Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:48:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708617.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_SRR1708617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708617.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:48:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,449,917
Mapped reads	2,514,845 / 72.9%
Unmapped reads	935,072 / 27.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	844 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	97,710 / 2.83%
Duplication rate	2.7%
Clipped reads	390,324 / 11.31%

2.2. ACGT Content

Number/percentage of A's	36,083,715 / 29.48%
Number/percentage of C's	23,011,961 / 18.8%
Number/percentage of T's	38,698,717 / 31.62%
Number/percentage of G's	24,592,956 / 20.09%
Number/percentage of N's	10,668 / 0.01%
GC Percentage	38.89%

2.3. Coverage

Mean	0.0395

Standard Deviation	0.4182

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

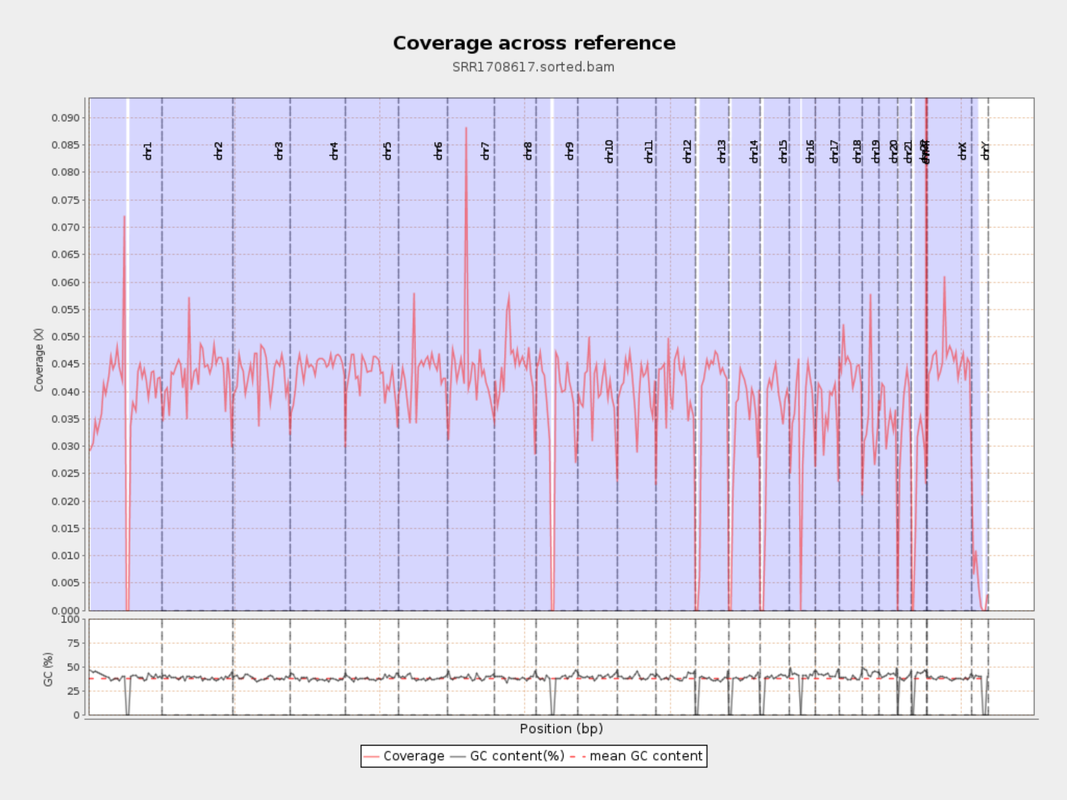
General error rate	0.64%
Mismatches	769,039
Insertions	5,692
Mapped reads with at least one insertion	0.23%
Deletions	15,576
Mapped reads with at least one deletion	0.62%
Homopolymer indels	48.45%

2.6. Chromosome stats

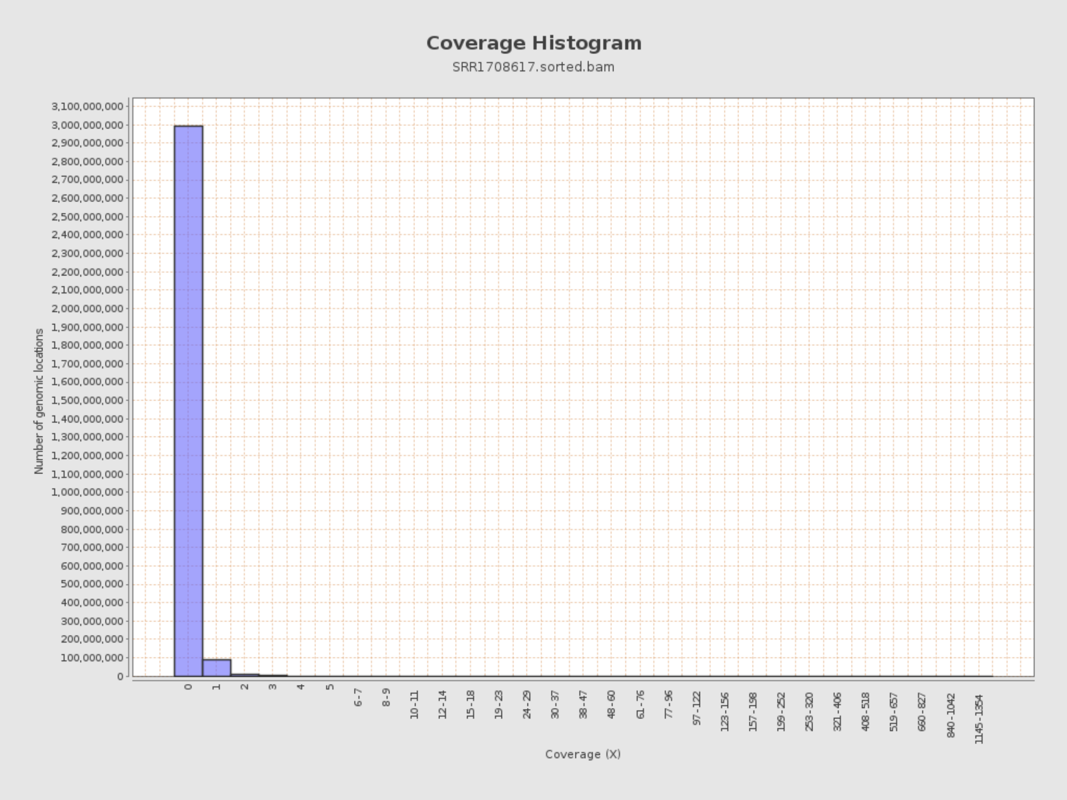
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9646724	0.0387	0.7544
chr2	243199373	10528684	0.0433	0.4182
chr3	198022430	8532578	0.0431	0.2418
chr4	191154276	8476338	0.0443	0.2497
chr5	180915260	7763366	0.0429	0.2442
chr6	171115067	7407805	0.0433	0.3309
chr7	159138663	7086072	0.0445	0.6516

chr8	146364022	6507580	0.0445	0.77
chr9	141213431	5151674	0.0365	0.3121
chr10	135534747	5470024	0.0404	0.3187
chr11	135006516	5481642	0.0406	0.3484
chr12	133851895	5487595	0.041	0.2444
chr13	115169878	4214976	0.0366	0.2255
chr14	107349540	3500972	0.0326	0.2285
chr15	102531392	3330667	0.0325	0.2099
chr16	90354753	3119669	0.0345	0.2284
chr17	81195210	2922233	0.036	0.269
chr18	78077248	3498075	0.0448	0.6487
chr19	59128983	2075491	0.0351	0.563
chr20	63025520	2217688	0.0352	0.2251
chr21	48129895	1547322	0.0321	0.2208
chr22	51304566	1148323	0.0224	0.172
chrMT	16571	12321	0.7435	1.0647
chrX	155270560	7016424	0.0452	0.2763
chrY	59373566	277520	0.0047	0.0851

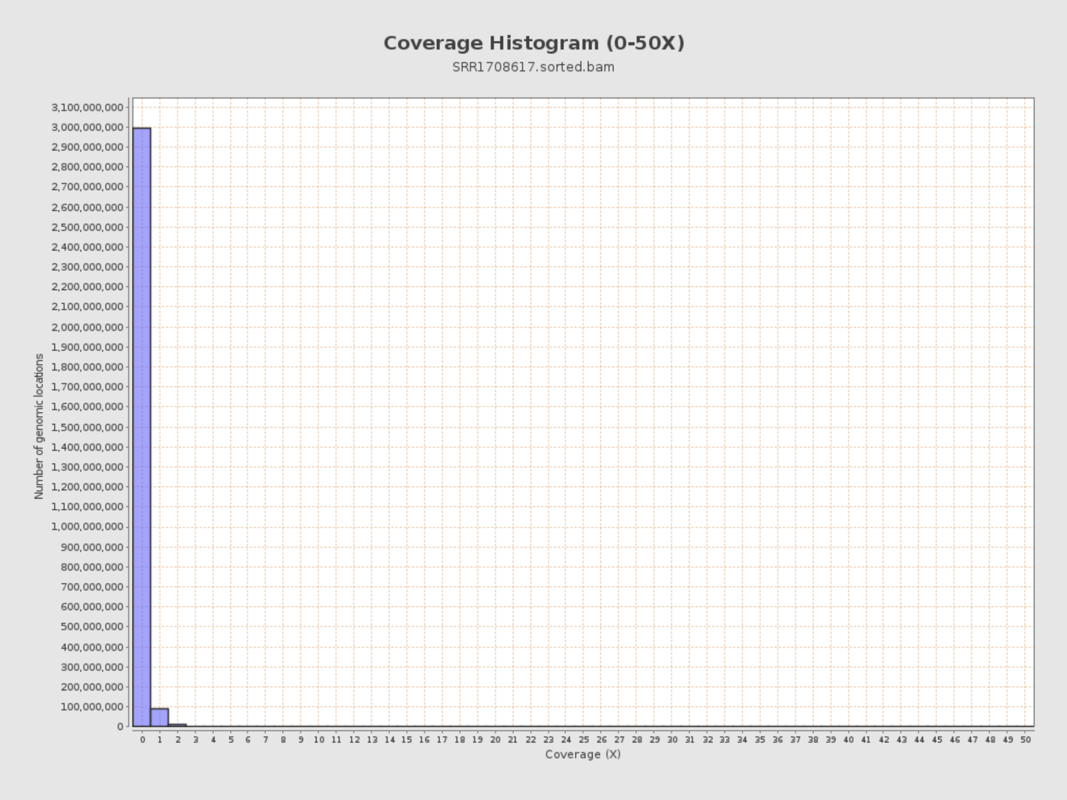
3. Results : Coverage across reference



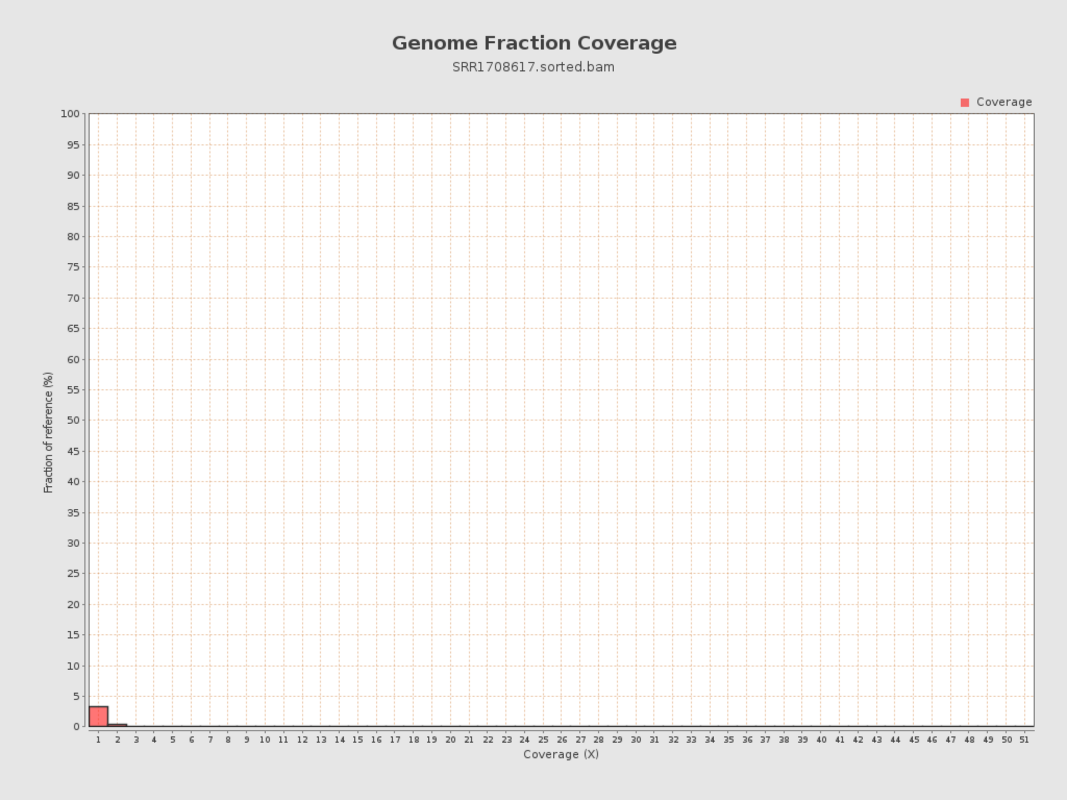
4. Results : Coverage Histogram



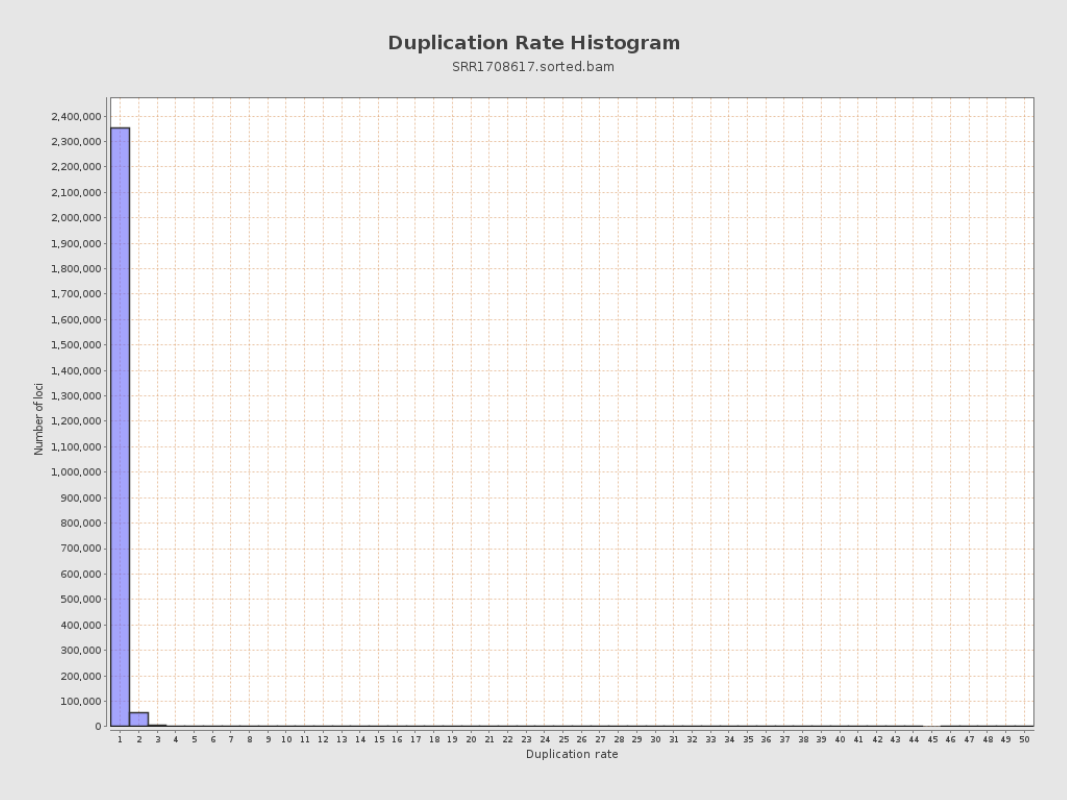
5. Results : Coverage Histogram (0-50X)



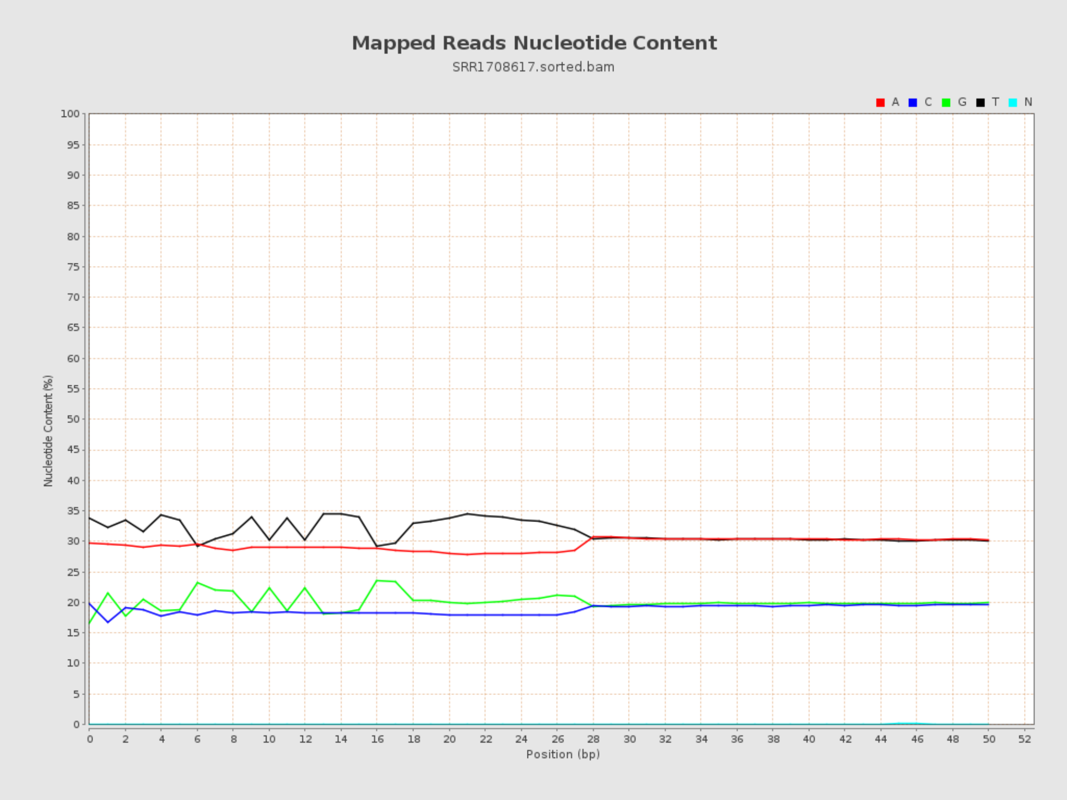
6. Results : Genome Fraction Coverage



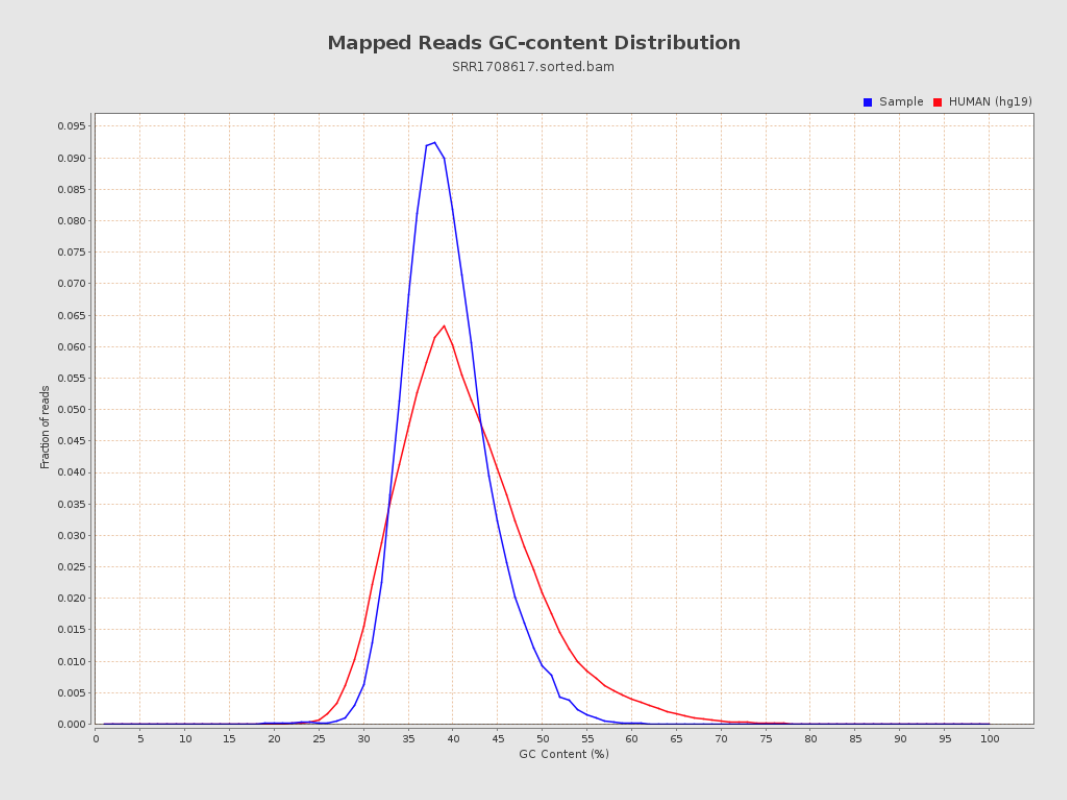
7. Results : Duplication Rate Histogram



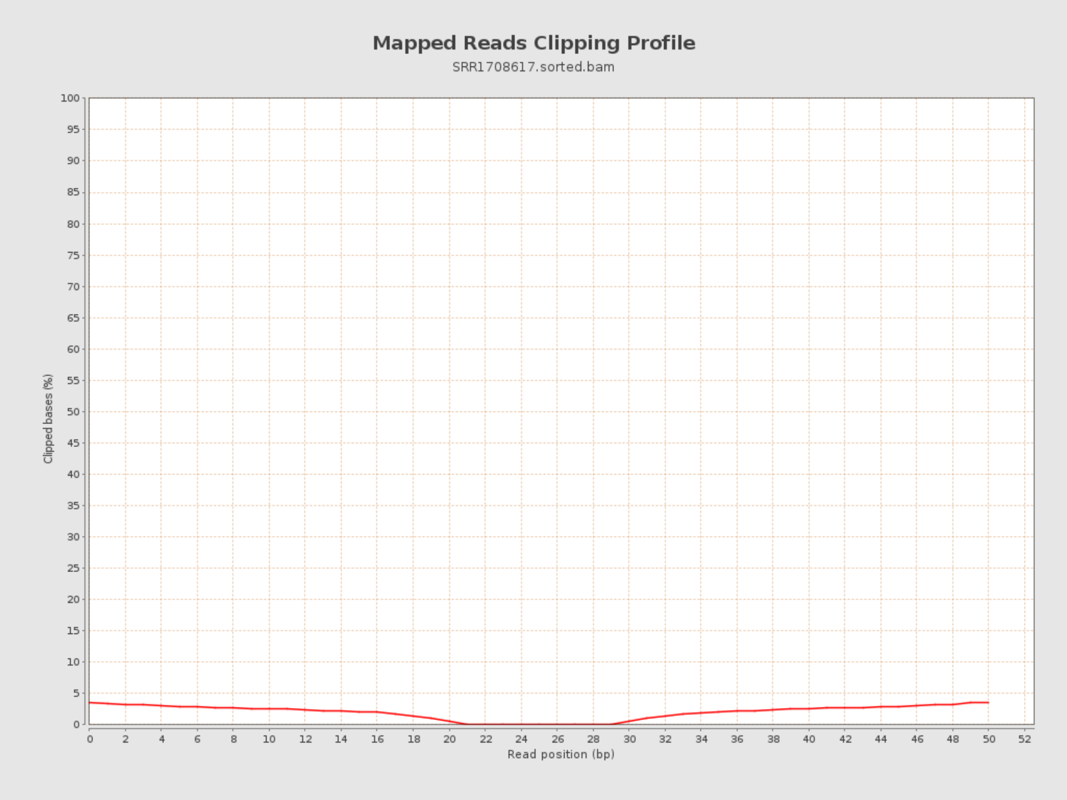
8. Results : Mapped Reads Nucleotide Content



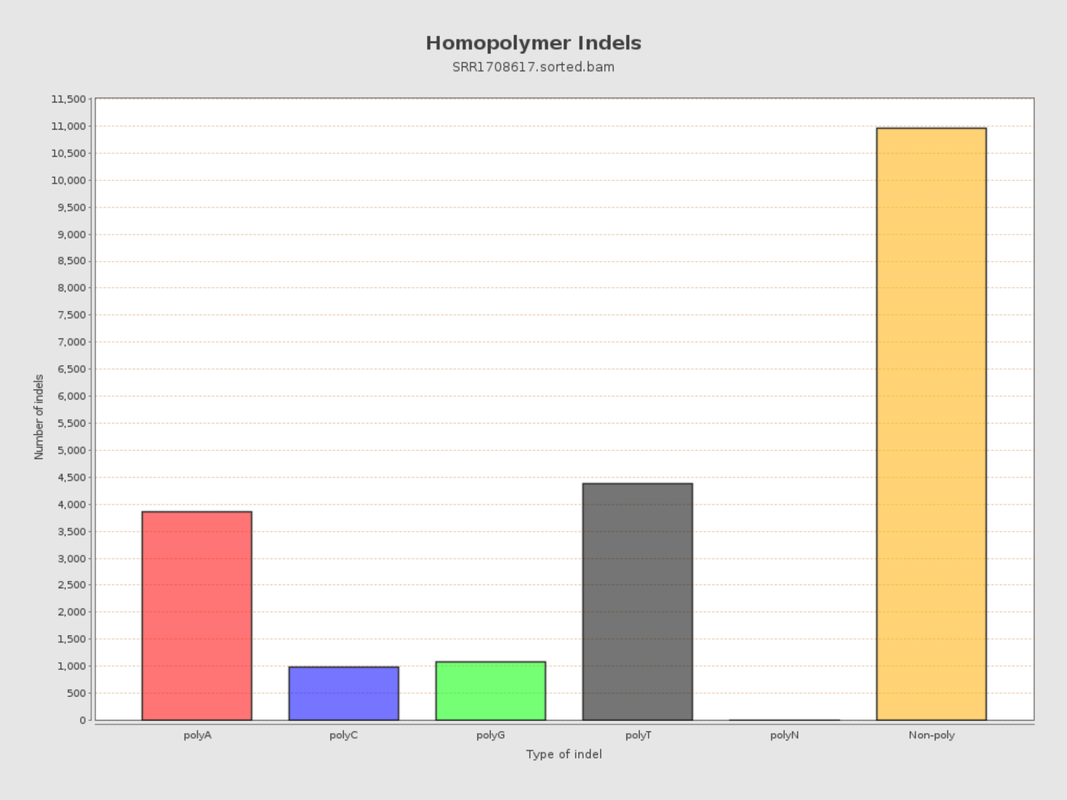
9. Results : Mapped Reads GC-content Distribution



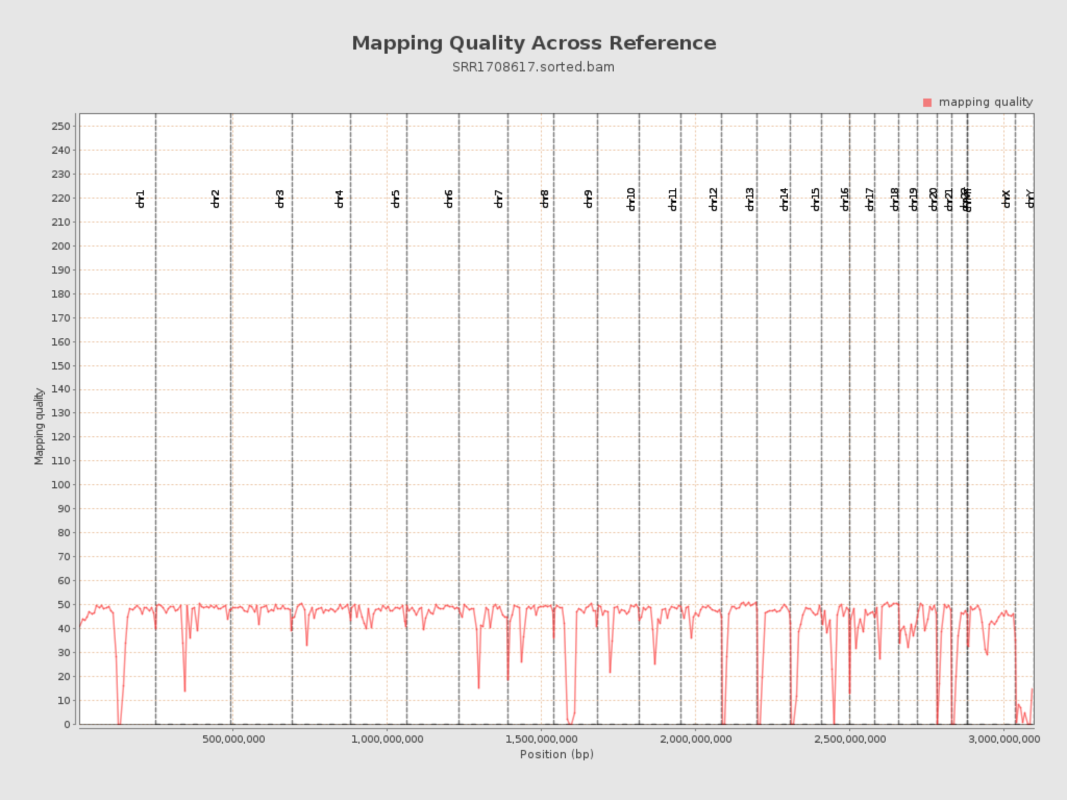
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram