

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:00:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231733.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_SRR6231733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231733.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,457,932
Mapped reads	5,149,967 / 94.36%
Unmapped reads	307,965 / 5.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	50,219 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	720,961 / 13.21%
Duplication rate	5.84%
Clipped reads	1,825,325 / 33.44%

2.2. ACGT Content

Number/percentage of A's	92,190,736 / 26.01%
Number/percentage of C's	63,927,506 / 18.03%
Number/percentage of T's	99,430,106 / 28.05%
Number/percentage of G's	98,872,881 / 27.89%
Number/percentage of N's	77,877 / 0.02%
GC Percentage	45.92%

2.3. Coverage

Mean	0.1146

Standard Deviation	53.861
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2.4. Mapping Quality

Mean Mapping Quality	45.94
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2.5. Mismatches and indels

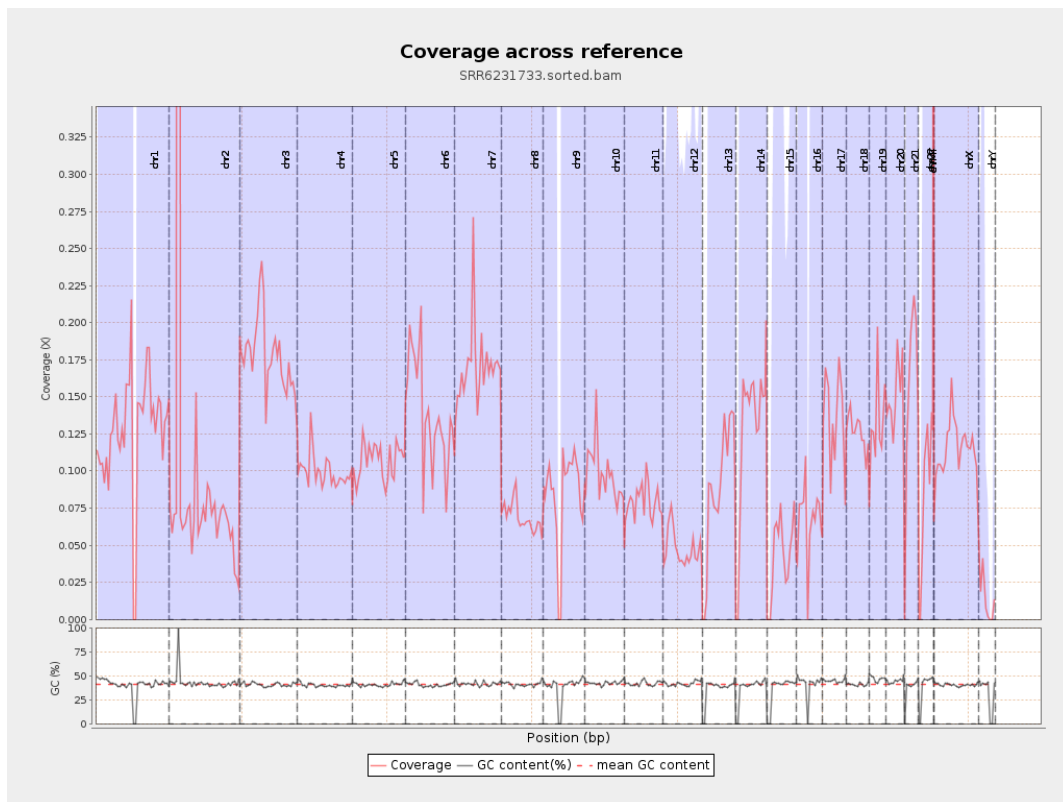
General error rate	0.63%
Mismatches	2,191,289
Insertions	24,075
Mapped reads with at least one insertion	0.46%
Deletions	75,796
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.65%

2.6. Chromosome stats

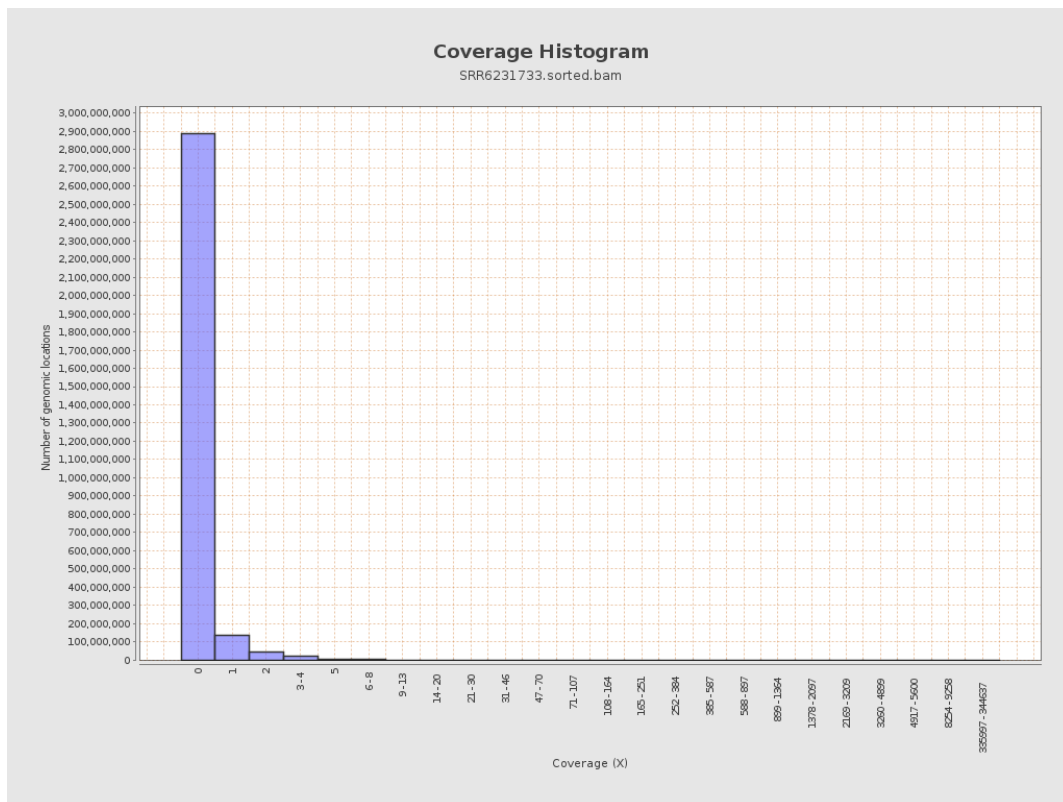
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31653233	0.127	1.7326
chr2	243199373	43404328	0.1785	192.1372
chr3	198022430	35468693	0.1791	0.622
chr4	191154276	18964405	0.0992	0.4919
chr5	180915260	19370559	0.1071	0.4787
chr6	171115067	23673044	0.1383	0.7323
chr7	159138663	27178178	0.1708	1.9615

chr8	146364022	10037129	0.0686	0.9107
chr9	141213431	11809072	0.0836	0.7768
chr10	135534747	13300772	0.0981	0.7331
chr11	135006516	10610913	0.0786	0.8076
chr12	133851895	6366930	0.0476	0.34
chr13	115169878	10143914	0.0881	0.4281
chr14	107349540	13468061	0.1255	0.6776
chr15	102531392	4555801	0.0444	0.3013
chr16	90354753	6101199	0.0675	0.4459
chr17	81195210	10819039	0.1332	0.6393
chr18	78077248	9894661	0.1267	1.6085
chr19	59128983	7935029	0.1342	1.0988
chr20	63025520	9416599	0.1494	0.5904
chr21	48129895	7517742	0.1562	0.6407
chr22	51304566	4262254	0.0831	0.4186
chrMT	16571	16486	0.9949	1.786
chrX	155270560	17826480	0.1148	0.5835
chrY	59373566	828733	0.014	0.2452

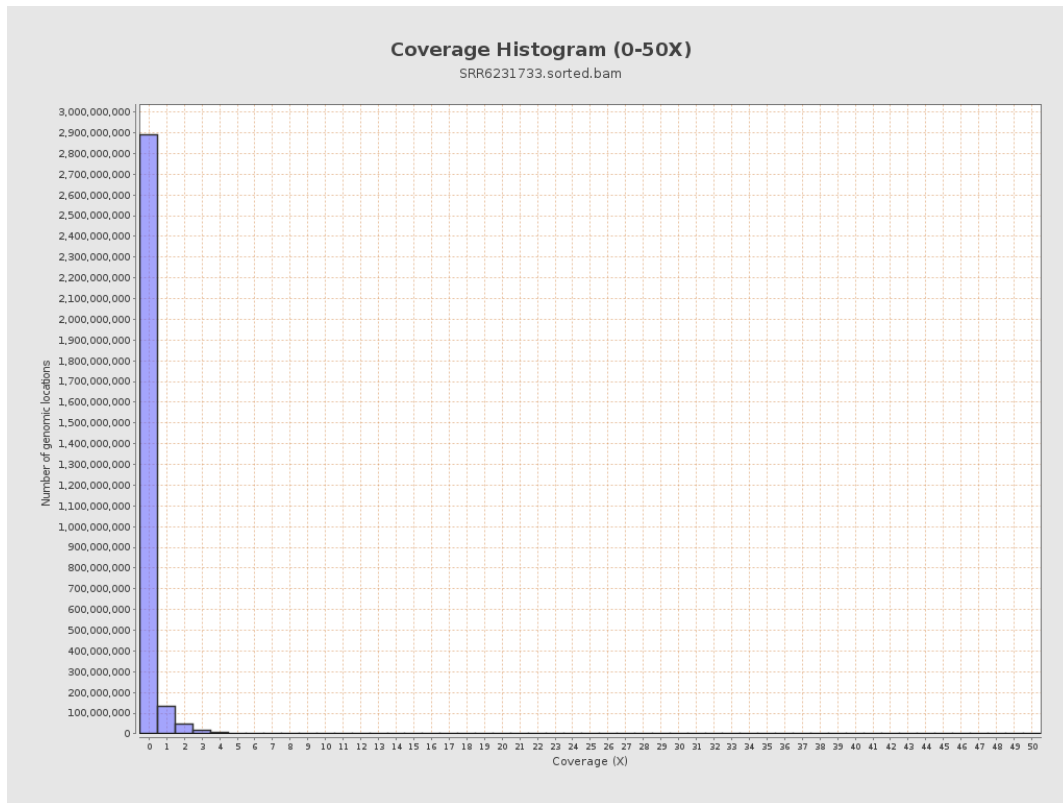
3. Results : Coverage across reference



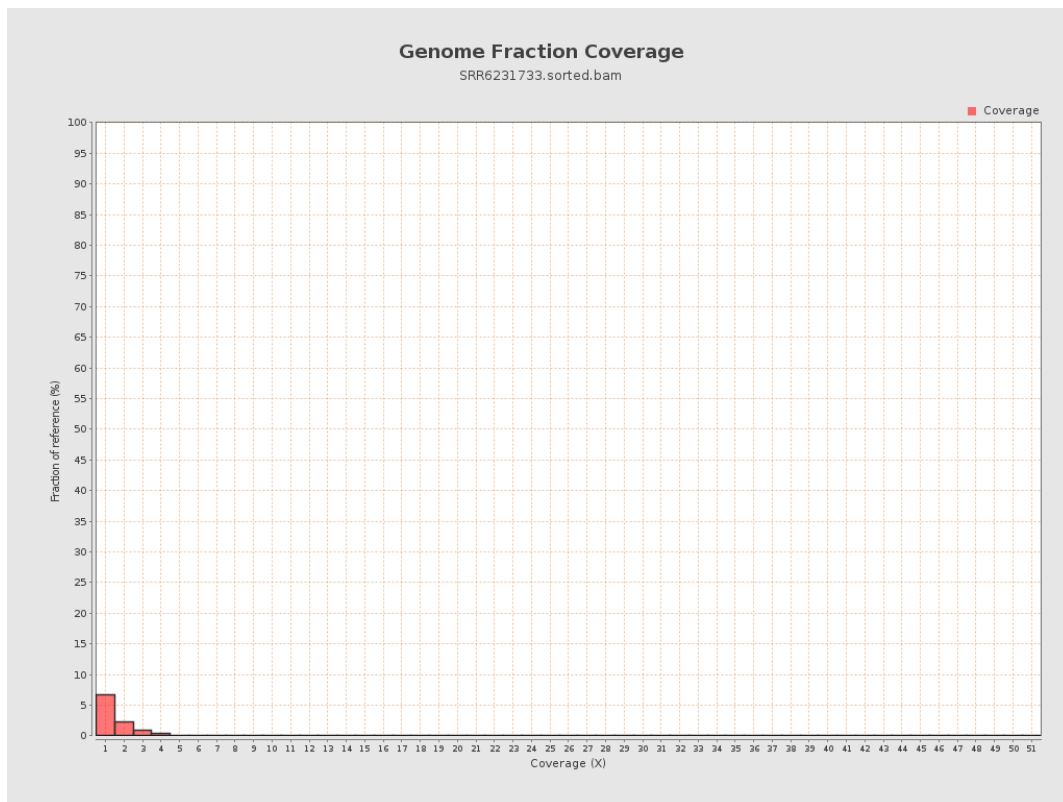
4. Results : Coverage Histogram



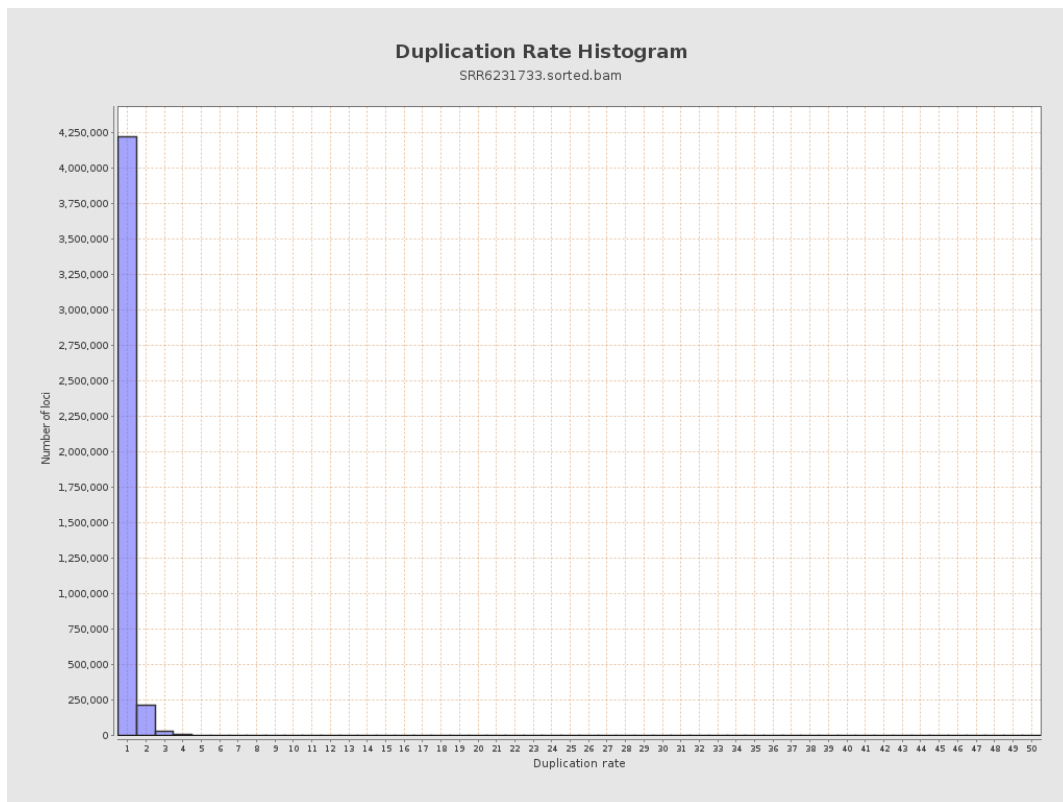
5. Results : Coverage Histogram (0-50X)



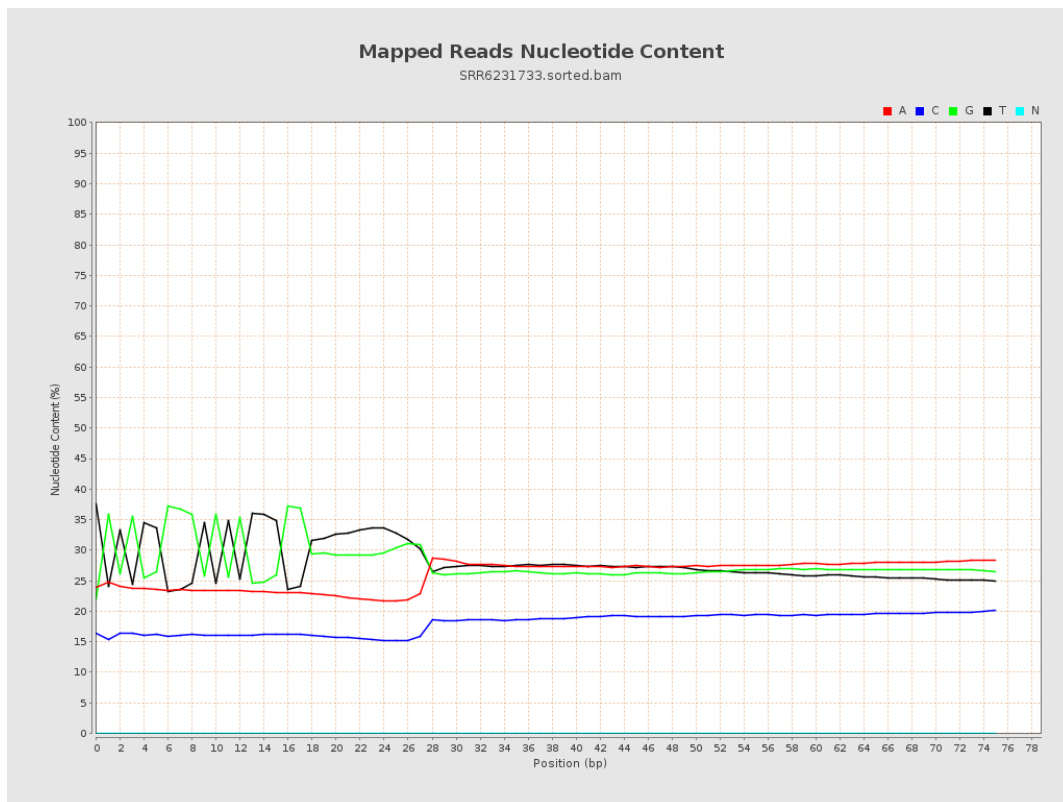
6. Results : Genome Fraction Coverage



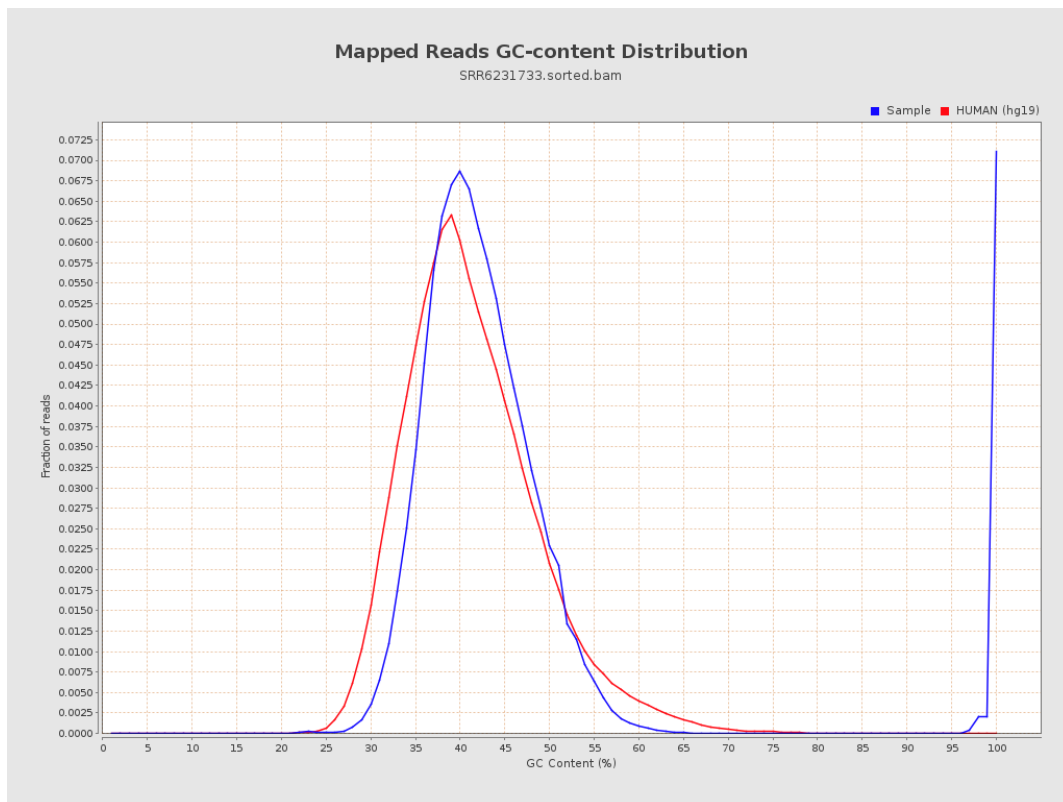
7. Results : Duplication Rate Histogram



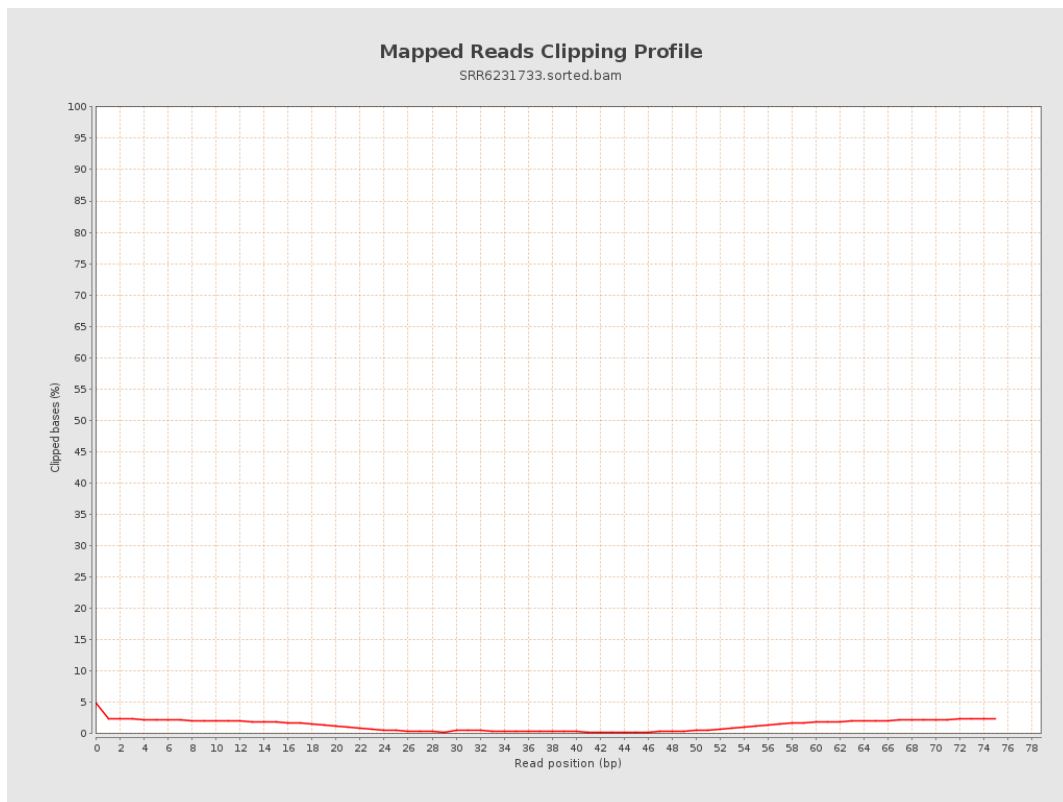
8. Results : Mapped Reads Nucleotide Content



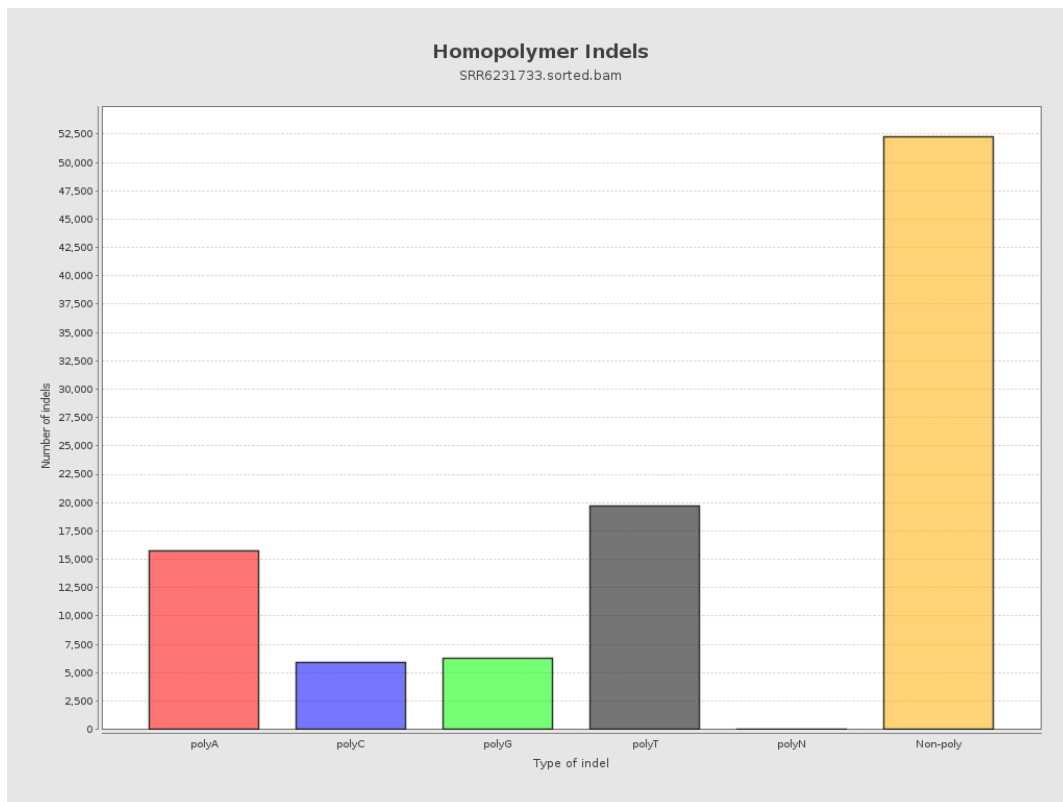
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

