

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:38:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231799.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_SRR6231799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:38:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,673,955
Mapped reads	2,149,787 / 80.4%
Unmapped reads	524,168 / 19.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,473 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	161,683 / 6.05%
Duplication rate	2.62%
Clipped reads	1,349,758 / 50.48%

2.2. ACGT Content

Number/percentage of A's	38,763,356 / 28.98%
Number/percentage of C's	25,489,063 / 19.05%
Number/percentage of T's	36,213,742 / 27.07%
Number/percentage of G's	33,295,250 / 24.89%
Number/percentage of N's	10,096 / 0.01%
GC Percentage	43.94%

2.3. Coverage

Mean	0.0432

Standard Deviation	11.8541
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2.4. Mapping Quality

Mean Mapping Quality	42.79
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2.5. Mismatches and indels

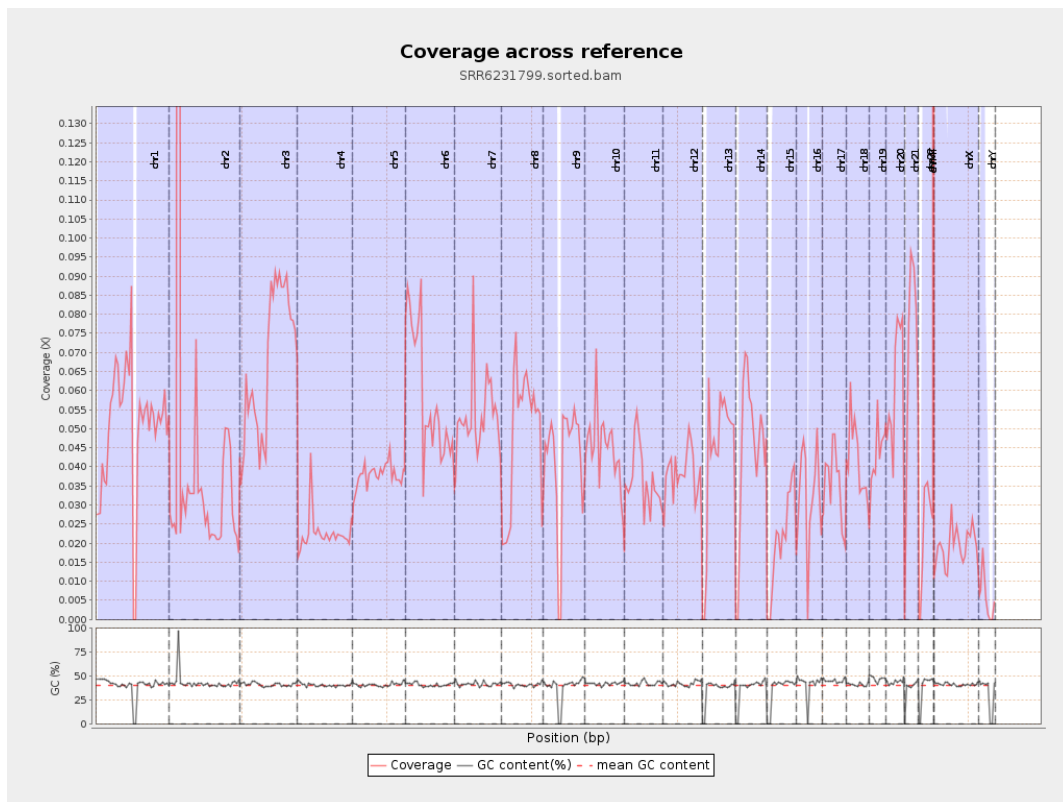
General error rate	0.7%
Mismatches	915,810
Insertions	9,955
Mapped reads with at least one insertion	0.46%
Deletions	31,260
Mapped reads with at least one deletion	1.44%
Homopolymer indels	42.79%

2.6. Chromosome stats

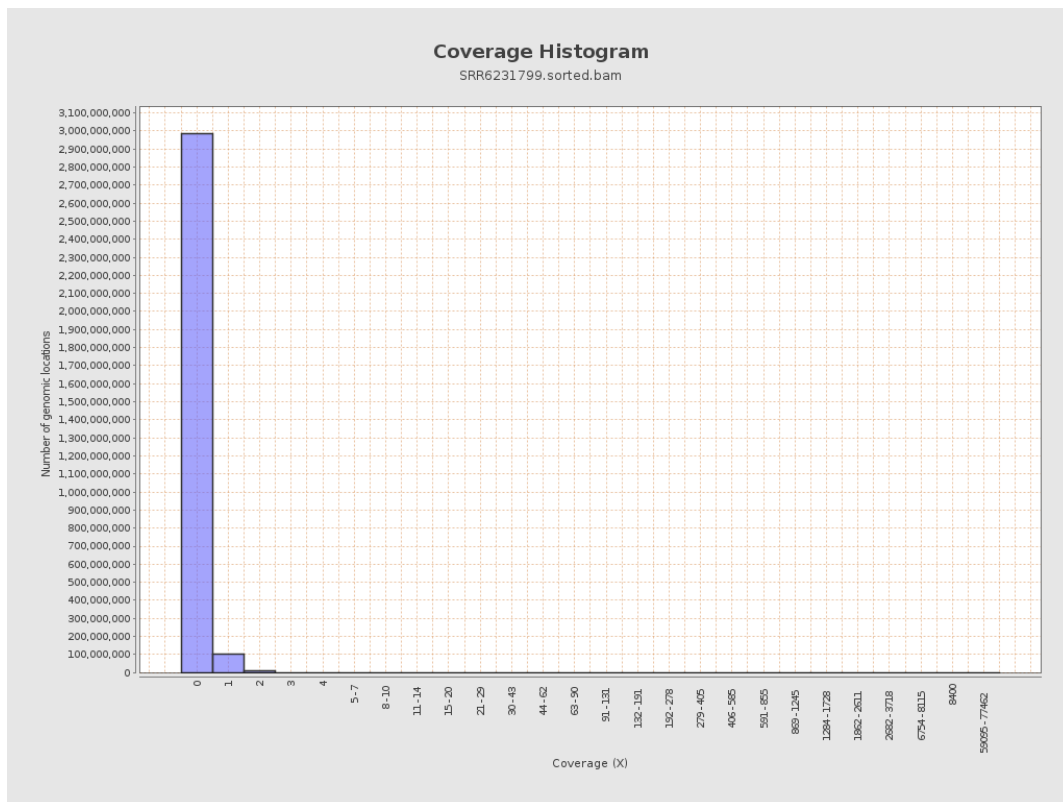
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12534088	0.0503	0.8085
chr2	243199373	13797266	0.0567	42.2684
chr3	198022430	13333422	0.0673	0.2858
chr4	191154276	4286922	0.0224	0.1873
chr5	180915260	6866589	0.038	0.2165
chr6	171115067	10041638	0.0587	0.3397
chr7	159138663	8567348	0.0538	0.6377

chr8	146364022	7016880	0.0479	0.6054
chr9	141213431	5921839	0.0419	0.3445
chr10	135534747	6105378	0.045	0.3846
chr11	135006516	4882483	0.0362	0.3441
chr12	133851895	5115669	0.0382	0.222
chr13	115169878	4969538	0.0431	0.2273
chr14	107349540	4817269	0.0449	0.3662
chr15	102531392	2183635	0.0213	0.1665
chr16	90354753	2971409	0.0329	0.2381
chr17	81195210	2828412	0.0348	0.2259
chr18	78077248	3263410	0.0418	0.7364
chr19	59128983	2572296	0.0435	0.5339
chr20	63025520	3867962	0.0614	0.2867
chr21	48129895	3283848	0.0682	0.301
chr22	51304566	1166900	0.0227	0.1635
chrMT	16571	123594	7.4585	5.3637
chrX	155270560	2980517	0.0192	0.2071
chrY	59373566	325162	0.0055	0.1149

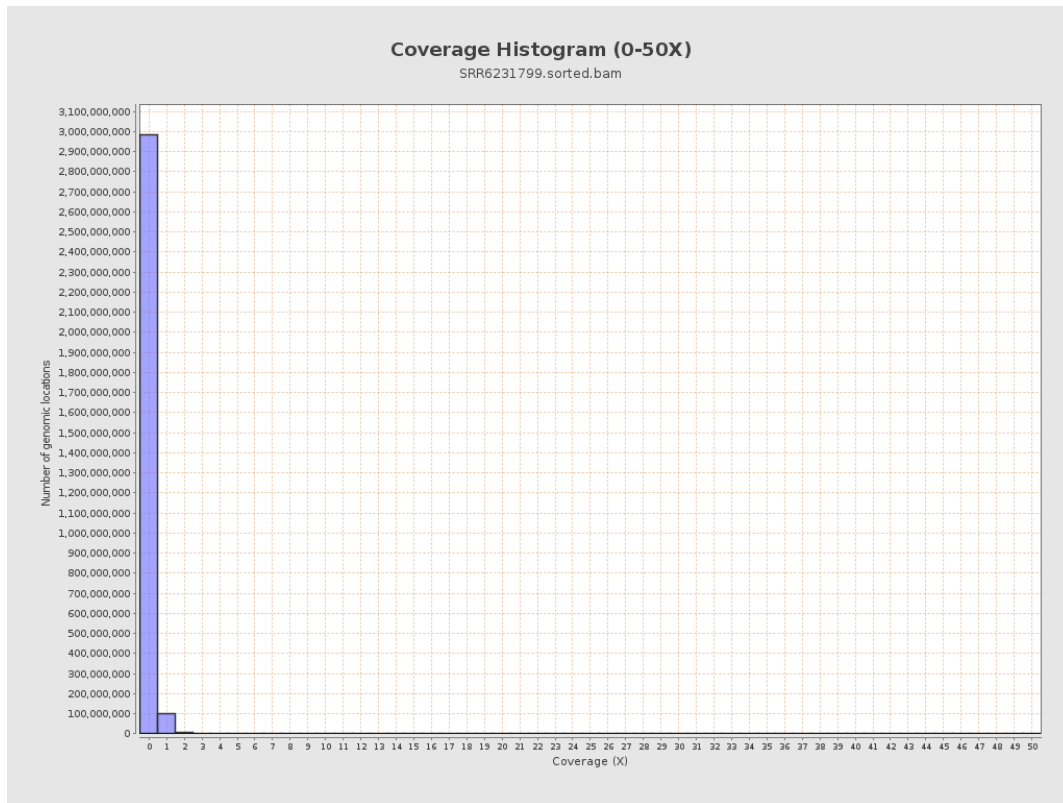
3. Results : Coverage across reference



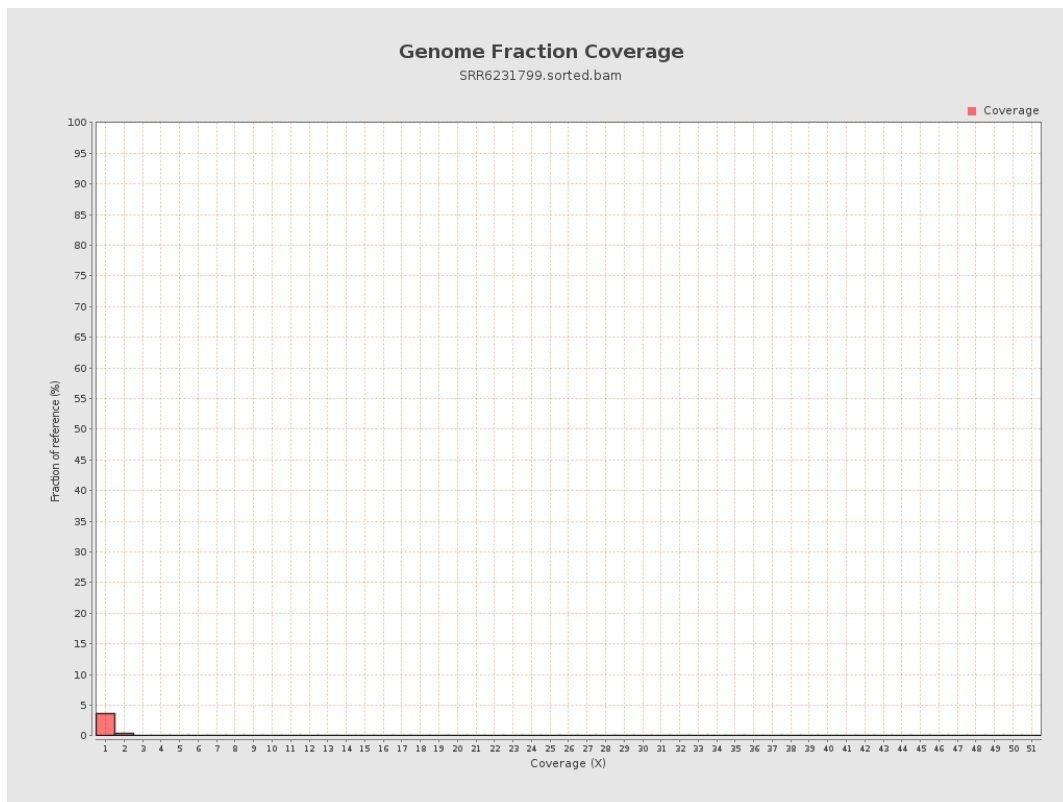
4. Results : Coverage Histogram



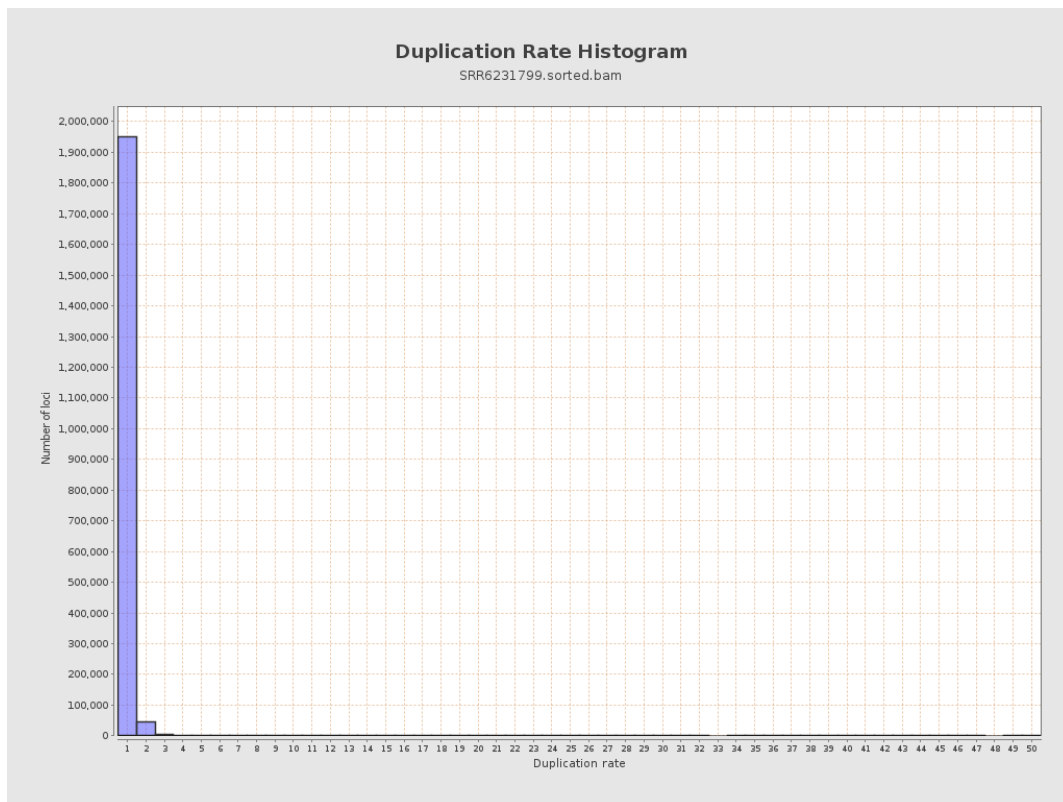
5. Results : Coverage Histogram (0-50X)



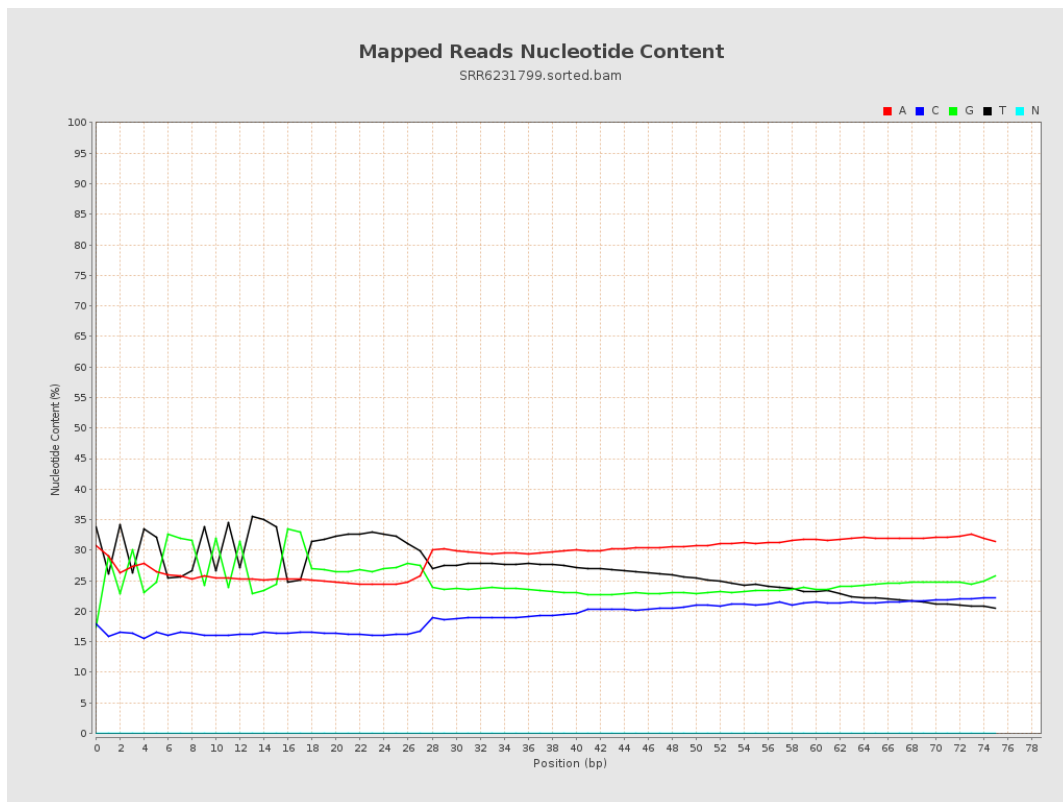
6. Results : Genome Fraction Coverage



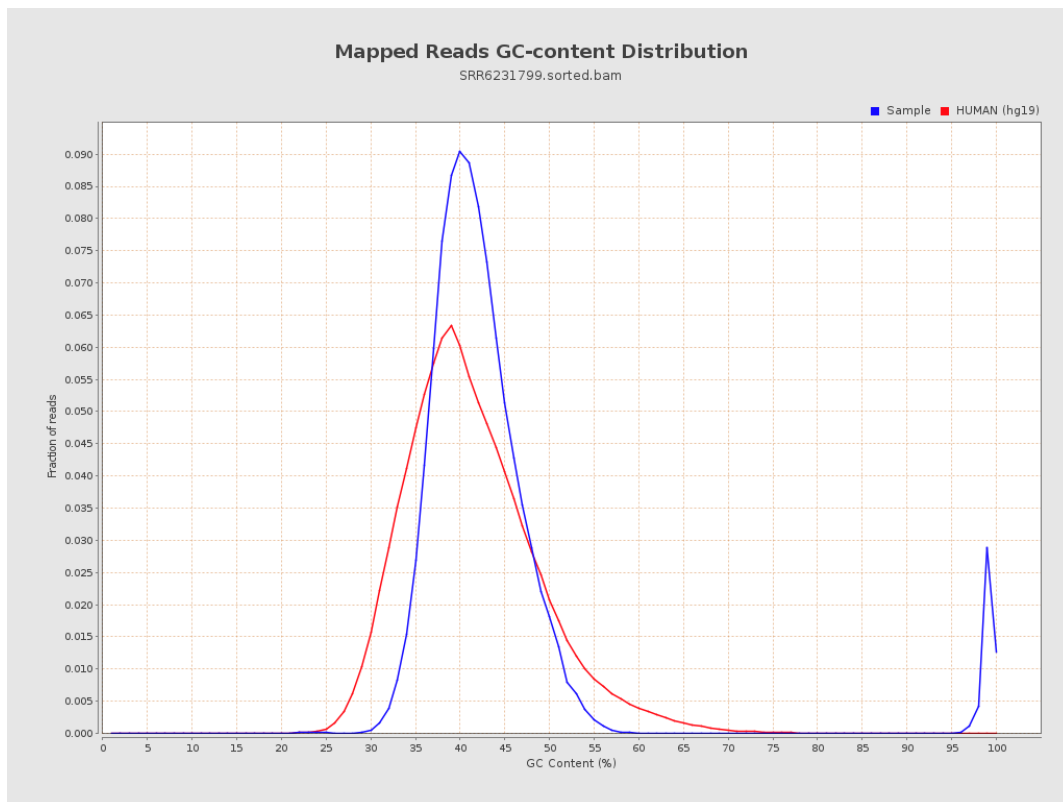
7. Results : Duplication Rate Histogram



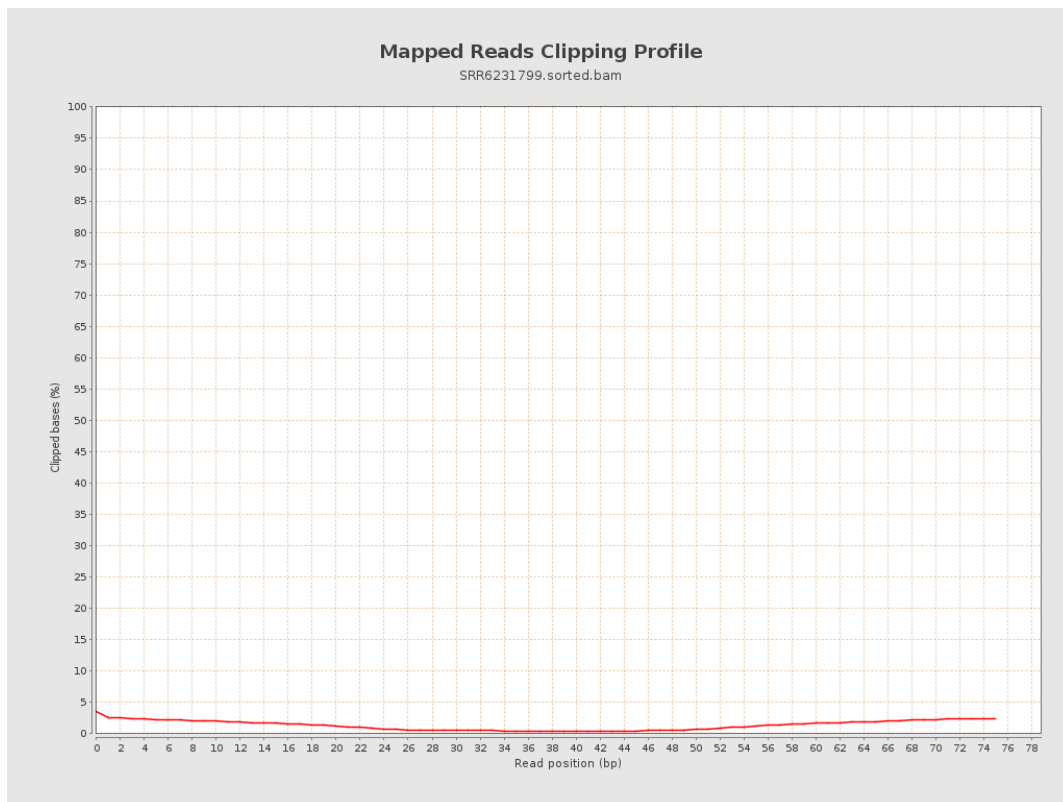
8. Results : Mapped Reads Nucleotide Content



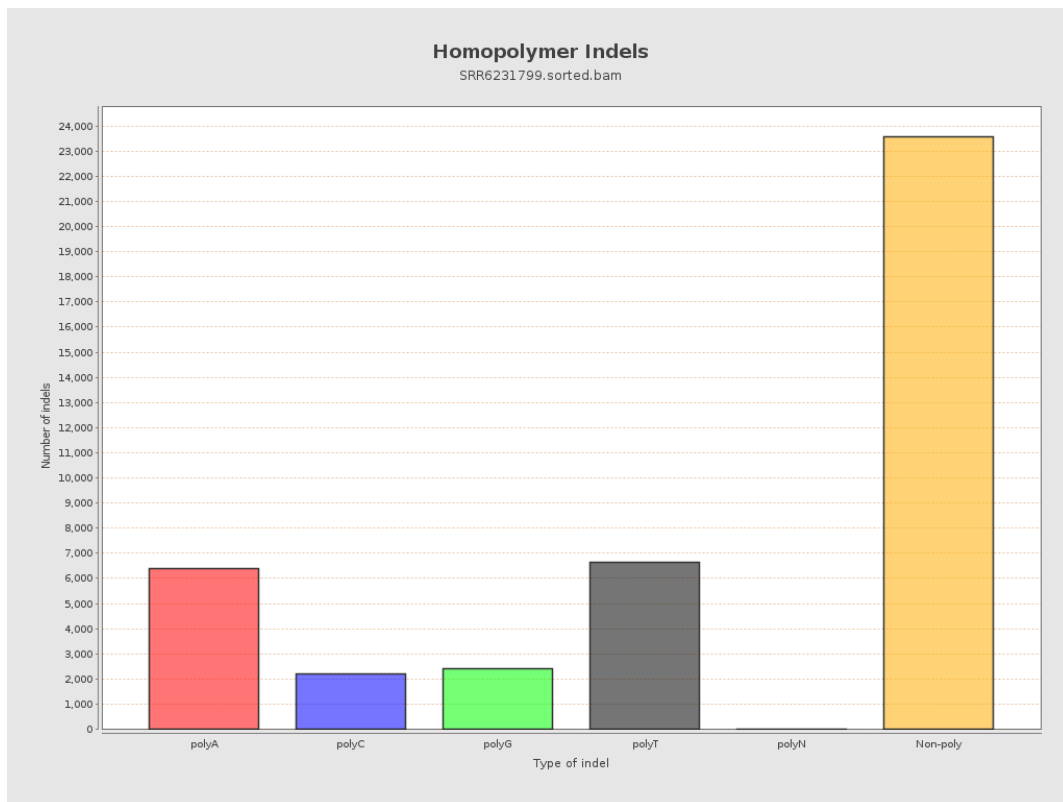
9. Results : Mapped Reads GC-content Distribution



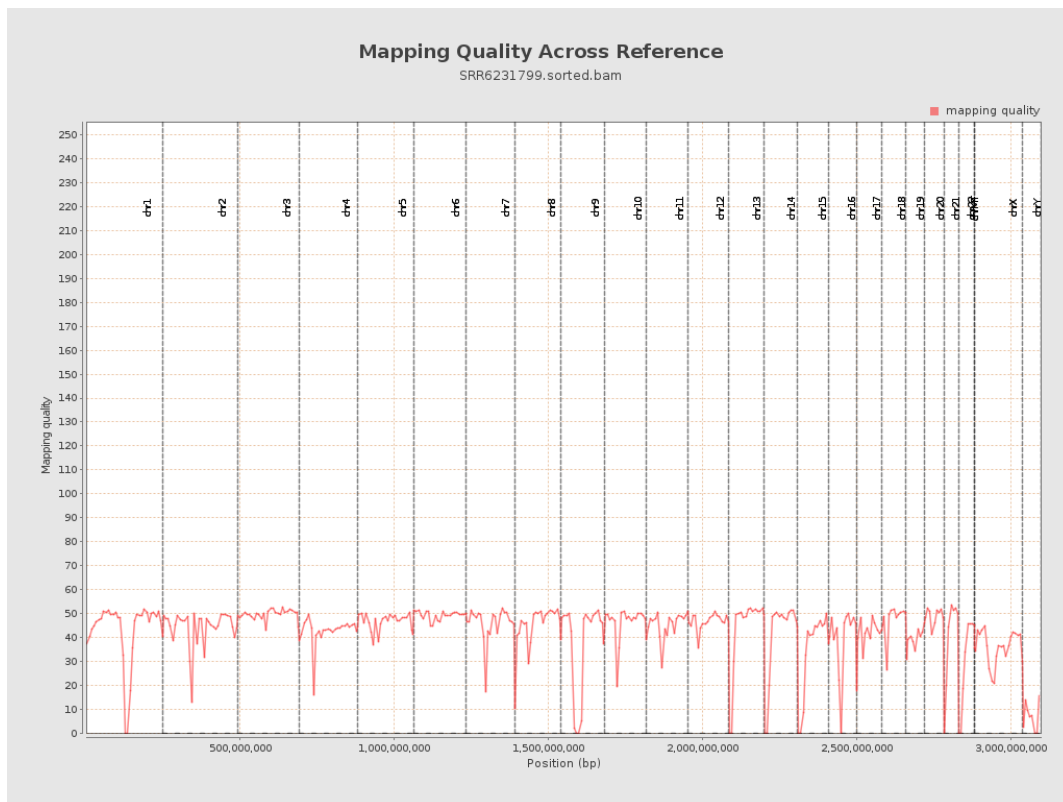
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

