Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:30:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708548.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_SRR1708548 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708548.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:30:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708548.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,959,604
Mapped reads	3,258,937 / 82.3%
Unmapped reads	700,667 / 17.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	84 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,010 / 0.38%
Duplication rate	0.46%
Clipped reads	44,159 / 1.12%

2.2. ACGT Content

Number/percentage of A's	50,359,307 / 30.99%
Number/percentage of C's	30,867,550 / 18.99%
Number/percentage of T's	50,093,915 / 30.83%
Number/percentage of G's	31,177,816 / 19.19%
Number/percentage of N's	7,297 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	0.0525

Standard Deviation	0.2358

2.4. Mapping Quality

Mean Mapping Quality	46.47

2.5. Mismatches and indels

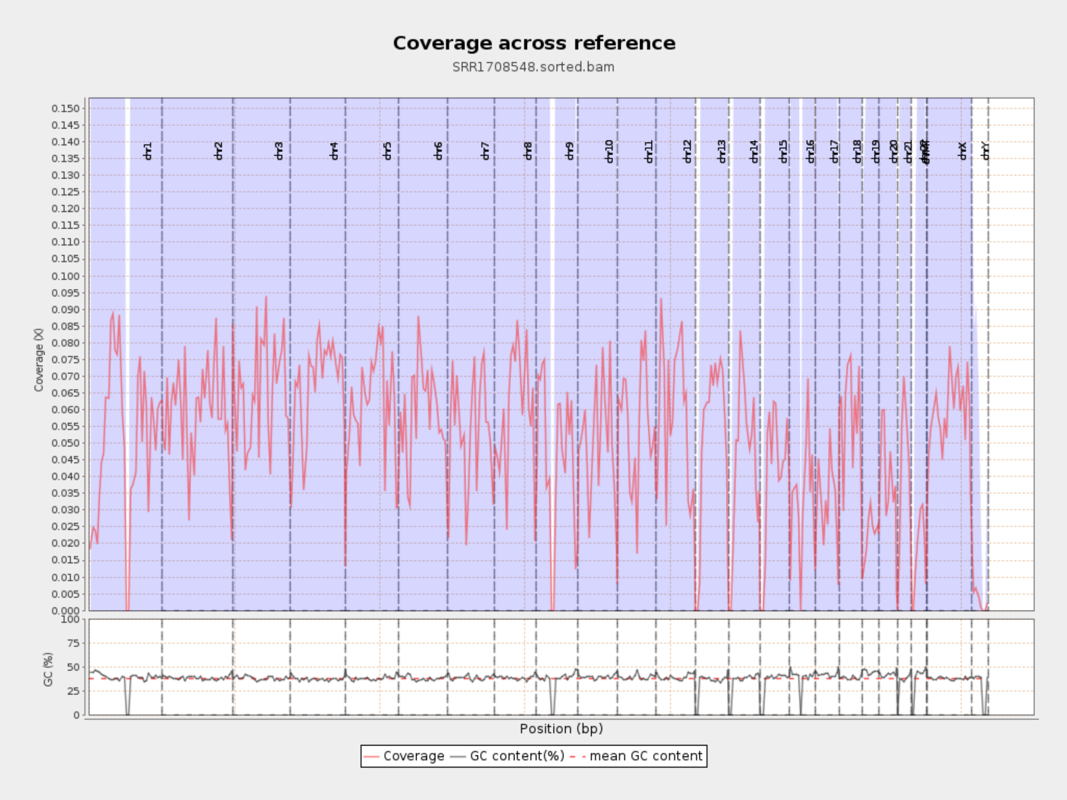
General error rate	0.17%
Mismatches	256,510
Insertions	10,727
Mapped reads with at least one insertion	0.33%
Deletions	8,702
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.52%

2.6. Chromosome stats

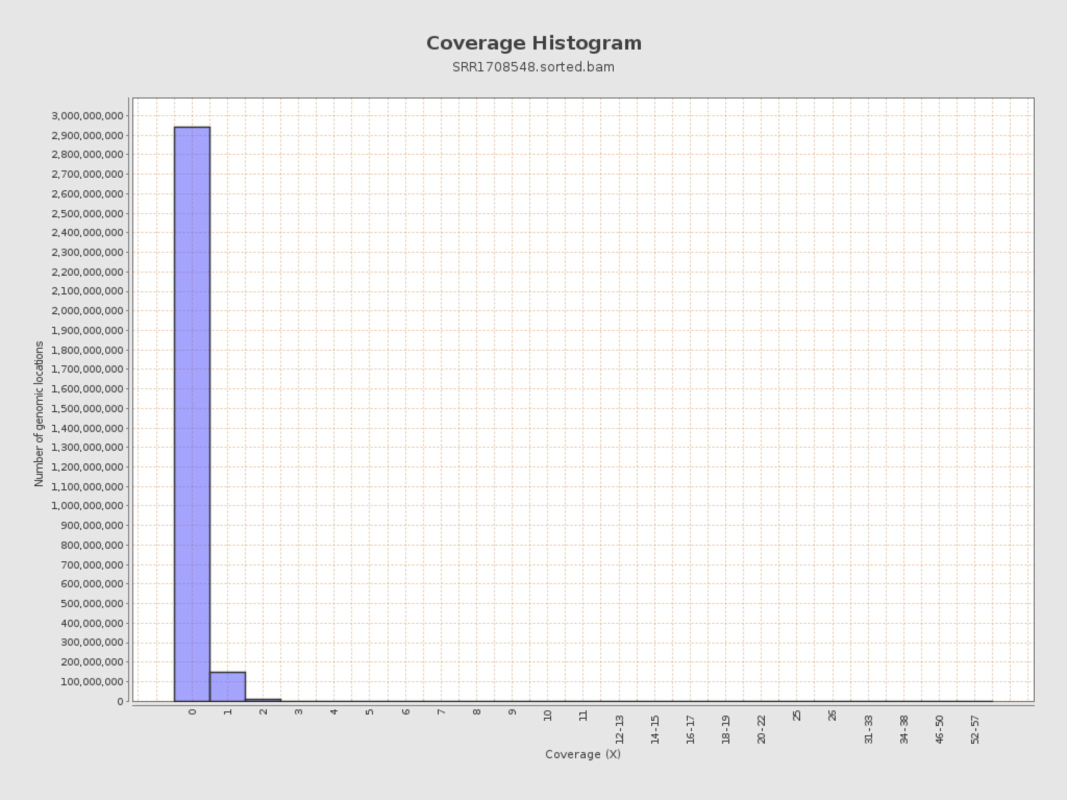
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12730025	0.0511	0.2338
chr2	243199373	14414403	0.0593	0.2498
chr3	198022430	13069456	0.066	0.2636
chr4	191154276	12983075	0.0679	0.2671
chr5	180915260	11226677	0.0621	0.2555
chr6	171115067	10060894	0.0588	0.2486
chr7	159138663	8735538	0.0549	0.2409

chr8	146364022	8857401	0.0605	0.2523
chr9	141213431	6569189	0.0465	0.2221
chr10	135534747	7073479	0.0522	0.2347
chr11	135006516	7453277	0.0552	0.2423
chr12	133851895	7868437	0.0588	0.249
chr13	115169878	6017240	0.0522	0.2349
chr14	107349540	4903229	0.0457	0.2206
chr15	102531392	4143661	0.0404	0.2066
chr16	90354753	3040489	0.0337	0.1886
chr17	81195210	2608798	0.0321	0.1842
chr18	78077248	4584811	0.0587	0.2482
chr19	59128983	1350575	0.0228	0.1542
chr20	63025520	2534808	0.0402	0.2063
chr21	48129895	1959448	0.0407	0.2083
chr22	51304566	905580	0.0177	0.1361
chrMT	16571	300	0.0181	0.1333
chrX	155270560	9210323	0.0593	0.2501
chrY	59373566	219725	0.0037	0.0631

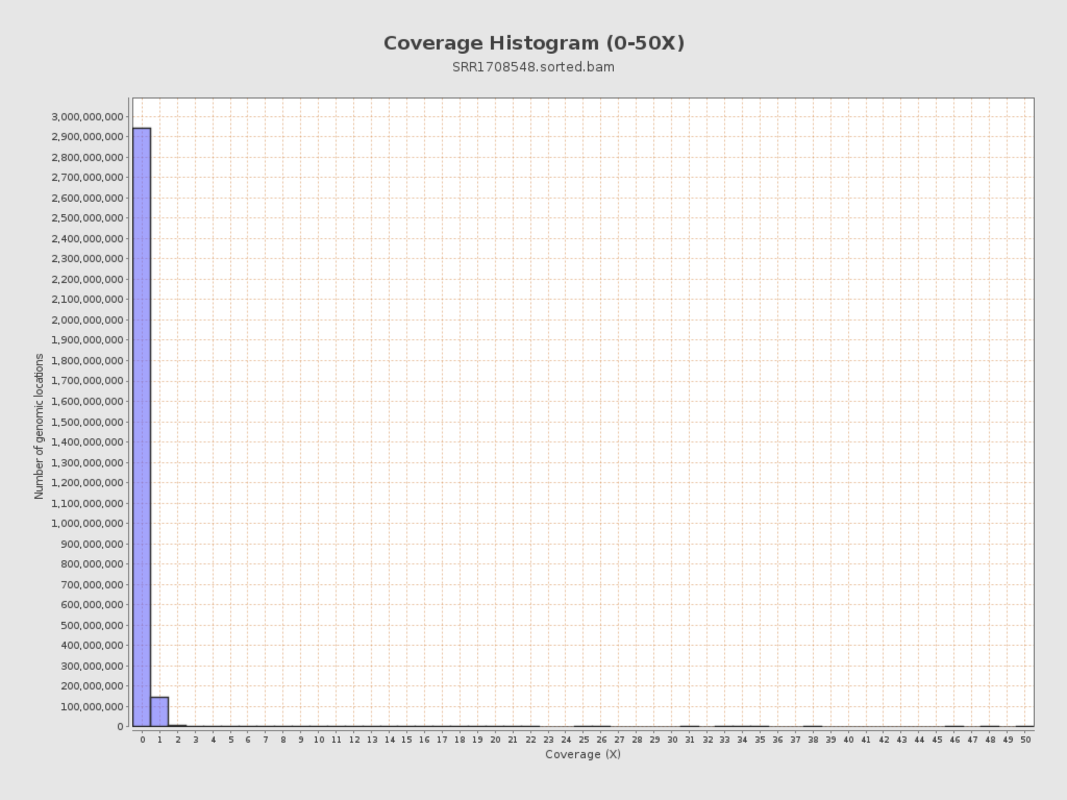
3. Results : Coverage across reference



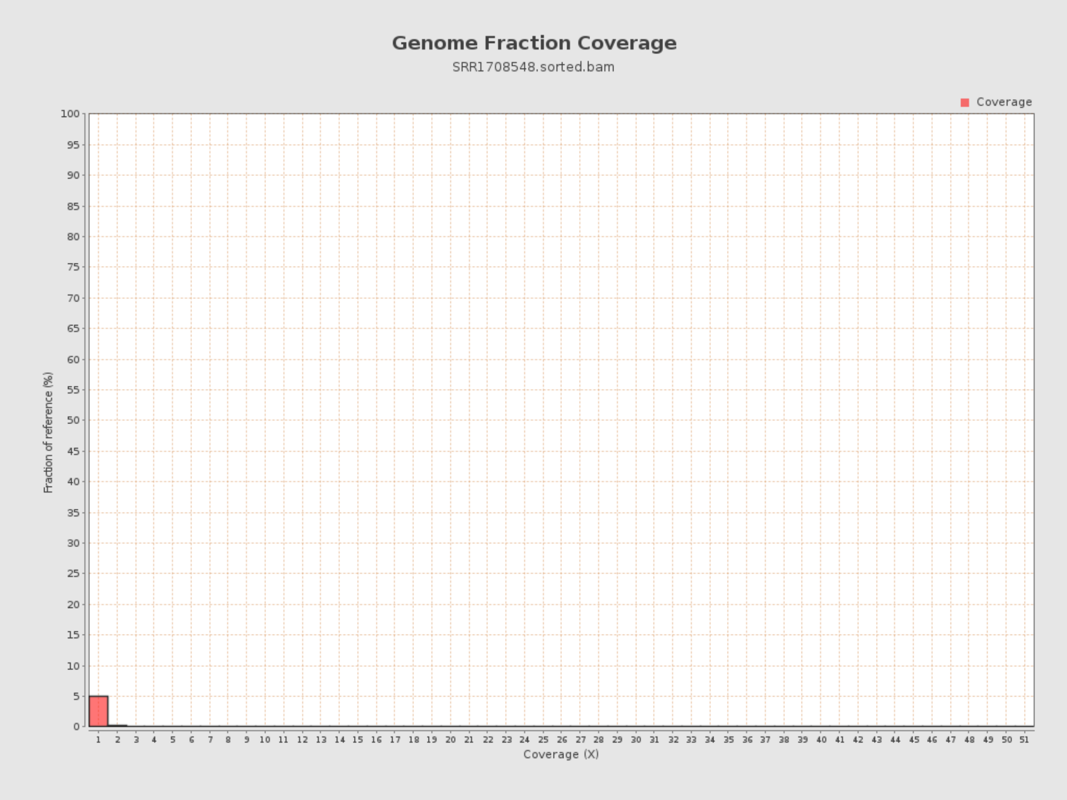
4. Results : Coverage Histogram



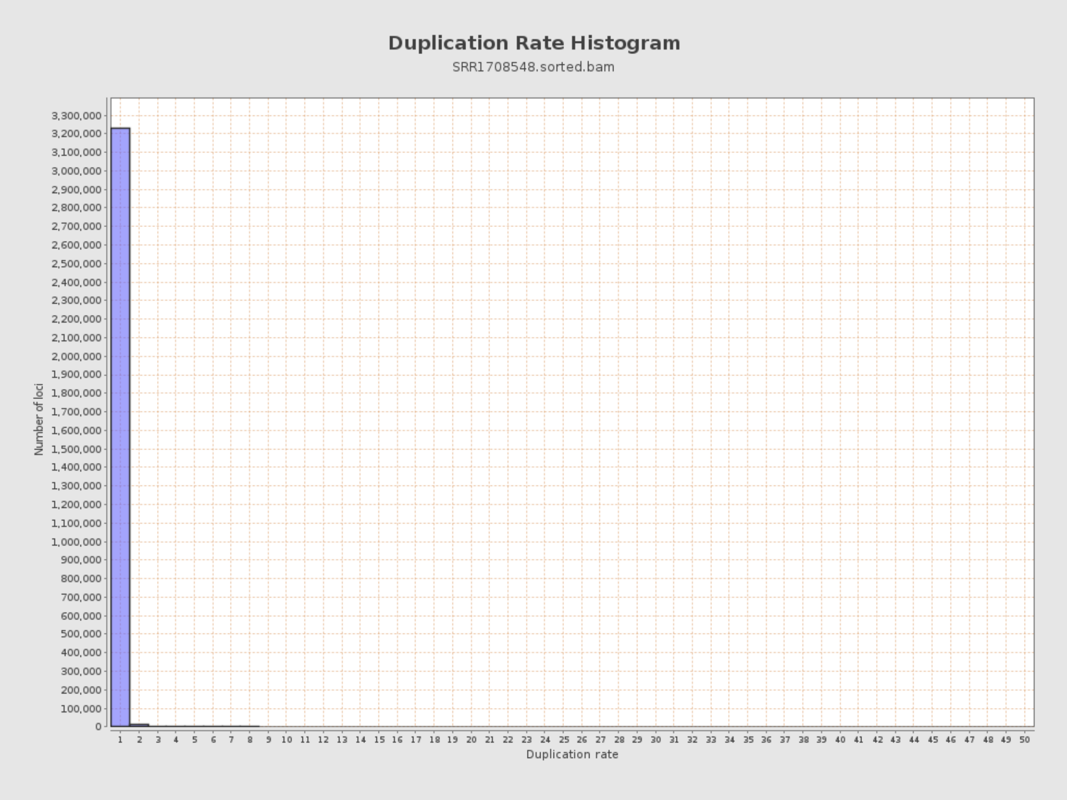
5. Results : Coverage Histogram (0-50X)



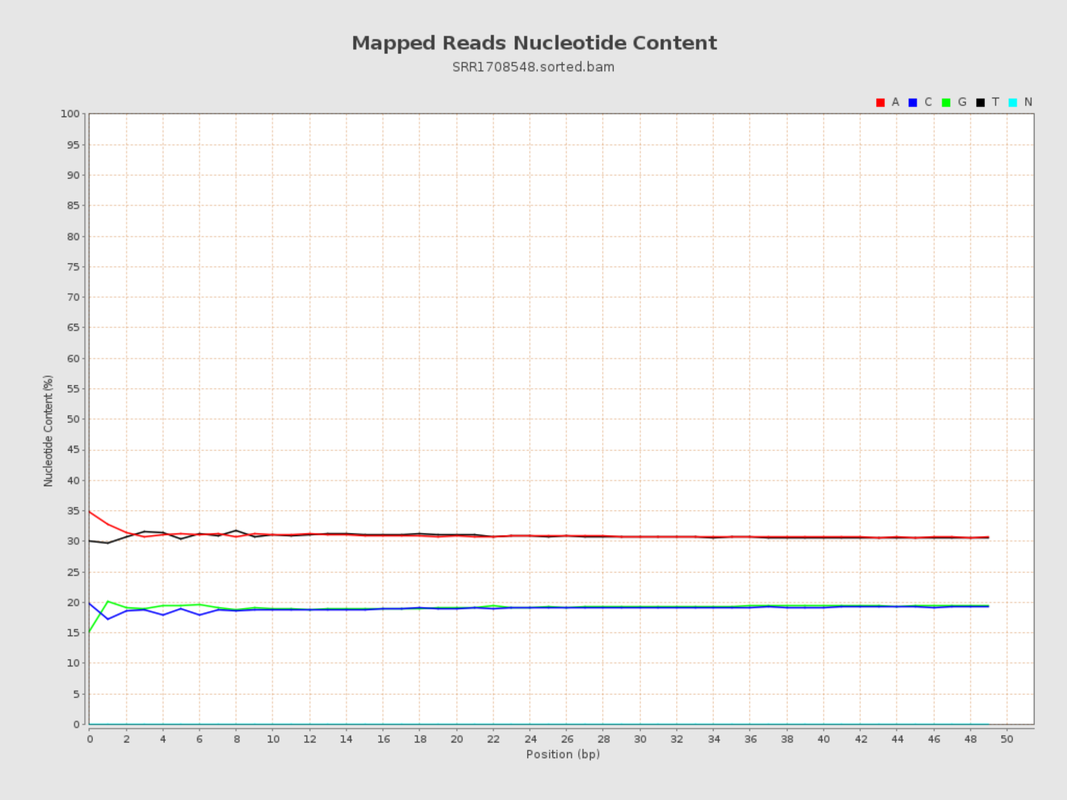
6. Results : Genome Fraction Coverage



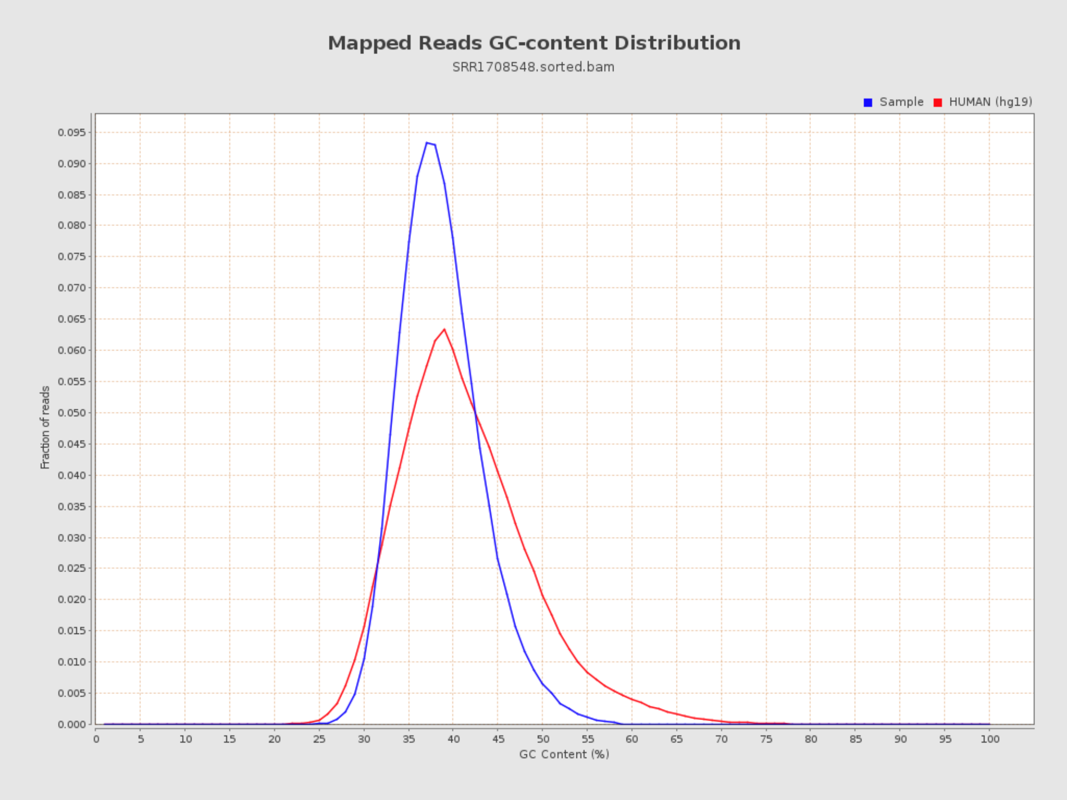
7. Results : Duplication Rate Histogram



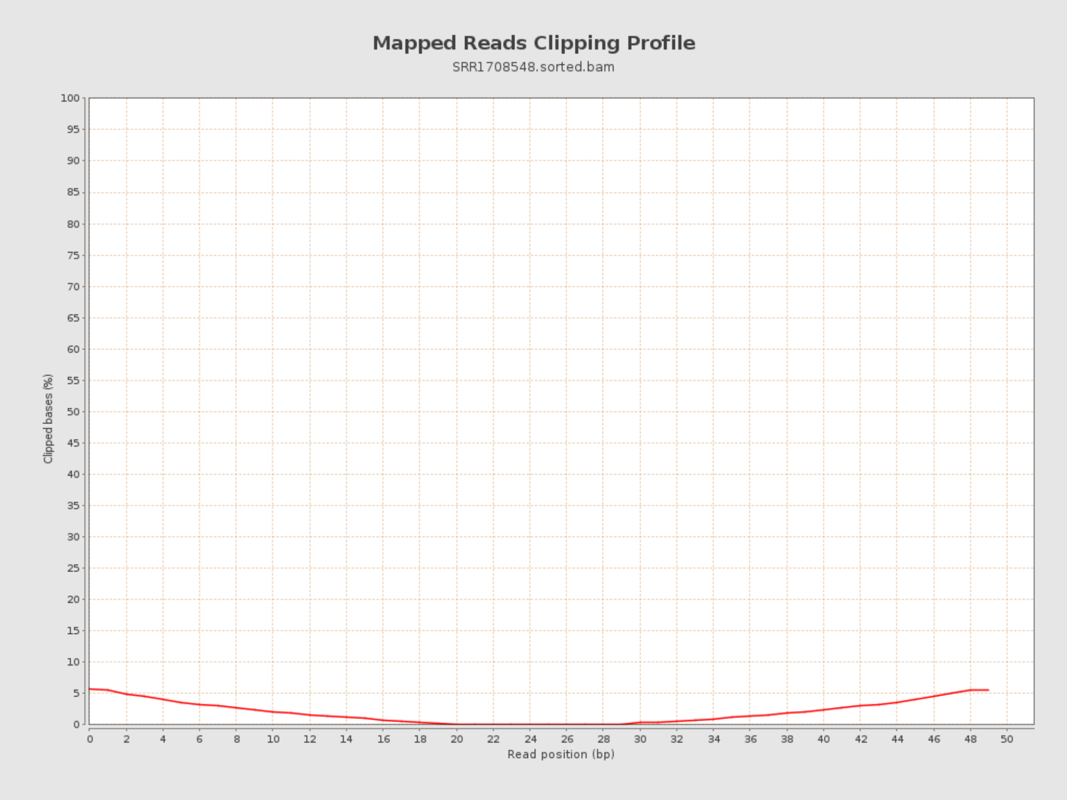
8. Results : Mapped Reads Nucleotide Content



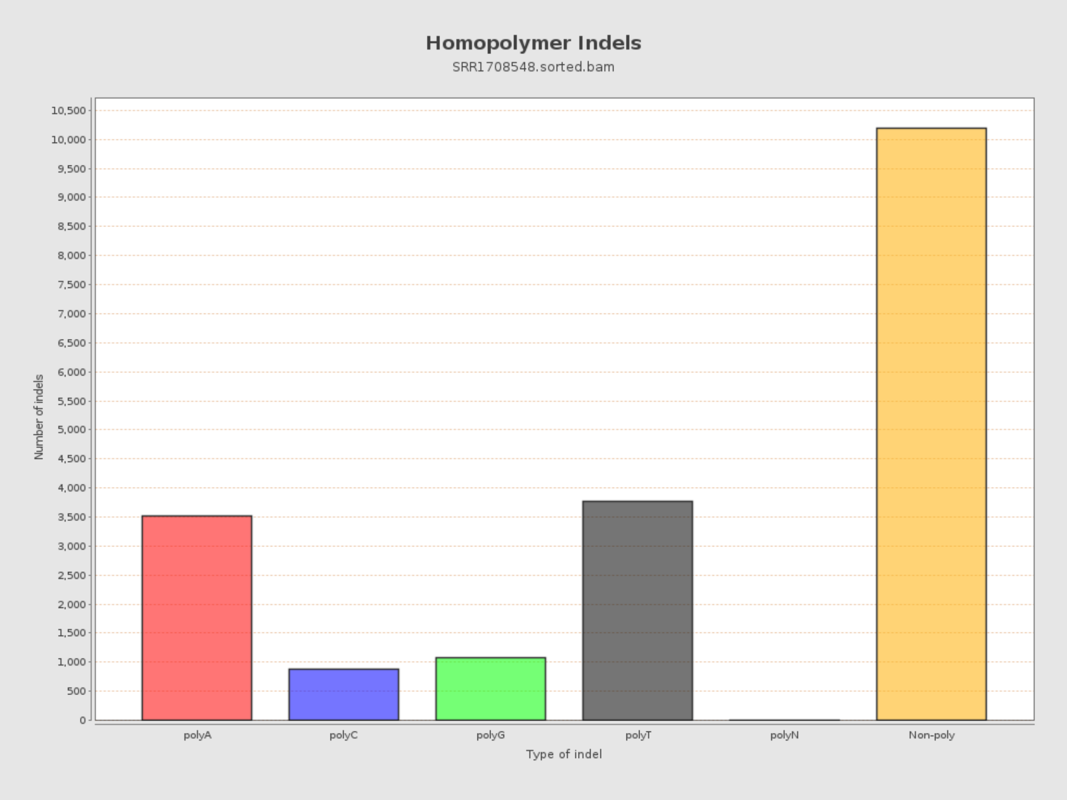
9. Results : Mapped Reads GC-content Distribution



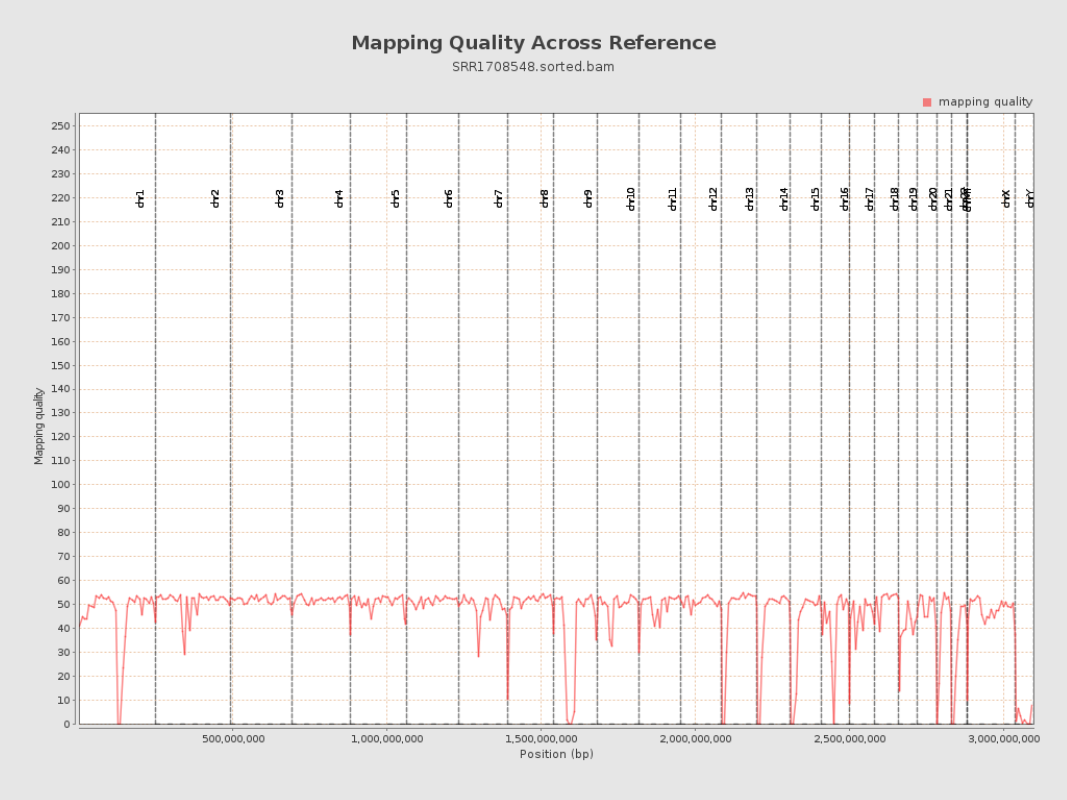
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram