Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:47:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708544.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_SRR1708544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708544.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,565,000
Mapped reads	22,720,707 / 96.42%
Unmapped reads	844,293 / 3.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	560 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	207,372 / 0.88%
Duplication rate	0.9%
Clipped reads	361,829 / 1.54%

2.2. ACGT Content

Number/percentage of A's	353,216,529 / 31.18%
Number/percentage of C's	211,421,611 / 18.66%
Number/percentage of T's	352,945,529 / 31.15%
Number/percentage of G's	214,922,843 / 18.97%
Number/percentage of N's	479,909 / 0.04%
GC Percentage	37.63%

2.3. Coverage

Mean	0.366

Standard Deviation	0.6762

2.4. Mapping Quality

Mean Mapping Quality	46.59

2.5. Mismatches and indels

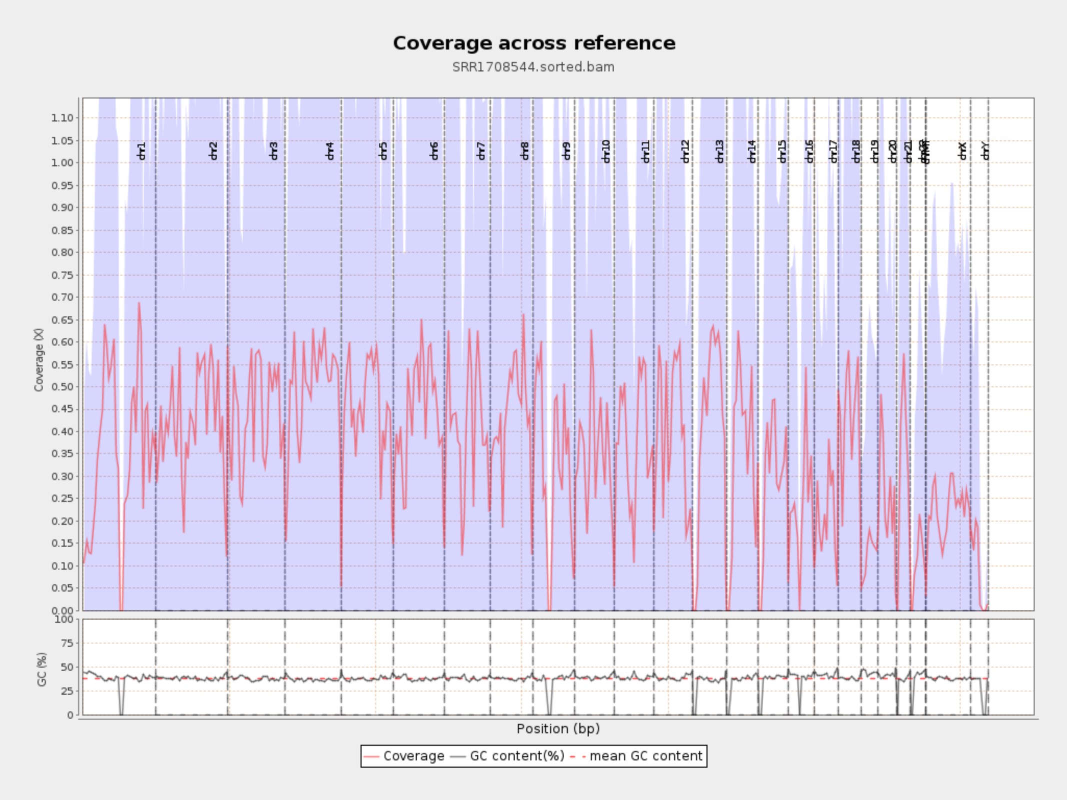
General error rate	0.36%
Mismatches	3,964,984
Insertions	63,176
Mapped reads with at least one insertion	0.28%
Deletions	58,613
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.36%

2.6. Chromosome stats

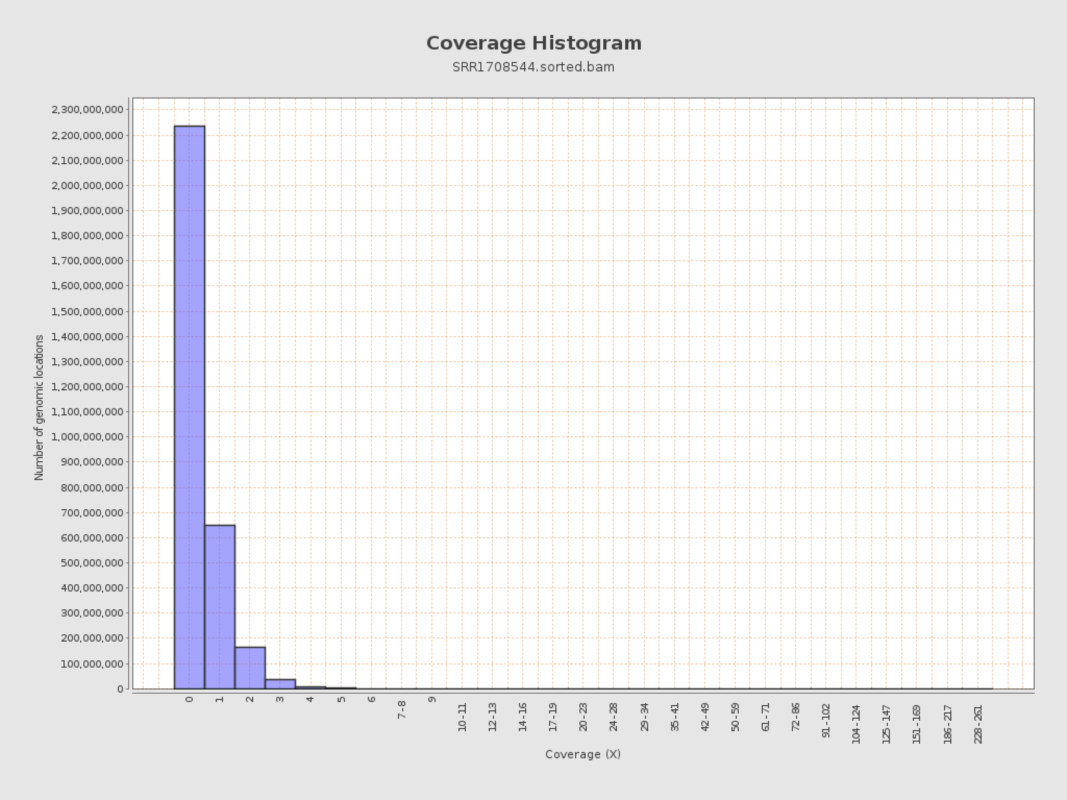
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	88652437	0.3557	0.6807
chr2	243199373	103033785	0.4237	0.7118
chr3	198022430	88012614	0.4445	0.7258
chr4	191154276	95603679	0.5001	0.767
chr5	180915260	80387950	0.4443	0.7255
chr6	171115067	76562961	0.4474	0.732
chr7	159138663	64741762	0.4068	0.709

chr8	146364022	64198057	0.4386	0.7249
chr9	141213431	47069901	0.3333	0.6519
chr10	135534747	48895760	0.3608	0.6591
chr11	135006516	51198668	0.3792	0.6881
chr12	133851895	52874238	0.395	0.7007
chr13	115169878	48061643	0.4173	0.7234
chr14	107349540	37162537	0.3462	0.6698
chr15	102531392	29621423	0.2889	0.6098
chr16	90354753	20553775	0.2275	0.5348
chr17	81195210	17312075	0.2132	0.5225
chr18	78077248	33931208	0.4346	0.7224
chr19	59128983	7558900	0.1278	0.3907
chr20	63025520	16894910	0.2681	0.5793
chr21	48129895	14990625	0.3115	0.6544
chr22	51304566	5618396	0.1095	0.3693
chrMT	16571	511	0.0308	0.1927
chrX	155270560	35003043	0.2254	0.5004
chrY	59373566	5141777	0.0866	0.331

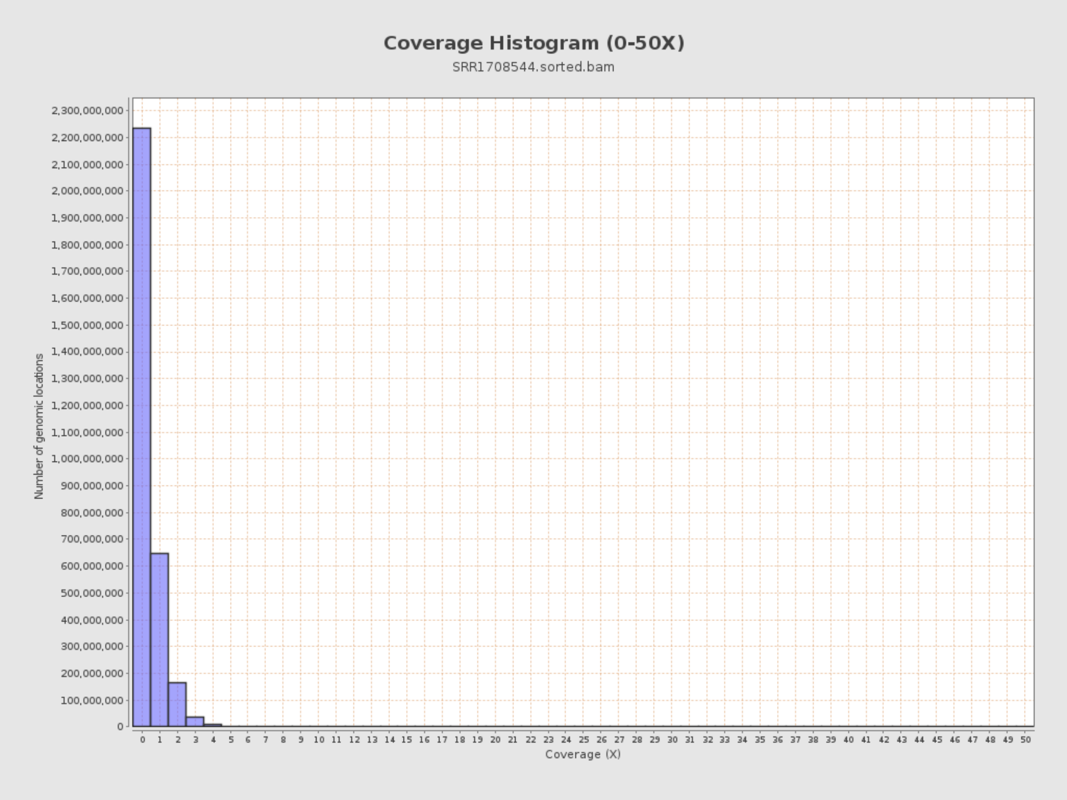
3. Results : Coverage across reference



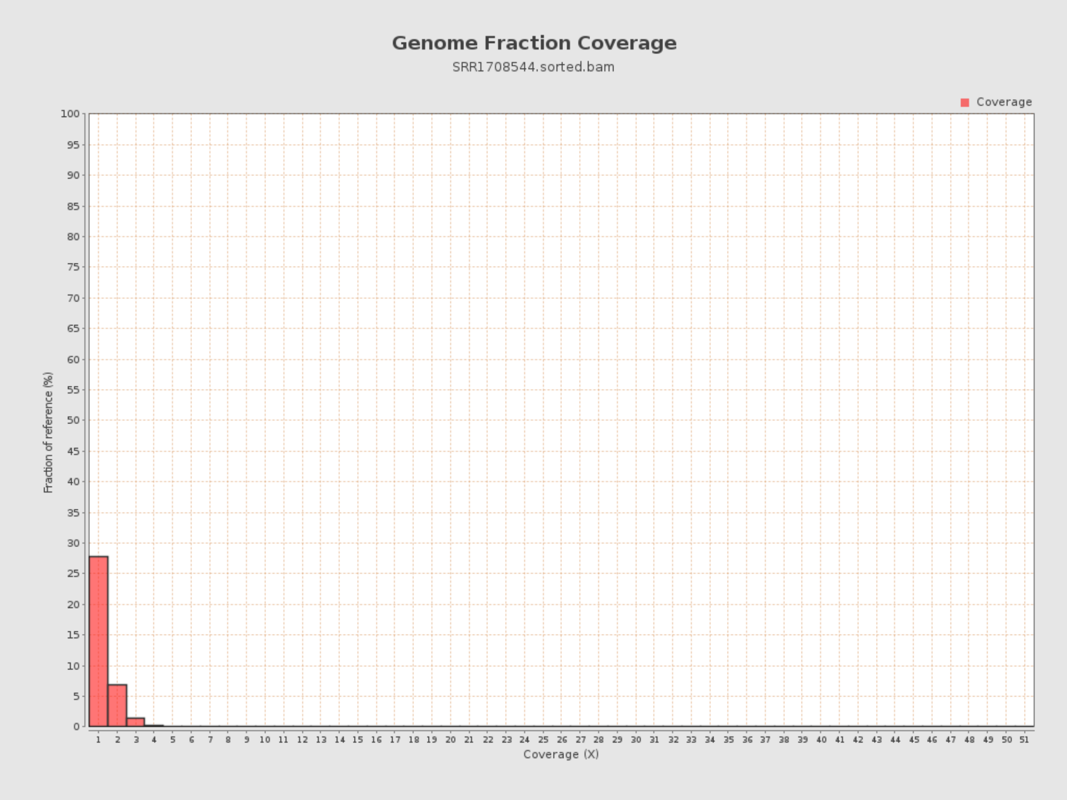
4. Results : Coverage Histogram



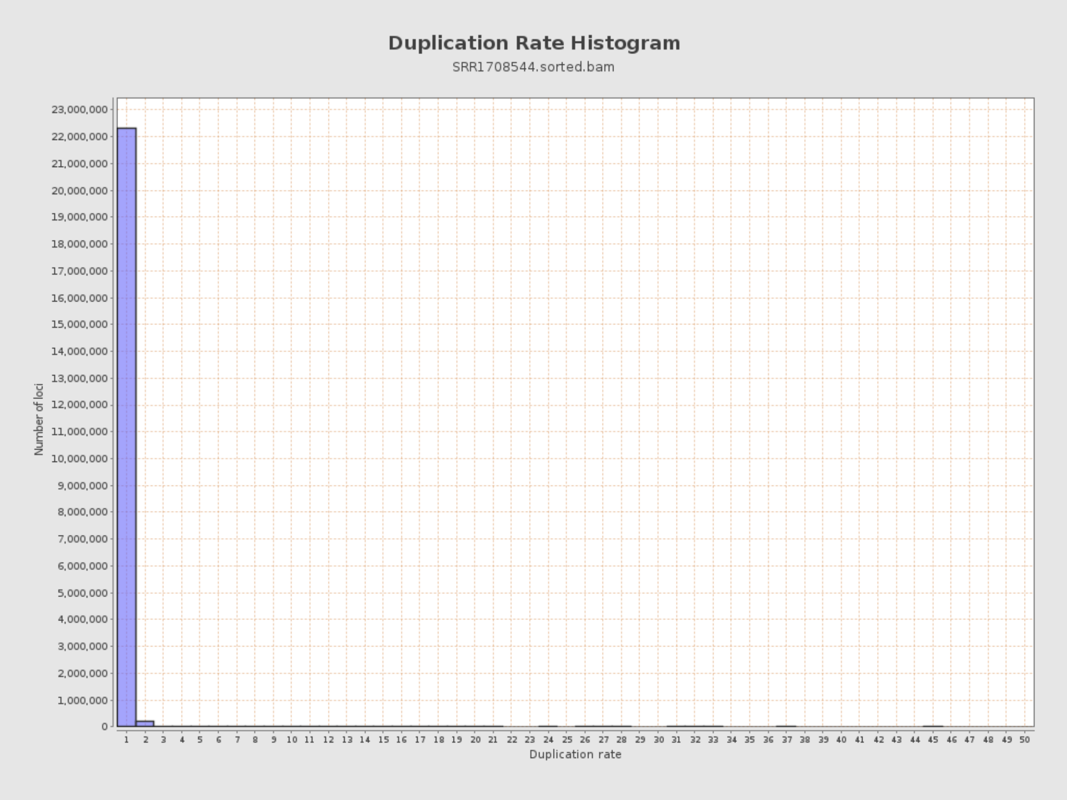
5. Results : Coverage Histogram (0-50X)



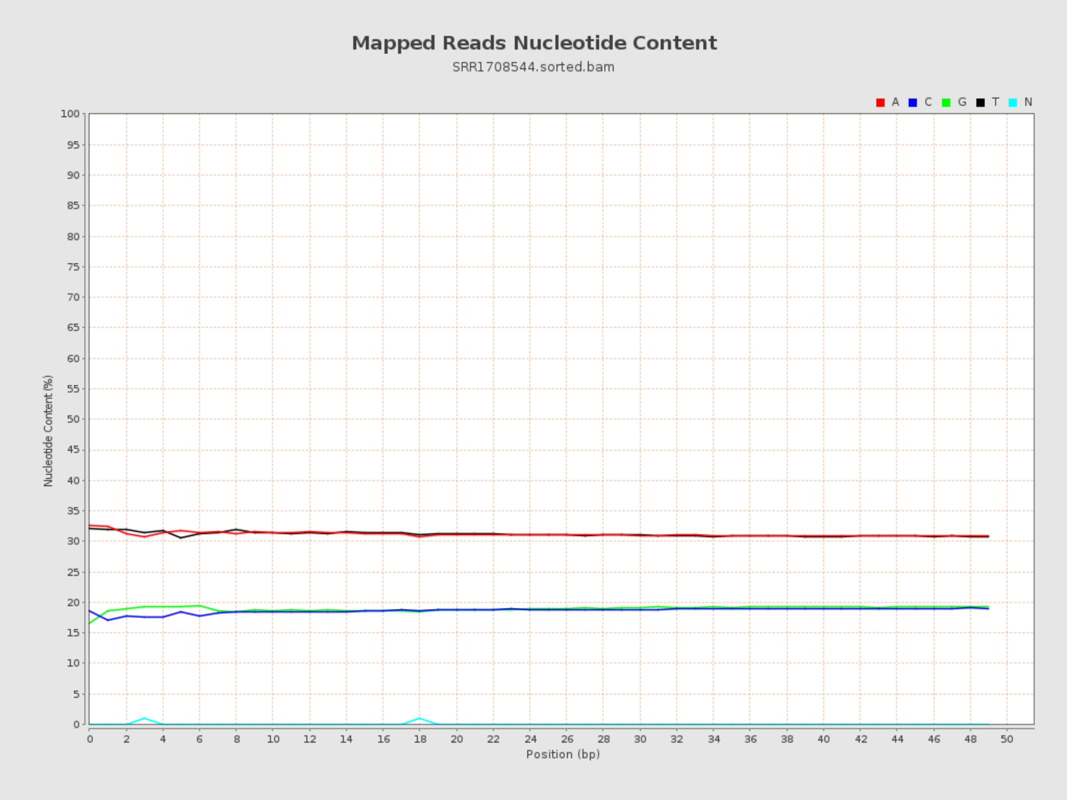
6. Results : Genome Fraction Coverage



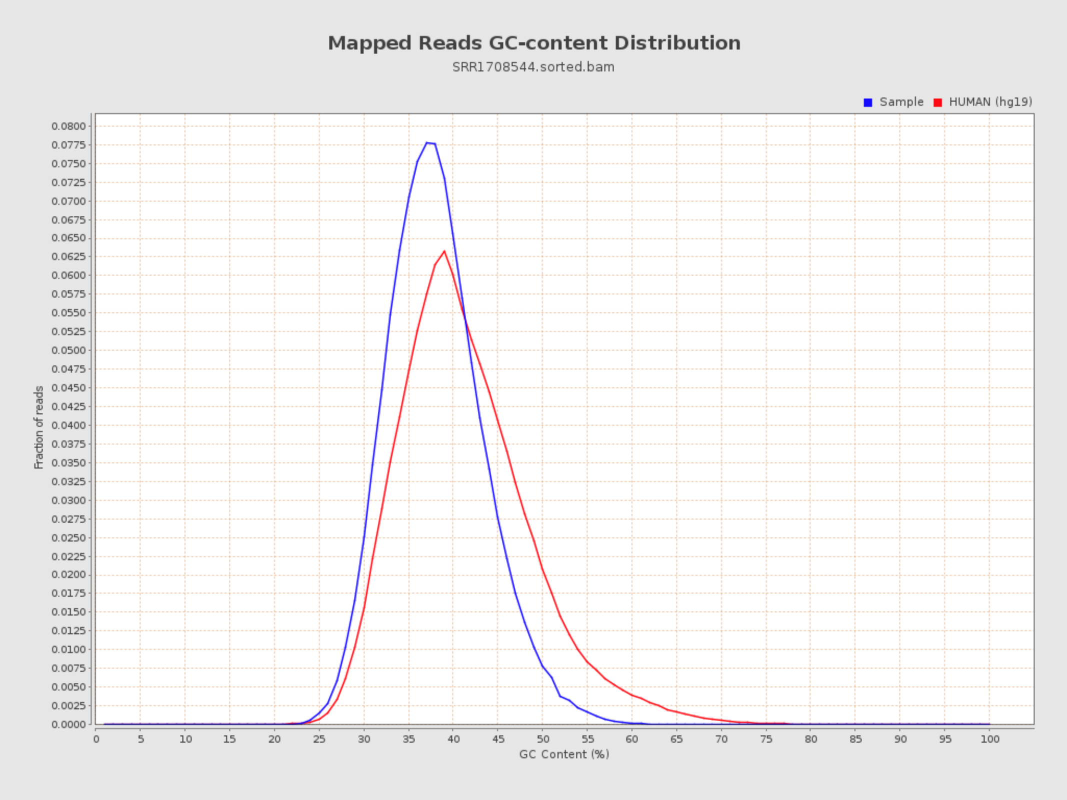
7. Results : Duplication Rate Histogram



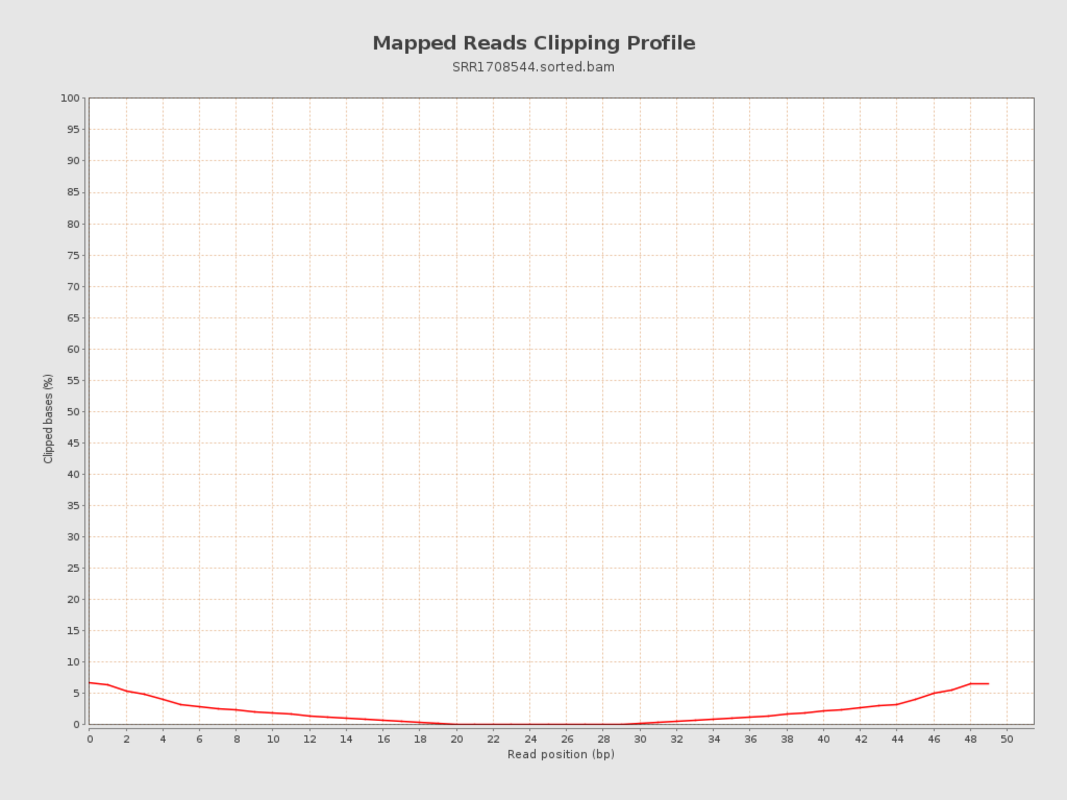
8. Results : Mapped Reads Nucleotide Content



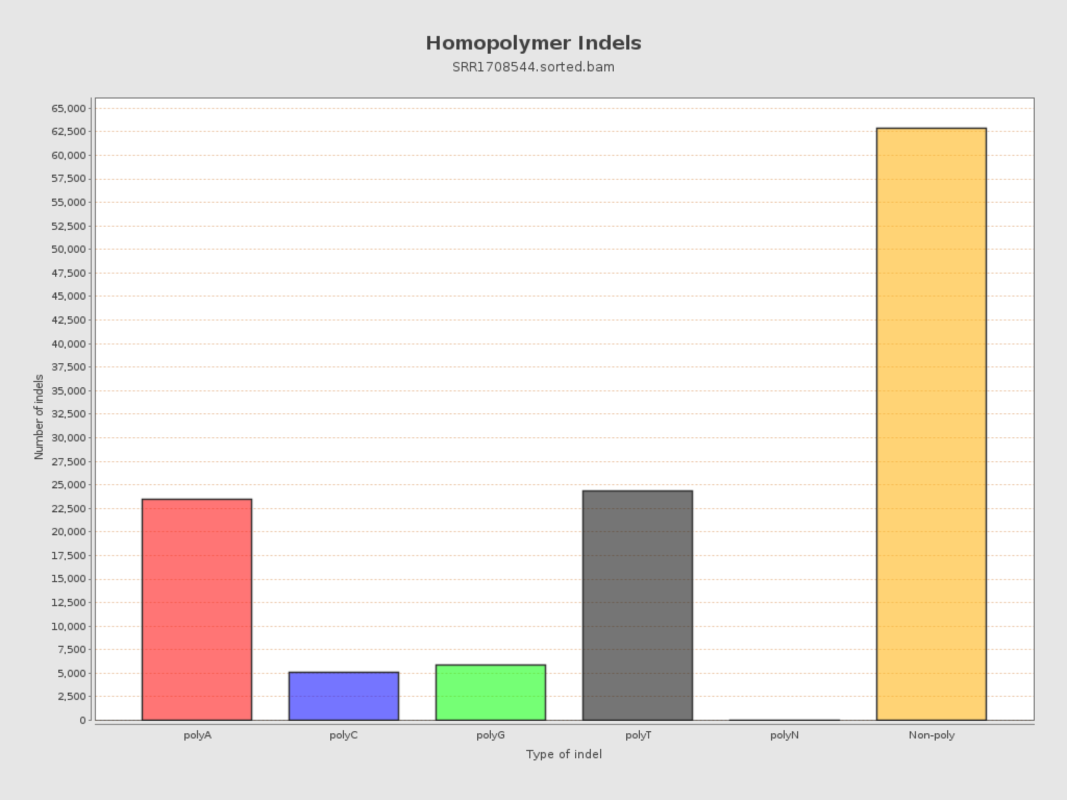
9. Results : Mapped Reads GC-content Distribution



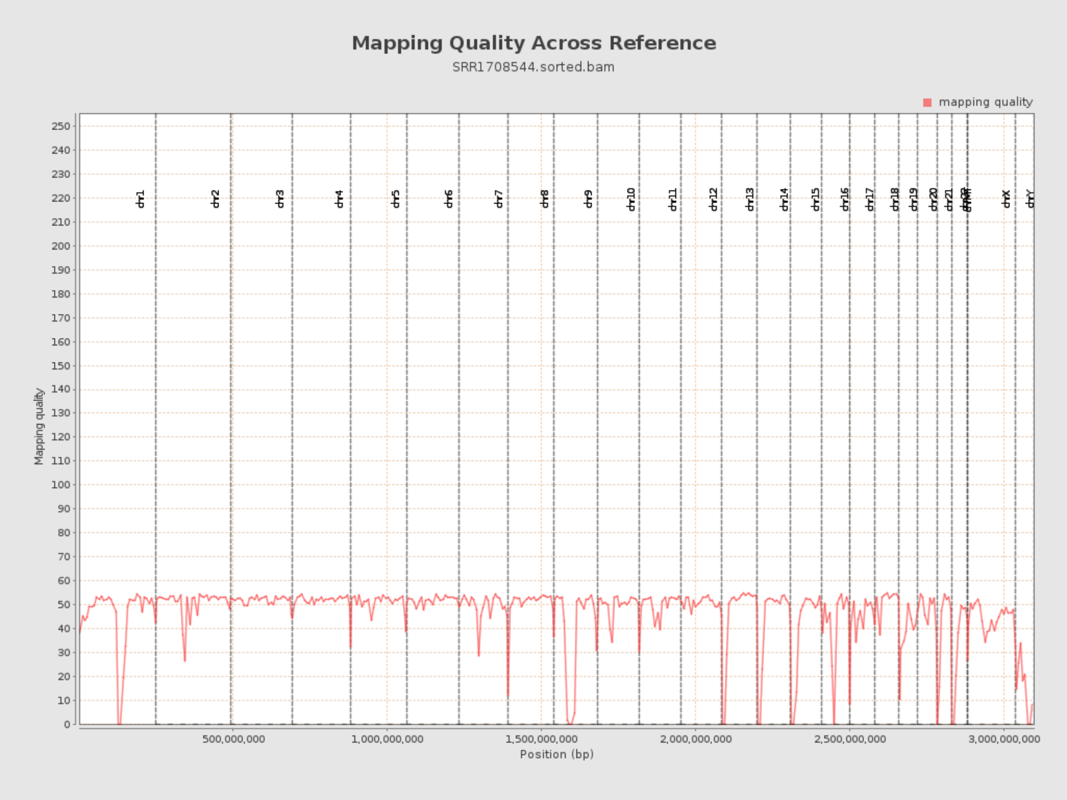
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram