

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:48:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237792.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_SRR6237792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:48:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,234,111
Mapped reads	3,665,729 / 86.58%
Unmapped reads	568,382 / 13.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,530 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	743,058 / 17.55%
Duplication rate	14.43%
Clipped reads	1,128,158 / 26.64%

2.2. ACGT Content

Number/percentage of A's	74,867,342 / 29.13%
Number/percentage of C's	49,385,212 / 19.21%
Number/percentage of T's	78,778,366 / 30.65%
Number/percentage of G's	53,580,616 / 20.85%
Number/percentage of N's	428,655 / 0.17%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0831

Standard Deviation	1.2654
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2.4. Mapping Quality

Mean Mapping Quality	47.4
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2.5. Mismatches and indels

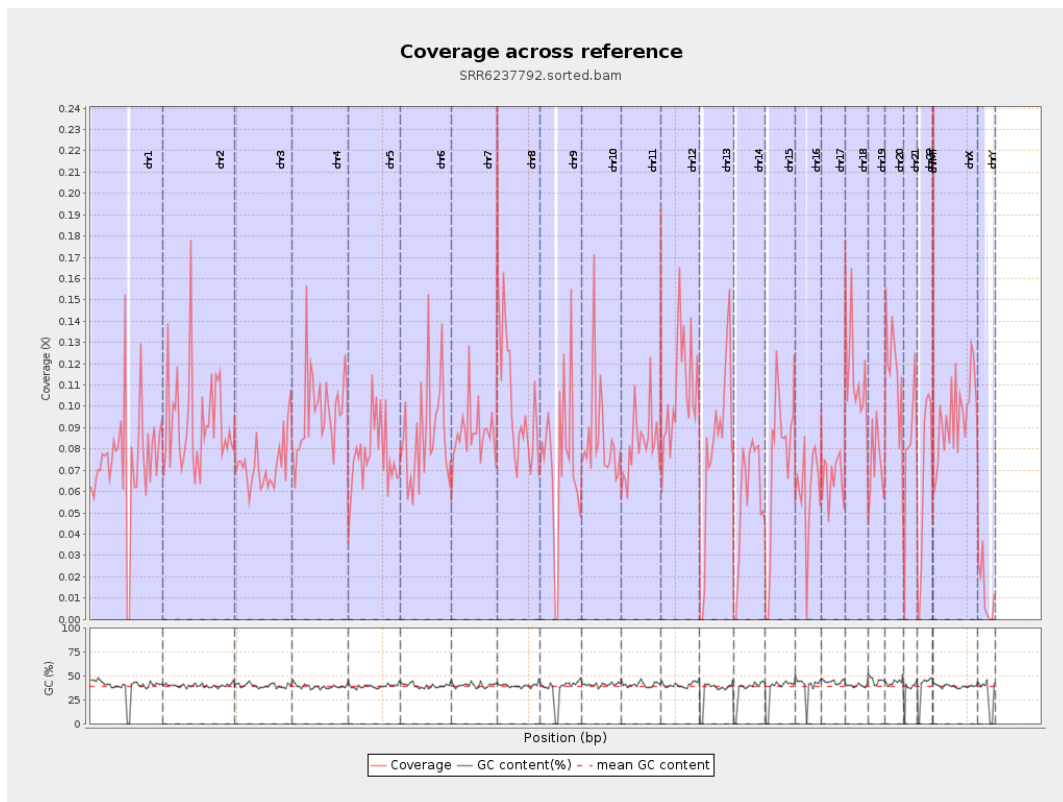
General error rate	0.84%
Mismatches	2,128,813
Insertions	19,151
Mapped reads with at least one insertion	0.52%
Deletions	60,085
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.3%

2.6. Chromosome stats

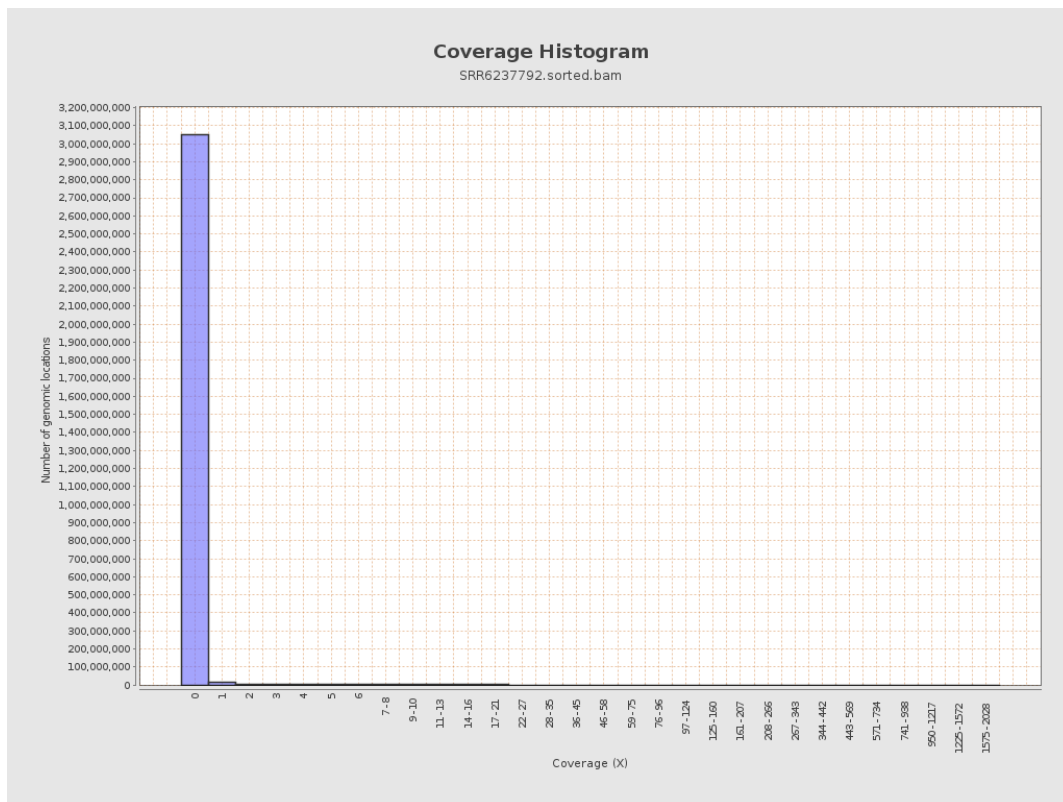
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18561812	0.0745	1.8661
chr2	243199373	22583798	0.0929	1.385
chr3	198022430	14454165	0.073	1.014
chr4	191154276	18684550	0.0977	1.2235
chr5	180915260	13991984	0.0773	1.0669
chr6	171115067	14906991	0.0871	1.1418
chr7	159138663	13812153	0.0868	1.359

chr8	146364022	14880564	0.1017	1.495
chr9	141213431	10528536	0.0746	1.14
chr10	135534747	11560624	0.0853	1.239
chr11	135006516	11192184	0.0829	1.1488
chr12	133851895	14313377	0.1069	1.2704
chr13	115169878	9349497	0.0812	1.0828
chr14	107349540	6215879	0.0579	0.9077
chr15	102531392	7595130	0.0741	1.0373
chr16	90354753	5406820	0.0598	0.9497
chr17	81195210	5414961	0.0667	1.0023
chr18	78077248	9044061	0.1158	1.7633
chr19	59128983	4391142	0.0743	1.305
chr20	63025520	7378229	0.1171	1.3845
chr21	48129895	3957857	0.0822	1.1222
chr22	51304566	3403031	0.0663	0.9841
chrMT	16571	121421	7.3273	9.5866
chrX	155270560	14676456	0.0945	1.1736
chrY	59373566	722356	0.0122	0.3709

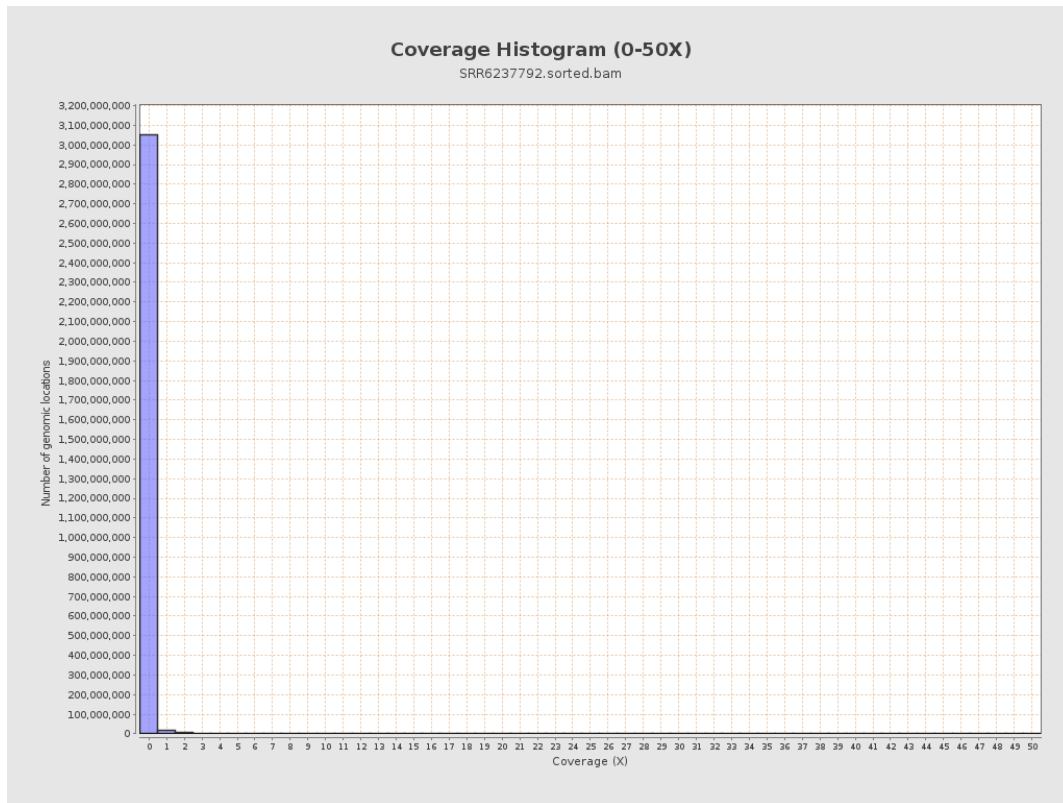
3. Results : Coverage across reference



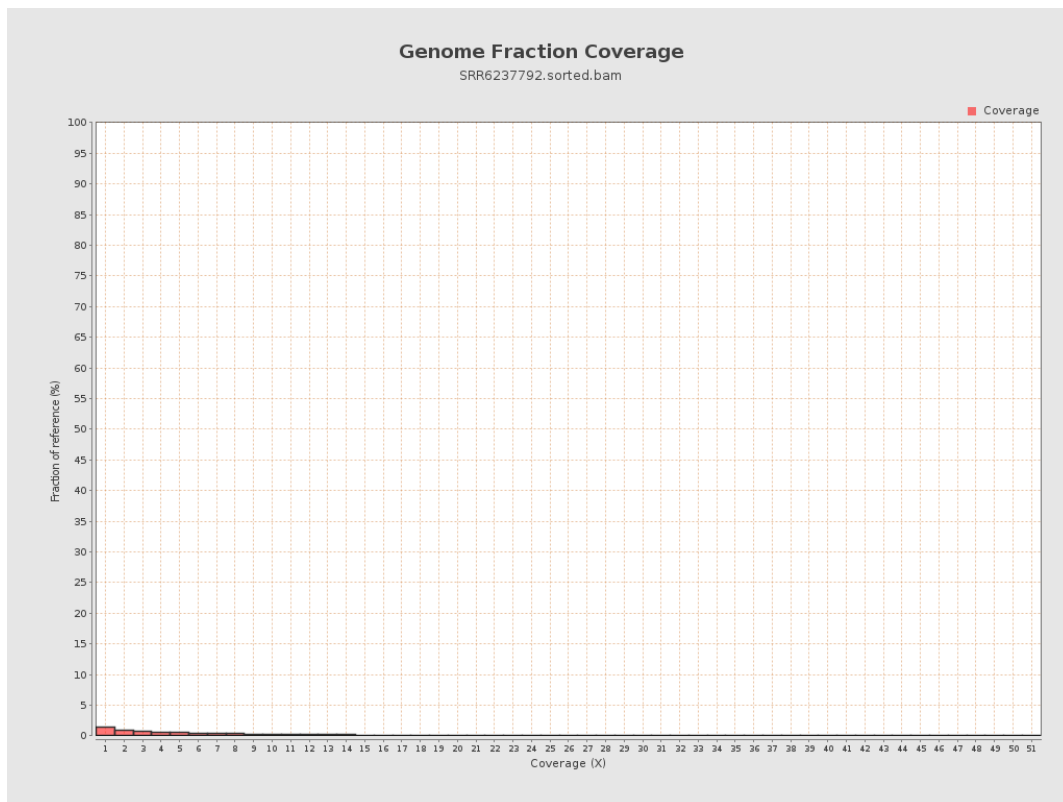
4. Results : Coverage Histogram



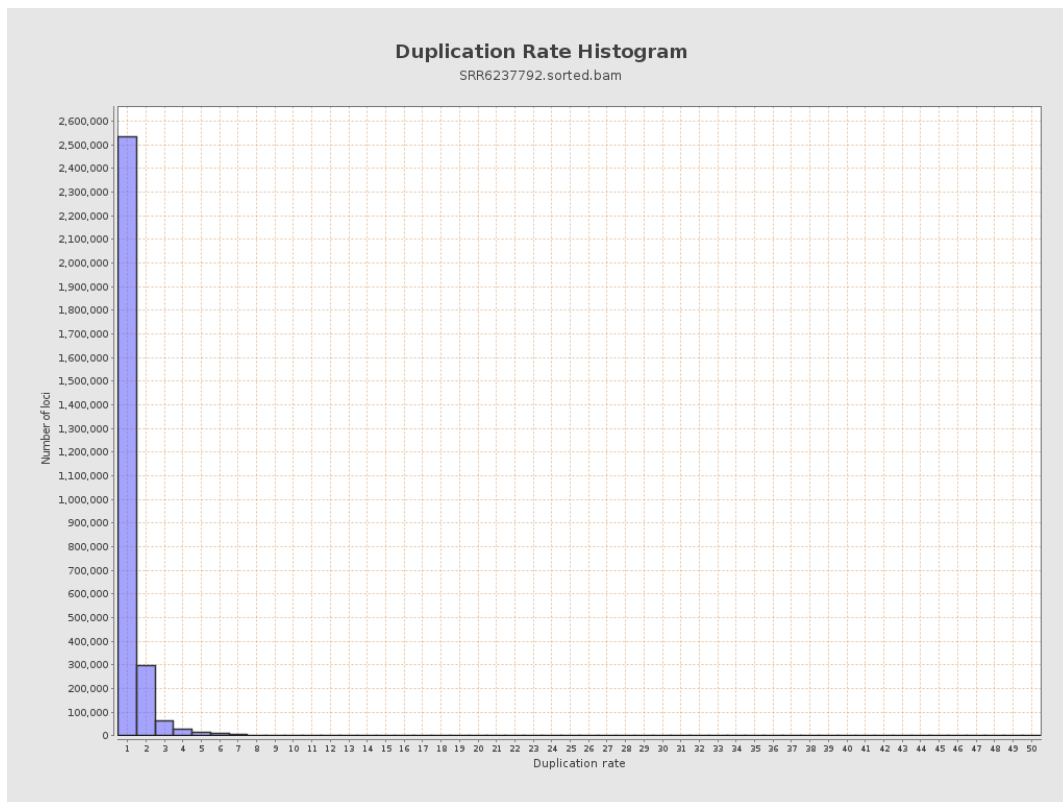
5. Results : Coverage Histogram (0-50X)



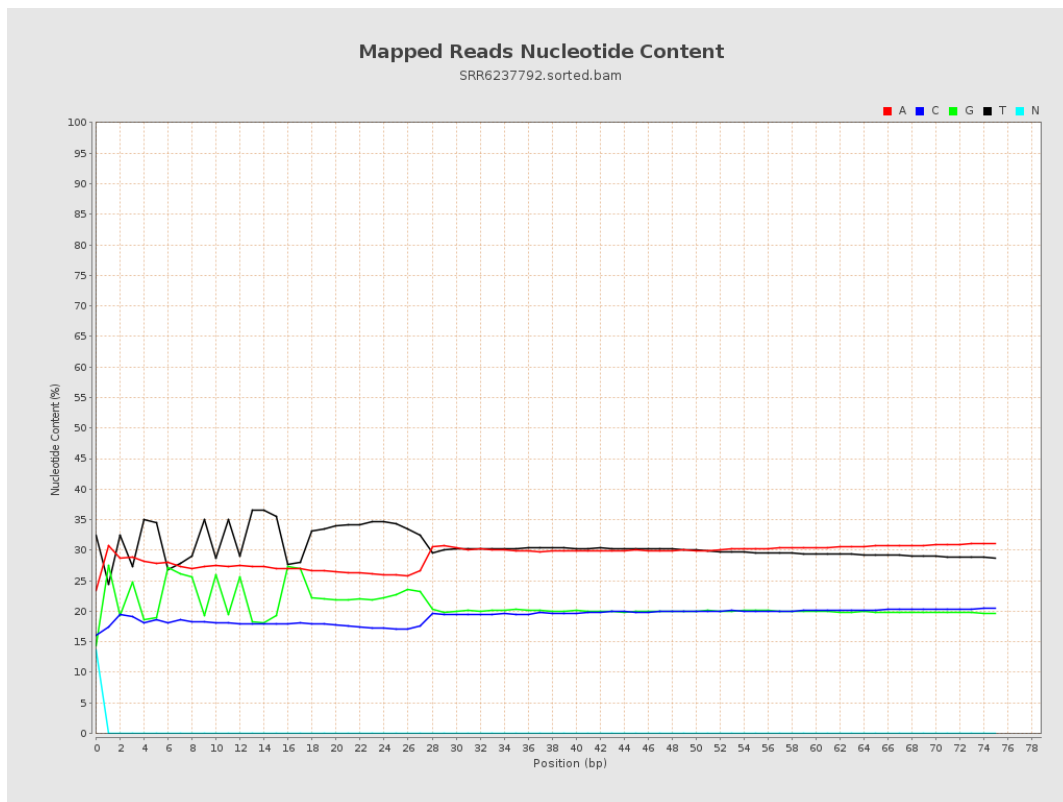
6. Results : Genome Fraction Coverage



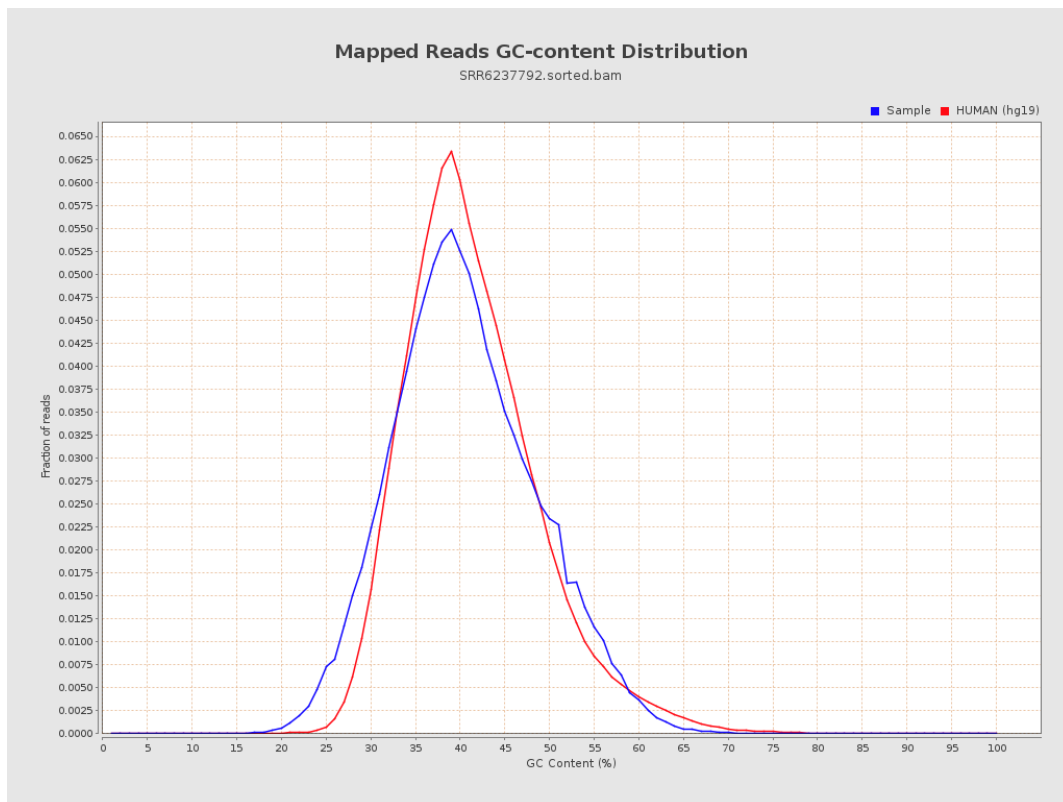
7. Results : Duplication Rate Histogram



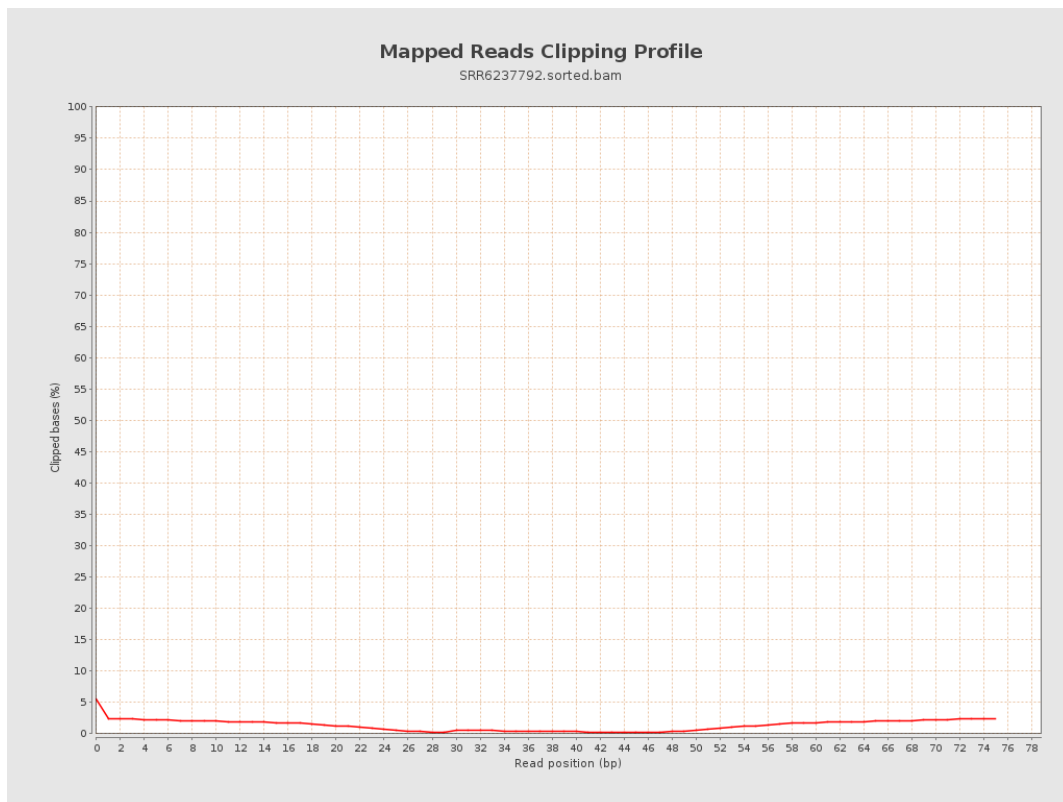
8. Results : Mapped Reads Nucleotide Content



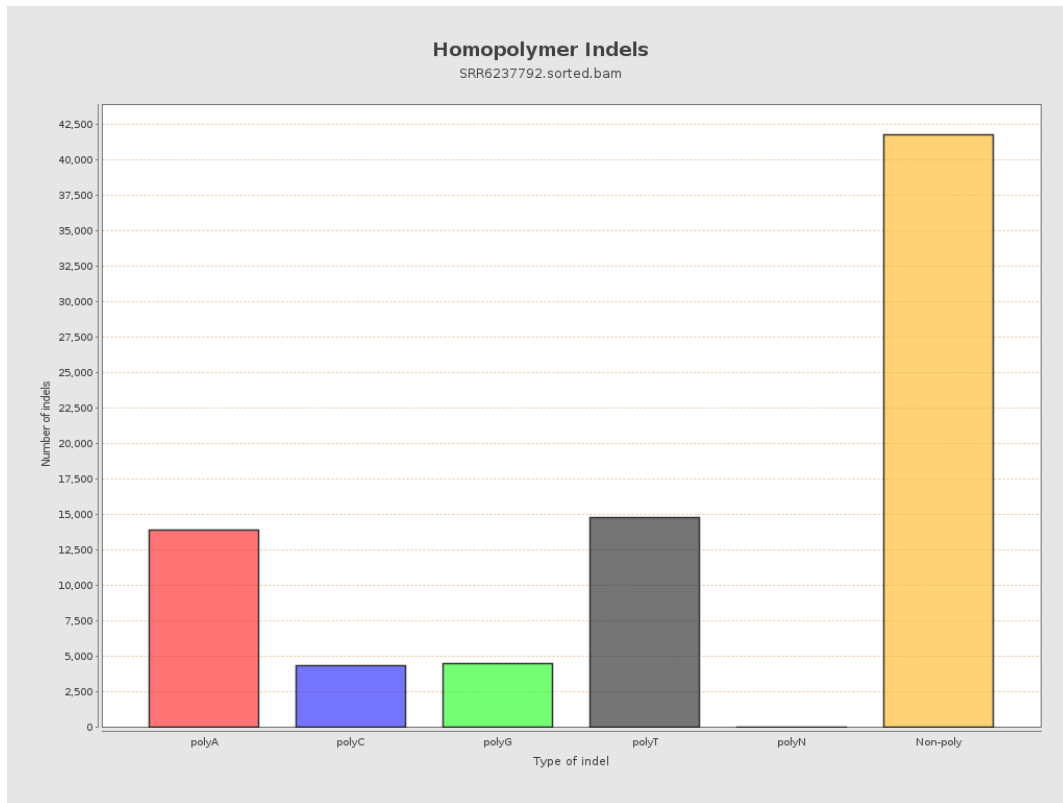
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

