

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 06:57:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867839.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_SRR9867839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867839.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 06:57:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,424,993
Mapped reads	2,247,732 / 92.69%
Unmapped reads	177,261 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,248 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	113,110 / 4.66%
Duplication rate	3.66%
Clipped reads	2,254,921 / 92.99%

2.2. ACGT Content

Number/percentage of A's	35,039,647 / 26.17%
Number/percentage of C's	27,545,634 / 20.57%
Number/percentage of T's	40,395,990 / 30.17%
Number/percentage of G's	30,885,720 / 23.07%
Number/percentage of N's	18,717 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.4017
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2.4. Mapping Quality

Mean Mapping Quality	46.12
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2.5. Mismatches and indels

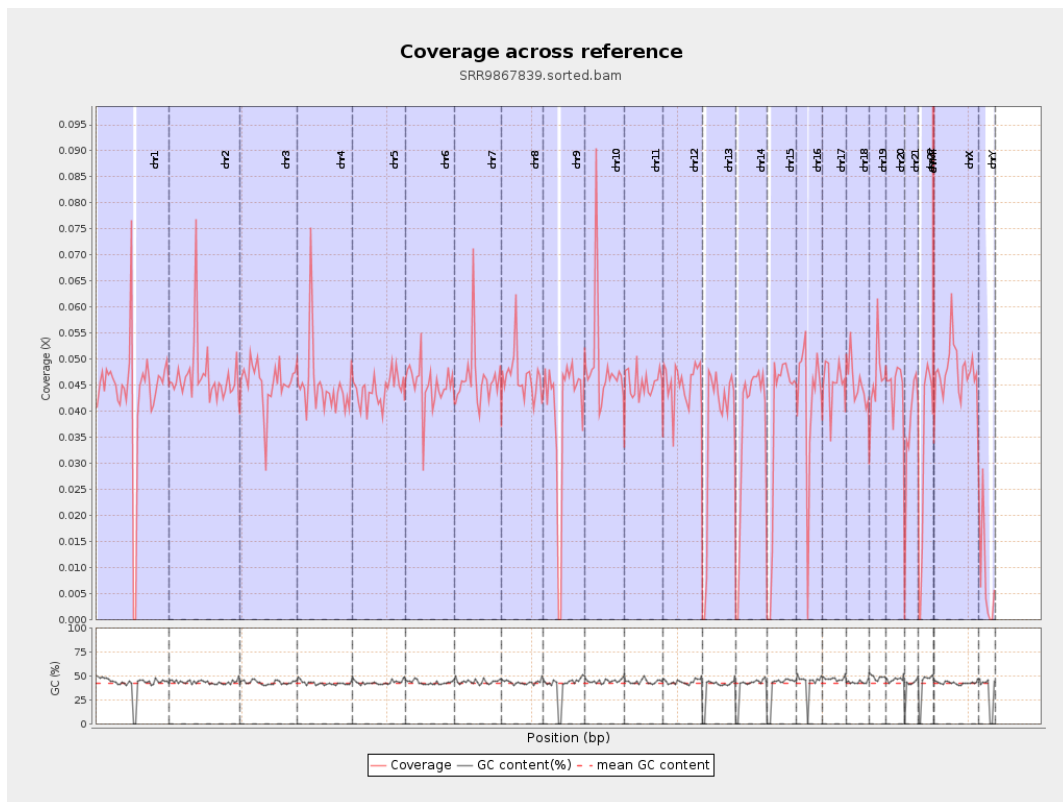
General error rate	0.51%
Mismatches	663,116
Insertions	8,808
Mapped reads with at least one insertion	0.39%
Deletions	25,007
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.92%

2.6. Chromosome stats

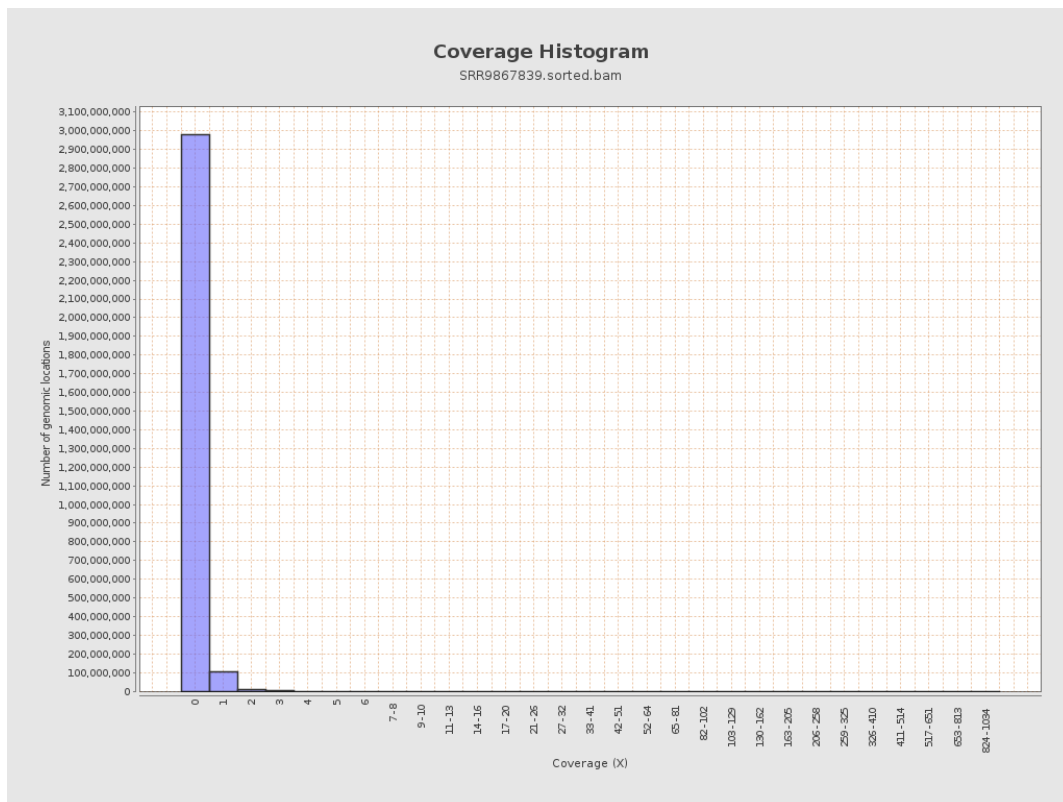
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10805636	0.0434	0.7791
chr2	243199373	11365848	0.0467	0.5391
chr3	198022430	8993469	0.0454	0.2379
chr4	191154276	8548156	0.0447	0.2826
chr5	180915260	7972918	0.0441	0.2361
chr6	171115067	7696556	0.045	0.2762
chr7	159138663	7369280	0.0463	0.4654

chr8	146364022	6817089	0.0466	0.4334
chr9	141213431	5624925	0.0398	0.3273
chr10	135534747	6563645	0.0484	0.4216
chr11	135006516	6085344	0.0451	0.3282
chr12	133851895	6073119	0.0454	0.2438
chr13	115169878	4214147	0.0366	0.2152
chr14	107349540	3992274	0.0372	0.2304
chr15	102531392	3874106	0.0378	0.2162
chr16	90354753	3857699	0.0427	0.2579
chr17	81195210	3673464	0.0452	0.2598
chr18	78077248	3566312	0.0457	0.6361
chr19	59128983	2757732	0.0466	0.569
chr20	63025520	2821994	0.0448	0.243
chr21	48129895	1753924	0.0364	0.2617
chr22	51304566	1633979	0.0318	0.1991
chrMT	16571	28377	1.7124	1.5558
chrX	155270560	7387647	0.0476	0.2767
chrY	59373566	447851	0.0075	0.2911

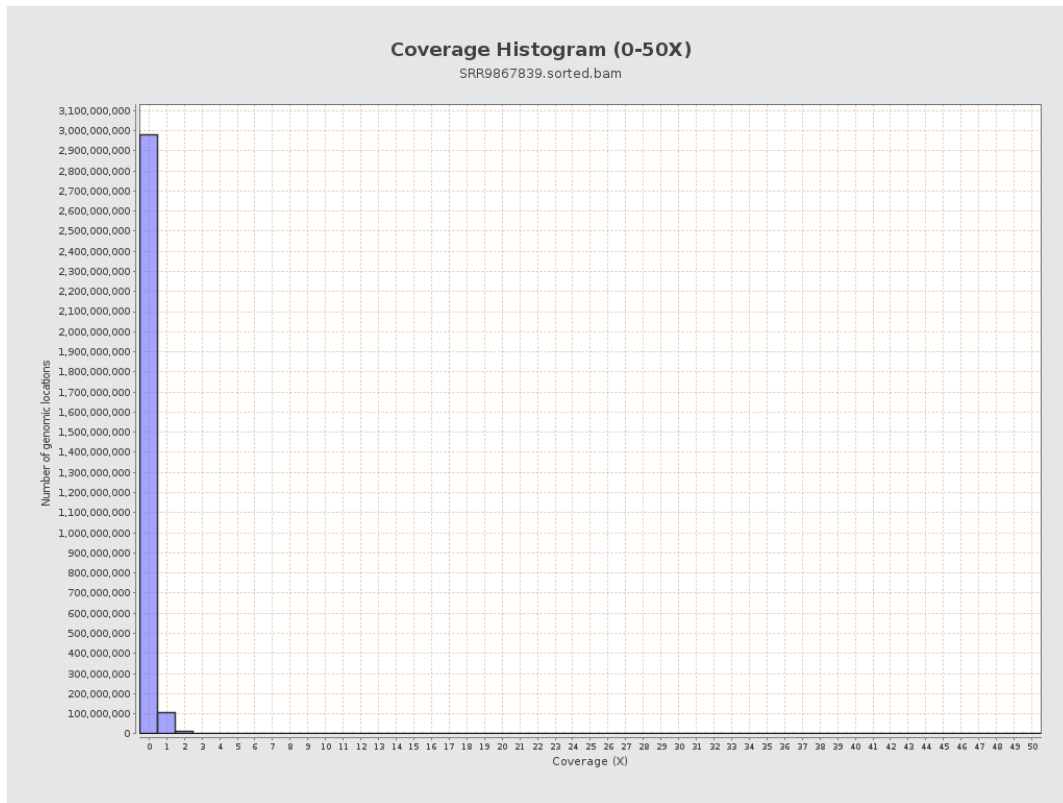
3. Results : Coverage across reference



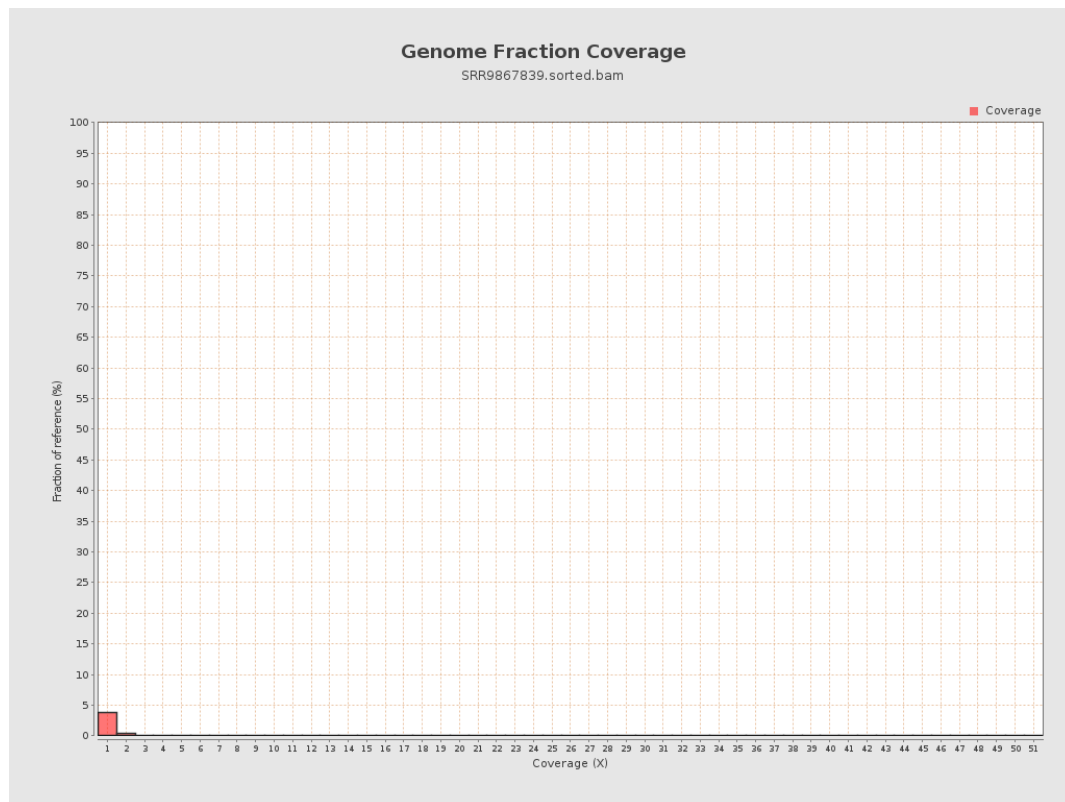
4. Results : Coverage Histogram



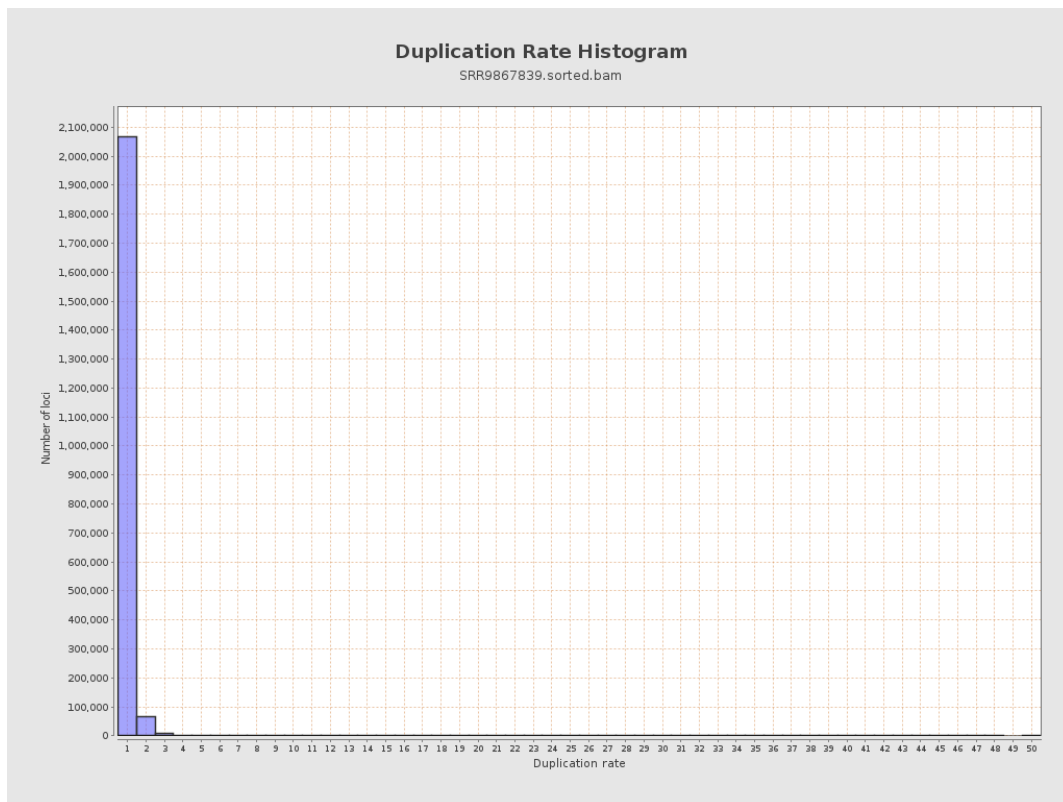
5. Results : Coverage Histogram (0-50X)



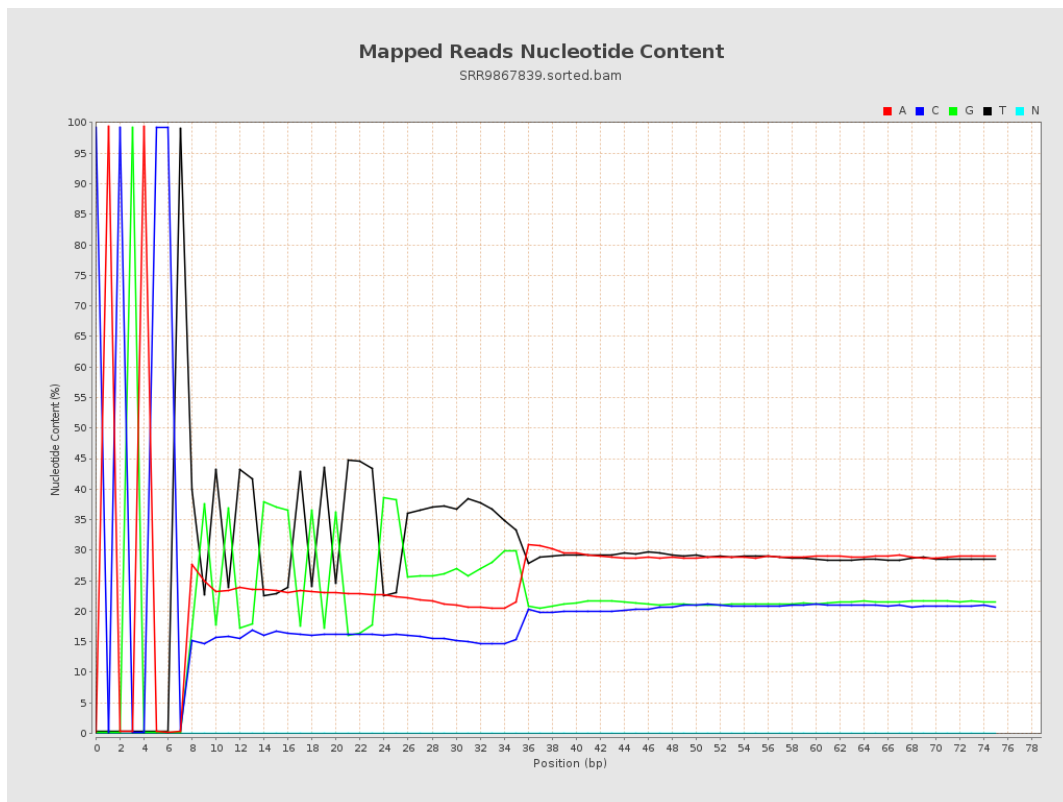
6. Results : Genome Fraction Coverage



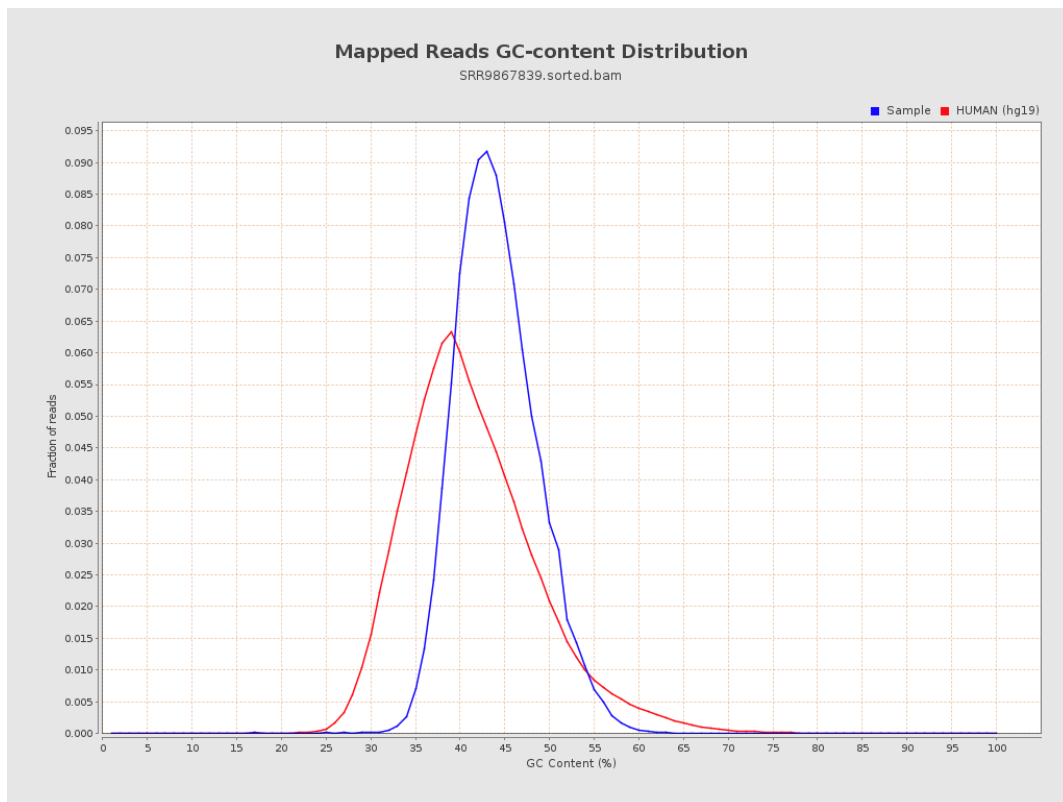
7. Results : Duplication Rate Histogram



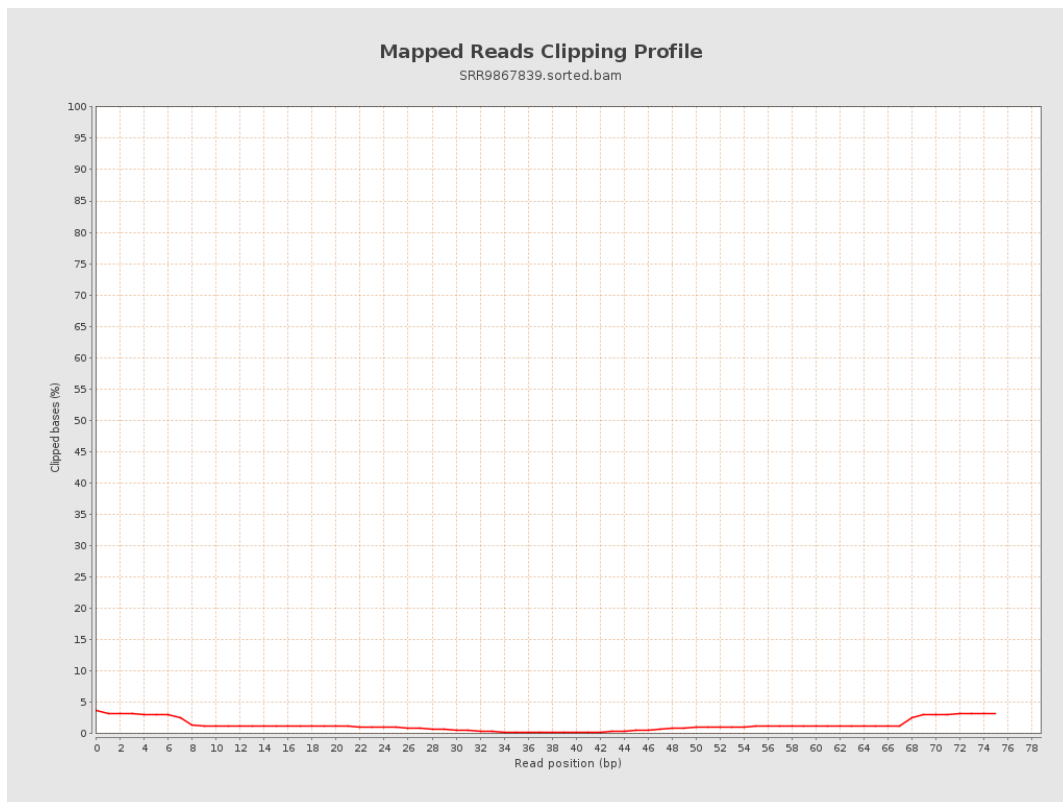
8. Results : Mapped Reads Nucleotide Content



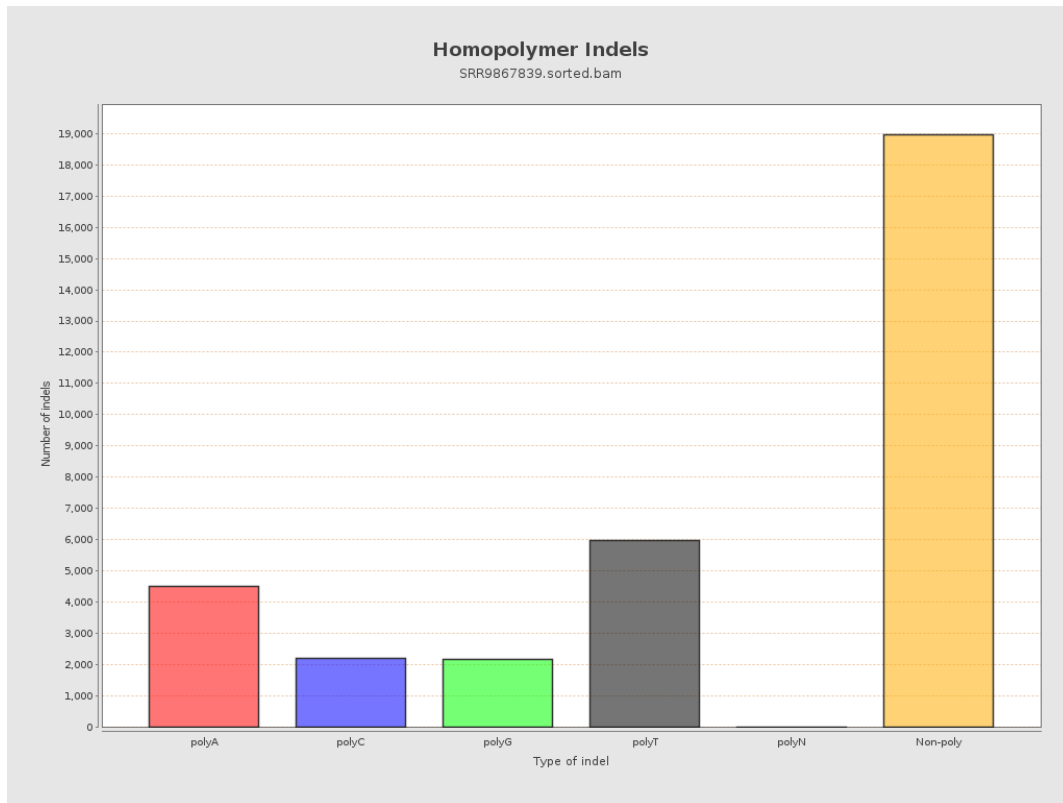
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

