Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:53:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524461.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_SRR10524461 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524461.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:53:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524461.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,071,505
Mapped reads	1,921,854 / 92.78%
Unmapped reads	149,651 / 7.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,202 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	95,293 / 4.6%
Duplication rate	3.82%
Clipped reads	1,923,753 / 92.87%

2.2. ACGT Content

Number/percentage of A's	27,877,871 / 24.81%
Number/percentage of C's	20,988,279 / 18.68%
Number/percentage of T's	35,867,372 / 31.92%
Number/percentage of G's	27,639,702 / 24.6%
Number/percentage of N's	2,315 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.316

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

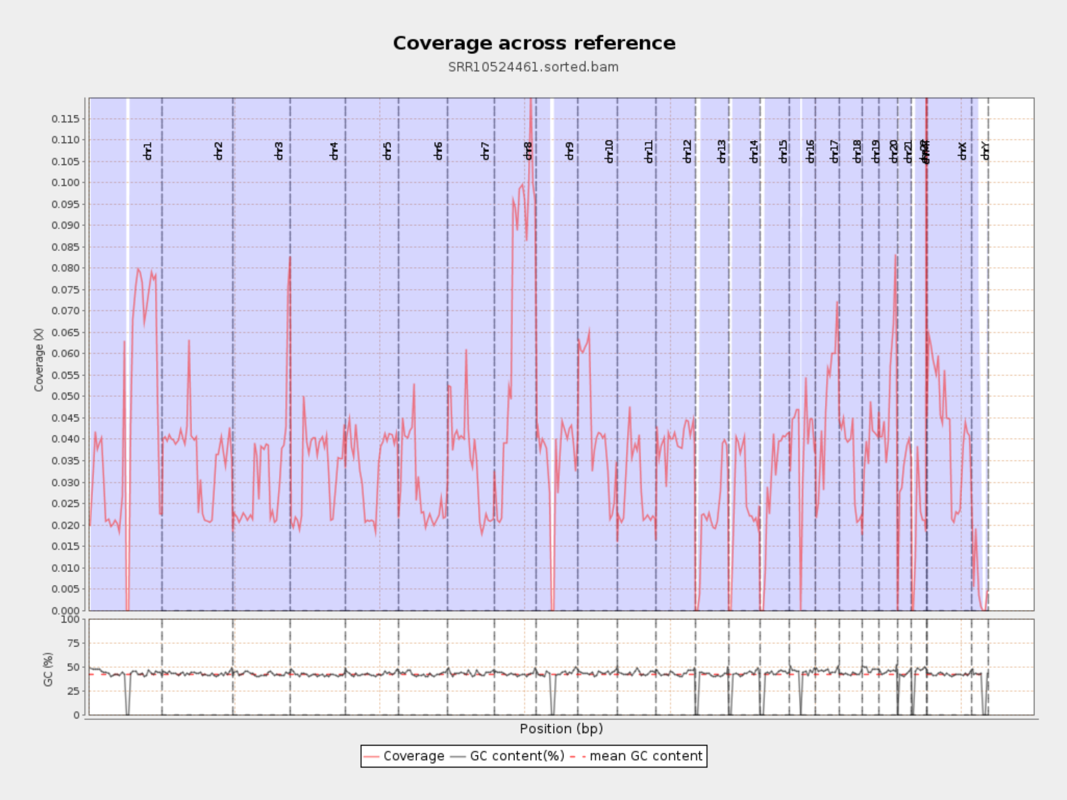
General error rate	0.47%
Mismatches	512,356
Insertions	5,992
Mapped reads with at least one insertion	0.31%
Deletions	19,703
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.49%

2.6. Chromosome stats

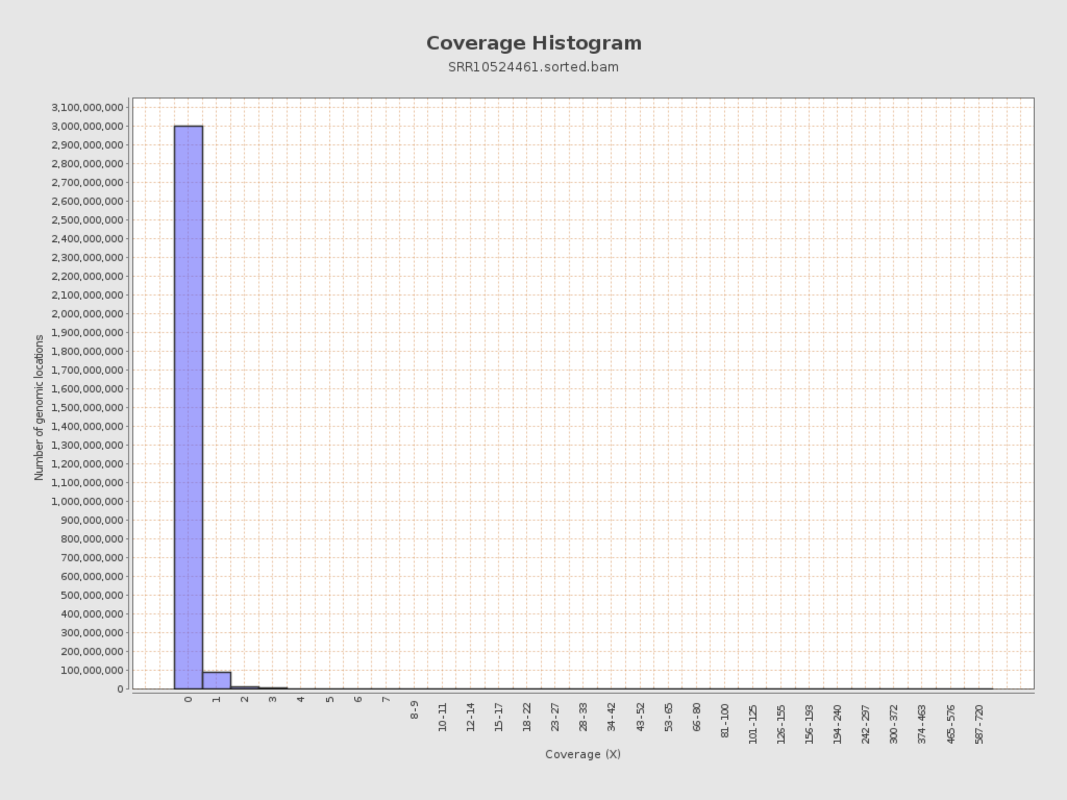
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10975104	0.044	0.5736
chr2	243199373	8801192	0.0362	0.3534
chr3	198022430	6097272	0.0308	0.2004
chr4	191154276	6284434	0.0329	0.2344
chr5	180915260	6155456	0.034	0.2099
chr6	171115067	4948160	0.0289	0.2469
chr7	159138663	5547884	0.0349	0.4146

chr8	146364022	10349422	0.0707	0.3495
chr9	141213431	4816602	0.0341	0.2725
chr10	135534747	5917074	0.0437	0.3236
chr11	135006516	3874367	0.0287	0.307
chr12	133851895	5354935	0.04	0.2278
chr13	115169878	2533437	0.022	0.1673
chr14	107349540	2667367	0.0248	0.1844
chr15	102531392	2965737	0.0289	0.2009
chr16	90354753	3542370	0.0392	0.2381
chr17	81195210	3875735	0.0477	0.2624
chr18	78077248	2733324	0.035	0.4977
chr19	59128983	2316339	0.0392	0.3893
chr20	63025520	3252000	0.0516	0.2625
chr21	48129895	1483313	0.0308	0.2188
chr22	51304566	935091	0.0182	0.1524
chrMT	16571	6773	0.4087	0.6947
chrX	155270560	6624829	0.0427	0.2643
chrY	59373566	351064	0.0059	0.1465

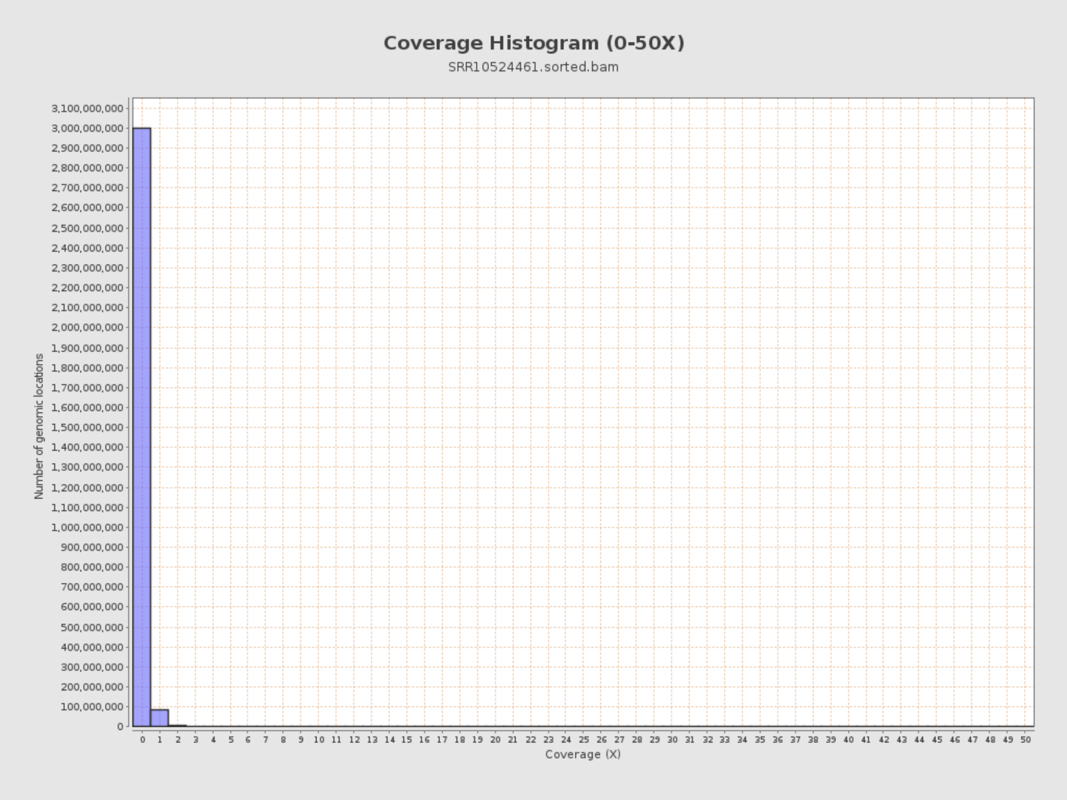
3. Results : Coverage across reference



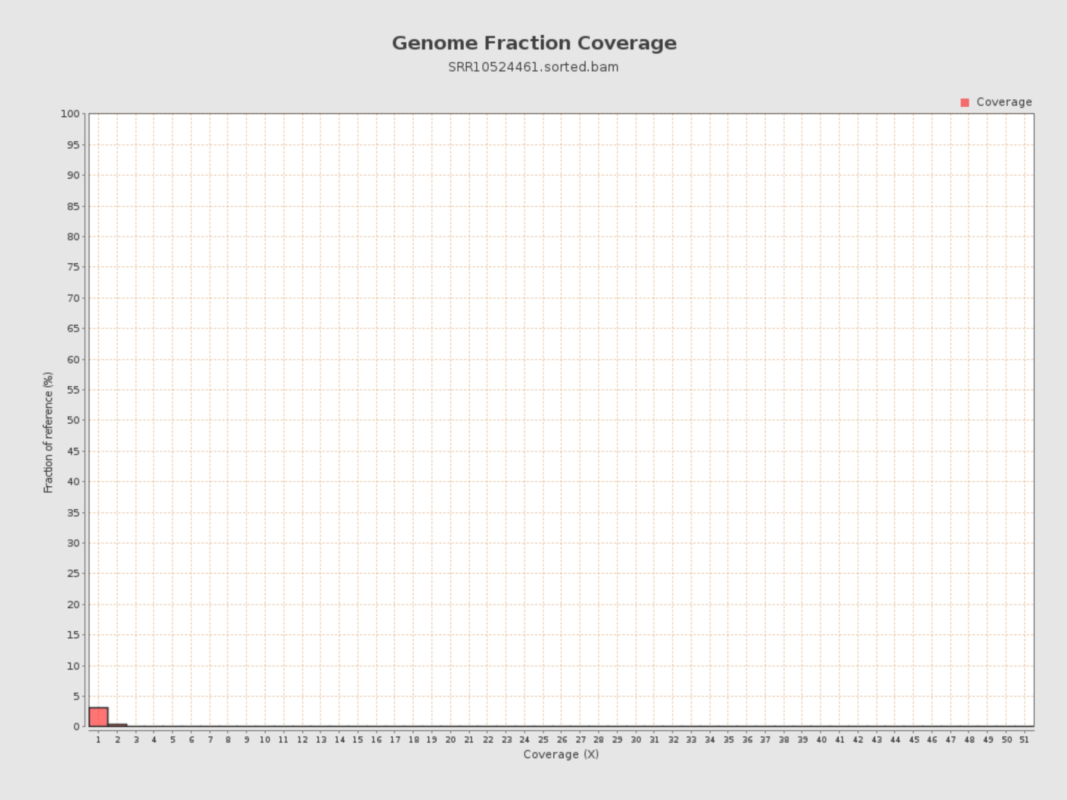
4. Results : Coverage Histogram



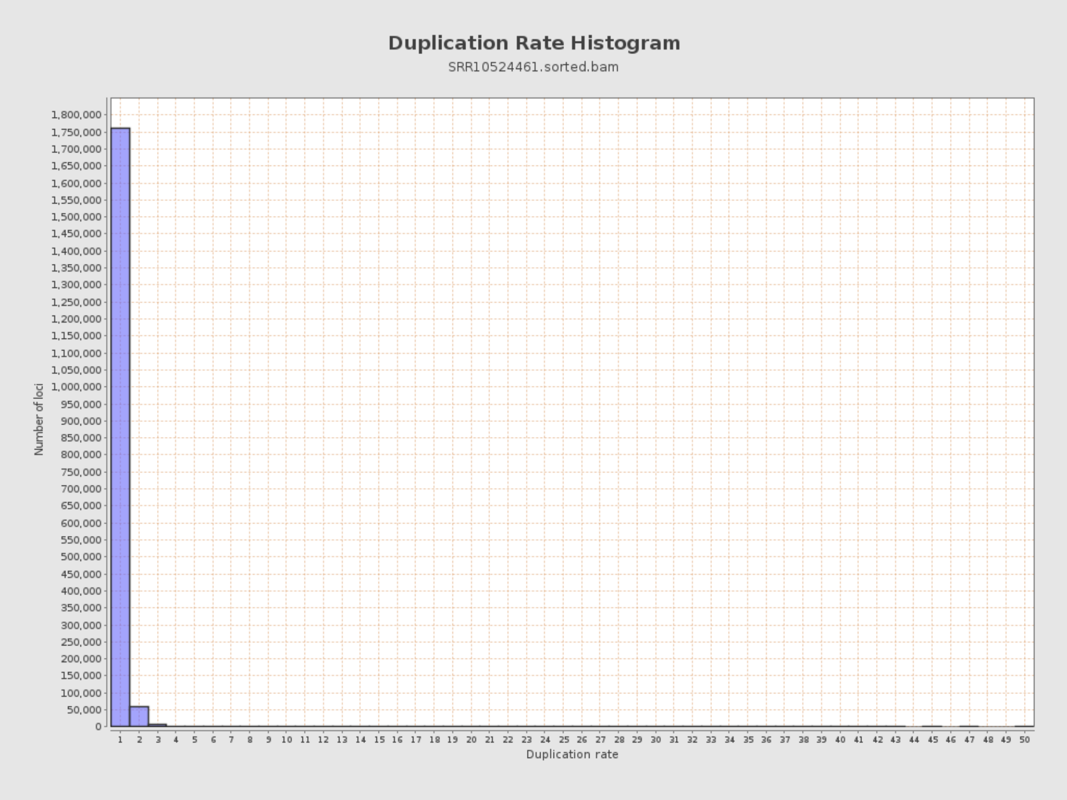
5. Results : Coverage Histogram (0-50X)



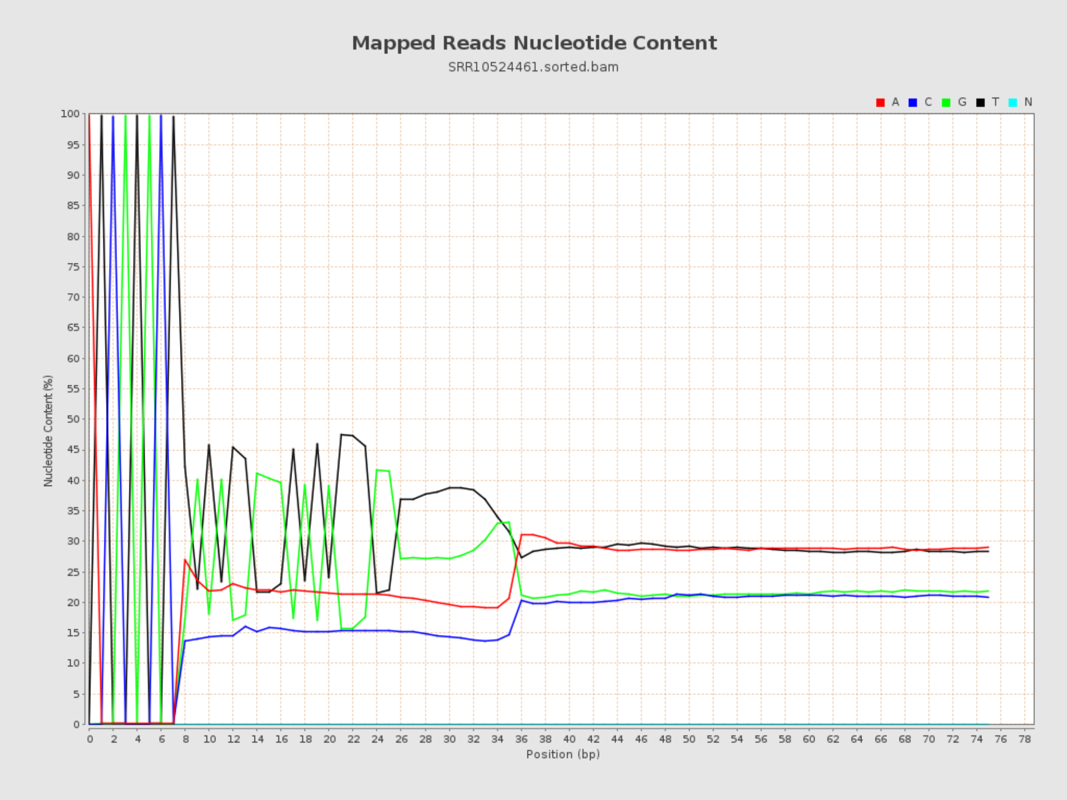
6. Results : Genome Fraction Coverage



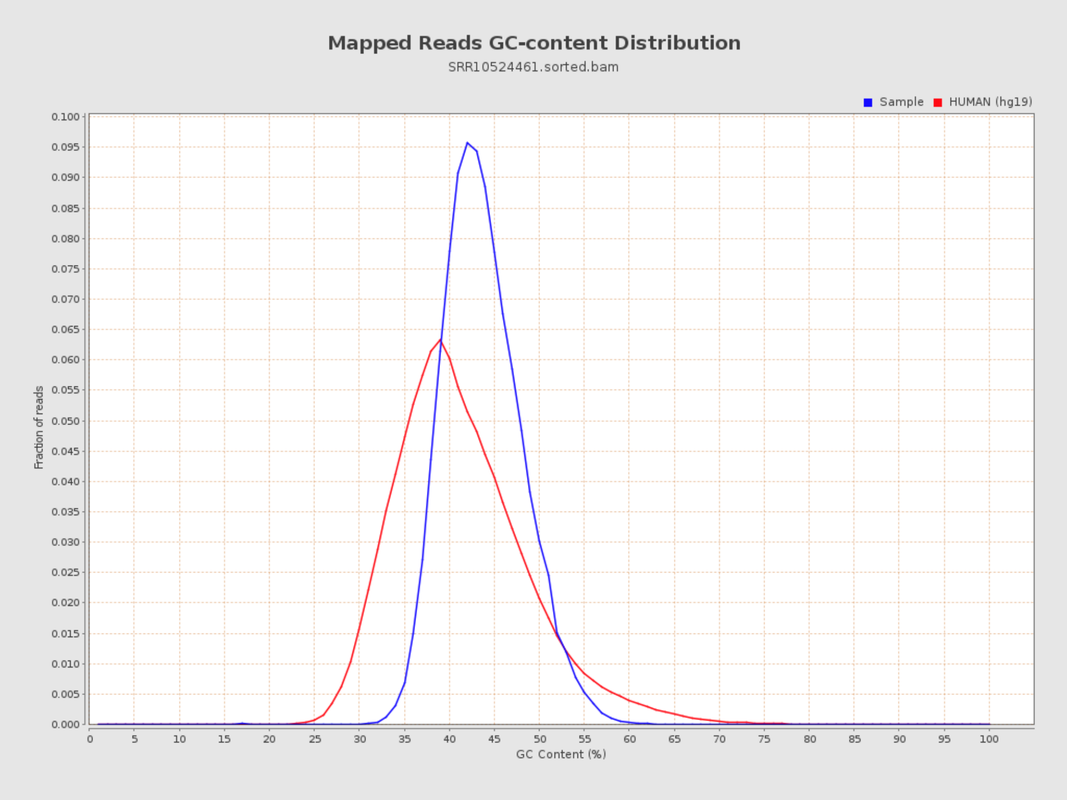
7. Results : Duplication Rate Histogram



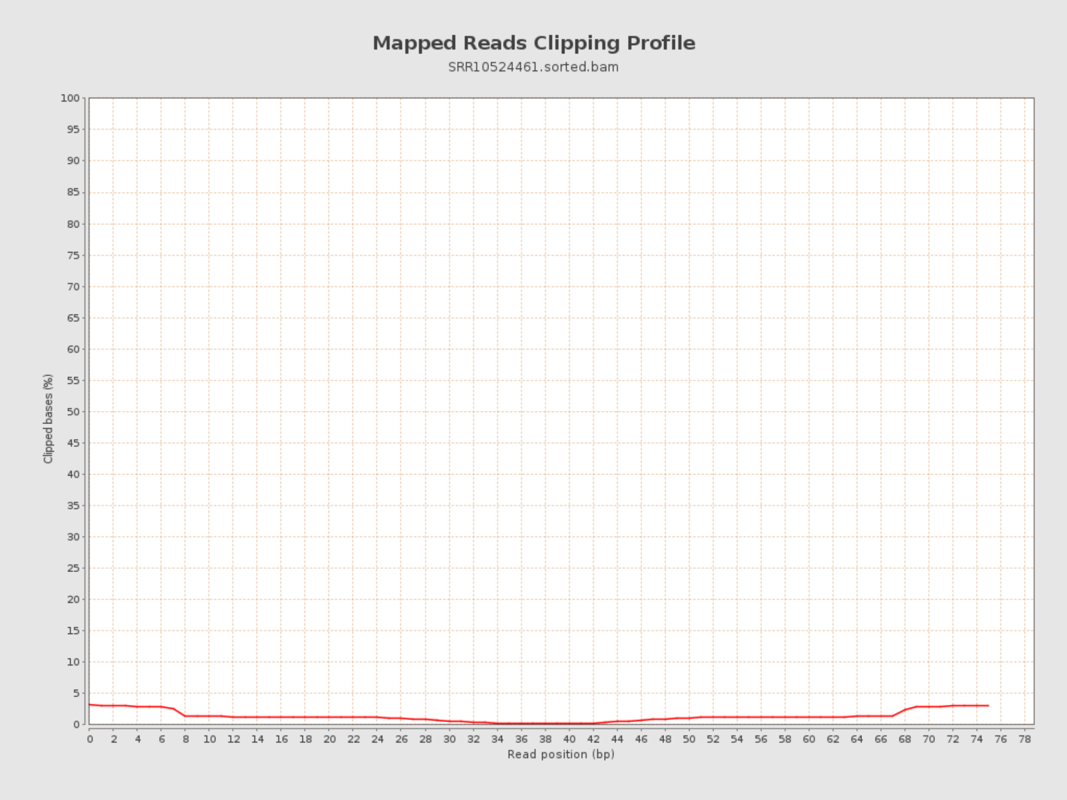
8. Results : Mapped Reads Nucleotide Content



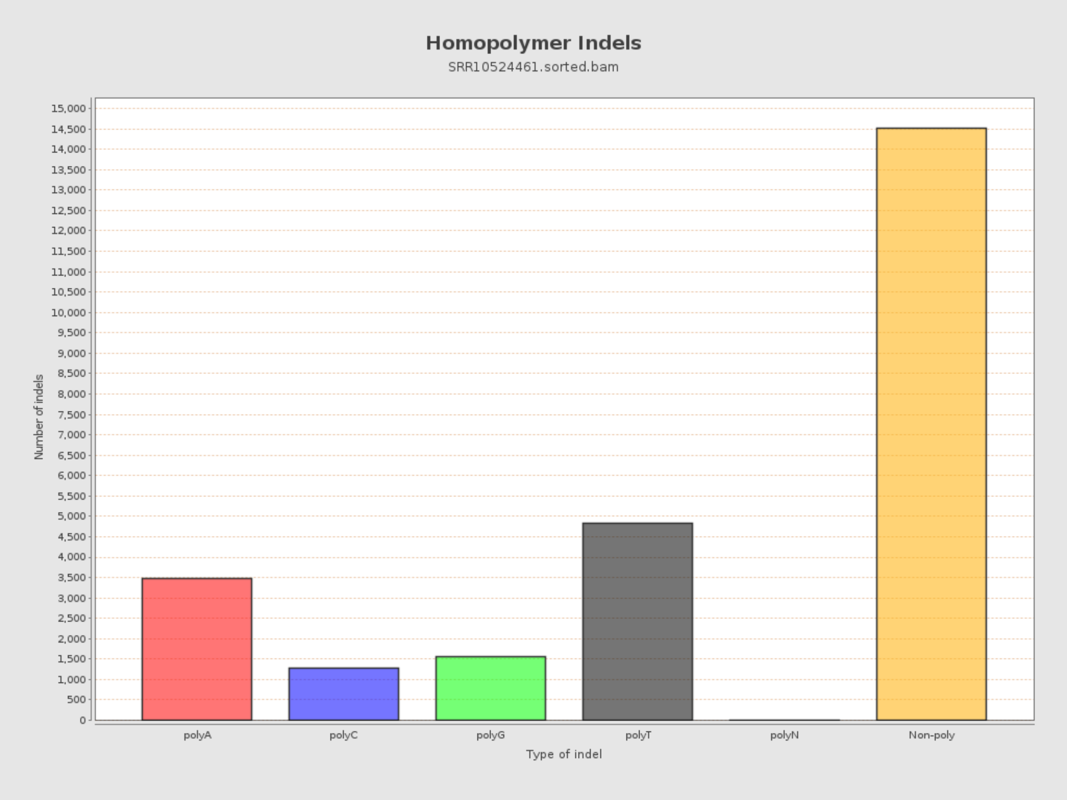
9. Results : Mapped Reads GC-content Distribution



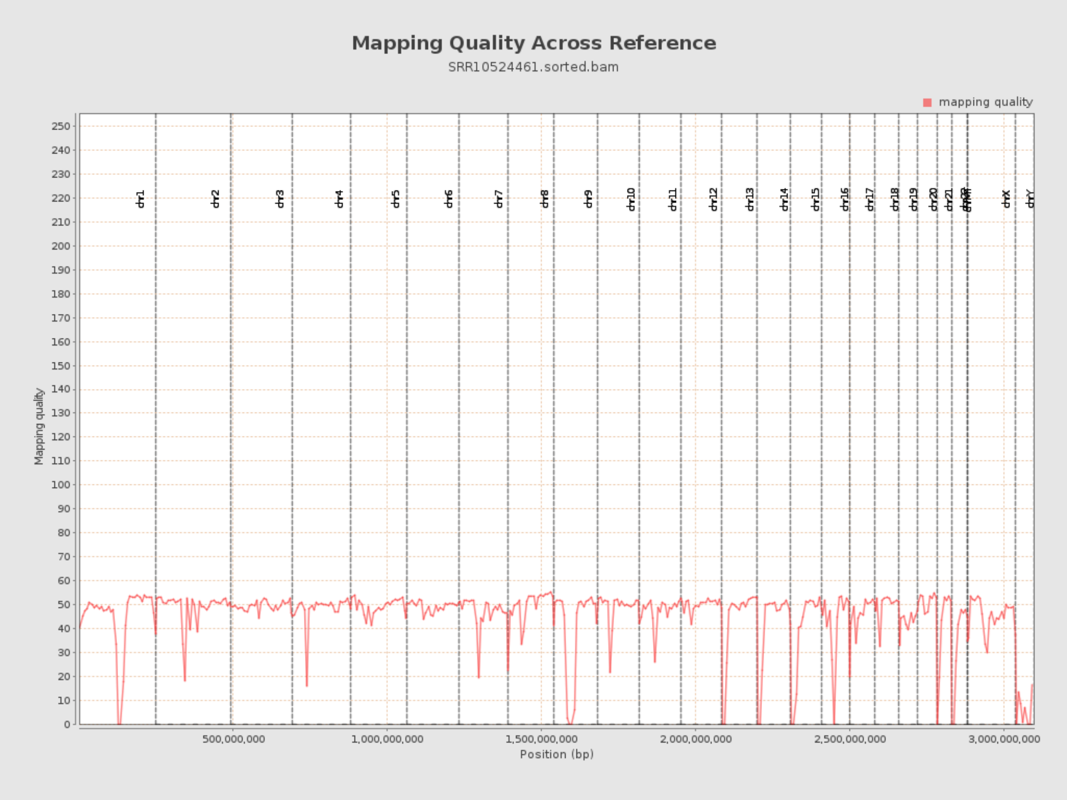
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram