Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:23:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524336.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_SRR10524336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:23:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,354,017
Mapped reads	1,236,829 / 91.35%
Unmapped reads	117,188 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,522 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	35,064 / 2.59%
Duplication rate	2.05%
Clipped reads	1,238,335 / 91.46%

2.2. ACGT Content

Number/percentage of A's	18,438,906 / 25.73%
Number/percentage of C's	13,593,603 / 18.97%
Number/percentage of T's	21,683,784 / 30.26%
Number/percentage of G's	17,924,626 / 25.02%
Number/percentage of N's	10,401 / 0.01%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2262

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

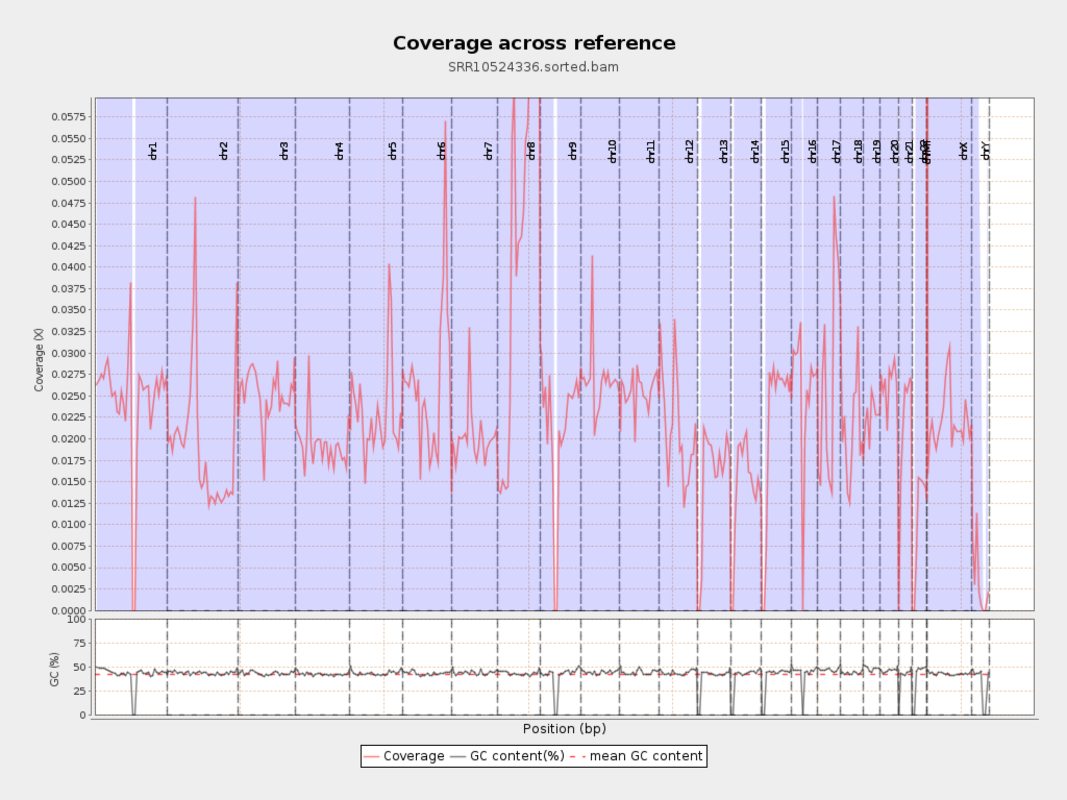
General error rate	0.52%
Mismatches	358,372
Insertions	5,502
Mapped reads with at least one insertion	0.44%
Deletions	11,218
Mapped reads with at least one deletion	0.9%
Homopolymer indels	41.63%

2.6. Chromosome stats

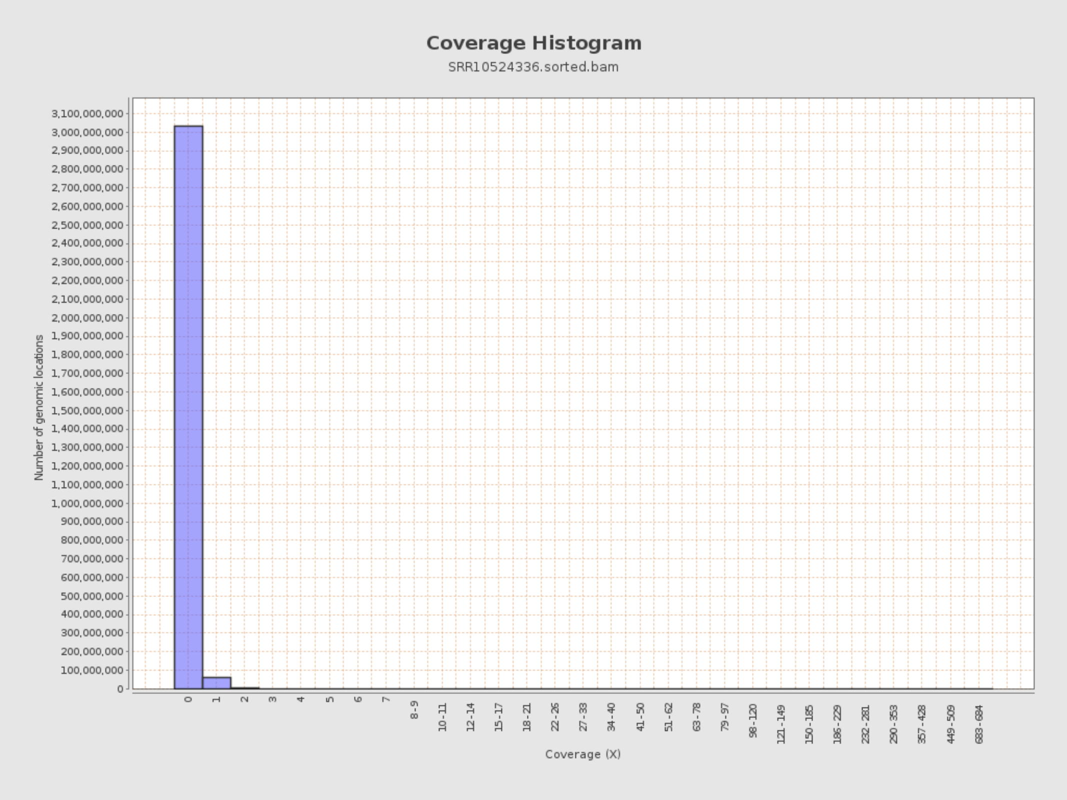
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6081736	0.0244	0.3907
chr2	243199373	4639793	0.0191	0.3097
chr3	198022430	4980807	0.0252	0.1694
chr4	191154276	3698415	0.0193	0.162
chr5	180915260	4207018	0.0233	0.163
chr6	171115067	4498994	0.0263	0.1816
chr7	159138663	3232166	0.0203	0.2506

chr8	146364022	7404003	0.0506	0.287
chr9	141213431	2974630	0.0211	0.1798
chr10	135534747	3634139	0.0268	0.2212
chr11	135006516	3458383	0.0256	0.1994
chr12	133851895	2814452	0.021	0.1565
chr13	115169878	1767232	0.0153	0.1319
chr14	107349540	1529472	0.0142	0.1318
chr15	102531392	2220195	0.0217	0.1577
chr16	90354753	2275648	0.0252	0.1761
chr17	81195210	2253865	0.0278	0.1919
chr18	78077248	1653883	0.0212	0.287
chr19	59128983	1336910	0.0226	0.261
chr20	63025520	1652114	0.0262	0.1746
chr21	48129895	1017777	0.0211	0.1624
chr22	51304566	539280	0.0105	0.1091
chrMT	16571	166173	10.0279	5.9659
chrX	155270560	3437856	0.0221	0.1712
chrY	59373566	194598	0.0033	0.0949

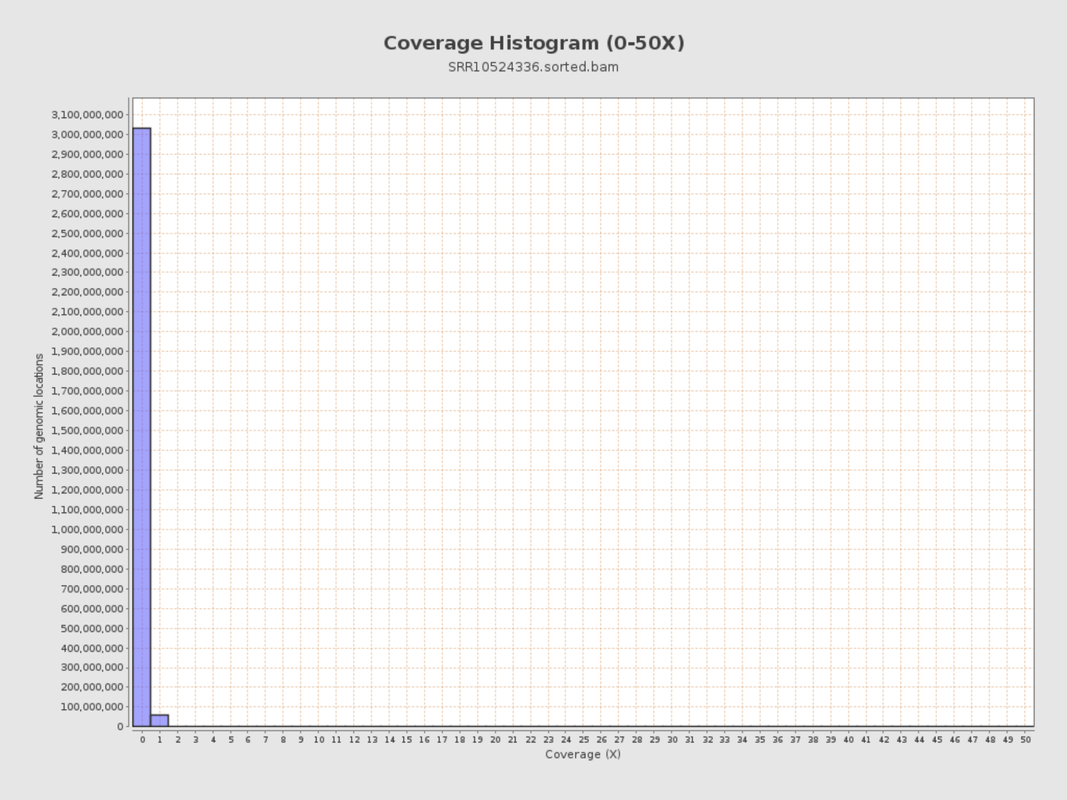
3. Results : Coverage across reference



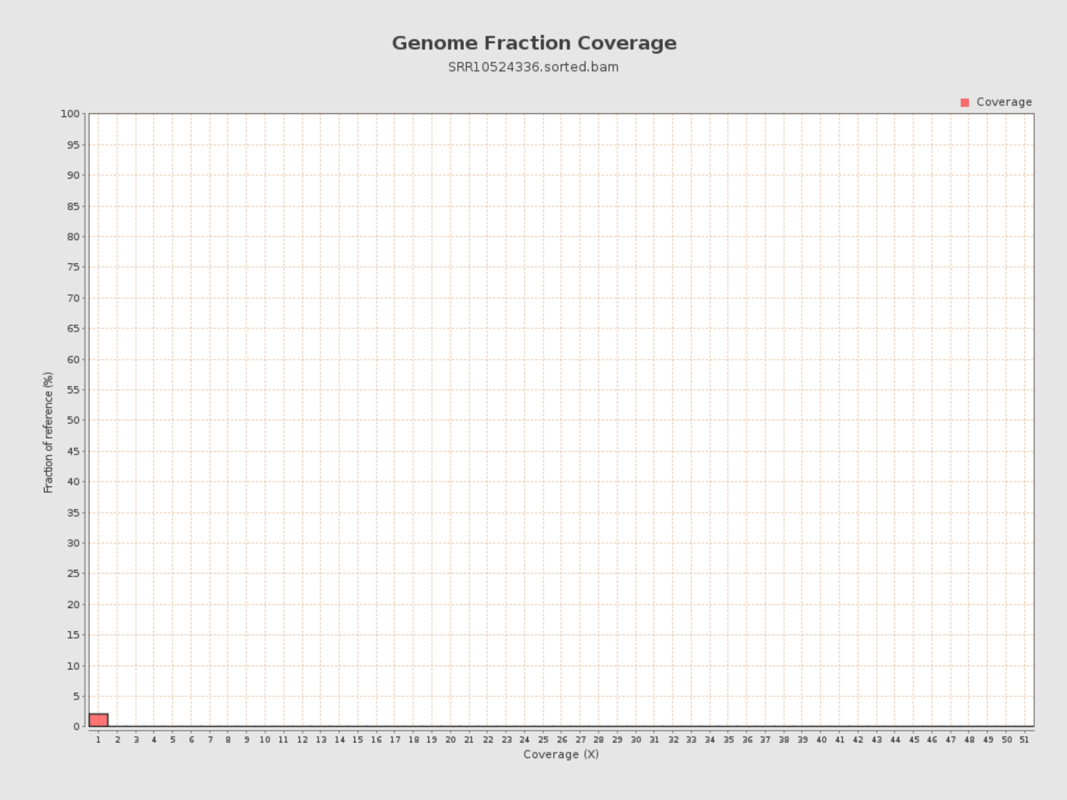
4. Results : Coverage Histogram



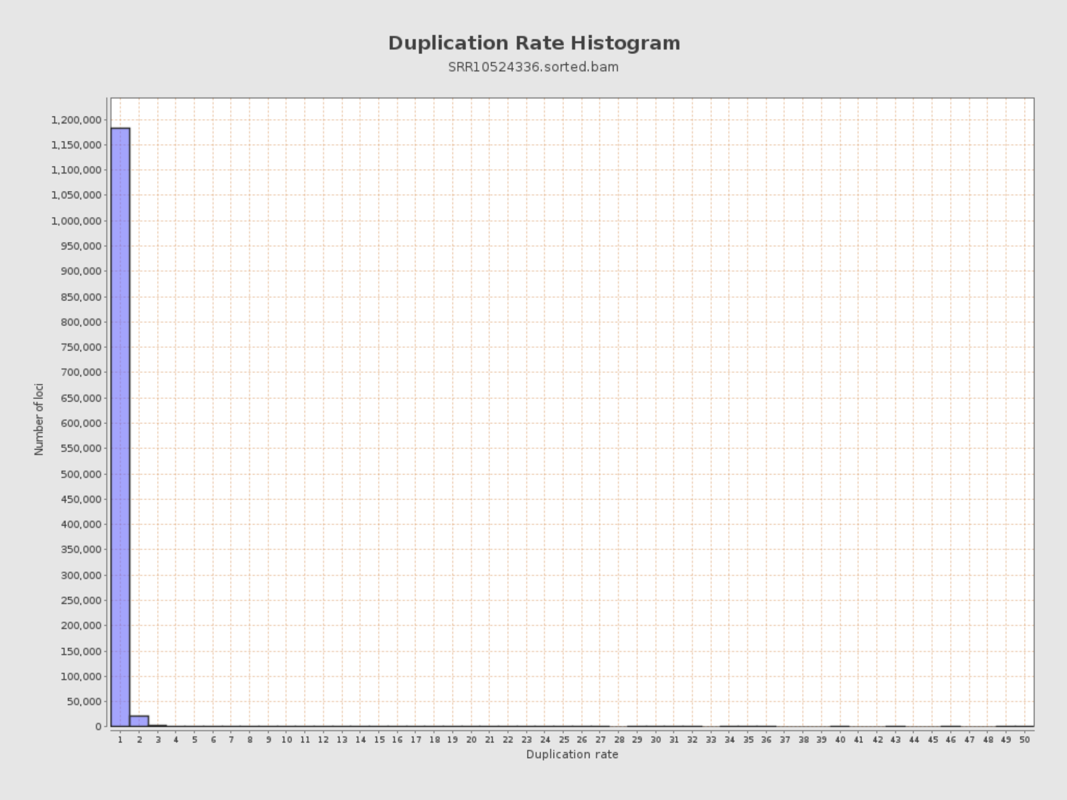
5. Results : Coverage Histogram (0-50X)



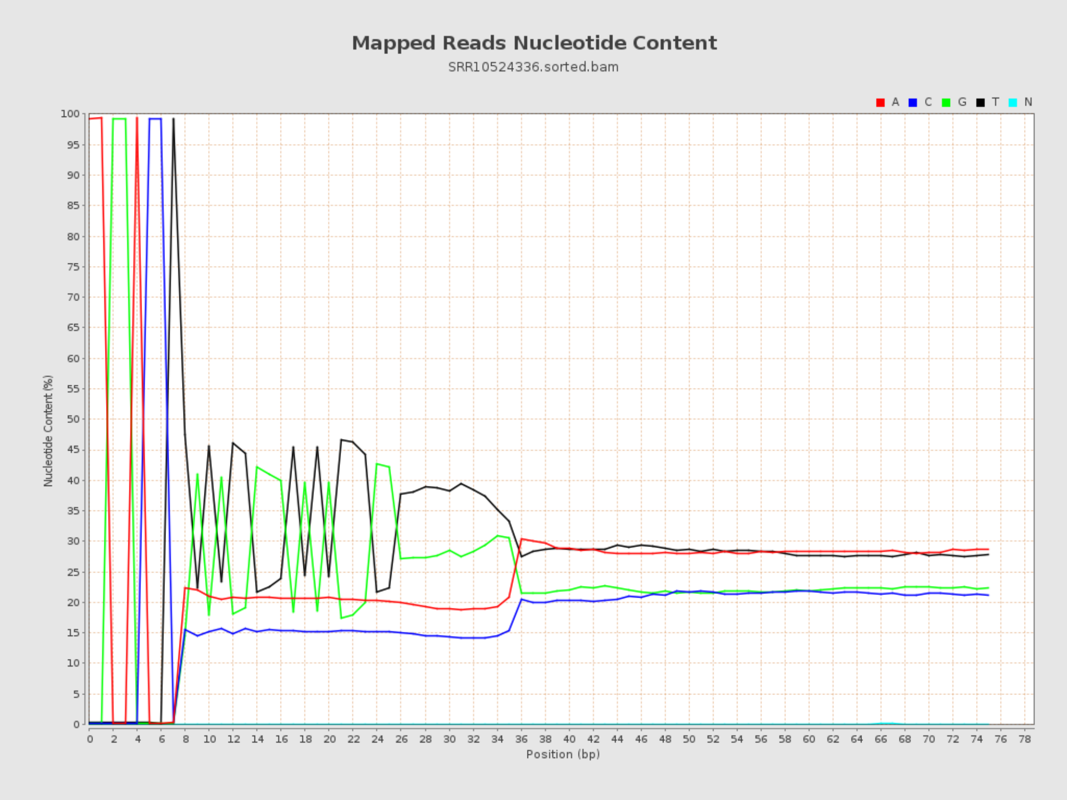
6. Results : Genome Fraction Coverage



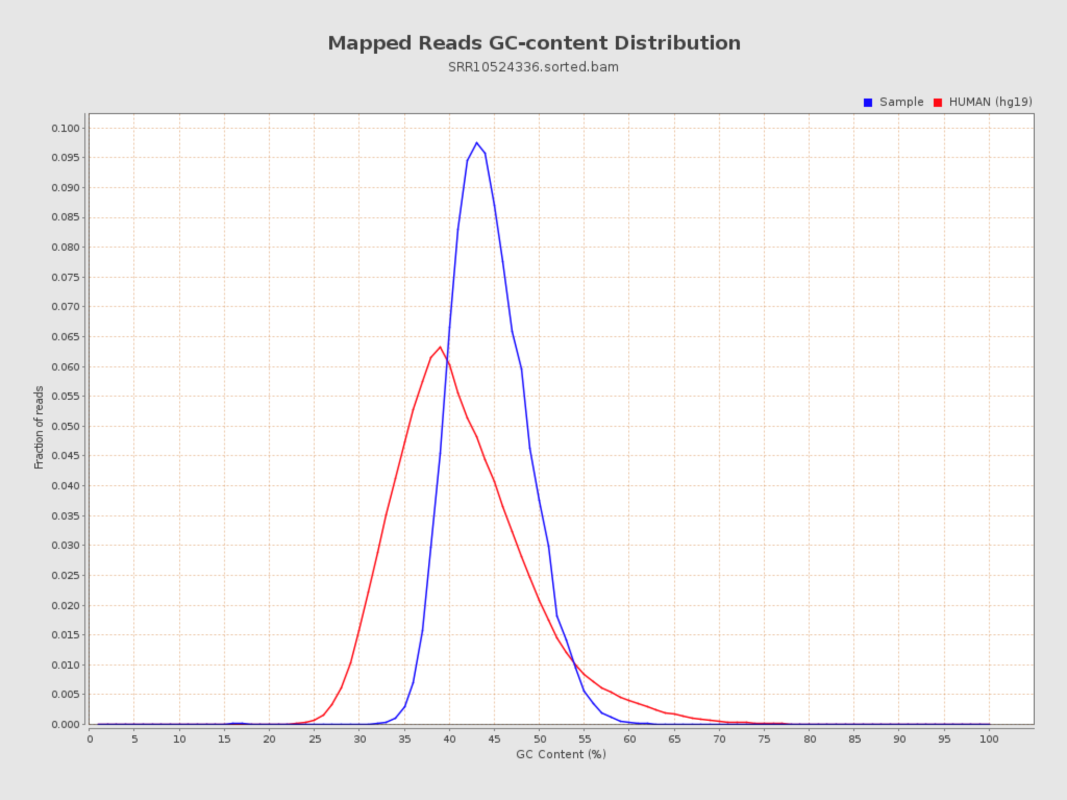
7. Results : Duplication Rate Histogram



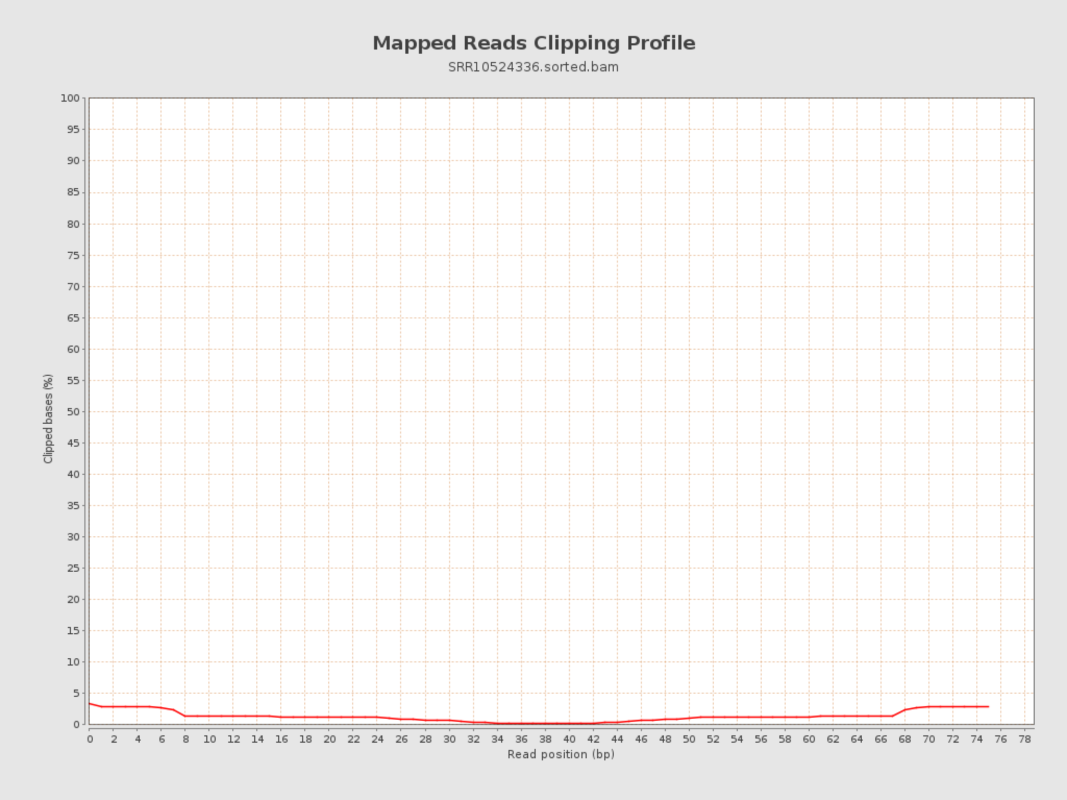
8. Results : Mapped Reads Nucleotide Content



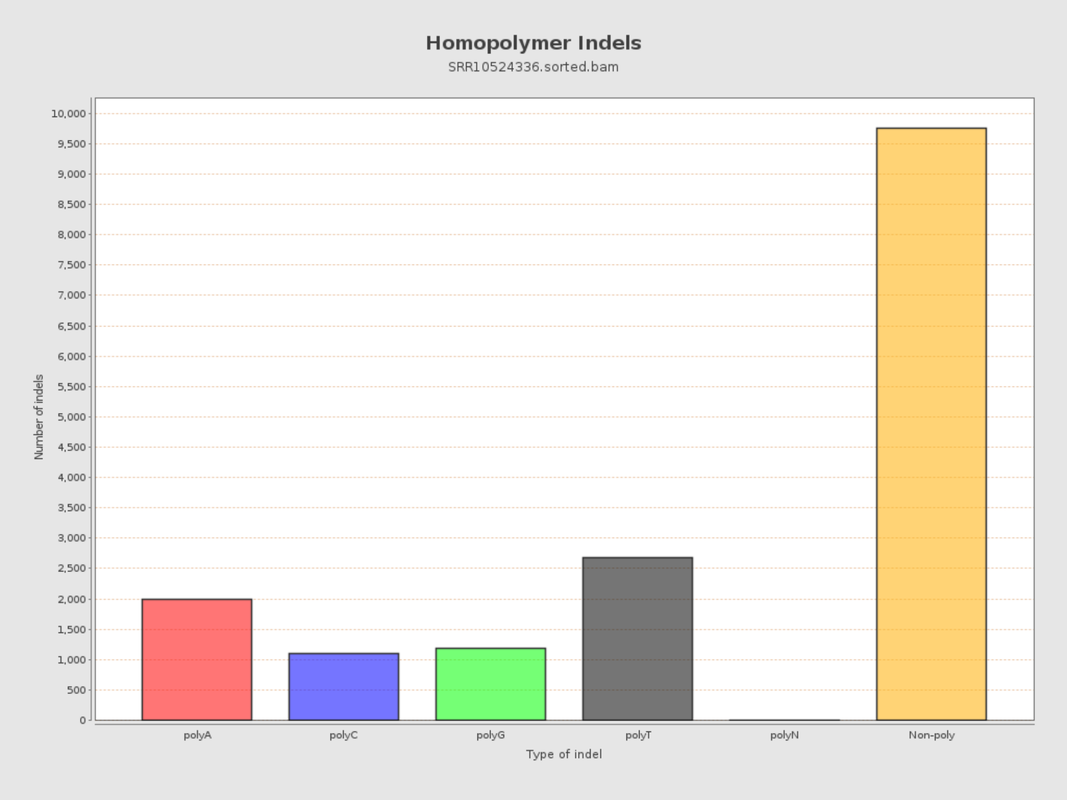
9. Results : Mapped Reads GC-content Distribution



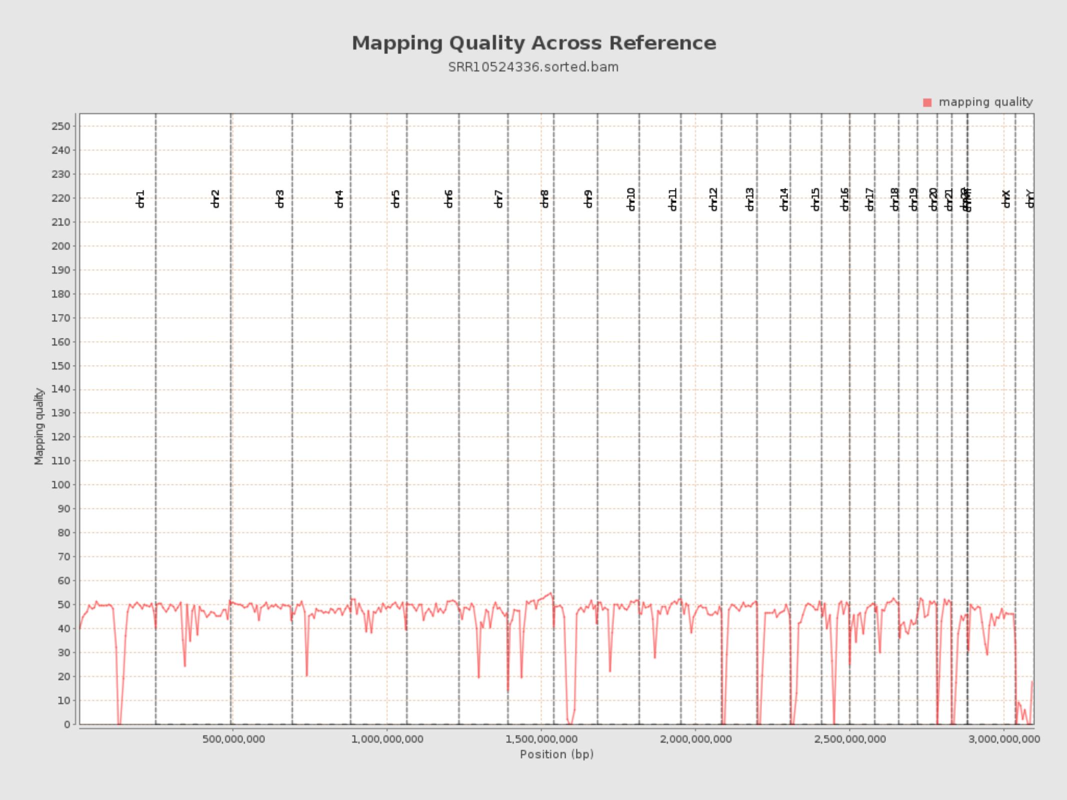
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram