Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:24:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524408.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_SRR10524408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524408.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:24:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,823,156
Mapped reads	1,684,699 / 92.41%
Unmapped reads	138,457 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,360 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	69,208 / 3.8%
Duplication rate	2.92%
Clipped reads	1,686,474 / 92.5%

2.2. ACGT Content

Number/percentage of A's	24,829,255 / 25.14%
Number/percentage of C's	18,402,193 / 18.64%
Number/percentage of T's	31,670,579 / 32.07%
Number/percentage of G's	23,836,319 / 24.14%
Number/percentage of N's	11,586 / 0.01%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.3329

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

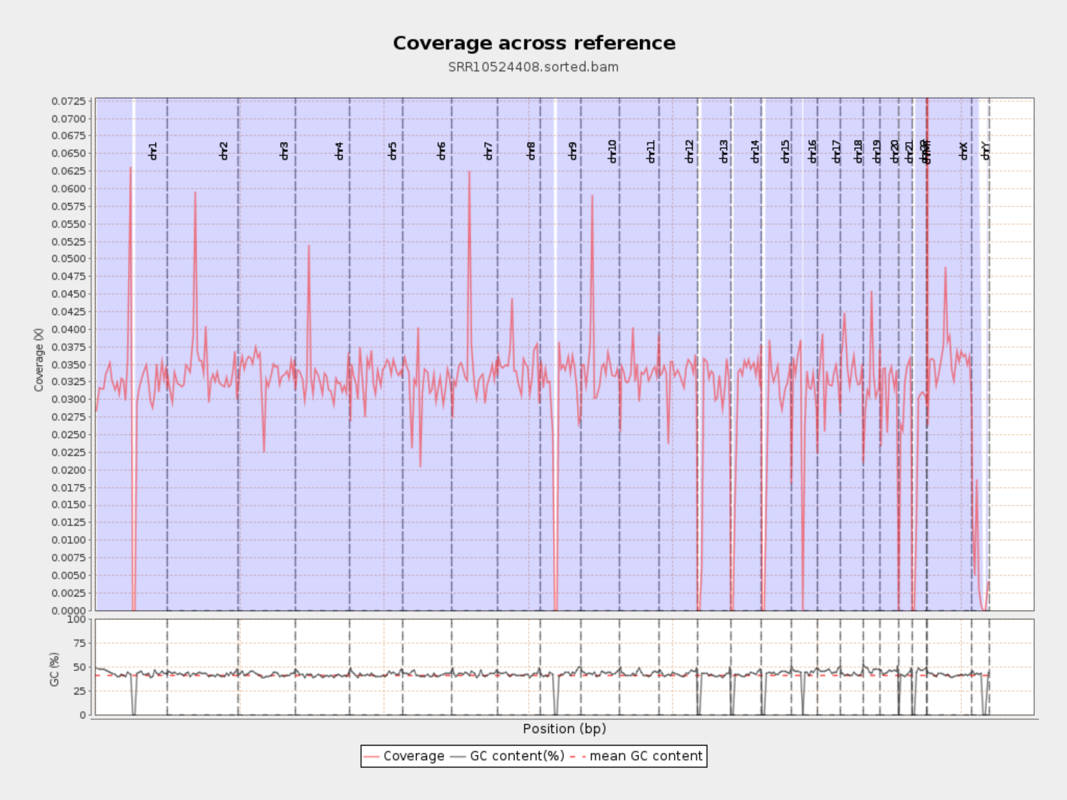
General error rate	0.5%
Mismatches	478,415
Insertions	7,607
Mapped reads with at least one insertion	0.45%
Deletions	17,931
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.1%

2.6. Chromosome stats

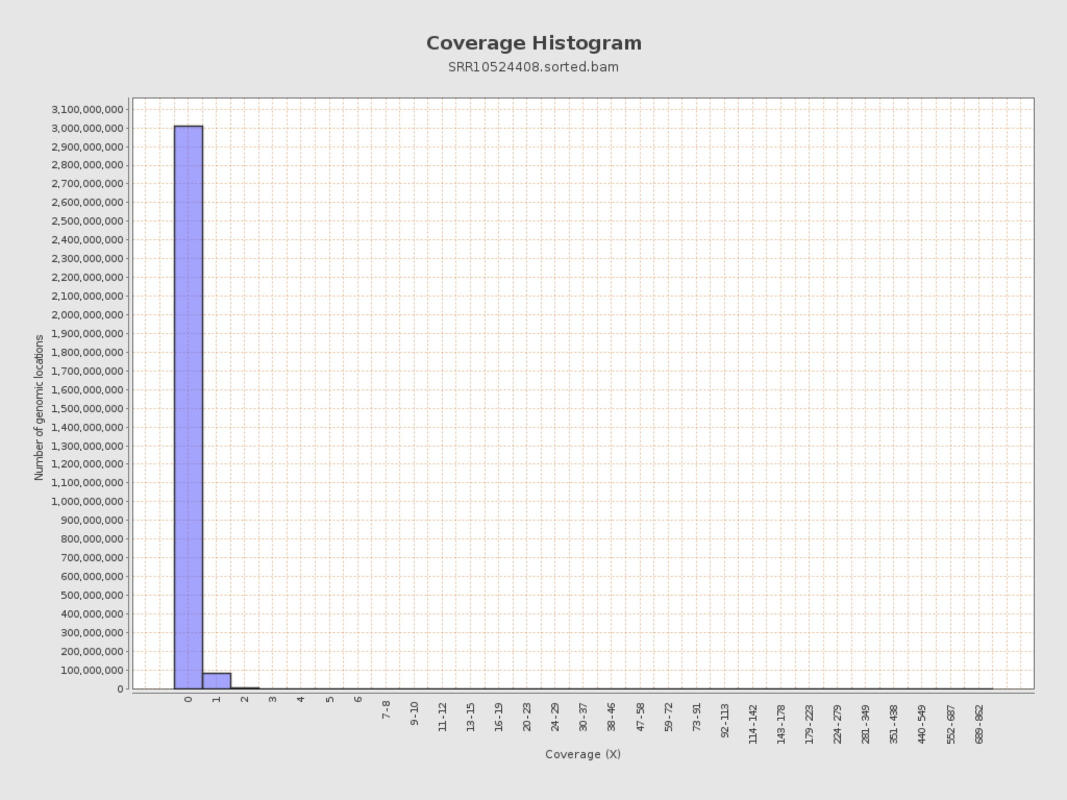
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7802502	0.0313	0.7065
chr2	243199373	8349112	0.0343	0.3626
chr3	198022430	6713339	0.0339	0.1995
chr4	191154276	6343369	0.0332	0.2259
chr5	180915260	6104896	0.0337	0.2003
chr6	171115067	5478061	0.032	0.2215
chr7	159138663	5500919	0.0346	0.4585

chr8	146364022	5098975	0.0348	0.2897
chr9	141213431	4184672	0.0296	0.2758
chr10	135534747	4788045	0.0353	0.294
chr11	135006516	4550316	0.0337	0.2777
chr12	133851895	4484612	0.0335	0.2052
chr13	115169878	3154467	0.0274	0.1801
chr14	107349540	3089191	0.0288	0.1943
chr15	102531392	2783533	0.0271	0.1799
chr16	90354753	2653305	0.0294	0.2022
chr17	81195210	2675522	0.033	0.2205
chr18	78077248	2732964	0.035	0.5175
chr19	59128983	1927083	0.0326	0.4741
chr20	63025520	1957778	0.0311	0.1971
chr21	48129895	1341719	0.0279	0.2098
chr22	51304566	1101771	0.0215	0.1585
chrMT	16571	70731	4.2684	2.8744
chrX	155270560	5582396	0.036	0.2321
chrY	59373566	309554	0.0052	0.1568

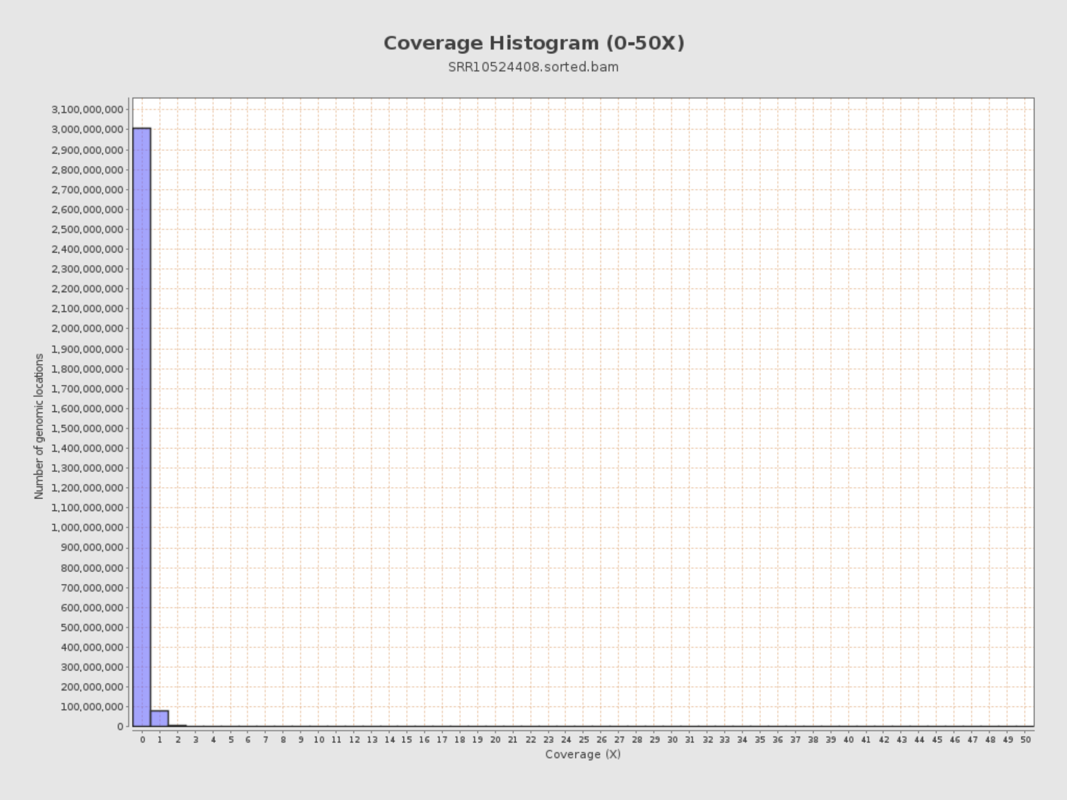
3. Results : Coverage across reference



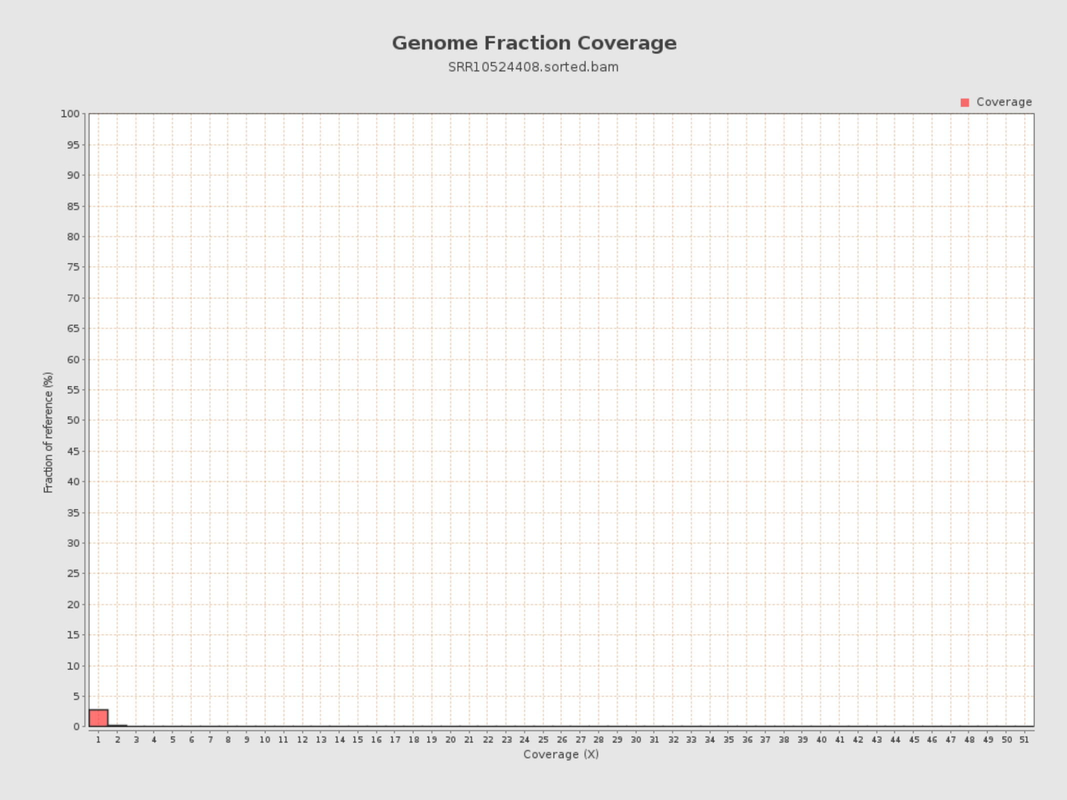
4. Results : Coverage Histogram



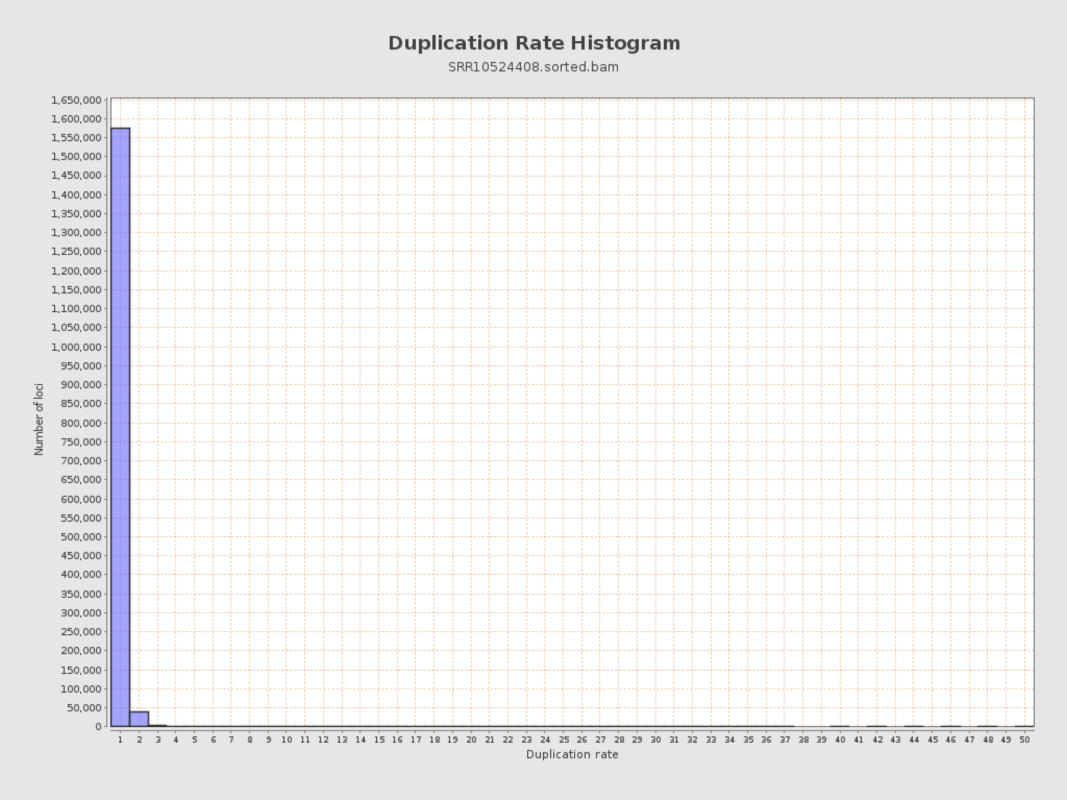
5. Results : Coverage Histogram (0-50X)



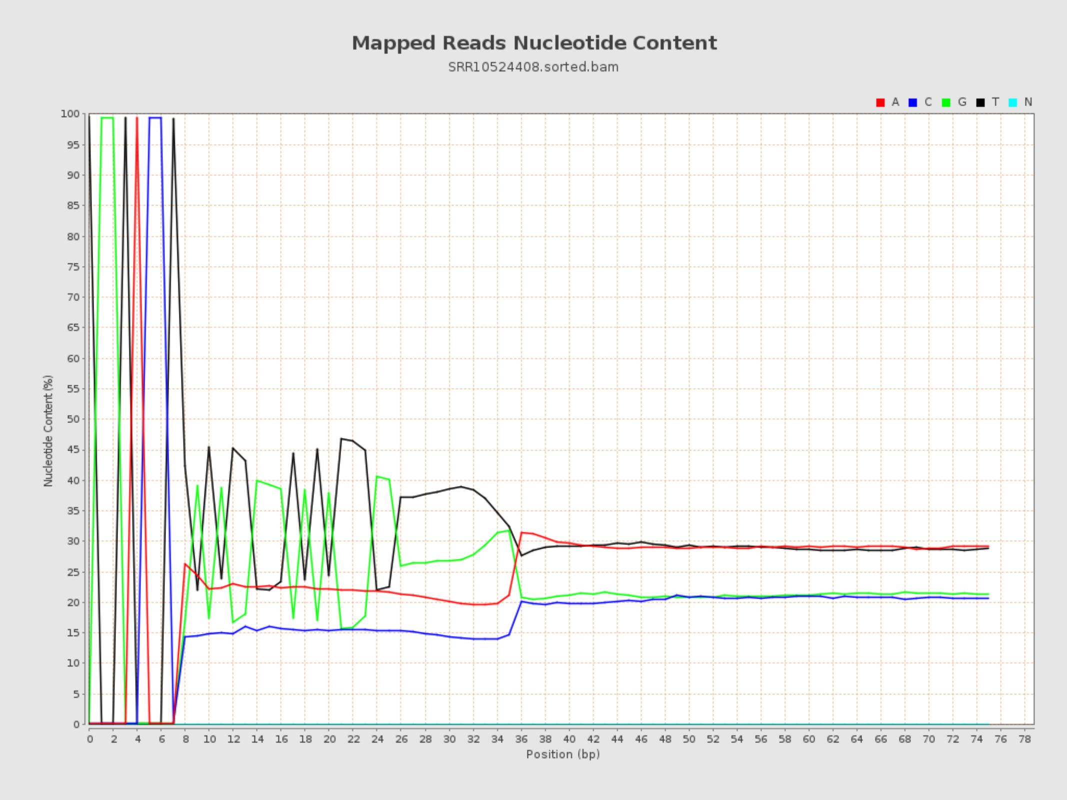
6. Results : Genome Fraction Coverage



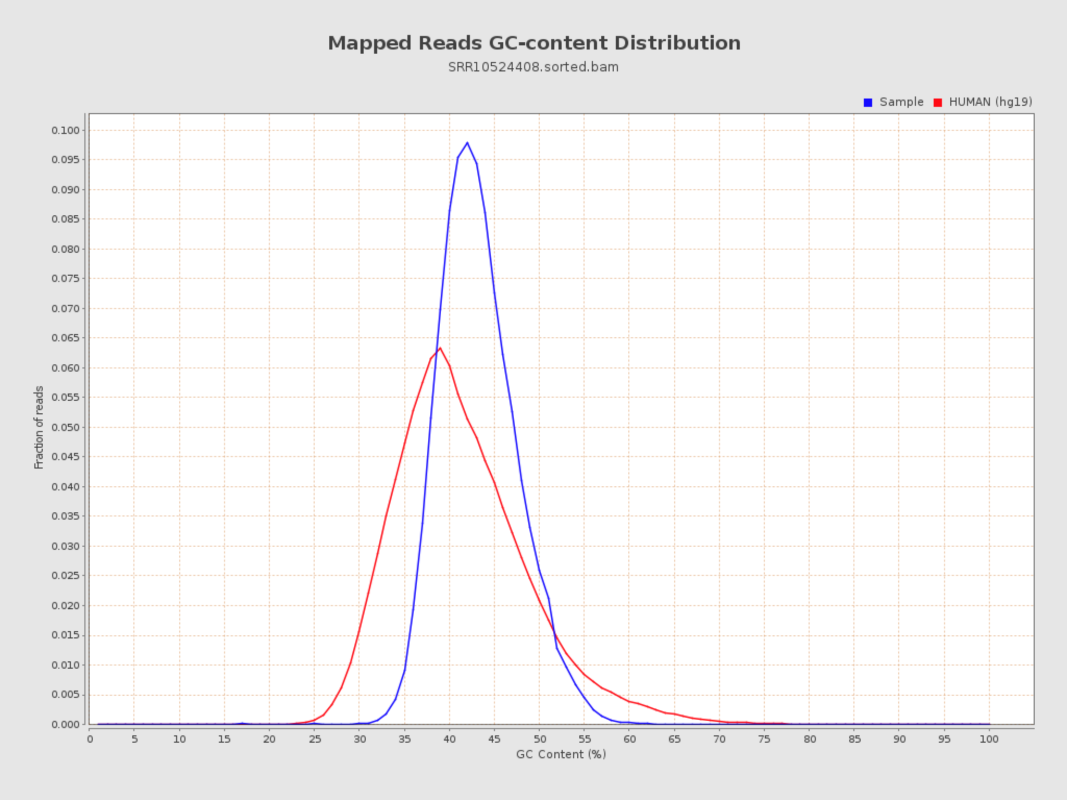
7. Results : Duplication Rate Histogram



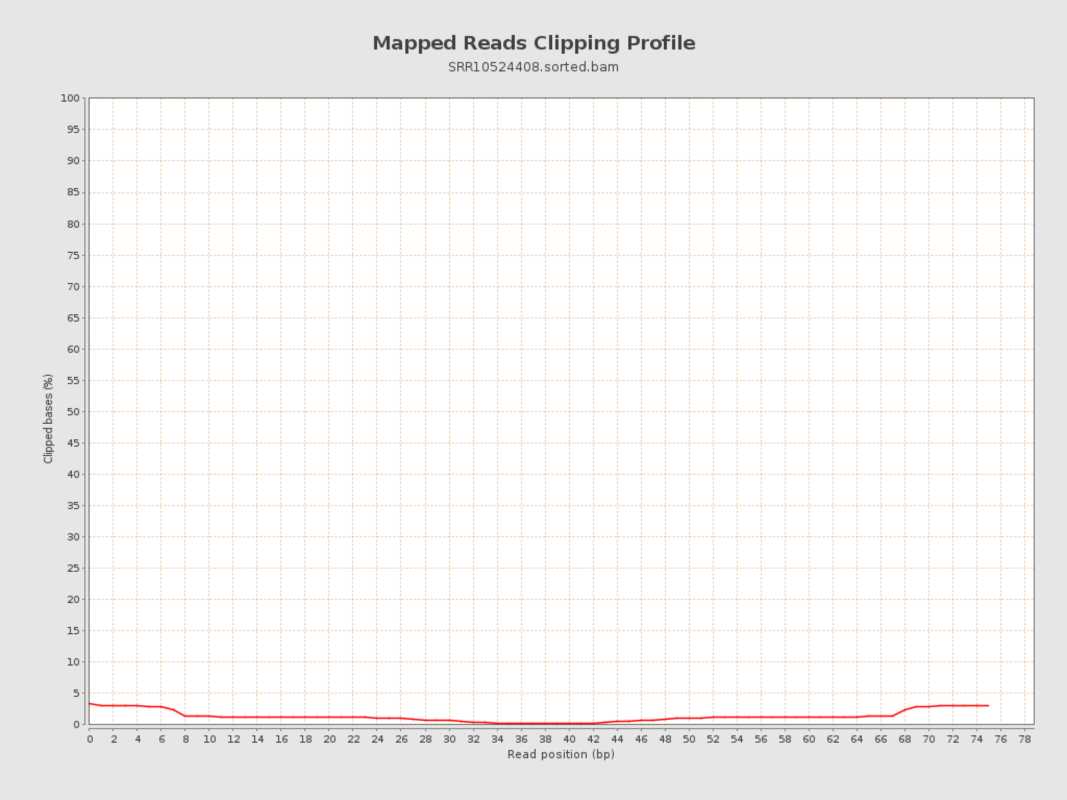
8. Results : Mapped Reads Nucleotide Content



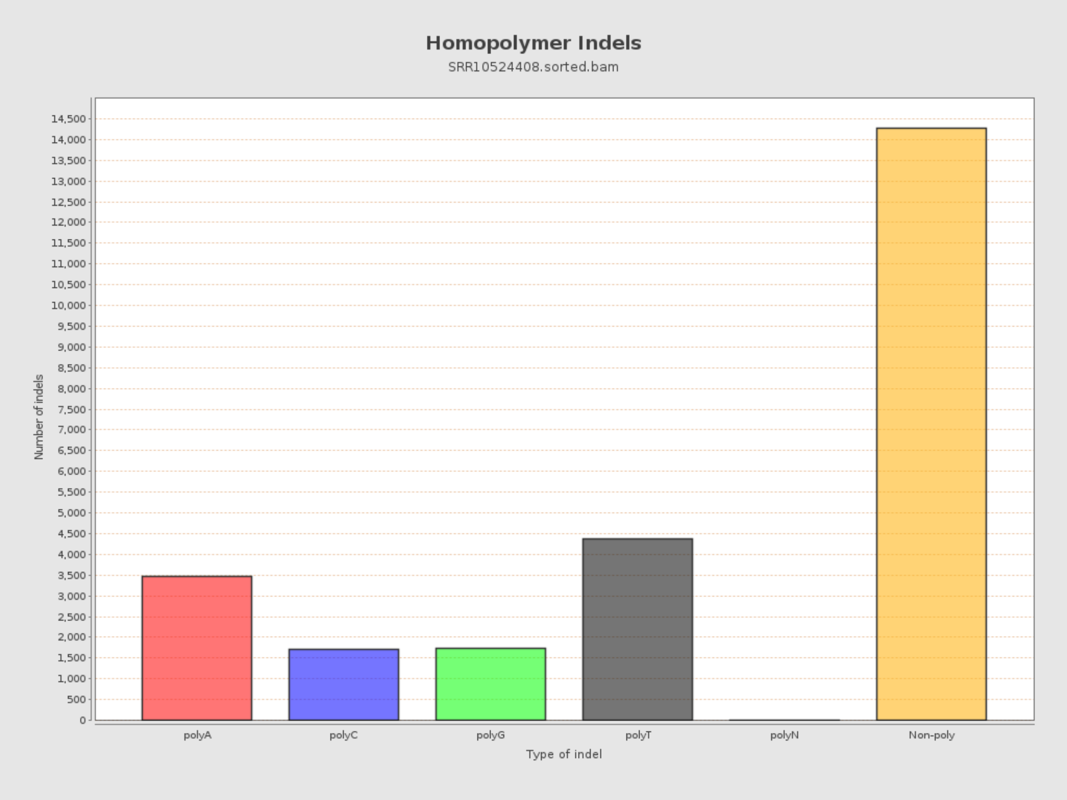
9. Results : Mapped Reads GC-content Distribution



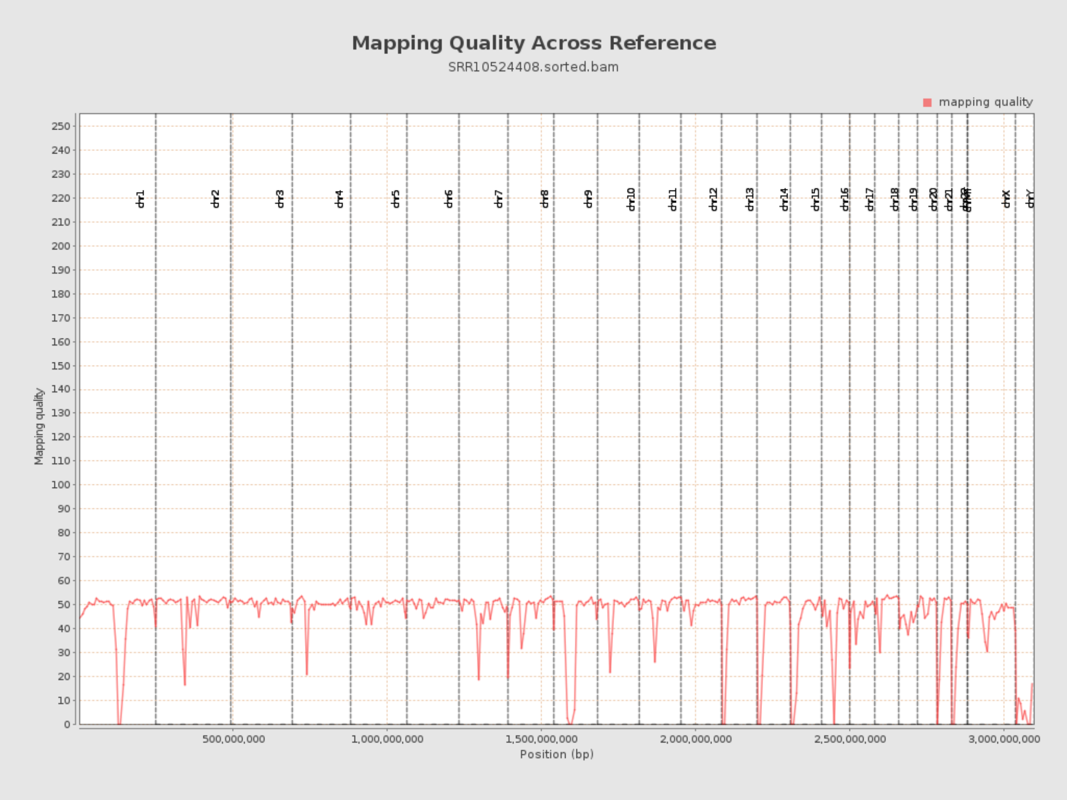
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram