Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:58:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524429.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_SRR10524429 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524429.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:58:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524429.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,869,228
Mapped reads	1,571,927 / 84.09%
Unmapped reads	297,301 / 15.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,962 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	72,212 / 3.86%
Duplication rate	3.44%
Clipped reads	1,574,186 / 84.22%

2.2. ACGT Content

Number/percentage of A's	22,992,154 / 25.01%
Number/percentage of C's	17,701,111 / 19.25%
Number/percentage of T's	29,229,607 / 31.79%
Number/percentage of G's	22,001,823 / 23.93%
Number/percentage of N's	9,143 / 0.01%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.2909

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

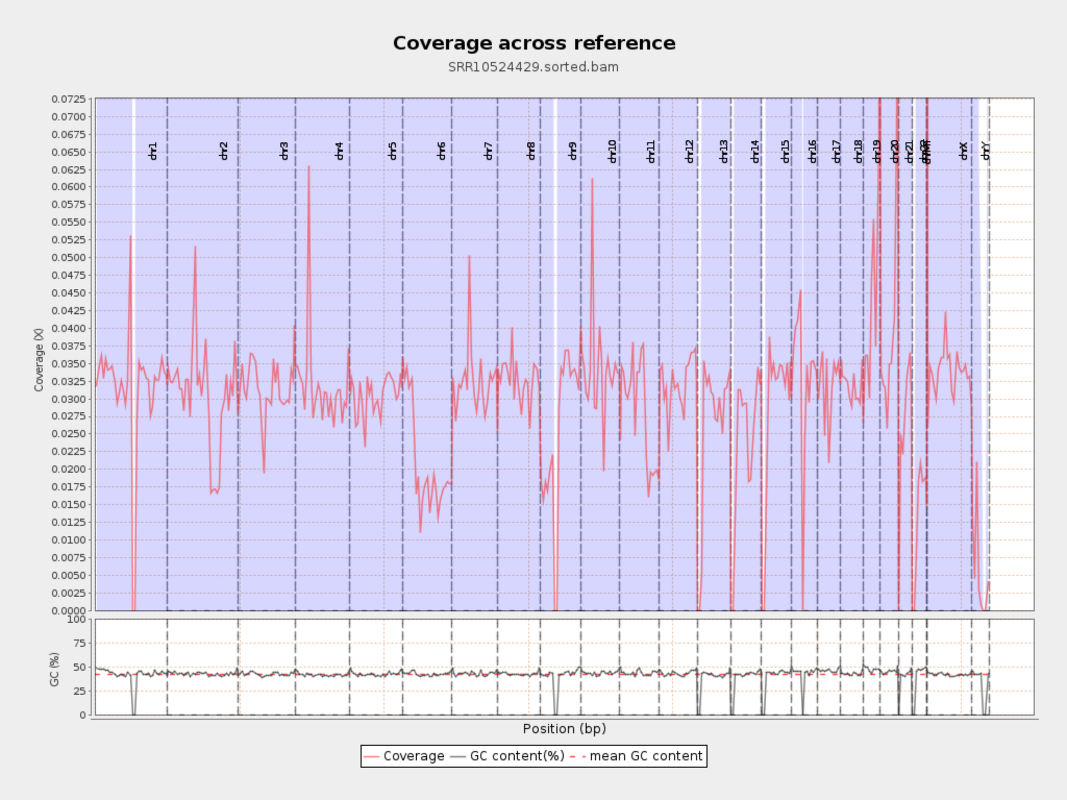
General error rate	0.52%
Mismatches	464,305
Insertions	6,464
Mapped reads with at least one insertion	0.41%
Deletions	16,033
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.61%

2.6. Chromosome stats

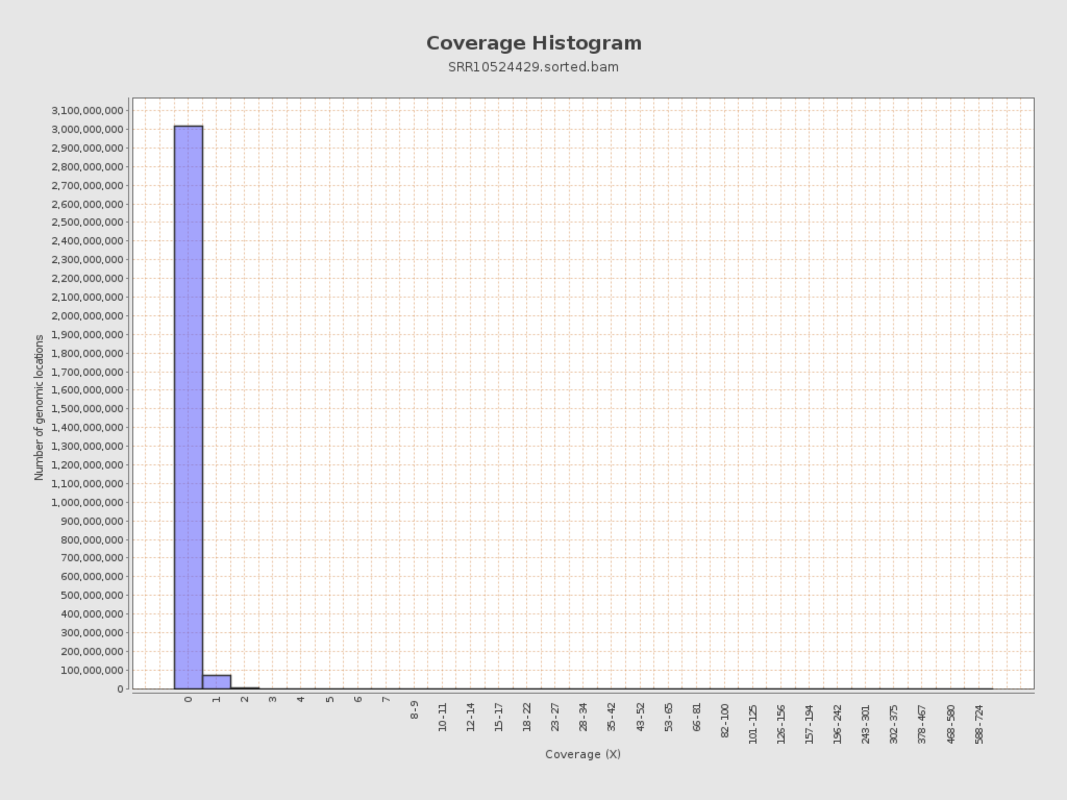
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7792329	0.0313	0.5645
chr2	243199373	7410685	0.0305	0.3867
chr3	198022430	6205914	0.0313	0.1973
chr4	191154276	6124403	0.032	0.2512
chr5	180915260	5530821	0.0306	0.1936
chr6	171115067	3522118	0.0206	0.1685
chr7	159138663	5196840	0.0327	0.3546

chr8	146364022	4784077	0.0327	0.2439
chr9	141213431	3518502	0.0249	0.2095
chr10	135534747	4639405	0.0342	0.33
chr11	135006516	3813764	0.0282	0.2212
chr12	133851895	4305936	0.0322	0.204
chr13	115169878	2951747	0.0256	0.1784
chr14	107349540	2531901	0.0236	0.175
chr15	102531392	2847411	0.0278	0.1852
chr16	90354753	2922021	0.0323	0.215
chr17	81195210	2580707	0.0318	0.2144
chr18	78077248	2472213	0.0317	0.3442
chr19	59128983	2704558	0.0457	0.3904
chr20	63025520	2555661	0.0405	0.2347
chr21	48129895	1273682	0.0265	0.2241
chr22	51304566	683733	0.0133	0.1298
chrMT	16571	6868	0.4145	0.8346
chrX	155270560	5257204	0.0339	0.2209
chrY	59373566	327191	0.0055	0.1778

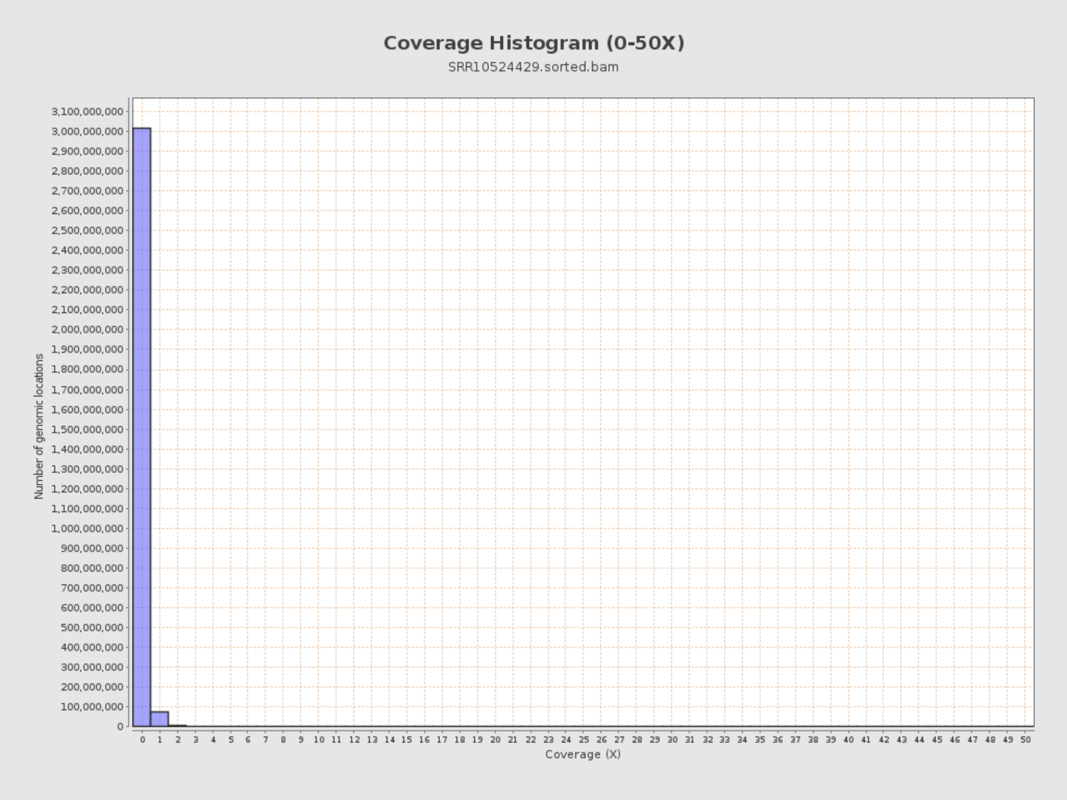
3. Results : Coverage across reference



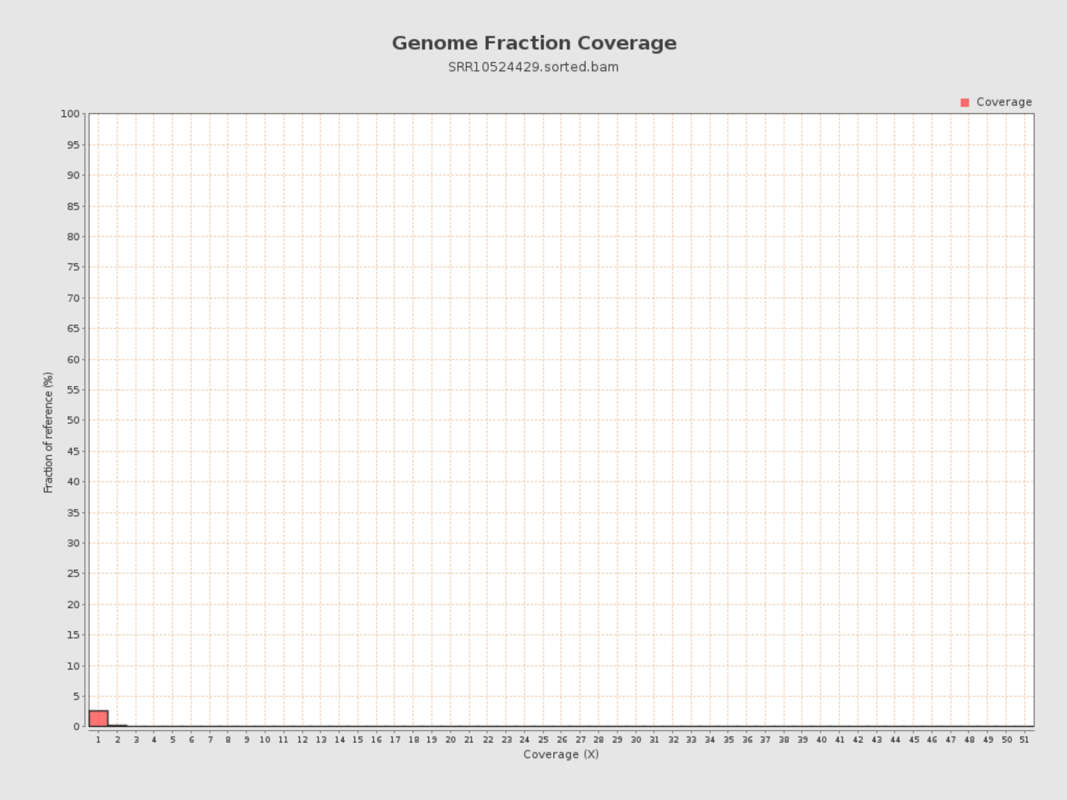
4. Results : Coverage Histogram



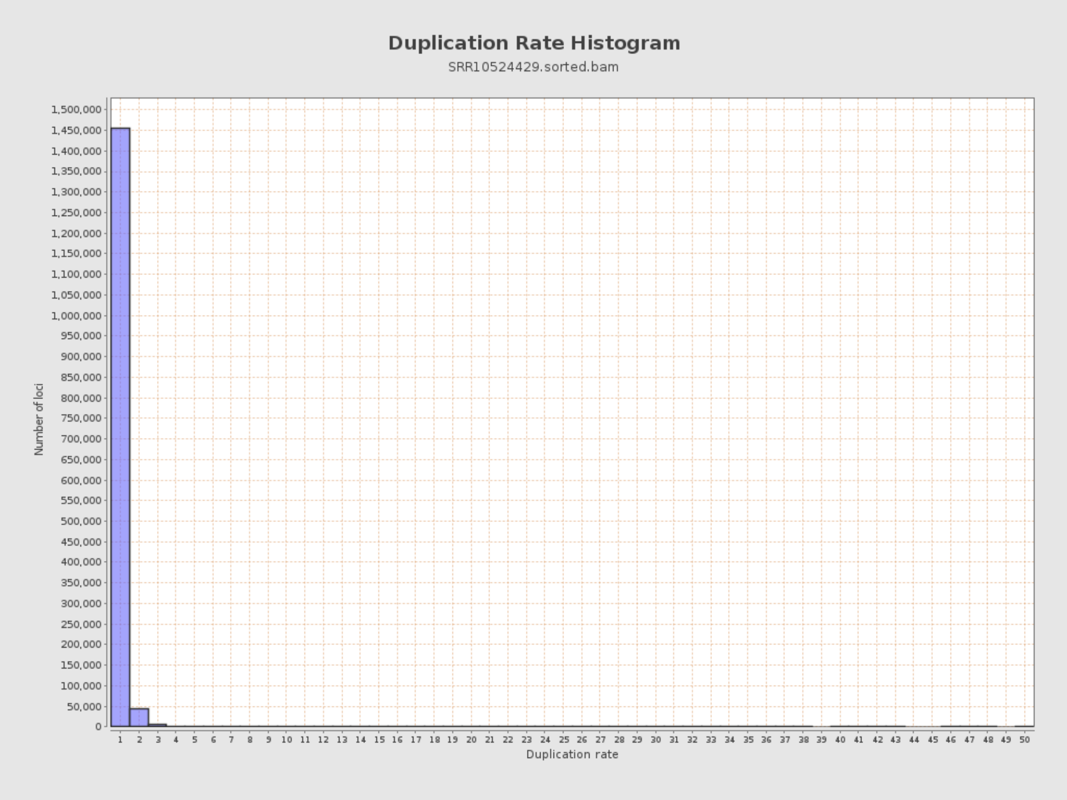
5. Results : Coverage Histogram (0-50X)



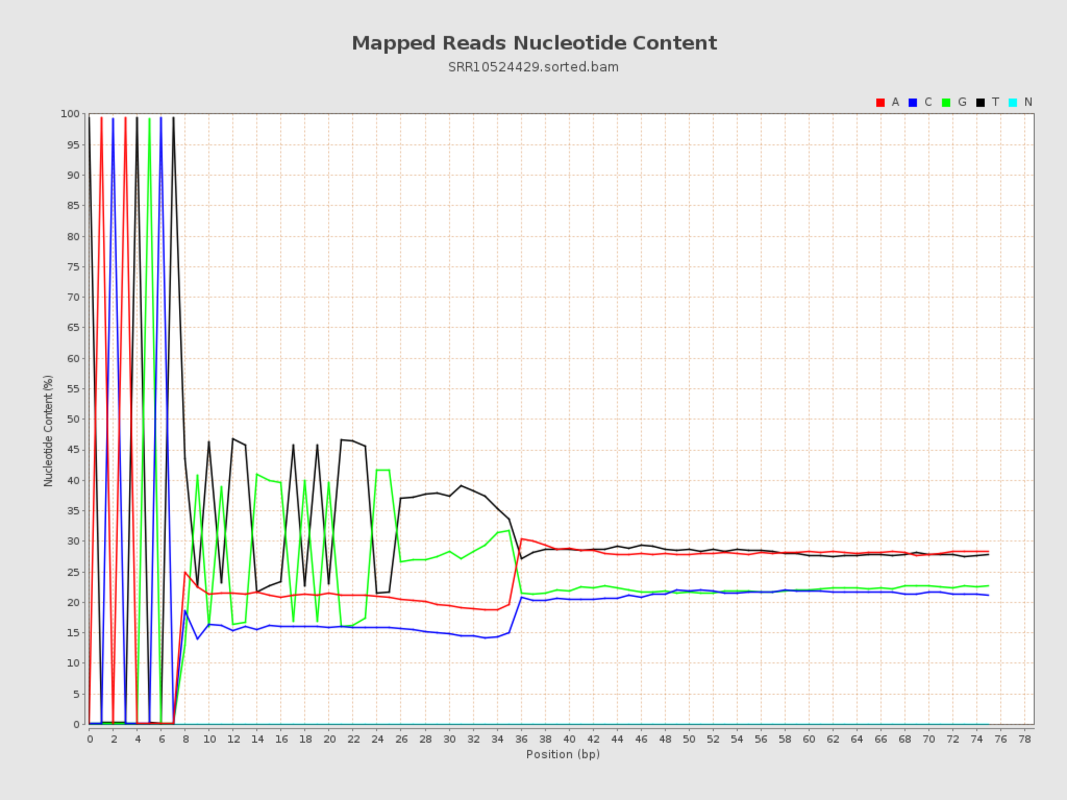
6. Results : Genome Fraction Coverage



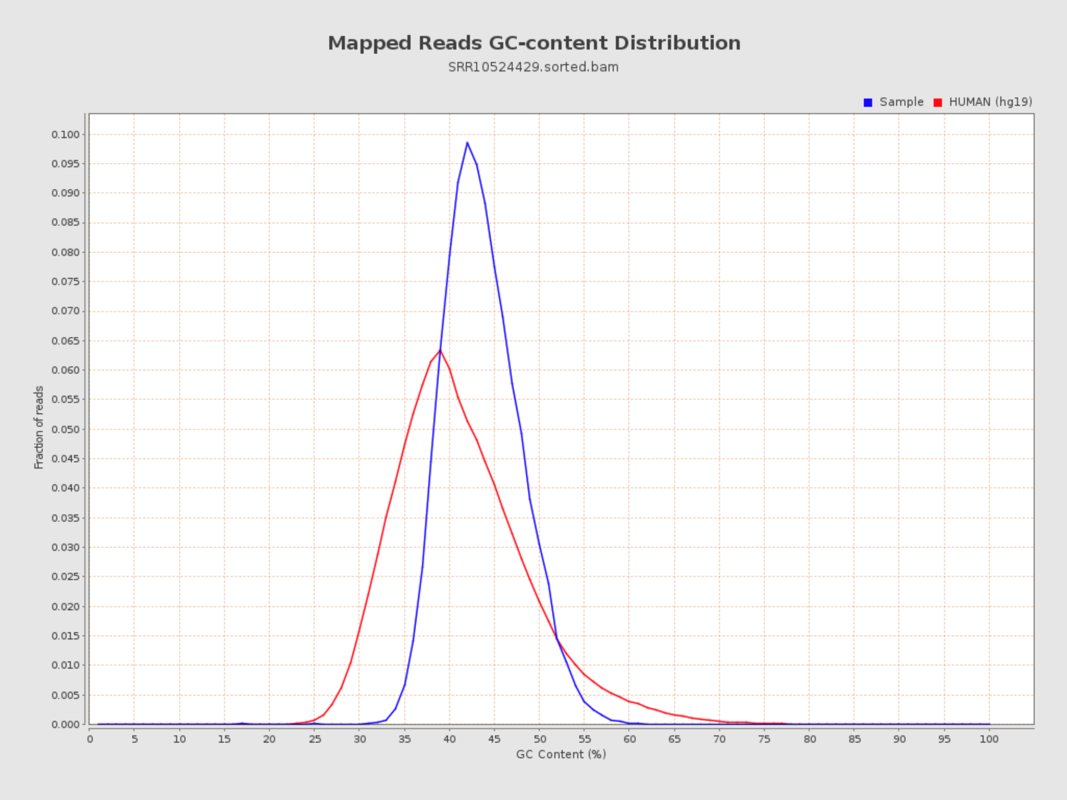
7. Results : Duplication Rate Histogram



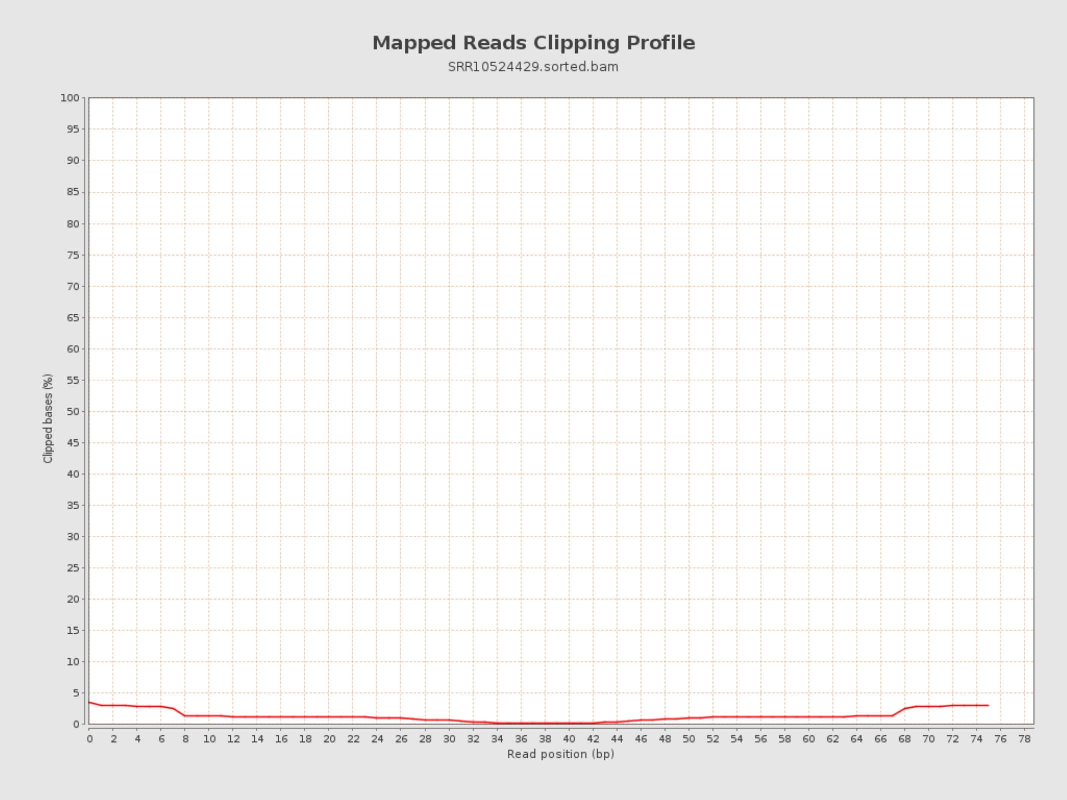
8. Results : Mapped Reads Nucleotide Content



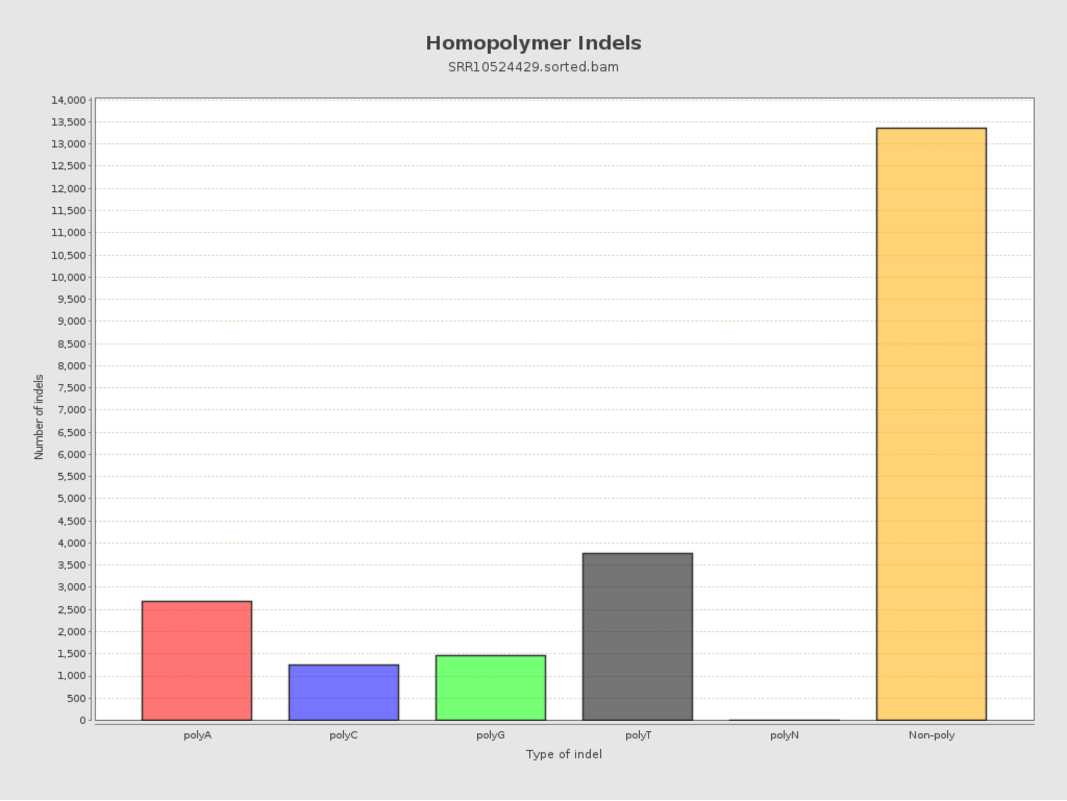
9. Results : Mapped Reads GC-content Distribution



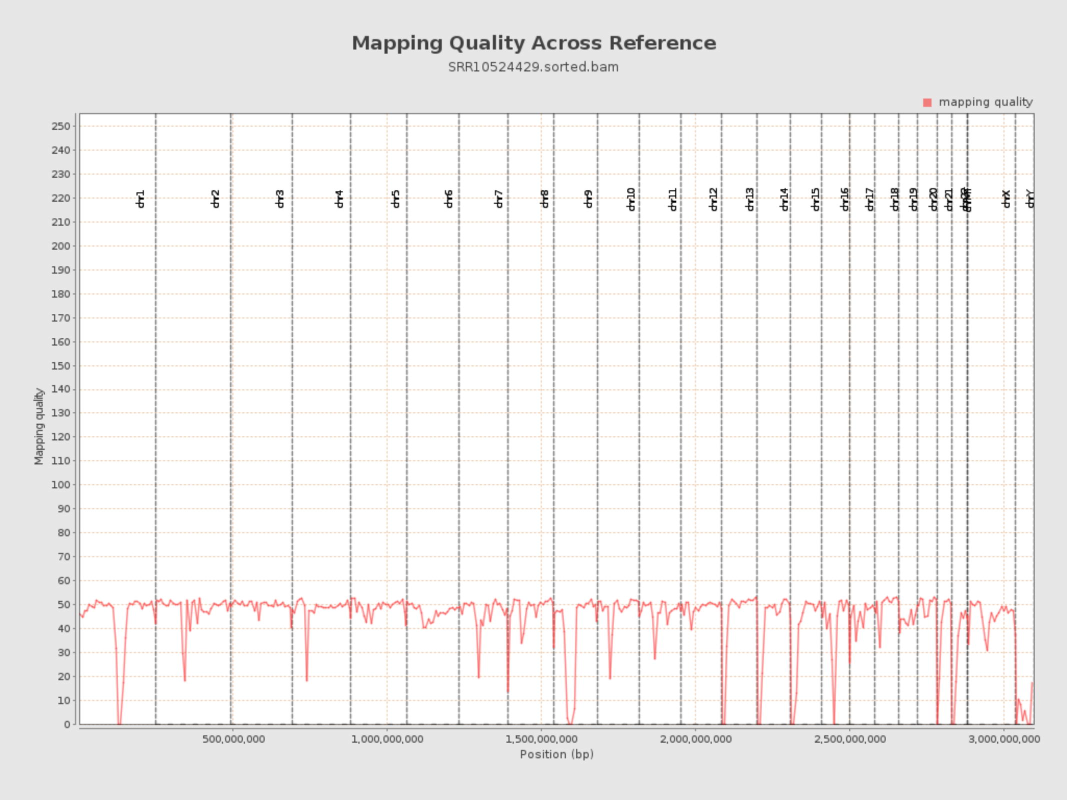
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram