Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:26:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708519.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_SRR1708519 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708519.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:26:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708519.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,147,914
Mapped reads	2,221,114 / 70.56%
Unmapped reads	926,800 / 29.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	412 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	99,941 / 3.17%
Duplication rate	3.42%
Clipped reads	389,995 / 12.39%

2.2. ACGT Content

Number/percentage of A's	31,470,738 / 29.33%
Number/percentage of C's	19,871,664 / 18.52%
Number/percentage of T's	34,356,866 / 32.02%
Number/percentage of G's	21,602,722 / 20.13%
Number/percentage of N's	1,560 / 0%
GC Percentage	38.65%

2.3. Coverage

Mean	0.0347

Standard Deviation	0.3769

2.4. Mapping Quality

Mean Mapping Quality	43.52

2.5. Mismatches and indels

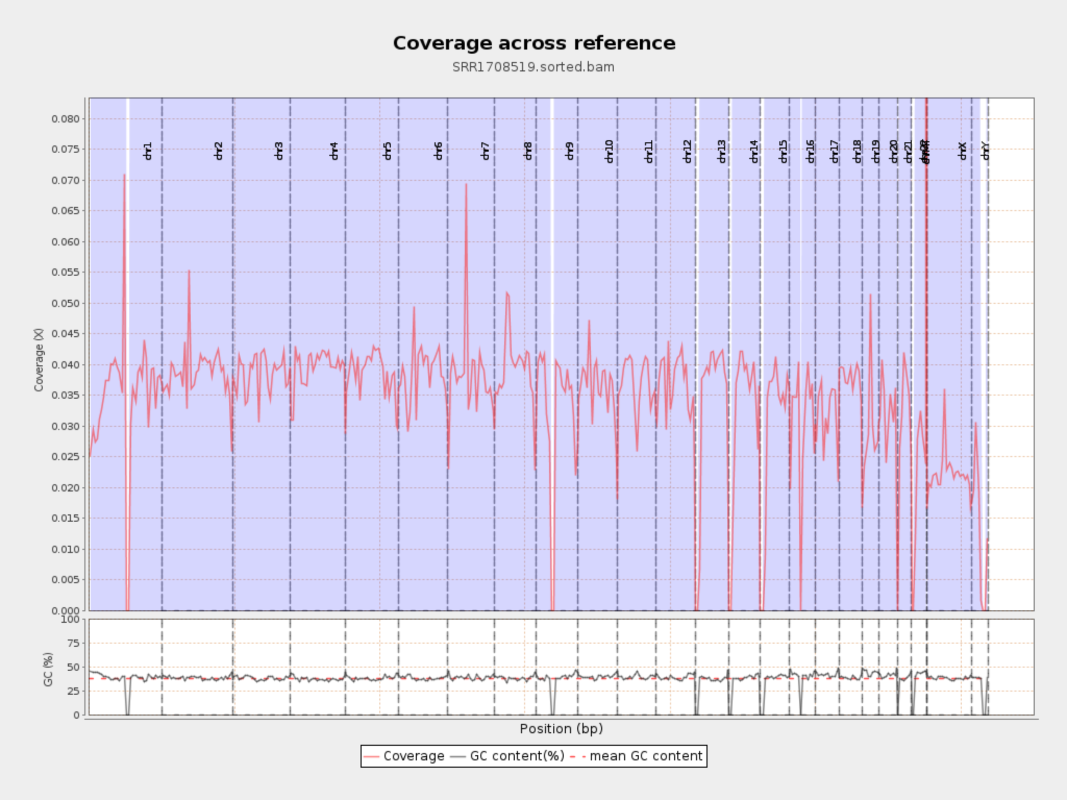
General error rate	0.5%
Mismatches	524,087
Insertions	5,121
Mapped reads with at least one insertion	0.23%
Deletions	12,743
Mapped reads with at least one deletion	0.57%
Homopolymer indels	48.07%

2.6. Chromosome stats

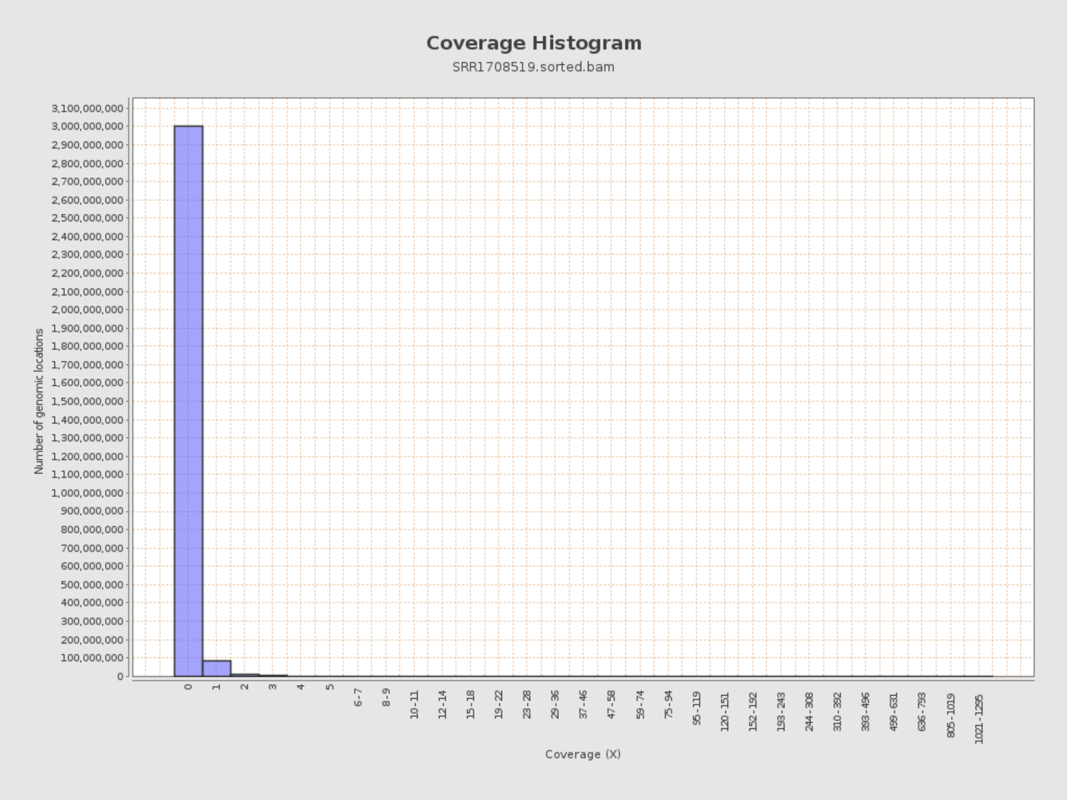
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8641994	0.0347	0.785
chr2	243199373	9444329	0.0388	0.2984
chr3	198022430	7634748	0.0386	0.2244
chr4	191154276	7582545	0.0397	0.2316
chr5	180915260	7021049	0.0388	0.227
chr6	171115067	6625538	0.0387	0.2672
chr7	159138663	6157087	0.0387	0.4665

chr8	146364022	5754453	0.0393	0.7341
chr9	141213431	4562366	0.0323	0.2532
chr10	135534747	4990709	0.0368	0.291
chr11	135006516	4945504	0.0366	0.3142
chr12	133851895	4937771	0.0369	0.2231
chr13	115169878	3800571	0.033	0.2076
chr14	107349540	3364817	0.0313	0.2062
chr15	102531392	2986076	0.0291	0.1925
chr16	90354753	2758884	0.0305	0.2083
chr17	81195210	2533778	0.0312	0.2502
chr18	78077248	2980458	0.0382	0.4254
chr19	59128983	1761256	0.0298	0.5334
chr20	63025520	2025237	0.0321	0.2058
chr21	48129895	1463998	0.0304	0.2294
chr22	51304566	1022912	0.0199	0.1784
chrMT	16571	120737	7.286	5.3697
chrX	155270560	3469745	0.0223	0.1955
chrY	59373566	736323	0.0124	0.1374

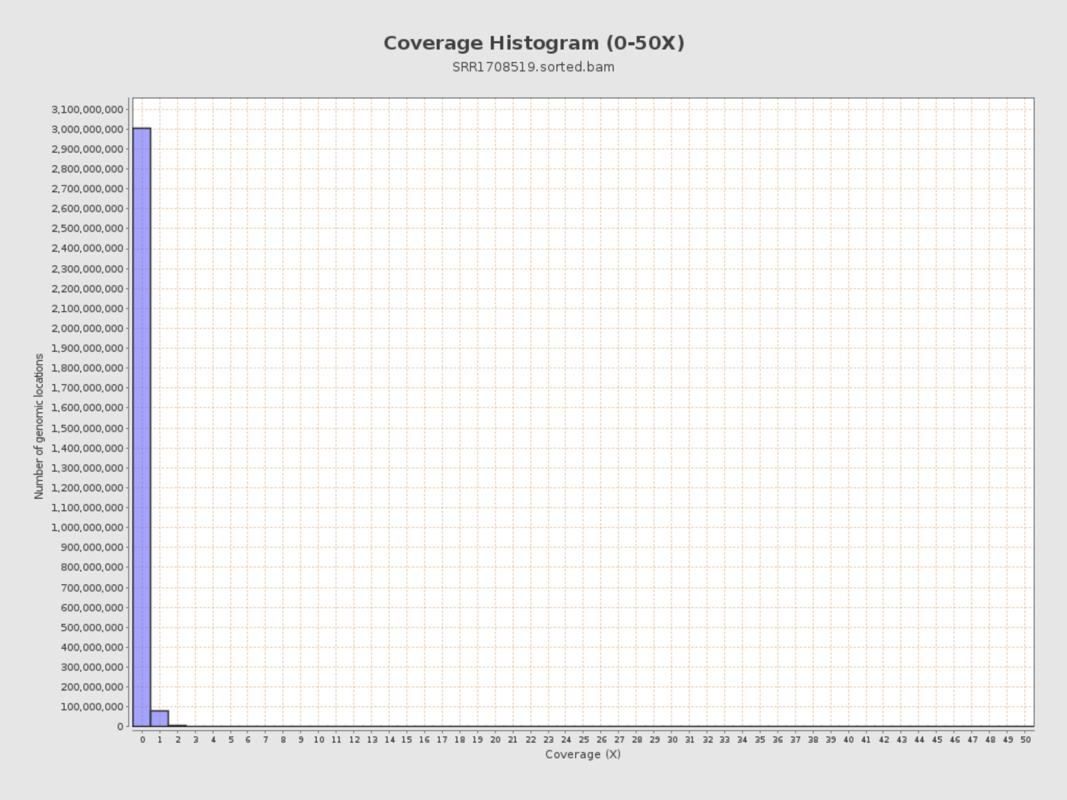
3. Results : Coverage across reference



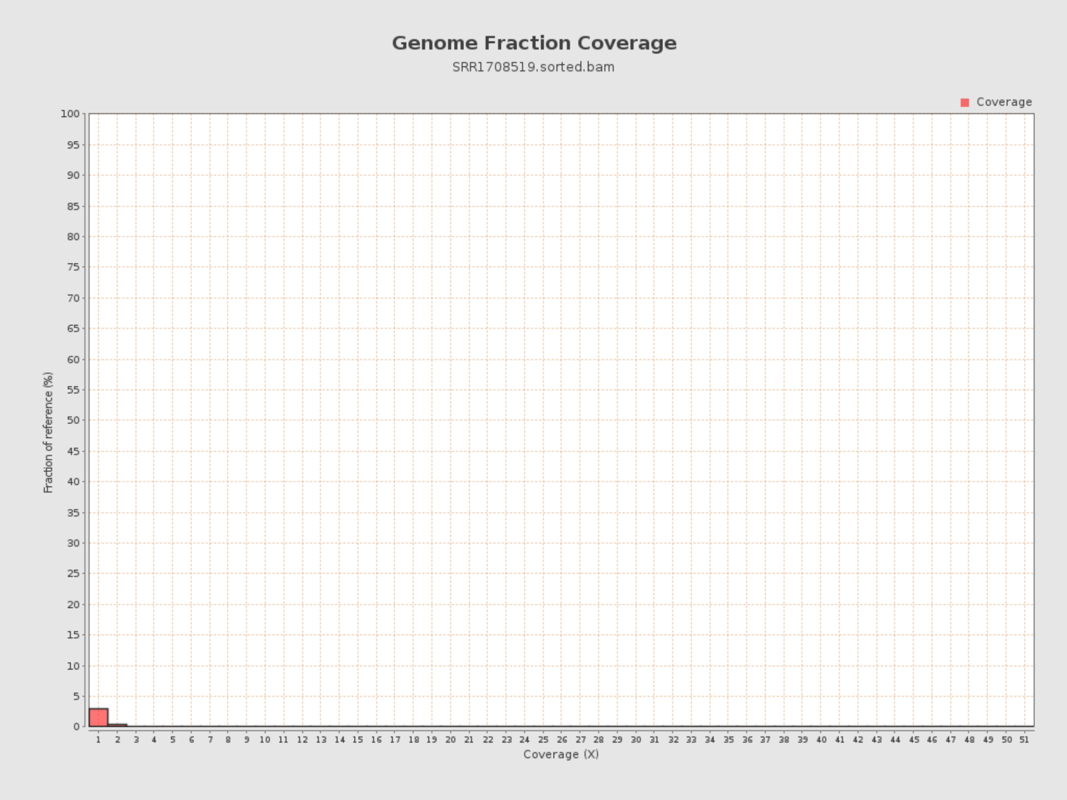
4. Results : Coverage Histogram



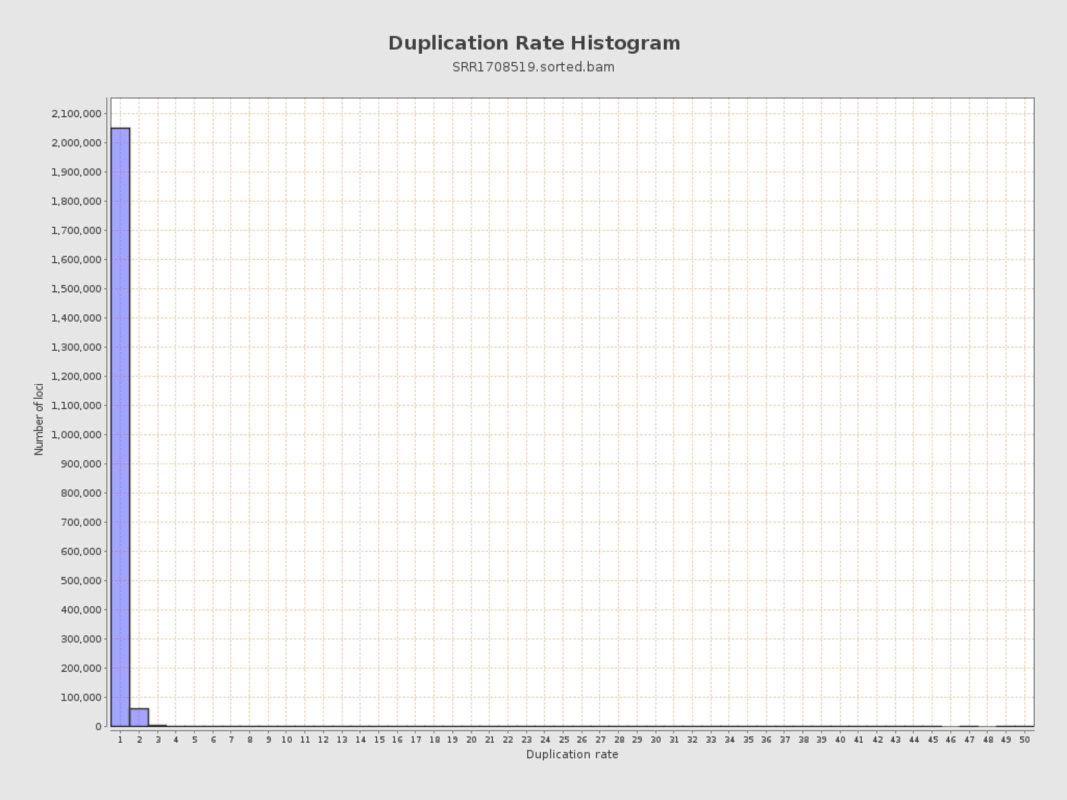
5. Results : Coverage Histogram (0-50X)



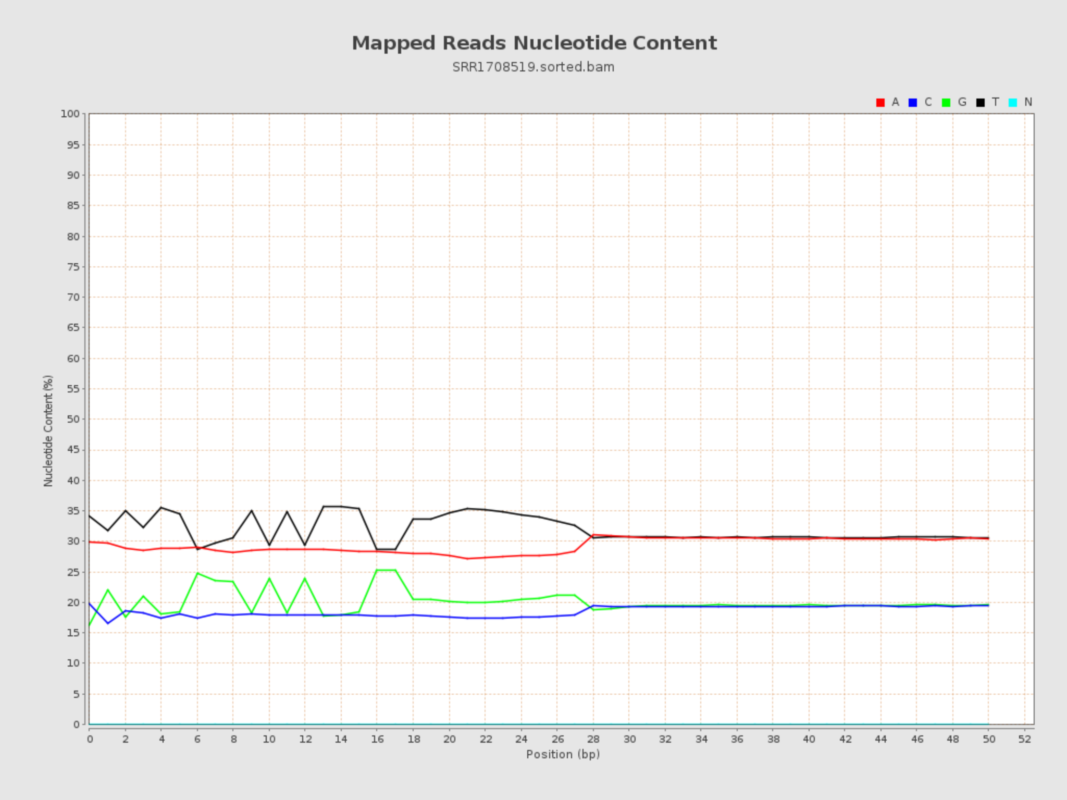
6. Results : Genome Fraction Coverage



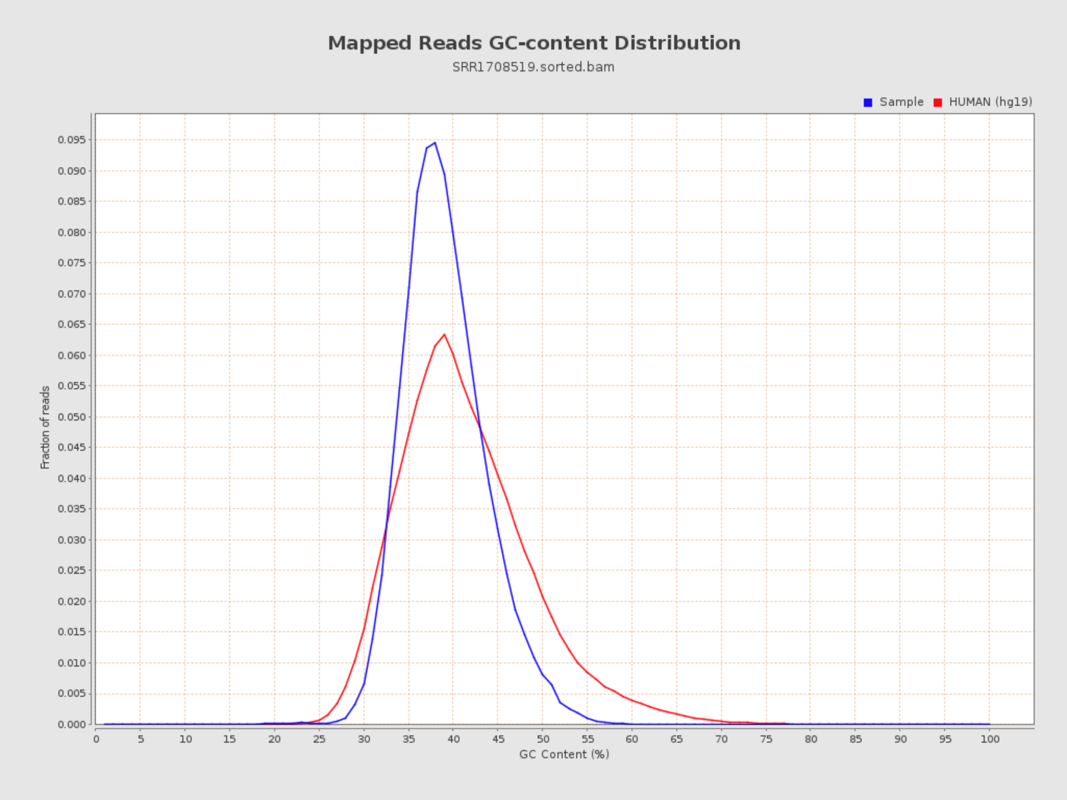
7. Results : Duplication Rate Histogram



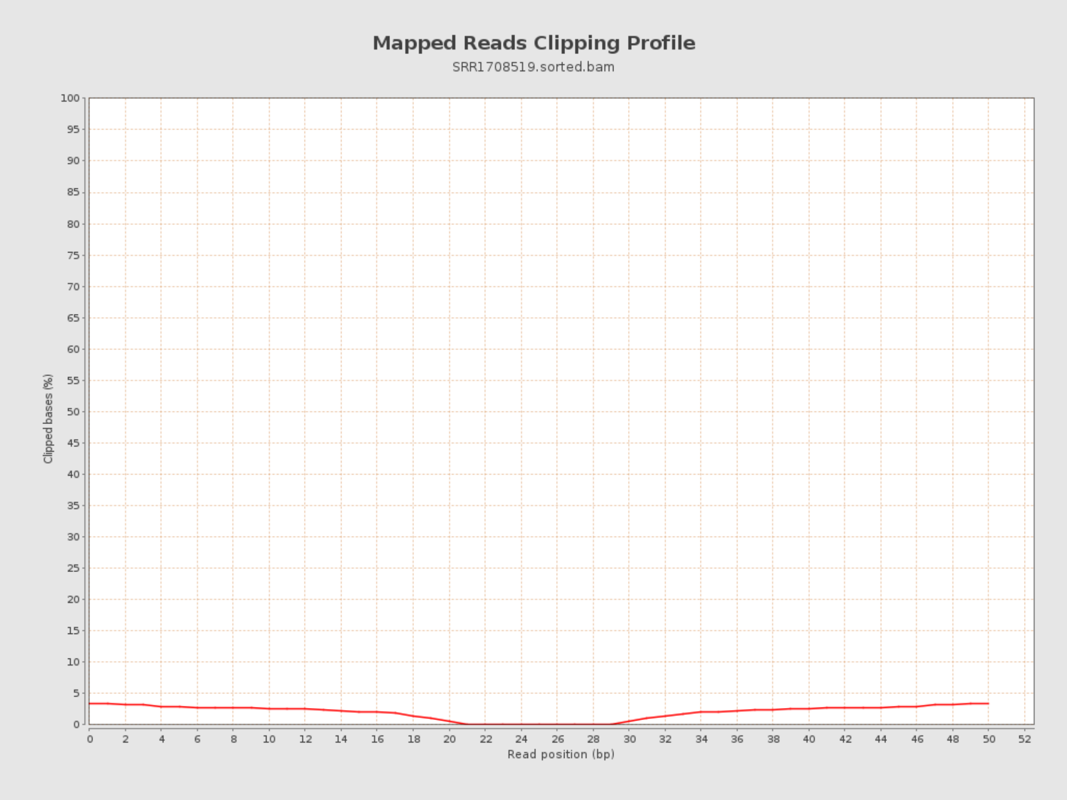
8. Results : Mapped Reads Nucleotide Content



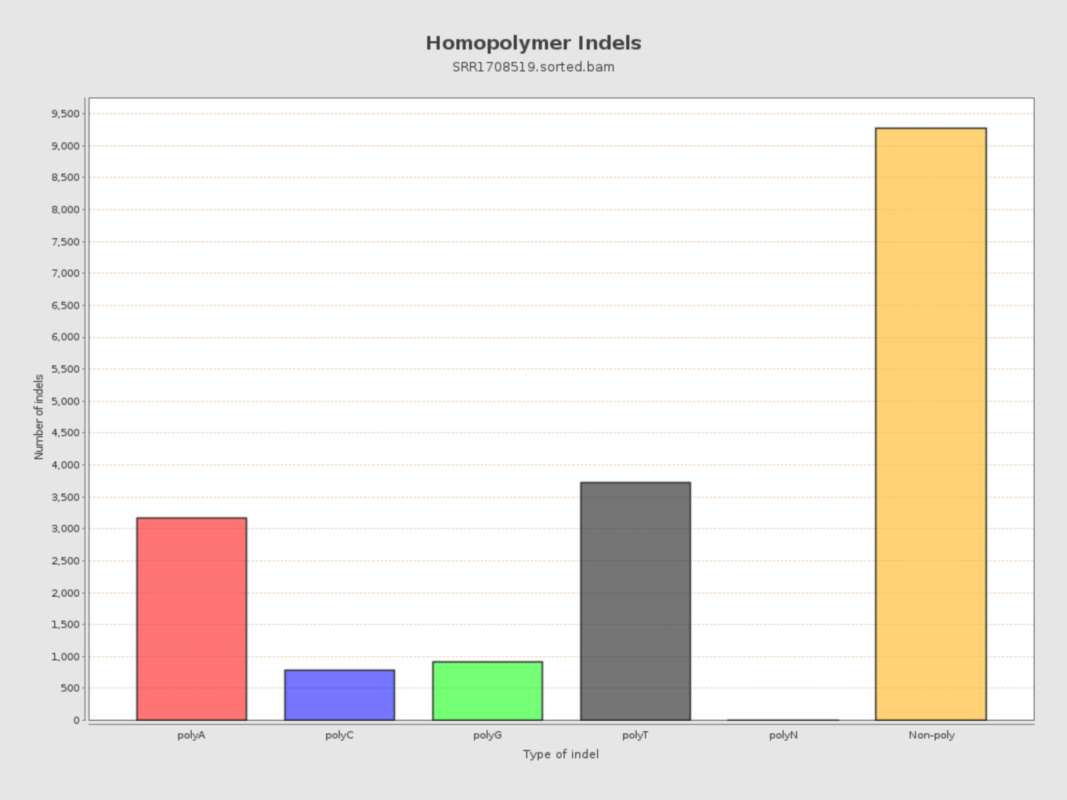
9. Results : Mapped Reads GC-content Distribution



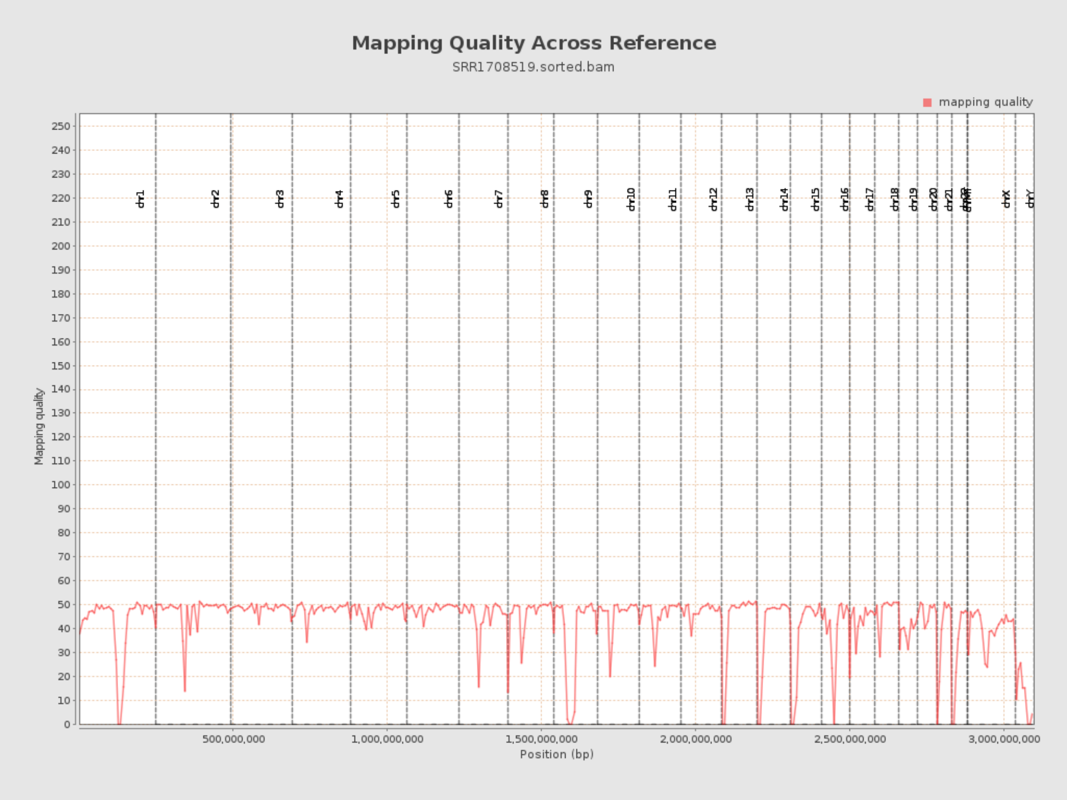
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram