Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:43:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708553.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_SRR1708553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708553.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:43:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,989,161
Mapped reads	3,289,035 / 82.45%
Unmapped reads	700,126 / 17.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	92 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,505 / 0.39%
Duplication rate	0.47%
Clipped reads	45,953 / 1.15%

2.2. ACGT Content

Number/percentage of A's	50,842,443 / 31%
Number/percentage of C's	31,122,406 / 18.98%
Number/percentage of T's	50,642,082 / 30.88%
Number/percentage of G's	31,378,593 / 19.13%
Number/percentage of N's	7,039 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	0.053

Standard Deviation	0.2382

2.4. Mapping Quality

Mean Mapping Quality	46.36

2.5. Mismatches and indels

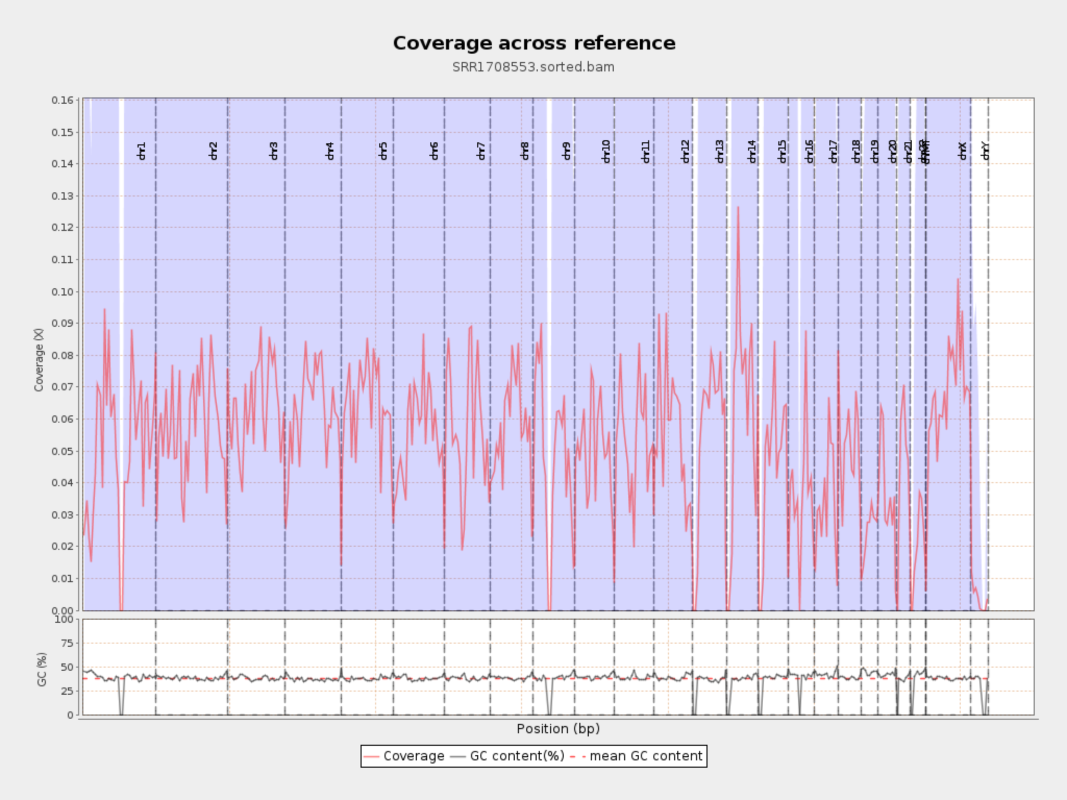
General error rate	0.17%
Mismatches	264,369
Insertions	11,305
Mapped reads with at least one insertion	0.34%
Deletions	8,857
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.84%

2.6. Chromosome stats

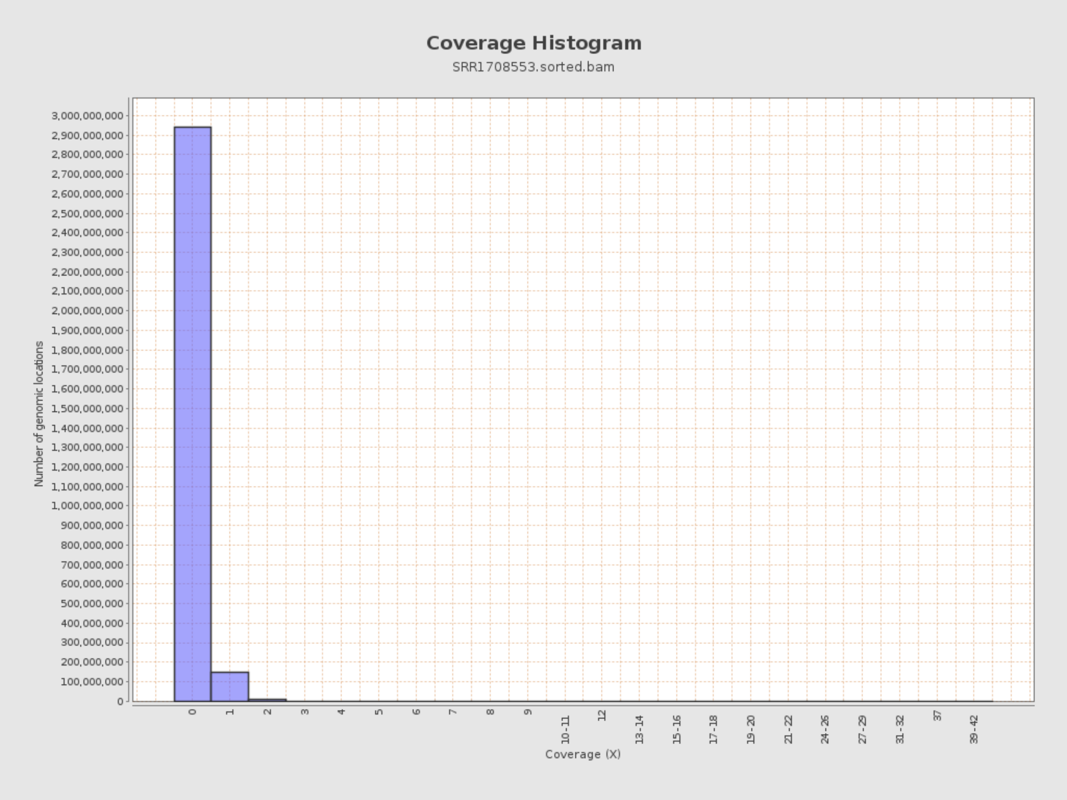
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12679697	0.0509	0.2345
chr2	243199373	13979592	0.0575	0.2473
chr3	198022430	12673090	0.064	0.2604
chr4	191154276	11906073	0.0623	0.2573
chr5	180915260	11498306	0.0636	0.2594
chr6	171115067	9573484	0.0559	0.244
chr7	159138663	8987528	0.0565	0.246

chr8	146364022	8523687	0.0582	0.2488
chr9	141213431	6935373	0.0491	0.23
chr10	135534747	6967828	0.0514	0.2333
chr11	135006516	7205866	0.0534	0.2389
chr12	133851895	7422169	0.0555	0.2438
chr13	115169878	6440838	0.0559	0.2447
chr14	107349540	6632206	0.0618	0.2585
chr15	102531392	4622359	0.0451	0.2203
chr16	90354753	3253390	0.036	0.1959
chr17	81195210	2812917	0.0346	0.1924
chr18	78077248	4022538	0.0515	0.2334
chr19	59128983	1484631	0.0251	0.1625
chr20	63025520	2399590	0.0381	0.202
chr21	48129895	2078997	0.0432	0.2174
chr22	51304566	1035858	0.0202	0.1465
chrMT	16571	100	0.006	0.0774
chrX	155270560	10639713	0.0685	0.2717
chrY	59373566	231947	0.0039	0.0655

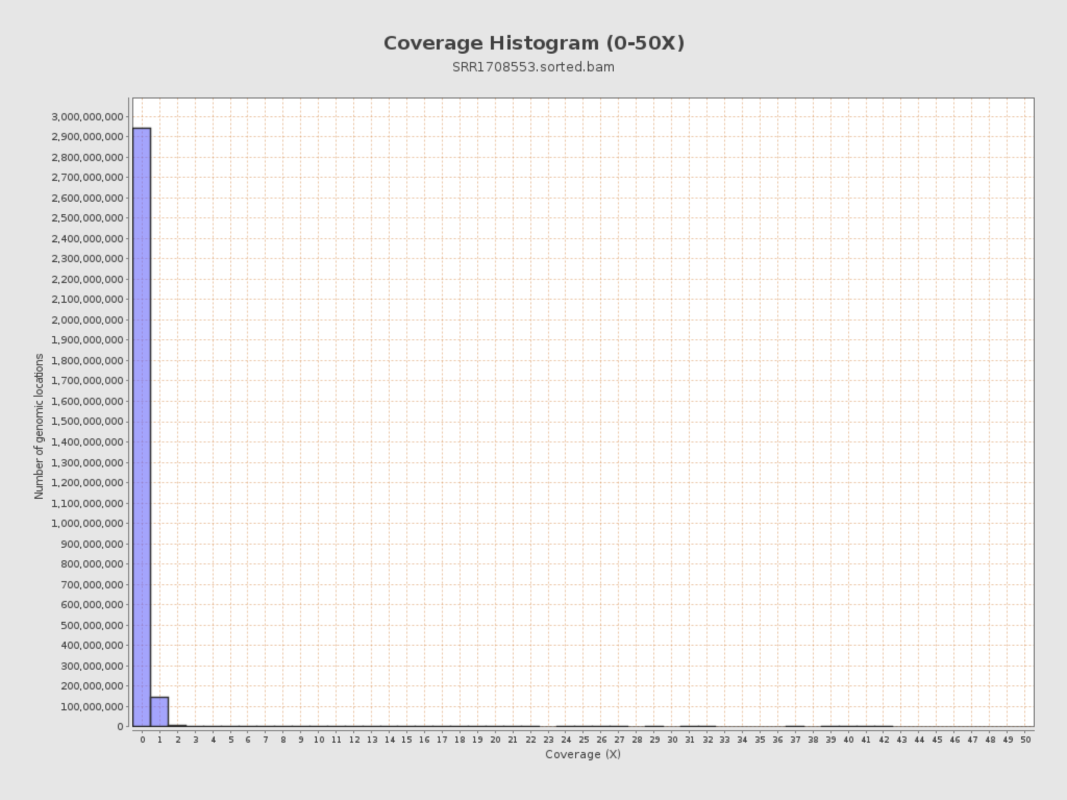
3. Results : Coverage across reference



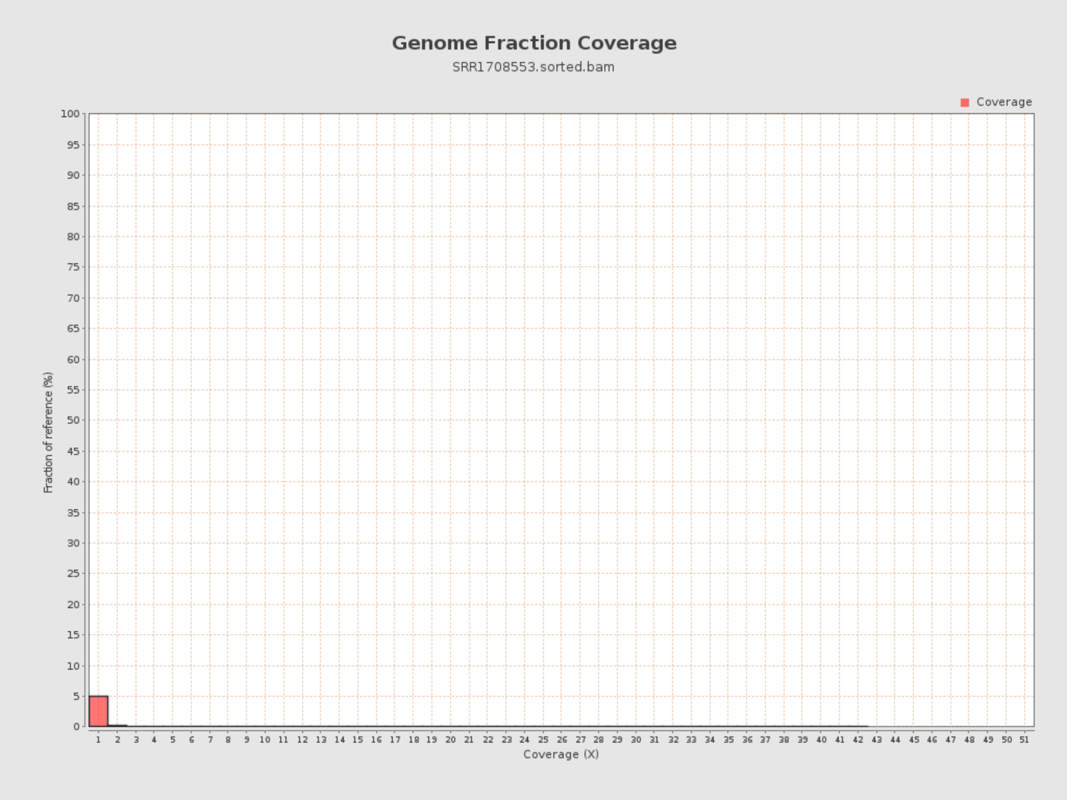
4. Results : Coverage Histogram



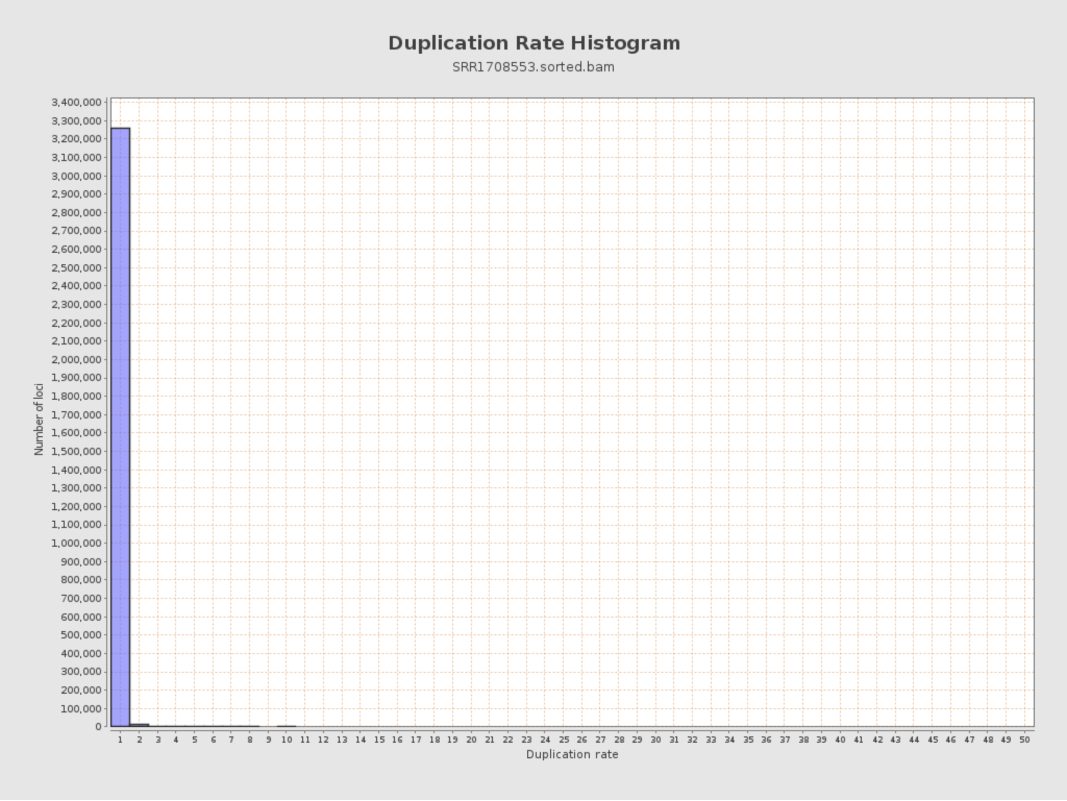
5. Results : Coverage Histogram (0-50X)



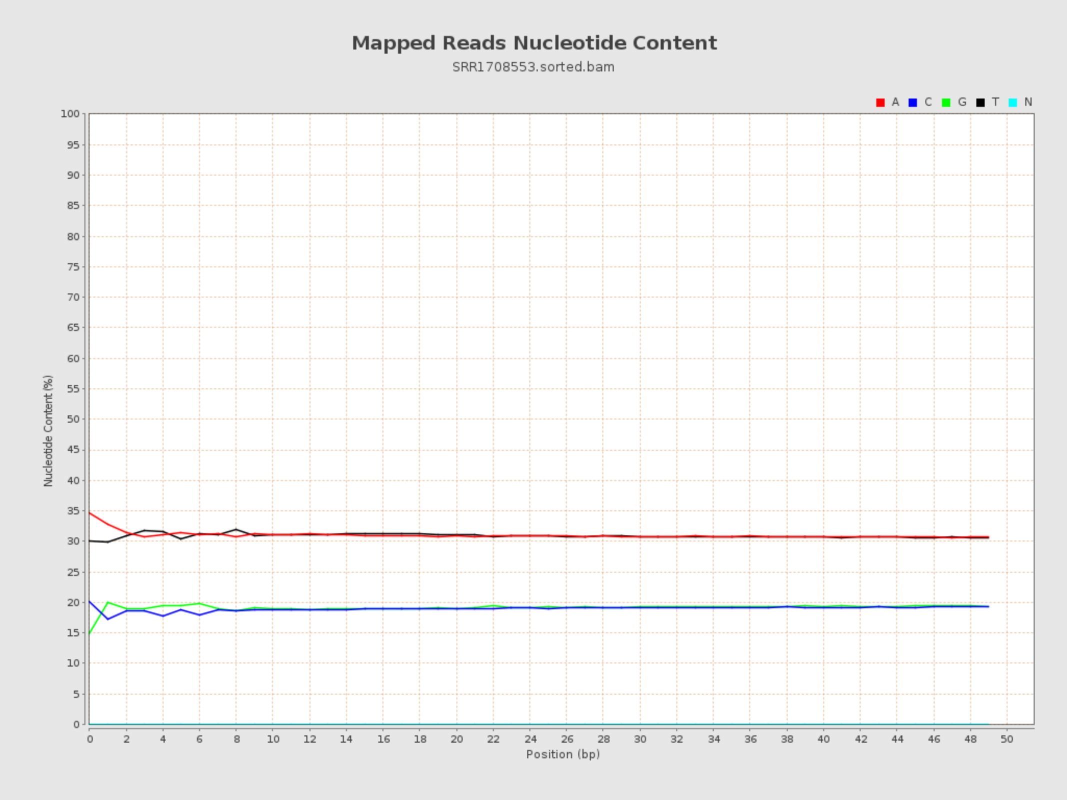
6. Results : Genome Fraction Coverage



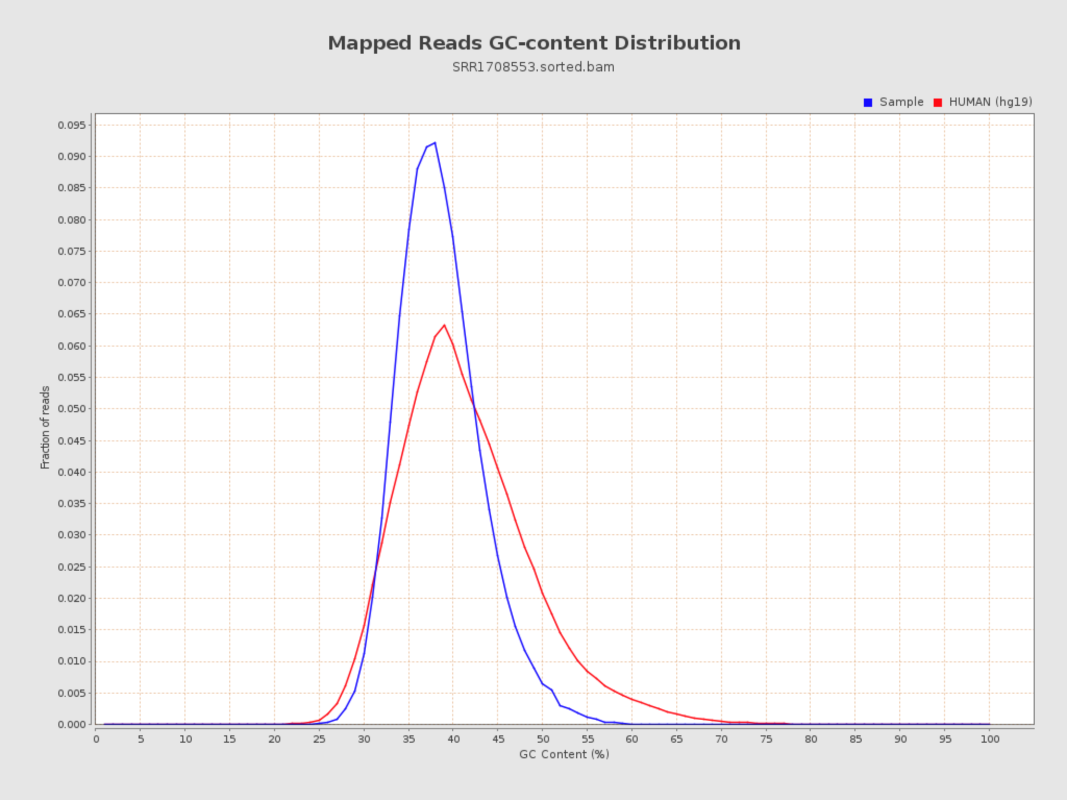
7. Results : Duplication Rate Histogram



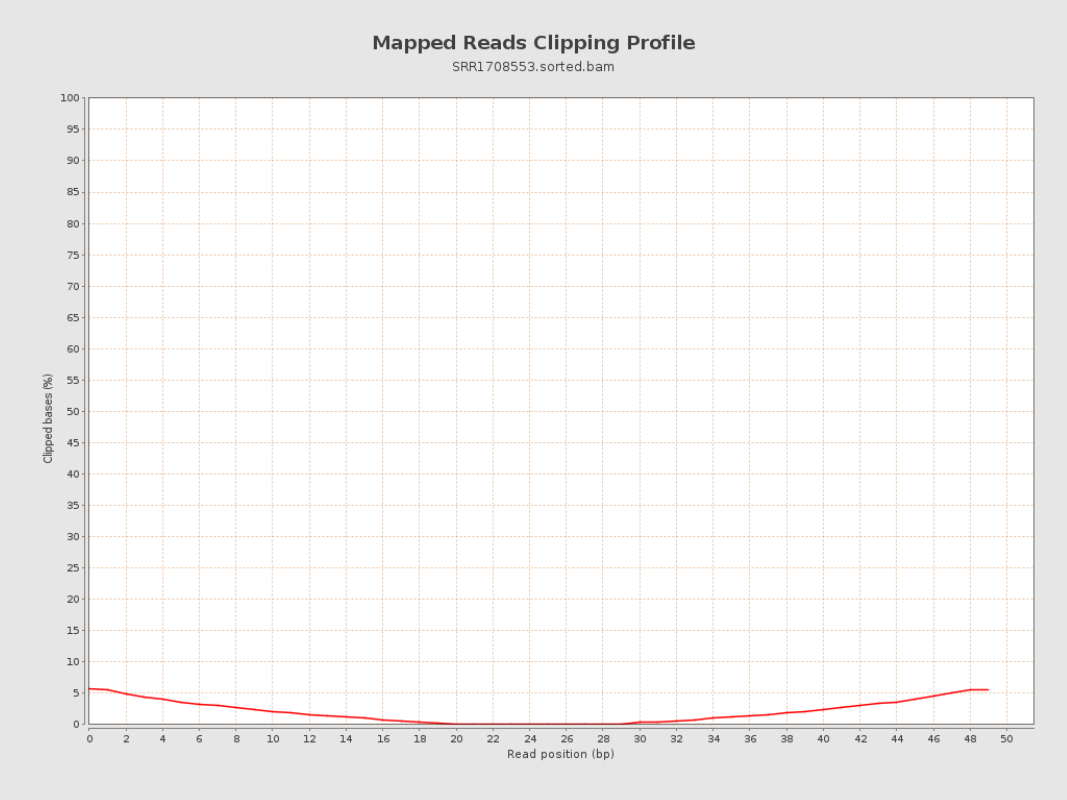
8. Results : Mapped Reads Nucleotide Content



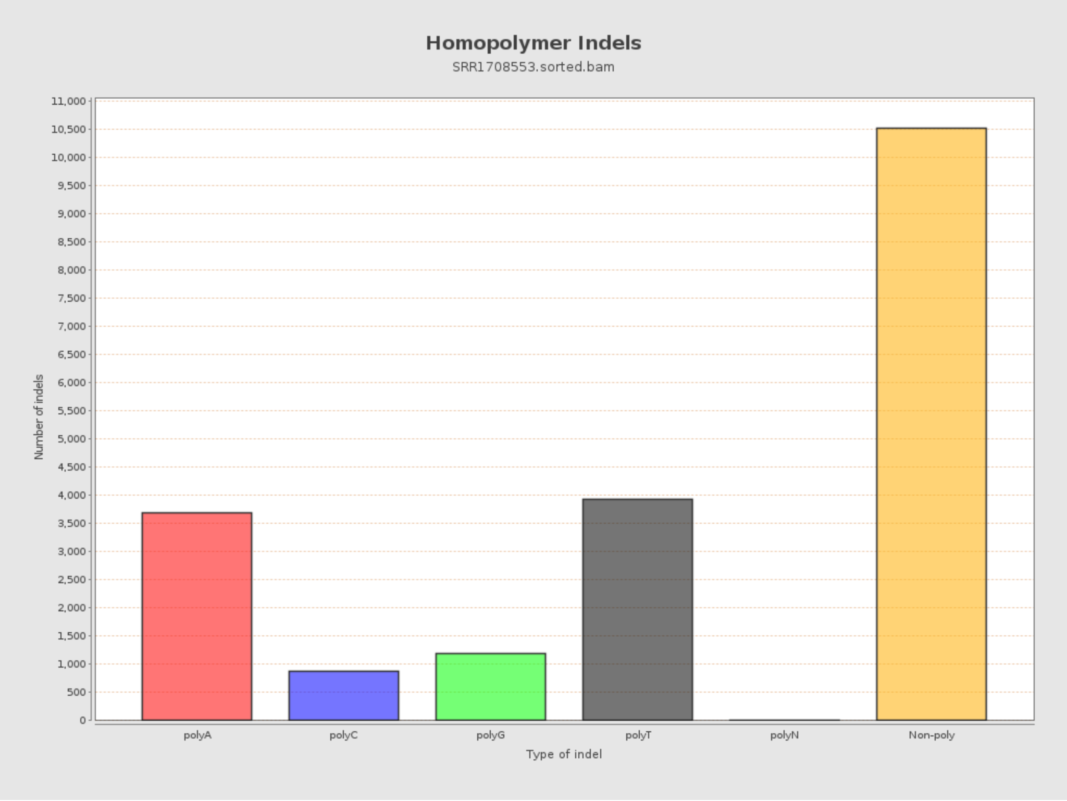
9. Results : Mapped Reads GC-content Distribution



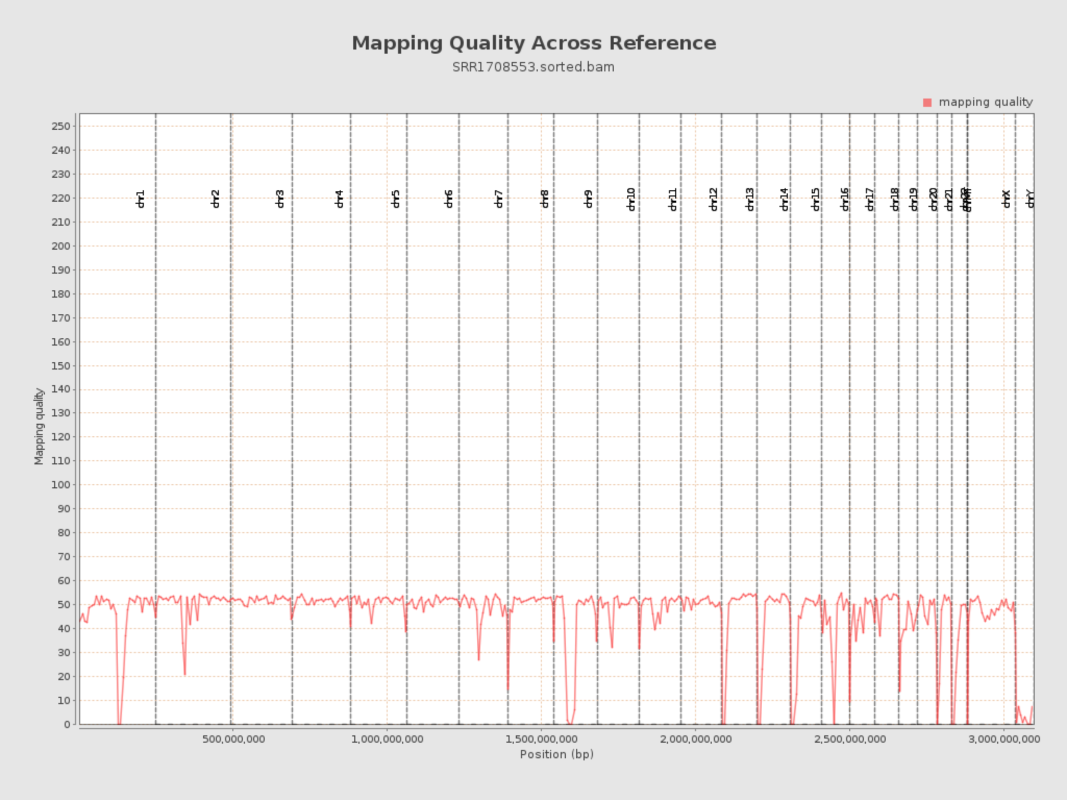
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram