Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:54:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524579.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_SRR10524579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524579.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:54:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,219,362
Mapped reads	1,118,282 / 91.71%
Unmapped reads	101,080 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,481 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	35,120 / 2.88%
Duplication rate	2.36%
Clipped reads	1,119,544 / 91.81%

2.2. ACGT Content

Number/percentage of A's	16,850,291 / 25.7%
Number/percentage of C's	12,394,035 / 18.91%
Number/percentage of T's	19,866,707 / 30.3%
Number/percentage of G's	16,446,828 / 25.09%
Number/percentage of N's	944 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.2089

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

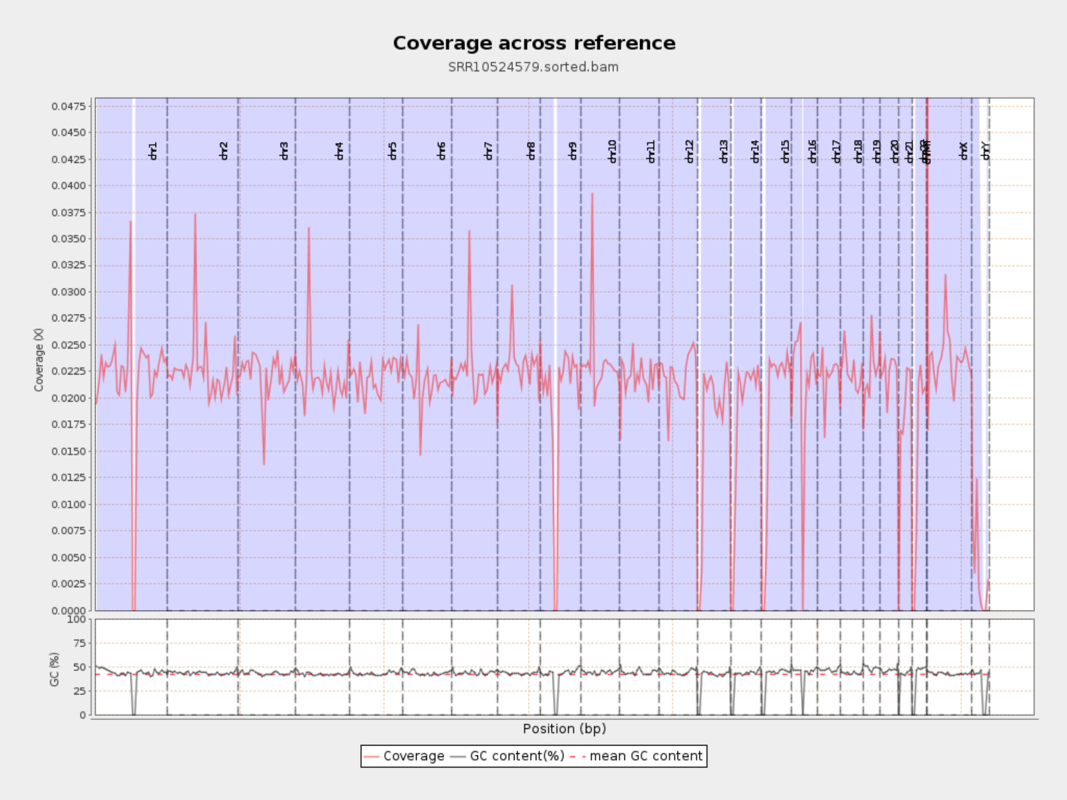
General error rate	0.52%
Mismatches	333,155
Insertions	4,613
Mapped reads with at least one insertion	0.41%
Deletions	12,921
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.41%

2.6. Chromosome stats

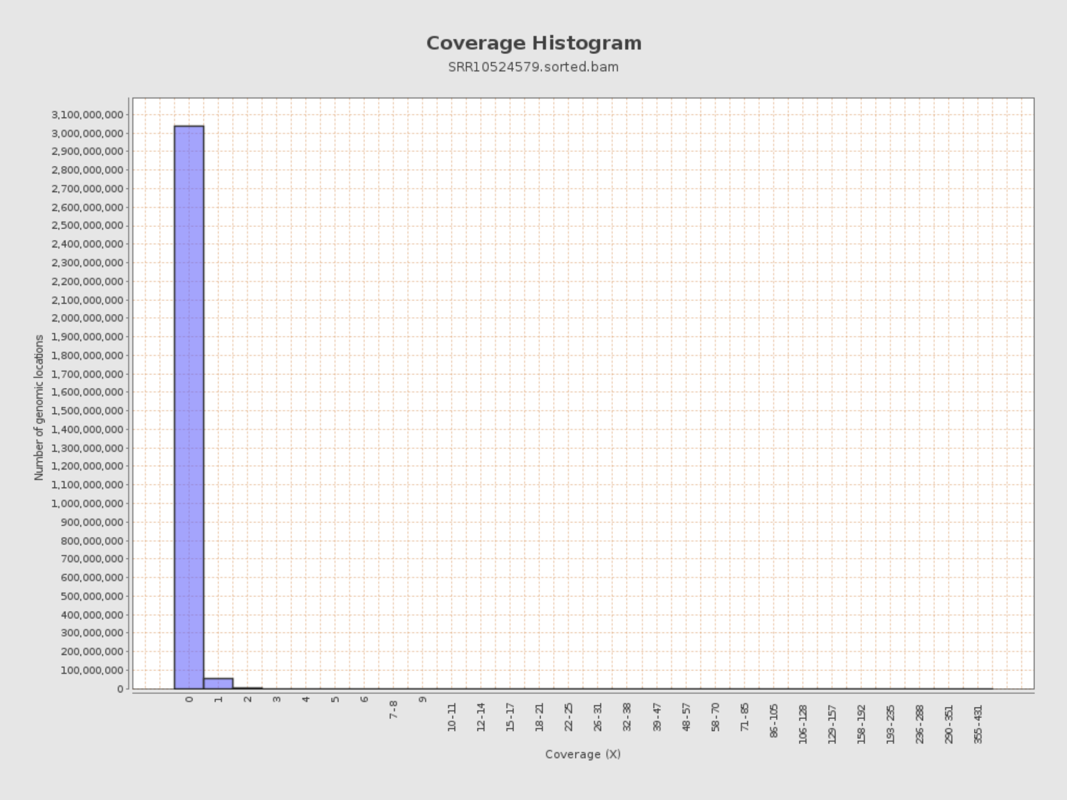
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5396395	0.0217	0.3565
chr2	243199373	5502957	0.0226	0.2343
chr3	198022430	4388322	0.0222	0.1594
chr4	191154276	4230625	0.0221	0.1744
chr5	180915260	4000187	0.0221	0.1586
chr6	171115067	3683305	0.0215	0.1758
chr7	159138663	3606029	0.0227	0.2623

chr8	146364022	3400124	0.0232	0.2156
chr9	141213431	2759509	0.0195	0.1811
chr10	135534747	3173941	0.0234	0.208
chr11	135006516	2983849	0.0221	0.1929
chr12	133851895	2962170	0.0221	0.1596
chr13	115169878	1996184	0.0173	0.1397
chr14	107349540	1940734	0.0181	0.1455
chr15	102531392	1893111	0.0185	0.1466
chr16	90354753	1889784	0.0209	0.1637
chr17	81195210	1786914	0.022	0.1669
chr18	78077248	1756379	0.0225	0.3192
chr19	59128983	1332536	0.0225	0.2648
chr20	63025520	1404158	0.0223	0.162
chr21	48129895	851130	0.0177	0.151
chr22	51304566	760703	0.0148	0.1292
chrMT	16571	4984	0.3008	0.6179
chrX	155270560	3668314	0.0236	0.1761
chrY	59373566	208100	0.0035	0.1098

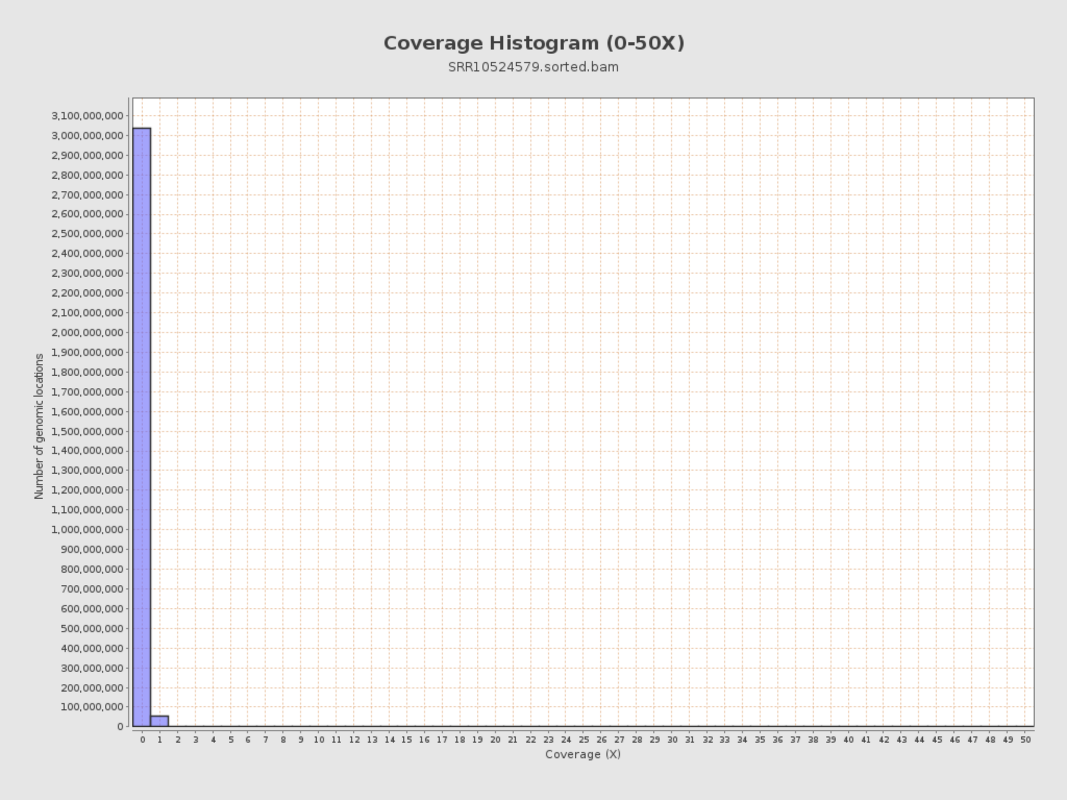
3. Results : Coverage across reference



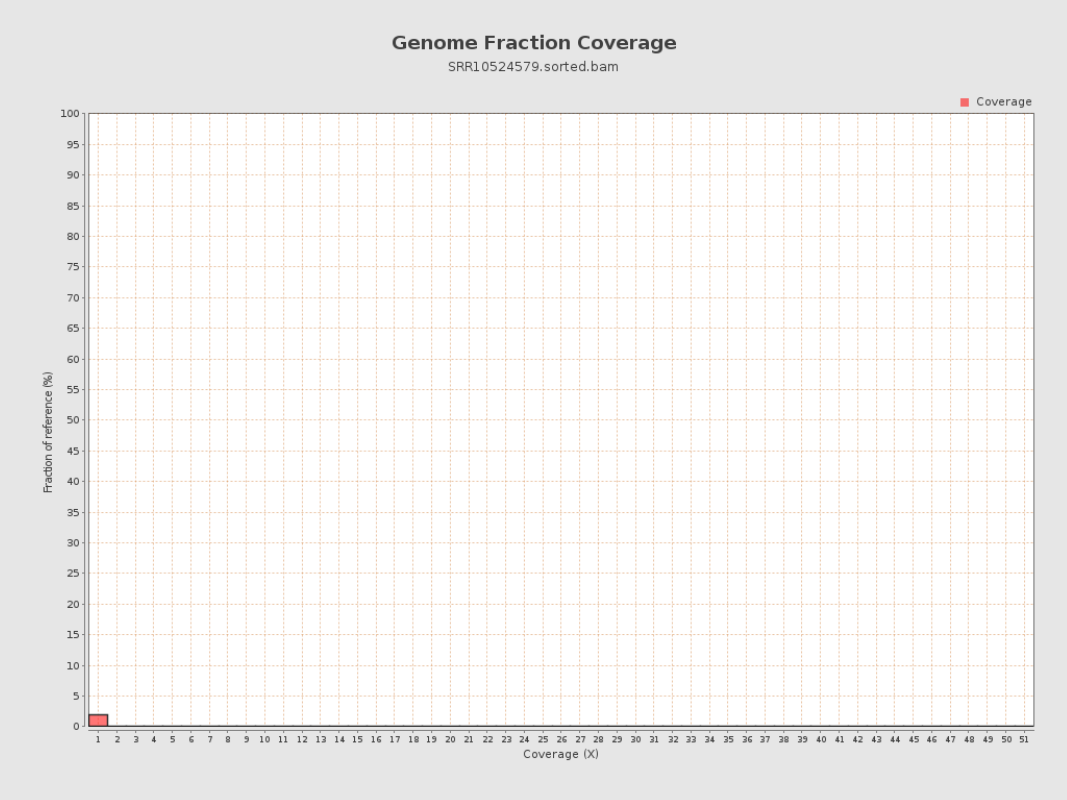
4. Results : Coverage Histogram



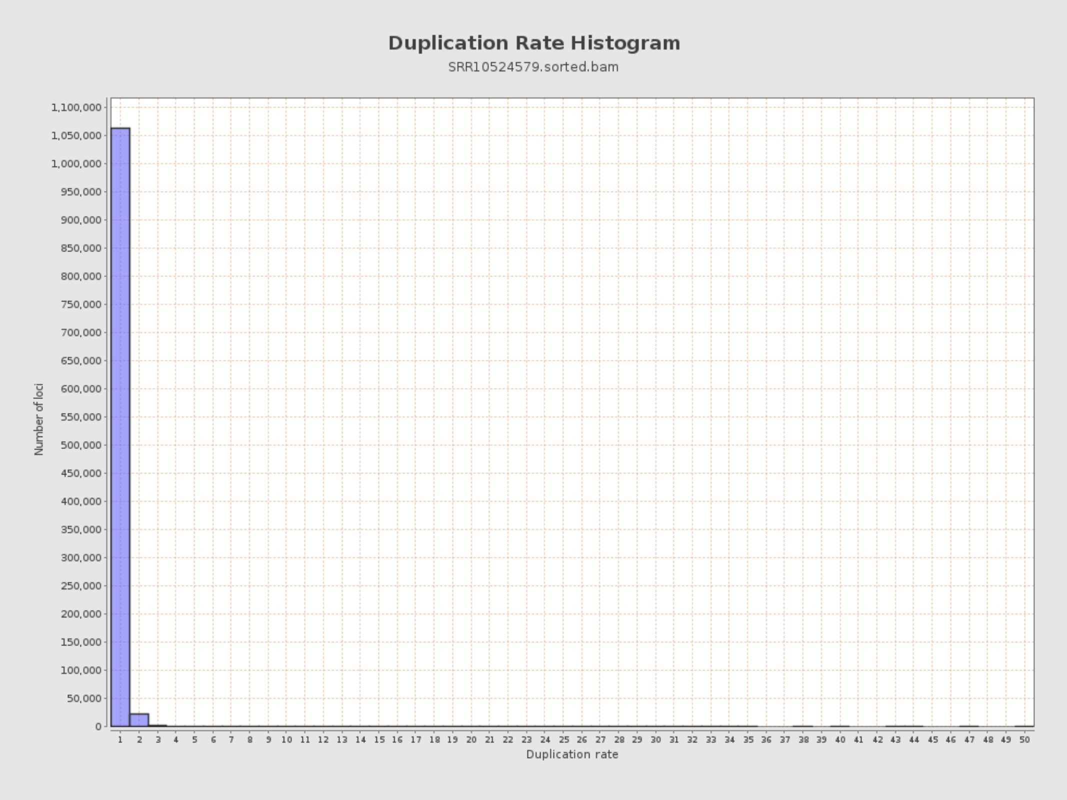
5. Results : Coverage Histogram (0-50X)



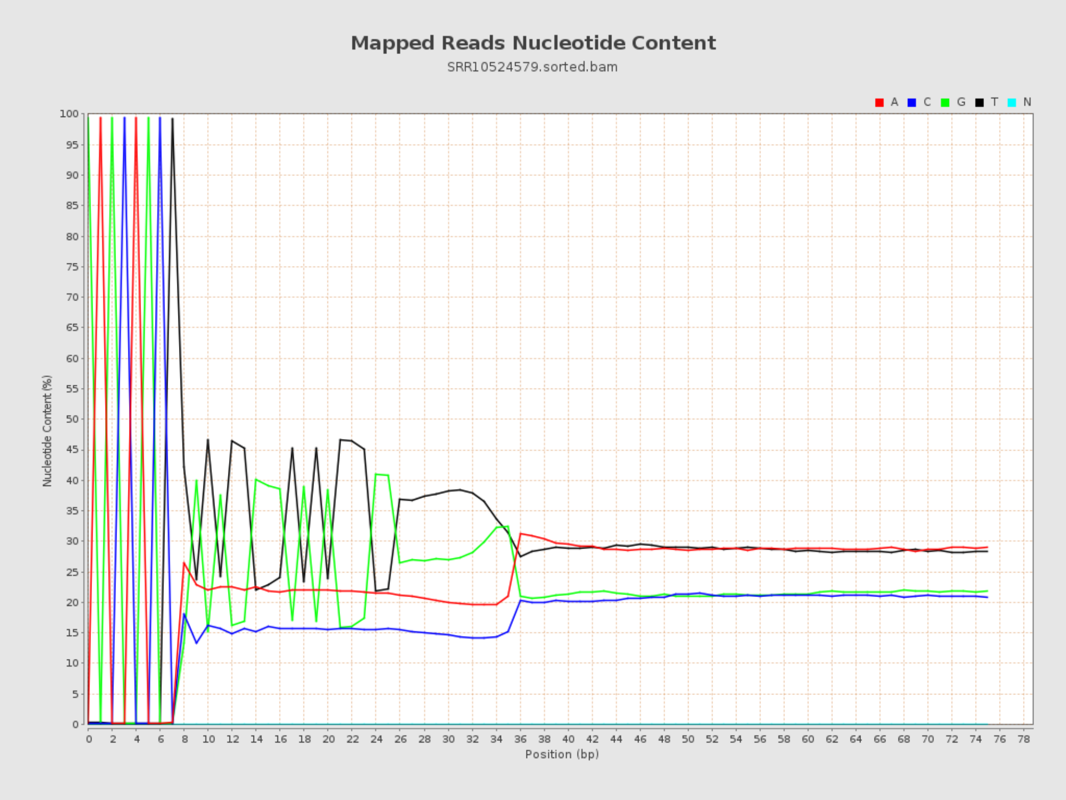
6. Results : Genome Fraction Coverage



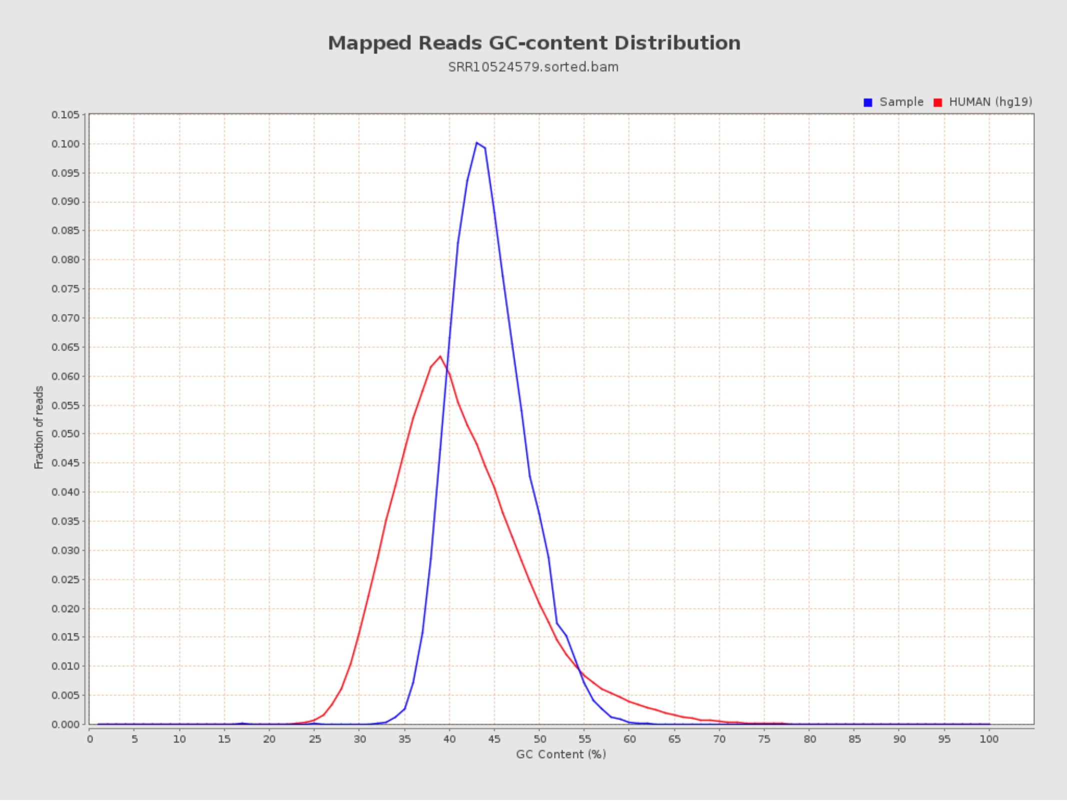
7. Results : Duplication Rate Histogram



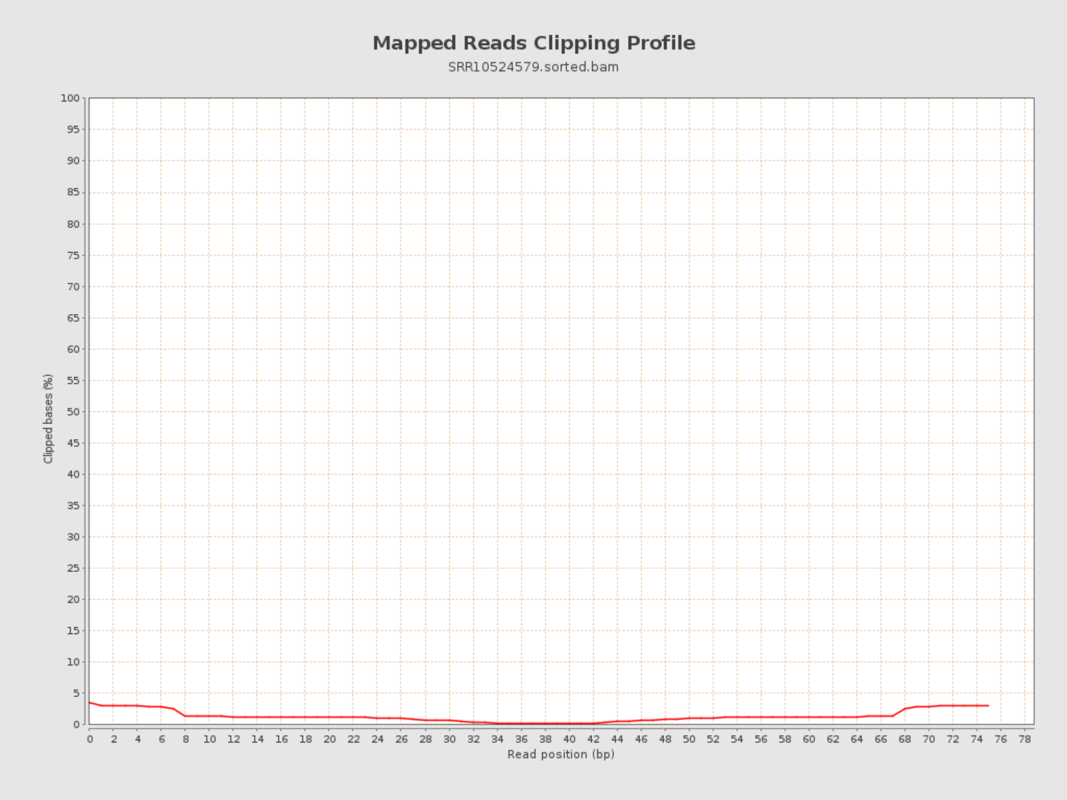
8. Results : Mapped Reads Nucleotide Content



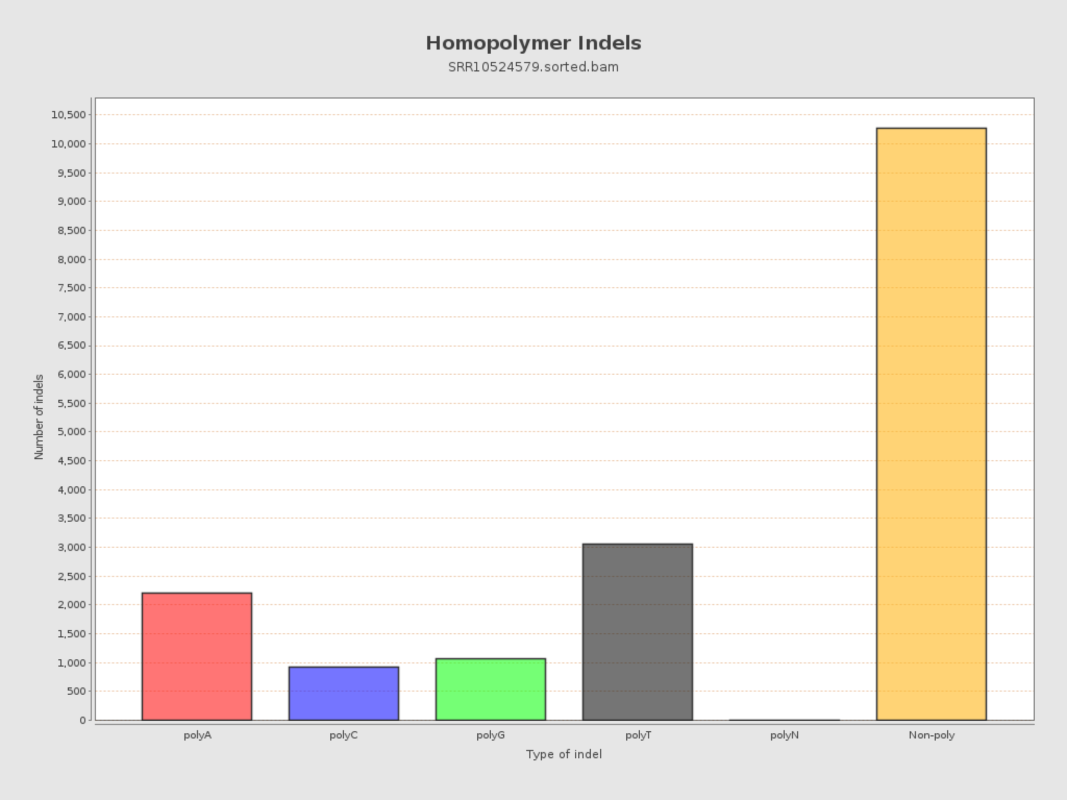
9. Results : Mapped Reads GC-content Distribution



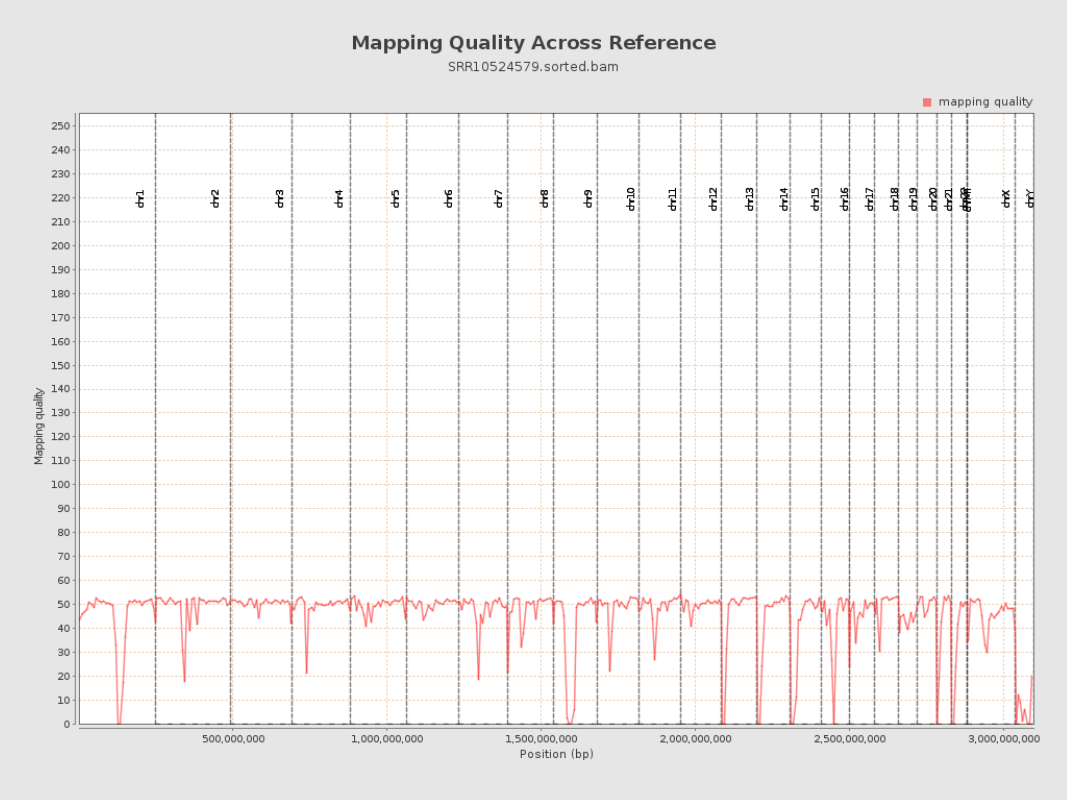
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram