Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:26:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708578.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_SRR1708578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708578.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:26:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,839,176
Mapped reads	3,753,335 / 97.76%
Unmapped reads	85,841 / 2.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	105 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	33,974 / 0.88%
Duplication rate	0.91%
Clipped reads	51,815 / 1.35%

2.2. ACGT Content

Number/percentage of A's	58,046,252 / 31.01%
Number/percentage of C's	35,422,150 / 18.92%
Number/percentage of T's	57,715,234 / 30.83%
Number/percentage of G's	35,989,470 / 19.23%
Number/percentage of N's	6,421 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0605

Standard Deviation	0.2544

2.4. Mapping Quality

Mean Mapping Quality	46.66

2.5. Mismatches and indels

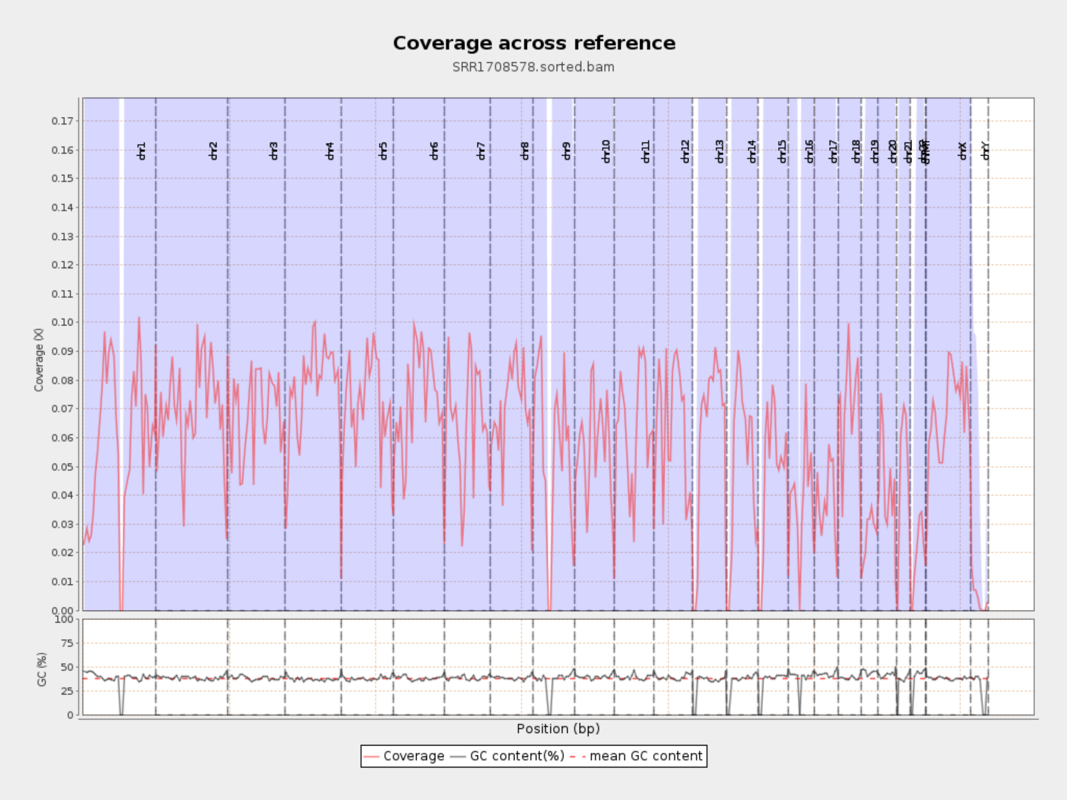
General error rate	0.16%
Mismatches	276,396
Insertions	12,023
Mapped reads with at least one insertion	0.32%
Deletions	9,471
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.97%

2.6. Chromosome stats

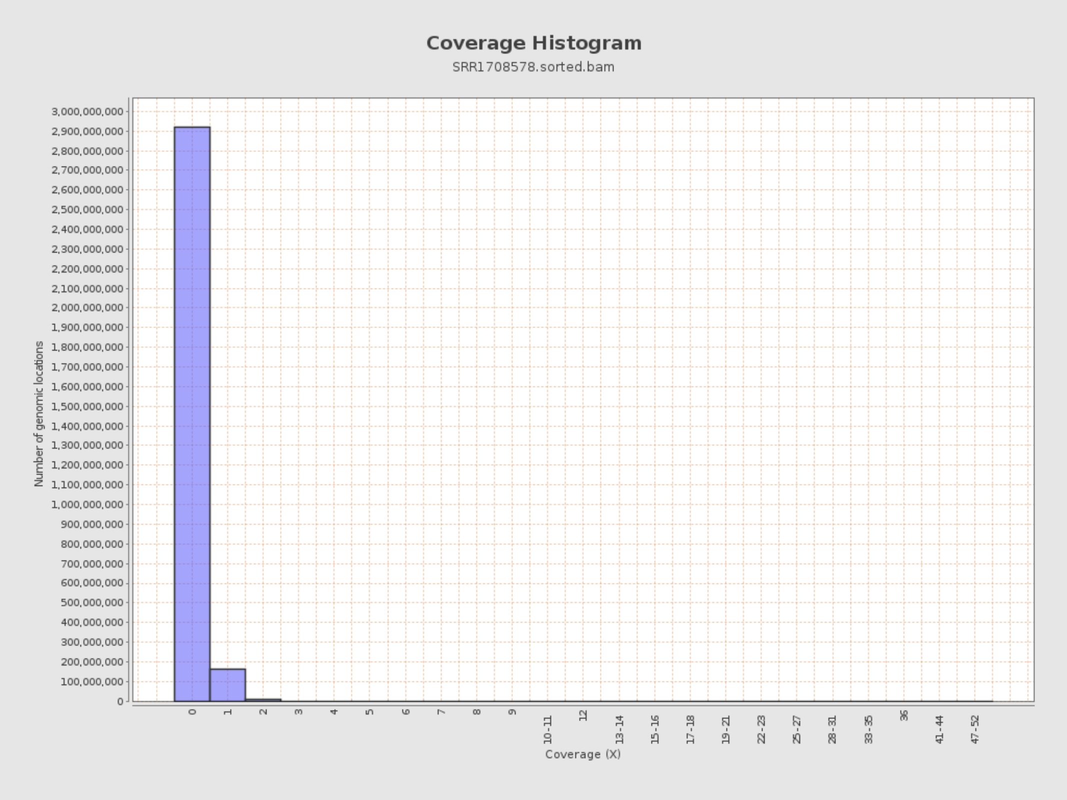
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14605363	0.0586	0.2517
chr2	243199373	17028500	0.07	0.273
chr3	198022430	13653634	0.0689	0.2704
chr4	191154276	14819164	0.0775	0.2865
chr5	180915260	12775303	0.0706	0.2734
chr6	171115067	12645194	0.0739	0.2803
chr7	159138663	10287330	0.0646	0.2627

chr8	146364022	10210721	0.0698	0.2721
chr9	141213431	7868528	0.0557	0.2445
chr10	135534747	7824632	0.0577	0.2475
chr11	135006516	8580414	0.0636	0.2618
chr12	133851895	8567561	0.064	0.2615
chr13	115169878	7189362	0.0624	0.2586
chr14	107349540	5627567	0.0524	0.237
chr15	102531392	4939955	0.0482	0.2276
chr16	90354753	3417878	0.0378	0.2007
chr17	81195210	3097554	0.0381	0.202
chr18	78077248	5545512	0.071	0.2751
chr19	59128983	1593723	0.027	0.169
chr20	63025520	2820993	0.0448	0.2187
chr21	48129895	2185918	0.0454	0.2222
chr22	51304566	1005736	0.0196	0.1439
chrMT	16571	336	0.0203	0.1409
chrX	155270560	10651405	0.0686	0.2699
chrY	59373566	253156	0.0043	0.0681

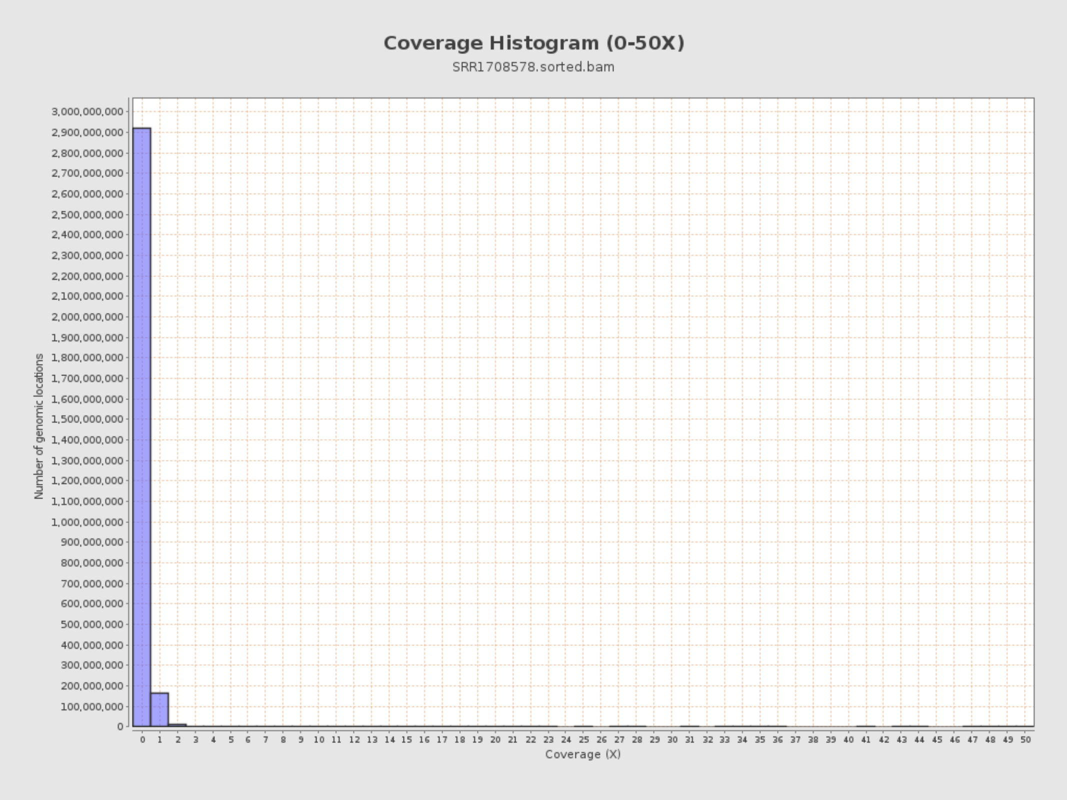
3. Results : Coverage across reference



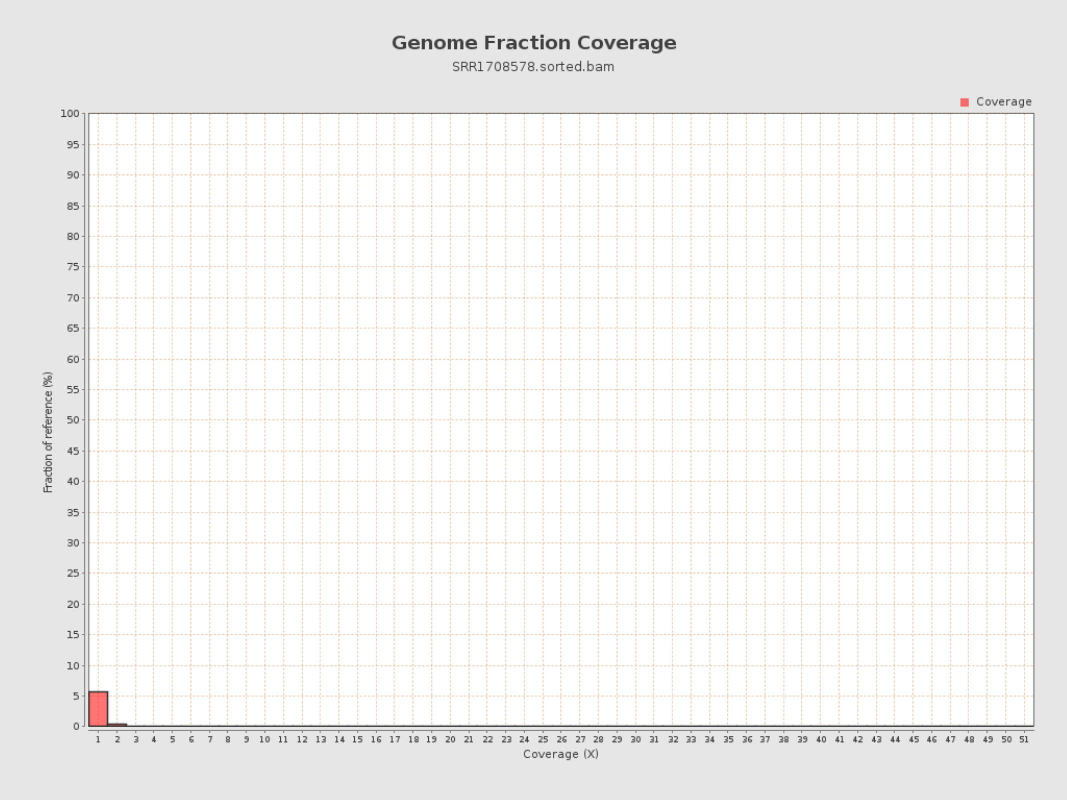
4. Results : Coverage Histogram



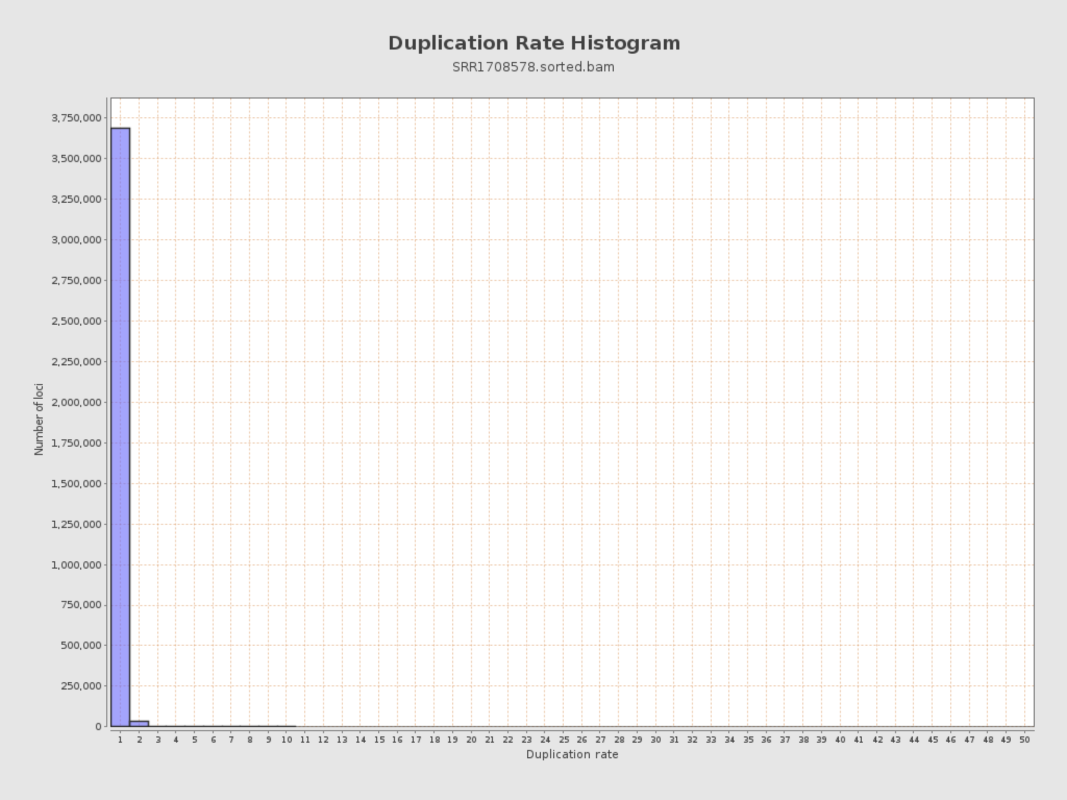
5. Results : Coverage Histogram (0-50X)



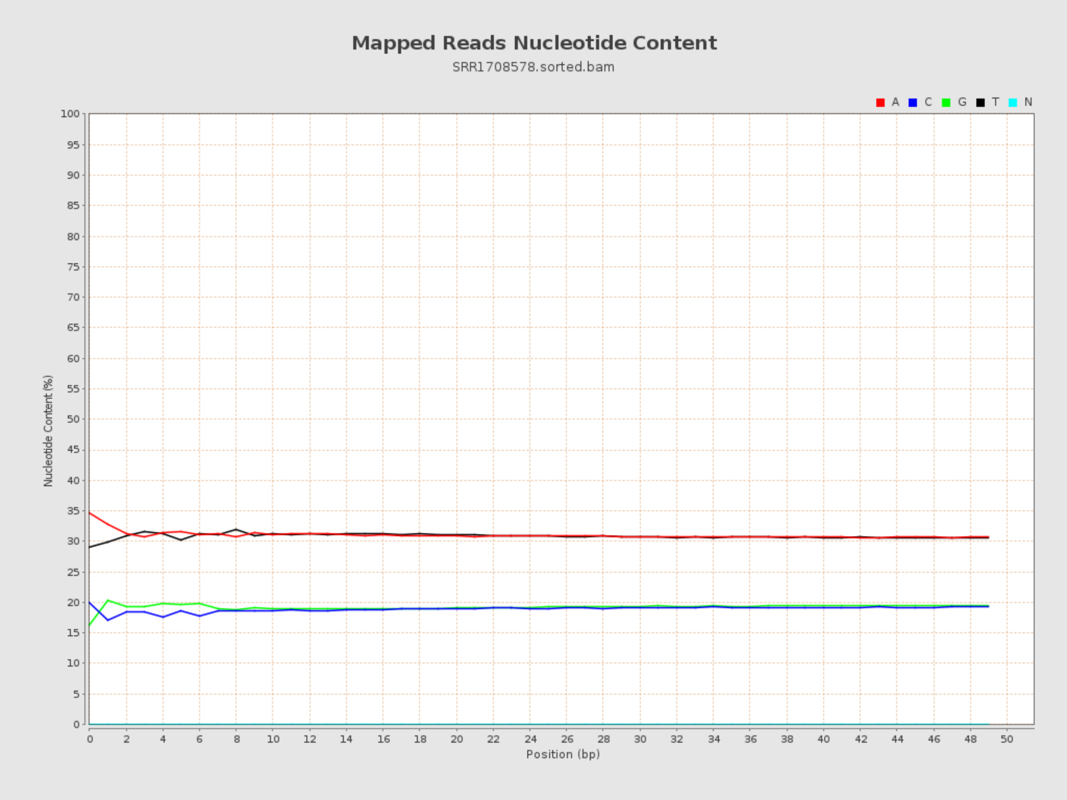
6. Results : Genome Fraction Coverage



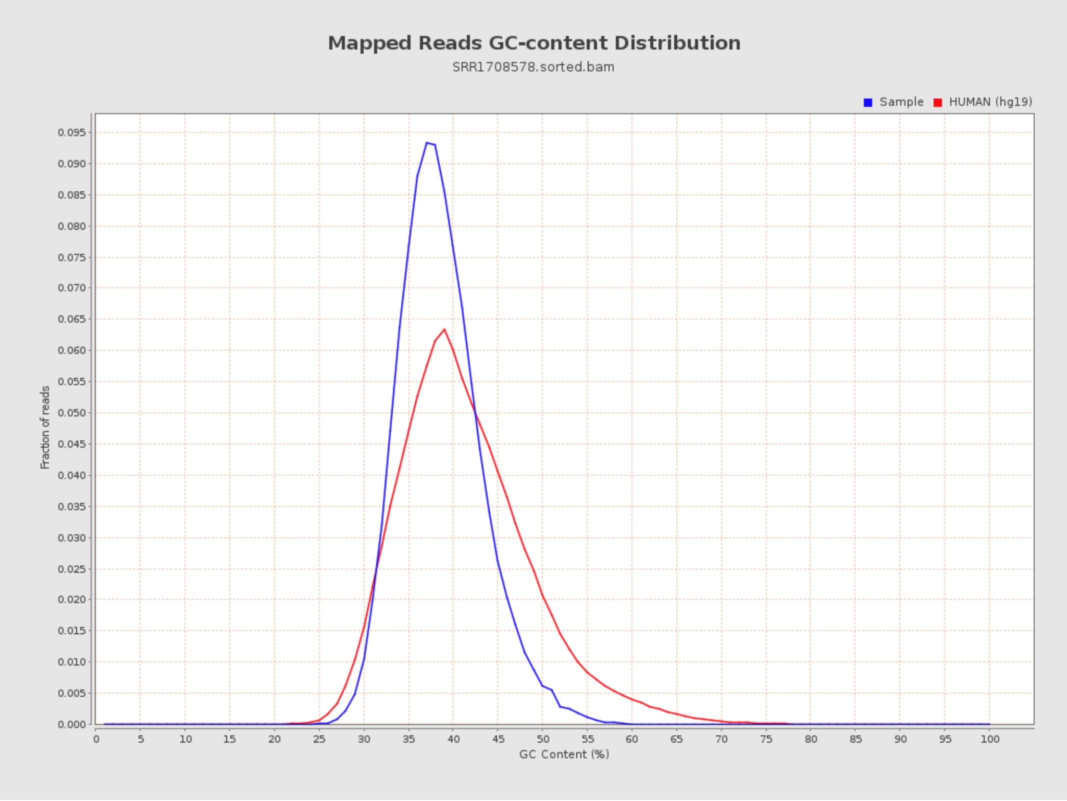
7. Results : Duplication Rate Histogram



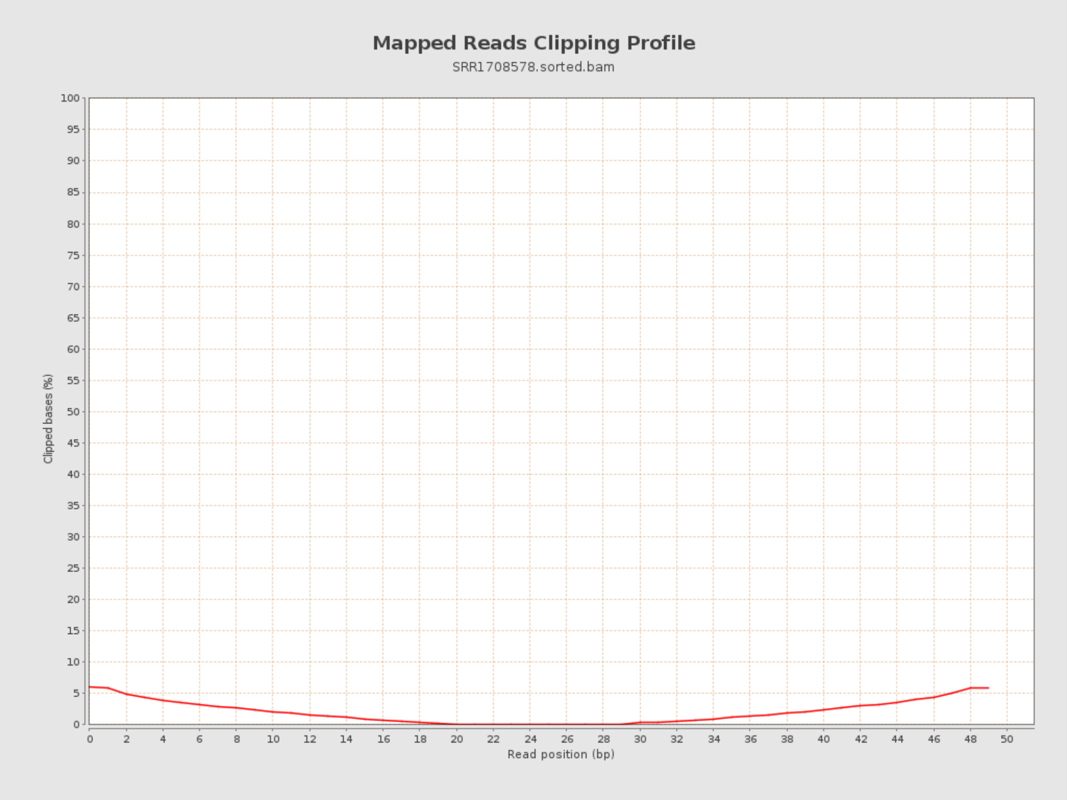
8. Results : Mapped Reads Nucleotide Content



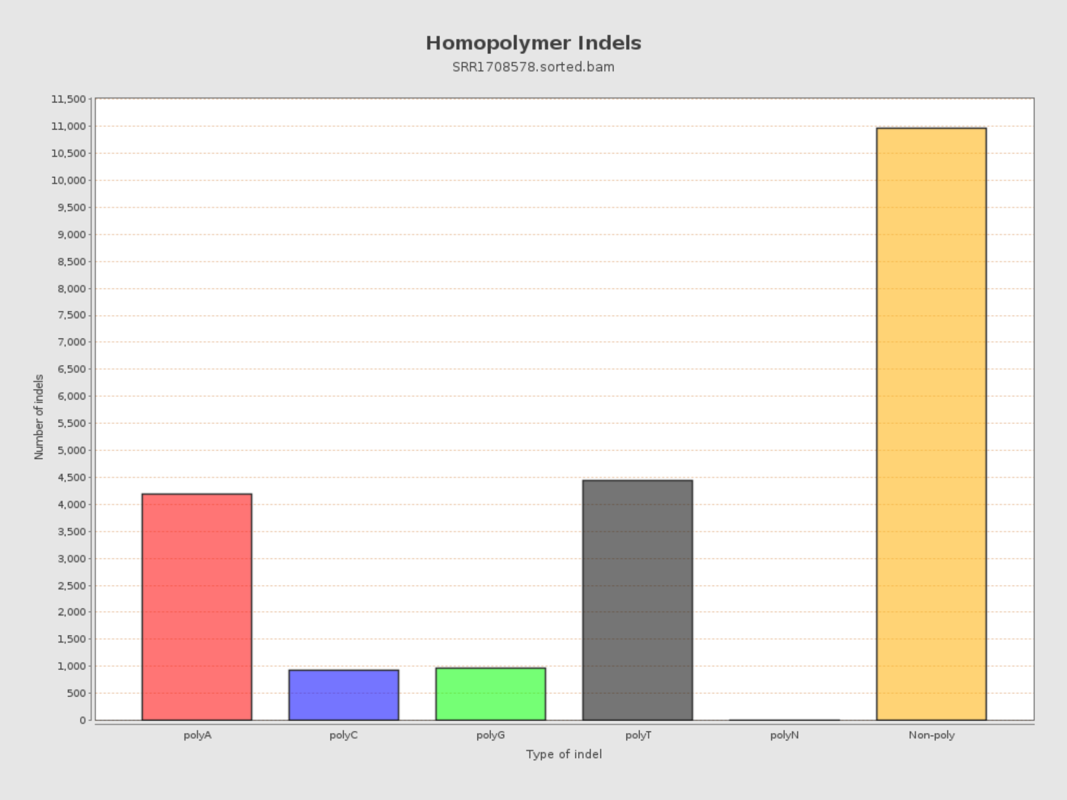
9. Results : Mapped Reads GC-content Distribution



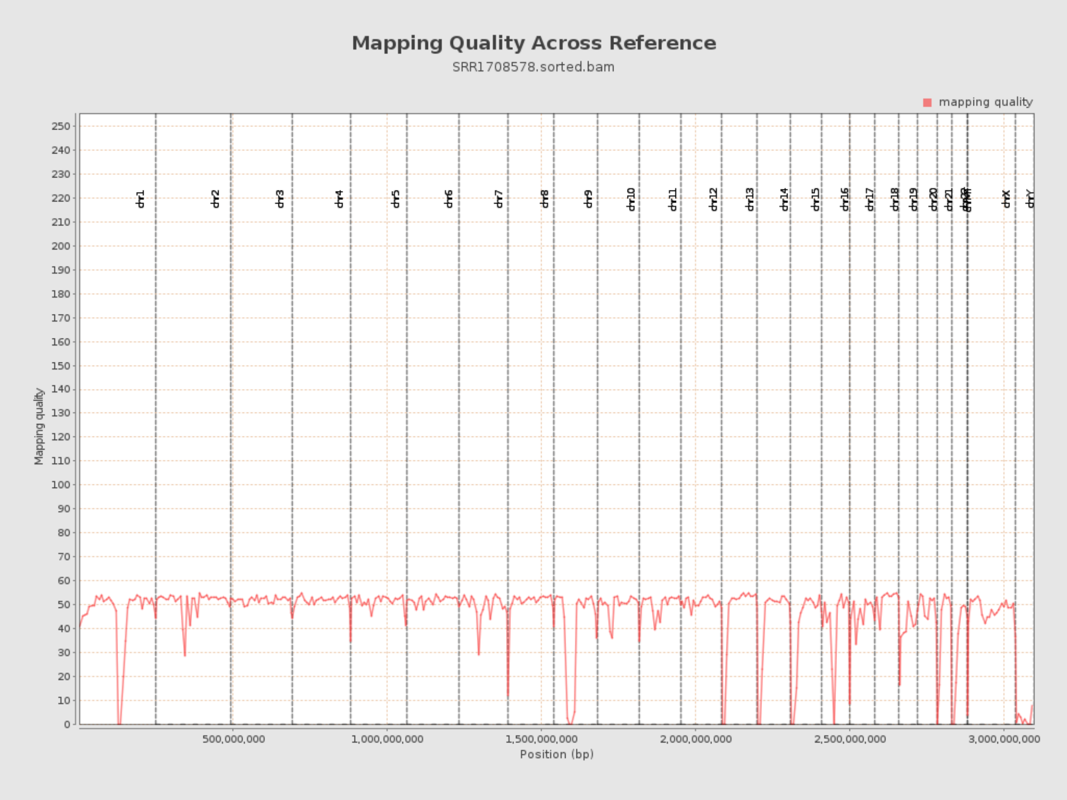
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram