Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:56:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524984.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_SRR10524984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:56:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	724,959
Mapped reads	668,944 / 92.27%
Unmapped reads	56,015 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,511 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	14,829 / 2.05%
Duplication rate	1.68%
Clipped reads	668,720 / 92.24%

2.2. ACGT Content

Number/percentage of A's	10,008,273 / 25.74%
Number/percentage of C's	7,487,829 / 19.26%
Number/percentage of T's	12,184,396 / 31.34%
Number/percentage of G's	9,202,287 / 23.67%
Number/percentage of N's	452 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0126

Standard Deviation	0.1405

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

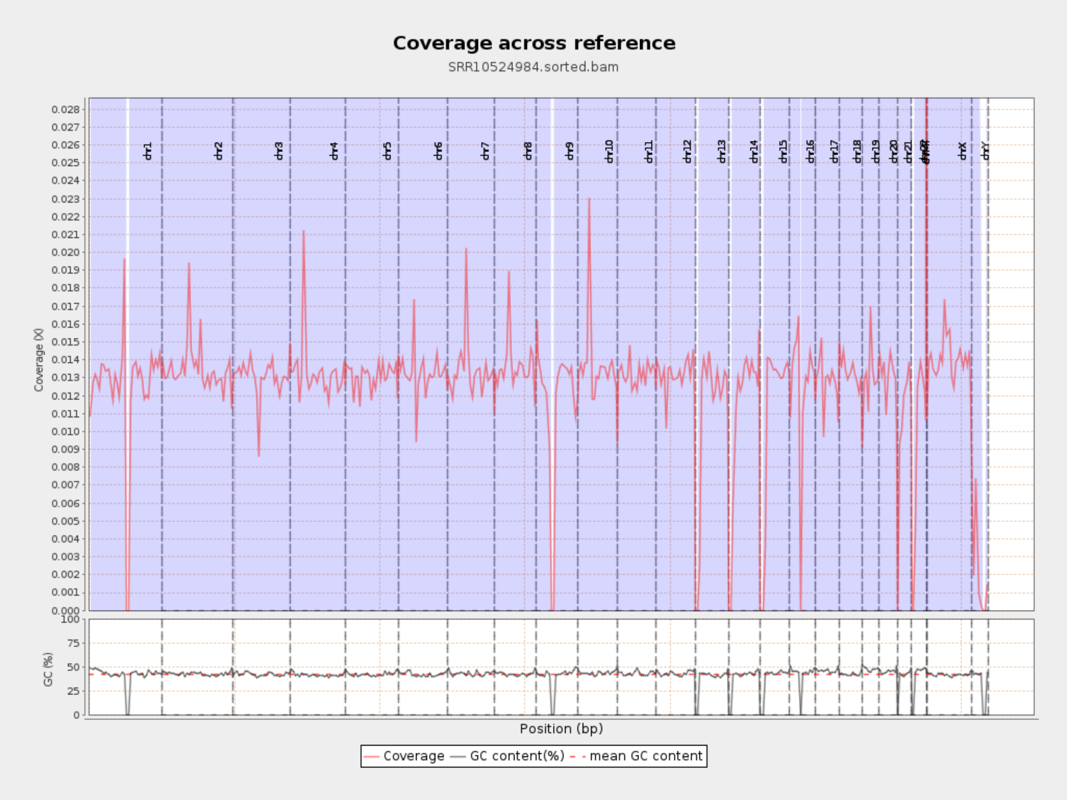
General error rate	0.5%
Mismatches	187,233
Insertions	2,817
Mapped reads with at least one insertion	0.42%
Deletions	7,255
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.25%

2.6. Chromosome stats

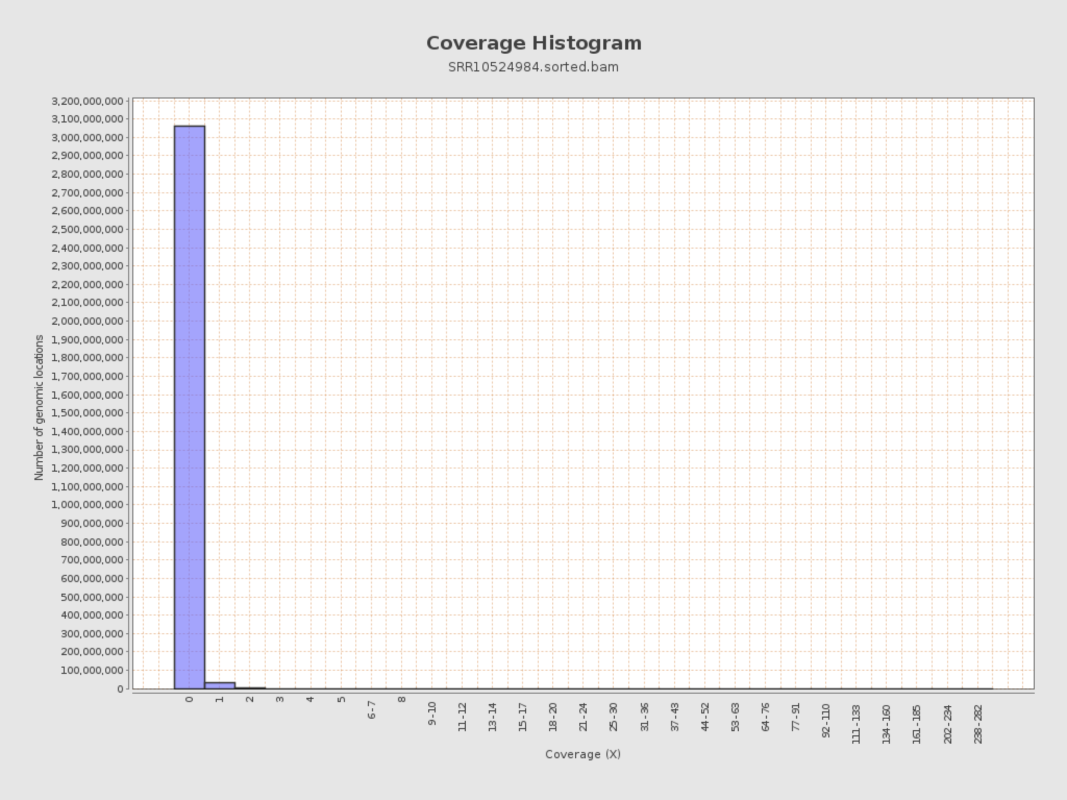
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3090640	0.0124	0.2148
chr2	243199373	3289792	0.0135	0.149
chr3	198022430	2578939	0.013	0.1192
chr4	191154276	2542369	0.0133	0.1273
chr5	180915260	2367868	0.0131	0.1191
chr6	171115067	2272535	0.0133	0.1332
chr7	159138663	2142243	0.0135	0.1666

chr8	146364022	2000727	0.0137	0.1535
chr9	141213431	1600818	0.0113	0.1254
chr10	135534747	1868844	0.0138	0.1458
chr11	135006516	1776577	0.0132	0.1353
chr12	133851895	1766905	0.0132	0.1201
chr13	115169878	1246777	0.0108	0.1088
chr14	107349540	1169997	0.0109	0.1106
chr15	102531392	1113606	0.0109	0.1114
chr16	90354753	1128126	0.0125	0.121
chr17	81195210	1032986	0.0127	0.1228
chr18	78077248	1043756	0.0134	0.1789
chr19	59128983	777568	0.0132	0.1567
chr20	63025520	825243	0.0131	0.1207
chr21	48129895	508625	0.0106	0.1117
chr22	51304566	455090	0.0089	0.098
chrMT	16571	1826	0.1102	0.3145
chrX	155270560	2175102	0.014	0.1292
chrY	59373566	118676	0.002	0.0712

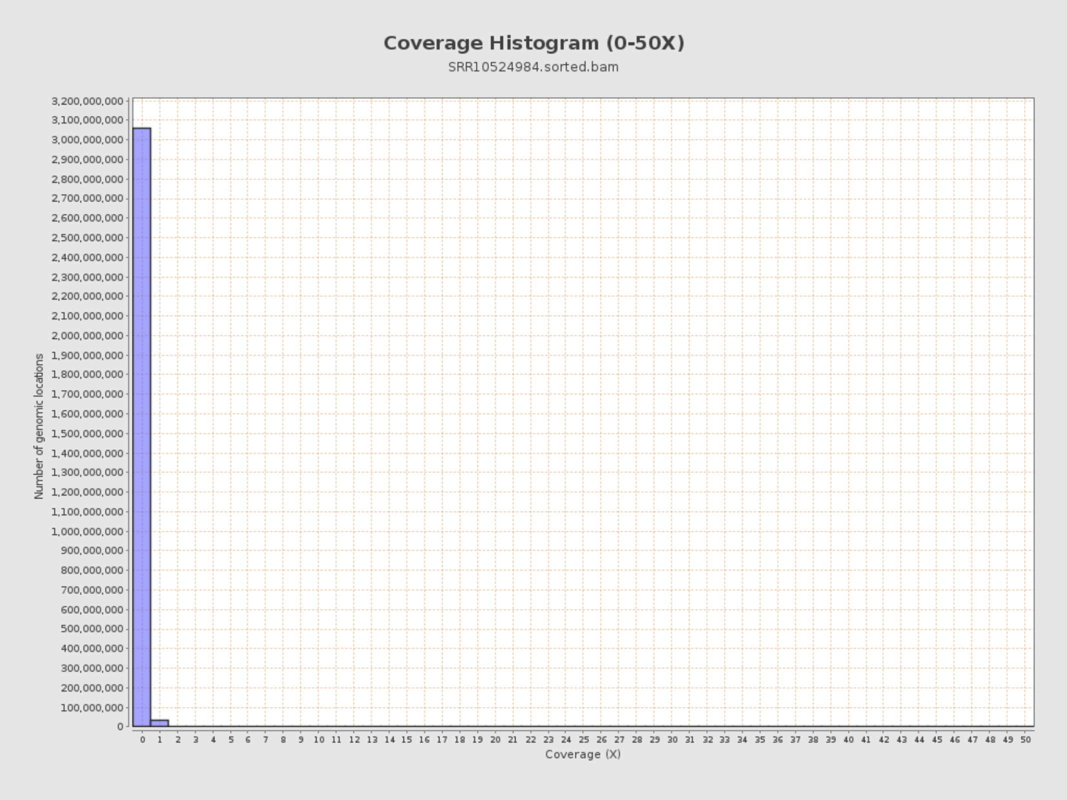
3. Results : Coverage across reference



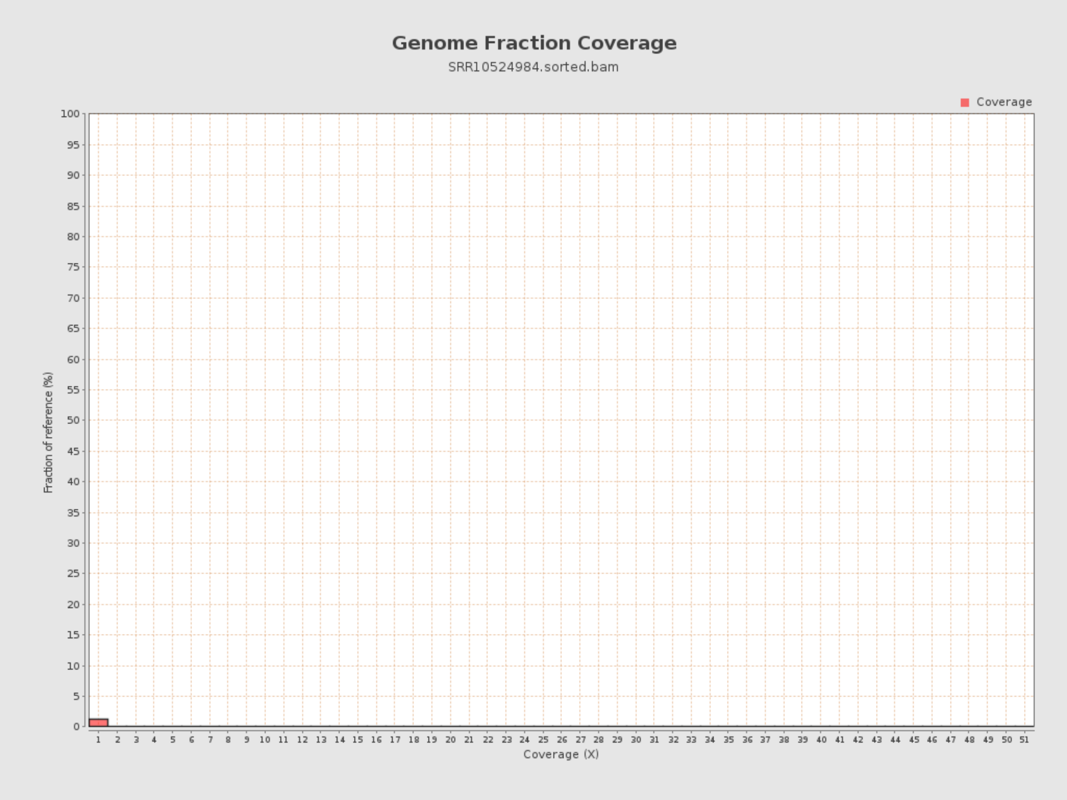
4. Results : Coverage Histogram



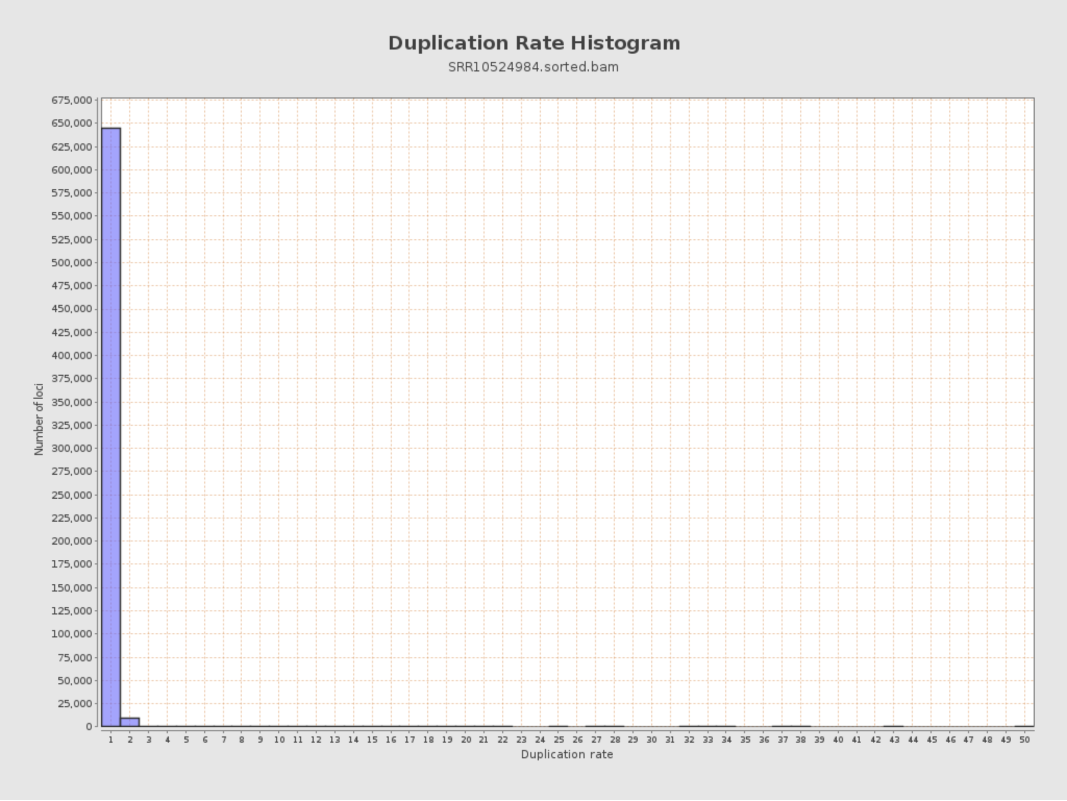
5. Results : Coverage Histogram (0-50X)



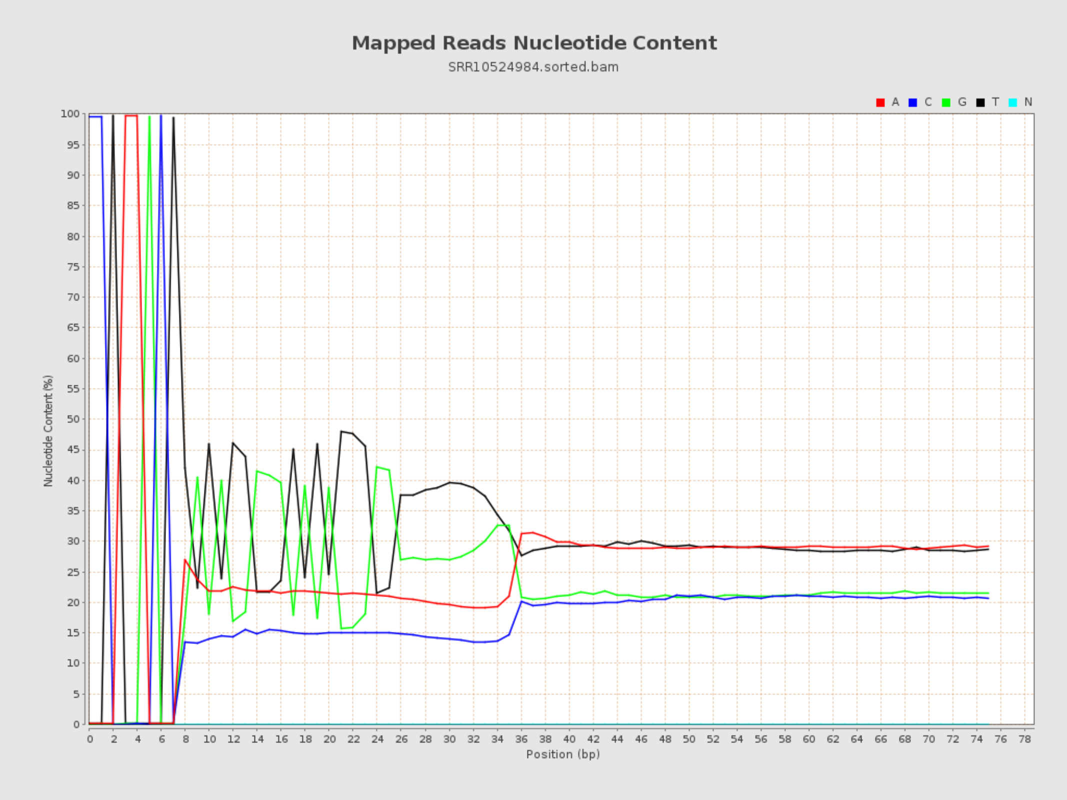
6. Results : Genome Fraction Coverage



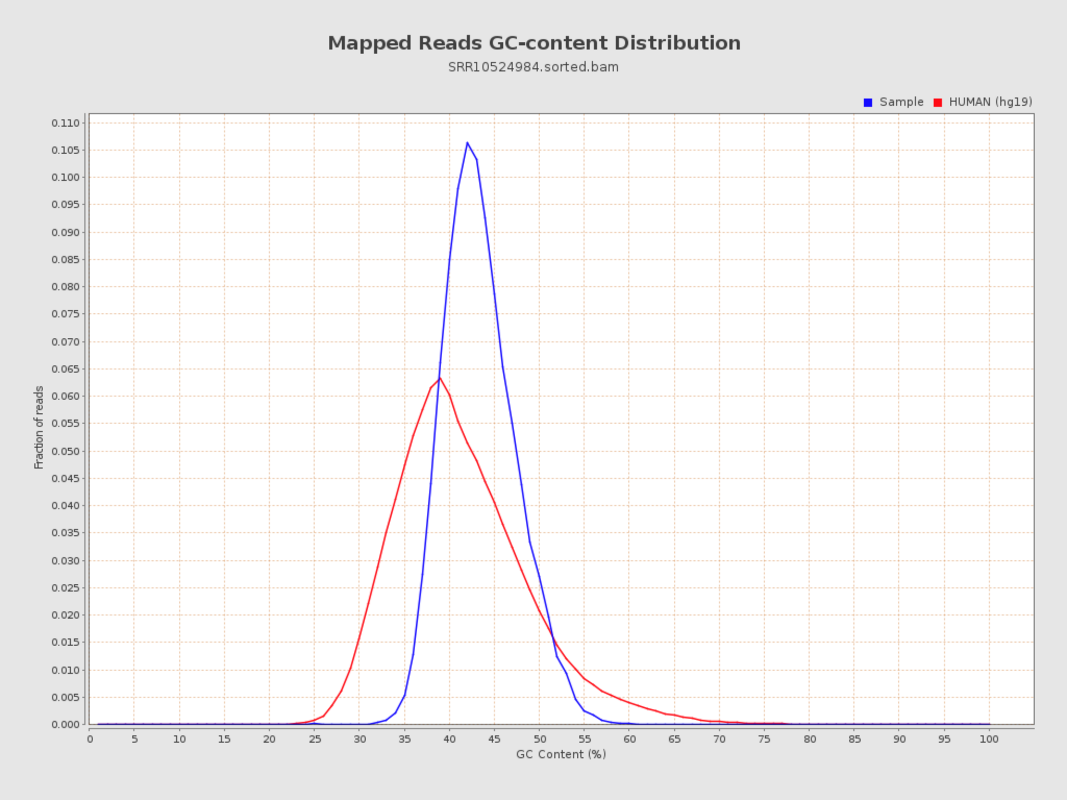
7. Results : Duplication Rate Histogram



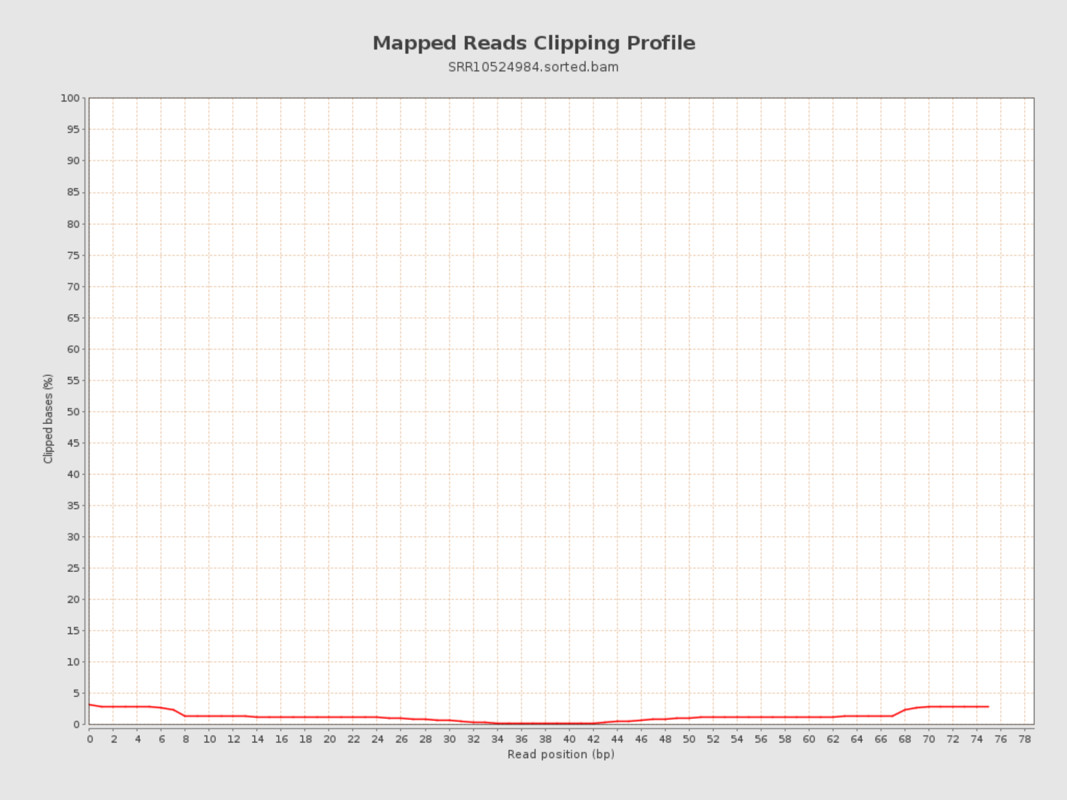
8. Results : Mapped Reads Nucleotide Content



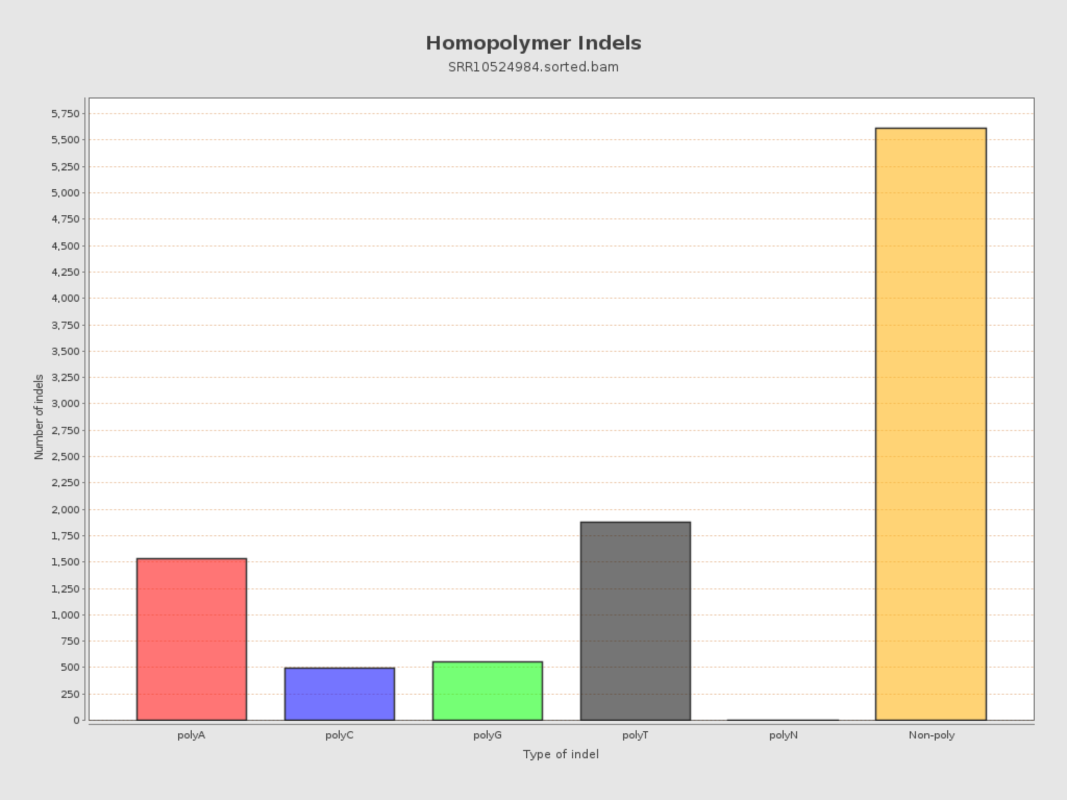
9. Results : Mapped Reads GC-content Distribution



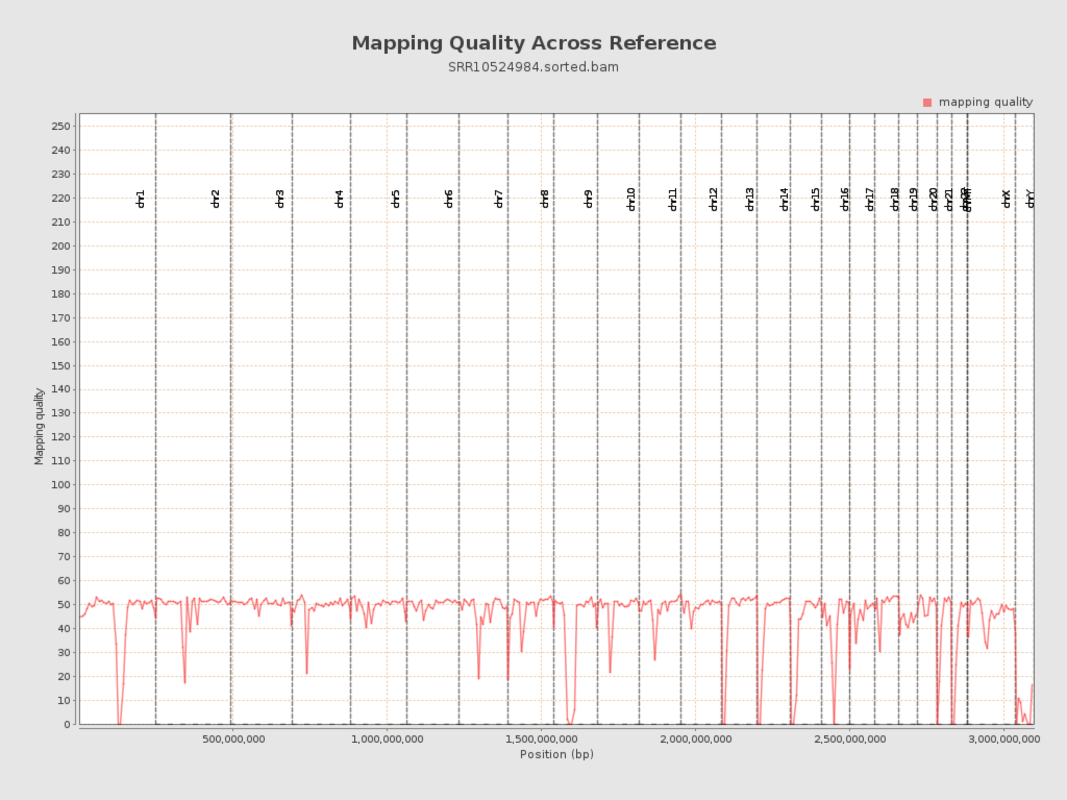
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram