

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:34:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068155.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_SRR6068155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:34:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,906,856
Mapped reads	4,668,226 / 95.14%
Unmapped reads	238,630 / 4.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,868 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	655,694 / 13.36%
Duplication rate	11.78%
Clipped reads	2,639,809 / 53.8%

2.2. ACGT Content

Number/percentage of A's	77,316,544 / 25.98%
Number/percentage of C's	54,798,787 / 18.42%
Number/percentage of T's	95,063,057 / 31.95%
Number/percentage of G's	70,360,809 / 23.64%
Number/percentage of N's	34,480 / 0.01%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0962

Standard Deviation	0.7309
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2.4. Mapping Quality

Mean Mapping Quality	41.6
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2.5. Mismatches and indels

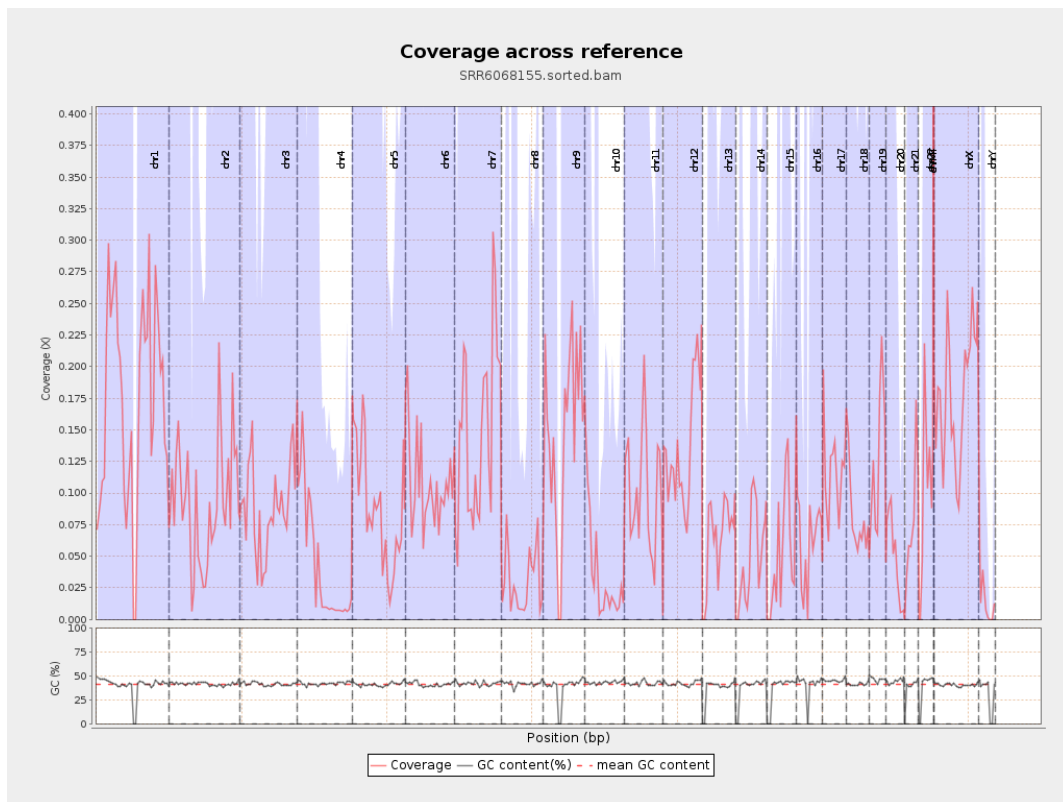
General error rate	0.55%
Mismatches	1,606,853
Insertions	18,774
Mapped reads with at least one insertion	0.4%
Deletions	70,205
Mapped reads with at least one deletion	1.49%
Homopolymer indels	44.55%

2.6. Chromosome stats

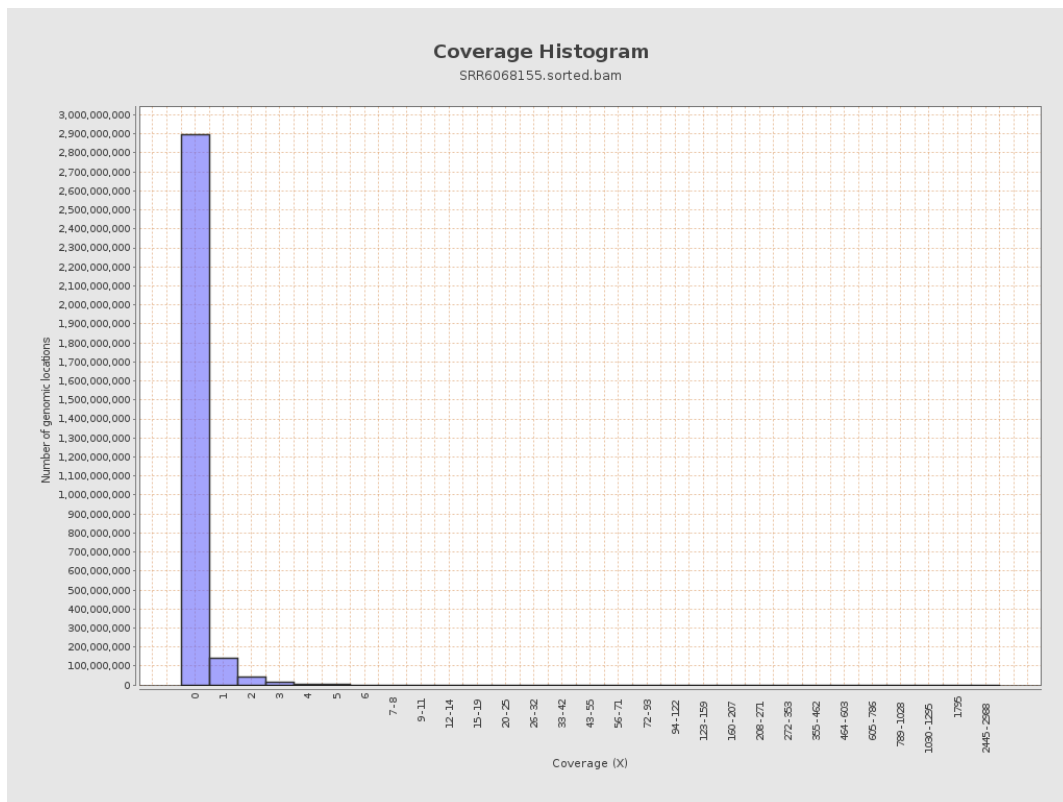
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	42908872	0.1722	1.142
chr2	243199373	22802462	0.0938	1.4718
chr3	198022430	17705190	0.0894	0.419
chr4	191154276	7925550	0.0415	0.3369
chr5	180915260	15706837	0.0868	0.416
chr6	171115067	18513561	0.1082	0.6552
chr7	159138663	23760052	0.1493	0.5809

chr8	146364022	4427222	0.0302	0.5504
chr9	141213431	20702278	0.1466	0.7759
chr10	135534747	4693343	0.0346	0.4712
chr11	135006516	13604951	0.1008	0.5527
chr12	133851895	18241074	0.1363	0.5392
chr13	115169878	7203582	0.0625	0.3901
chr14	107349540	5016688	0.0467	0.3599
chr15	102531392	5324145	0.0519	0.3743
chr16	90354753	5352296	0.0592	0.3974
chr17	81195210	9716439	0.1197	0.5228
chr18	78077248	6452058	0.0826	1.1877
chr19	59128983	7269783	0.1229	0.8949
chr20	63025520	3132062	0.0497	0.3215
chr21	48129895	3699283	0.0769	0.4164
chr22	51304566	4866309	0.0949	0.4268
chrMT	16571	14171	0.8552	1.282
chrX	155270560	27771458	0.1789	0.6608
chrY	59373566	886553	0.0149	0.3865

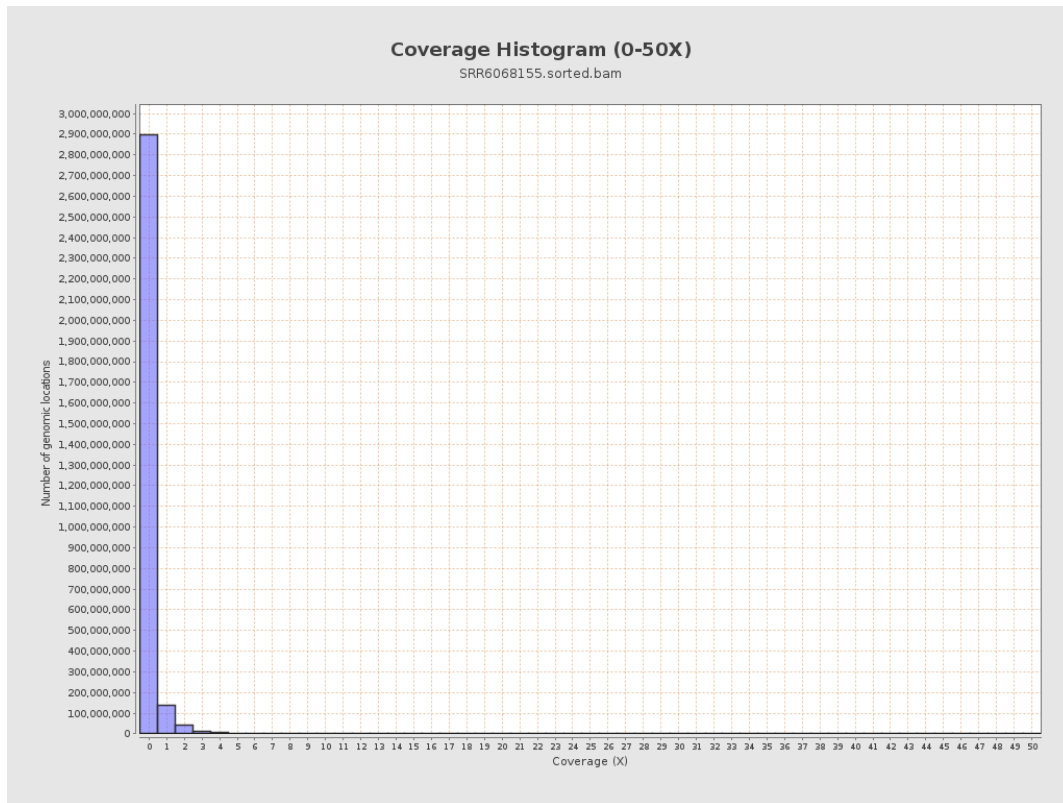
3. Results : Coverage across reference



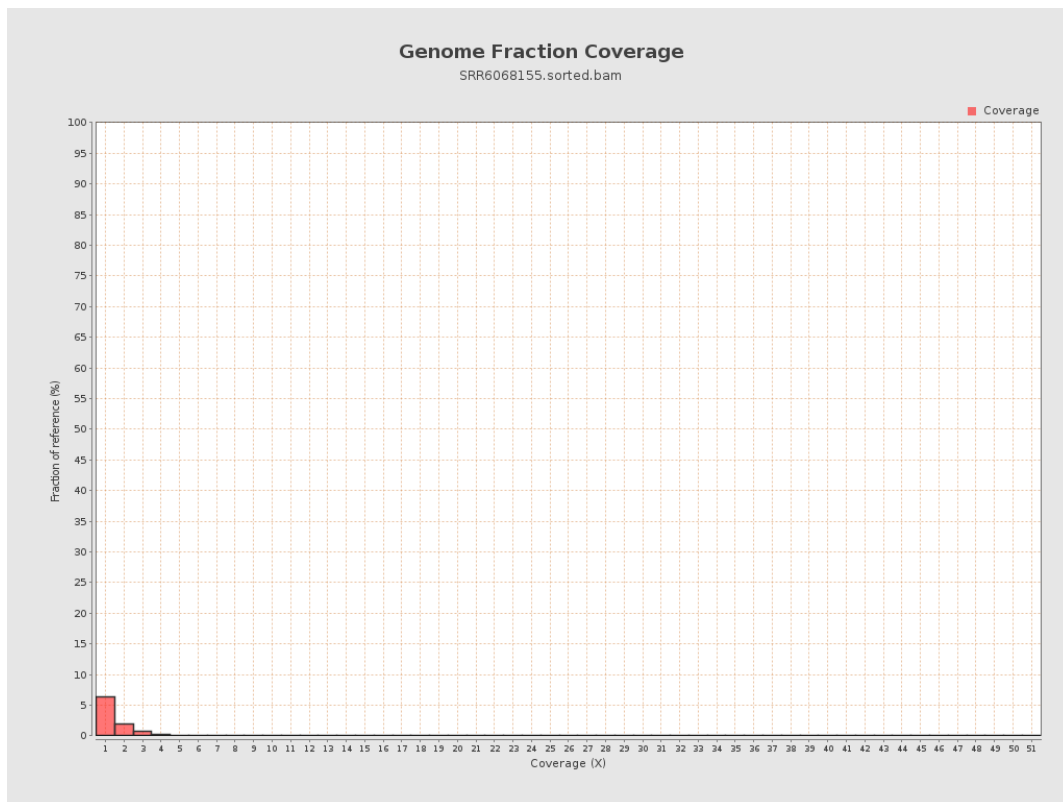
4. Results : Coverage Histogram



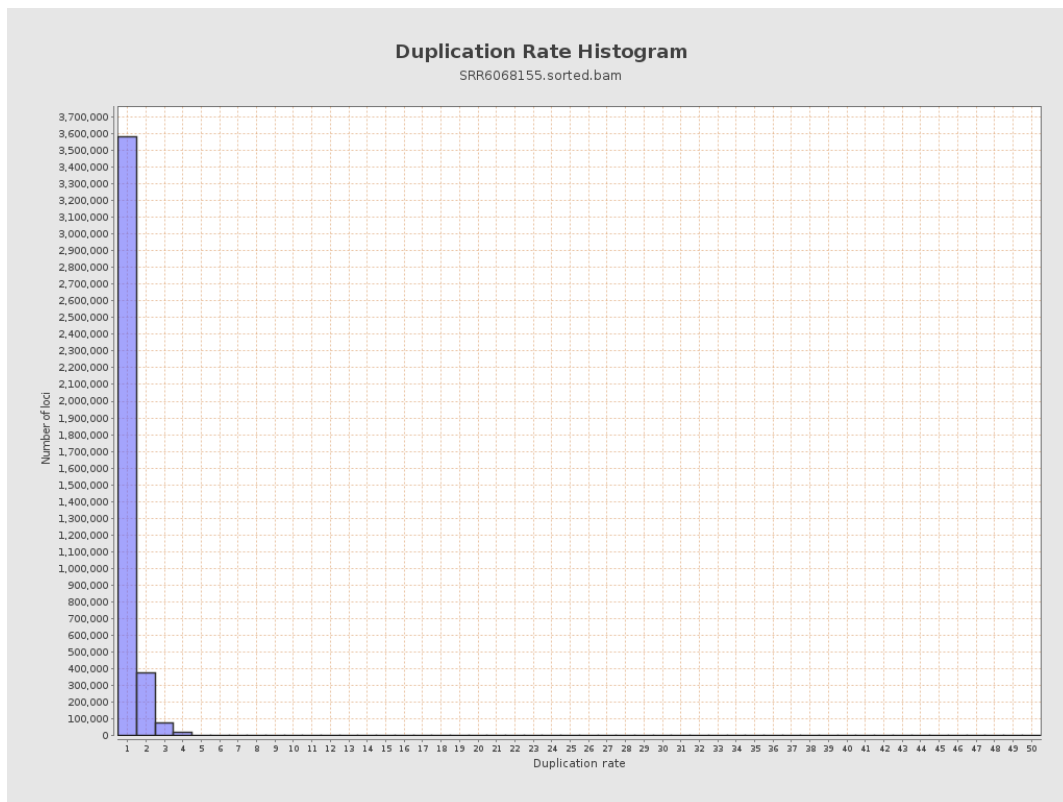
5. Results : Coverage Histogram (0-50X)



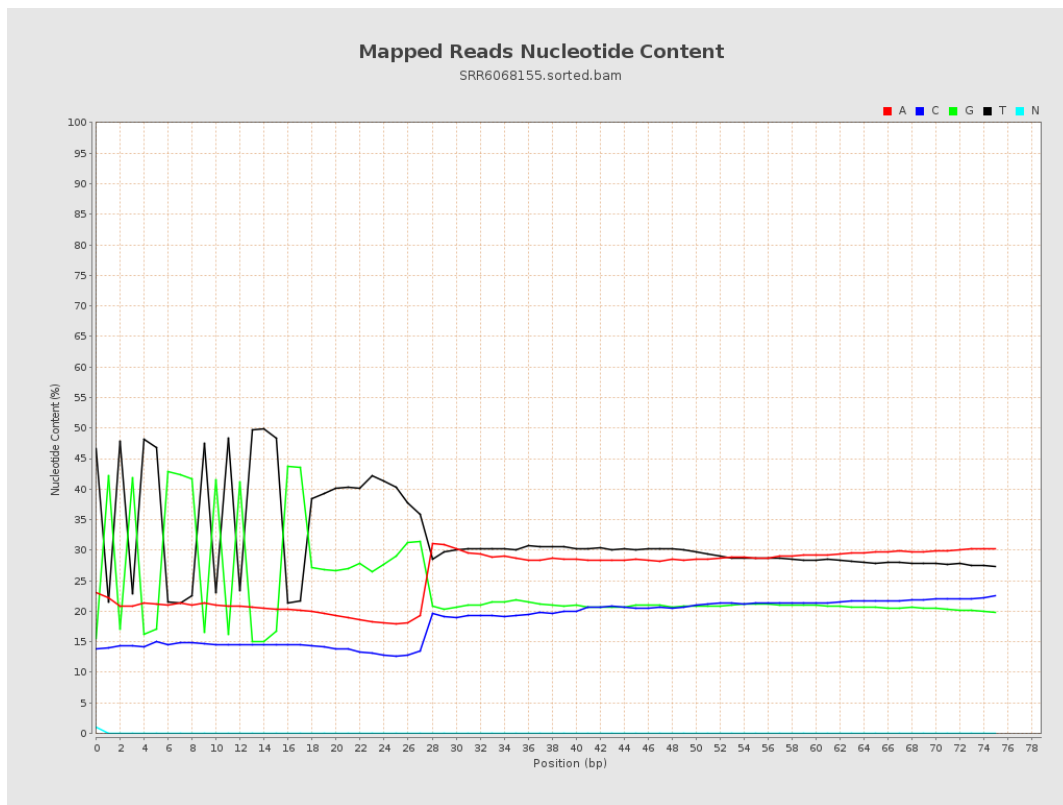
6. Results : Genome Fraction Coverage



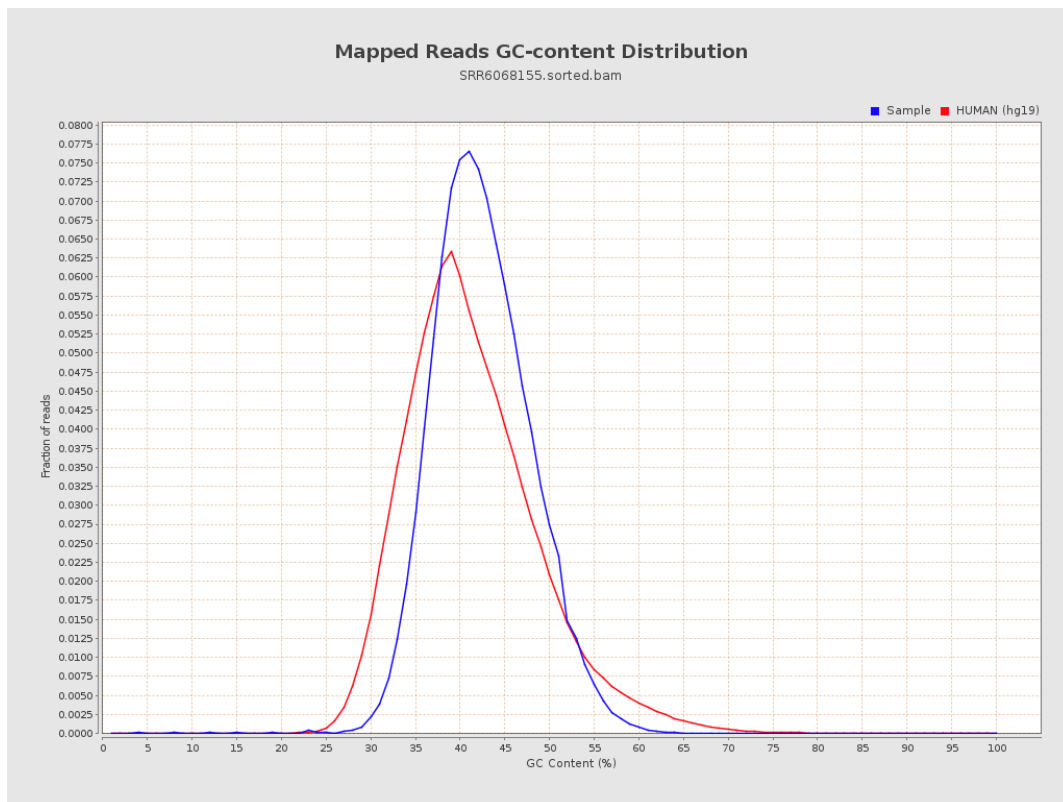
7. Results : Duplication Rate Histogram



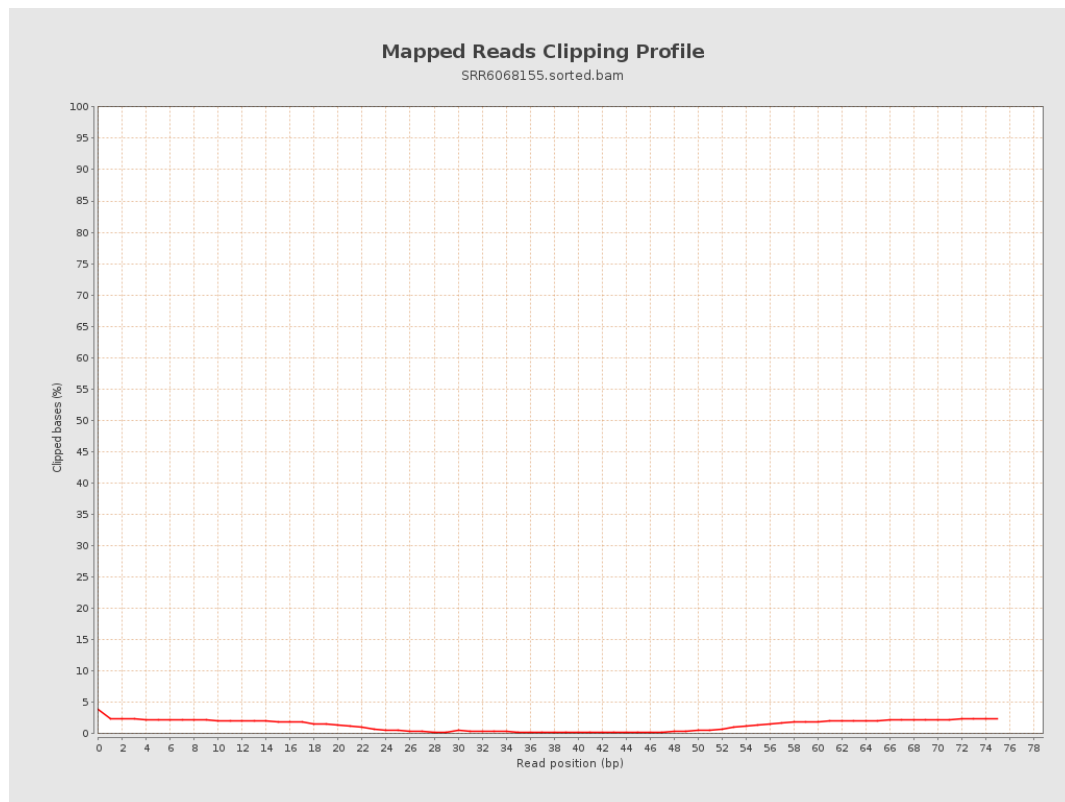
8. Results : Mapped Reads Nucleotide Content



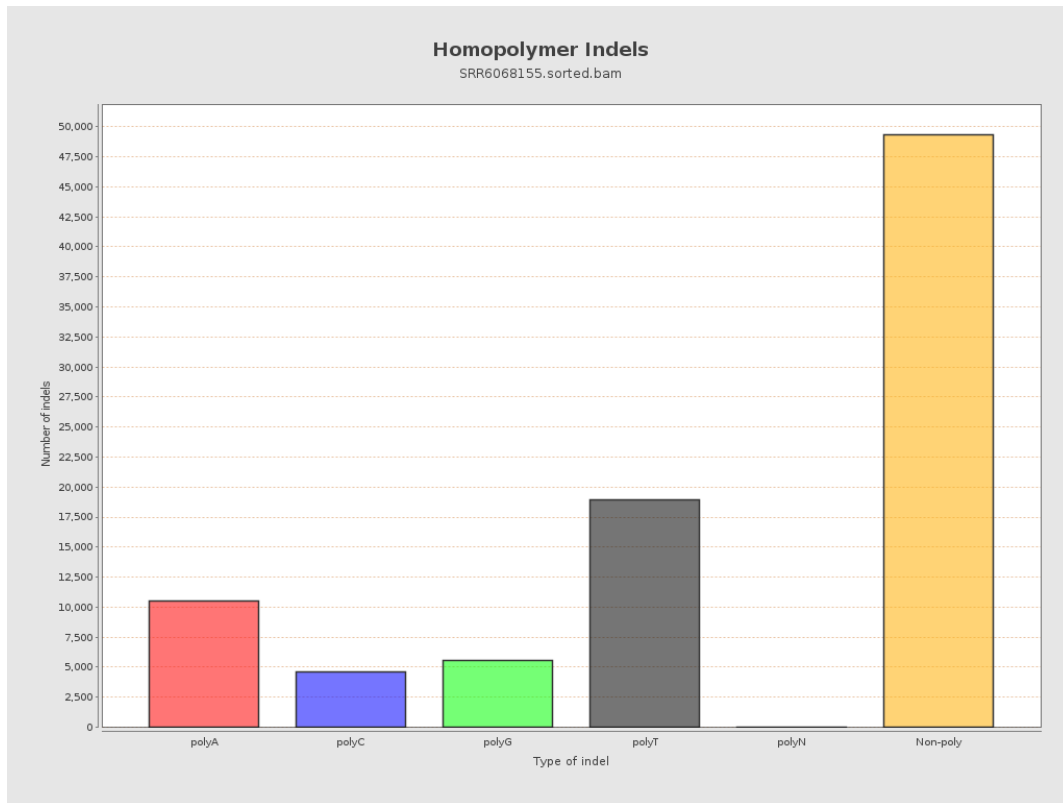
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

