Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:01:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524746.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_SRR10524746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:01:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,401,395
Mapped reads	1,274,658 / 90.96%
Unmapped reads	126,737 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,478 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	44,407 / 3.17%
Duplication rate	2.66%
Clipped reads	1,275,641 / 91.03%

2.2. ACGT Content

Number/percentage of A's	17,062,755 / 23.29%
Number/percentage of C's	13,018,923 / 17.77%
Number/percentage of T's	24,277,845 / 33.13%
Number/percentage of G's	18,906,839 / 25.8%
Number/percentage of N's	9,009 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2169

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

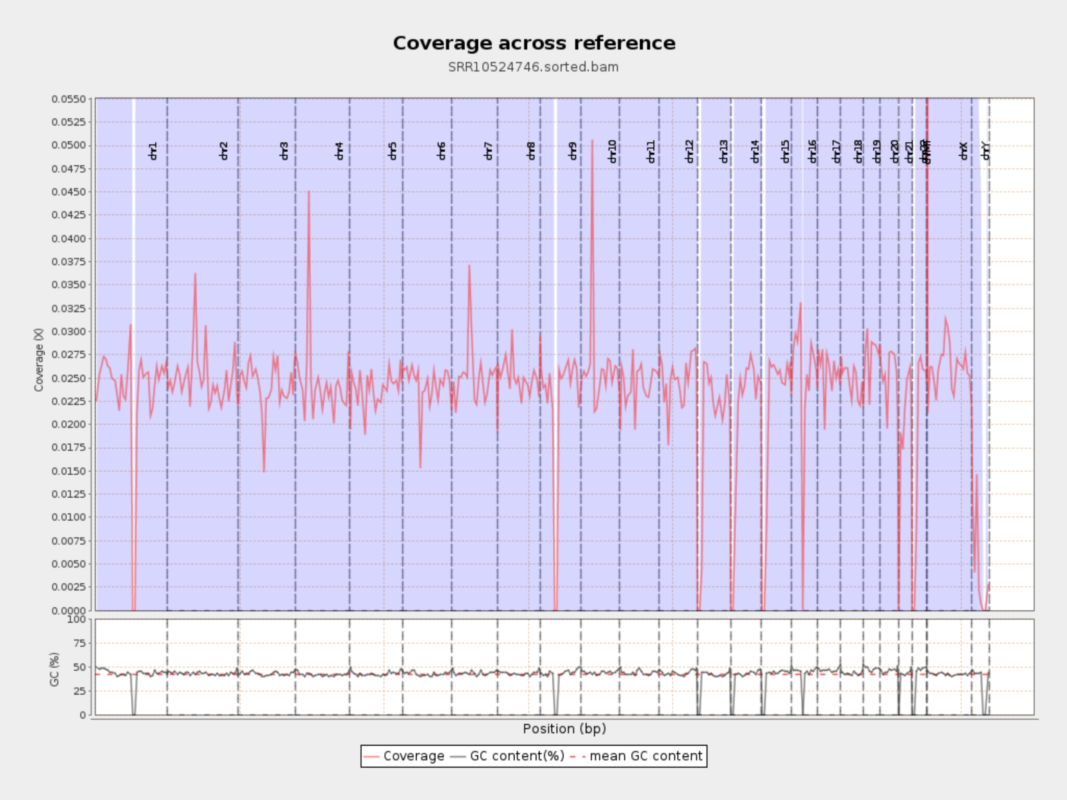
General error rate	0.53%
Mismatches	381,395
Insertions	5,523
Mapped reads with at least one insertion	0.43%
Deletions	15,787
Mapped reads with at least one deletion	1.23%
Homopolymer indels	40.92%

2.6. Chromosome stats

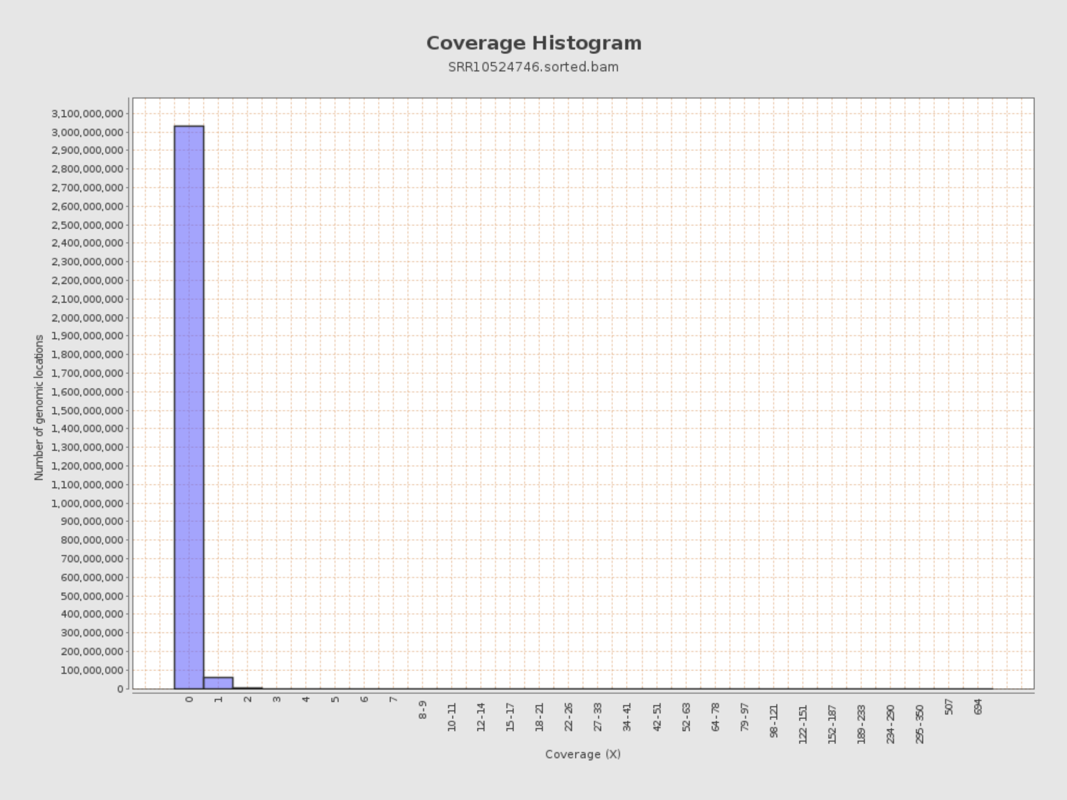
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5841287	0.0234	0.2833
chr2	243199373	6102659	0.0251	0.3397
chr3	198022430	4781463	0.0241	0.1715
chr4	191154276	4711996	0.0247	0.1919
chr5	180915260	4339990	0.024	0.1684
chr6	171115067	4153051	0.0243	0.1823
chr7	159138663	4044948	0.0254	0.2601

chr8	146364022	3671126	0.0251	0.2024
chr9	141213431	3128867	0.0222	0.185
chr10	135534747	3595823	0.0265	0.2587
chr11	135006516	3301588	0.0245	0.194
chr12	133851895	3327554	0.0249	0.1732
chr13	115169878	2260698	0.0196	0.1518
chr14	107349540	2207935	0.0206	0.1581
chr15	102531392	2129120	0.0208	0.1576
chr16	90354753	2235336	0.0247	0.1858
chr17	81195210	2085311	0.0257	0.1801
chr18	78077248	1927380	0.0247	0.2786
chr19	59128983	1623804	0.0275	0.2444
chr20	63025520	1598198	0.0254	0.1828
chr21	48129895	959677	0.0199	0.1668
chr22	51304566	931597	0.0182	0.1475
chrMT	16571	27341	1.6499	1.663
chrX	155270560	4064941	0.0262	0.1856
chrY	59373566	249777	0.0042	0.1246

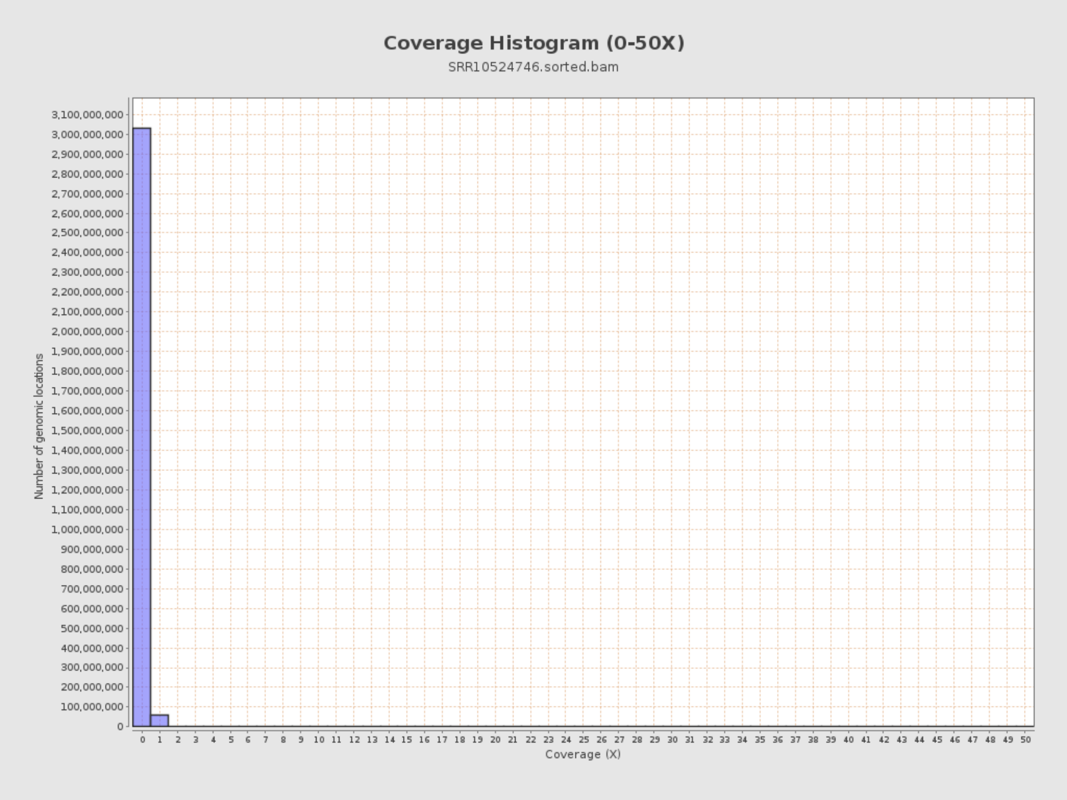
3. Results : Coverage across reference



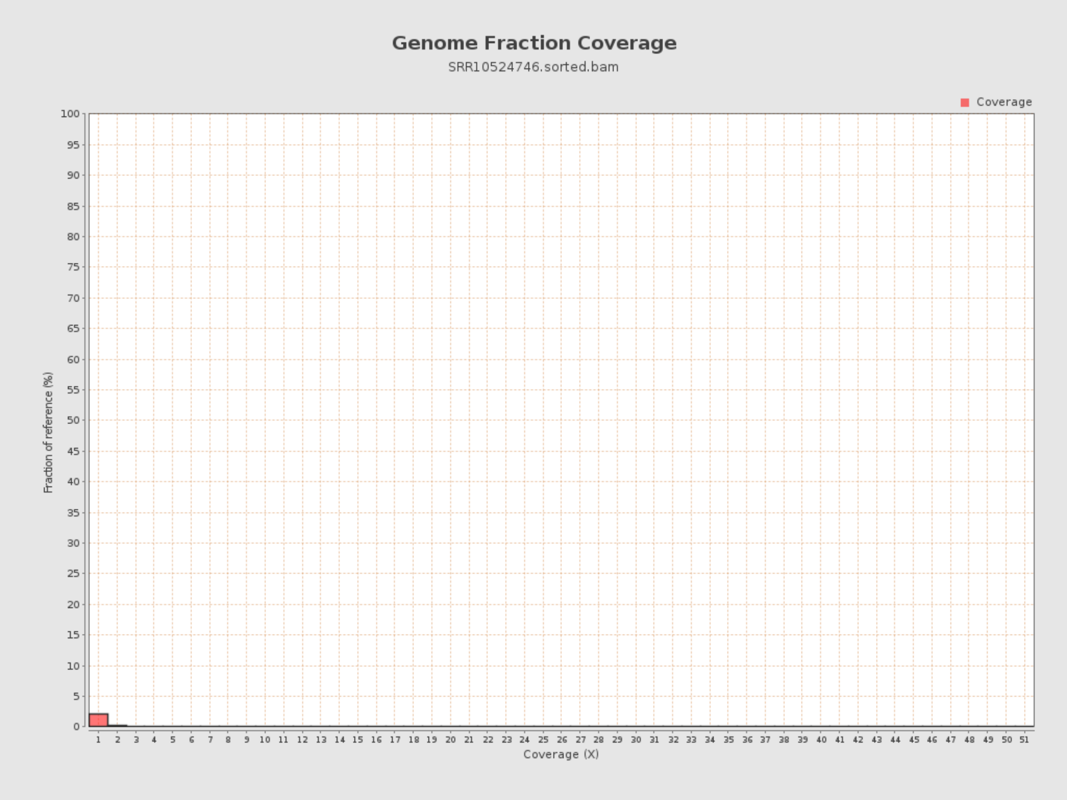
4. Results : Coverage Histogram



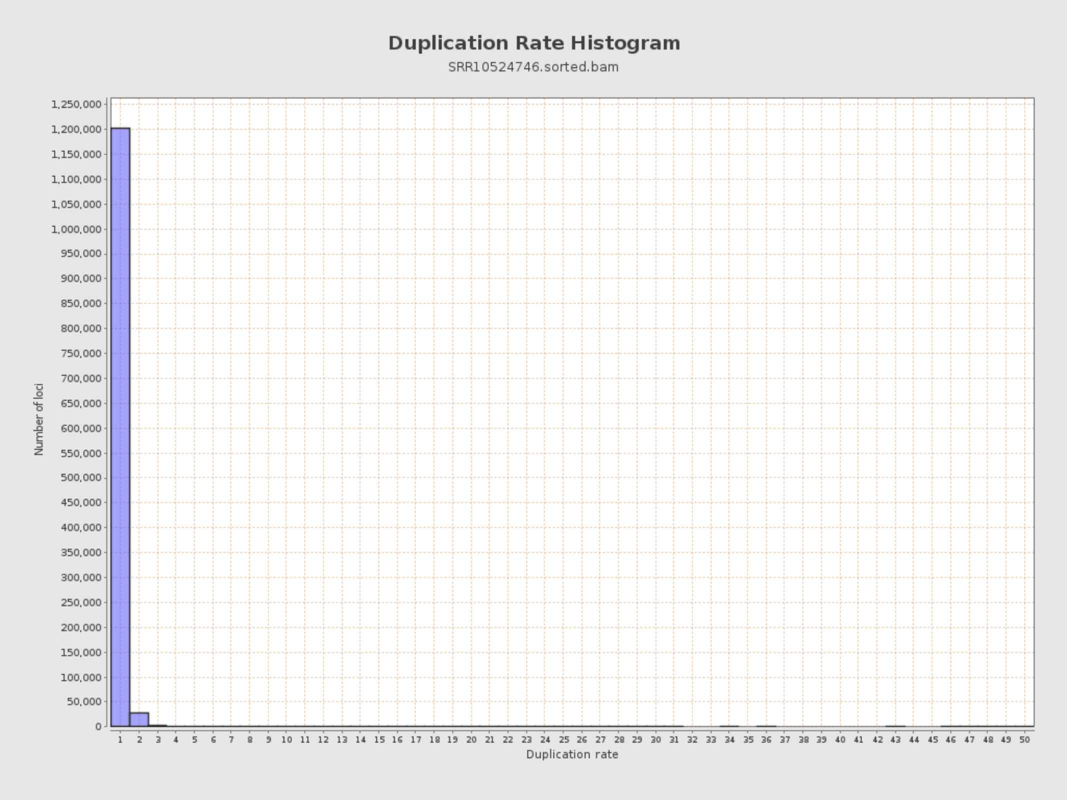
5. Results : Coverage Histogram (0-50X)



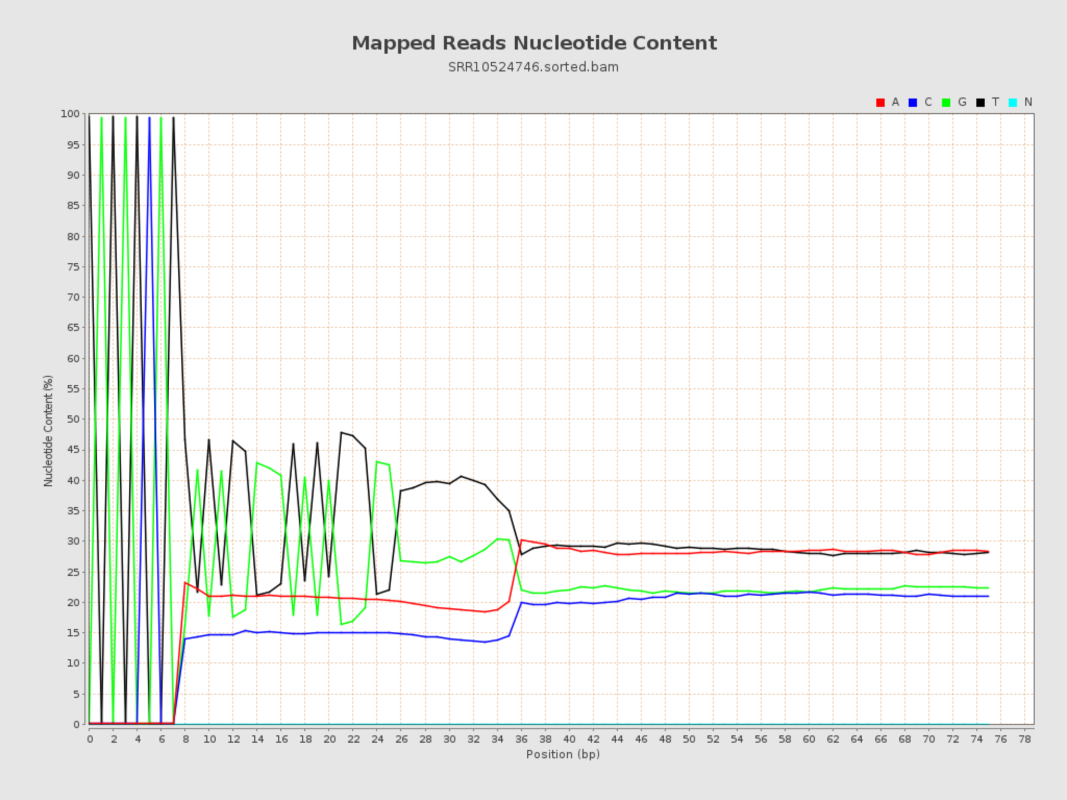
6. Results : Genome Fraction Coverage



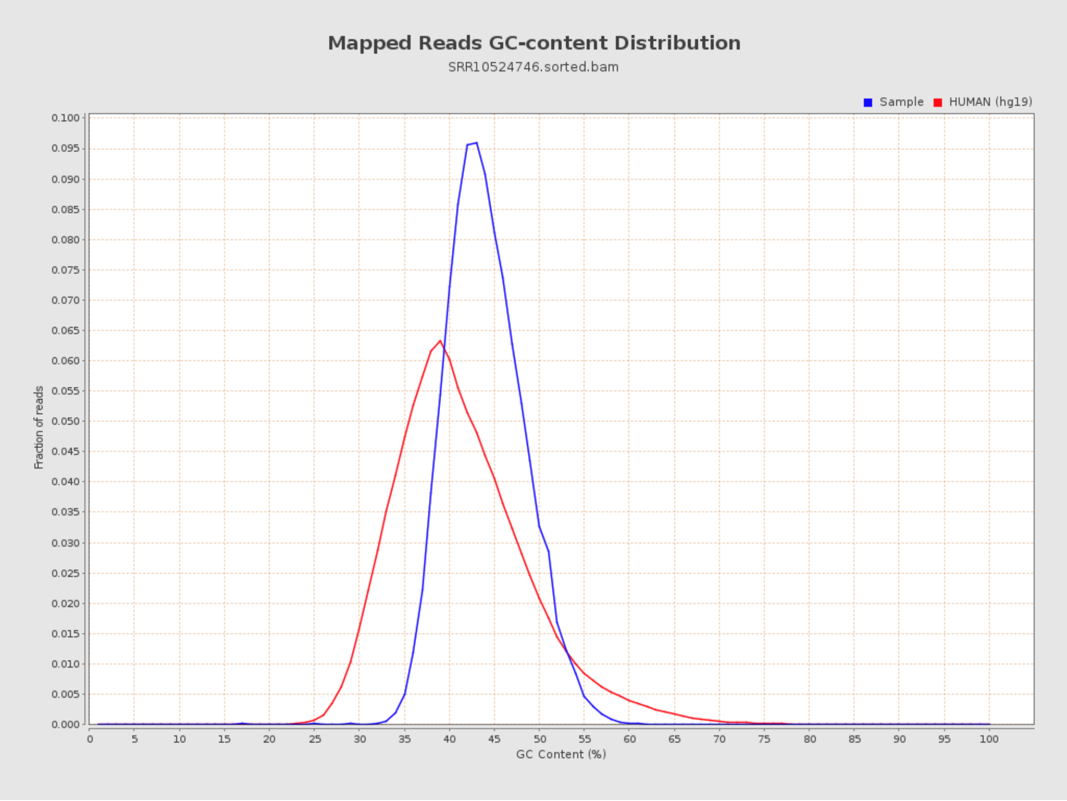
7. Results : Duplication Rate Histogram



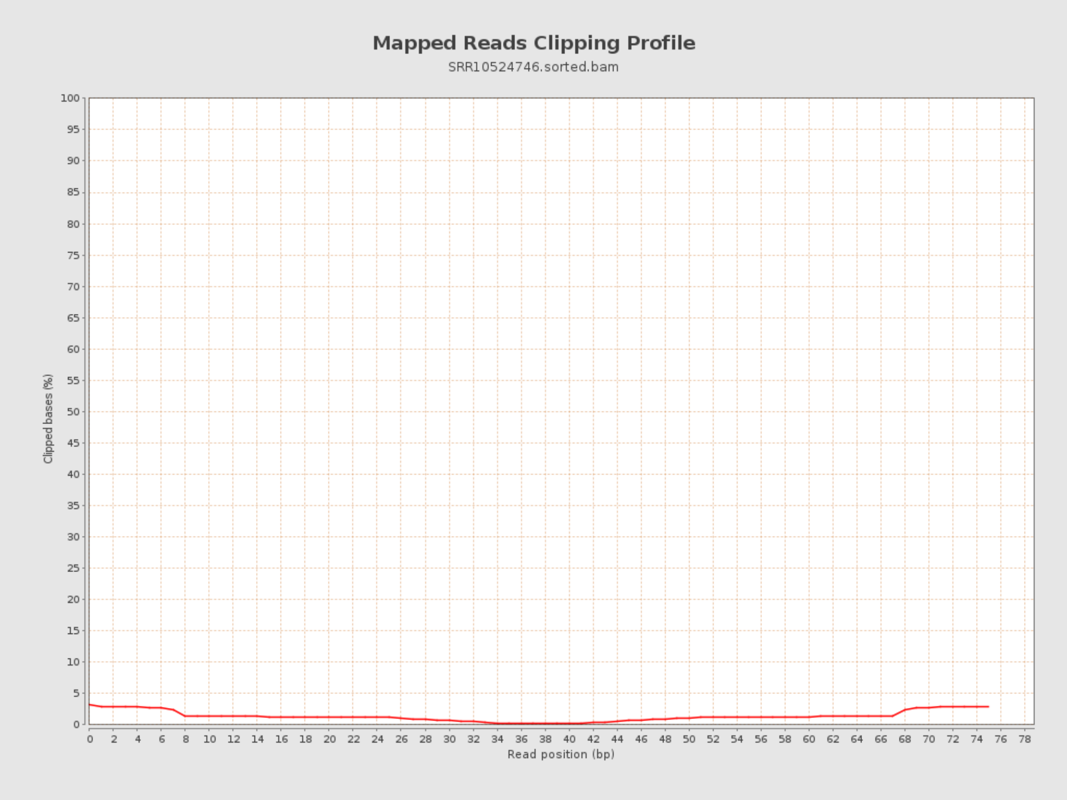
8. Results : Mapped Reads Nucleotide Content



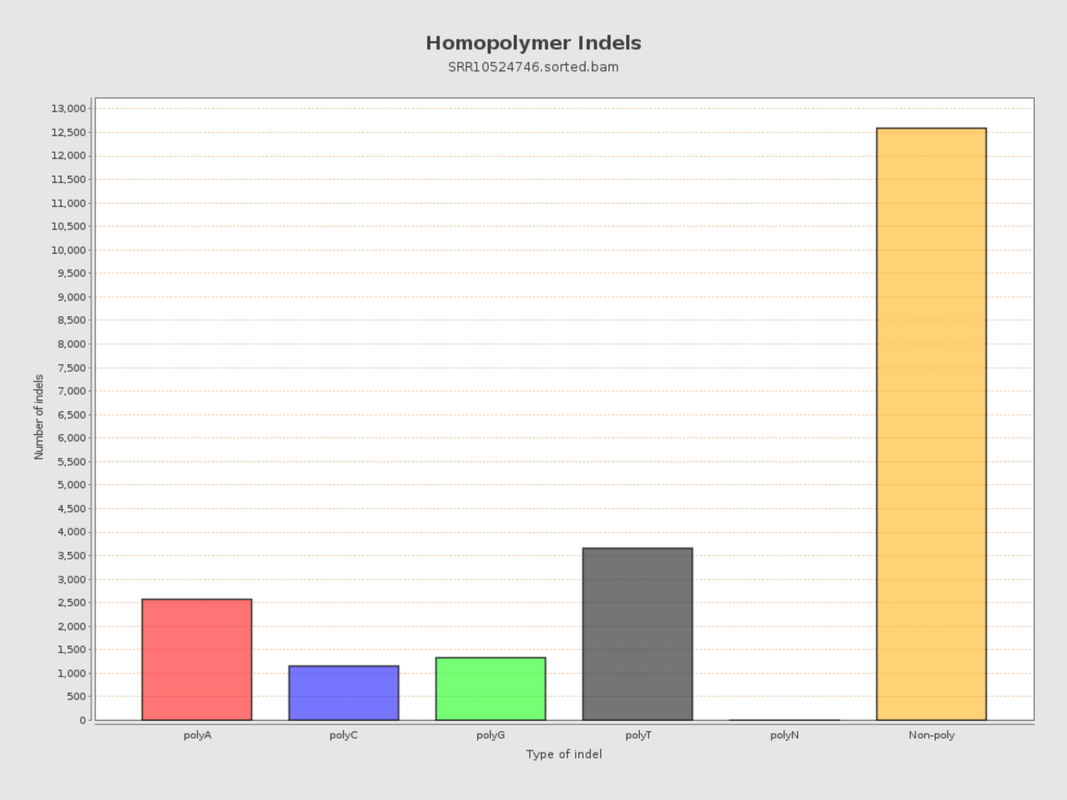
9. Results : Mapped Reads GC-content Distribution



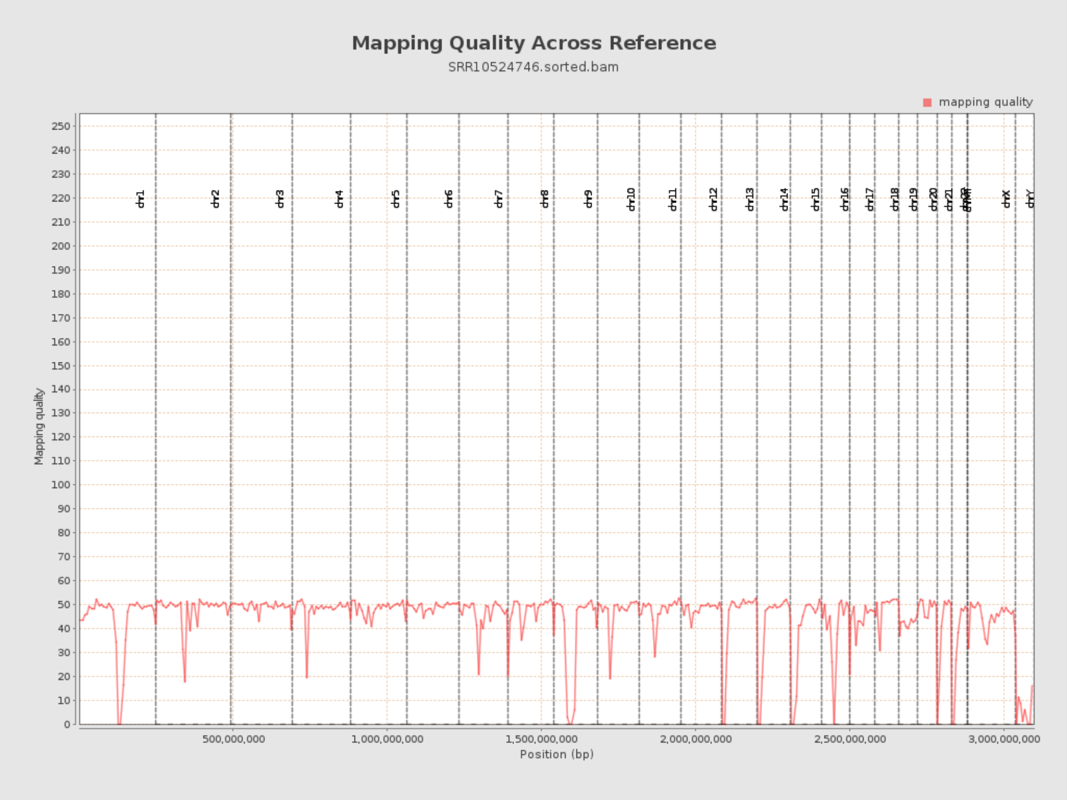
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram