

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:52:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008795.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_SRR6008795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:52:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,437,471
Mapped reads	1,190,203 / 82.8%
Unmapped reads	247,268 / 17.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,937 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	169,996 / 11.83%
Duplication rate	10.59%
Clipped reads	609,269 / 42.38%

2.2. ACGT Content

Number/percentage of A's	20,460,407 / 26.39%
Number/percentage of C's	14,522,638 / 18.73%
Number/percentage of T's	24,281,942 / 31.32%
Number/percentage of G's	18,226,546 / 23.51%
Number/percentage of N's	29,244 / 0.04%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2894
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2.4. Mapping Quality

Mean Mapping Quality	44.82
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2.5. Mismatches and indels

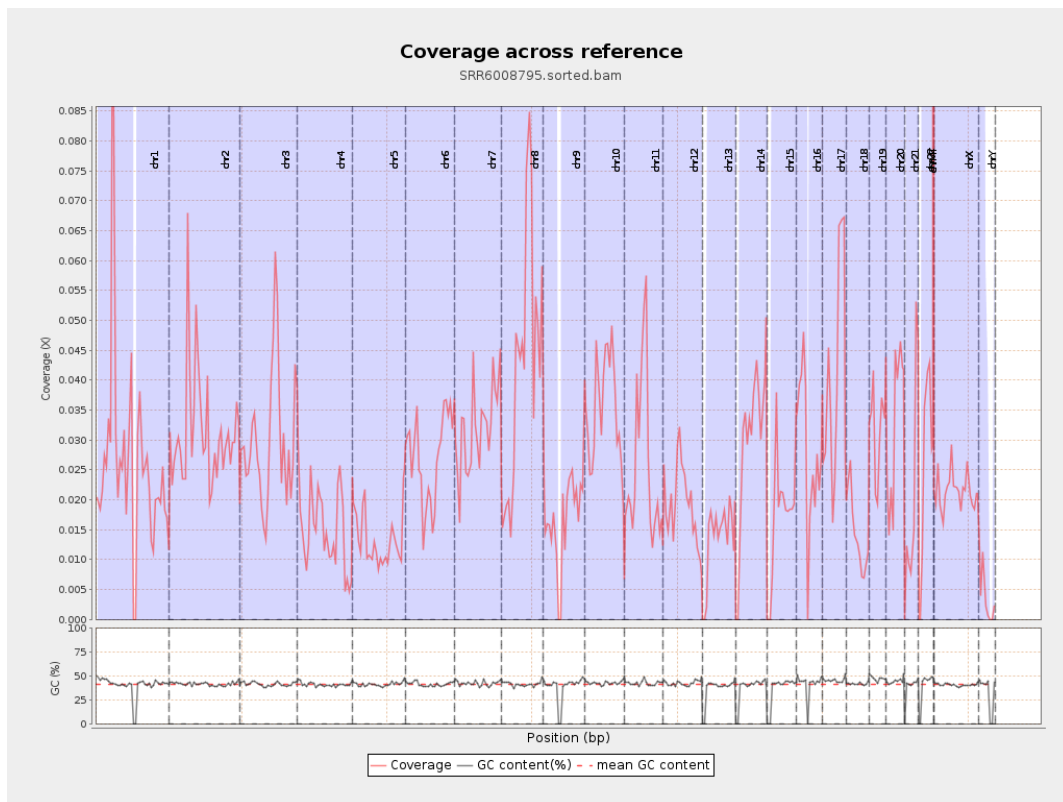
General error rate	0.81%
Mismatches	616,719
Insertions	5,584
Mapped reads with at least one insertion	0.46%
Deletions	17,969
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.3%

2.6. Chromosome stats

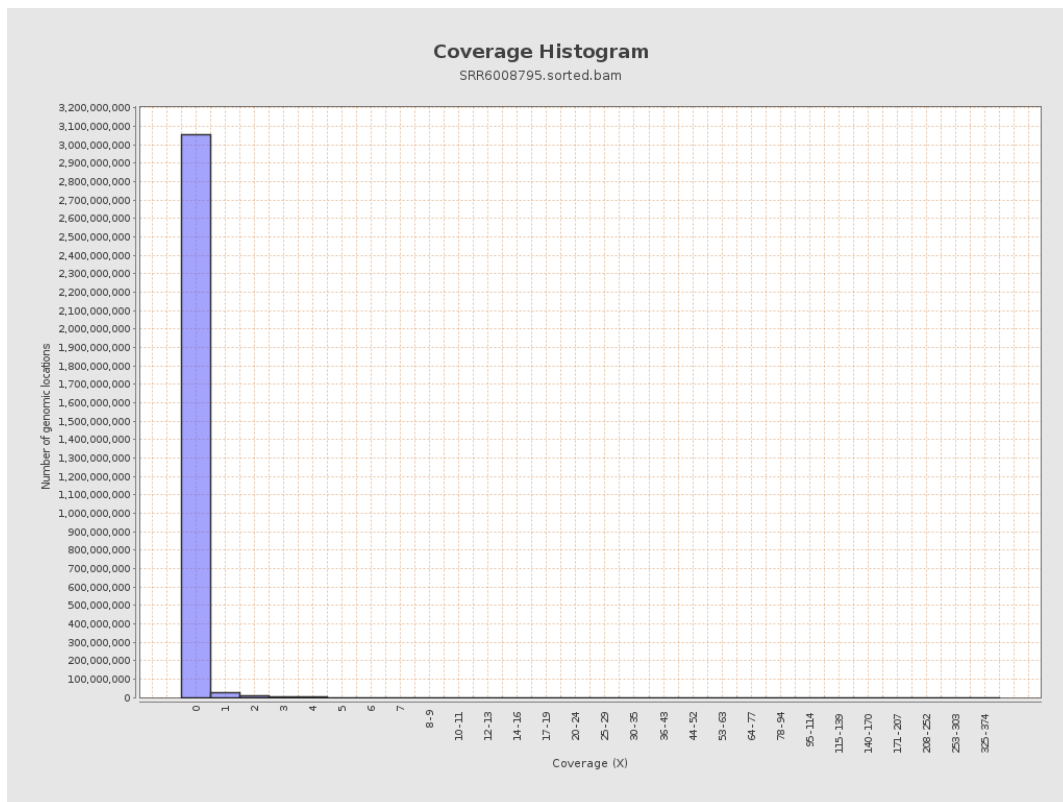
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6448302	0.0259	0.3349
chr2	243199373	7642029	0.0314	0.3484
chr3	198022430	5909389	0.0298	0.2821
chr4	191154276	2825171	0.0148	0.1999
chr5	180915260	2426907	0.0134	0.1839
chr6	171115067	4645638	0.0271	0.2752
chr7	159138663	5094851	0.032	0.3623

chr8	146364022	6206041	0.0424	0.4046
chr9	141213431	2321244	0.0164	0.2381
chr10	135534747	4775077	0.0352	0.329
chr11	135006516	3441381	0.0255	0.3233
chr12	133851895	2614705	0.0195	0.2245
chr13	115169878	1539247	0.0134	0.1857
chr14	107349540	3145285	0.0293	0.281
chr15	102531392	1808943	0.0176	0.2141
chr16	90354753	2538195	0.0281	0.2747
chr17	81195210	3287787	0.0405	0.3521
chr18	78077248	1122949	0.0144	0.3393
chr19	59128983	1867279	0.0316	0.3121
chr20	63025520	2015669	0.032	0.2964
chr21	48129895	984897	0.0205	0.2352
chr22	51304566	1298377	0.0253	0.2564
chrMT	16571	29966	1.8083	2.9719
chrX	155270560	3343419	0.0215	0.2471
chrY	59373566	219443	0.0037	0.1098

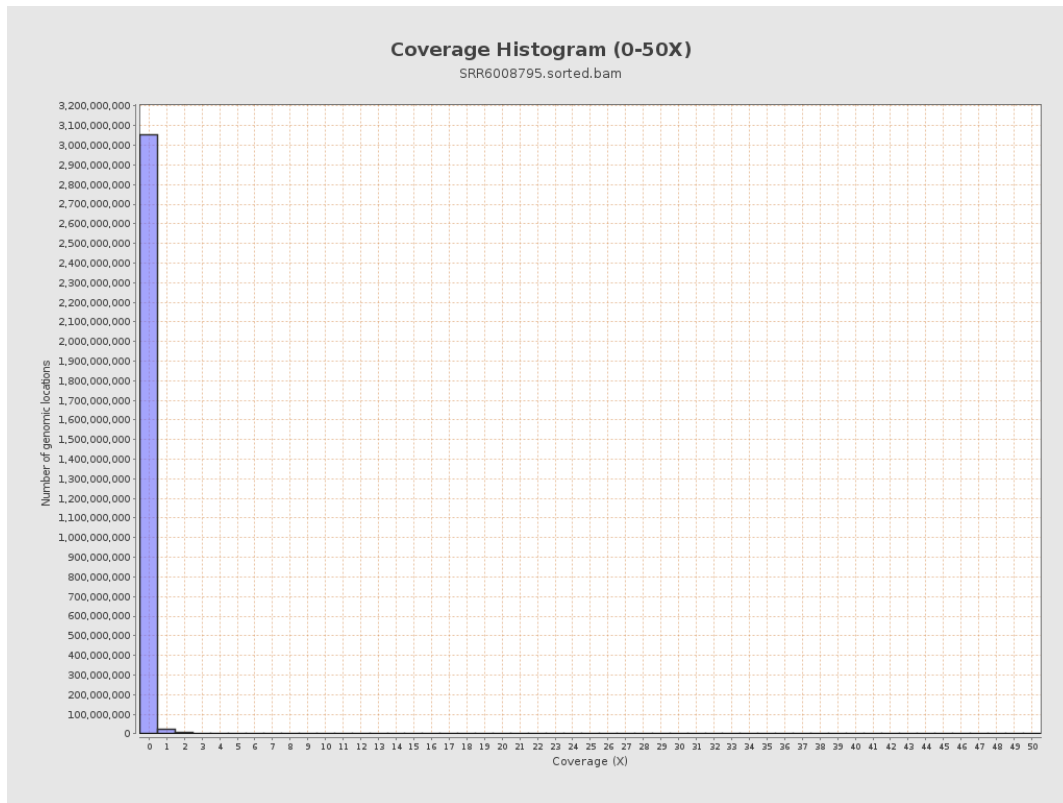
3. Results : Coverage across reference



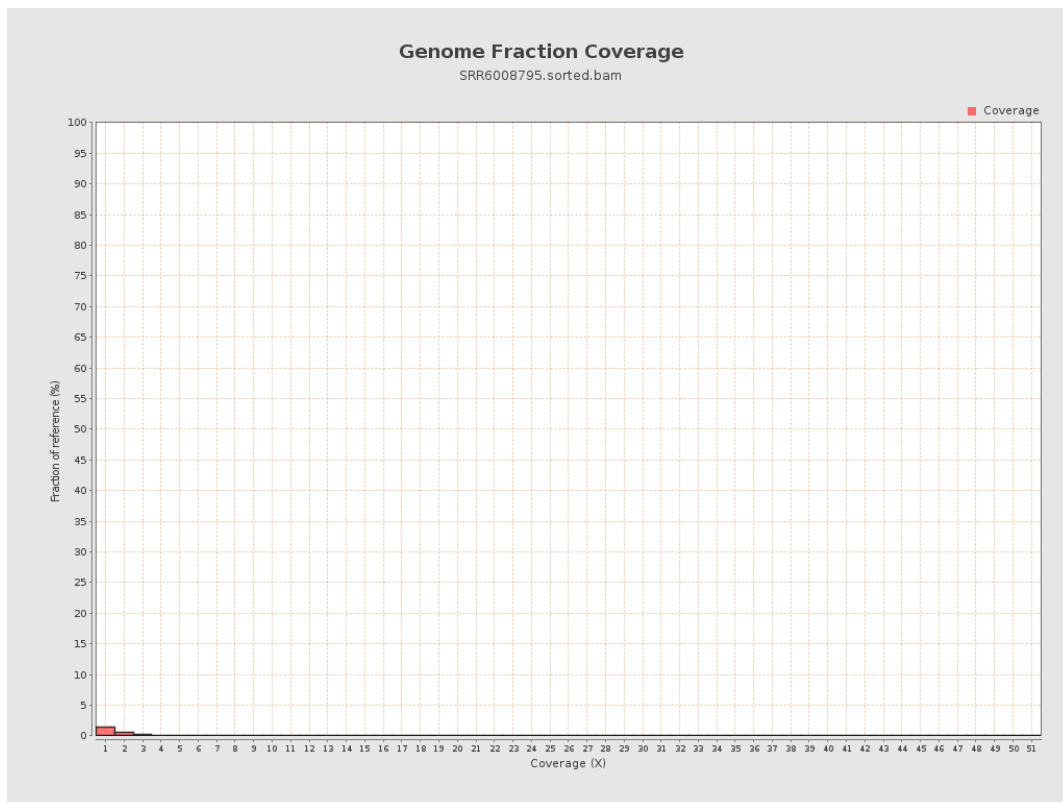
4. Results : Coverage Histogram



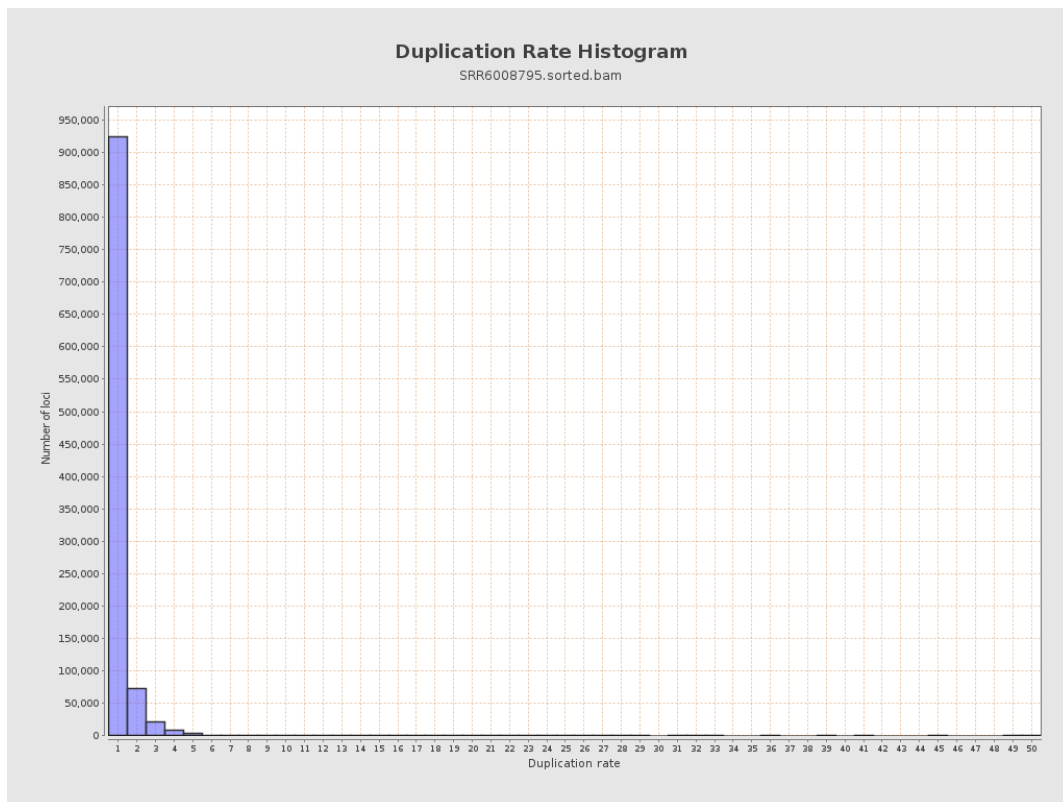
5. Results : Coverage Histogram (0-50X)



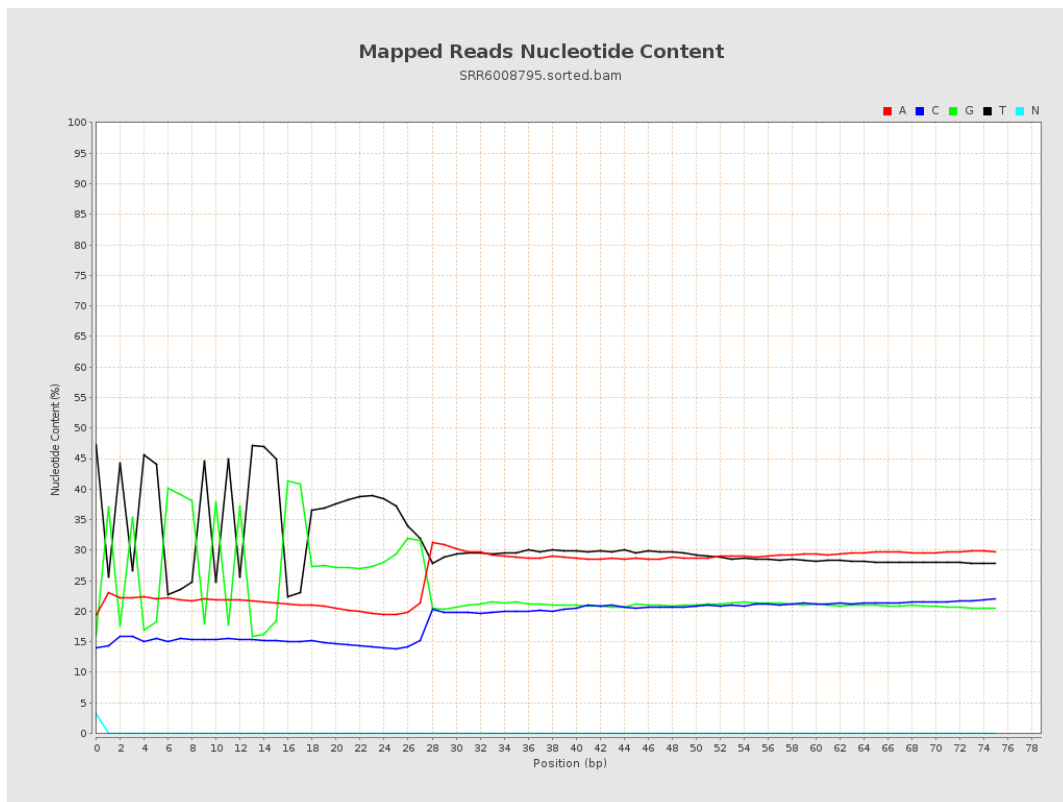
6. Results : Genome Fraction Coverage



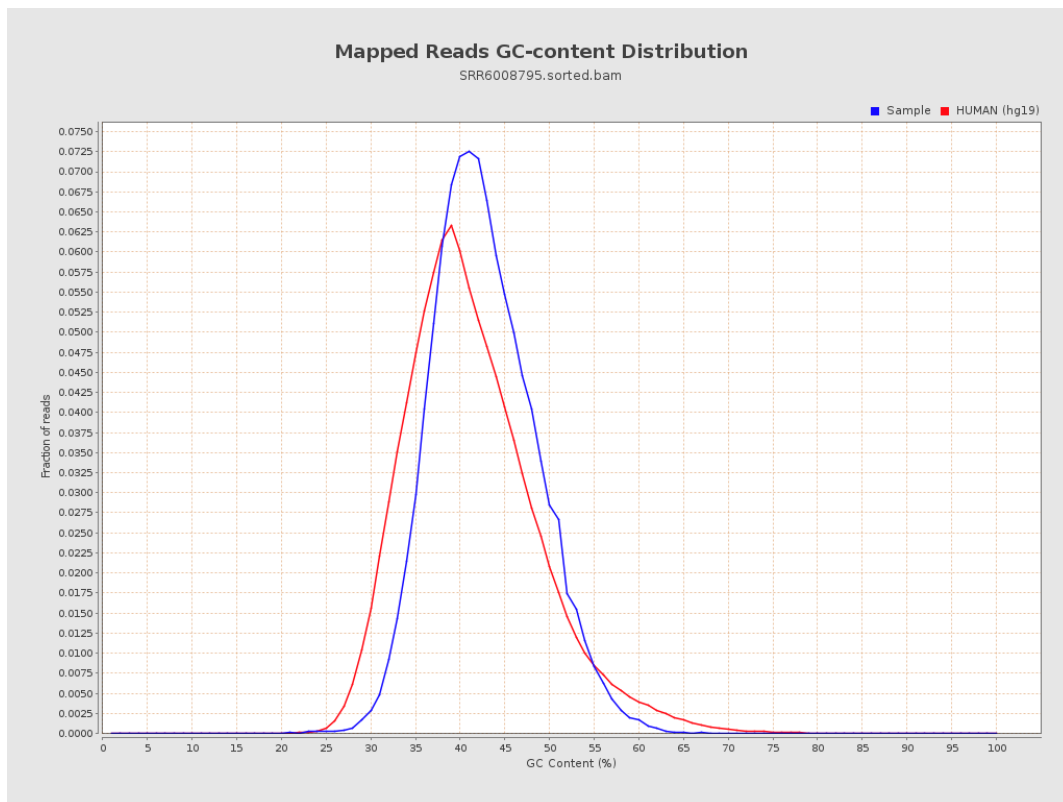
7. Results : Duplication Rate Histogram



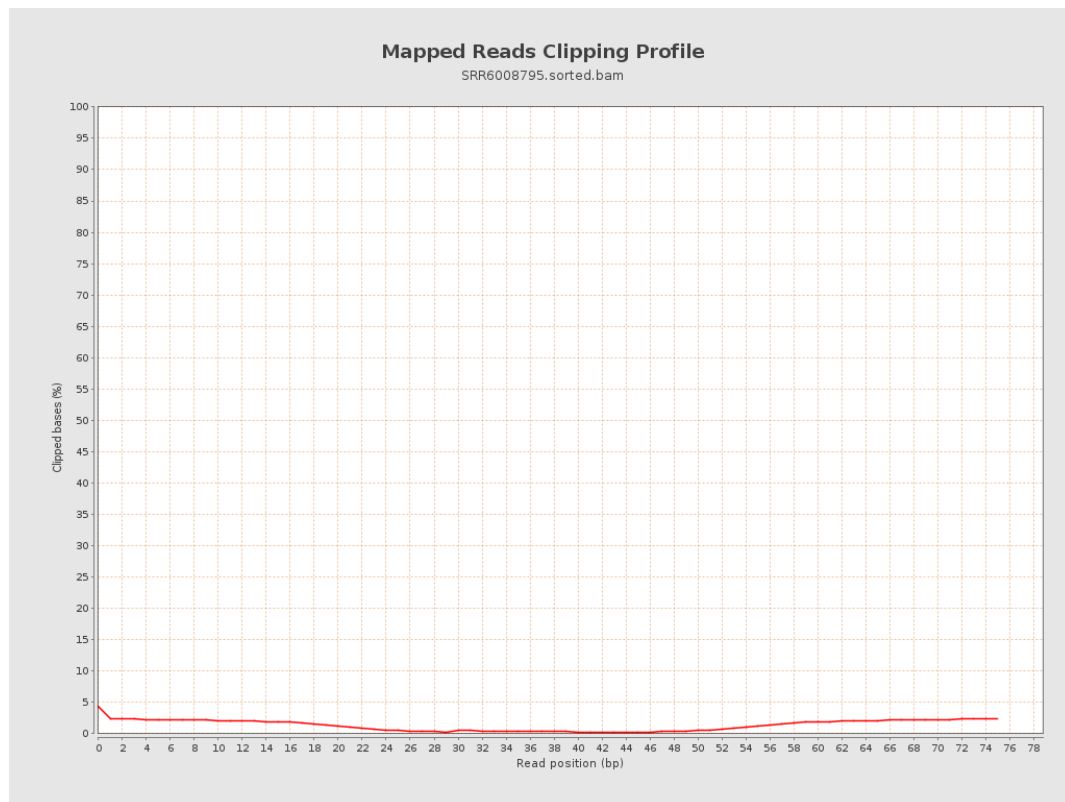
8. Results : Mapped Reads Nucleotide Content



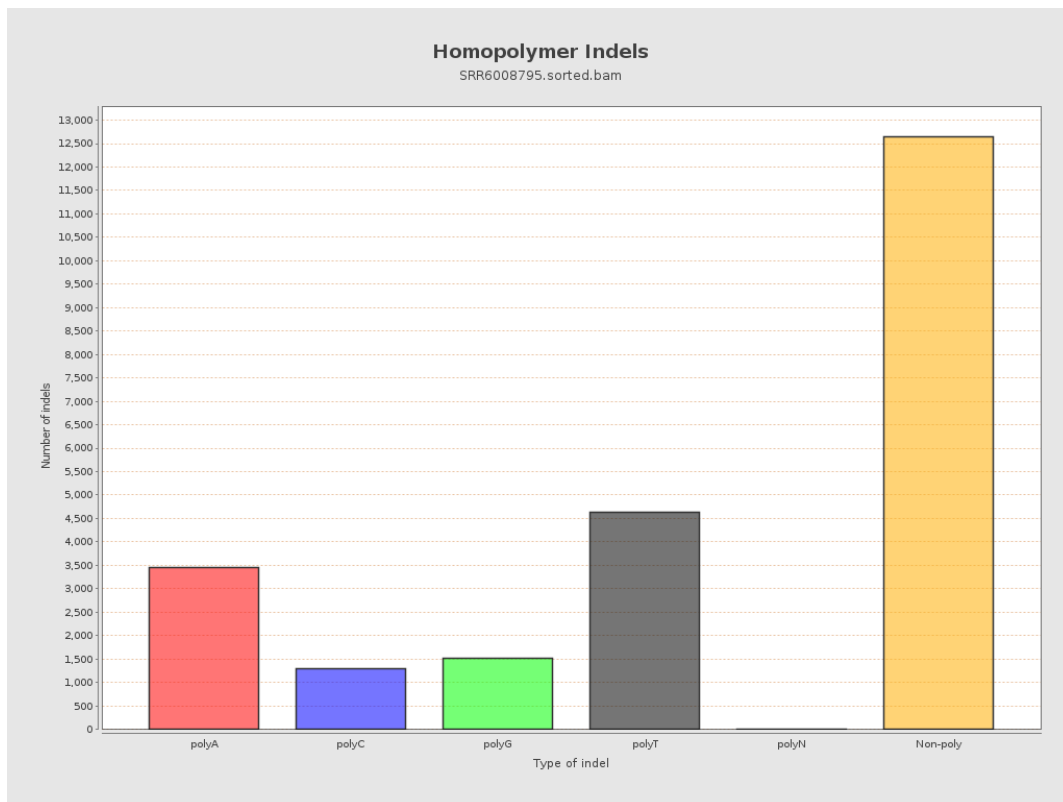
9. Results : Mapped Reads GC-content Distribution



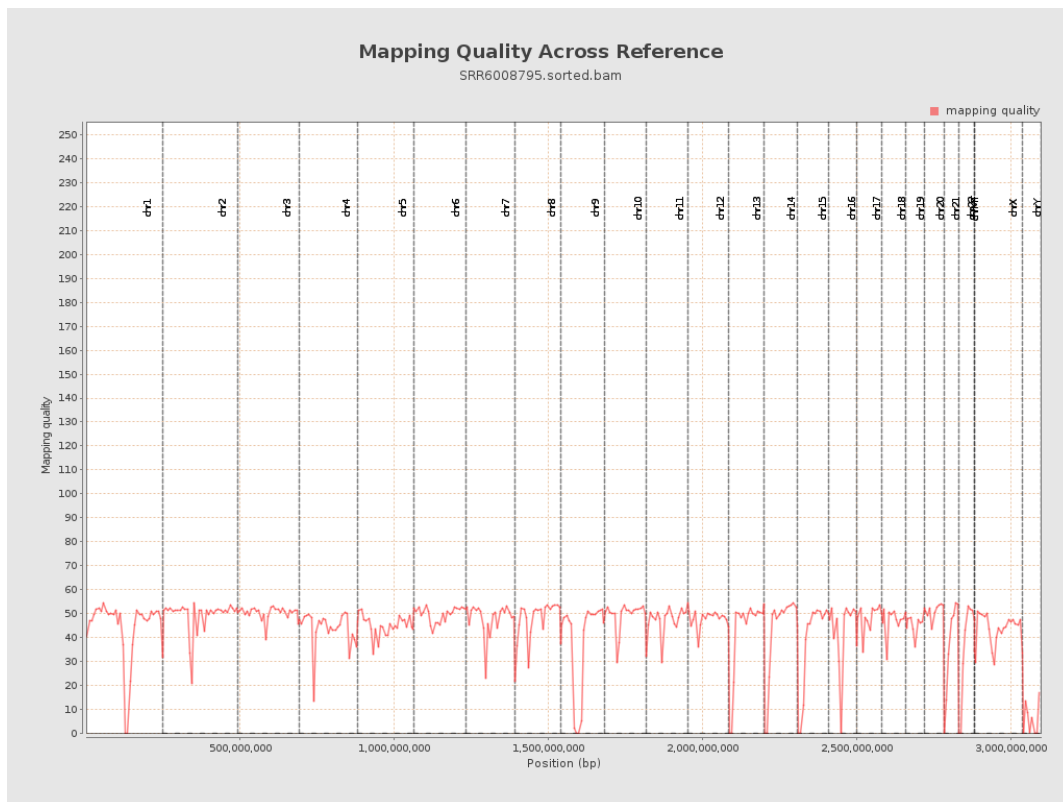
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

