Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:59:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524327.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_SRR10524327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:59:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,123,364
Mapped reads	2,856,783 / 91.46%
Unmapped reads	266,581 / 8.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,963 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	126,796 / 4.06%
Duplication rate	3.12%
Clipped reads	2,861,762 / 91.62%

2.2. ACGT Content

Number/percentage of A's	41,668,072 / 25.13%
Number/percentage of C's	29,995,411 / 18.09%
Number/percentage of T's	51,683,355 / 31.18%
Number/percentage of G's	42,411,284 / 25.58%
Number/percentage of N's	23,921 / 0.01%
GC Percentage	43.68%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.4557

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Mismatches and indels

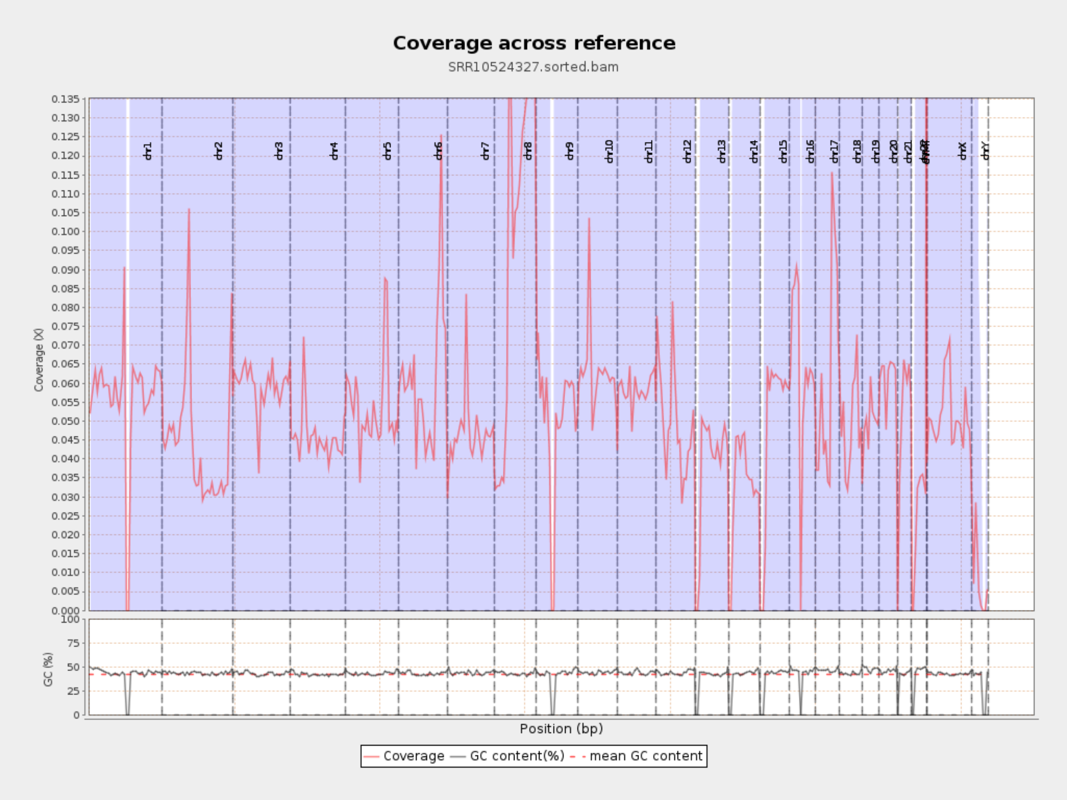
General error rate	0.52%
Mismatches	844,340
Insertions	11,060
Mapped reads with at least one insertion	0.39%
Deletions	28,639
Mapped reads with at least one deletion	1%
Homopolymer indels	41.79%

2.6. Chromosome stats

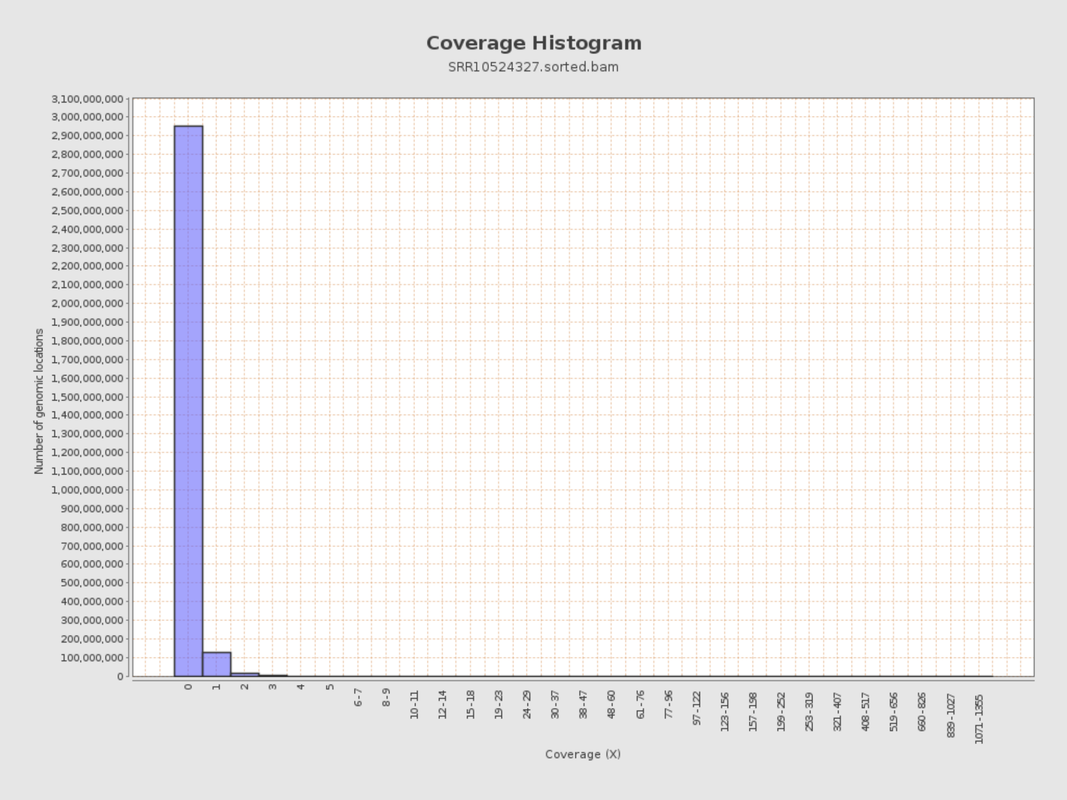
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13962404	0.056	0.8948
chr2	243199373	10788870	0.0444	0.6137
chr3	198022430	11747287	0.0593	0.2789
chr4	191154276	8696137	0.0455	0.285
chr5	180915260	9786116	0.0541	0.2643
chr6	171115067	10400369	0.0608	0.3125
chr7	159138663	7524196	0.0473	0.596

chr8	146364022	16477785	0.1126	0.5396
chr9	141213431	6993937	0.0495	0.3539
chr10	135534747	8543895	0.063	0.4526
chr11	135006516	7856496	0.0582	0.366
chr12	133851895	6654185	0.0497	0.2605
chr13	115169878	4345578	0.0377	0.2188
chr14	107349540	3492010	0.0325	0.2276
chr15	102531392	5019051	0.049	0.2601
chr16	90354753	5790534	0.0641	0.3134
chr17	81195210	4898349	0.0603	0.3197
chr18	78077248	3920134	0.0502	0.6686
chr19	59128983	2954969	0.05	0.5873
chr20	63025520	3858044	0.0612	0.2922
chr21	48129895	2435318	0.0506	0.2878
chr22	51304566	1234395	0.0241	0.1776
chrMT	16571	9456	0.5706	0.8622
chrX	155270560	7968516	0.0513	0.3051
chrY	59373566	469298	0.0079	0.2166

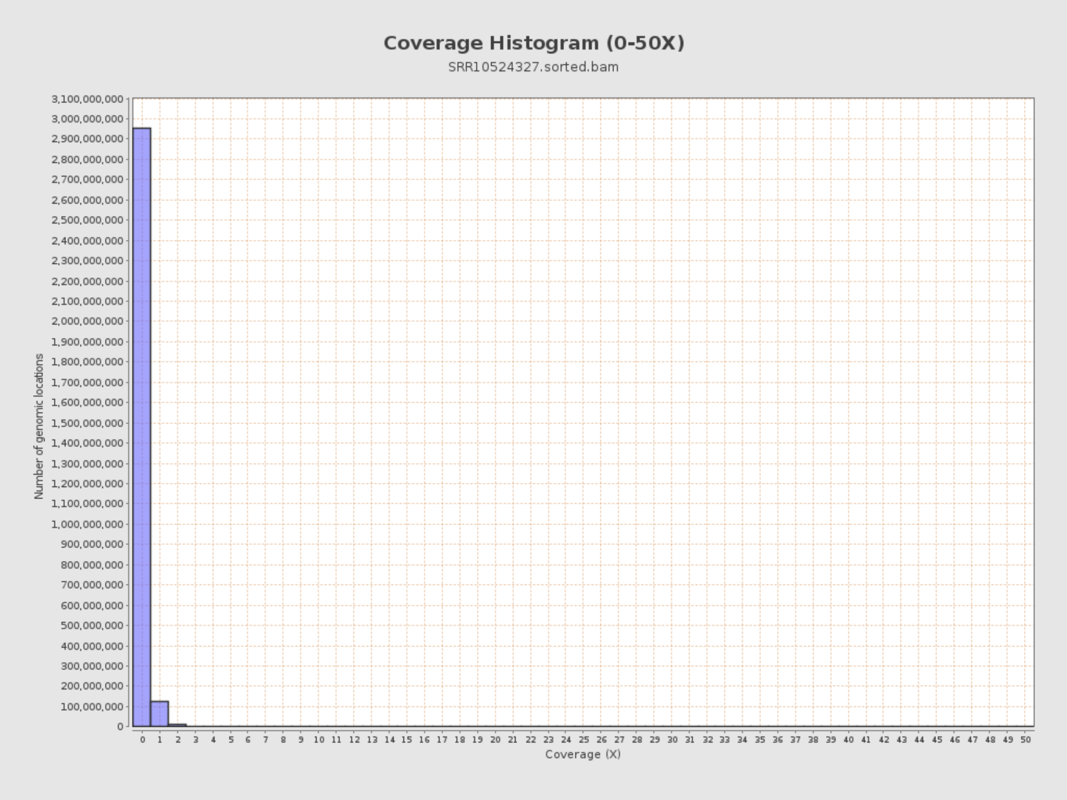
3. Results : Coverage across reference



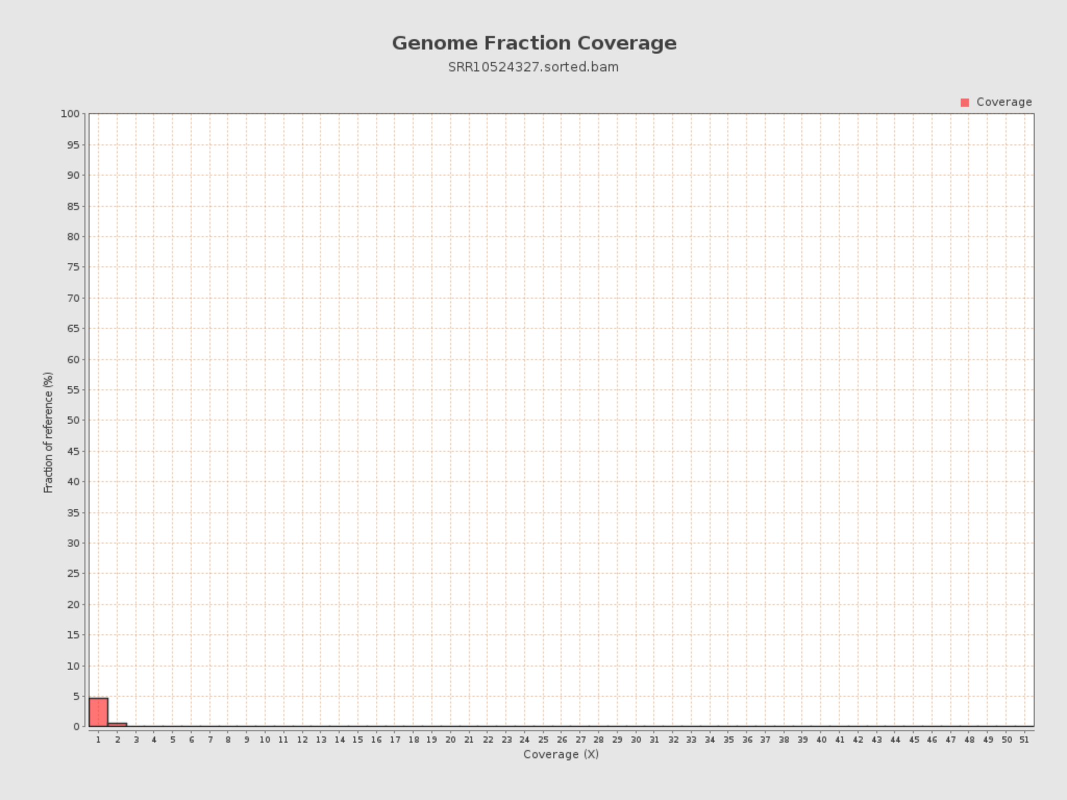
4. Results : Coverage Histogram



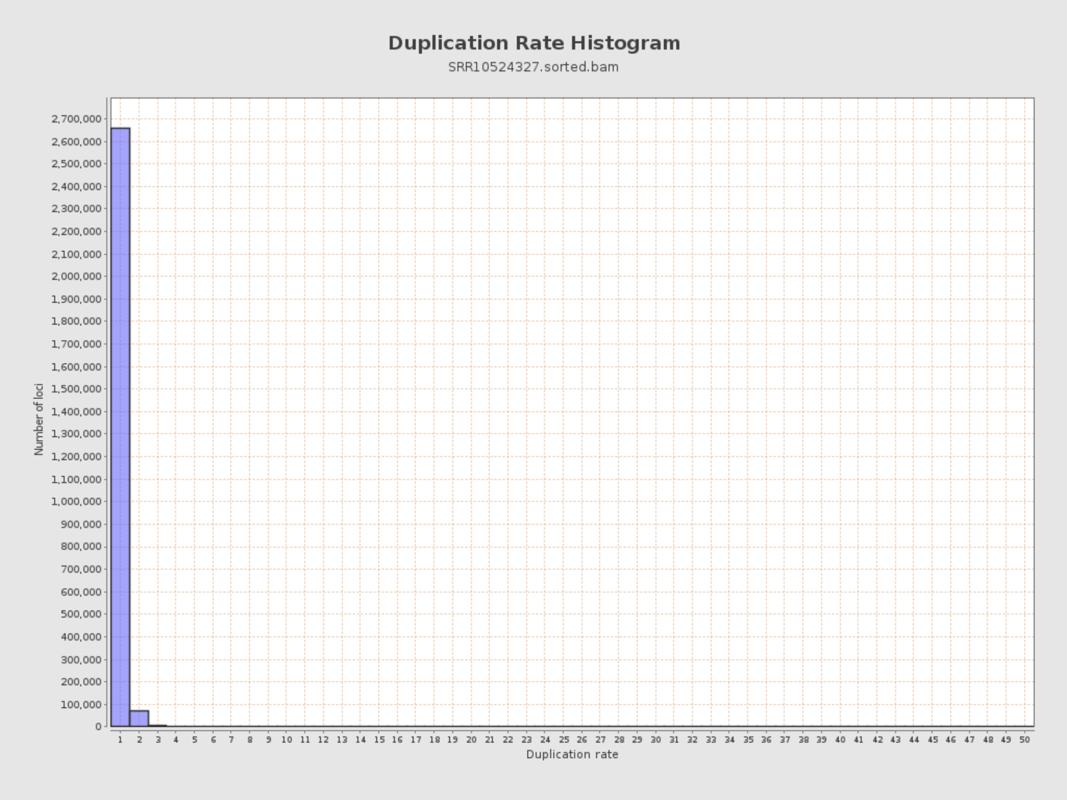
5. Results : Coverage Histogram (0-50X)



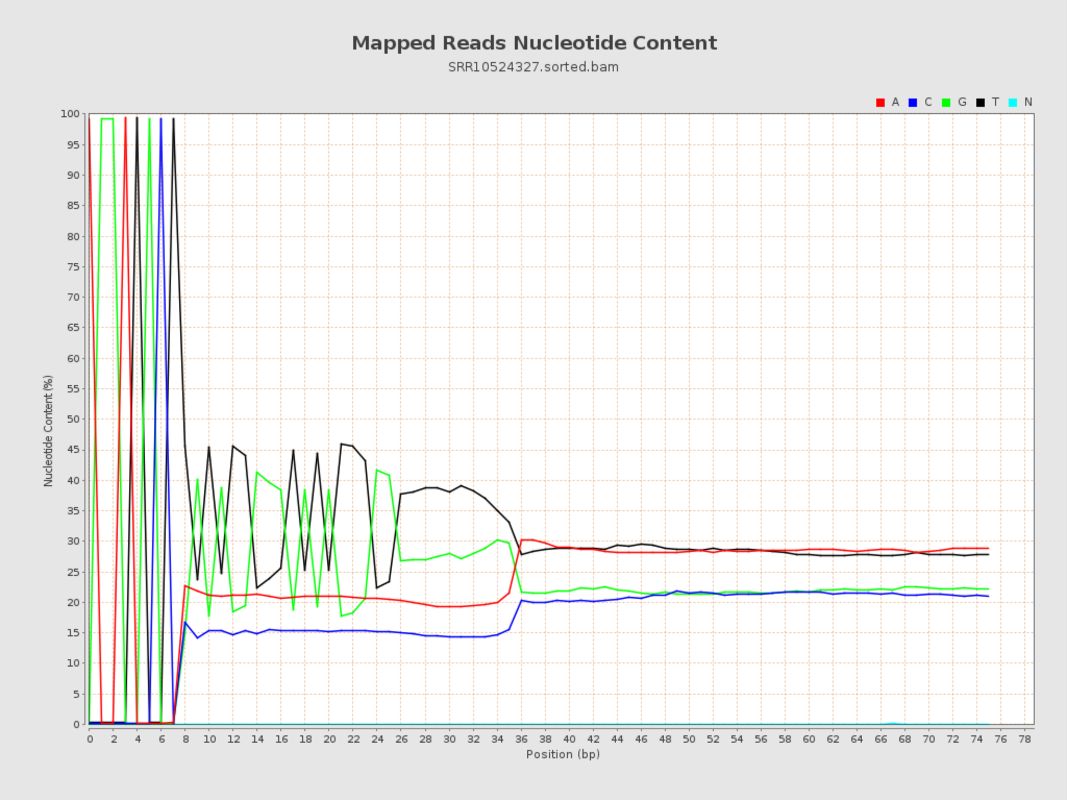
6. Results : Genome Fraction Coverage



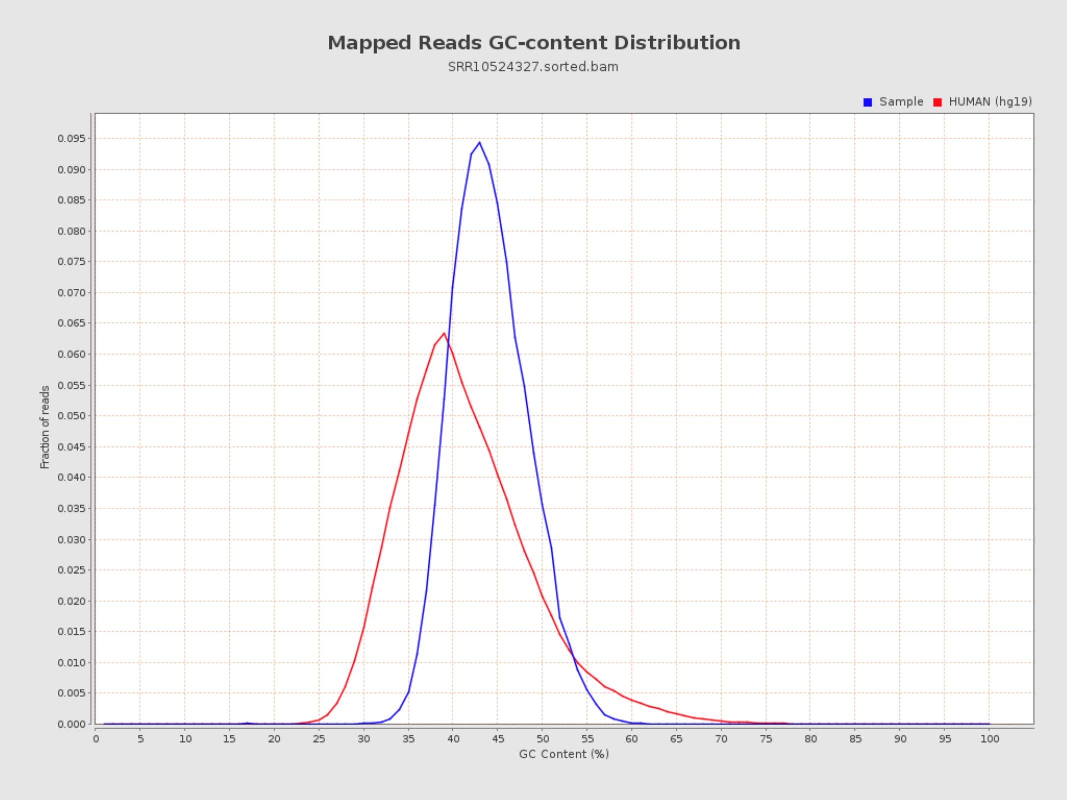
7. Results : Duplication Rate Histogram



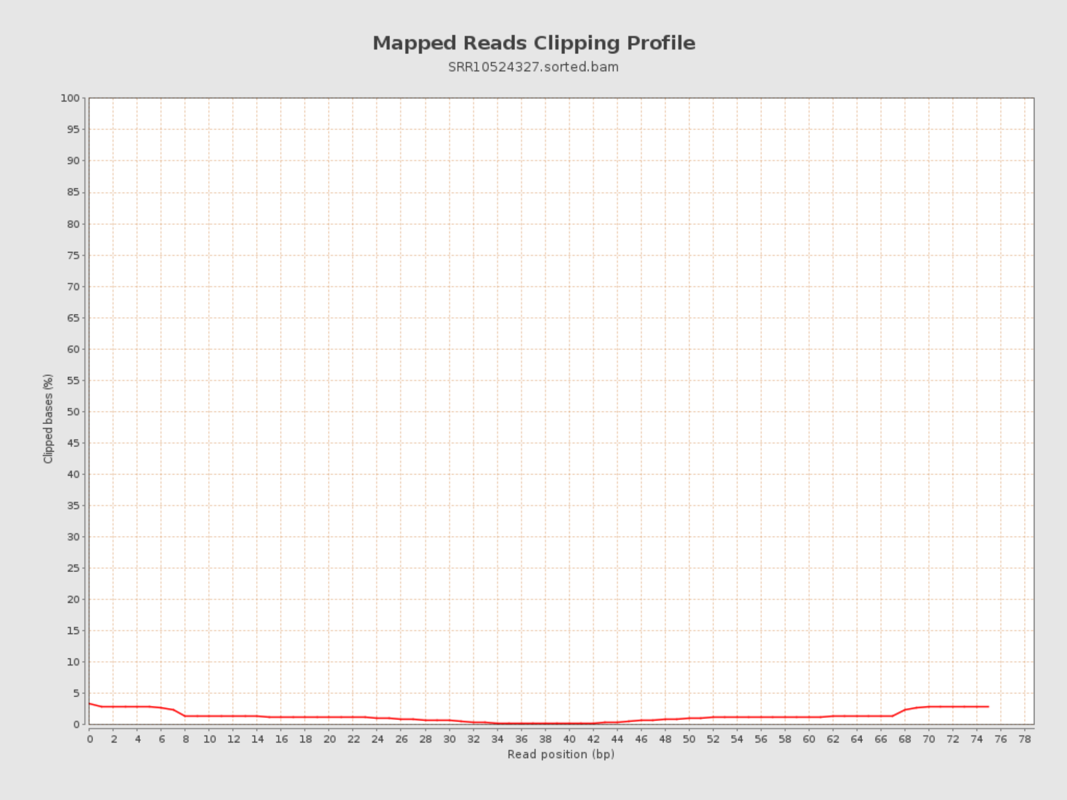
8. Results : Mapped Reads Nucleotide Content



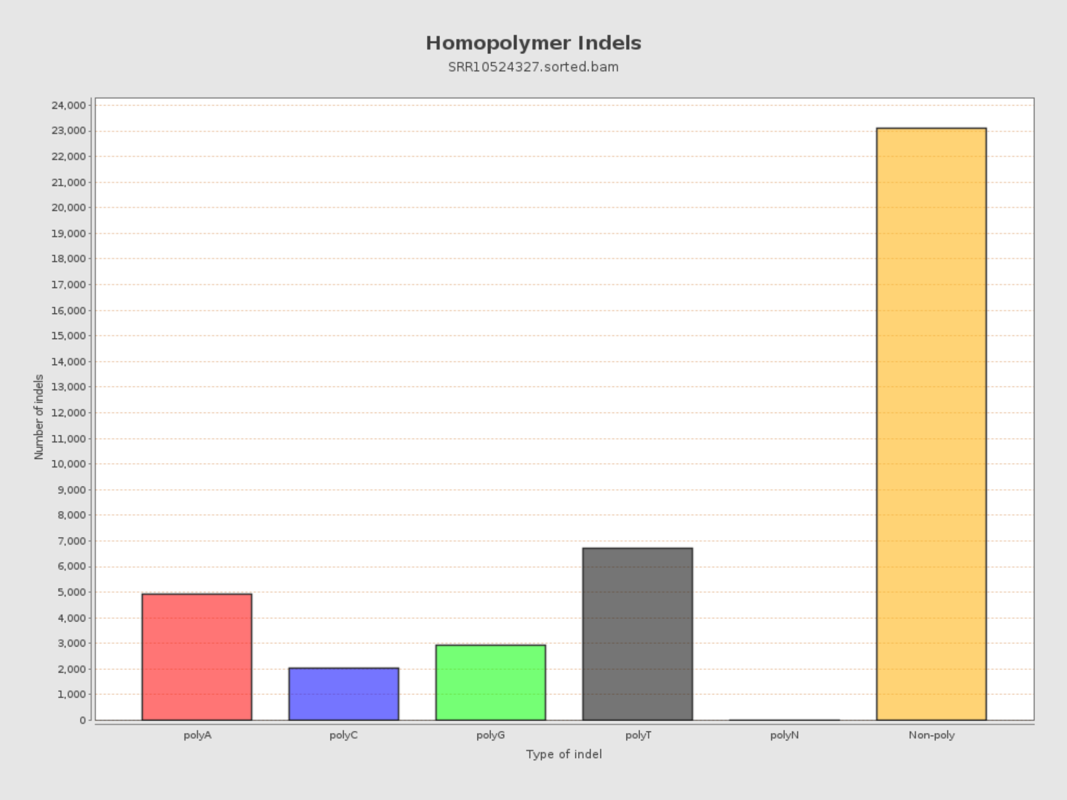
9. Results : Mapped Reads GC-content Distribution



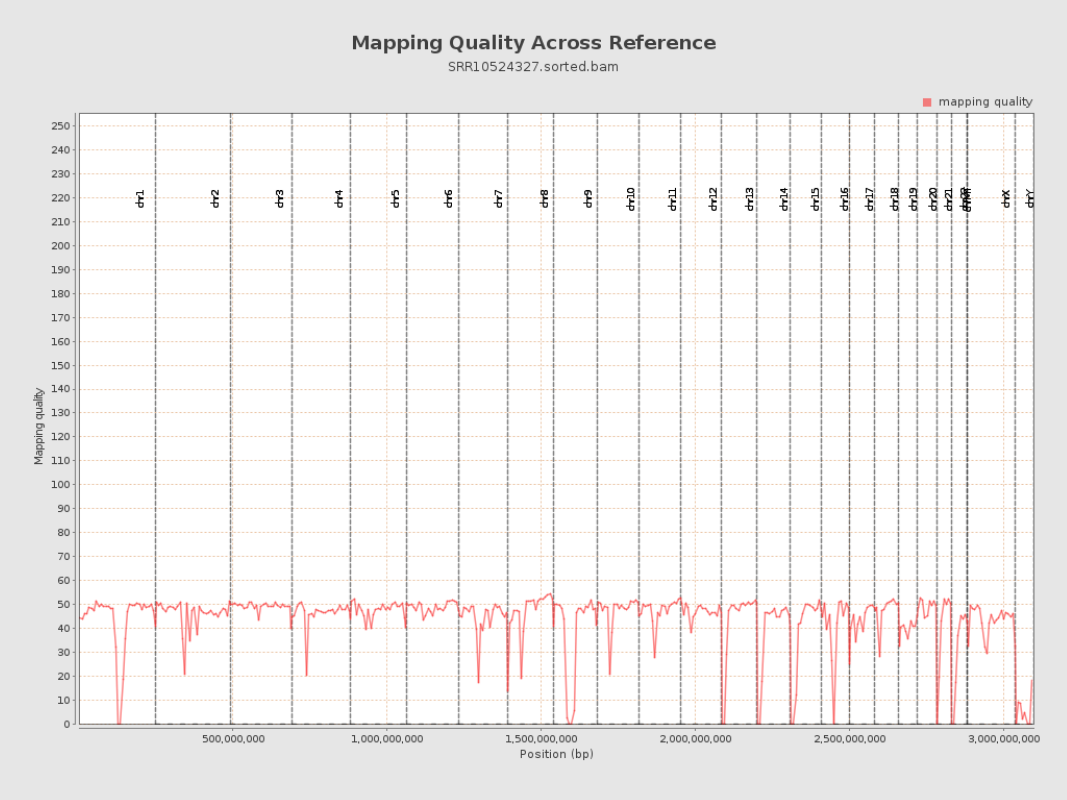
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram