

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:44:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008792.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_SRR6008792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:44:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,420,886
Mapped reads	1,260,382 / 88.7%
Unmapped reads	160,504 / 11.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,269 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	115,187 / 8.11%
Duplication rate	7.24%
Clipped reads	541,865 / 38.14%

2.2. ACGT Content

Number/percentage of A's	23,459,258 / 27.78%
Number/percentage of C's	15,526,998 / 18.39%
Number/percentage of T's	26,901,177 / 31.86%
Number/percentage of G's	18,520,675 / 21.93%
Number/percentage of N's	29,087 / 0.03%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.3104
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2.4. Mapping Quality

Mean Mapping Quality	46.07
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2.5. Mismatches and indels

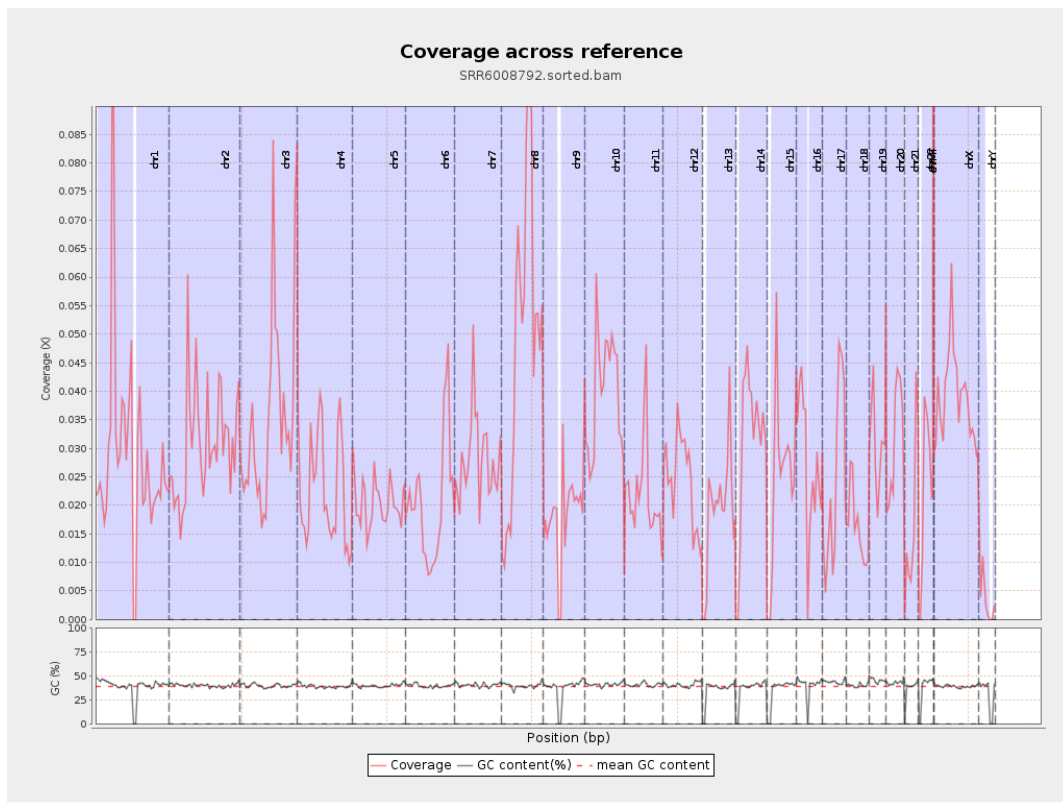
General error rate	0.78%
Mismatches	649,233
Insertions	6,430
Mapped reads with at least one insertion	0.51%
Deletions	20,256
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.99%

2.6. Chromosome stats

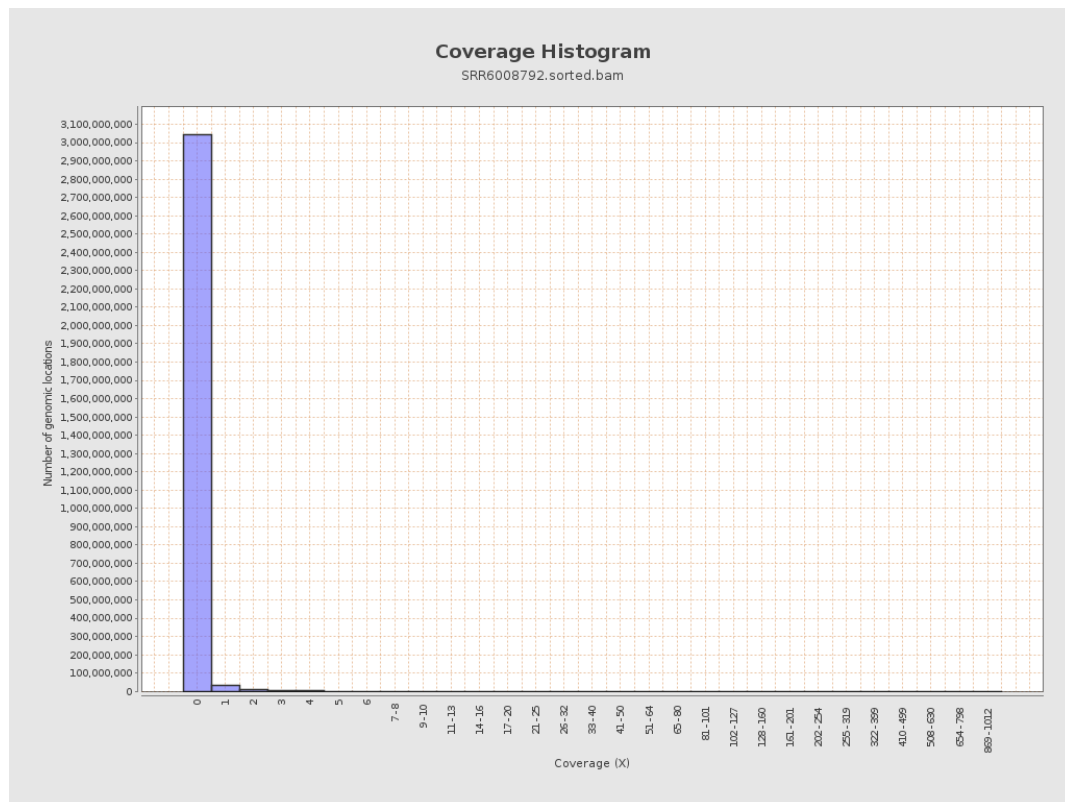
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7070154	0.0284	0.3515
chr2	243199373	7469889	0.0307	0.3284
chr3	198022430	6959950	0.0351	0.277
chr4	191154276	4282005	0.0224	0.2356
chr5	180915260	3705395	0.0205	0.209
chr6	171115067	3498253	0.0204	0.2171
chr7	159138663	4471574	0.0281	0.3609

chr8	146364022	7117646	0.0486	0.6704
chr9	141213431	2537387	0.018	0.2697
chr10	135534747	5347979	0.0395	0.3311
chr11	135006516	2949192	0.0218	0.2613
chr12	133851895	3282362	0.0245	0.2298
chr13	115169878	2211349	0.0192	0.2023
chr14	107349540	3344850	0.0312	0.2658
chr15	102531392	2559786	0.025	0.2303
chr16	90354753	2424597	0.0268	0.2452
chr17	81195210	1969084	0.0243	0.2335
chr18	78077248	1267795	0.0162	0.4014
chr19	59128983	1845544	0.0312	0.2952
chr20	63025520	1958266	0.0311	0.2644
chr21	48129895	821429	0.0171	0.1974
chr22	51304566	1095970	0.0214	0.209
chrMT	16571	6974	0.4209	1.0447
chrX	155270560	6048137	0.039	0.3279
chrY	59373566	227720	0.0038	0.1124

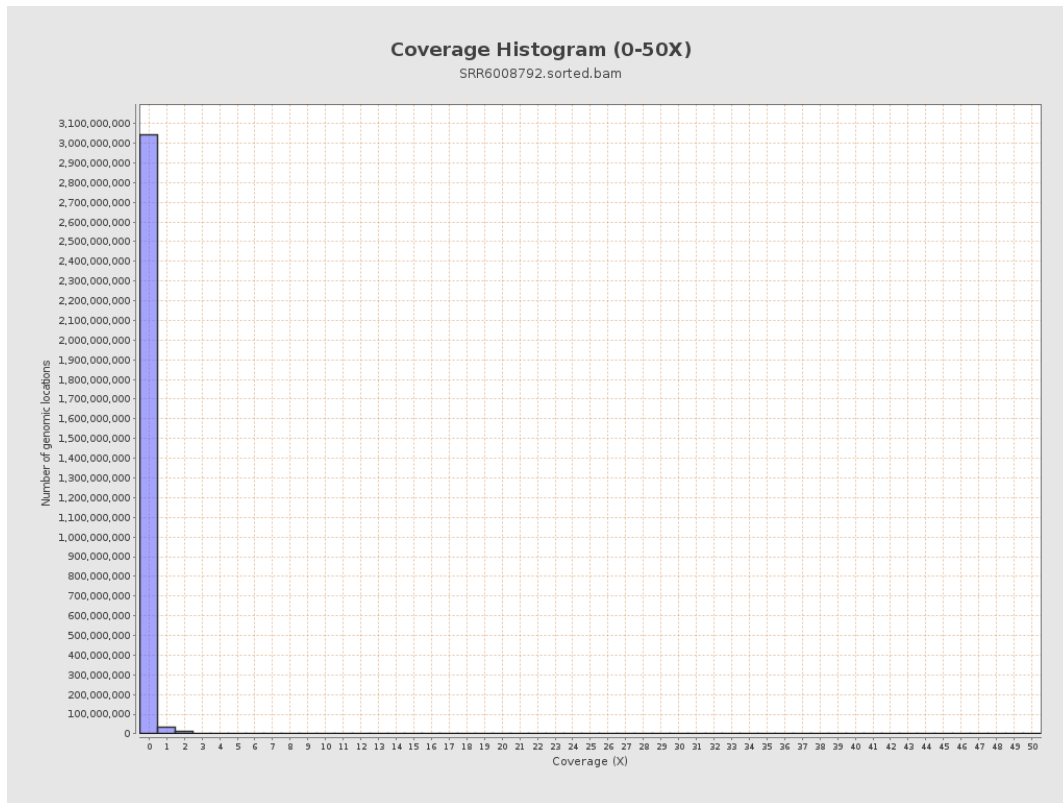
3. Results : Coverage across reference



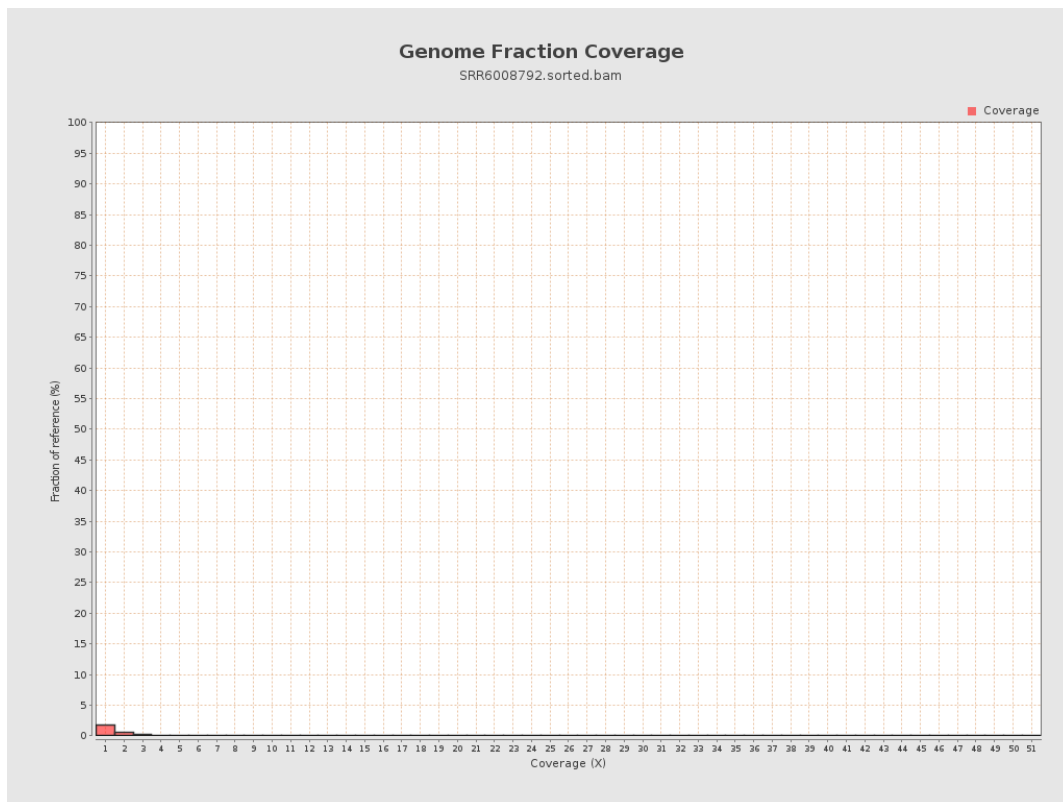
4. Results : Coverage Histogram



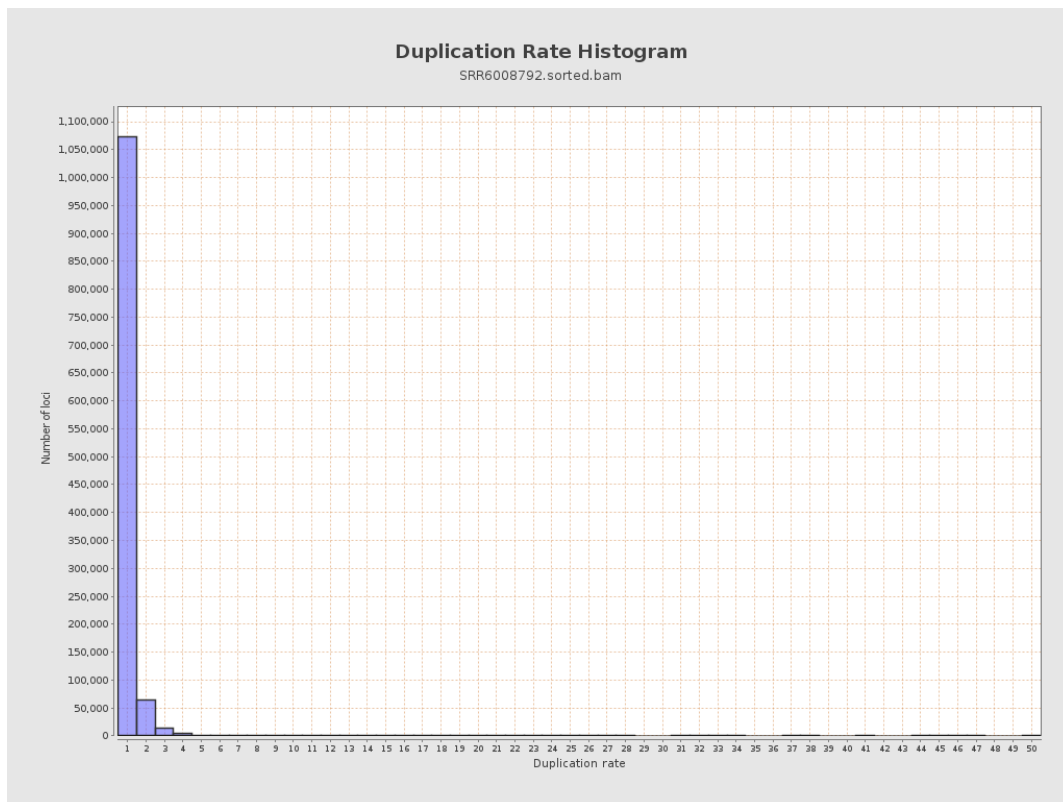
5. Results : Coverage Histogram (0-50X)



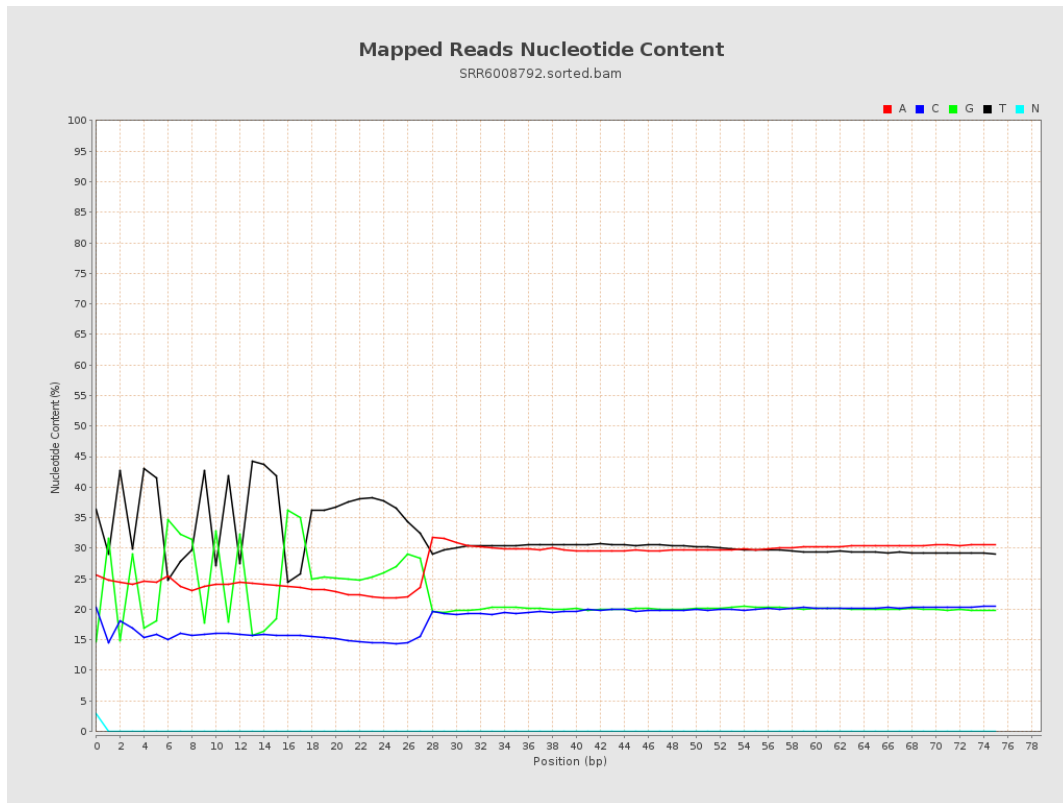
6. Results : Genome Fraction Coverage



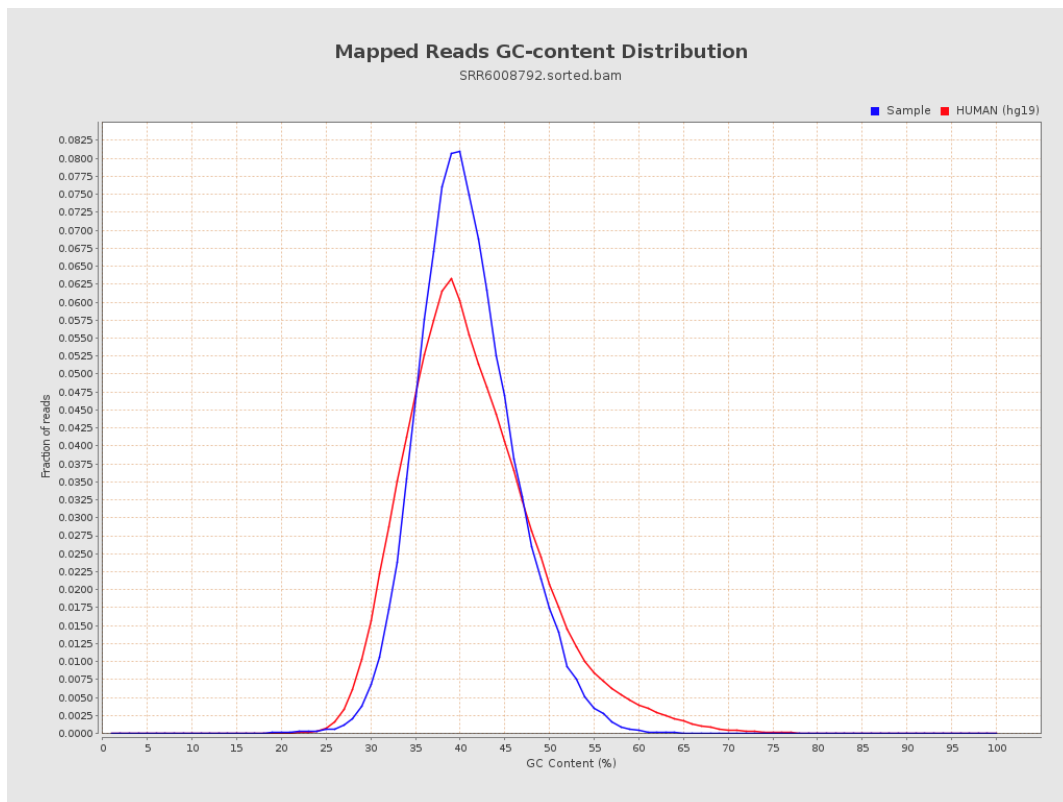
7. Results : Duplication Rate Histogram



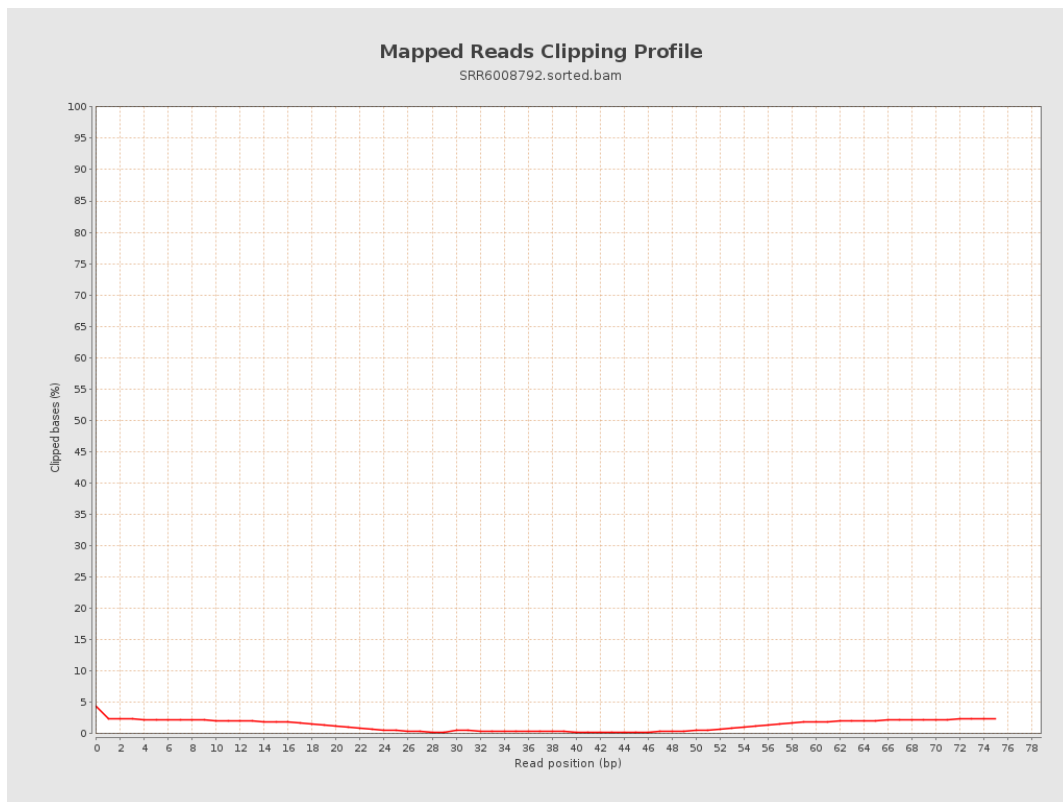
8. Results : Mapped Reads Nucleotide Content



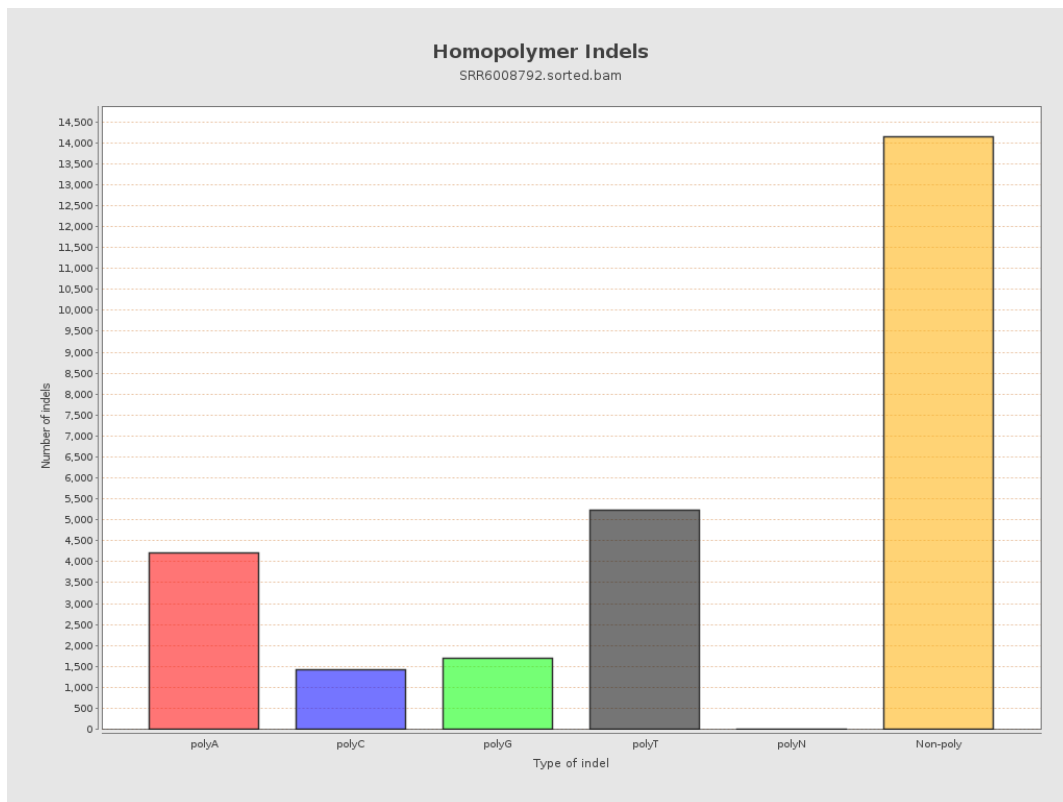
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

