Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:10:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524730.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_SRR10524730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524730.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:10:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	614,363
Mapped reads	460,926 / 75.03%
Unmapped reads	153,437 / 24.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,091 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	7,330 / 1.19%
Duplication rate	1.14%
Clipped reads	461,490 / 75.12%

2.2. ACGT Content

Number/percentage of A's	6,387,085 / 24.24%
Number/percentage of C's	4,890,610 / 18.56%
Number/percentage of T's	8,464,091 / 32.12%
Number/percentage of G's	6,608,488 / 25.08%
Number/percentage of N's	3,199 / 0.01%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0085

Standard Deviation	0.109

2.4. Mapping Quality

Mean Mapping Quality	43.36

2.5. Mismatches and indels

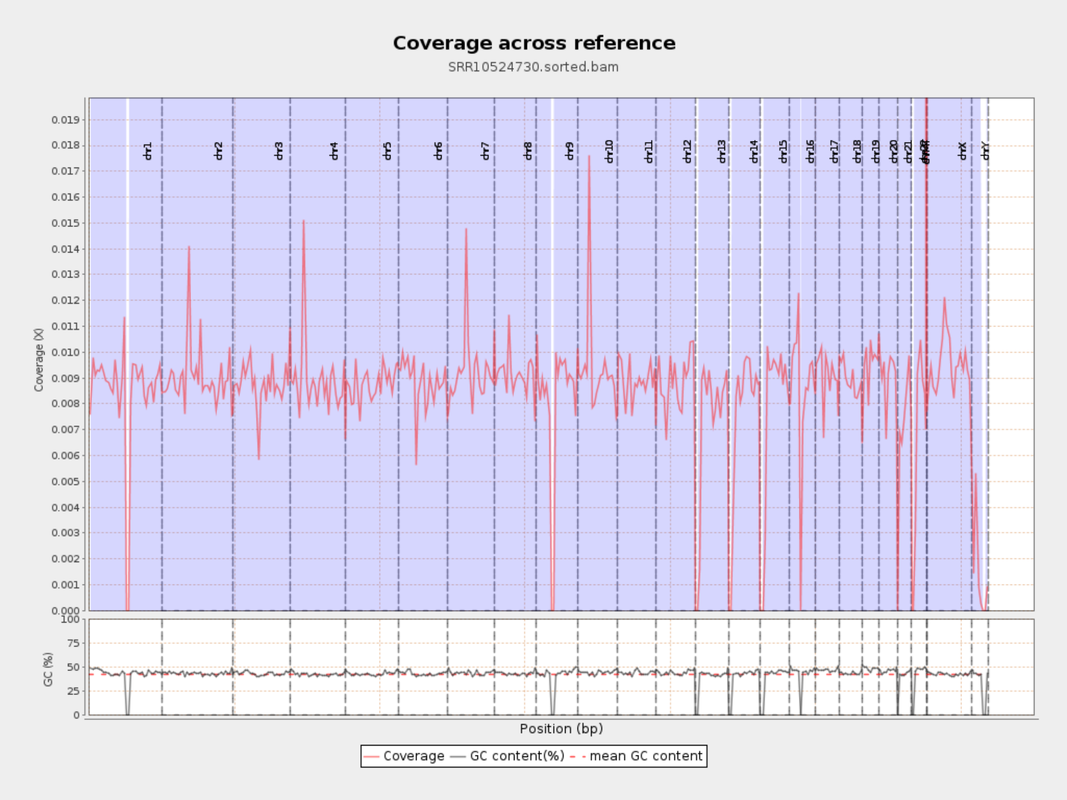
General error rate	0.54%
Mismatches	136,629
Insertions	2,227
Mapped reads with at least one insertion	0.48%
Deletions	5,395
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.27%

2.6. Chromosome stats

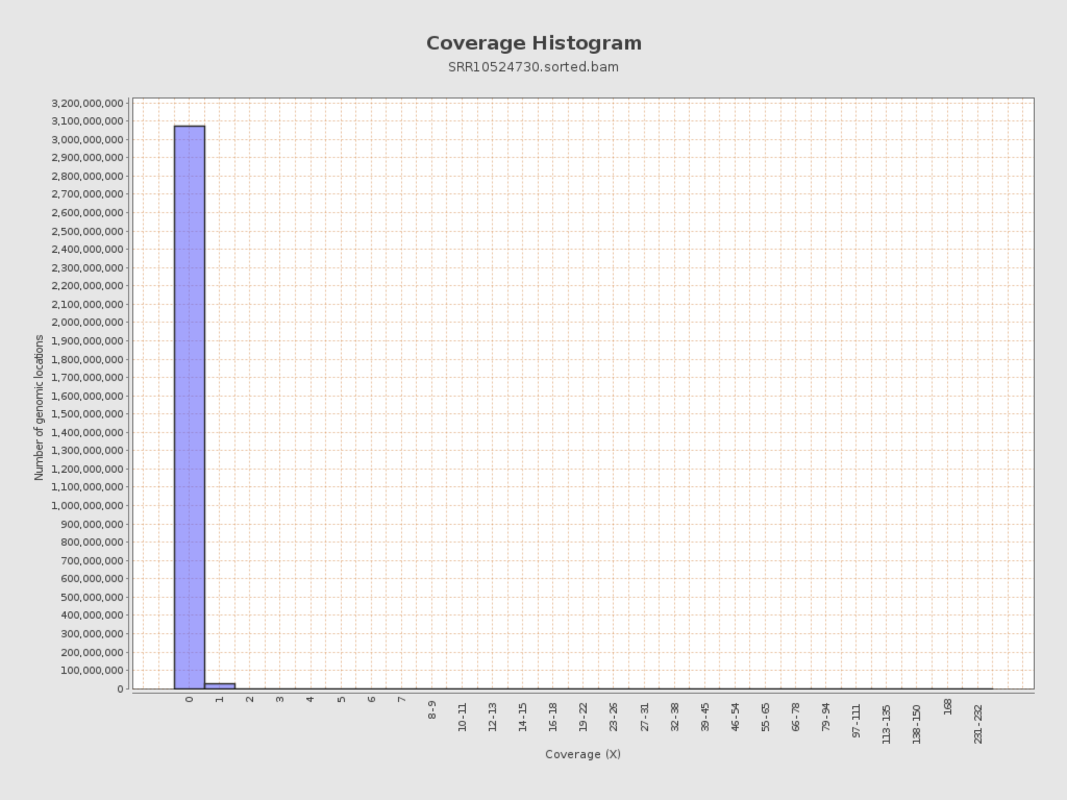
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2095233	0.0084	0.1324
chr2	243199373	2205931	0.0091	0.1421
chr3	198022430	1726239	0.0087	0.097
chr4	191154276	1700590	0.0089	0.1018
chr5	180915260	1584789	0.0088	0.0966
chr6	171115067	1509455	0.0088	0.0995
chr7	159138663	1472305	0.0093	0.1306

chr8	146364022	1335989	0.0091	0.1079
chr9	141213431	1119885	0.0079	0.1018
chr10	135534747	1269873	0.0094	0.1204
chr11	135006516	1198384	0.0089	0.1048
chr12	133851895	1183845	0.0088	0.0976
chr13	115169878	817808	0.0071	0.0869
chr14	107349540	793106	0.0074	0.0907
chr15	102531392	774744	0.0076	0.0901
chr16	90354753	778250	0.0086	0.099
chr17	81195210	734764	0.009	0.0997
chr18	78077248	699827	0.009	0.1327
chr19	59128983	562589	0.0095	0.1172
chr20	63025520	567135	0.009	0.0992
chr21	48129895	341419	0.0071	0.09
chr22	51304566	324104	0.0063	0.082
chrMT	16571	8605	0.5193	0.8133
chrX	155270560	1469494	0.0095	0.1039
chrY	59373566	87774	0.0015	0.0533

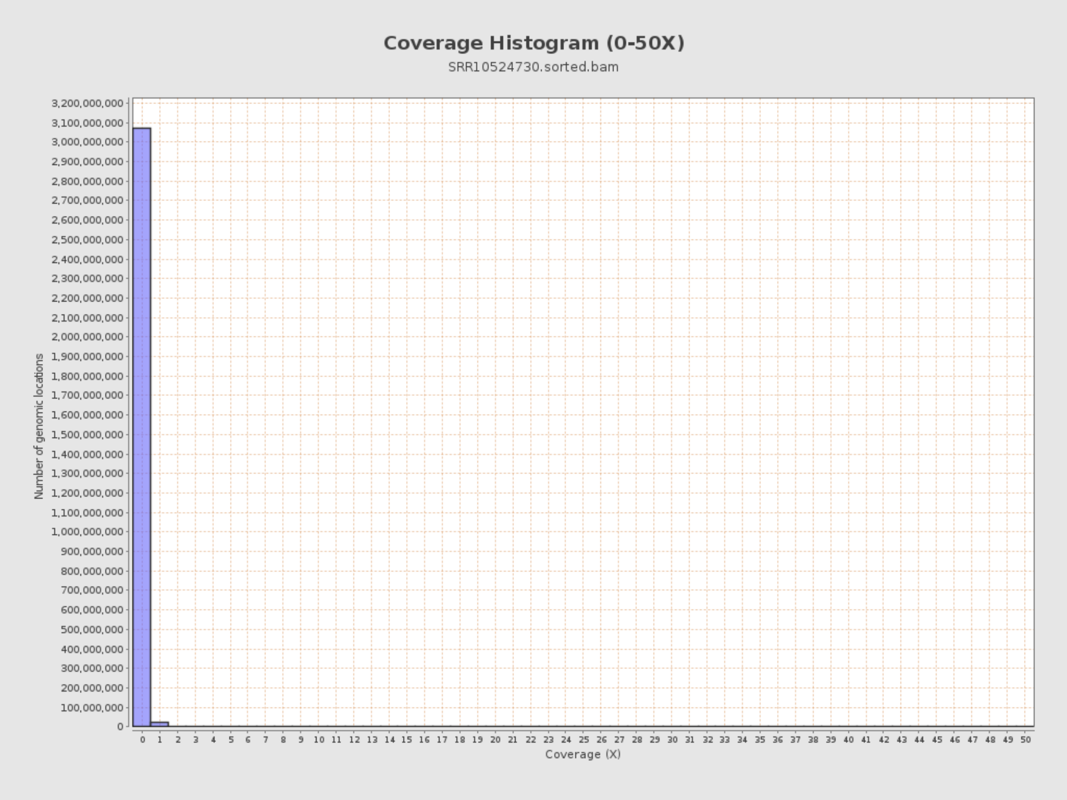
3. Results : Coverage across reference



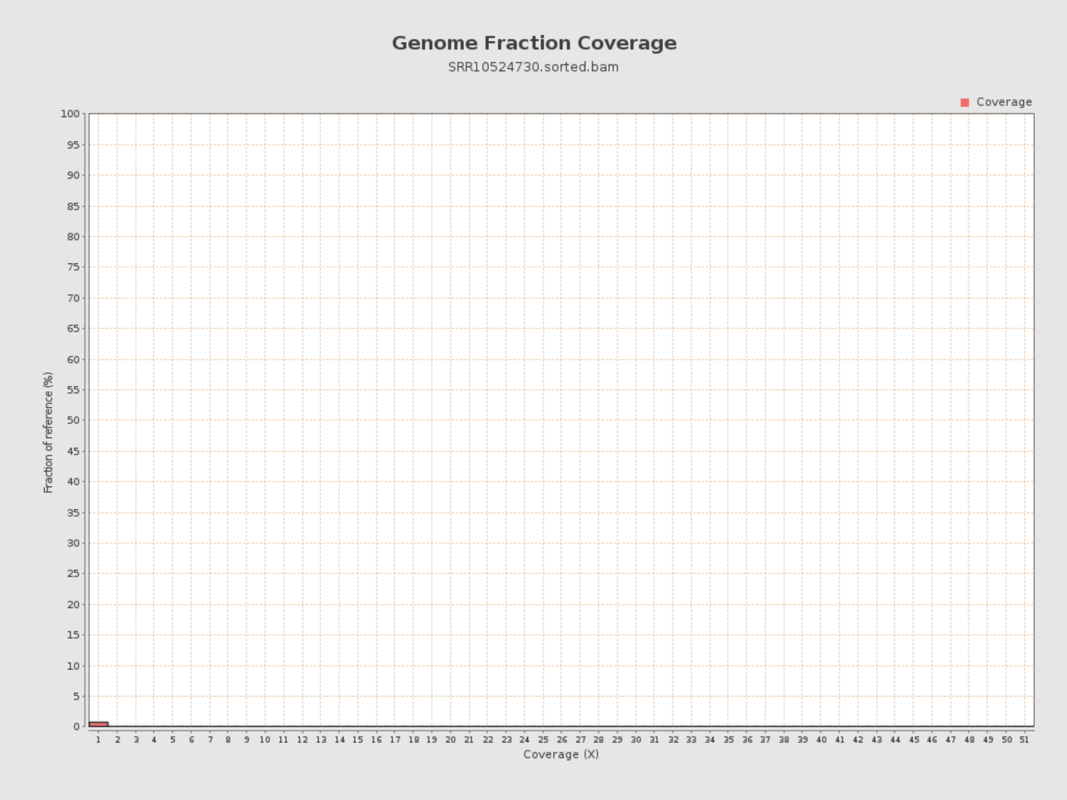
4. Results : Coverage Histogram



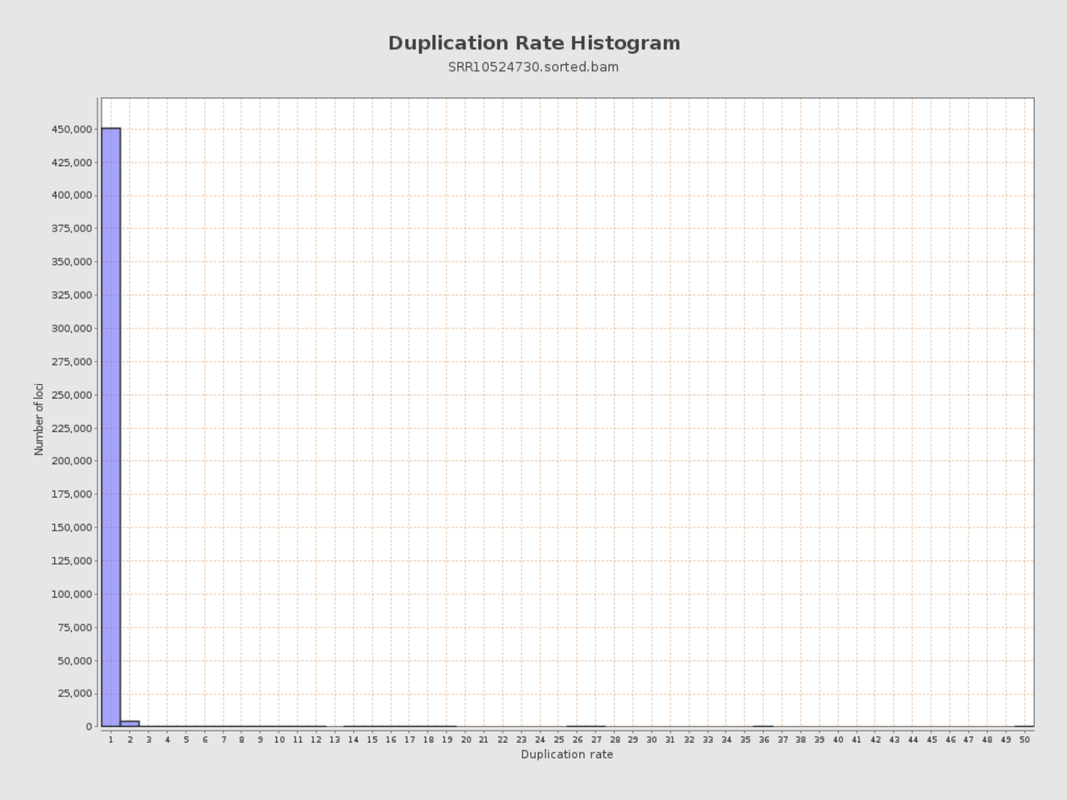
5. Results : Coverage Histogram (0-50X)



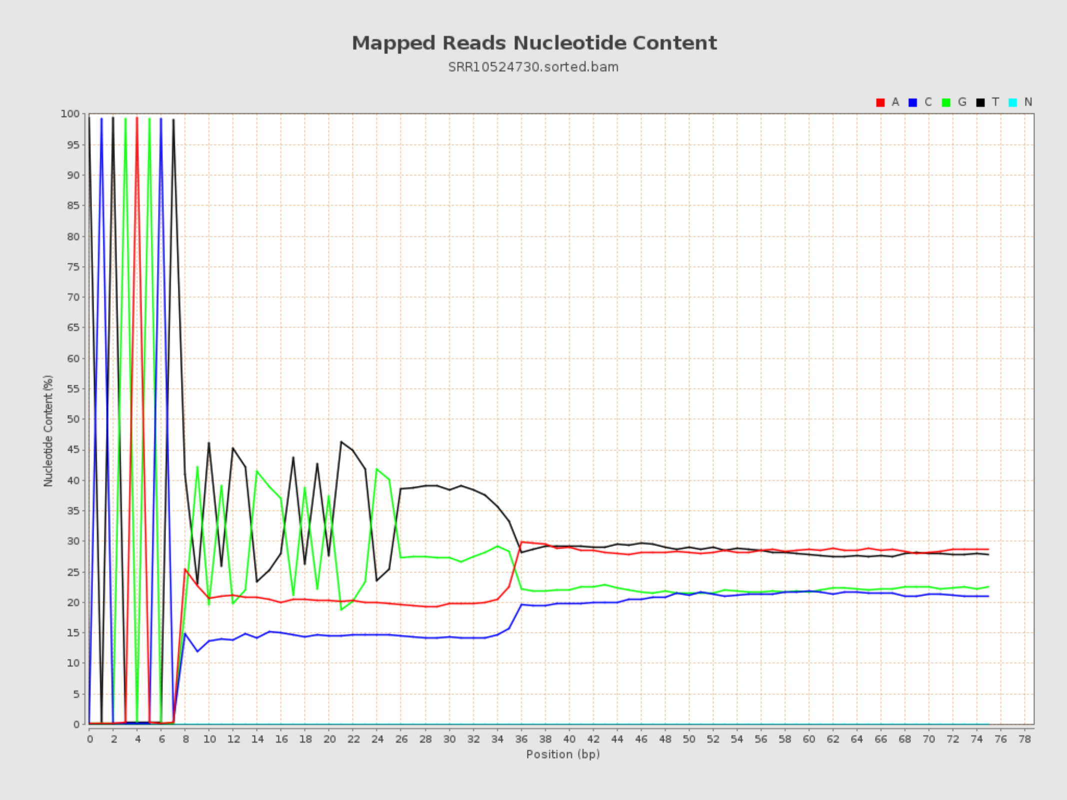
6. Results : Genome Fraction Coverage



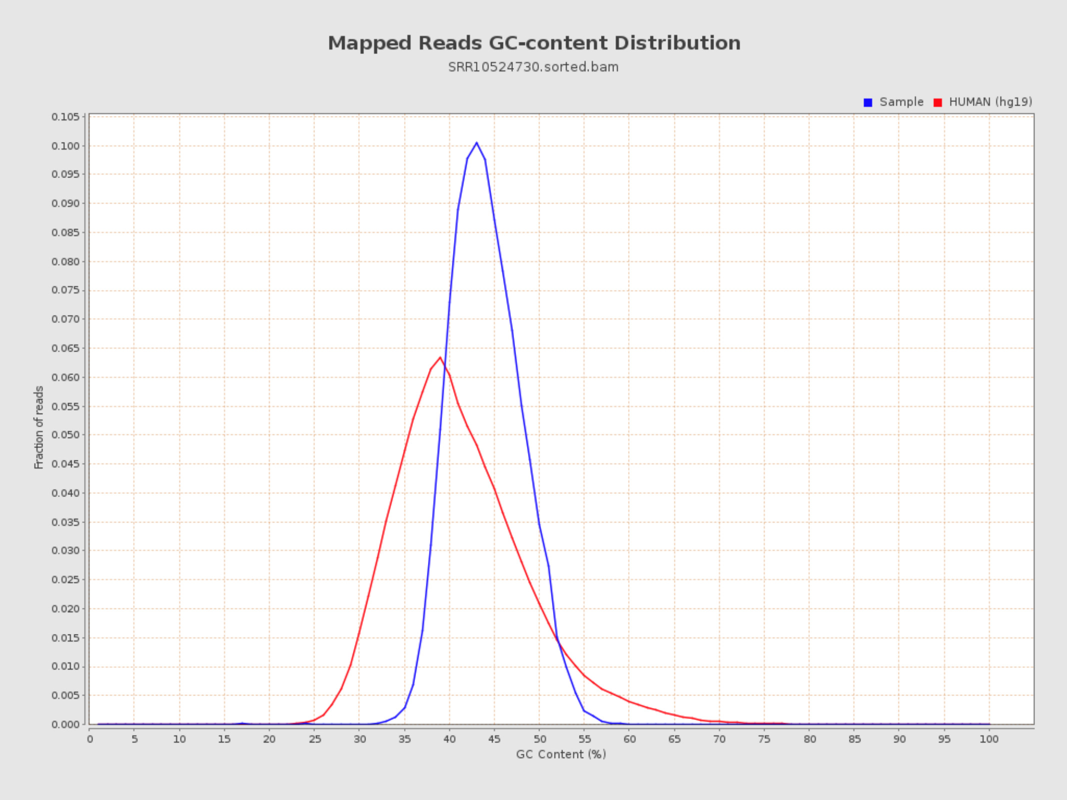
7. Results : Duplication Rate Histogram



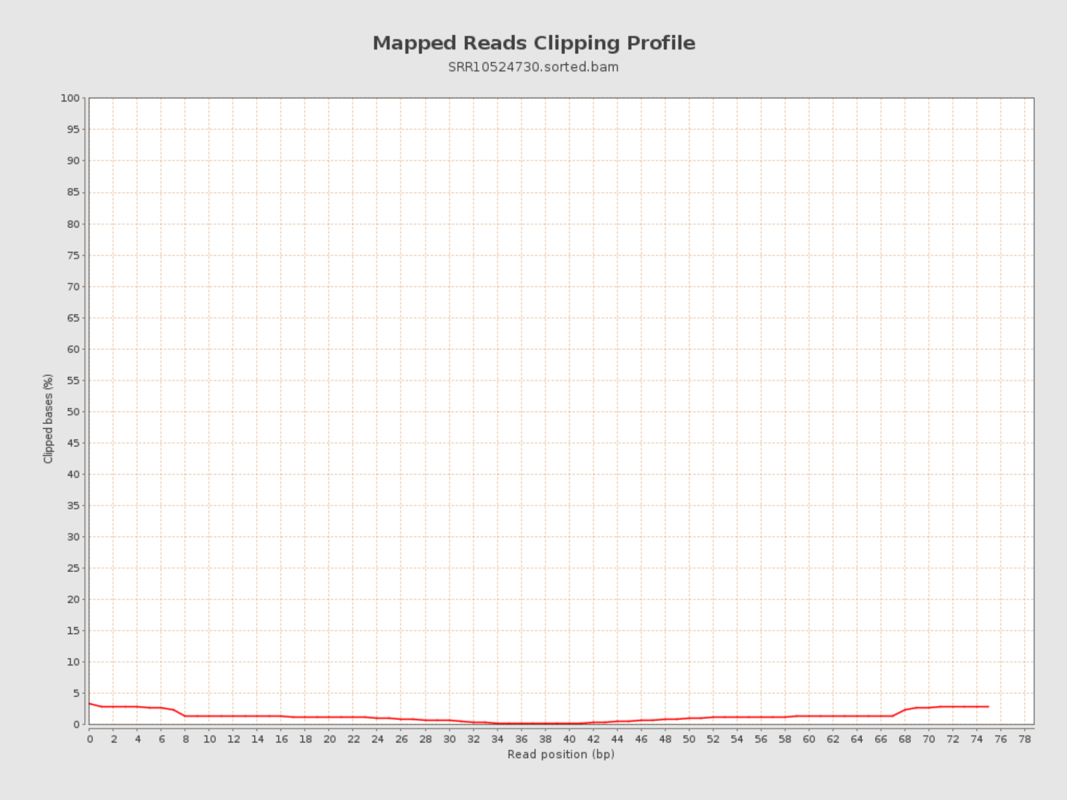
8. Results : Mapped Reads Nucleotide Content



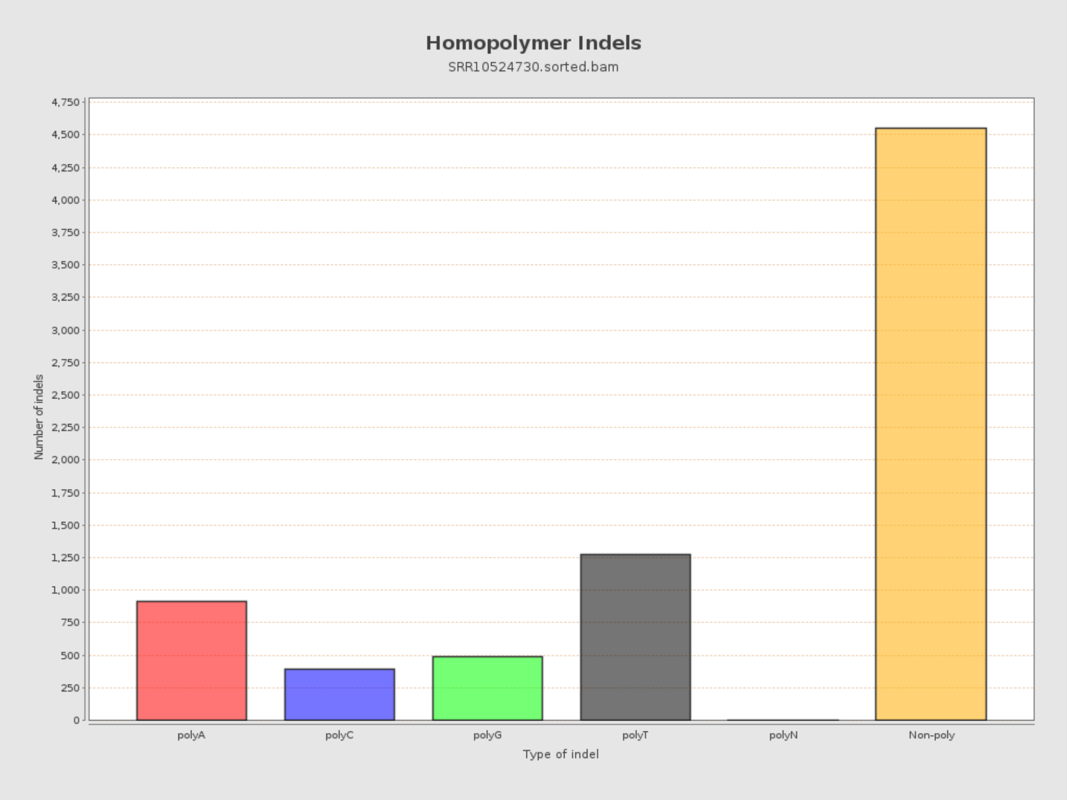
9. Results : Mapped Reads GC-content Distribution



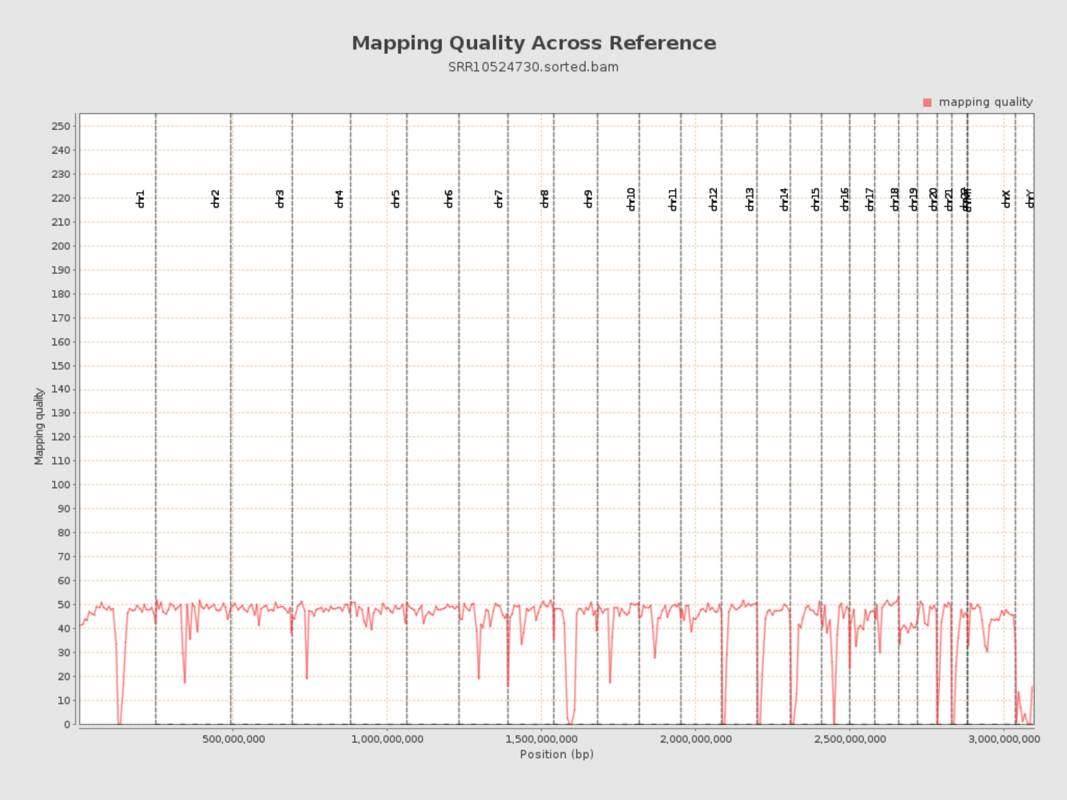
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram