

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:36:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008768.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_SRR6008768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008768.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:36:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,080,929
Mapped reads	8,329,335 / 91.72%
Unmapped reads	751,594 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,455 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,097,921 / 12.09%
Duplication rate	9.39%
Clipped reads	3,594,152 / 39.58%

2.2. ACGT Content

Number/percentage of A's	151,321,043 / 27.25%
Number/percentage of C's	102,076,143 / 18.38%
Number/percentage of T's	176,278,671 / 31.74%
Number/percentage of G's	125,594,244 / 22.61%
Number/percentage of N's	102,102 / 0.02%
GC Percentage	40.99%

2.3. Coverage

Mean	0.1795

Standard Deviation	1.845
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2.4. Mapping Quality

Mean Mapping Quality	44.16
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2.5. Mismatches and indels

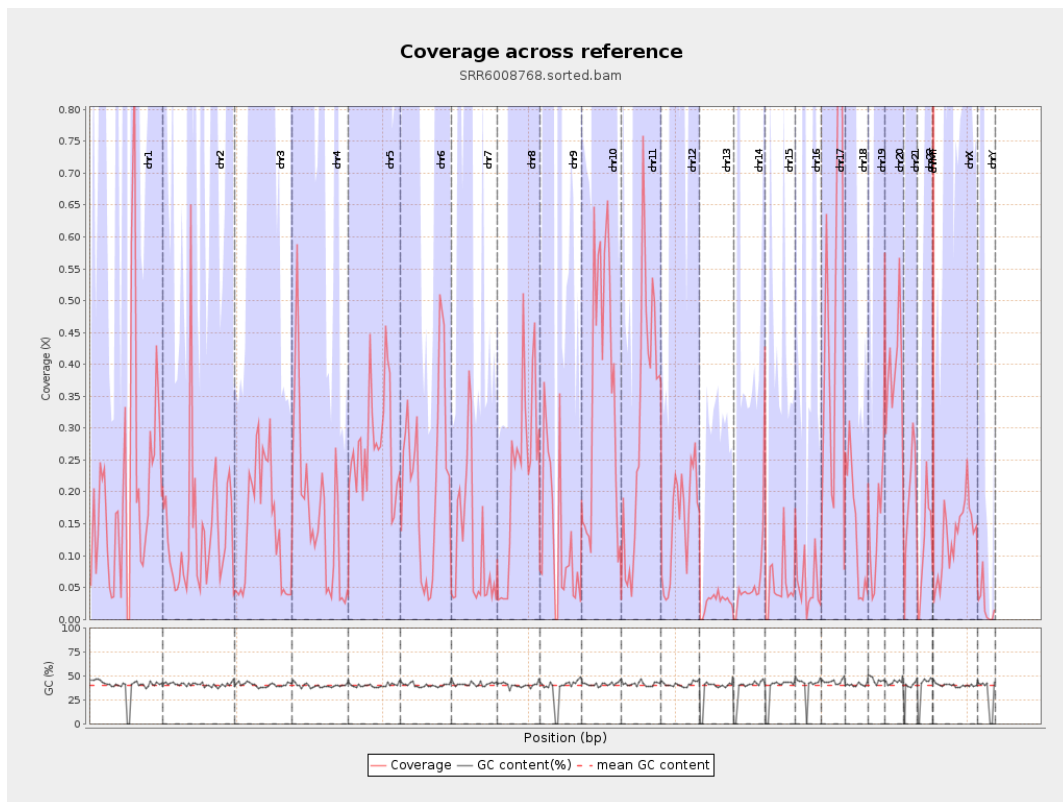
General error rate	0.77%
Mismatches	4,195,744
Insertions	48,200
Mapped reads with at least one insertion	0.57%
Deletions	140,670
Mapped reads with at least one deletion	1.67%
Homopolymer indels	47.44%

2.6. Chromosome stats

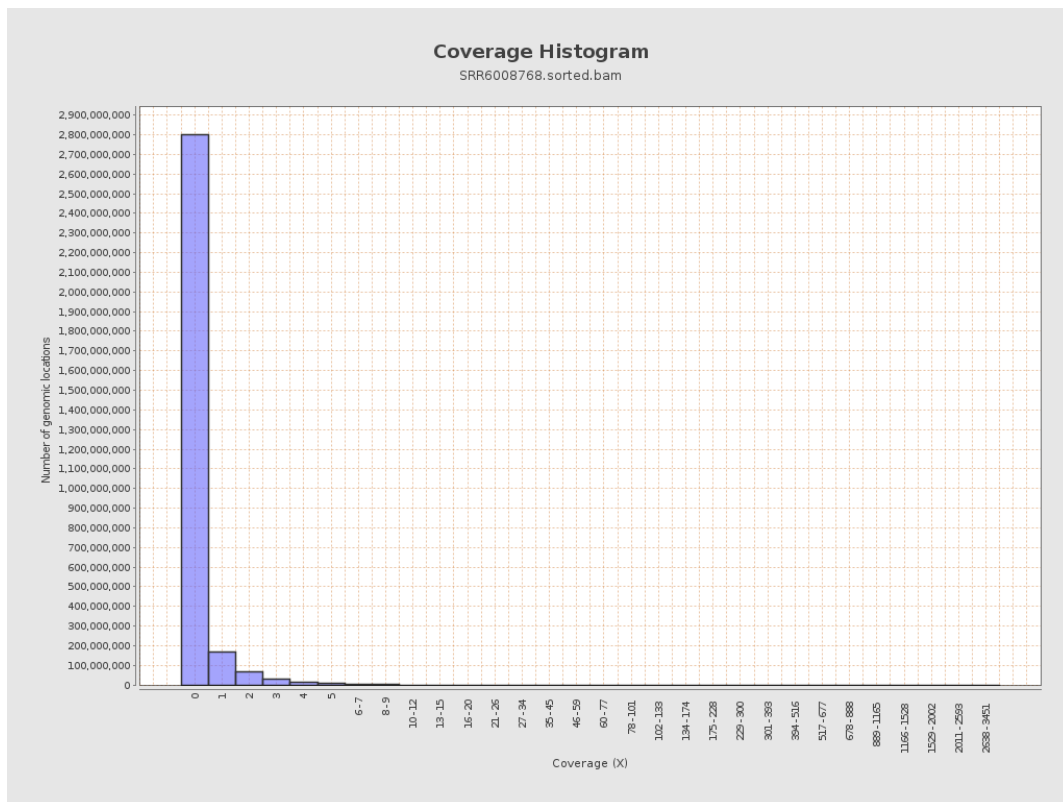
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	49443916	0.1984	2.2666
chr2	243199373	33433482	0.1375	3.5631
chr3	198022430	28614790	0.1445	0.6887
chr4	191154276	33237041	0.1739	0.821
chr5	180915260	49453707	0.2734	0.8754
chr6	171115067	38342019	0.2241	1.0374
chr7	159138663	18404474	0.1157	2.365

chr8	146364022	33089719	0.2261	2.3015
chr9	141213431	18717657	0.1325	2.4398
chr10	135534747	48273808	0.3562	2.2858
chr11	135006516	41195229	0.3051	1.3715
chr12	133851895	20782551	0.1553	0.7743
chr13	115169878	3137706	0.0272	0.2566
chr14	107349540	5441535	0.0507	0.5904
chr15	102531392	5313267	0.0518	0.3918
chr16	90354753	5005119	0.0554	0.8985
chr17	81195210	41682133	0.5134	2.7753
chr18	78077248	11227802	0.1438	3.2264
chr19	59128983	9150440	0.1548	1.622
chr20	63025520	25027163	0.3971	1.1496
chr21	48129895	8924141	0.1854	0.8386
chr22	51304566	6179774	0.1205	0.5416
chrMT	16571	170623	10.2965	6.5017
chrX	155270560	19982035	0.1287	0.9929
chrY	59373566	1372560	0.0231	0.6981

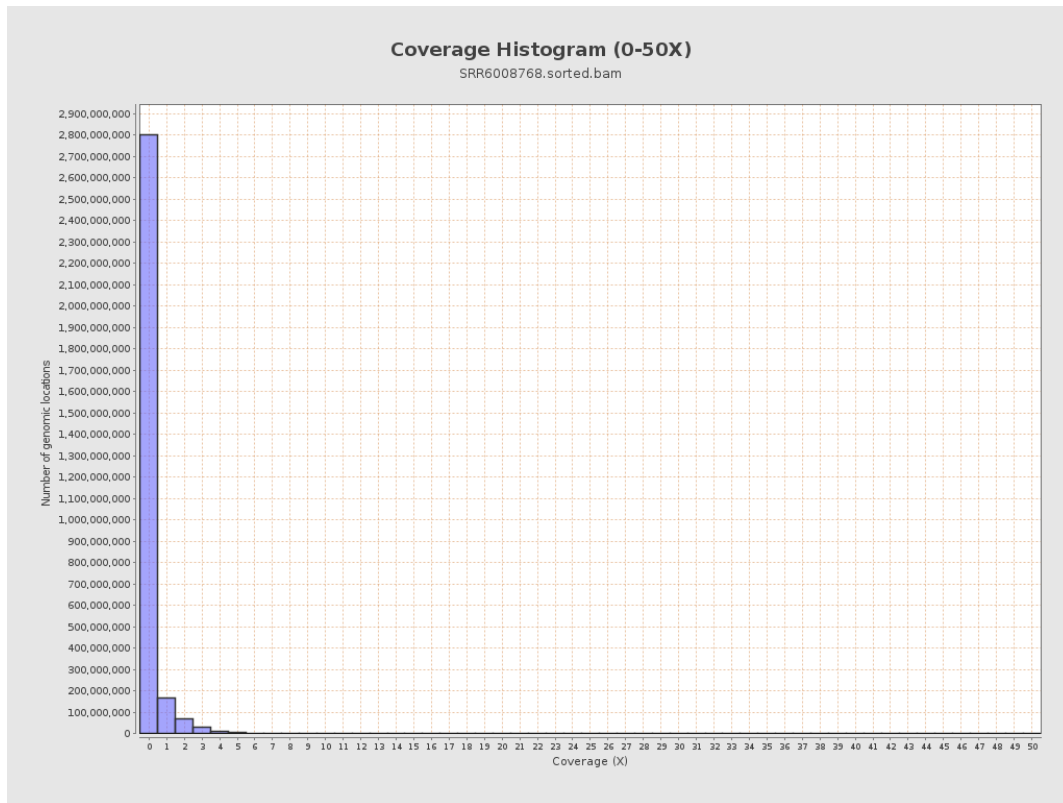
3. Results : Coverage across reference



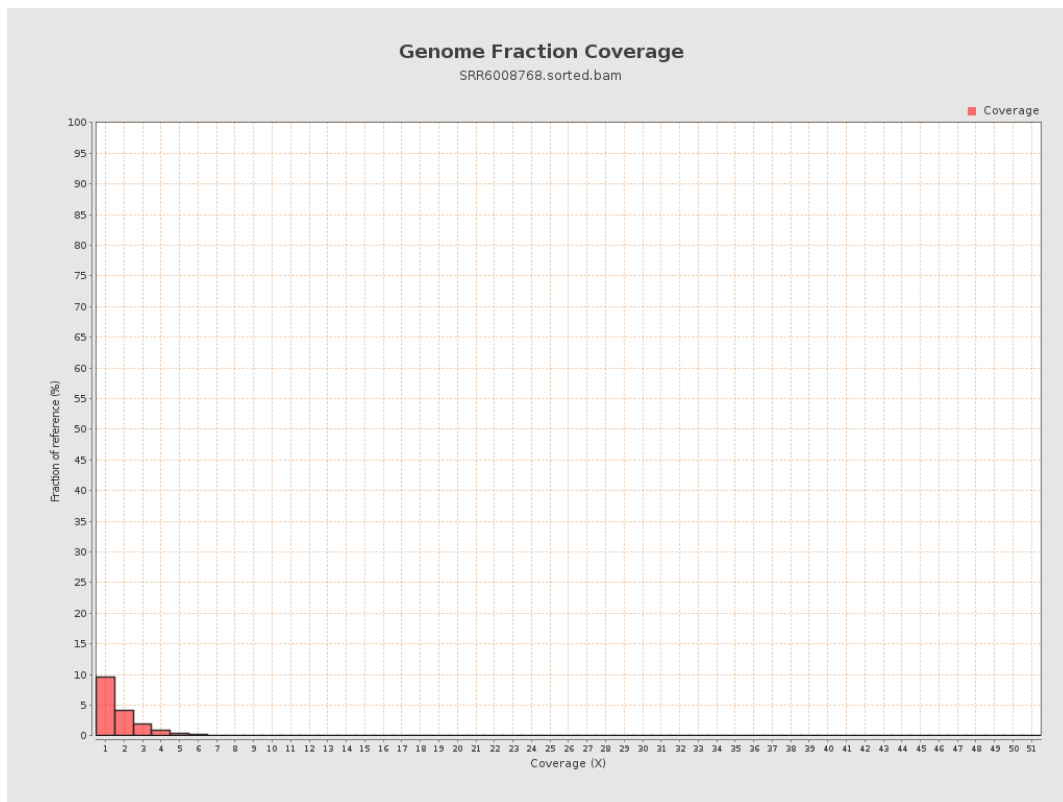
4. Results : Coverage Histogram



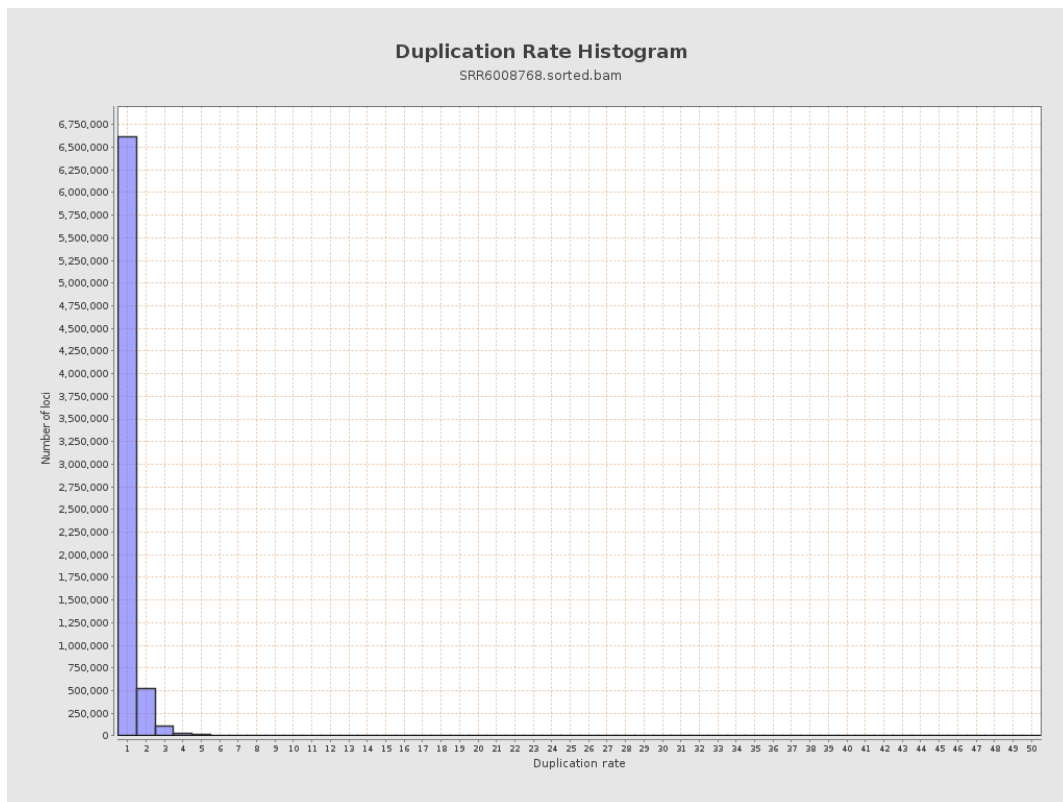
5. Results : Coverage Histogram (0-50X)



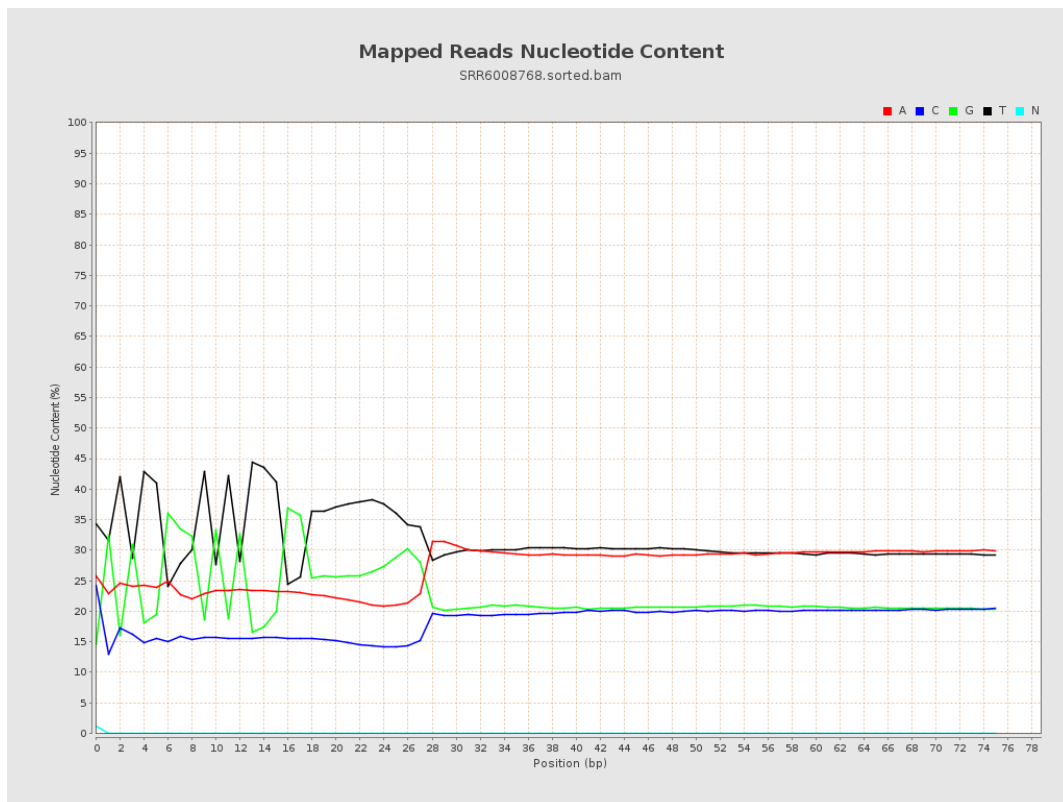
6. Results : Genome Fraction Coverage



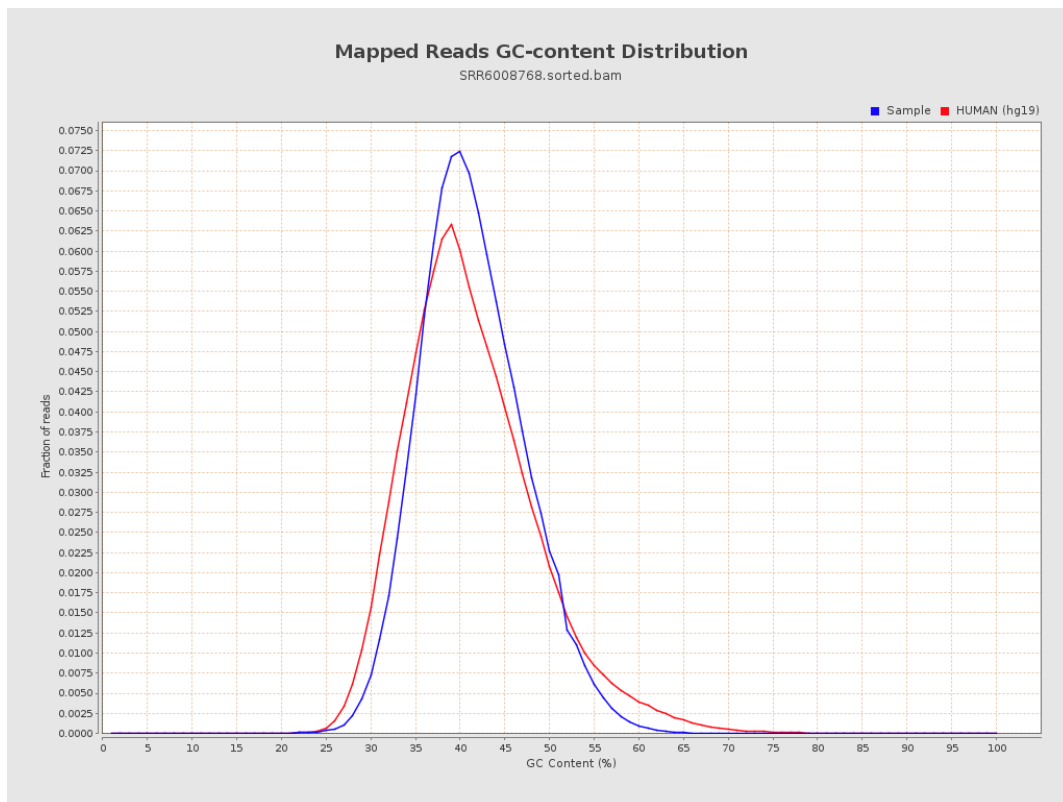
7. Results : Duplication Rate Histogram



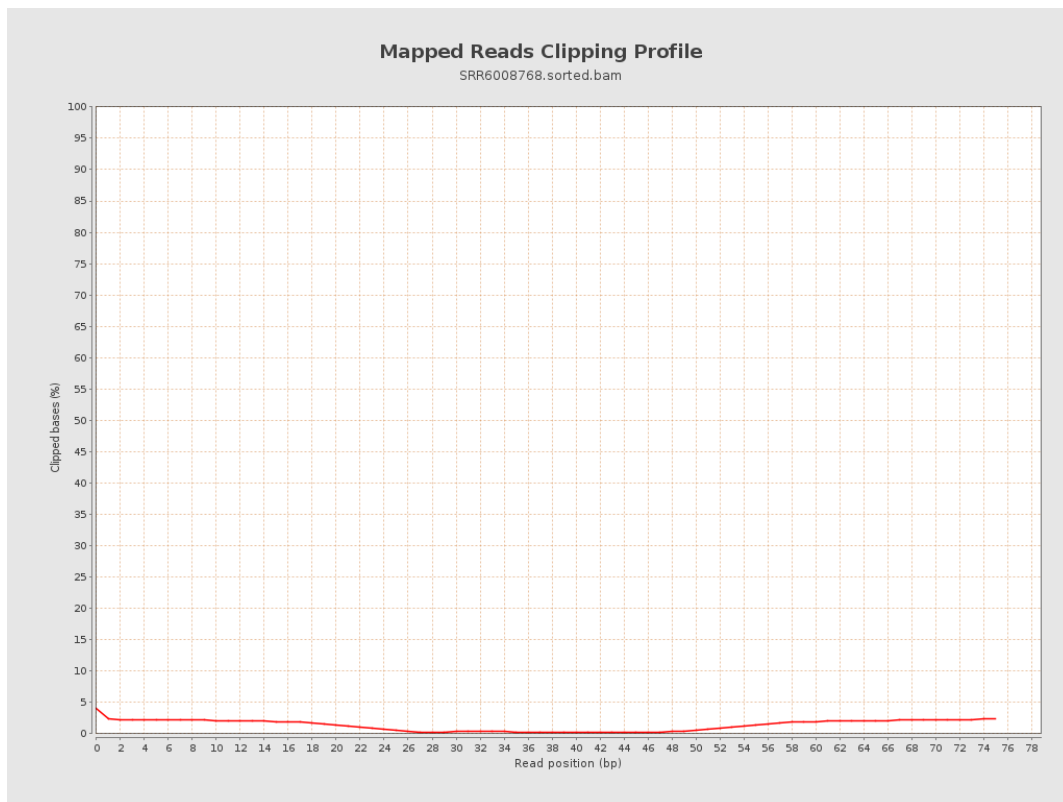
8. Results : Mapped Reads Nucleotide Content



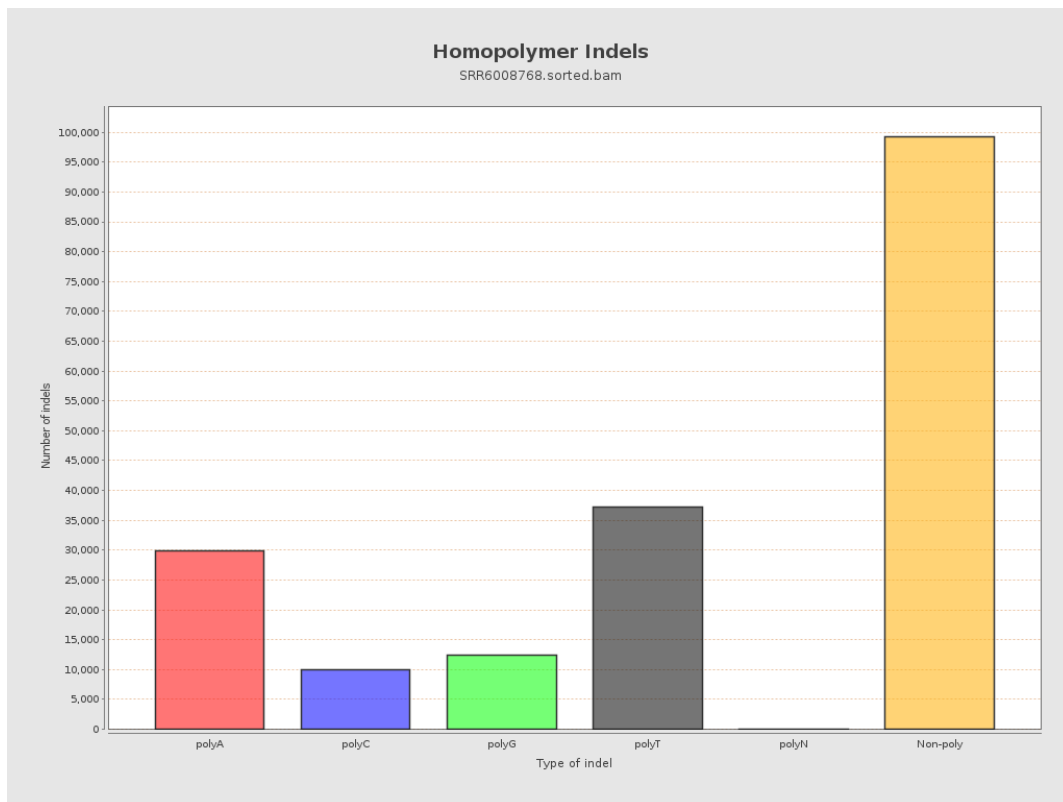
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

