

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:13:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068955.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_SRR6068955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:13:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,098,757
Mapped reads	1,743,636 / 83.08%
Unmapped reads	355,121 / 16.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,687 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	56,397 / 2.69%
Duplication rate	2.06%
Clipped reads	903,770 / 43.06%

2.2. ACGT Content

Number/percentage of A's	30,334,734 / 26.71%
Number/percentage of C's	19,645,960 / 17.3%
Number/percentage of T's	37,267,917 / 32.82%
Number/percentage of G's	26,028,030 / 22.92%
Number/percentage of N's	273,461 / 0.24%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.3861
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2.4. Mapping Quality

Mean Mapping Quality	44.25
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2.5. Mismatches and indels

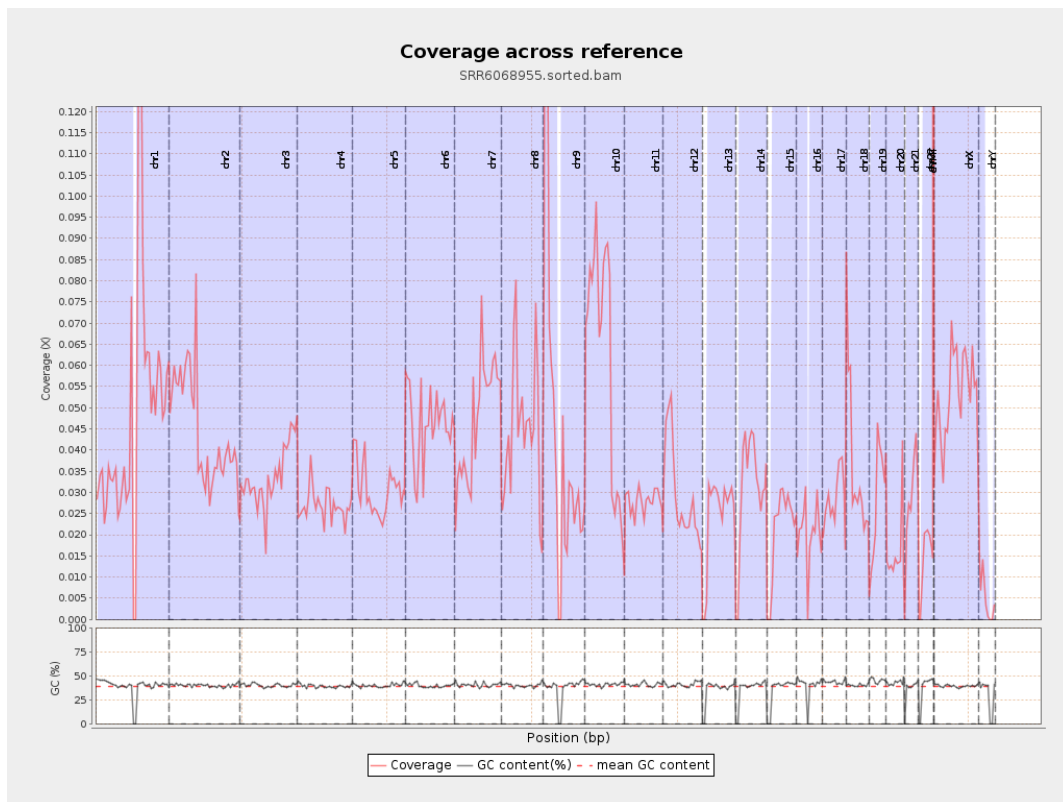
General error rate	0.95%
Mismatches	1,055,779
Insertions	10,589
Mapped reads with at least one insertion	0.6%
Deletions	30,227
Mapped reads with at least one deletion	1.71%
Homopolymer indels	48.41%

2.6. Chromosome stats

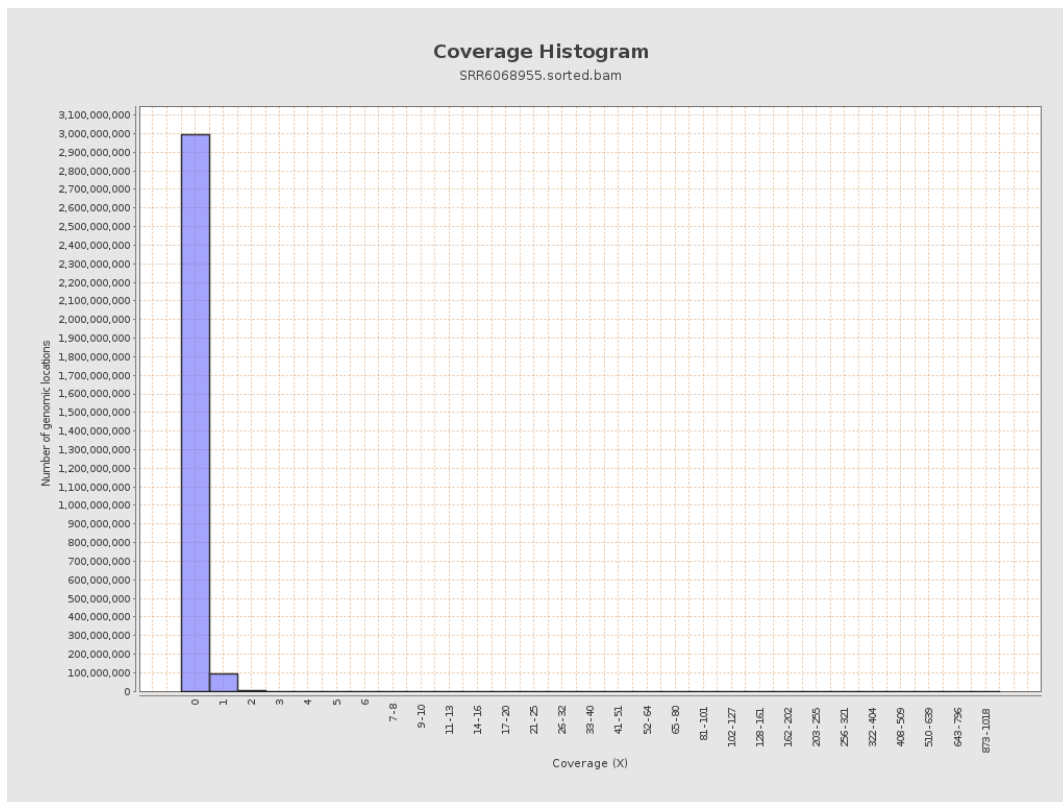
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11828244	0.0475	0.7659
chr2	243199373	10897093	0.0448	0.3817
chr3	198022430	6638952	0.0335	0.209
chr4	191154276	5109533	0.0267	0.1973
chr5	180915260	5524372	0.0305	0.1924
chr6	171115067	7906282	0.0462	0.3069
chr7	159138663	7595987	0.0477	0.3907

chr8	146364022	6574190	0.0449	0.5875
chr9	141213431	6531689	0.0463	0.4356
chr10	135534747	8560585	0.0632	0.4698
chr11	135006516	3702670	0.0274	0.3019
chr12	133851895	3912185	0.0292	0.1969
chr13	115169878	2777679	0.0241	0.165
chr14	107349540	3303838	0.0308	0.231
chr15	102531392	2189159	0.0214	0.1585
chr16	90354753	1835545	0.0203	0.2171
chr17	81195210	2280404	0.0281	0.1994
chr18	78077248	2785970	0.0357	0.6764
chr19	59128983	1691020	0.0286	0.4417
chr20	63025520	1039311	0.0165	0.1663
chr21	48129895	1357835	0.0282	0.2032
chr22	51304566	712888	0.0139	0.1279
chrMT	16571	290575	17.5352	9.7904
chrX	155270560	8263362	0.0532	0.2899
chrY	59373566	290985	0.0049	0.125

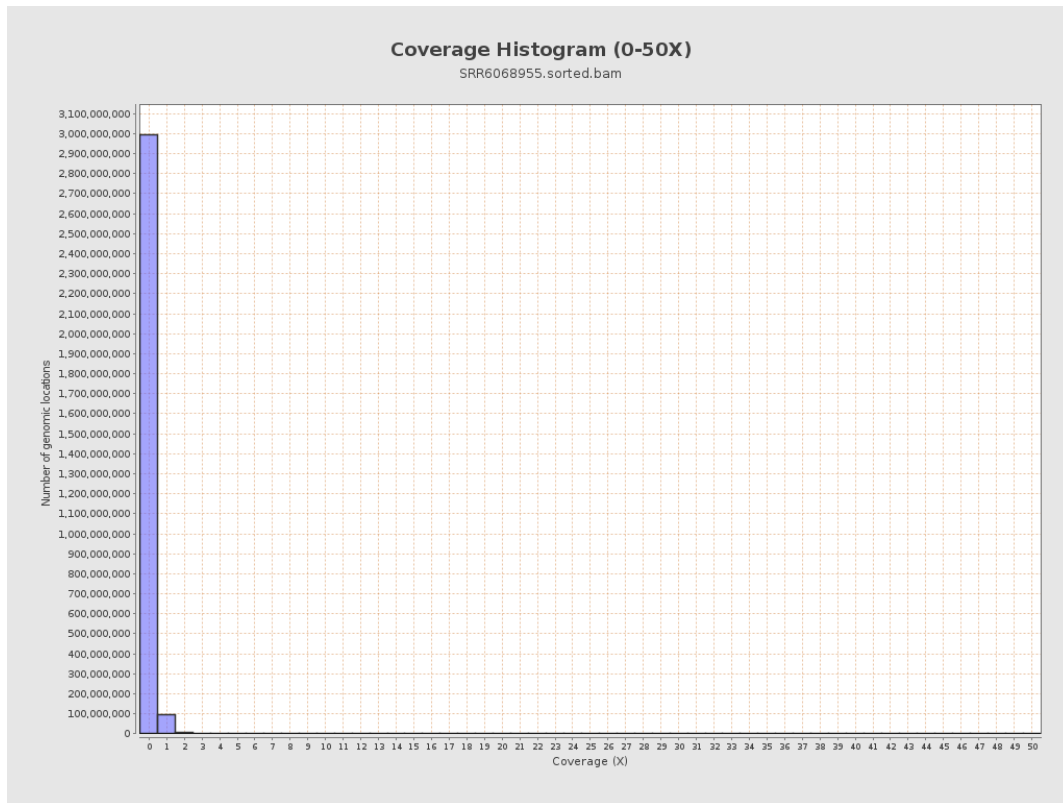
3. Results : Coverage across reference



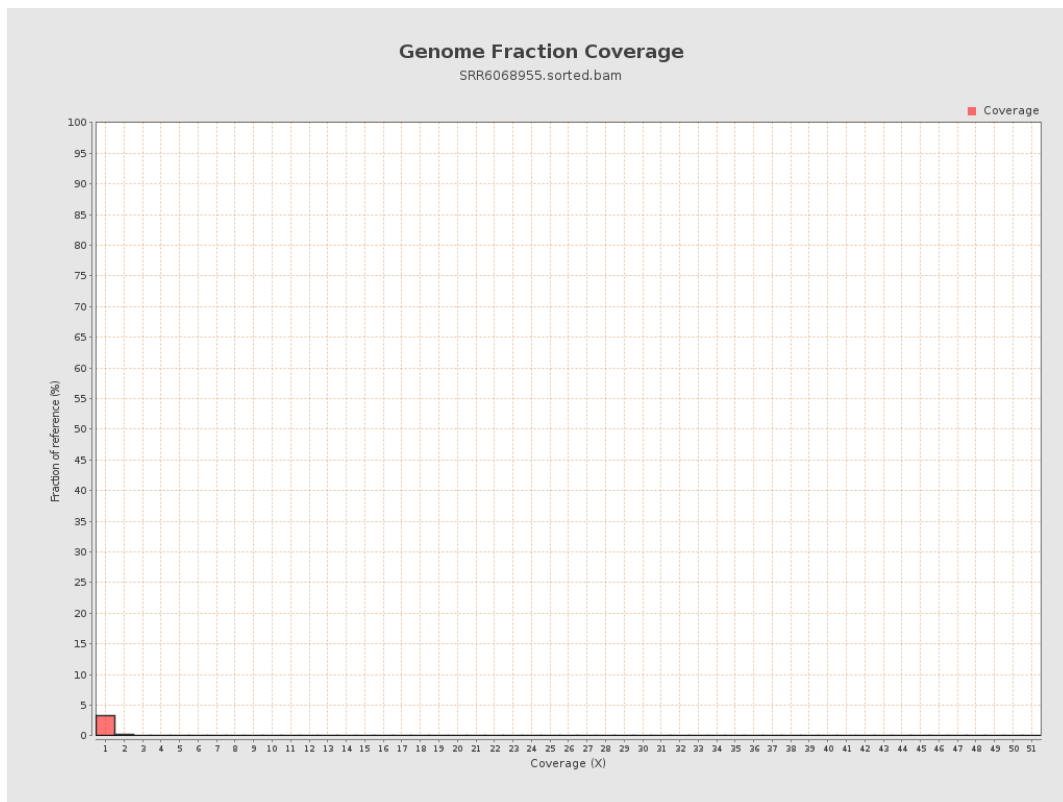
4. Results : Coverage Histogram



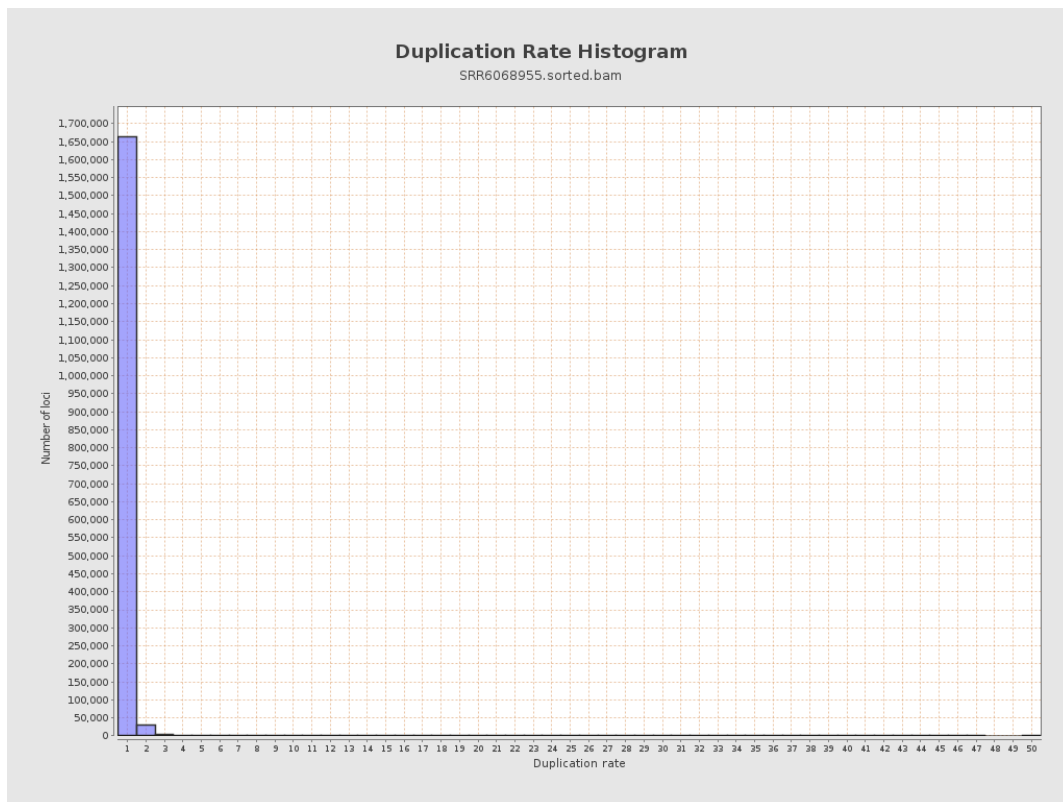
5. Results : Coverage Histogram (0-50X)



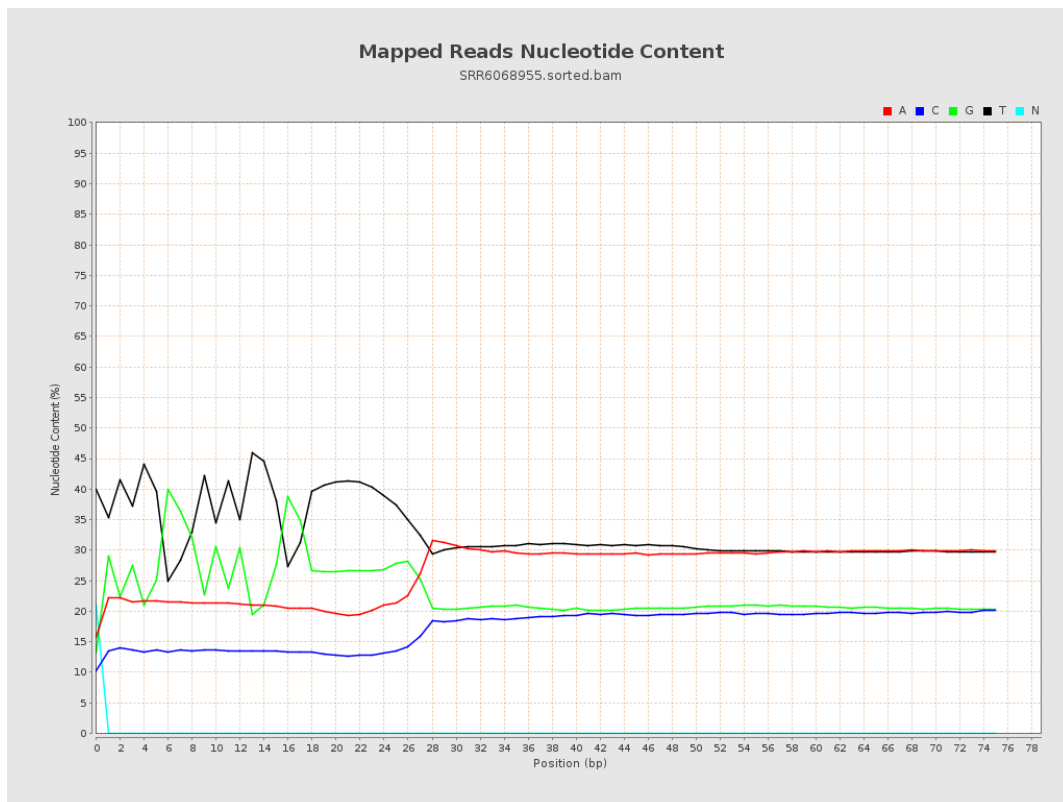
6. Results : Genome Fraction Coverage



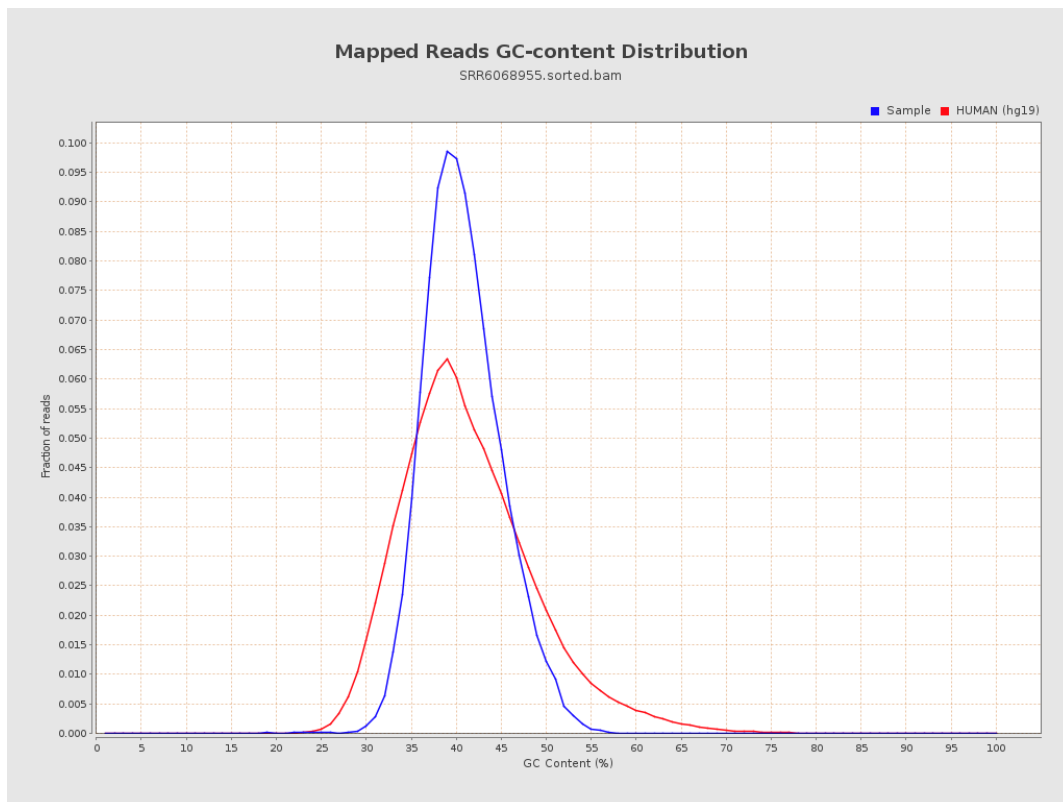
7. Results : Duplication Rate Histogram



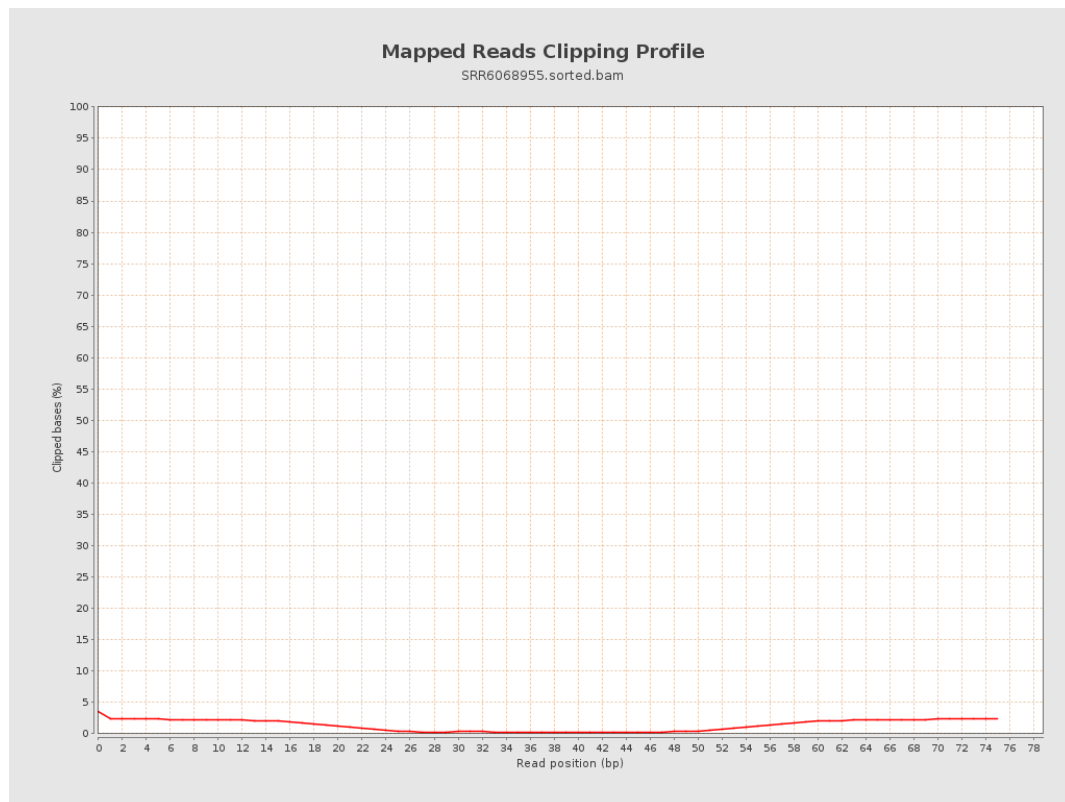
8. Results : Mapped Reads Nucleotide Content



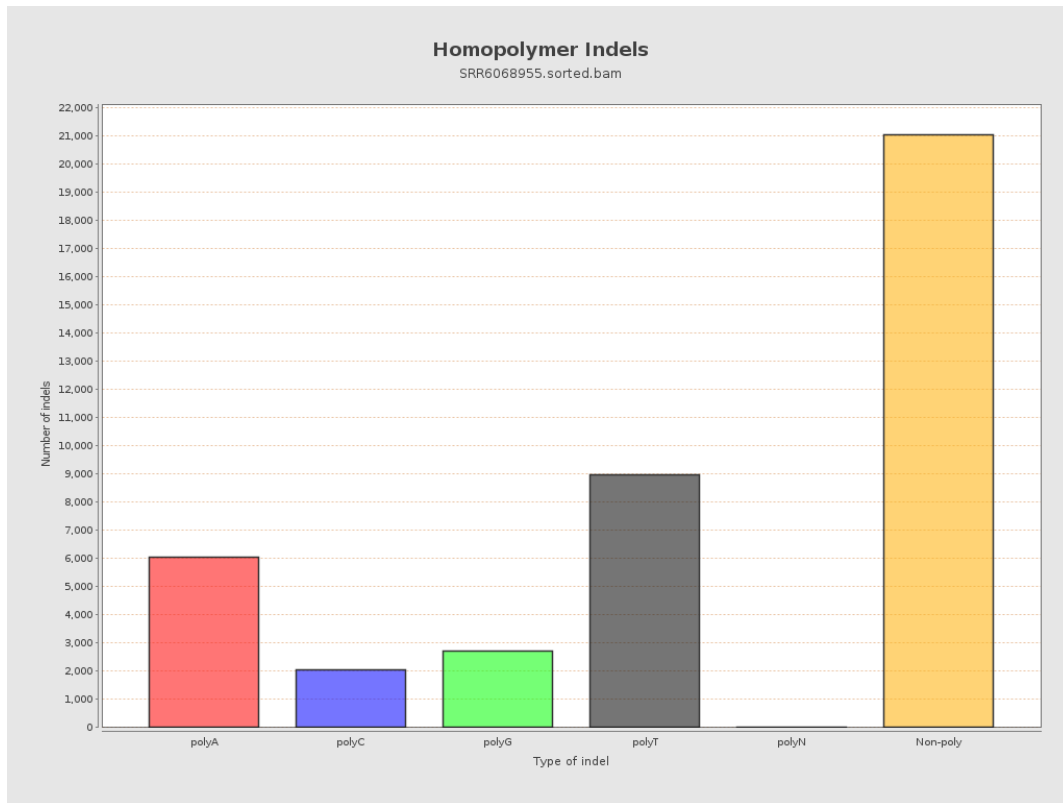
9. Results : Mapped Reads GC-content Distribution



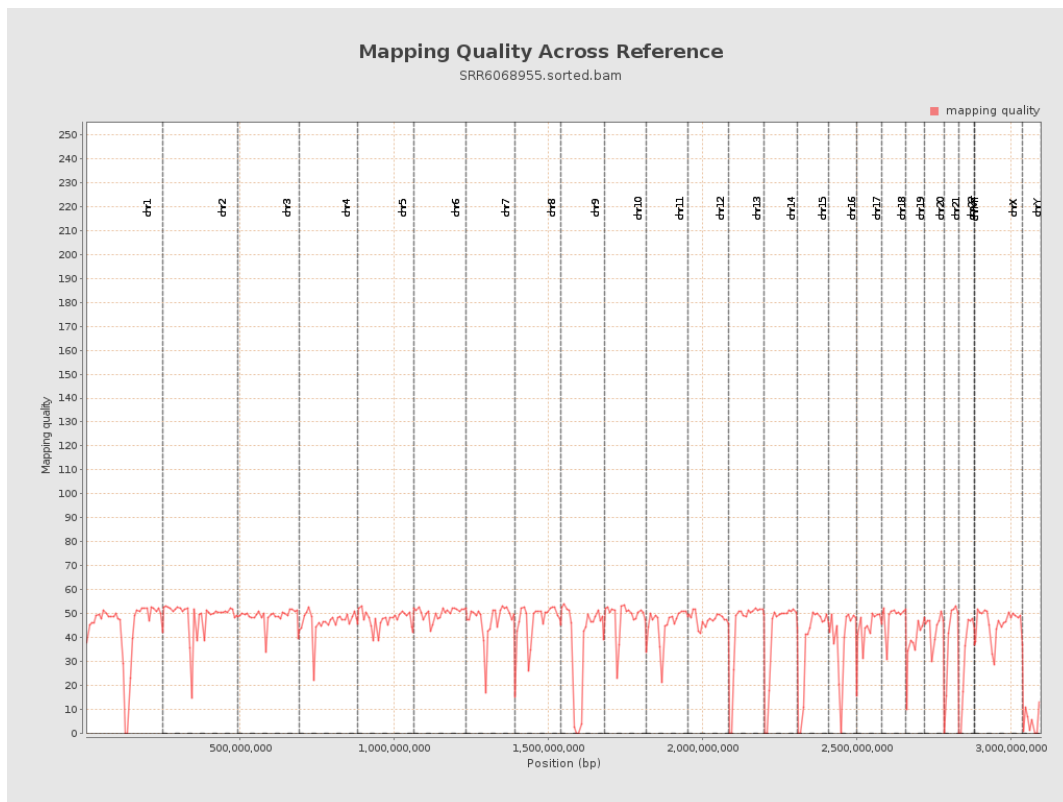
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

