Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:33:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708613.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_SRR1708613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:33:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,246,367
Mapped reads	1,284,290 / 57.17%
Unmapped reads	962,077 / 42.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	274 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	51,018 / 2.27%
Duplication rate	3.23%
Clipped reads	242,164 / 10.78%

2.2. ACGT Content

Number/percentage of A's	17,895,600 / 28.95%
Number/percentage of C's	11,787,634 / 19.07%
Number/percentage of T's	19,350,523 / 31.3%
Number/percentage of G's	12,779,979 / 20.67%
Number/percentage of N's	5,239 / 0.01%
GC Percentage	39.74%

2.3. Coverage

Mean	0.02

Standard Deviation	0.2135

2.4. Mapping Quality

Mean Mapping Quality	41.75

2.5. Mismatches and indels

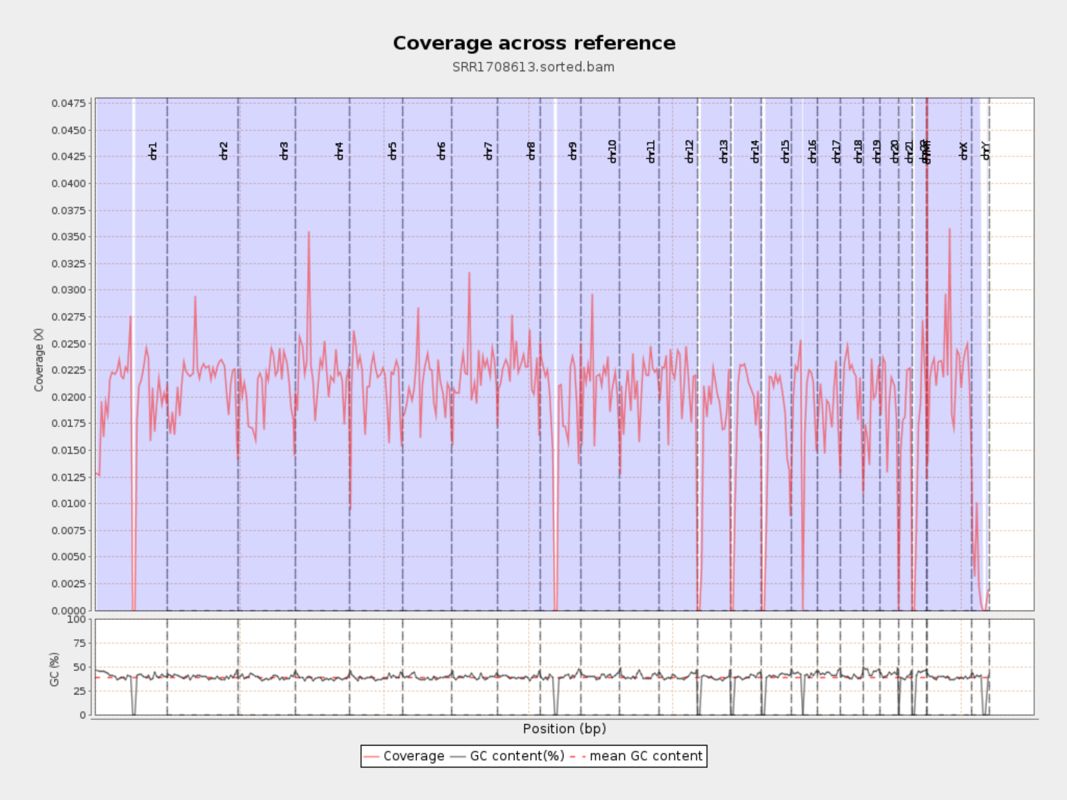
General error rate	0.7%
Mismatches	427,781
Insertions	3,196
Mapped reads with at least one insertion	0.25%
Deletions	10,570
Mapped reads with at least one deletion	0.82%
Homopolymer indels	48.97%

2.6. Chromosome stats

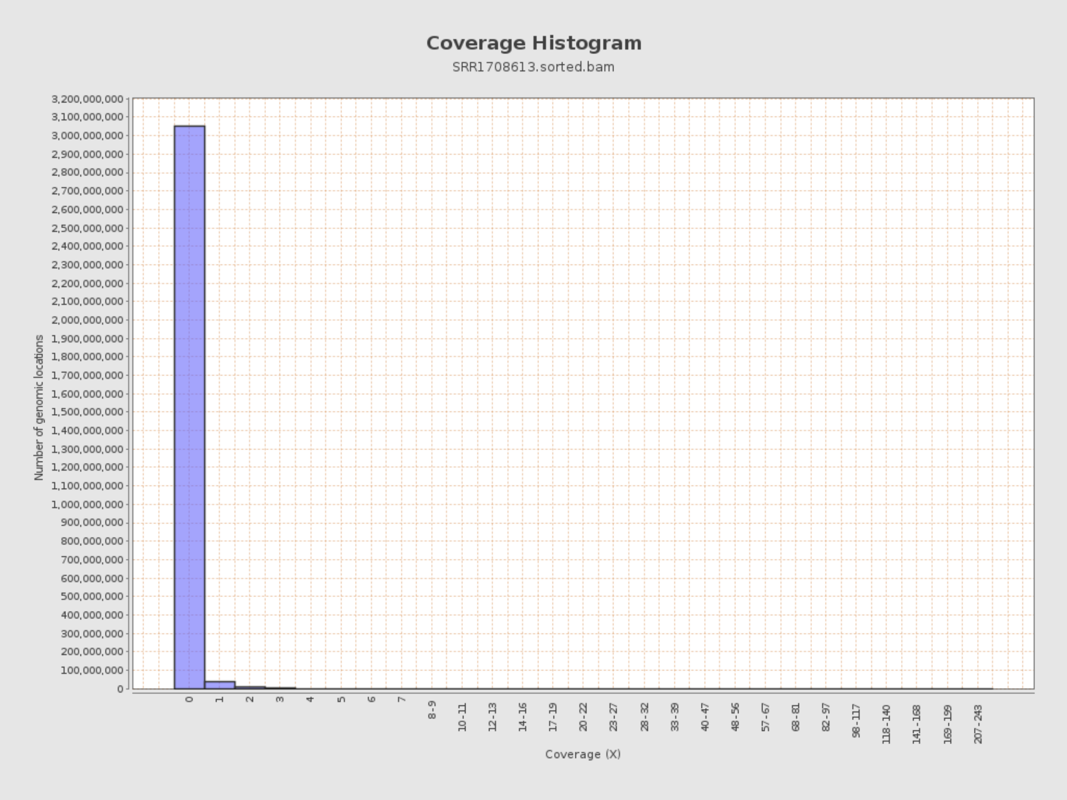
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4779308	0.0192	0.2535
chr2	243199373	5247506	0.0216	0.2357
chr3	198022430	4113471	0.0208	0.1892
chr4	191154276	4313120	0.0226	0.2047
chr5	180915260	3919900	0.0217	0.1945
chr6	171115067	3579643	0.0209	0.2061
chr7	159138663	3557758	0.0224	0.2685

chr8	146364022	3322577	0.0227	0.2334
chr9	141213431	2539866	0.018	0.2027
chr10	135534747	2886943	0.0213	0.2089
chr11	135006516	2838469	0.021	0.2253
chr12	133851895	2876734	0.0215	0.1935
chr13	115169878	1903365	0.0165	0.1696
chr14	107349540	1868315	0.0174	0.1782
chr15	102531392	1610274	0.0157	0.1639
chr16	90354753	1692237	0.0187	0.1823
chr17	81195210	1523914	0.0188	0.1983
chr18	78077248	1654611	0.0212	0.2993
chr19	59128983	1108420	0.0187	0.2789
chr20	63025520	1220936	0.0194	0.1864
chr21	48129895	812701	0.0169	0.1793
chr22	51304566	738137	0.0144	0.156
chrMT	16571	1173	0.0708	0.2907
chrX	155270560	3550747	0.0229	0.2059
chrY	59373566	175410	0.003	0.0862

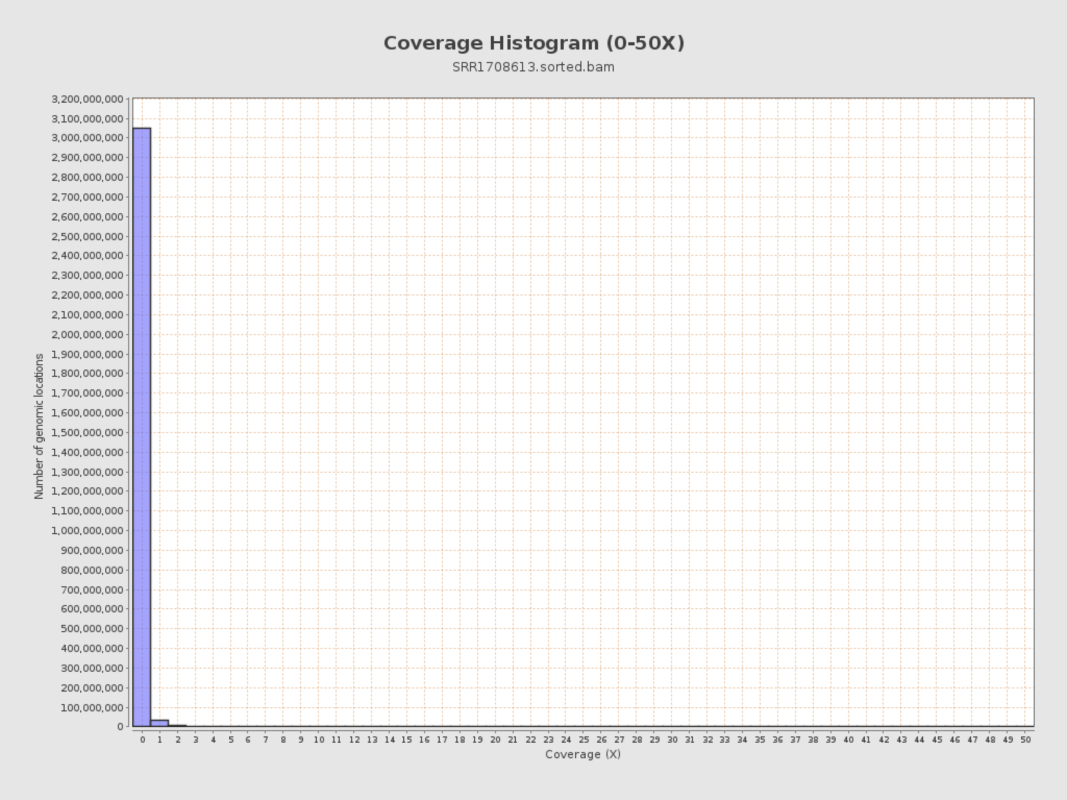
3. Results : Coverage across reference



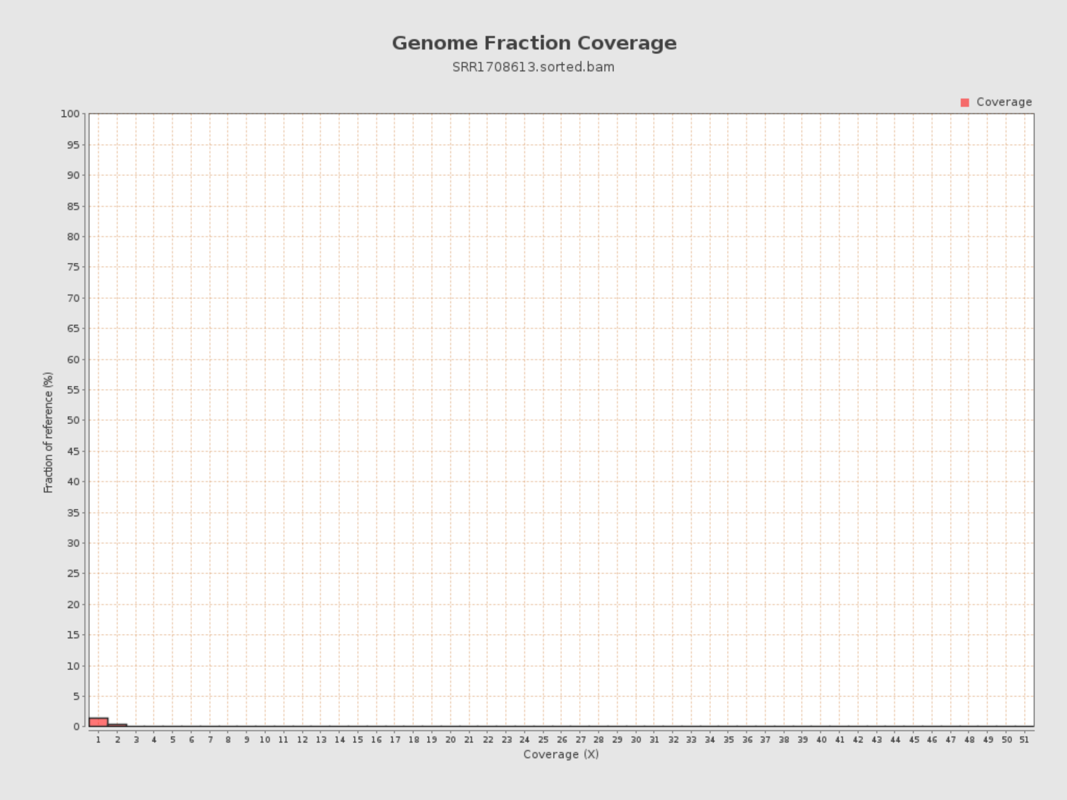
4. Results : Coverage Histogram



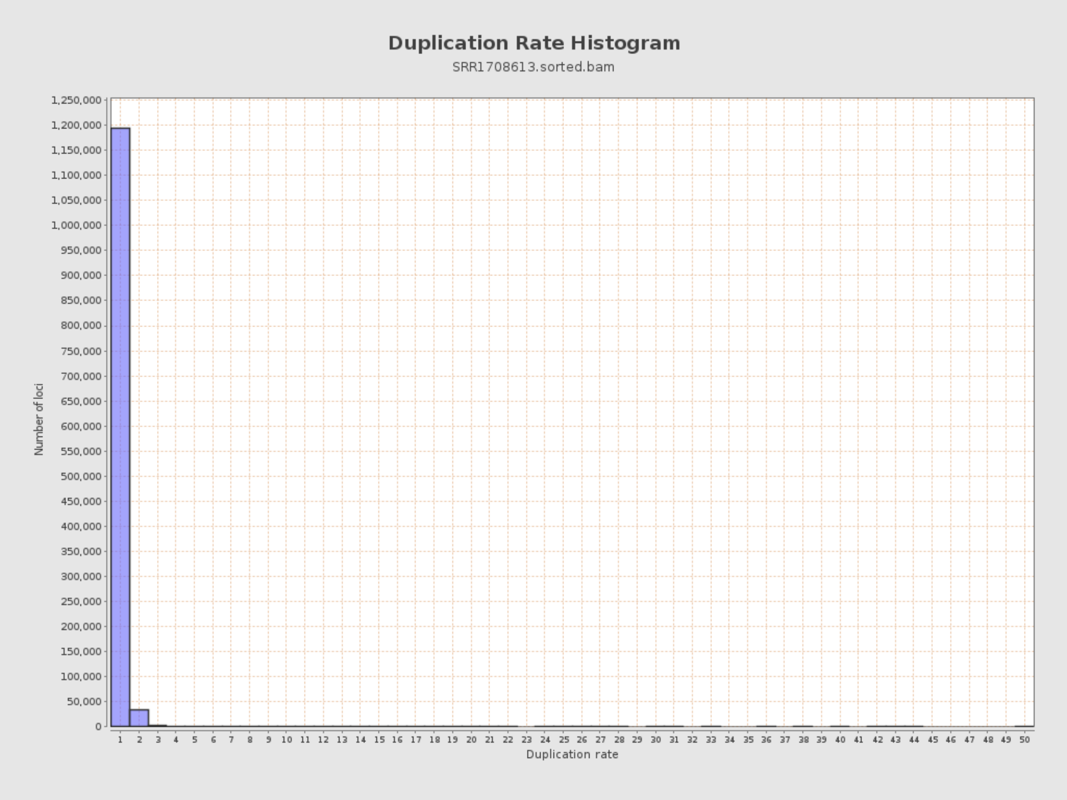
5. Results : Coverage Histogram (0-50X)



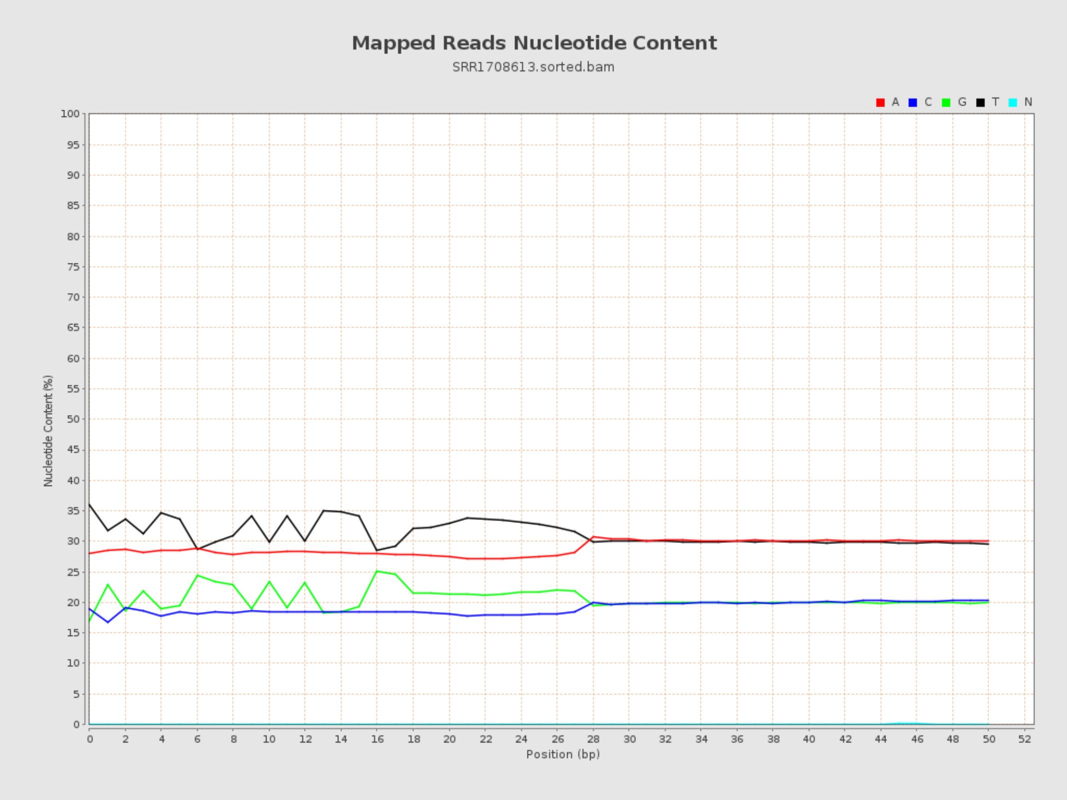
6. Results : Genome Fraction Coverage



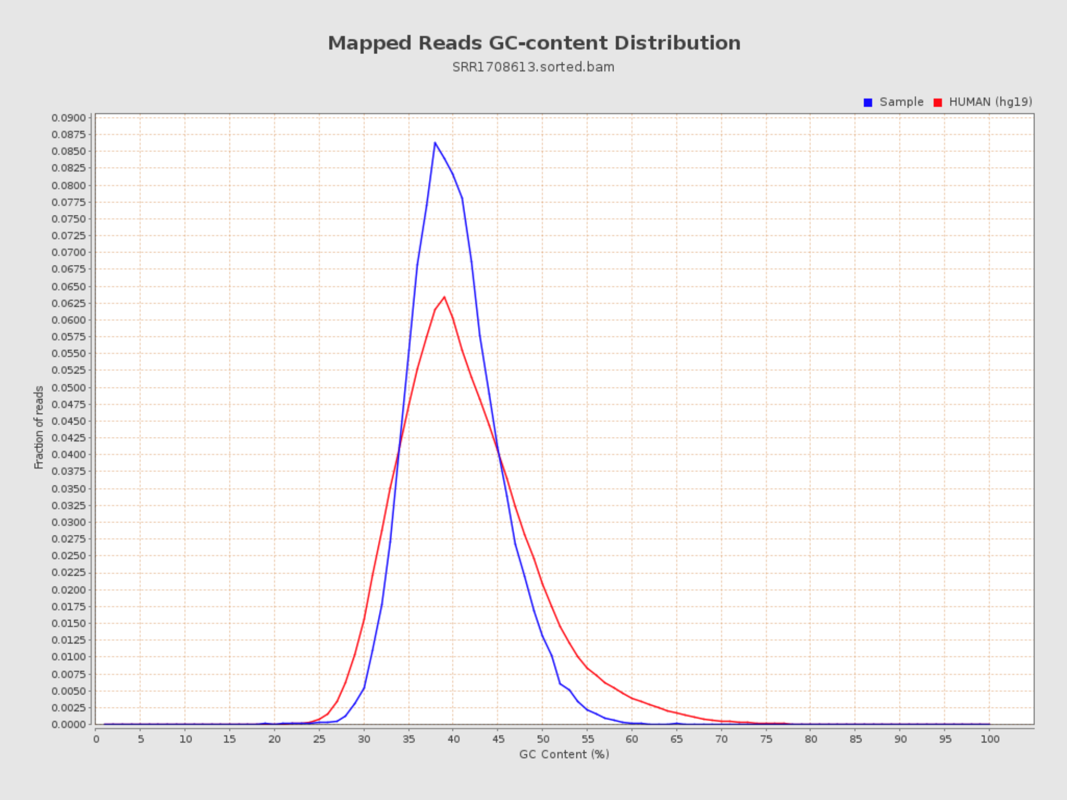
7. Results : Duplication Rate Histogram



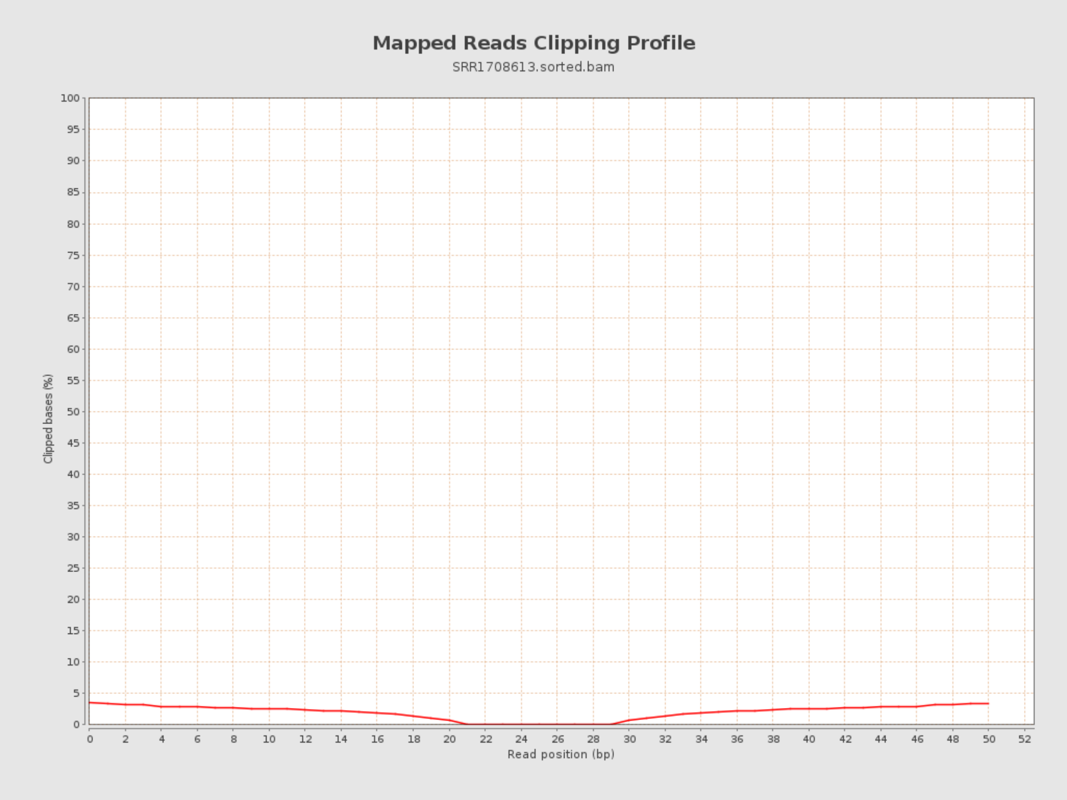
8. Results : Mapped Reads Nucleotide Content



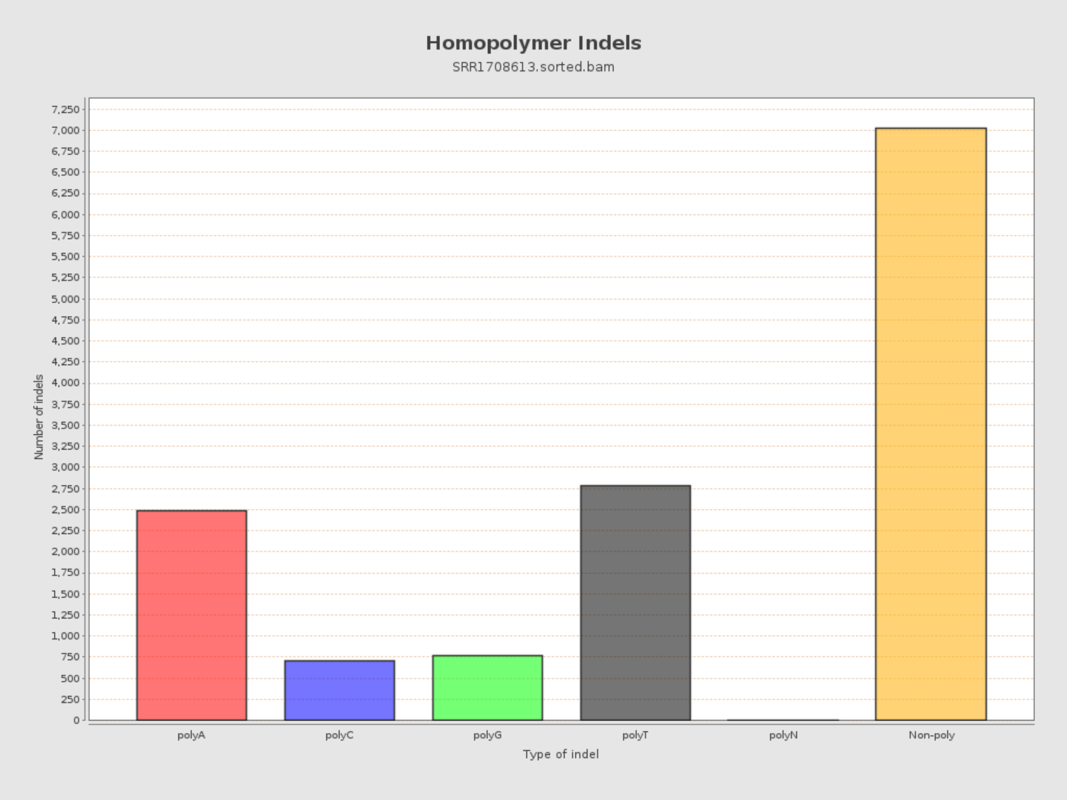
9. Results : Mapped Reads GC-content Distribution



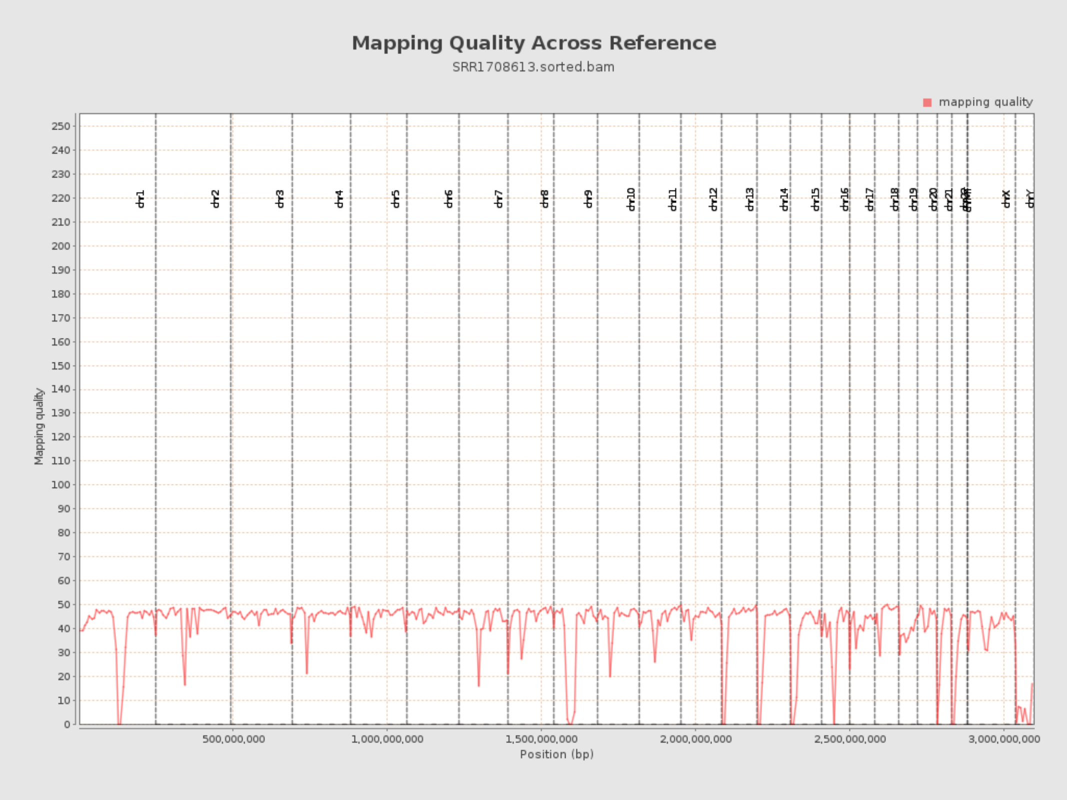
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram