

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:21:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818795.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_SRR1818795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:21:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,673,322
Mapped reads	2,603,705 / 97.4%
Unmapped reads	69,617 / 2.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,968 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,301,210 / 48.67%
Duplication rate	42.08%
Clipped reads	2,594,992 / 97.07%

2.2. ACGT Content

Number/percentage of A's	48,673,028 / 27.51%
Number/percentage of C's	37,133,322 / 20.98%
Number/percentage of T's	51,201,407 / 28.93%
Number/percentage of G's	39,940,522 / 22.57%
Number/percentage of N's	10,187 / 0.01%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0572

Standard Deviation	0.6933
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2.4. Mapping Quality

Mean Mapping Quality	47.56
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2.5. Mismatches and indels

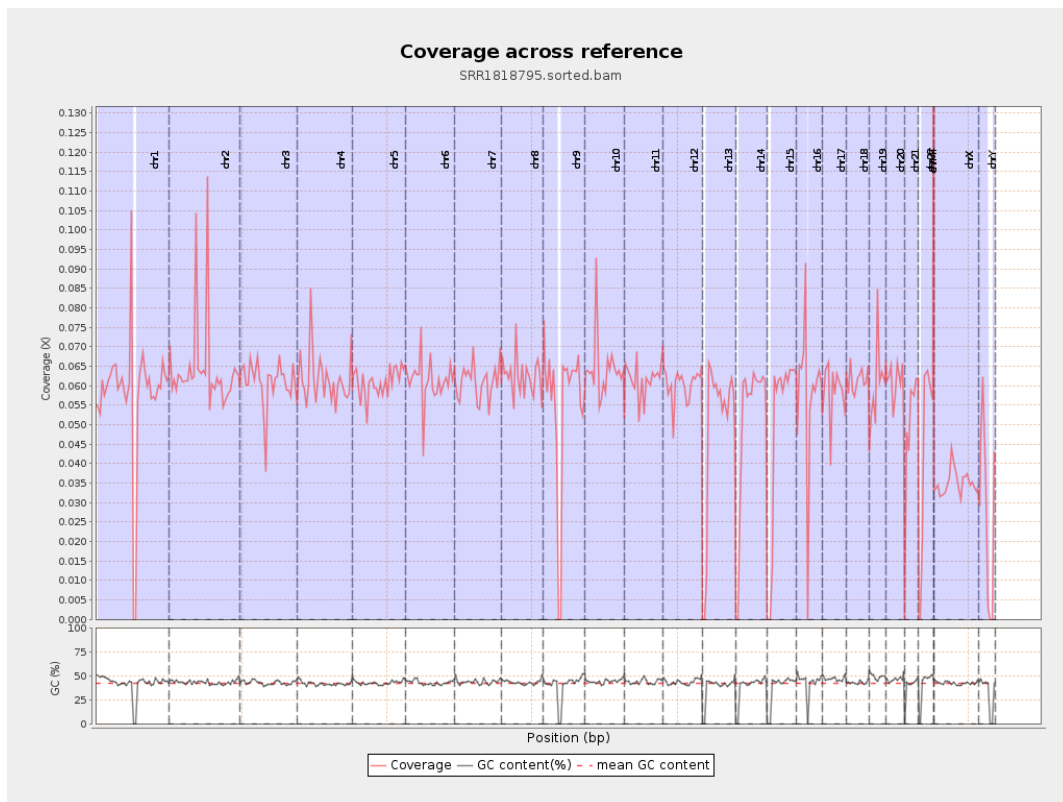
General error rate	0.52%
Mismatches	878,916
Insertions	20,410
Mapped reads with at least one insertion	0.77%
Deletions	44,674
Mapped reads with at least one deletion	1.7%
Homopolymer indels	41.08%

2.6. Chromosome stats

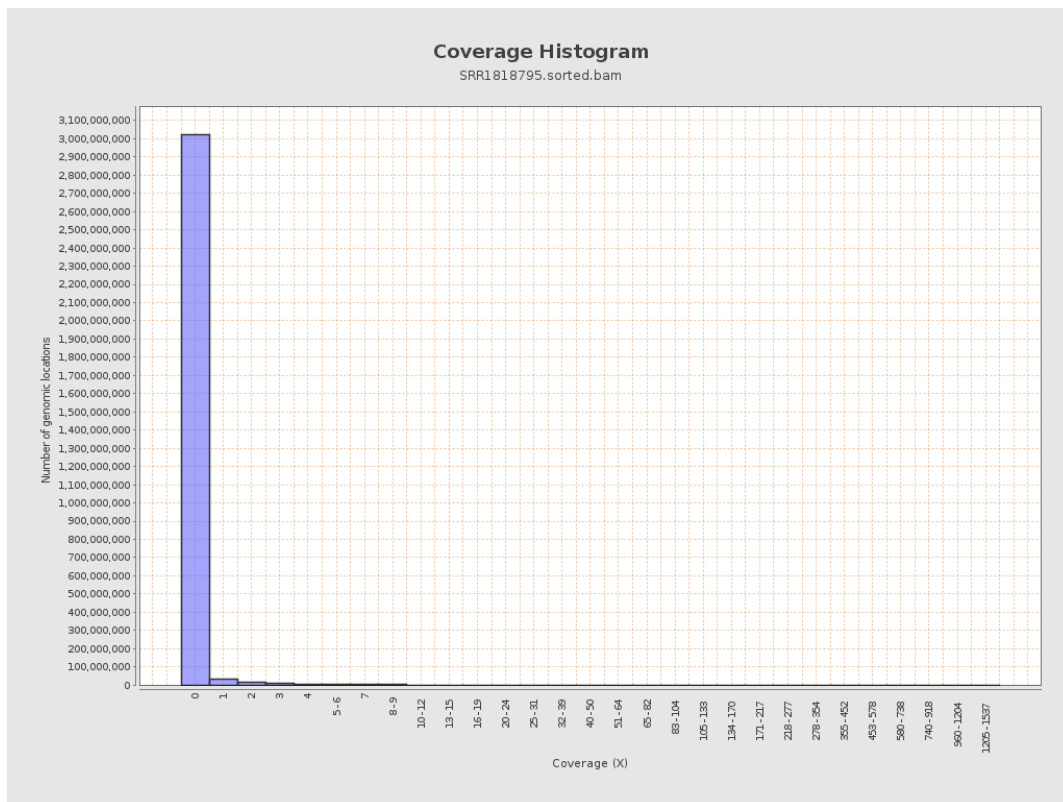
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14479583	0.0581	1.1226
chr2	243199373	15633179	0.0643	1.0699
chr3	198022430	12067051	0.0609	0.4931
chr4	191154276	11770852	0.0616	0.5782
chr5	180915260	10997839	0.0608	0.5077
chr6	171115067	10505394	0.0614	0.5538
chr7	159138663	9683324	0.0608	0.6272

chr8	146364022	9137750	0.0624	0.5928
chr9	141213431	7683910	0.0544	0.5842
chr10	135534747	8681752	0.0641	0.7286
chr11	135006516	8302166	0.0615	0.5715
chr12	133851895	8046979	0.0601	0.5251
chr13	115169878	5657555	0.0491	0.4425
chr14	107349540	5429121	0.0506	0.5014
chr15	102531392	5089916	0.0496	0.4498
chr16	90354753	5272496	0.0584	0.7255
chr17	81195210	4727935	0.0582	0.5262
chr18	78077248	4810753	0.0616	0.8036
chr19	59128983	3592681	0.0608	0.8911
chr20	63025520	3838548	0.0609	0.5308
chr21	48129895	2390179	0.0497	0.4778
chr22	51304566	2173939	0.0424	0.4548
chrMT	16571	3638	0.2195	0.729
chrX	155270560	5443699	0.0351	0.4344
chrY	59373566	1611007	0.0271	1.0274

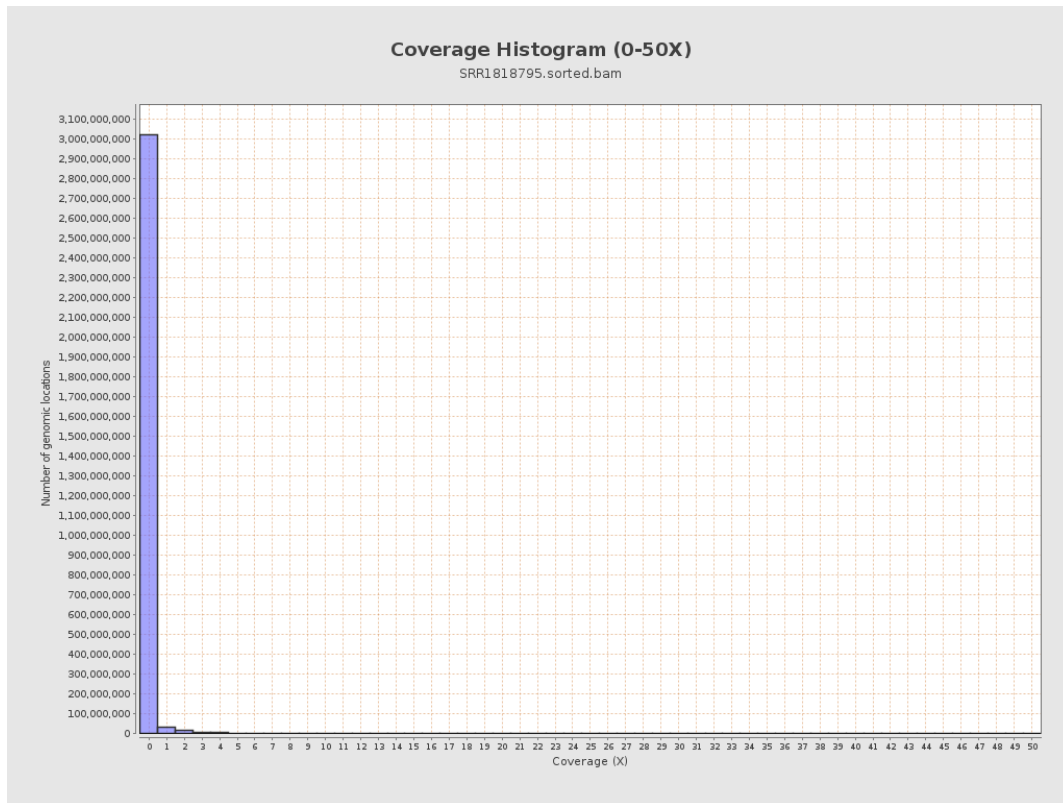
3. Results : Coverage across reference



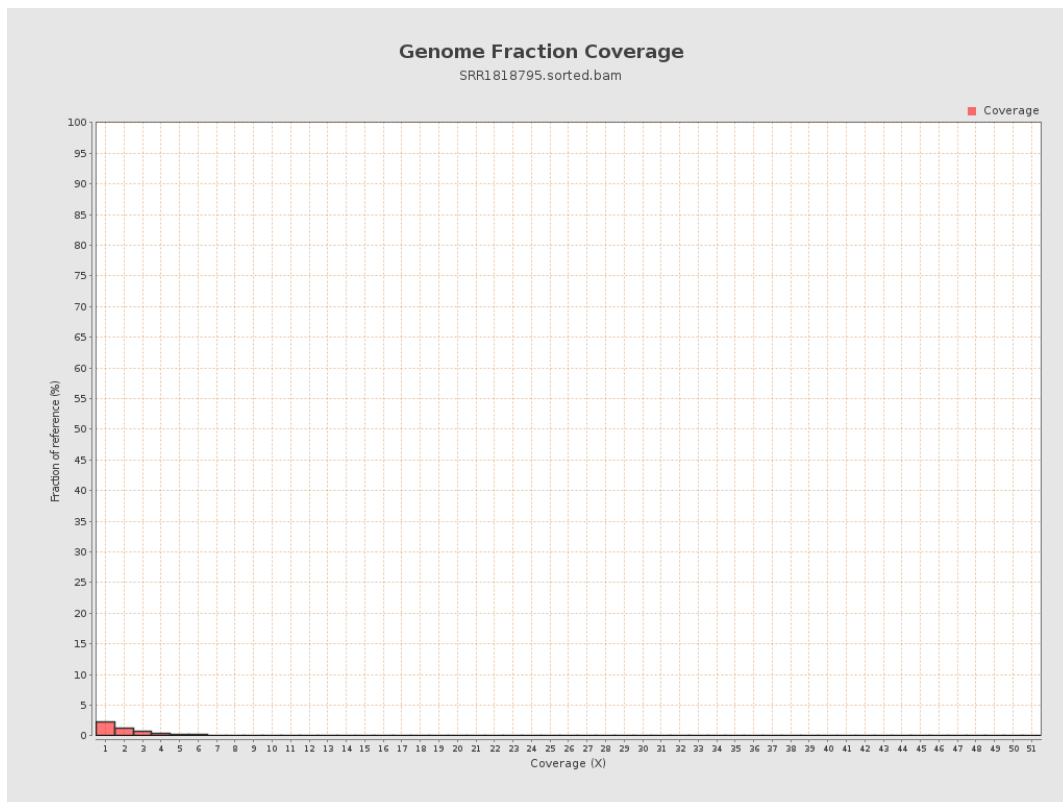
4. Results : Coverage Histogram



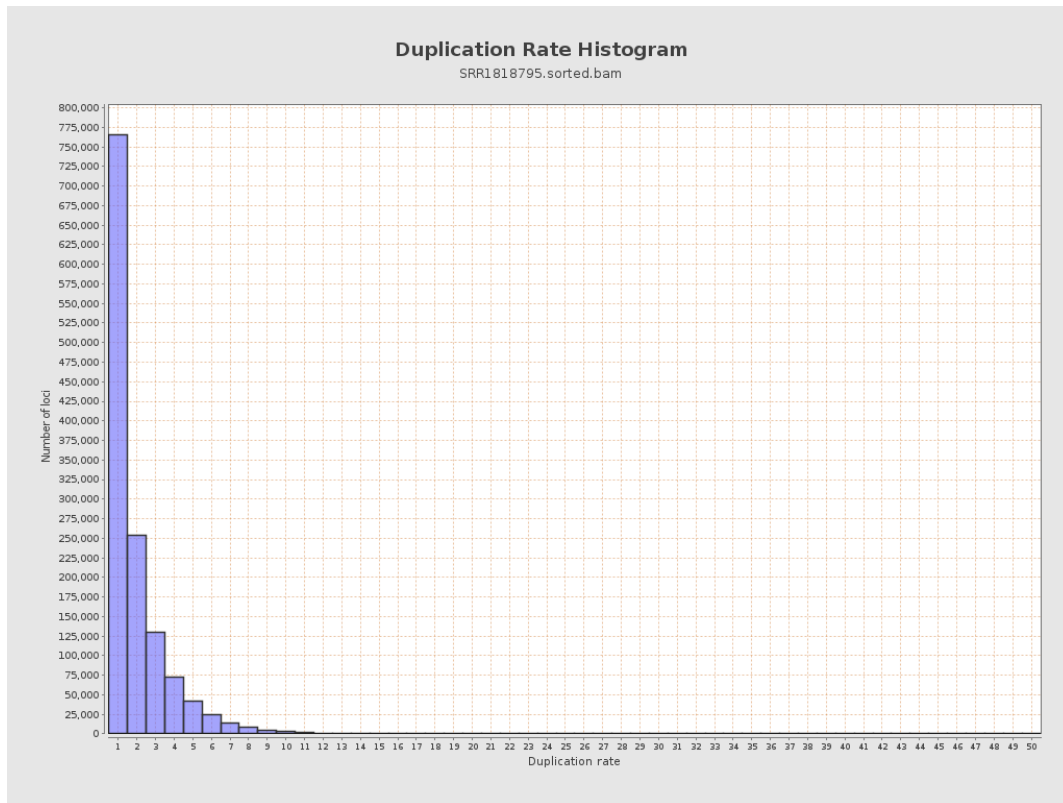
5. Results : Coverage Histogram (0-50X)



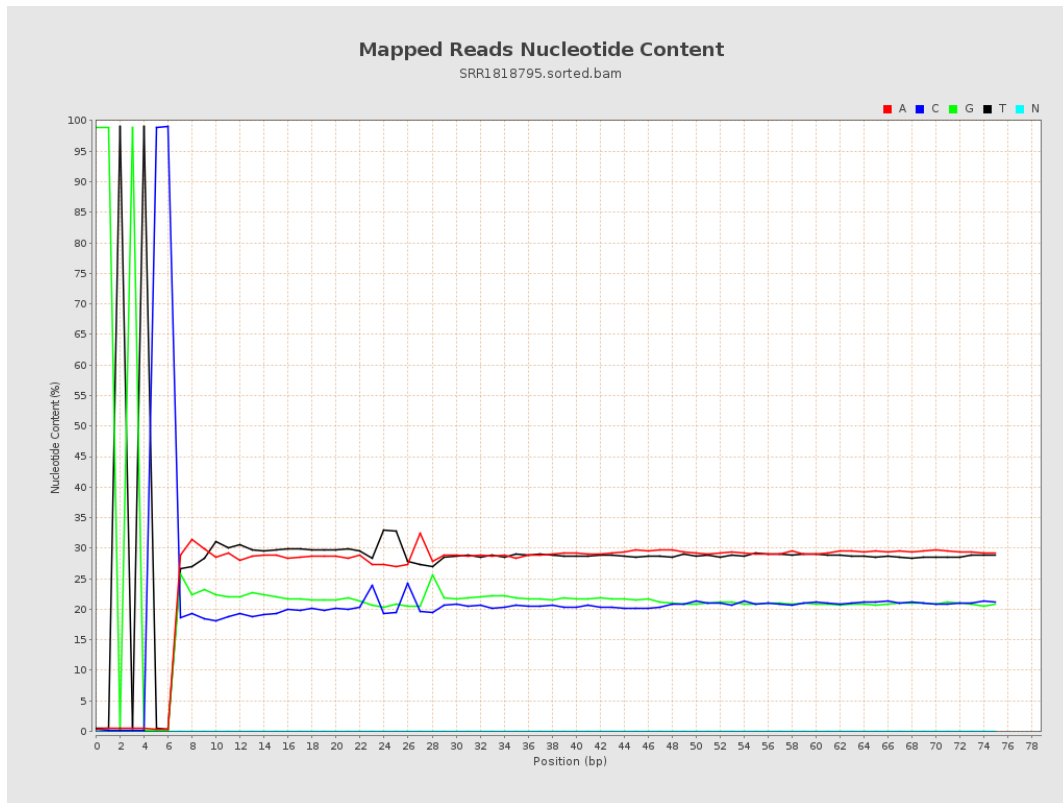
6. Results : Genome Fraction Coverage



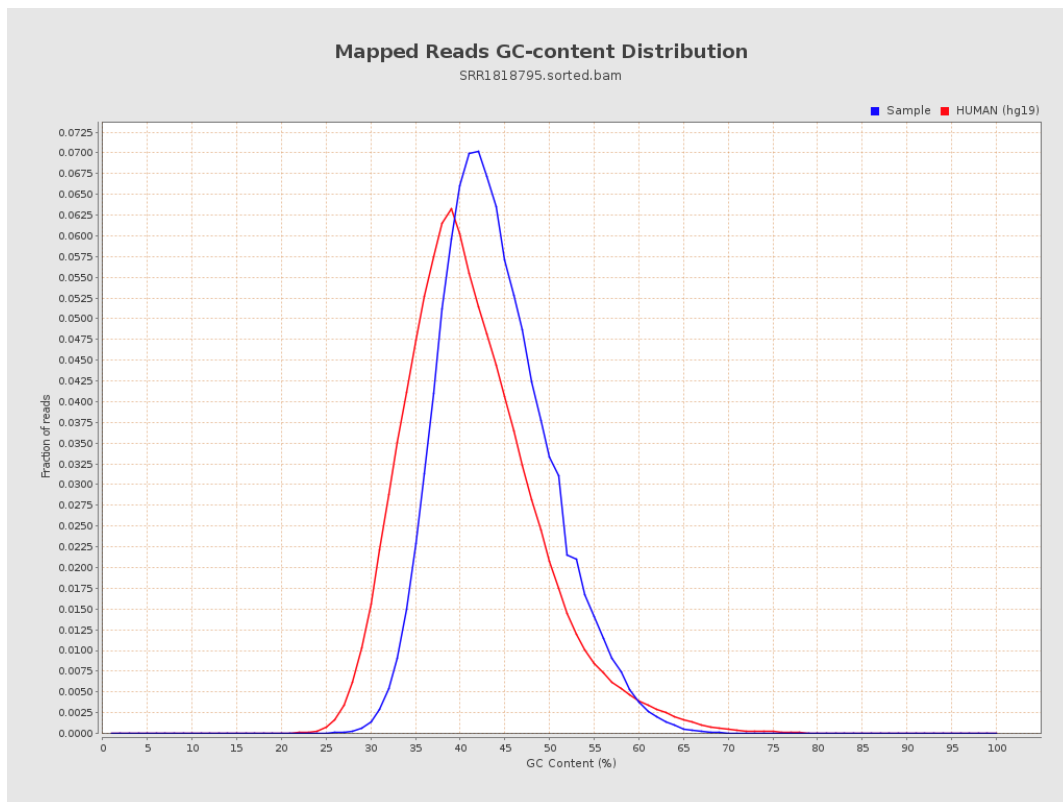
7. Results : Duplication Rate Histogram



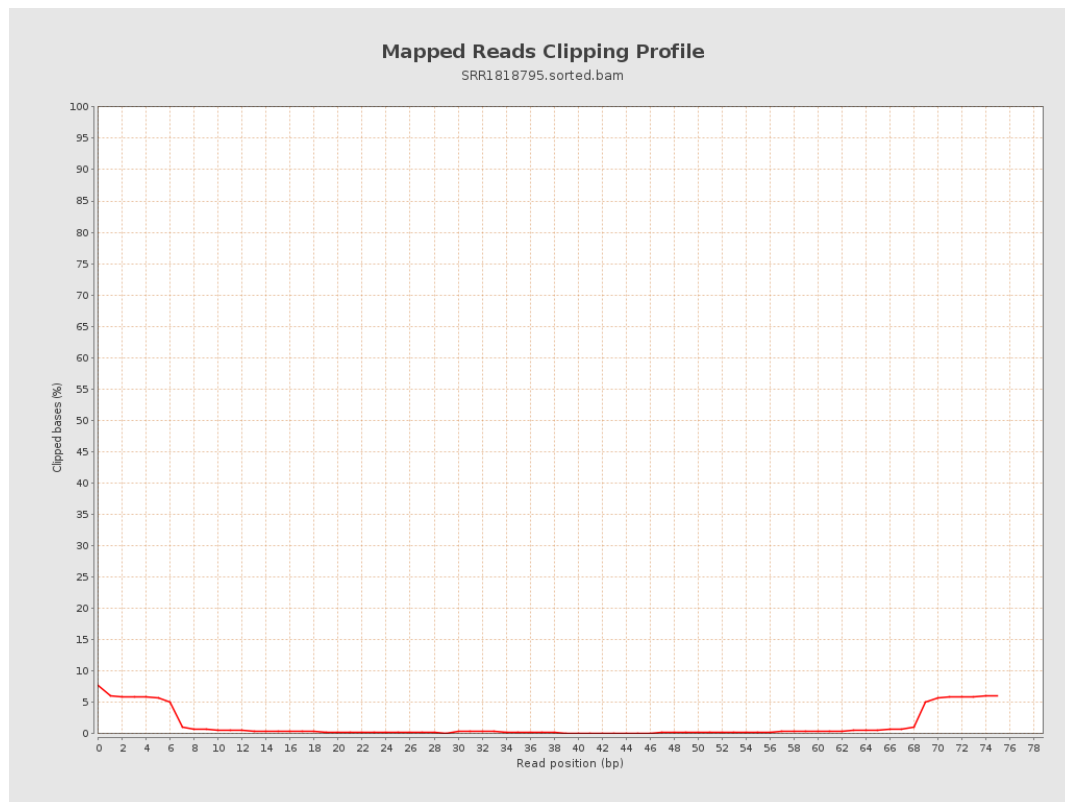
8. Results : Mapped Reads Nucleotide Content



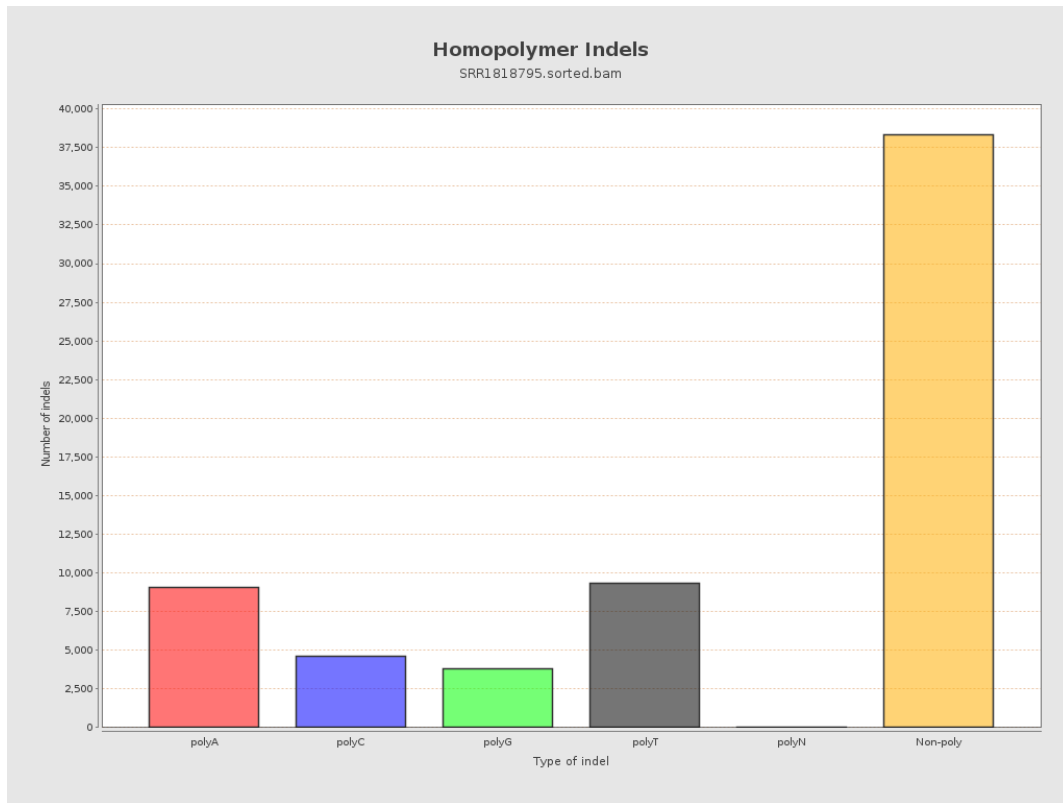
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

