

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:55:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818798.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_SRR1818798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:55:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,089,878
Mapped reads	1,056,010 / 96.89%
Unmapped reads	33,868 / 3.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,665 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	378,368 / 34.72%
Duplication rate	30.94%
Clipped reads	1,056,977 / 96.98%

2.2. ACGT Content

Number/percentage of A's	20,351,722 / 28.44%
Number/percentage of C's	15,235,862 / 21.29%
Number/percentage of T's	20,617,526 / 28.81%
Number/percentage of G's	15,347,850 / 21.45%
Number/percentage of N's	4,521 / 0.01%
GC Percentage	42.74%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.3354
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2.4. Mapping Quality

Mean Mapping Quality	47.95
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2.5. Mismatches and indels

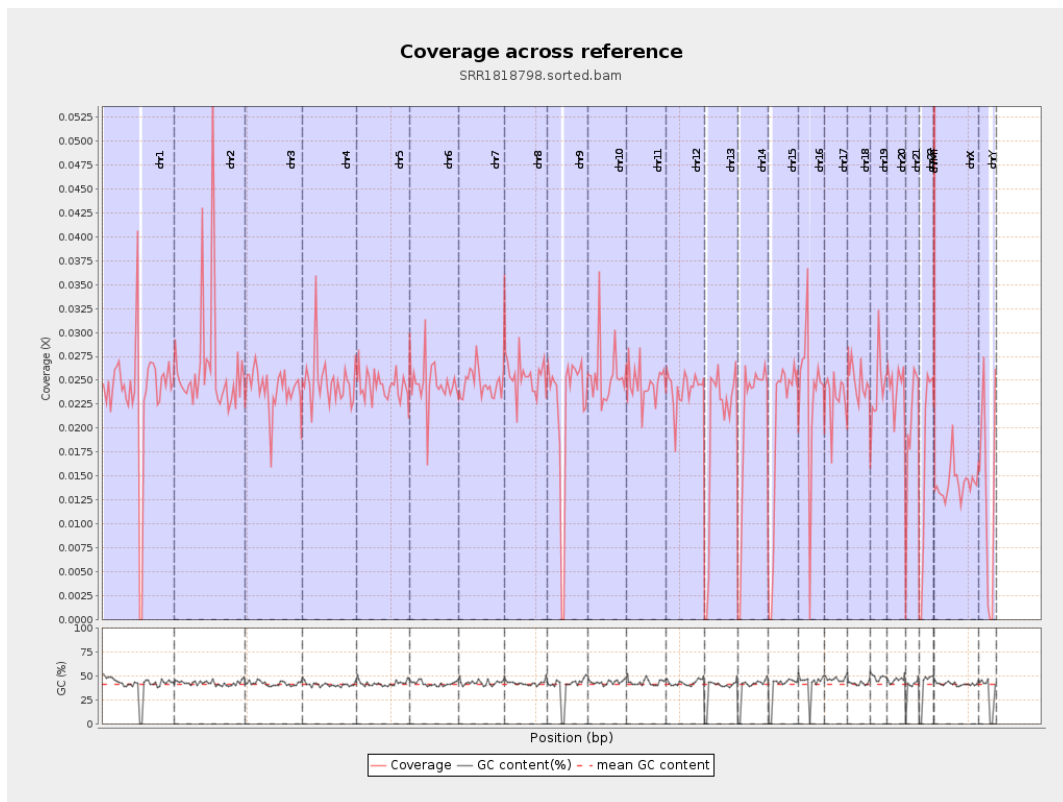
General error rate	0.55%
Mismatches	370,051
Insertions	9,703
Mapped reads with at least one insertion	0.91%
Deletions	18,516
Mapped reads with at least one deletion	1.74%
Homopolymer indels	39.9%

2.6. Chromosome stats

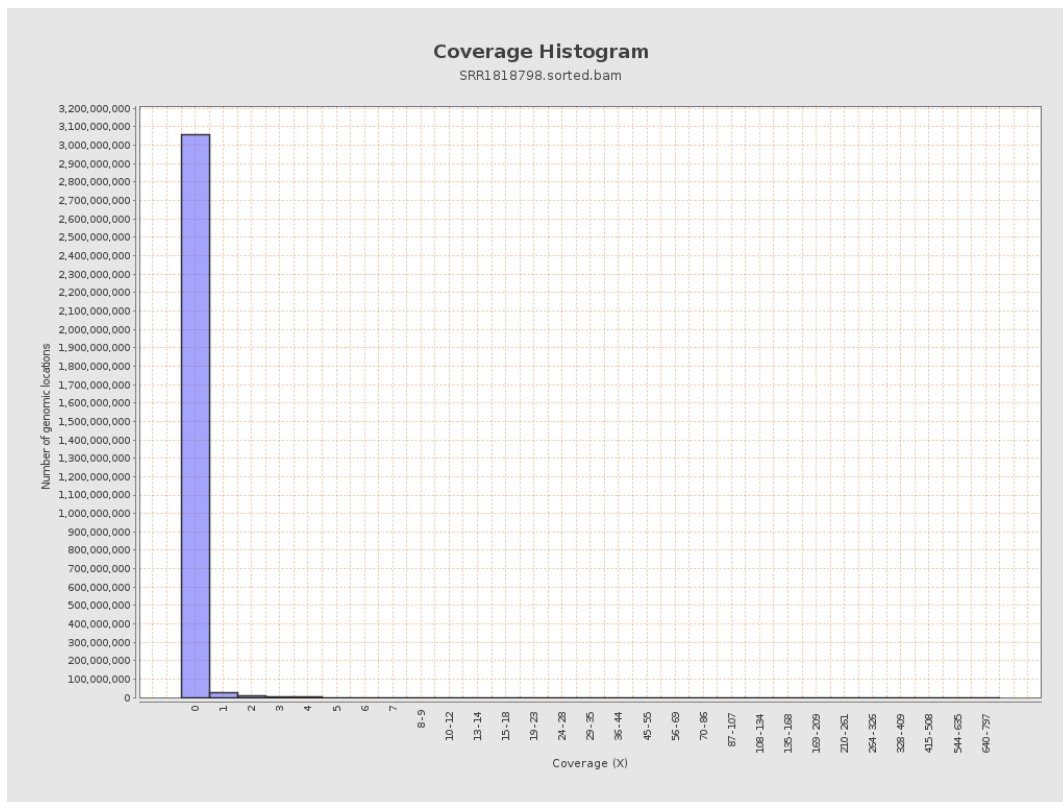
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5870606	0.0236	0.4218
chr2	243199373	6382309	0.0262	0.5864
chr3	198022430	4780620	0.0241	0.2456
chr4	191154276	4755233	0.0249	0.2802
chr5	180915260	4427500	0.0245	0.2567
chr6	171115067	4218355	0.0247	0.2721
chr7	159138663	3931646	0.0247	0.2889

chr8	146364022	3714586	0.0254	0.2759
chr9	141213431	3111839	0.022	0.2697
chr10	135534747	3453100	0.0255	0.357
chr11	135006516	3330844	0.0247	0.2787
chr12	133851895	3221221	0.0241	0.256
chr13	115169878	2295037	0.0199	0.2217
chr14	107349540	2232652	0.0208	0.258
chr15	102531392	2061024	0.0201	0.227
chr16	90354753	2130396	0.0236	0.3703
chr17	81195210	1883709	0.0232	0.2531
chr18	78077248	1949851	0.025	0.3424
chr19	59128983	1437542	0.0243	0.3669
chr20	63025520	1531819	0.0243	0.2699
chr21	48129895	983651	0.0204	0.236
chr22	51304566	862345	0.0168	0.2242
chrMT	16571	17253	1.0412	1.7969
chrX	155270560	2227410	0.0143	0.2079
chrY	59373566	777249	0.0131	0.6879

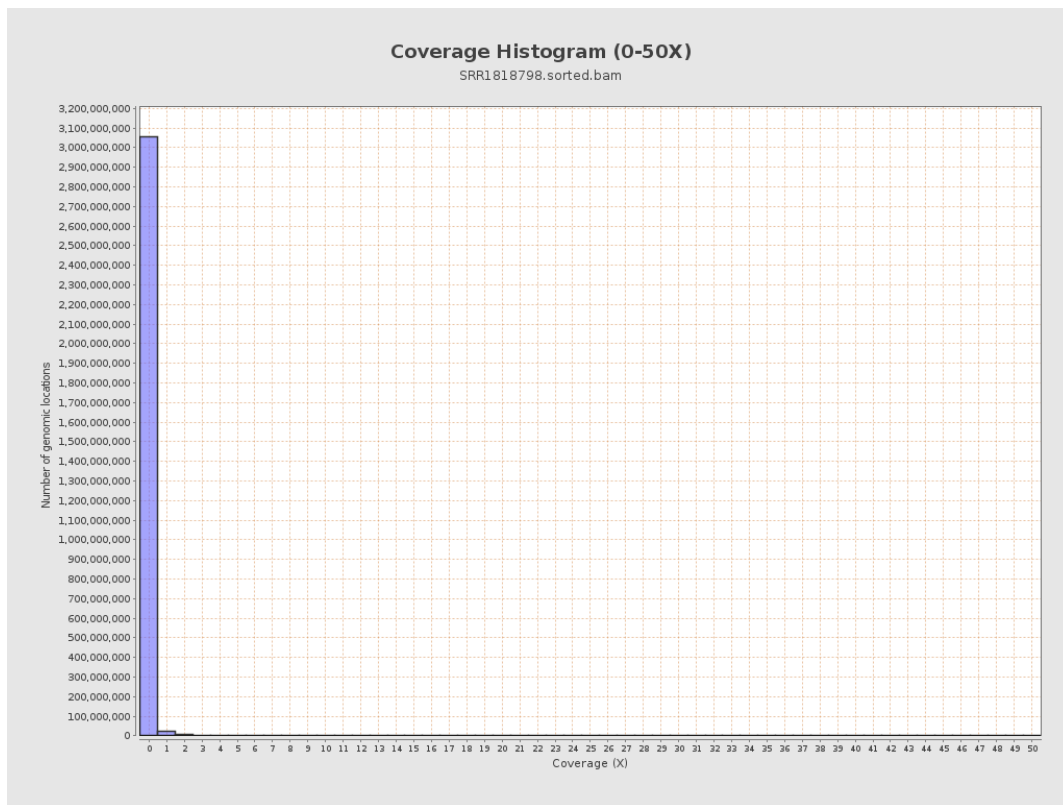
3. Results : Coverage across reference



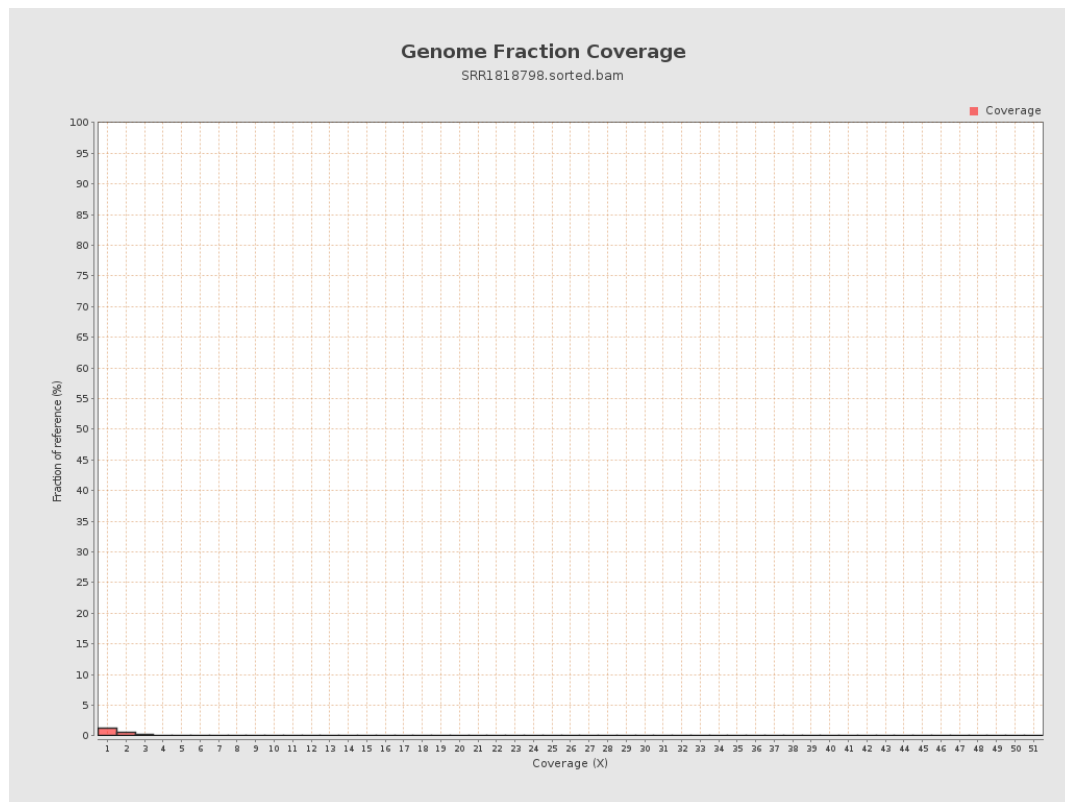
4. Results : Coverage Histogram



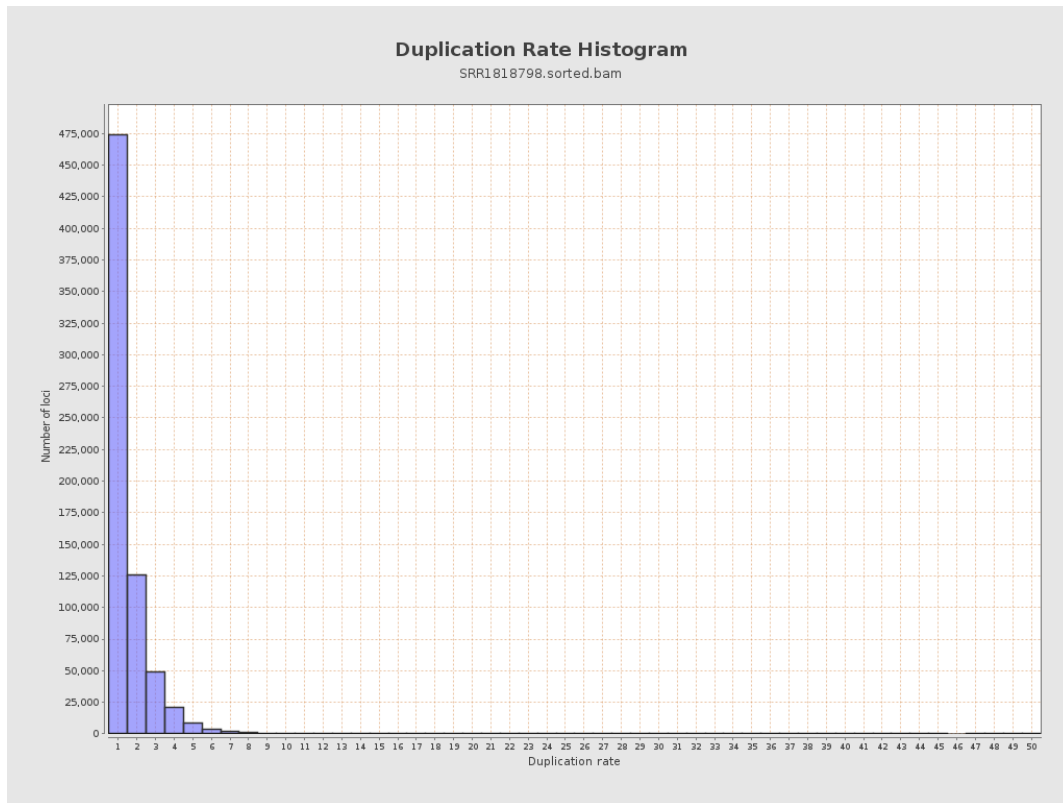
5. Results : Coverage Histogram (0-50X)



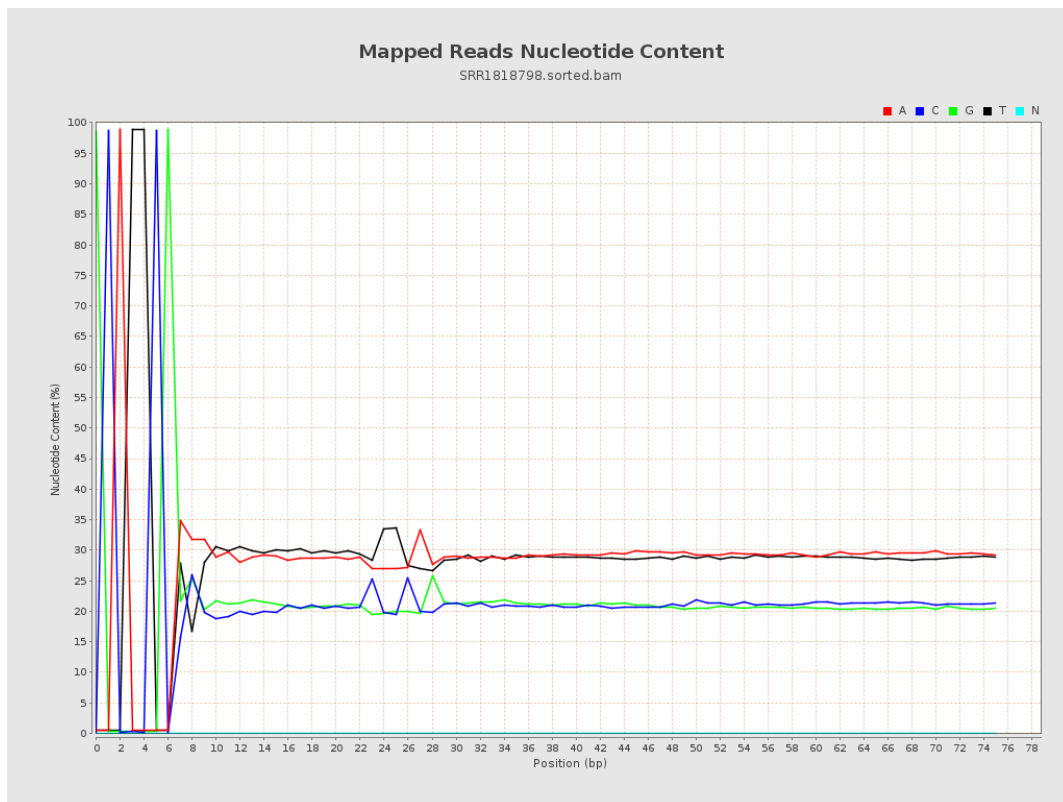
6. Results : Genome Fraction Coverage



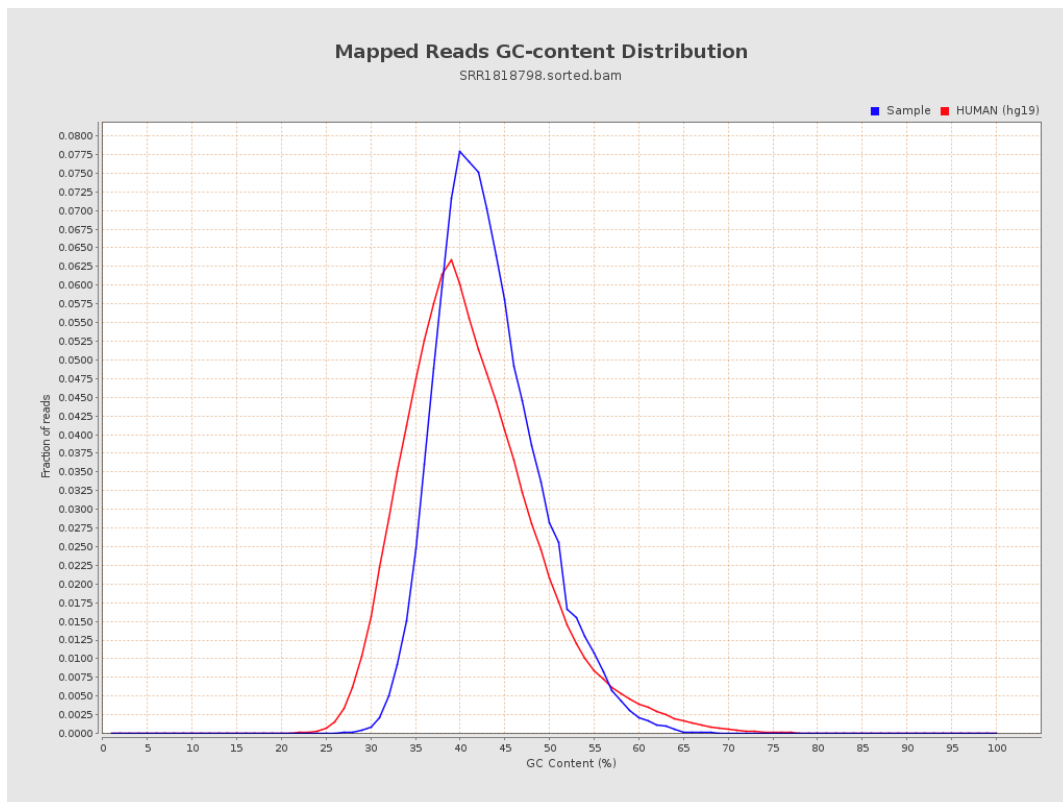
7. Results : Duplication Rate Histogram



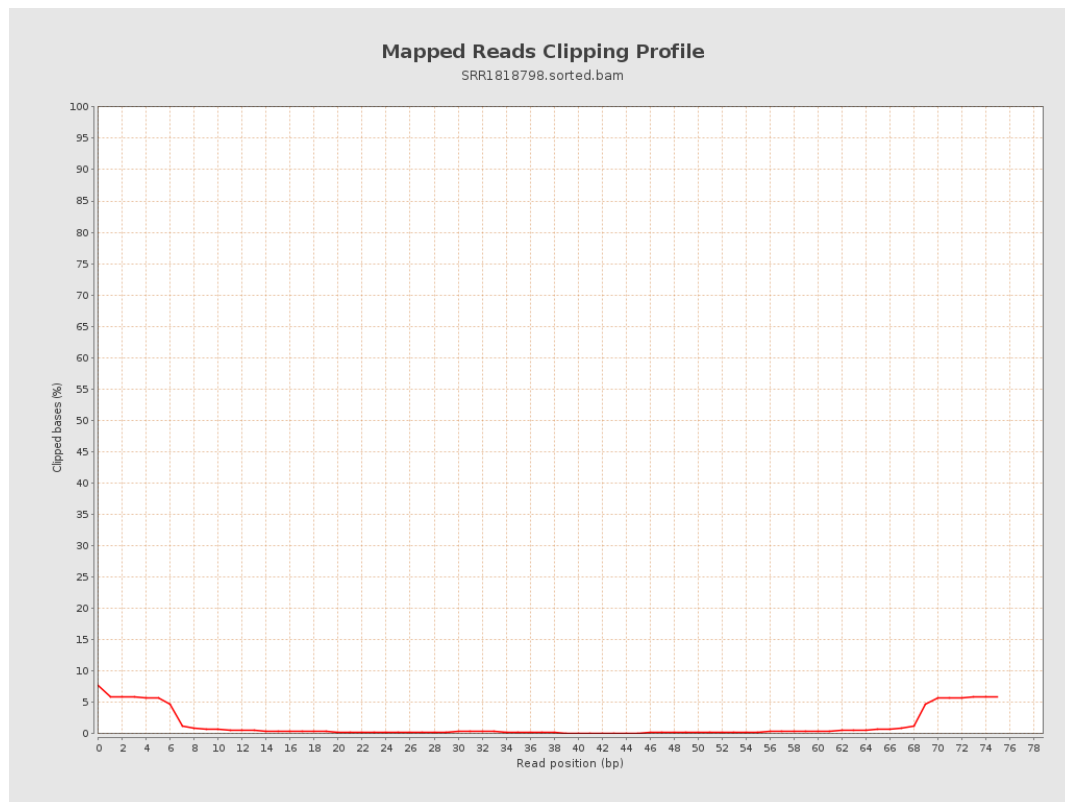
8. Results : Mapped Reads Nucleotide Content



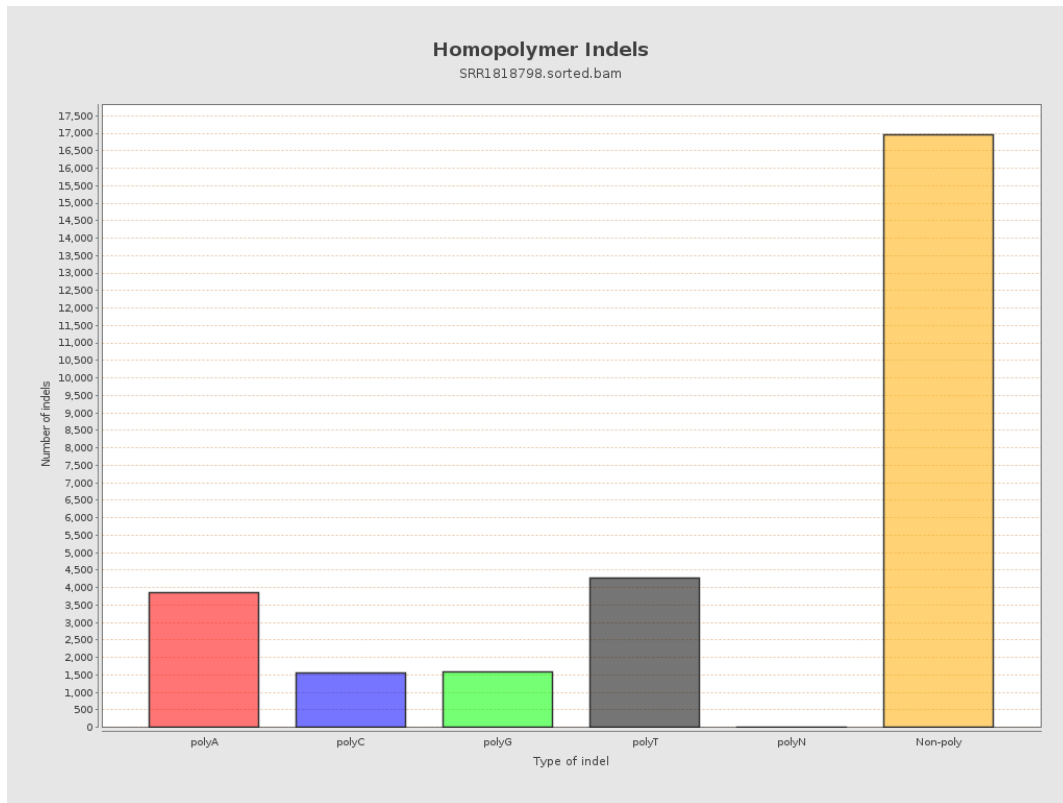
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

