

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:23:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068105.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_SRR6068105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:23:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,632,214
Mapped reads	5,367,471 / 95.3%
Unmapped reads	264,743 / 4.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,349 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	757,289 / 13.45%
Duplication rate	11.68%
Clipped reads	2,505,147 / 44.48%

2.2. ACGT Content

Number/percentage of A's	96,022,943 / 27.25%
Number/percentage of C's	62,936,683 / 17.86%
Number/percentage of T's	115,128,845 / 32.67%
Number/percentage of G's	78,256,403 / 22.21%
Number/percentage of N's	41,973 / 0.01%
GC Percentage	40.07%

2.3. Coverage

Mean	0.1139

Standard Deviation	1.1496
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2.4. Mapping Quality

Mean Mapping Quality	46.71
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2.5. Mismatches and indels

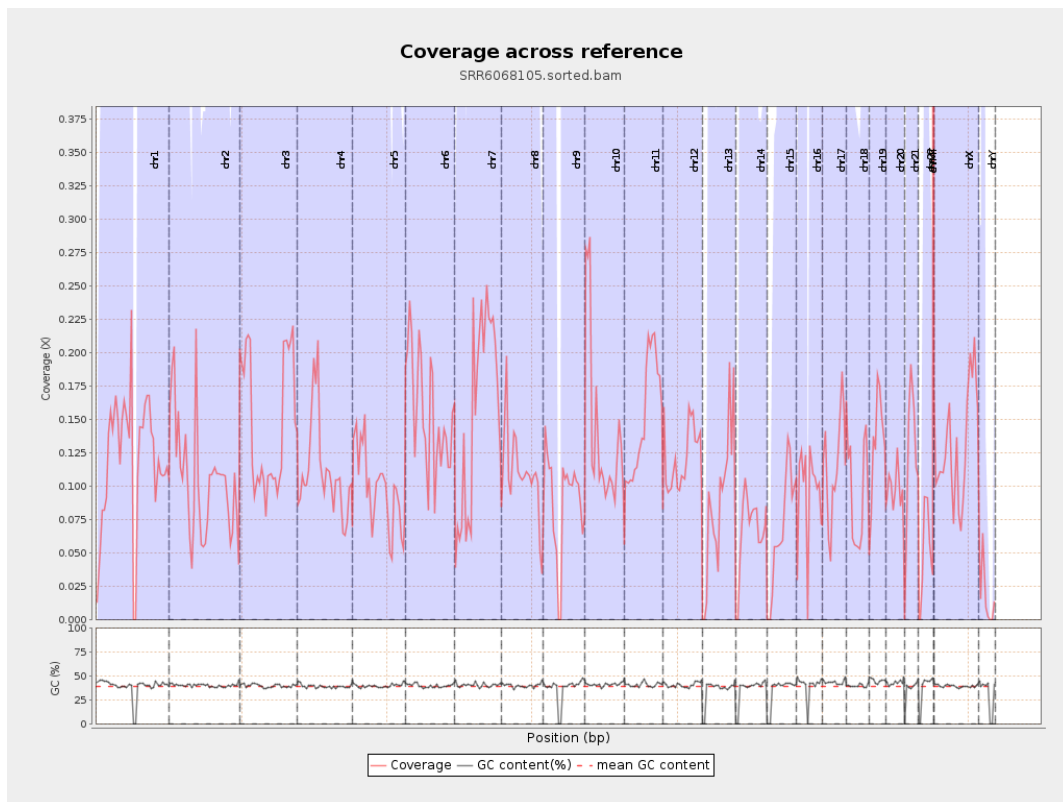
General error rate	0.56%
Mismatches	1,934,211
Insertions	23,501
Mapped reads with at least one insertion	0.43%
Deletions	90,467
Mapped reads with at least one deletion	1.67%
Homopolymer indels	45.5%

2.6. Chromosome stats

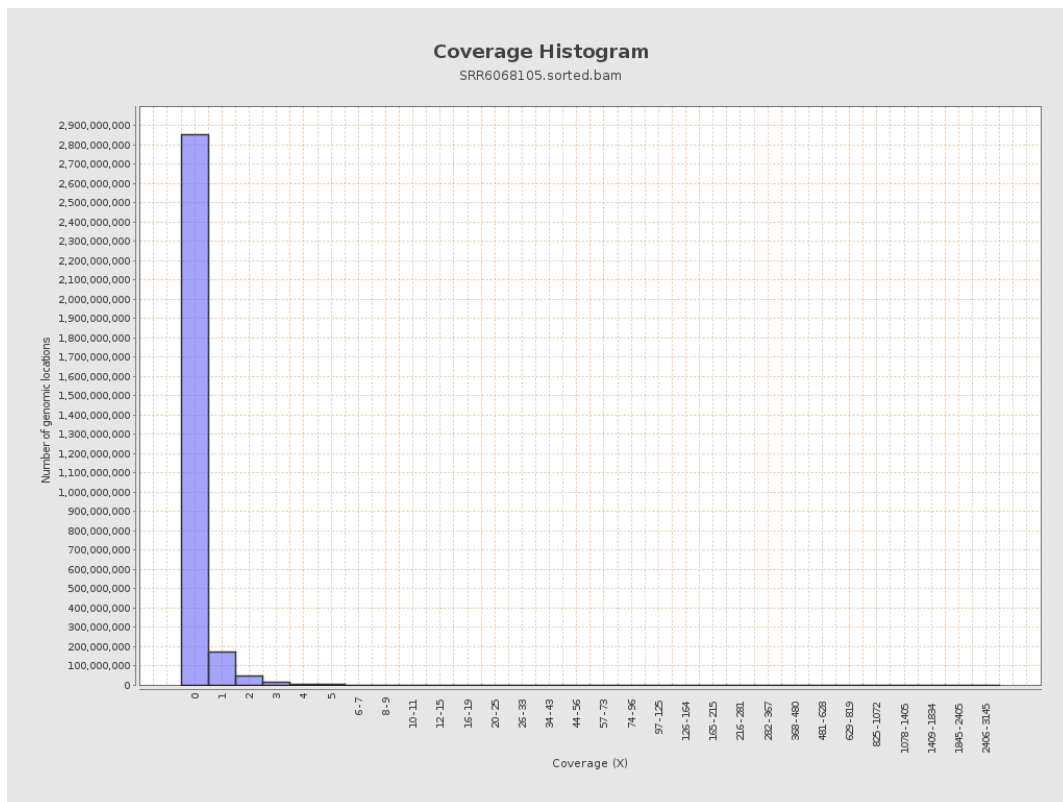
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29891586	0.1199	2.634
chr2	243199373	25467385	0.1047	1.2638
chr3	198022430	29148164	0.1472	0.5202
chr4	191154276	21152118	0.1107	0.5111
chr5	180915260	17669268	0.0977	0.4299
chr6	171115067	26468997	0.1547	0.7176
chr7	159138663	25013963	0.1572	1.6525

chr8	146364022	16063218	0.1097	1.7418
chr9	141213431	12620324	0.0894	0.8153
chr10	135534747	19138538	0.1412	0.8564
chr11	135006516	20312130	0.1505	0.7397
chr12	133851895	16390969	0.1225	0.5204
chr13	115169878	10141107	0.0881	0.4287
chr14	107349540	7007970	0.0653	0.427
chr15	102531392	6970451	0.068	0.3899
chr16	90354753	8583598	0.095	0.482
chr17	81195210	9311663	0.1147	0.5024
chr18	78077248	7371633	0.0944	1.4419
chr19	59128983	7937745	0.1342	1.7825
chr20	63025520	6128593	0.0972	0.4755
chr21	48129895	5846176	0.1215	0.5137
chr22	51304566	2461586	0.048	0.2854
chrMT	16571	48427	2.9224	2.4717
chrX	155270560	20363951	0.1312	0.5729
chrY	59373566	1036912	0.0175	0.7457

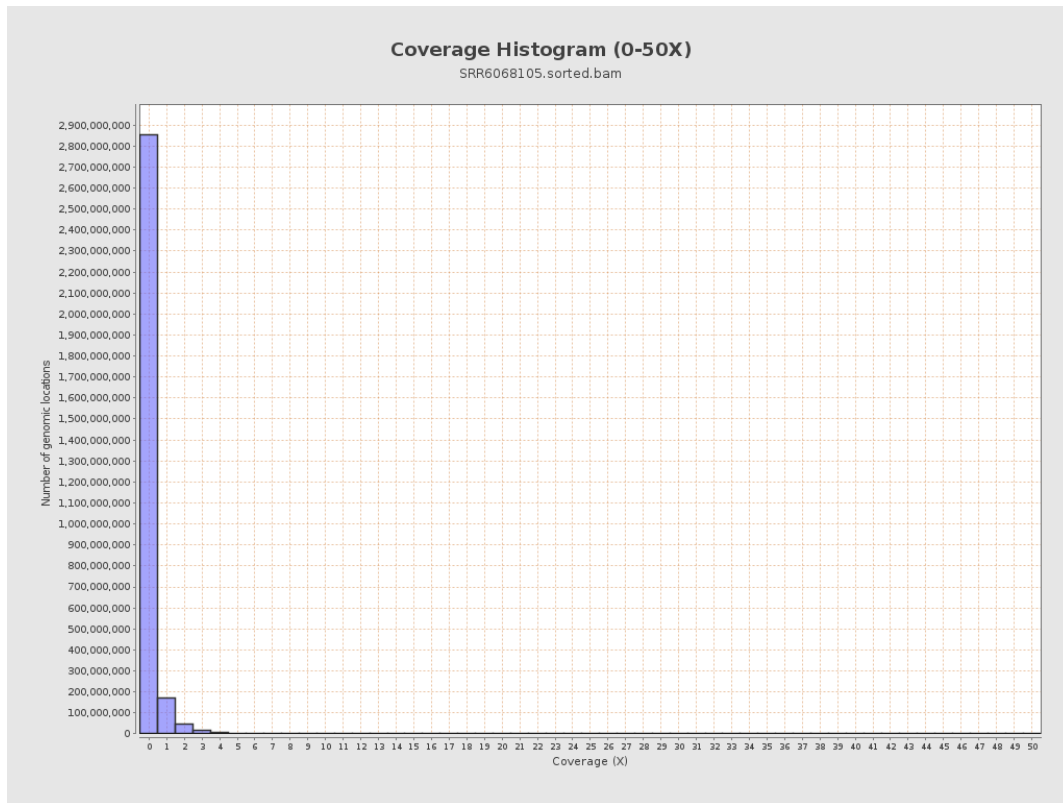
3. Results : Coverage across reference



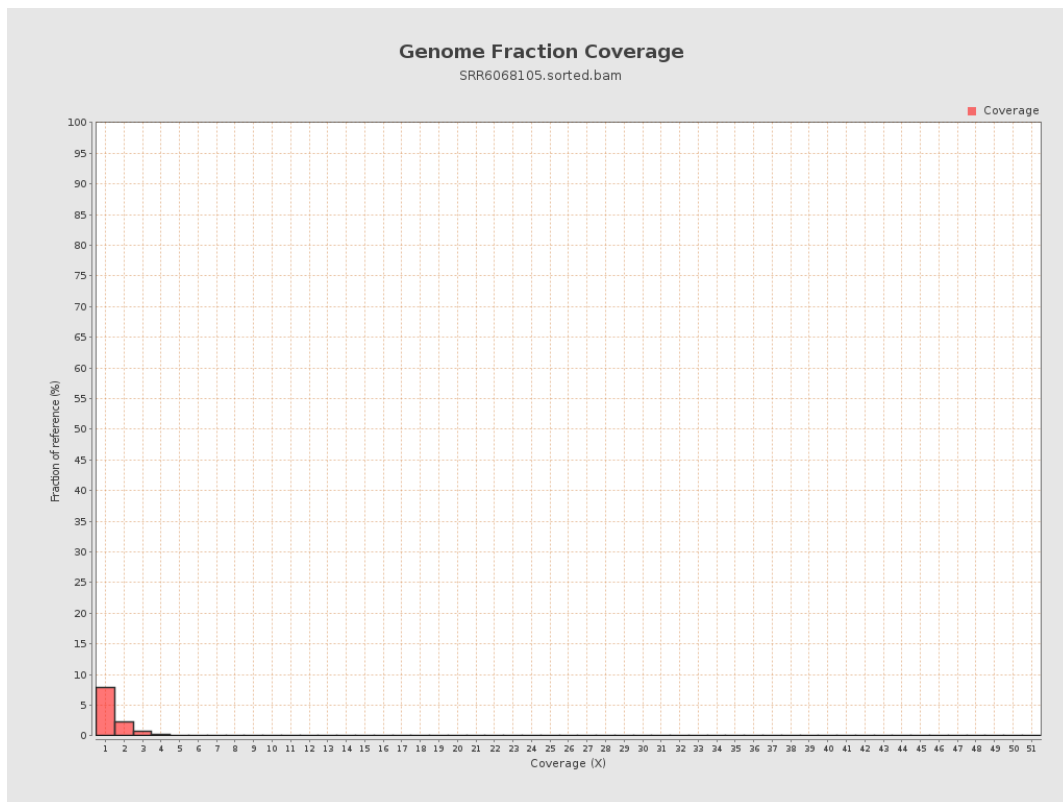
4. Results : Coverage Histogram



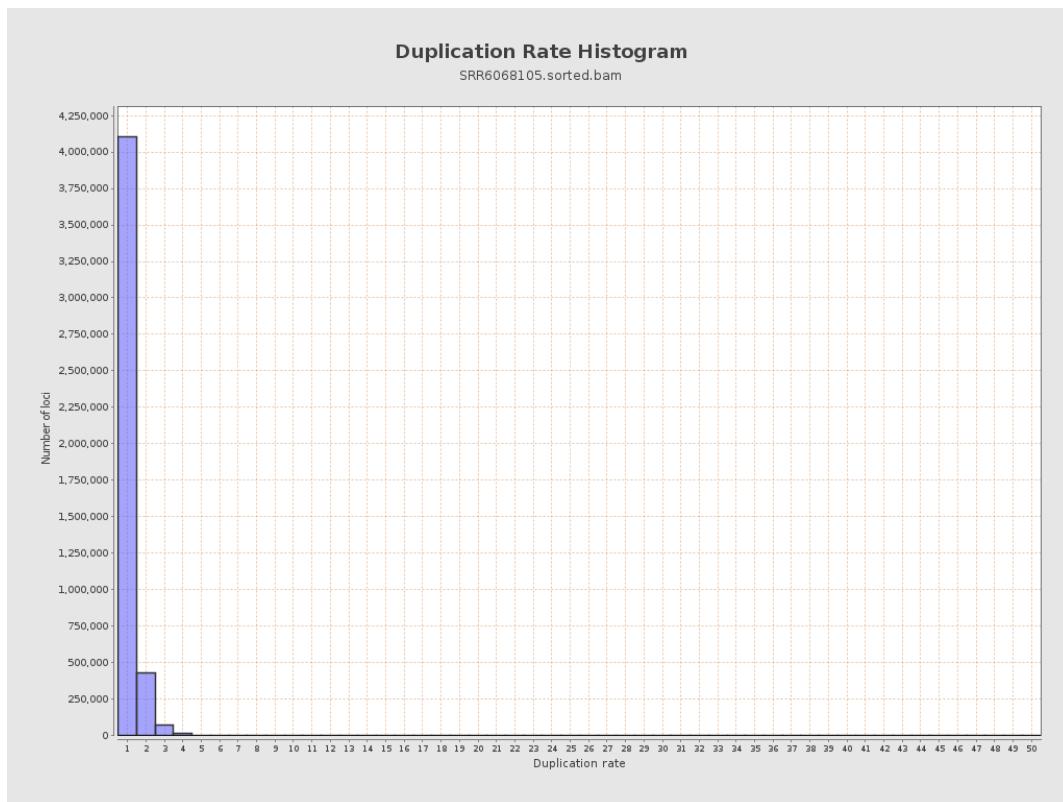
5. Results : Coverage Histogram (0-50X)



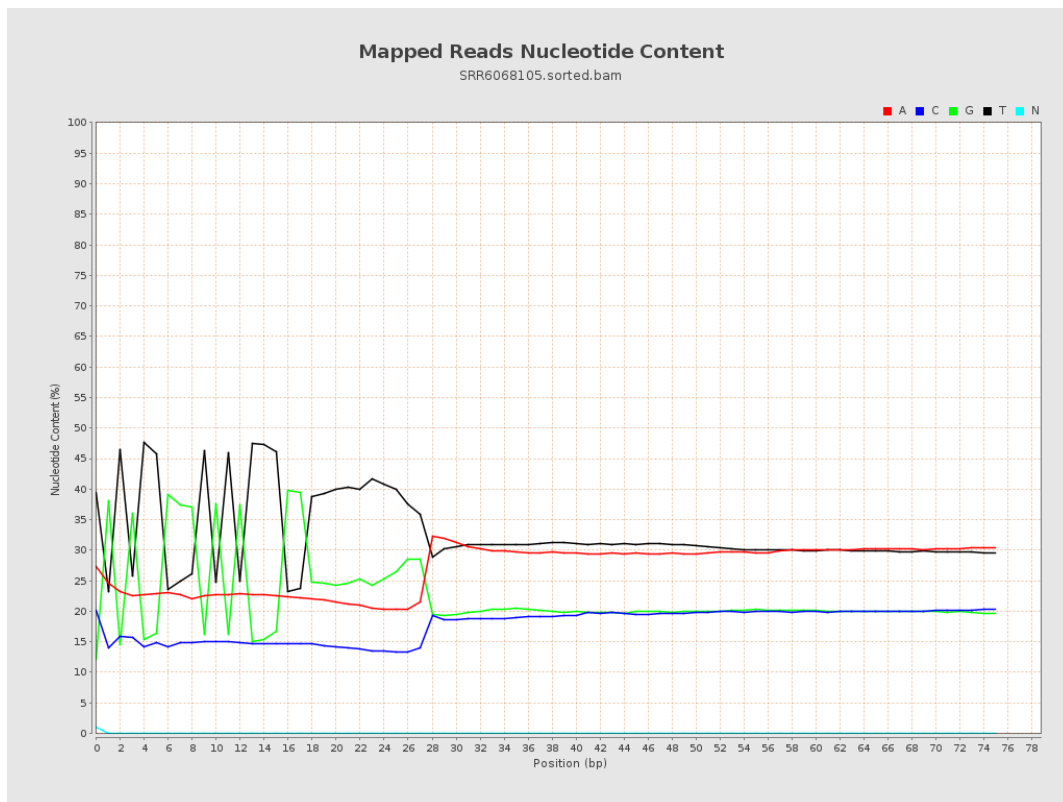
6. Results : Genome Fraction Coverage



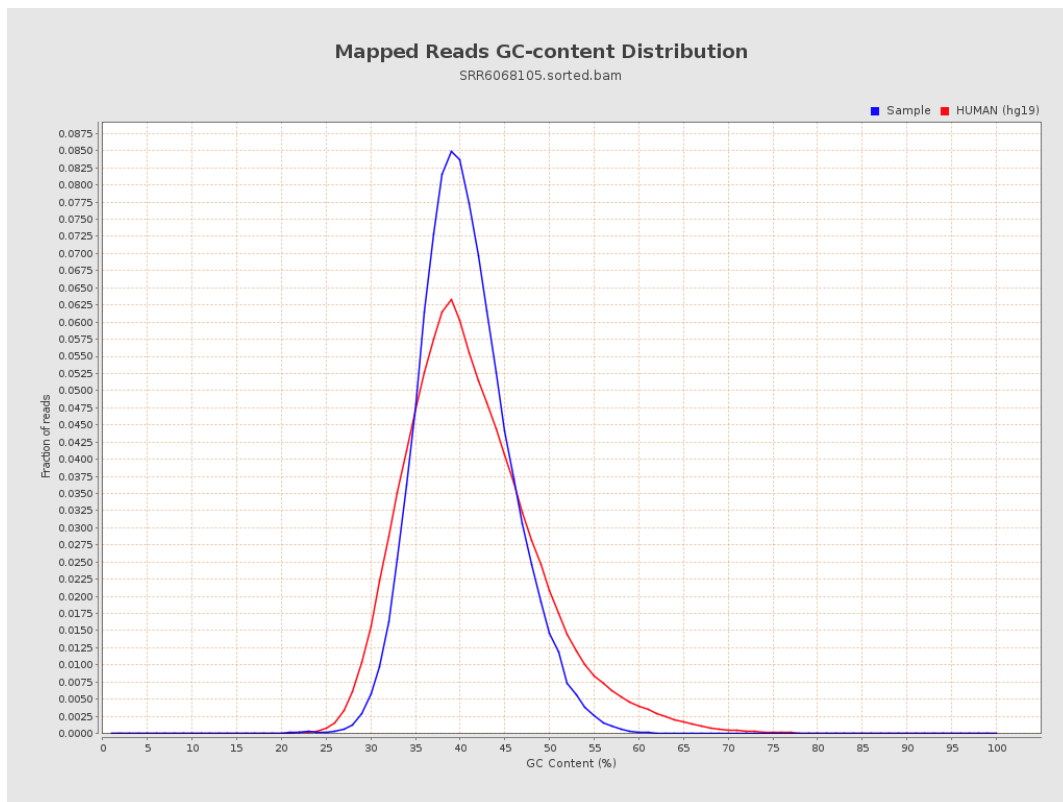
7. Results : Duplication Rate Histogram



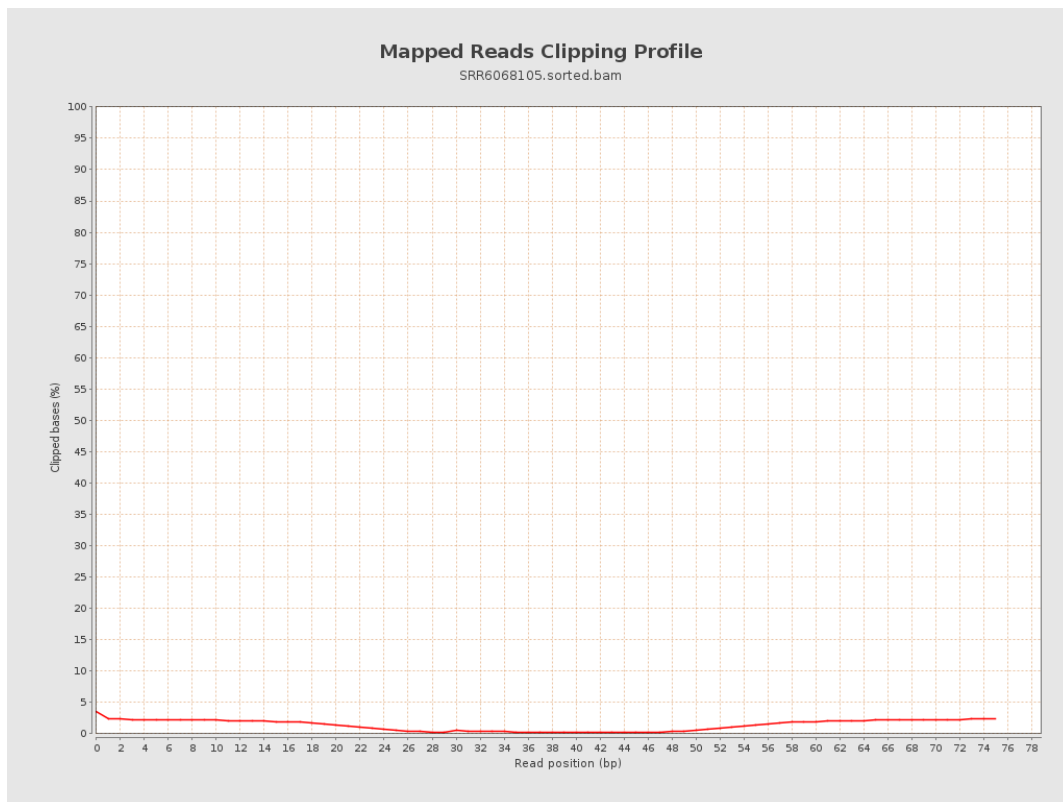
8. Results : Mapped Reads Nucleotide Content



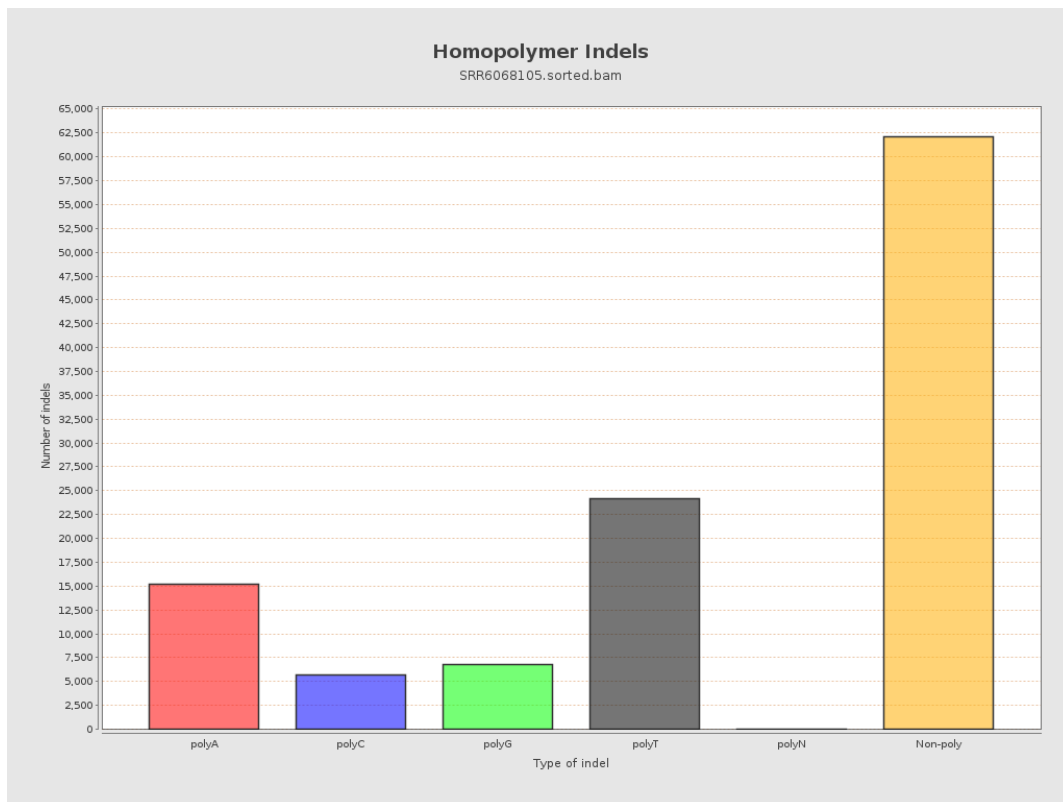
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

