Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:52:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708618.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_SRR1708618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708618.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:52:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,113,899
Mapped reads	2,243,636 / 72.05%
Unmapped reads	870,263 / 27.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	715 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	83,751 / 2.69%
Duplication rate	2.62%
Clipped reads	352,630 / 11.32%

2.2. ACGT Content

Number/percentage of A's	32,111,348 / 29.43%
Number/percentage of C's	20,511,606 / 18.8%
Number/percentage of T's	34,498,720 / 31.61%
Number/percentage of G's	21,997,322 / 20.16%
Number/percentage of N's	9,523 / 0.01%
GC Percentage	38.95%

2.3. Coverage

Mean	0.0353

Standard Deviation	0.375

2.4. Mapping Quality

Mean Mapping Quality	43.26

2.5. Mismatches and indels

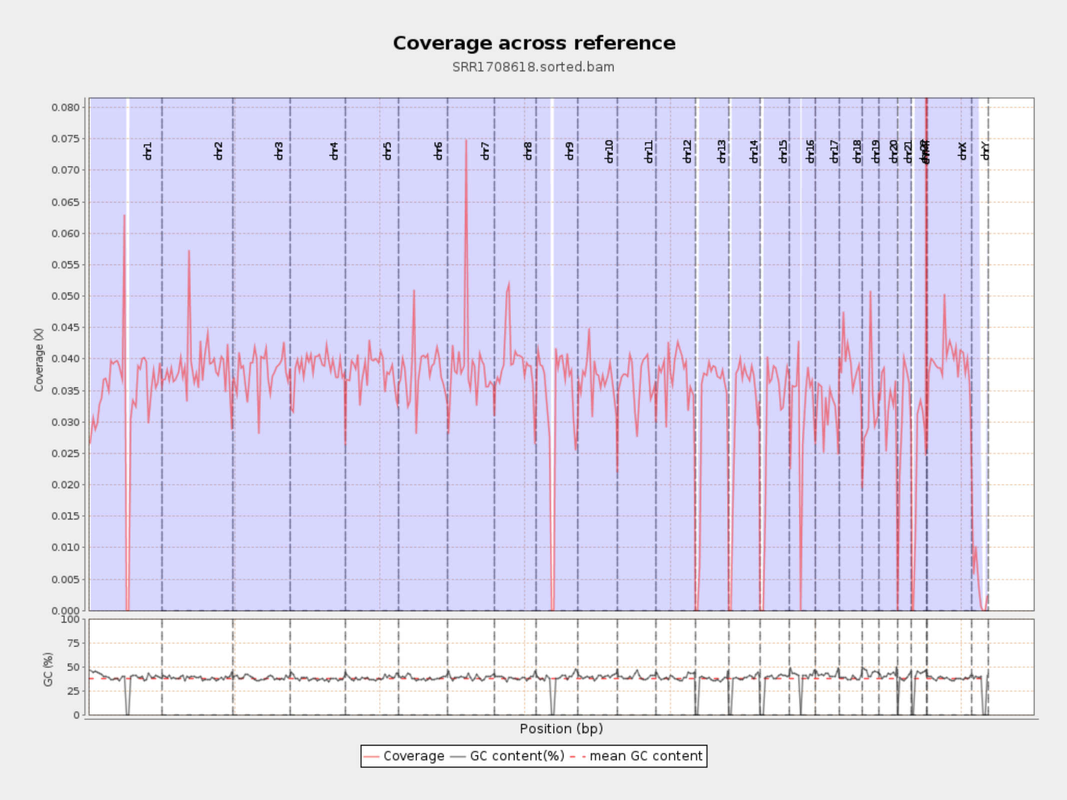
General error rate	0.63%
Mismatches	683,745
Insertions	4,991
Mapped reads with at least one insertion	0.22%
Deletions	13,417
Mapped reads with at least one deletion	0.6%
Homopolymer indels	48.44%

2.6. Chromosome stats

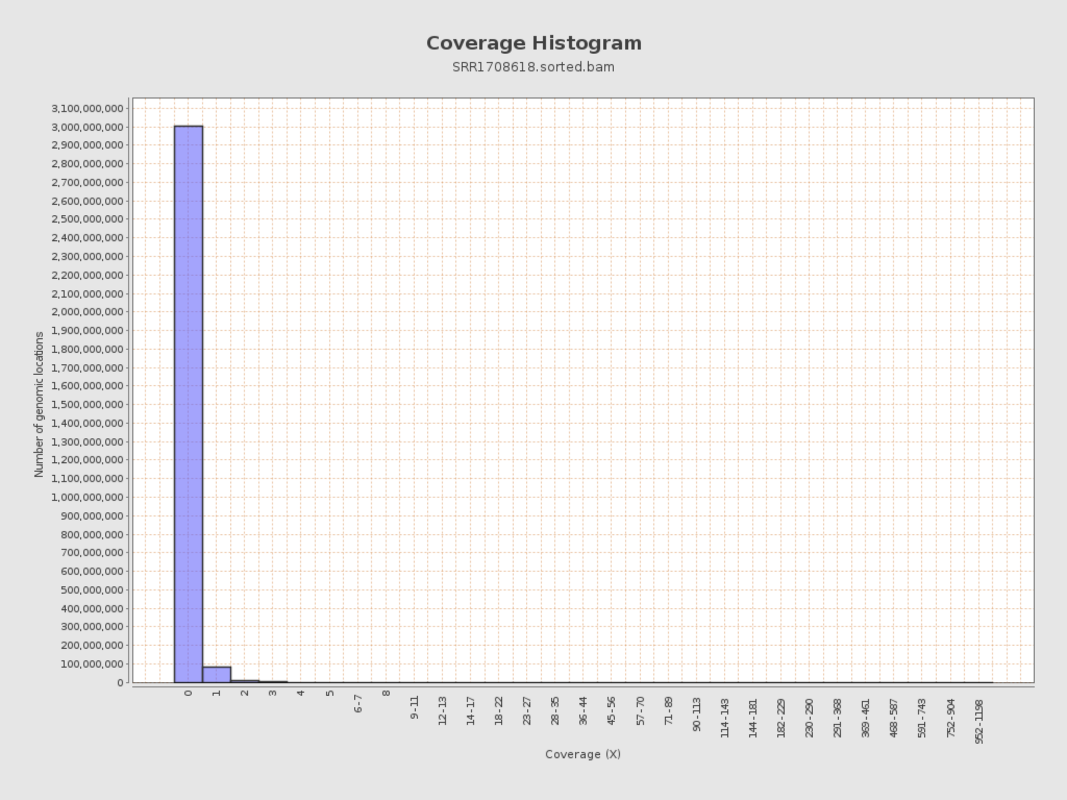
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8538796	0.0343	0.6681
chr2	243199373	9403730	0.0387	0.3797
chr3	198022430	7531446	0.038	0.2251
chr4	191154276	7385408	0.0386	0.2294
chr5	180915260	6887925	0.0381	0.2276
chr6	171115067	6516941	0.0381	0.2964
chr7	159138663	6253679	0.0393	0.5435

chr8	146364022	5759418	0.0393	0.6927
chr9	141213431	4621361	0.0327	0.2945
chr10	135534747	5014814	0.037	0.2899
chr11	135006516	4891098	0.0362	0.3202
chr12	133851895	5011595	0.0374	0.2306
chr13	115169878	3583507	0.0311	0.2038
chr14	107349540	3309118	0.0308	0.2151
chr15	102531392	3054740	0.0298	0.1984
chr16	90354753	2840887	0.0314	0.2174
chr17	81195210	2574817	0.0317	0.2442
chr18	78077248	3060182	0.0392	0.5939
chr19	59128983	1911190	0.0323	0.5051
chr20	63025520	2097526	0.0333	0.2169
chr21	48129895	1419121	0.0295	0.2147
chr22	51304566	1108829	0.0216	0.1668
chrMT	16571	8958	0.5406	0.8756
chrX	155270560	6120431	0.0394	0.2552
chrY	59373566	243525	0.0041	0.0809

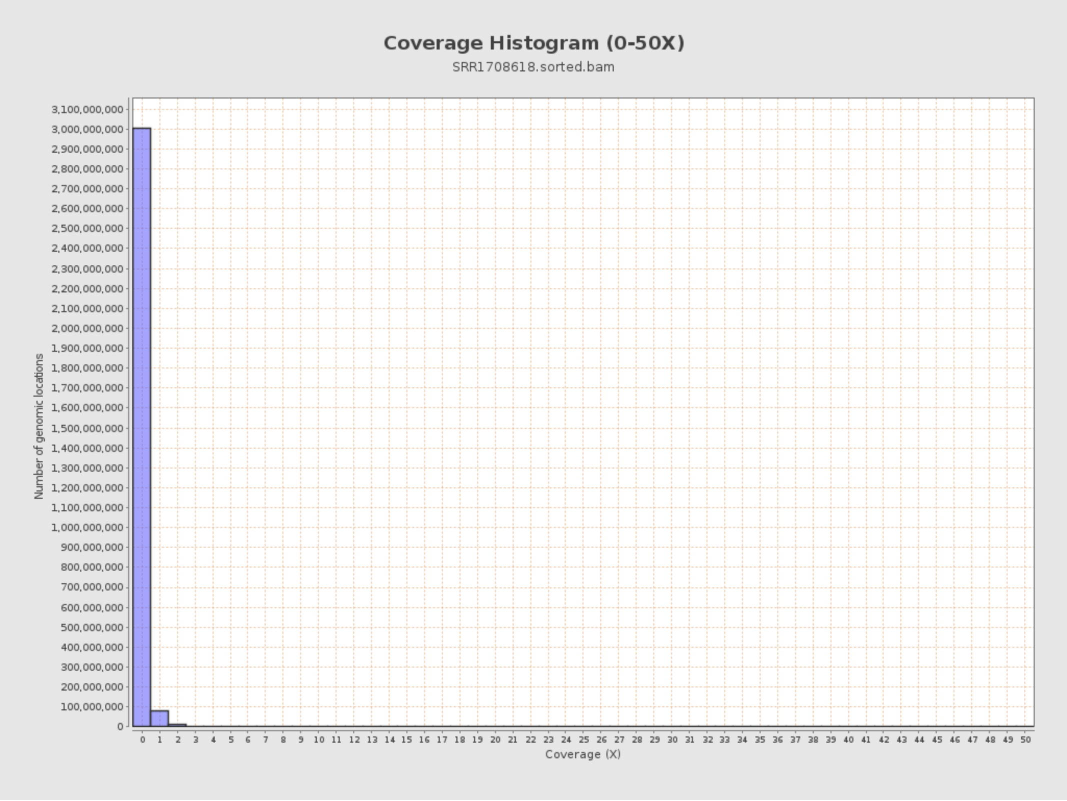
3. Results : Coverage across reference



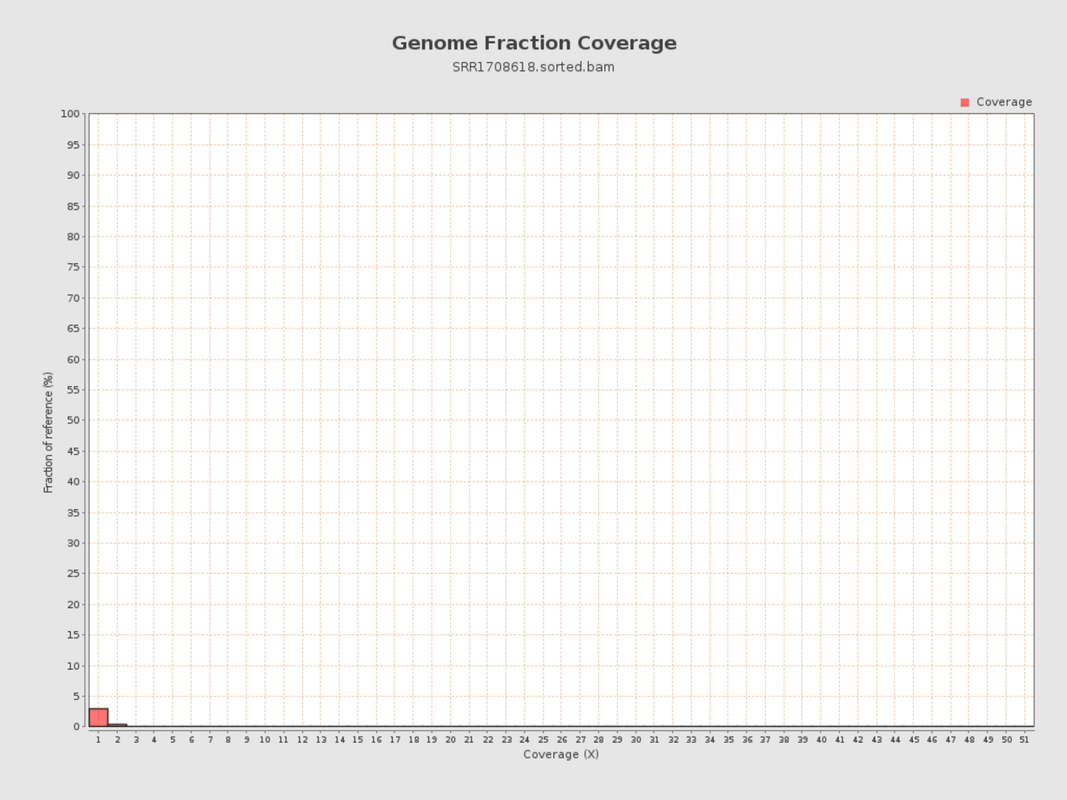
4. Results : Coverage Histogram



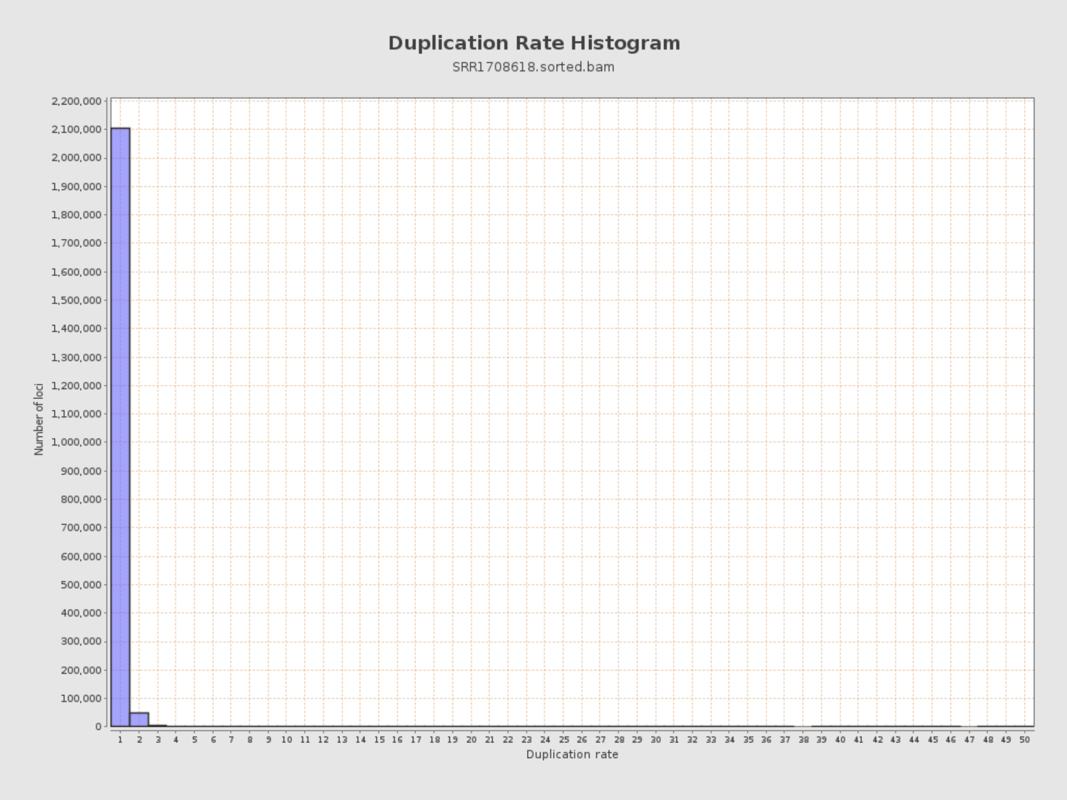
5. Results : Coverage Histogram (0-50X)



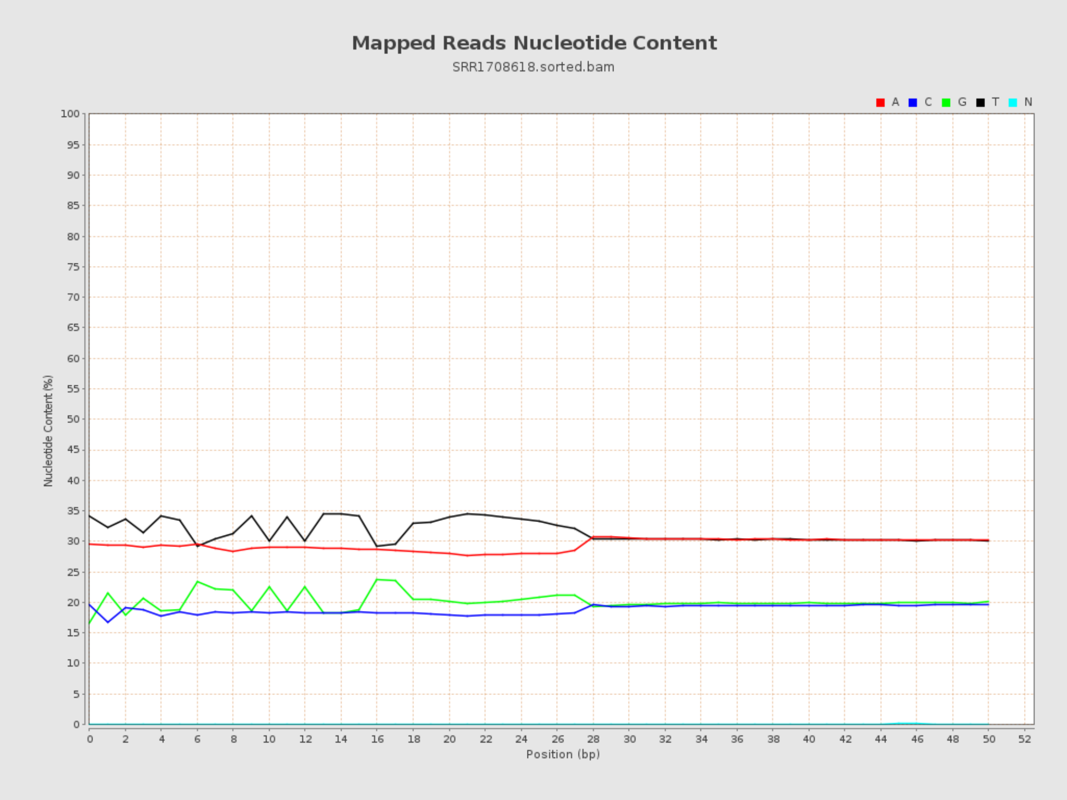
6. Results : Genome Fraction Coverage



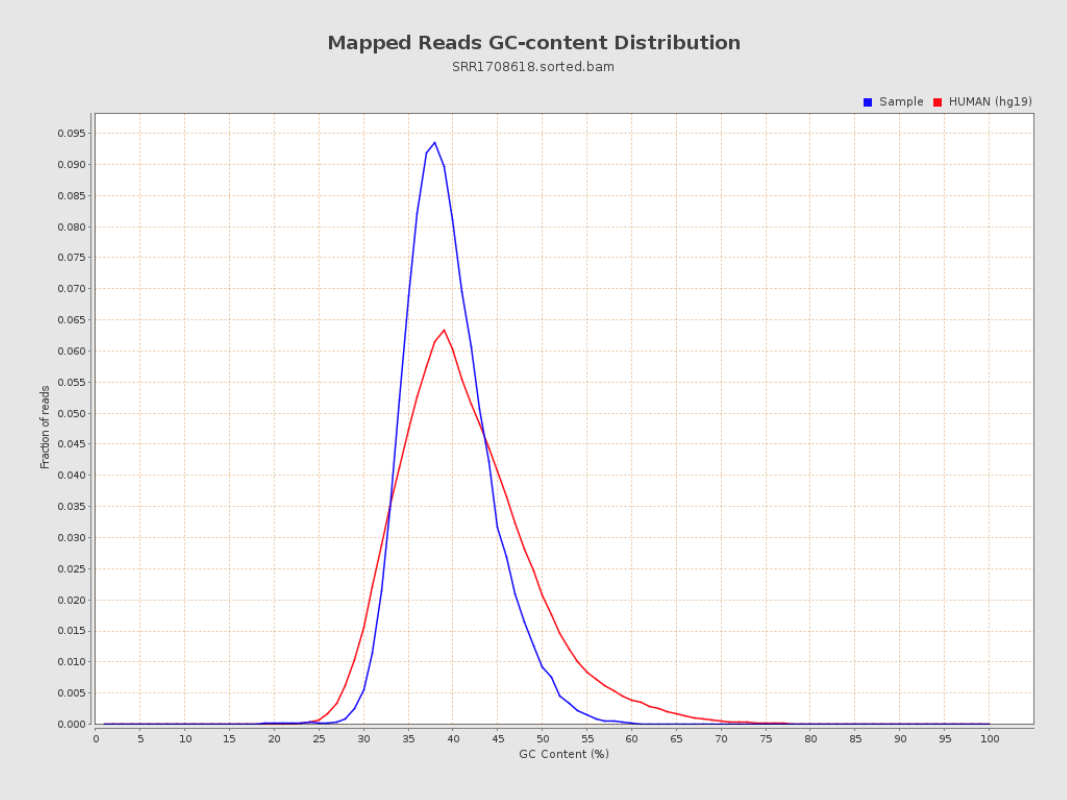
7. Results : Duplication Rate Histogram



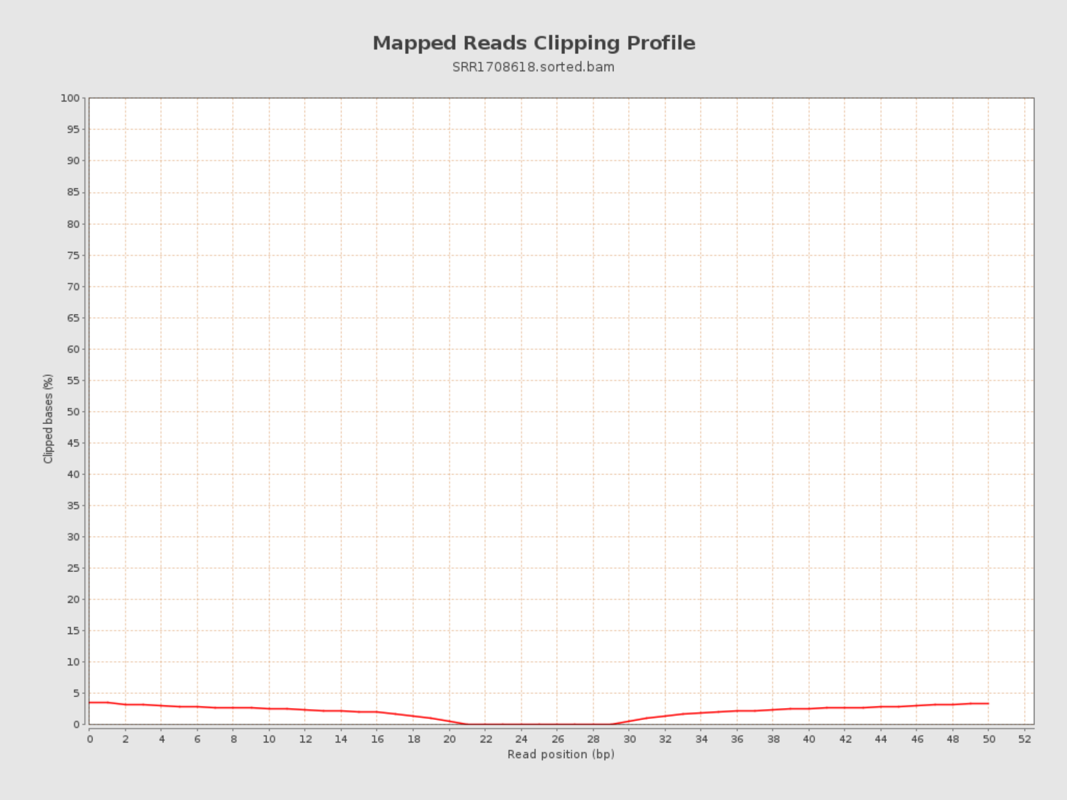
8. Results : Mapped Reads Nucleotide Content



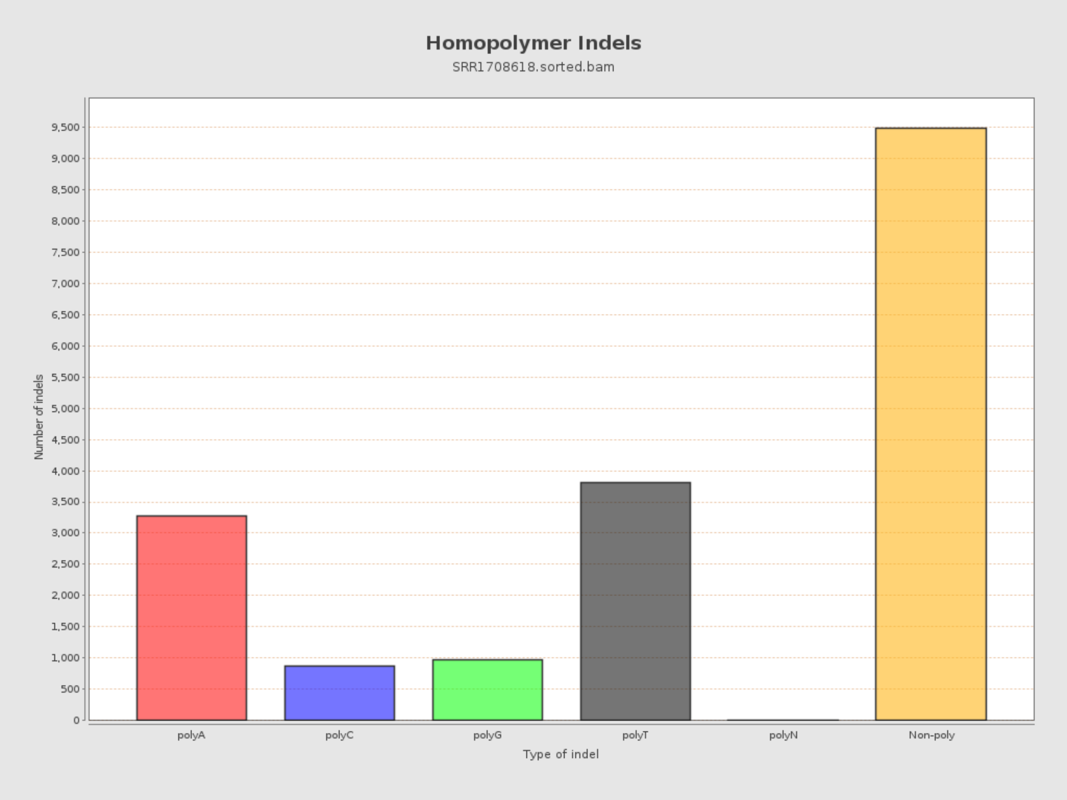
9. Results : Mapped Reads GC-content Distribution



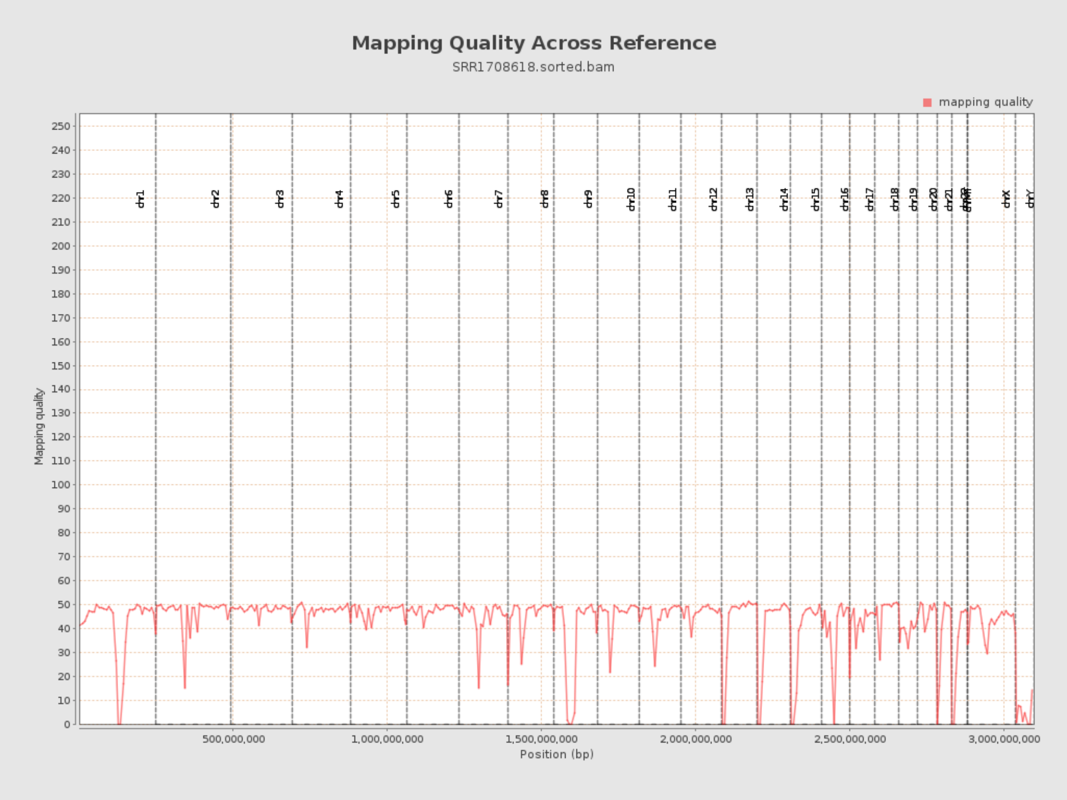
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram