Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:45:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708652.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_SRR1708652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:45:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,948,608
Mapped reads	22,381,330 / 97.53%
Unmapped reads	567,278 / 2.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	546 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	248,521 / 1.08%
Duplication rate	1.1%
Clipped reads	282,985 / 1.23%

2.2. ACGT Content

Number/percentage of A's	339,235,774 / 30.39%
Number/percentage of C's	217,269,590 / 19.46%
Number/percentage of T's	337,613,441 / 30.24%
Number/percentage of G's	222,281,949 / 19.91%
Number/percentage of N's	39,189 / 0%
GC Percentage	39.37%

2.3. Coverage

Mean	0.3607

Standard Deviation	0.7086

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

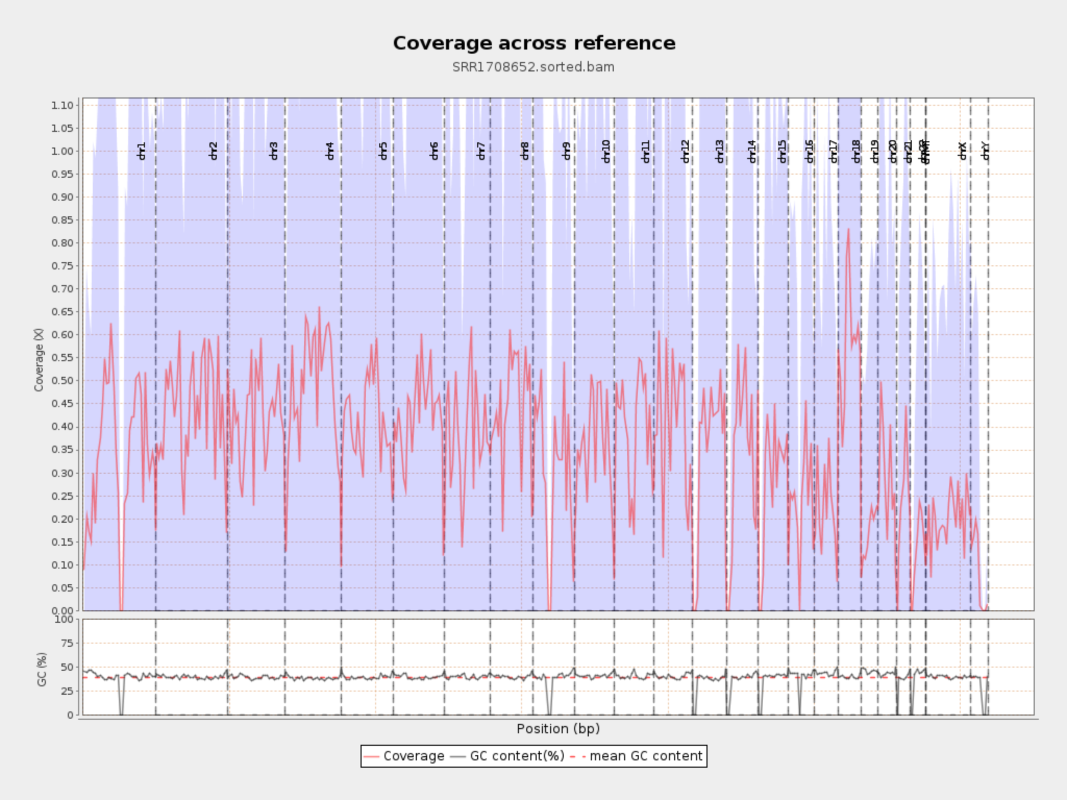
General error rate	0.22%
Mismatches	2,317,748
Insertions	68,301
Mapped reads with at least one insertion	0.3%
Deletions	60,498
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48.67%

2.6. Chromosome stats

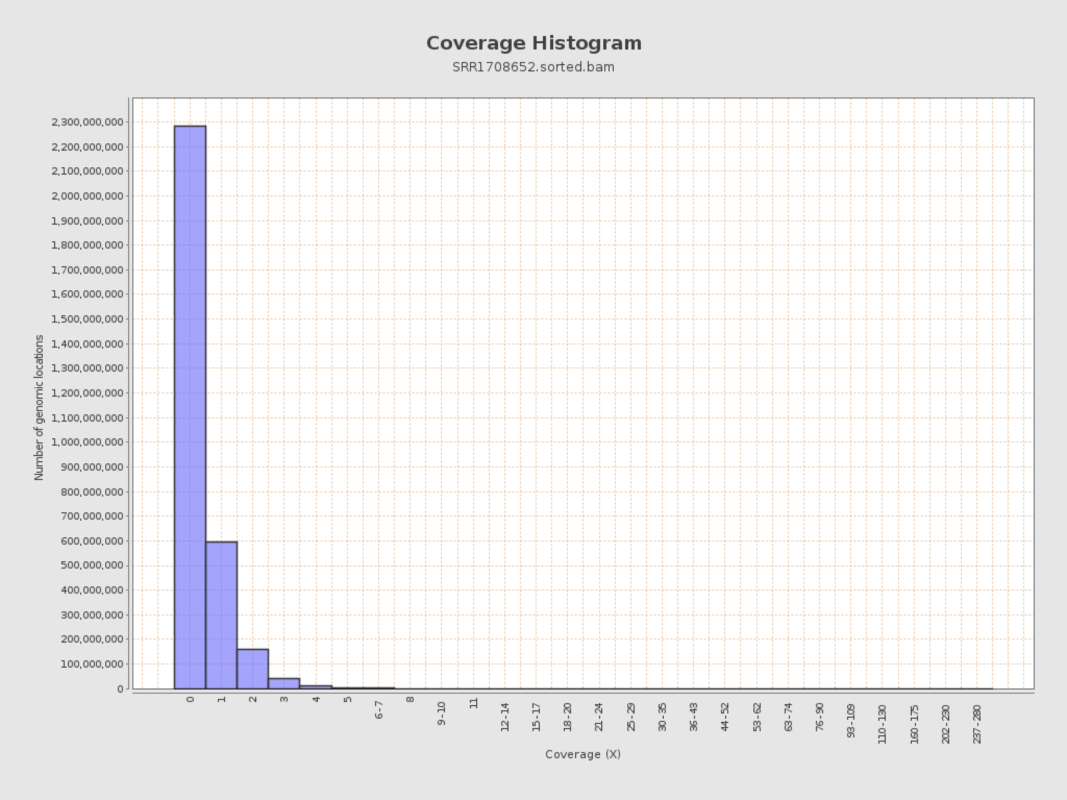
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	83869519	0.3365	0.6979
chr2	243199373	106031724	0.436	0.7688
chr3	198022430	83832087	0.4233	0.749
chr4	191154276	93389311	0.4886	0.8136
chr5	180915260	75055280	0.4149	0.74
chr6	171115067	73725707	0.4309	0.7561
chr7	159138663	61141784	0.3842	0.7253

chr8	146364022	65374537	0.4467	0.7762
chr9	141213431	43691437	0.3094	0.6559
chr10	135534747	49290083	0.3637	0.6941
chr11	135006516	53229345	0.3943	0.7422
chr12	133851895	54493001	0.4071	0.7467
chr13	115169878	40687973	0.3533	0.6974
chr14	107349540	35128380	0.3272	0.6793
chr15	102531392	28629139	0.2792	0.6287
chr16	90354753	21362076	0.2364	0.5694
chr17	81195210	18491388	0.2277	0.5483
chr18	78077248	45717392	0.5855	0.9139
chr19	59128983	10051052	0.17	0.4657
chr20	63025520	18855128	0.2992	0.6402
chr21	48129895	11571980	0.2404	0.5941
chr22	51304566	6835631	0.1332	0.4269
chrMT	16571	2758	0.1664	0.4132
chrX	155270560	31134507	0.2005	0.5096
chrY	59373566	4950874	0.0834	0.3409

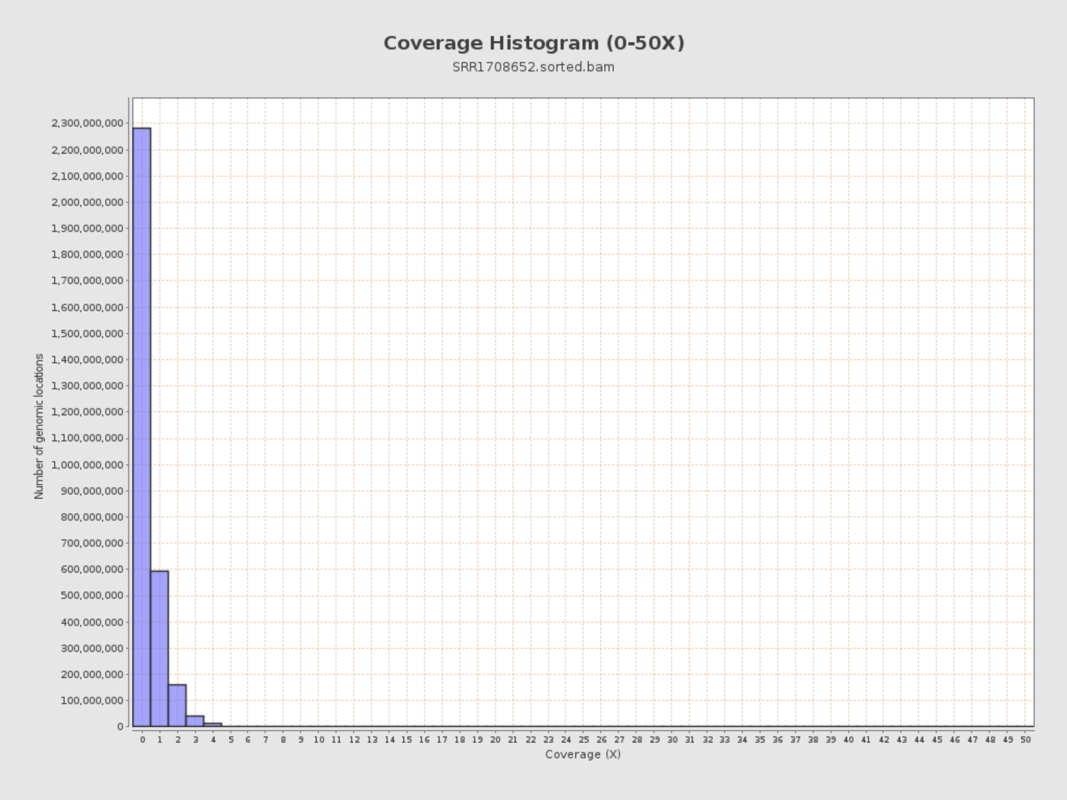
3. Results : Coverage across reference



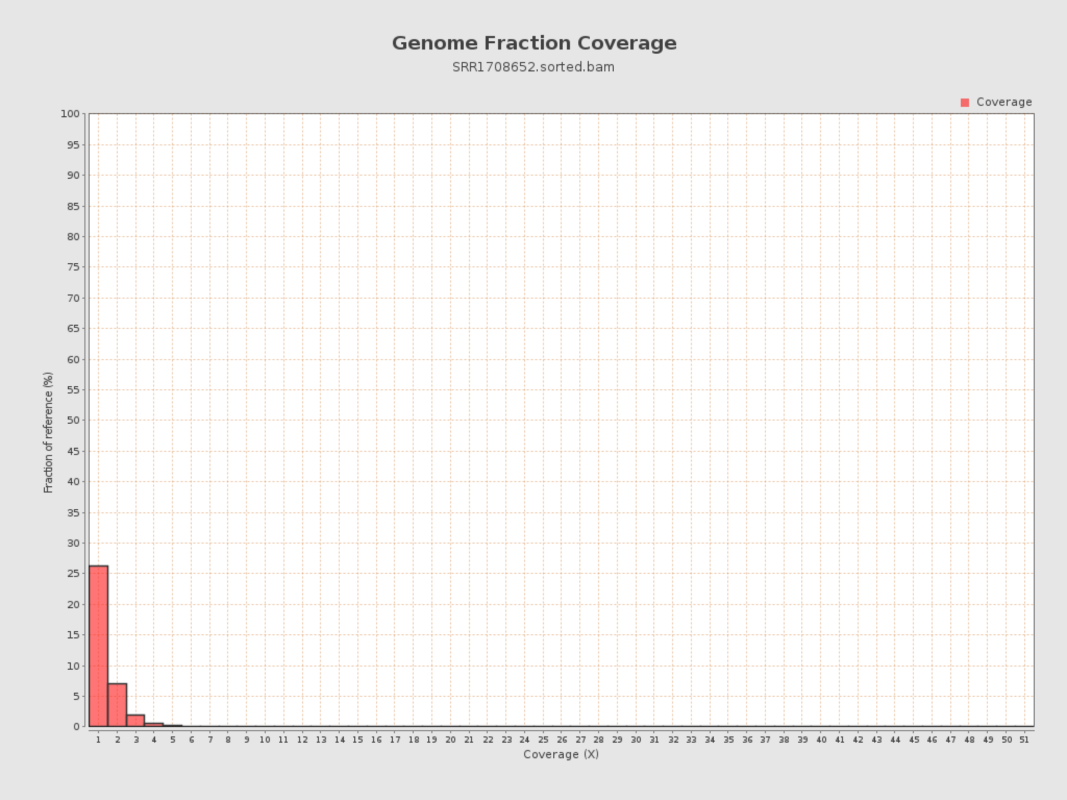
4. Results : Coverage Histogram



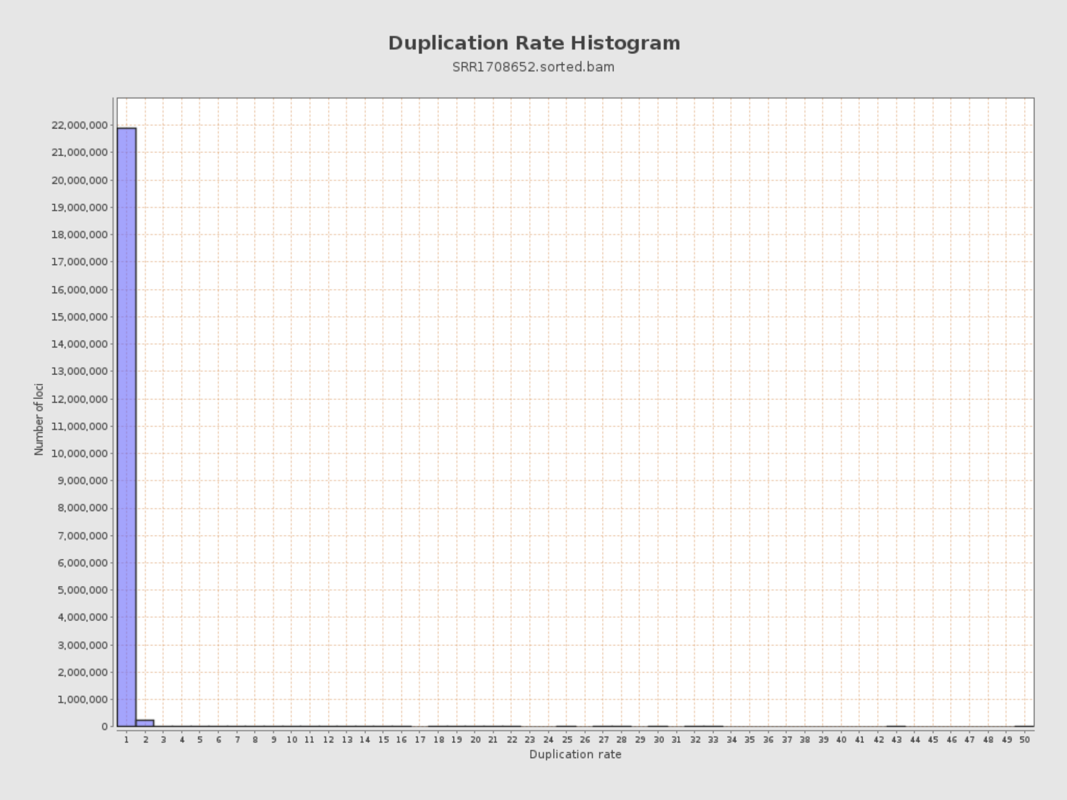
5. Results : Coverage Histogram (0-50X)



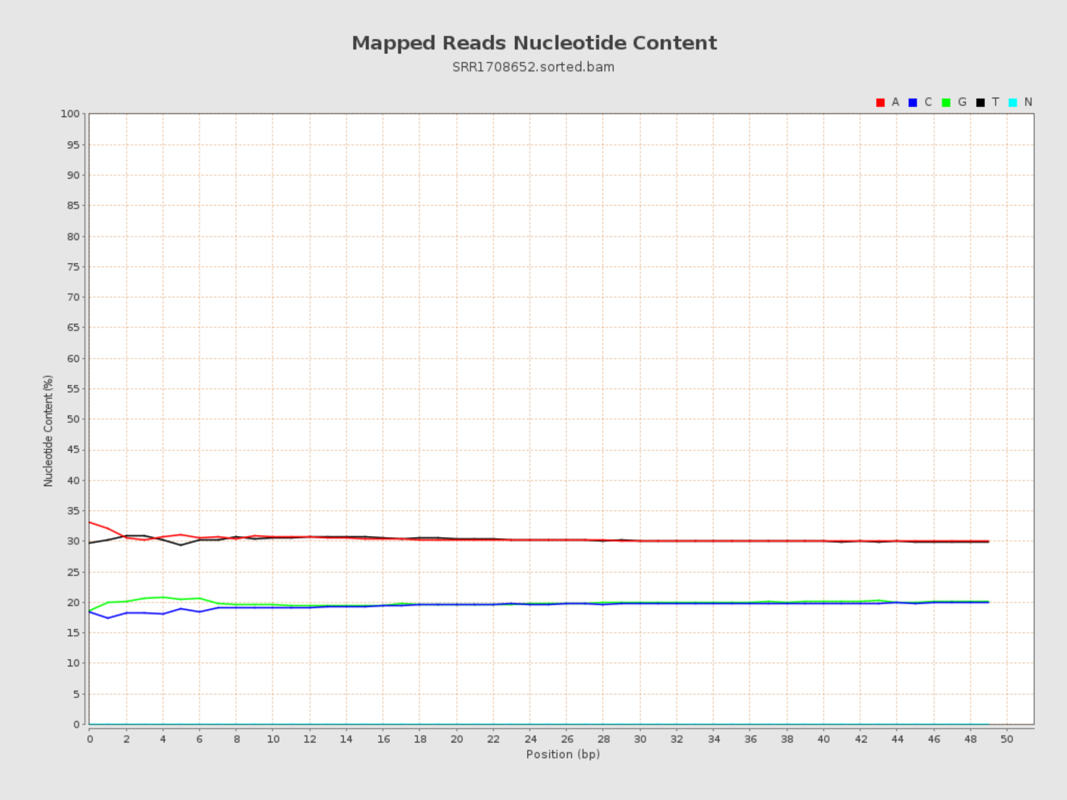
6. Results : Genome Fraction Coverage



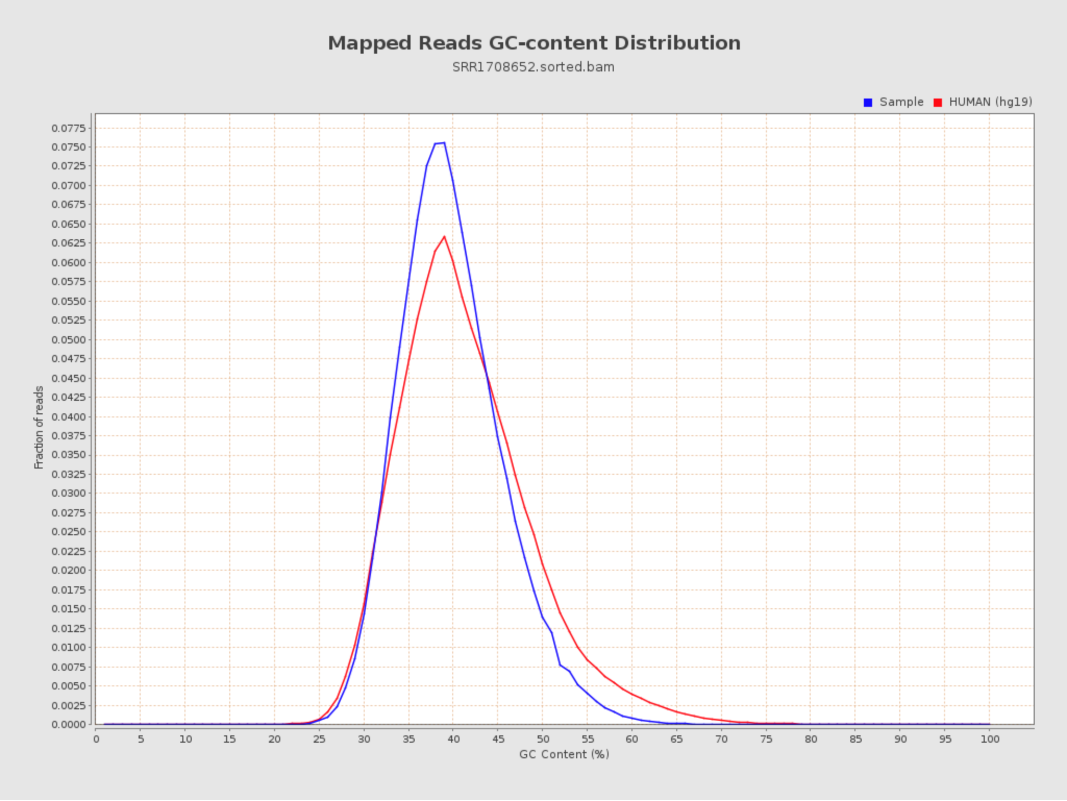
7. Results : Duplication Rate Histogram



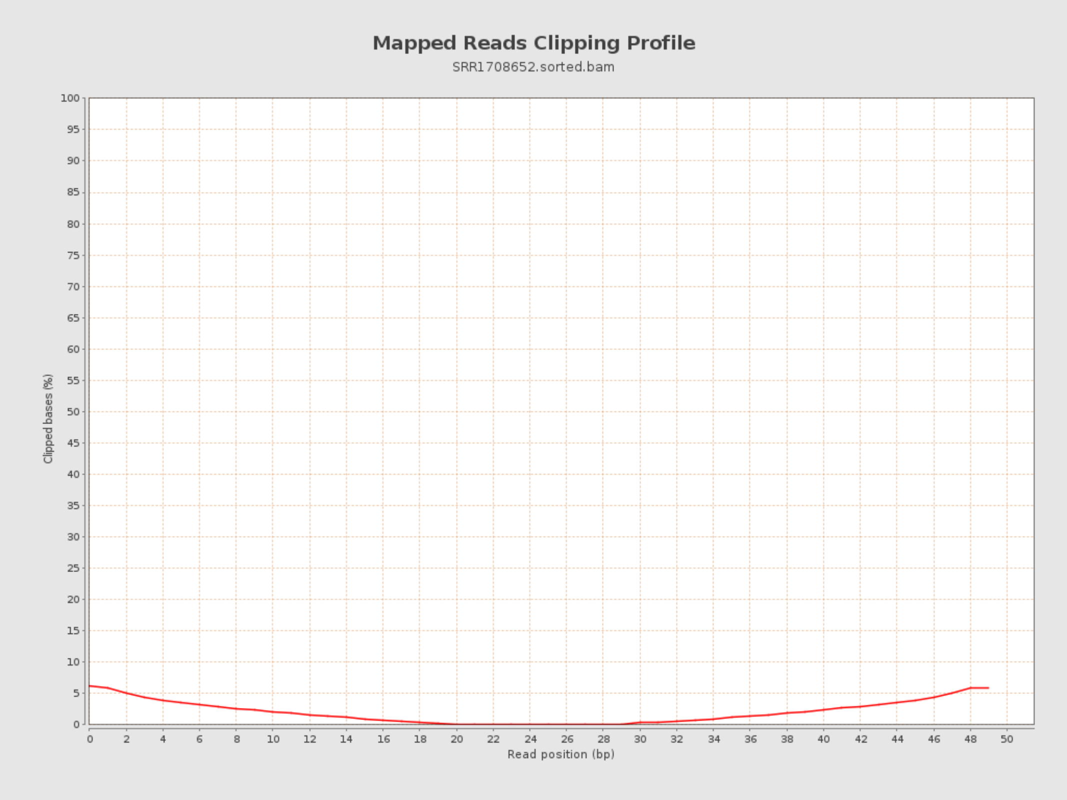
8. Results : Mapped Reads Nucleotide Content



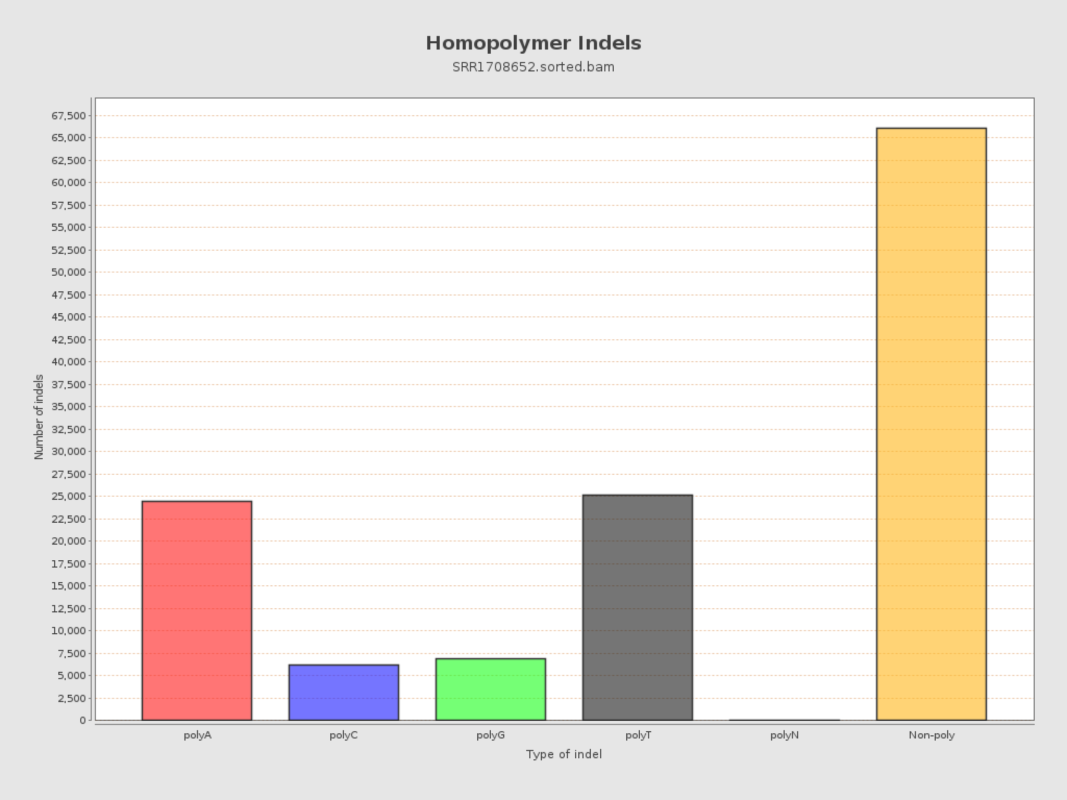
9. Results : Mapped Reads GC-content Distribution



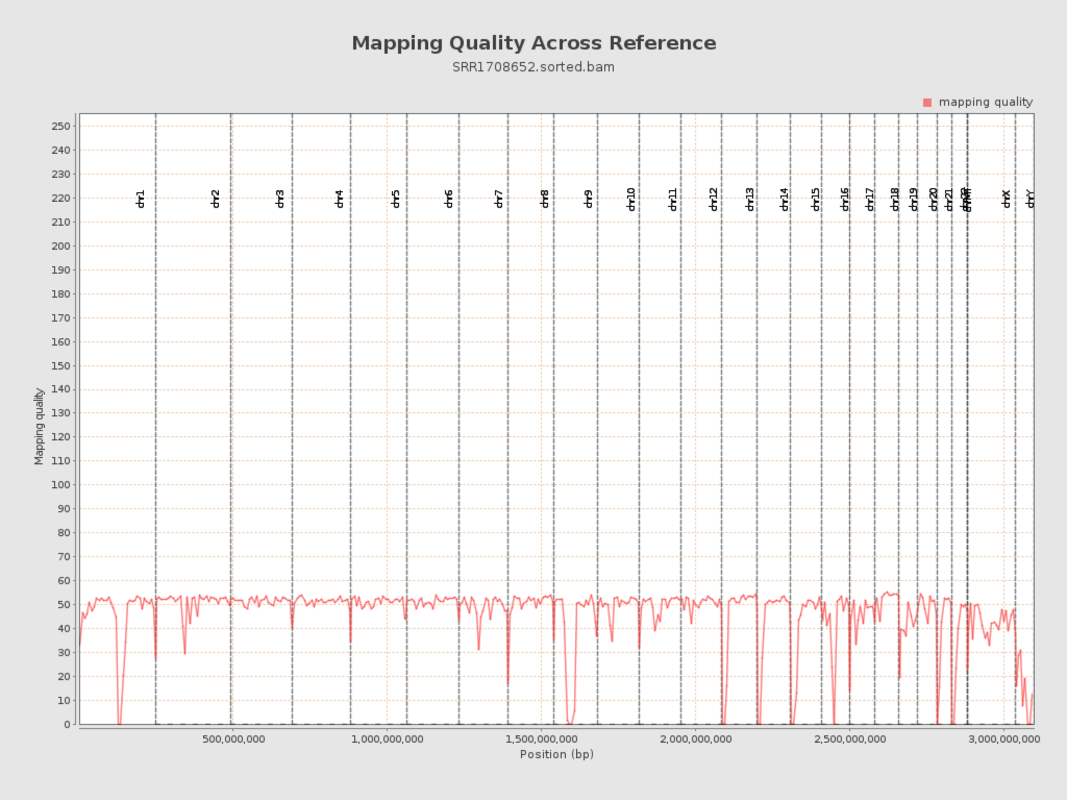
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram