Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:20:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708572.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_SRR1708572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:20:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,272,512
Mapped reads	3,488,368 / 81.65%
Unmapped reads	784,144 / 18.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	90 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,739 / 0.39%
Duplication rate	0.48%
Clipped reads	46,824 / 1.1%

2.2. ACGT Content

Number/percentage of A's	53,964,379 / 31.02%
Number/percentage of C's	33,009,634 / 18.98%
Number/percentage of T's	53,666,187 / 30.85%
Number/percentage of G's	33,305,883 / 19.15%
Number/percentage of N's	7,333 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.2445

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

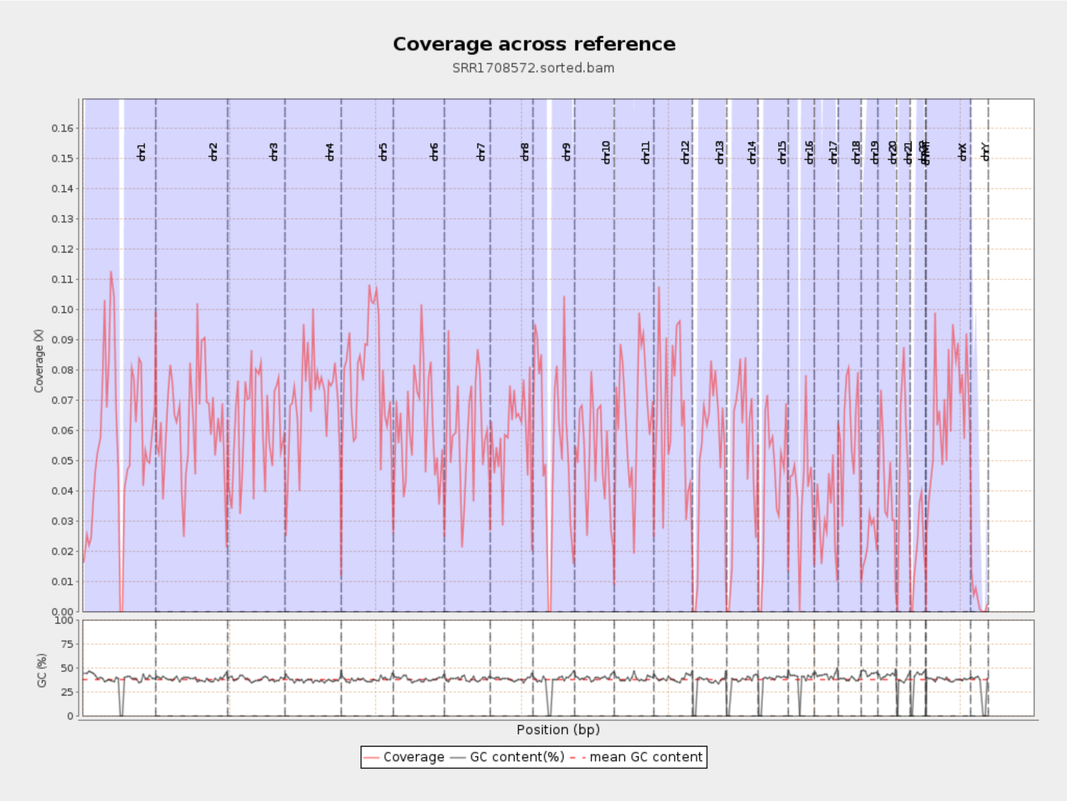
General error rate	0.17%
Mismatches	272,264
Insertions	11,610
Mapped reads with at least one insertion	0.33%
Deletions	9,455
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48.04%

2.6. Chromosome stats

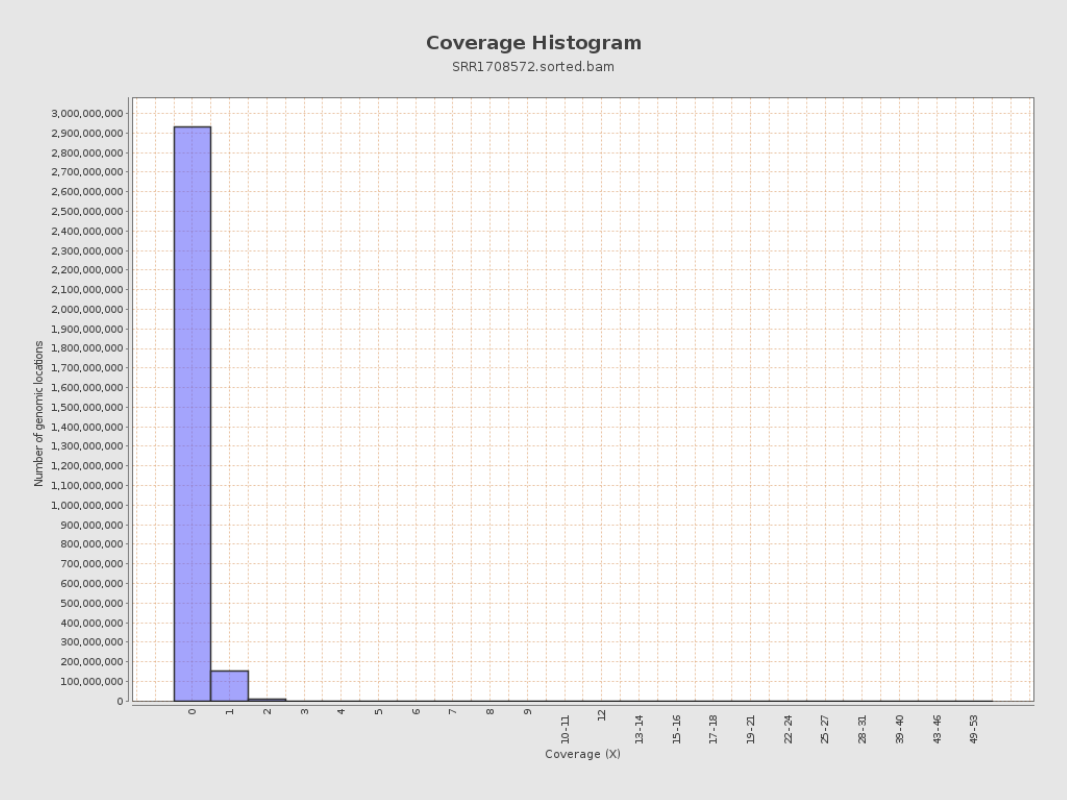
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13977687	0.0561	0.2454
chr2	243199373	15095525	0.0621	0.2558
chr3	198022430	12181116	0.0615	0.255
chr4	191154276	13426635	0.0702	0.2722
chr5	180915260	13914194	0.0769	0.2847
chr6	171115067	10559299	0.0617	0.2552
chr7	159138663	9199141	0.0578	0.2477

chr8	146364022	8524518	0.0582	0.2477
chr9	141213431	7930212	0.0562	0.2448
chr10	135534747	7056425	0.0521	0.234
chr11	135006516	8848044	0.0655	0.2646
chr12	133851895	8650047	0.0646	0.2622
chr13	115169878	6038637	0.0524	0.2357
chr14	107349540	5445413	0.0507	0.2322
chr15	102531392	4399975	0.0429	0.2138
chr16	90354753	3559444	0.0394	0.2044
chr17	81195210	2548247	0.0314	0.182
chr18	78077248	4673830	0.0599	0.2511
chr19	59128983	1383574	0.0234	0.1565
chr20	63025520	2640312	0.0419	0.2107
chr21	48129895	2302986	0.0478	0.2279
chr22	51304566	1044058	0.0204	0.1466
chrMT	16571	0	0	0
chrX	155270560	10343958	0.0666	0.2668
chrY	59373566	225832	0.0038	0.0641

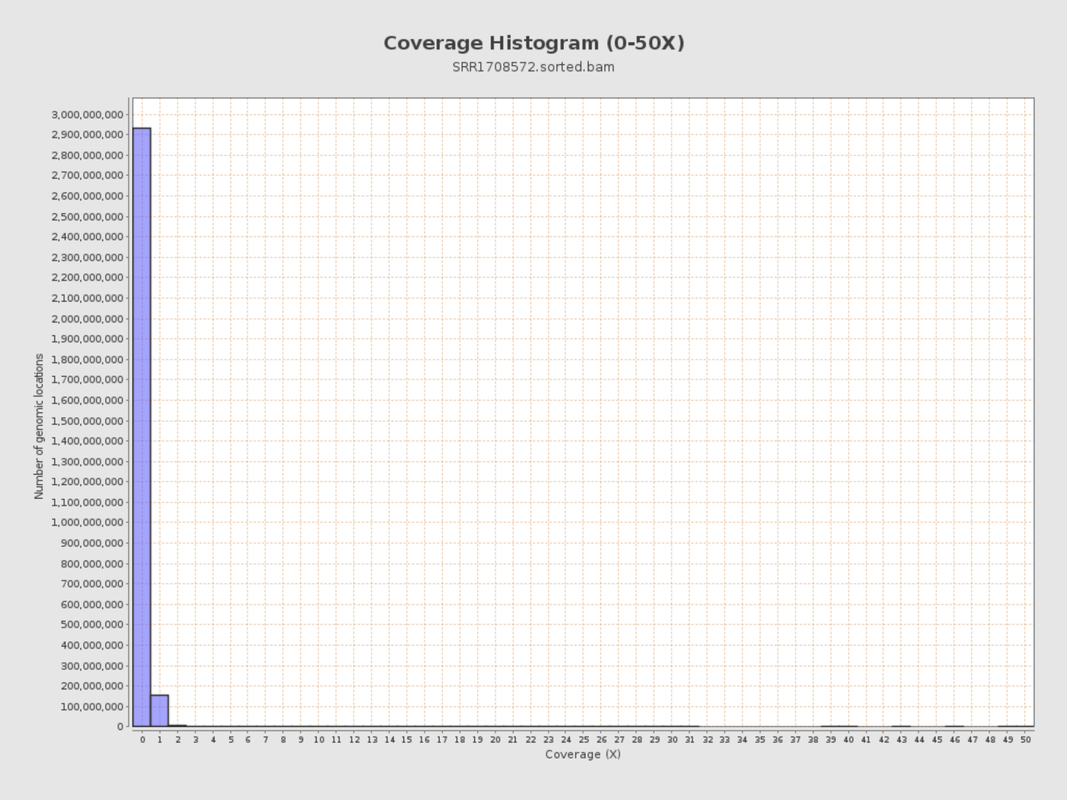
3. Results : Coverage across reference



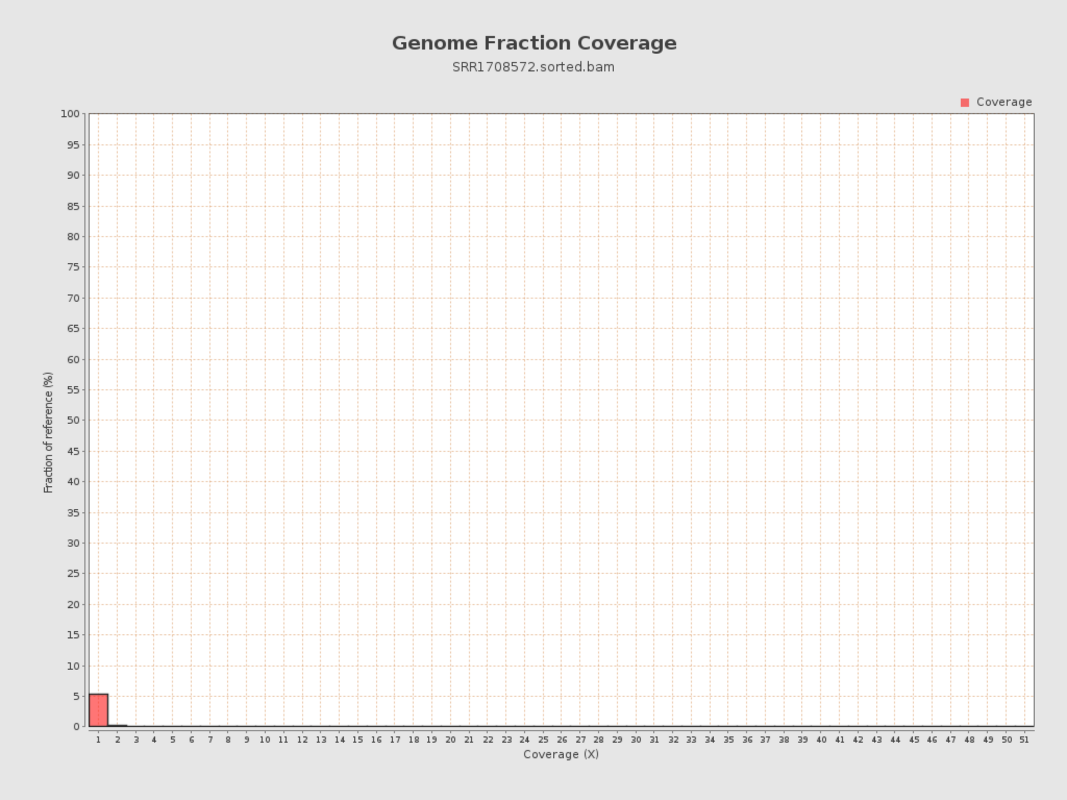
4. Results : Coverage Histogram



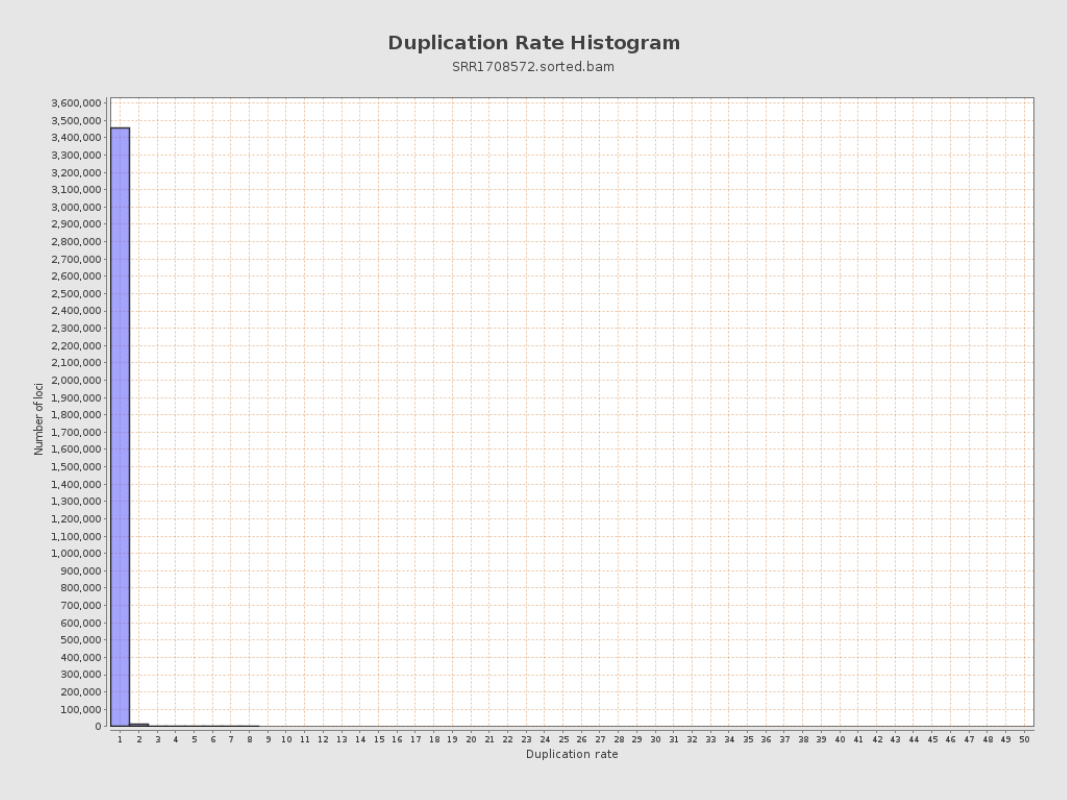
5. Results : Coverage Histogram (0-50X)



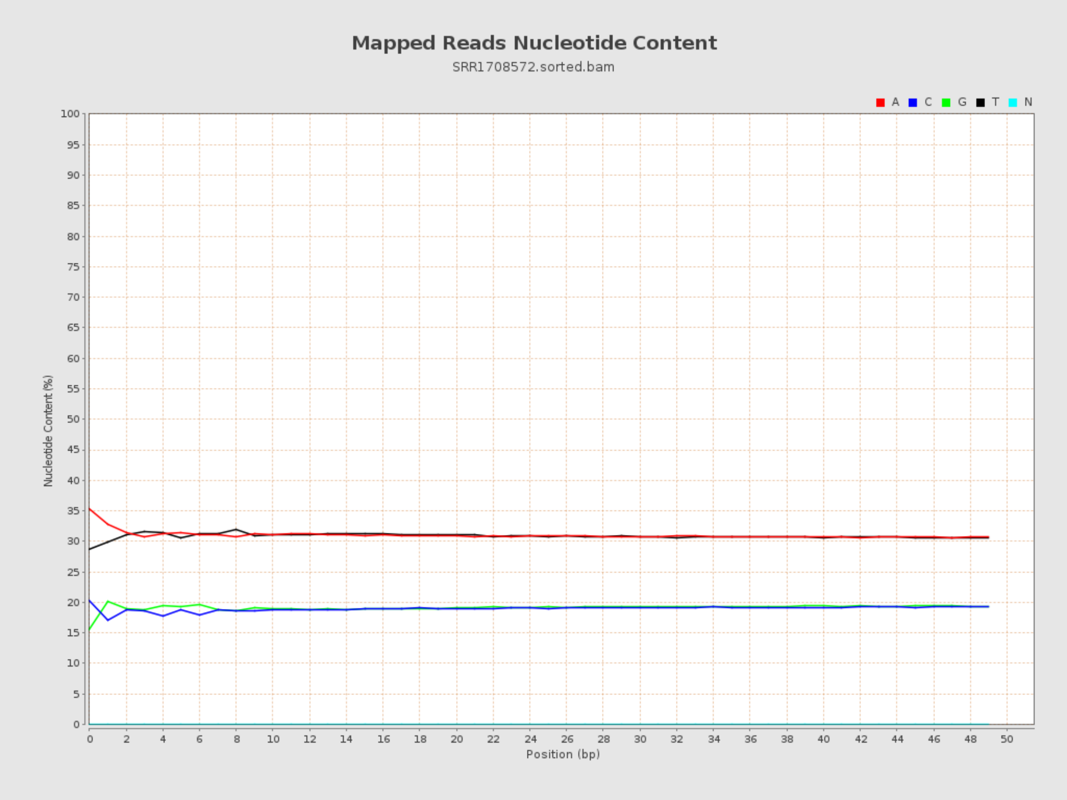
6. Results : Genome Fraction Coverage



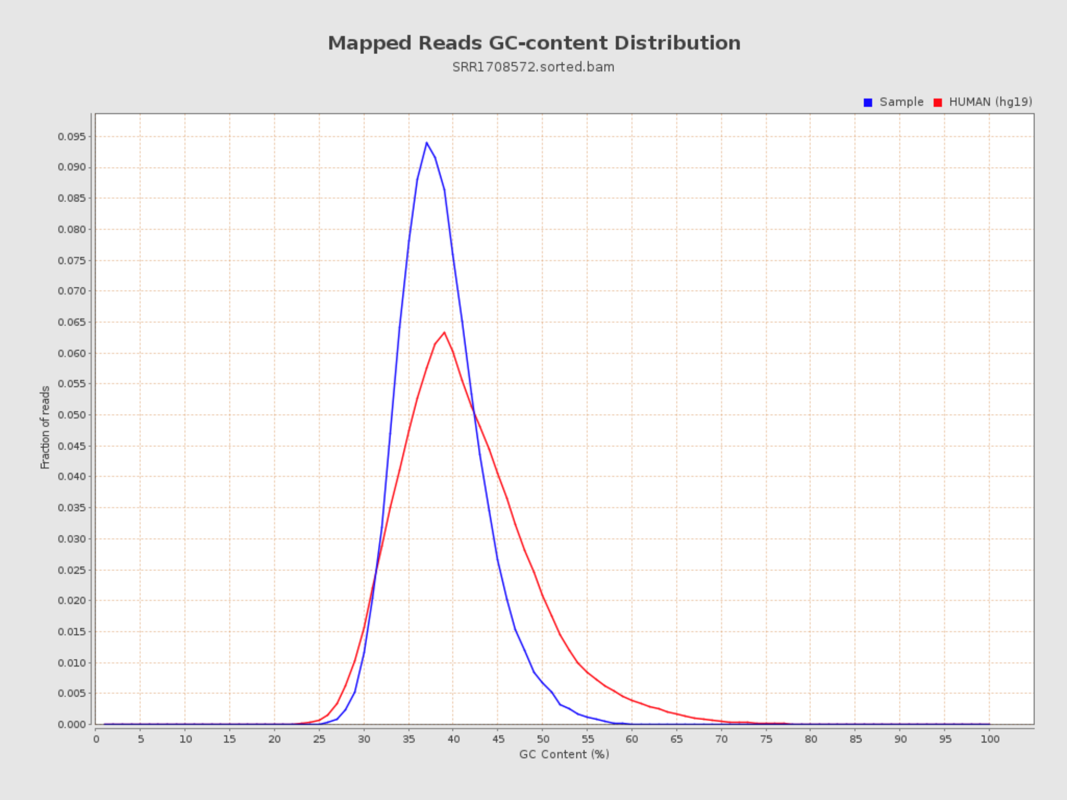
7. Results : Duplication Rate Histogram



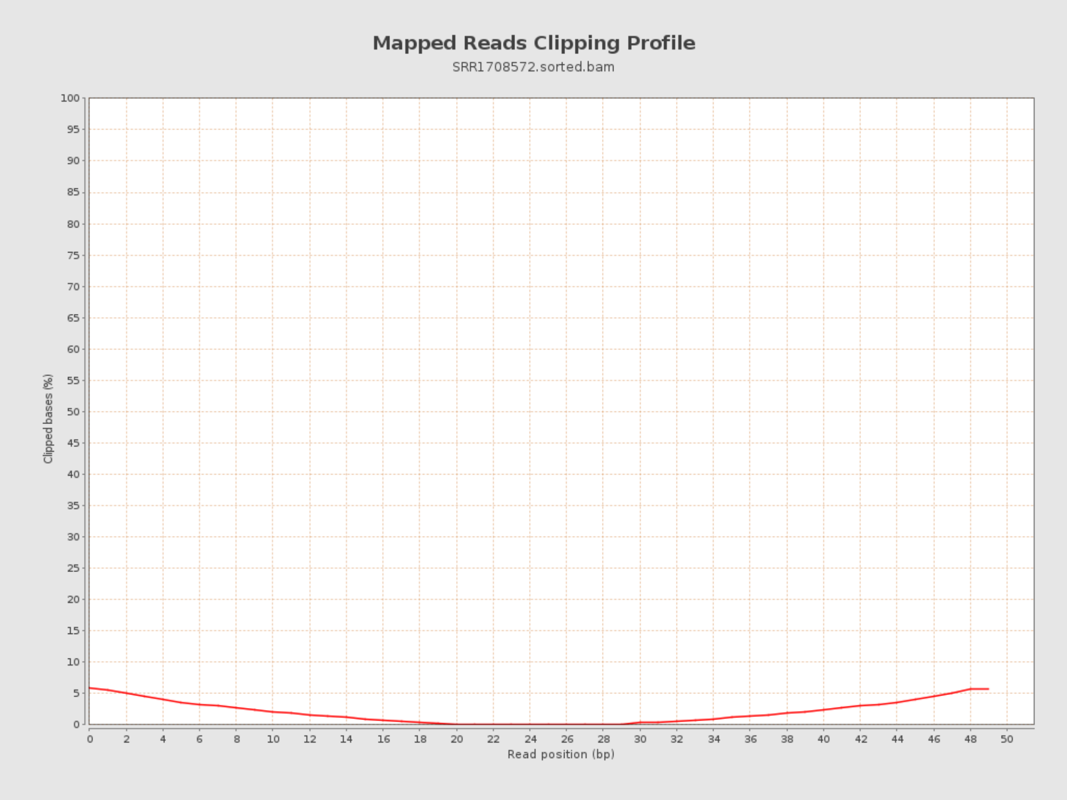
8. Results : Mapped Reads Nucleotide Content



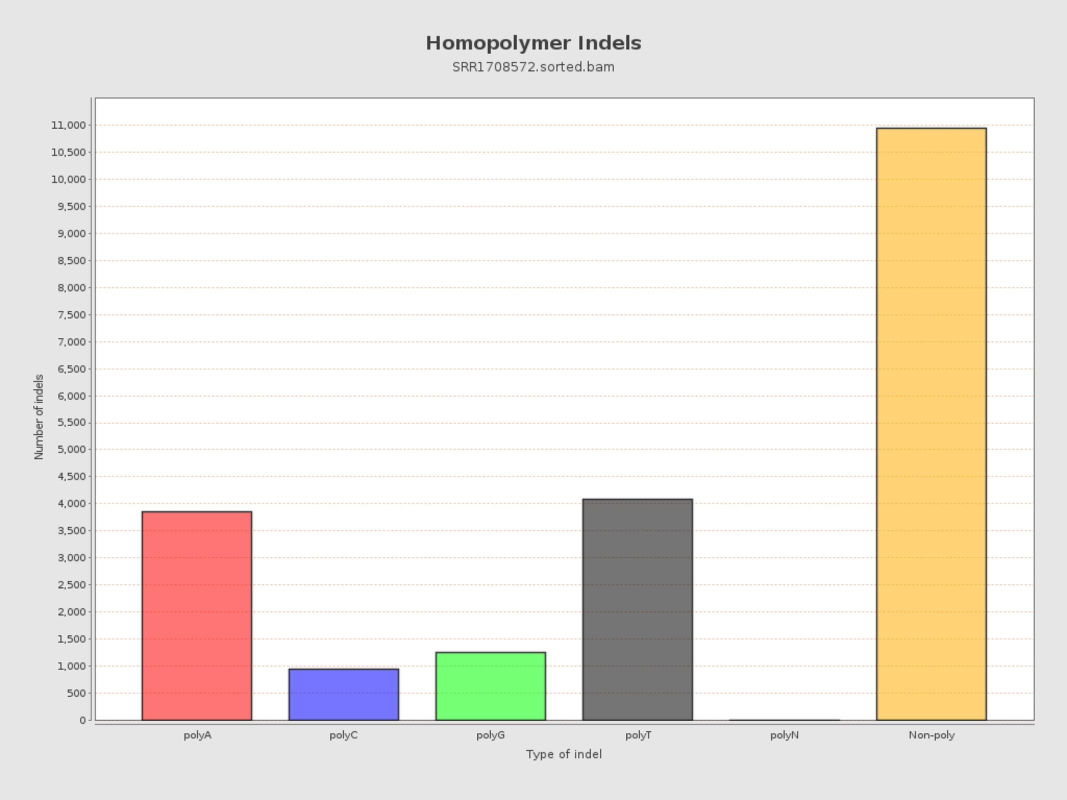
9. Results : Mapped Reads GC-content Distribution



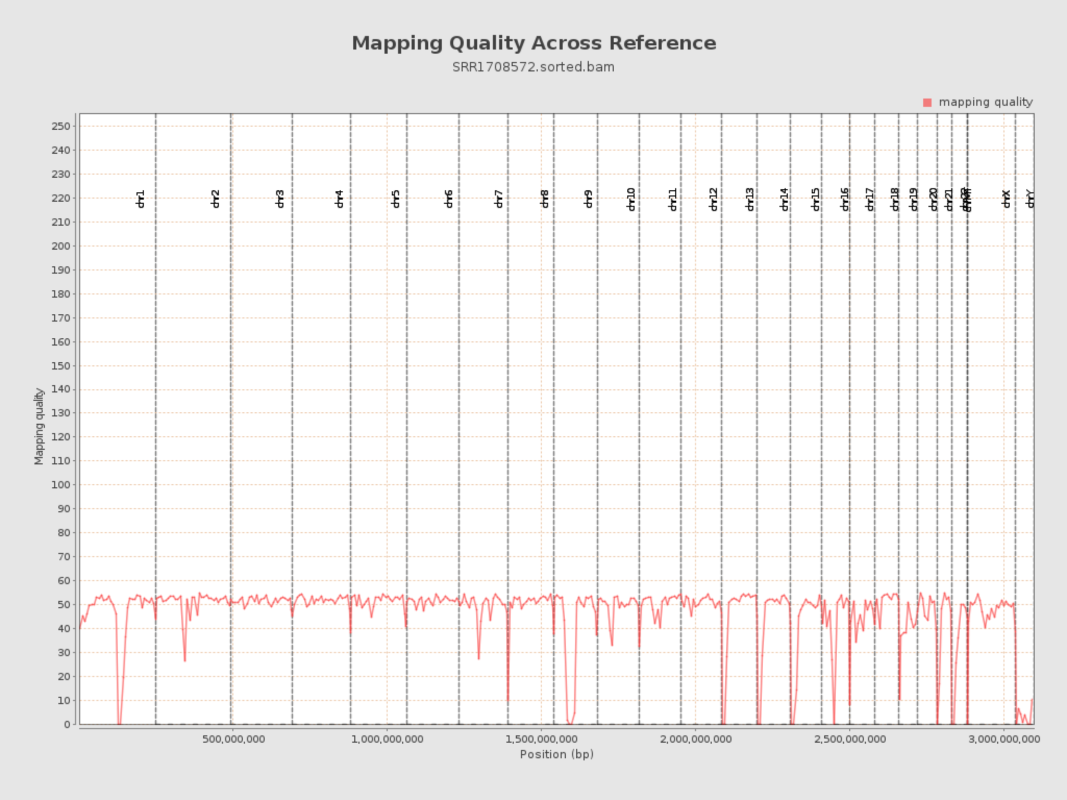
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram