Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:27:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524709.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_SRR10524709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524709.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:27:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524709.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,142,632
Mapped reads	1,056,256 / 92.44%
Unmapped reads	86,376 / 7.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,962 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	33,338 / 2.92%
Duplication rate	2.29%
Clipped reads	1,056,864 / 92.49%

2.2. ACGT Content

Number/percentage of A's	15,809,132 / 25.36%
Number/percentage of C's	11,636,396 / 18.66%
Number/percentage of T's	20,030,699 / 32.13%
Number/percentage of G's	14,858,329 / 23.83%
Number/percentage of N's	8,885 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2136

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

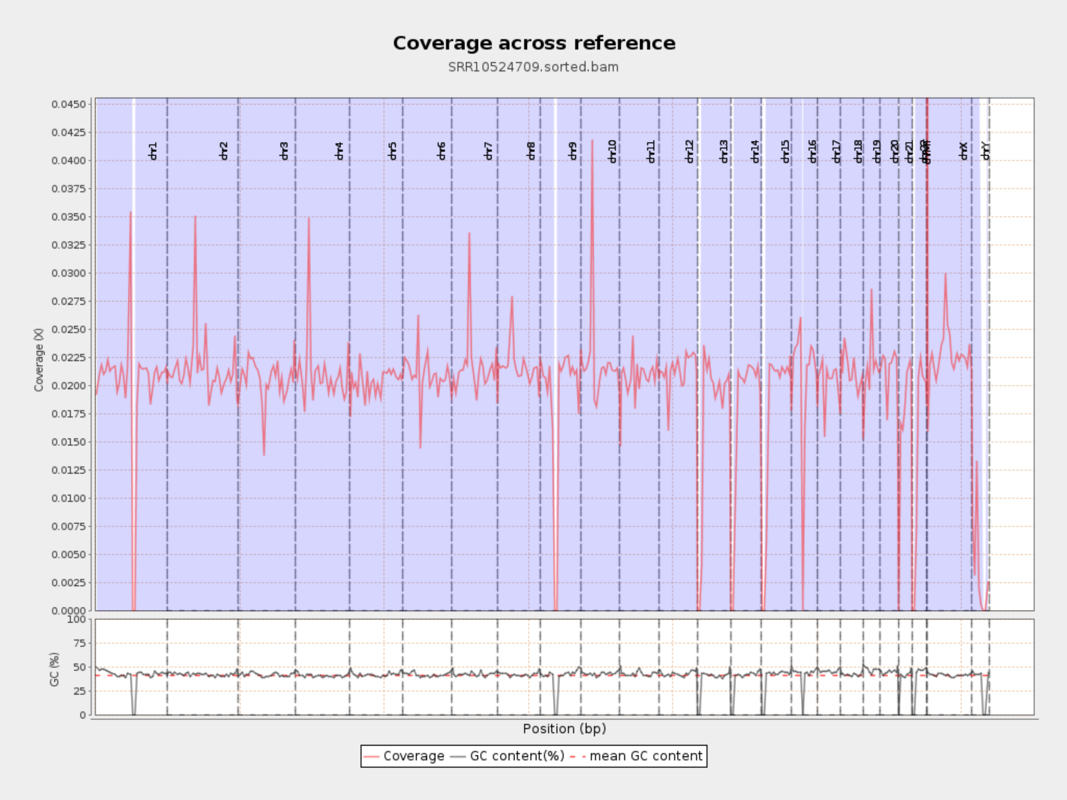
General error rate	0.52%
Mismatches	315,182
Insertions	4,725
Mapped reads with at least one insertion	0.44%
Deletions	12,231
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.64%

2.6. Chromosome stats

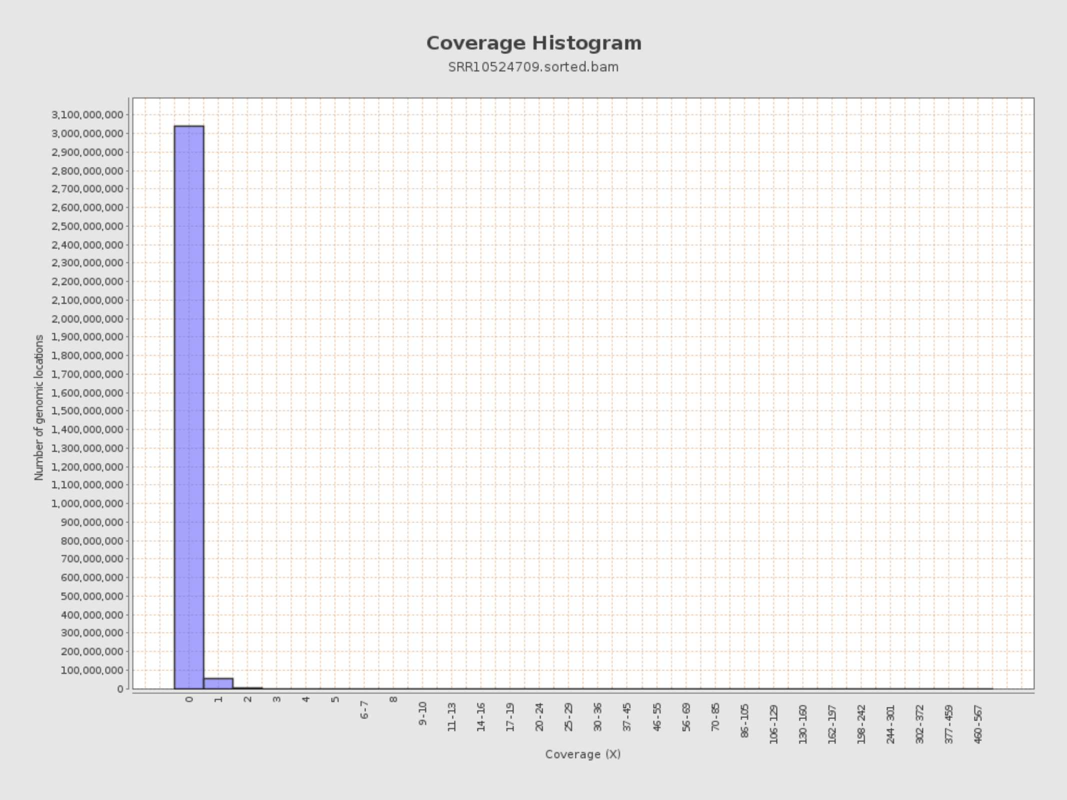
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4994485	0.02	0.3656
chr2	243199373	5252336	0.0216	0.2899
chr3	198022430	4063772	0.0205	0.1531
chr4	191154276	4046404	0.0212	0.17
chr5	180915260	3701617	0.0205	0.1529
chr6	171115067	3575433	0.0209	0.1688
chr7	159138663	3461672	0.0218	0.2392

chr8	146364022	3198117	0.0219	0.2353
chr9	141213431	2623552	0.0186	0.1803
chr10	135534747	3028264	0.0223	0.223
chr11	135006516	2814755	0.0208	0.1812
chr12	133851895	2858661	0.0214	0.1563
chr13	115169878	1975585	0.0172	0.1397
chr14	107349540	1870435	0.0174	0.1464
chr15	102531392	1768793	0.0173	0.1402
chr16	90354753	1824101	0.0202	0.1601
chr17	81195210	1653758	0.0204	0.1569
chr18	78077248	1659558	0.0213	0.2965
chr19	59128983	1287356	0.0218	0.2877
chr20	63025520	1349542	0.0214	0.1579
chr21	48129895	834613	0.0173	0.1531
chr22	51304566	744556	0.0145	0.128
chrMT	16571	32819	1.9805	1.8987
chrX	155270560	3534229	0.0228	0.172
chrY	59373566	208784	0.0035	0.1343

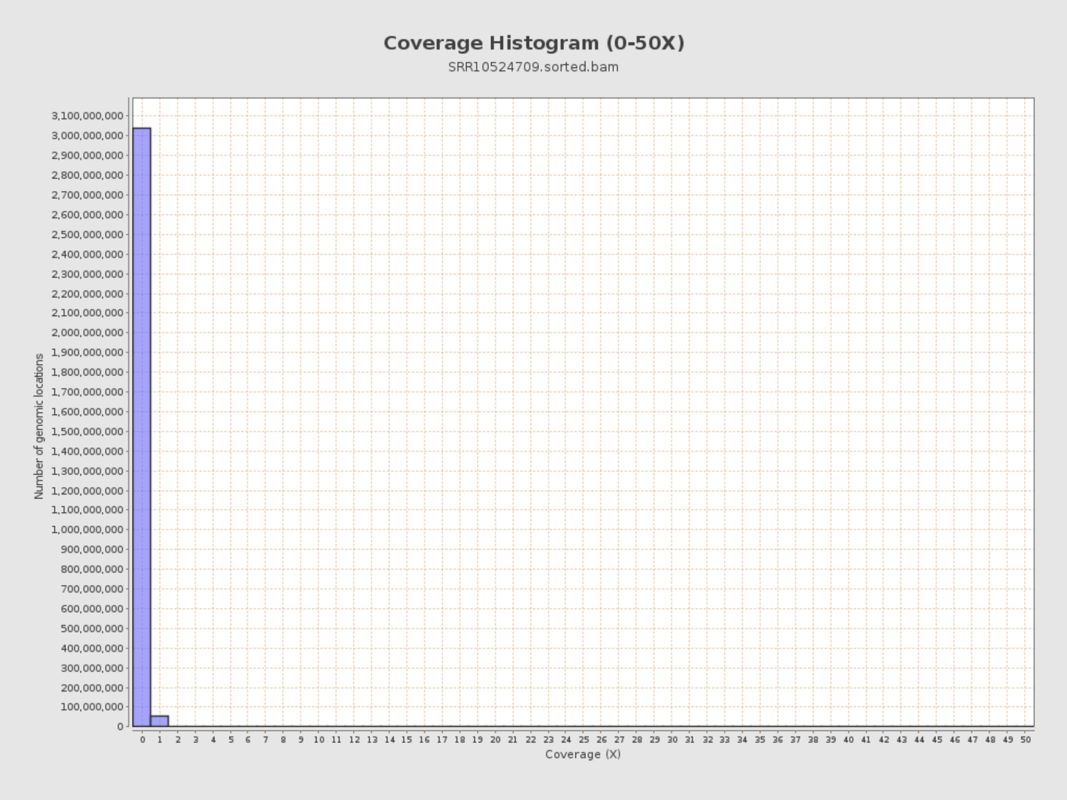
3. Results : Coverage across reference



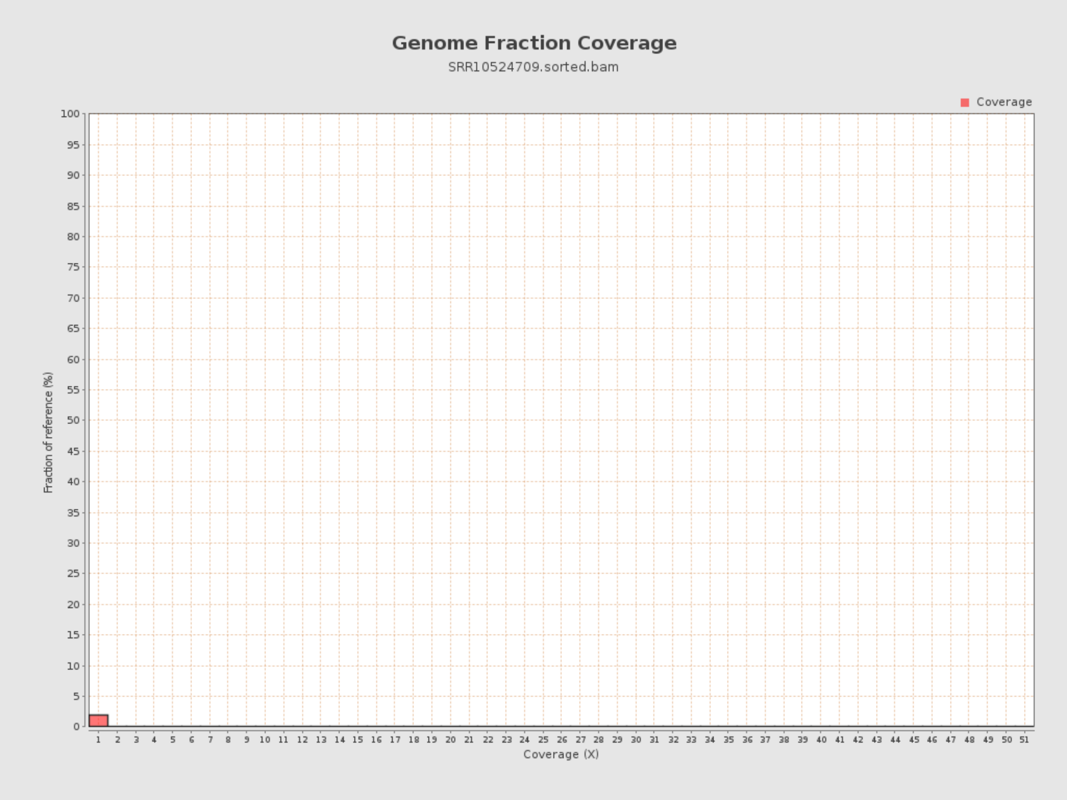
4. Results : Coverage Histogram



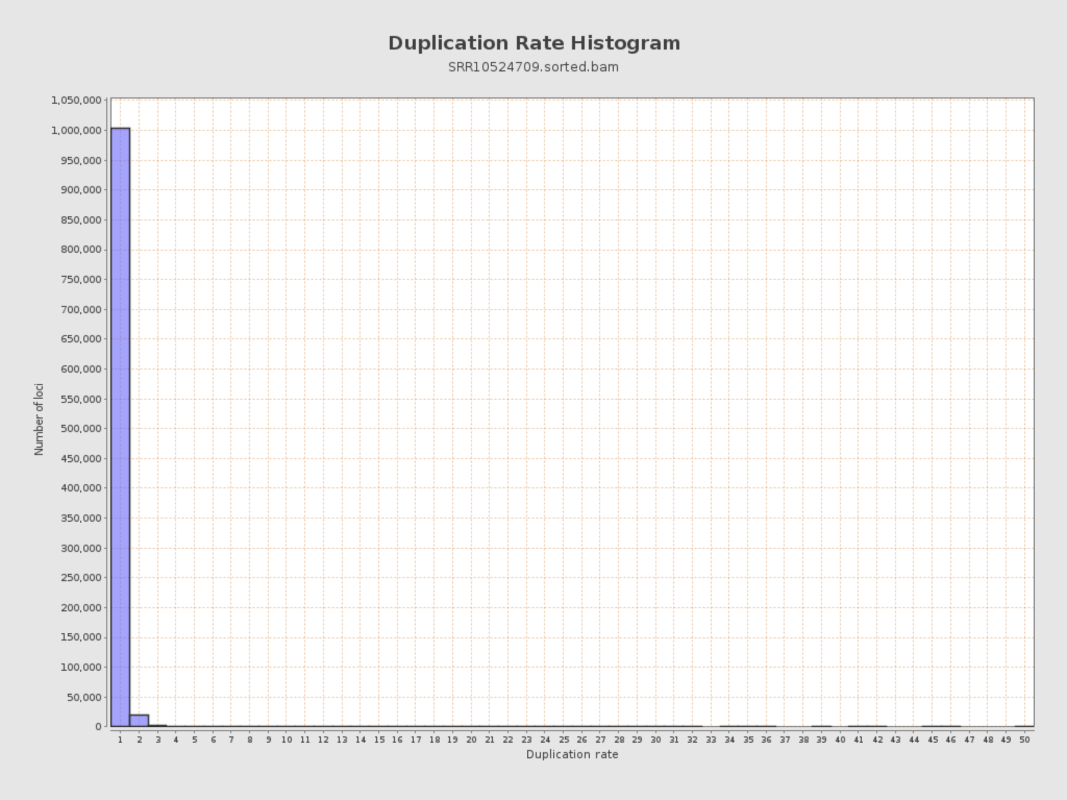
5. Results : Coverage Histogram (0-50X)



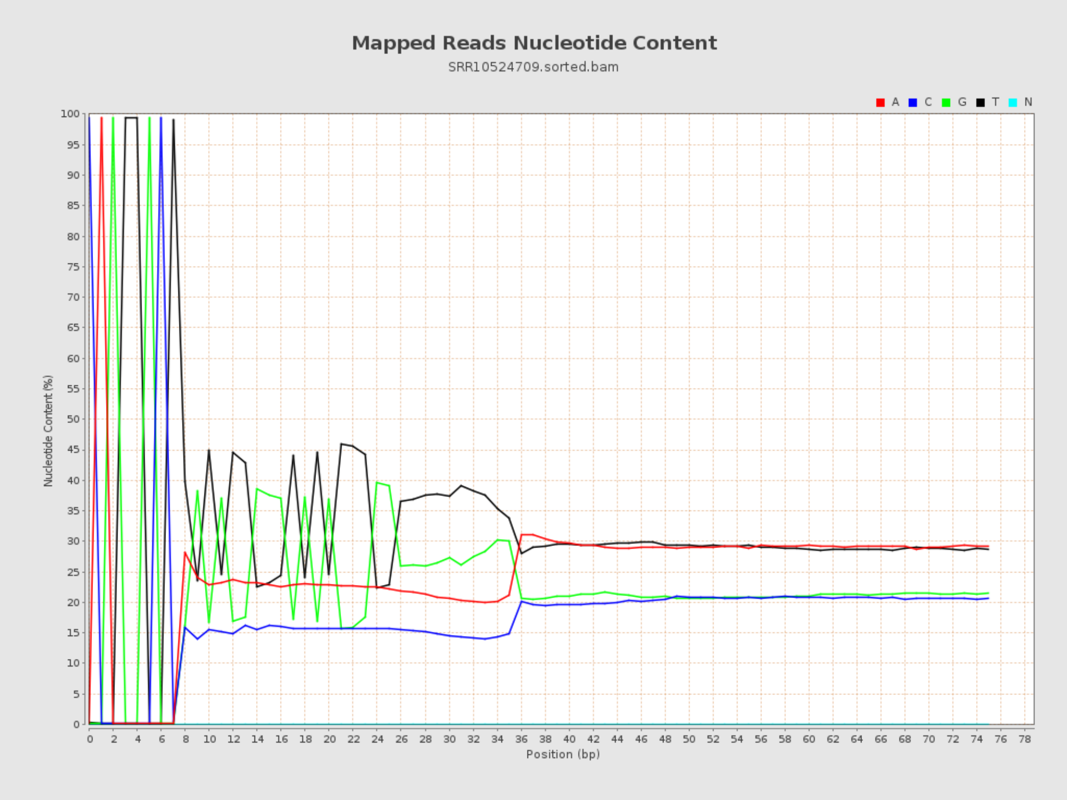
6. Results : Genome Fraction Coverage



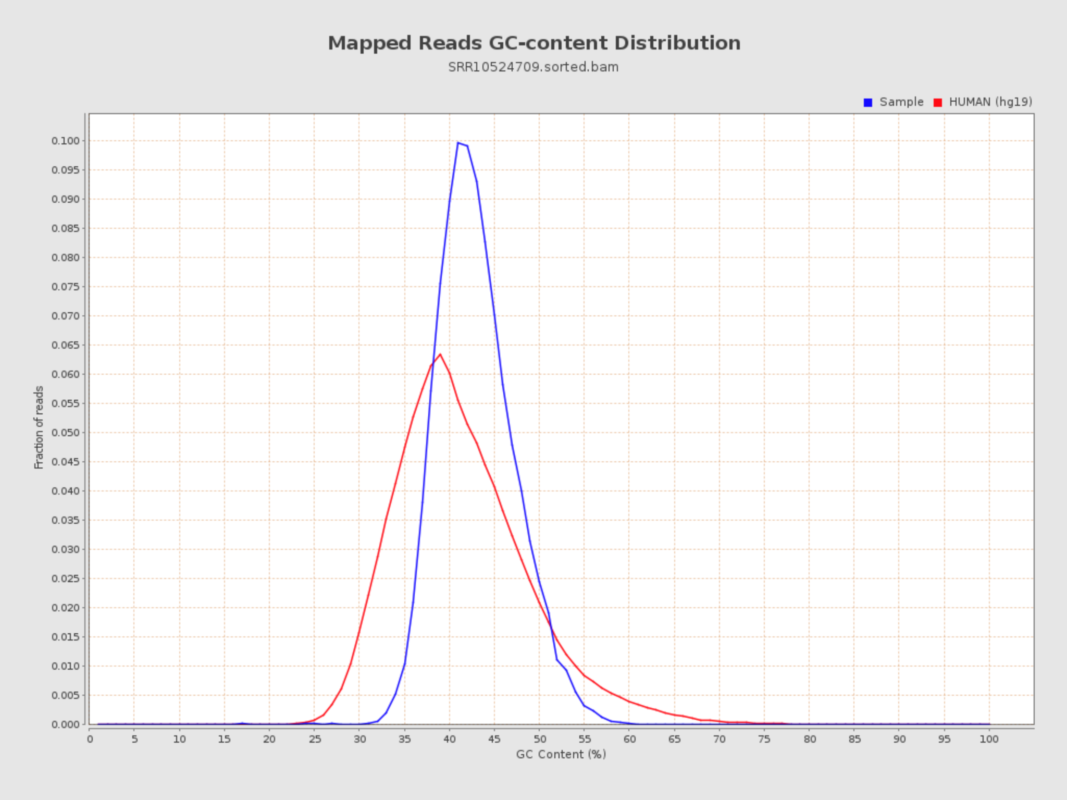
7. Results : Duplication Rate Histogram



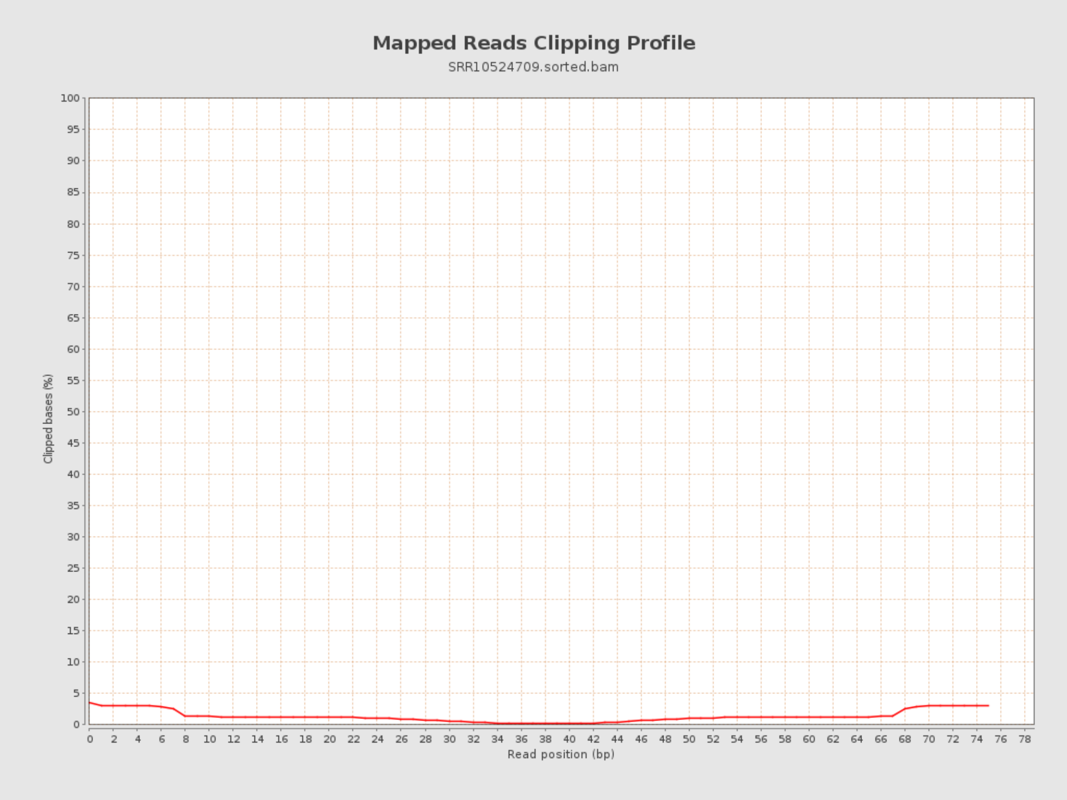
8. Results : Mapped Reads Nucleotide Content



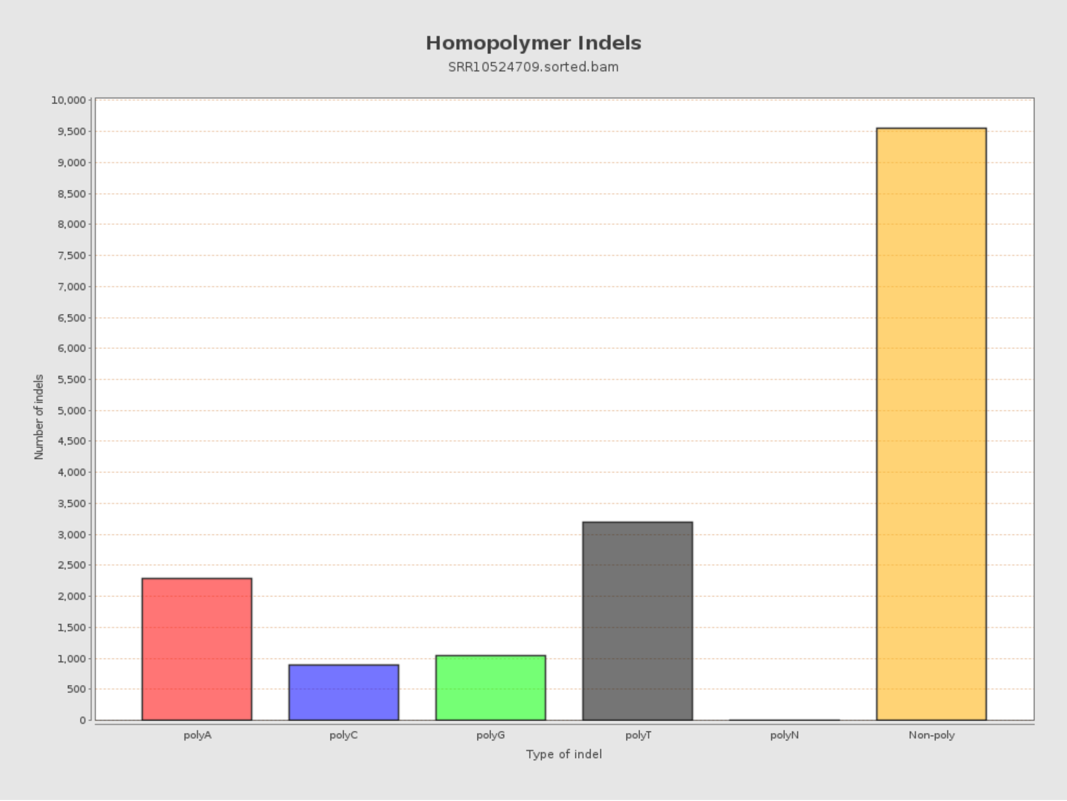
9. Results : Mapped Reads GC-content Distribution



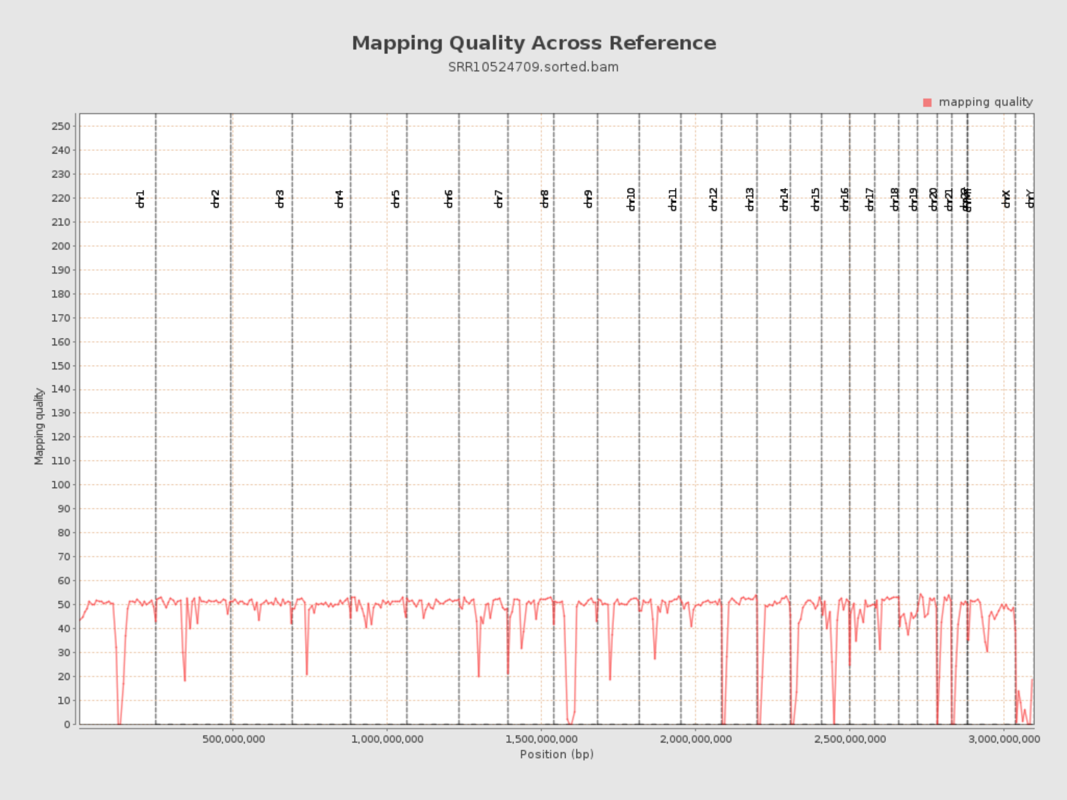
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram