

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:17:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068165.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_SRR6068165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068165.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:17:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,715,891
Mapped reads	1,598,389 / 93.15%
Unmapped reads	117,502 / 6.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,494 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	60,068 / 3.5%
Duplication rate	3.03%
Clipped reads	603,853 / 35.19%

2.2. ACGT Content

Number/percentage of A's	32,051,713 / 29.21%
Number/percentage of C's	20,948,557 / 19.09%
Number/percentage of T's	33,884,478 / 30.88%
Number/percentage of G's	22,708,914 / 20.7%
Number/percentage of N's	128,967 / 0.12%
GC Percentage	39.79%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.3765
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2.4. Mapping Quality

Mean Mapping Quality	43.2
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2.5. Mismatches and indels

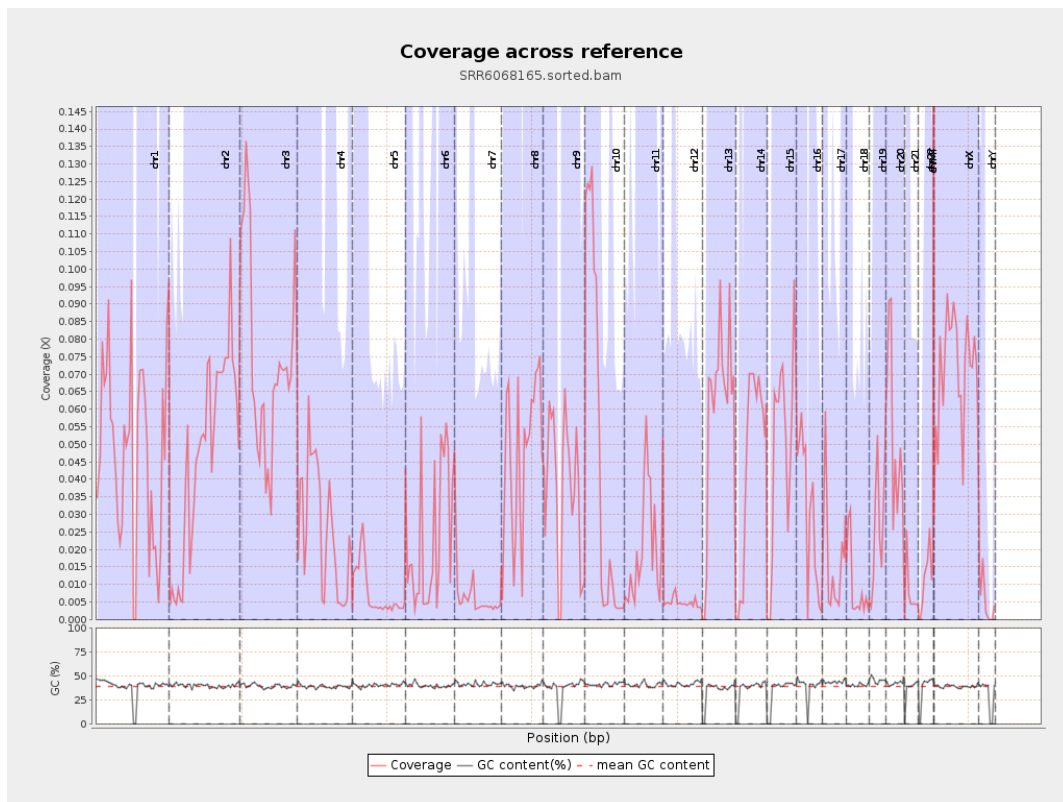
General error rate	0.85%
Mismatches	914,060
Insertions	7,408
Mapped reads with at least one insertion	0.46%
Deletions	25,481
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.88%

2.6. Chromosome stats

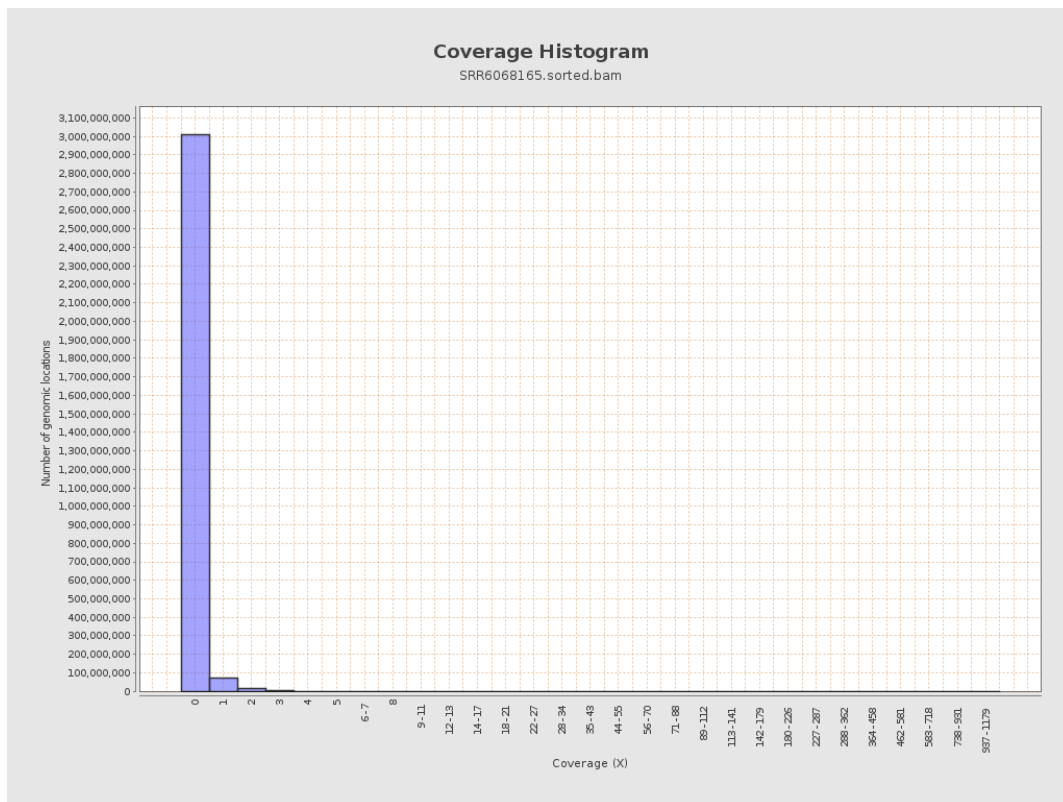
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11775891	0.0472	0.9366
chr2	243199373	11471848	0.0472	0.3578
chr3	198022430	14913809	0.0753	0.3341
chr4	191154276	4815886	0.0252	0.1984
chr5	180915260	1385867	0.0077	0.1101
chr6	171115067	4023586	0.0235	0.2332
chr7	159138663	928319	0.0058	0.1125

chr8	146364022	6958045	0.0475	0.2918
chr9	141213431	5277881	0.0374	0.3102
chr10	135534747	6195731	0.0457	0.3787
chr11	135006516	2786254	0.0206	0.1825
chr12	133851895	643143	0.0048	0.0955
chr13	115169878	6854209	0.0595	0.2934
chr14	107349540	4836345	0.0451	0.2706
chr15	102531392	5030113	0.0491	0.2648
chr16	90354753	2619055	0.029	0.2356
chr17	81195210	1347539	0.0166	0.1537
chr18	78077248	761428	0.0098	0.4062
chr19	59128983	1596555	0.027	0.5662
chr20	63025520	3296460	0.0523	0.2809
chr21	48129895	376044	0.0078	0.1386
chr22	51304566	579337	0.0113	0.1247
chrMT	16571	4387	0.2647	0.5687
chrX	155270560	10988588	0.0708	0.3687
chrY	59373566	301452	0.0051	0.1707

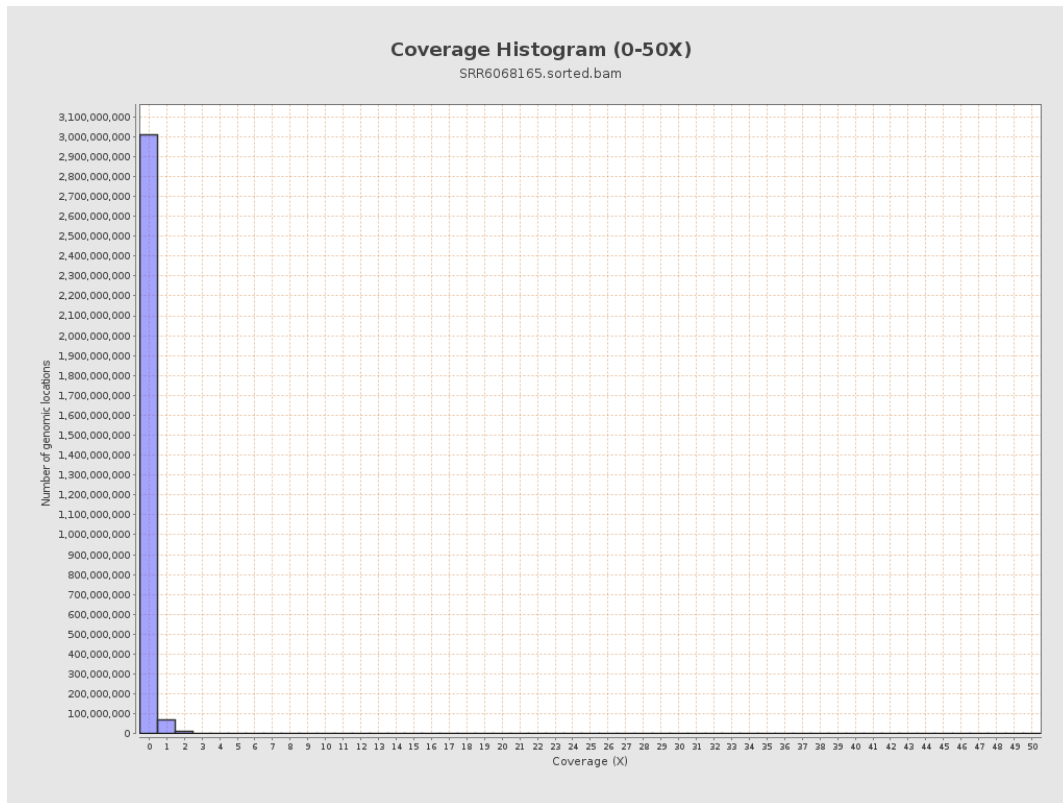
3. Results : Coverage across reference



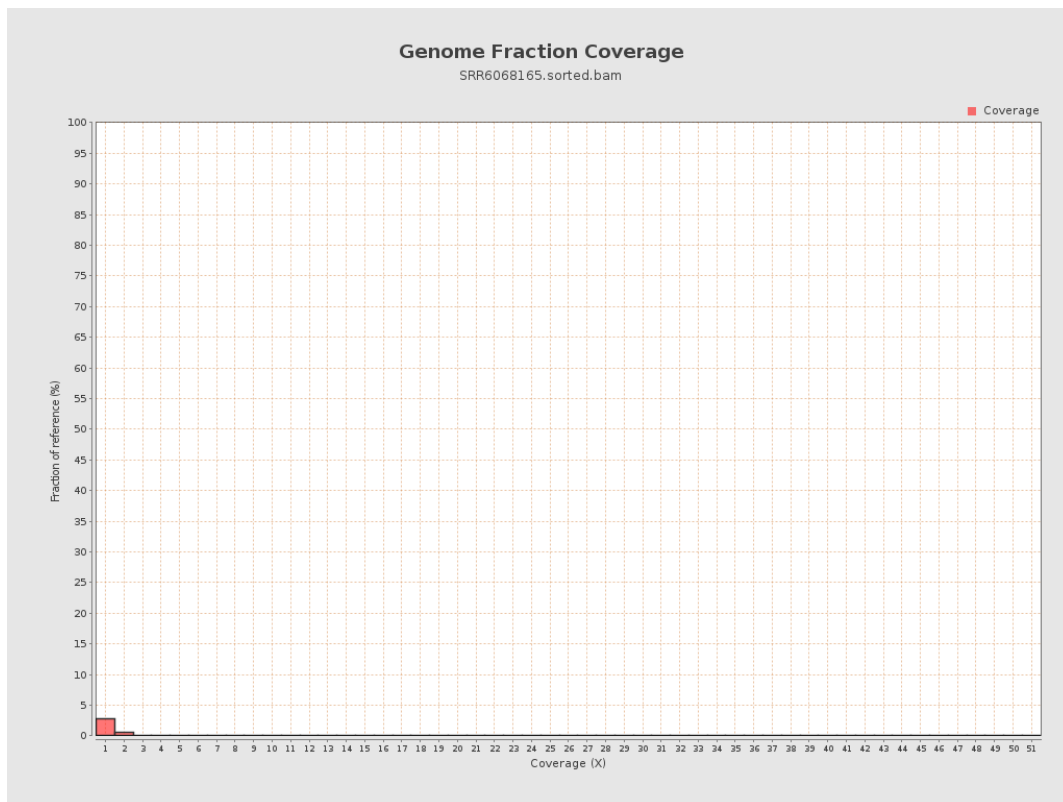
4. Results : Coverage Histogram



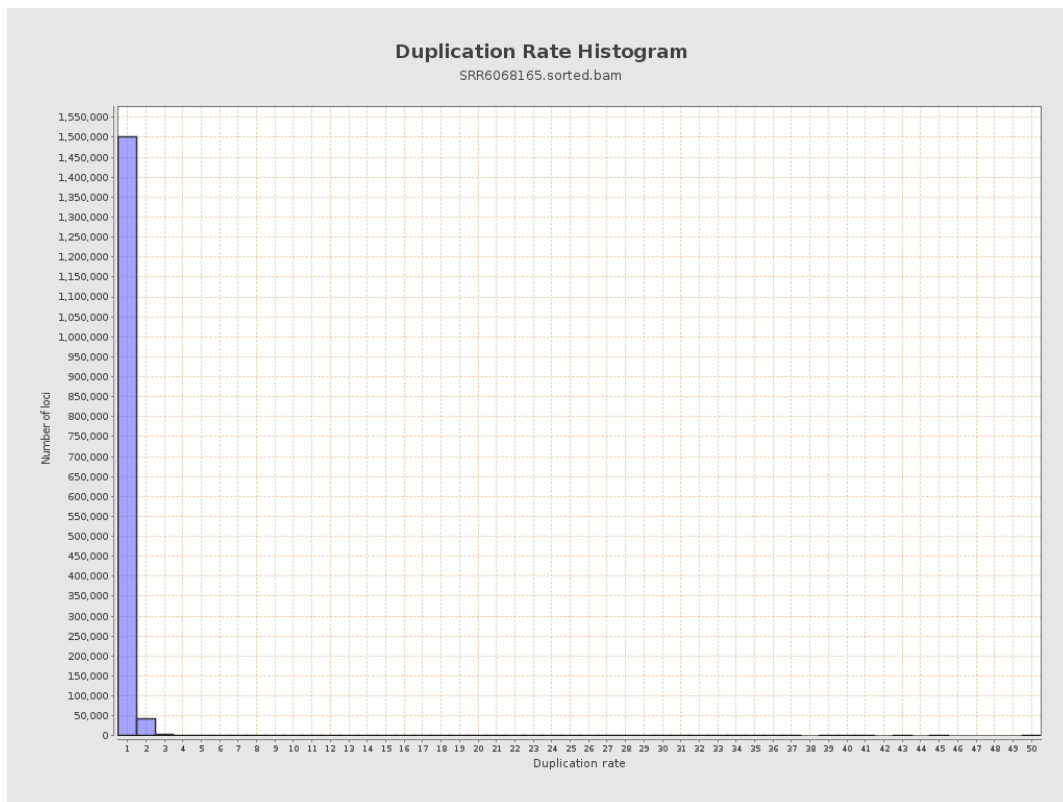
5. Results : Coverage Histogram (0-50X)



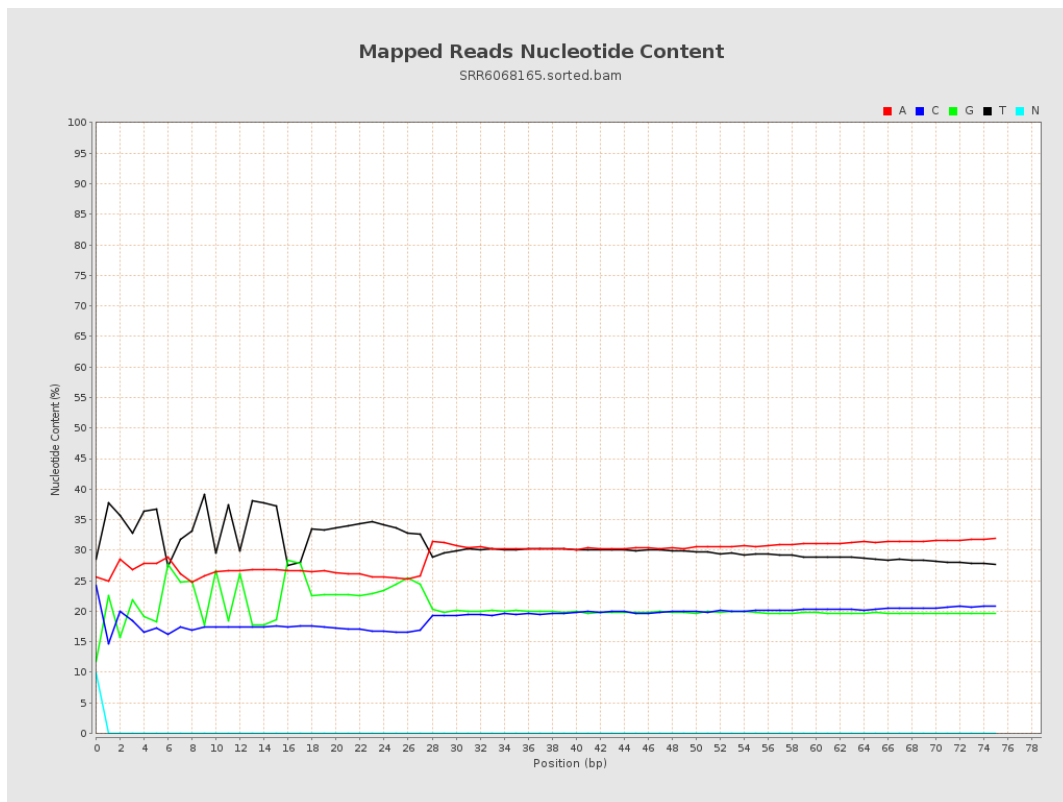
6. Results : Genome Fraction Coverage



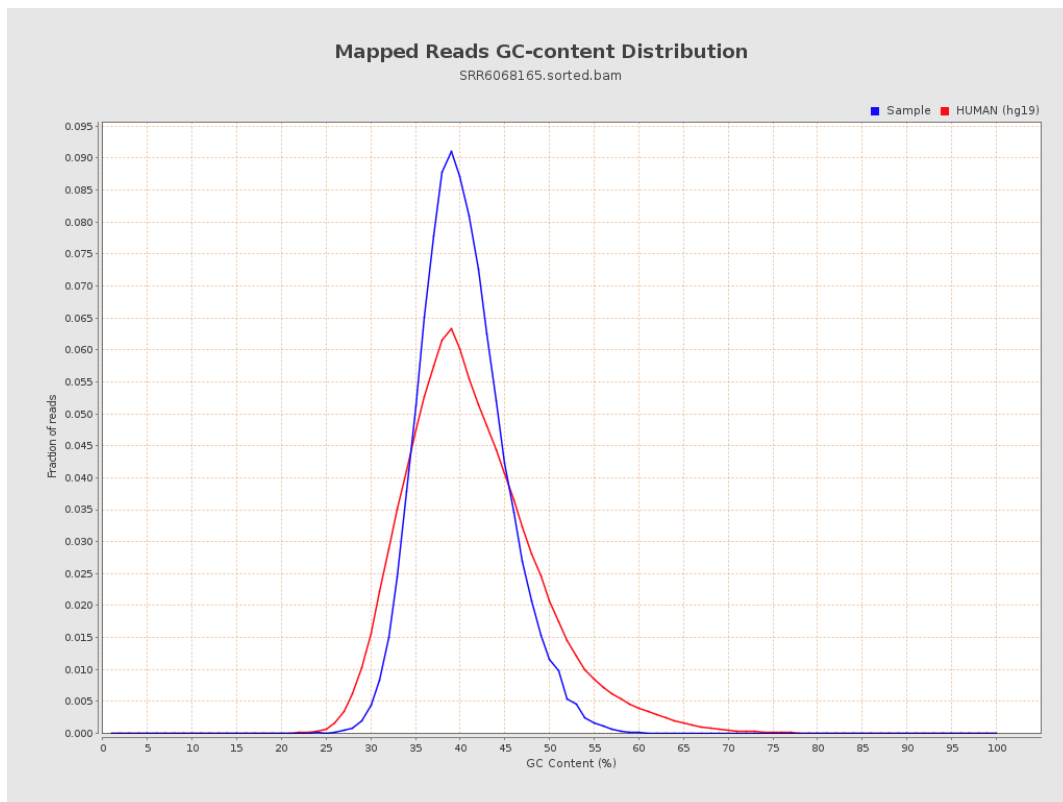
7. Results : Duplication Rate Histogram



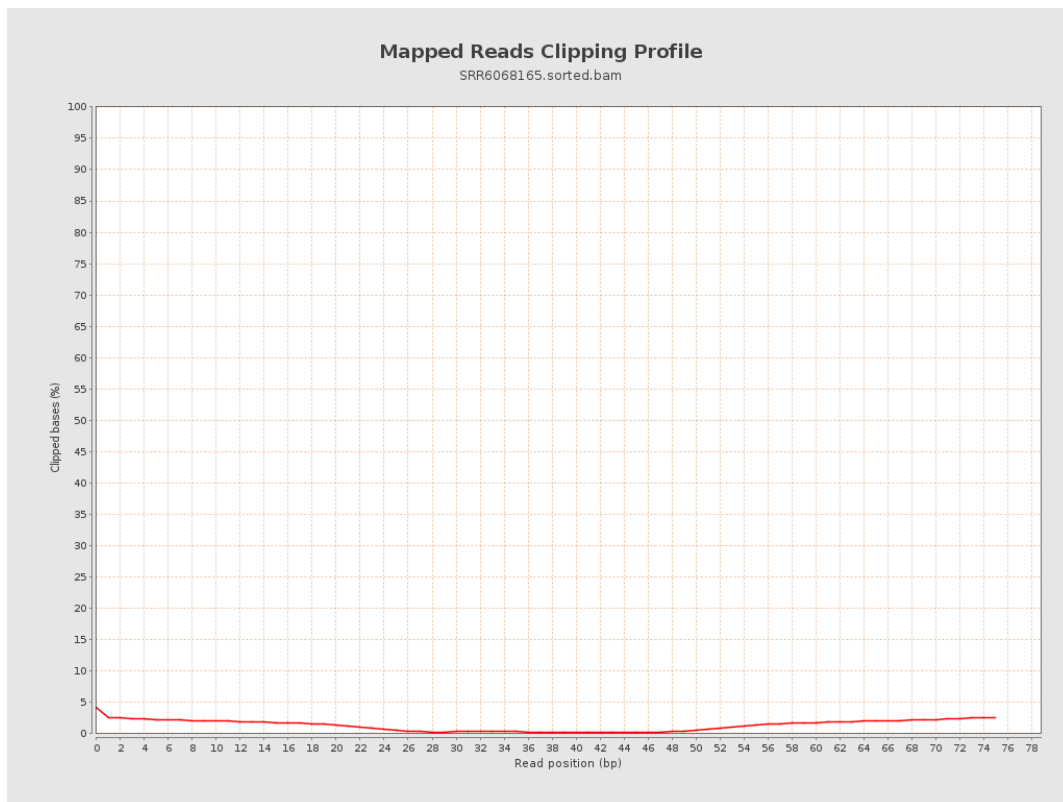
8. Results : Mapped Reads Nucleotide Content



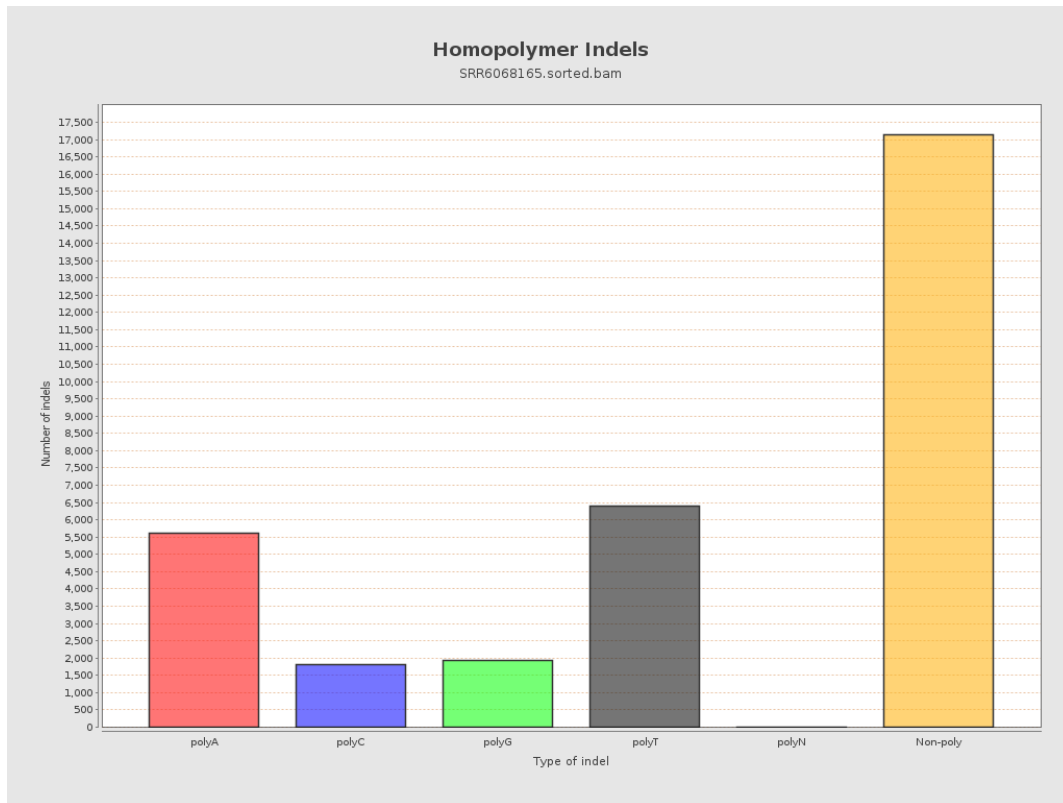
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

