Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:14:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708637.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_SRR1708637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708637.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:14:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,762,812
Mapped reads	4,407,836 / 92.55%
Unmapped reads	354,976 / 7.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	116 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	21,292 / 0.45%
Duplication rate	0.48%
Clipped reads	56,471 / 1.19%

2.2. ACGT Content

Number/percentage of A's	67,905,765 / 30.89%
Number/percentage of C's	41,831,703 / 19.03%
Number/percentage of T's	67,804,685 / 30.84%
Number/percentage of G's	42,294,472 / 19.24%
Number/percentage of N's	7,728 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	0.071

Standard Deviation	0.2782

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

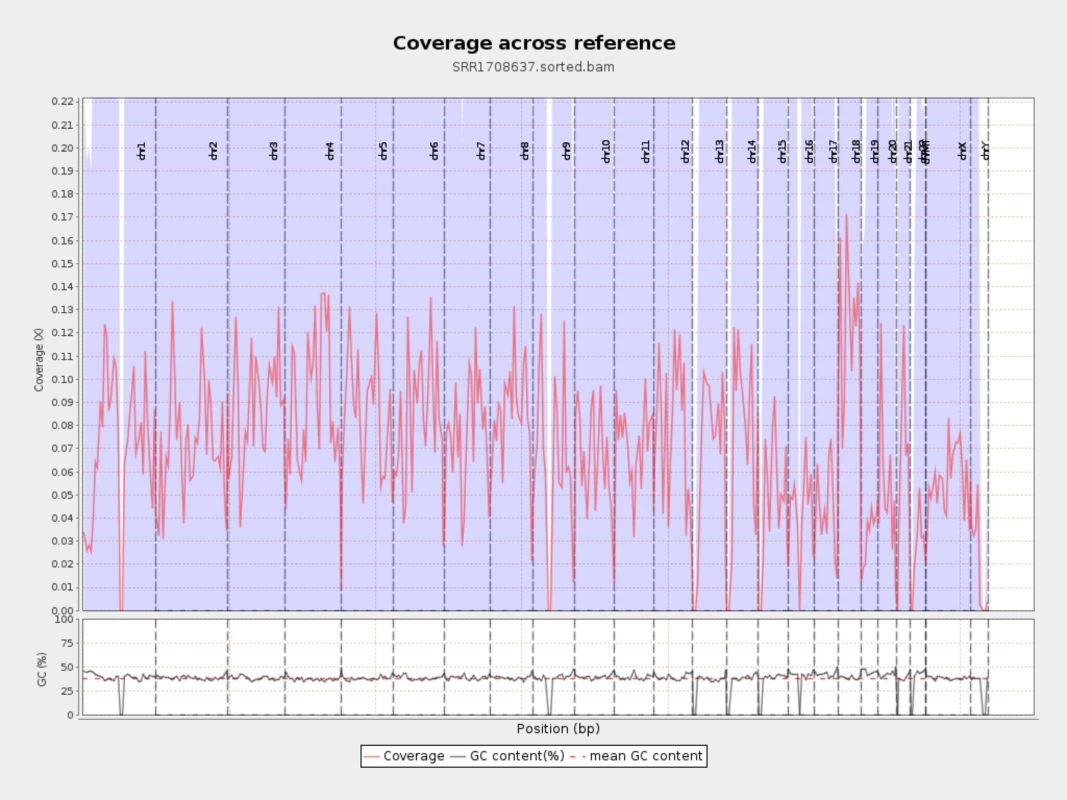
General error rate	0.17%
Mismatches	359,817
Insertions	13,902
Mapped reads with at least one insertion	0.31%
Deletions	12,651
Mapped reads with at least one deletion	0.29%
Homopolymer indels	48.7%

2.6. Chromosome stats

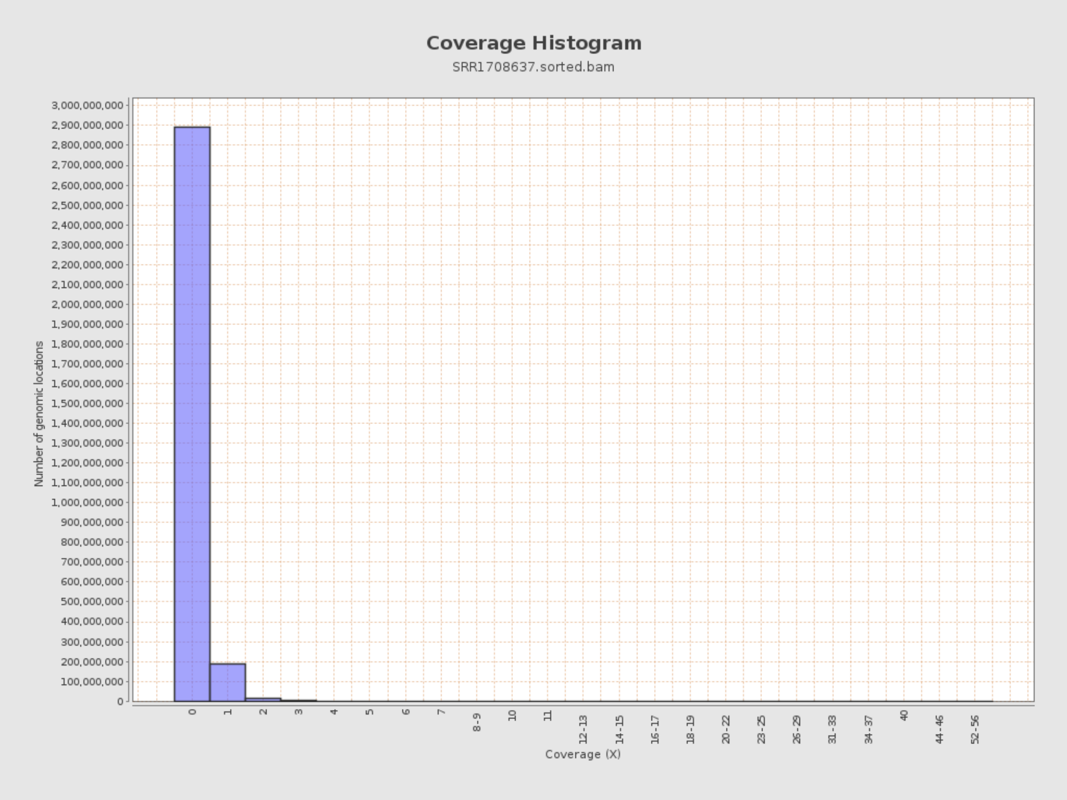
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17520780	0.0703	0.2778
chr2	243199373	17716331	0.0728	0.2797
chr3	198022430	17505599	0.0884	0.3087
chr4	191154276	17156319	0.0898	0.312
chr5	180915260	15306904	0.0846	0.3023
chr6	171115067	14505079	0.0848	0.3034
chr7	159138663	12089011	0.076	0.2866

chr8	146364022	12480673	0.0853	0.3033
chr9	141213431	9057782	0.0641	0.2646
chr10	135534747	9104191	0.0672	0.2686
chr11	135006516	9652245	0.0715	0.2797
chr12	133851895	10421185	0.0779	0.2906
chr13	115169878	7826363	0.068	0.271
chr14	107349540	7737875	0.0721	0.2816
chr15	102531392	4933698	0.0481	0.2288
chr16	90354753	3841589	0.0425	0.2129
chr17	81195210	3661960	0.0451	0.2208
chr18	78077248	9713502	0.1244	0.3705
chr19	59128983	1960507	0.0332	0.1878
chr20	63025520	3463660	0.055	0.2458
chr21	48129895	2937109	0.061	0.2611
chr22	51304566	1346399	0.0262	0.1679
chrMT	16571	400	0.0241	0.1535
chrX	155270560	8751672	0.0564	0.2458
chrY	59373566	1175518	0.0198	0.1467

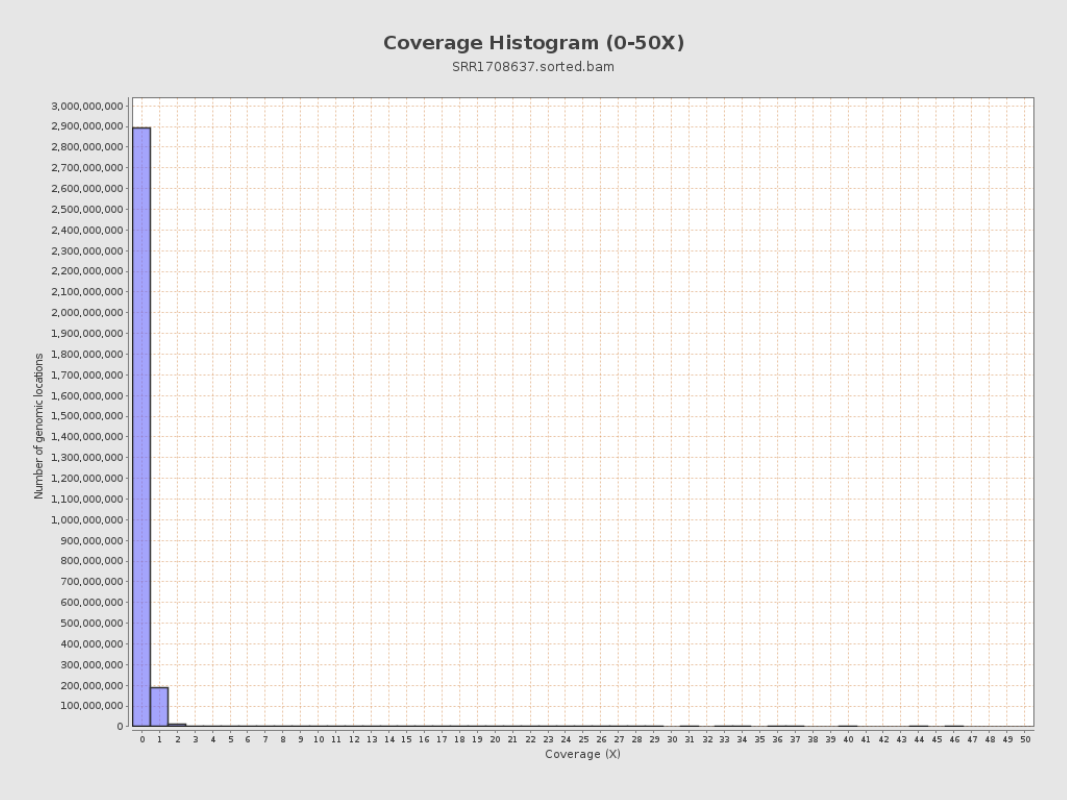
3. Results : Coverage across reference



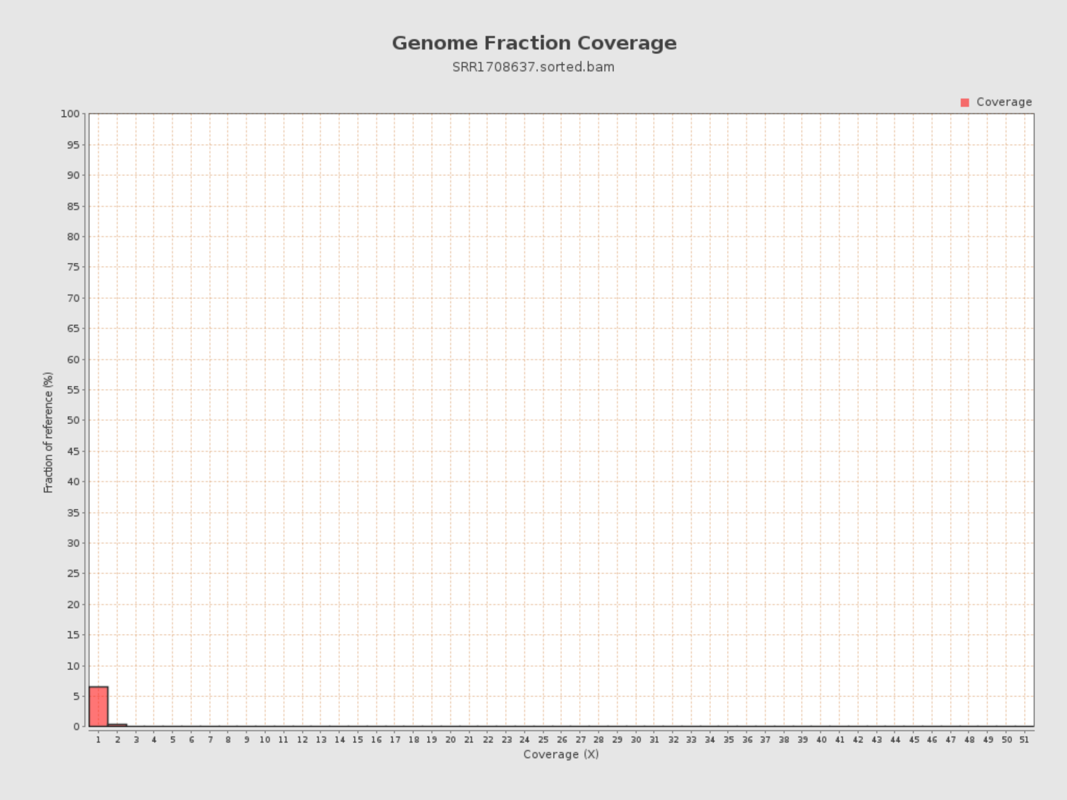
4. Results : Coverage Histogram



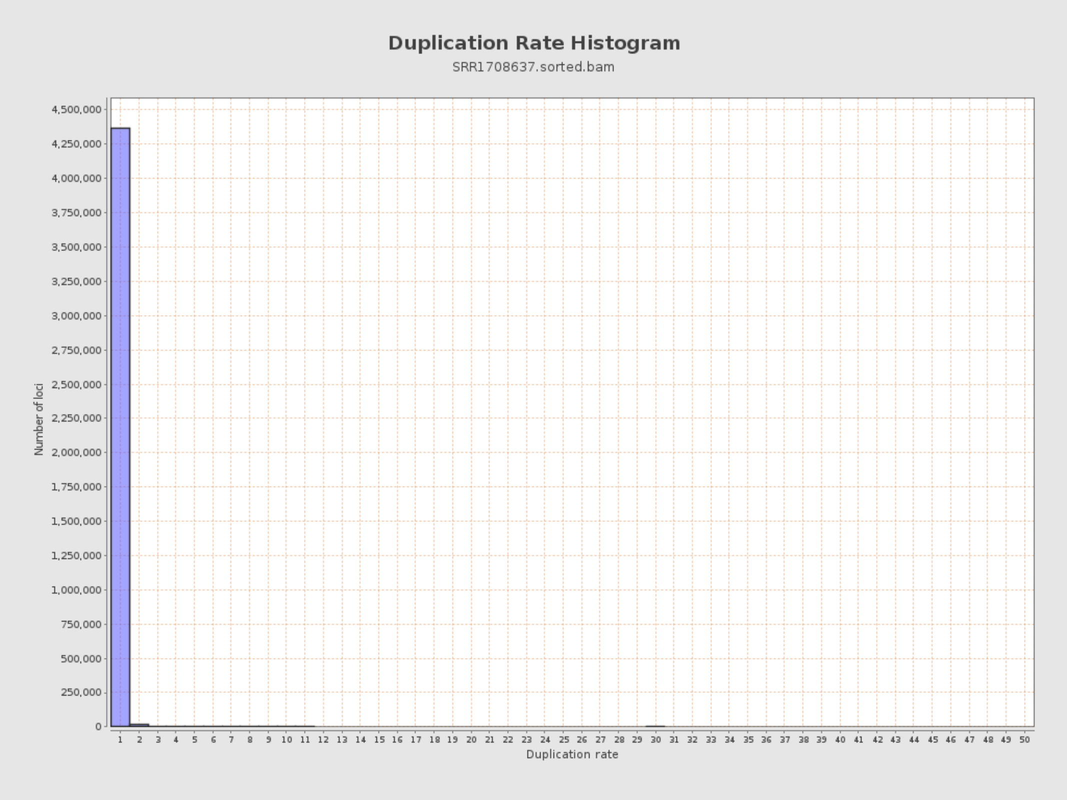
5. Results : Coverage Histogram (0-50X)



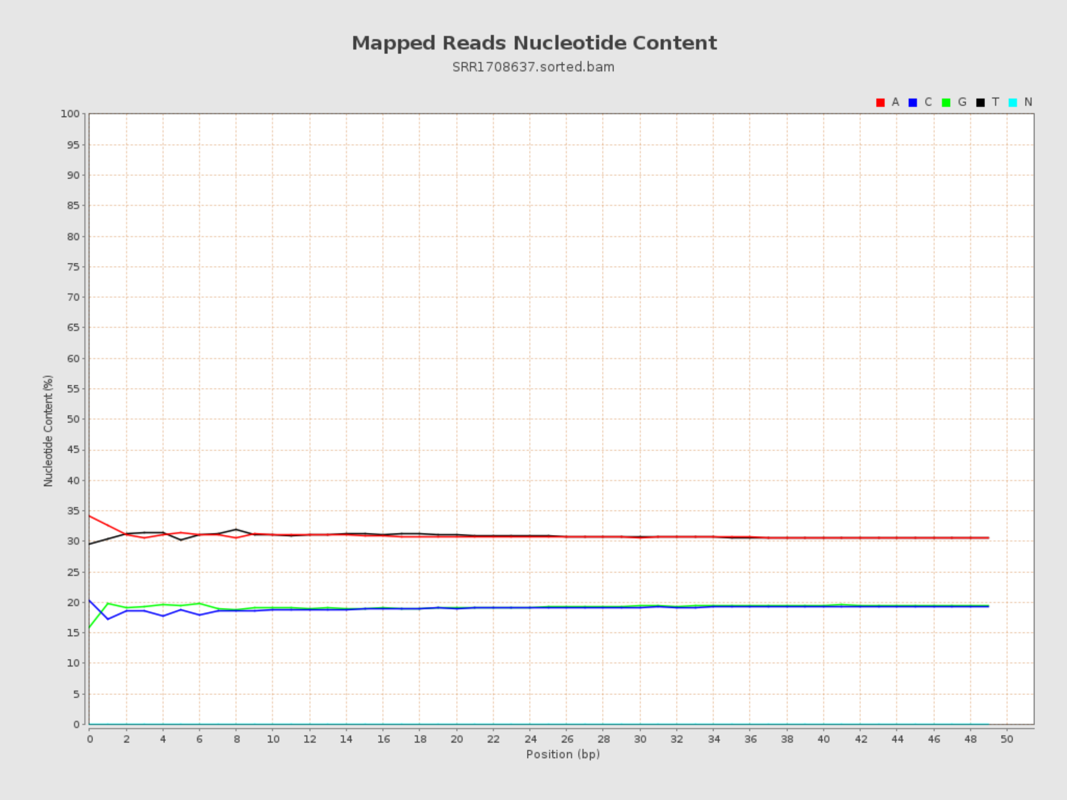
6. Results : Genome Fraction Coverage



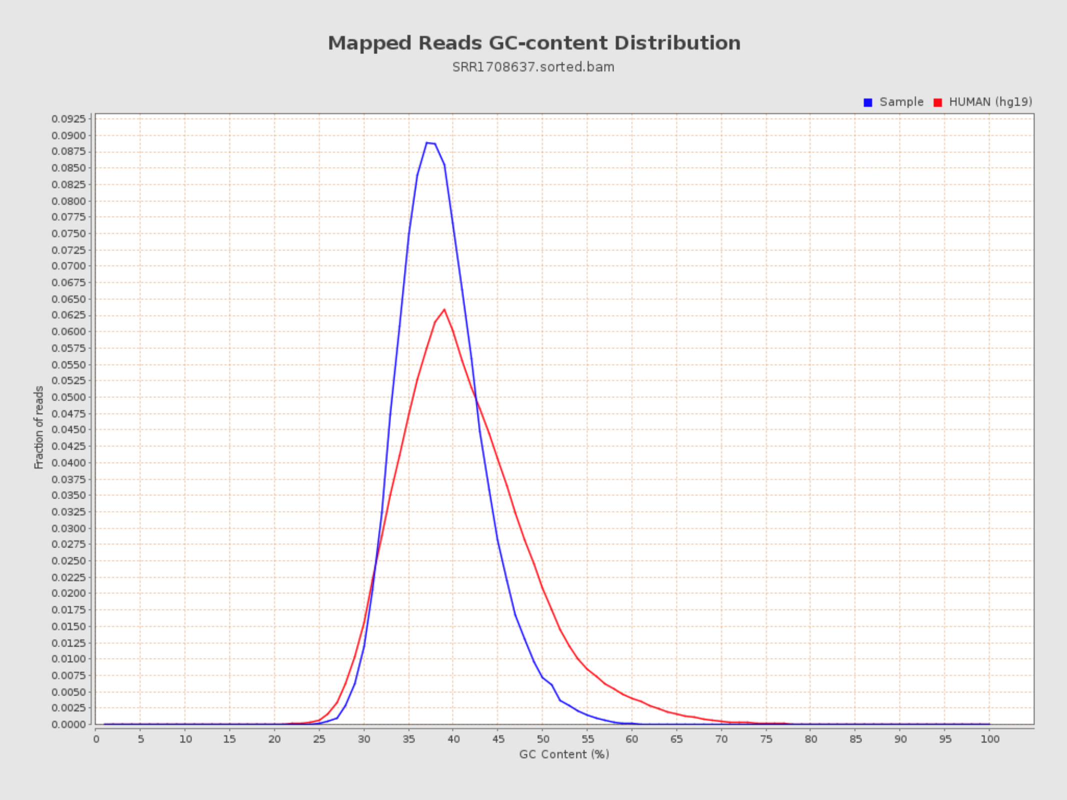
7. Results : Duplication Rate Histogram



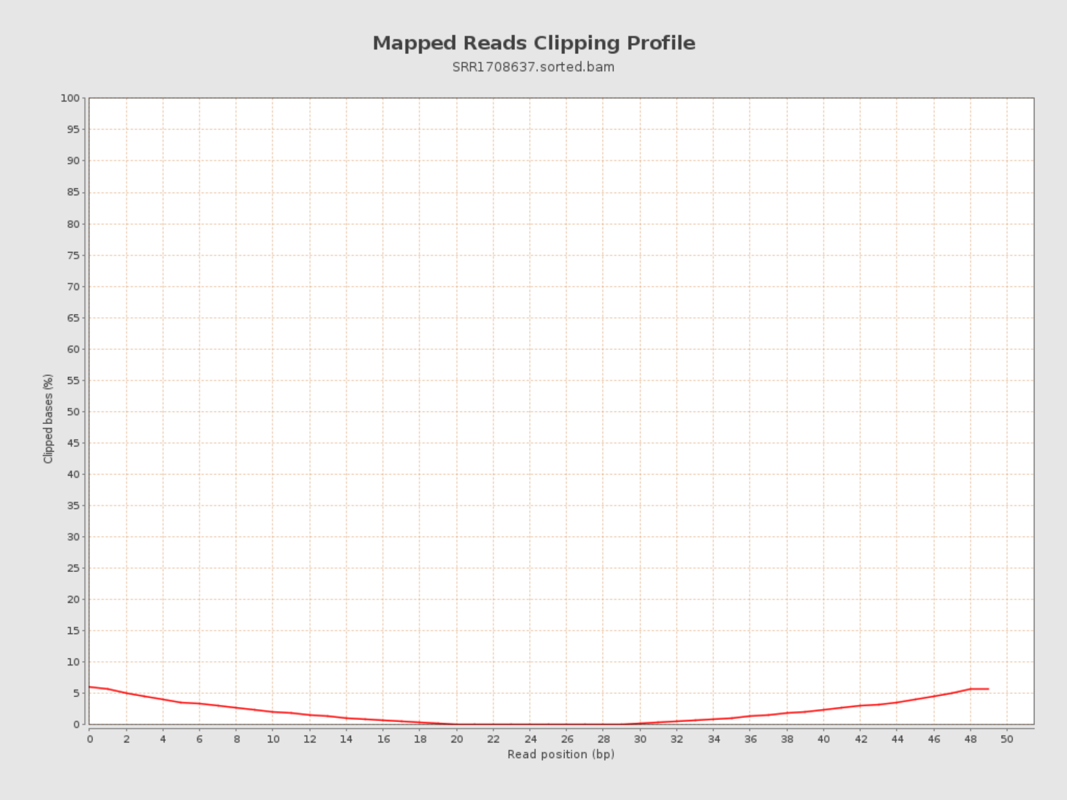
8. Results : Mapped Reads Nucleotide Content



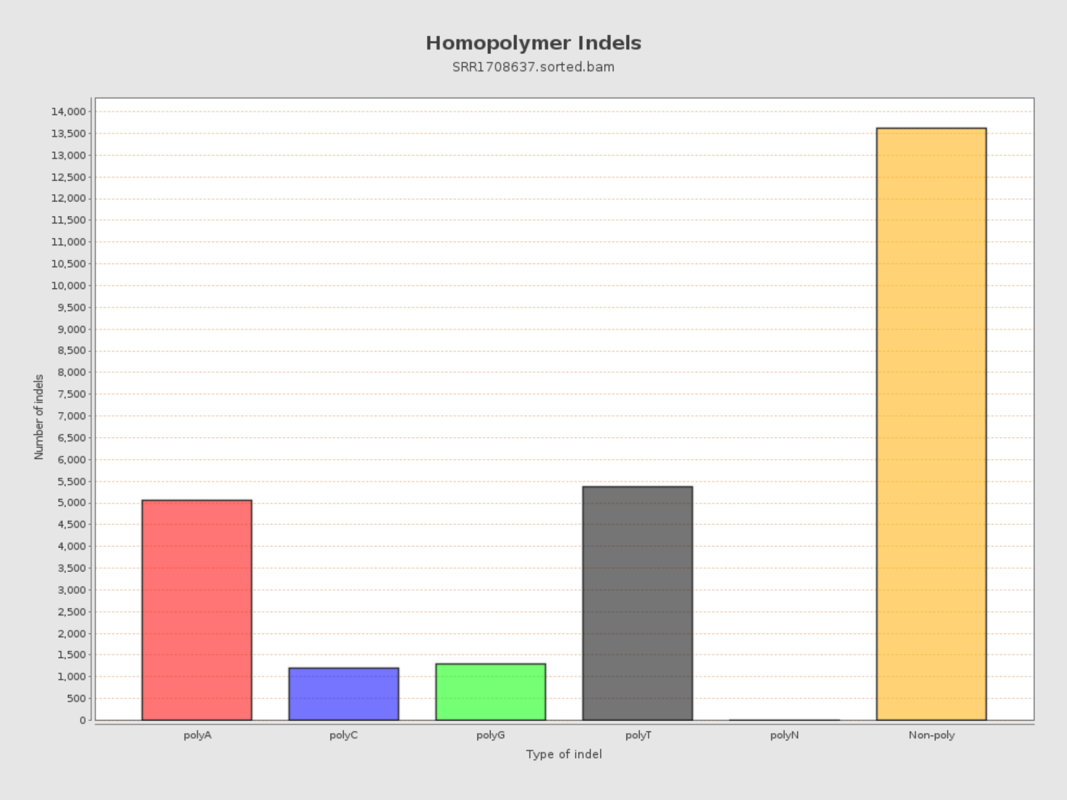
9. Results : Mapped Reads GC-content Distribution



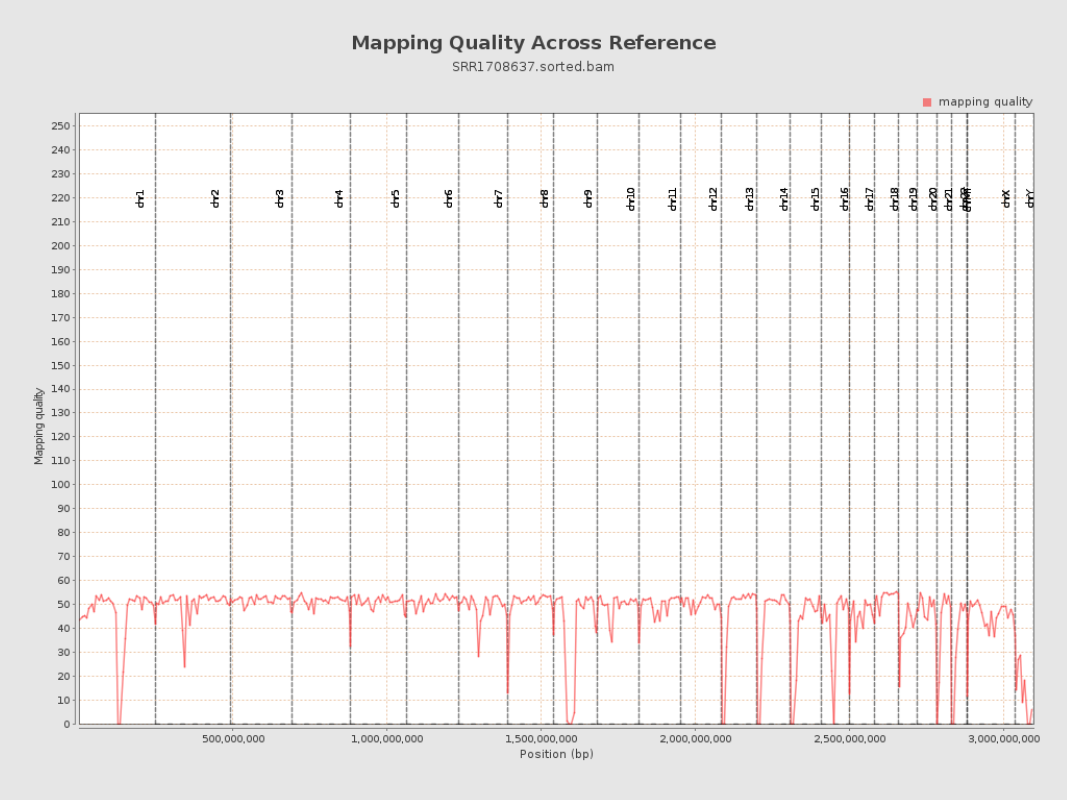
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram