Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:00:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818898.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_SRR1818898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818898.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:00:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	952,366
Mapped reads	937,890 / 98.48%
Unmapped reads	14,476 / 1.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,706 / 1.44%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	148,073 / 15.55%
Duplication rate	12.98%
Clipped reads	944,614 / 99.19%

2.2. ACGT Content

Number/percentage of A's	25,124,050 / 28.95%
Number/percentage of C's	18,920,282 / 21.8%
Number/percentage of T's	24,146,998 / 27.82%
Number/percentage of G's	18,598,250 / 21.43%
Number/percentage of N's	1,099 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.3846

2.4. Mapping Quality

Mean Mapping Quality	49.24

2.5. Mismatches and indels

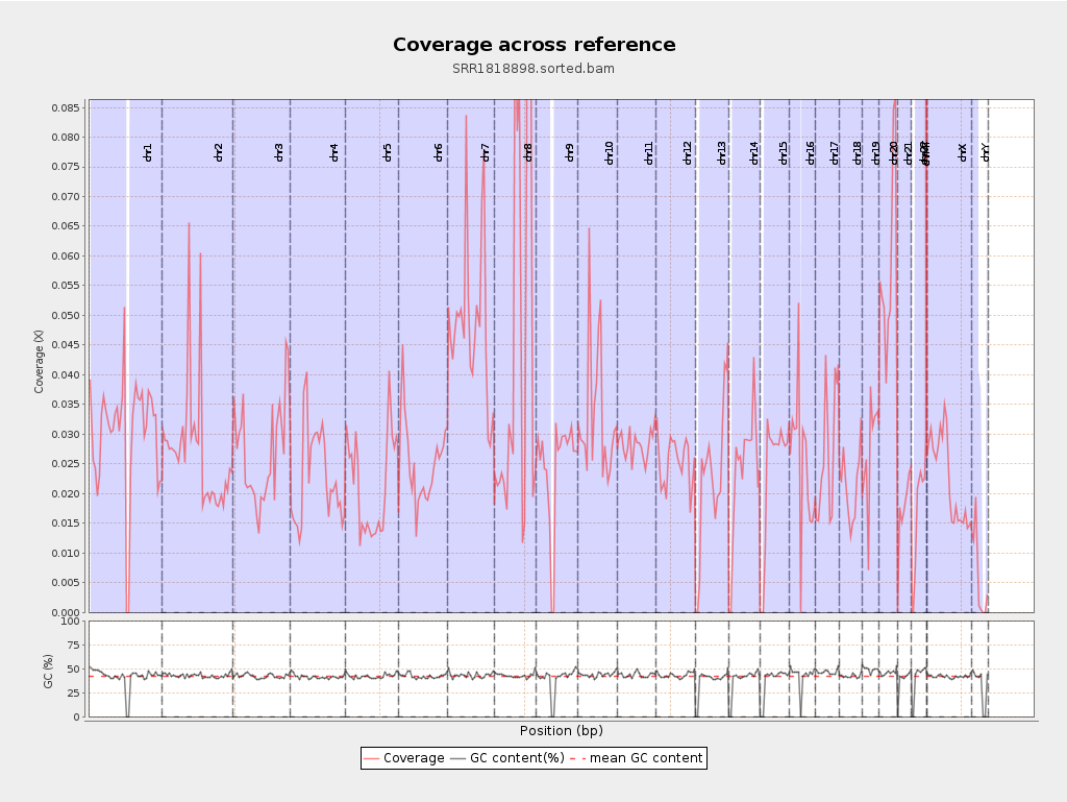
General error rate	0.66%
Mismatches	535,044
Insertions	13,772
Mapped reads with at least one insertion	1.42%
Deletions	29,031
Mapped reads with at least one deletion	3.01%
Homopolymer indels	39.67%

2.6. Chromosome stats

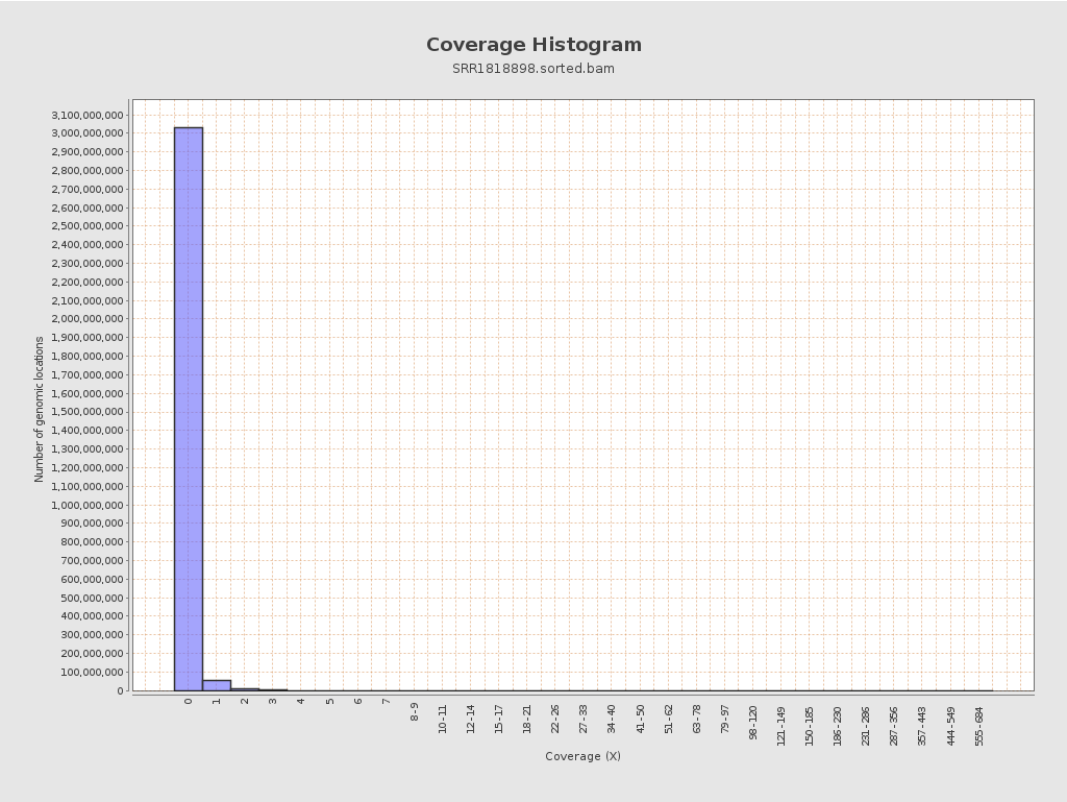
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7491170	0.0301	0.5176
chr2	243199373	6617221	0.0272	0.6277
chr3	198022430	5320873	0.0269	0.1999
chr4	191154276	4314790	0.0226	0.2309
chr5	180915260	3864897	0.0214	0.1915
chr6	171115067	4279867	0.025	0.2119
chr7	159138663	7797639	0.049	0.7858

chr8	146364022	7487136	0.0512	0.3195
chr9	141213431	3439215	0.0244	0.2989
chr10	135534747	4462993	0.0329	0.4981
chr11	135006516	3810834	0.0282	0.2405
chr12	133851895	3414917	0.0255	0.1954
chr13	115169878	2595916	0.0225	0.1814
chr14	107349540	2550503	0.0238	0.2096
chr15	102531392	2437464	0.0238	0.1873
chr16	90354753	2248800	0.0249	0.4544
chr17	81195210	2208626	0.0272	0.2507
chr18	78077248	1663774	0.0213	0.3353
chr19	59128983	1605907	0.0272	0.4822
chr20	63025520	3681245	0.0584	0.3164
chr21	48129895	846026	0.0176	0.1846
chr22	51304566	809744	0.0158	0.1685
chrMT	16571	47789	2.8839	2.5381
chrX	155270560	3506273	0.0226	0.2082
chrY	59373566	345814	0.0058	0.5103

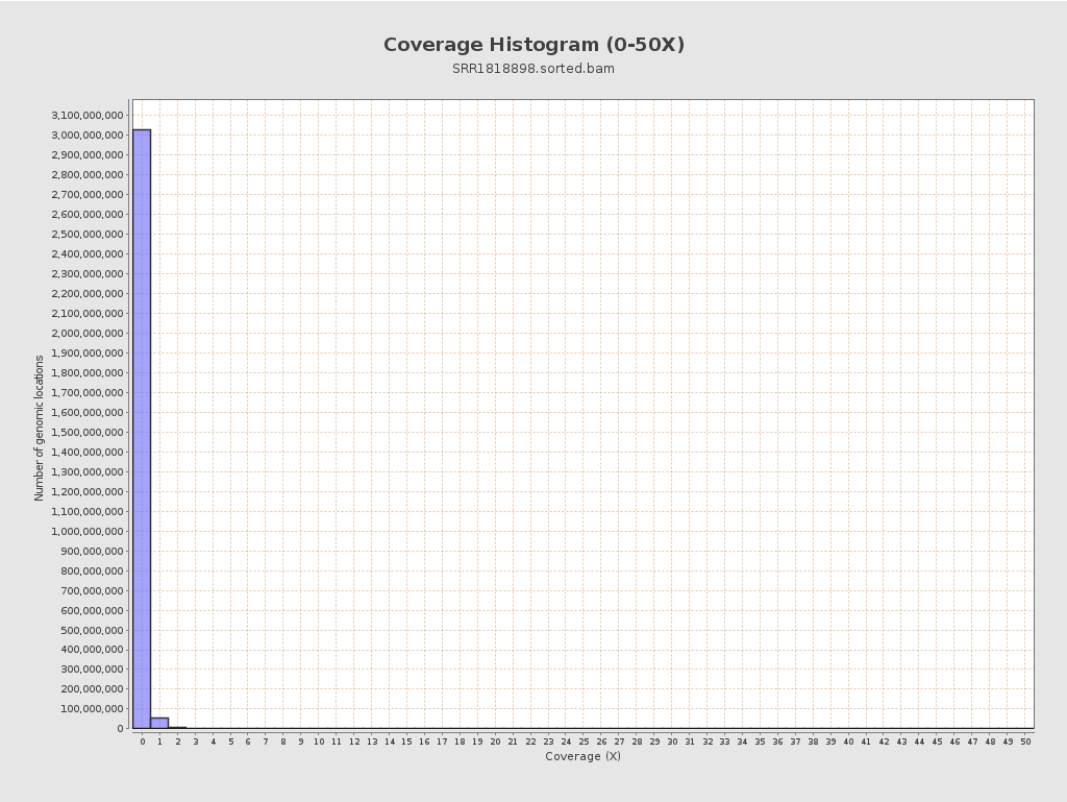
3. Results : Coverage across reference



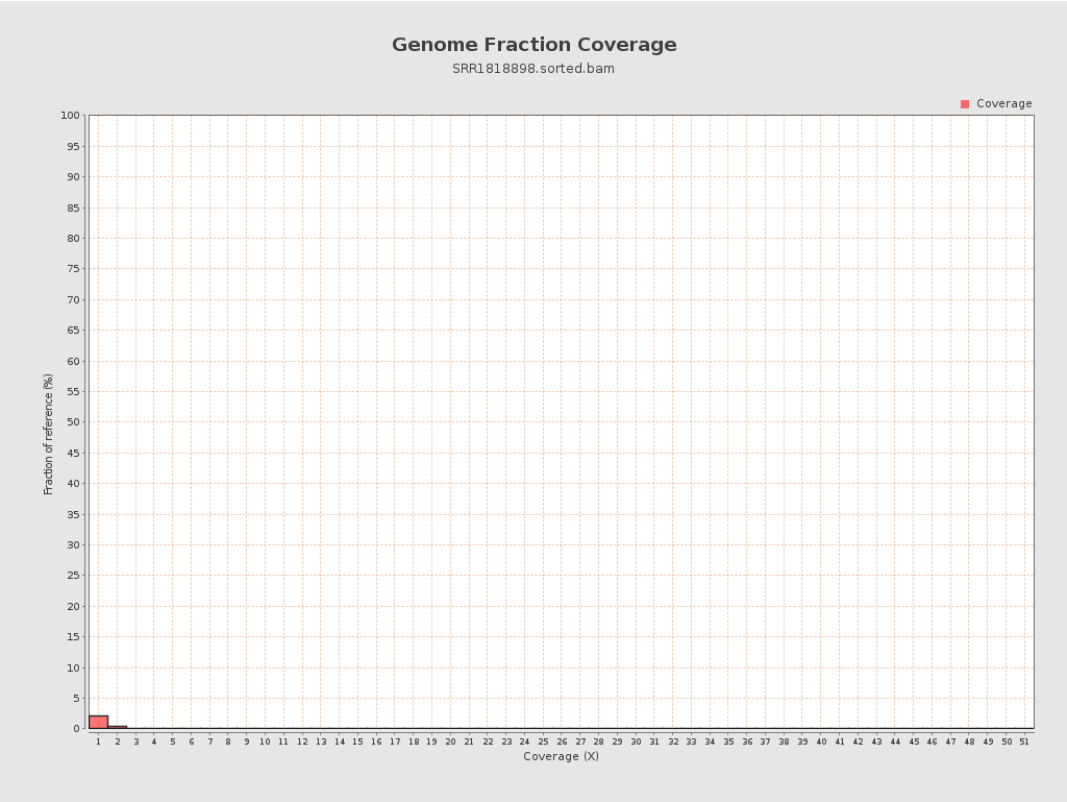
4. Results : Coverage Histogram



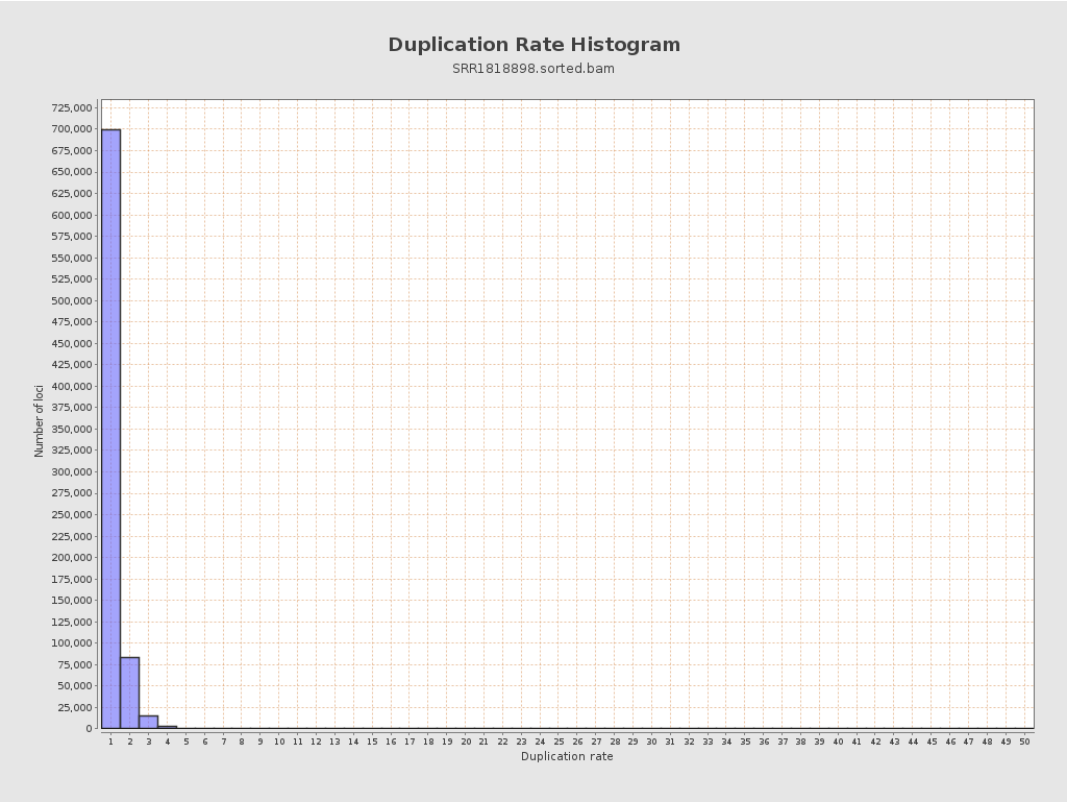
5. Results : Coverage Histogram (0-50X)



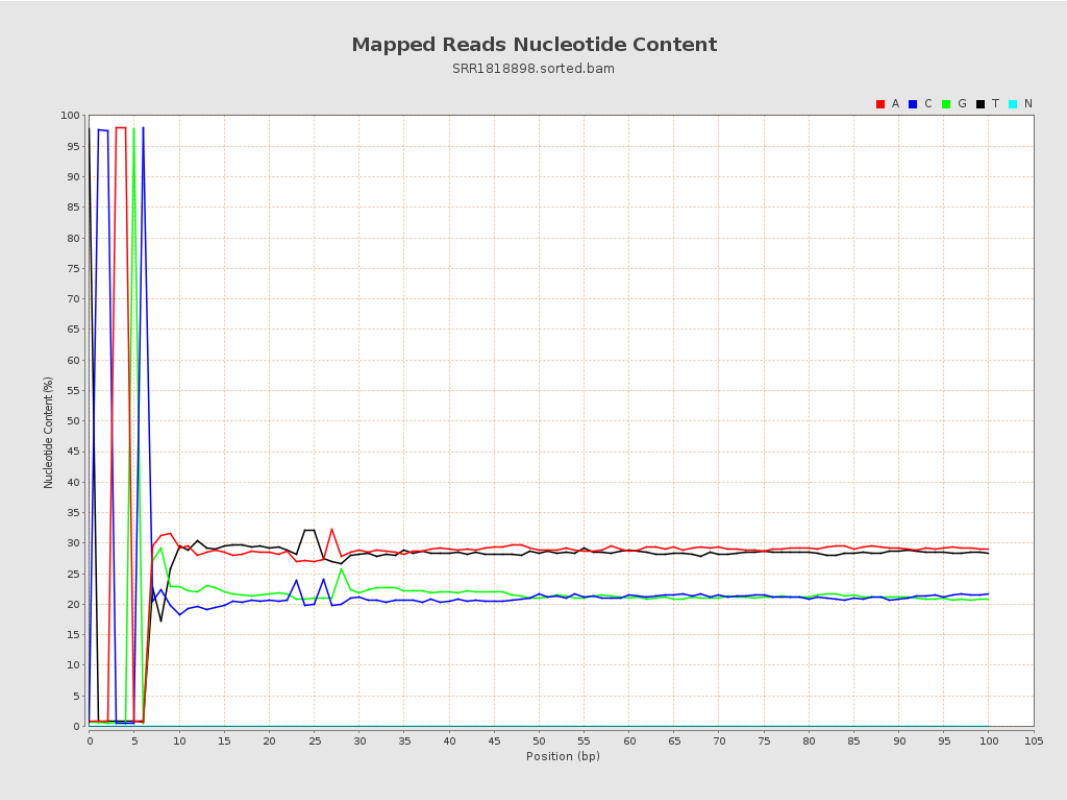
6. Results : Genome Fraction Coverage



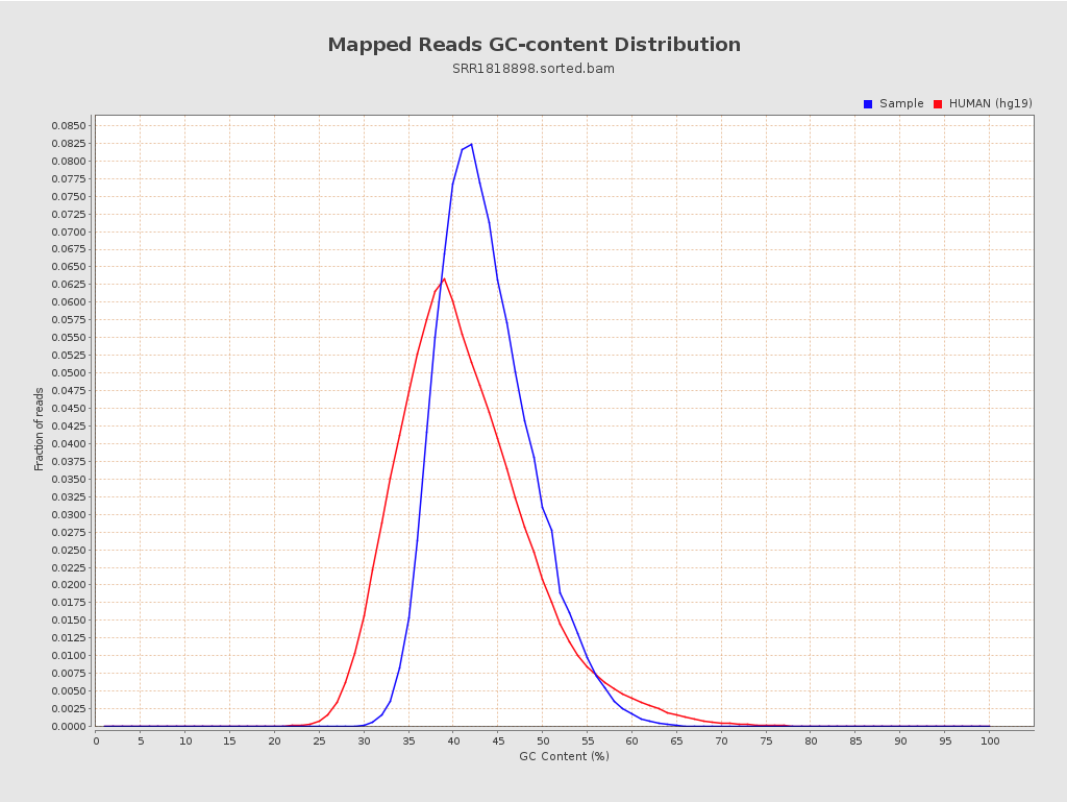
7. Results : Duplication Rate Histogram



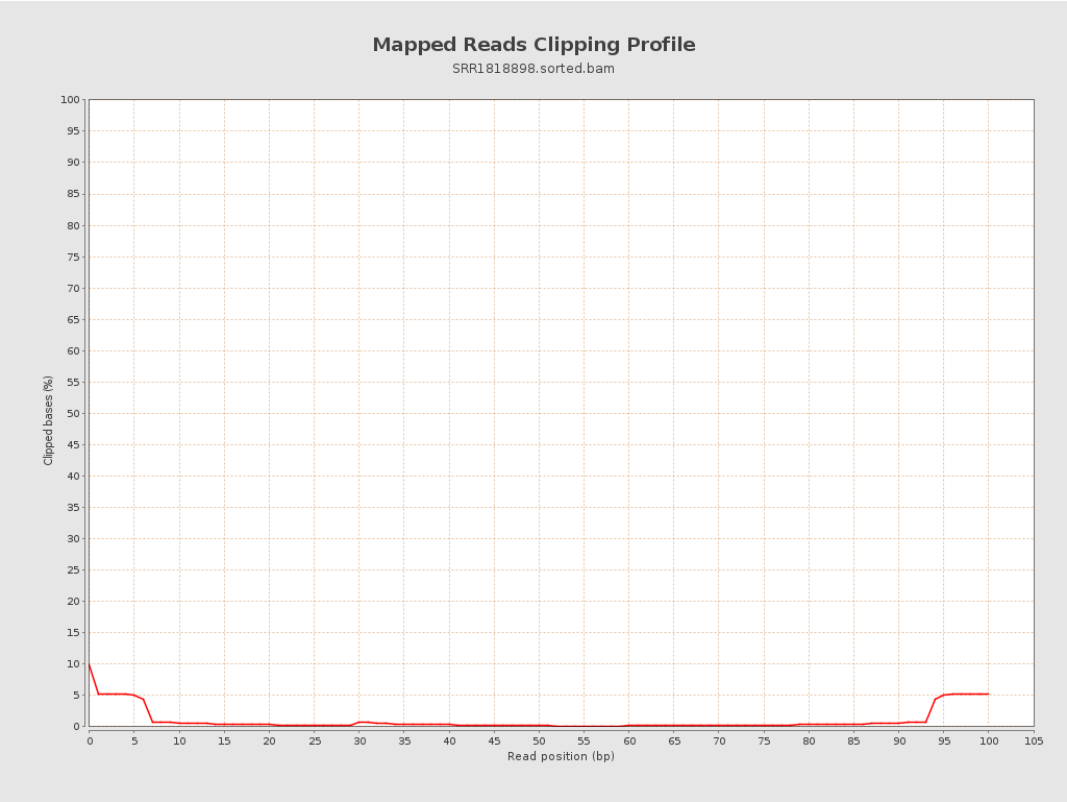
8. Results : Mapped Reads Nucleotide Content



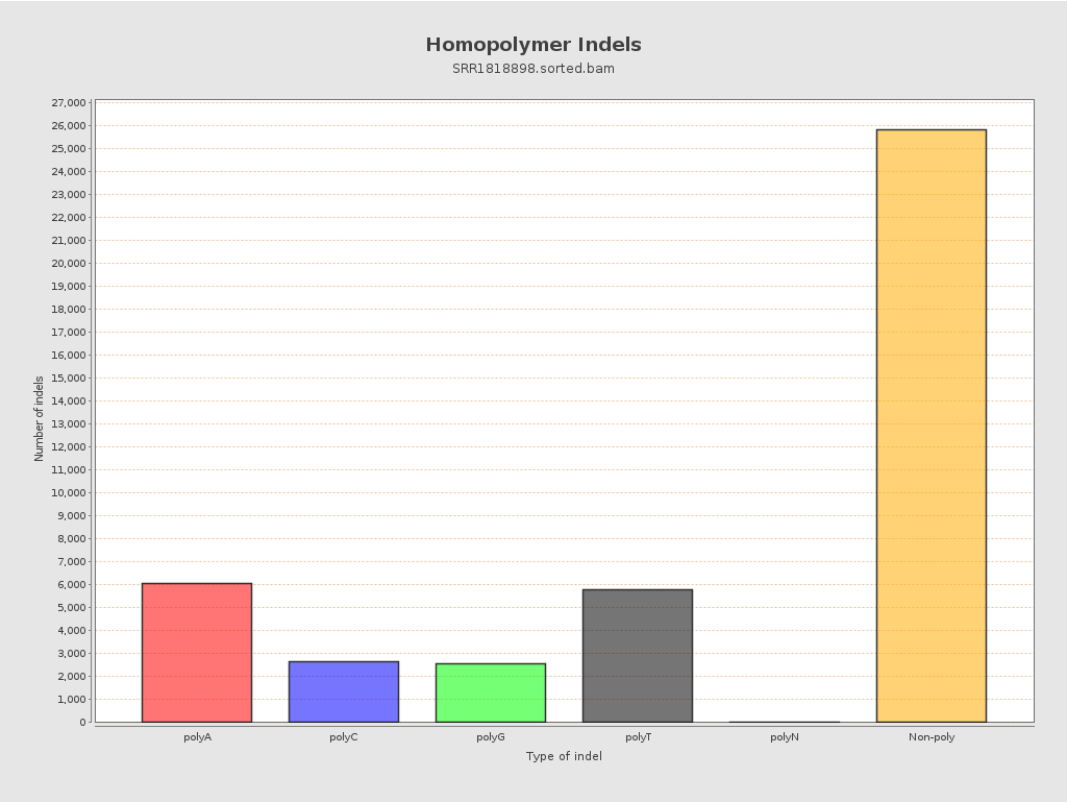
9. Results : Mapped Reads GC-content Distribution



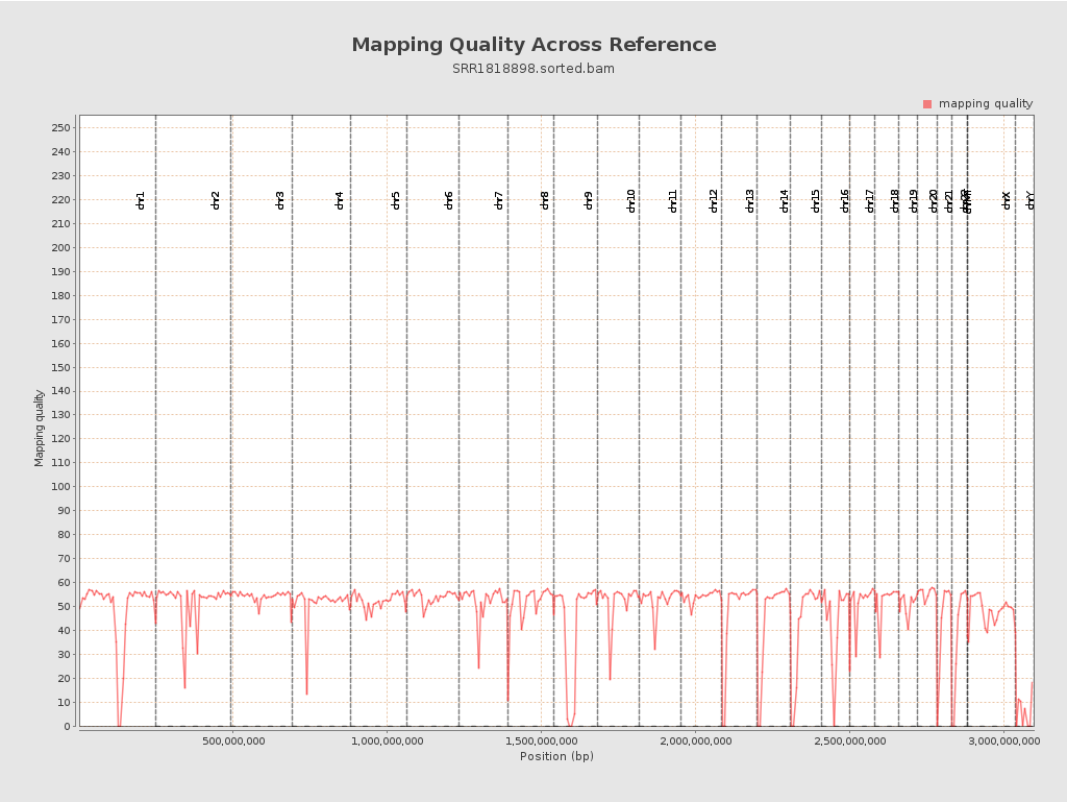
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram