

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:44:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818895.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_SRR1818895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818895.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:44:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,248,404
Mapped reads	1,231,584 / 98.65%
Unmapped reads	16,820 / 1.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,864 / 1.59%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	215,011 / 17.22%
Duplication rate	14.39%
Clipped reads	1,247,664 / 99.94%

2.2. ACGT Content

Number/percentage of A's	33,157,301 / 29.13%
Number/percentage of C's	25,143,648 / 22.09%
Number/percentage of T's	31,700,049 / 27.85%
Number/percentage of G's	23,820,885 / 20.93%
Number/percentage of N's	1,504 / 0%
GC Percentage	43.02%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.4816
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2.4. Mapping Quality

Mean Mapping Quality	49.12
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2.5. Mismatches and indels

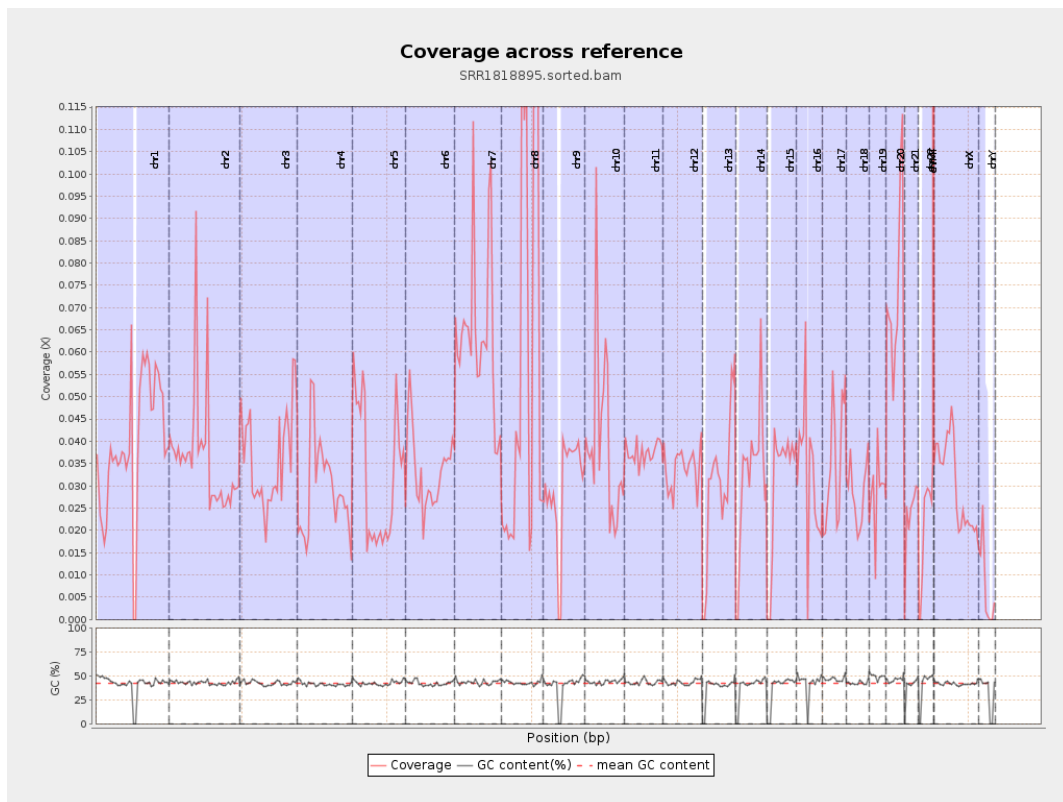
General error rate	0.65%
Mismatches	706,231
Insertions	14,459
Mapped reads with at least one insertion	1.13%
Deletions	38,397
Mapped reads with at least one deletion	3.04%
Homopolymer indels	41.84%

2.6. Chromosome stats

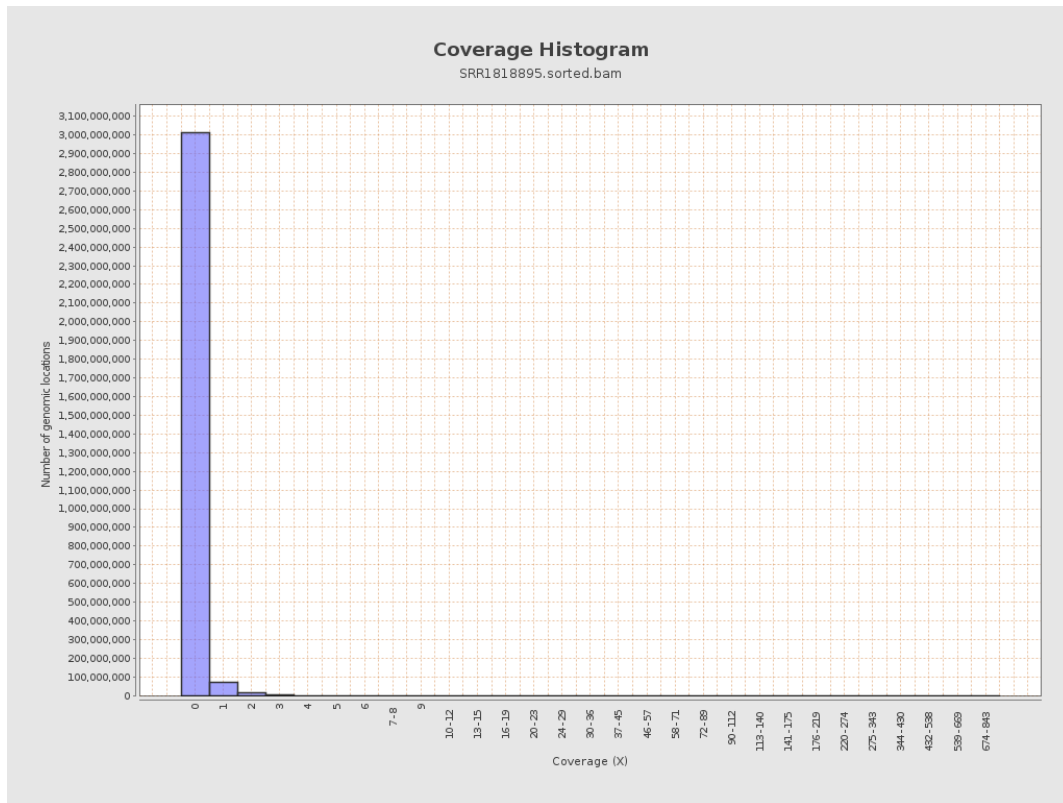
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9738491	0.0391	0.7059
chr2	243199373	8843159	0.0364	0.7206
chr3	198022430	7150803	0.0361	0.2382
chr4	191154276	5497505	0.0288	0.2864
chr5	180915260	5823385	0.0322	0.237
chr6	171115067	5677960	0.0332	0.2515
chr7	159138663	10217090	0.0642	1.023

chr8	146364022	9875923	0.0675	0.4082
chr9	141213431	4198021	0.0297	0.3724
chr10	135534747	5375586	0.0397	0.6845
chr11	135006516	5061930	0.0375	0.2943
chr12	133851895	4559953	0.0341	0.2331
chr13	115169878	3481941	0.0302	0.2134
chr14	107349540	3443271	0.0321	0.248
chr15	102531392	3177235	0.031	0.219
chr16	90354753	2871573	0.0318	0.4963
chr17	81195210	2882811	0.0355	0.3047
chr18	78077248	2214721	0.0284	0.4417
chr19	59128983	1692512	0.0286	0.5781
chr20	63025520	4647335	0.0737	0.3678
chr21	48129895	1134118	0.0236	0.2365
chr22	51304566	1016798	0.0198	0.1984
chrMT	16571	164777	9.9437	6.9603
chrX	155270560	4715131	0.0304	0.2533
chrY	59373566	436757	0.0074	0.5645

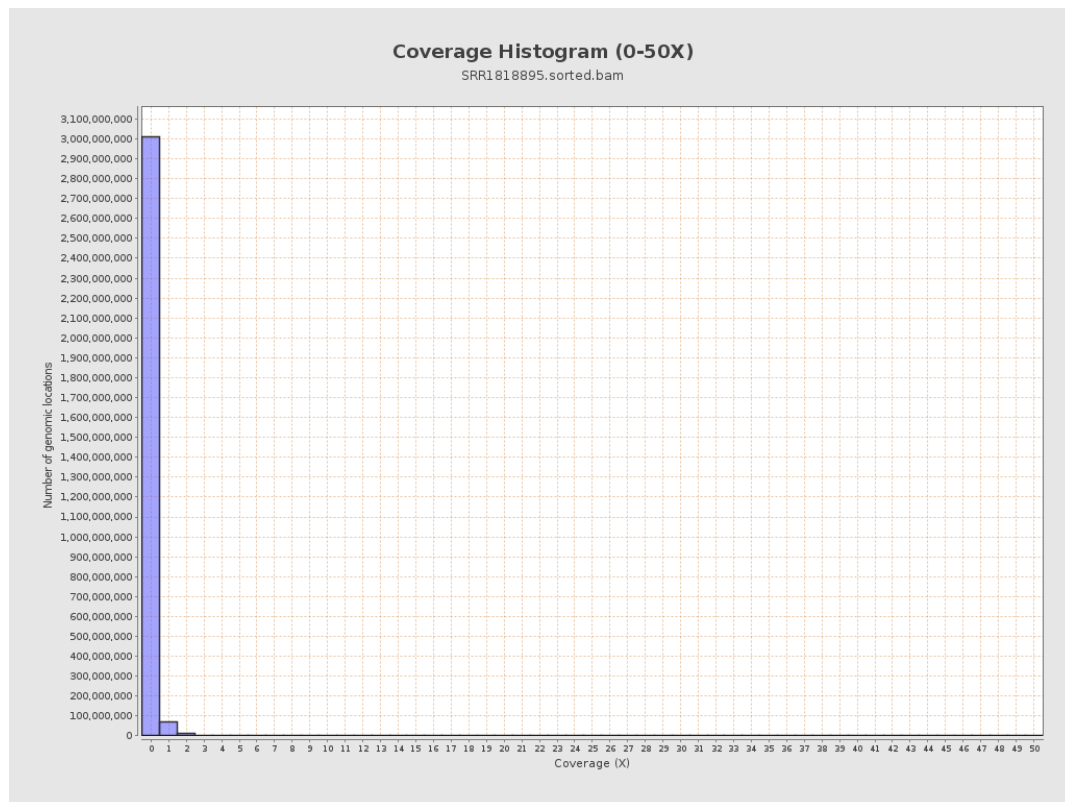
3. Results : Coverage across reference



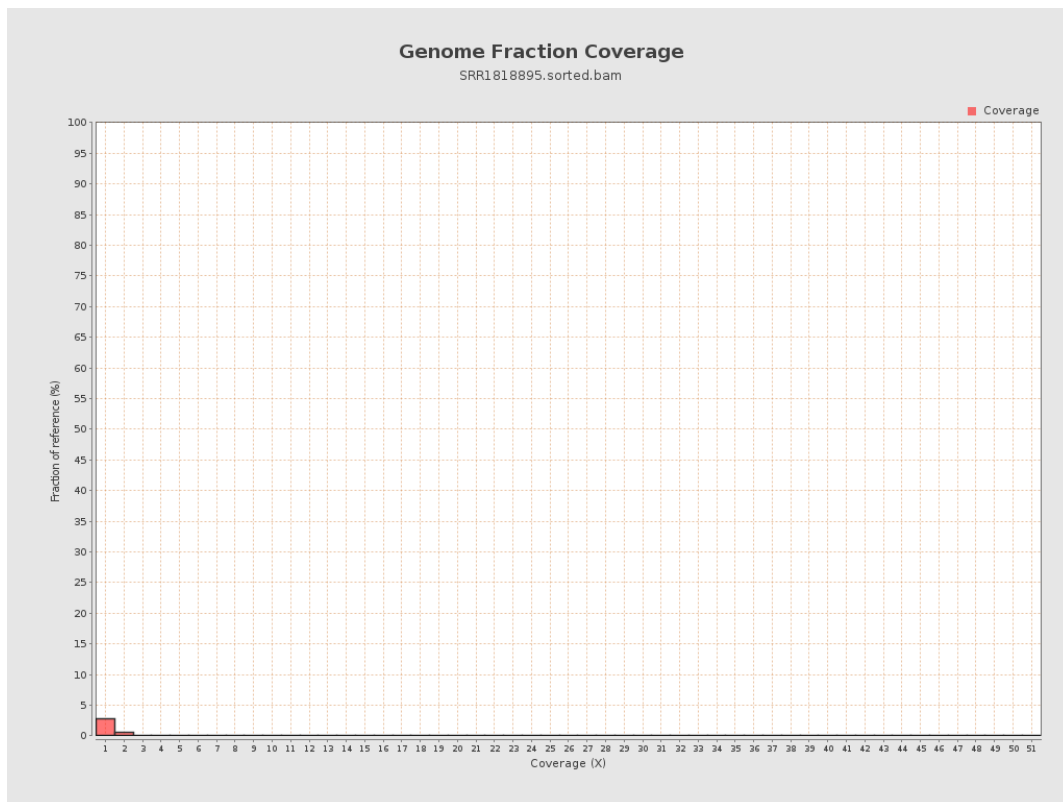
4. Results : Coverage Histogram



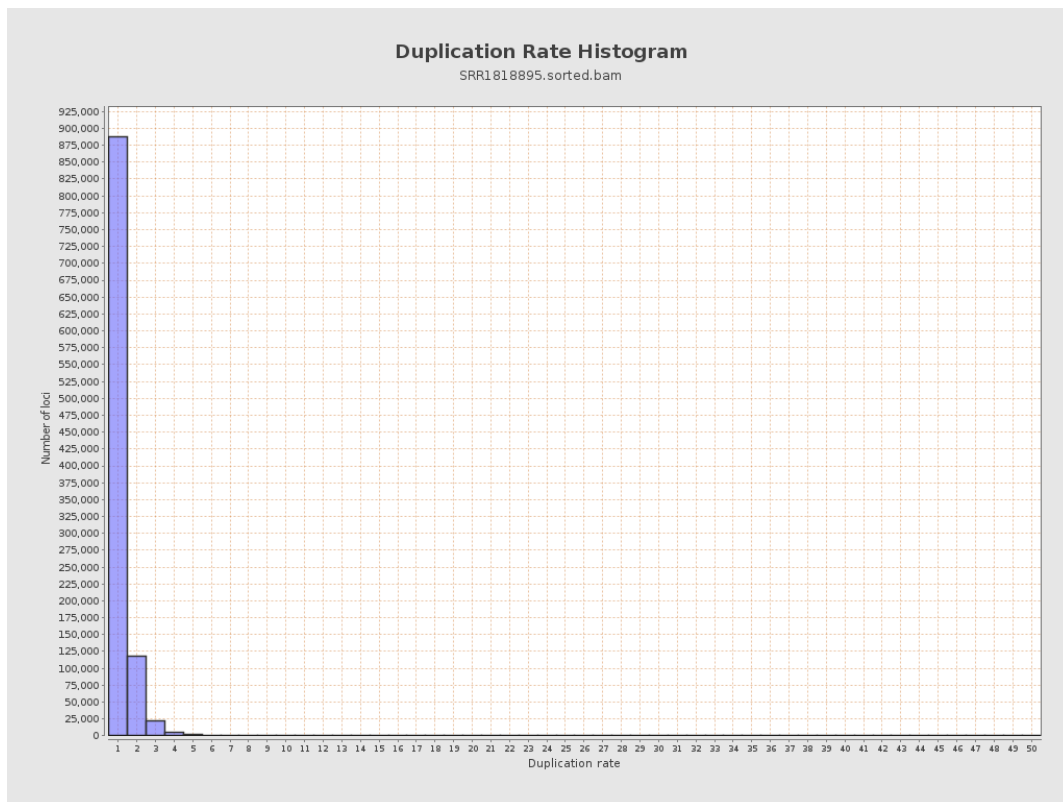
5. Results : Coverage Histogram (0-50X)



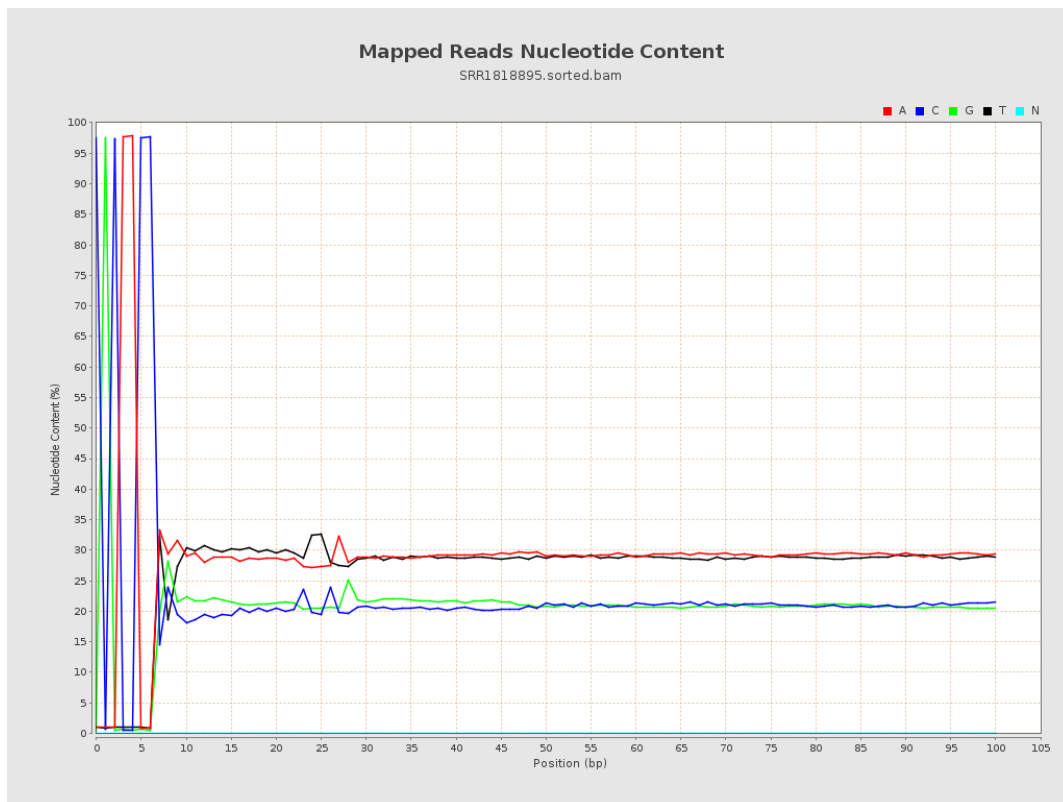
6. Results : Genome Fraction Coverage



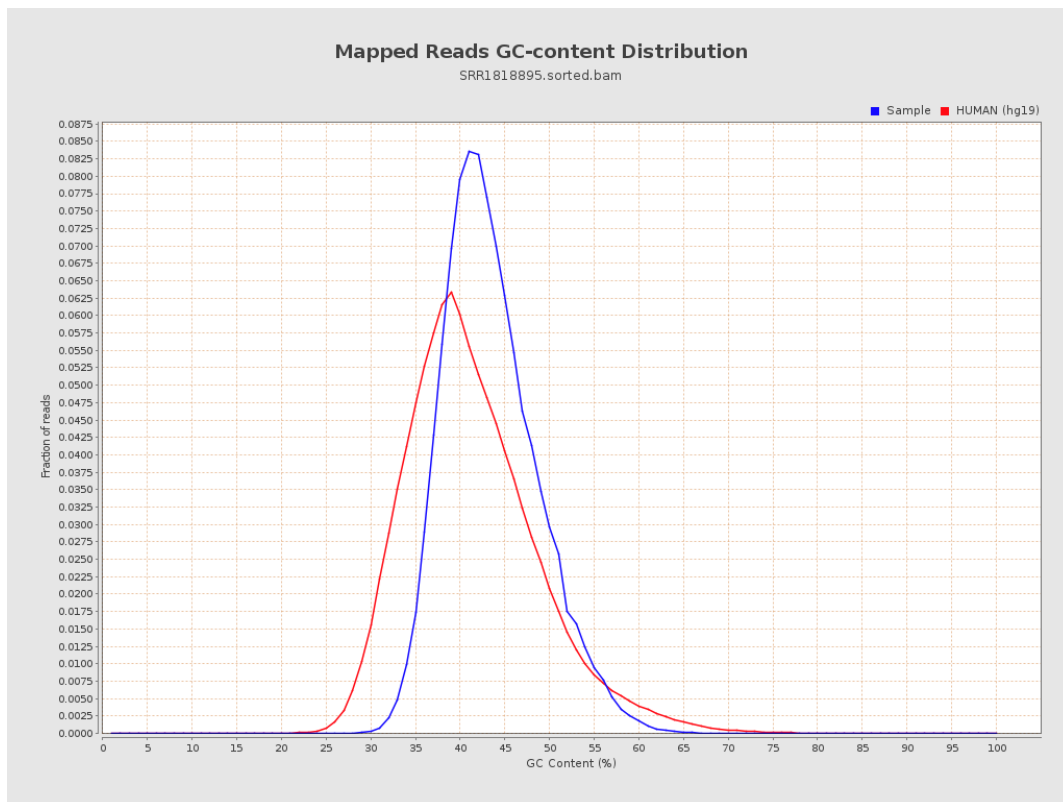
7. Results : Duplication Rate Histogram



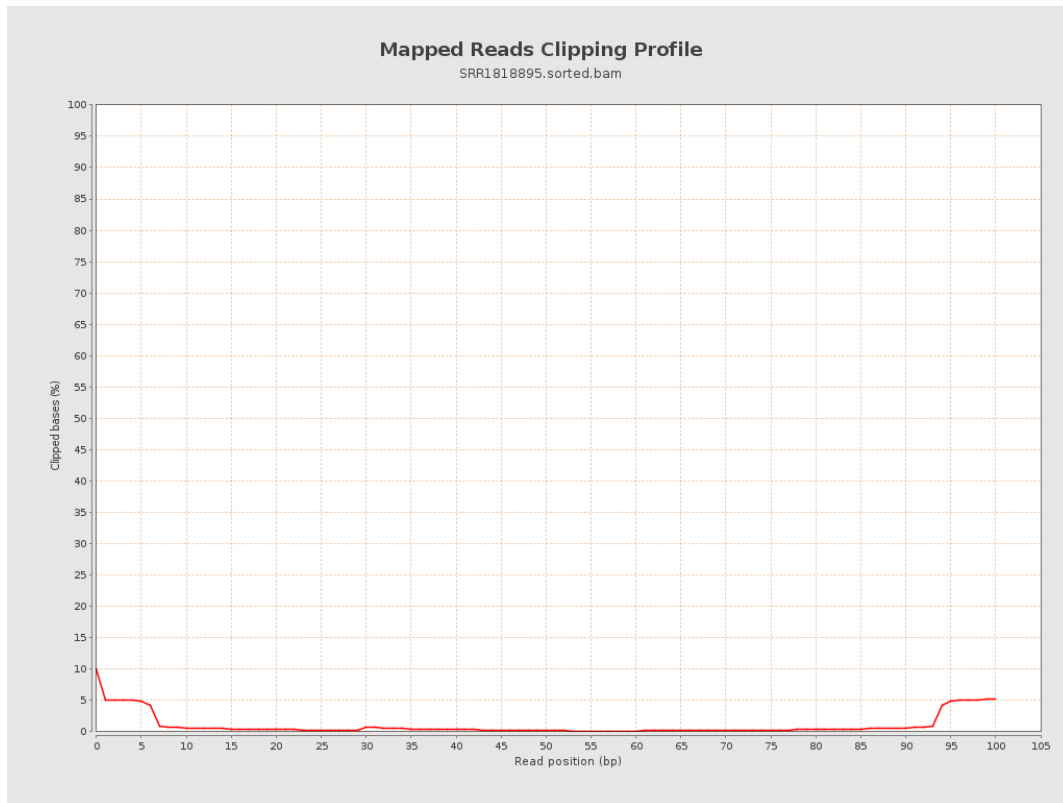
8. Results : Mapped Reads Nucleotide Content



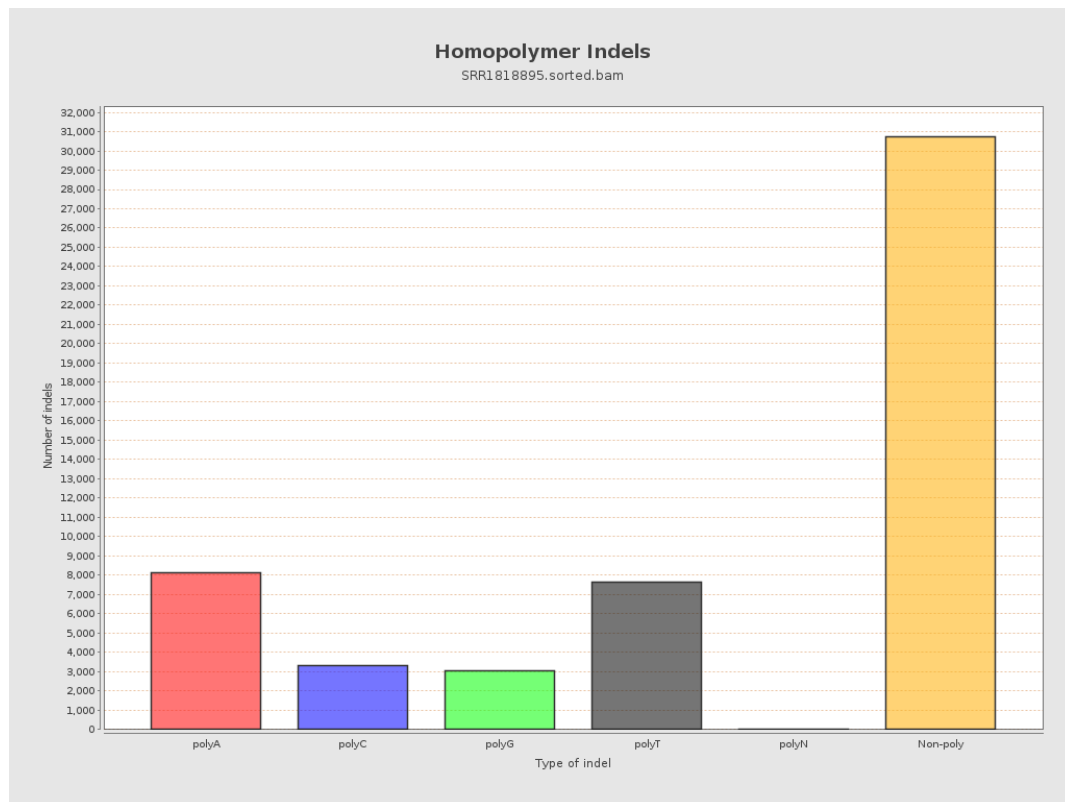
9. Results : Mapped Reads GC-content Distribution



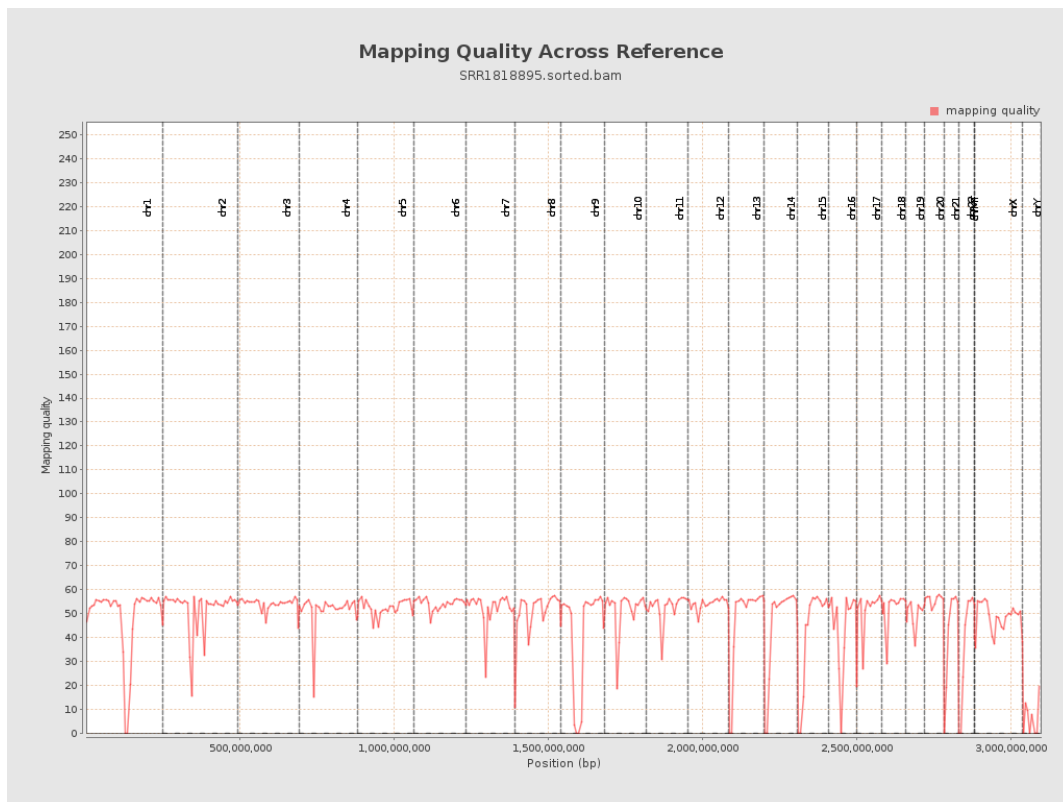
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

