Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524352.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_SRR10524352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524352.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,065
Mapped reads	2,019,510 / 91.42%
Unmapped reads	189,555 / 8.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,683 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	116,561 / 5.28%
Duplication rate	4.31%
Clipped reads	2,024,001 / 91.62%

2.2. ACGT Content

Number/percentage of A's	30,176,052 / 25.47%
Number/percentage of C's	20,619,260 / 17.4%
Number/percentage of T's	37,731,639 / 31.84%
Number/percentage of G's	29,942,608 / 25.27%
Number/percentage of N's	16,261 / 0.01%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3647

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

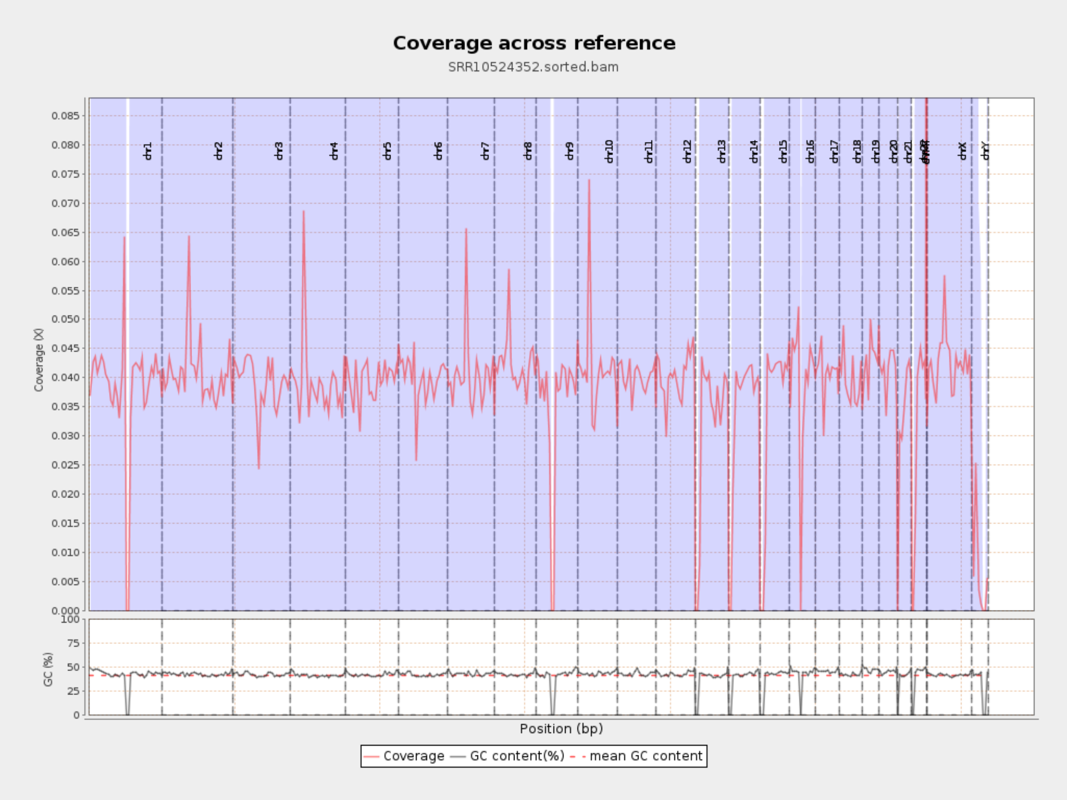
General error rate	0.53%
Mismatches	605,516
Insertions	8,619
Mapped reads with at least one insertion	0.42%
Deletions	20,376
Mapped reads with at least one deletion	1%
Homopolymer indels	42.18%

2.6. Chromosome stats

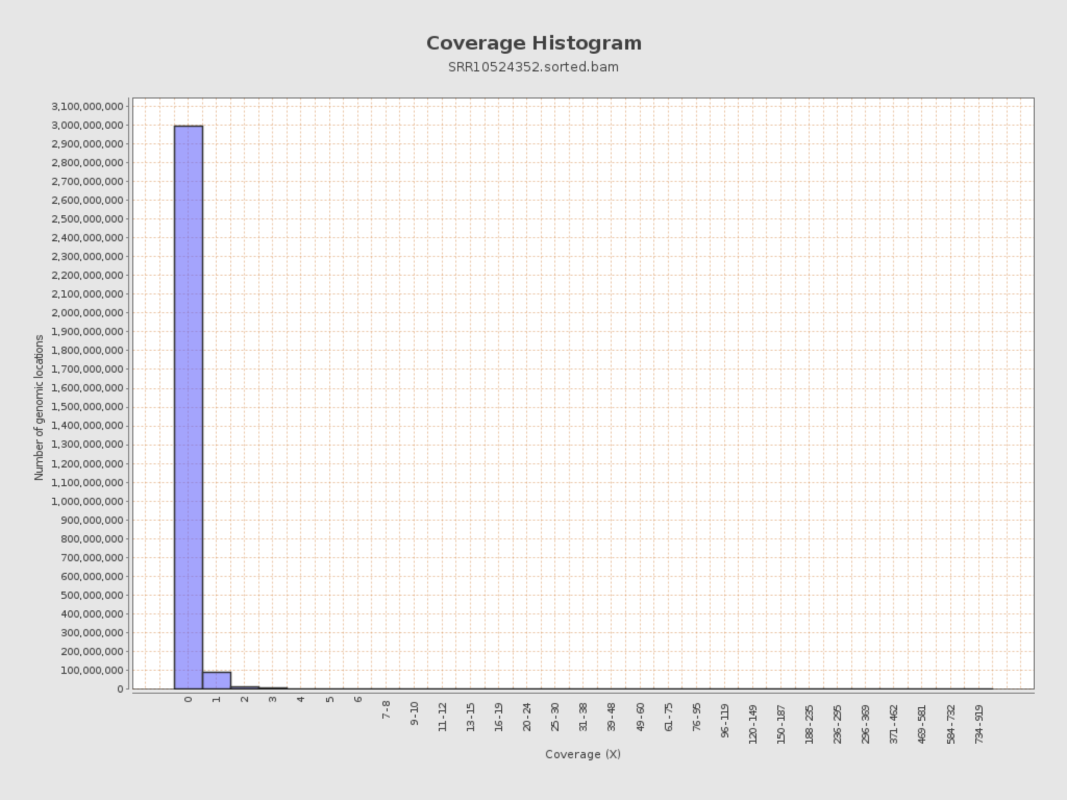
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9507821	0.0381	0.7096
chr2	243199373	9989931	0.0411	0.4704
chr3	198022430	7741545	0.0391	0.2255
chr4	191154276	7456911	0.039	0.2755
chr5	180915260	7127051	0.0394	0.2265
chr6	171115067	6839782	0.04	0.2518
chr7	159138663	6453253	0.0406	0.4515

chr8	146364022	6196421	0.0423	0.3371
chr9	141213431	4886309	0.0346	0.2951
chr10	135534747	5647683	0.0417	0.3646
chr11	135006516	5404813	0.04	0.3098
chr12	133851895	5391849	0.0403	0.2366
chr13	115169878	3637733	0.0316	0.2014
chr14	107349540	3603384	0.0336	0.2292
chr15	102531392	3465917	0.0338	0.2096
chr16	90354753	3523813	0.039	0.2457
chr17	81195210	3301837	0.0407	0.2544
chr18	78077248	3096478	0.0397	0.5948
chr19	59128983	2544114	0.043	0.4583
chr20	63025520	2599162	0.0412	0.2415
chr21	48129895	1576993	0.0328	0.2459
chr22	51304566	1506943	0.0294	0.1973
chrMT	16571	12639	0.7627	1.0037
chrX	155270560	6594250	0.0425	0.268
chrY	59373566	411628	0.0069	0.2039

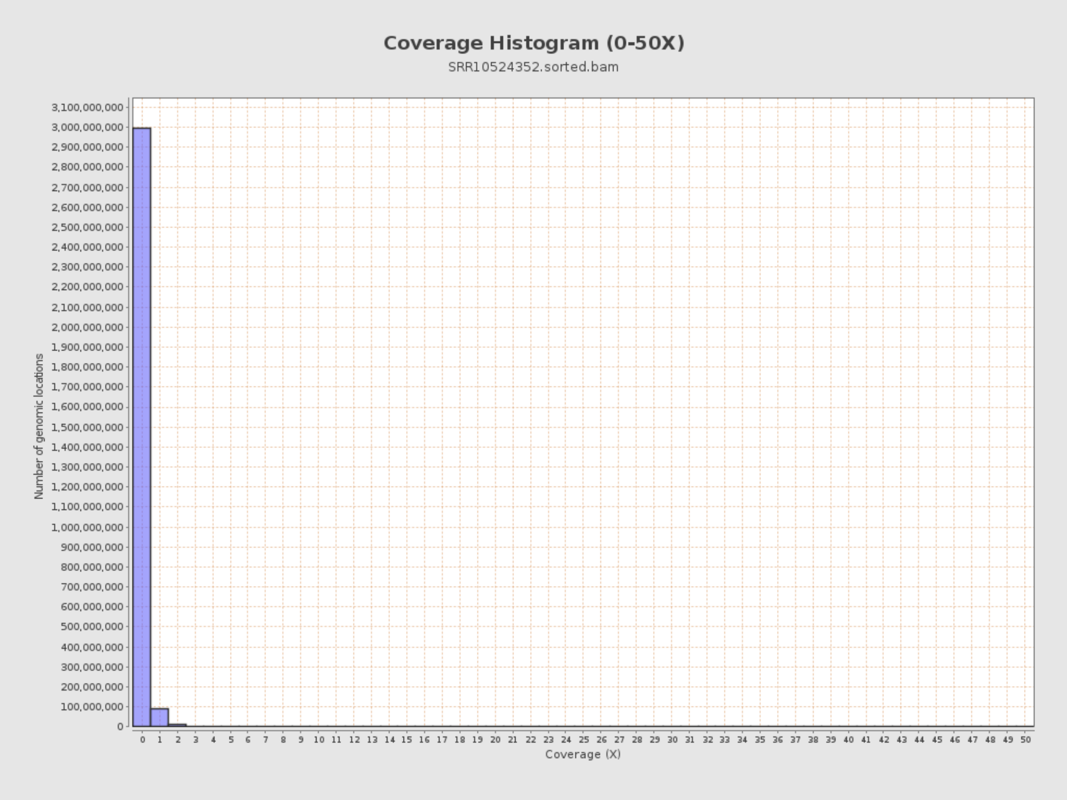
3. Results : Coverage across reference



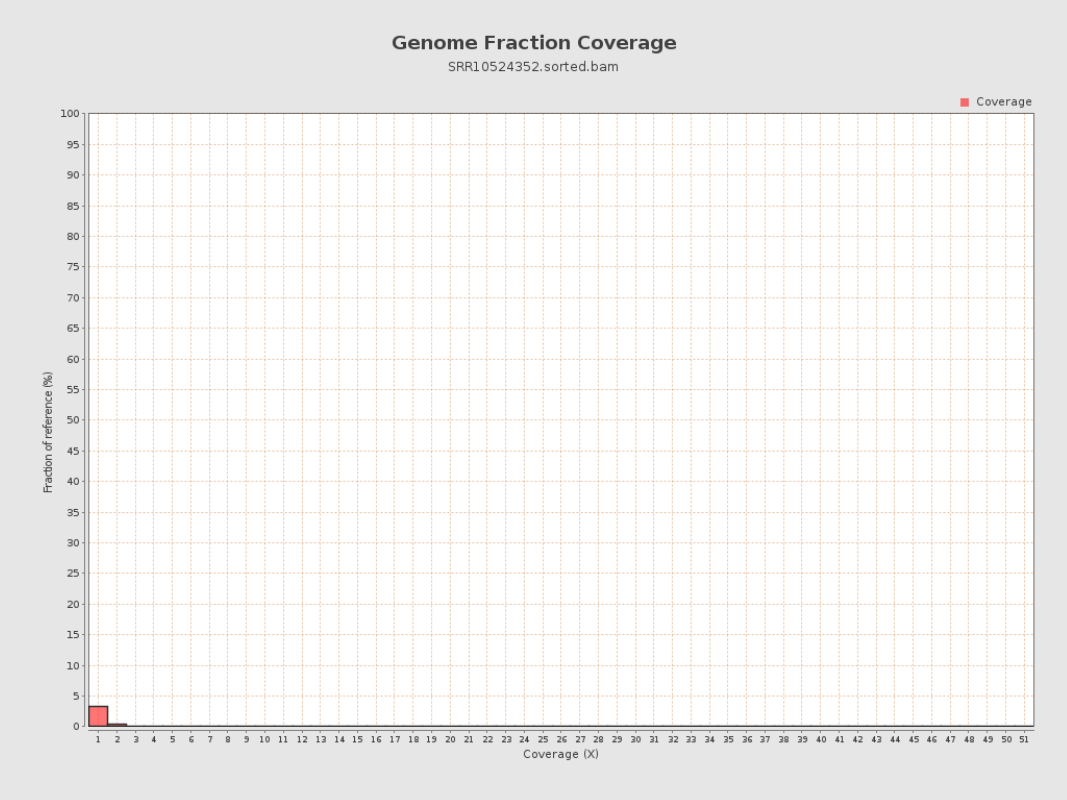
4. Results : Coverage Histogram



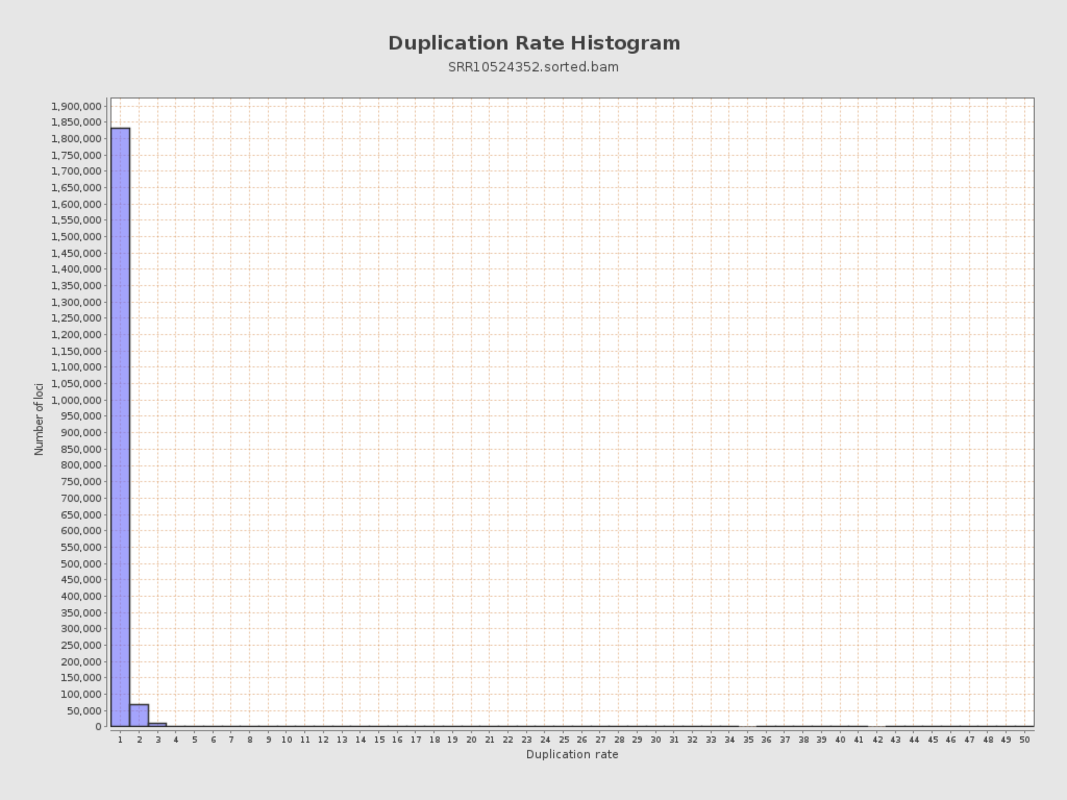
5. Results : Coverage Histogram (0-50X)



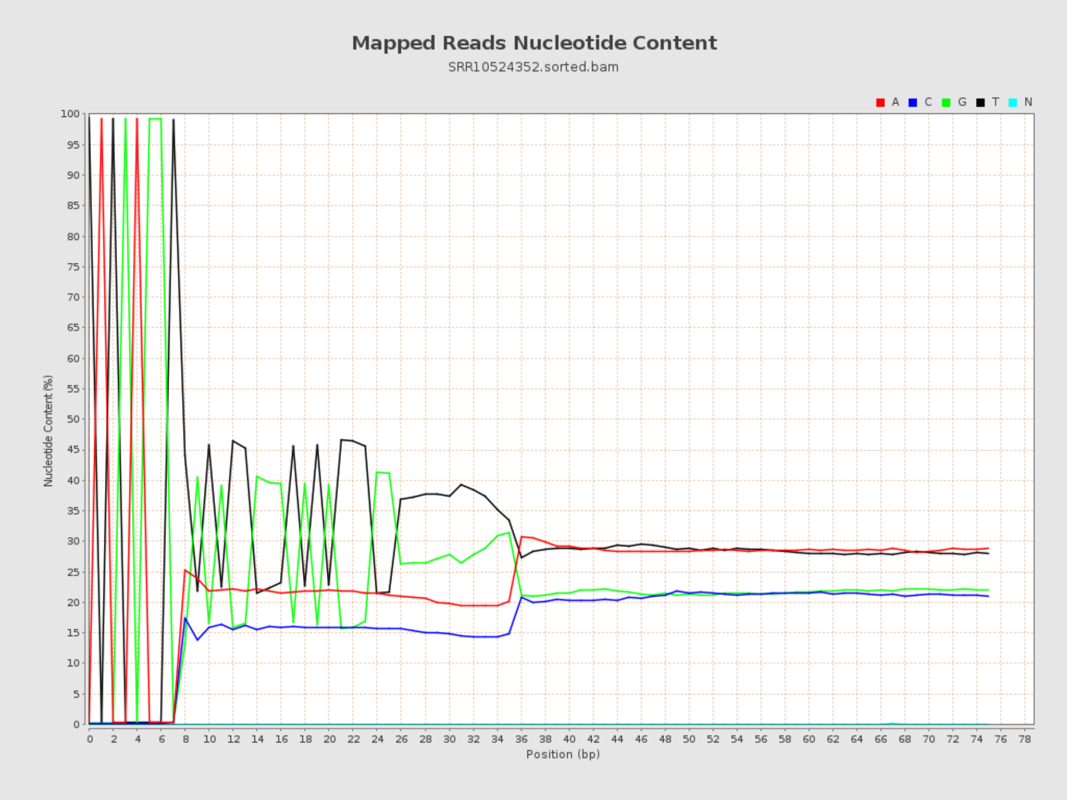
6. Results : Genome Fraction Coverage



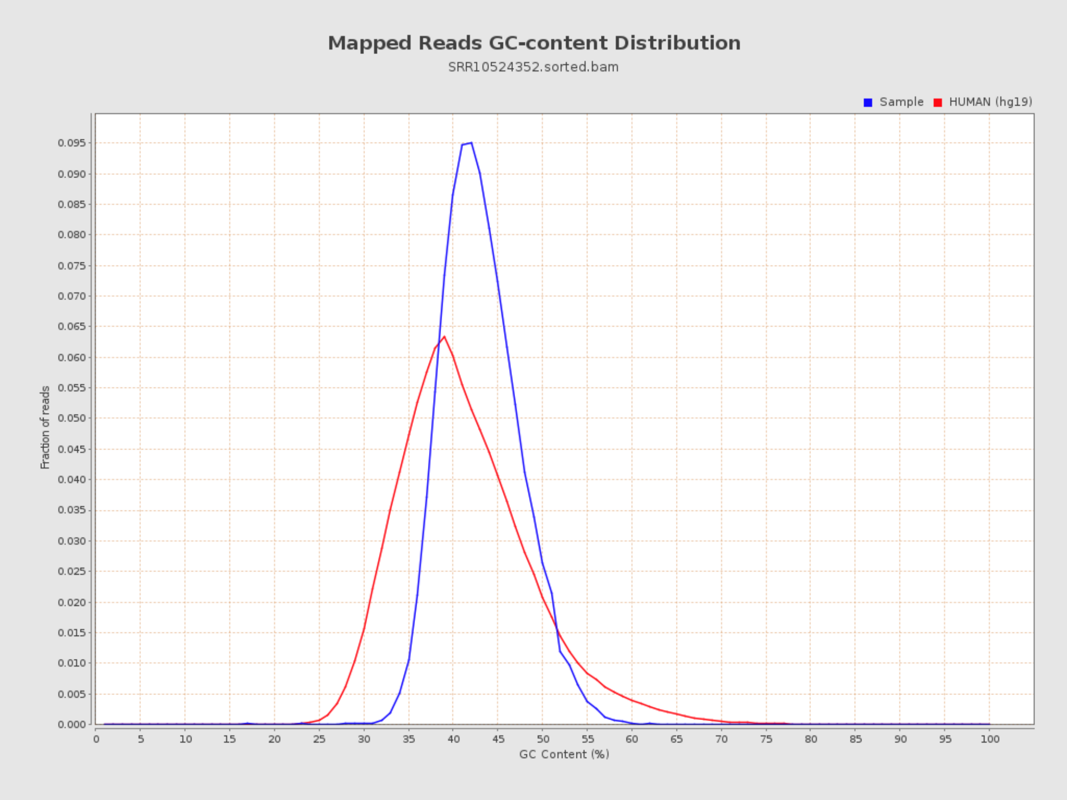
7. Results : Duplication Rate Histogram



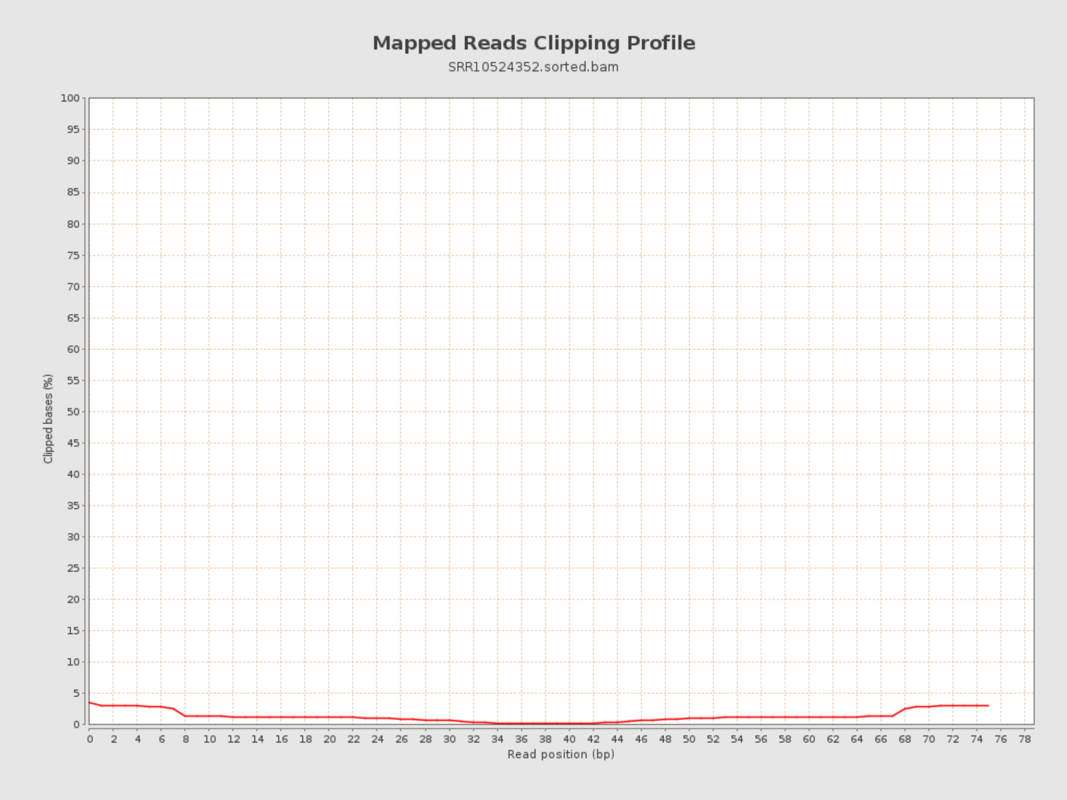
8. Results : Mapped Reads Nucleotide Content



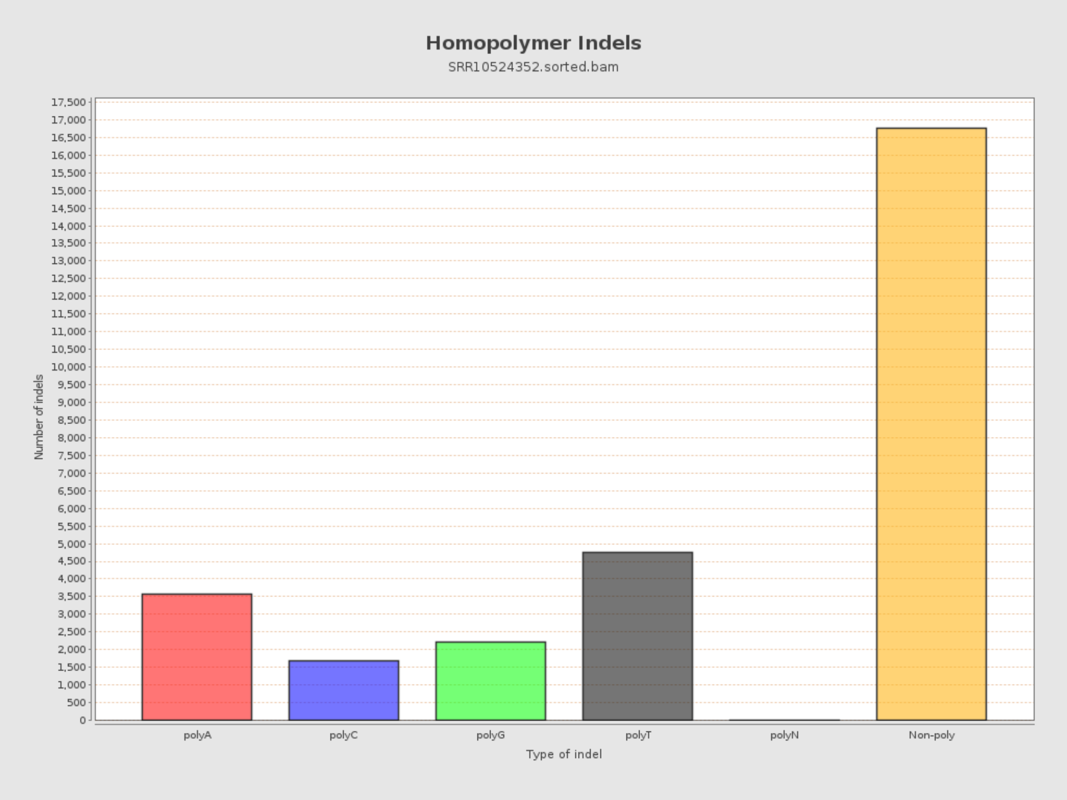
9. Results : Mapped Reads GC-content Distribution



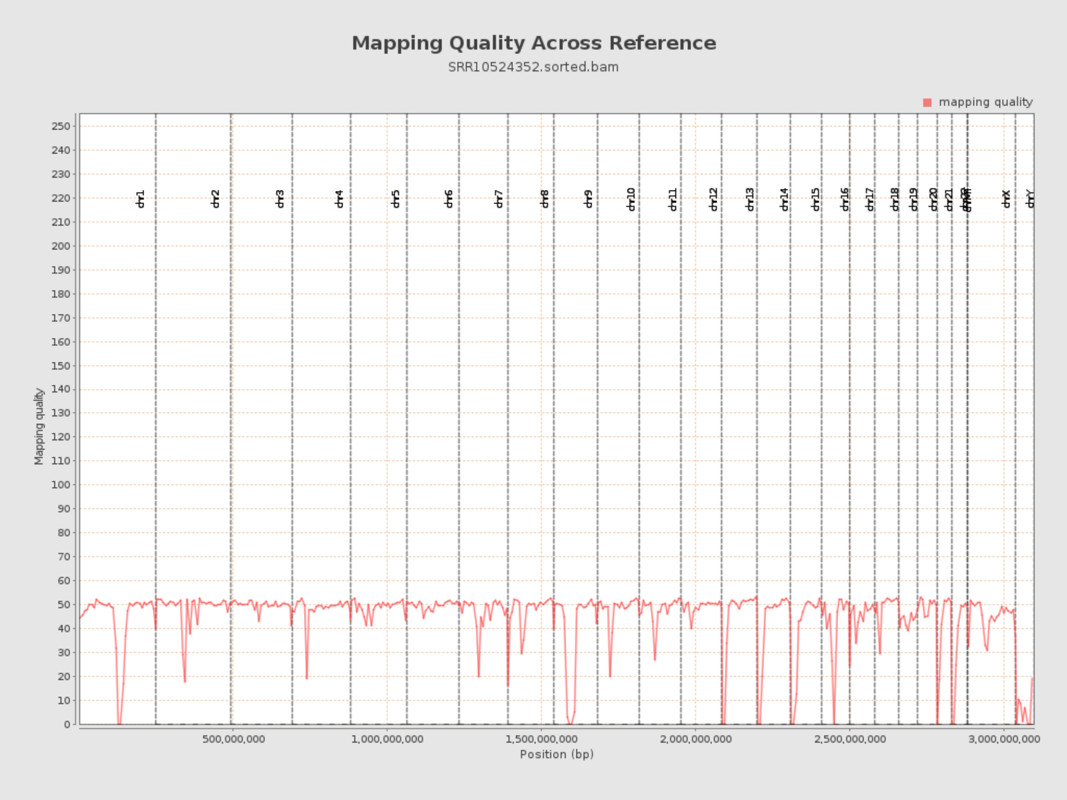
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram