Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:04:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524457.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_SRR10524457 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524457.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:04:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524457.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,755,798
Mapped reads	2,550,449 / 92.55%
Unmapped reads	205,349 / 7.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,043 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	152,817 / 5.55%
Duplication rate	4.55%
Clipped reads	2,550,344 / 92.54%

2.2. ACGT Content

Number/percentage of A's	38,029,618 / 25.63%
Number/percentage of C's	28,820,163 / 19.43%
Number/percentage of T's	46,227,142 / 31.16%
Number/percentage of G's	35,272,420 / 23.78%
Number/percentage of N's	3,019 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.4104

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

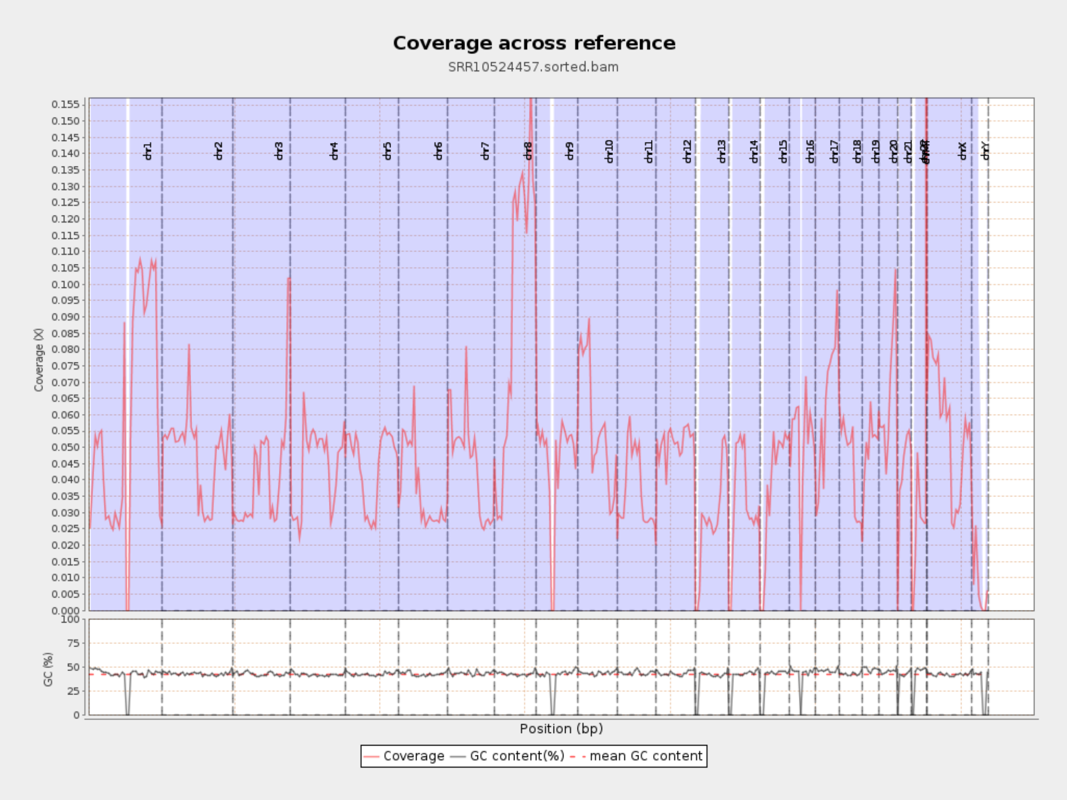
General error rate	0.47%
Mismatches	683,470
Insertions	8,847
Mapped reads with at least one insertion	0.35%
Deletions	26,317
Mapped reads with at least one deletion	1.02%
Homopolymer indels	44.36%

2.6. Chromosome stats

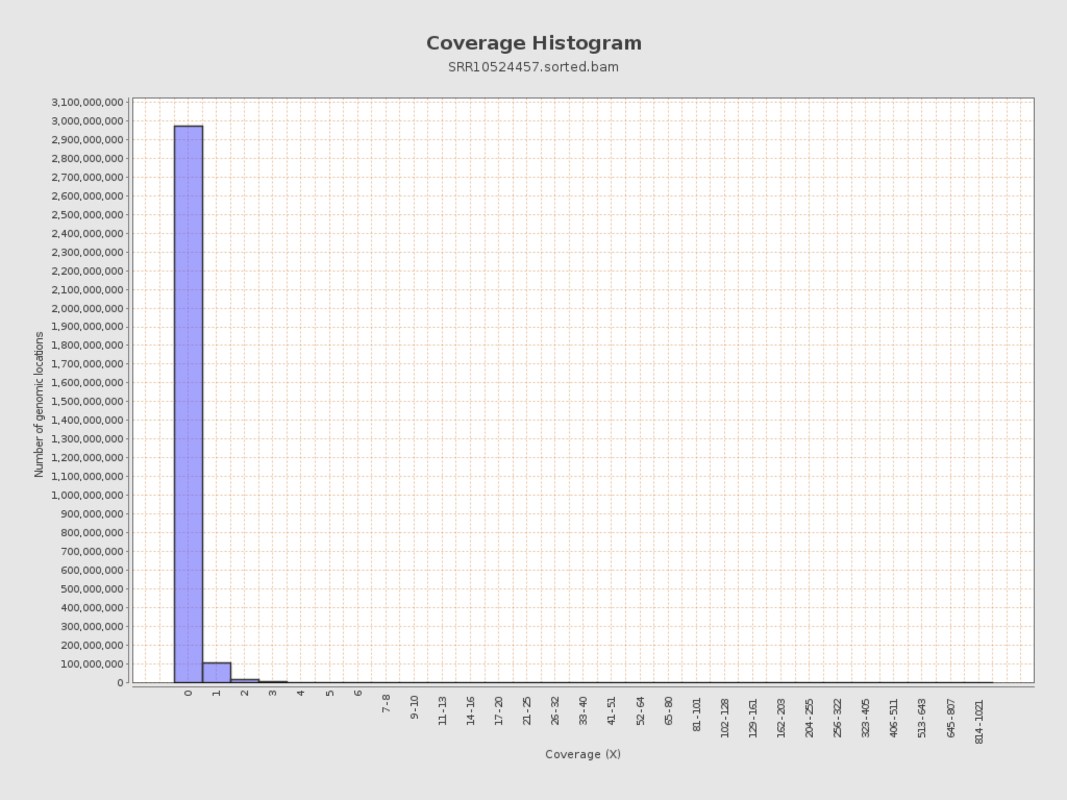
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14675854	0.0589	0.7983
chr2	243199373	11784128	0.0485	0.4654
chr3	198022430	8110814	0.041	0.2394
chr4	191154276	8405780	0.044	0.2838
chr5	180915260	8081636	0.0447	0.248
chr6	171115067	6355157	0.0371	0.3102
chr7	159138663	7229105	0.0454	0.5337

chr8	146364022	13764174	0.094	0.432
chr9	141213431	6358878	0.045	0.358
chr10	135534747	7814607	0.0577	0.4214
chr11	135006516	5004901	0.0371	0.3717
chr12	133851895	6918560	0.0517	0.2681
chr13	115169878	3265472	0.0284	0.1969
chr14	107349540	3528966	0.0329	0.2191
chr15	102531392	3886105	0.0379	0.2441
chr16	90354753	4657513	0.0515	0.2932
chr17	81195210	5203723	0.0641	0.315
chr18	78077248	3524175	0.0451	0.6304
chr19	59128983	2989476	0.0506	0.5694
chr20	63025520	4226932	0.0671	0.307
chr21	48129895	2042255	0.0424	0.2673
chr22	51304566	1193823	0.0233	0.1774
chrMT	16571	69102	4.1701	3.6367
chrX	155270560	8832533	0.0569	0.3215
chrY	59373566	473671	0.008	0.2009

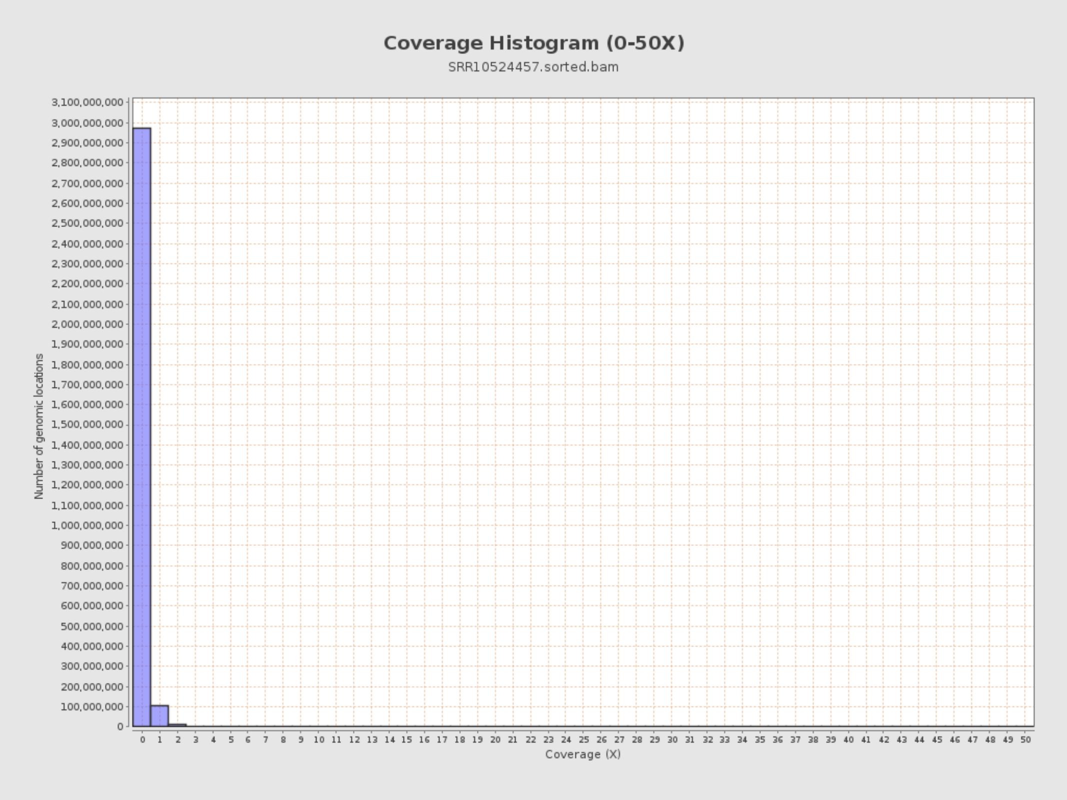
3. Results : Coverage across reference



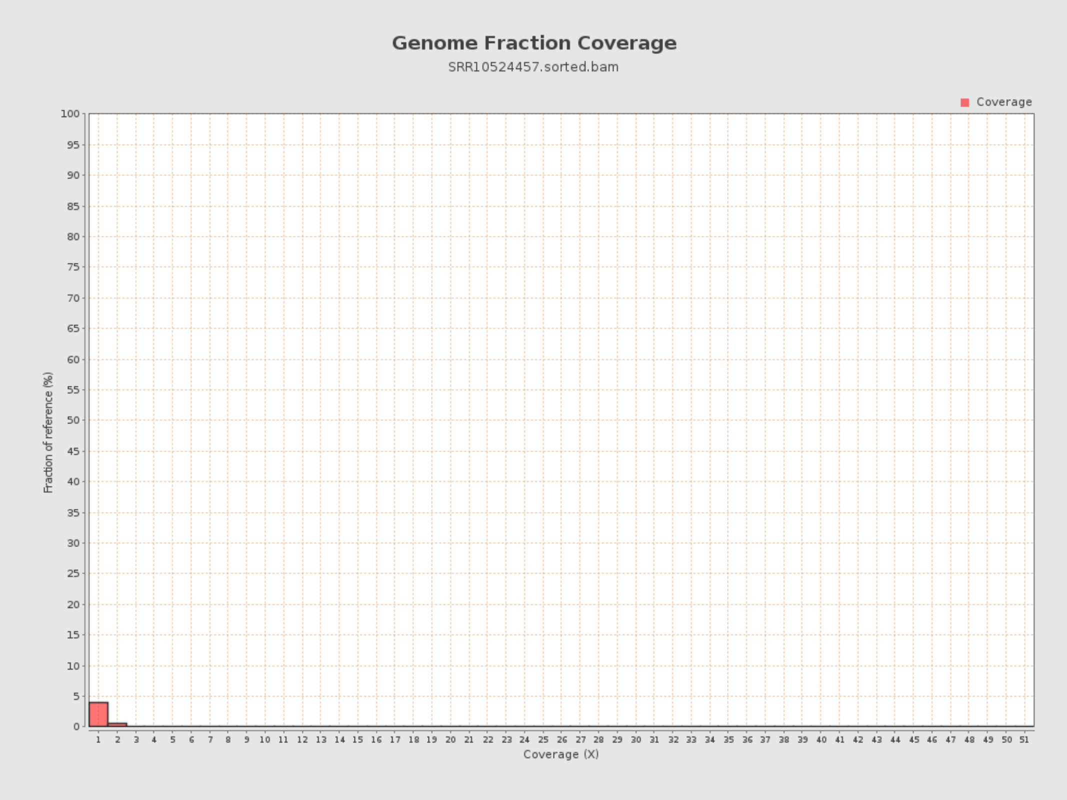
4. Results : Coverage Histogram



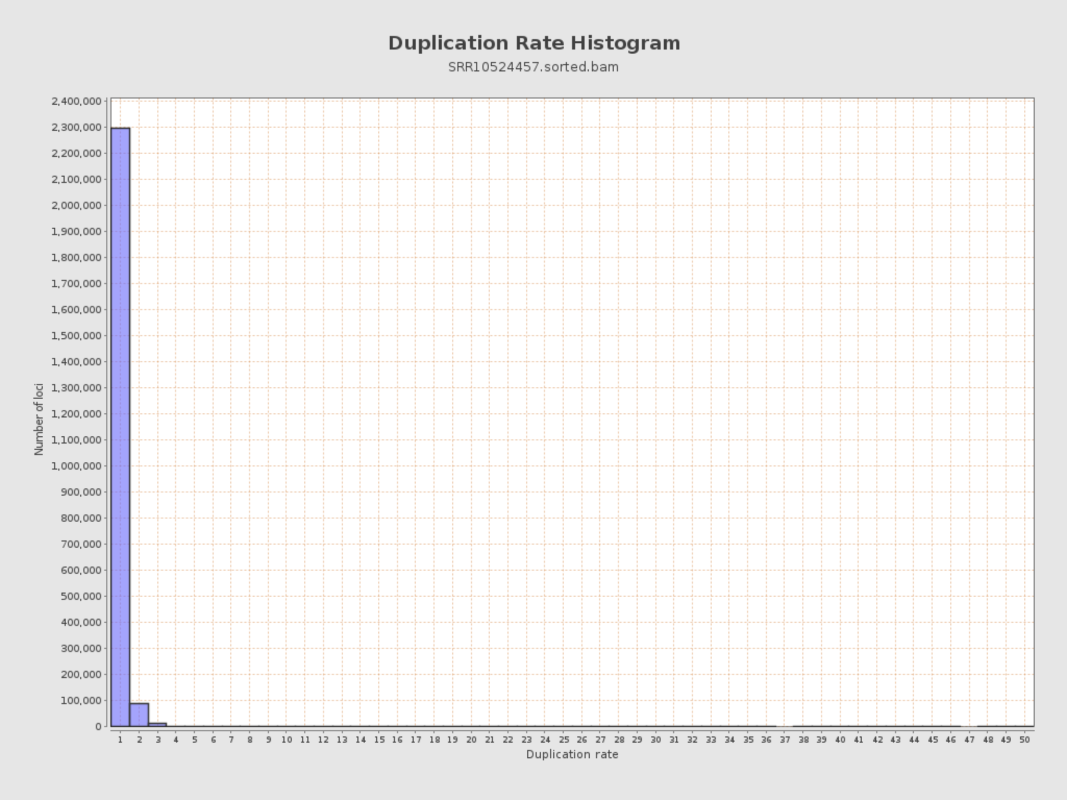
5. Results : Coverage Histogram (0-50X)



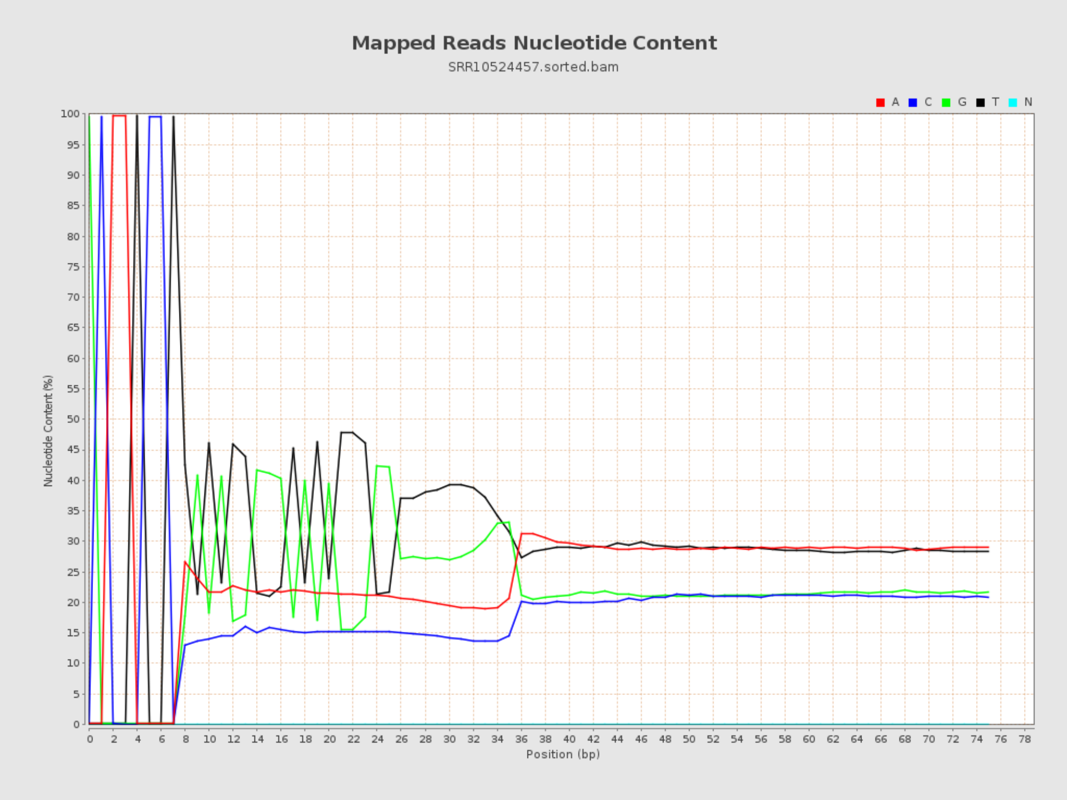
6. Results : Genome Fraction Coverage



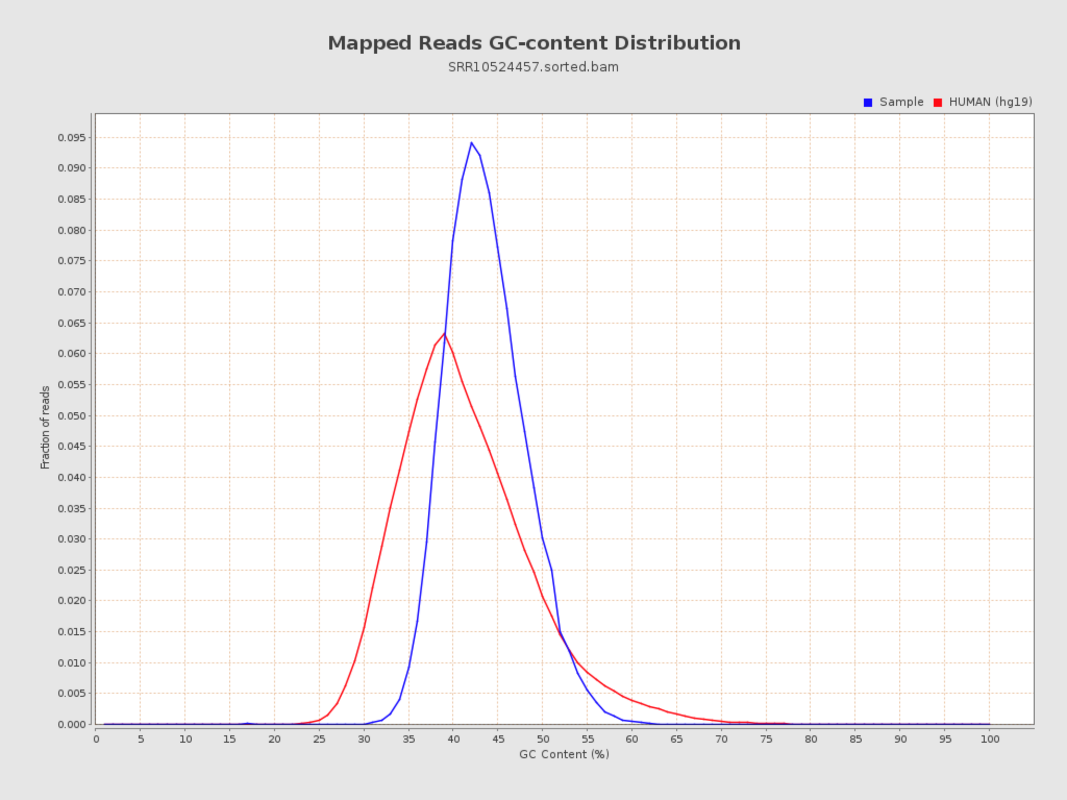
7. Results : Duplication Rate Histogram



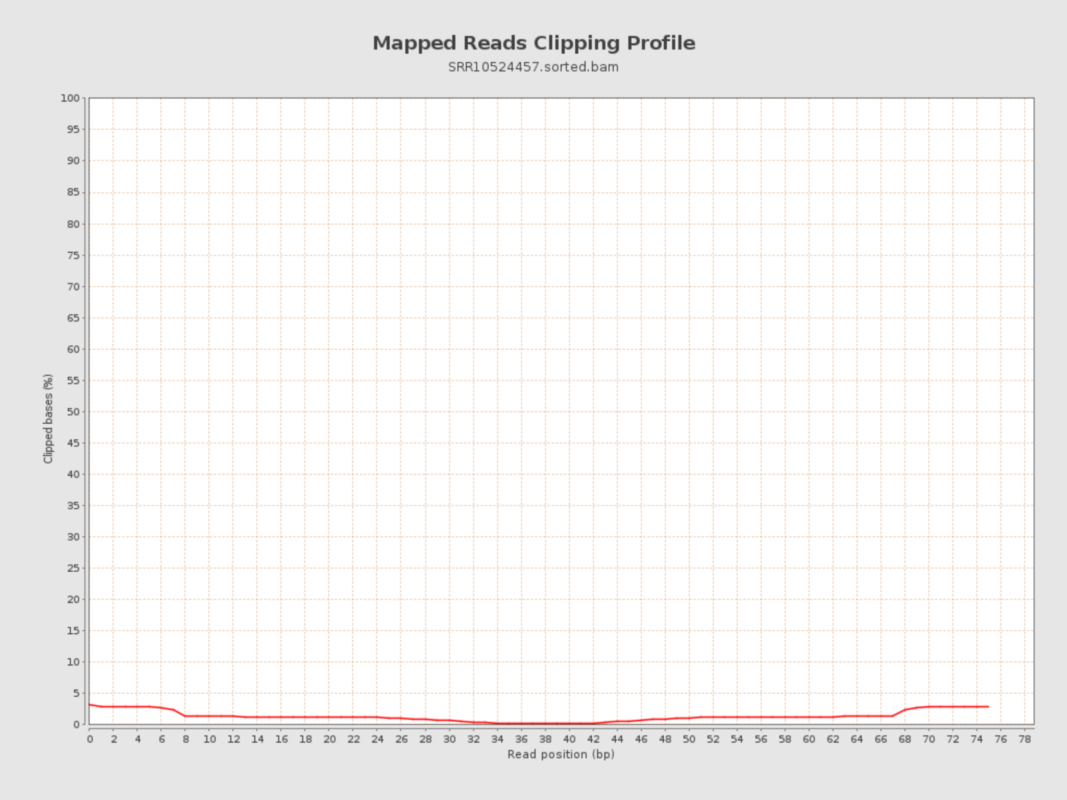
8. Results : Mapped Reads Nucleotide Content



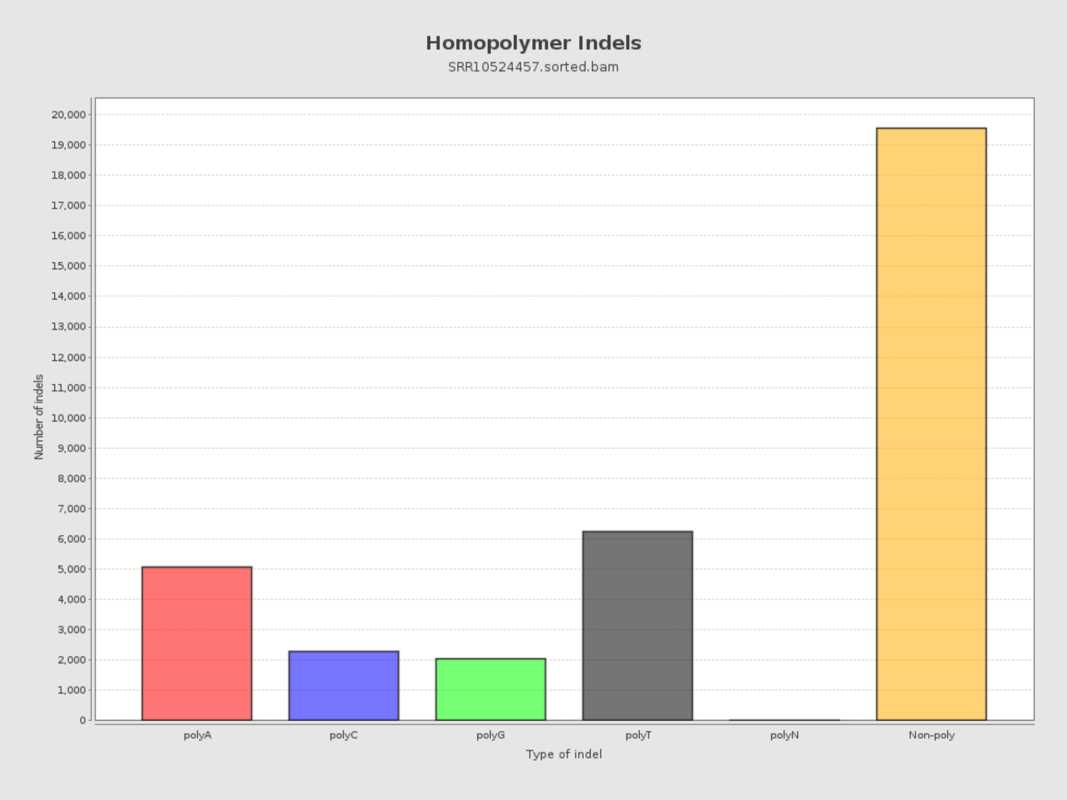
9. Results : Mapped Reads GC-content Distribution



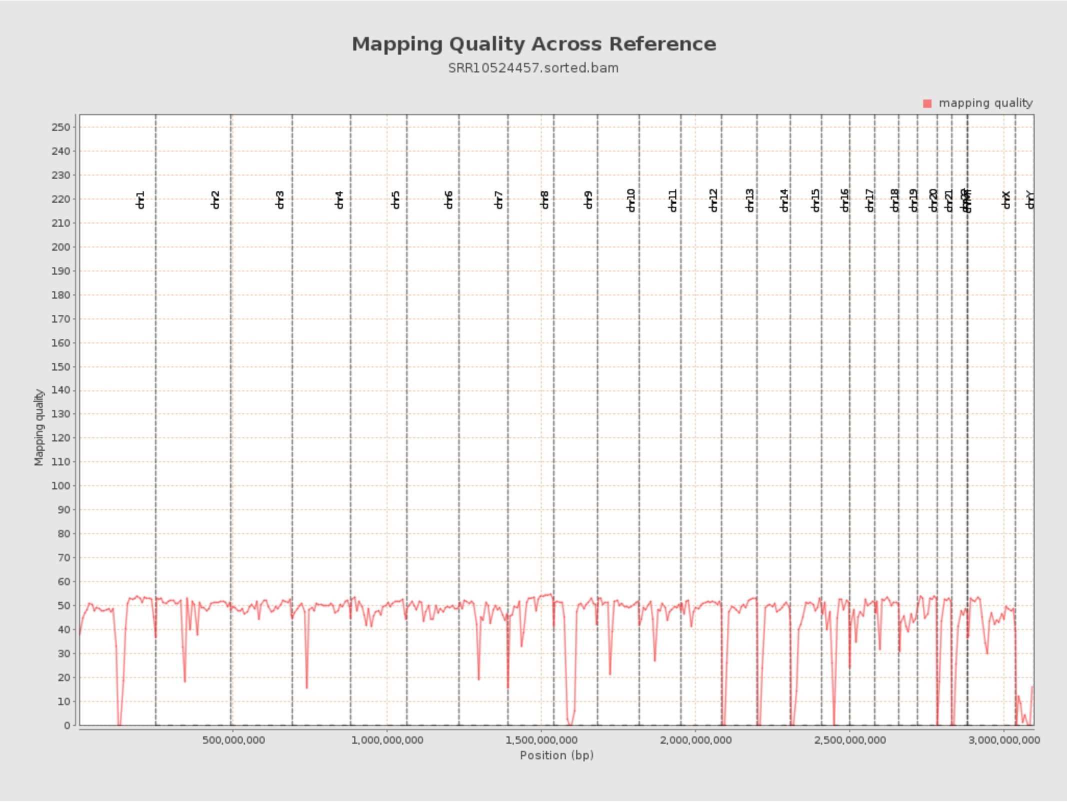
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram