Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:27:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524833.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_SRR10524833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:27:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	875,207
Mapped reads	802,021 / 91.64%
Unmapped reads	73,186 / 8.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,366 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	19,816 / 2.26%
Duplication rate	1.81%
Clipped reads	803,390 / 91.79%

2.2. ACGT Content

Number/percentage of A's	11,955,879 / 25.78%
Number/percentage of C's	8,801,988 / 18.98%
Number/percentage of T's	14,813,268 / 31.94%
Number/percentage of G's	10,799,177 / 23.29%
Number/percentage of N's	921 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1714

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

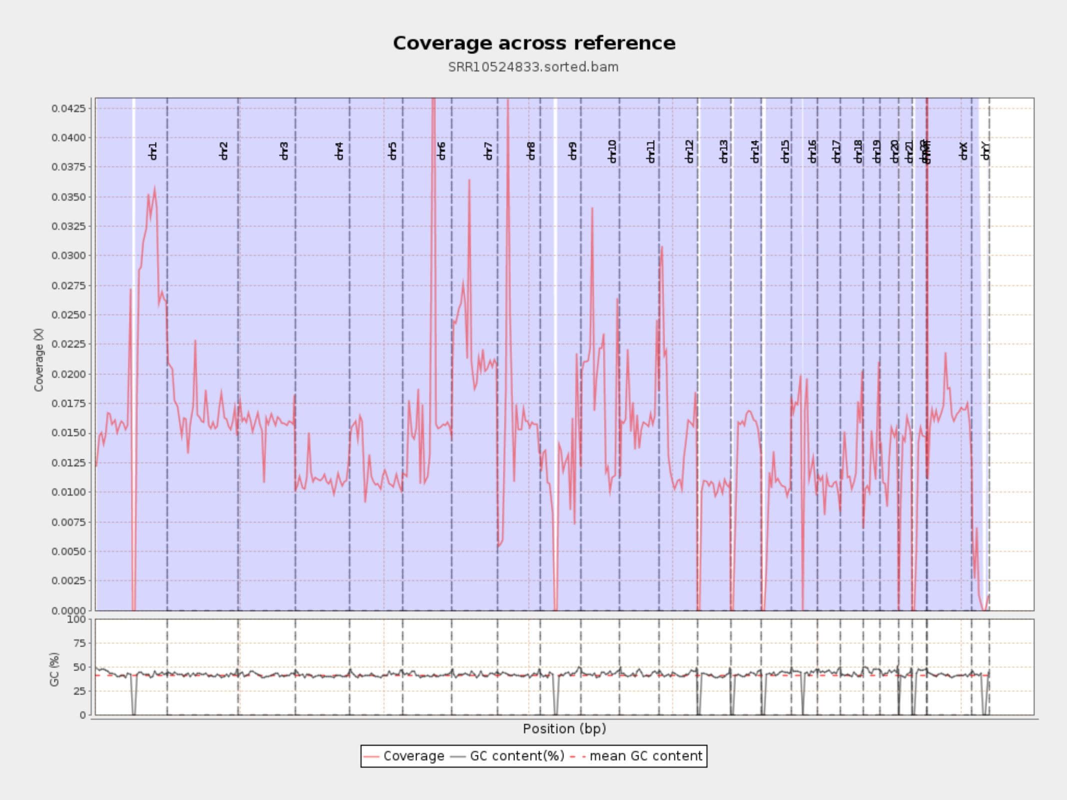
General error rate	0.52%
Mismatches	233,089
Insertions	3,514
Mapped reads with at least one insertion	0.44%
Deletions	9,863
Mapped reads with at least one deletion	1.22%
Homopolymer indels	42.52%

2.6. Chromosome stats

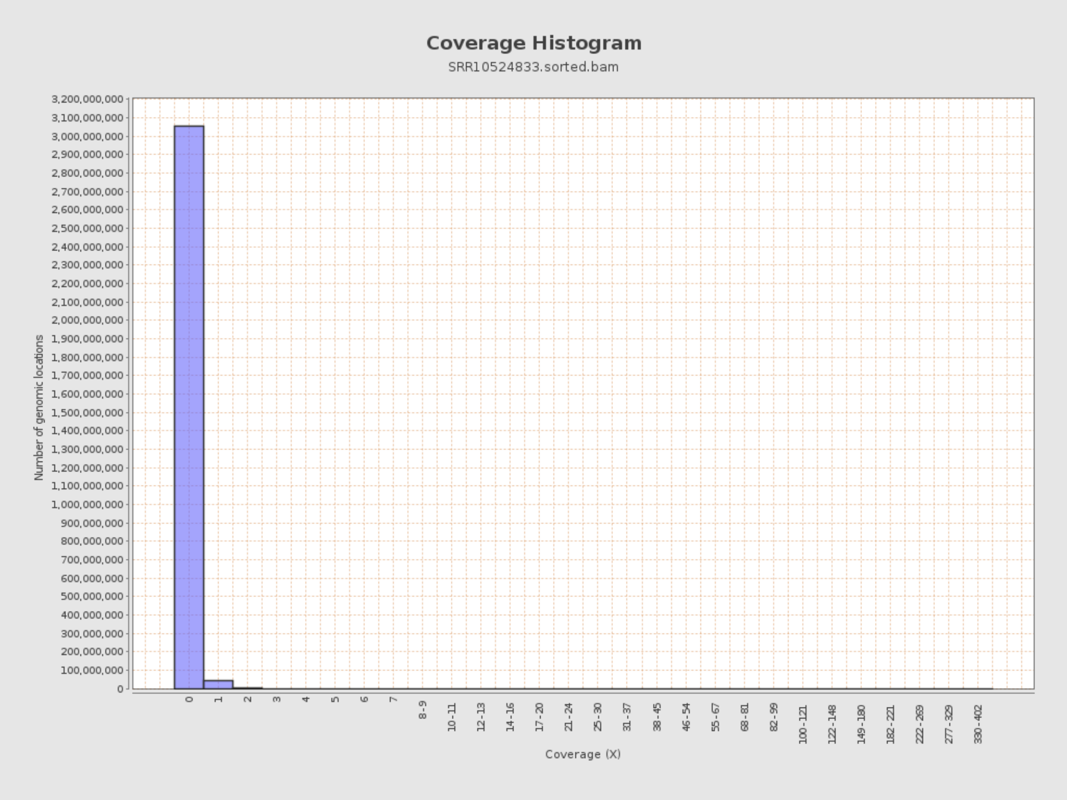
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5257278	0.0211	0.2865
chr2	243199373	4086071	0.0168	0.2129
chr3	198022430	3144373	0.0159	0.1332
chr4	191154276	2128638	0.0111	0.1139
chr5	180915260	2205419	0.0122	0.1151
chr6	171115067	2976654	0.0174	0.1479
chr7	159138663	3644426	0.0229	0.2931

chr8	146364022	2357360	0.0161	0.157
chr9	141213431	1598663	0.0113	0.1276
chr10	135534747	2597669	0.0192	0.1885
chr11	135006516	2231170	0.0165	0.149
chr12	133851895	2158654	0.0161	0.1334
chr13	115169878	1080045	0.0094	0.103
chr14	107349540	1418351	0.0132	0.1219
chr15	102531392	903549	0.0088	0.0991
chr16	90354753	1282663	0.0142	0.1318
chr17	81195210	849821	0.0105	0.1097
chr18	78077248	1031578	0.0132	0.2043
chr19	59128983	752234	0.0127	0.198
chr20	63025520	803535	0.0127	0.1184
chr21	48129895	611041	0.0127	0.1201
chr22	51304566	520310	0.0101	0.105
chrMT	16571	1340	0.0809	0.3028
chrX	155270560	2614598	0.0168	0.1425
chrY	59373566	131366	0.0022	0.0689

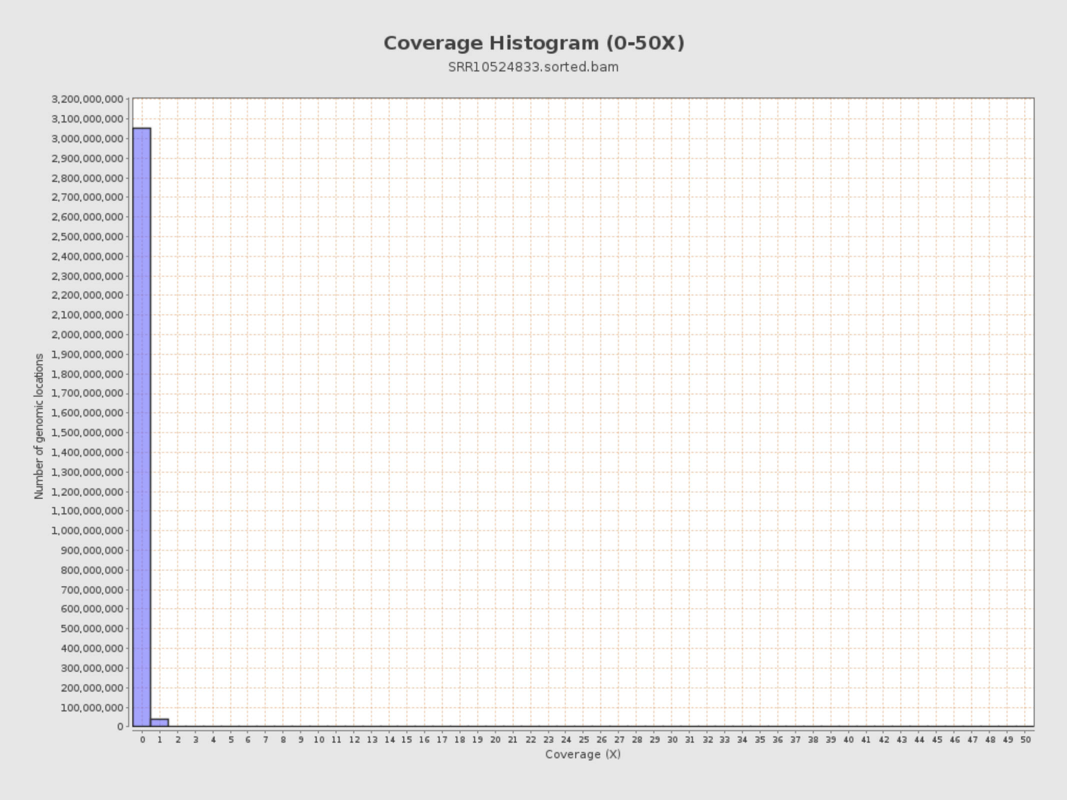
3. Results : Coverage across reference



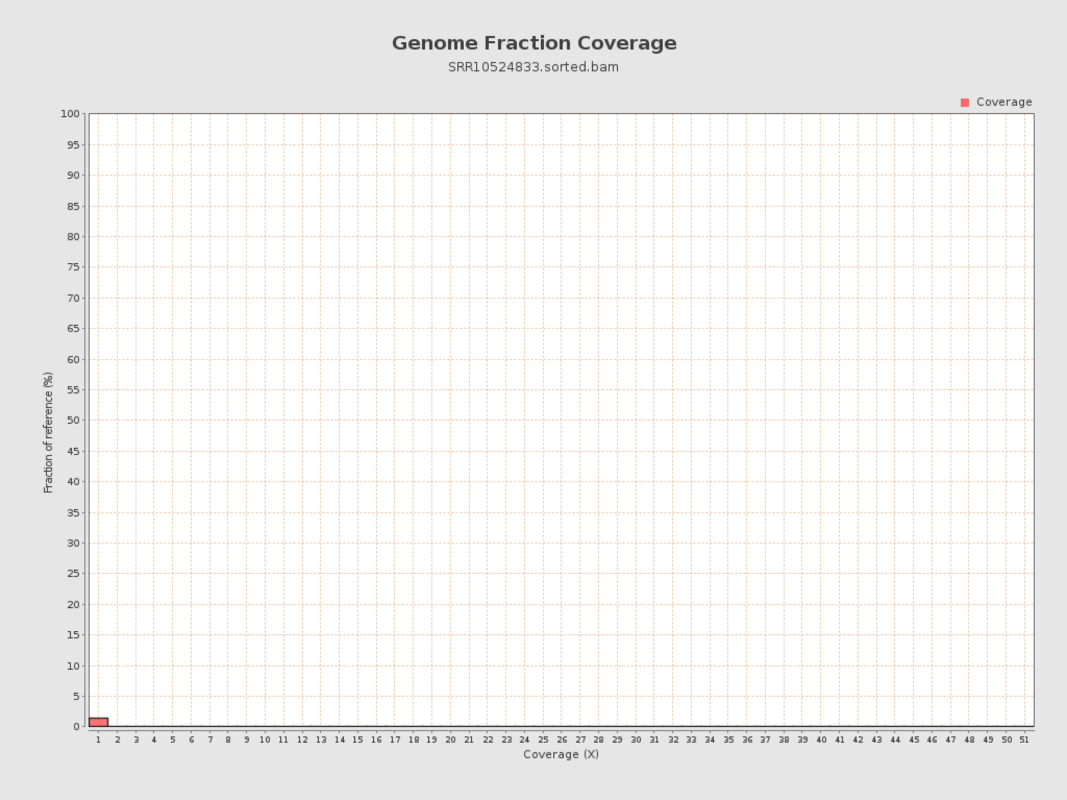
4. Results : Coverage Histogram



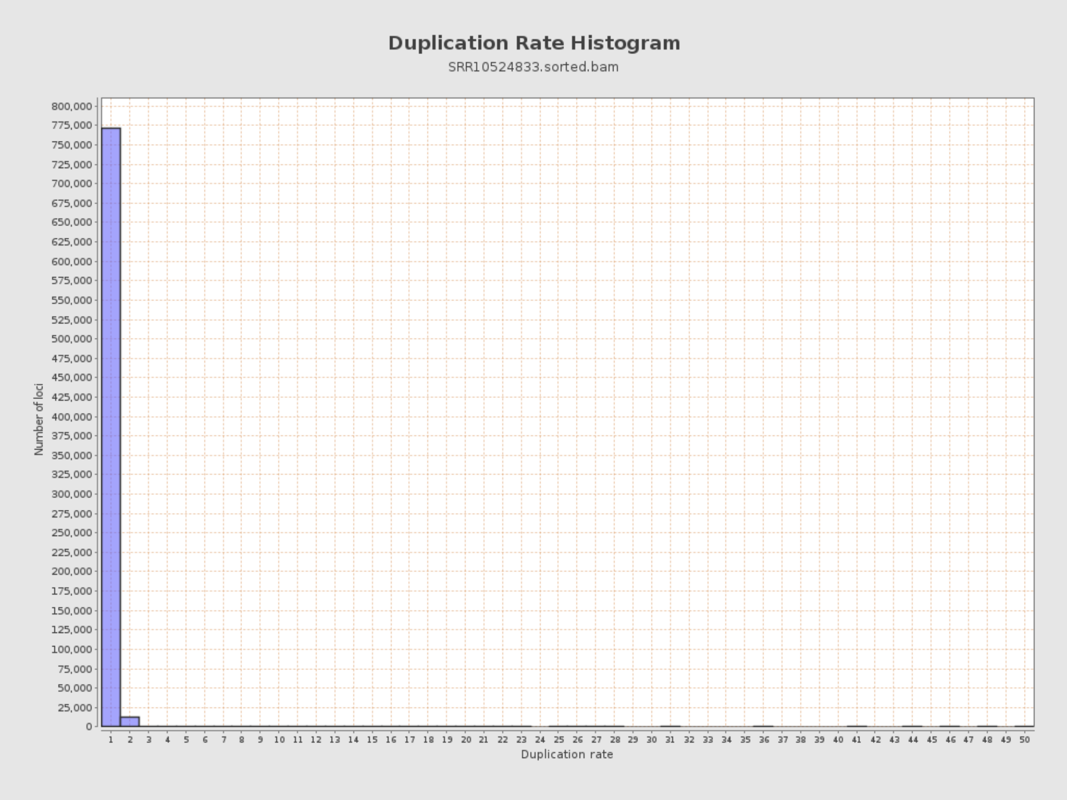
5. Results : Coverage Histogram (0-50X)



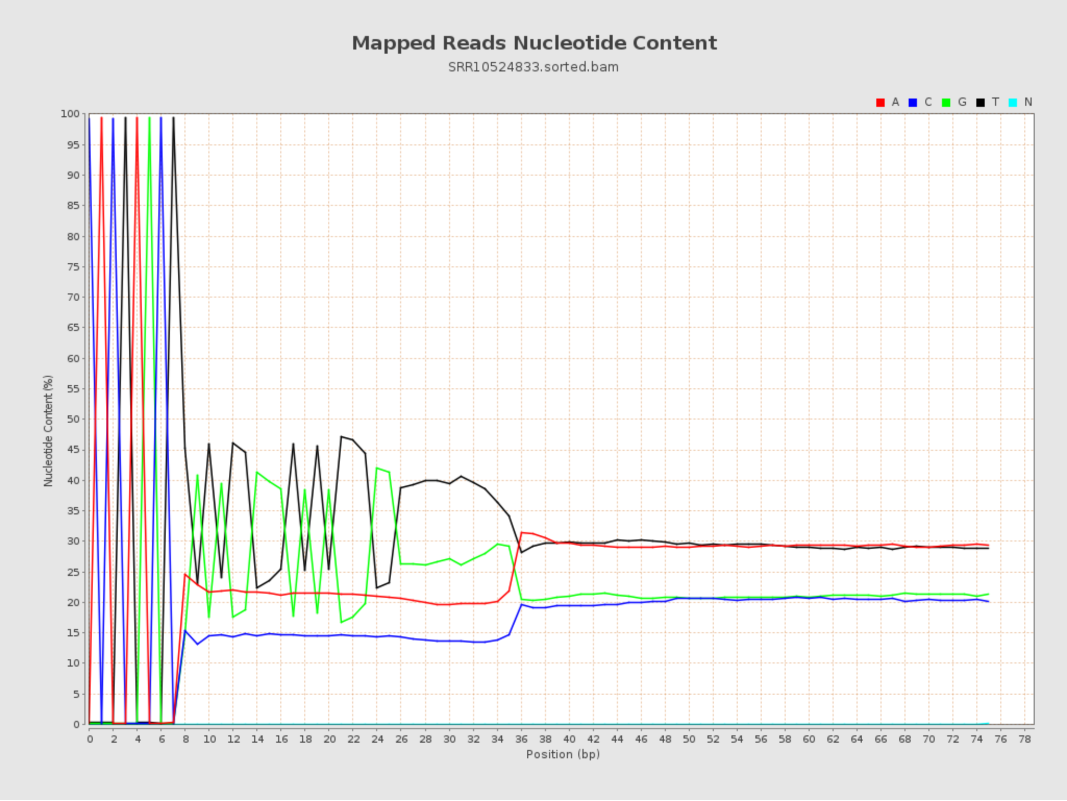
6. Results : Genome Fraction Coverage



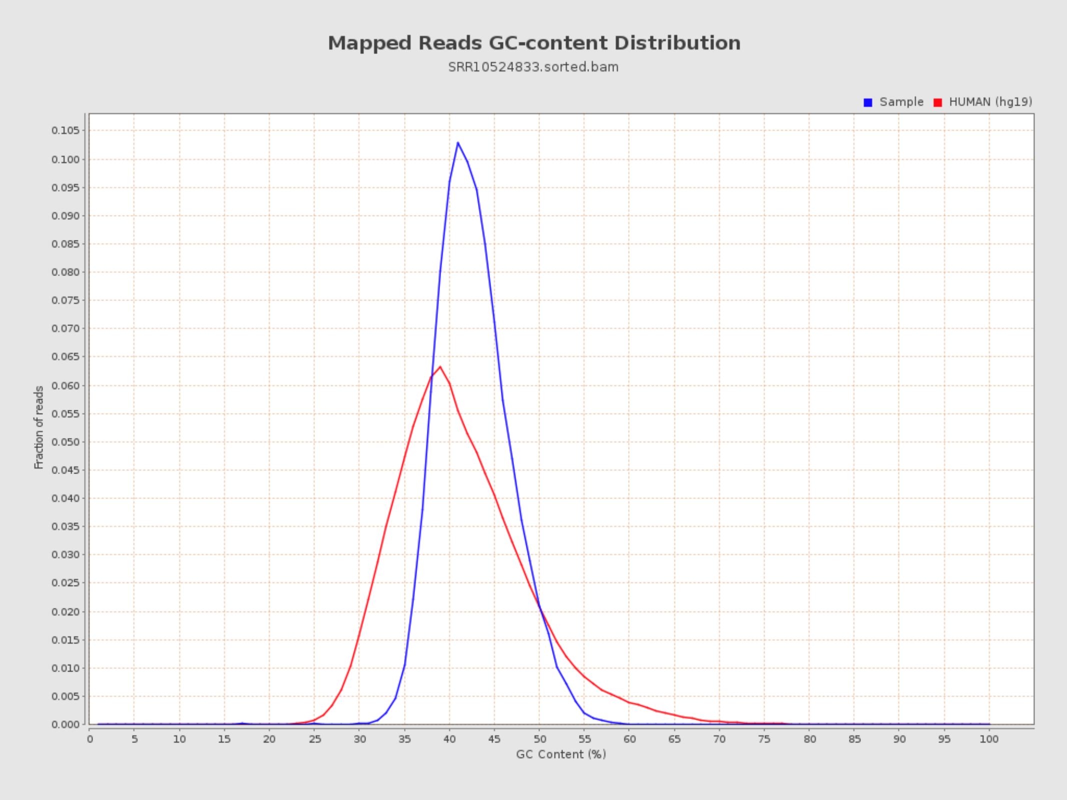
7. Results : Duplication Rate Histogram



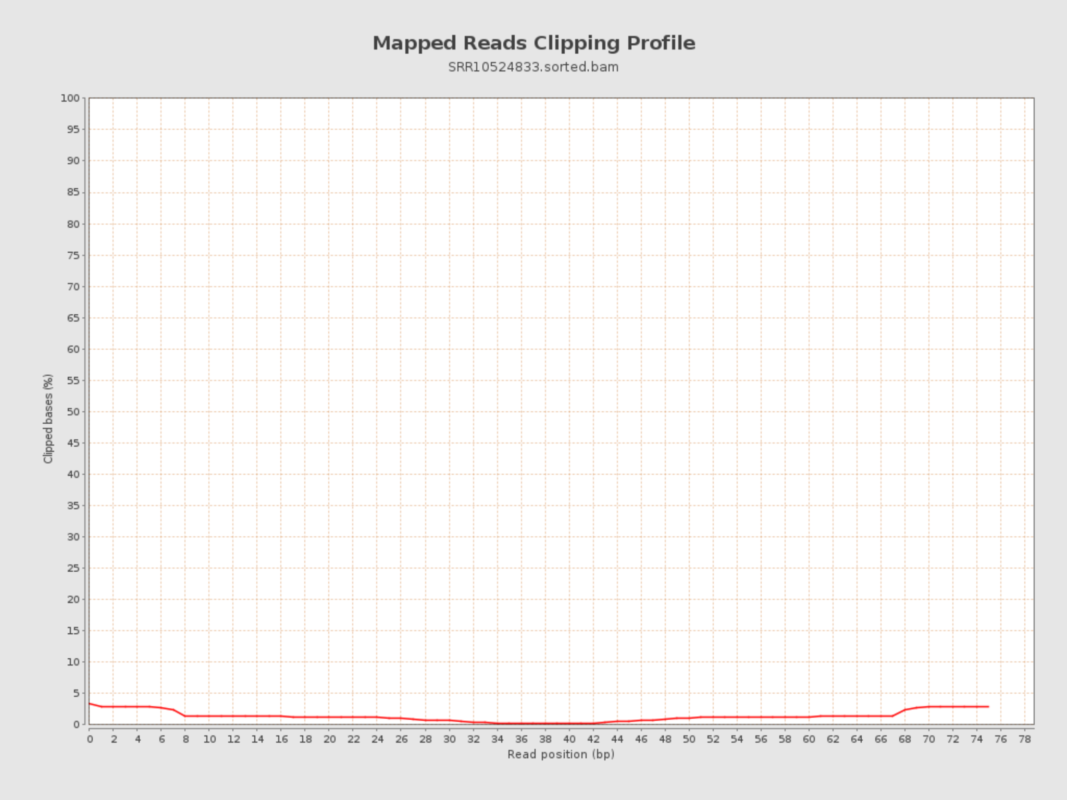
8. Results : Mapped Reads Nucleotide Content



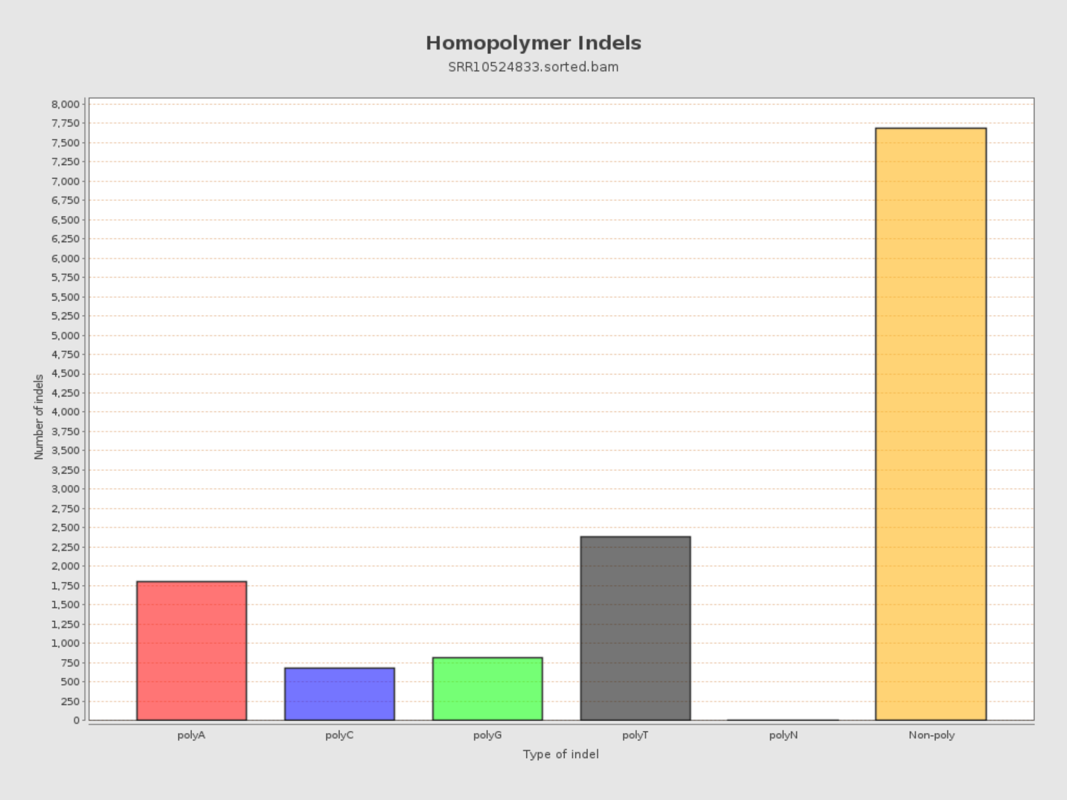
9. Results : Mapped Reads GC-content Distribution



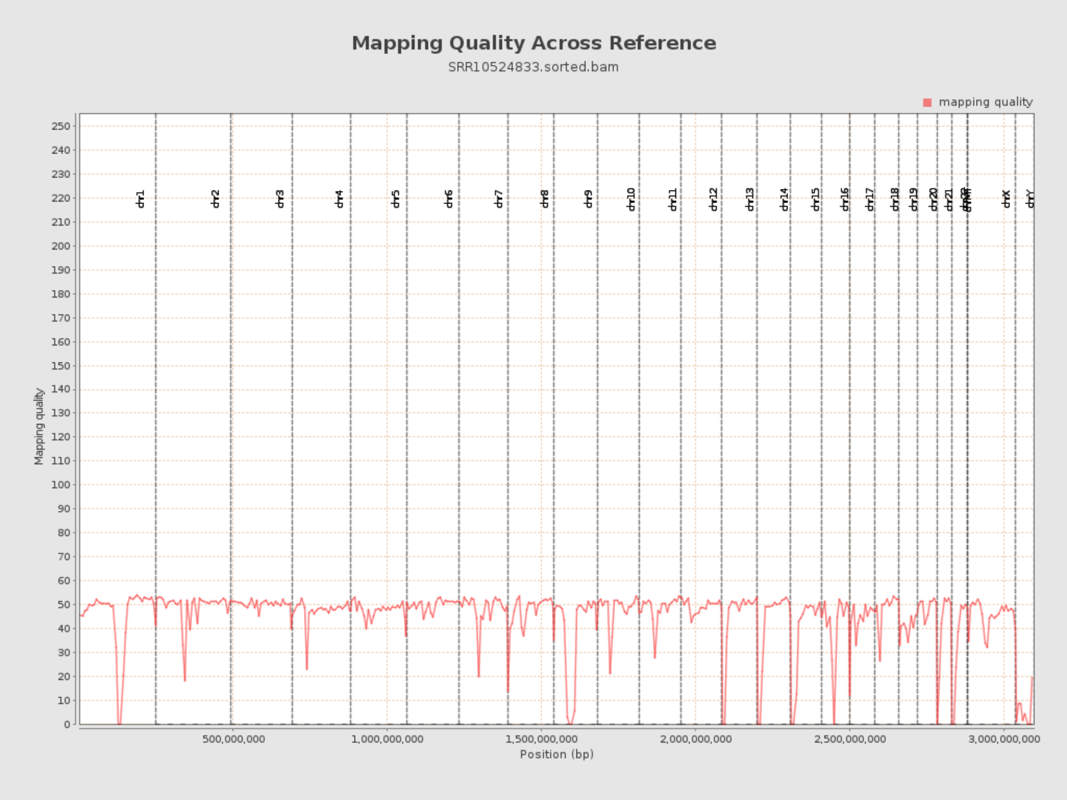
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram