Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:33:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524296.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_SRR10524296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524296.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:33:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,107,316
Mapped reads	1,915,084 / 90.88%
Unmapped reads	192,232 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,950 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	65,033 / 3.09%
Duplication rate	2.28%
Clipped reads	1,918,052 / 91.02%

2.2. ACGT Content

Number/percentage of A's	26,110,049 / 23.64%
Number/percentage of C's	20,534,074 / 18.59%
Number/percentage of T's	35,631,476 / 32.26%
Number/percentage of G's	28,157,804 / 25.49%
Number/percentage of N's	14,860 / 0.01%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3393

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Mismatches and indels

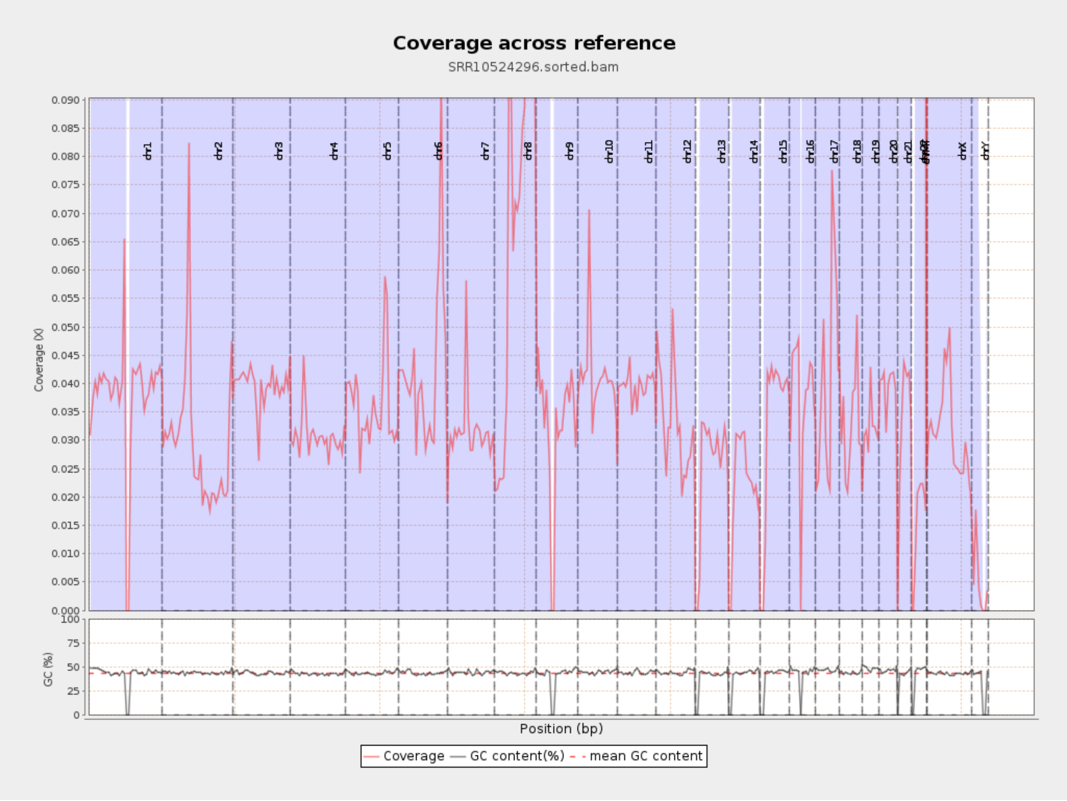
General error rate	0.52%
Mismatches	566,850
Insertions	6,947
Mapped reads with at least one insertion	0.36%
Deletions	19,286
Mapped reads with at least one deletion	1%
Homopolymer indels	42.68%

2.6. Chromosome stats

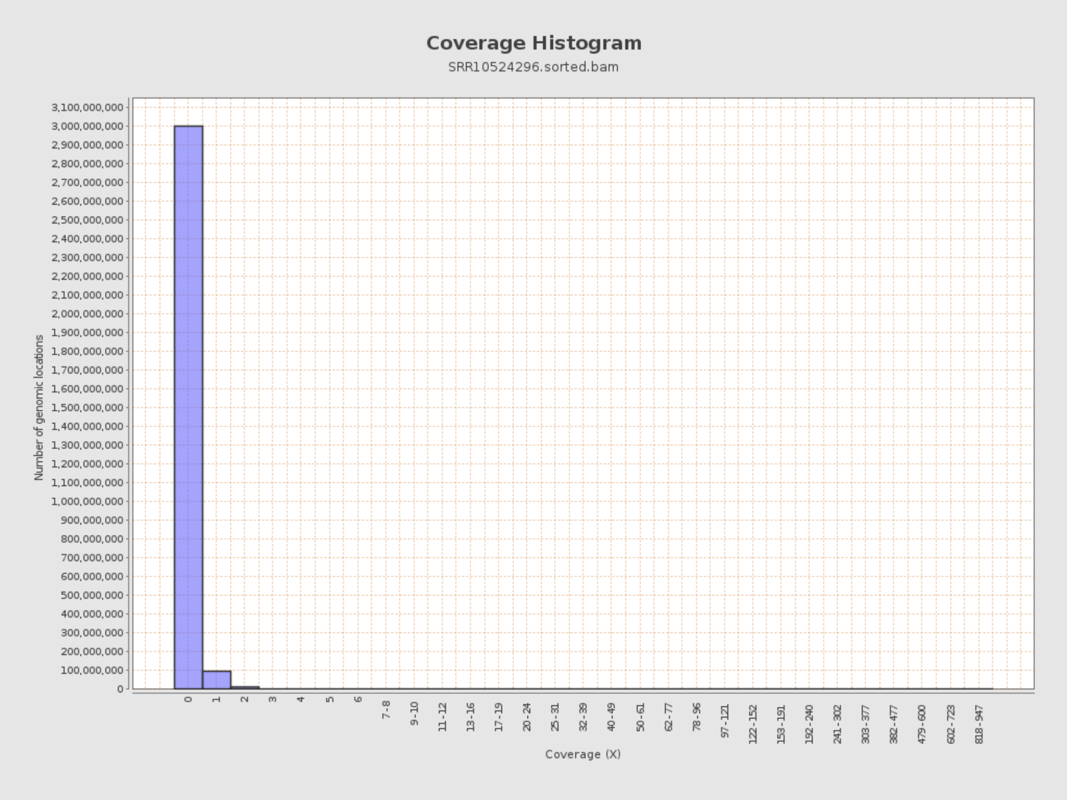
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9436307	0.0379	0.6782
chr2	243199373	7178841	0.0295	0.4369
chr3	198022430	7822747	0.0395	0.2188
chr4	191154276	5848936	0.0306	0.2109
chr5	180915260	6562673	0.0363	0.2085
chr6	171115067	7240335	0.0423	0.246
chr7	159138663	5082589	0.0319	0.4227

chr8	146364022	11535424	0.0788	0.4045
chr9	141213431	4525658	0.032	0.2596
chr10	135534747	5616762	0.0414	0.3331
chr11	135006516	5318428	0.0394	0.2812
chr12	133851895	4439087	0.0332	0.2023
chr13	115169878	2876301	0.025	0.1751
chr14	107349540	2356008	0.0219	0.1731
chr15	102531392	3369354	0.0329	0.2089
chr16	90354753	3382601	0.0374	0.2267
chr17	81195210	3304020	0.0407	0.2492
chr18	78077248	2622910	0.0336	0.466
chr19	59128983	1899231	0.0321	0.4551
chr20	63025520	2464315	0.0391	0.2173
chr21	48129895	1591703	0.0331	0.2124
chr22	51304566	771229	0.015	0.1338
chrMT	16571	50081	3.0222	2.6819
chrX	155270560	4884540	0.0315	0.2271
chrY	59373566	298714	0.005	0.1346

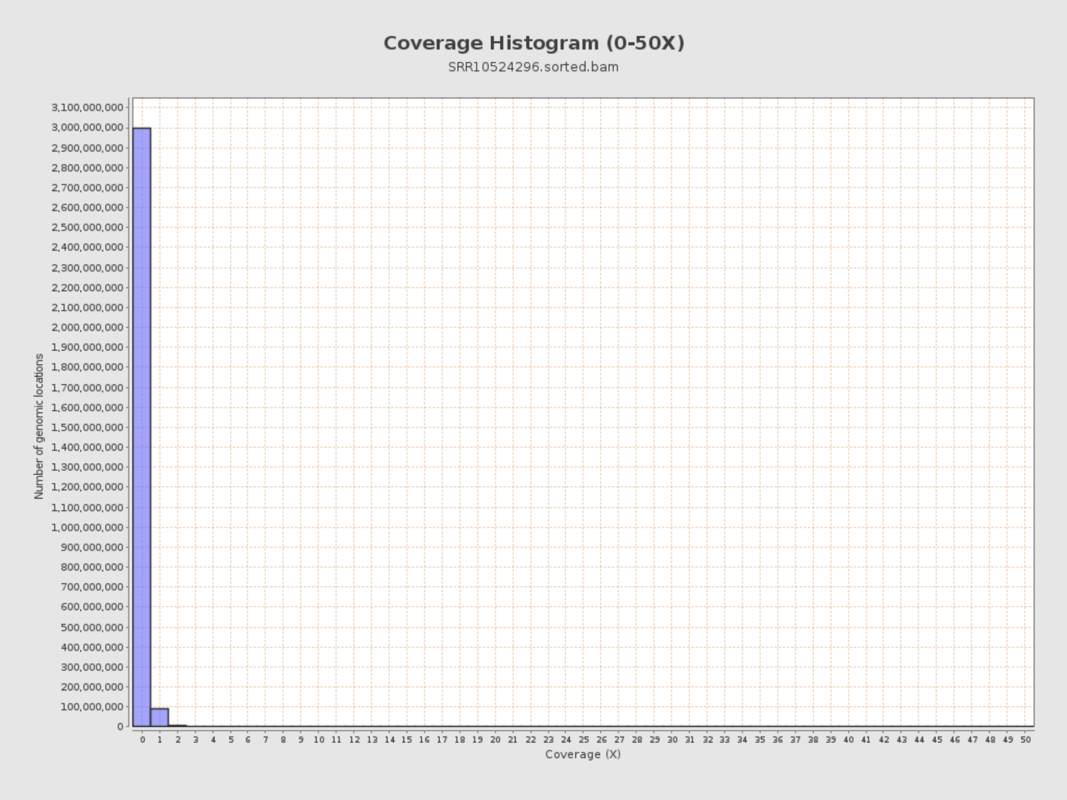
3. Results : Coverage across reference



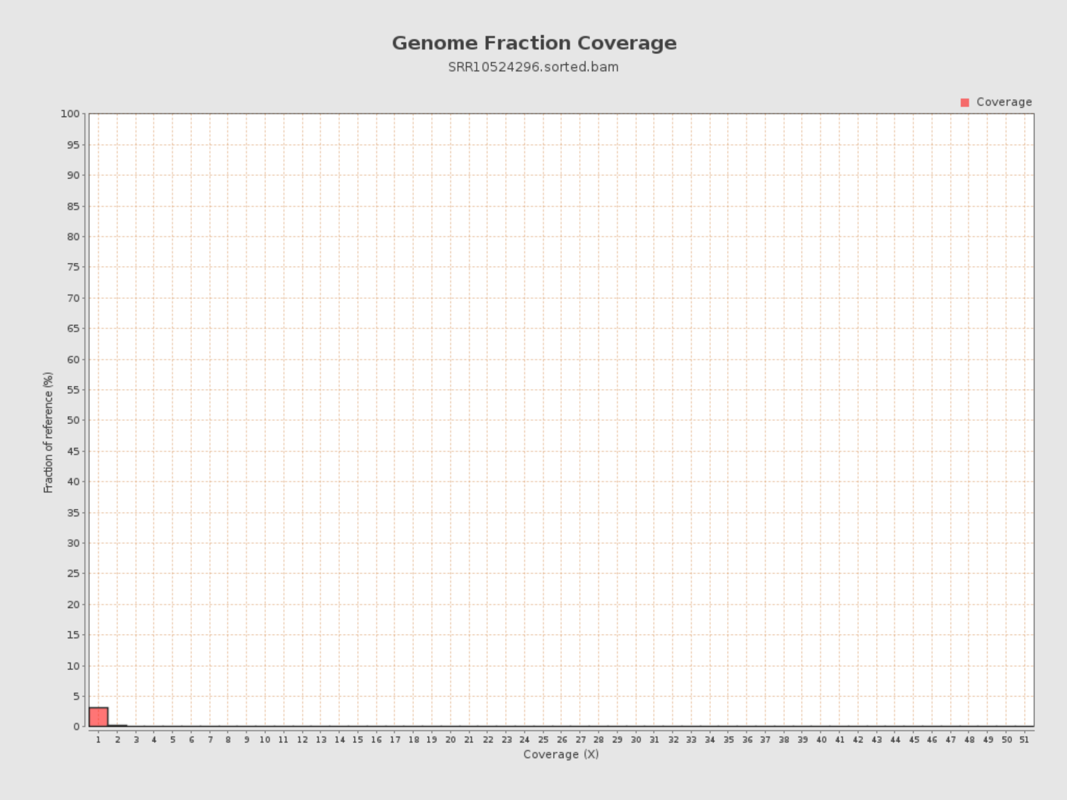
4. Results : Coverage Histogram



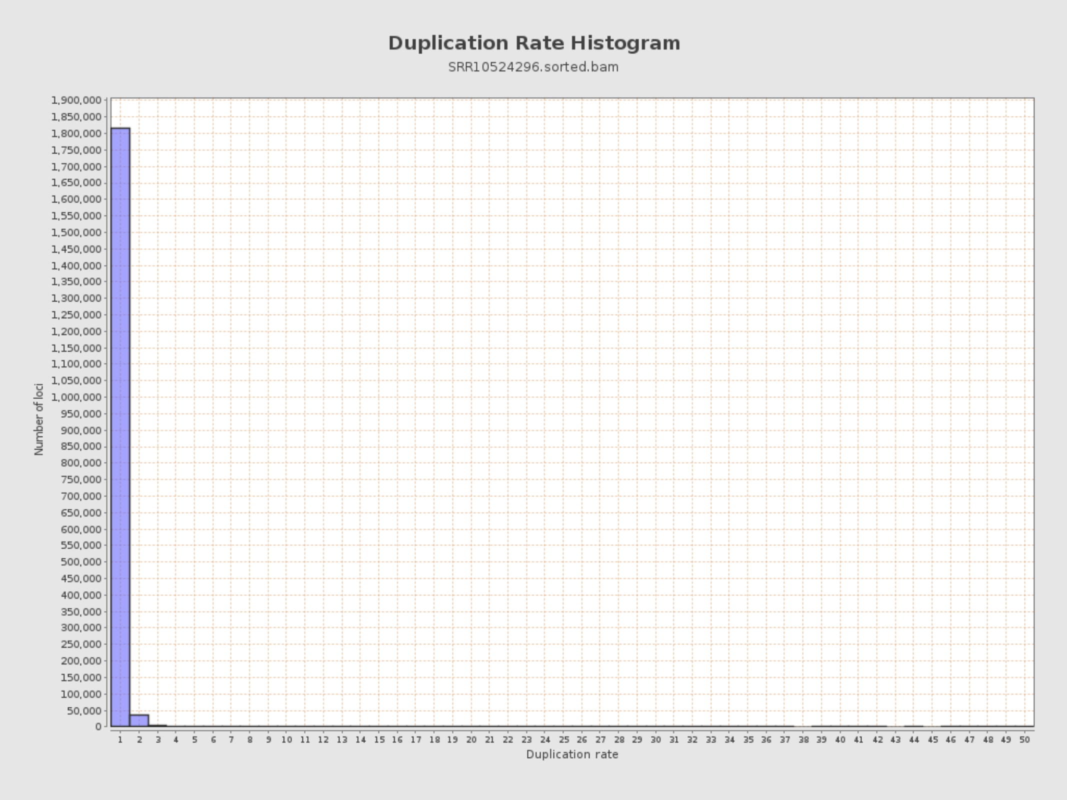
5. Results : Coverage Histogram (0-50X)



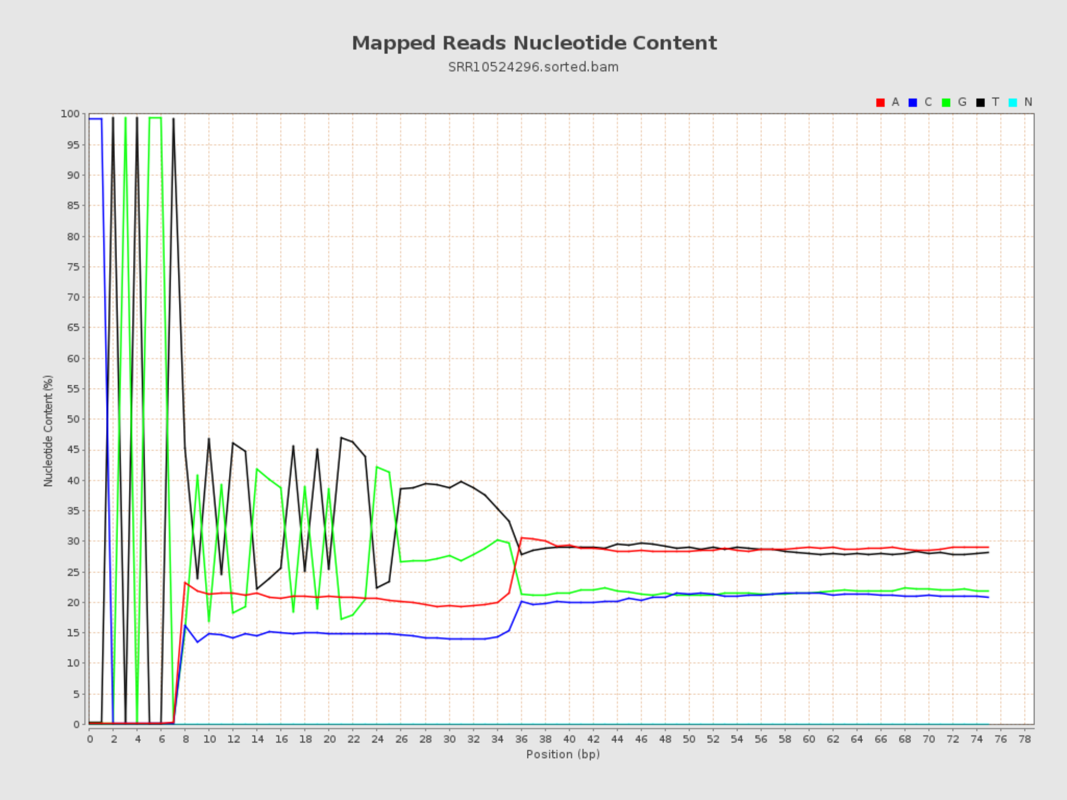
6. Results : Genome Fraction Coverage



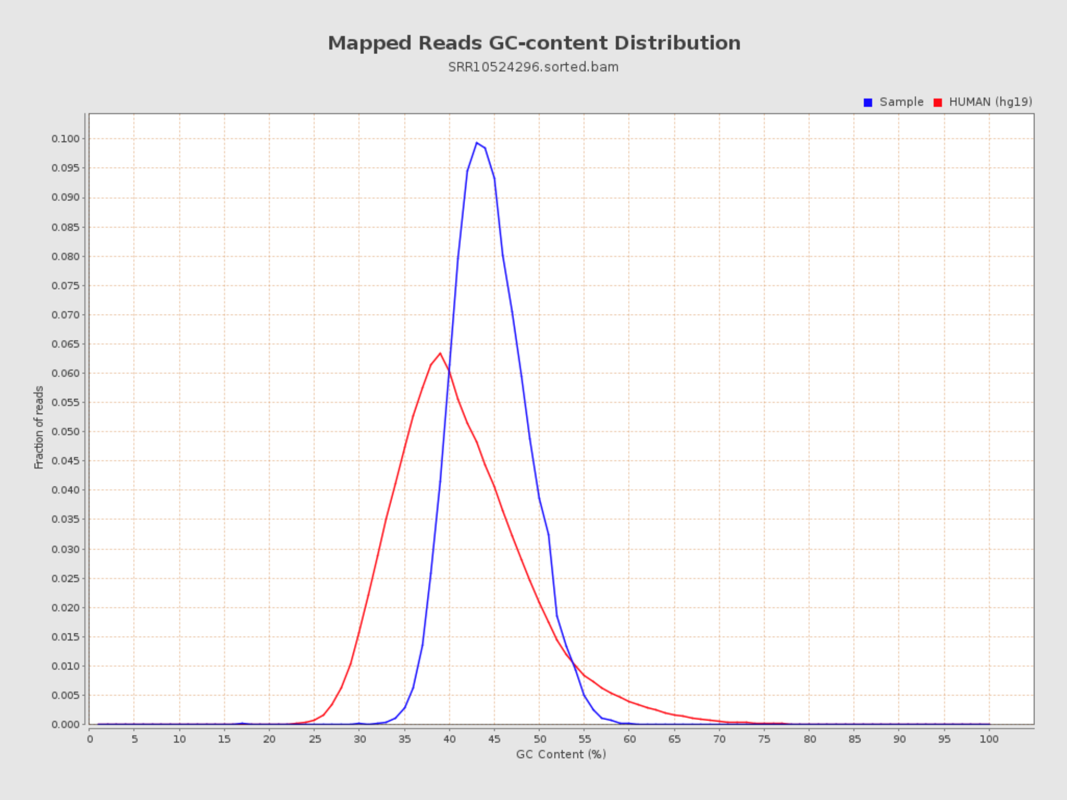
7. Results : Duplication Rate Histogram



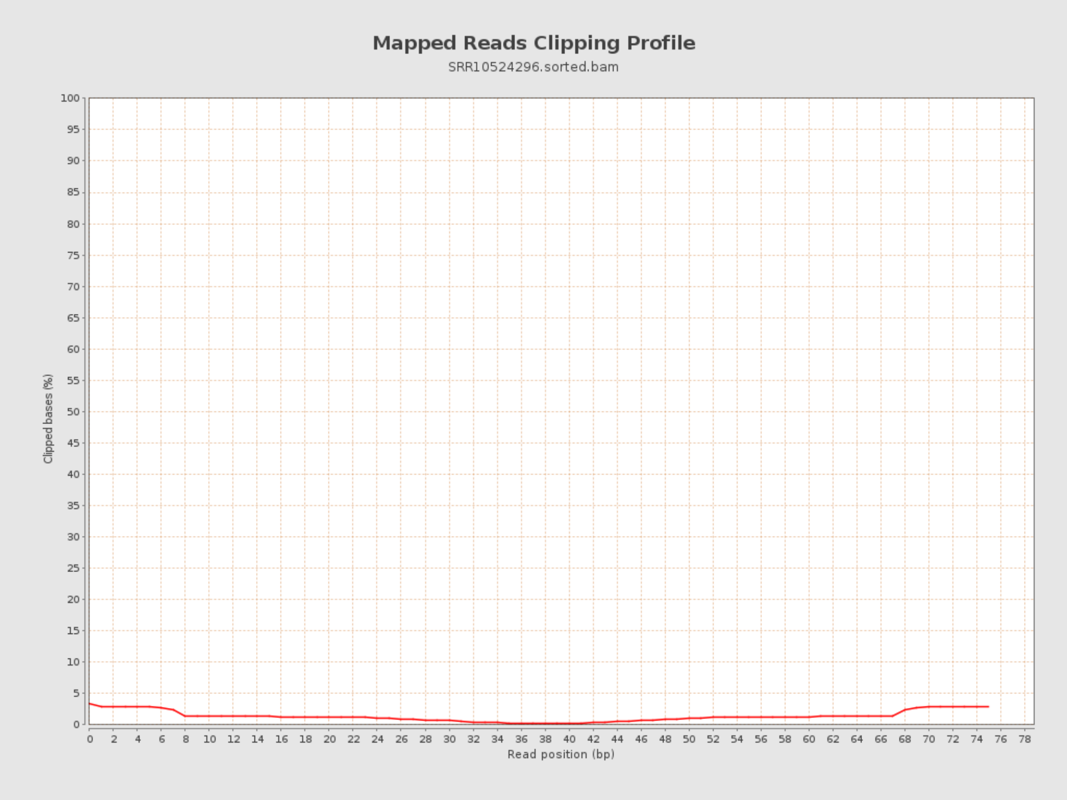
8. Results : Mapped Reads Nucleotide Content



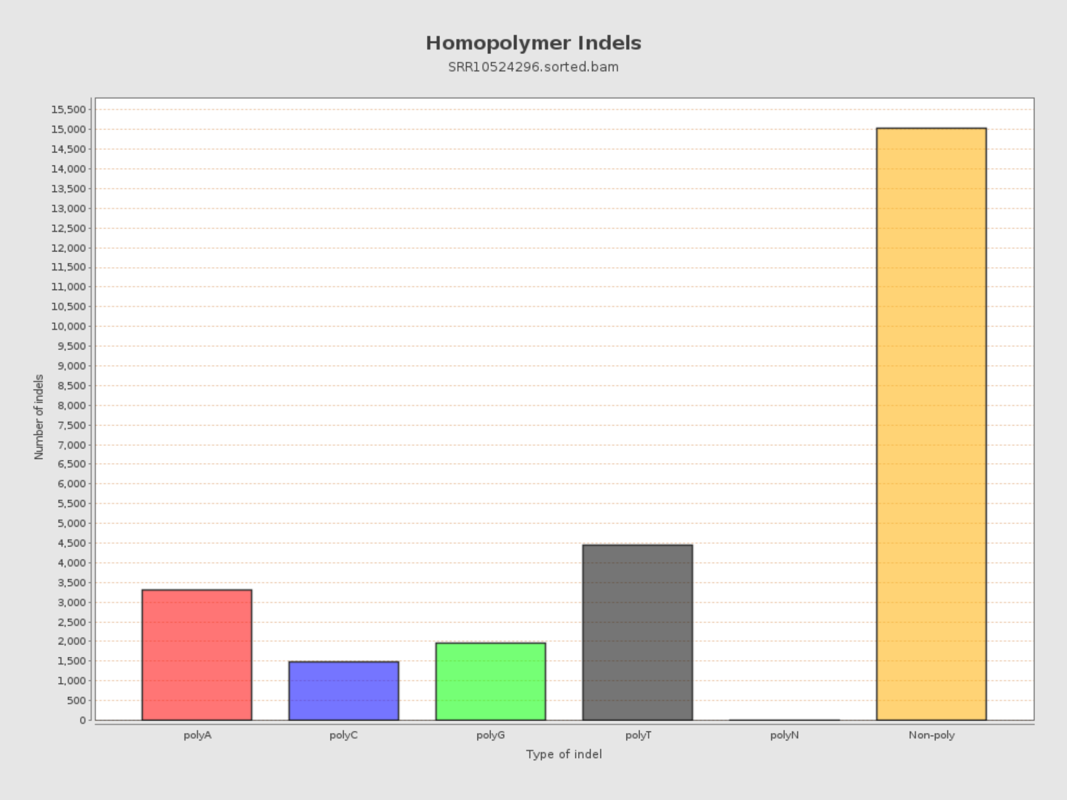
9. Results : Mapped Reads GC-content Distribution



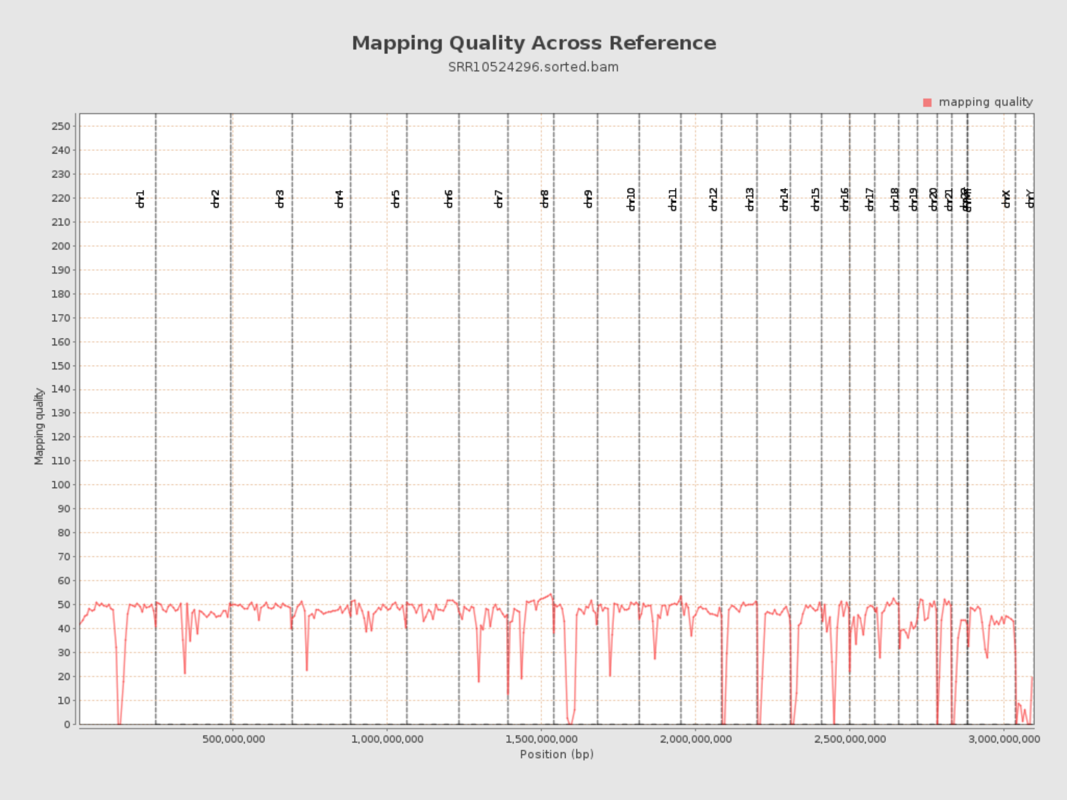
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram