Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:52:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524578.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_SRR10524578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524578.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:52:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,825,579
Mapped reads	1,678,969 / 91.97%
Unmapped reads	146,610 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,157 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	65,852 / 3.61%
Duplication rate	2.91%
Clipped reads	1,680,451 / 92.05%

2.2. ACGT Content

Number/percentage of A's	23,344,678 / 23.82%
Number/percentage of C's	20,118,588 / 20.53%
Number/percentage of T's	31,246,835 / 31.89%
Number/percentage of G's	23,282,310 / 23.76%
Number/percentage of N's	1,384 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.2886

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

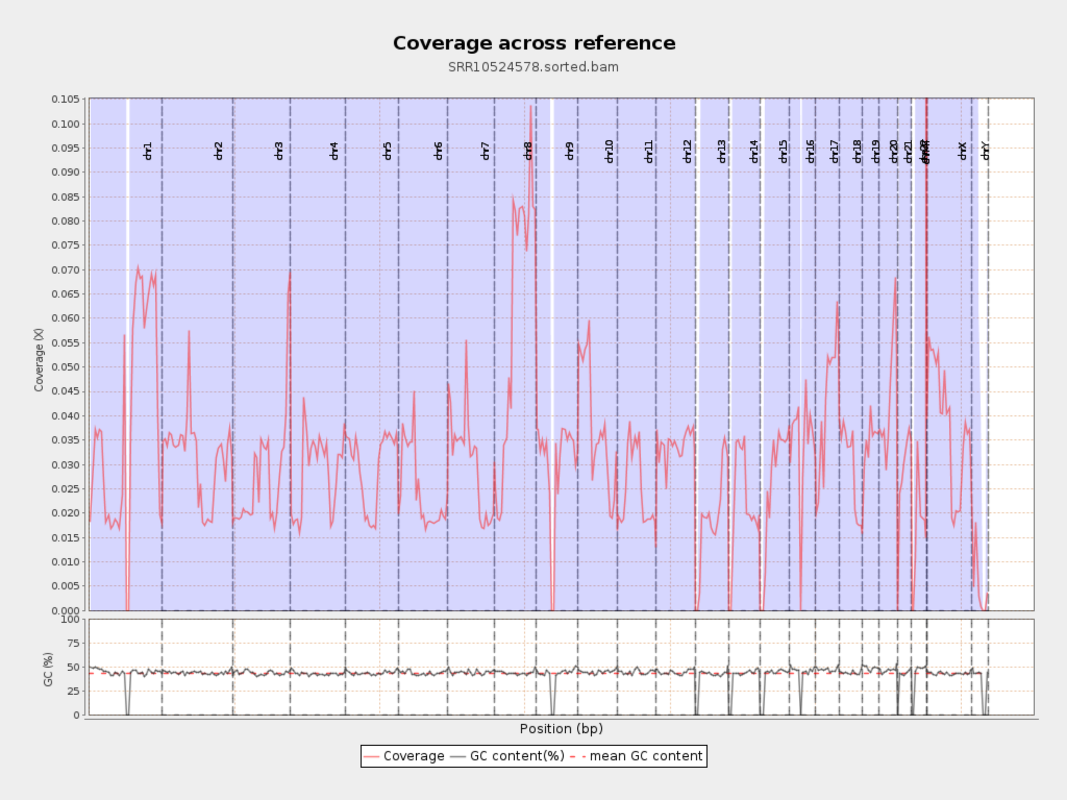
General error rate	0.52%
Mismatches	494,072
Insertions	6,845
Mapped reads with at least one insertion	0.41%
Deletions	18,847
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.5%

2.6. Chromosome stats

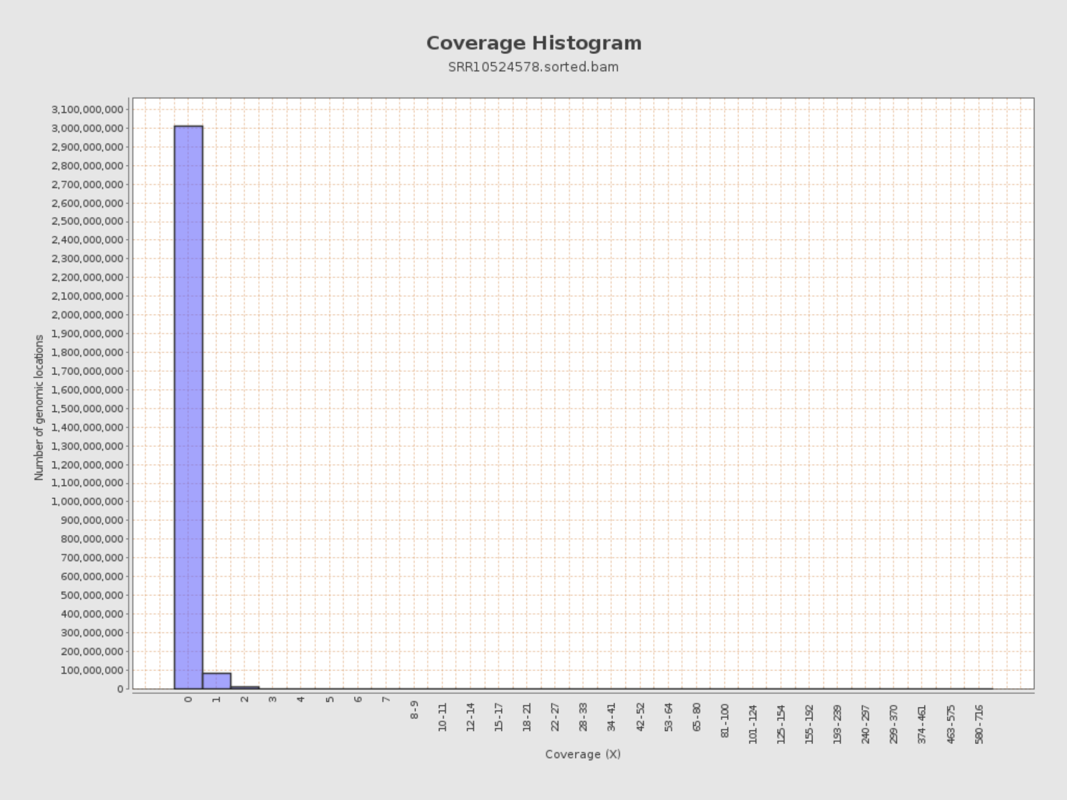
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9673592	0.0388	0.5405
chr2	243199373	7669718	0.0315	0.33
chr3	198022430	5391956	0.0272	0.184
chr4	191154276	5448299	0.0285	0.2095
chr5	180915260	5341270	0.0295	0.1888
chr6	171115067	4201829	0.0246	0.2209
chr7	159138663	4873623	0.0306	0.364

chr8	146364022	8877302	0.0607	0.3146
chr9	141213431	4189059	0.0297	0.2418
chr10	135534747	5165177	0.0381	0.2932
chr11	135006516	3368126	0.0249	0.2647
chr12	133851895	4563154	0.0341	0.2038
chr13	115169878	2172080	0.0189	0.1515
chr14	107349540	2336300	0.0218	0.1686
chr15	102531392	2602848	0.0254	0.1795
chr16	90354753	3095849	0.0343	0.2177
chr17	81195210	3487720	0.043	0.2418
chr18	78077248	2325903	0.0298	0.4386
chr19	59128983	2037181	0.0345	0.3705
chr20	63025520	2801512	0.0445	0.2343
chr21	48129895	1353681	0.0281	0.2015
chr22	51304566	823046	0.016	0.1381
chrMT	16571	6617	0.3993	0.6998
chrX	155270560	5904646	0.038	0.2398
chrY	59373566	314379	0.0053	0.1493

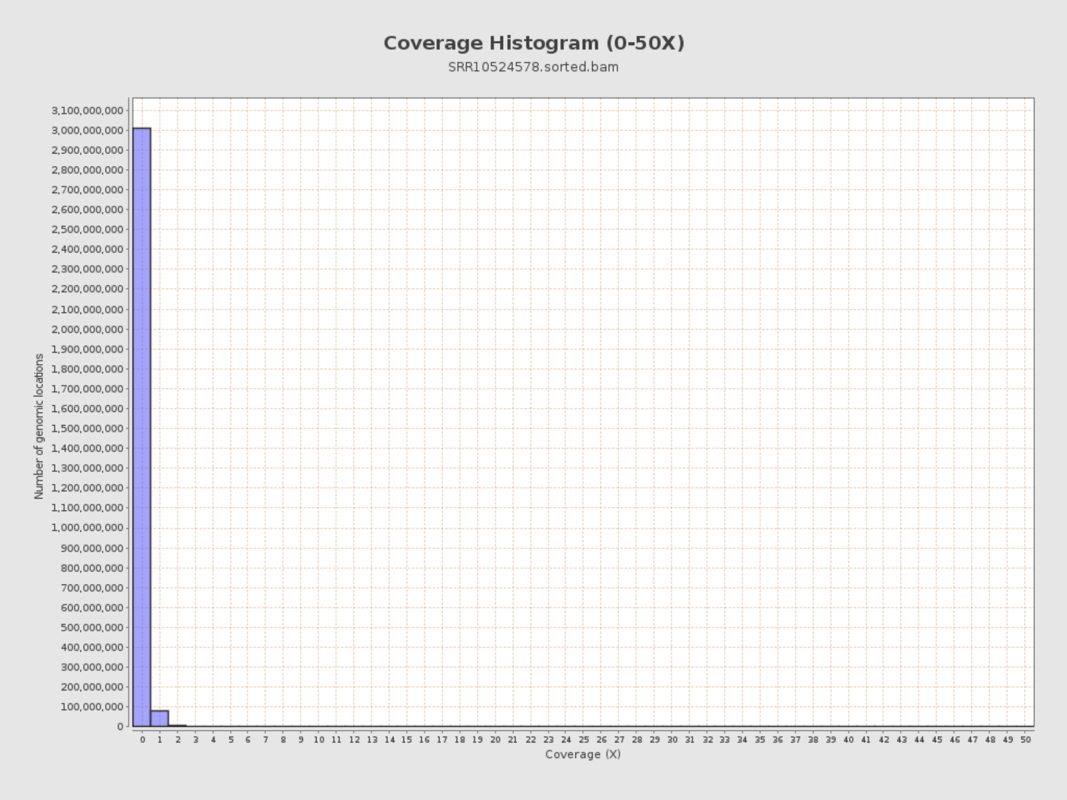
3. Results : Coverage across reference



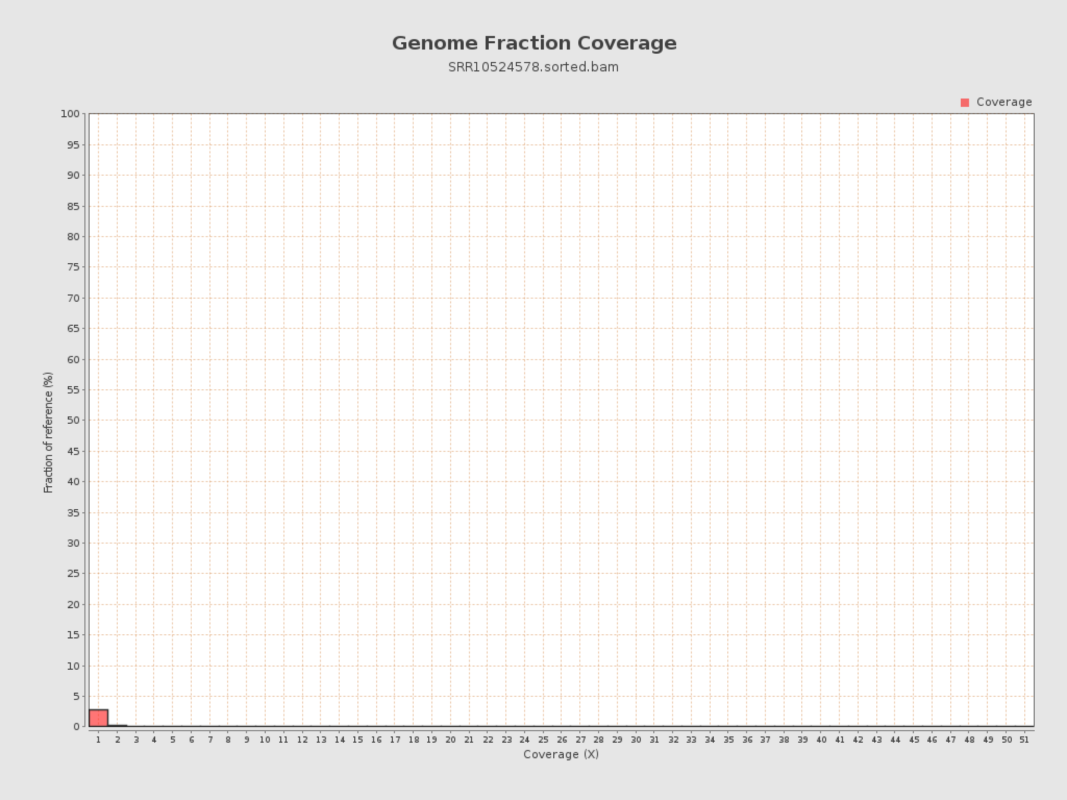
4. Results : Coverage Histogram



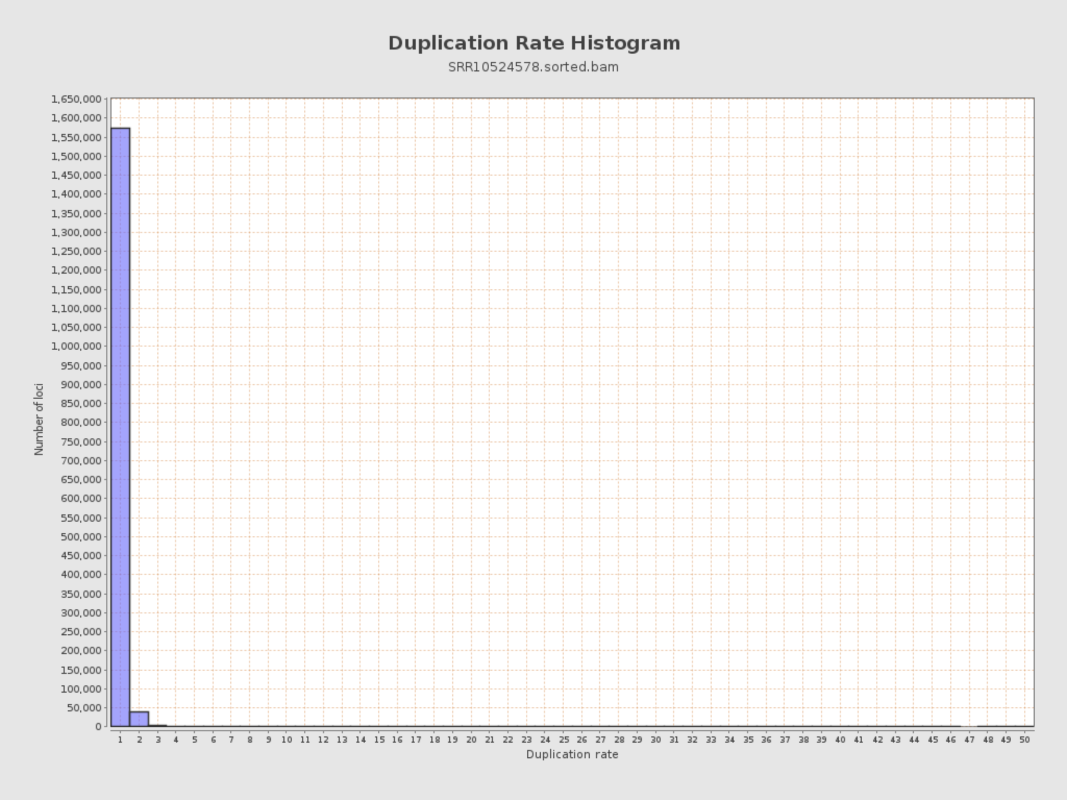
5. Results : Coverage Histogram (0-50X)



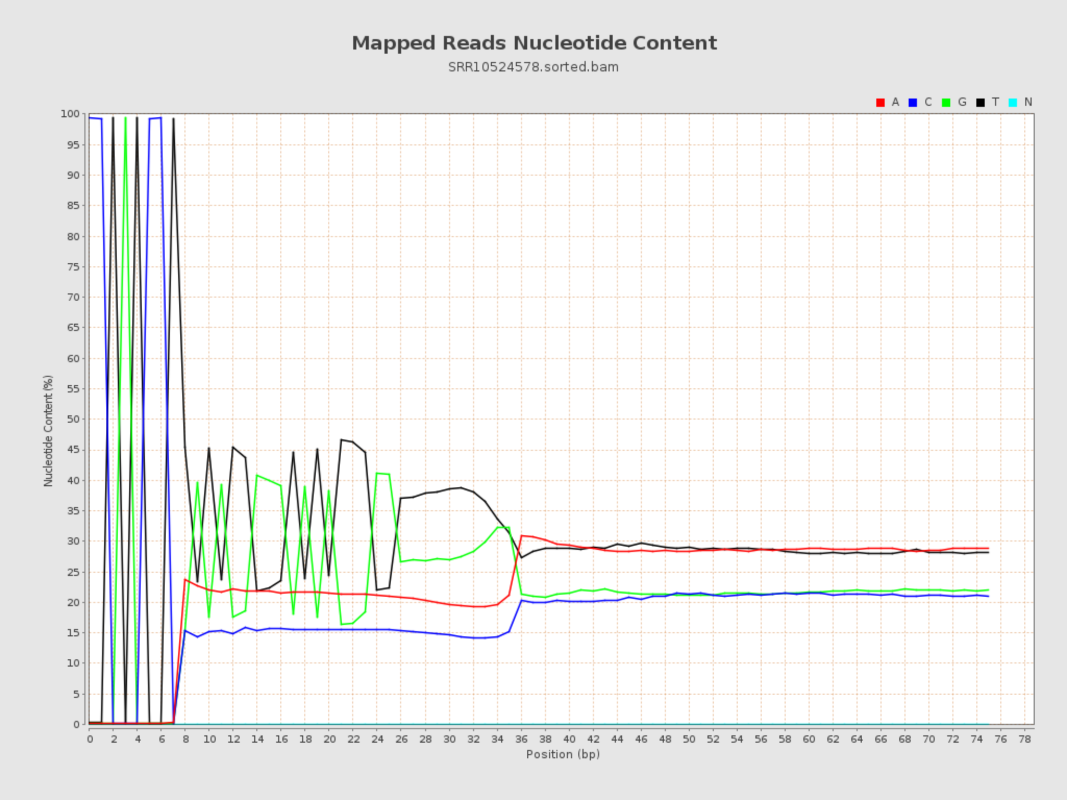
6. Results : Genome Fraction Coverage



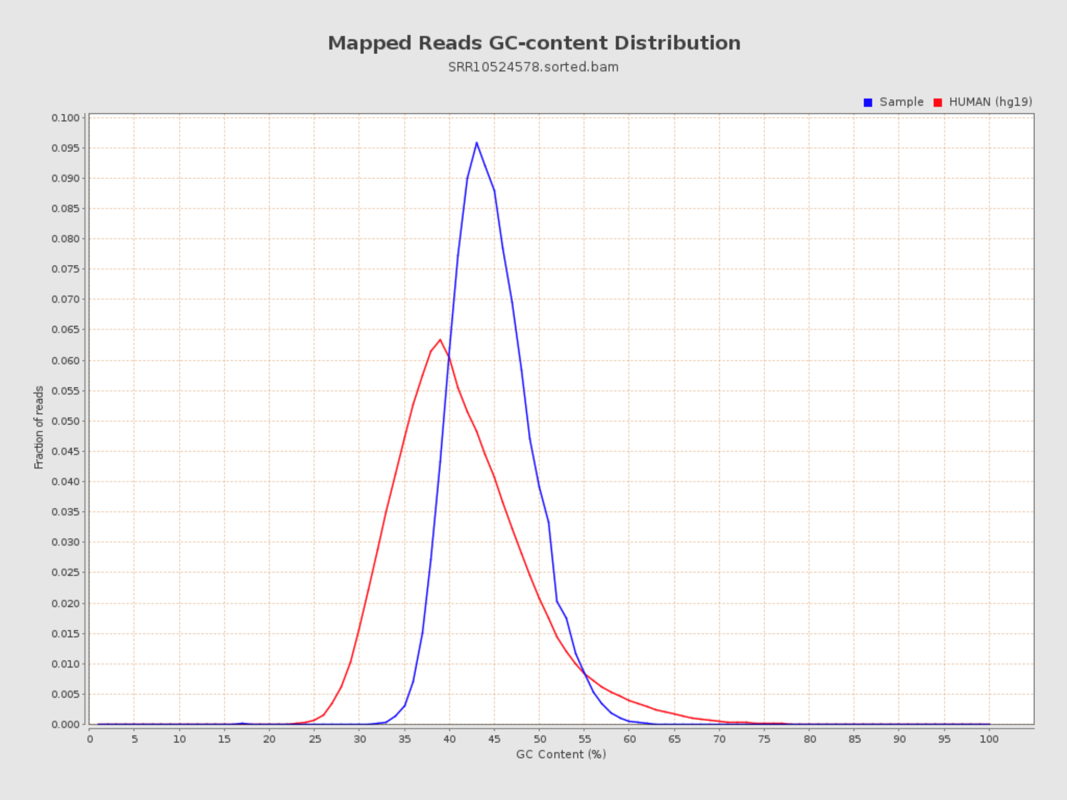
7. Results : Duplication Rate Histogram



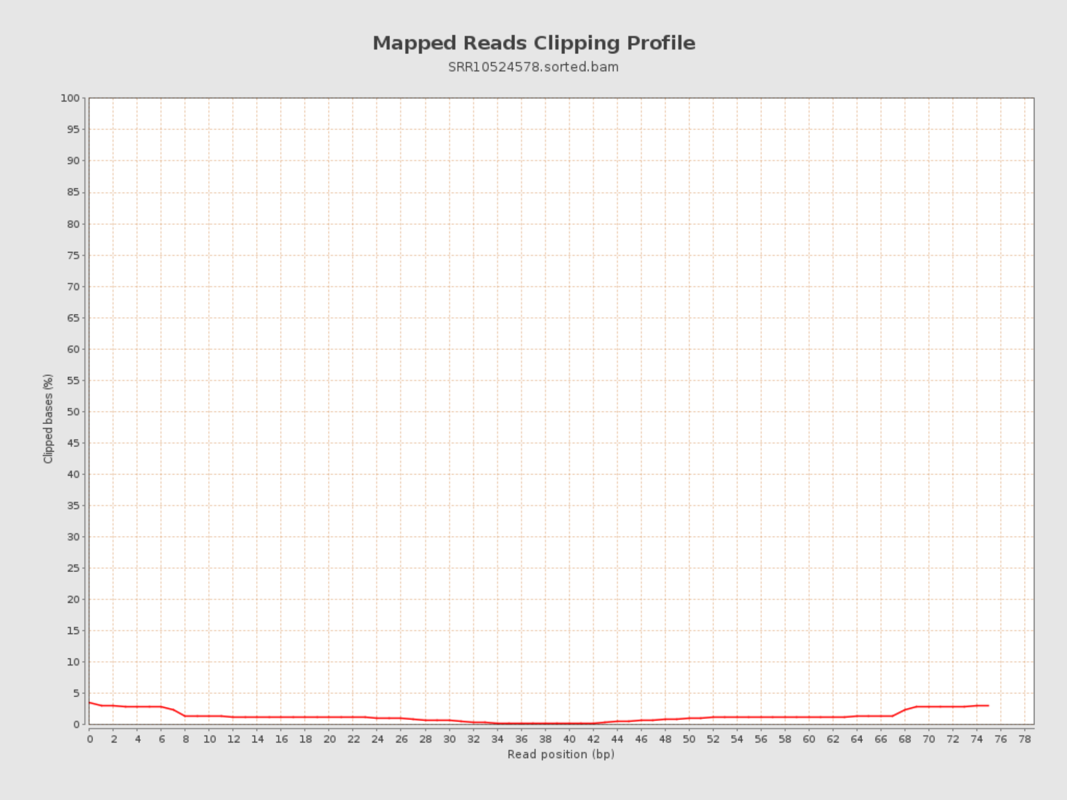
8. Results : Mapped Reads Nucleotide Content



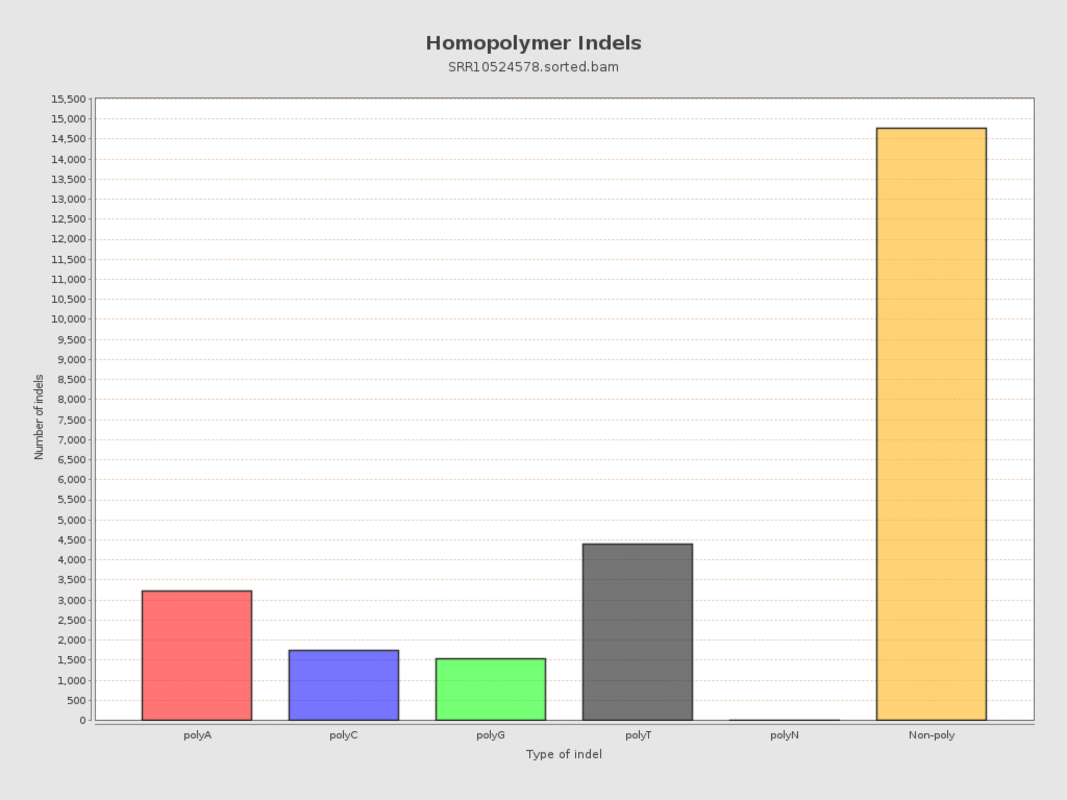
9. Results : Mapped Reads GC-content Distribution



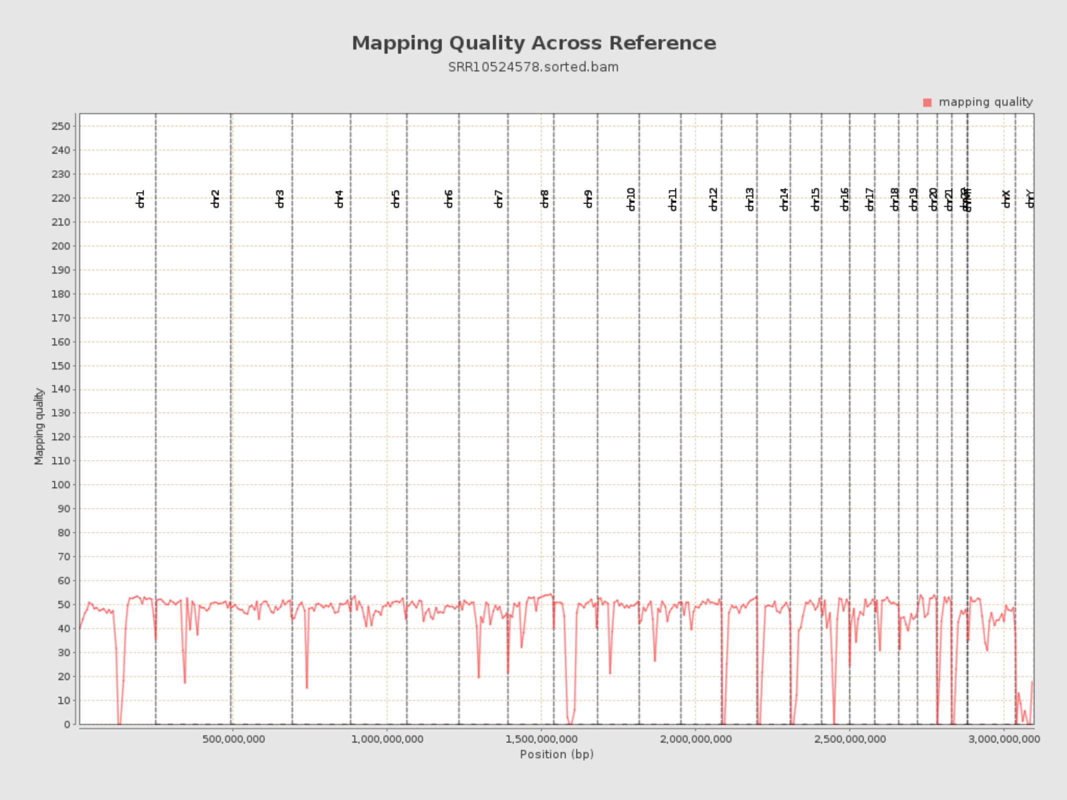
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram