Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:15:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708648.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_SRR1708648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:15:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,390,026
Mapped reads	4,167,744 / 94.94%
Unmapped reads	222,282 / 5.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	129 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	21,541 / 0.49%
Duplication rate	0.51%
Clipped reads	56,018 / 1.28%

2.2. ACGT Content

Number/percentage of A's	64,075,117 / 30.83%
Number/percentage of C's	39,692,686 / 19.1%
Number/percentage of T's	64,049,948 / 30.82%
Number/percentage of G's	40,025,304 / 19.26%
Number/percentage of N's	7,007 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	0.0671

Standard Deviation	0.2749

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

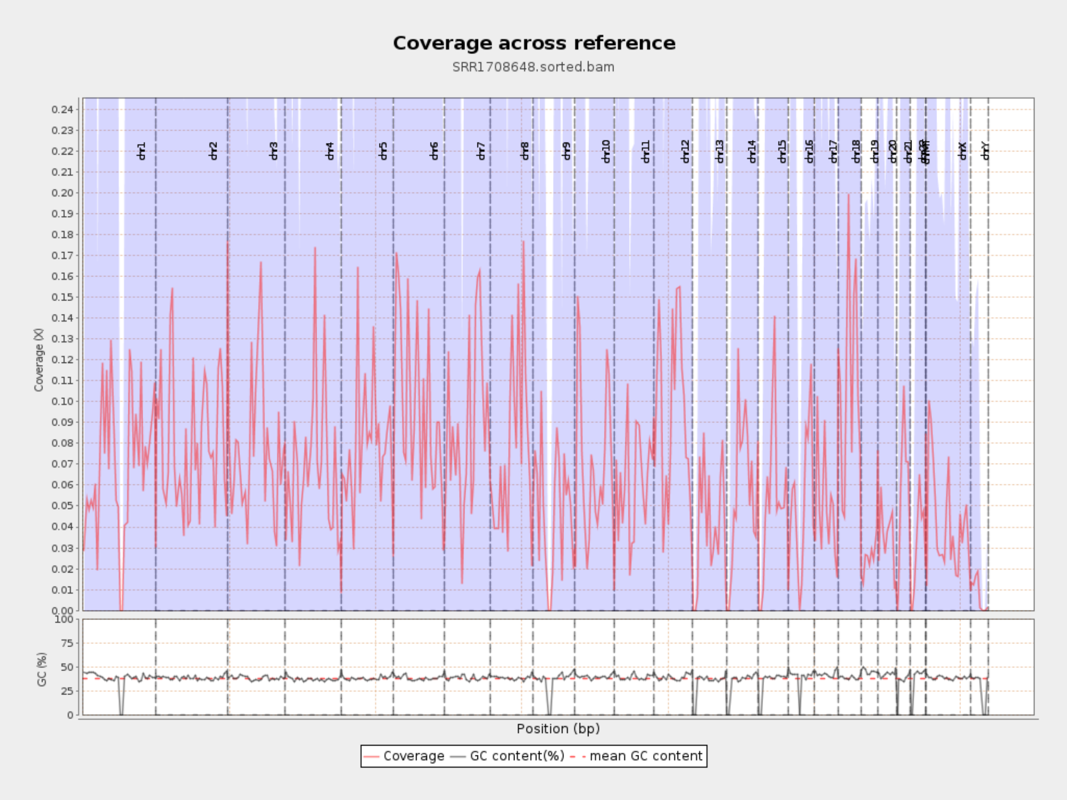
General error rate	0.17%
Mismatches	338,727
Insertions	14,256
Mapped reads with at least one insertion	0.34%
Deletions	11,865
Mapped reads with at least one deletion	0.28%
Homopolymer indels	49.39%

2.6. Chromosome stats

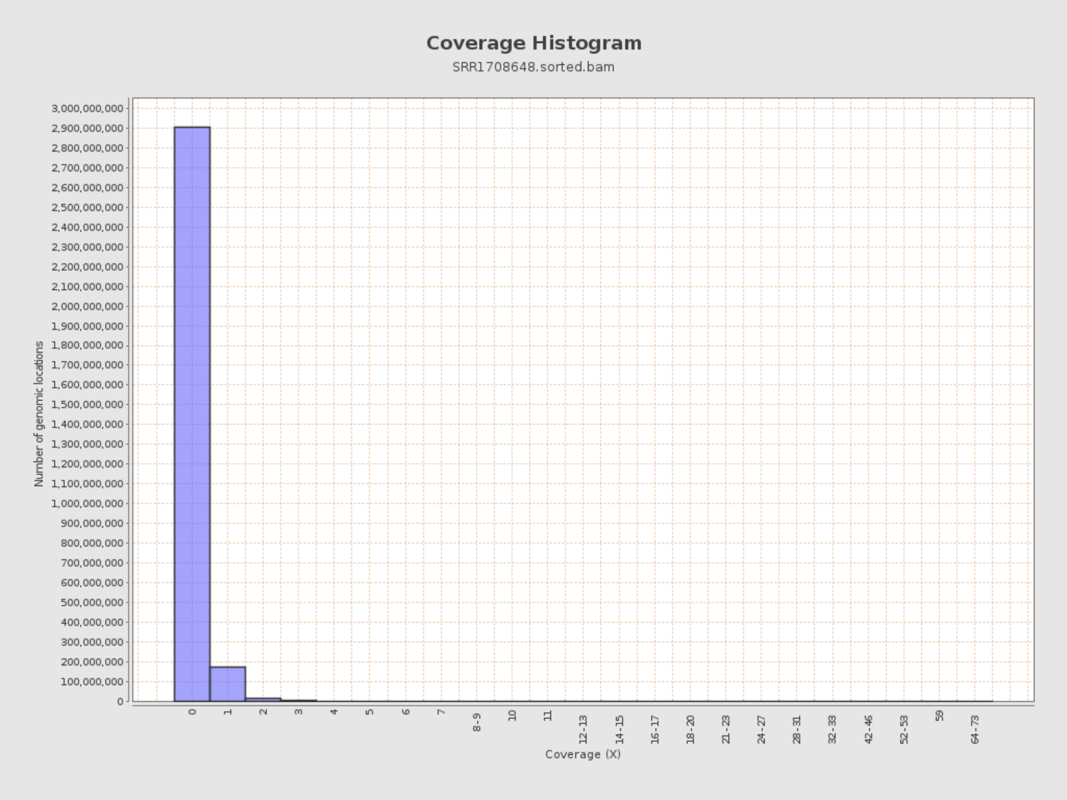
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17506697	0.0702	0.282
chr2	243199373	19654907	0.0808	0.3009
chr3	198022430	15684583	0.0792	0.2961
chr4	191154276	12930570	0.0676	0.2741
chr5	180915260	14278667	0.0789	0.2961
chr6	171115067	16638707	0.0972	0.3322
chr7	159138663	13913377	0.0874	0.3135

chr8	146364022	11504427	0.0786	0.2973
chr9	141213431	6800545	0.0482	0.2312
chr10	135534747	9627664	0.071	0.2827
chr11	135006516	8020368	0.0594	0.2587
chr12	133851895	12662725	0.0946	0.3249
chr13	115169878	4754855	0.0413	0.2125
chr14	107349540	6096677	0.0568	0.2522
chr15	102531392	5403261	0.0527	0.2434
chr16	90354753	4466278	0.0494	0.2338
chr17	81195210	4044713	0.0498	0.2351
chr18	78077248	8724135	0.1117	0.3549
chr19	59128983	1611109	0.0272	0.1714
chr20	63025520	2212572	0.0351	0.1936
chr21	48129895	2633190	0.0547	0.2484
chr22	51304566	1664284	0.0324	0.189
chrMT	16571	1400	0.0845	0.3018
chrX	155270560	6574116	0.0423	0.2168
chrY	59373566	460488	0.0078	0.0903

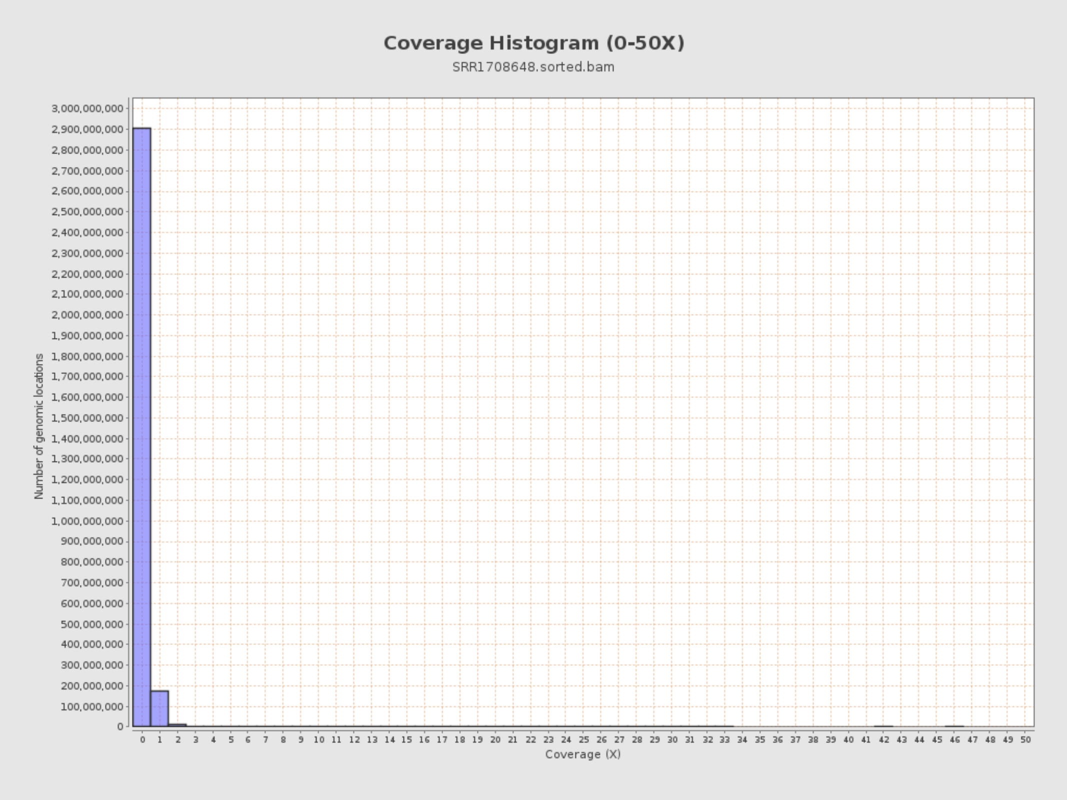
3. Results : Coverage across reference



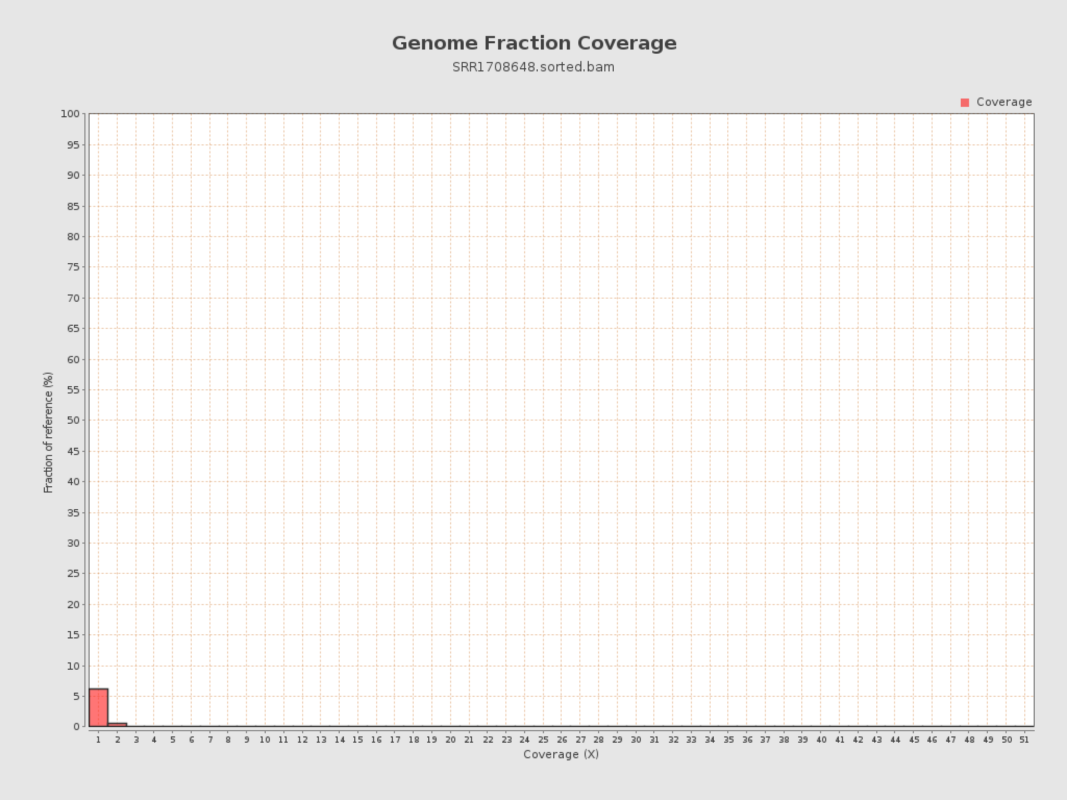
4. Results : Coverage Histogram



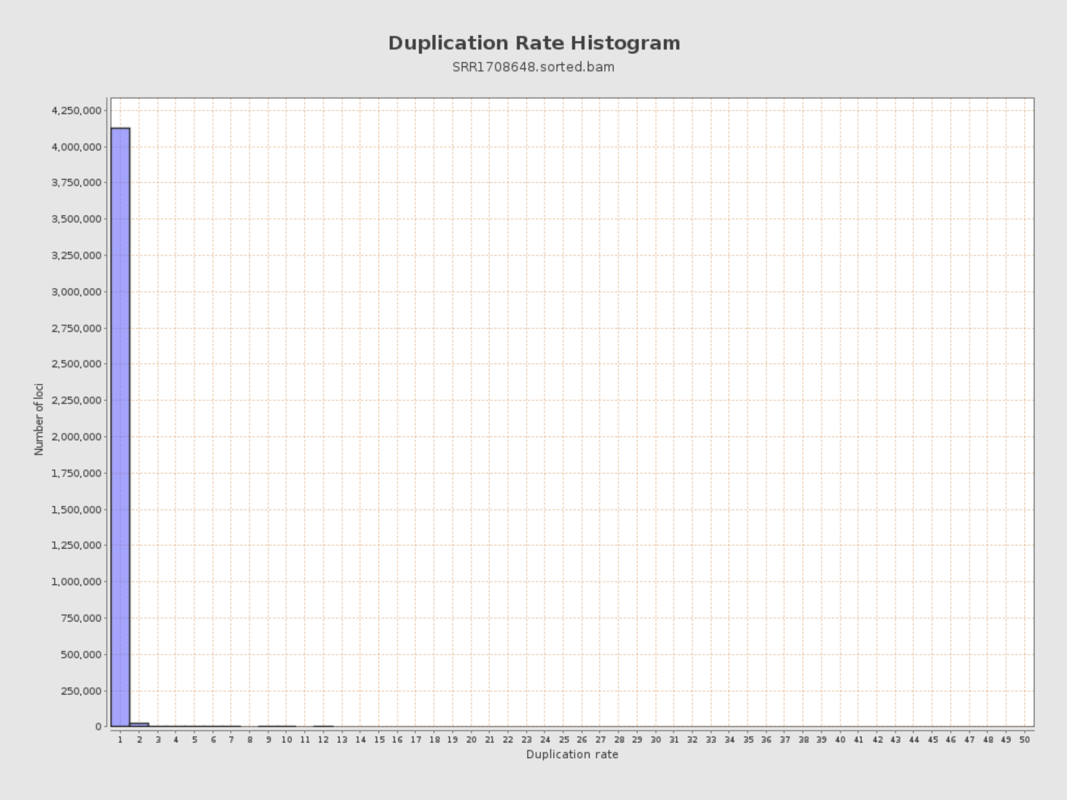
5. Results : Coverage Histogram (0-50X)



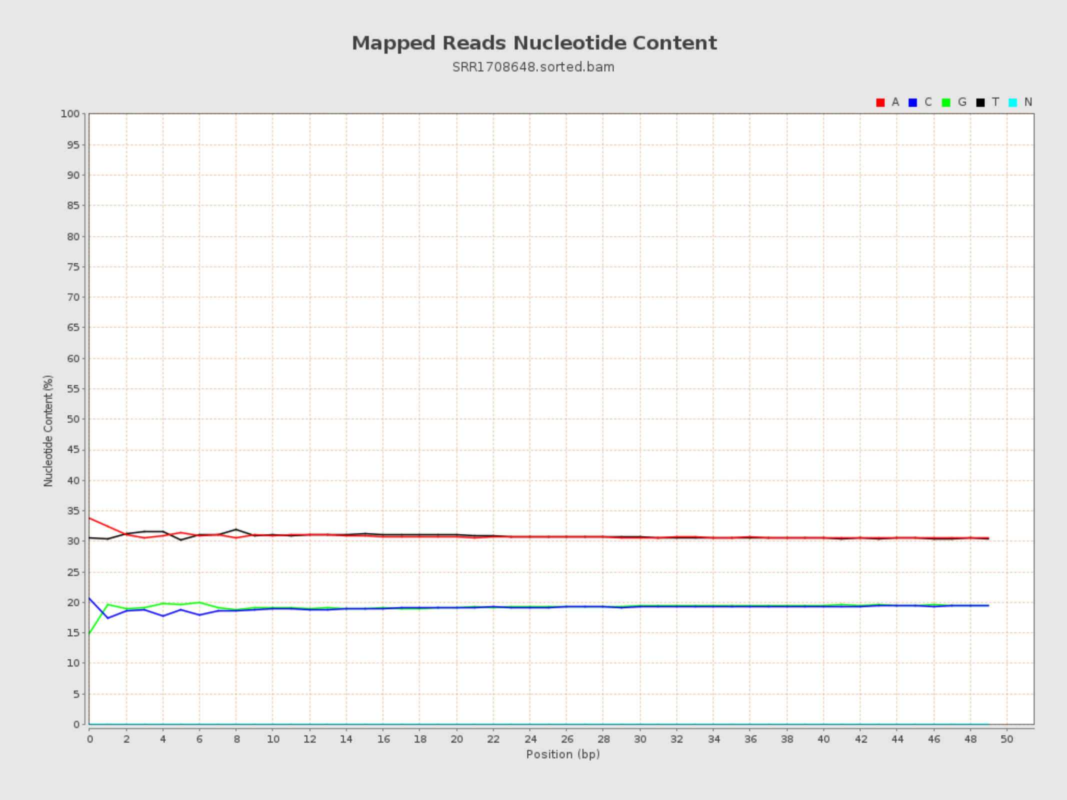
6. Results : Genome Fraction Coverage



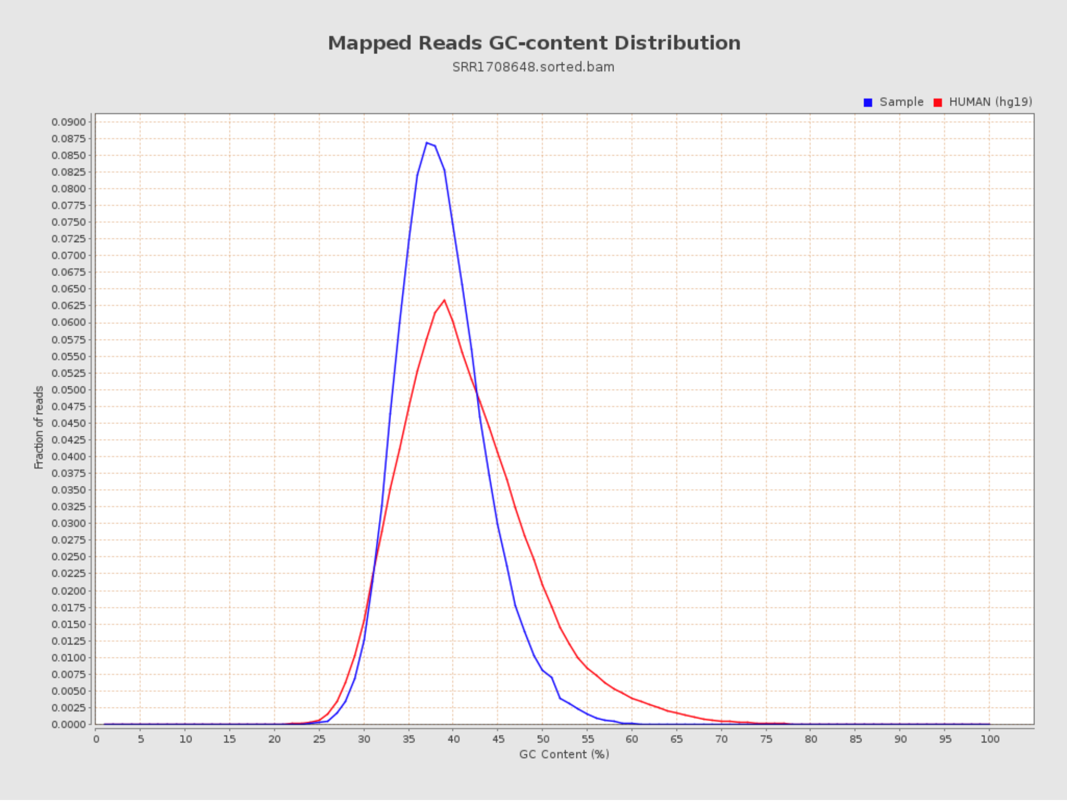
7. Results : Duplication Rate Histogram



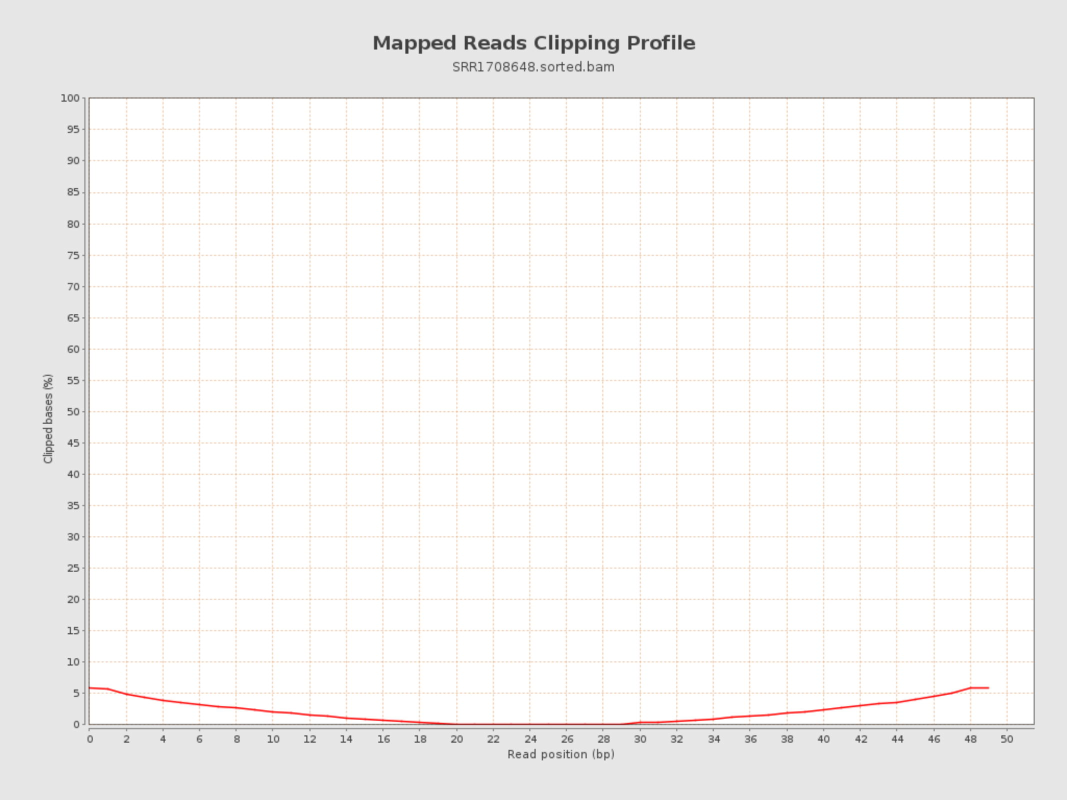
8. Results : Mapped Reads Nucleotide Content



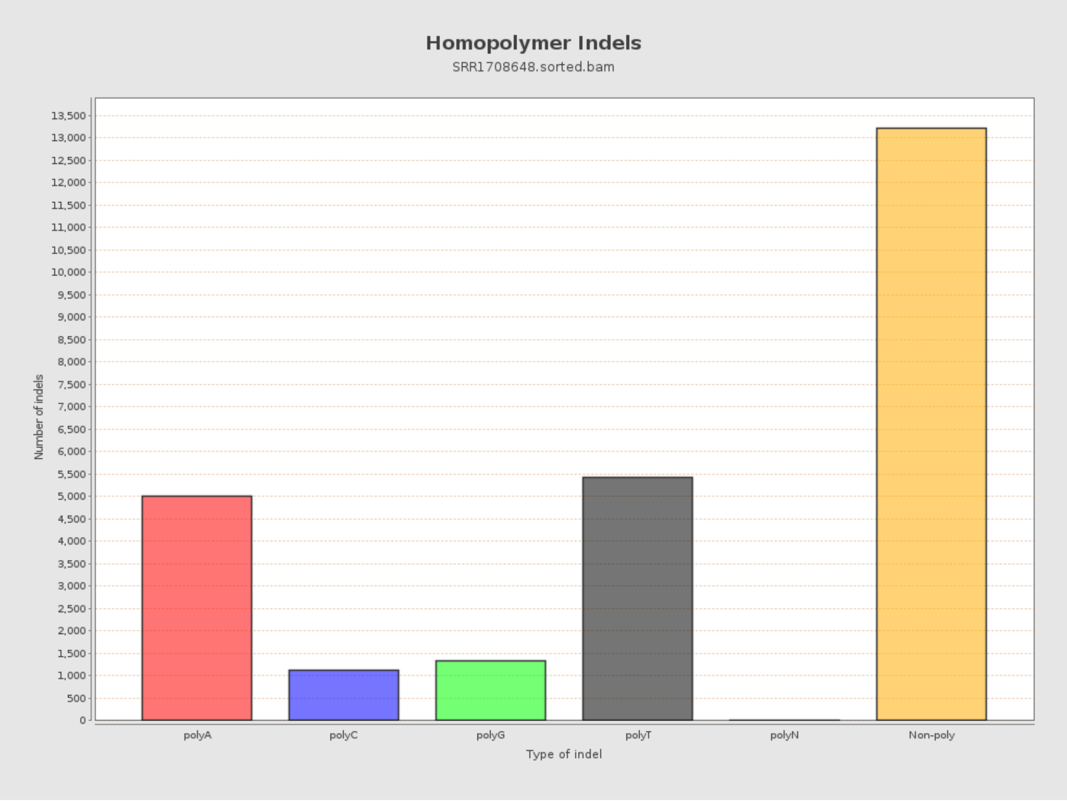
9. Results : Mapped Reads GC-content Distribution



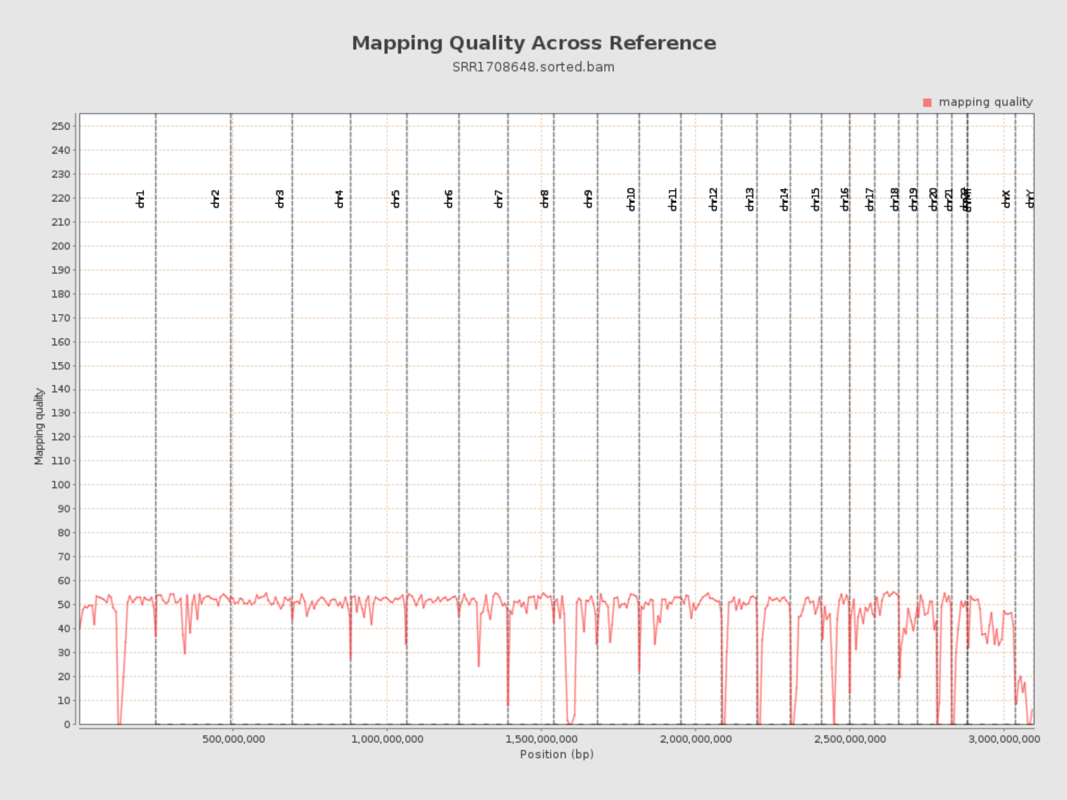
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram