Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:28:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708601.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_SRR1708601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:28:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,156,460
Mapped reads	4,044,025 / 97.29%
Unmapped reads	112,435 / 2.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	95 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	38,799 / 0.93%
Duplication rate	0.96%
Clipped reads	52,044 / 1.25%

2.2. ACGT Content

Number/percentage of A's	62,503,676 / 30.99%
Number/percentage of C's	38,243,127 / 18.96%
Number/percentage of T's	62,213,759 / 30.84%
Number/percentage of G's	38,742,196 / 19.21%
Number/percentage of N's	7,266 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	0.0652

Standard Deviation	0.2648

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

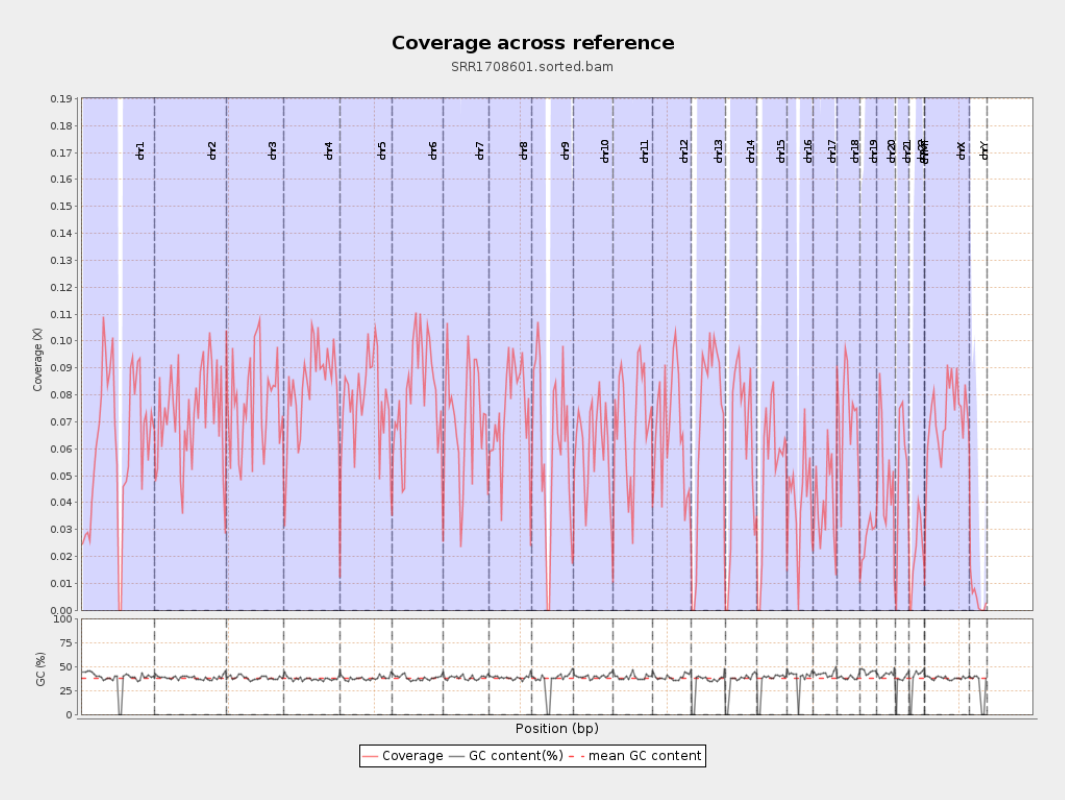
General error rate	0.15%
Mismatches	295,147
Insertions	12,931
Mapped reads with at least one insertion	0.32%
Deletions	10,313
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.27%

2.6. Chromosome stats

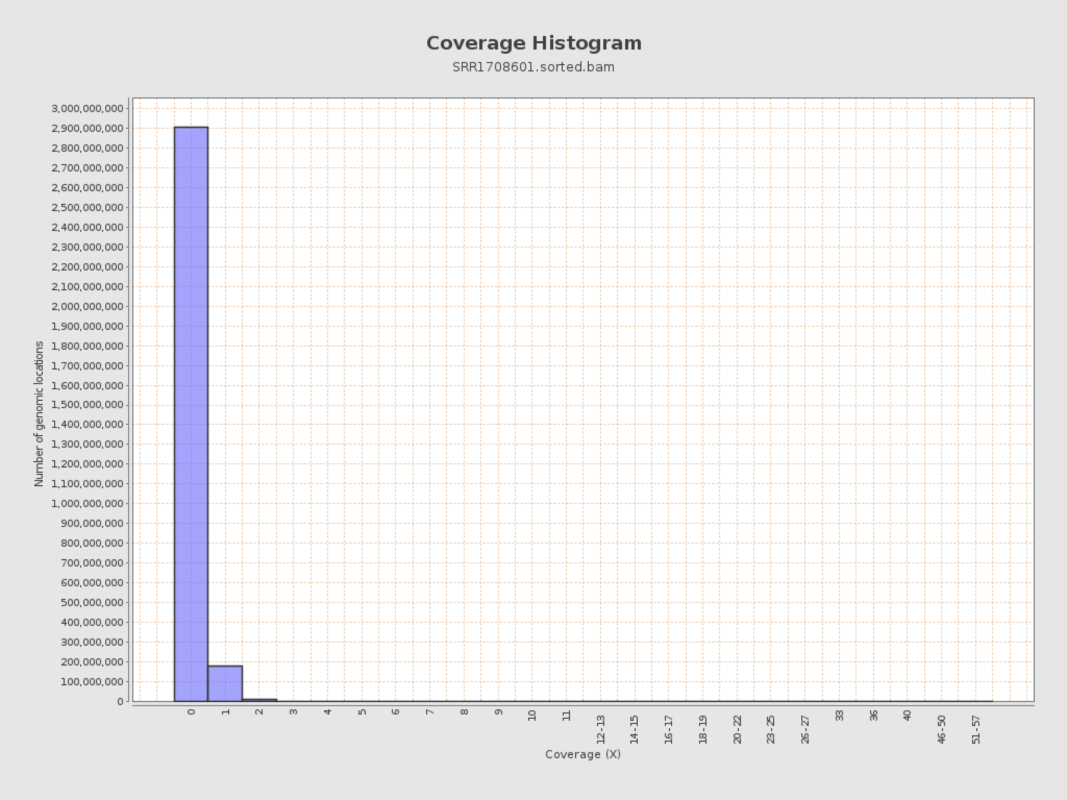
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15538928	0.0623	0.2603
chr2	243199373	17639263	0.0725	0.2784
chr3	198022430	15386592	0.0777	0.2877
chr4	191154276	15843442	0.0829	0.2972
chr5	180915260	13907964	0.0769	0.2859
chr6	171115067	13875396	0.0811	0.2945
chr7	159138663	11126975	0.0699	0.2737

chr8	146364022	10763049	0.0735	0.2803
chr9	141213431	8697220	0.0616	0.2579
chr10	135534747	8334442	0.0615	0.2559
chr11	135006516	9412671	0.0697	0.2747
chr12	133851895	8881258	0.0664	0.2669
chr13	115169878	8111249	0.0704	0.2756
chr14	107349540	6540307	0.0609	0.2568
chr15	102531392	5337746	0.0521	0.2373
chr16	90354753	3643243	0.0403	0.2078
chr17	81195210	3260412	0.0402	0.2074
chr18	78077248	5646790	0.0723	0.2778
chr19	59128983	1610851	0.0272	0.17
chr20	63025520	3205342	0.0509	0.2336
chr21	48129895	2407985	0.05	0.234
chr22	51304566	1106363	0.0216	0.1518
chrMT	16571	150	0.0091	0.0947
chrX	155270560	11193591	0.0721	0.2775
chrY	59373566	256338	0.0043	0.0688

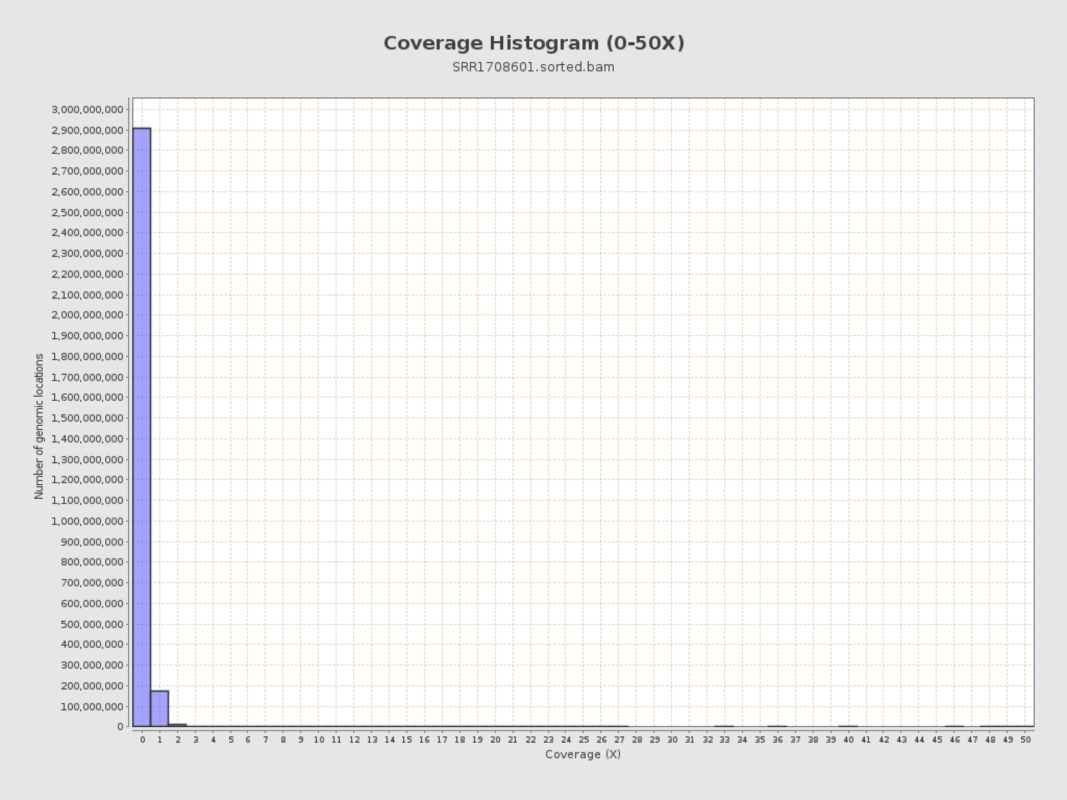
3. Results : Coverage across reference



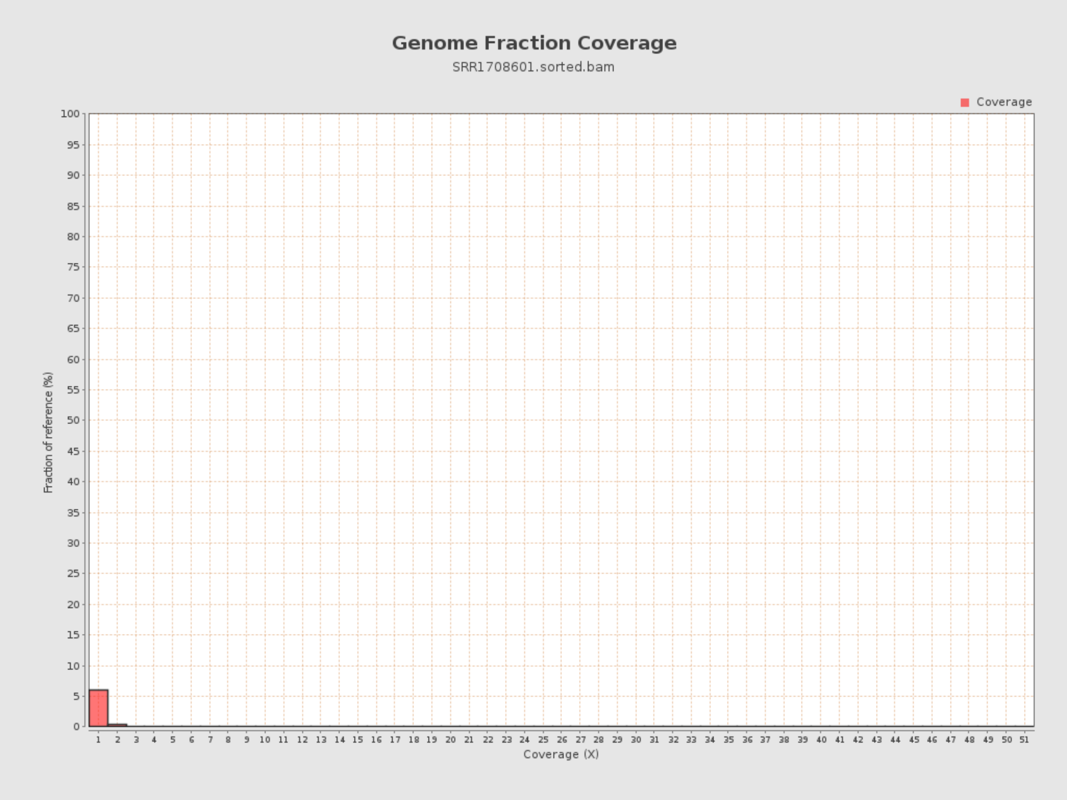
4. Results : Coverage Histogram



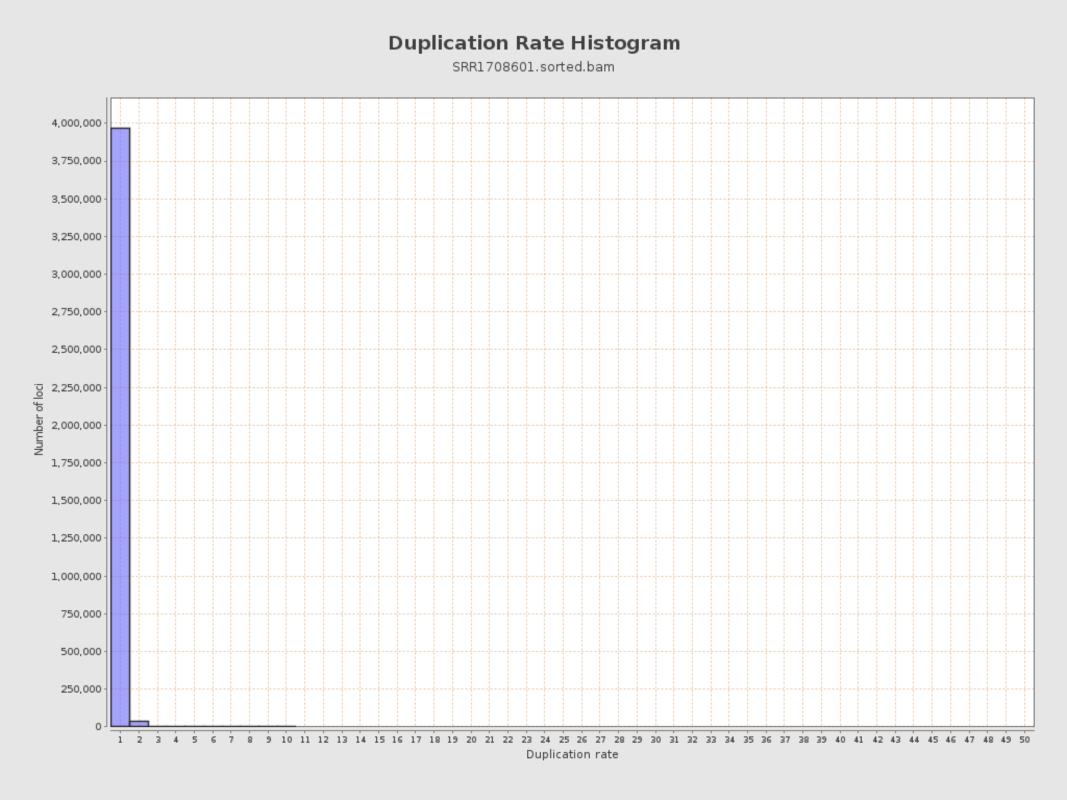
5. Results : Coverage Histogram (0-50X)



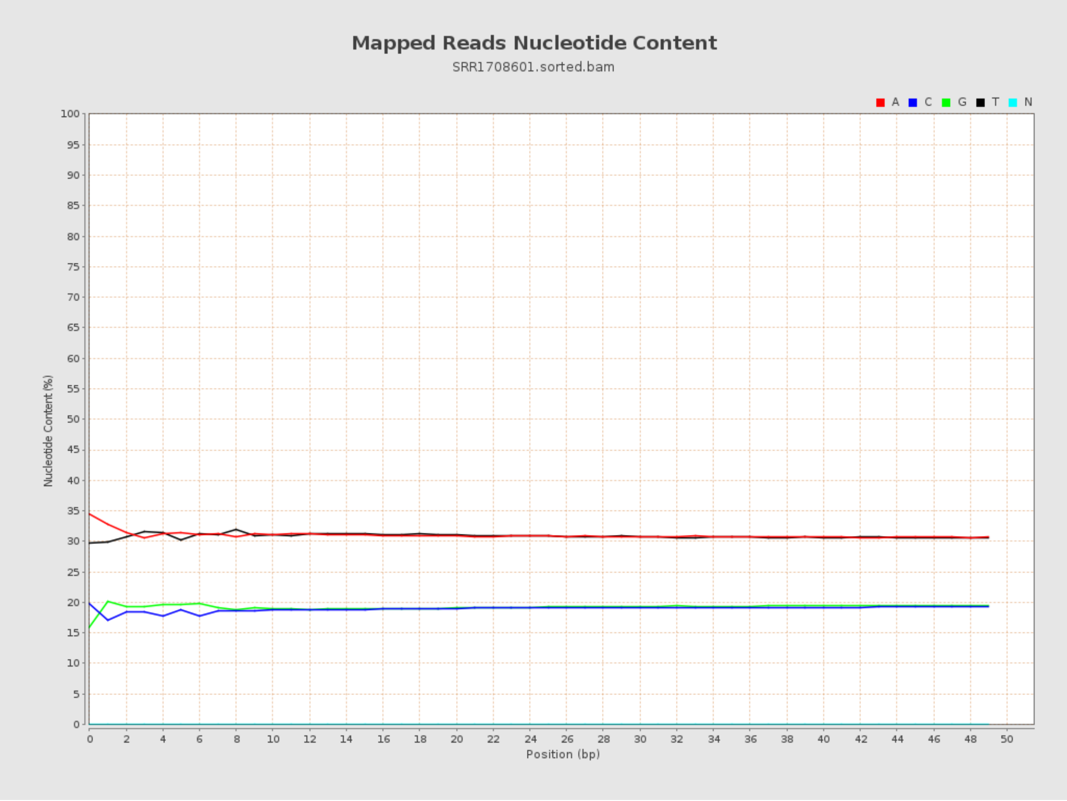
6. Results : Genome Fraction Coverage



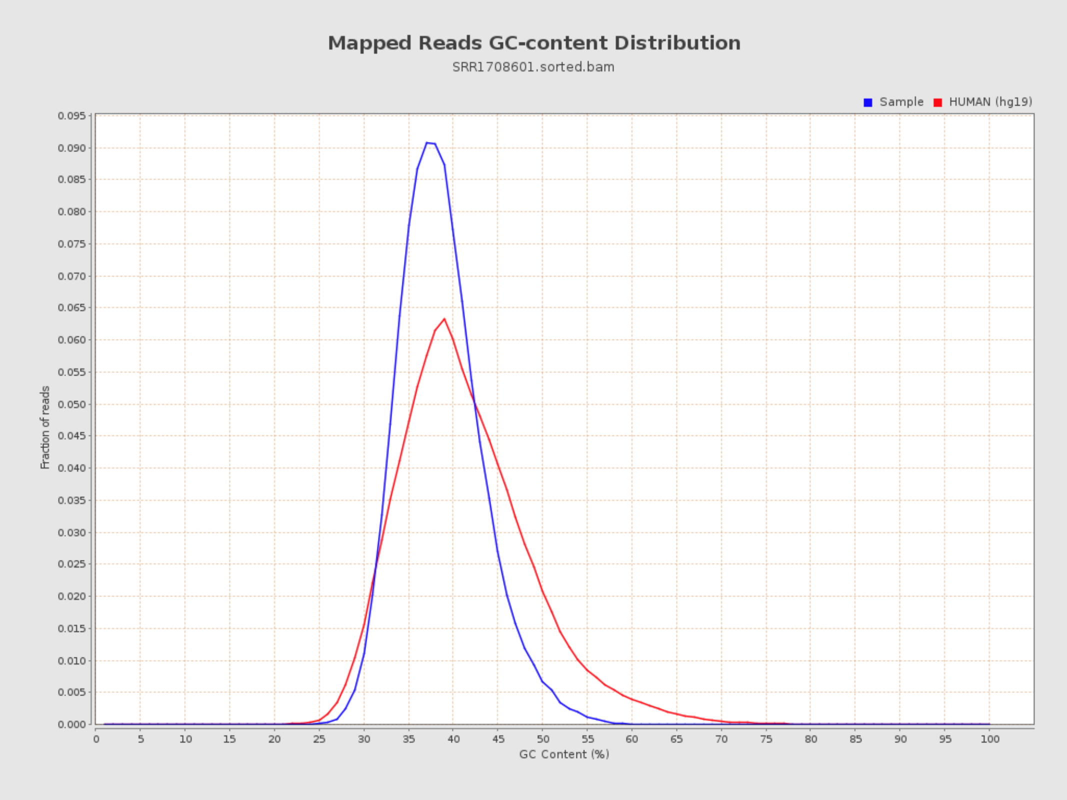
7. Results : Duplication Rate Histogram



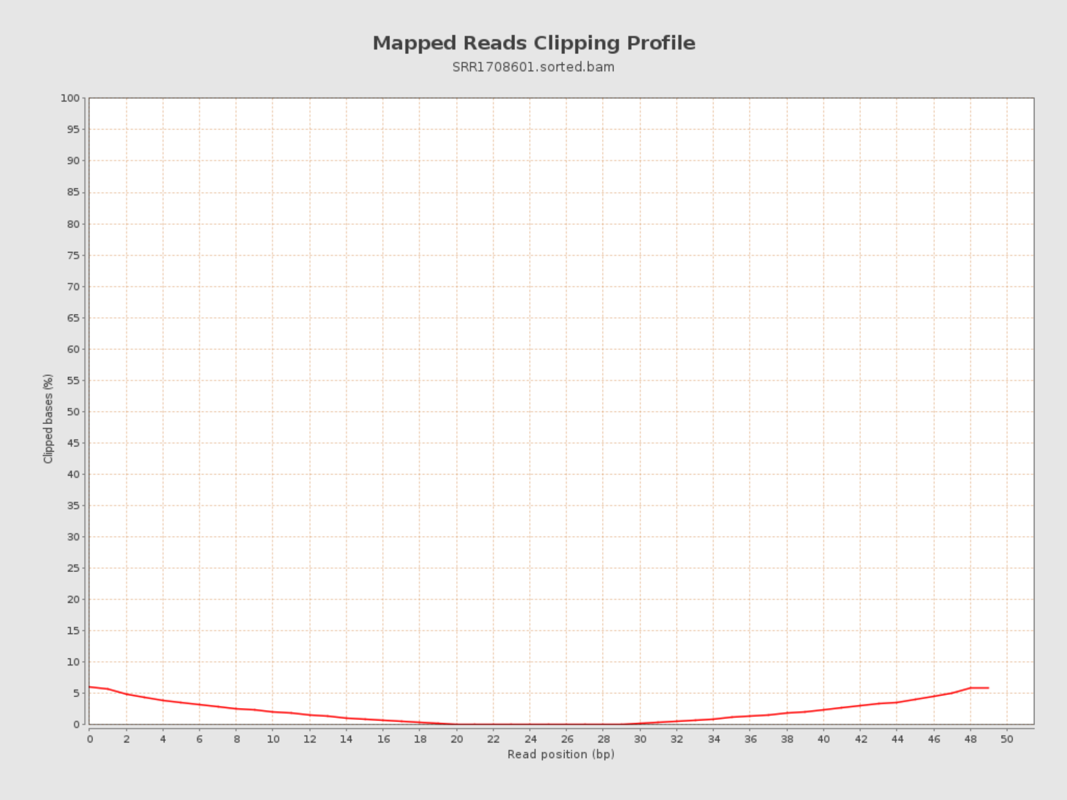
8. Results : Mapped Reads Nucleotide Content



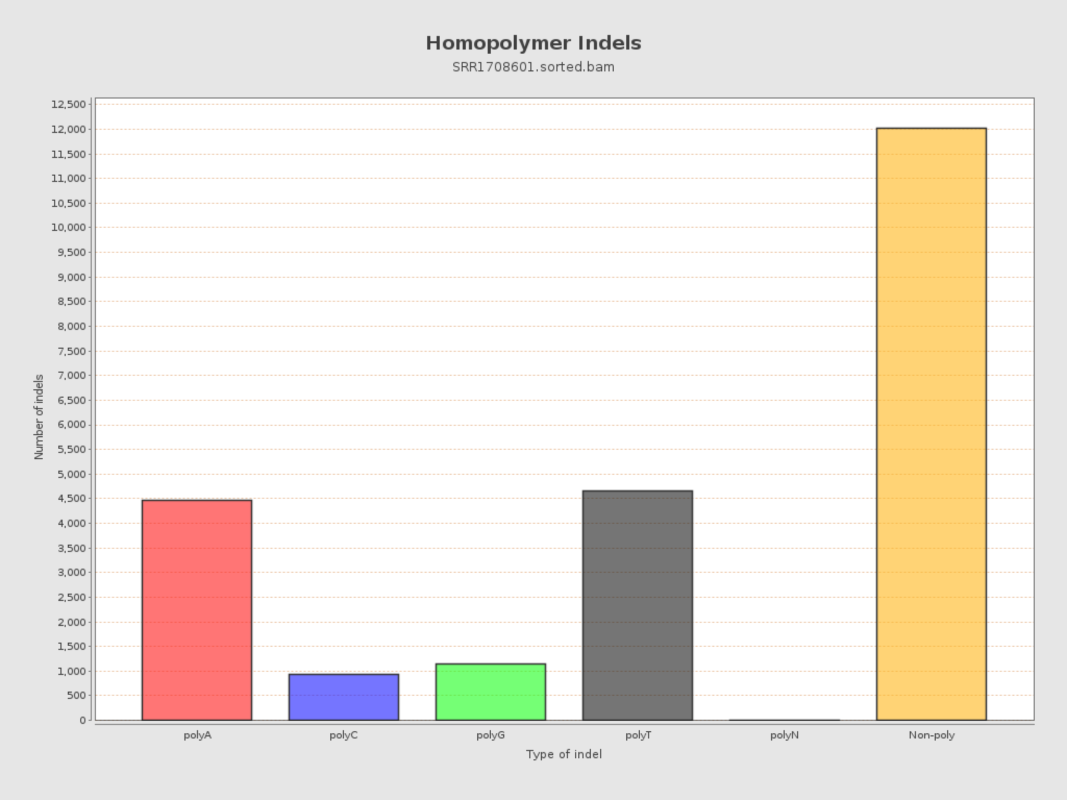
9. Results : Mapped Reads GC-content Distribution



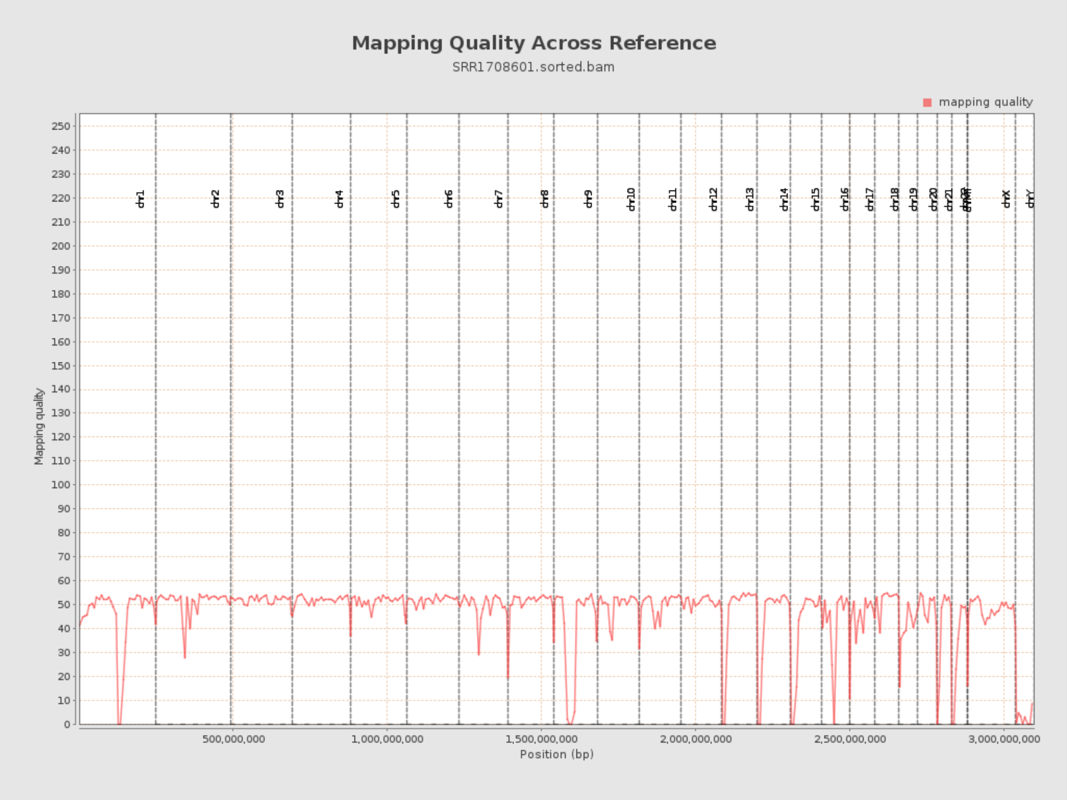
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram