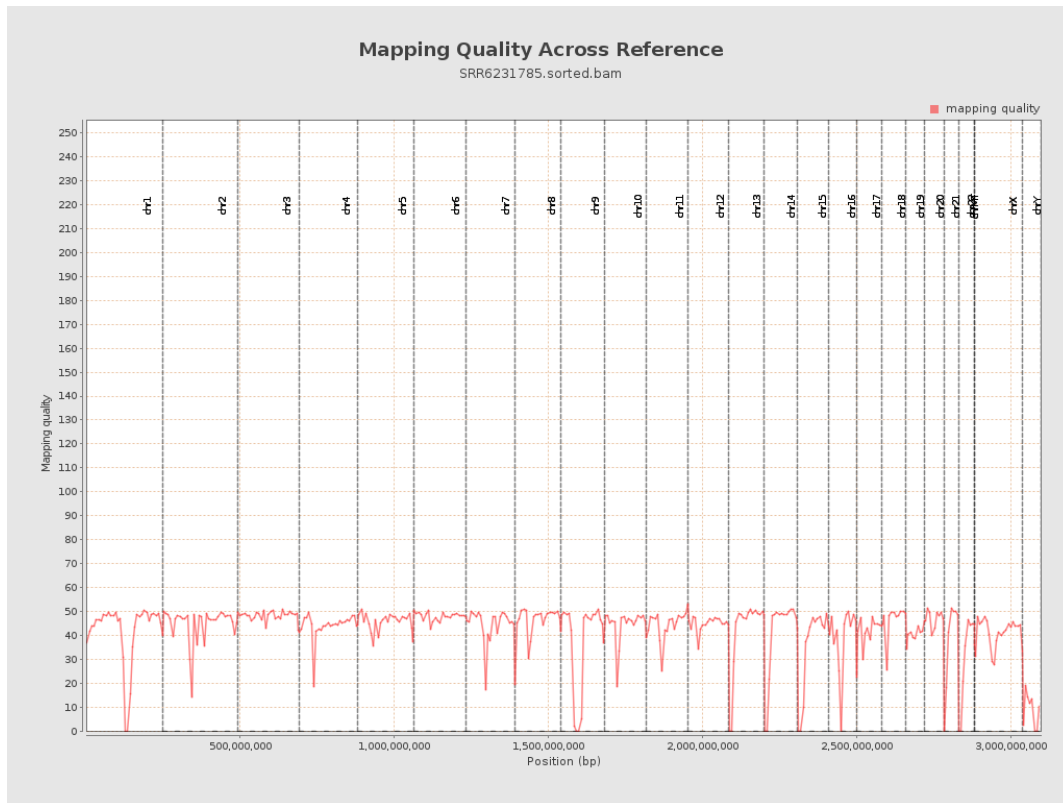
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

