Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:42:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708539.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_SRR1708539 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708539.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:42:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,228,568
Mapped reads	24,342,989 / 96.49%
Unmapped reads	885,579 / 3.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	526 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	232,830 / 0.92%
Duplication rate	0.94%
Clipped reads	388,009 / 1.54%

2.2. ACGT Content

Number/percentage of A's	378,514,791 / 31.18%
Number/percentage of C's	226,852,774 / 18.69%
Number/percentage of T's	376,970,289 / 31.06%
Number/percentage of G's	231,011,113 / 19.03%
Number/percentage of N's	486,095 / 0.04%
GC Percentage	37.72%

2.3. Coverage

Mean	0.3921

Standard Deviation	0.7033

2.4. Mapping Quality

Mean Mapping Quality	46.55

2.5. Mismatches and indels

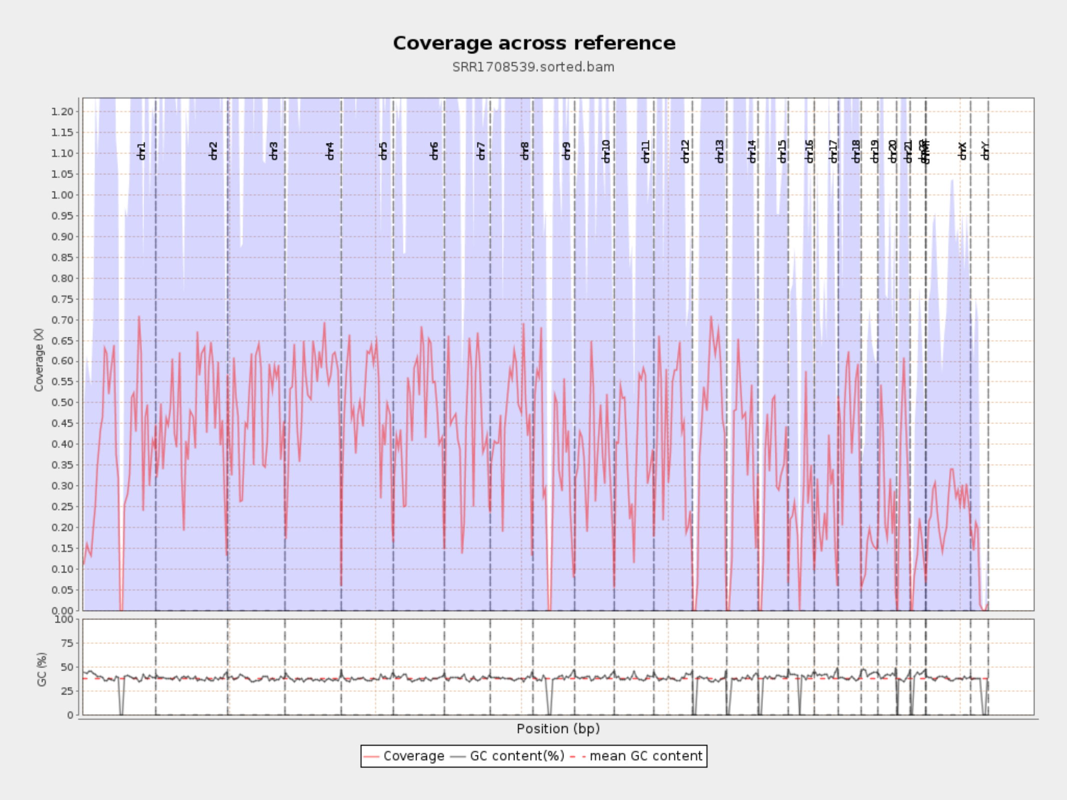
General error rate	0.35%
Mismatches	4,199,821
Insertions	66,043
Mapped reads with at least one insertion	0.27%
Deletions	63,673
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.36%

2.6. Chromosome stats

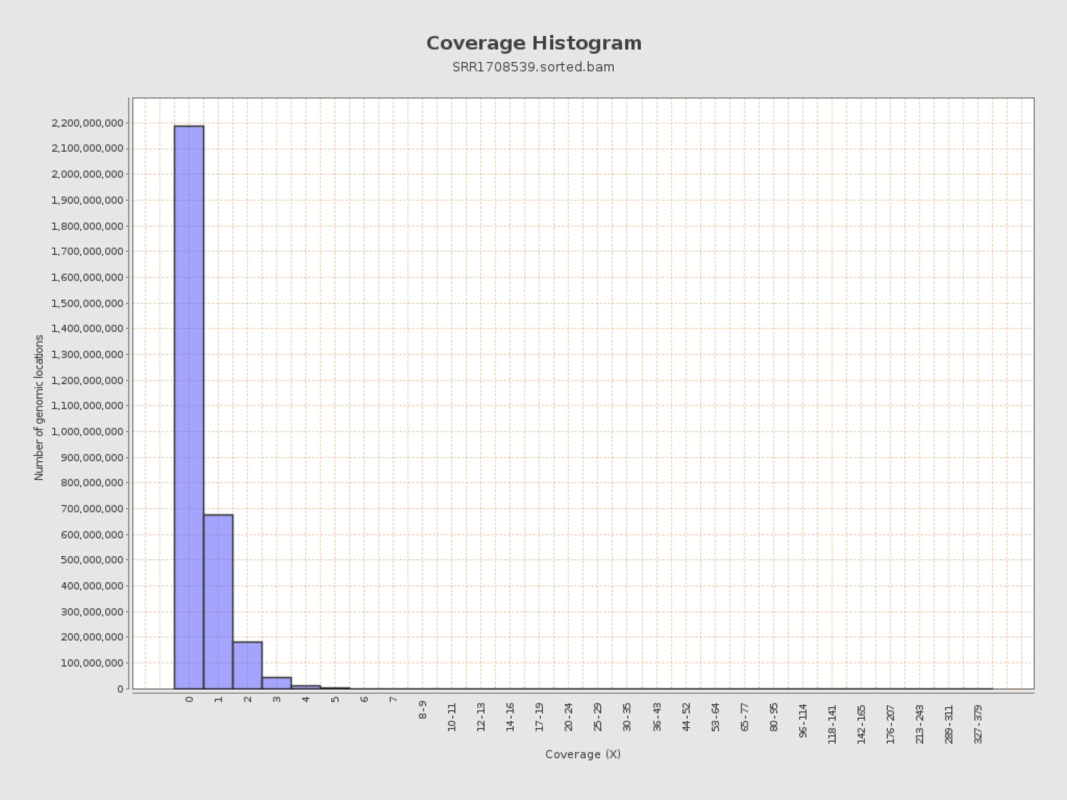
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	92738041	0.3721	0.7034
chr2	243199373	112449119	0.4624	0.7472
chr3	198022430	94186899	0.4756	0.7521
chr4	191154276	102422321	0.5358	0.7959
chr5	180915260	87632831	0.4844	0.7603
chr6	171115067	82904612	0.4845	0.7639
chr7	159138663	69802956	0.4386	0.7402

chr8	146364022	67782333	0.4631	0.7461
chr9	141213431	50475424	0.3574	0.6793
chr10	135534747	51558978	0.3804	0.6763
chr11	135006516	53903126	0.3993	0.7162
chr12	133851895	56103370	0.4191	0.7235
chr13	115169878	51707132	0.449	0.7533
chr14	107349540	38705656	0.3606	0.6818
chr15	102531392	32228000	0.3143	0.6407
chr16	90354753	21384222	0.2367	0.5458
chr17	81195210	18883519	0.2326	0.551
chr18	78077248	36825566	0.4717	0.7537
chr19	59128983	8217120	0.139	0.4091
chr20	63025520	18174344	0.2884	0.6043
chr21	48129895	15708309	0.3264	0.6728
chr22	51304566	5936727	0.1157	0.3798
chrMT	16571	1113	0.0672	0.2623
chrX	155270560	38698320	0.2492	0.528
chrY	59373566	5510051	0.0928	0.3442

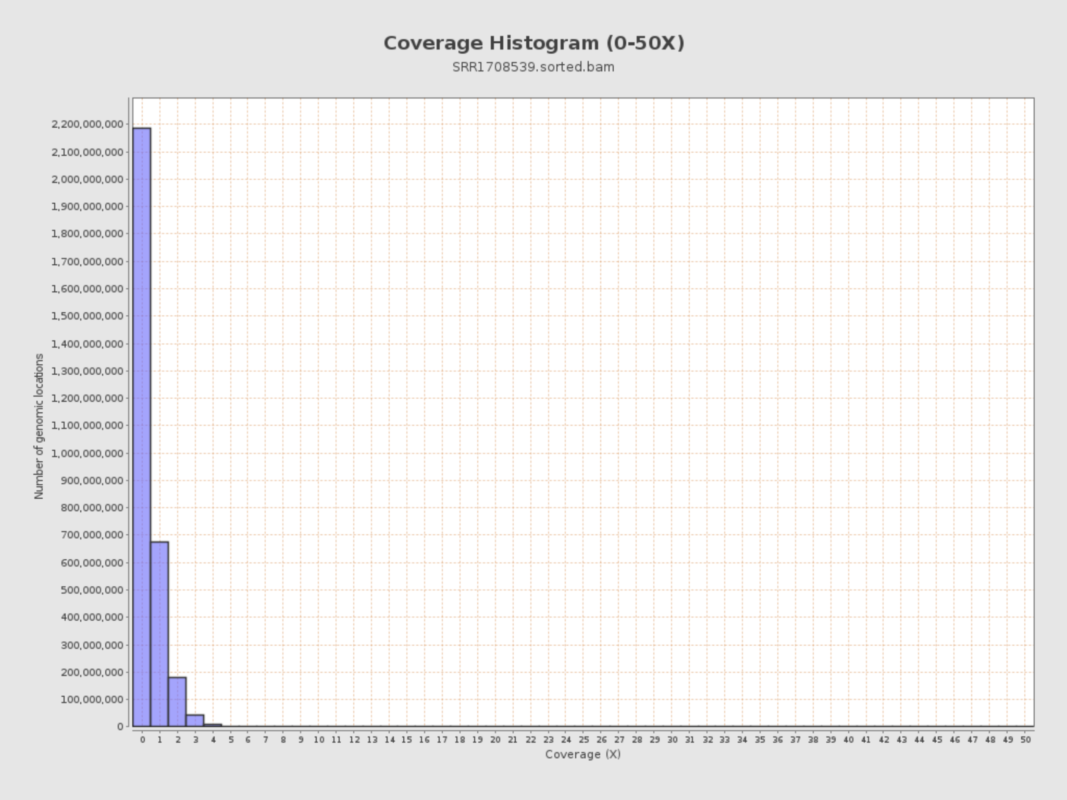
3. Results : Coverage across reference



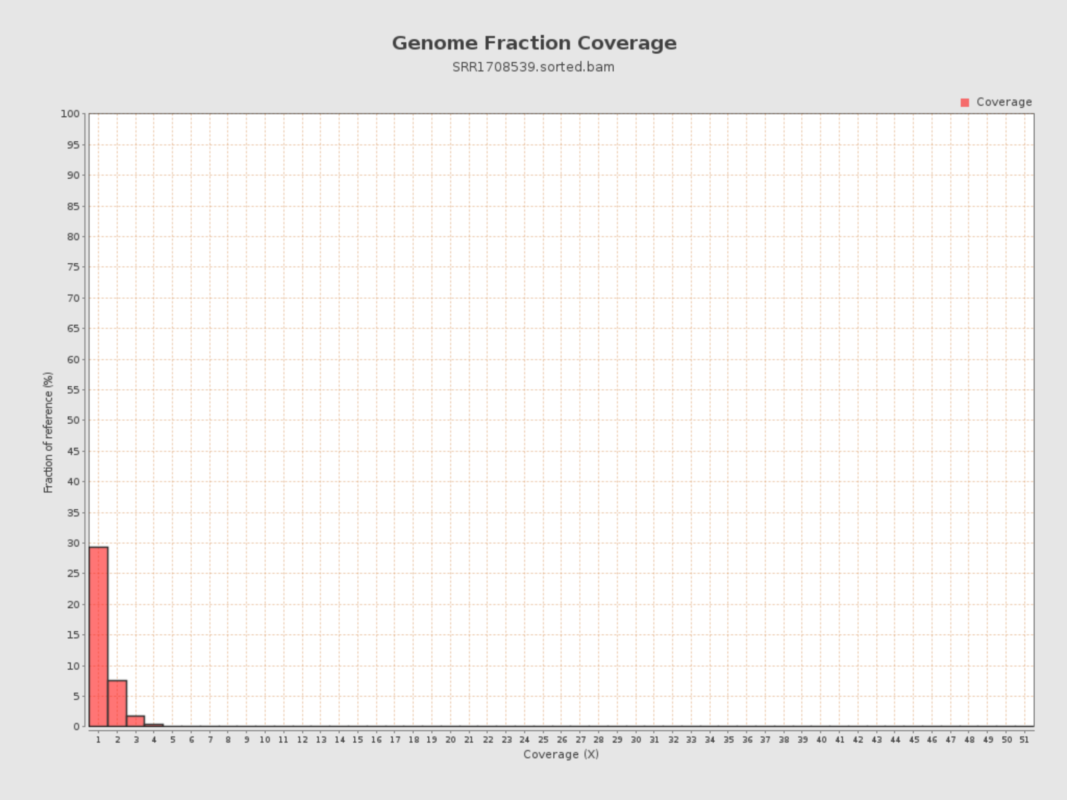
4. Results : Coverage Histogram



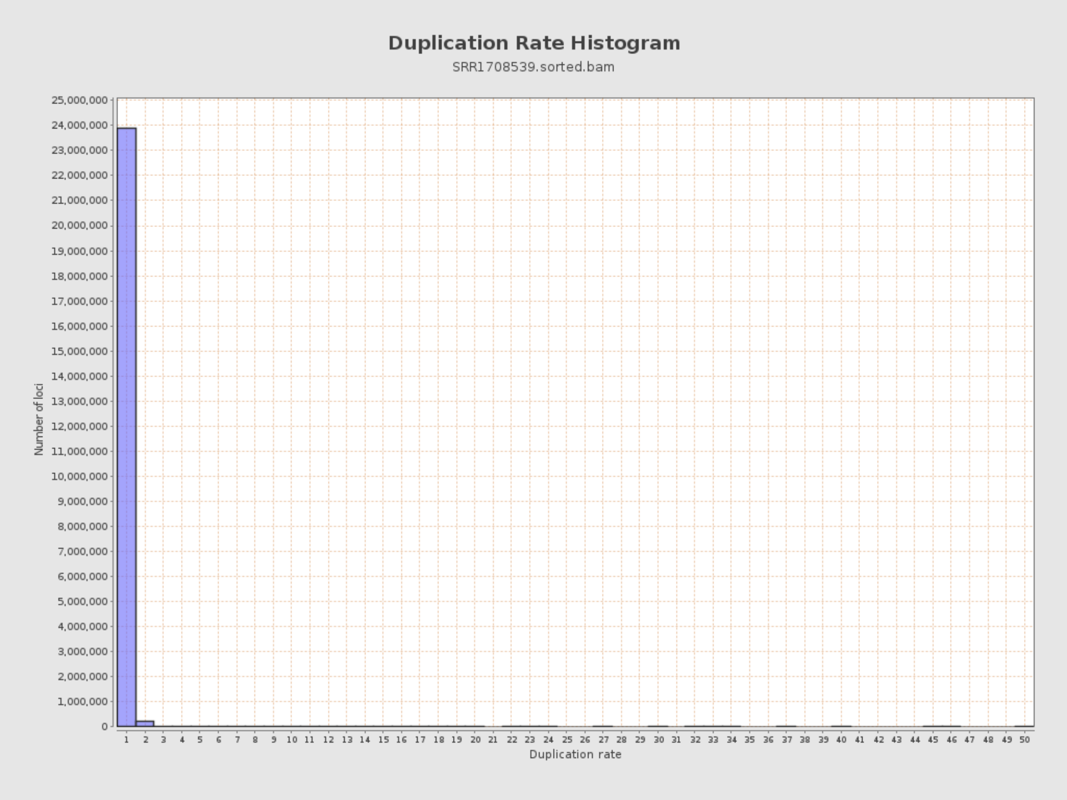
5. Results : Coverage Histogram (0-50X)



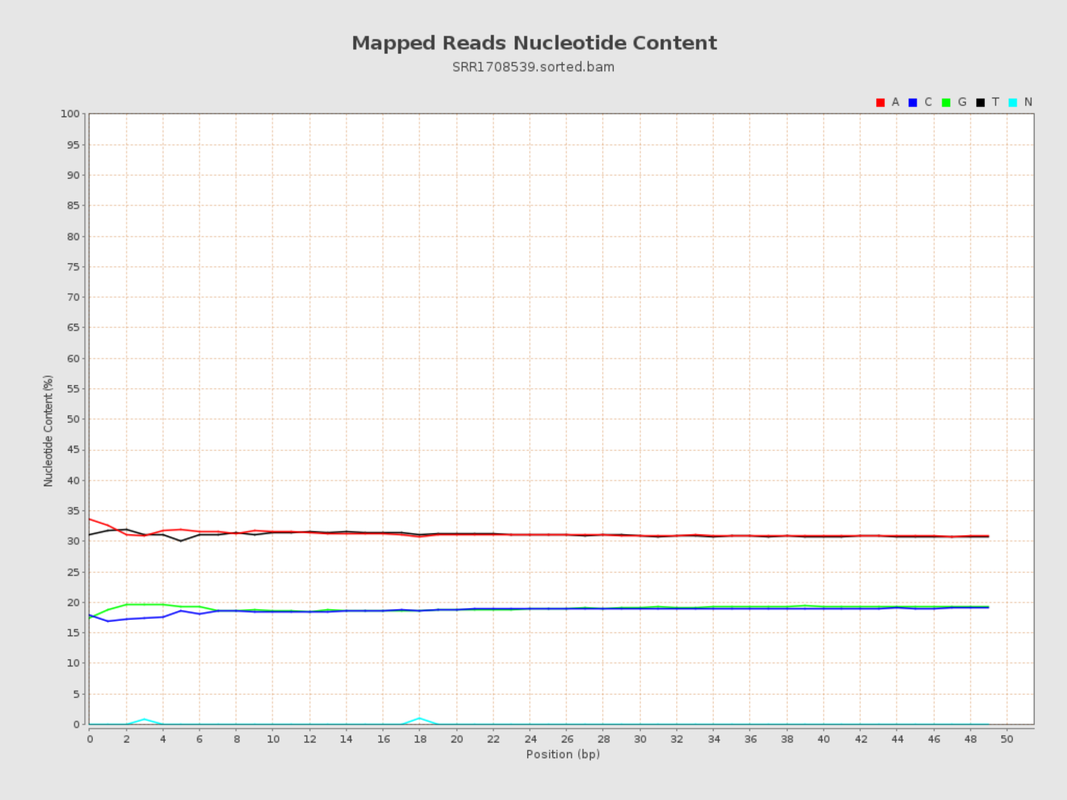
6. Results : Genome Fraction Coverage



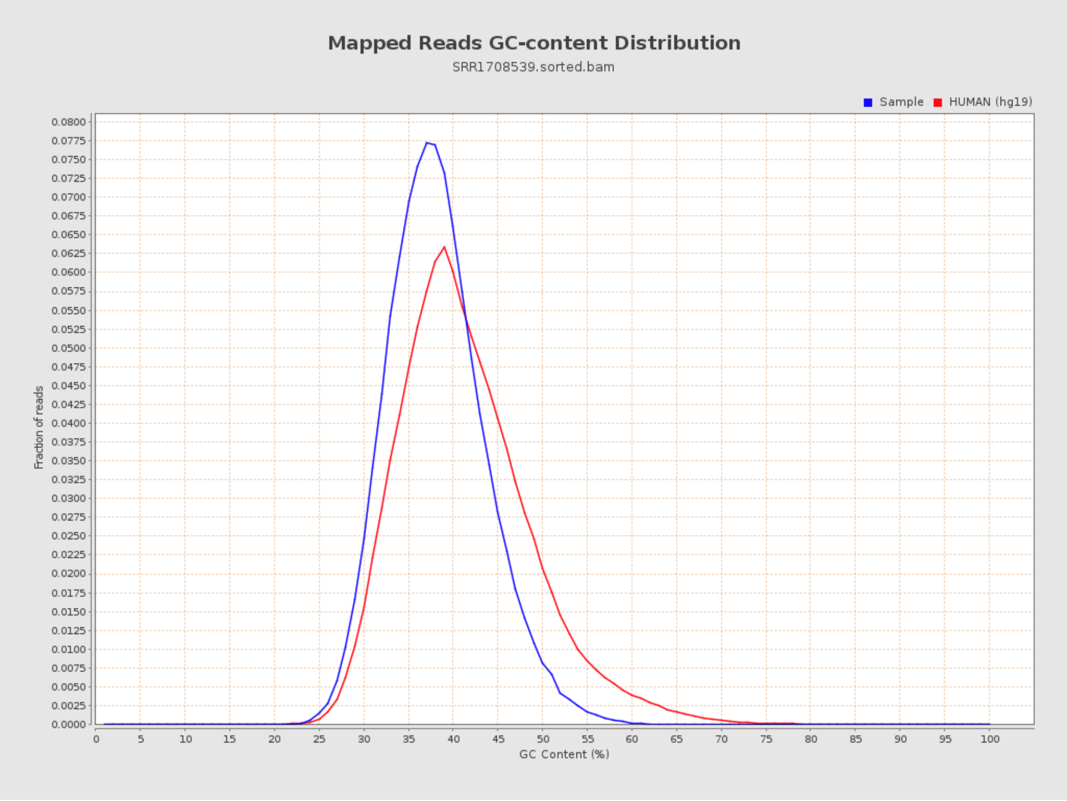
7. Results : Duplication Rate Histogram



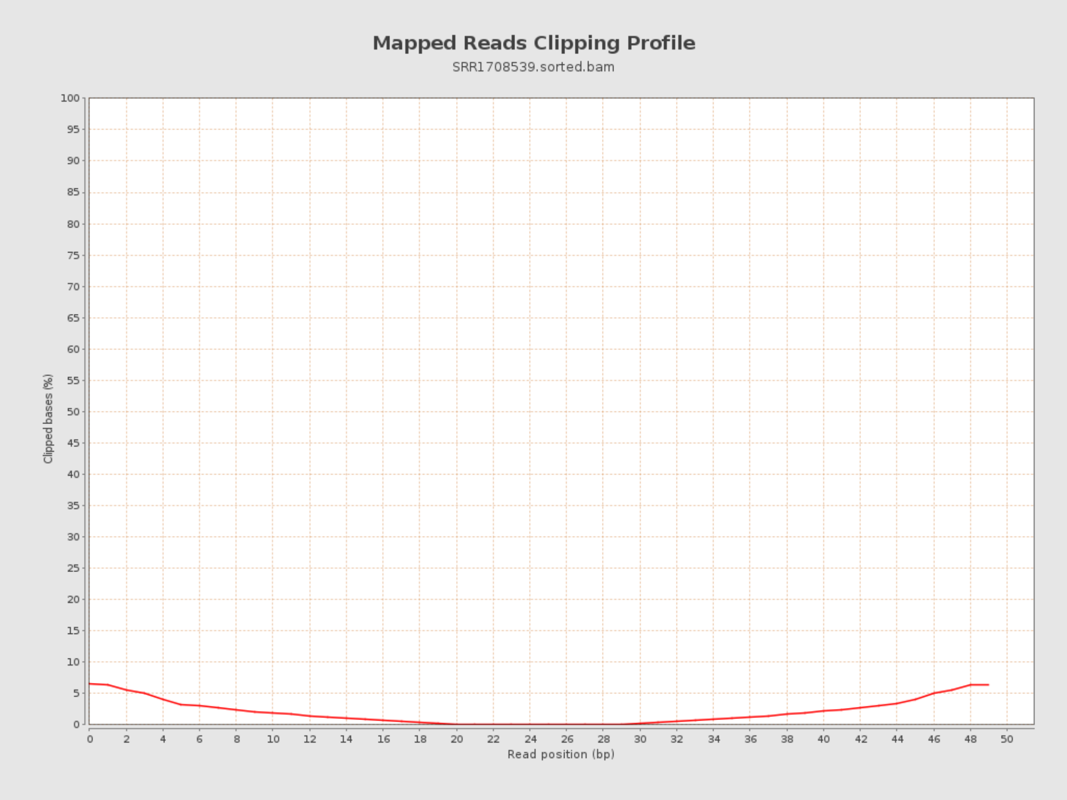
8. Results : Mapped Reads Nucleotide Content



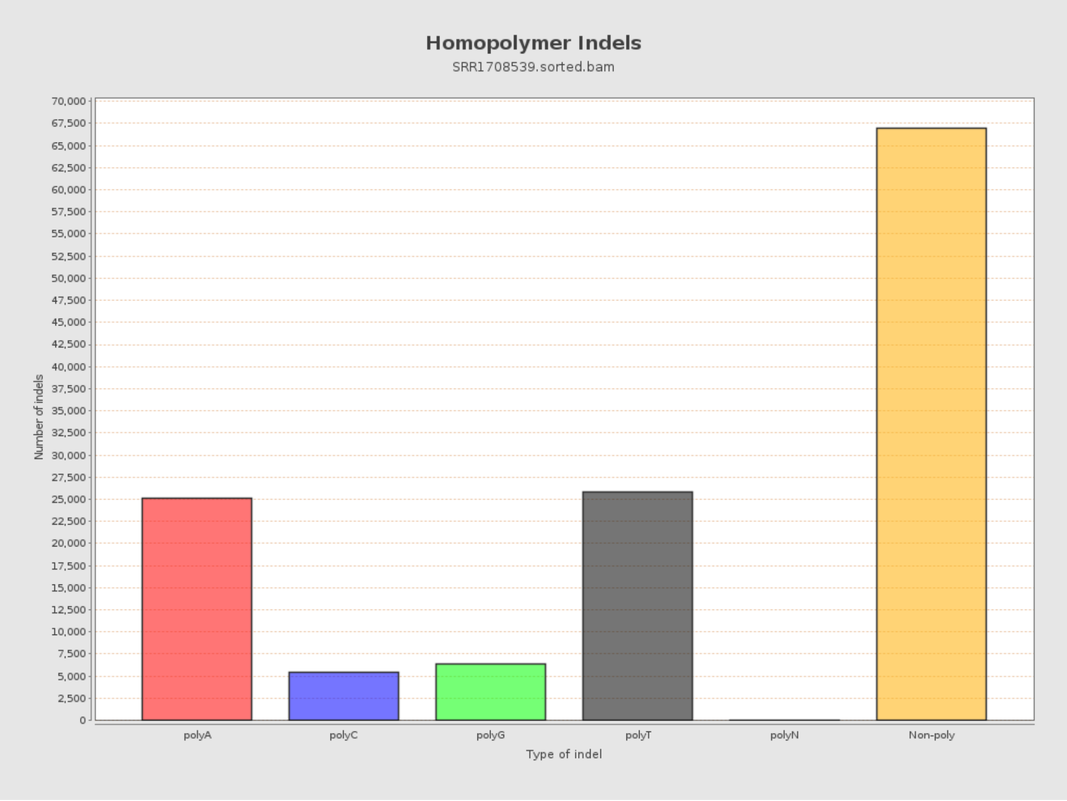
9. Results : Mapped Reads GC-content Distribution



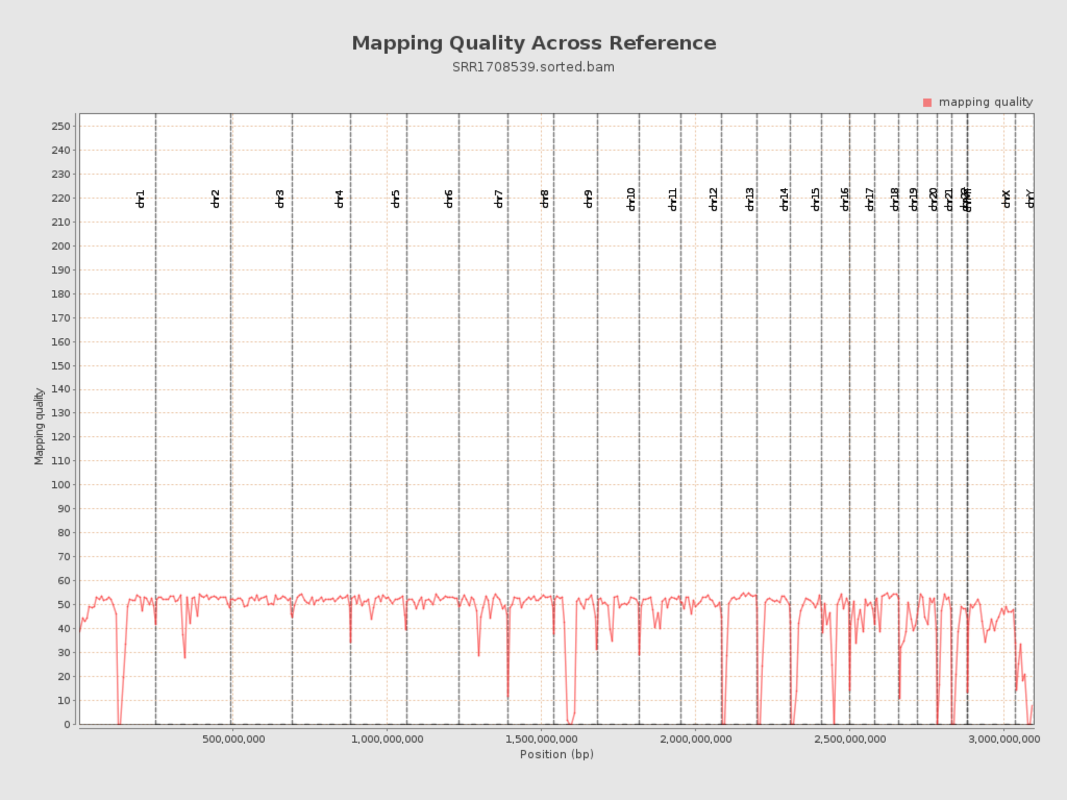
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram