Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:39:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524298.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_SRR10524298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524298.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:39:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,573,454
Mapped reads	1,438,204 / 91.4%
Unmapped reads	135,250 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,372 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	41,028 / 2.61%
Duplication rate	1.96%
Clipped reads	1,439,150 / 91.46%

2.2. ACGT Content

Number/percentage of A's	20,584,841 / 24.58%
Number/percentage of C's	15,842,738 / 18.92%
Number/percentage of T's	26,780,088 / 31.98%
Number/percentage of G's	20,516,855 / 24.5%
Number/percentage of N's	11,769 / 0.01%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2608

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

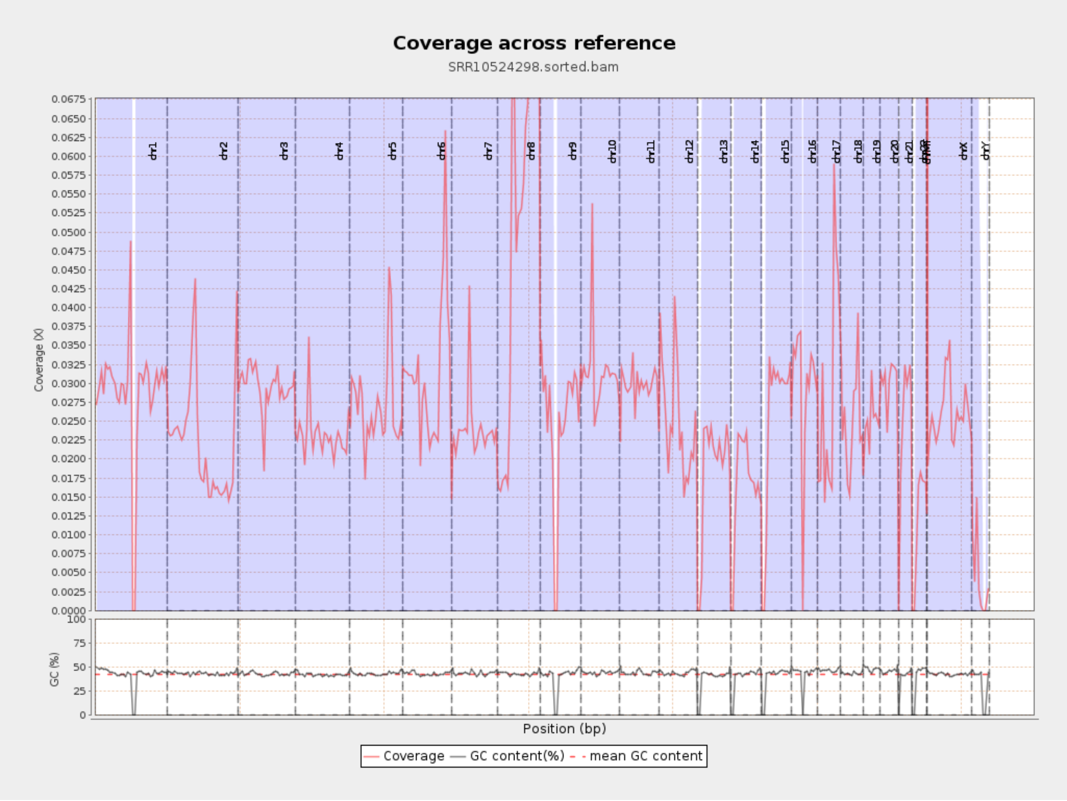
General error rate	0.52%
Mismatches	424,475
Insertions	6,468
Mapped reads with at least one insertion	0.45%
Deletions	14,302
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.8%

2.6. Chromosome stats

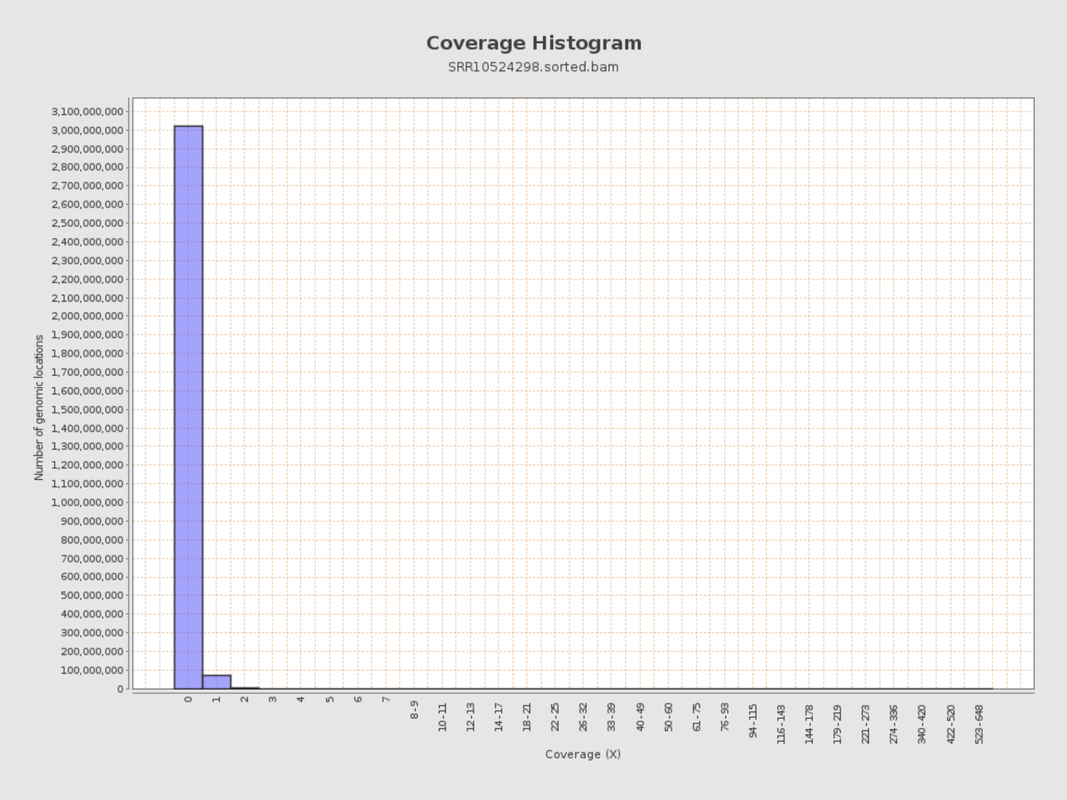
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7129289	0.0286	0.4967
chr2	243199373	5353289	0.022	0.3085
chr3	198022430	5851780	0.0296	0.1848
chr4	191154276	4431381	0.0232	0.1804
chr5	180915260	4923765	0.0272	0.1779
chr6	171115067	5314435	0.0311	0.2023
chr7	159138663	3835796	0.0241	0.3223

chr8	146364022	8770084	0.0599	0.3291
chr9	141213431	3488122	0.0247	0.2041
chr10	135534747	4283626	0.0316	0.2656
chr11	135006516	4037805	0.0299	0.2202
chr12	133851895	3343117	0.025	0.1724
chr13	115169878	2123844	0.0184	0.1448
chr14	107349540	1760801	0.0164	0.1483
chr15	102531392	2560608	0.025	0.1709
chr16	90354753	2627178	0.0291	0.1919
chr17	81195210	2372045	0.0292	0.1998
chr18	78077248	1956411	0.0251	0.3438
chr19	59128983	1484124	0.0251	0.3315
chr20	63025520	1891187	0.03	0.1881
chr21	48129895	1211420	0.0252	0.1818
chr22	51304566	617327	0.012	0.1164
chrMT	16571	76574	4.621	3.2436
chrX	155270560	4071224	0.0262	0.19
chrY	59373566	243756	0.0041	0.1267

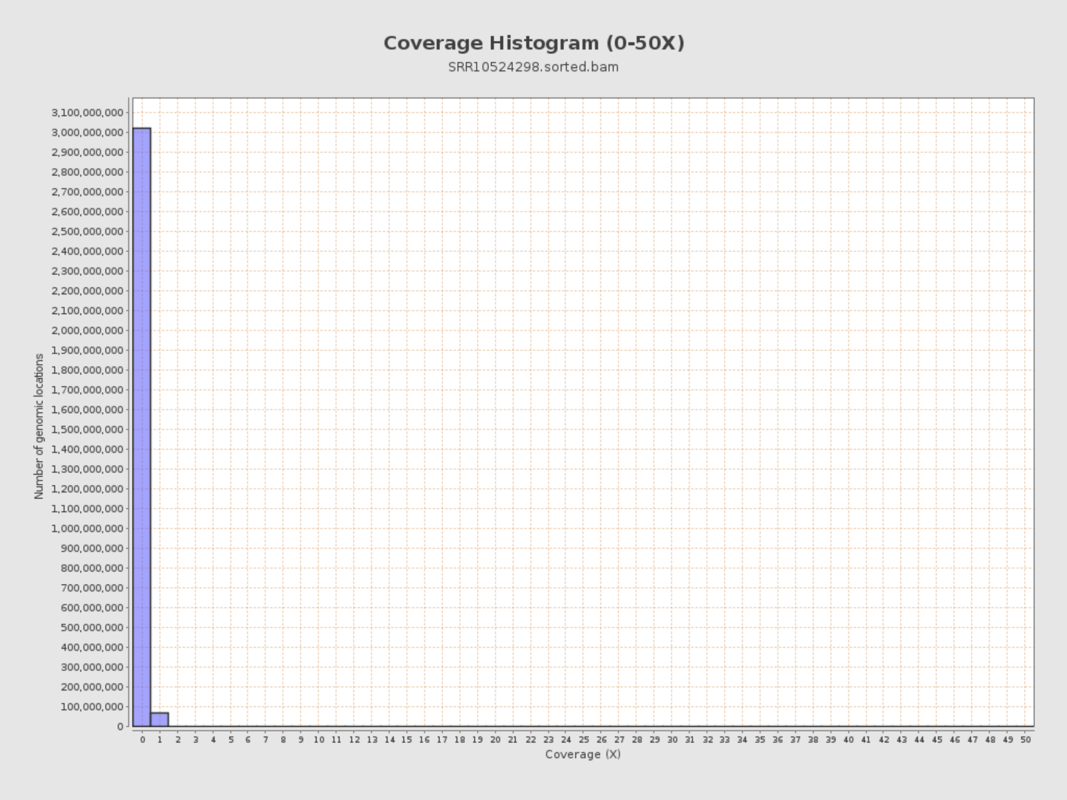
3. Results : Coverage across reference



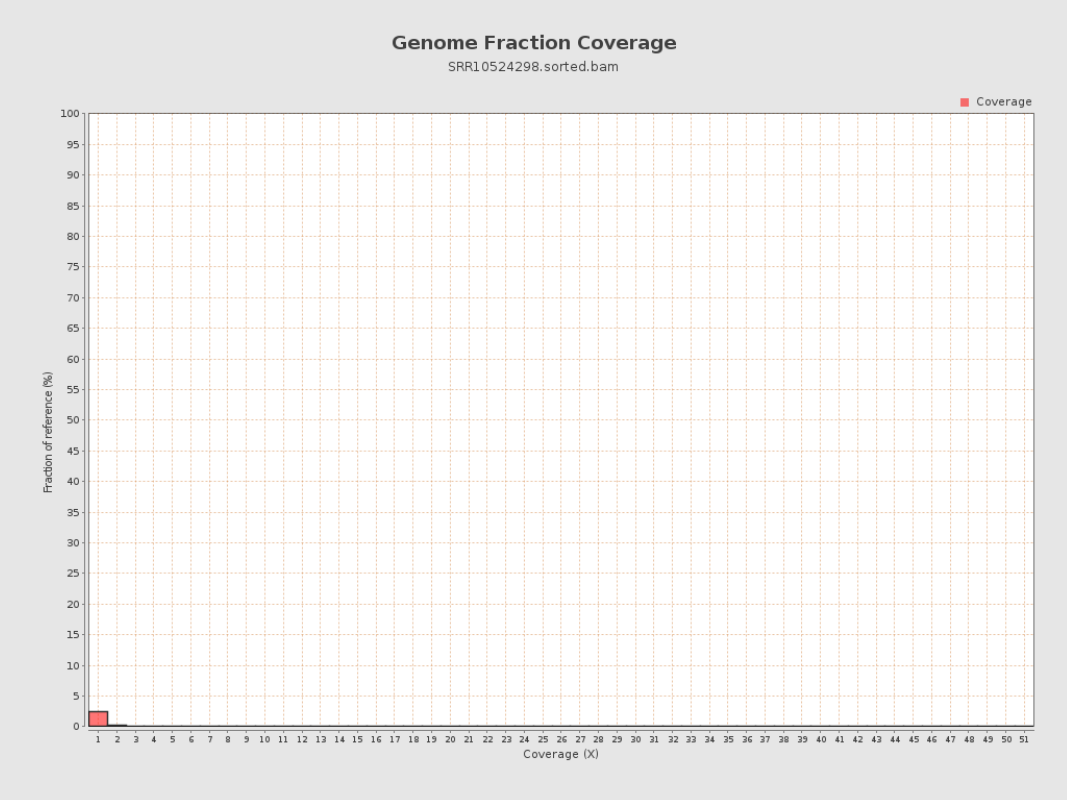
4. Results : Coverage Histogram



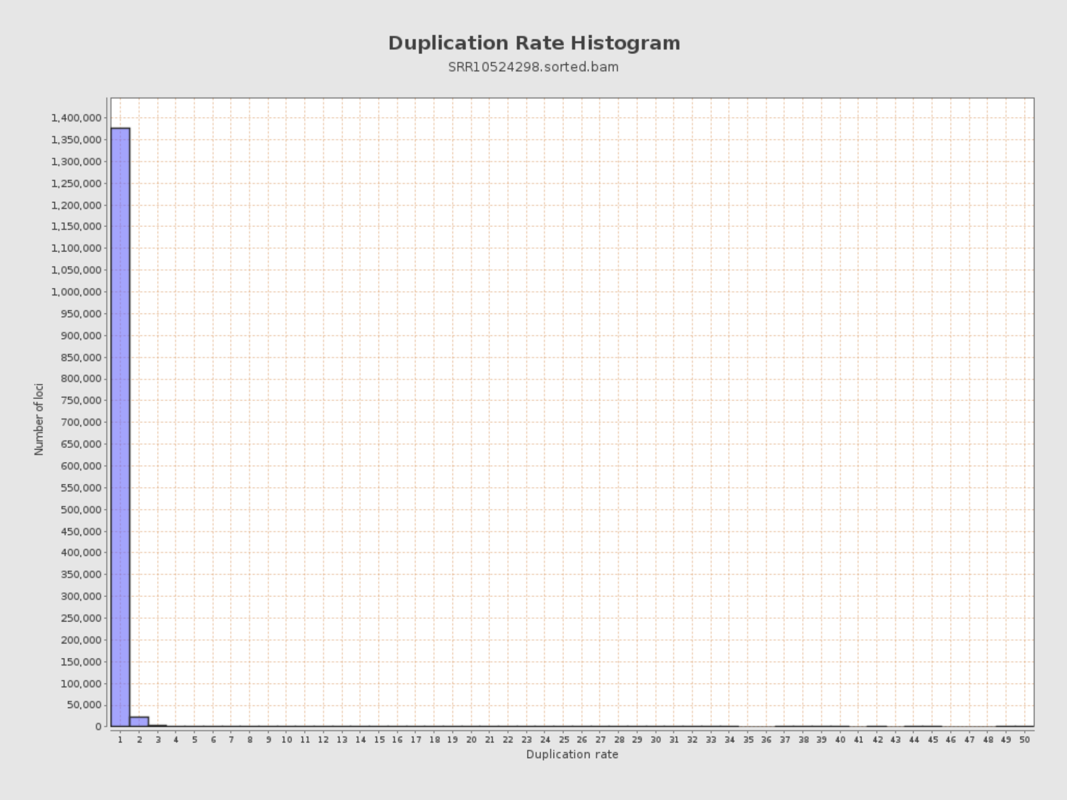
5. Results : Coverage Histogram (0-50X)



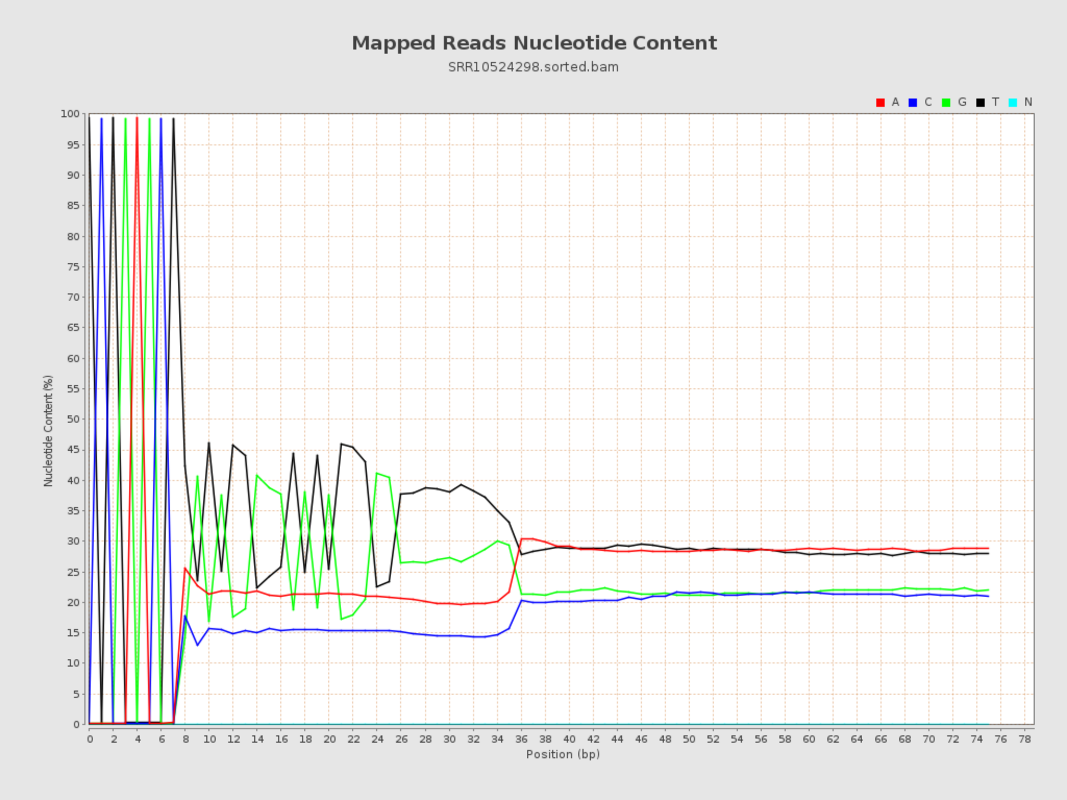
6. Results : Genome Fraction Coverage



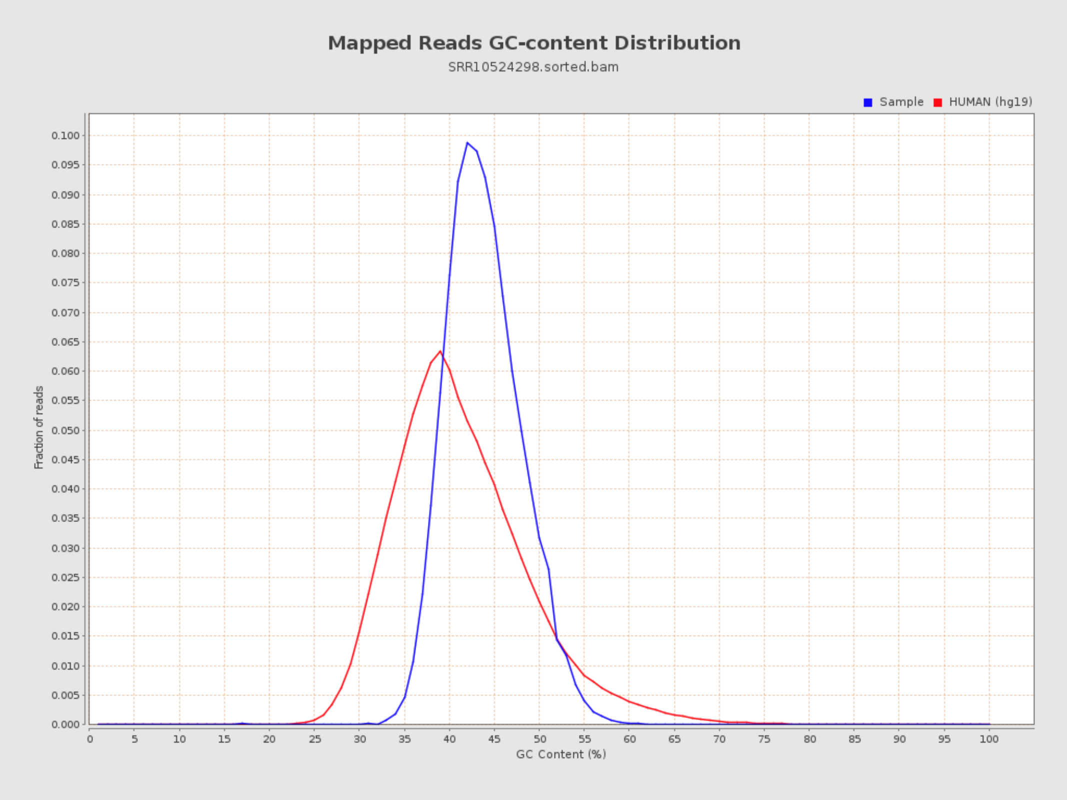
7. Results : Duplication Rate Histogram



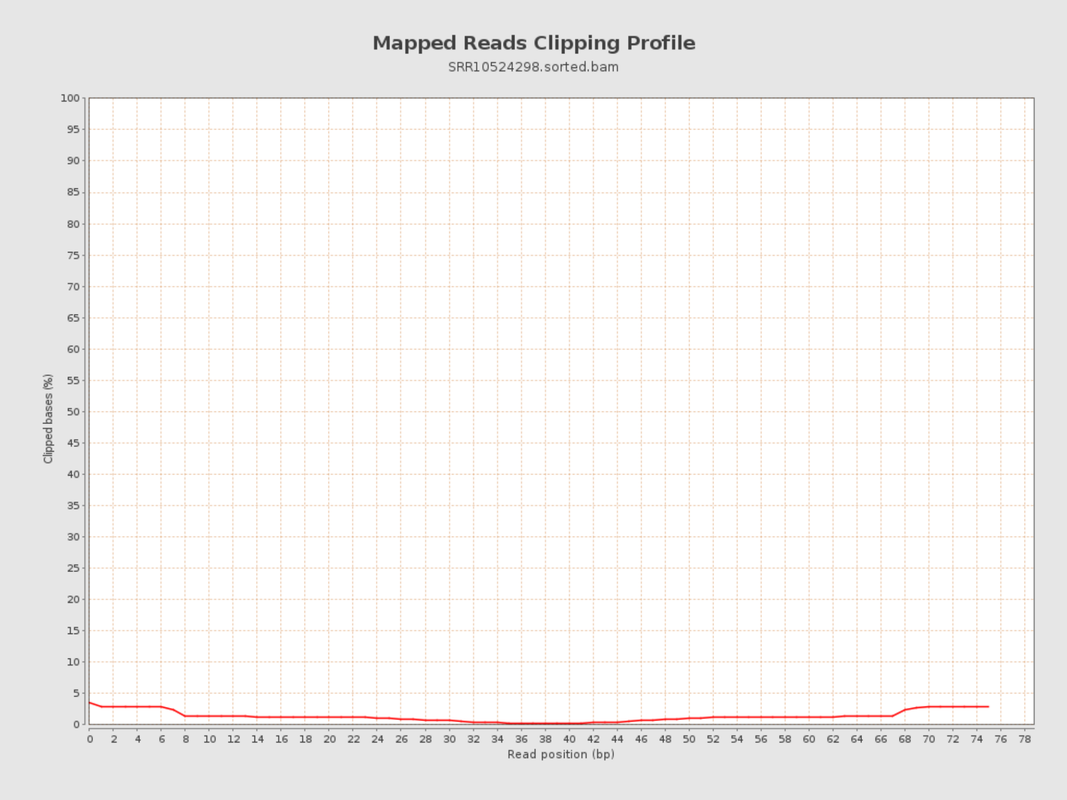
8. Results : Mapped Reads Nucleotide Content



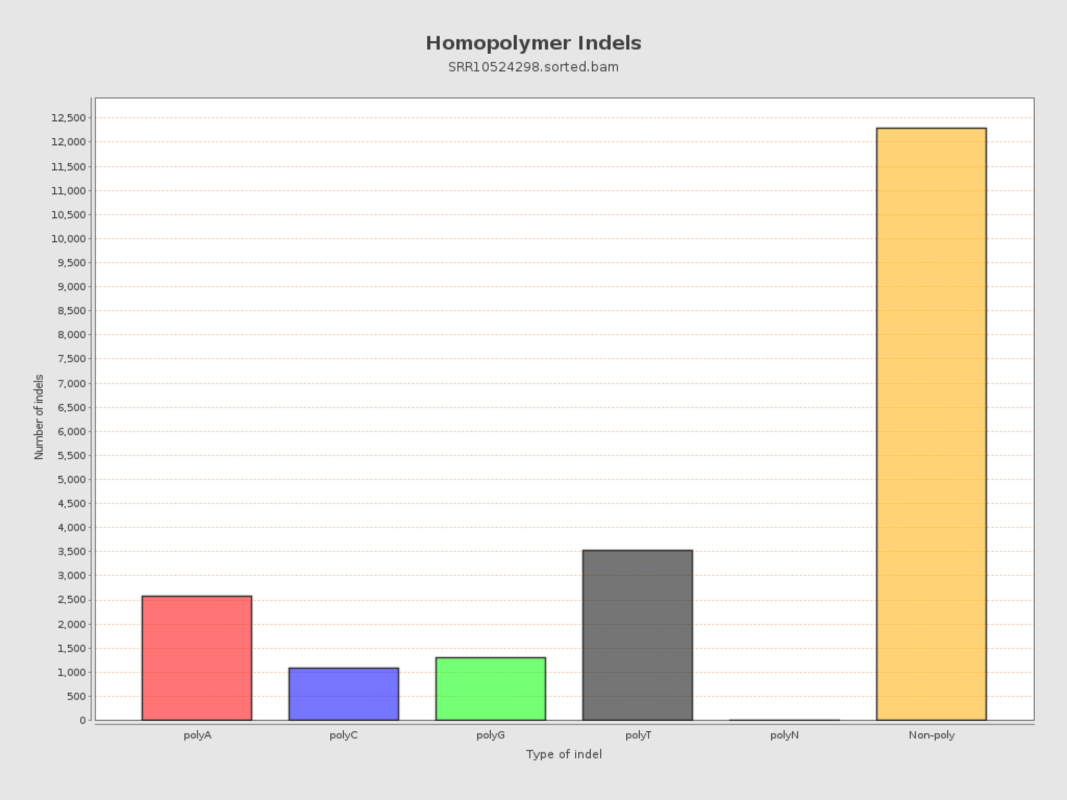
9. Results : Mapped Reads GC-content Distribution



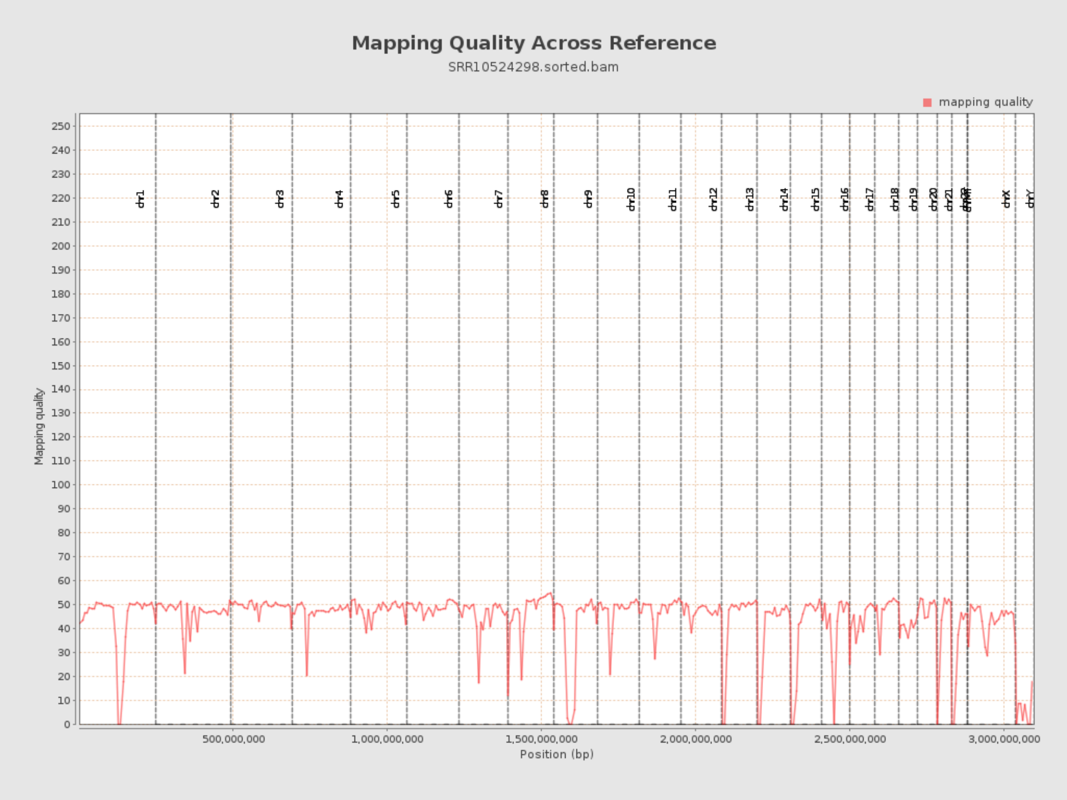
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram