Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:38:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524644.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_SRR10524644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524644.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:38:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,600,673
Mapped reads	1,487,644 / 92.94%
Unmapped reads	113,029 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,612 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	54,890 / 3.43%
Duplication rate	2.79%
Clipped reads	1,489,937 / 93.08%

2.2. ACGT Content

Number/percentage of A's	22,002,063 / 25.24%
Number/percentage of C's	17,837,751 / 20.46%
Number/percentage of T's	26,257,693 / 30.12%
Number/percentage of G's	21,066,062 / 24.17%
Number/percentage of N's	2,676 / 0%
GC Percentage	44.63%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2601

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

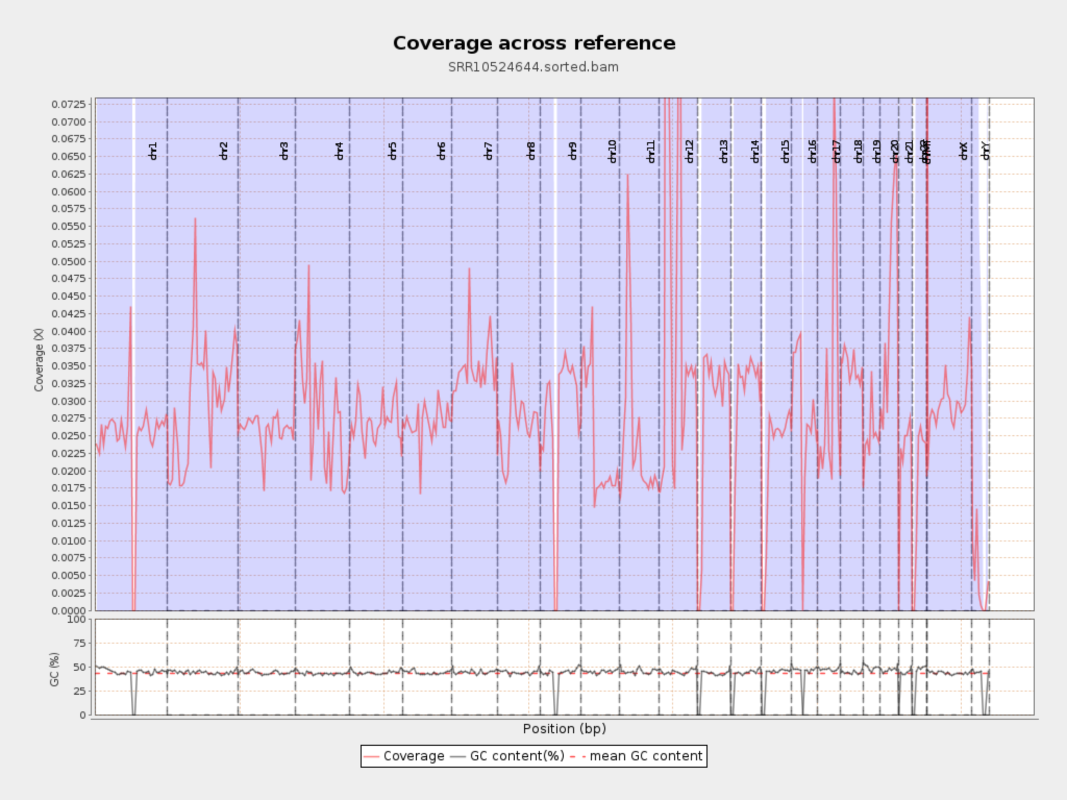
General error rate	0.49%
Mismatches	413,528
Insertions	5,800
Mapped reads with at least one insertion	0.39%
Deletions	13,732
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.44%

2.6. Chromosome stats

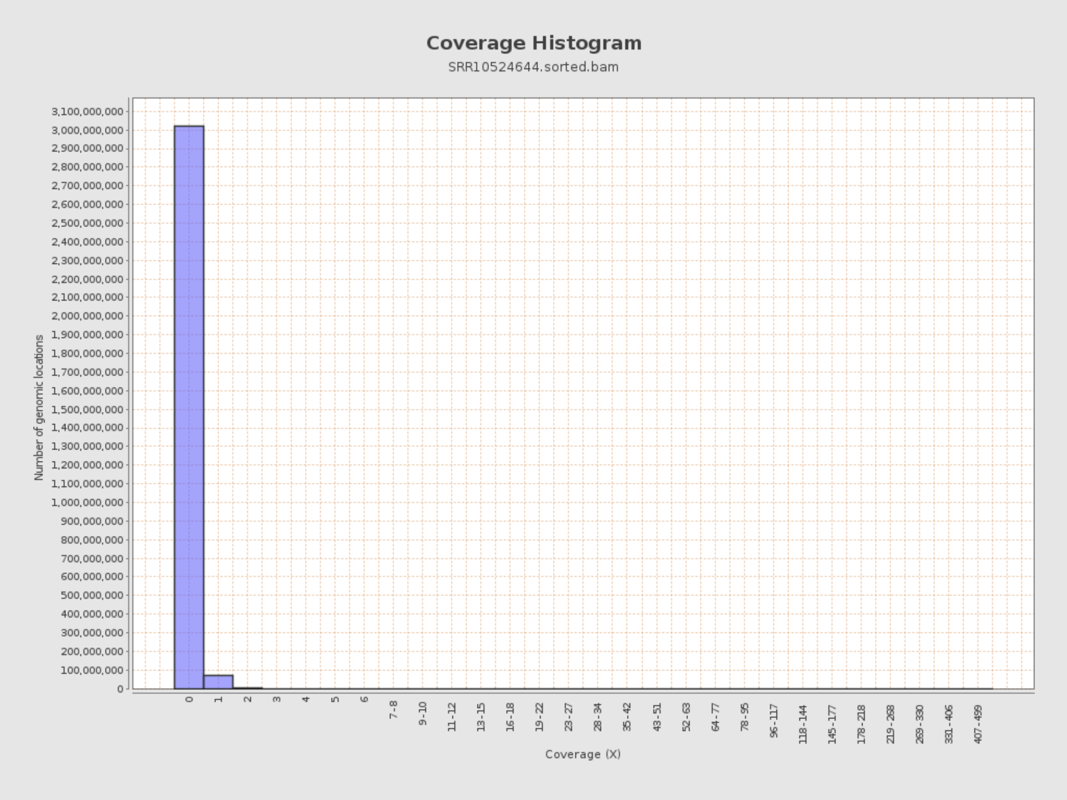
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6171680	0.0248	0.4397
chr2	243199373	7315956	0.0301	0.2816
chr3	198022430	5130296	0.0259	0.1748
chr4	191154276	5391536	0.0282	0.208
chr5	180915260	4899571	0.0271	0.1803
chr6	171115067	4584359	0.0268	0.1906
chr7	159138663	5564872	0.035	0.3311

chr8	146364022	3877503	0.0265	0.2823
chr9	141213431	3912151	0.0277	0.2562
chr10	135534747	3275971	0.0242	0.2519
chr11	135006516	3318301	0.0246	0.2163
chr12	133851895	6298407	0.0471	0.2637
chr13	115169878	3242151	0.0282	0.1823
chr14	107349540	3048362	0.0284	0.197
chr15	102531392	2187005	0.0213	0.1584
chr16	90354753	2493708	0.0276	0.191
chr17	81195210	2634917	0.0325	0.2064
chr18	78077248	2722035	0.0349	0.4375
chr19	59128983	1491748	0.0252	0.3343
chr20	63025520	2787946	0.0442	0.2346
chr21	48129895	1064867	0.0221	0.1838
chr22	51304566	887077	0.0173	0.1425
chrMT	16571	5872	0.3544	0.637
chrX	155270560	4631643	0.0298	0.2125
chrY	59373566	251209	0.0042	0.1141

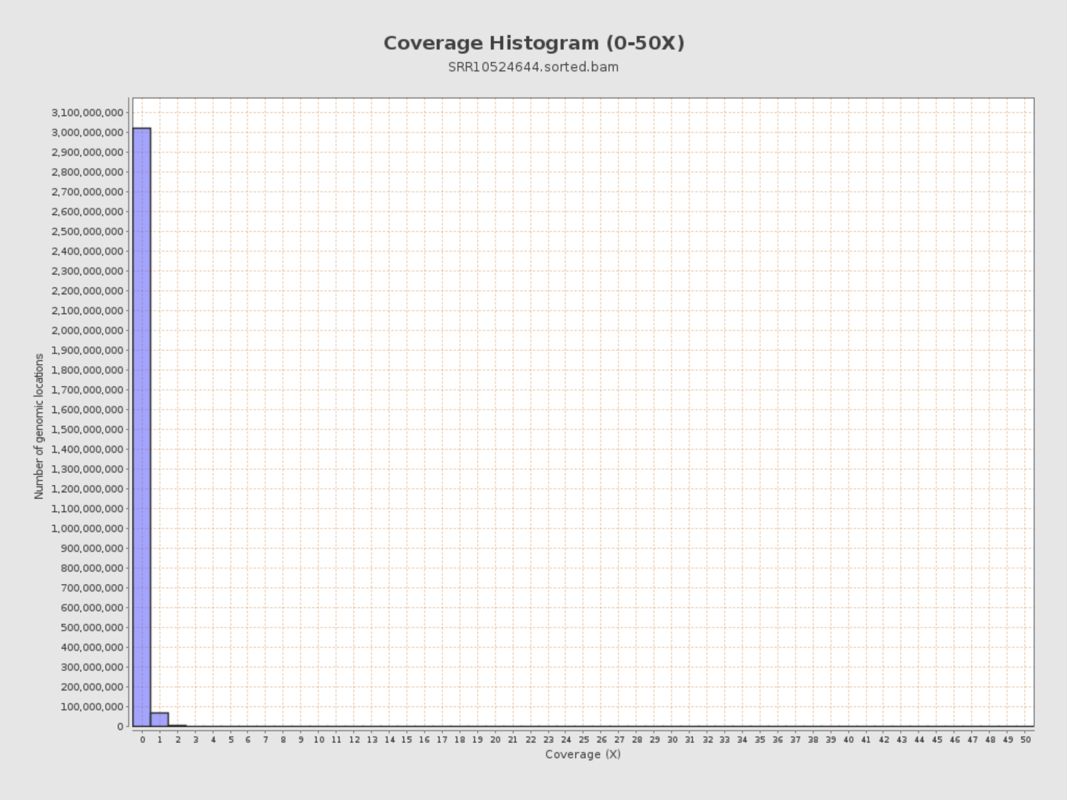
3. Results : Coverage across reference



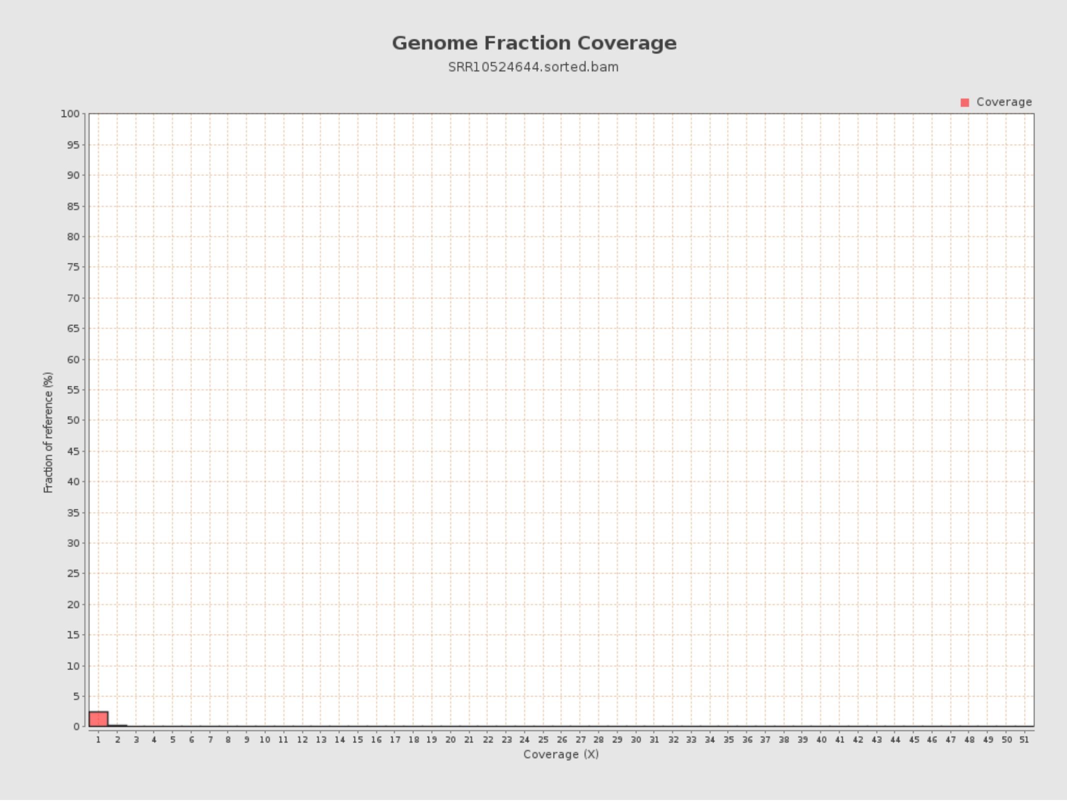
4. Results : Coverage Histogram



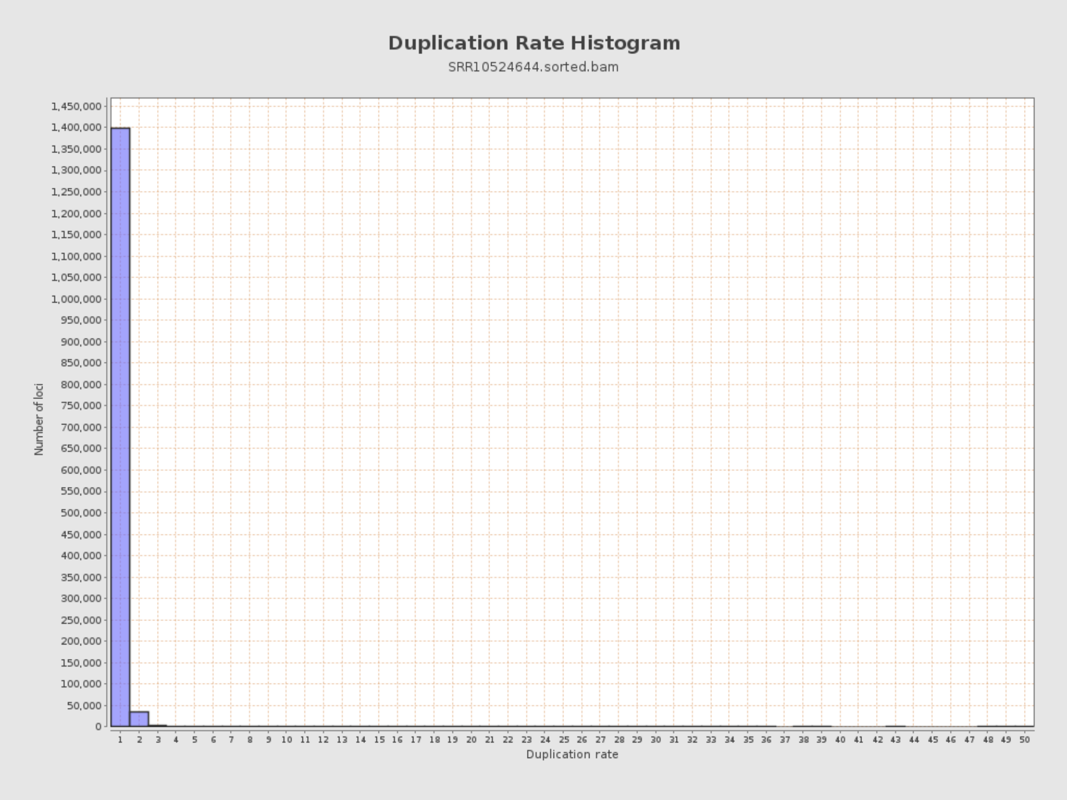
5. Results : Coverage Histogram (0-50X)



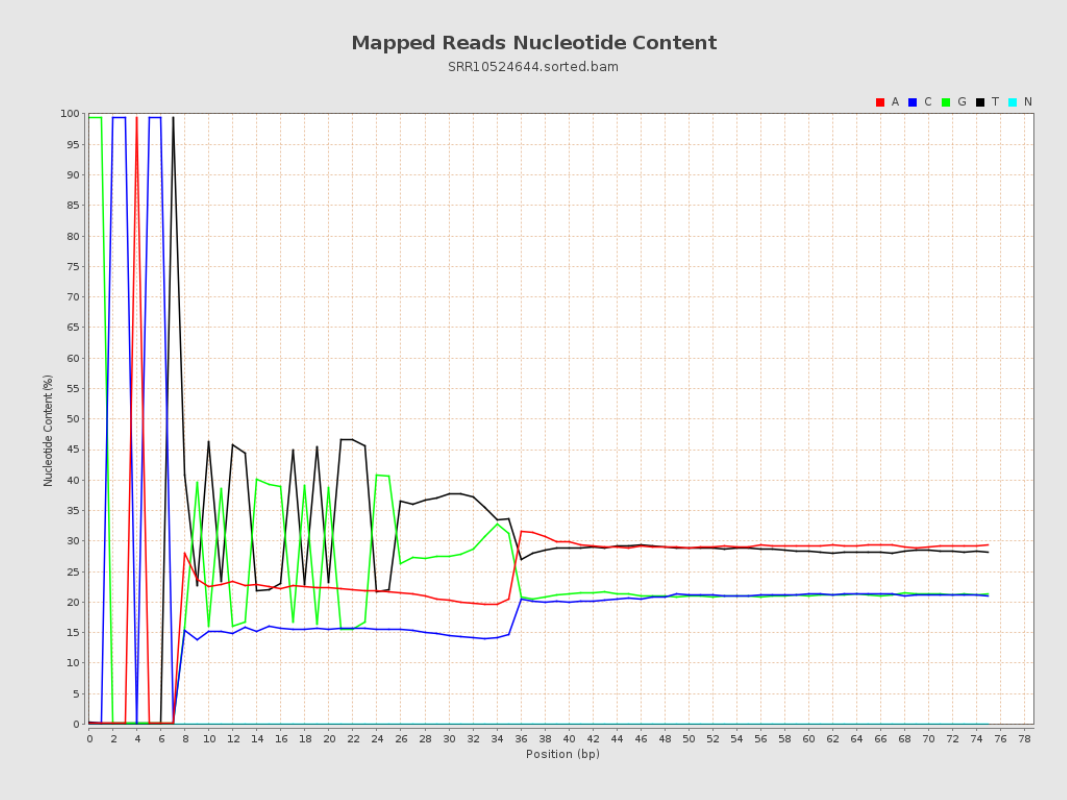
6. Results : Genome Fraction Coverage



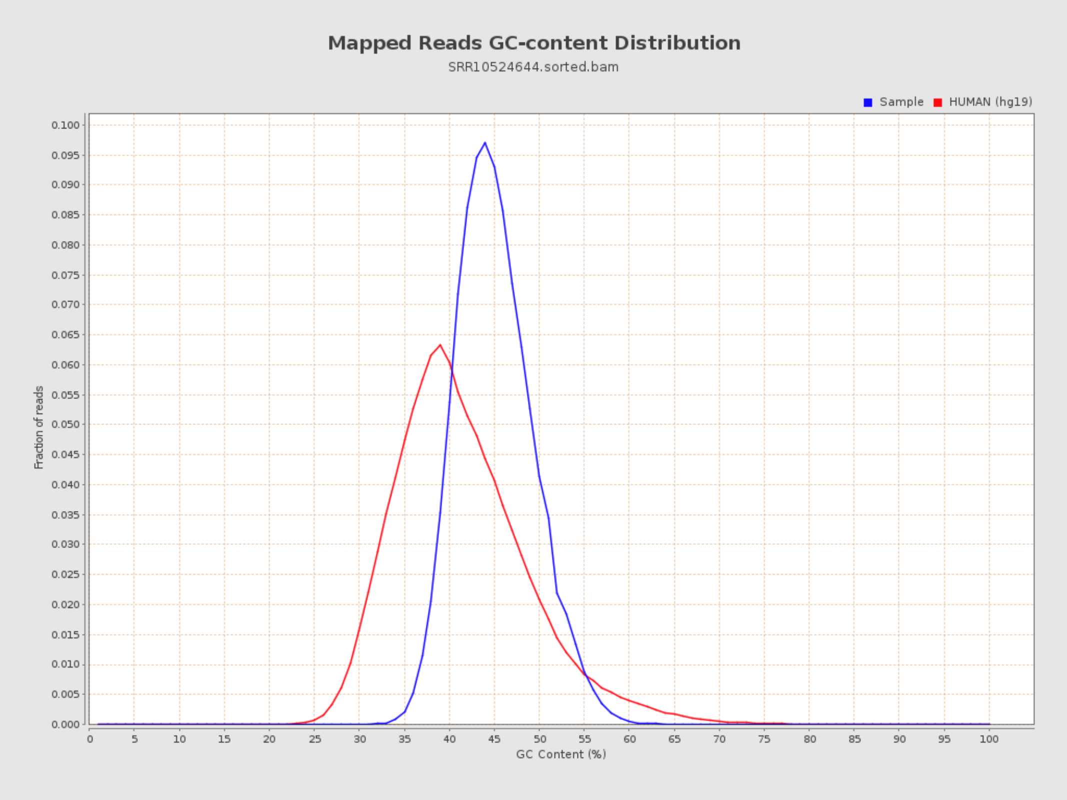
7. Results : Duplication Rate Histogram



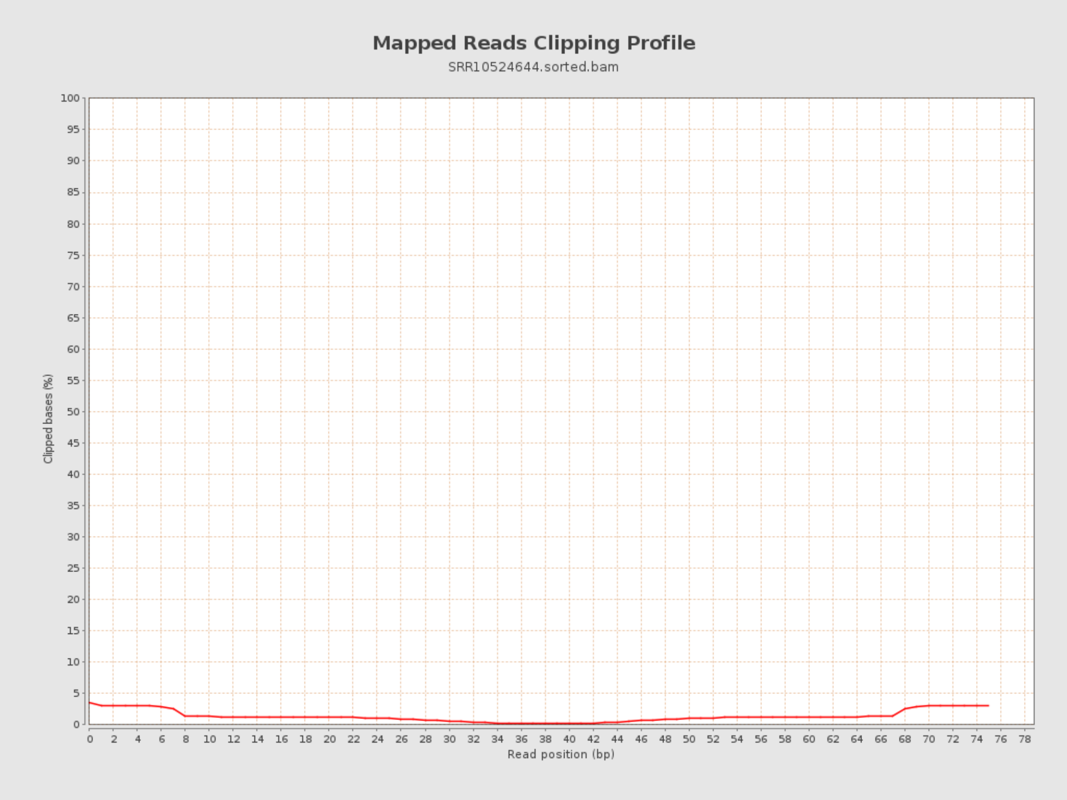
8. Results : Mapped Reads Nucleotide Content



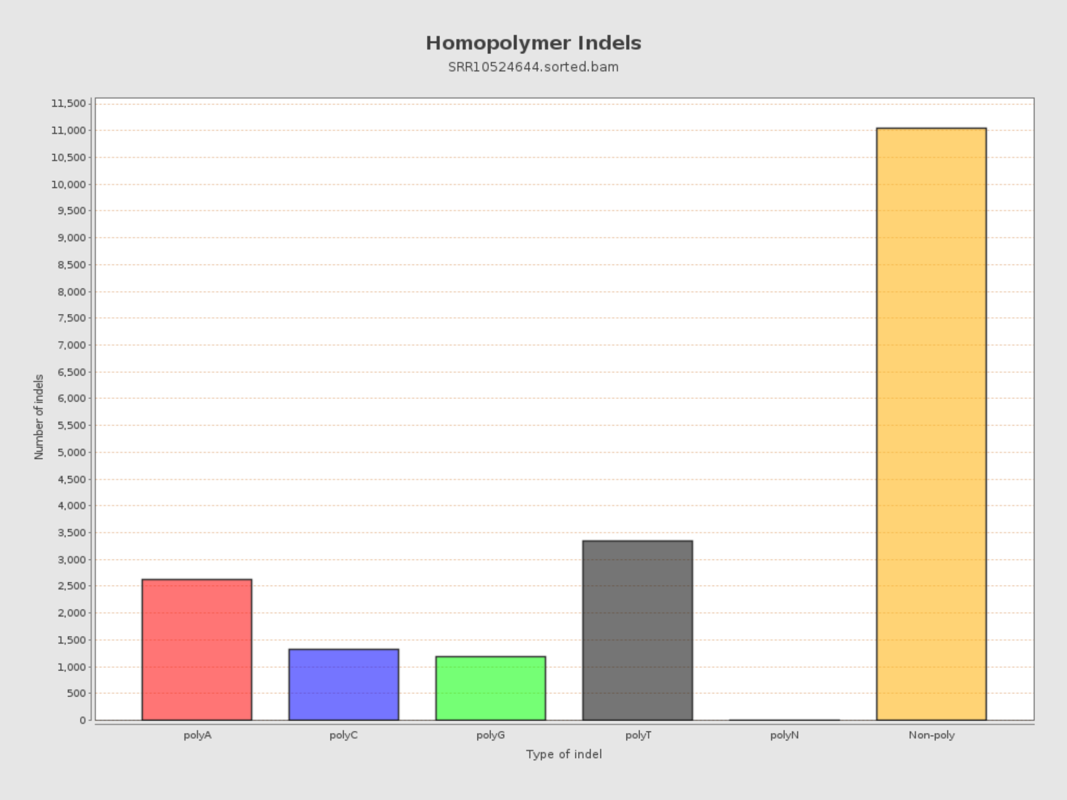
9. Results : Mapped Reads GC-content Distribution



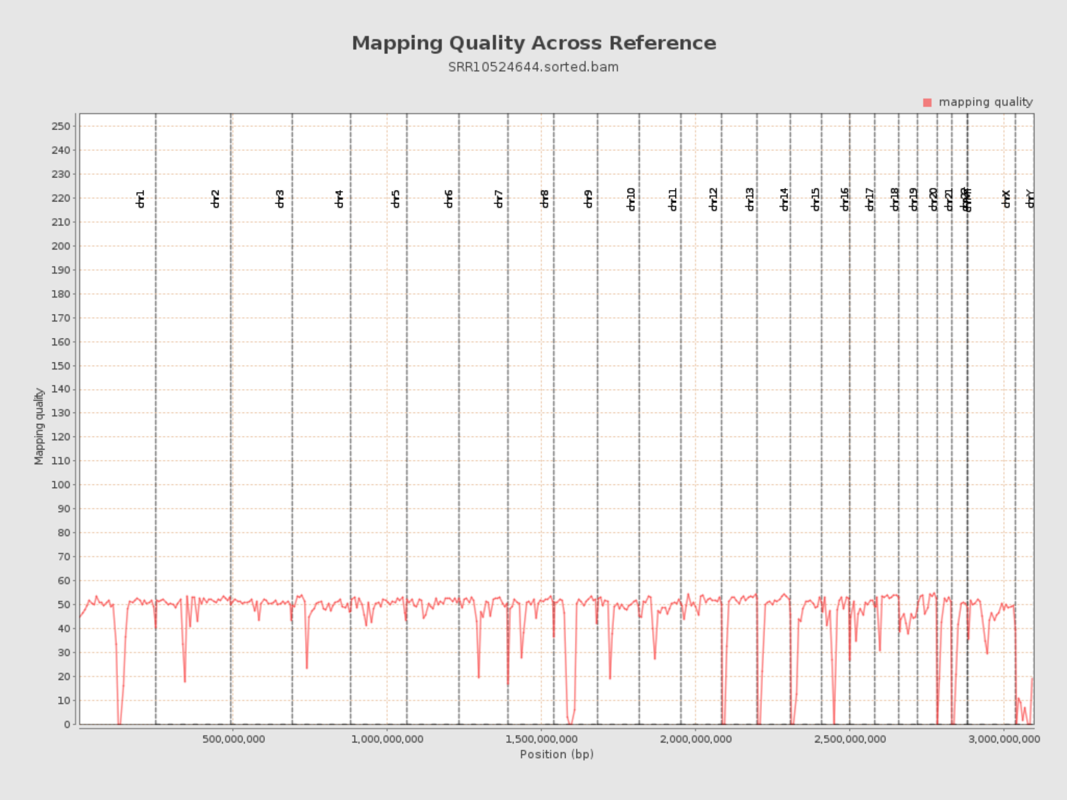
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram