

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:02:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008799.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_SRR6008799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:02:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,310,772
Mapped reads	1,994,415 / 86.31%
Unmapped reads	316,357 / 13.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,261 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	290,101 / 12.55%
Duplication rate	10.42%
Clipped reads	958,996 / 41.5%

2.2. ACGT Content

Number/percentage of A's	35,905,800 / 27.22%
Number/percentage of C's	25,196,668 / 19.1%
Number/percentage of T's	40,725,498 / 30.87%
Number/percentage of G's	30,038,357 / 22.77%
Number/percentage of N's	48,634 / 0.04%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.4697
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2.4. Mapping Quality

Mean Mapping Quality	45.2
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2.5. Mismatches and indels

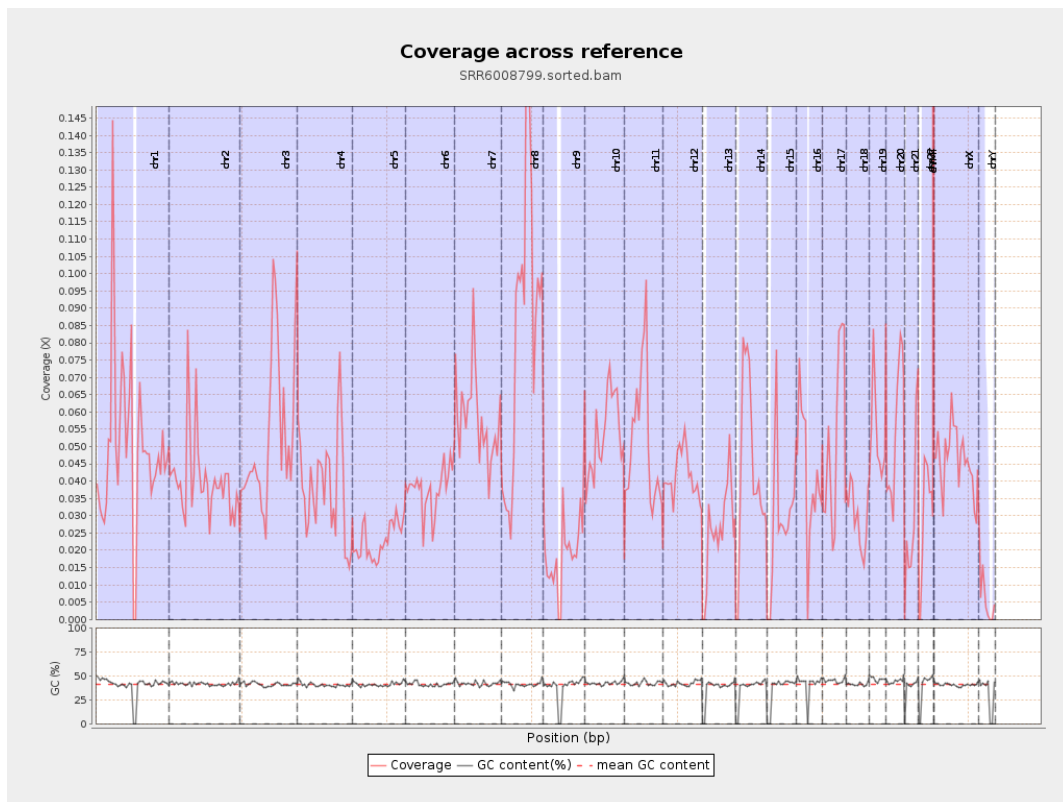
General error rate	0.77%
Mismatches	1,004,572
Insertions	9,061
Mapped reads with at least one insertion	0.45%
Deletions	27,439
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.77%

2.6. Chromosome stats

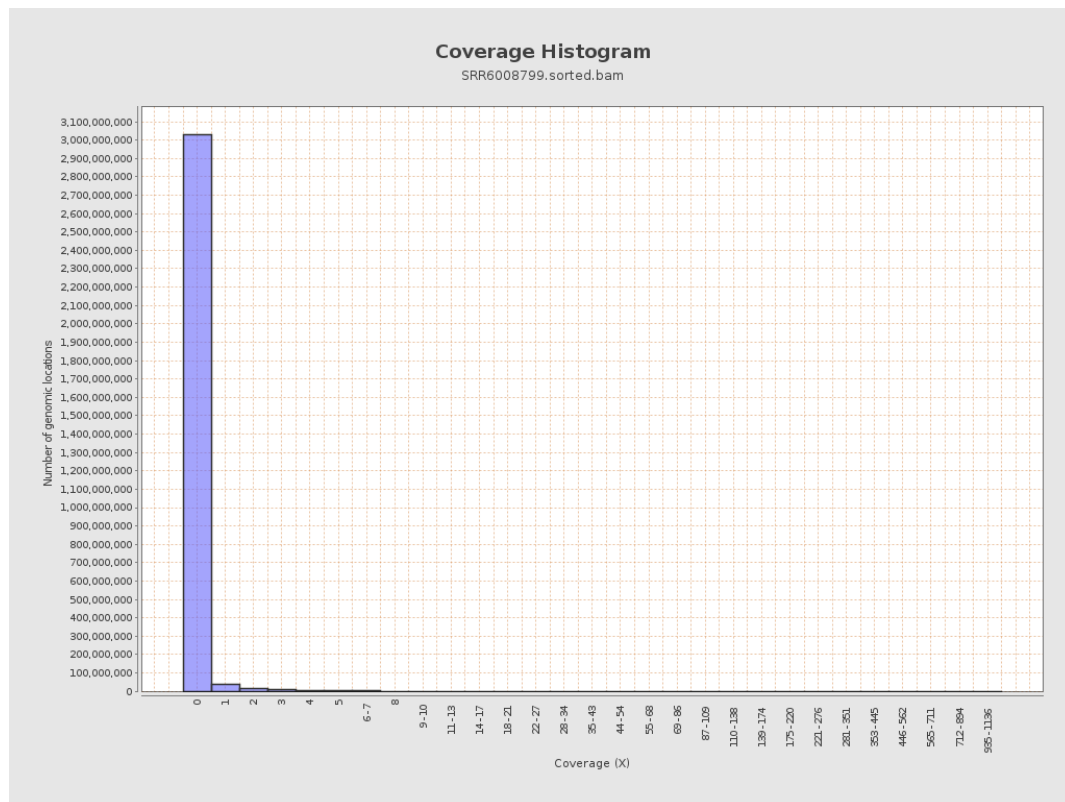
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12162751	0.0488	0.7434
chr2	243199373	9826303	0.0404	0.4598
chr3	198022430	10414222	0.0526	0.3946
chr4	191154276	7173533	0.0375	0.3347
chr5	180915260	4135612	0.0229	0.254
chr6	171115067	6433875	0.0376	0.3445
chr7	159138663	9238348	0.0581	0.6481

chr8	146364022	12140699	0.0829	0.8296
chr9	141213431	2618725	0.0185	0.3185
chr10	135534747	7228441	0.0533	0.4265
chr11	135006516	6879958	0.051	0.5547
chr12	133851895	5571751	0.0416	0.3459
chr13	115169878	2960254	0.0257	0.2743
chr14	107349540	4728991	0.0441	0.361
chr15	102531392	3027617	0.0295	0.2884
chr16	90354753	3808335	0.0421	0.3562
chr17	81195210	4125392	0.0508	0.4441
chr18	78077248	2265427	0.029	0.5534
chr19	59128983	3261608	0.0552	0.5357
chr20	63025520	3426047	0.0544	0.4053
chr21	48129895	1470024	0.0305	0.3032
chr22	51304566	1480768	0.0289	0.2849
chrMT	16571	71596	4.3206	5.4237
chrX	155270560	7153998	0.0461	0.3957
chrY	59373566	357868	0.006	0.1412

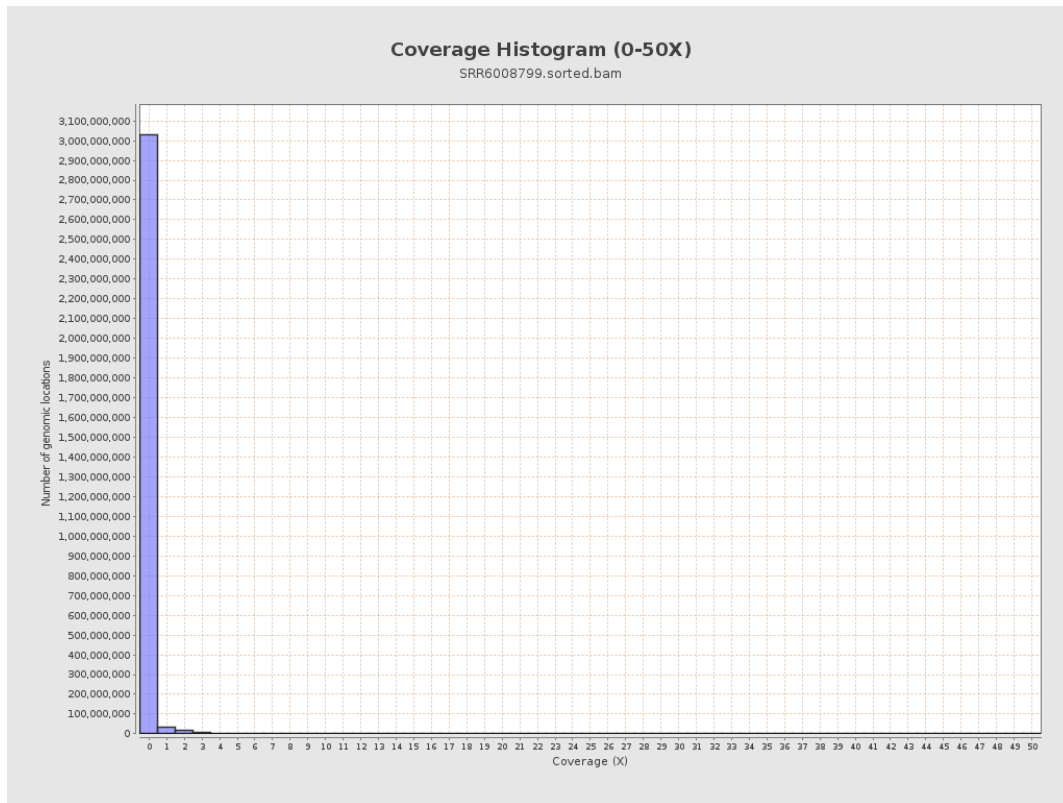
3. Results : Coverage across reference



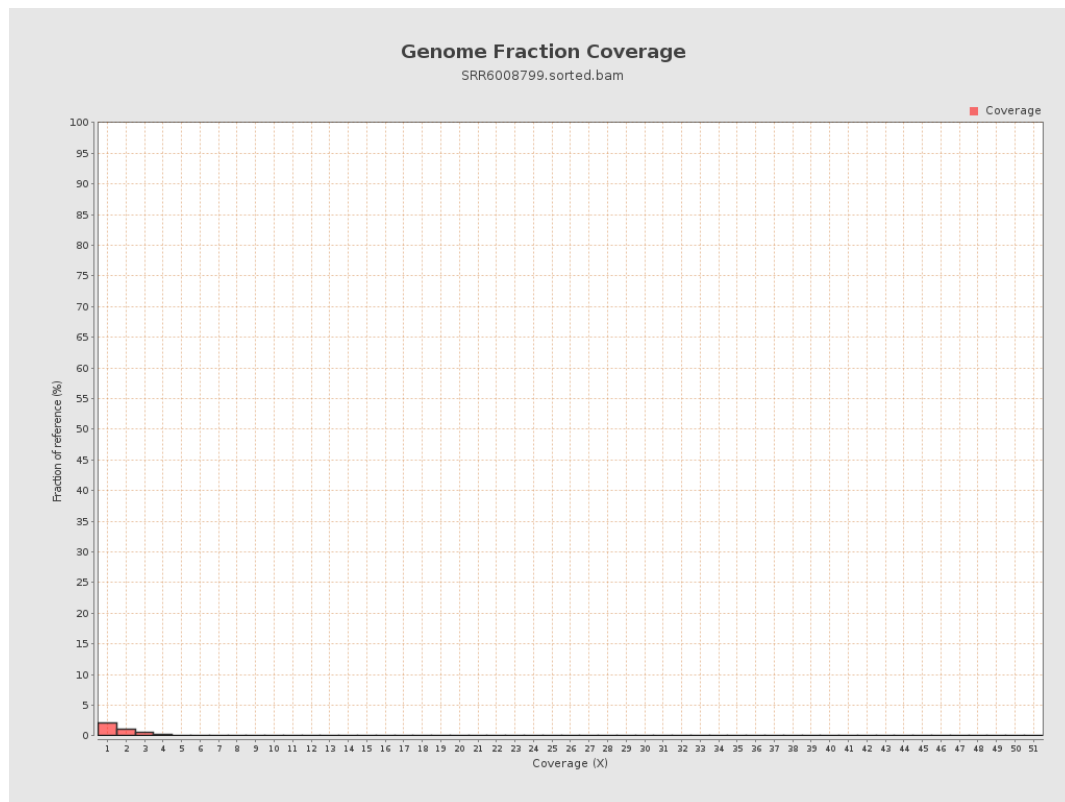
4. Results : Coverage Histogram



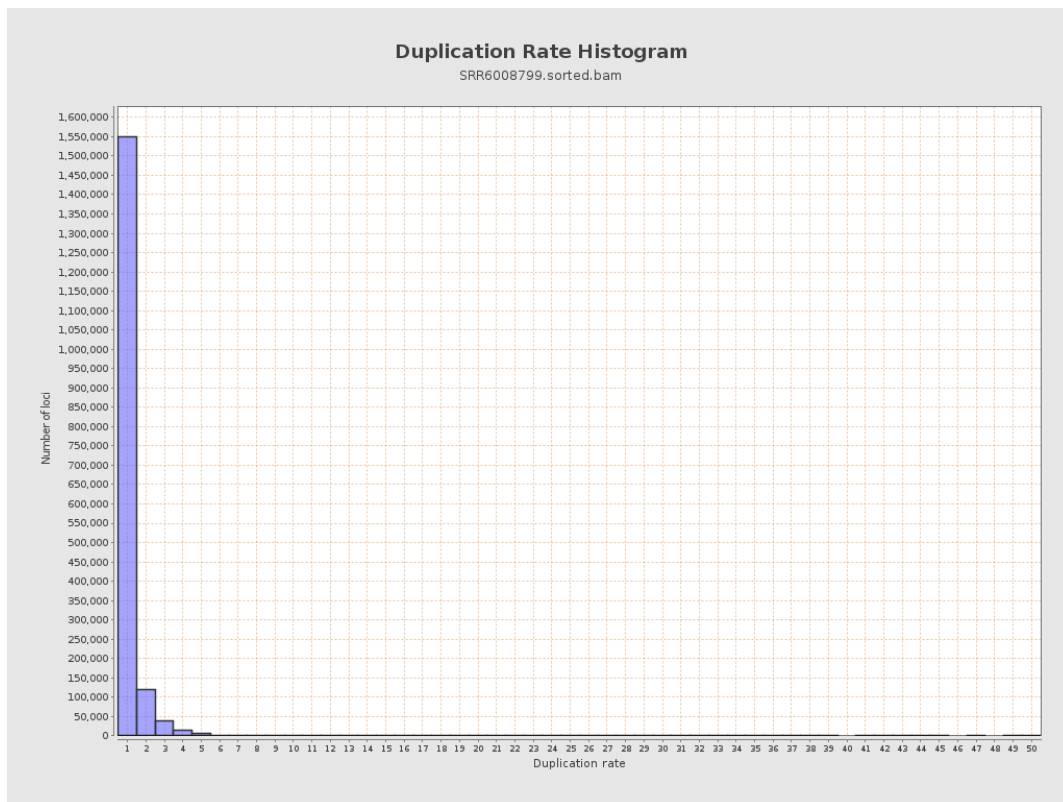
5. Results : Coverage Histogram (0-50X)



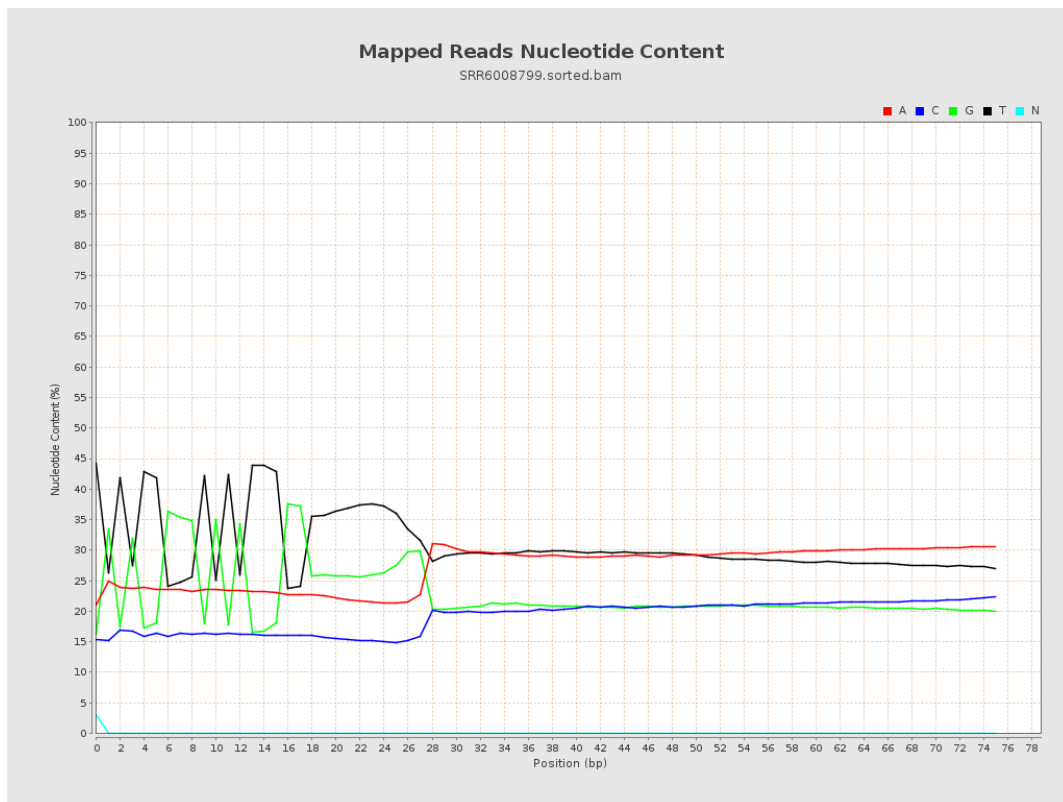
6. Results : Genome Fraction Coverage



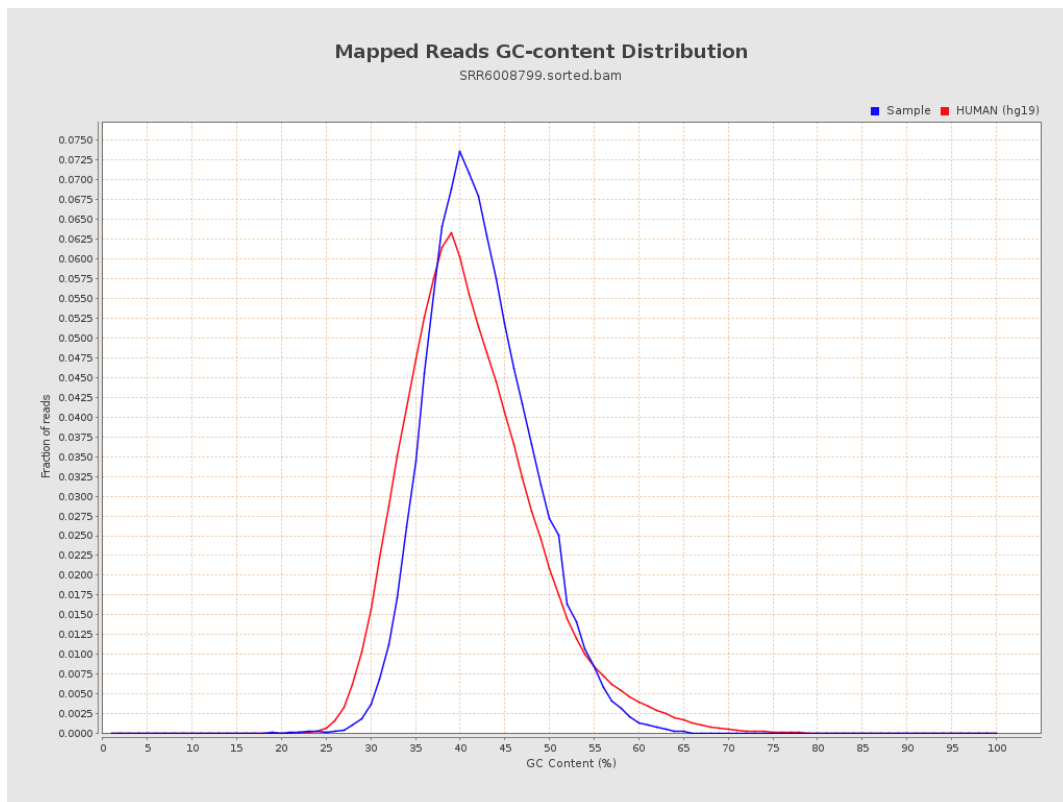
7. Results : Duplication Rate Histogram



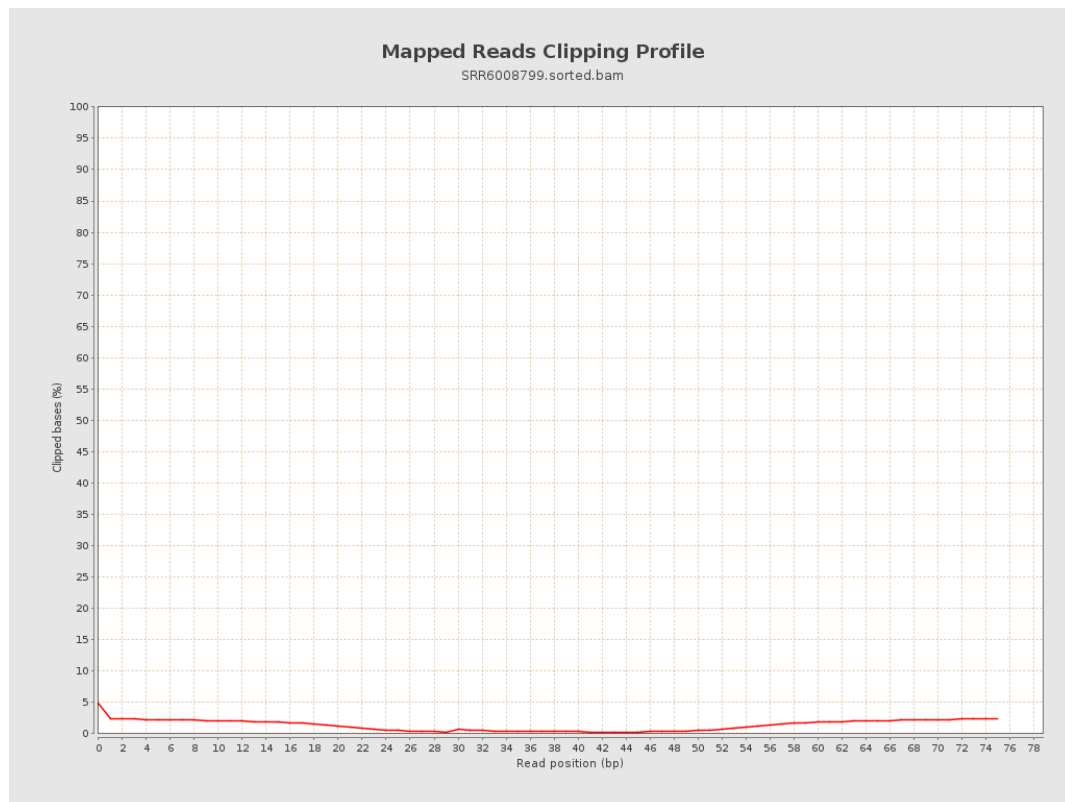
8. Results : Mapped Reads Nucleotide Content



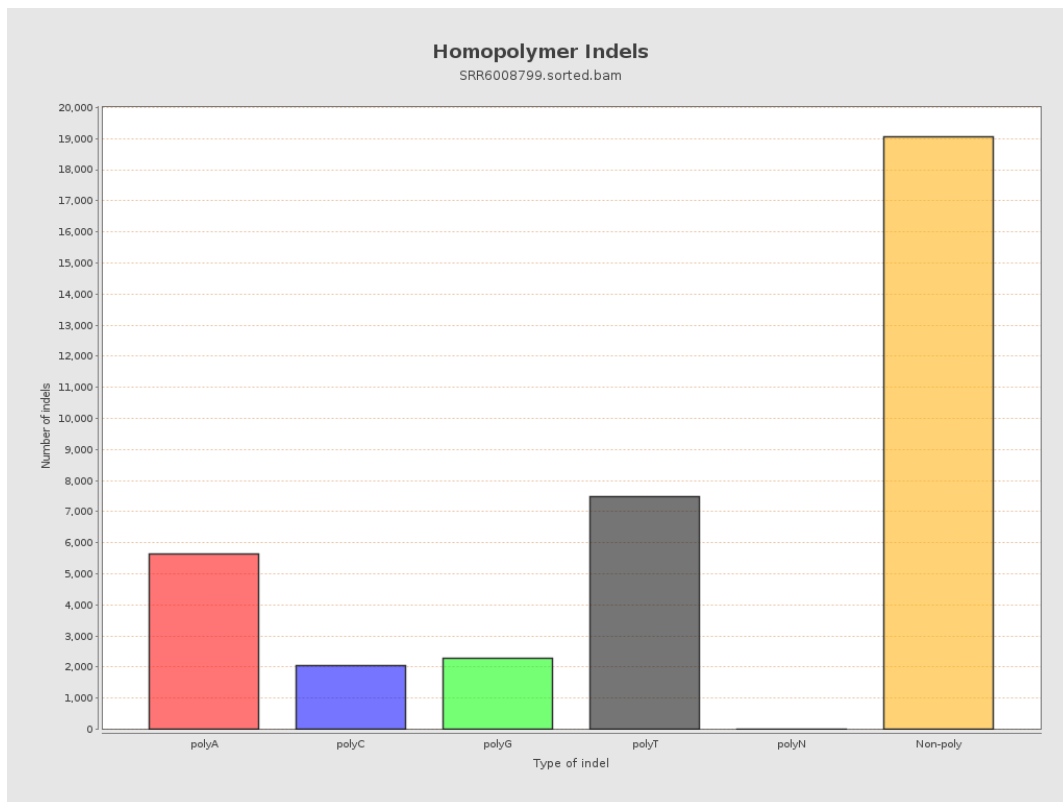
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

