Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:57:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524696.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_SRR10524696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524696.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:57:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	157,985
Mapped reads	143,354 / 90.74%
Unmapped reads	14,631 / 9.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	508 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	1,685 / 1.07%
Duplication rate	0.89%
Clipped reads	143,487 / 90.82%

2.2. ACGT Content

Number/percentage of A's	2,207,768 / 26.25%
Number/percentage of C's	1,551,517 / 18.45%
Number/percentage of T's	2,710,112 / 32.23%
Number/percentage of G's	1,939,173 / 23.06%
Number/percentage of N's	1,080 / 0.01%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0027

Standard Deviation	0.057

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

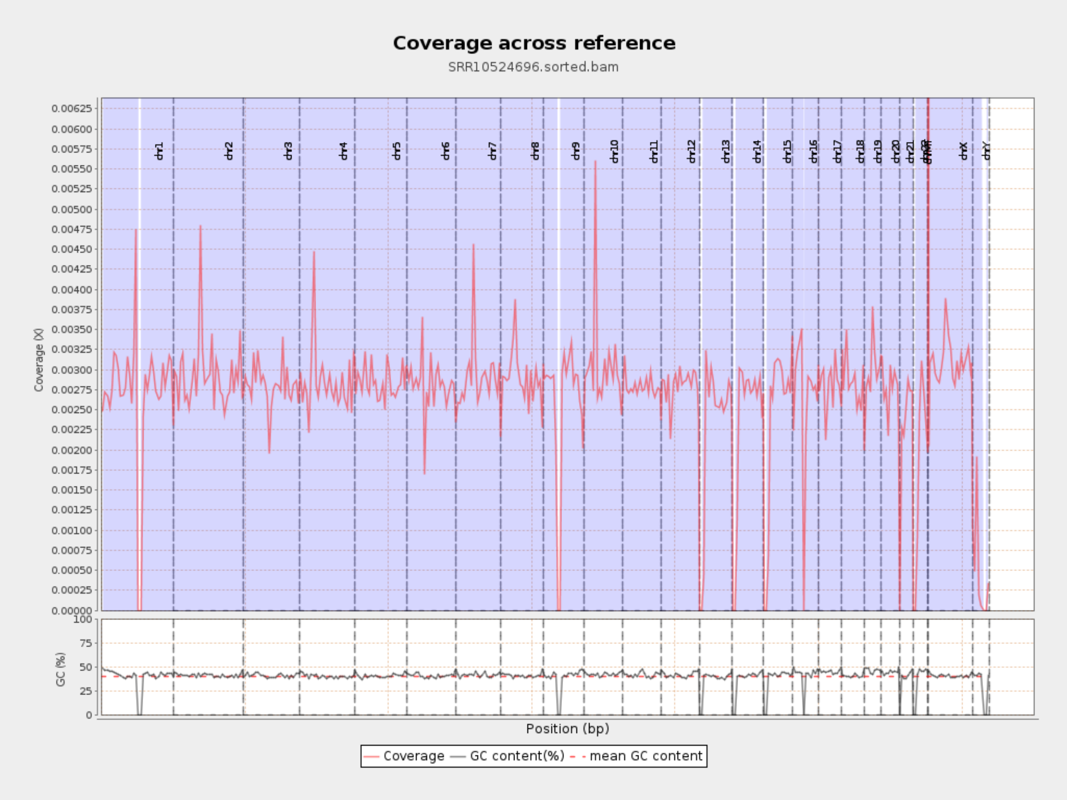
General error rate	0.53%
Mismatches	43,617
Insertions	652
Mapped reads with at least one insertion	0.45%
Deletions	1,626
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.88%

2.6. Chromosome stats

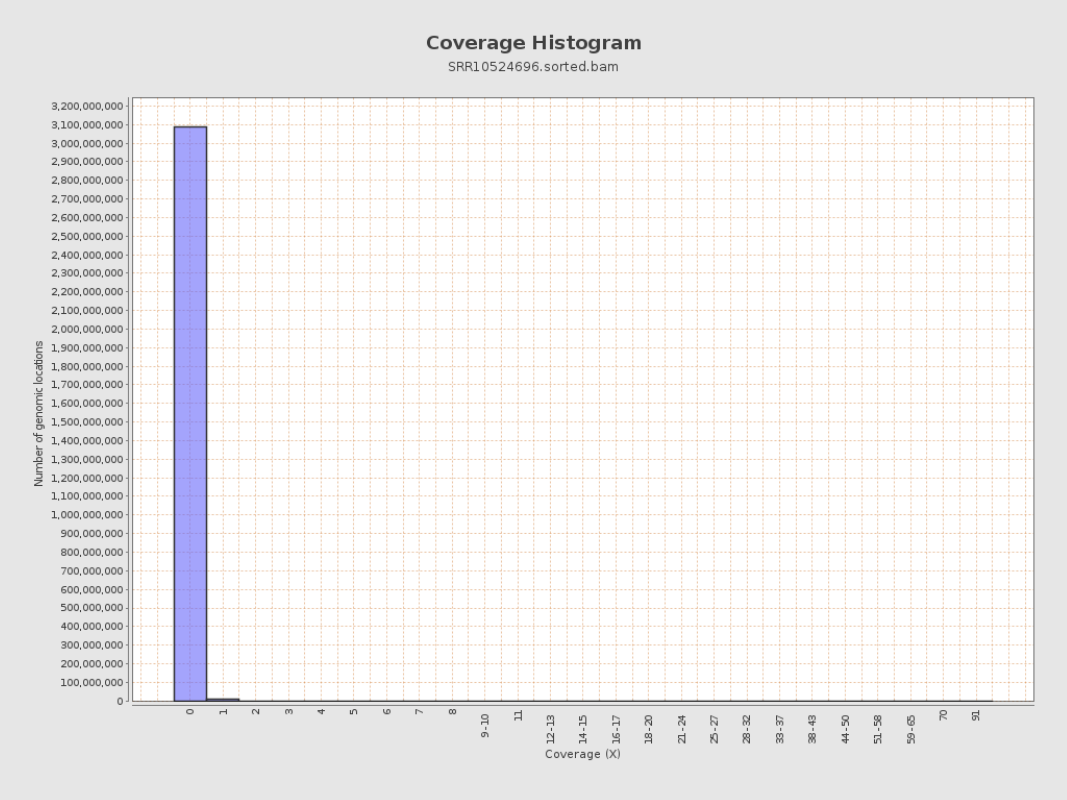
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	682293	0.0027	0.0706
chr2	243199373	716587	0.0029	0.0663
chr3	198022430	553941	0.0028	0.0535
chr4	191154276	542695	0.0028	0.0546
chr5	180915260	513425	0.0028	0.0539
chr6	171115067	481498	0.0028	0.0547
chr7	159138663	464060	0.0029	0.0619

chr8	146364022	426838	0.0029	0.0597
chr9	141213431	360259	0.0026	0.0529
chr10	135534747	416963	0.0031	0.0597
chr11	135006516	377042	0.0028	0.0552
chr12	133851895	376716	0.0028	0.0539
chr13	115169878	261725	0.0023	0.0484
chr14	107349540	249334	0.0023	0.0491
chr15	102531392	238074	0.0023	0.0487
chr16	90354753	238453	0.0026	0.0524
chr17	81195210	227661	0.0028	0.0538
chr18	78077248	222256	0.0028	0.0644
chr19	59128983	177674	0.003	0.0628
chr20	63025520	173665	0.0028	0.0534
chr21	48129895	110857	0.0023	0.0494
chr22	51304566	93903	0.0018	0.0432
chrMT	16571	1052	0.0635	0.2674
chrX	155270560	476677	0.0031	0.057
chrY	59373566	28564	0.0005	0.0279

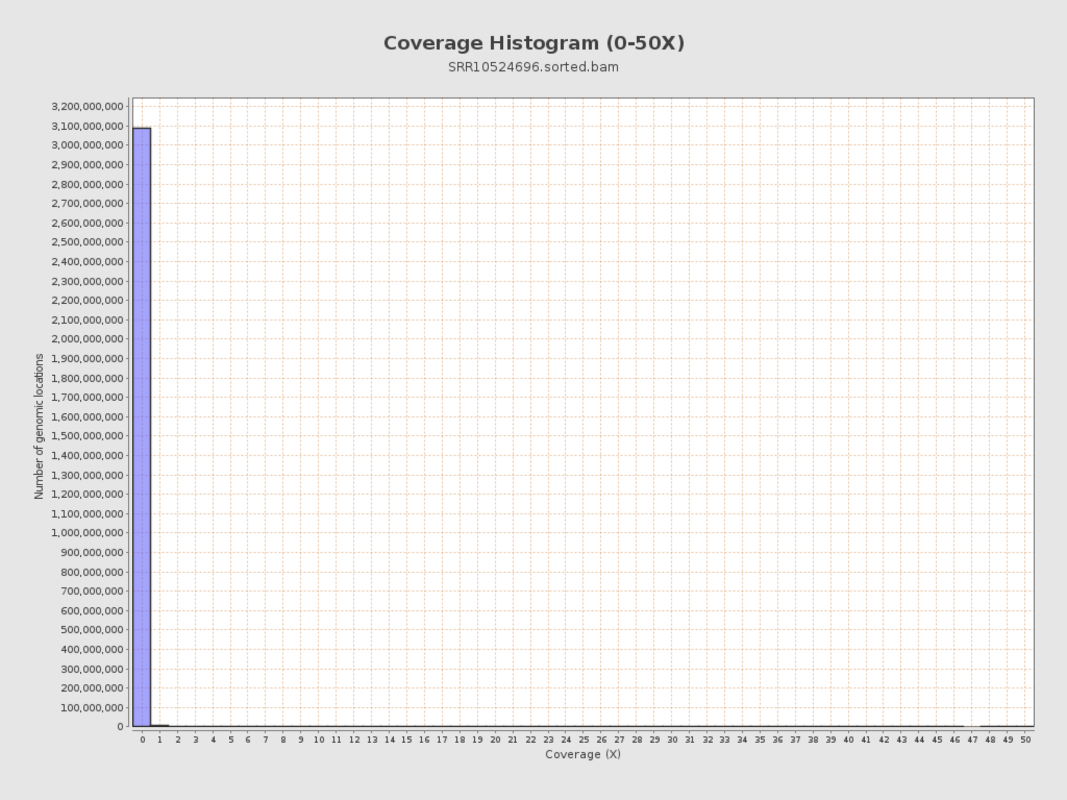
3. Results : Coverage across reference



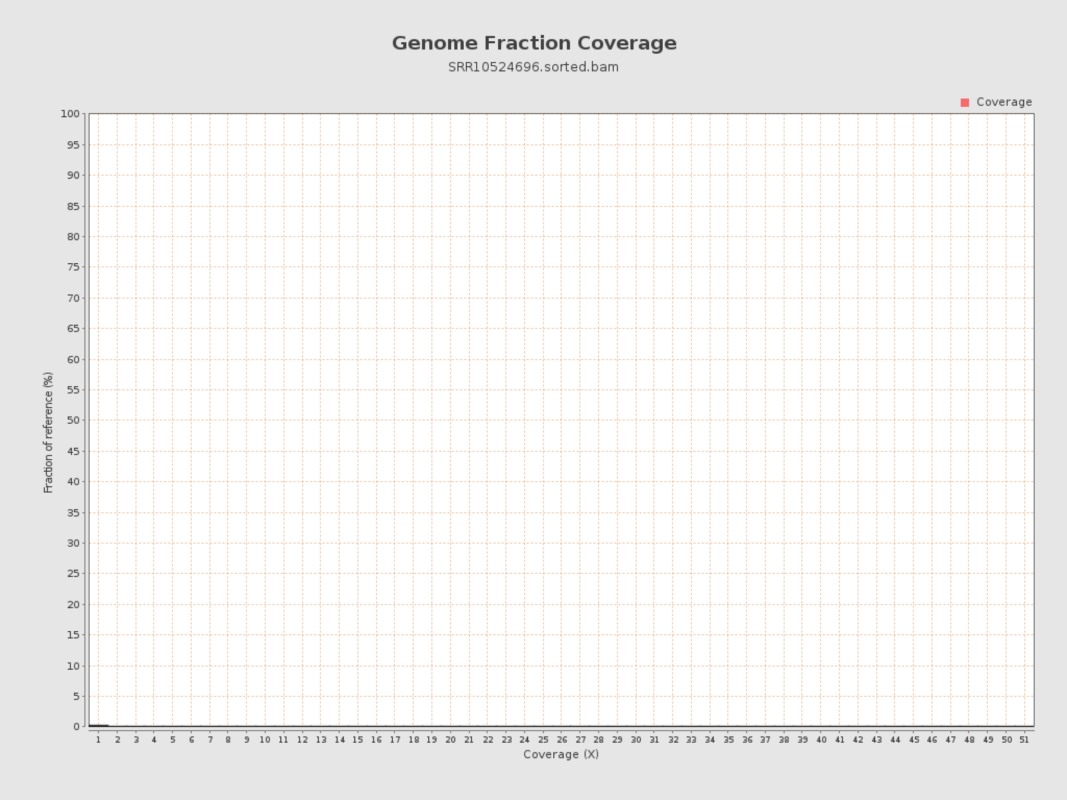
4. Results : Coverage Histogram



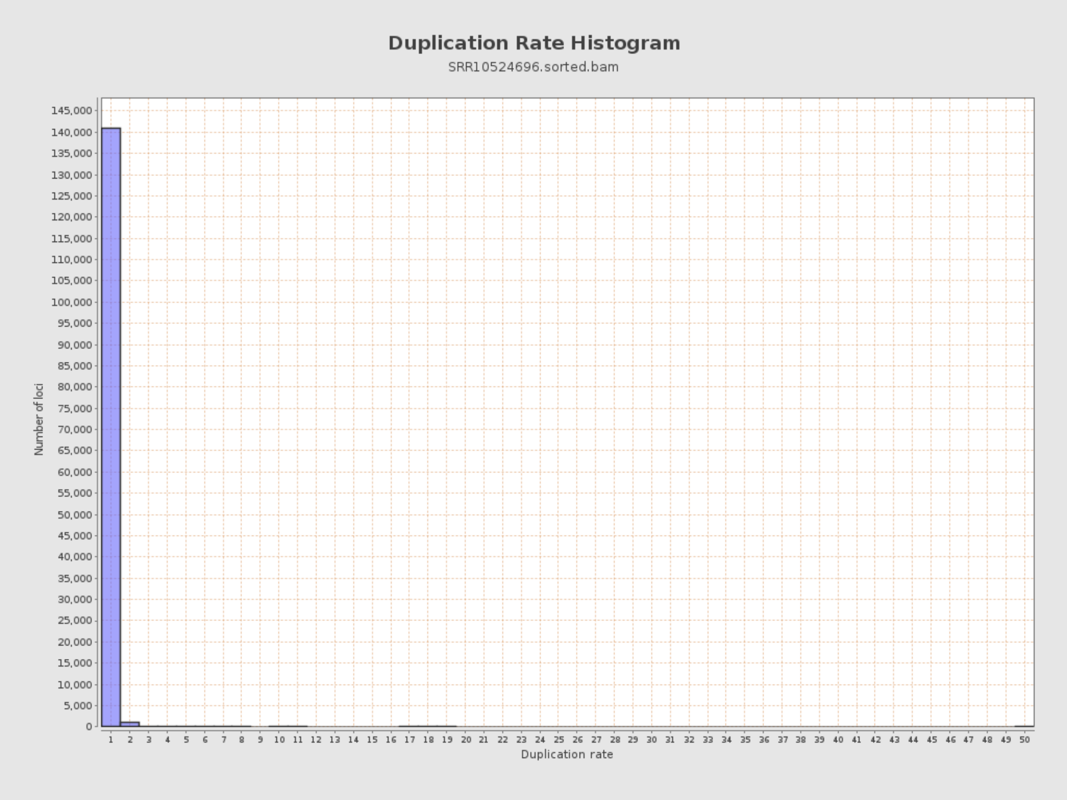
5. Results : Coverage Histogram (0-50X)



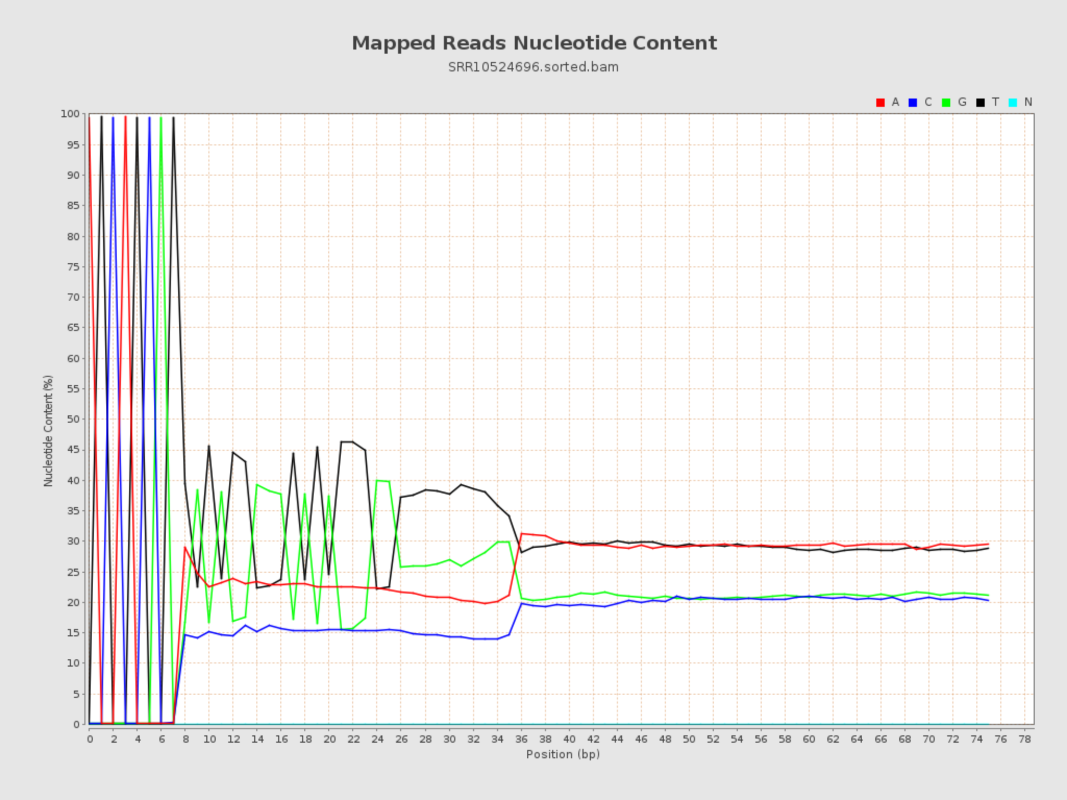
6. Results : Genome Fraction Coverage



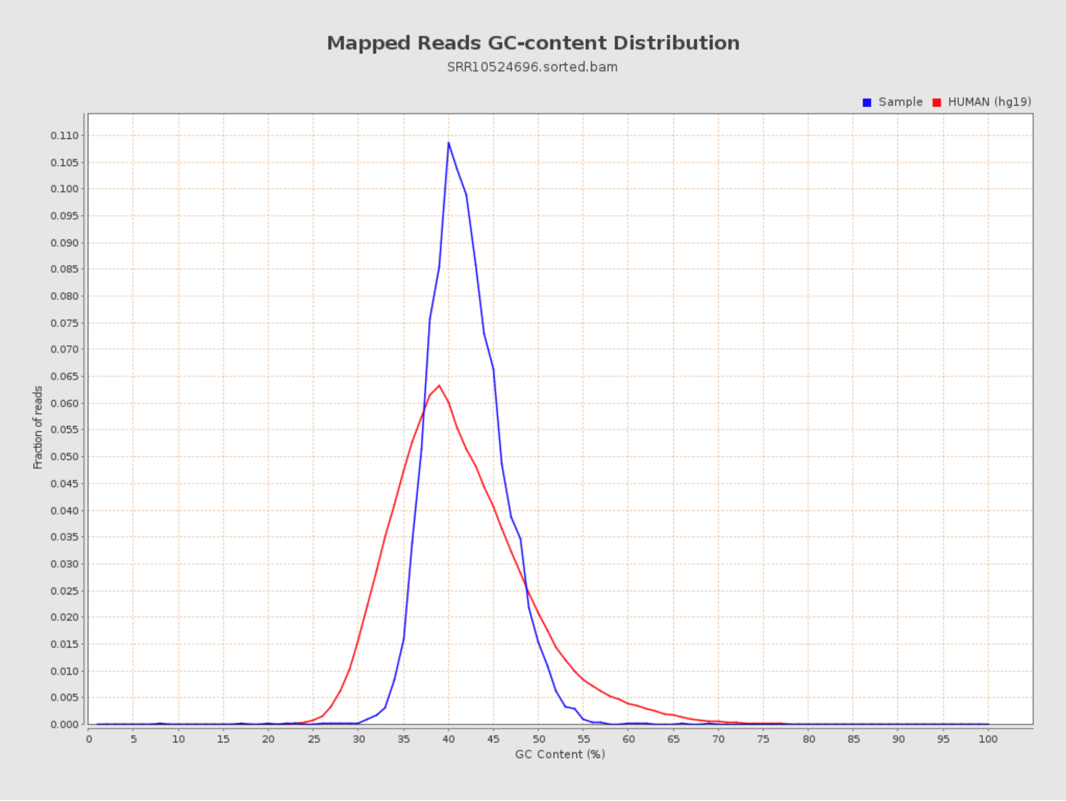
7. Results : Duplication Rate Histogram



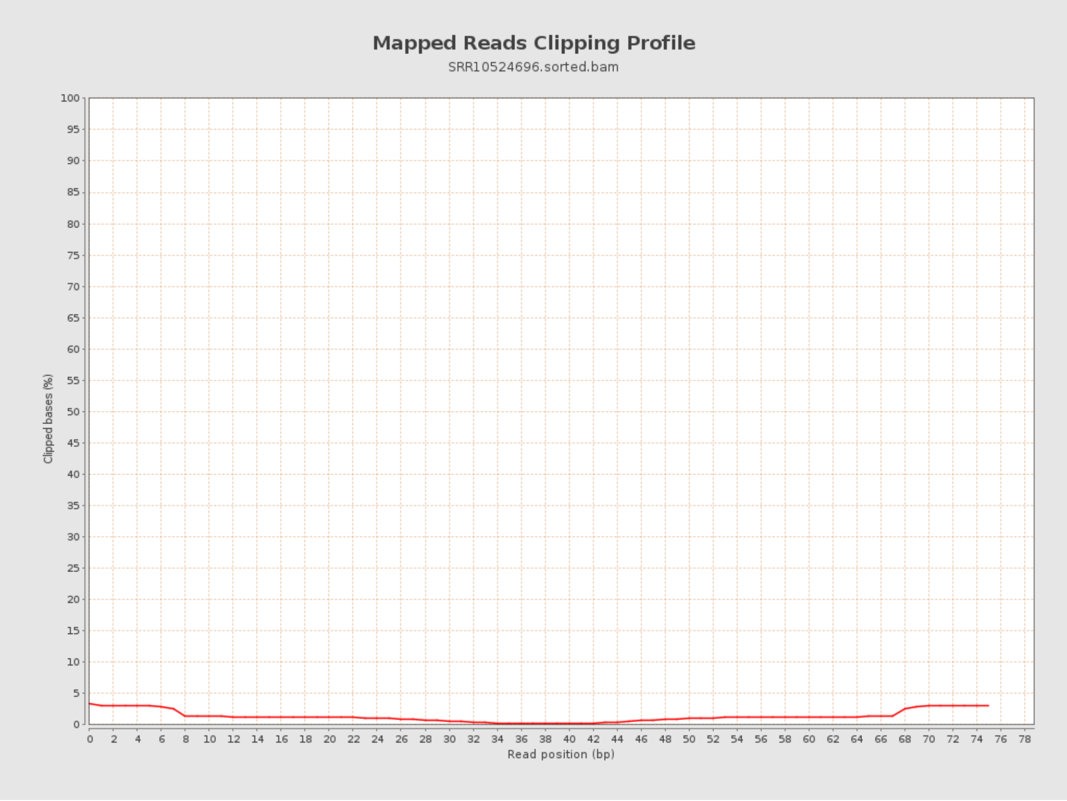
8. Results : Mapped Reads Nucleotide Content



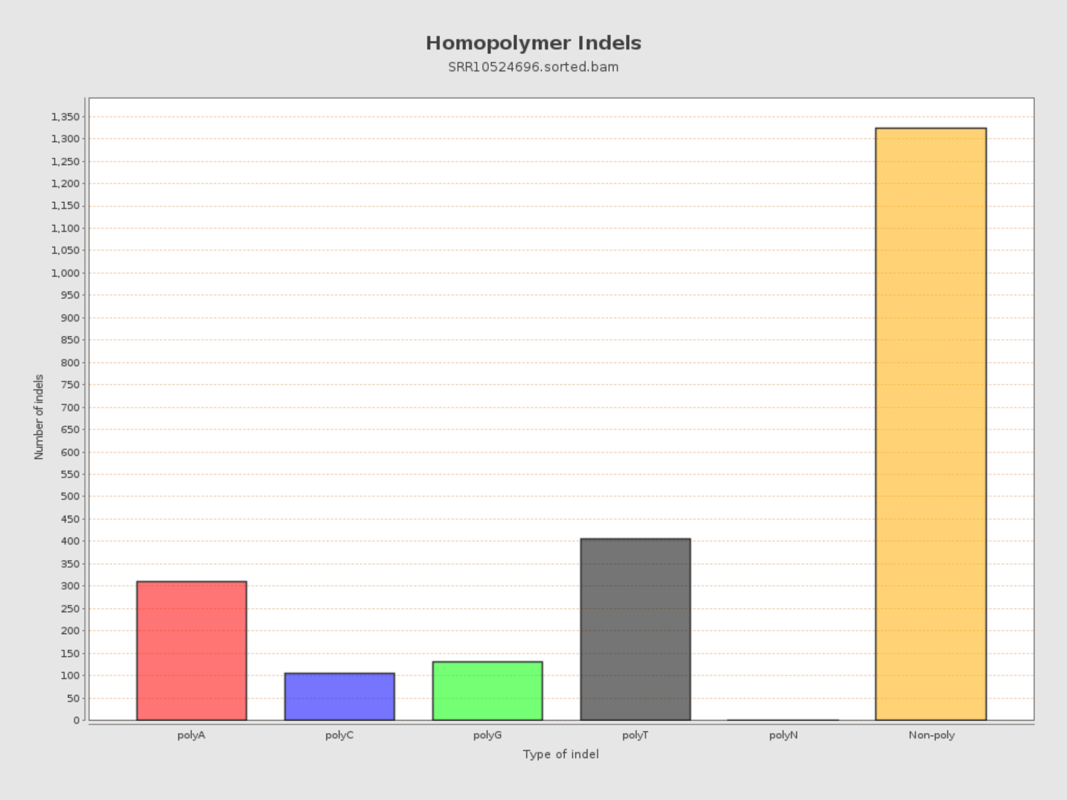
9. Results : Mapped Reads GC-content Distribution



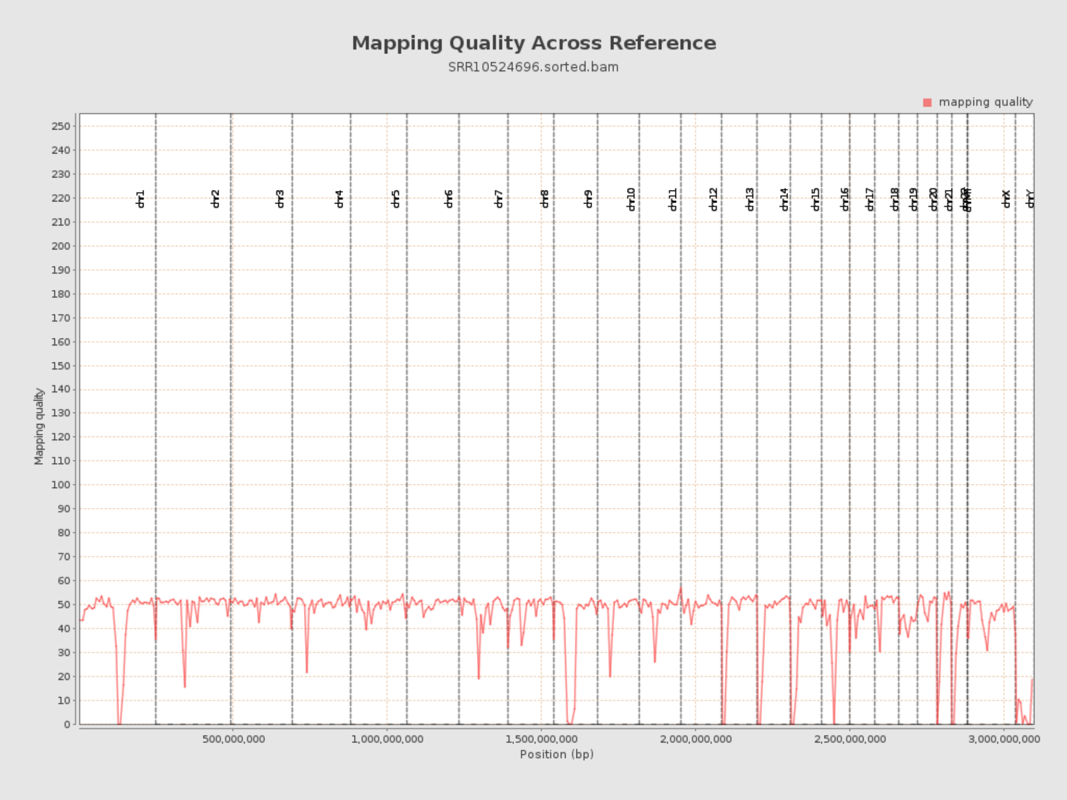
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram