Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:35:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524499.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_SRR10524499 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524499.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:35:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524499.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,159,078
Mapped reads	1,072,524 / 92.53%
Unmapped reads	86,554 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,416 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	36,450 / 3.14%
Duplication rate	2.63%
Clipped reads	1,071,694 / 92.46%

2.2. ACGT Content

Number/percentage of A's	16,213,383 / 25.82%
Number/percentage of C's	11,738,215 / 18.69%
Number/percentage of T's	19,029,551 / 30.3%
Number/percentage of G's	15,821,721 / 25.19%
Number/percentage of N's	1,449 / 0%
GC Percentage	43.88%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.2036

2.4. Mapping Quality

Mean Mapping Quality	45.57

2.5. Mismatches and indels

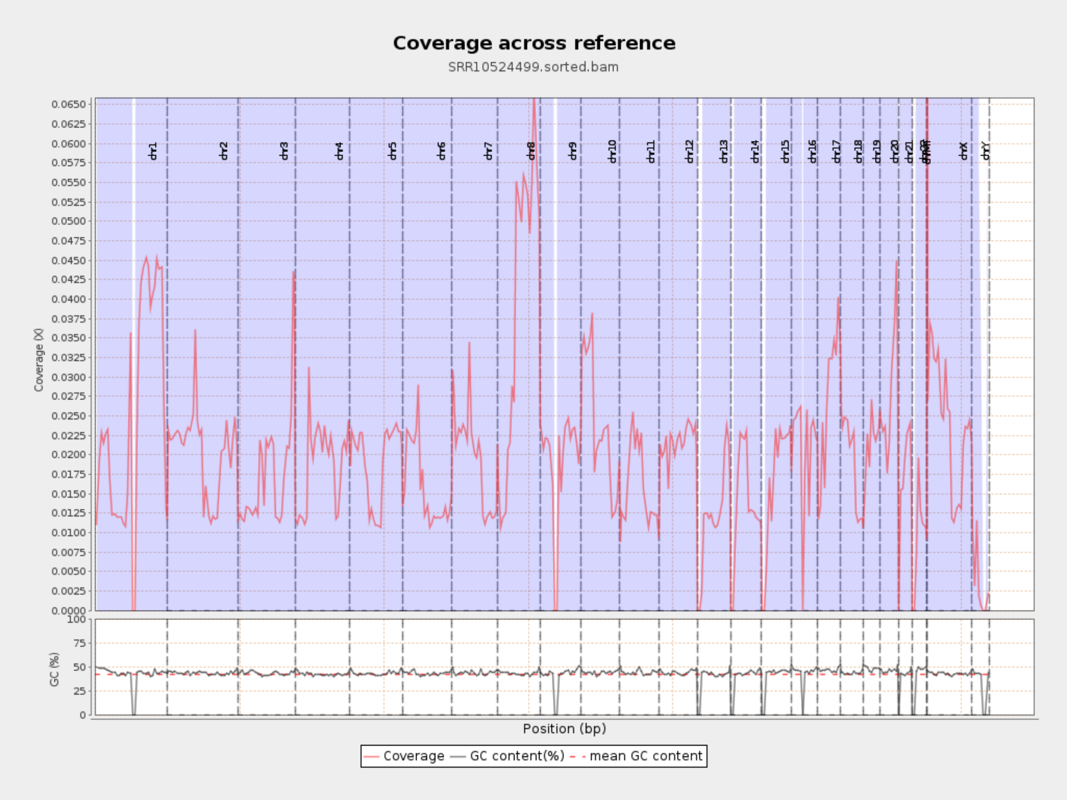
General error rate	0.48%
Mismatches	291,580
Insertions	4,421
Mapped reads with at least one insertion	0.41%
Deletions	11,819
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.54%

2.6. Chromosome stats

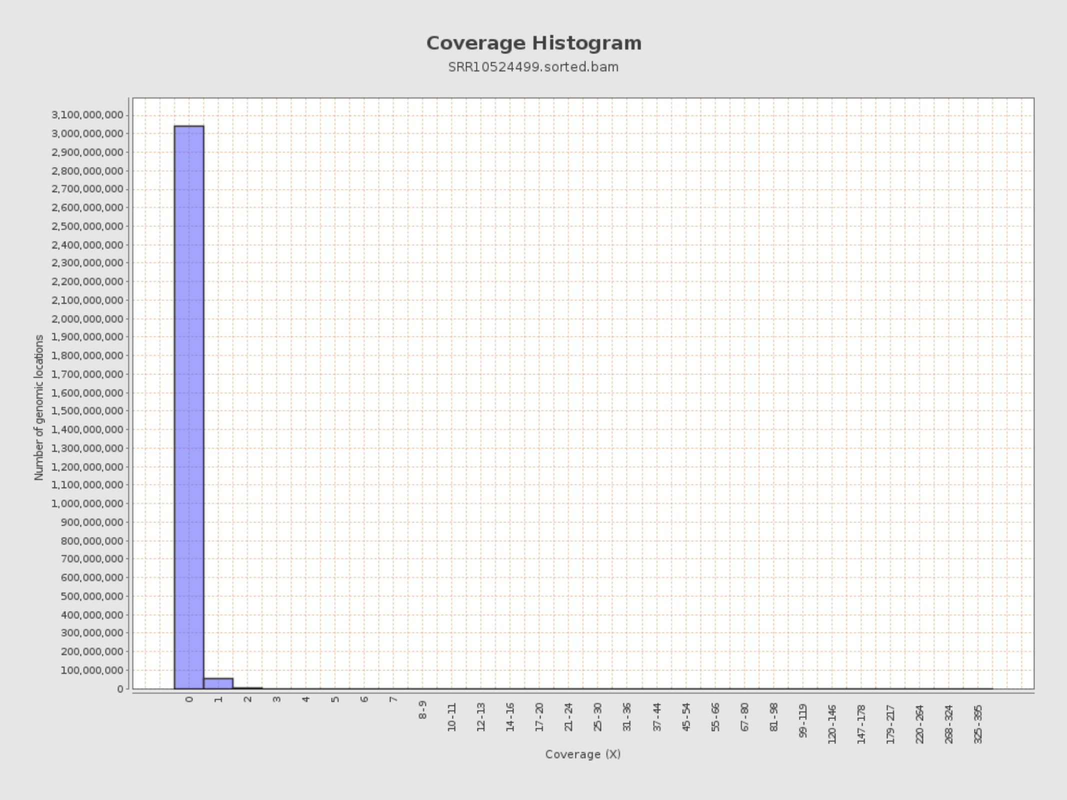
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6208176	0.0249	0.3441
chr2	243199373	4977969	0.0205	0.2203
chr3	198022430	3432487	0.0173	0.1427
chr4	191154276	3579288	0.0187	0.1635
chr5	180915260	3466938	0.0192	0.1498
chr6	171115067	2719268	0.0159	0.1622
chr7	159138663	3148369	0.0198	0.2568

chr8	146364022	5756928	0.0393	0.2358
chr9	141213431	2687695	0.019	0.1851
chr10	135534747	3298896	0.0243	0.2144
chr11	135006516	2178587	0.0161	0.1916
chr12	133851895	2909245	0.0217	0.159
chr13	115169878	1407187	0.0122	0.1186
chr14	107349540	1486340	0.0138	0.1296
chr15	102531392	1673173	0.0163	0.143
chr16	90354753	1851465	0.0205	0.1628
chr17	81195210	2179749	0.0268	0.1834
chr18	78077248	1499665	0.0192	0.2992
chr19	59128983	1269245	0.0215	0.2584
chr20	63025520	1771699	0.0281	0.1845
chr21	48129895	846864	0.0176	0.1533
chr22	51304566	493160	0.0096	0.1051
chrMT	16571	5283	0.3188	0.5991
chrX	155270560	3772432	0.0243	0.1816
chrY	59373566	204369	0.0034	0.0984

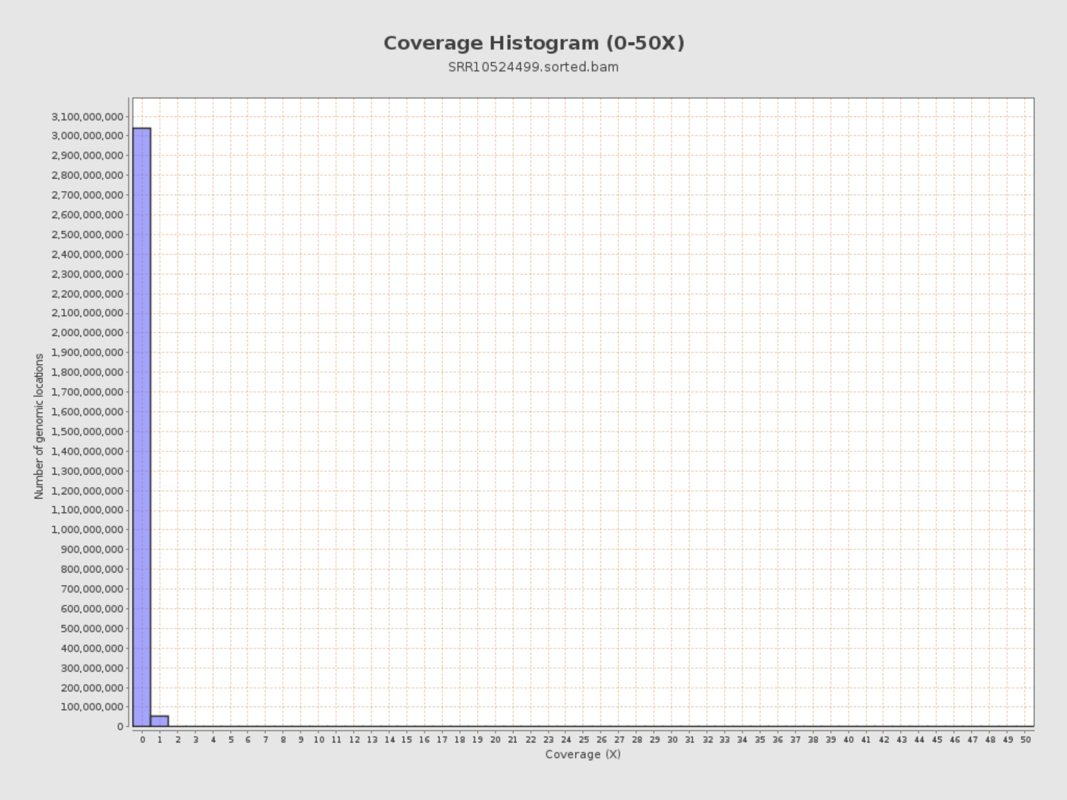
3. Results : Coverage across reference



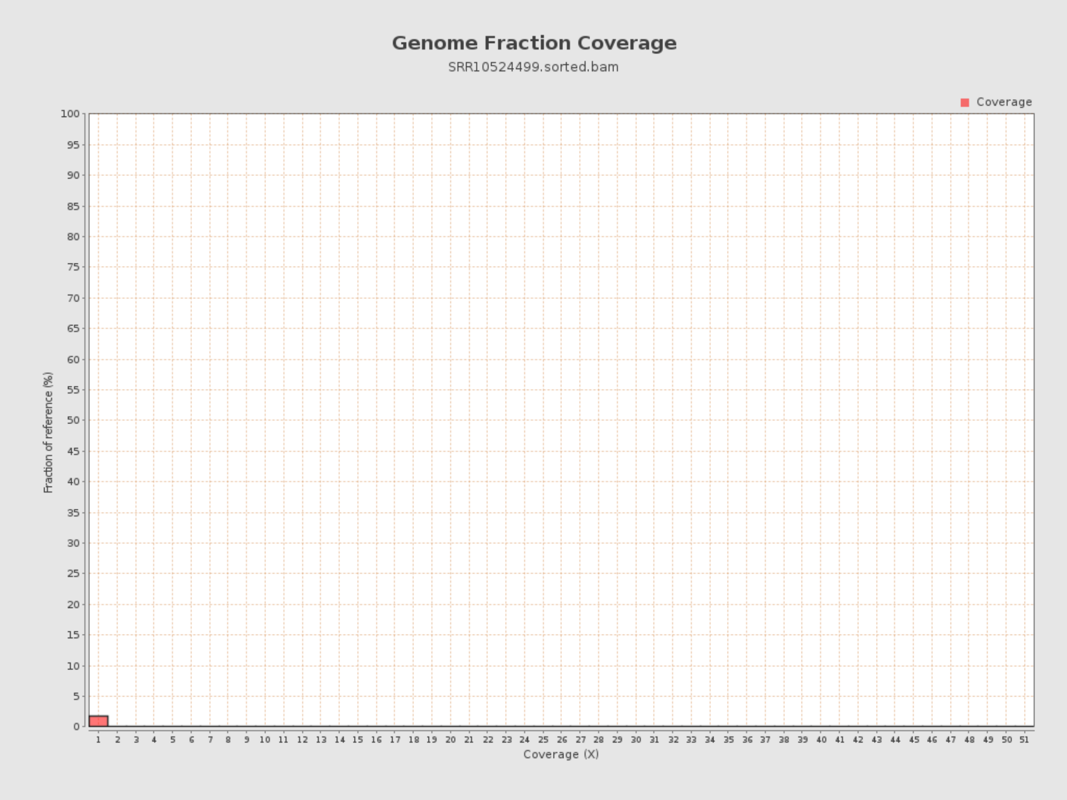
4. Results : Coverage Histogram



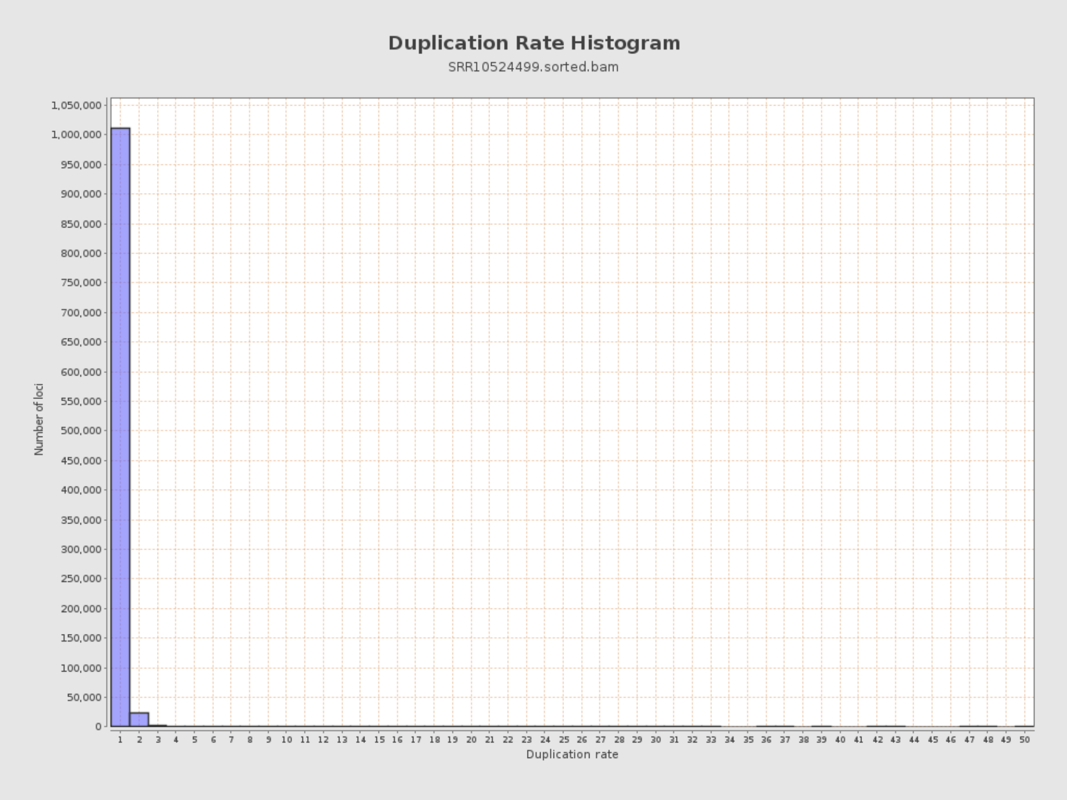
5. Results : Coverage Histogram (0-50X)



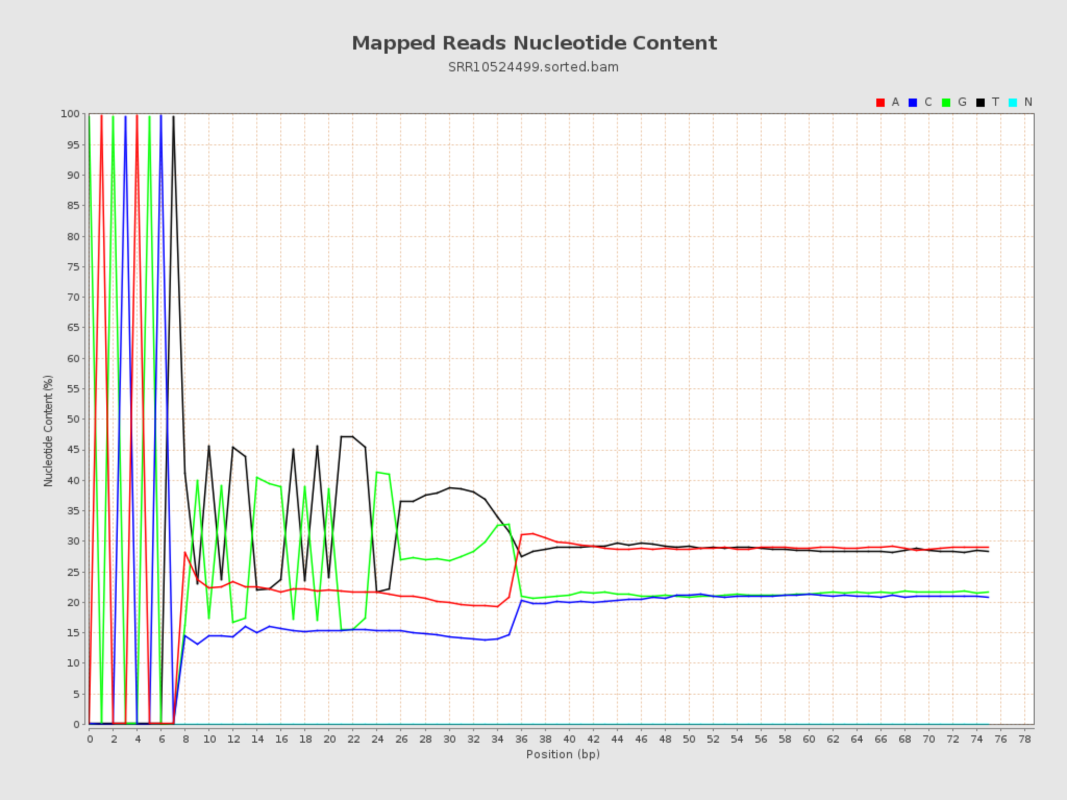
6. Results : Genome Fraction Coverage



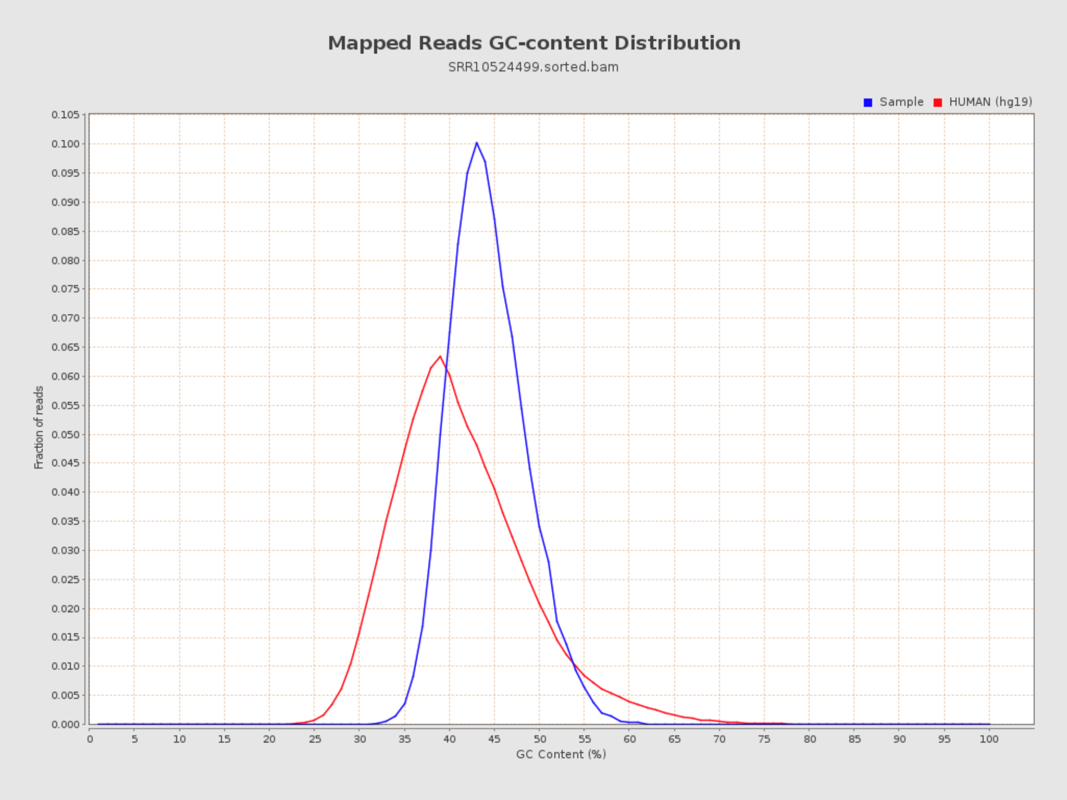
7. Results : Duplication Rate Histogram



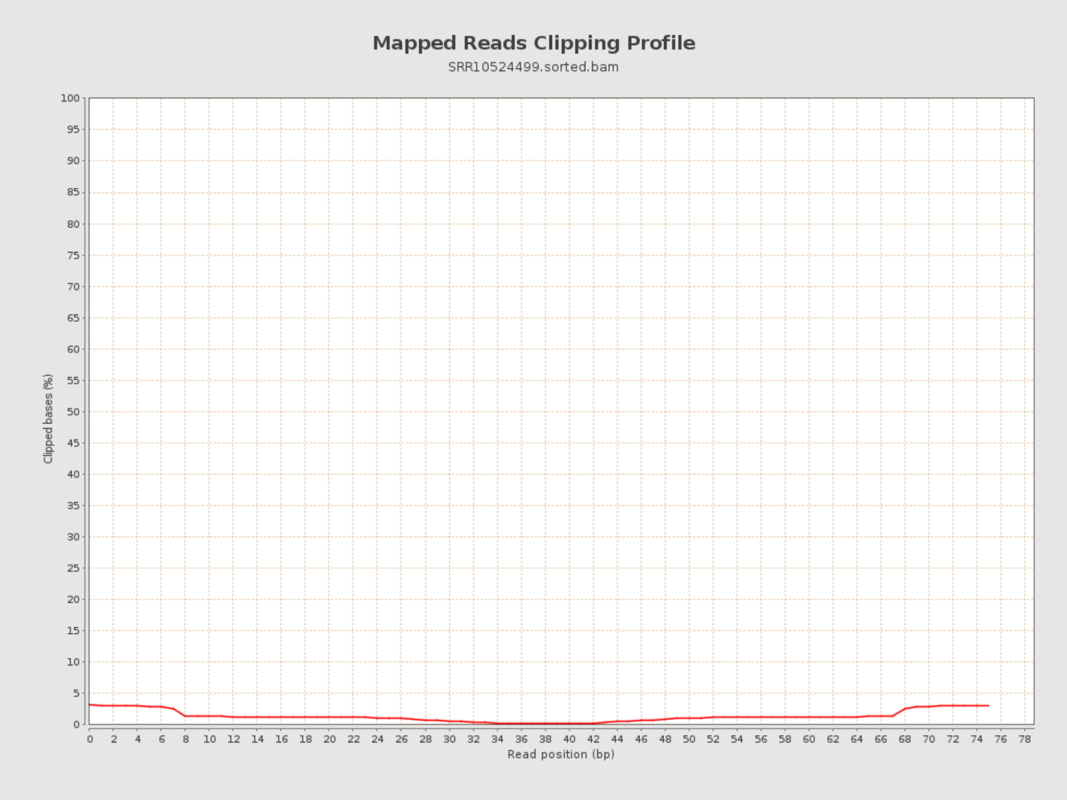
8. Results : Mapped Reads Nucleotide Content



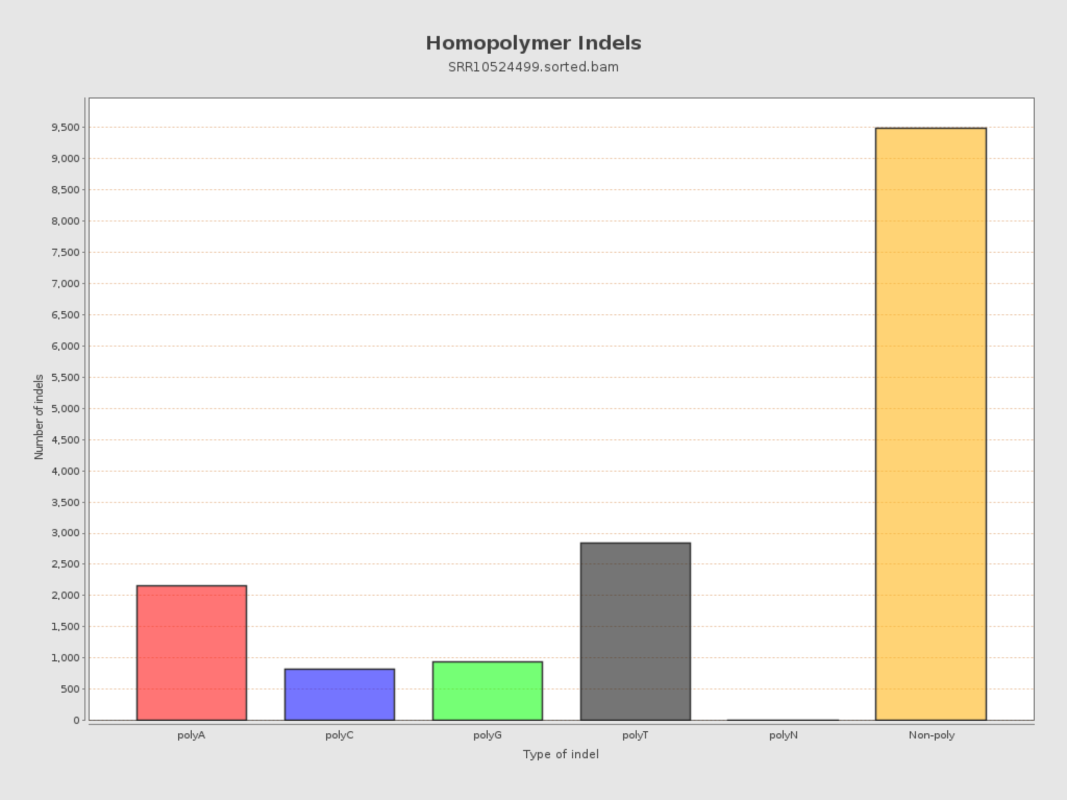
9. Results : Mapped Reads GC-content Distribution



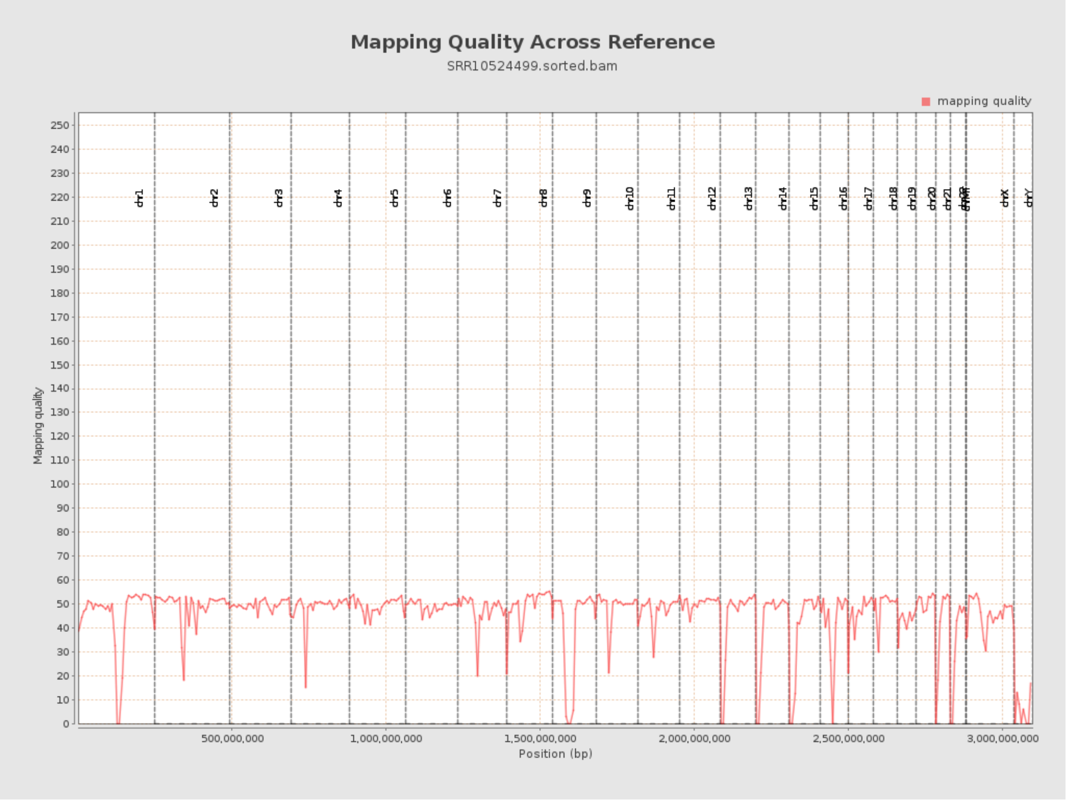
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram