

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:52:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708565.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_SRR1708565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708565.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:52:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708565.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,187,669
Mapped reads	3,430,974 / 81.93%
Unmapped reads	756,695 / 18.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	94 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,358 / 0.37%
Duplication rate	0.44%
Clipped reads	46,912 / 1.12%

2.2. ACGT Content

Number/percentage of A's	52,992,819 / 30.98%
Number/percentage of C's	32,498,850 / 19%
Number/percentage of T's	52,758,733 / 30.84%
Number/percentage of G's	32,826,516 / 19.19%
Number/percentage of N's	4,781 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	0.0553

Standard Deviation	0.2417
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2.4. Mapping Quality

Mean Mapping Quality	46.53
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2.5. Mismatches and indels

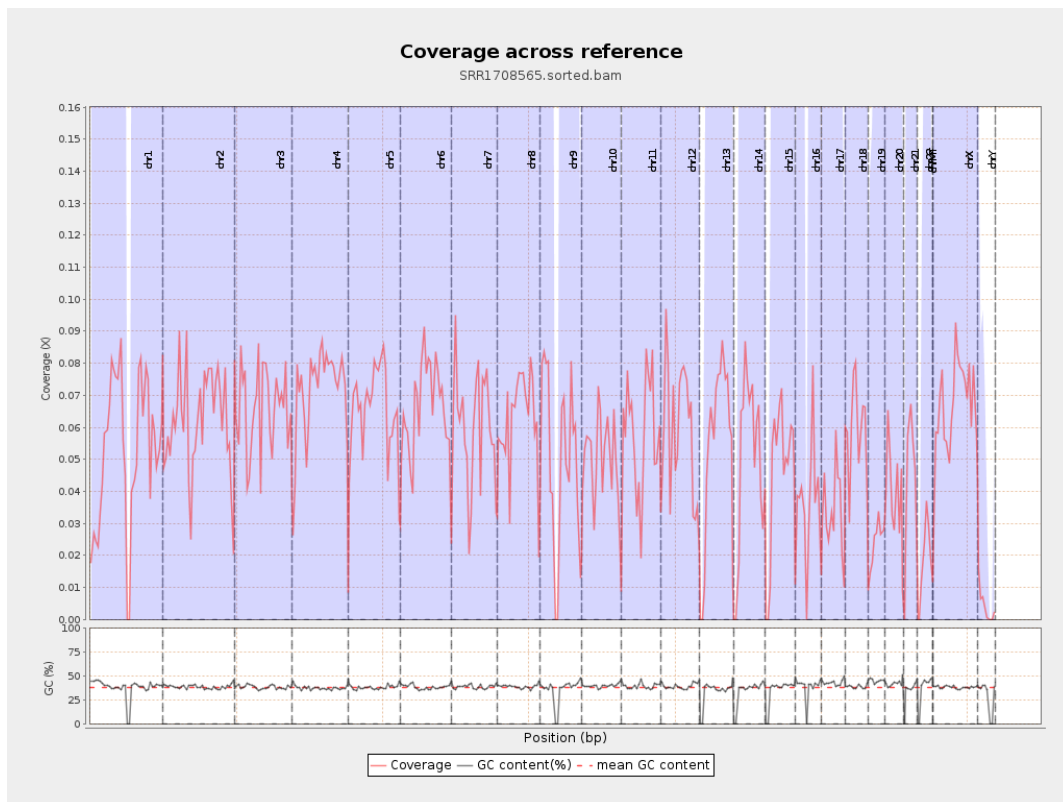
General error rate	0.17%
Mismatches	272,093
Insertions	11,829
Mapped reads with at least one insertion	0.34%
Deletions	9,038
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.47%

2.6. Chromosome stats

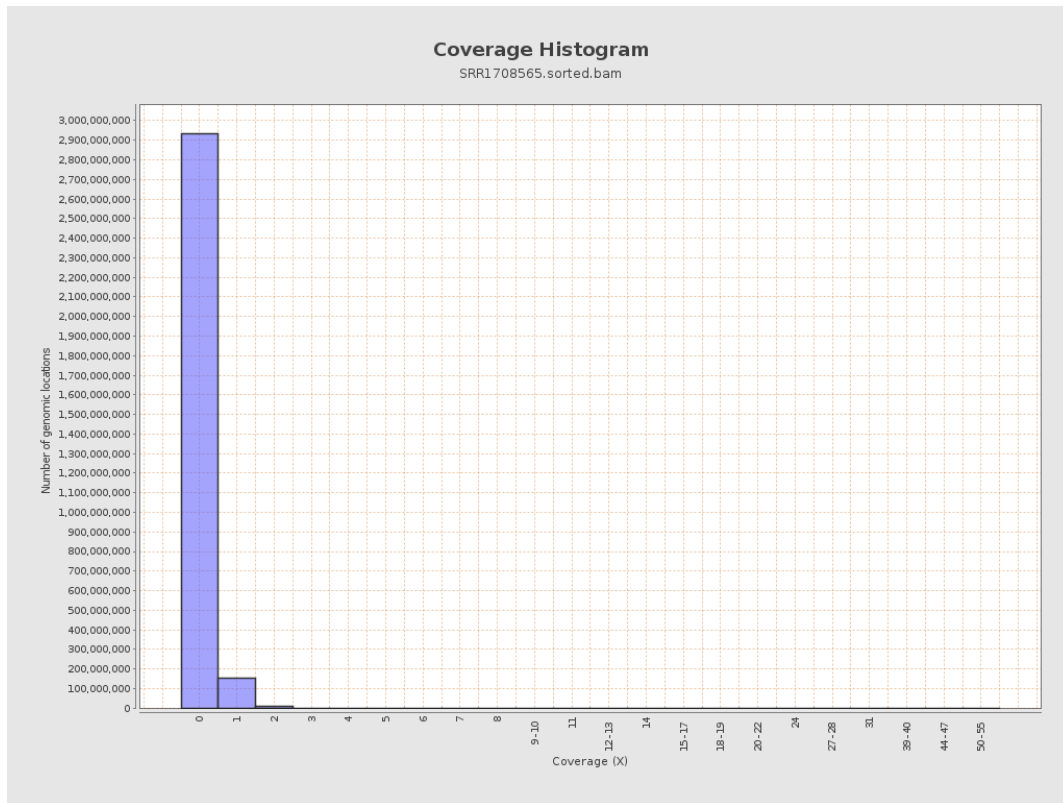
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13160003	0.0528	0.2373
chr2	243199373	15032790	0.0618	0.2549
chr3	198022430	13056055	0.0659	0.263
chr4	191154276	13705349	0.0717	0.274
chr5	180915260	11703410	0.0647	0.2602
chr6	171115067	11418481	0.0667	0.2647
chr7	159138663	9401575	0.0591	0.2496

chr8	146364022	9186870	0.0628	0.2564
chr9	141213431	7117449	0.0504	0.2311
chr10	135534747	6877261	0.0507	0.2305
chr11	135006516	7770992	0.0576	0.2471
chr12	133851895	7902813	0.059	0.2494
chr13	115169878	6340468	0.0551	0.2411
chr14	107349540	5421693	0.0505	0.2316
chr15	102531392	4667269	0.0455	0.2203
chr16	90354753	3236052	0.0358	0.1943
chr17	81195210	2803867	0.0345	0.1913
chr18	78077248	4647606	0.0595	0.2493
chr19	59128983	1436945	0.0243	0.1592
chr20	63025520	2570632	0.0408	0.2071
chr21	48129895	2024437	0.0421	0.2126
chr22	51304566	962052	0.0188	0.1403
chrMT	16571	200	0.0121	0.1092
chrX	155270560	10413333	0.0671	0.2659
chrY	59373566	239060	0.004	0.0658

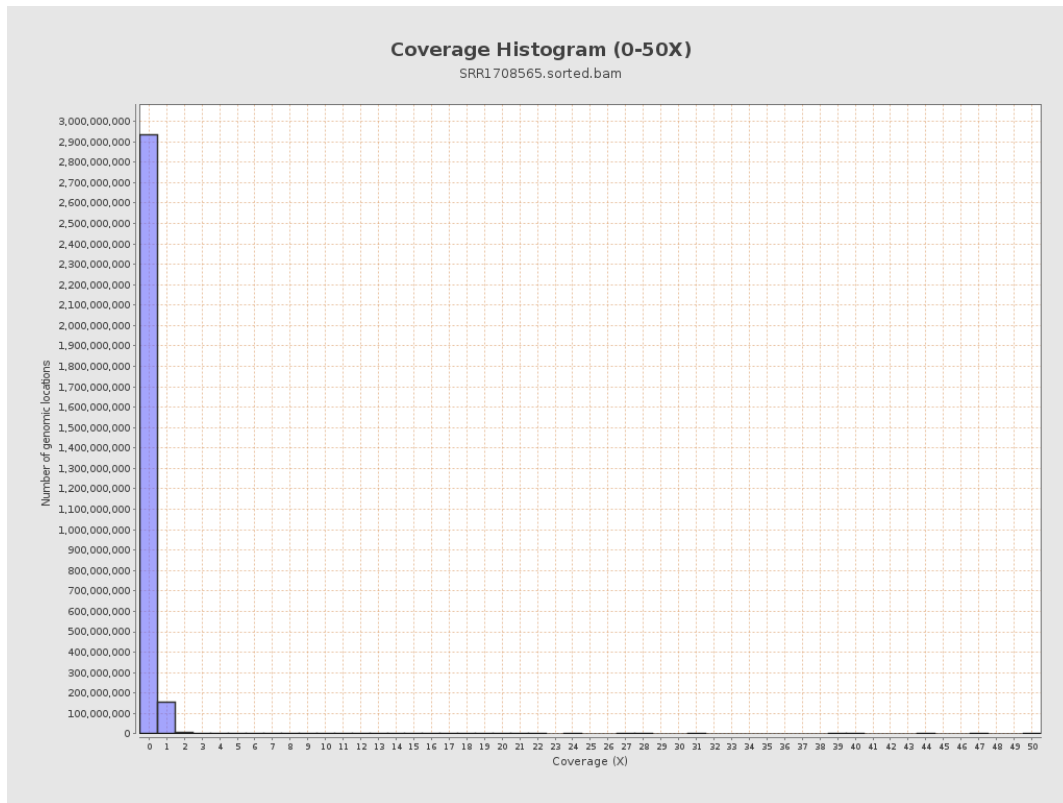
3. Results : Coverage across reference



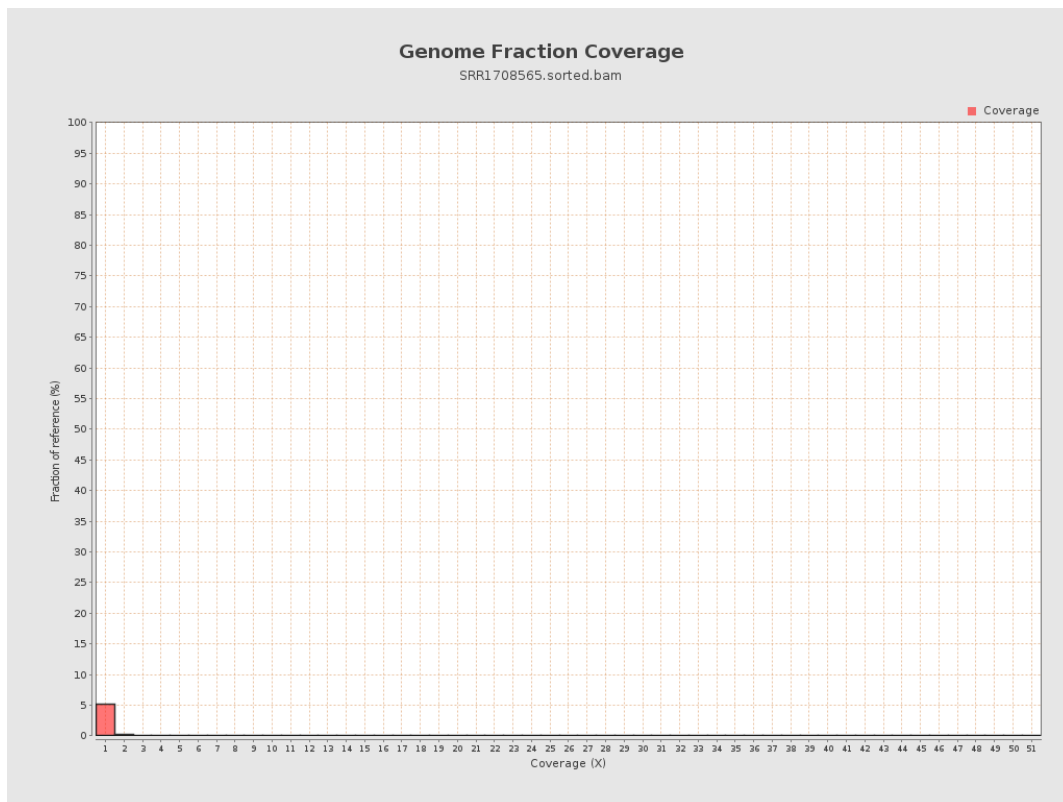
4. Results : Coverage Histogram



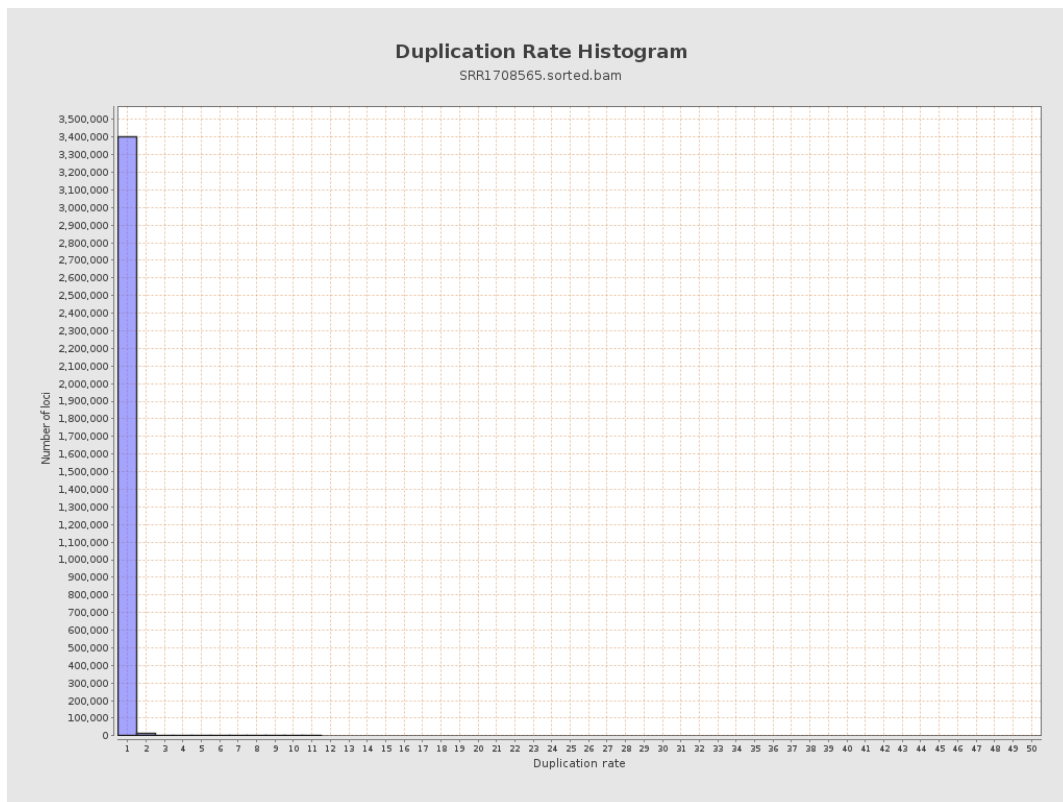
5. Results : Coverage Histogram (0-50X)



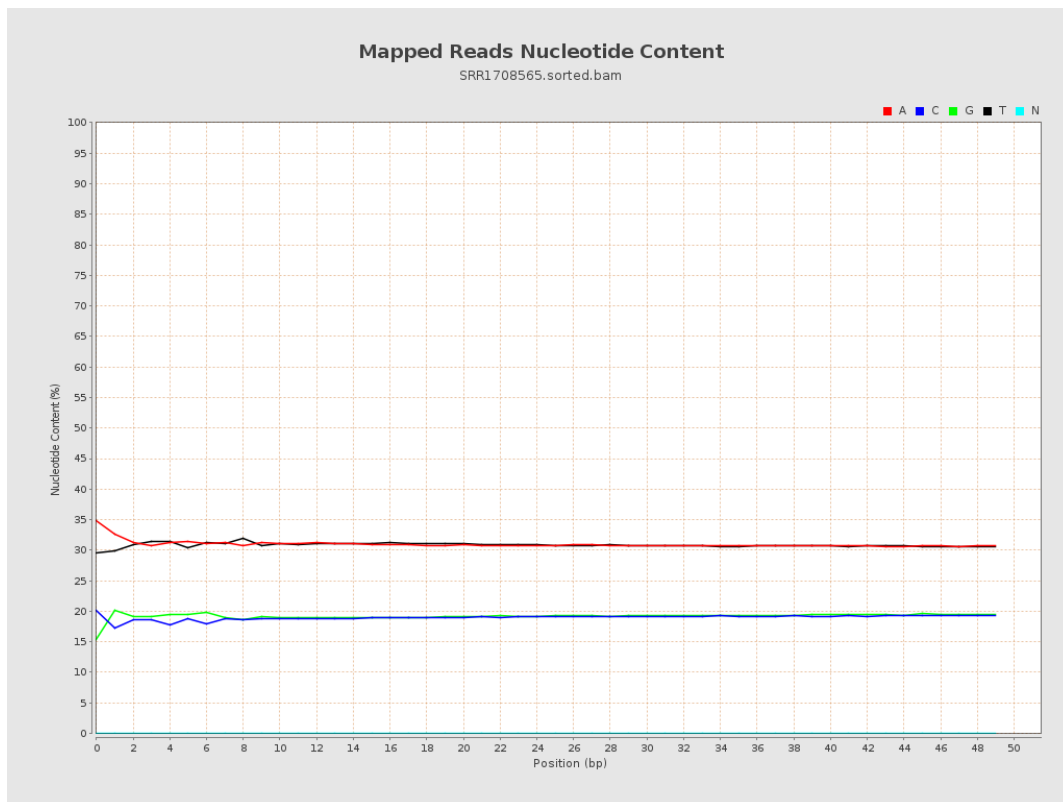
6. Results : Genome Fraction Coverage



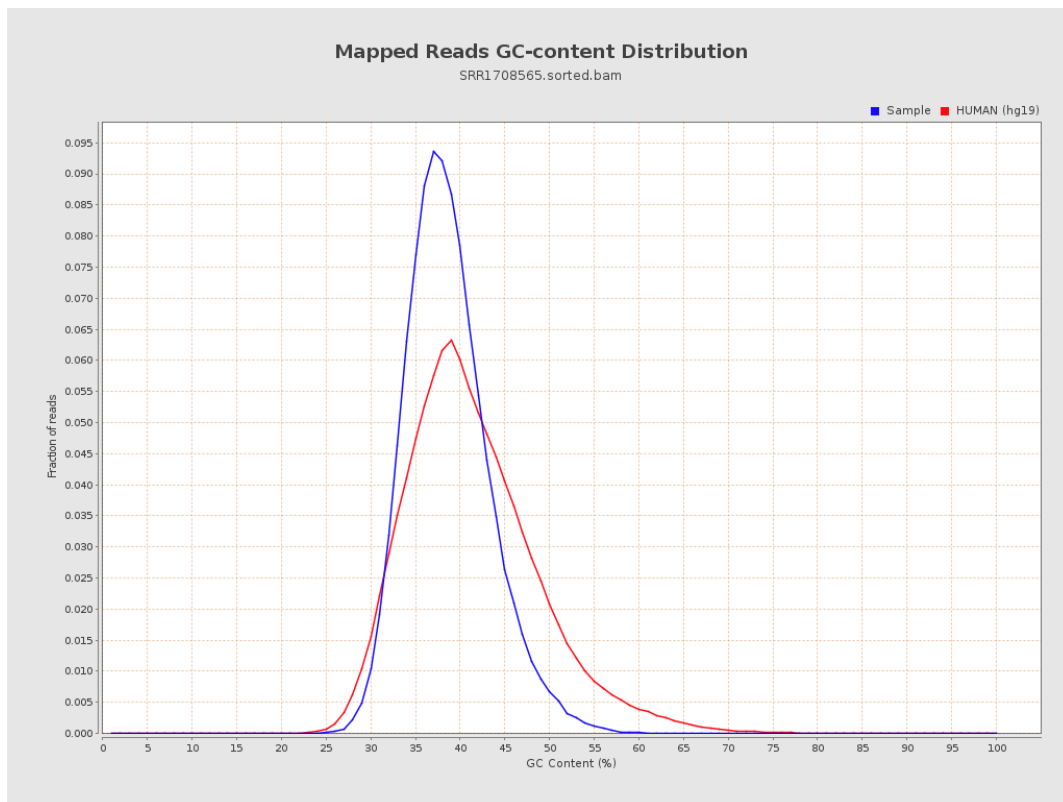
7. Results : Duplication Rate Histogram



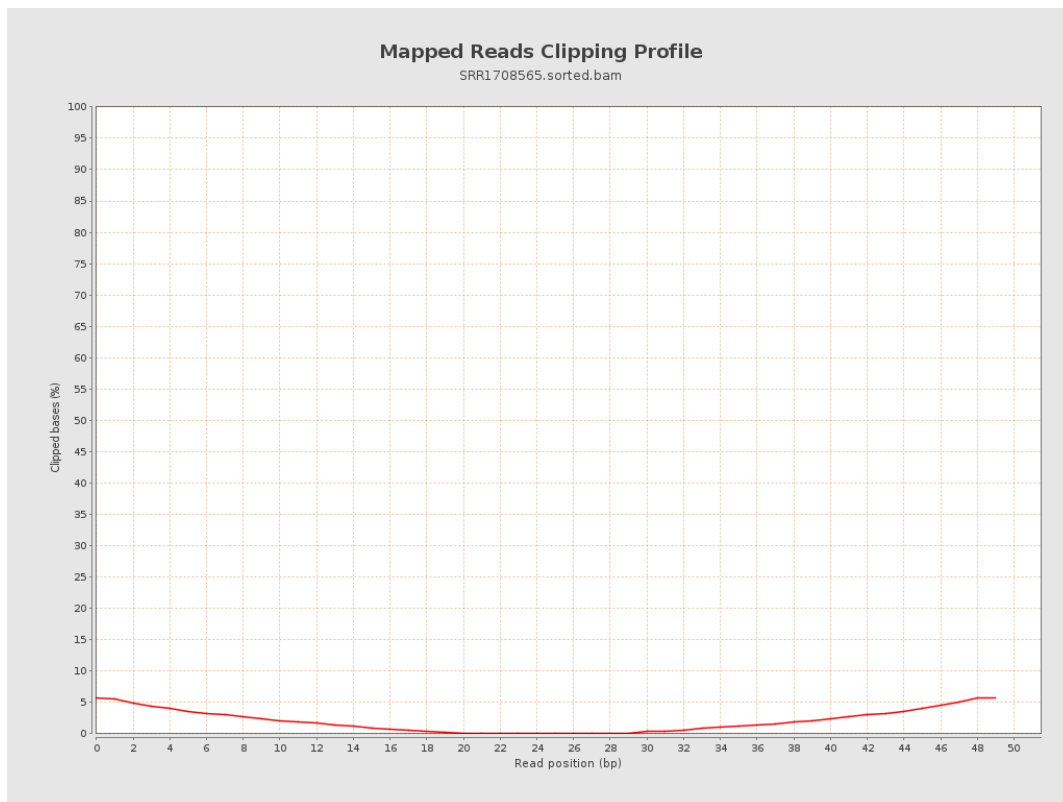
8. Results : Mapped Reads Nucleotide Content



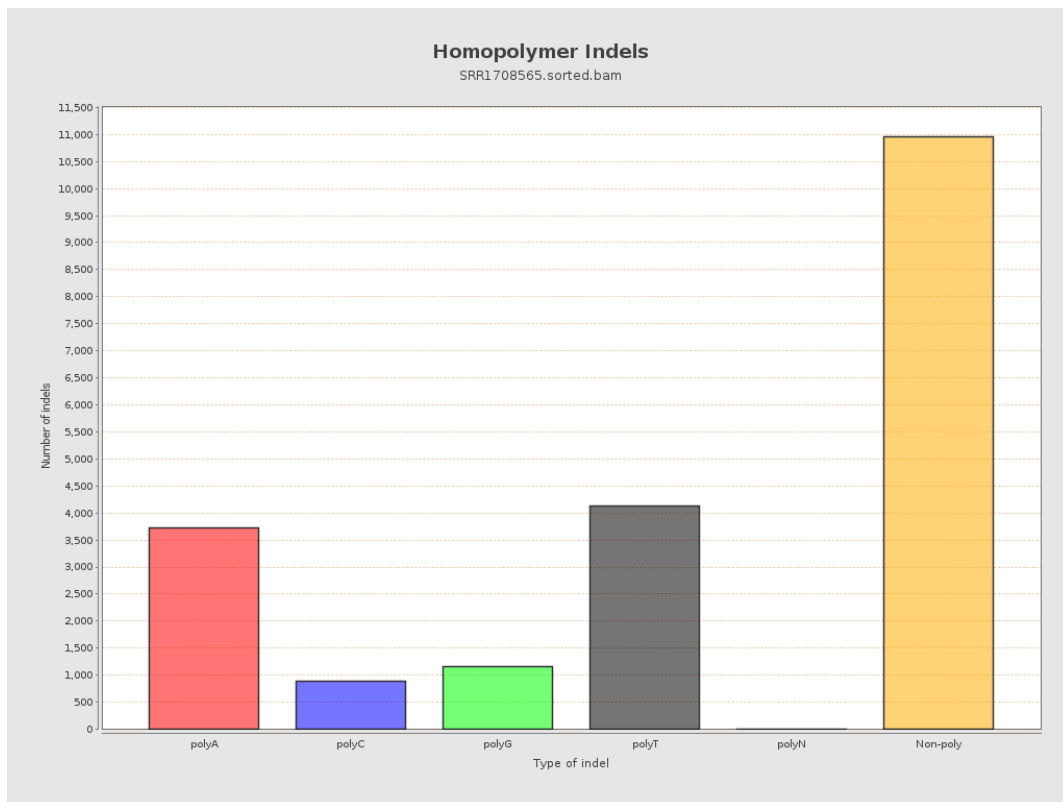
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

