Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:57:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708634.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_SRR1708634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:57:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,579,839
Mapped reads	2,561,348 / 71.55%
Unmapped reads	1,018,491 / 28.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	832 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	90,506 / 2.53%
Duplication rate	2.42%
Clipped reads	400,089 / 11.18%

2.2. ACGT Content

Number/percentage of A's	36,886,523 / 29.59%
Number/percentage of C's	23,360,815 / 18.74%
Number/percentage of T's	39,484,256 / 31.67%
Number/percentage of G's	24,932,438 / 20%
Number/percentage of N's	10,872 / 0.01%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3975

2.4. Mapping Quality

Mean Mapping Quality	43.18

2.5. Mismatches and indels

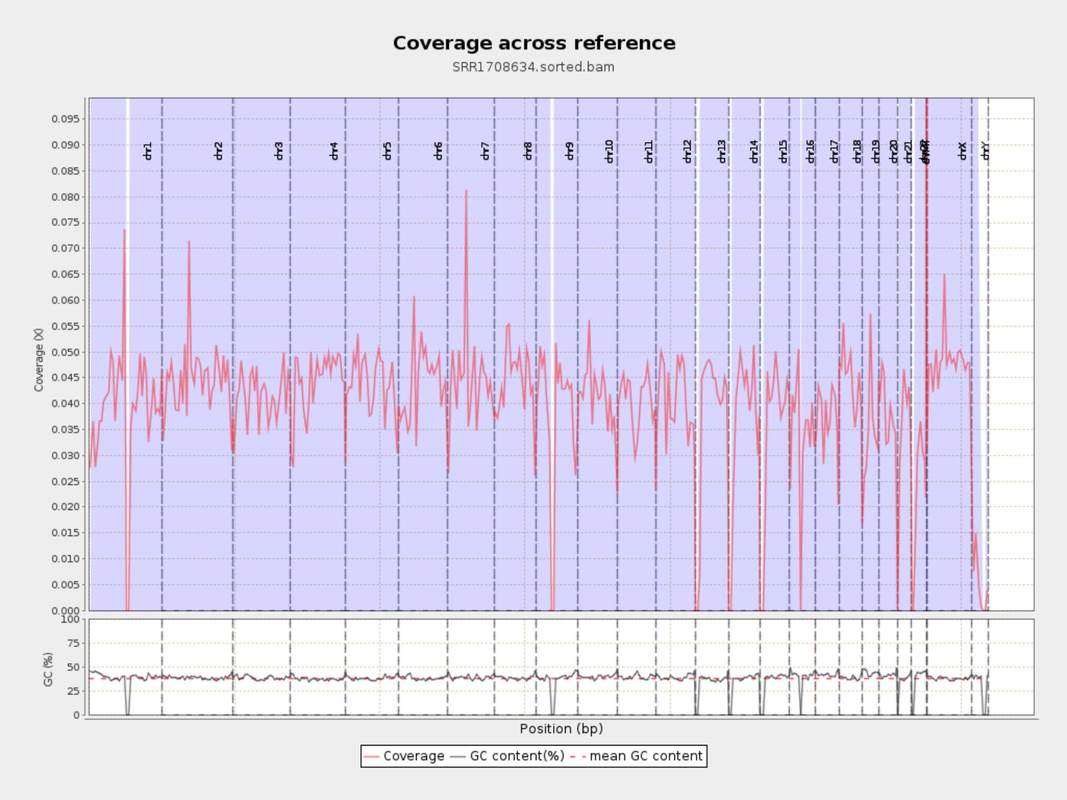
General error rate	0.65%
Mismatches	803,901
Insertions	5,838
Mapped reads with at least one insertion	0.23%
Deletions	16,045
Mapped reads with at least one deletion	0.62%
Homopolymer indels	47.51%

2.6. Chromosome stats

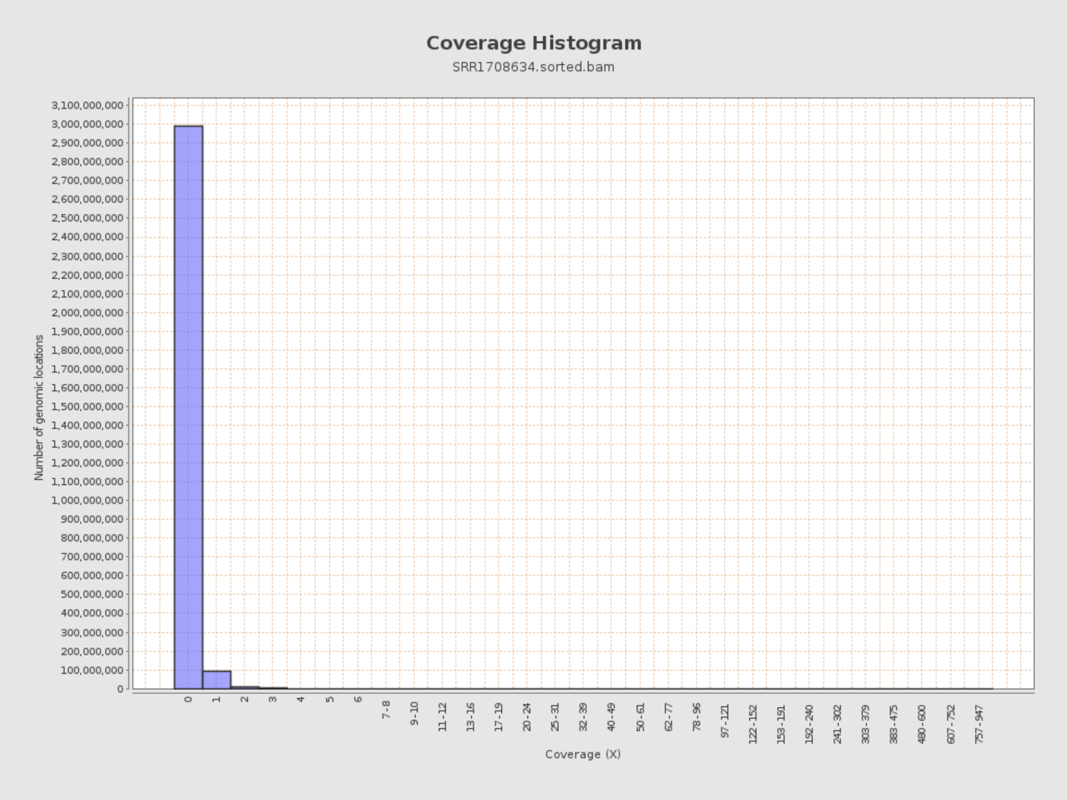
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9681448	0.0388	0.7826
chr2	243199373	10920896	0.0449	0.4036
chr3	198022430	8227630	0.0415	0.2334
chr4	191154276	8494233	0.0444	0.2428
chr5	180915260	7948679	0.0439	0.2418
chr6	171115067	7544708	0.0441	0.3101
chr7	159138663	7198987	0.0452	0.5574

chr8	146364022	6486476	0.0443	0.5731
chr9	141213431	5366556	0.038	0.3279
chr10	135534747	5668215	0.0418	0.3102
chr11	135006516	5433656	0.0402	0.3217
chr12	133851895	5488609	0.041	0.235
chr13	115169878	4250875	0.0369	0.2178
chr14	107349540	3864695	0.036	0.2311
chr15	102531392	3561725	0.0347	0.2117
chr16	90354753	3083128	0.0341	0.2258
chr17	81195210	2997331	0.0369	0.2529
chr18	78077248	3502793	0.0449	0.6776
chr19	59128983	2066519	0.0349	0.5638
chr20	63025520	2373843	0.0377	0.2286
chr21	48129895	1654169	0.0344	0.2328
chr22	51304566	1130212	0.022	0.1654
chrMT	16571	4449	0.2685	0.5875
chrX	155270560	7424950	0.0478	0.2806
chrY	59373566	324776	0.0055	0.1048

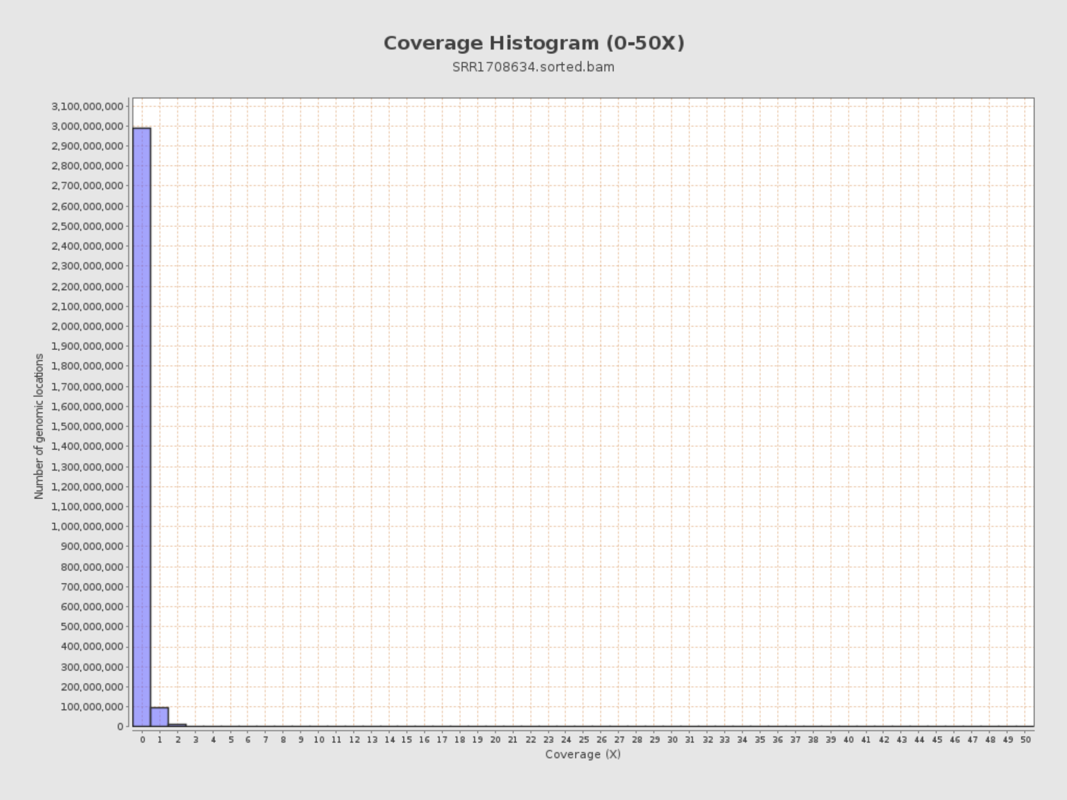
3. Results : Coverage across reference



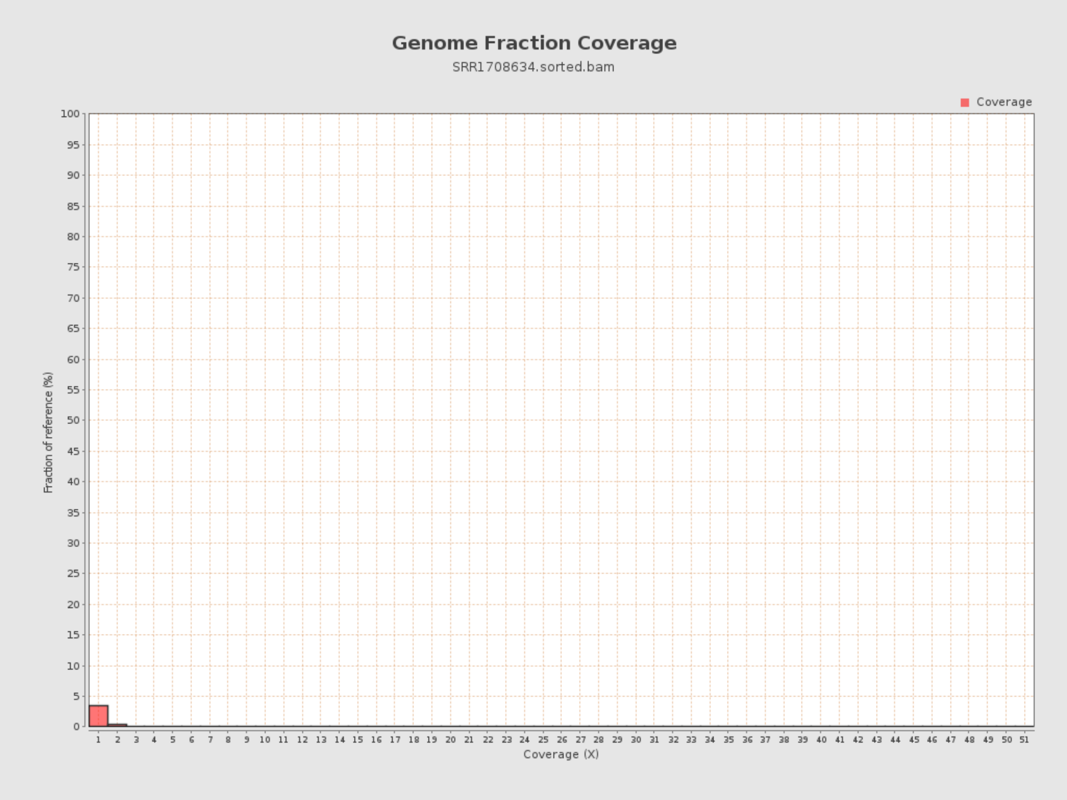
4. Results : Coverage Histogram



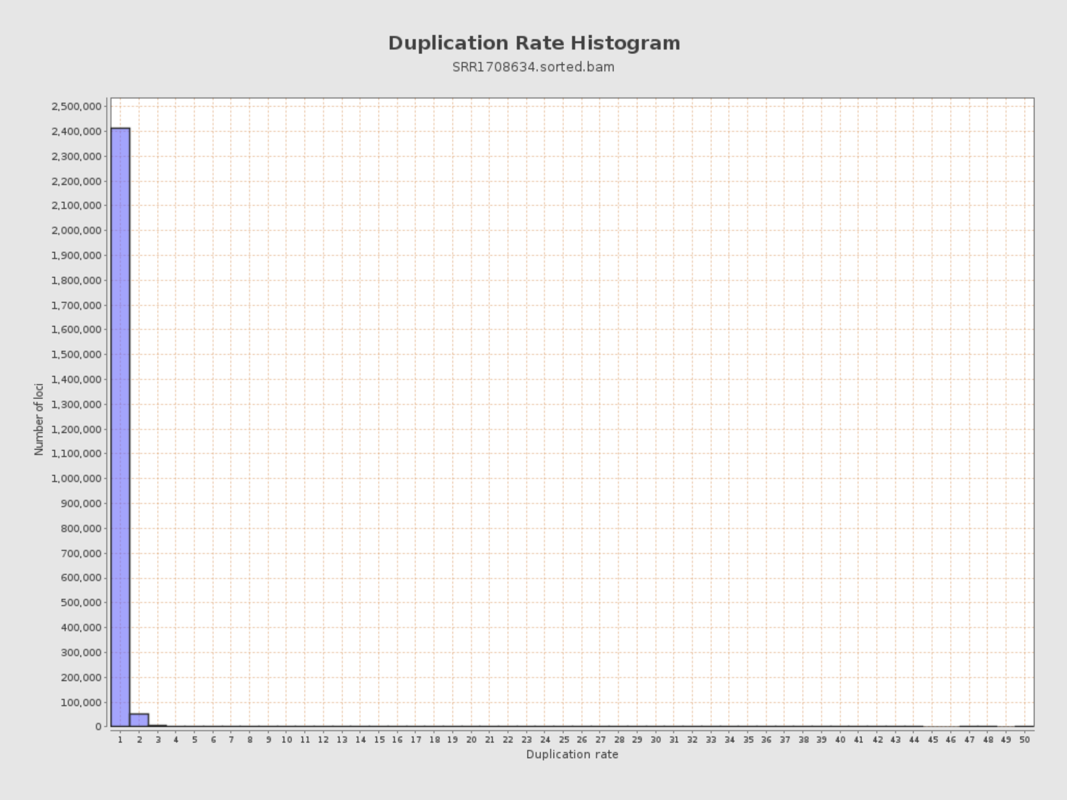
5. Results : Coverage Histogram (0-50X)



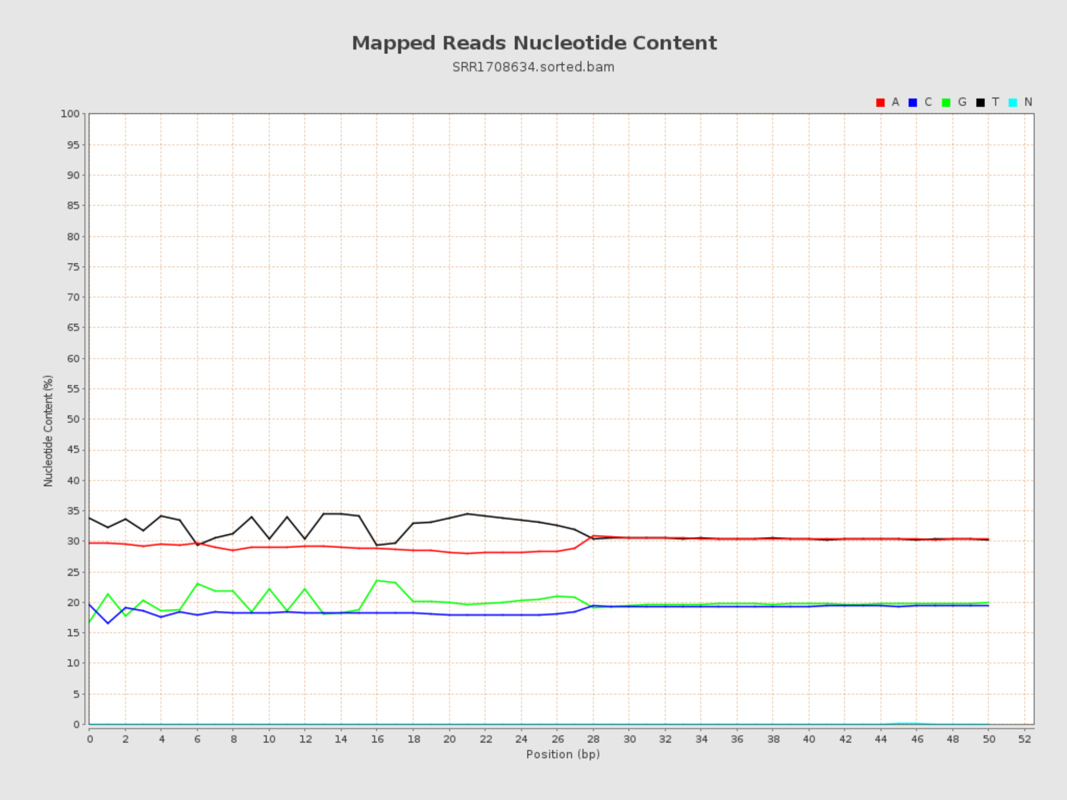
6. Results : Genome Fraction Coverage



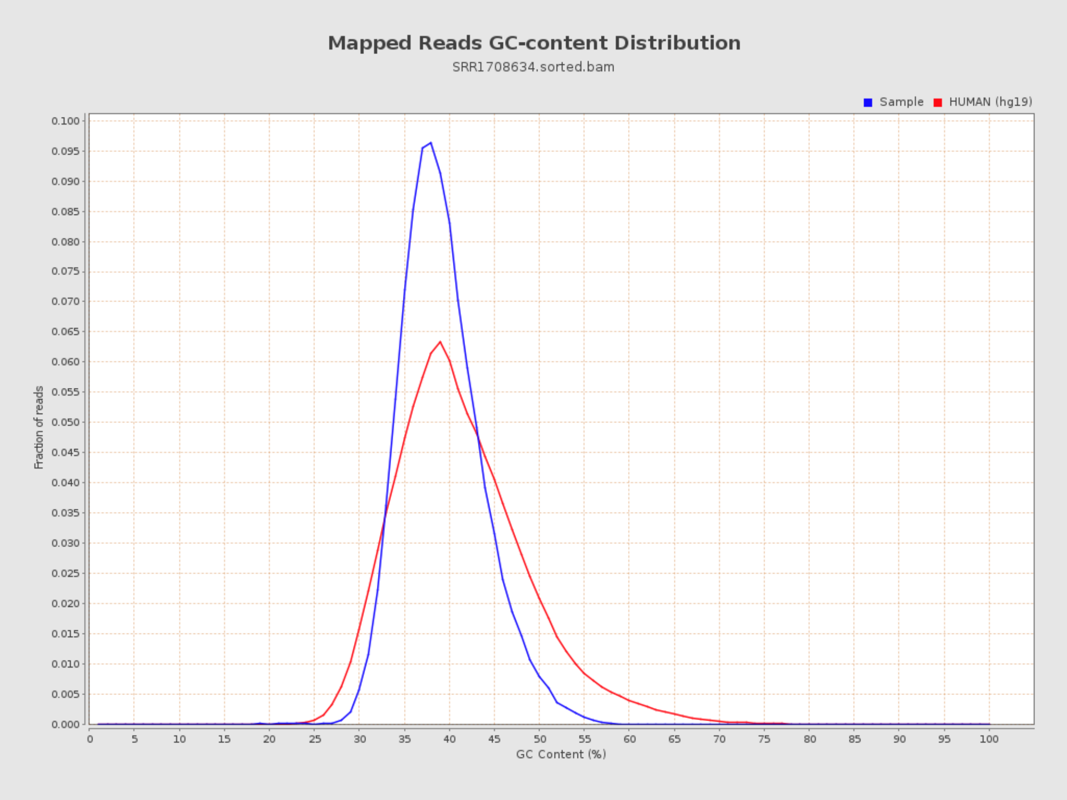
7. Results : Duplication Rate Histogram



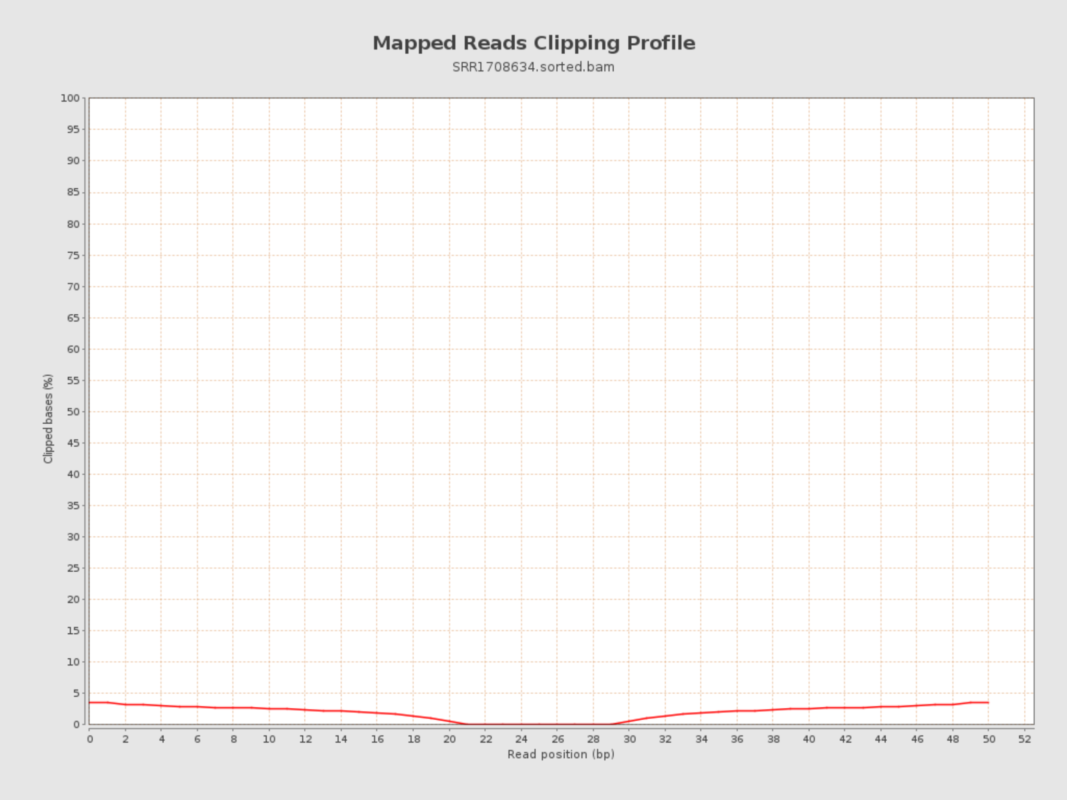
8. Results : Mapped Reads Nucleotide Content



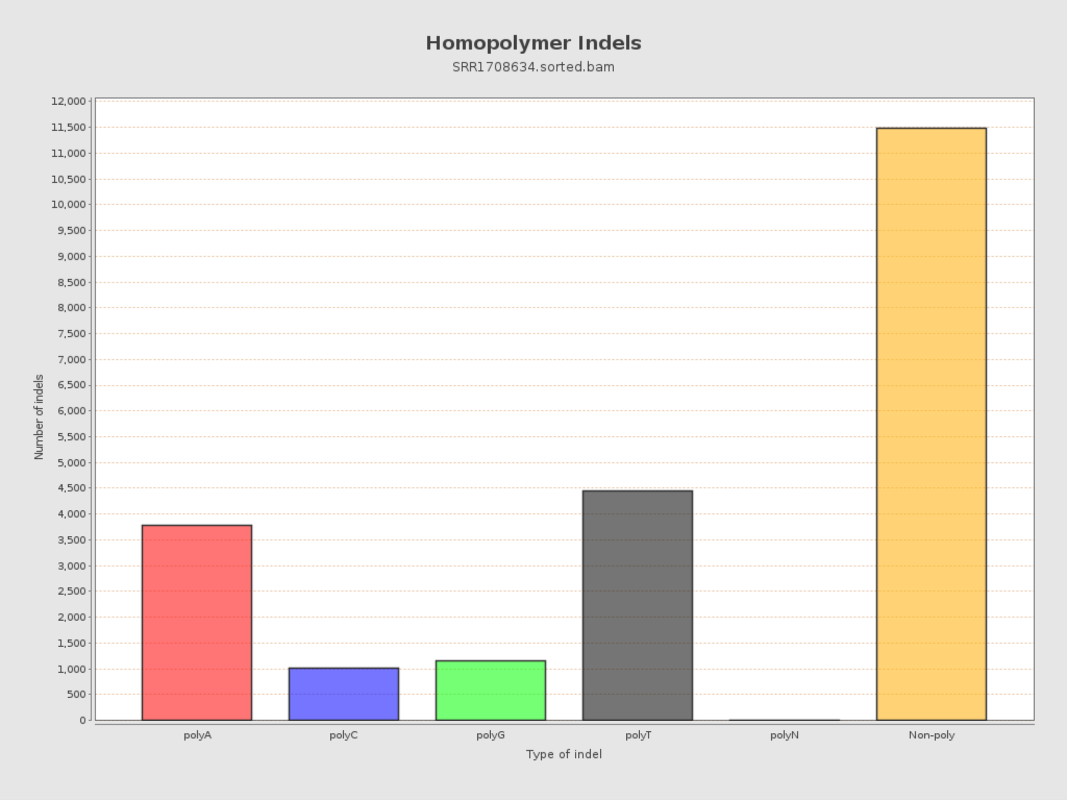
9. Results : Mapped Reads GC-content Distribution



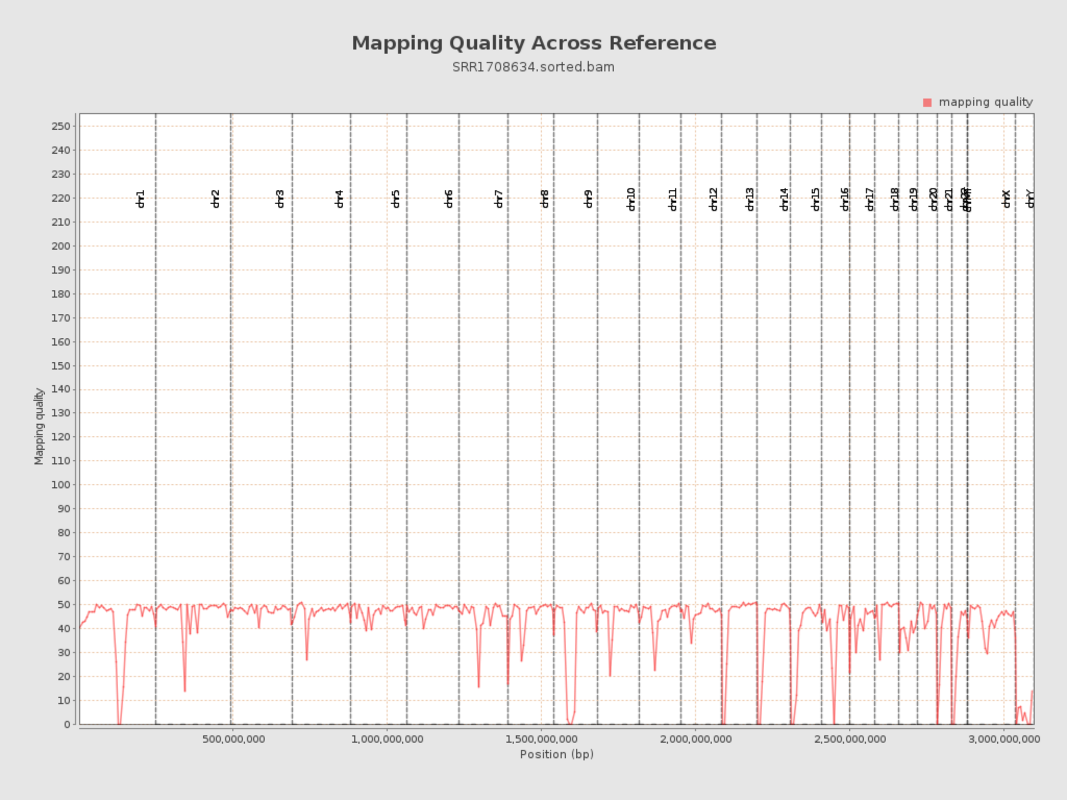
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram