

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:05:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231792.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_SRR6231792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:05:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,575,337
Mapped reads	2,981,530 / 83.39%
Unmapped reads	593,807 / 16.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,083 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	771,574 / 21.58%
Duplication rate	17.98%
Clipped reads	1,756,354 / 49.12%

2.2. ACGT Content

Number/percentage of A's	47,125,535 / 25.25%
Number/percentage of C's	33,409,495 / 17.9%
Number/percentage of T's	61,670,872 / 33.04%
Number/percentage of G's	44,371,626 / 23.77%
Number/percentage of N's	68,496 / 0.04%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0603

Standard Deviation	0.9286
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2.4. Mapping Quality

Mean Mapping Quality	40.14
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2.5. Mismatches and indels

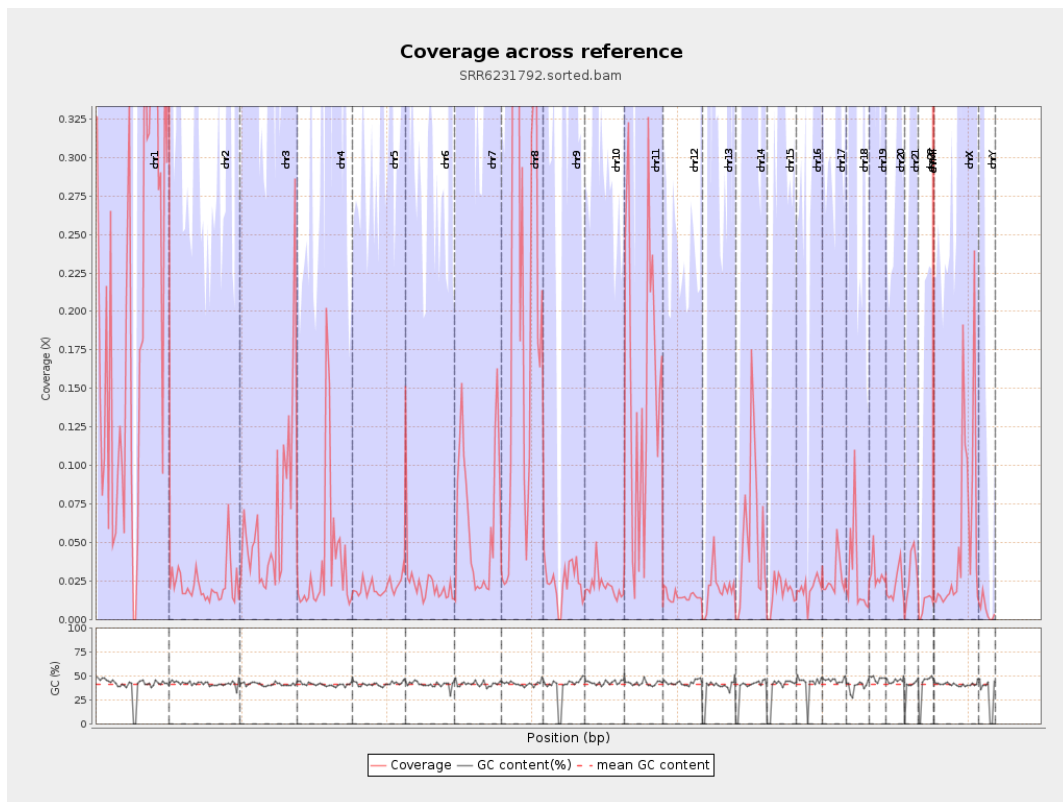
General error rate	0.69%
Mismatches	1,275,145
Insertions	11,909
Mapped reads with at least one insertion	0.4%
Deletions	52,467
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.18%

2.6. Chromosome stats

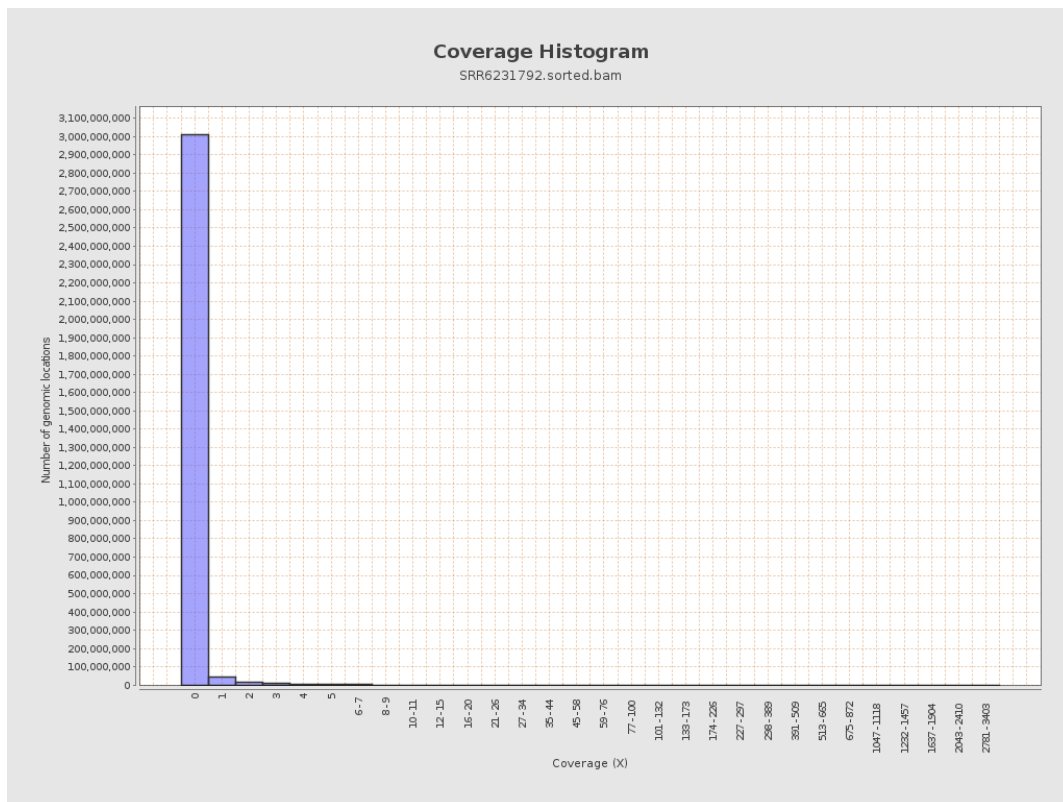
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	49615427	0.1991	0.9995
chr2	243199373	5437380	0.0224	1.5913
chr3	198022430	12909426	0.0652	0.5088
chr4	191154276	7051260	0.0369	0.3577
chr5	180915260	3789188	0.0209	0.282
chr6	171115067	4202740	0.0246	0.8155
chr7	159138663	10097010	0.0634	0.5842

chr8	146364022	33484392	0.2288	1.5415
chr9	141213431	3411387	0.0242	0.3113
chr10	135534747	2935168	0.0217	0.3683
chr11	135006516	20340244	0.1507	0.7511
chr12	133851895	2023987	0.0151	0.2339
chr13	115169878	2243623	0.0195	0.6362
chr14	107349540	6023148	0.0561	0.4632
chr15	102531392	1820435	0.0178	0.3169
chr16	90354753	1842544	0.0204	0.2954
chr17	81195210	2198024	0.0271	0.3046
chr18	78077248	2239847	0.0287	2.9964
chr19	59128983	1759037	0.0297	0.4187
chr20	63025520	1357525	0.0215	0.2735
chr21	48129895	1386503	0.0288	0.3099
chr22	51304566	505875	0.0099	0.171
chrMT	16571	1592522	96.103	63.3121
chrX	155270560	8119630	0.0523	0.4352
chrY	59373566	344226	0.0058	0.2595

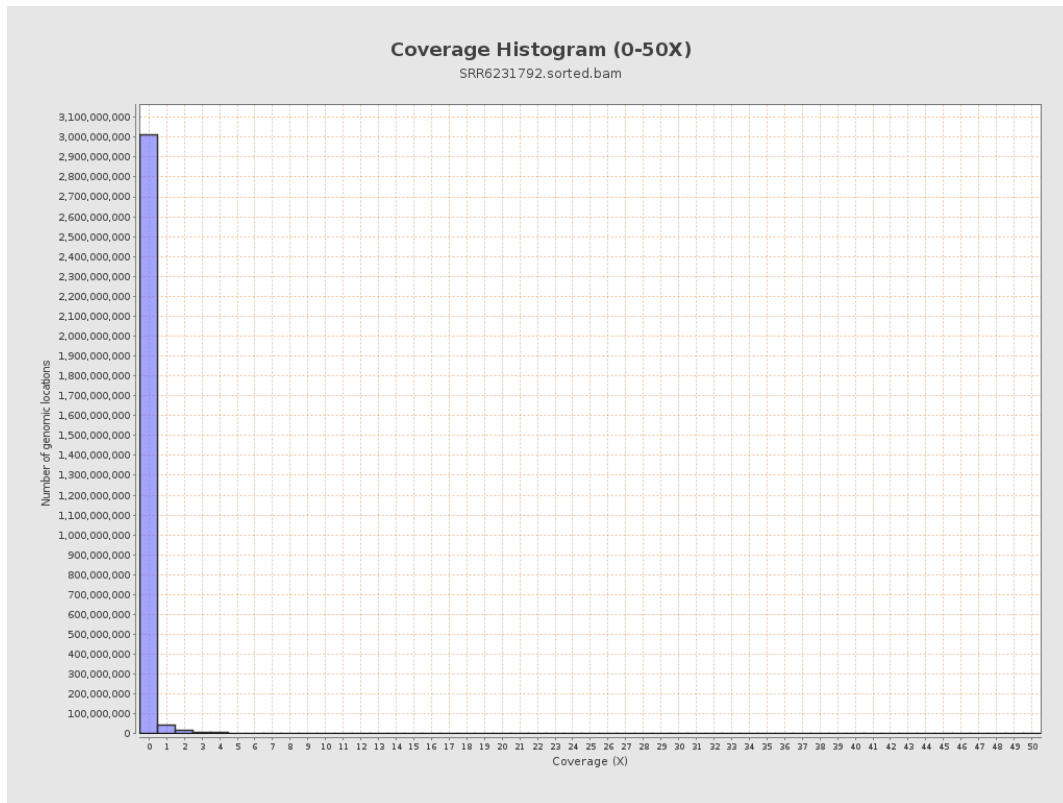
3. Results : Coverage across reference



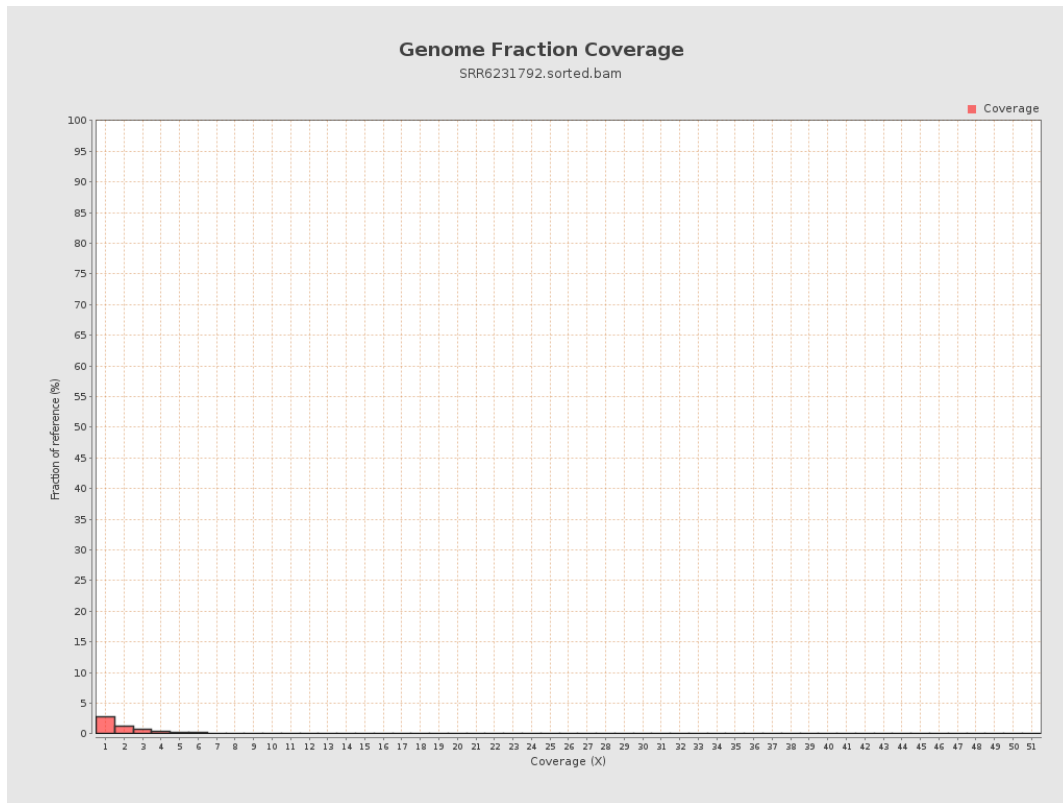
4. Results : Coverage Histogram



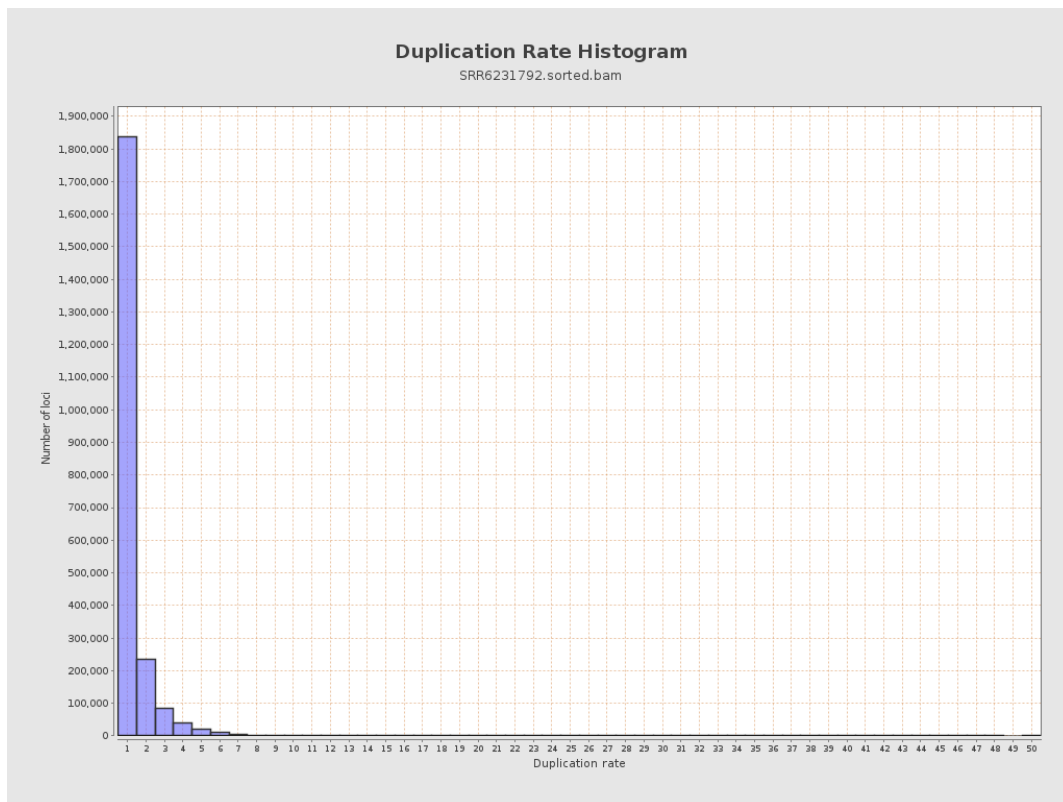
5. Results : Coverage Histogram (0-50X)



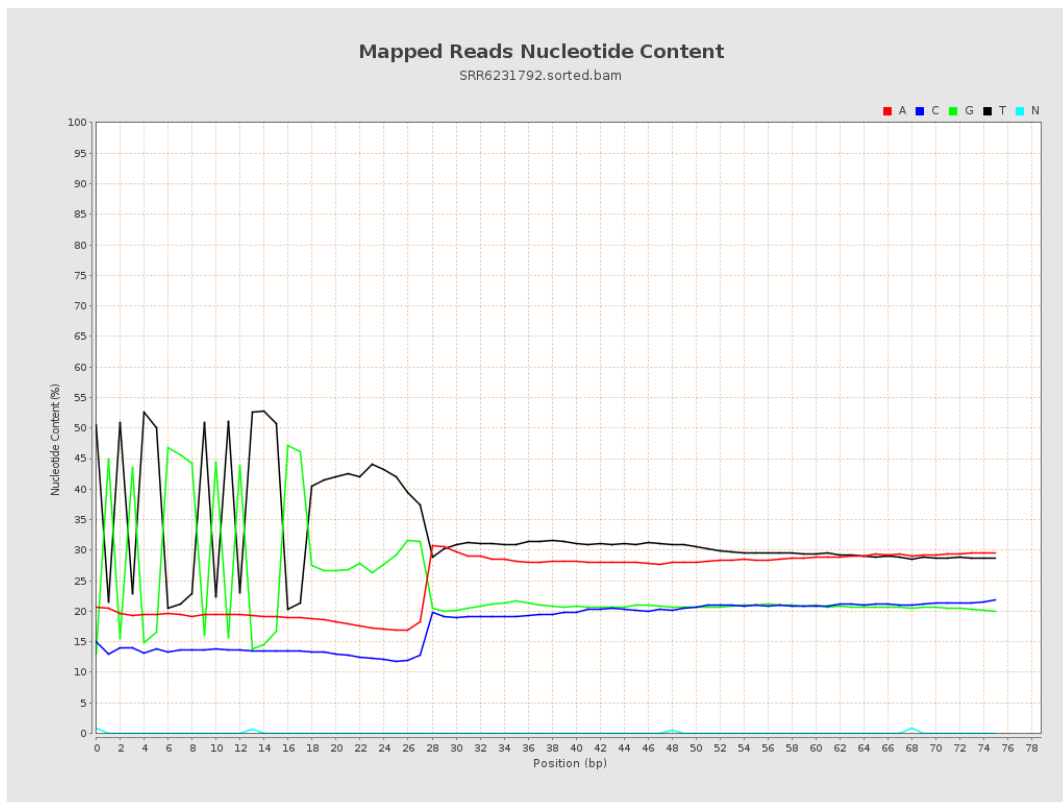
6. Results : Genome Fraction Coverage



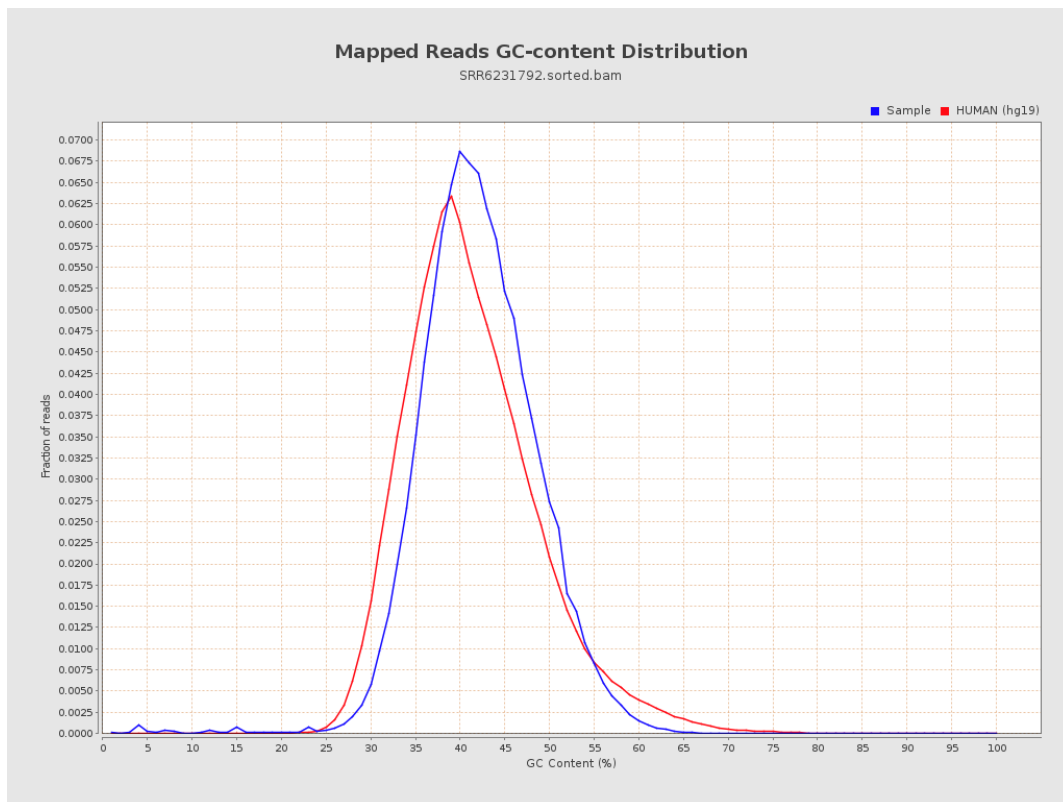
7. Results : Duplication Rate Histogram



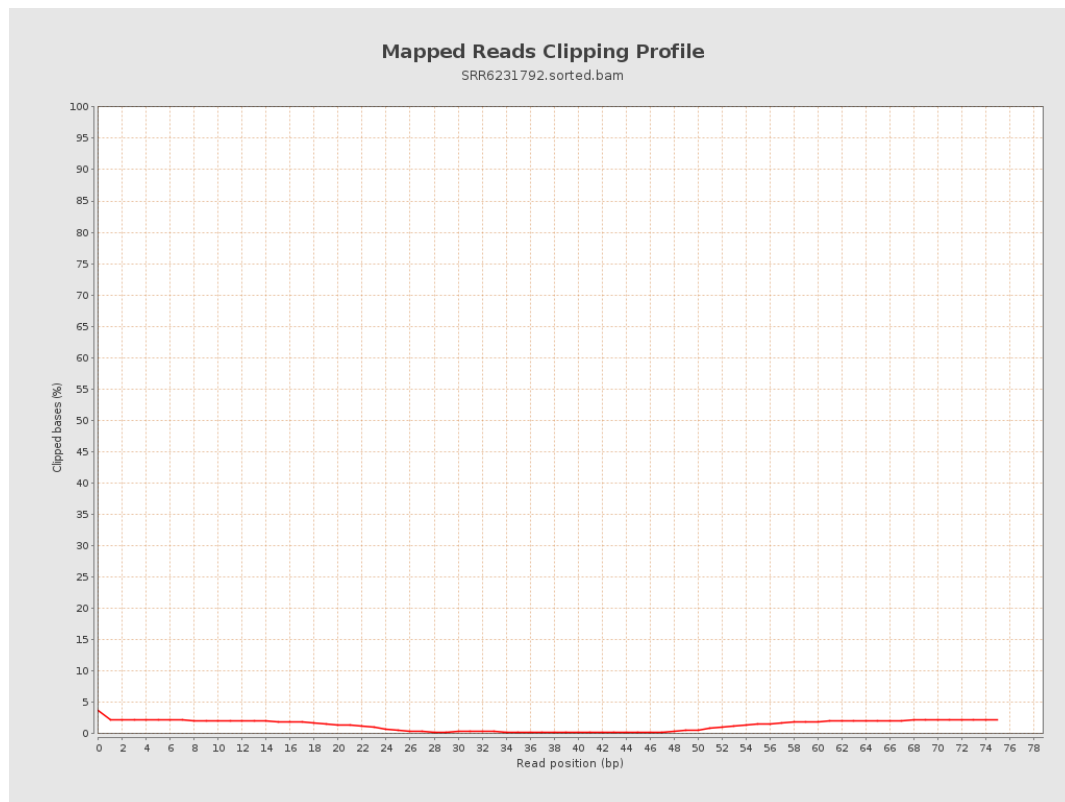
8. Results : Mapped Reads Nucleotide Content



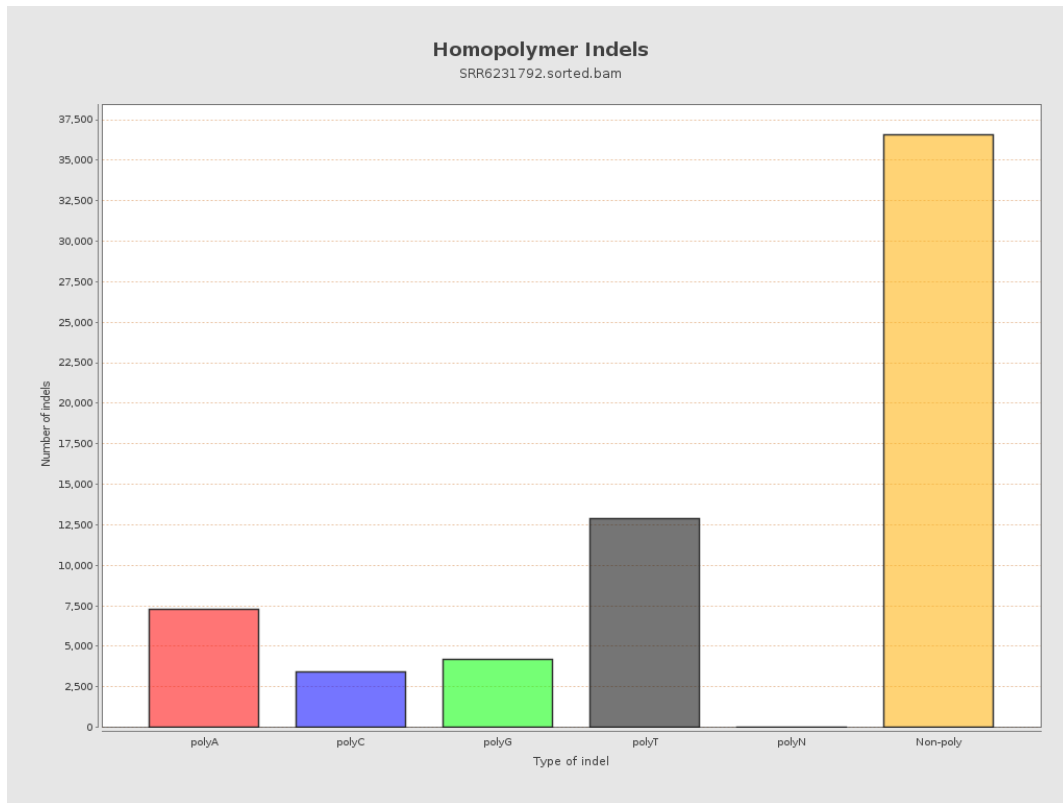
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

