

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:21:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231740.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_SRR6231740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:21:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,908,691
Mapped reads	1,481,996 / 77.64%
Unmapped reads	426,695 / 22.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,635 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	189,300 / 9.92%
Duplication rate	9.4%
Clipped reads	634,128 / 33.22%

2.2. ACGT Content

Number/percentage of A's	28,541,896 / 28.76%
Number/percentage of C's	17,141,046 / 17.27%
Number/percentage of T's	32,985,115 / 33.24%
Number/percentage of G's	20,542,668 / 20.7%
Number/percentage of N's	30,237 / 0.03%
GC Percentage	37.97%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.6359
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2.4. Mapping Quality

Mean Mapping Quality	47.03
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2.5. Mismatches and indels

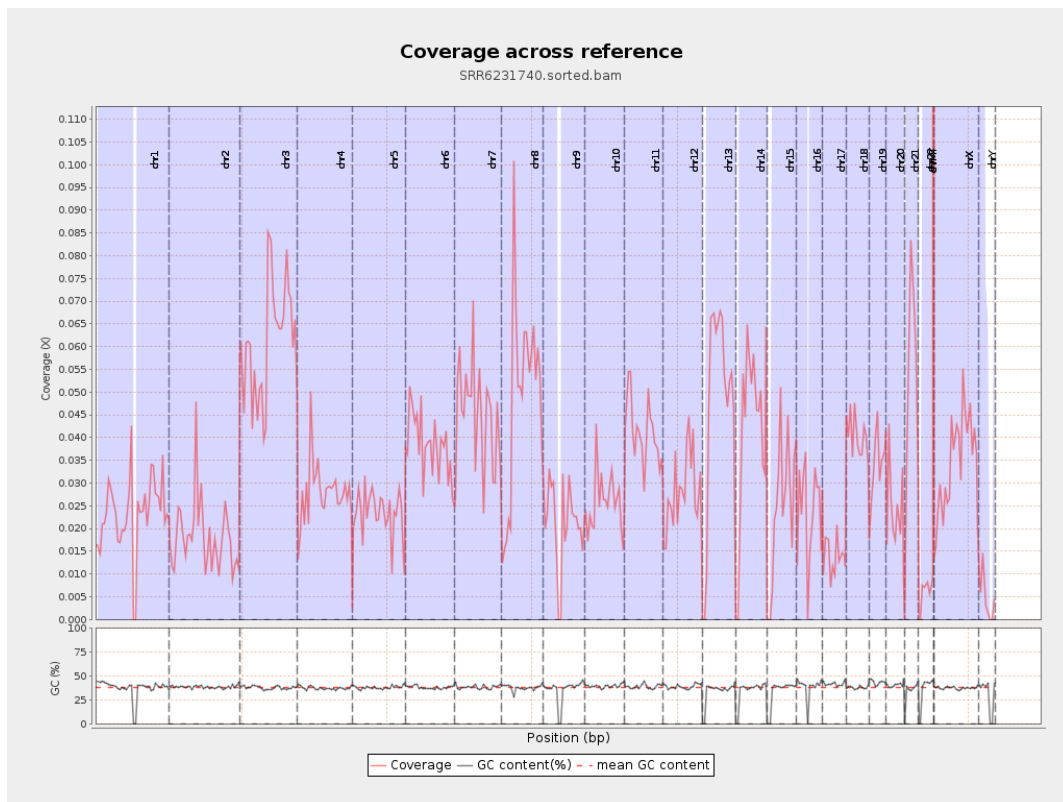
General error rate	0.86%
Mismatches	837,171
Insertions	8,515
Mapped reads with at least one insertion	0.57%
Deletions	28,484
Mapped reads with at least one deletion	1.9%
Homopolymer indels	45.27%

2.6. Chromosome stats

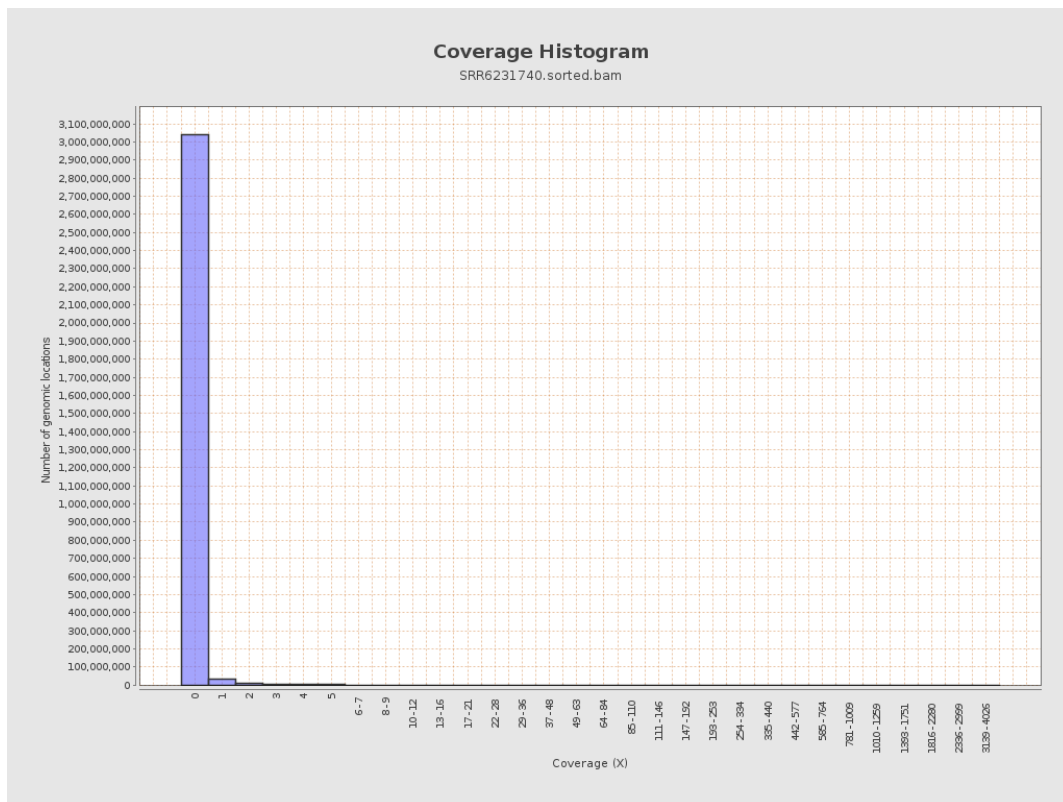
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5807483	0.0233	0.5249
chr2	243199373	4370489	0.018	0.3197
chr3	198022430	12079228	0.061	0.4094
chr4	191154276	5320707	0.0278	0.2862
chr5	180915260	4214159	0.0233	0.2506
chr6	171115067	6528327	0.0382	0.3391
chr7	159138663	7181372	0.0451	0.576

chr8	146364022	7051747	0.0482	2.4005
chr9	141213431	2949730	0.0209	0.2934
chr10	135534747	3486109	0.0257	0.315
chr11	135006516	5501702	0.0408	0.4365
chr12	133851895	3789388	0.0283	0.2756
chr13	115169878	5492325	0.0477	0.3667
chr14	107349540	4396764	0.041	0.3433
chr15	102531392	2548332	0.0249	0.2533
chr16	90354753	2154483	0.0238	0.2695
chr17	81195210	1099142	0.0135	0.2139
chr18	78077248	3144213	0.0403	0.6508
chr19	59128983	2037556	0.0345	0.3831
chr20	63025520	1542723	0.0245	0.2717
chr21	48129895	2503926	0.052	0.3832
chr22	51304566	297629	0.0058	0.1118
chrMT	16571	187103	11.291	9.3544
chrX	155270560	5335933	0.0344	0.3279
chrY	59373566	270410	0.0046	0.1187

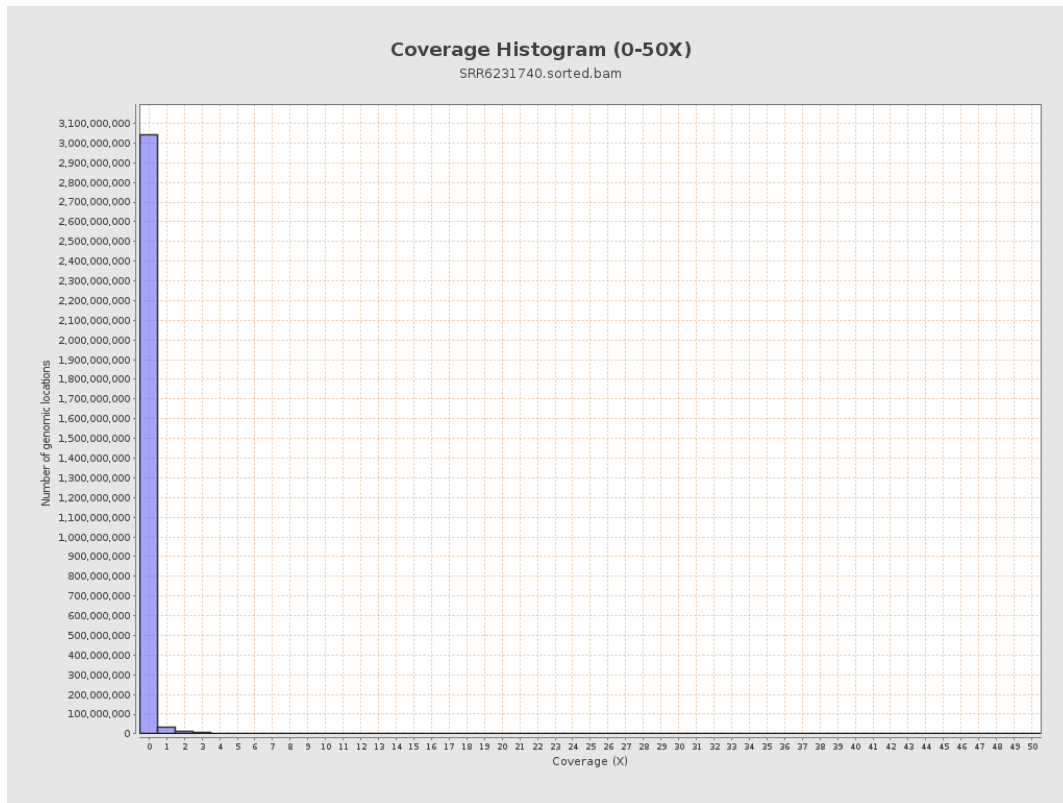
3. Results : Coverage across reference



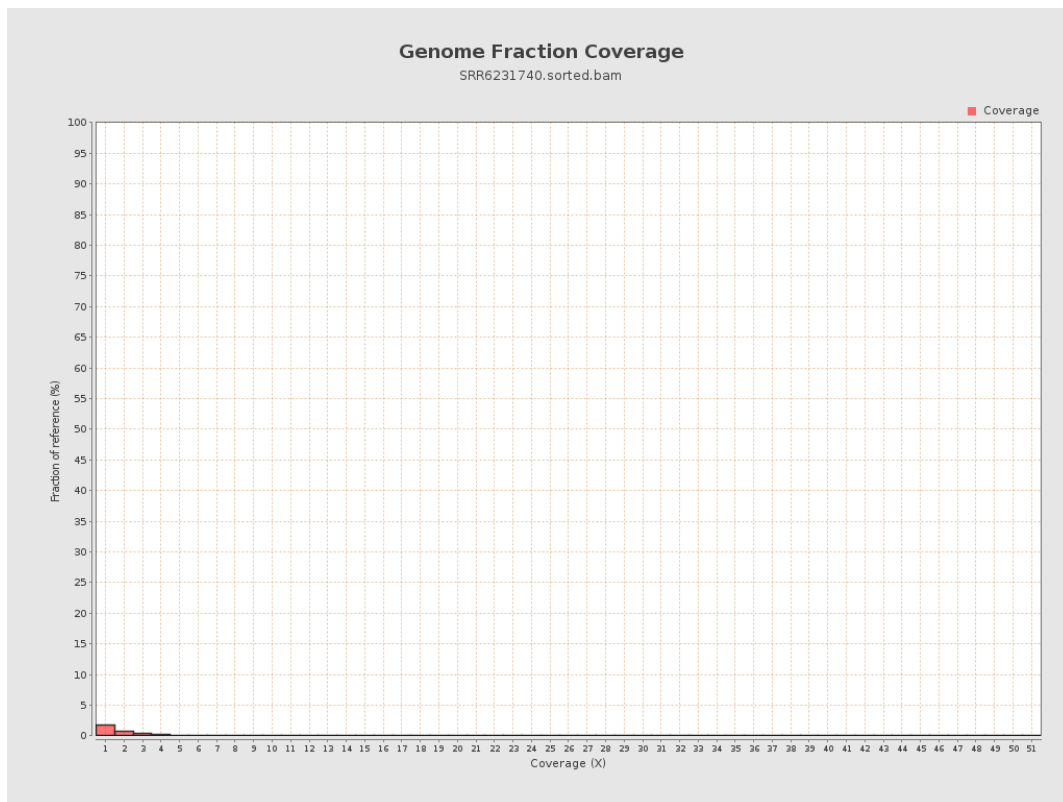
4. Results : Coverage Histogram



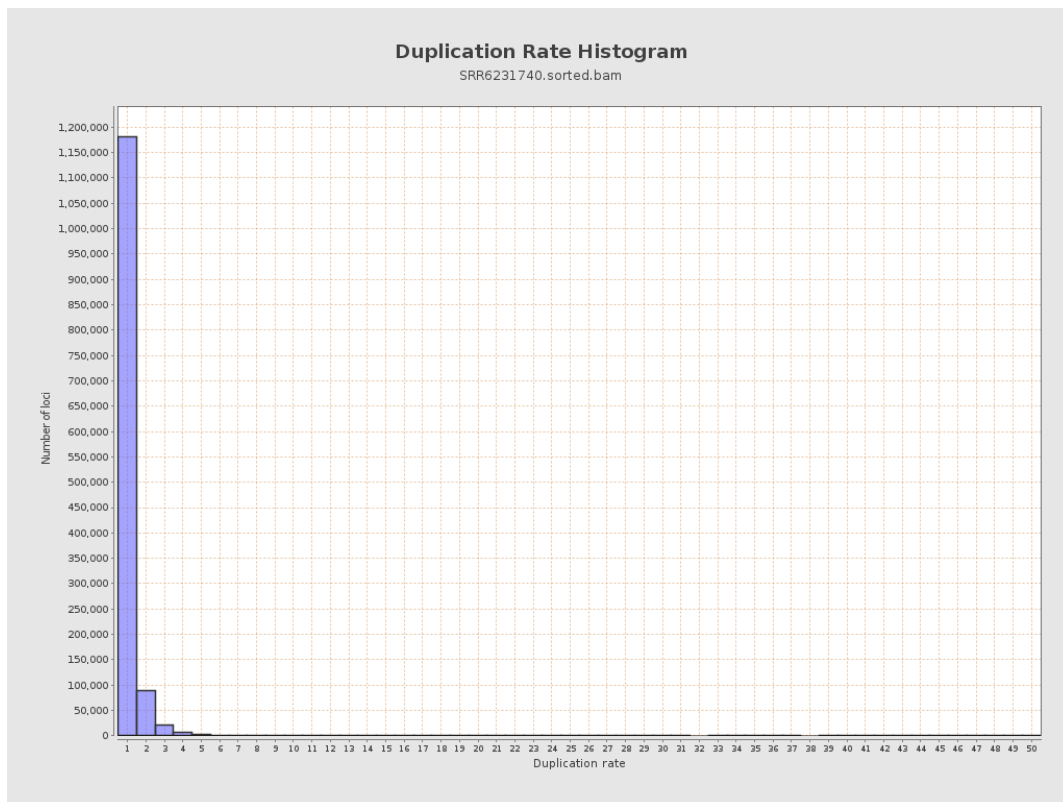
5. Results : Coverage Histogram (0-50X)



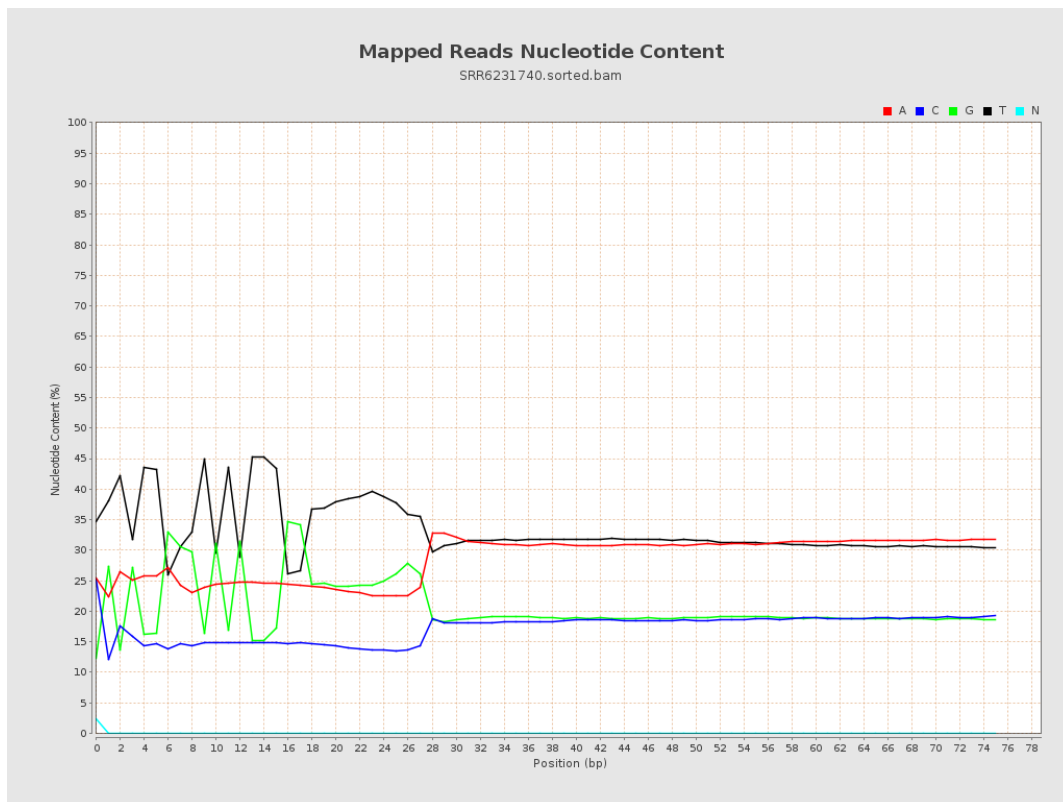
6. Results : Genome Fraction Coverage



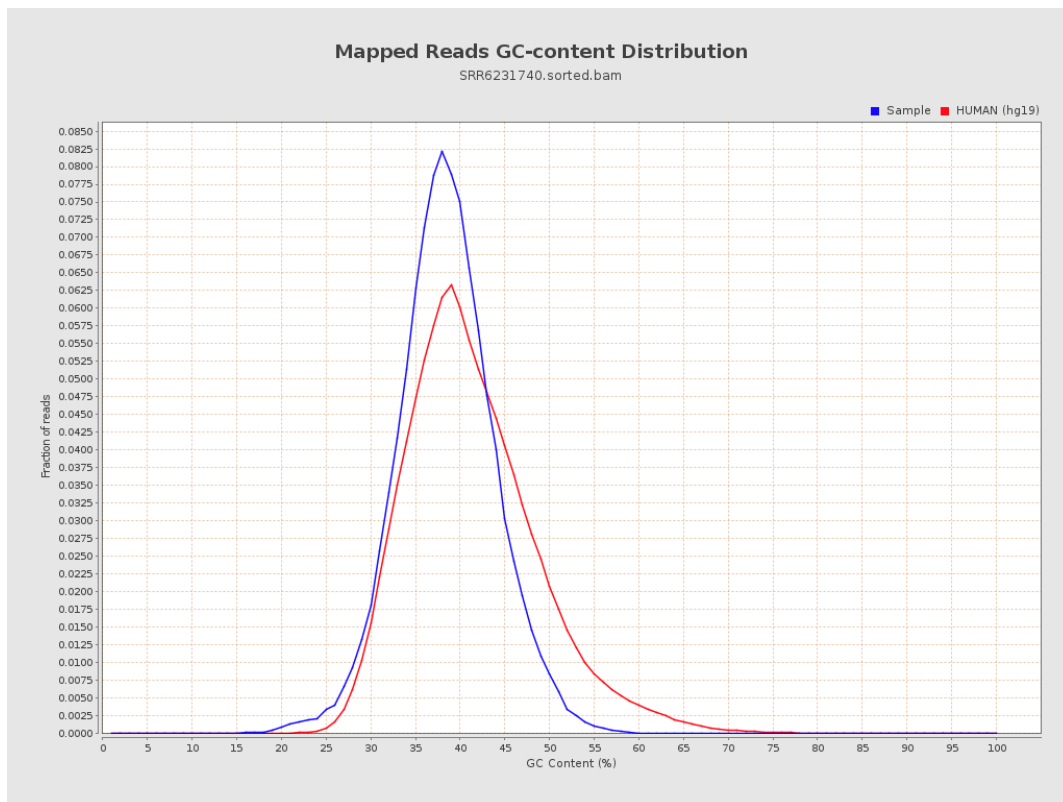
7. Results : Duplication Rate Histogram



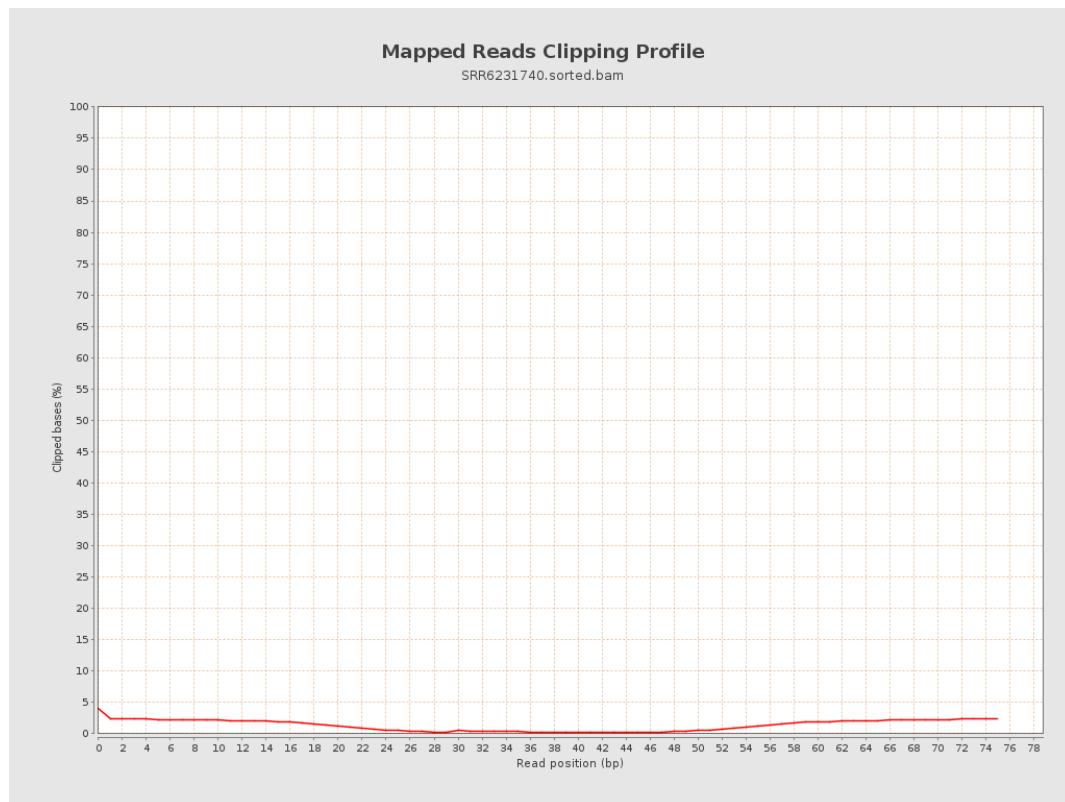
8. Results : Mapped Reads Nucleotide Content



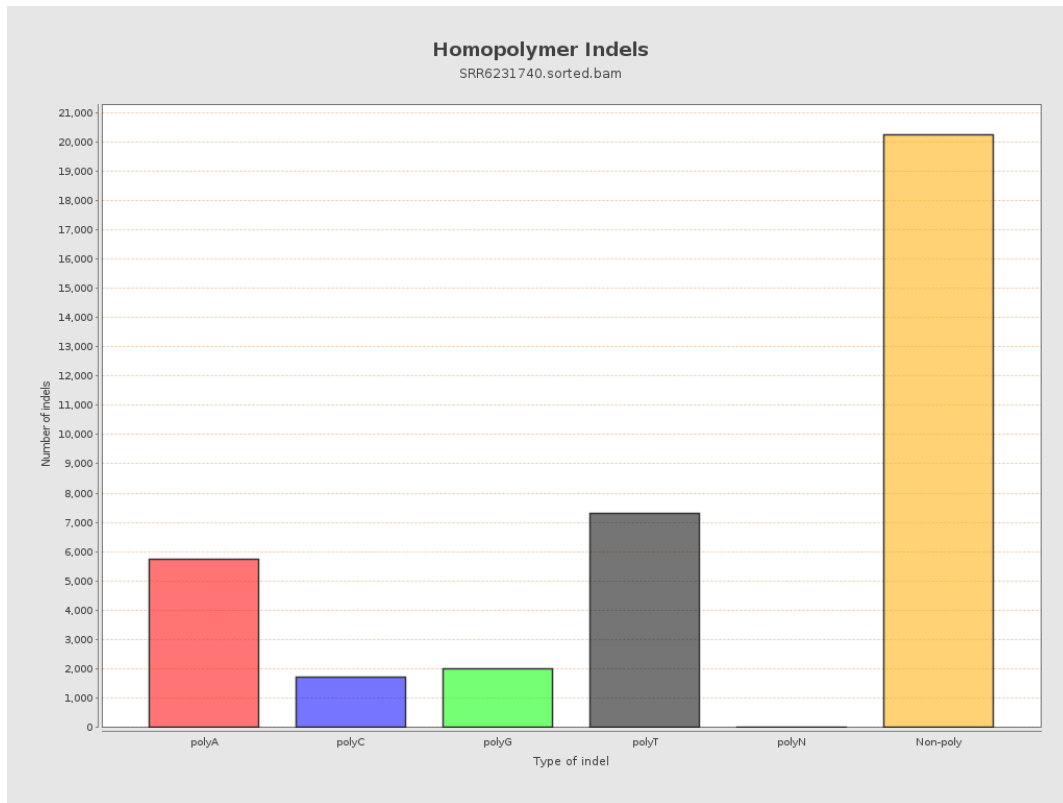
9. Results : Mapped Reads GC-content Distribution



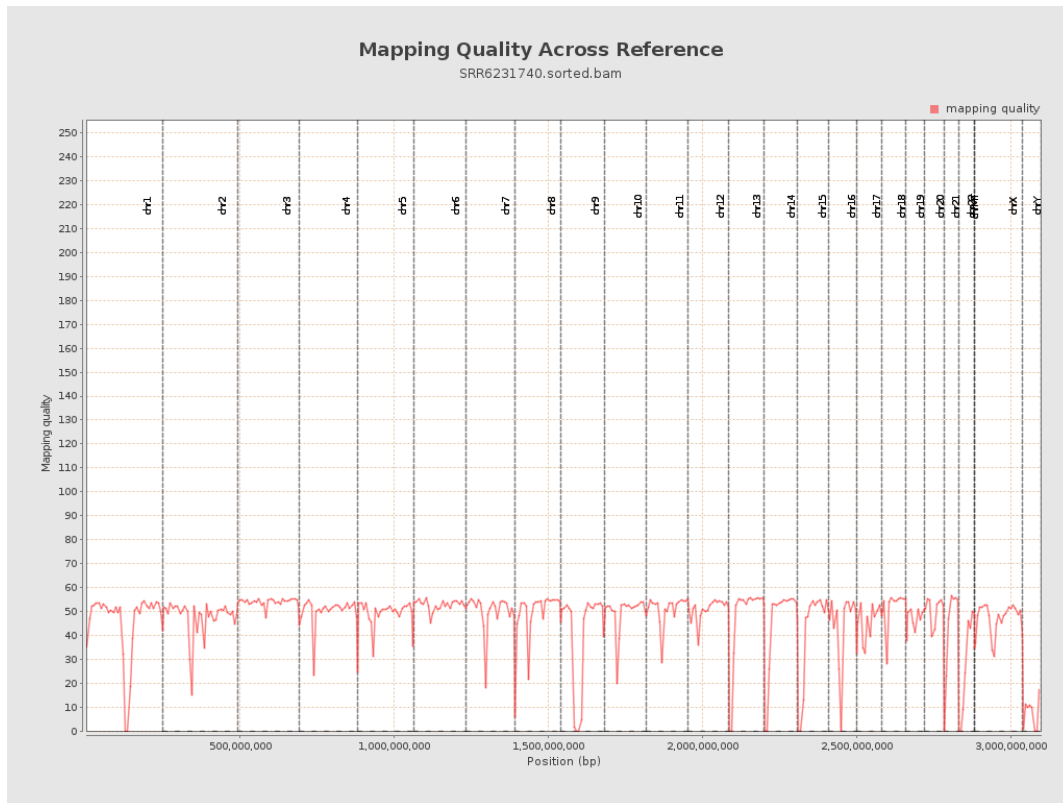
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

