Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818947.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_SRR1818947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818947.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:14:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,525,896
Mapped reads	1,277,899 / 83.75%
Unmapped reads	247,997 / 16.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,427 / 1.21%
Read min/max/mean length	30 / 101 / 101.46
Duplicated reads (estimated)	404,549 / 26.51%
Duplication rate	27.7%
Clipped reads	1,291,570 / 84.64%

2.2. ACGT Content

Number/percentage of A's	34,915,908 / 29.54%
Number/percentage of C's	24,050,038 / 20.35%
Number/percentage of T's	33,625,795 / 28.45%
Number/percentage of G's	25,592,033 / 21.65%
Number/percentage of N's	5,476 / 0%
GC Percentage	42%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.4486

2.4. Mapping Quality

Mean Mapping Quality	49.35

2.5. Mismatches and indels

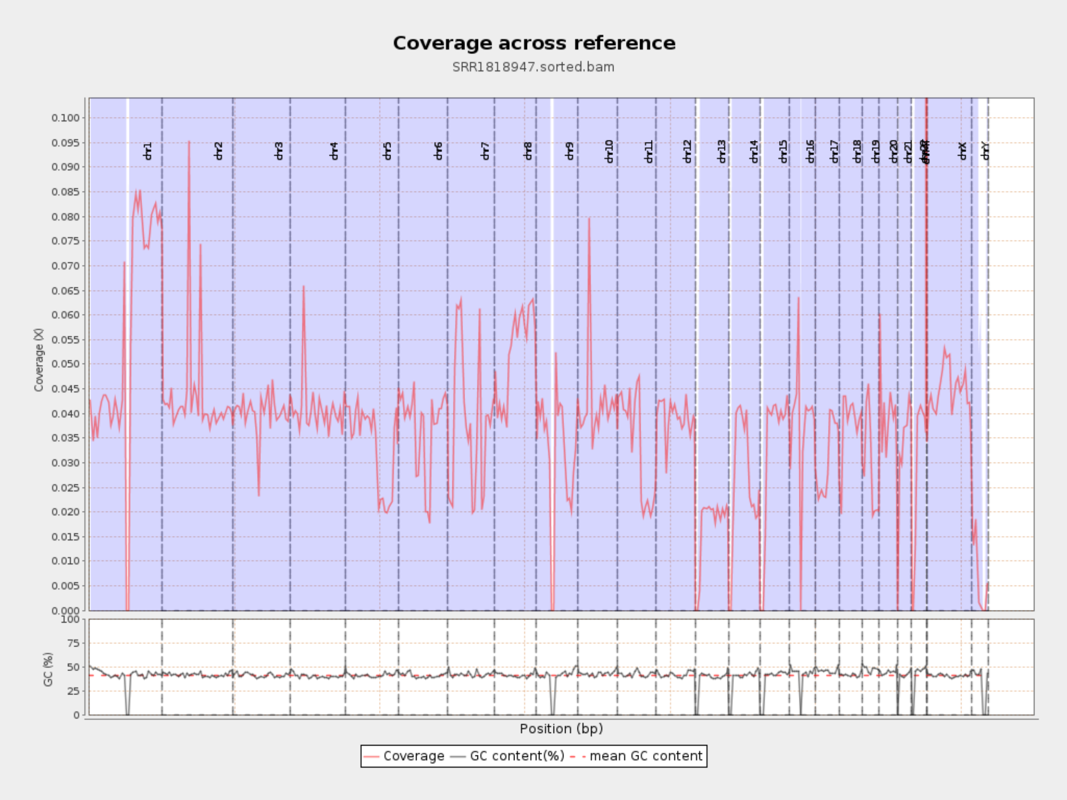
General error rate	0.67%
Mismatches	759,741
Insertions	14,668
Mapped reads with at least one insertion	1.11%
Deletions	37,661
Mapped reads with at least one deletion	2.88%
Homopolymer indels	43.28%

2.6. Chromosome stats

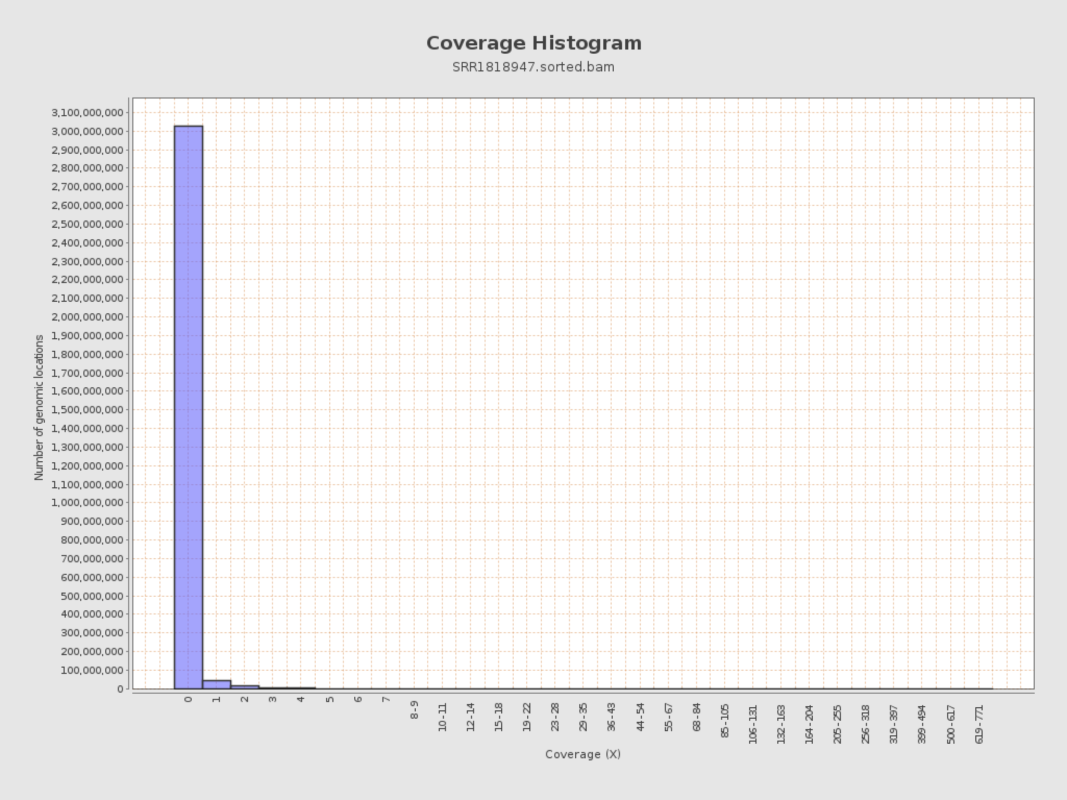
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13785951	0.0553	0.7298
chr2	243199373	10586951	0.0435	0.6931
chr3	198022430	7946149	0.0401	0.3022
chr4	191154276	7811922	0.0409	0.3386
chr5	180915260	6085186	0.0336	0.2811
chr6	171115067	6375331	0.0373	0.3126
chr7	159138663	6038593	0.0379	0.3754

chr8	146364022	7743188	0.0529	0.4075
chr9	141213431	4423829	0.0313	0.497
chr10	135534747	5703548	0.0421	0.5501
chr11	135006516	4538620	0.0336	0.3254
chr12	133851895	5260754	0.0393	0.3052
chr13	115169878	1947100	0.0169	0.1933
chr14	107349540	2816959	0.0262	0.2693
chr15	102531392	3370055	0.0329	0.273
chr16	90354753	3438640	0.0381	0.5274
chr17	81195210	2505089	0.0309	0.2961
chr18	78077248	2939976	0.0377	0.5631
chr19	59128983	1767286	0.0299	0.6066
chr20	63025520	2520251	0.04	0.315
chr21	48129895	1589611	0.033	0.2957
chr22	51304566	1418881	0.0277	0.267
chrMT	16571	299001	18.0436	12.0428
chrX	155270560	6956716	0.0448	0.3779
chrY	59373566	389446	0.0066	0.4125

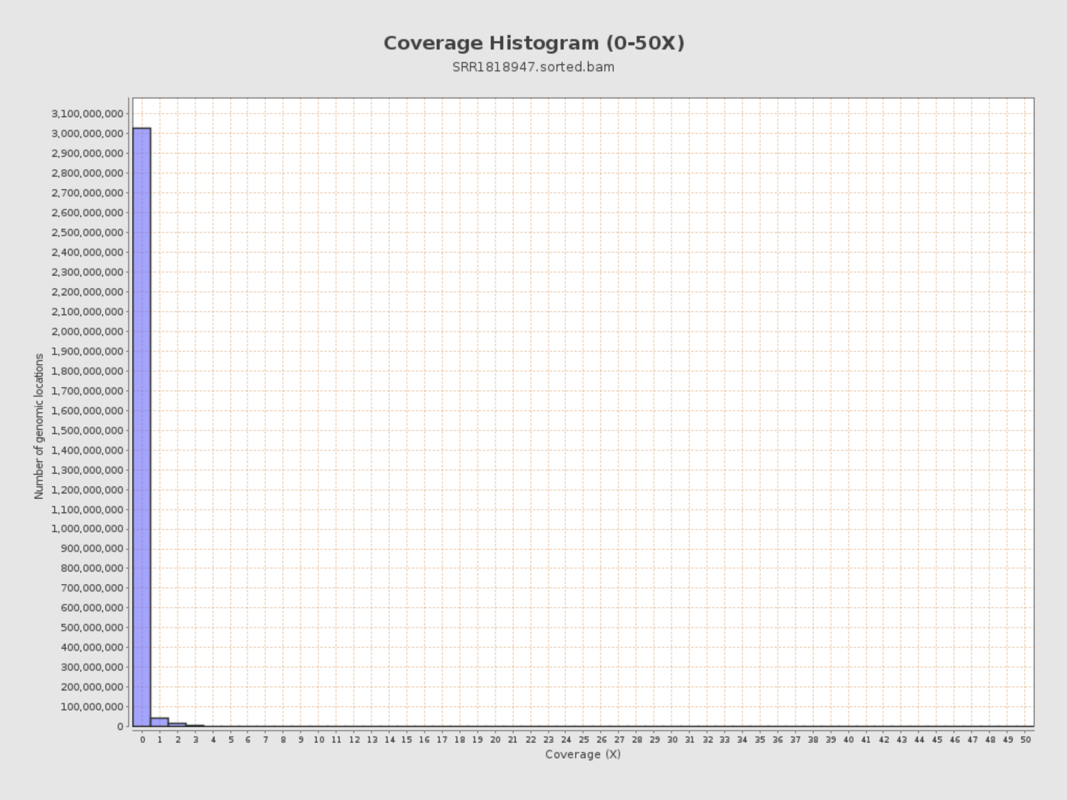
3. Results : Coverage across reference



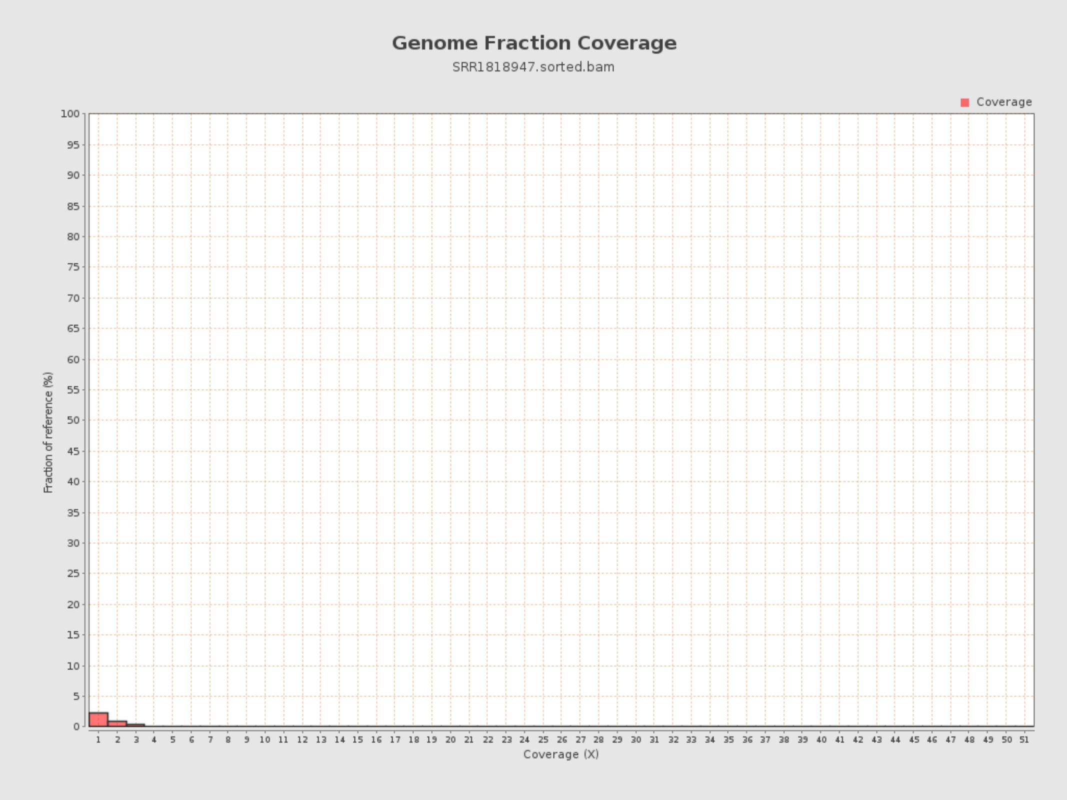
4. Results : Coverage Histogram



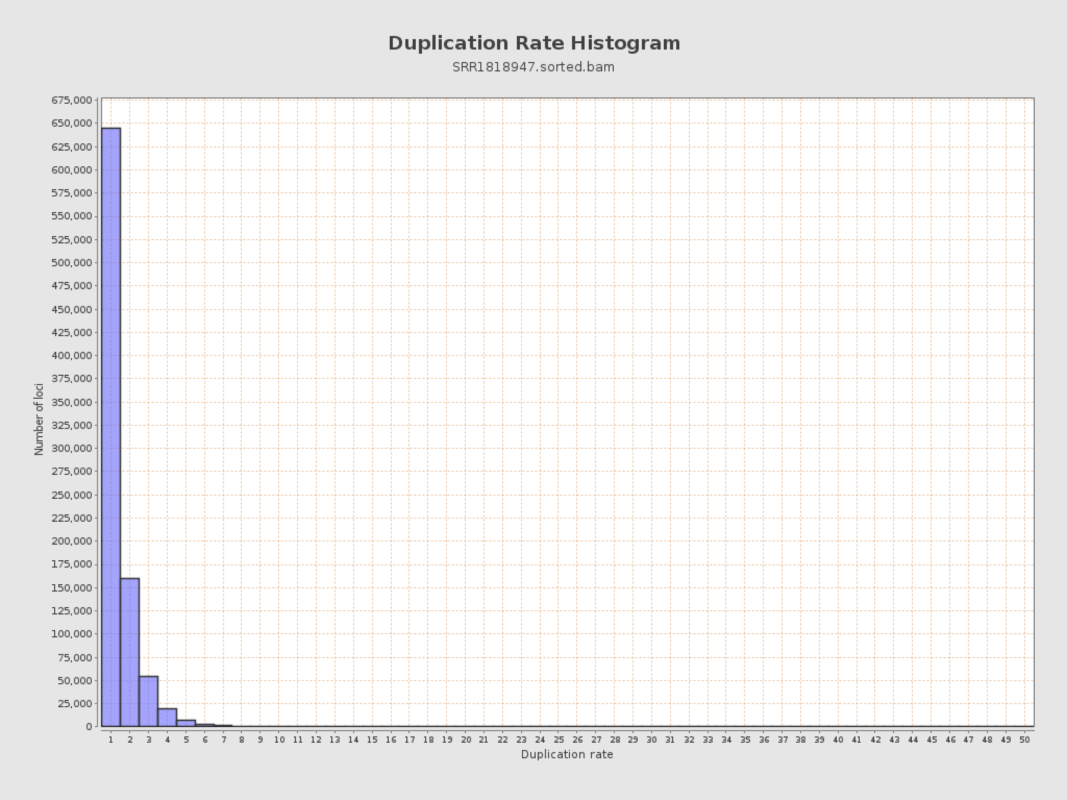
5. Results : Coverage Histogram (0-50X)



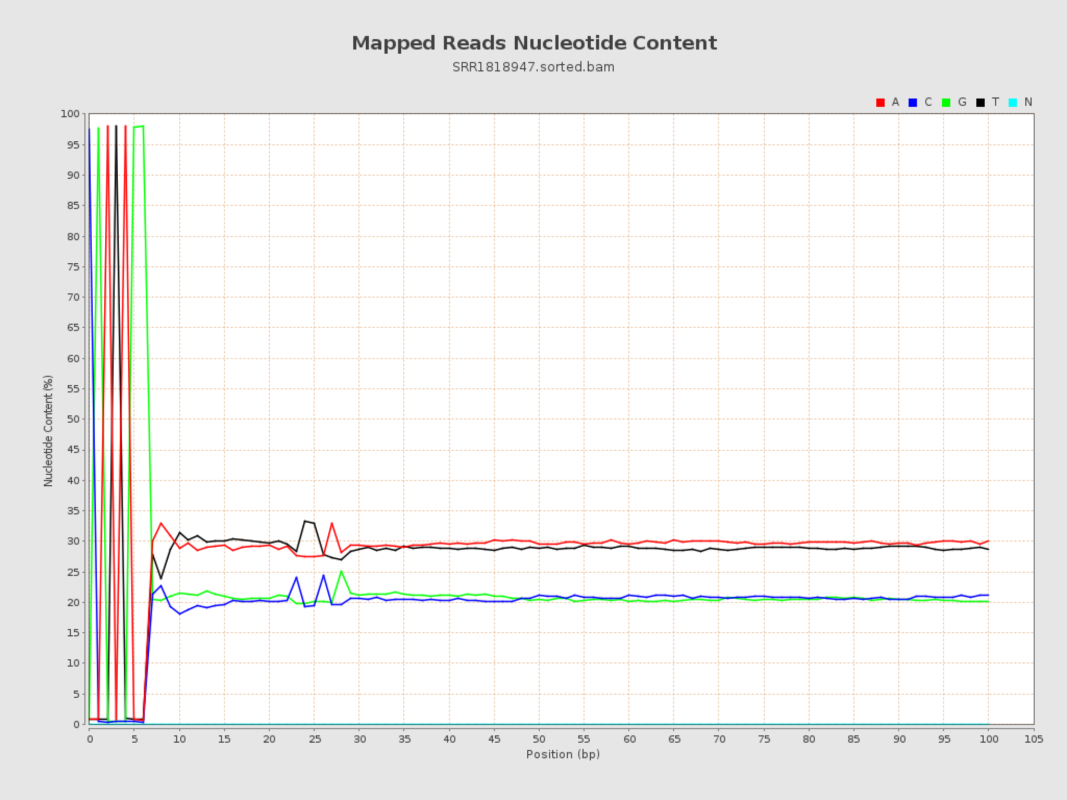
6. Results : Genome Fraction Coverage



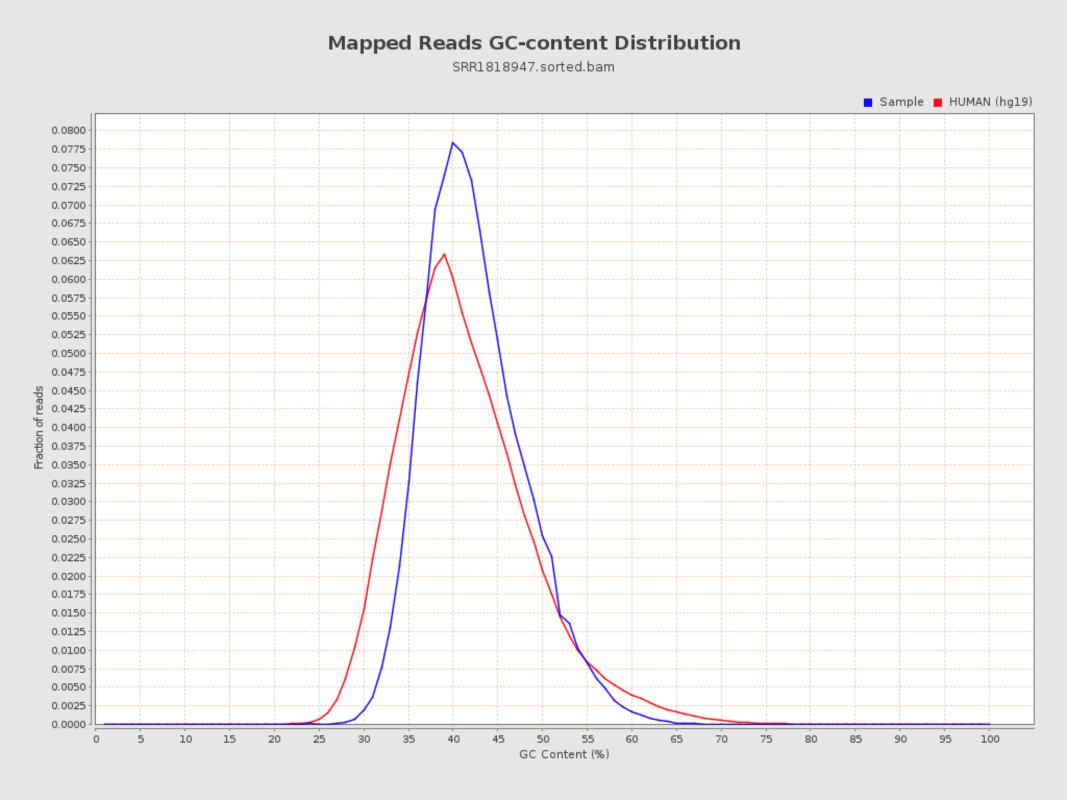
7. Results : Duplication Rate Histogram



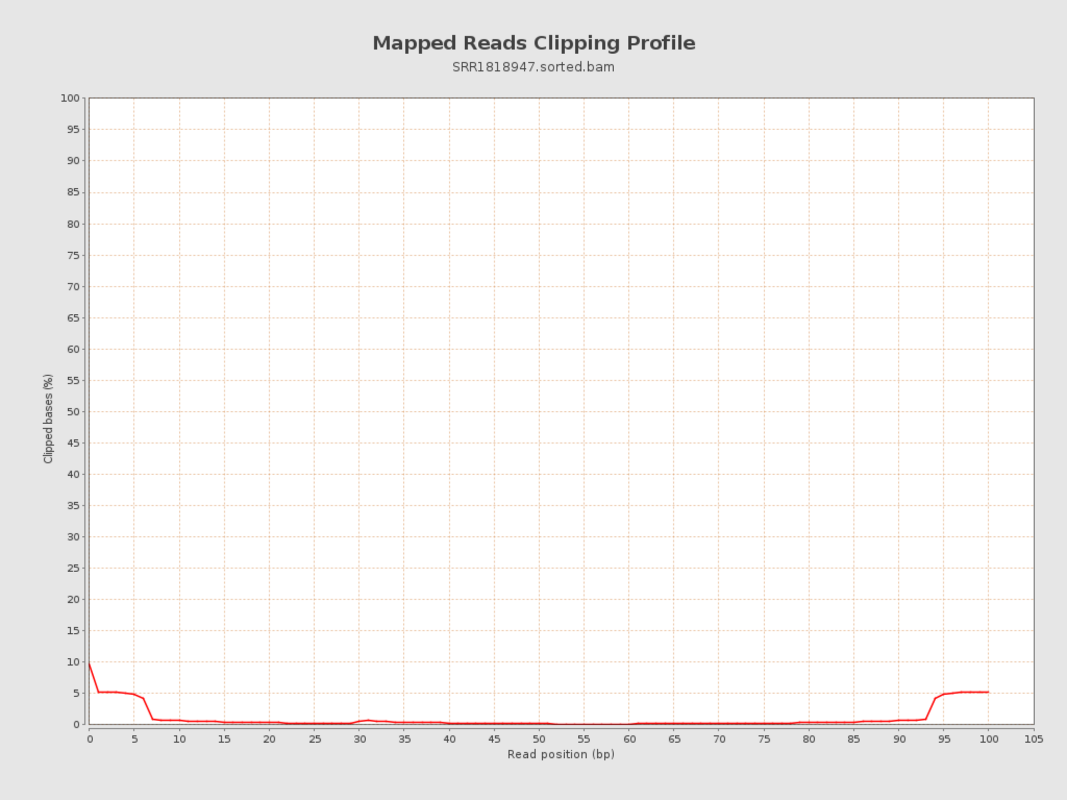
8. Results : Mapped Reads Nucleotide Content



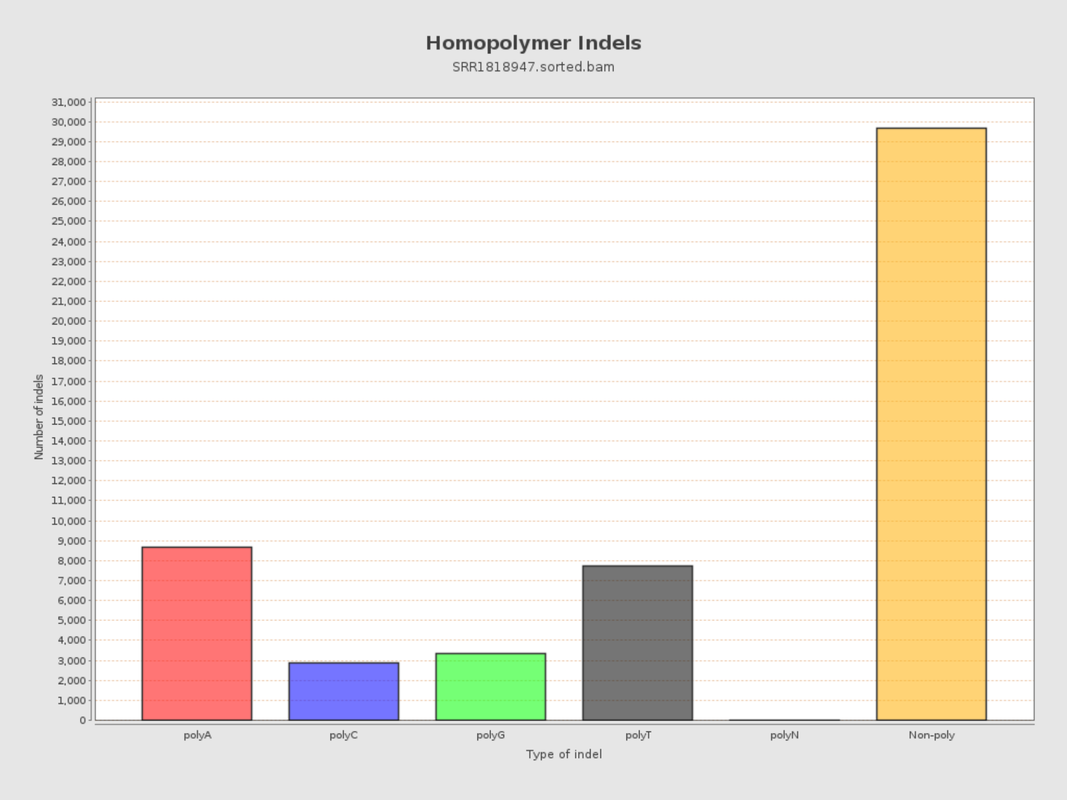
9. Results : Mapped Reads GC-content Distribution



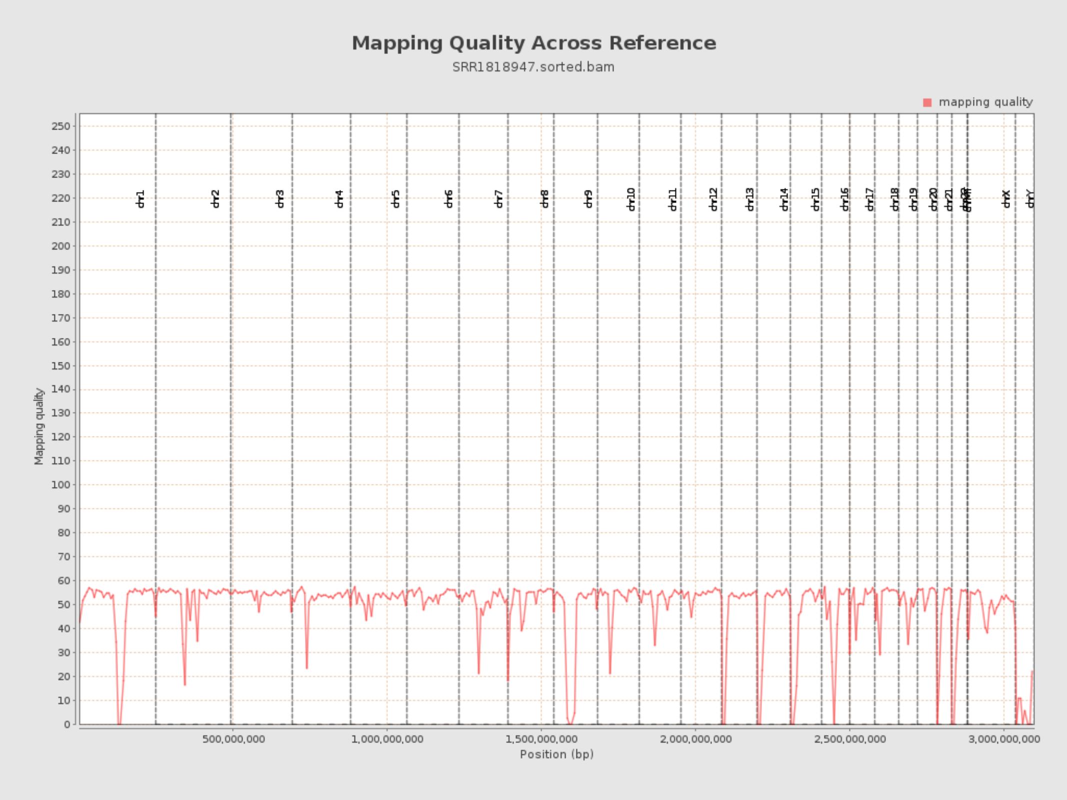
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram