Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:55:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708644.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_SRR1708644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708644.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:55:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,202,992
Mapped reads	4,020,701 / 95.66%
Unmapped reads	182,291 / 4.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	122 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	18,489 / 0.44%
Duplication rate	0.46%
Clipped reads	54,163 / 1.29%

2.2. ACGT Content

Number/percentage of A's	62,002,591 / 30.92%
Number/percentage of C's	38,088,571 / 19%
Number/percentage of T's	61,954,588 / 30.9%
Number/percentage of G's	38,464,033 / 19.18%
Number/percentage of N's	6,816 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	0.0648

Standard Deviation	0.2637

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

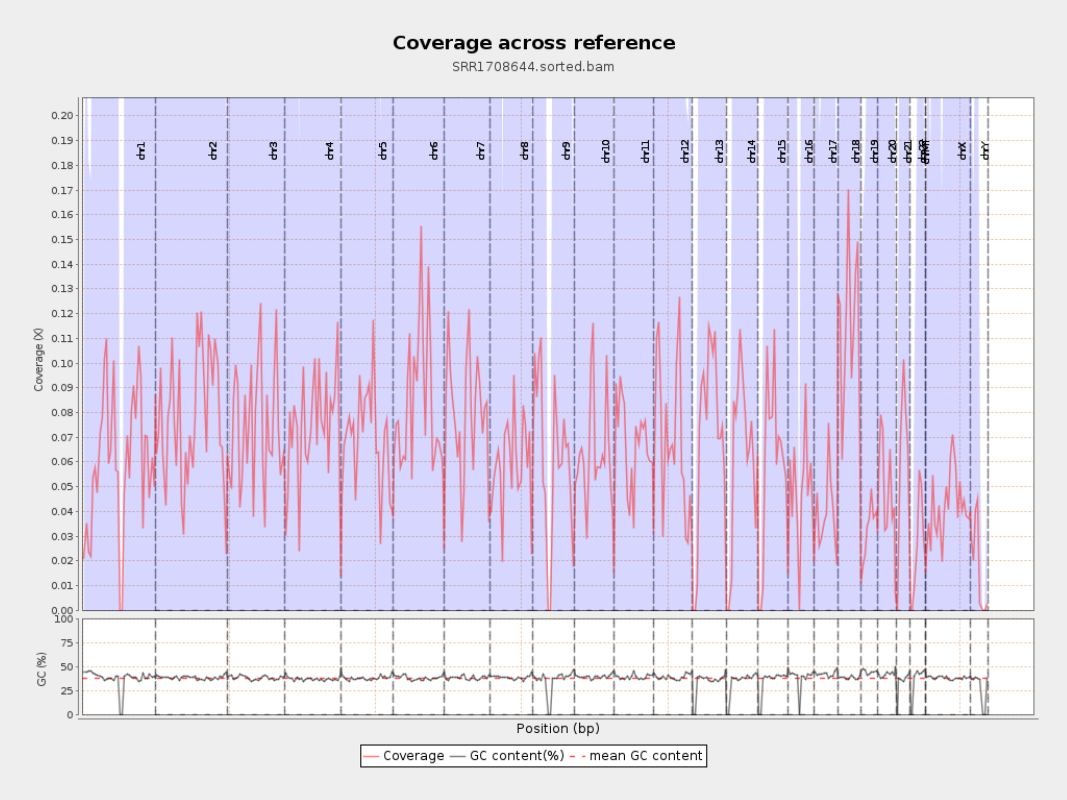
General error rate	0.17%
Mismatches	328,943
Insertions	13,787
Mapped reads with at least one insertion	0.34%
Deletions	11,648
Mapped reads with at least one deletion	0.29%
Homopolymer indels	49.13%

2.6. Chromosome stats

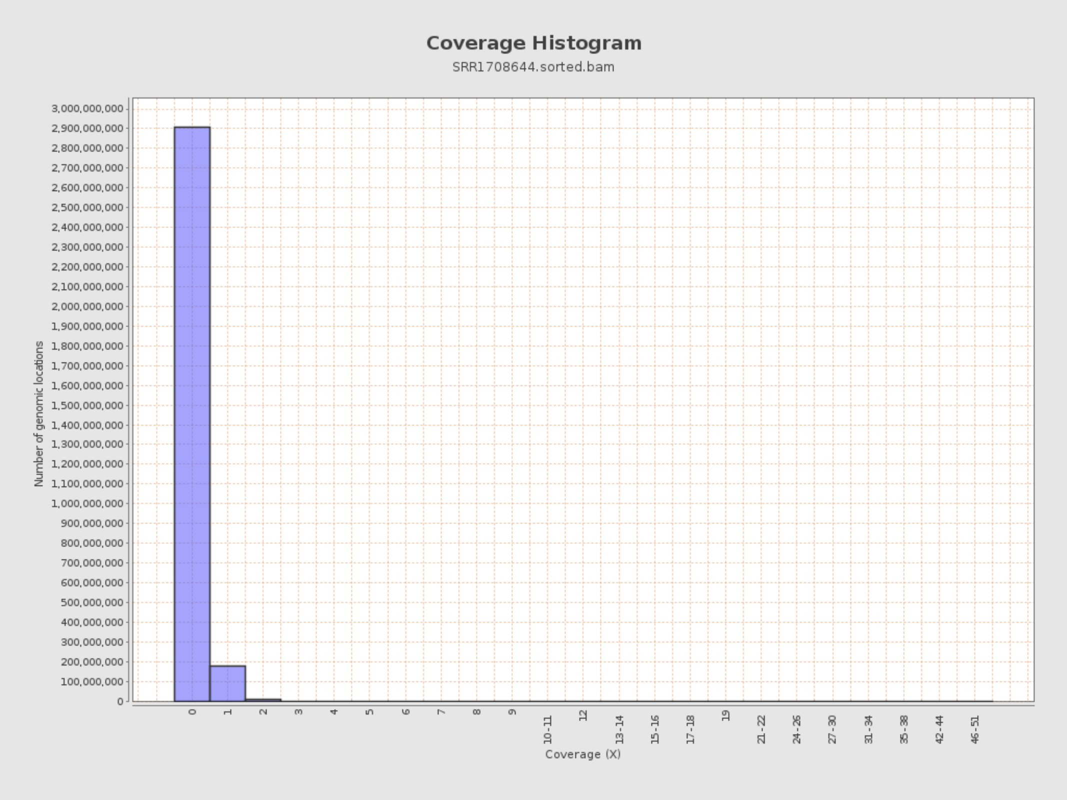
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14942822	0.06	0.2544
chr2	243199373	18909489	0.0778	0.2884
chr3	198022430	14771137	0.0746	0.2817
chr4	191154276	14173595	0.0741	0.28
chr5	180915260	12383761	0.0685	0.2691
chr6	171115067	14451763	0.0845	0.3005
chr7	159138663	12397676	0.0779	0.2894

chr8	146364022	8719848	0.0596	0.2504
chr9	141213431	8681643	0.0615	0.257
chr10	135534747	8747477	0.0645	0.2618
chr11	135006516	9028684	0.0669	0.2681
chr12	133851895	9180921	0.0686	0.2708
chr13	115169878	8252387	0.0717	0.2772
chr14	107349540	6660371	0.062	0.2588
chr15	102531392	6010898	0.0586	0.253
chr16	90354753	4247615	0.047	0.2244
chr17	81195210	3257651	0.0401	0.2072
chr18	78077248	8995229	0.1152	0.3529
chr19	59128983	1942578	0.0329	0.1871
chr20	63025520	3131426	0.0497	0.2299
chr21	48129895	2730054	0.0567	0.2476
chr22	51304566	1374793	0.0268	0.1698
chrMT	16571	246	0.0148	0.1209
chrX	155270560	6533544	0.0421	0.2104
chrY	59373566	1011074	0.017	0.1348

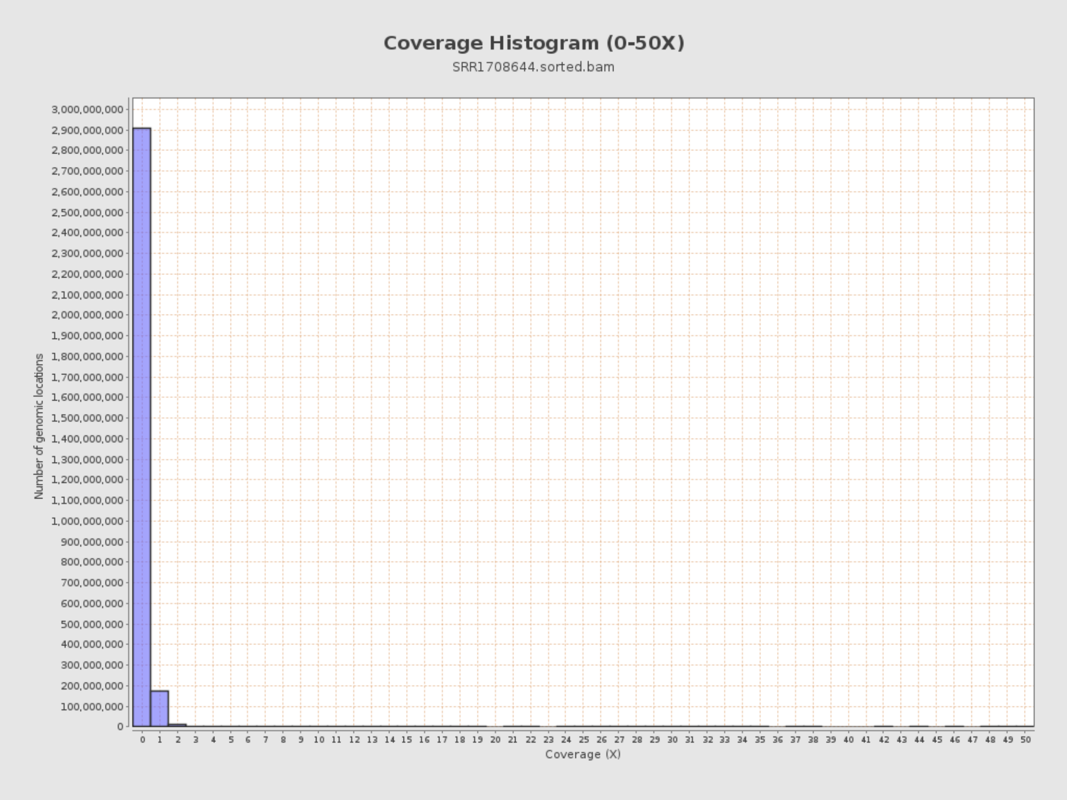
3. Results : Coverage across reference



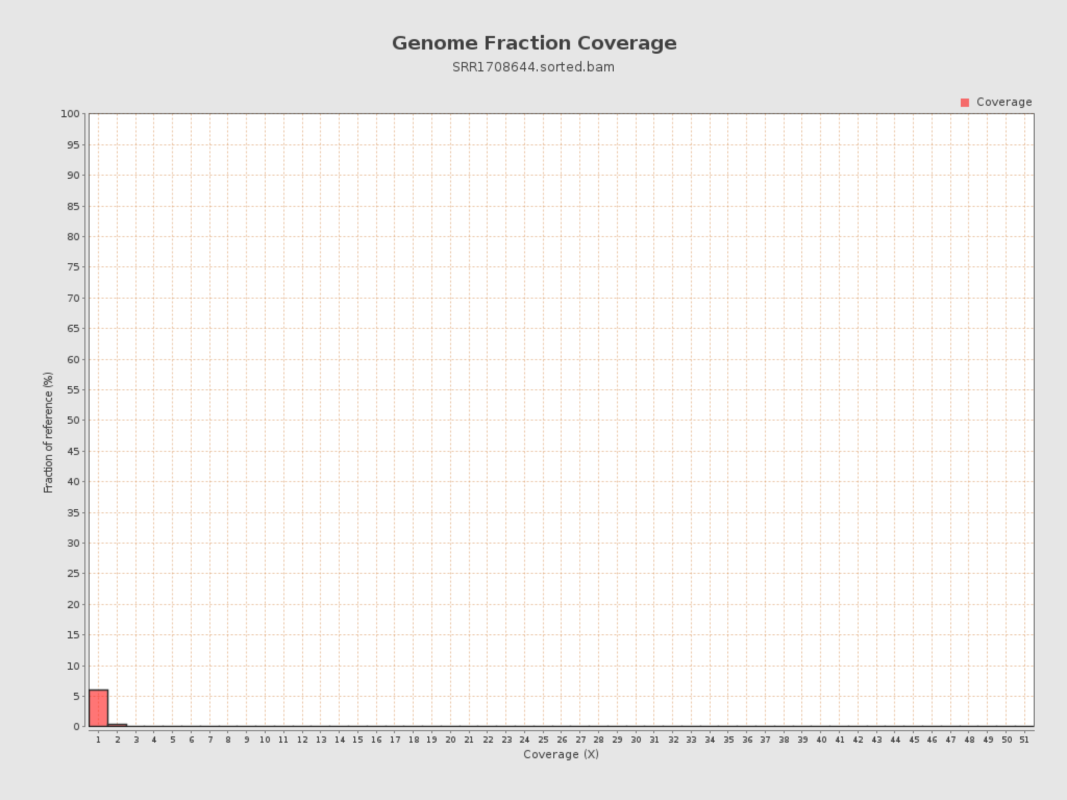
4. Results : Coverage Histogram



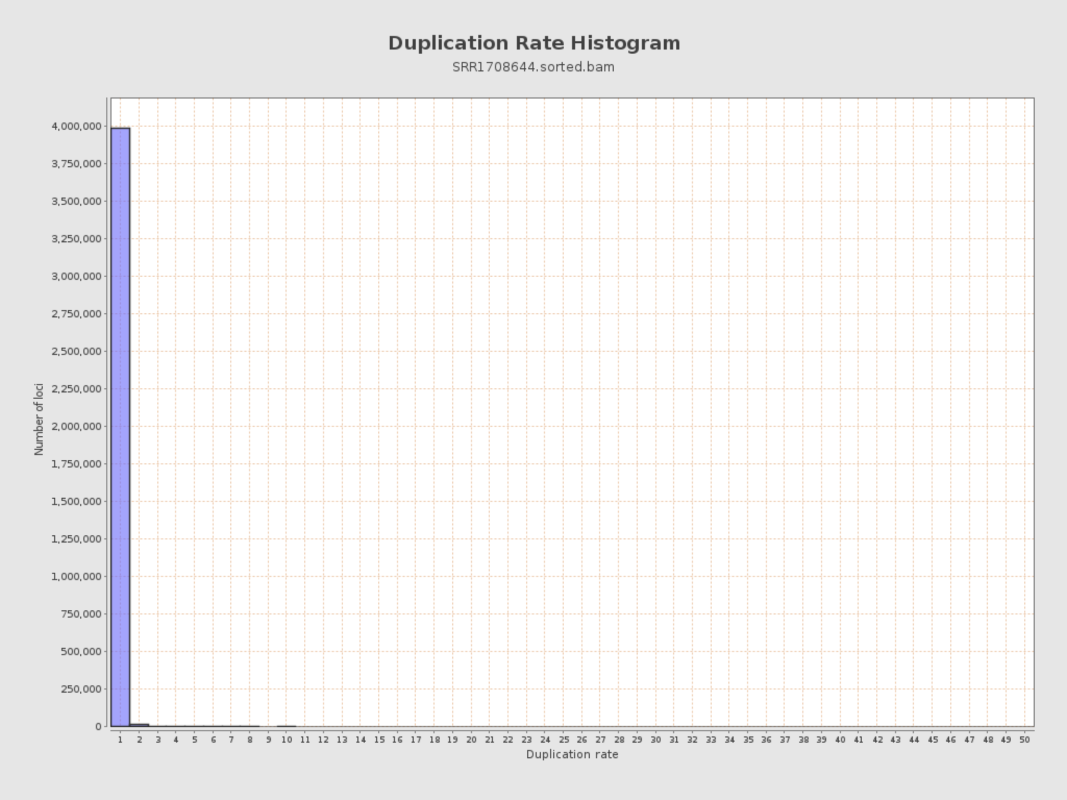
5. Results : Coverage Histogram (0-50X)



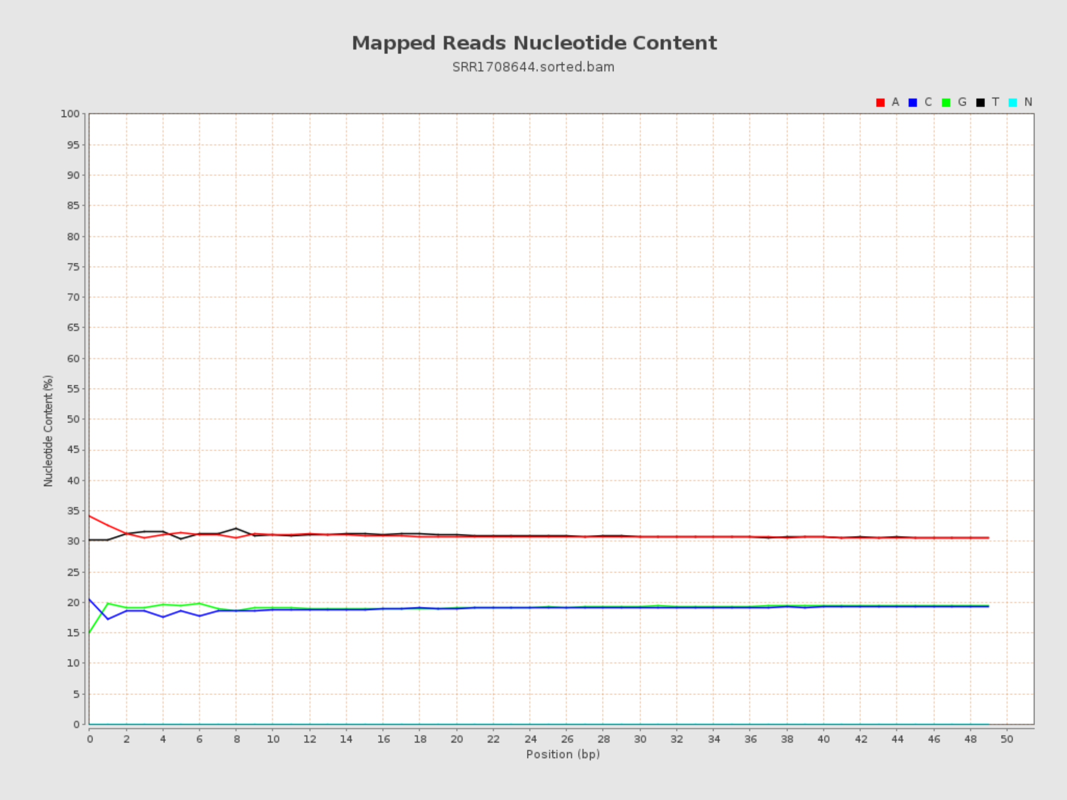
6. Results : Genome Fraction Coverage



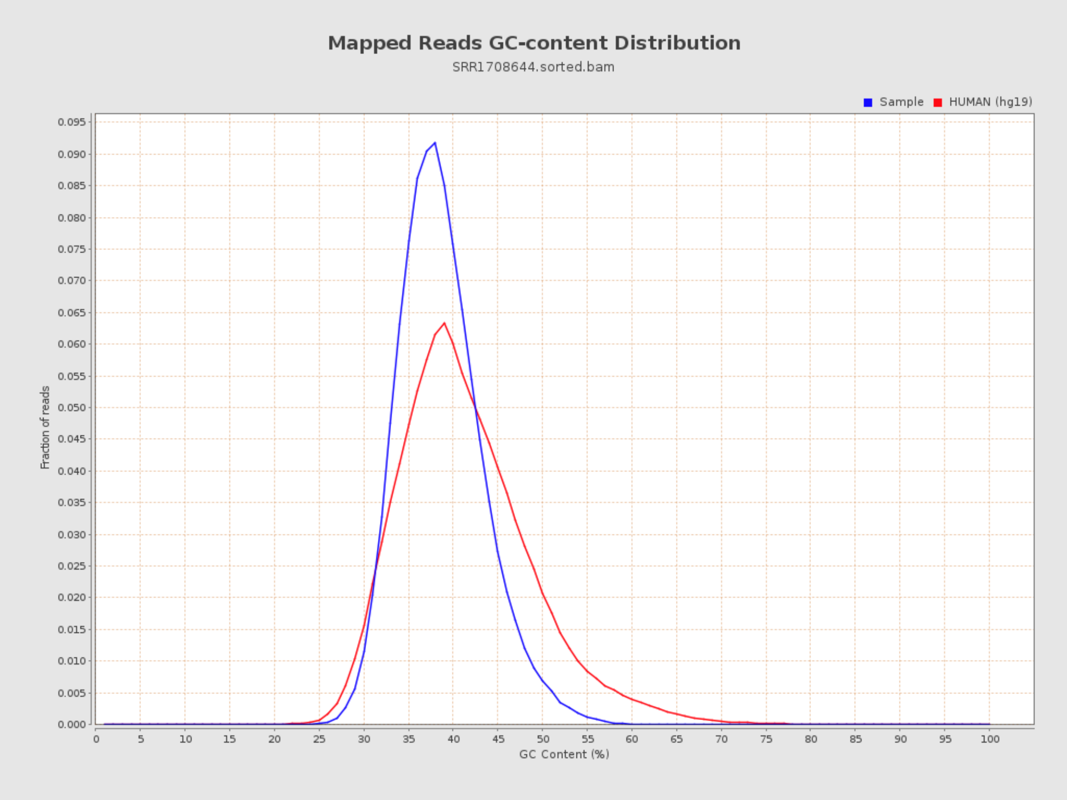
7. Results : Duplication Rate Histogram



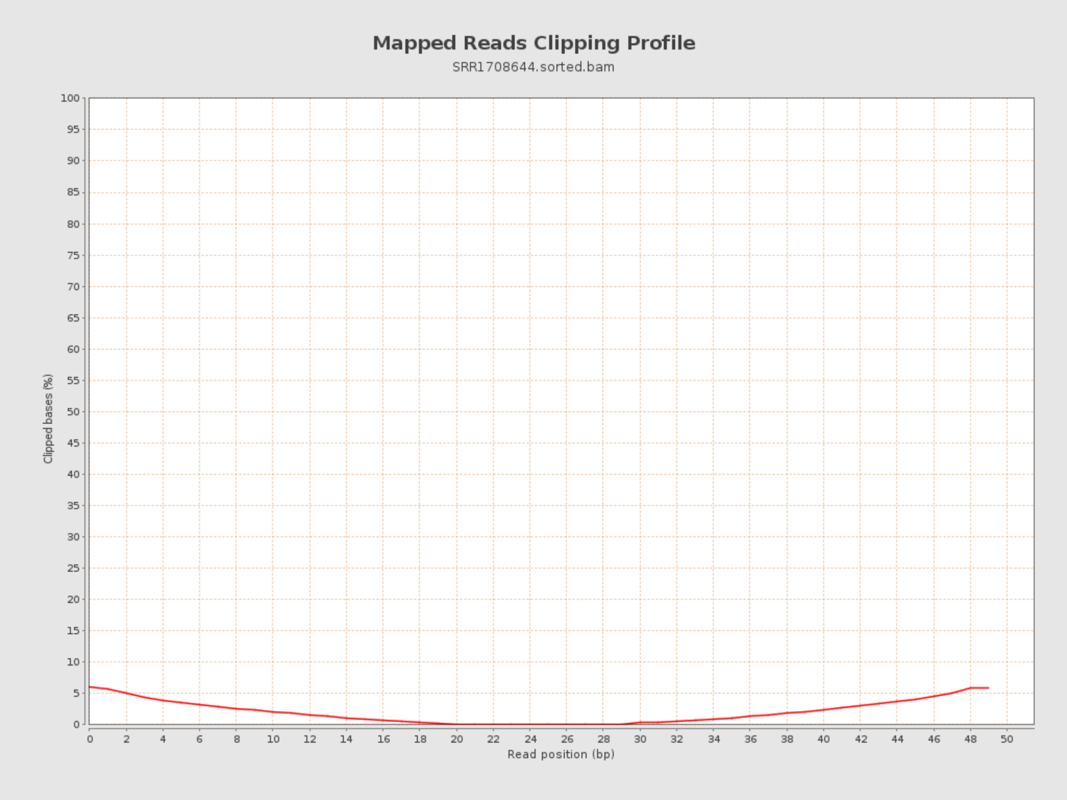
8. Results : Mapped Reads Nucleotide Content



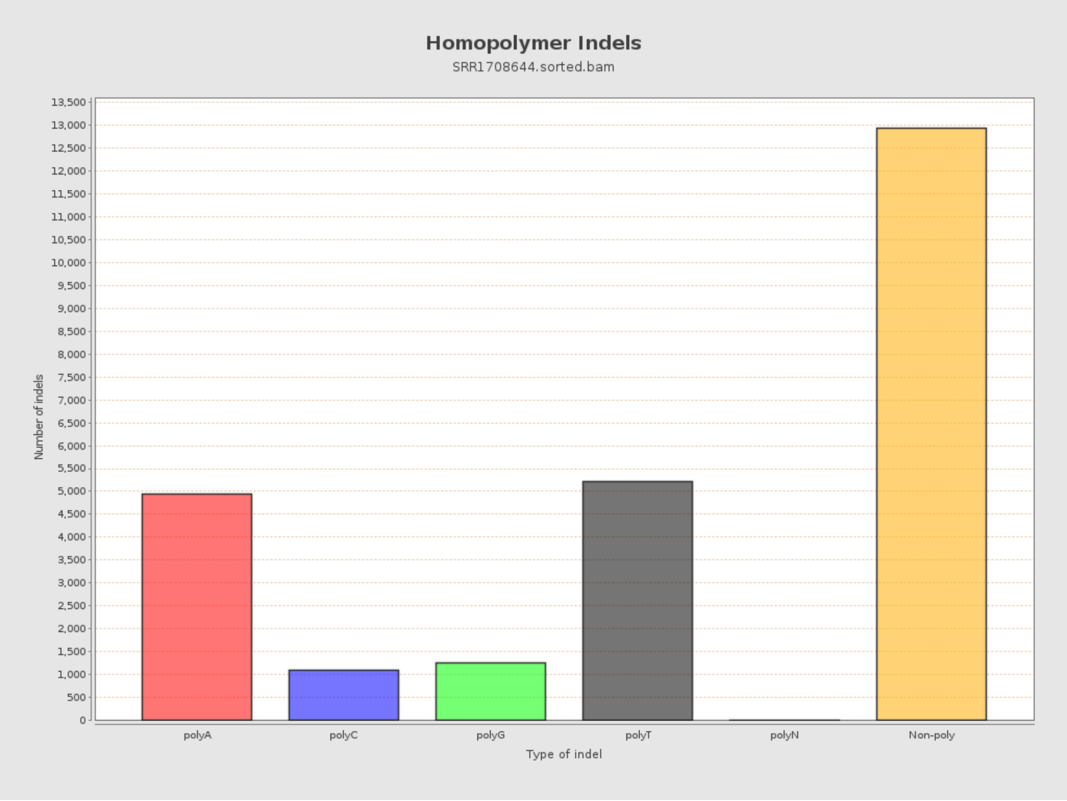
9. Results : Mapped Reads GC-content Distribution



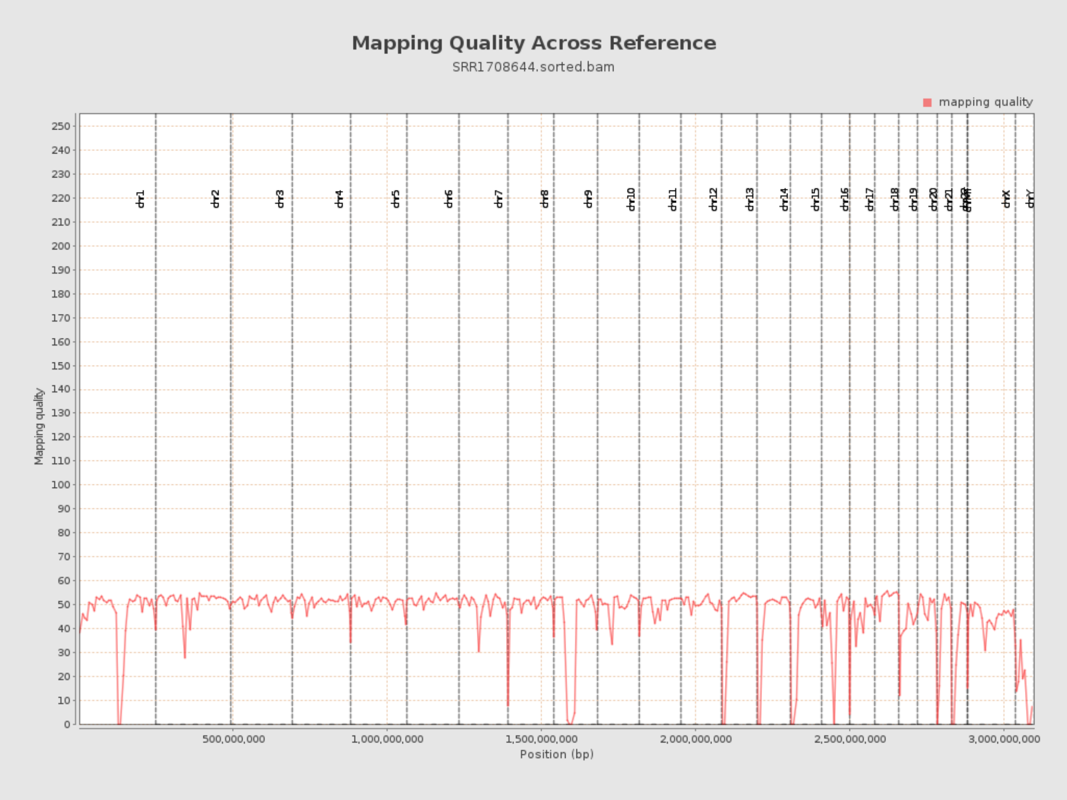
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram