Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:11:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708518.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_SRR1708518 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708518.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708518.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,128,577
Mapped reads	2,286,517 / 73.08%
Unmapped reads	842,060 / 26.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	461 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	92,130 / 2.94%
Duplication rate	3.11%
Clipped reads	356,301 / 11.39%

2.2. ACGT Content

Number/percentage of A's	32,962,101 / 29.61%
Number/percentage of C's	21,021,912 / 18.88%
Number/percentage of T's	35,120,279 / 31.55%
Number/percentage of G's	22,222,787 / 19.96%
Number/percentage of N's	1,638 / 0%
GC Percentage	38.84%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3549

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Mismatches and indels

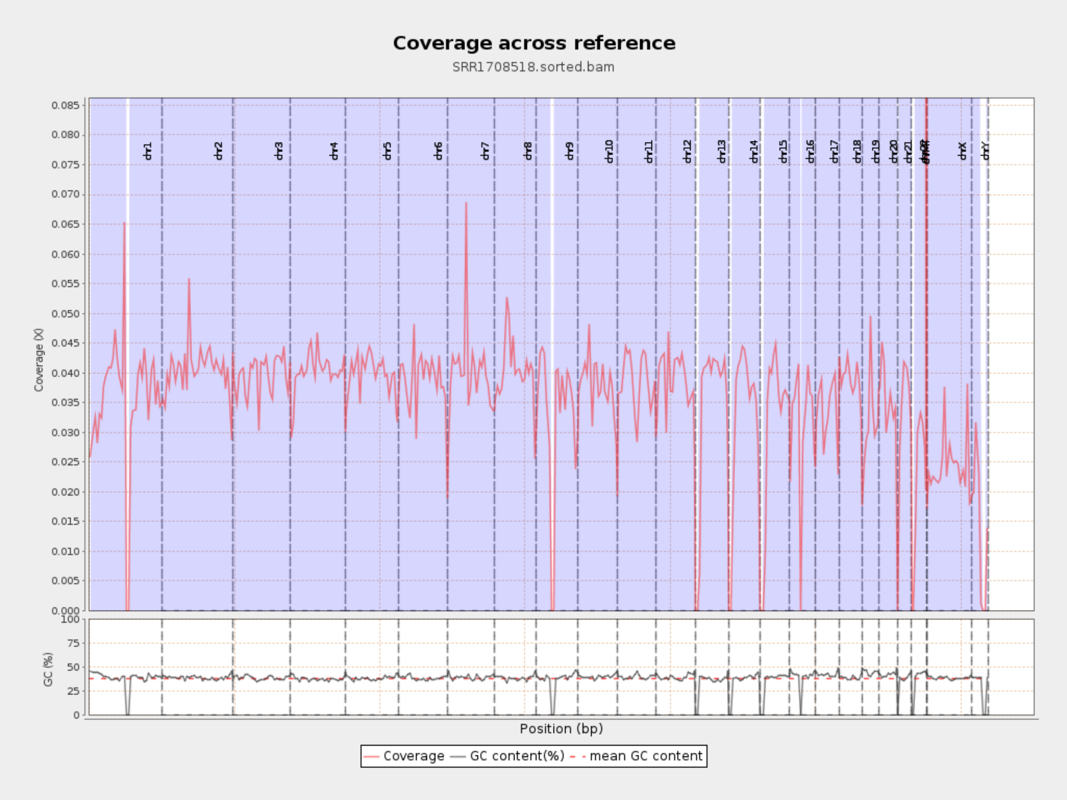
General error rate	0.5%
Mismatches	551,466
Insertions	5,439
Mapped reads with at least one insertion	0.24%
Deletions	13,724
Mapped reads with at least one deletion	0.6%
Homopolymer indels	49.31%

2.6. Chromosome stats

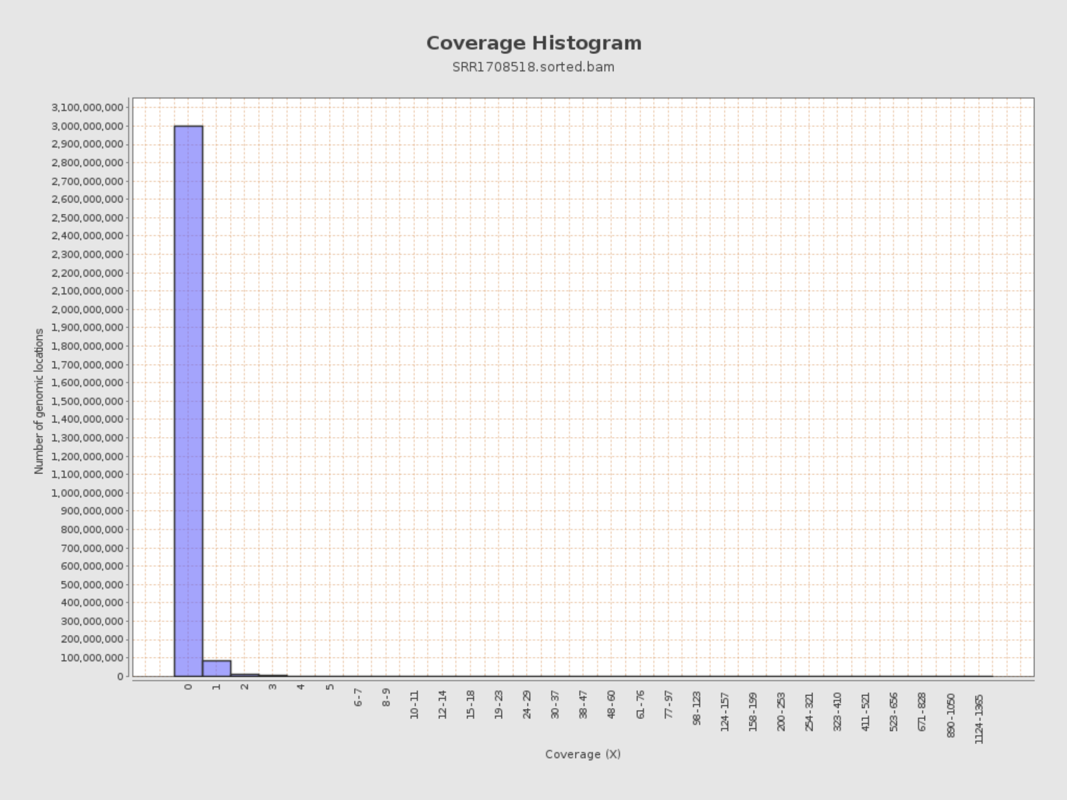
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8889343	0.0357	0.632
chr2	243199373	9873316	0.0406	0.2899
chr3	198022430	7850529	0.0396	0.2294
chr4	191154276	7707039	0.0403	0.2325
chr5	180915260	7228948	0.04	0.2289
chr6	171115067	6646055	0.0388	0.2719
chr7	159138663	6461416	0.0406	0.4612

chr8	146364022	5906900	0.0404	0.76
chr9	141213431	4647499	0.0329	0.2591
chr10	135534747	5180408	0.0382	0.286
chr11	135006516	5176896	0.0383	0.3168
chr12	133851895	5199478	0.0388	0.2273
chr13	115169878	3885088	0.0337	0.209
chr14	107349540	3466899	0.0323	0.2113
chr15	102531392	3143358	0.0307	0.1989
chr16	90354753	2860766	0.0317	0.2109
chr17	81195210	2698607	0.0332	0.2552
chr18	78077248	3049739	0.0391	0.4399
chr19	59128983	1901542	0.0322	0.4515
chr20	63025520	2227671	0.0353	0.2188
chr21	48129895	1559230	0.0324	0.2478
chr22	51304566	1086787	0.0212	0.1911
chrMT	16571	131709	7.9482	5.5956
chrX	155270560	3774769	0.0243	0.2054
chrY	59373566	795820	0.0134	0.1447

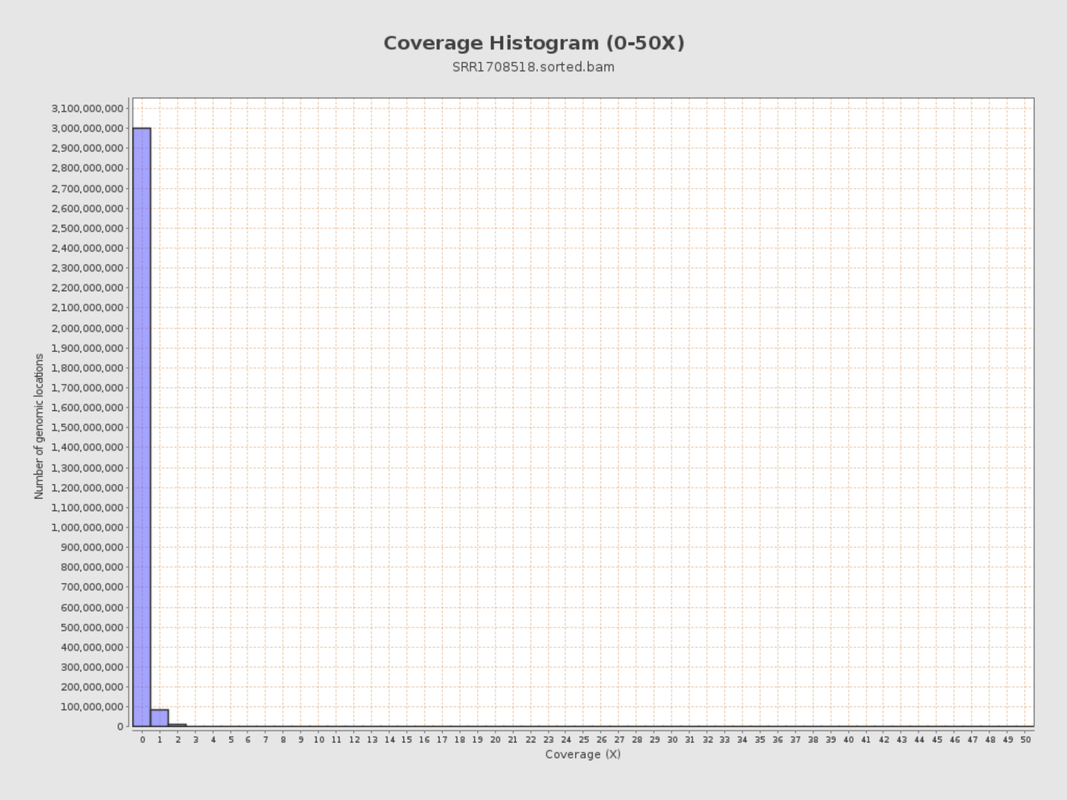
3. Results : Coverage across reference



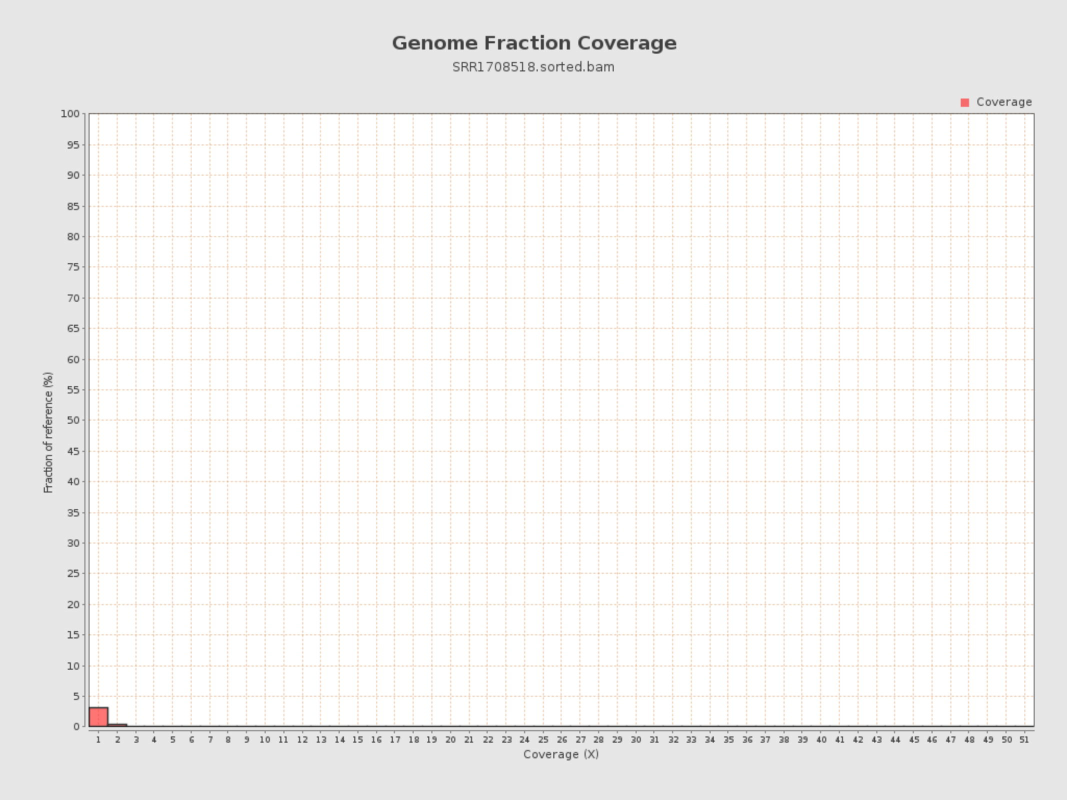
4. Results : Coverage Histogram



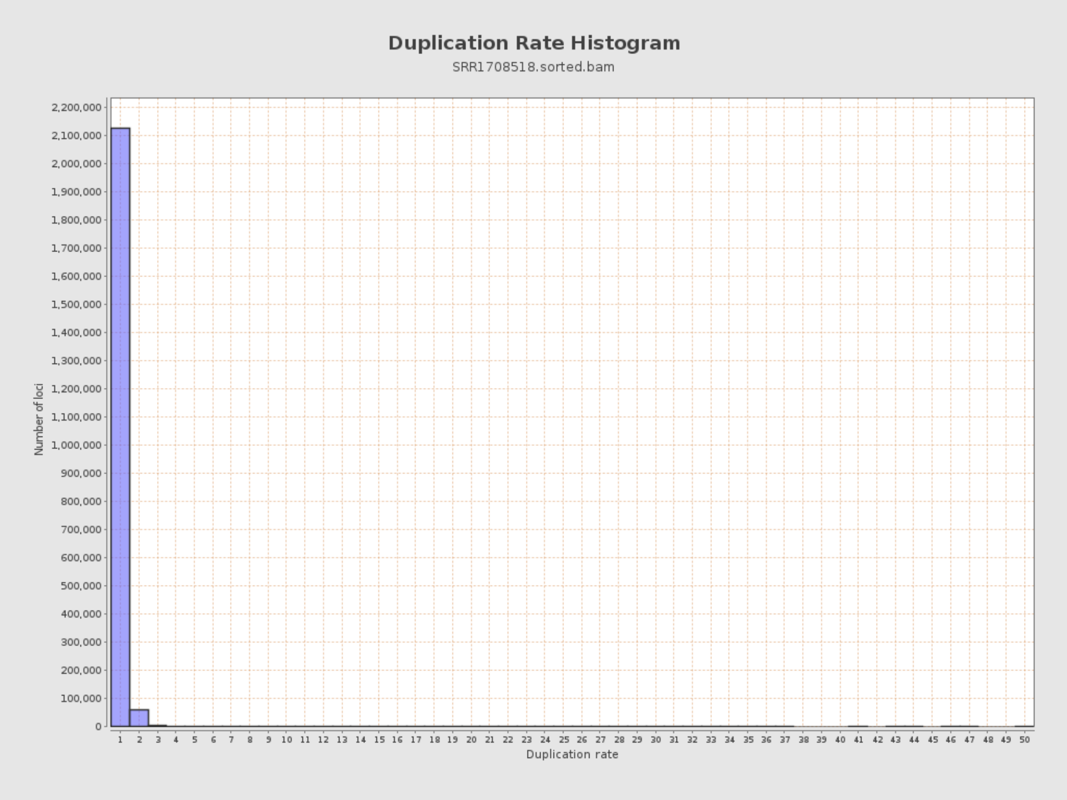
5. Results : Coverage Histogram (0-50X)



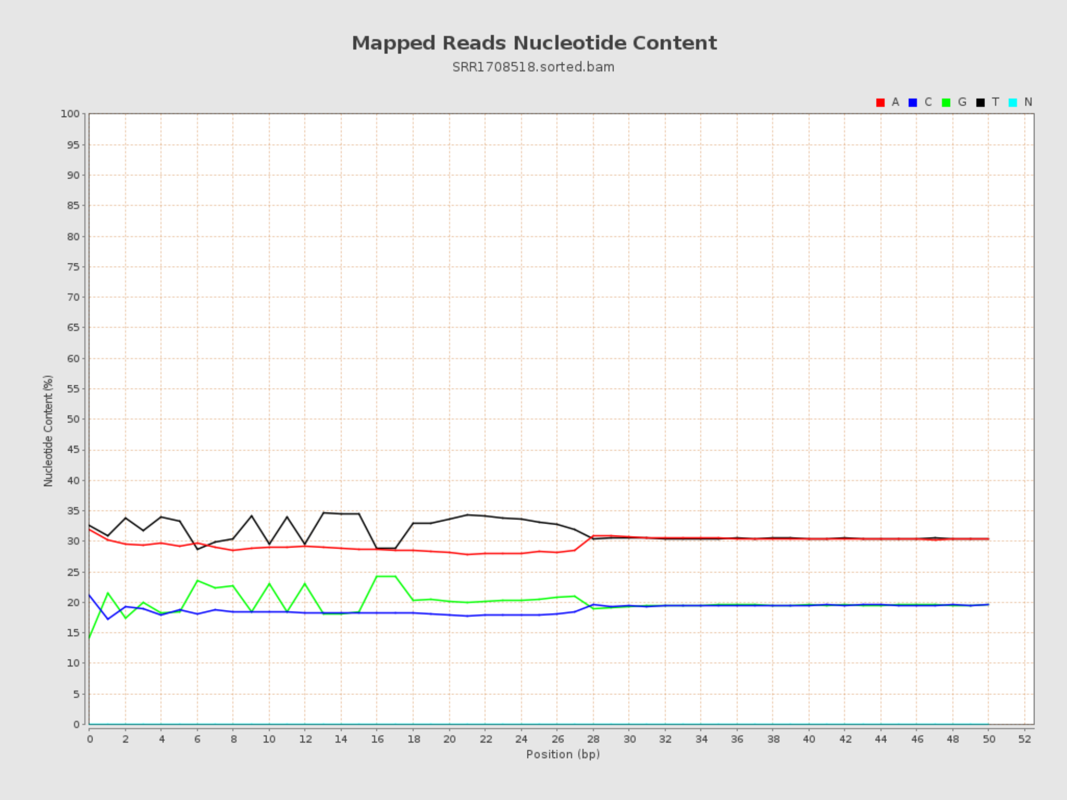
6. Results : Genome Fraction Coverage



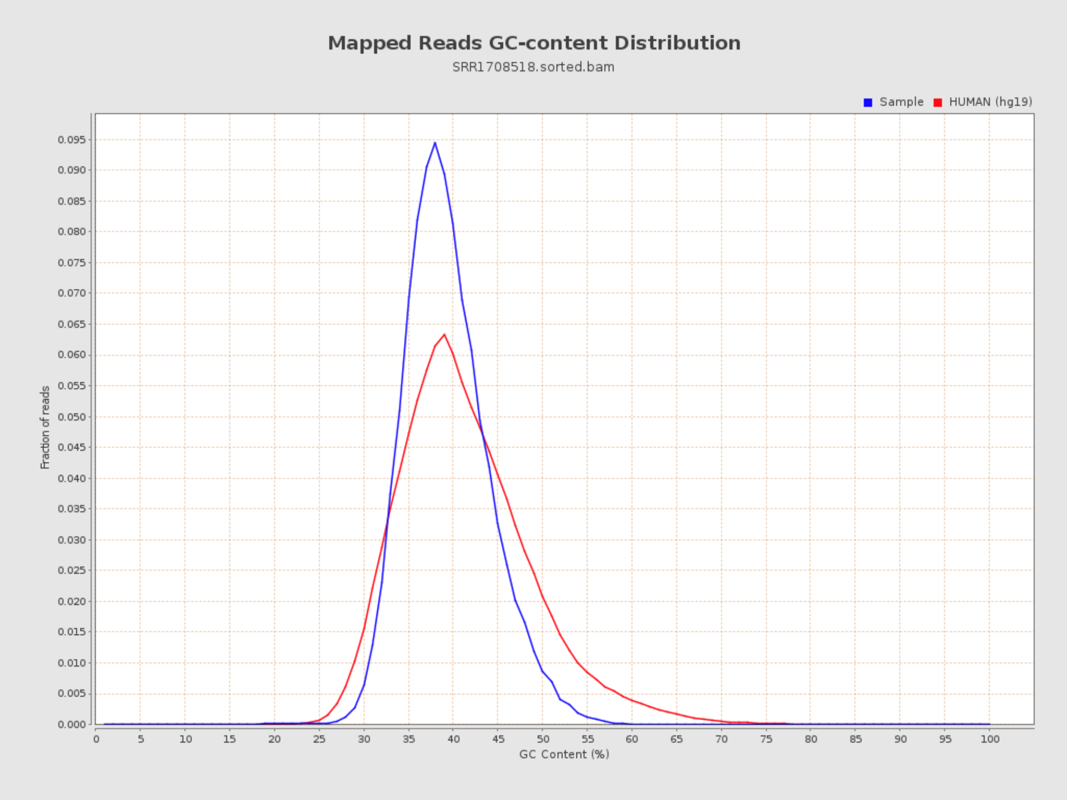
7. Results : Duplication Rate Histogram



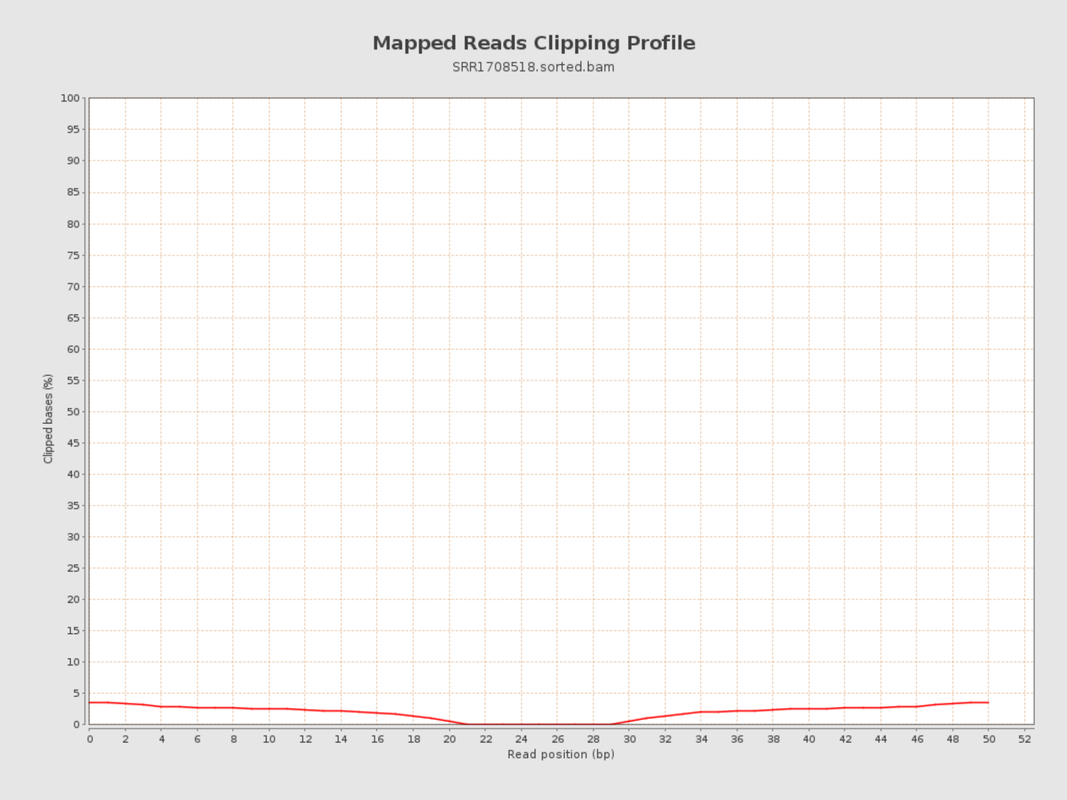
8. Results : Mapped Reads Nucleotide Content



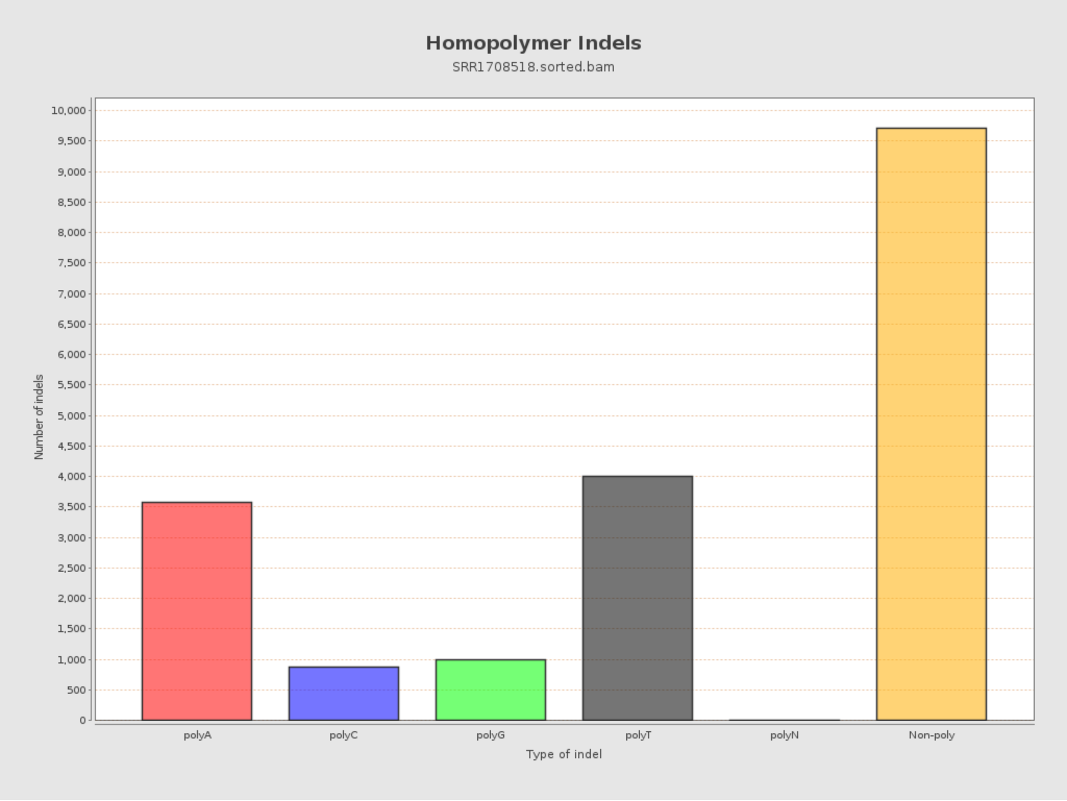
9. Results : Mapped Reads GC-content Distribution



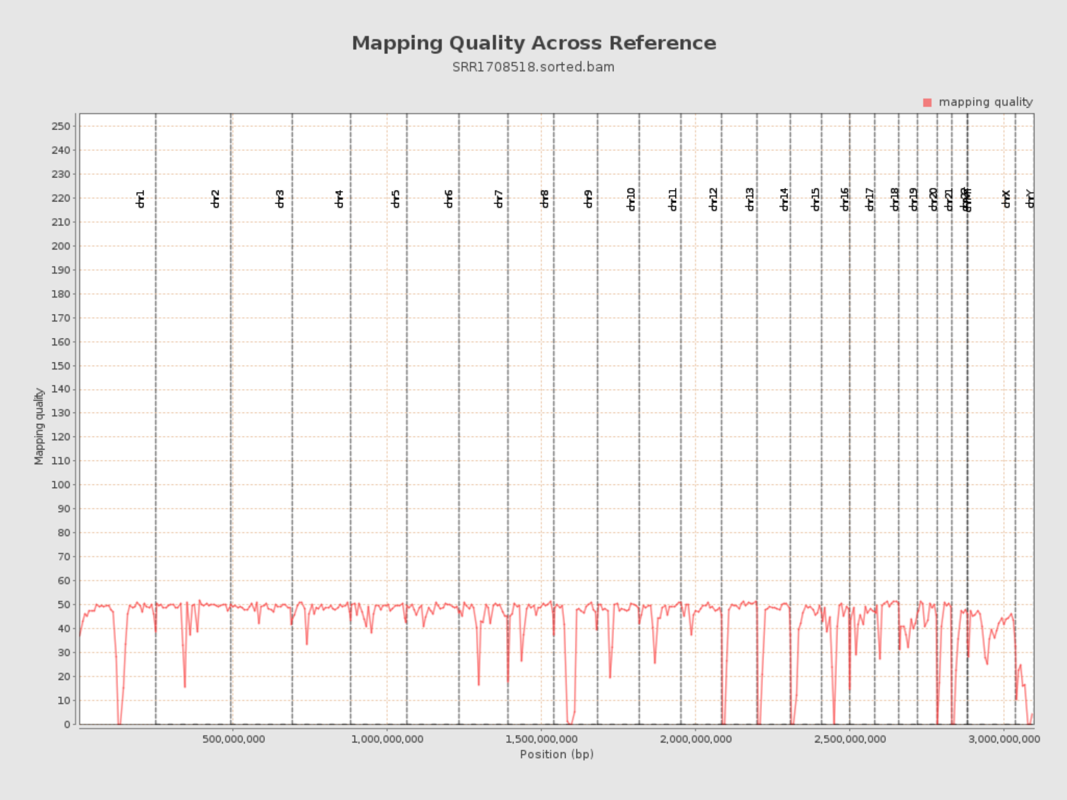
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram