Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:05:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708646.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_SRR1708646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:05:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,815,581
Mapped reads	3,673,920 / 96.29%
Unmapped reads	141,661 / 3.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	132 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	22,100 / 0.58%
Duplication rate	0.6%
Clipped reads	50,095 / 1.31%

2.2. ACGT Content

Number/percentage of A's	56,710,072 / 30.95%
Number/percentage of C's	34,780,560 / 18.98%
Number/percentage of T's	56,653,744 / 30.92%
Number/percentage of G's	35,066,913 / 19.14%
Number/percentage of N's	5,991 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.2693

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

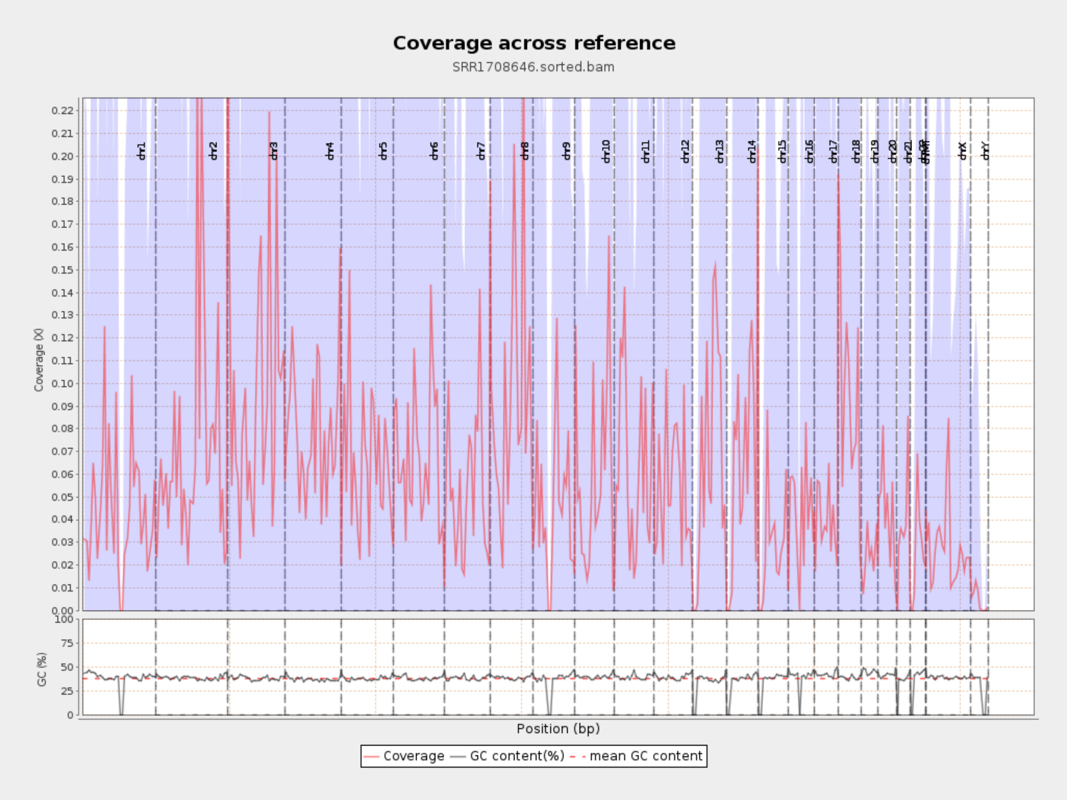
General error rate	0.17%
Mismatches	301,154
Insertions	12,907
Mapped reads with at least one insertion	0.35%
Deletions	10,512
Mapped reads with at least one deletion	0.29%
Homopolymer indels	48.49%

2.6. Chromosome stats

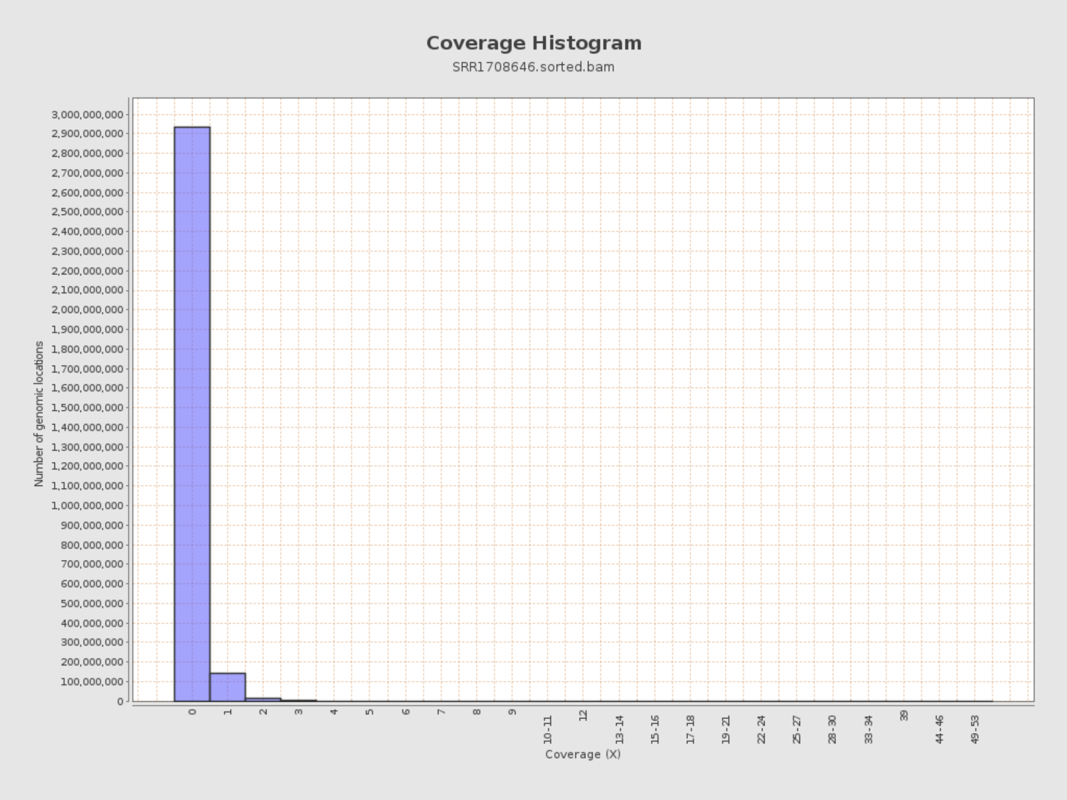
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11087097	0.0445	0.2322
chr2	243199373	17212688	0.0708	0.2968
chr3	198022430	18985505	0.0959	0.349
chr4	191154276	15148384	0.0792	0.3091
chr5	180915260	11652846	0.0644	0.2789
chr6	171115067	11845900	0.0692	0.2872
chr7	159138663	8388577	0.0527	0.2517

chr8	146364022	13979355	0.0955	0.345
chr9	141213431	6688875	0.0474	0.2378
chr10	135534747	8400088	0.062	0.2737
chr11	135006516	8661321	0.0642	0.2807
chr12	133851895	7113017	0.0531	0.2495
chr13	115169878	7739190	0.0672	0.2904
chr14	107349540	6842449	0.0637	0.2789
chr15	102531392	2978533	0.029	0.1881
chr16	90354753	3822087	0.0423	0.2211
chr17	81195210	3192158	0.0393	0.2157
chr18	78077248	7609036	0.0975	0.3444
chr19	59128983	1422383	0.0241	0.1649
chr20	63025520	2765728	0.0439	0.2258
chr21	48129895	1741345	0.0362	0.2062
chr22	51304566	1343883	0.0262	0.1765
chrMT	16571	738	0.0445	0.2177
chrX	155270560	4333826	0.0279	0.1804
chrY	59373566	280291	0.0047	0.0717

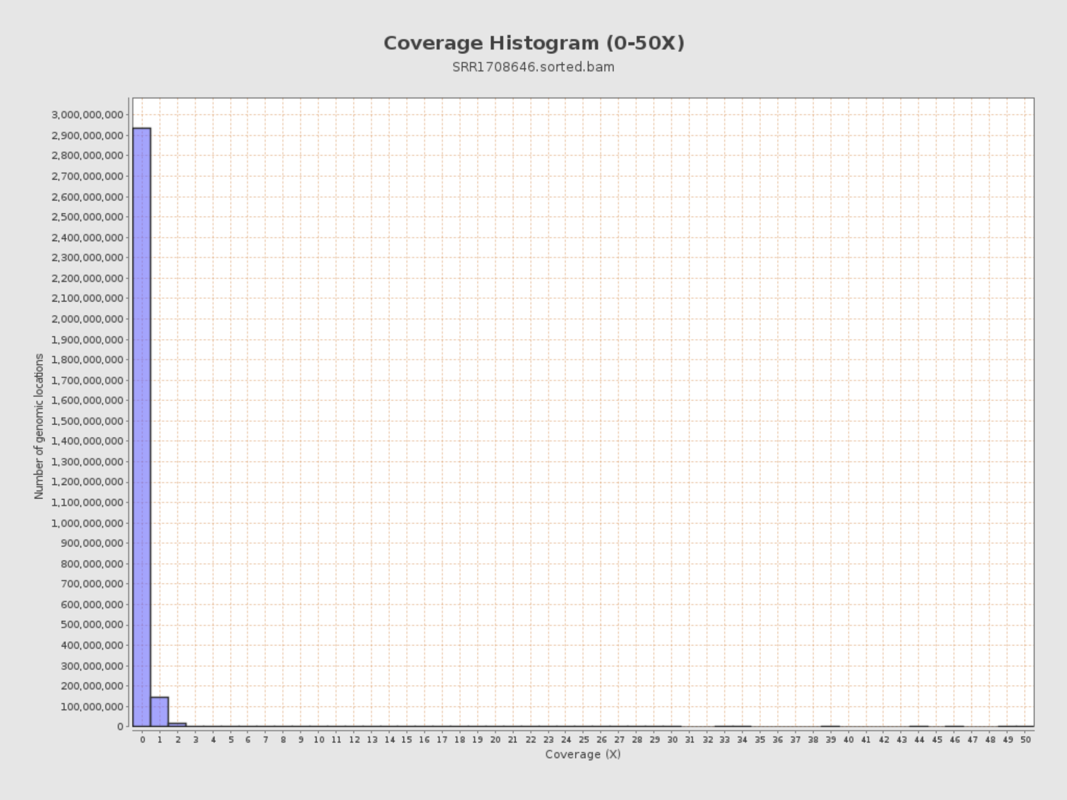
3. Results : Coverage across reference



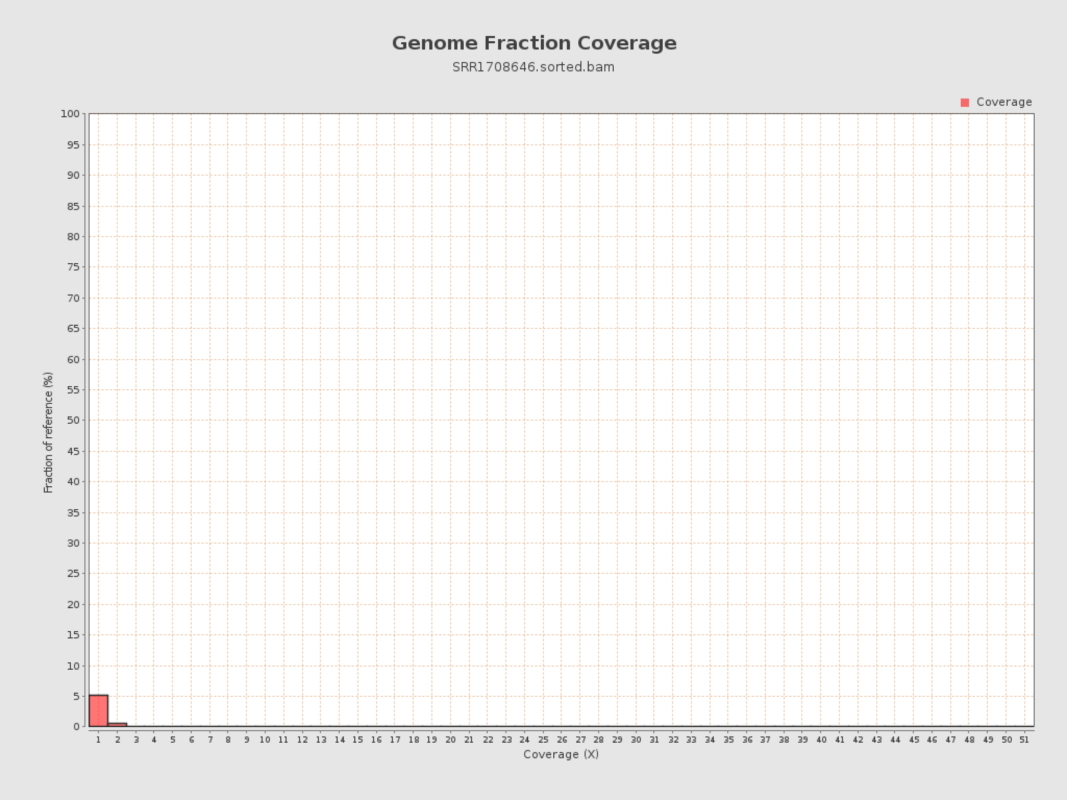
4. Results : Coverage Histogram



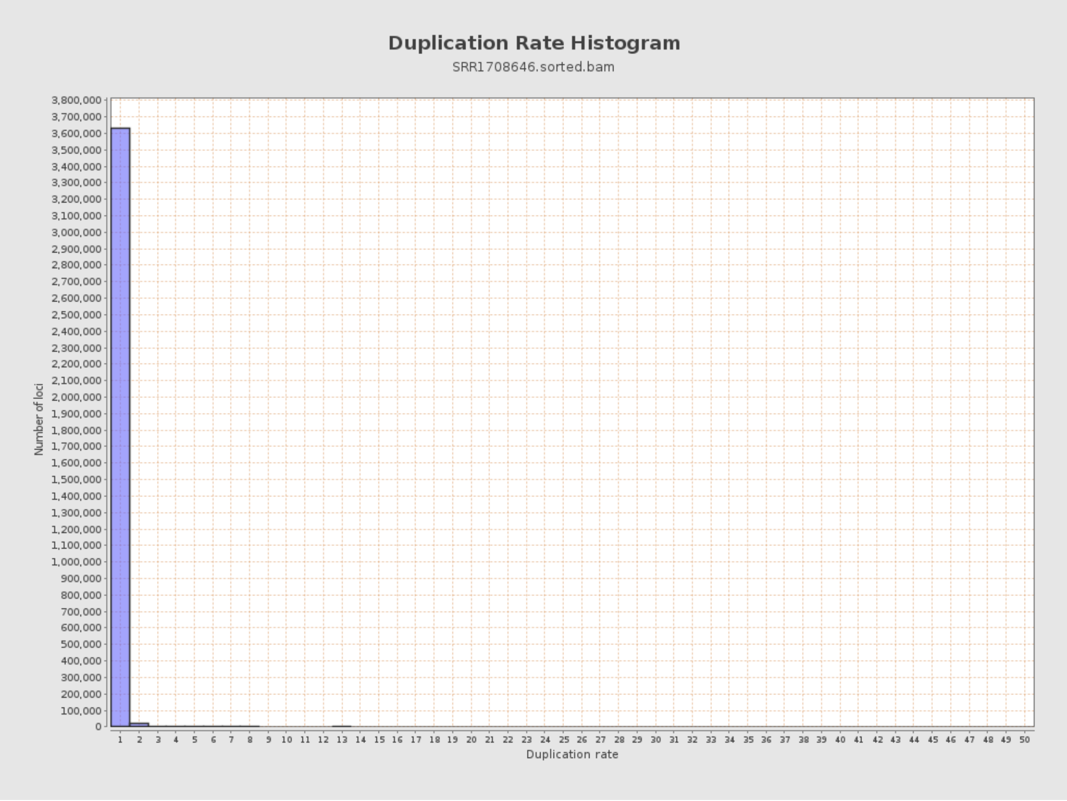
5. Results : Coverage Histogram (0-50X)



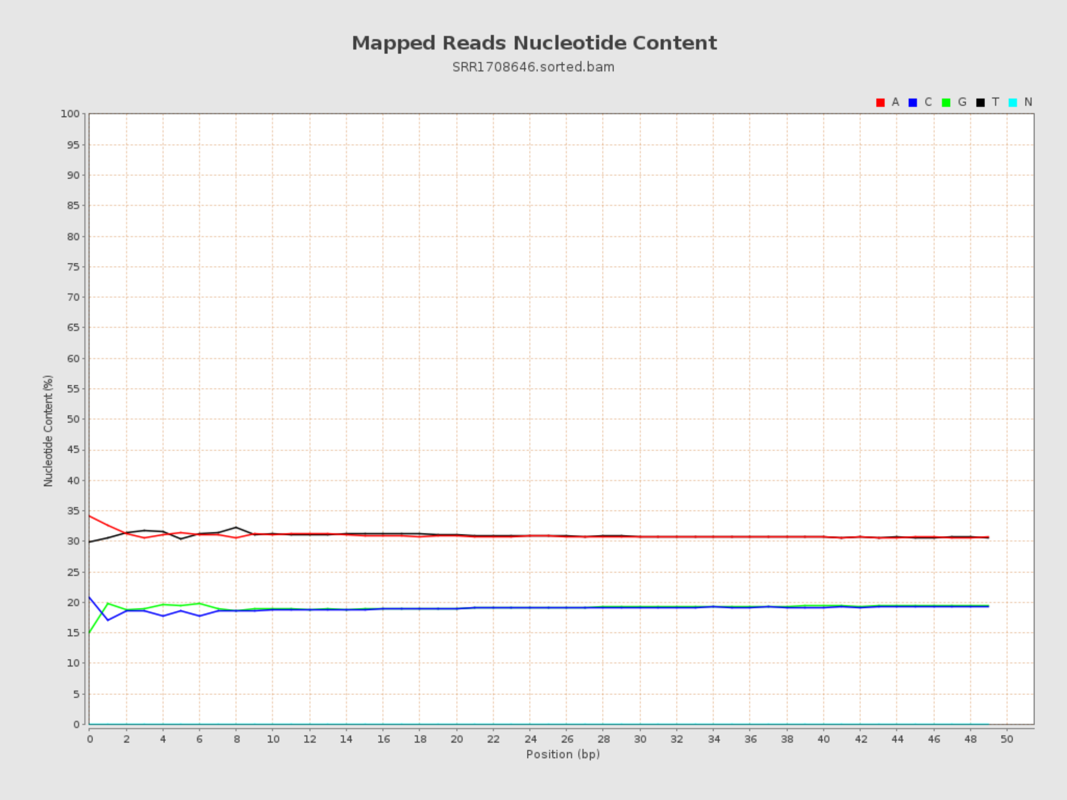
6. Results : Genome Fraction Coverage



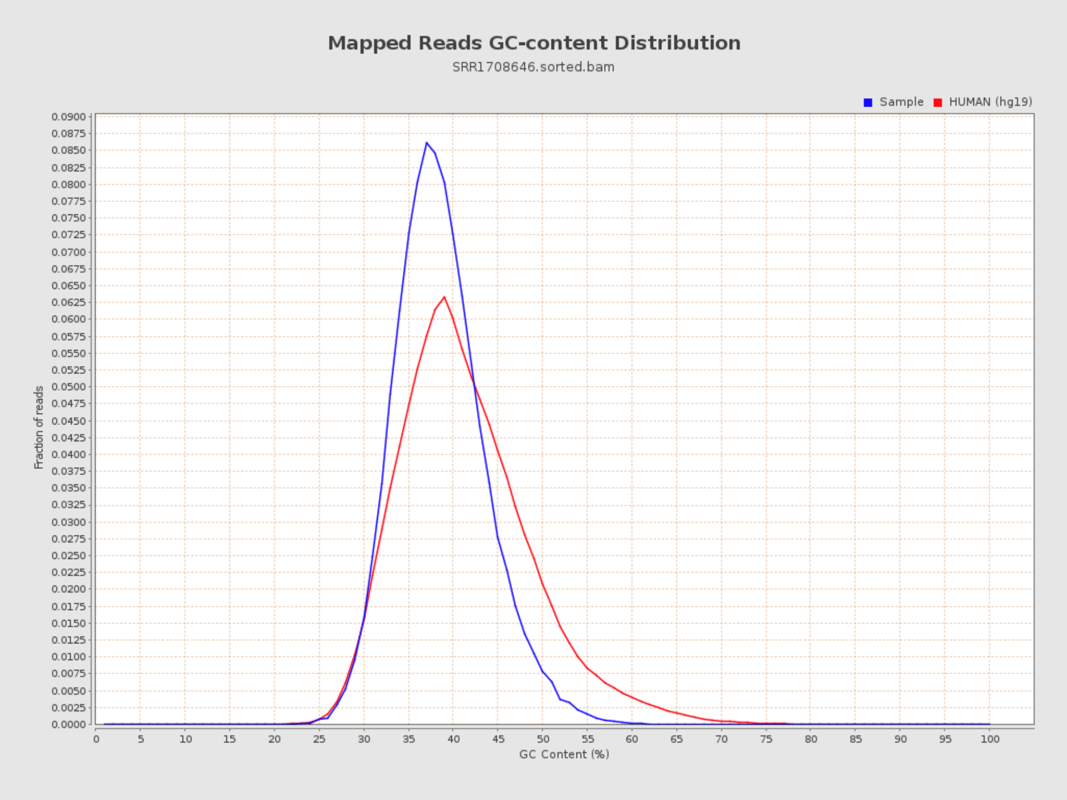
7. Results : Duplication Rate Histogram



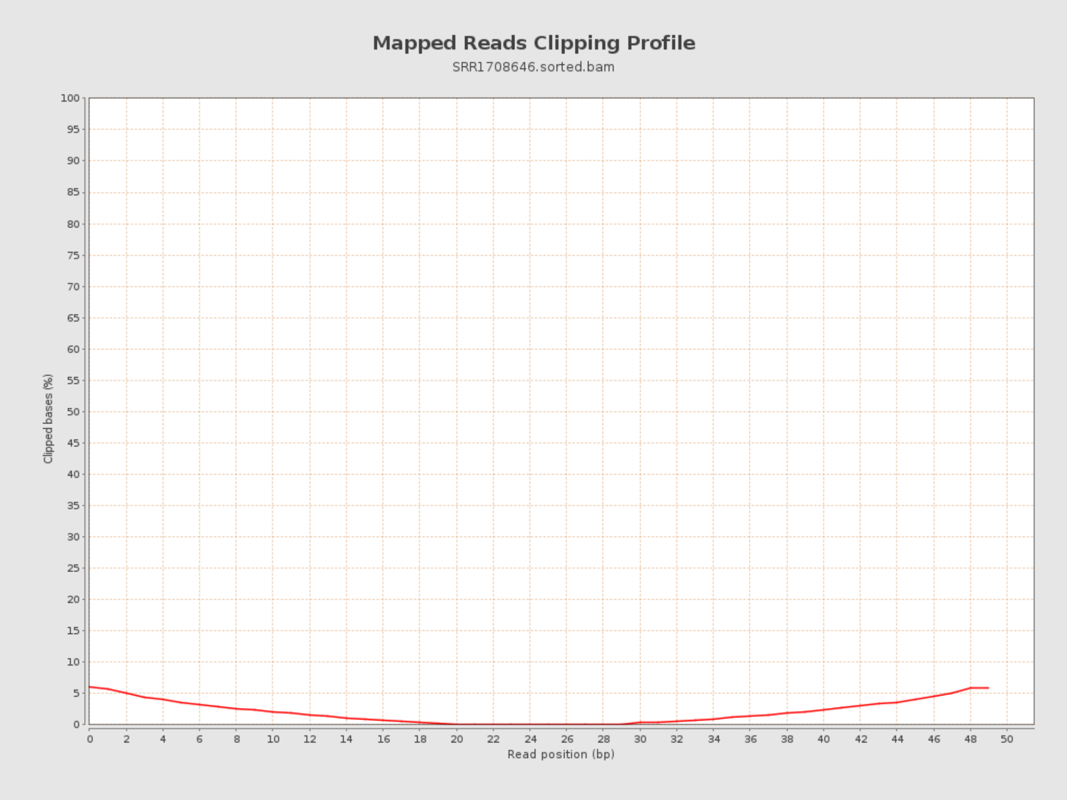
8. Results : Mapped Reads Nucleotide Content



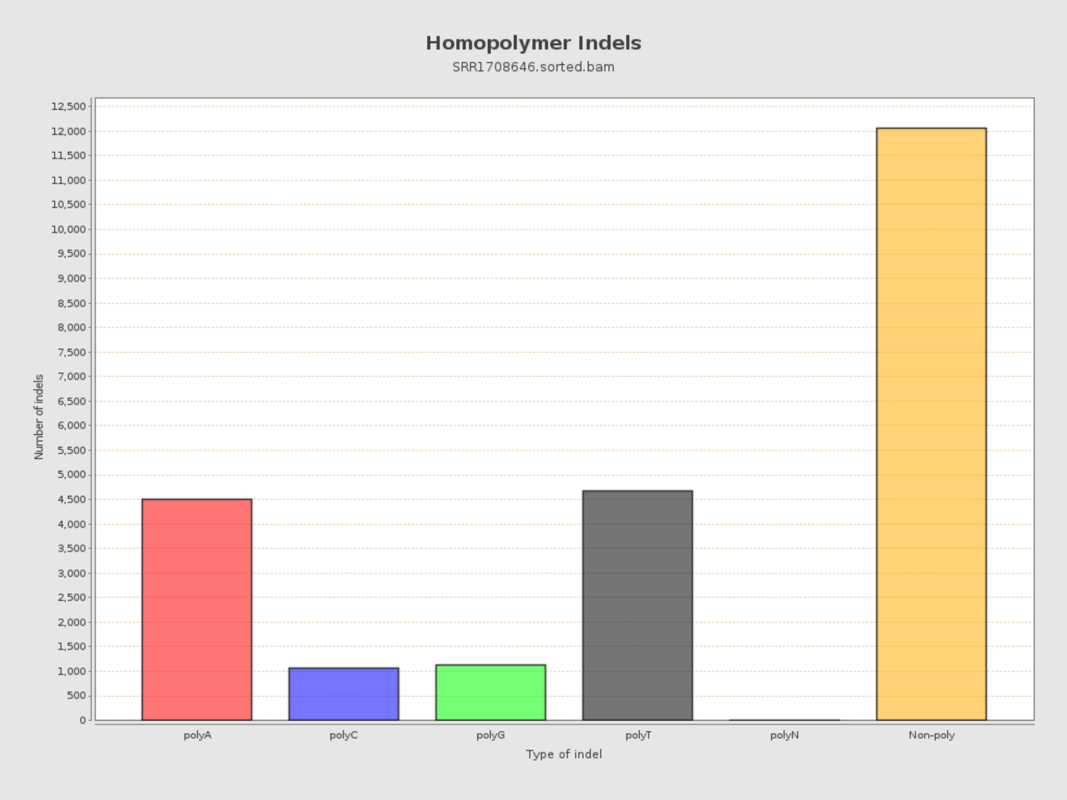
9. Results : Mapped Reads GC-content Distribution



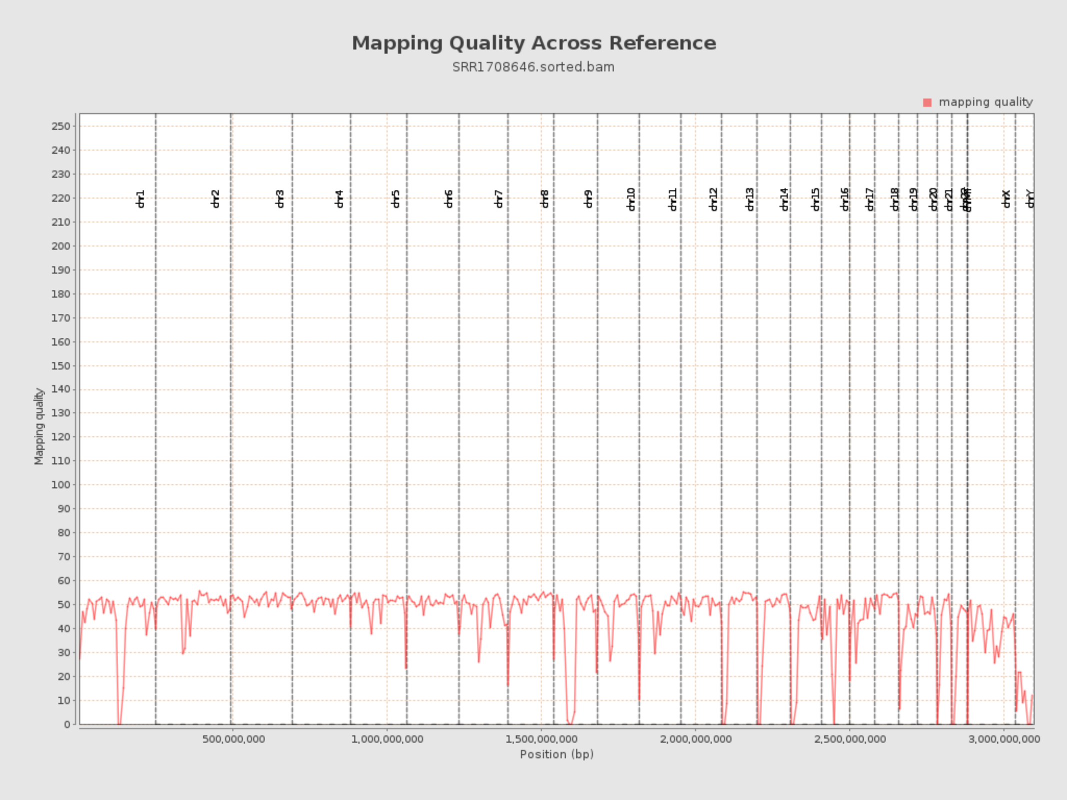
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram