

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:13:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080698.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_SRR3080698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080698.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:13:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,033,109
Mapped reads	2,555,017 / 84.24%
Unmapped reads	478,092 / 15.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,588 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	182,623 / 6.02%
Duplication rate	5.91%
Clipped reads	975,225 / 32.15%

2.2. ACGT Content

Number/percentage of A's	51,921,402 / 29.64%
Number/percentage of C's	32,316,909 / 18.45%
Number/percentage of T's	54,459,133 / 31.09%
Number/percentage of G's	36,471,585 / 20.82%
Number/percentage of N's	2,461 / 0%
GC Percentage	39.27%

2.3. Coverage

Mean	0.0566

Standard Deviation	0.4986
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2.4. Mapping Quality

Mean Mapping Quality	47.22
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2.5. Mismatches and indels

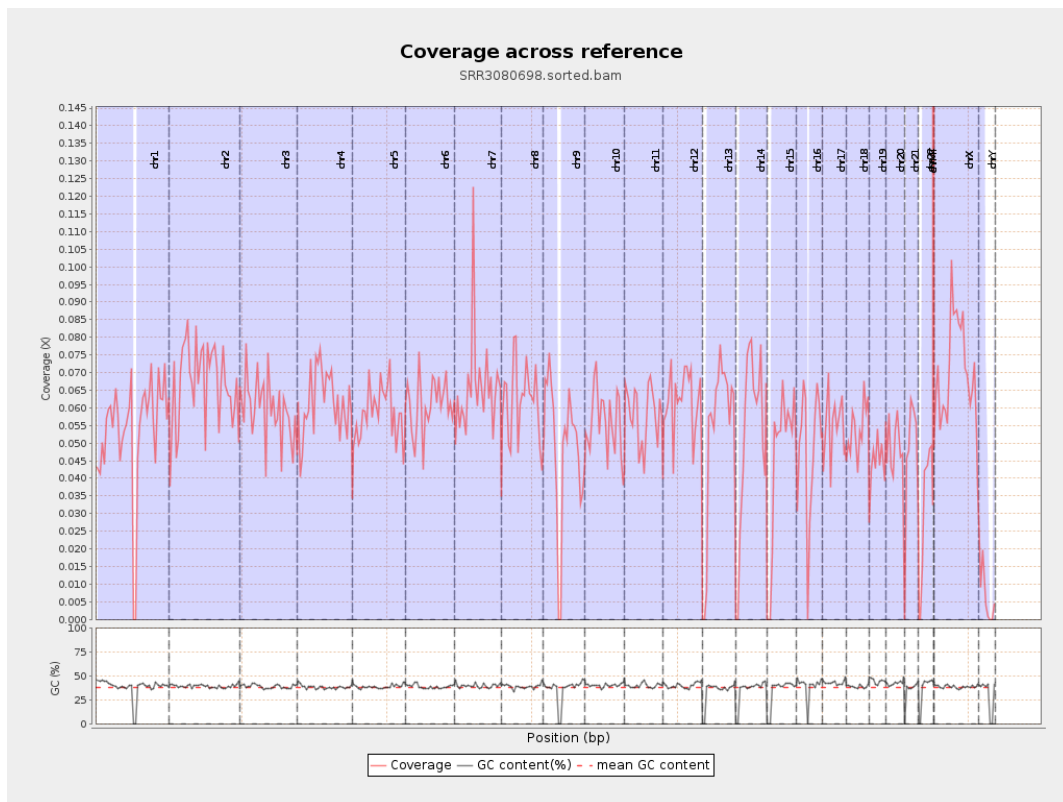
General error rate	0.84%
Mismatches	1,448,747
Insertions	13,468
Mapped reads with at least one insertion	0.52%
Deletions	37,522
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.43%

2.6. Chromosome stats

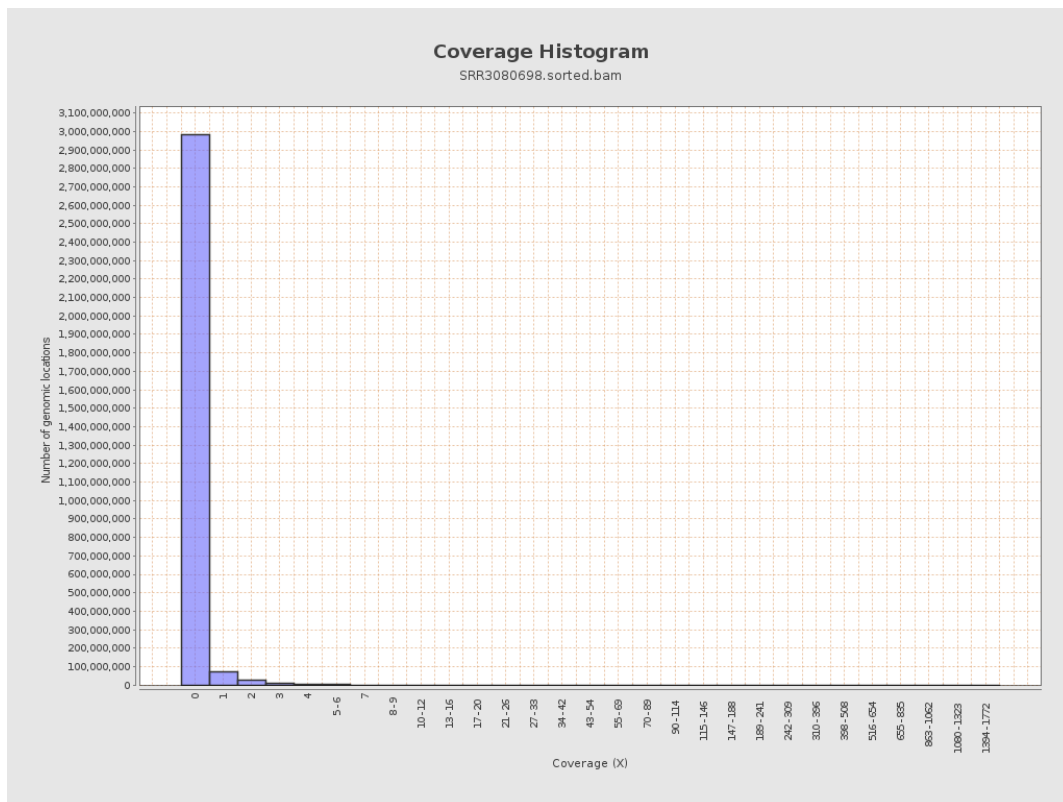
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13393693	0.0537	0.5307
chr2	243199373	16233361	0.0667	0.476
chr3	198022430	11803850	0.0596	0.3494
chr4	191154276	11786942	0.0617	0.3633
chr5	180915260	10551542	0.0583	0.3463
chr6	171115067	10457358	0.0611	0.3632
chr7	159138663	10478234	0.0658	0.9016

chr8	146364022	9026739	0.0617	1.1355
chr9	141213431	6835315	0.0484	0.3498
chr10	135534747	7611986	0.0562	0.4198
chr11	135006516	7825174	0.058	0.3784
chr12	133851895	8258481	0.0617	0.3554
chr13	115169878	6110151	0.0531	0.3333
chr14	107349540	5633624	0.0525	0.3327
chr15	102531392	4697051	0.0458	0.3024
chr16	90354753	4392118	0.0486	0.3176
chr17	81195210	4375142	0.0539	0.3692
chr18	78077248	4223862	0.0541	0.4397
chr19	59128983	2678222	0.0453	0.3985
chr20	63025520	3022480	0.048	0.3106
chr21	48129895	2253011	0.0468	0.3174
chr22	51304566	1599341	0.0312	0.2454
chrMT	16571	673904	40.6677	23.4928
chrX	155270560	10912562	0.0703	0.3972
chrY	59373566	403399	0.0068	0.1433

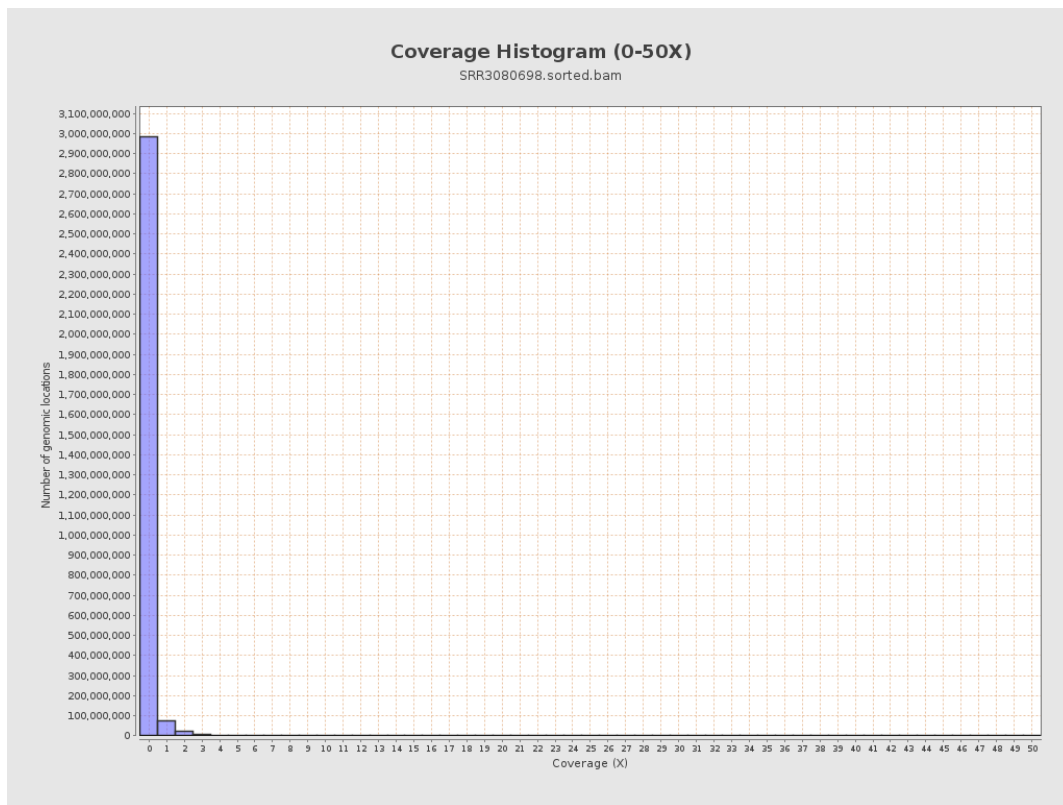
3. Results : Coverage across reference



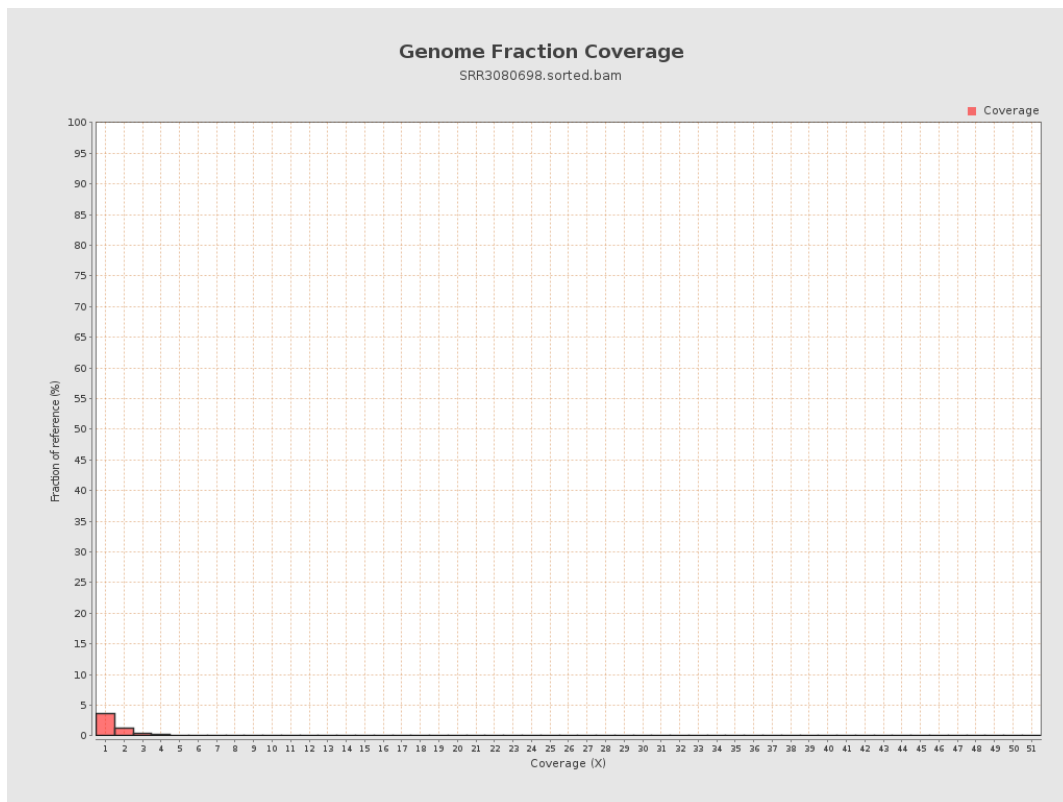
4. Results : Coverage Histogram



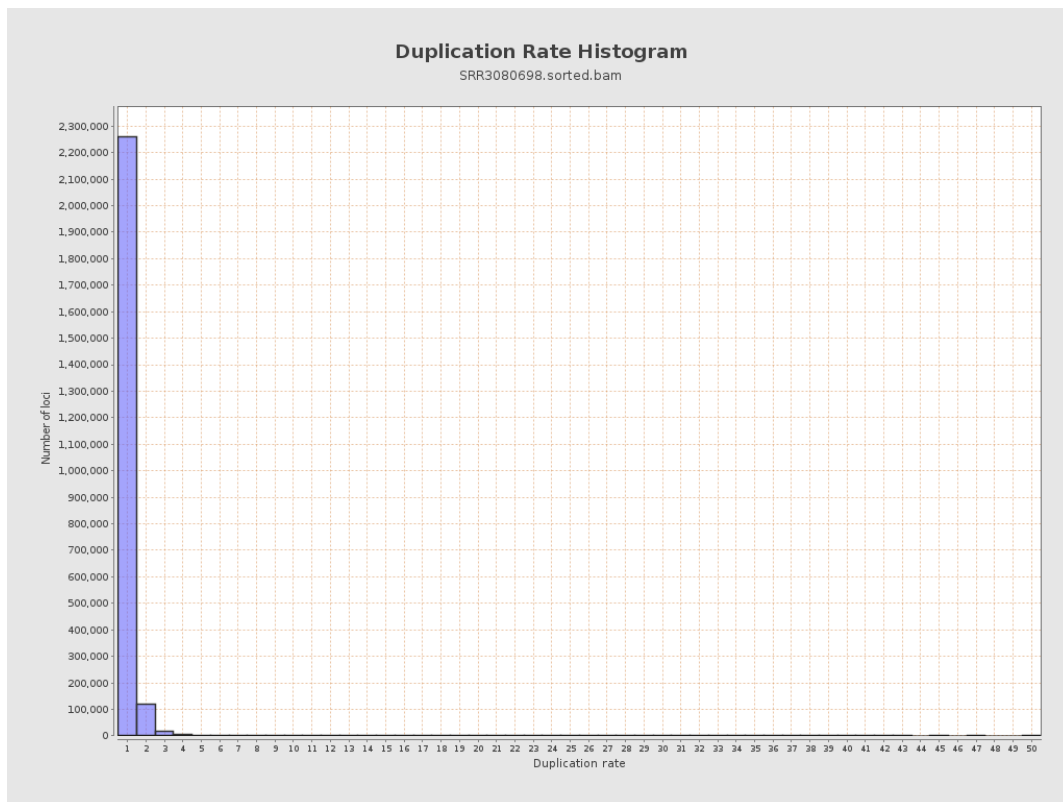
5. Results : Coverage Histogram (0-50X)



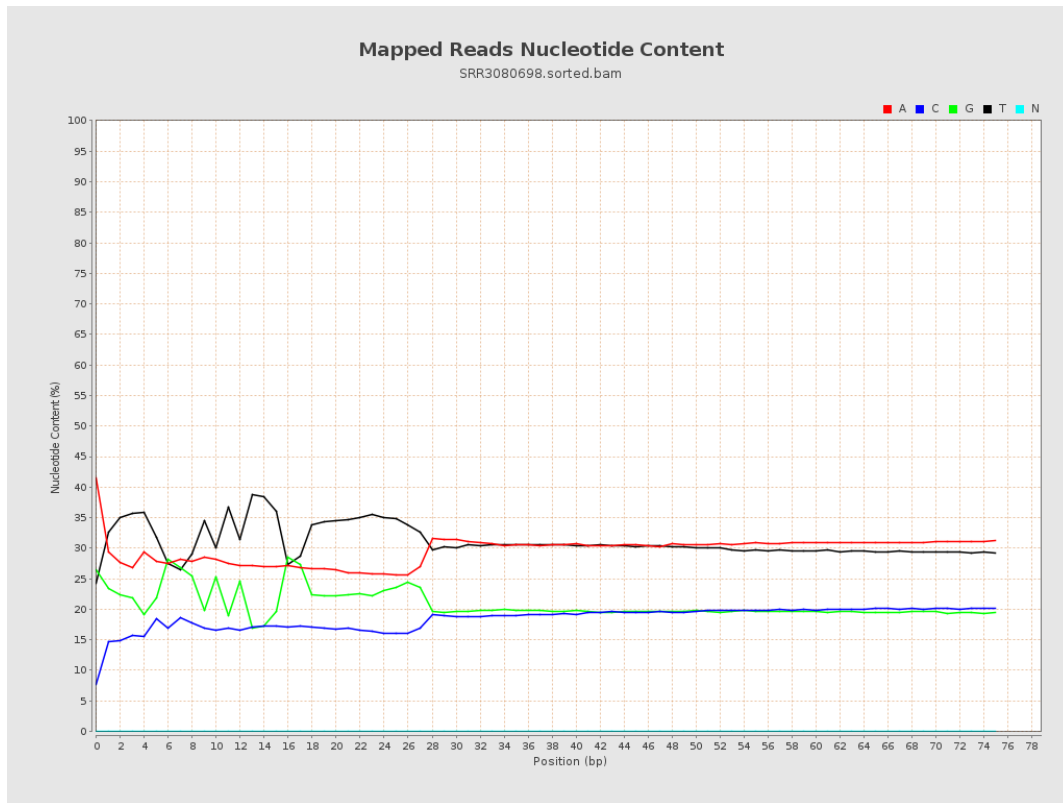
6. Results : Genome Fraction Coverage



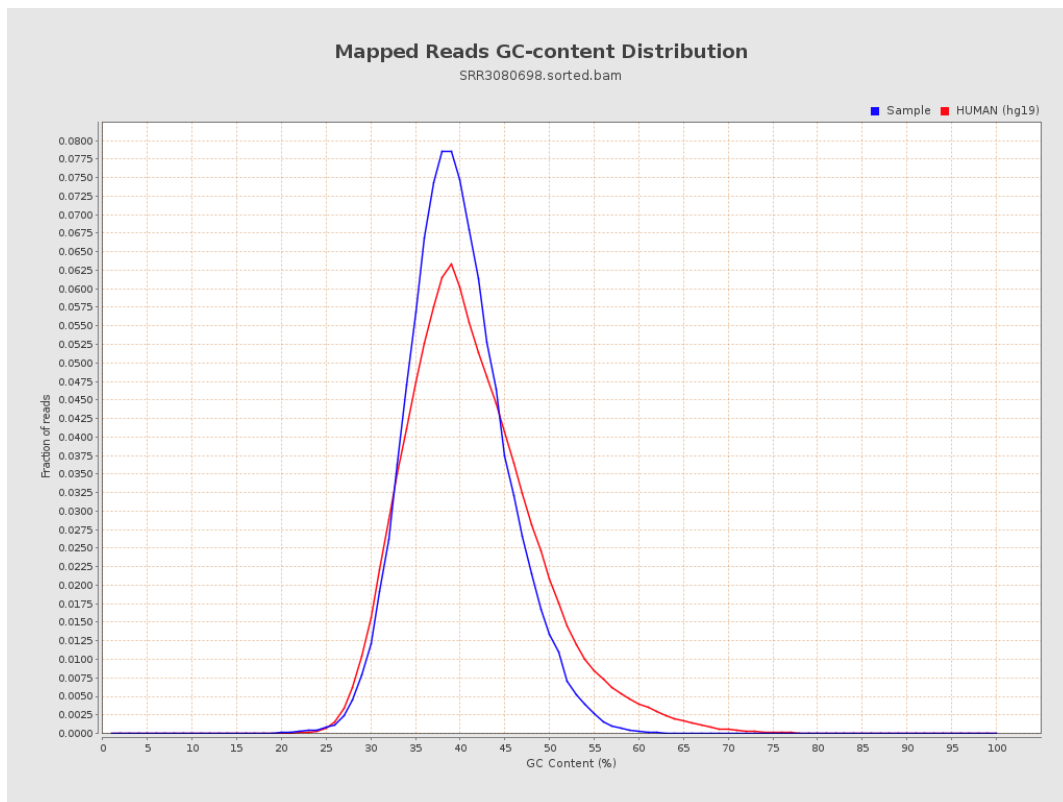
7. Results : Duplication Rate Histogram



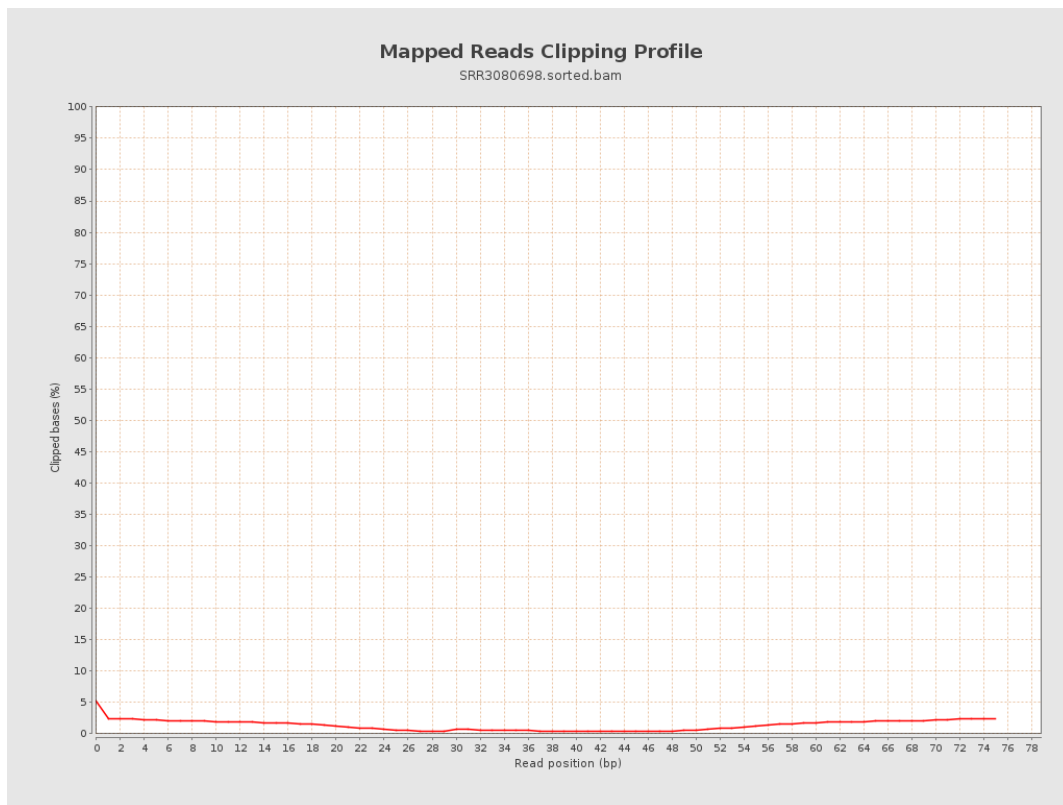
8. Results : Mapped Reads Nucleotide Content



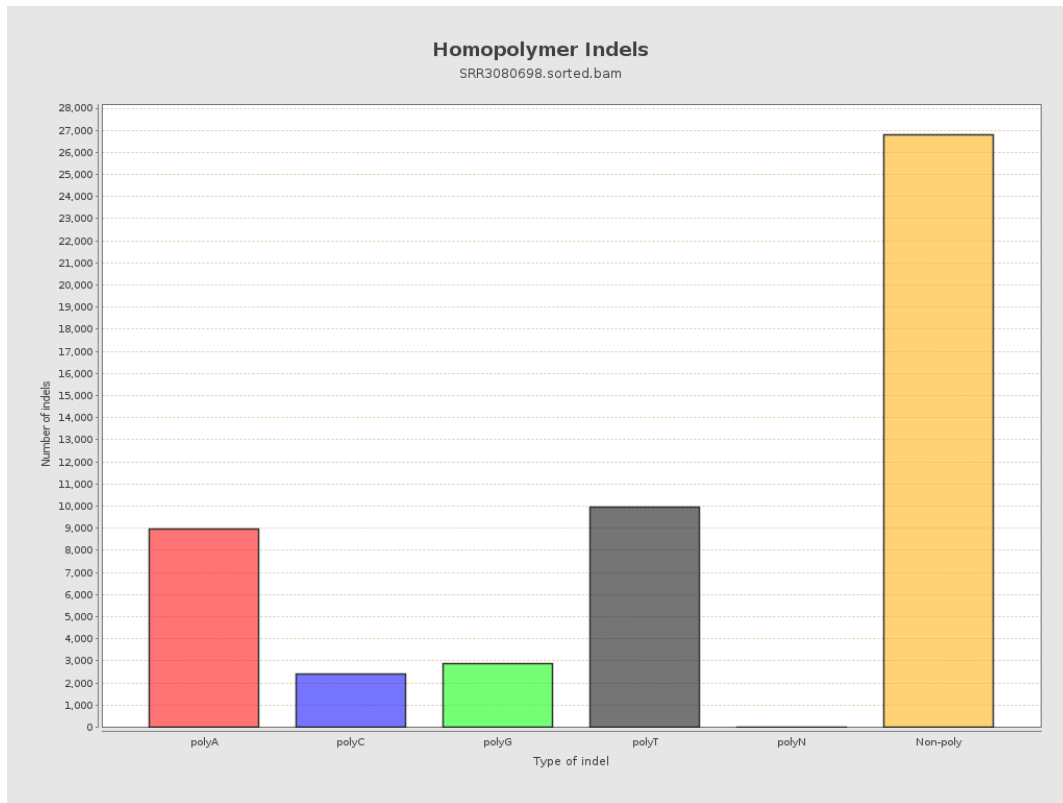
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

