

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:12:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013192.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_SRR6013192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013192.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:12:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,647,241
Mapped reads	2,143,157 / 80.96%
Unmapped reads	504,084 / 19.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,829 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	207,607 / 7.84%
Duplication rate	7.47%
Clipped reads	1,096,378 / 41.42%

2.2. ACGT Content

Number/percentage of A's	37,691,397 / 27.13%
Number/percentage of C's	25,346,201 / 18.24%
Number/percentage of T's	44,540,204 / 32.06%
Number/percentage of G's	31,351,107 / 22.57%
Number/percentage of N's	1,882 / 0%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0449

Standard Deviation	0.5813
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2.4. Mapping Quality

Mean Mapping Quality	46.16
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2.5. Mismatches and indels

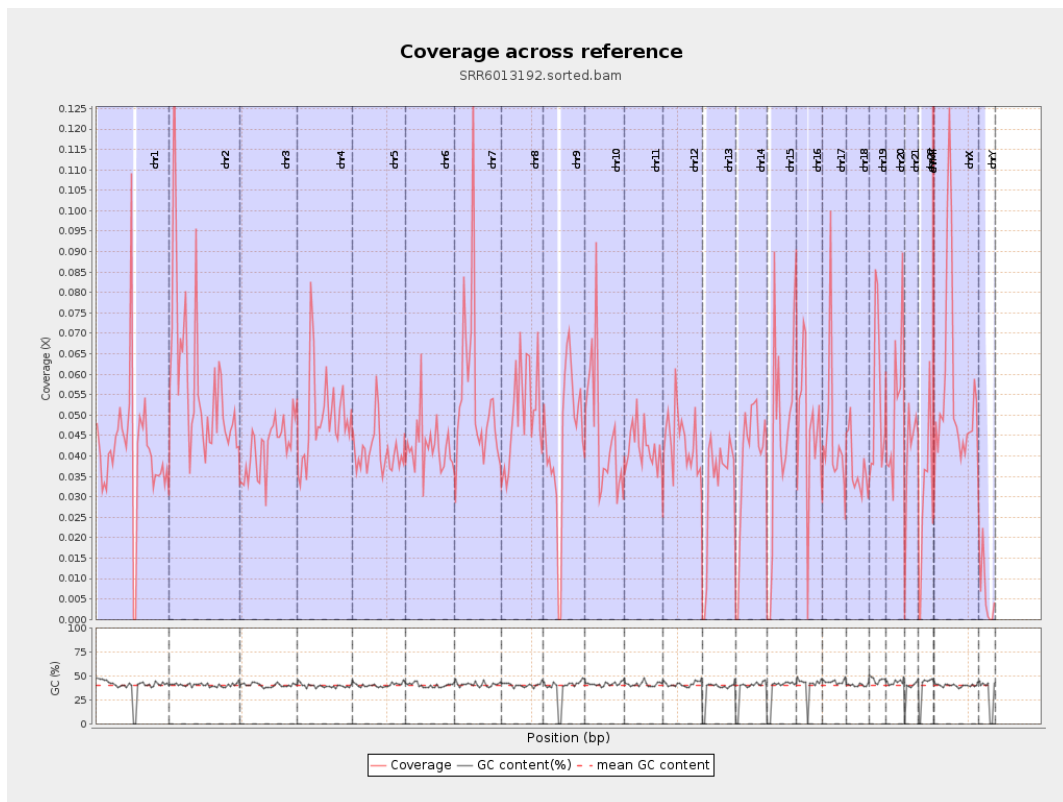
General error rate	0.78%
Mismatches	1,063,236
Insertions	9,964
Mapped reads with at least one insertion	0.46%
Deletions	38,571
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.96%

2.6. Chromosome stats

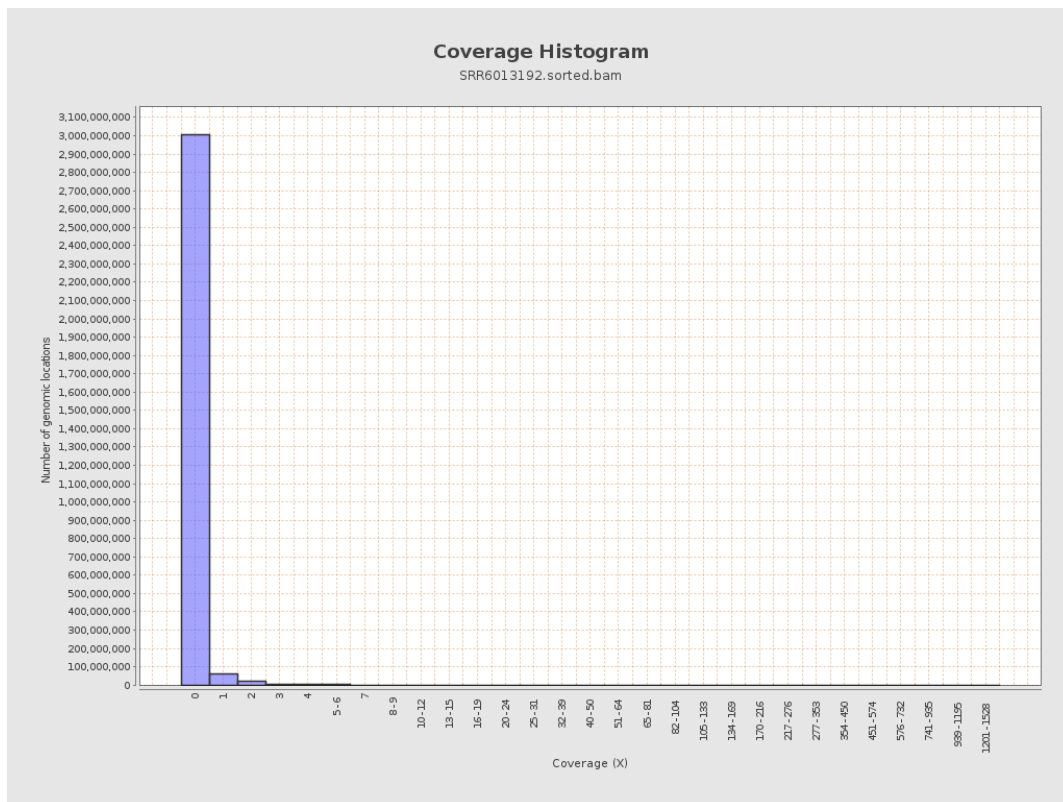
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10152726	0.0407	1.3069
chr2	243199373	14024635	0.0577	0.5293
chr3	198022430	8327646	0.0421	0.3018
chr4	191154276	9356718	0.0489	0.3461
chr5	180915260	7454406	0.0412	0.2994
chr6	171115067	7245161	0.0423	0.3745
chr7	159138663	8754467	0.055	1.0207

chr8	146364022	7340343	0.0502	0.6227
chr9	141213431	6160387	0.0436	0.394
chr10	135534747	6113528	0.0451	0.4881
chr11	135006516	5688438	0.0421	0.3678
chr12	133851895	5848887	0.0437	0.3068
chr13	115169878	3769110	0.0327	0.2639
chr14	107349540	4184403	0.039	0.3137
chr15	102531392	4623664	0.0451	0.3108
chr16	90354753	4203982	0.0465	0.3396
chr17	81195210	3648133	0.0449	0.3647
chr18	78077248	2907086	0.0372	0.6681
chr19	59128983	3233678	0.0547	0.7807
chr20	63025520	3337748	0.053	0.3462
chr21	48129895	1980919	0.0412	0.3146
chr22	51304566	1561303	0.0304	0.2509
chrMT	16571	52943	3.1949	2.8911
chrX	155270560	8665134	0.0558	0.4002
chrY	59373566	362783	0.0061	0.18

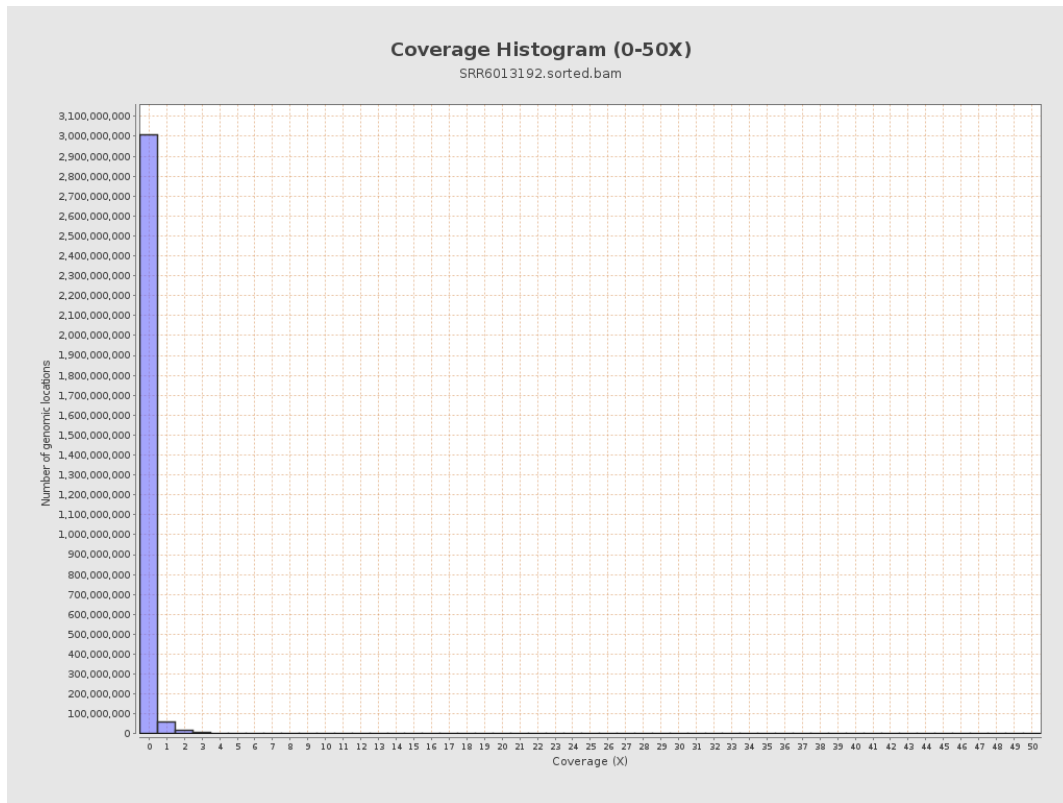
3. Results : Coverage across reference



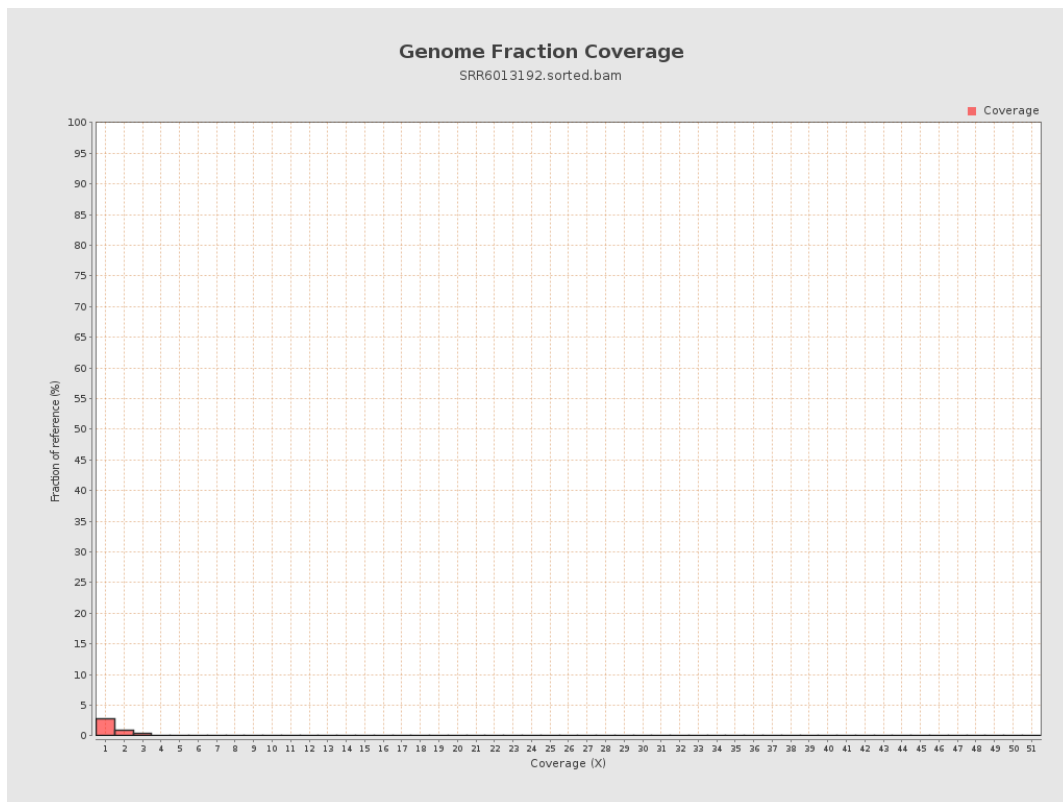
4. Results : Coverage Histogram



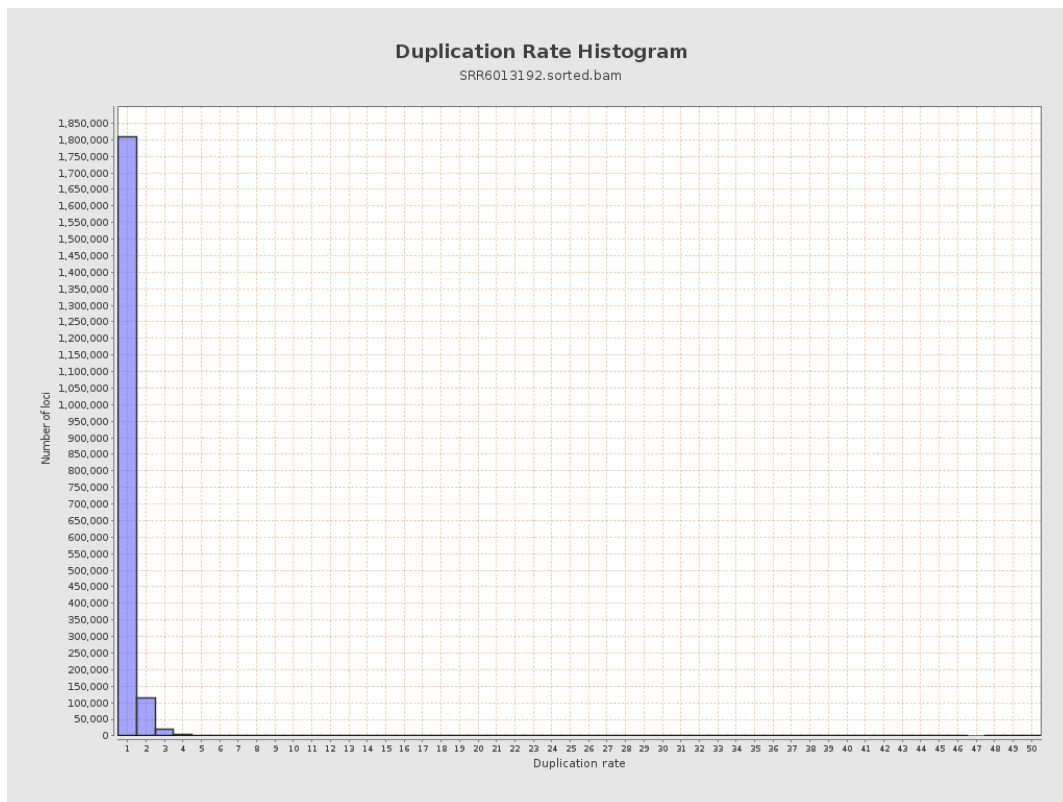
5. Results : Coverage Histogram (0-50X)



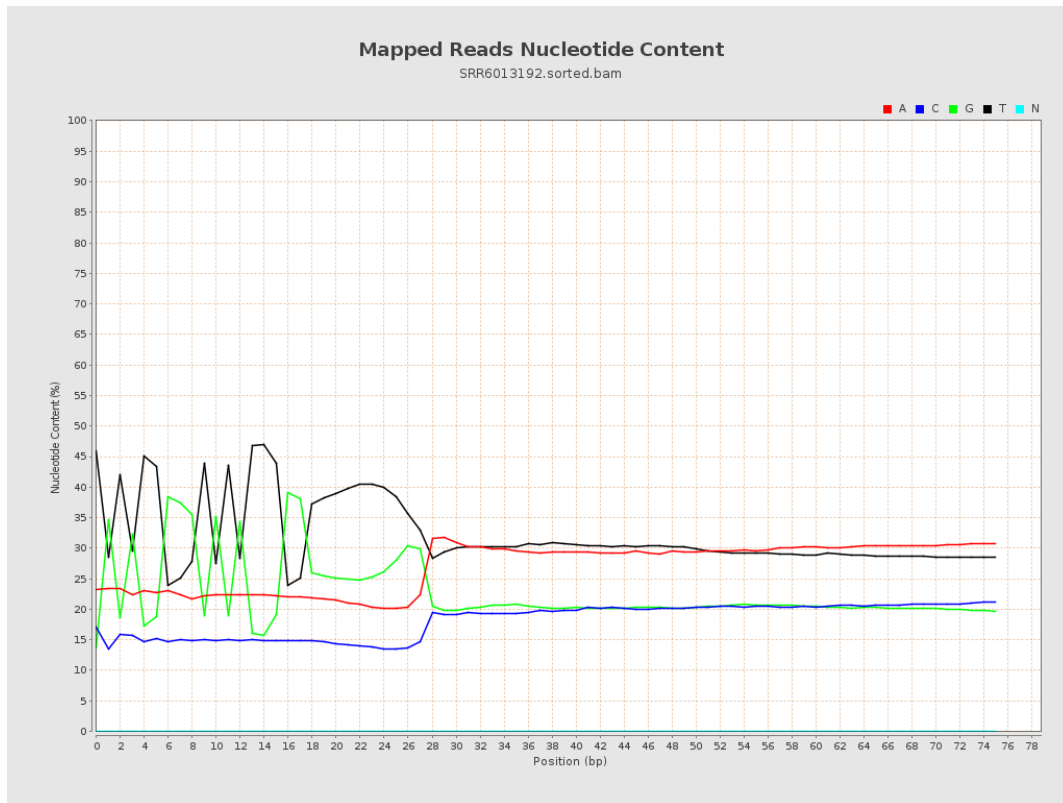
6. Results : Genome Fraction Coverage



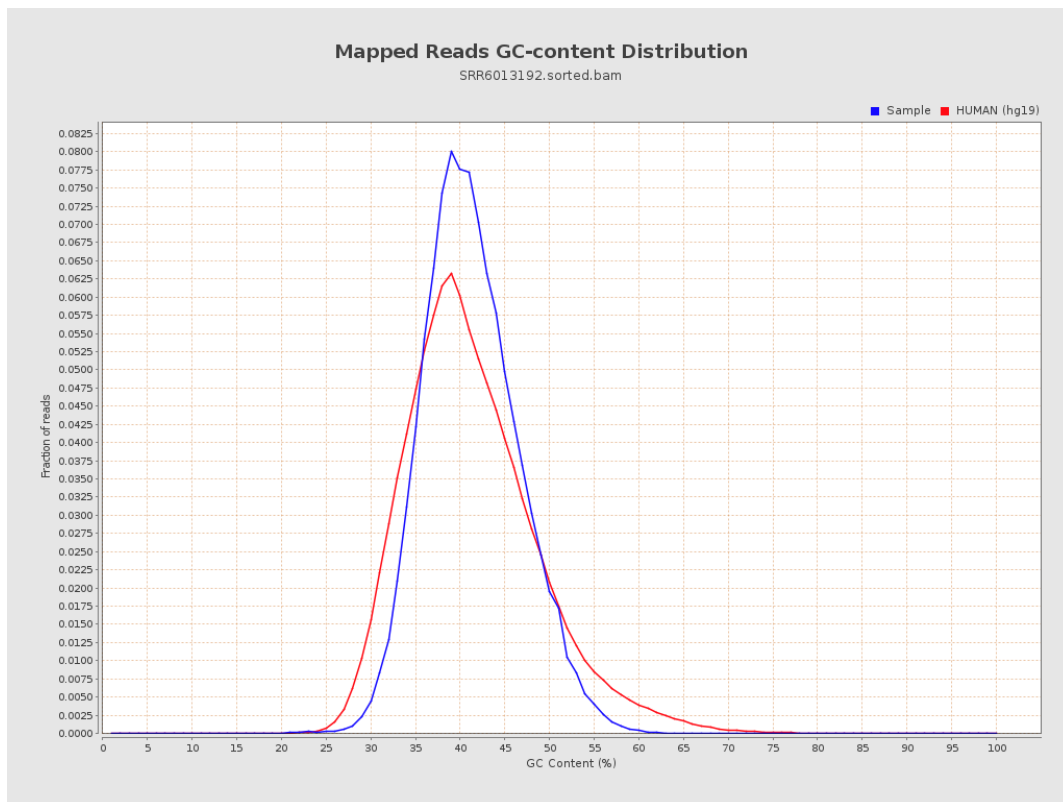
7. Results : Duplication Rate Histogram



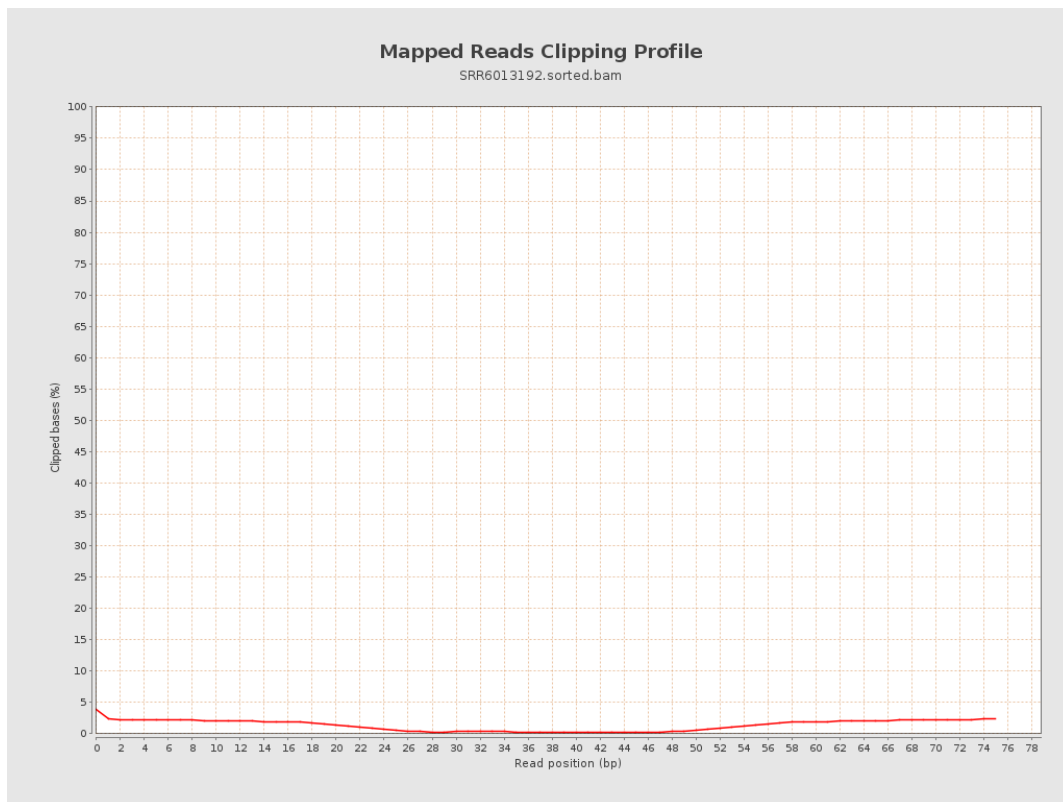
8. Results : Mapped Reads Nucleotide Content



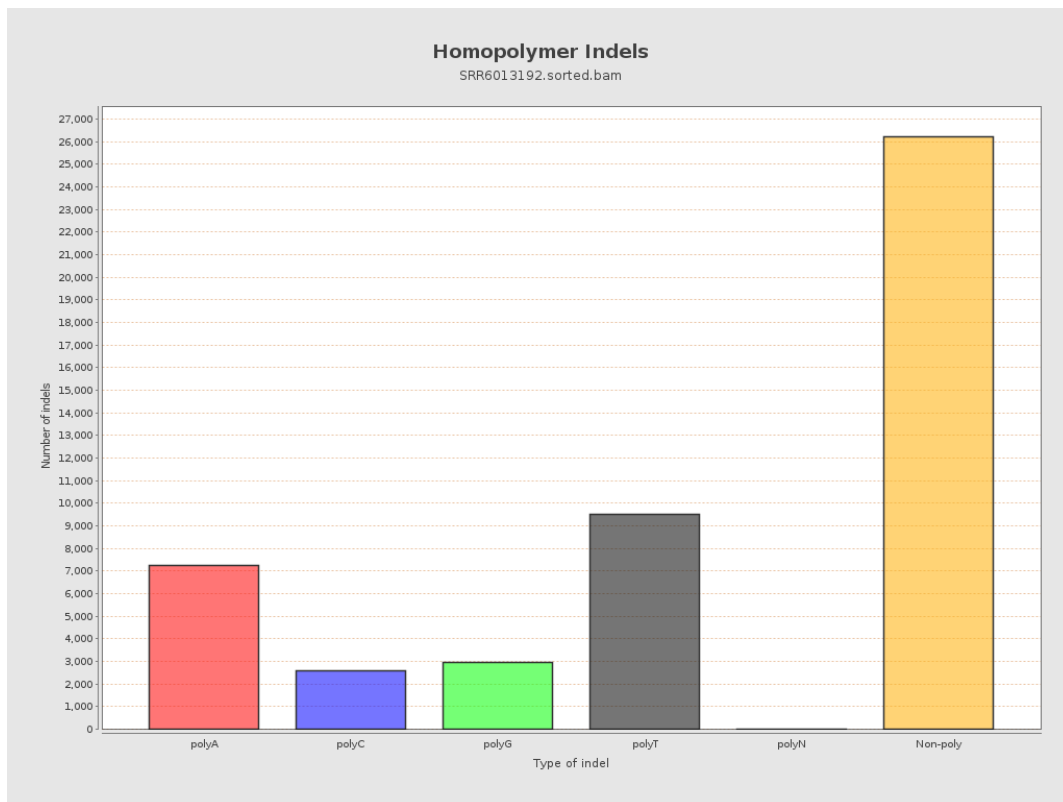
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

