Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:01:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524798.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_SRR10524798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:01:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,448,181
Mapped reads	1,300,101 / 89.77%
Unmapped reads	148,080 / 10.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,043 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	45,067 / 3.11%
Duplication rate	2.63%
Clipped reads	1,299,759 / 89.75%

2.2. ACGT Content

Number/percentage of A's	17,384,748 / 23.65%
Number/percentage of C's	14,646,537 / 19.93%
Number/percentage of T's	24,049,470 / 32.72%
Number/percentage of G's	17,415,211 / 23.69%
Number/percentage of N's	8,477 / 0.01%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2196

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Mismatches and indels

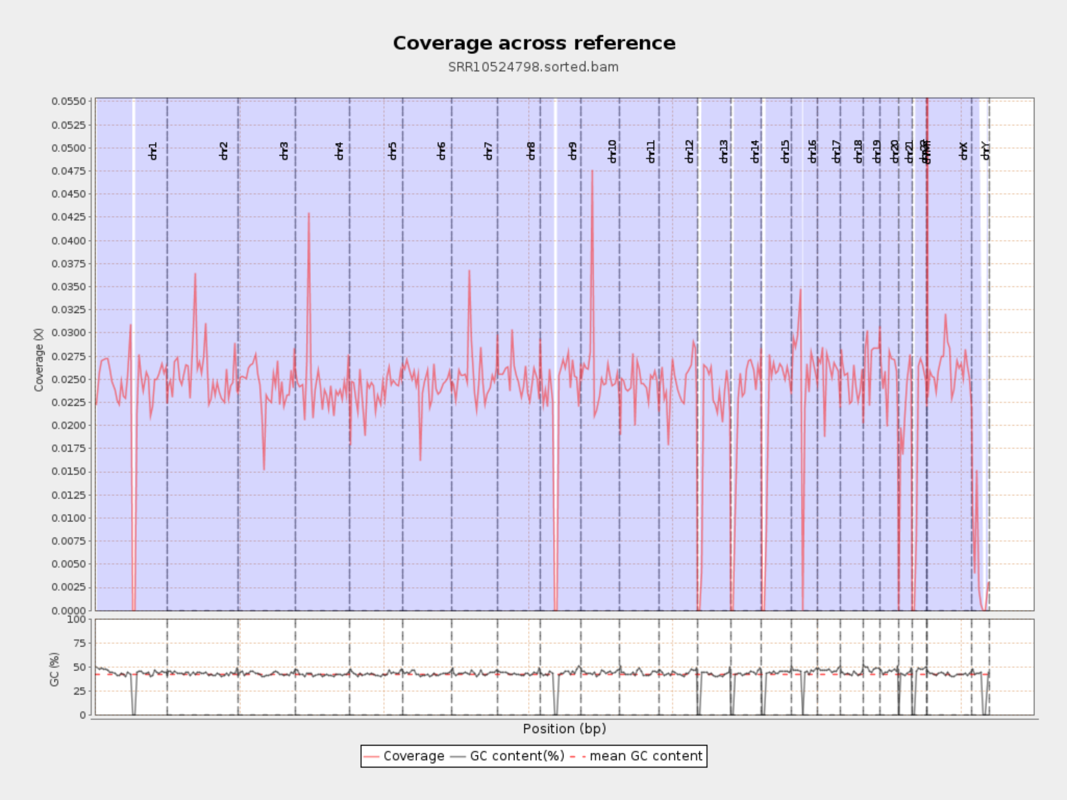
General error rate	0.53%
Mismatches	376,914
Insertions	6,165
Mapped reads with at least one insertion	0.47%
Deletions	14,446
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.18%

2.6. Chromosome stats

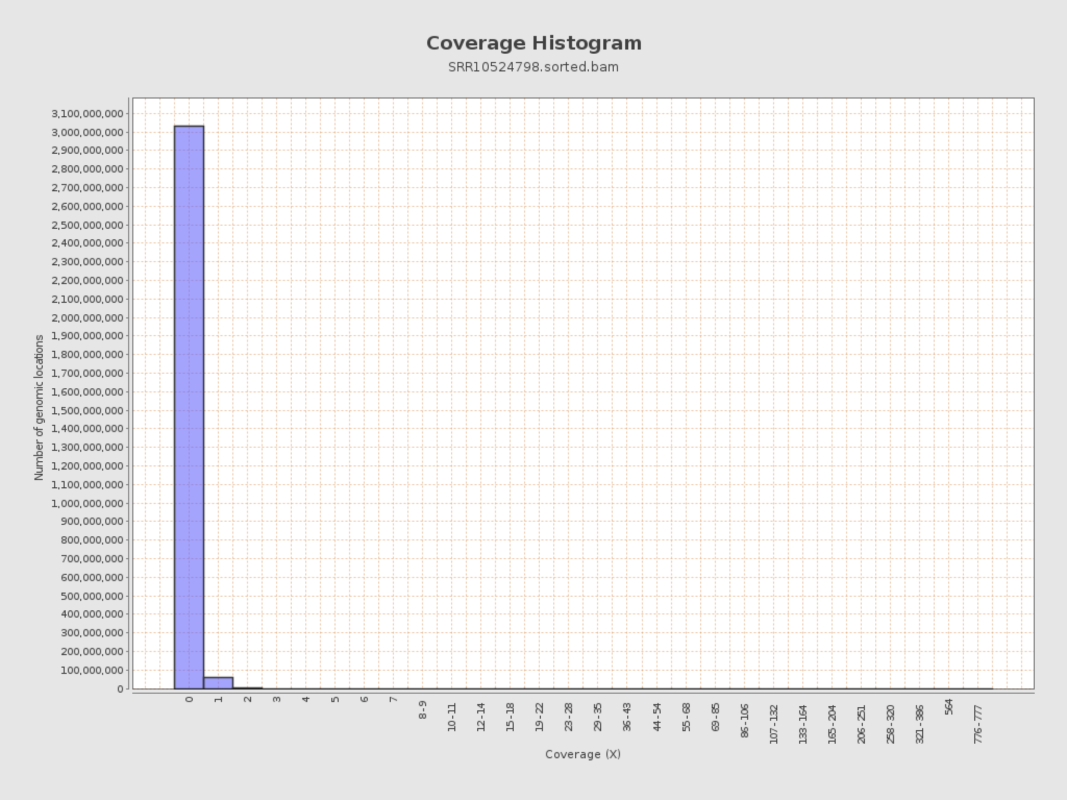
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5835251	0.0234	0.2831
chr2	243199373	6225469	0.0256	0.3633
chr3	198022430	4797795	0.0242	0.1722
chr4	191154276	4700643	0.0246	0.1915
chr5	180915260	4322678	0.0239	0.1676
chr6	171115067	4190612	0.0245	0.1856
chr7	159138663	4045140	0.0254	0.2602

chr8	146364022	3686459	0.0252	0.1984
chr9	141213431	3141675	0.0222	0.189
chr10	135534747	3540291	0.0261	0.2458
chr11	135006516	3313954	0.0245	0.198
chr12	133851895	3292288	0.0246	0.1726
chr13	115169878	2307620	0.02	0.154
chr14	107349540	2248514	0.0209	0.16
chr15	102531392	2154355	0.021	0.1598
chr16	90354753	2248872	0.0249	0.1879
chr17	81195210	2093939	0.0258	0.1814
chr18	78077248	1929460	0.0247	0.2734
chr19	59128983	1625269	0.0275	0.2399
chr20	63025520	1597507	0.0253	0.1786
chr21	48129895	973691	0.0202	0.1708
chr22	51304566	919498	0.0179	0.1466
chrMT	16571	13389	0.808	1.0529
chrX	155270560	4071437	0.0262	0.1909
chrY	59373566	251686	0.0042	0.1195

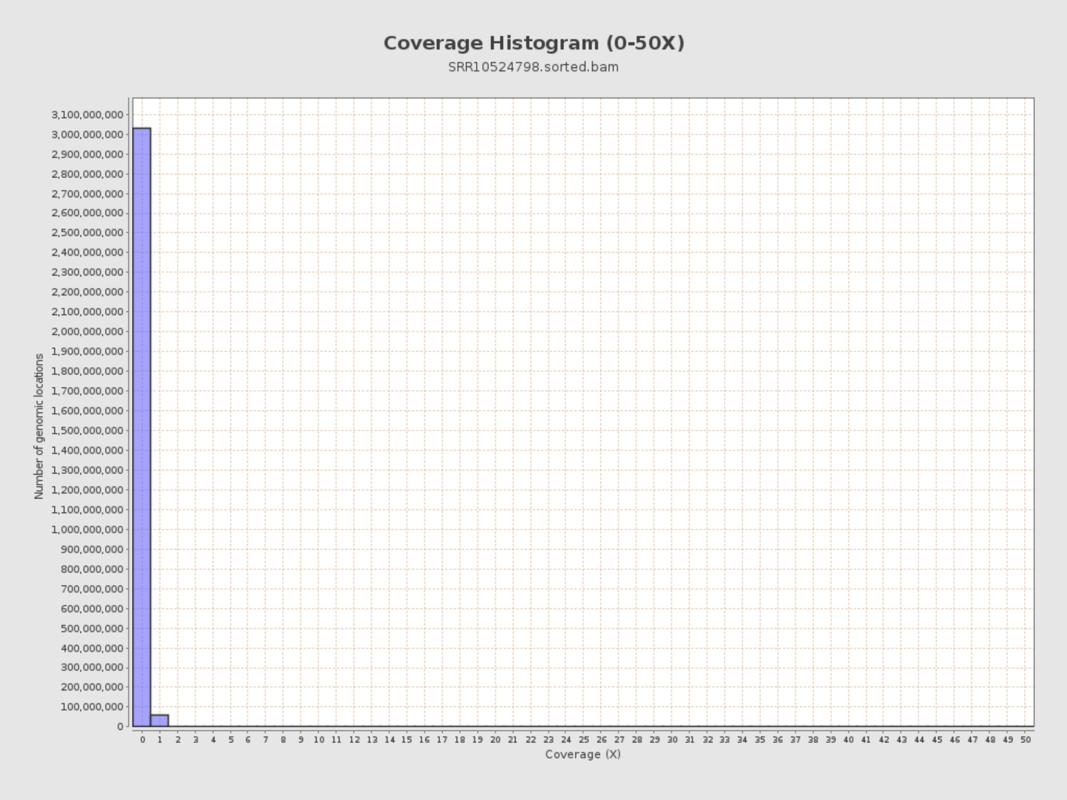
3. Results : Coverage across reference



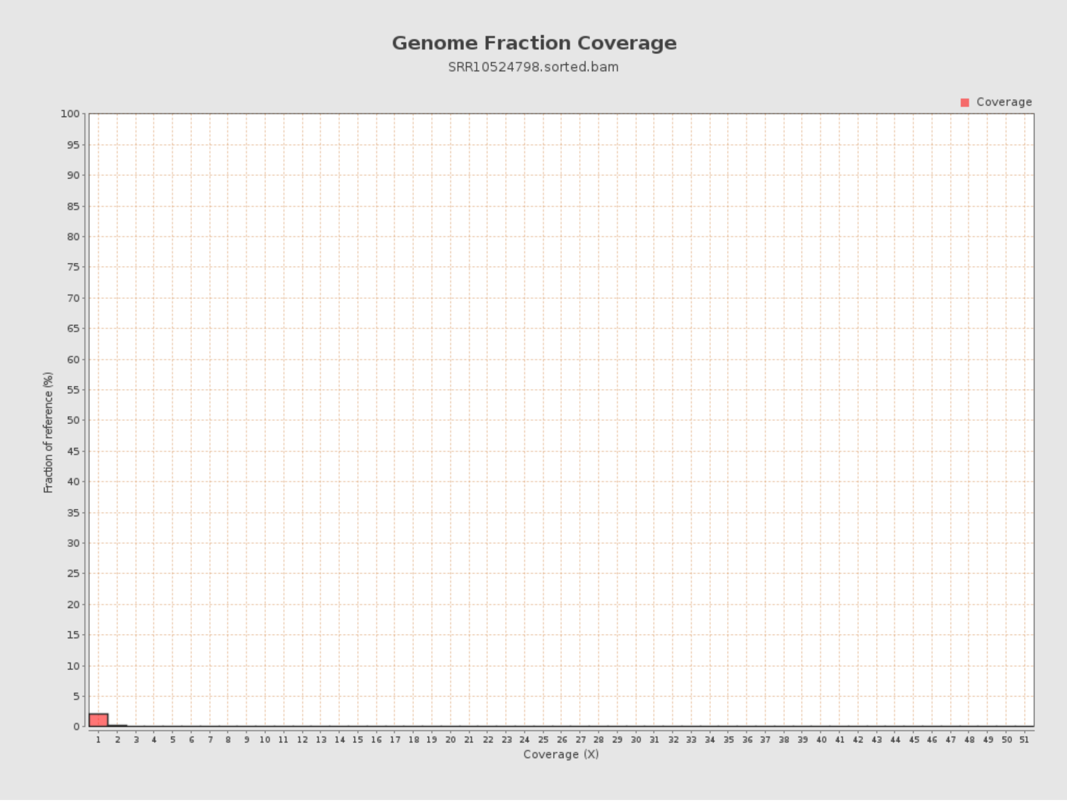
4. Results : Coverage Histogram



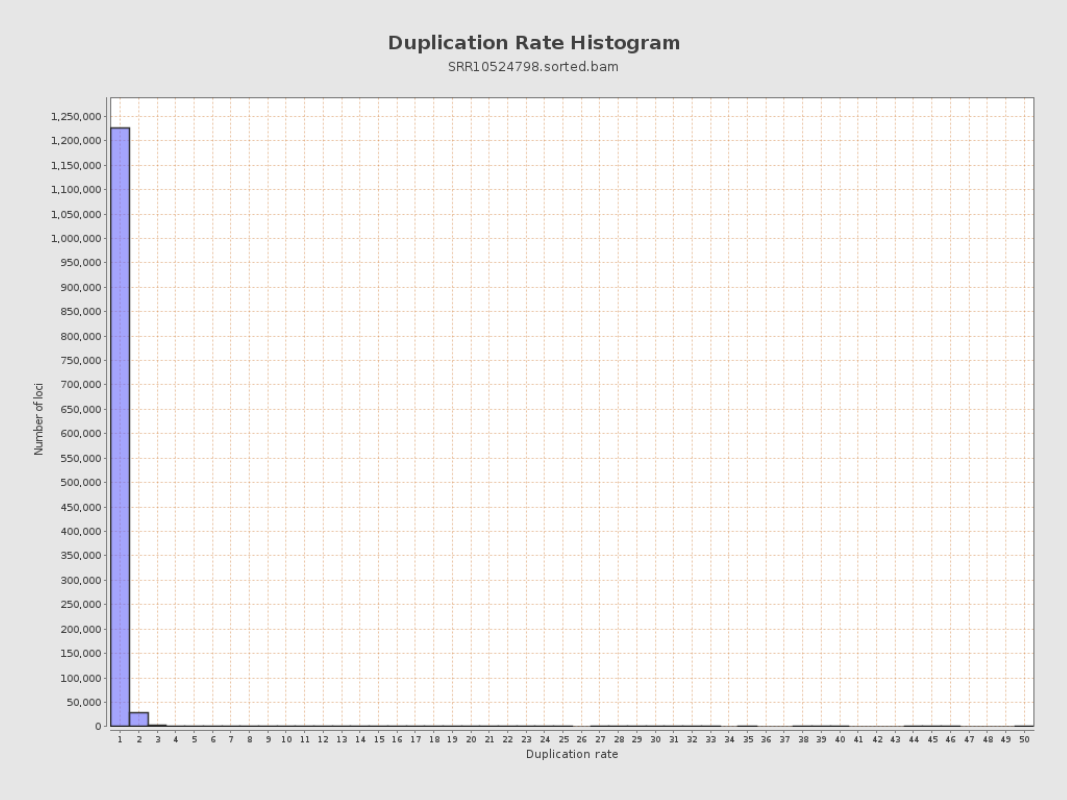
5. Results : Coverage Histogram (0-50X)



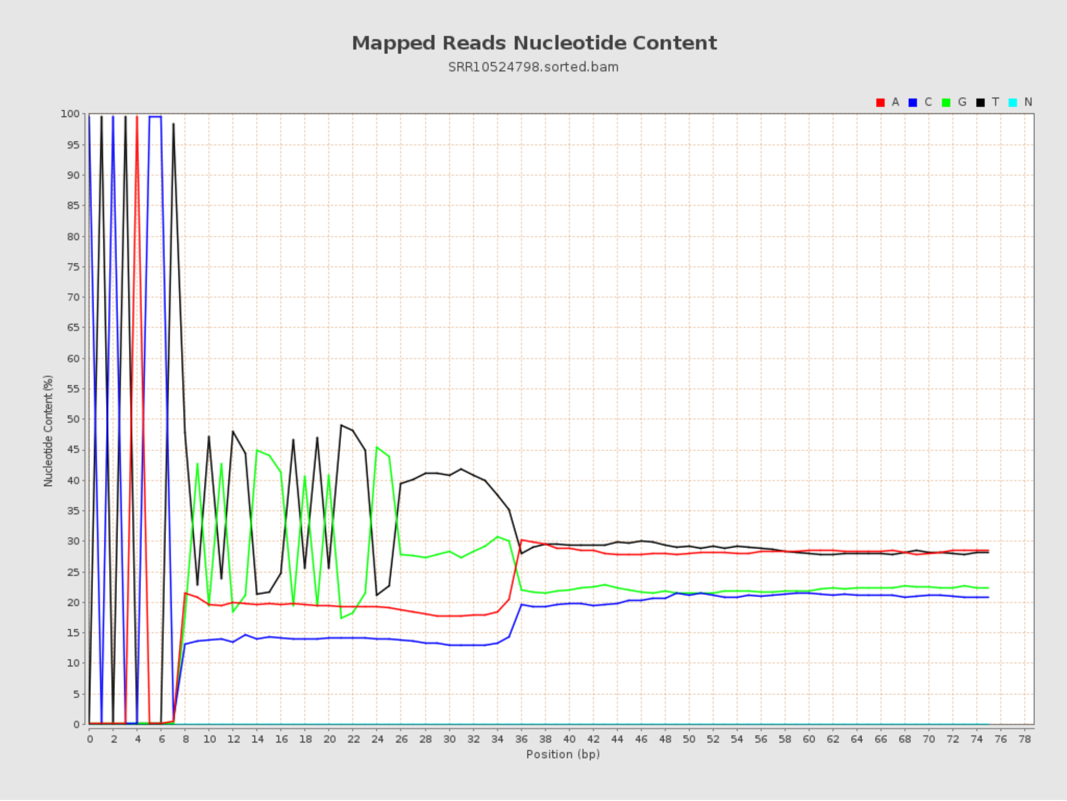
6. Results : Genome Fraction Coverage



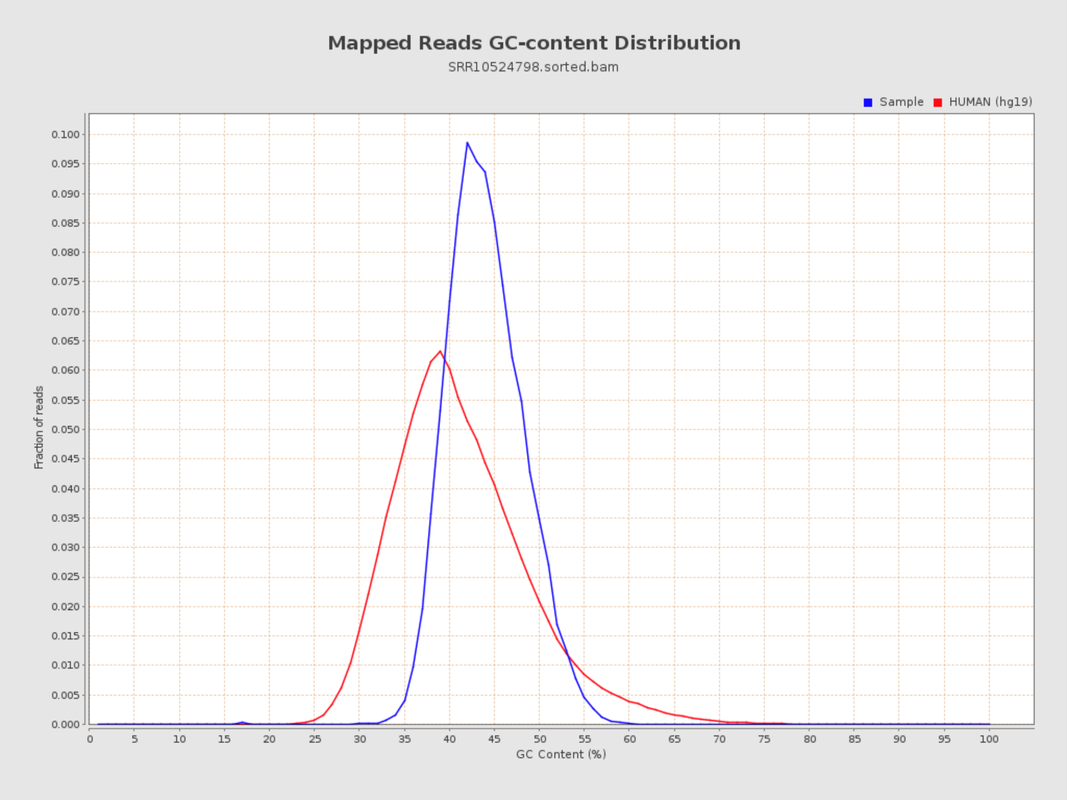
7. Results : Duplication Rate Histogram



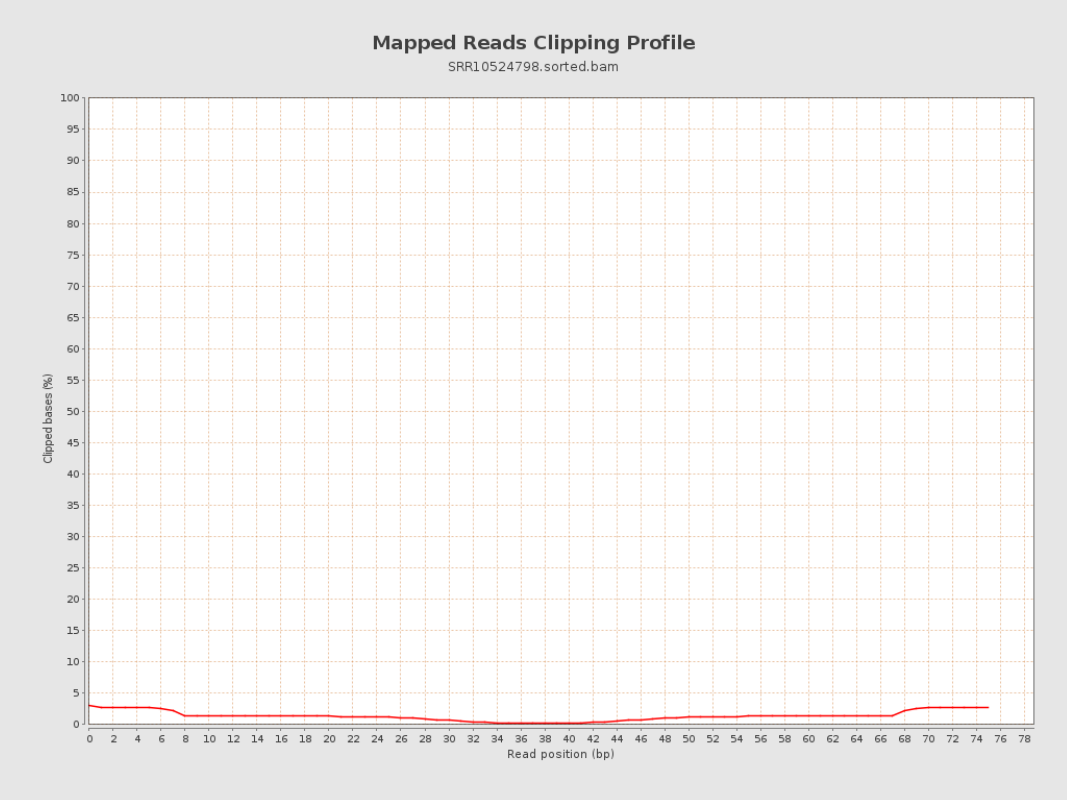
8. Results : Mapped Reads Nucleotide Content



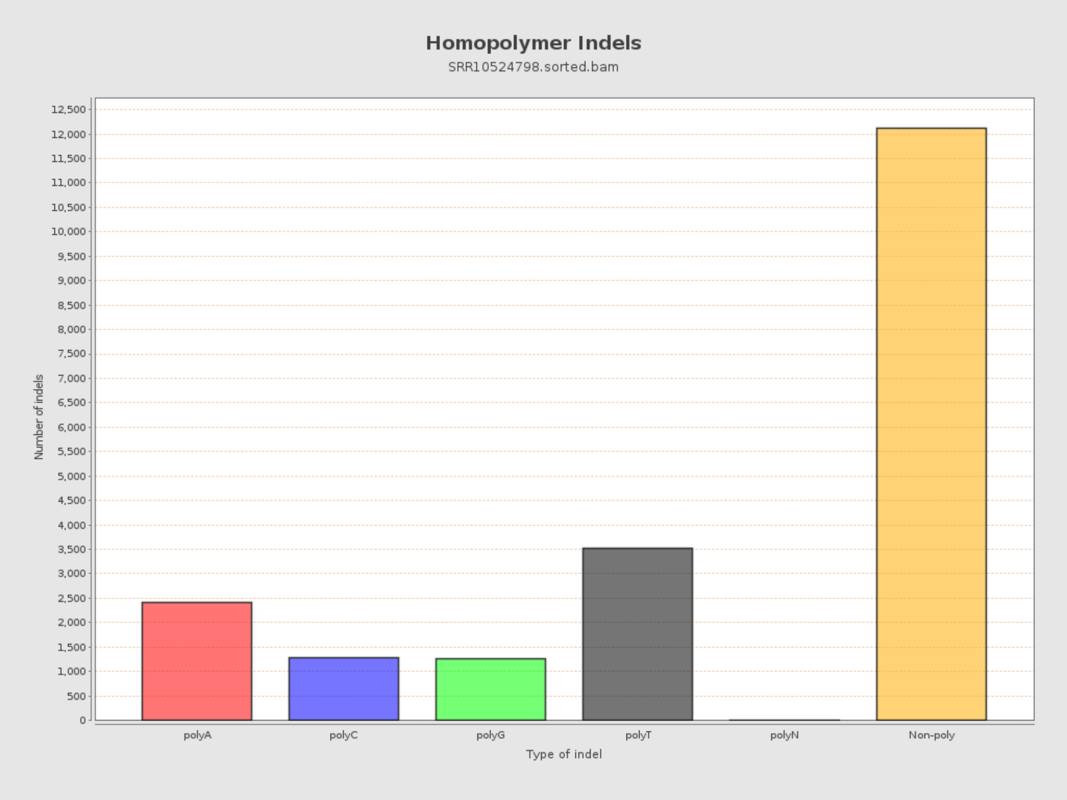
9. Results : Mapped Reads GC-content Distribution



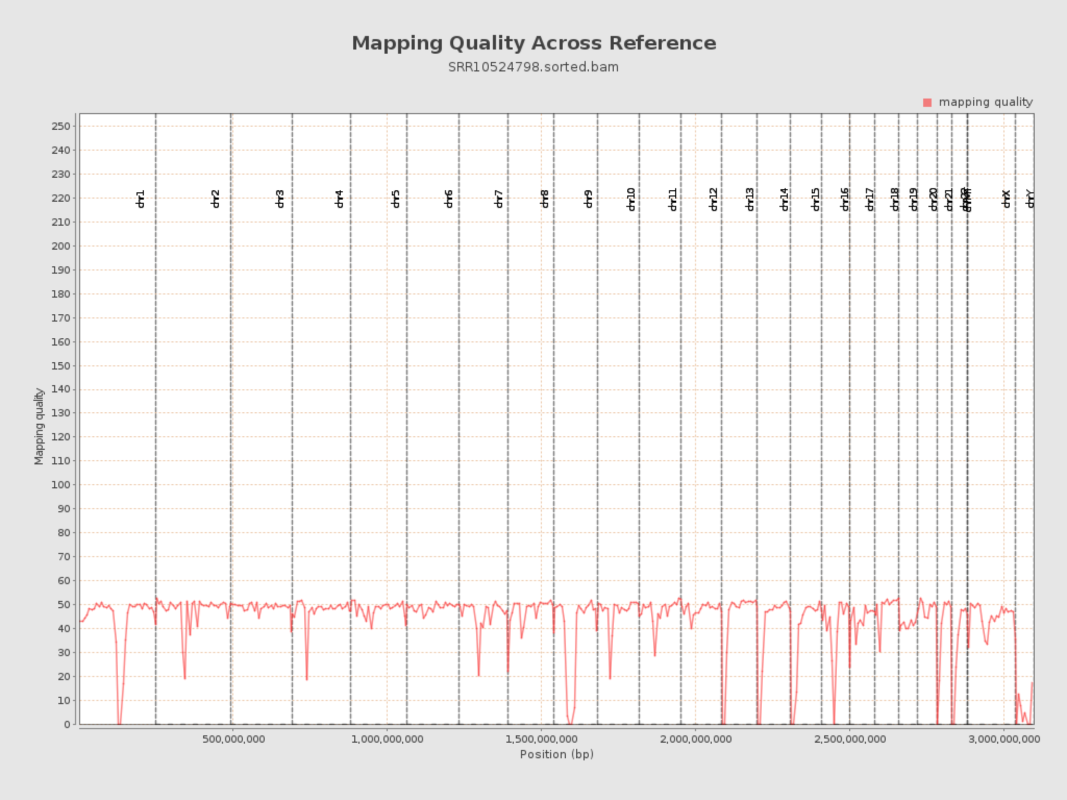
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram