Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:42:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524299.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_SRR10524299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:42:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,955,106
Mapped reads	2,689,735 / 91.02%
Unmapped reads	265,371 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,600 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	120,452 / 4.08%
Duplication rate	3.16%
Clipped reads	2,692,048 / 91.1%

2.2. ACGT Content

Number/percentage of A's	38,602,967 / 24.89%
Number/percentage of C's	26,601,836 / 17.15%
Number/percentage of T's	49,685,741 / 32.04%
Number/percentage of G's	40,167,491 / 25.9%
Number/percentage of N's	21,899 / 0.01%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.4353

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

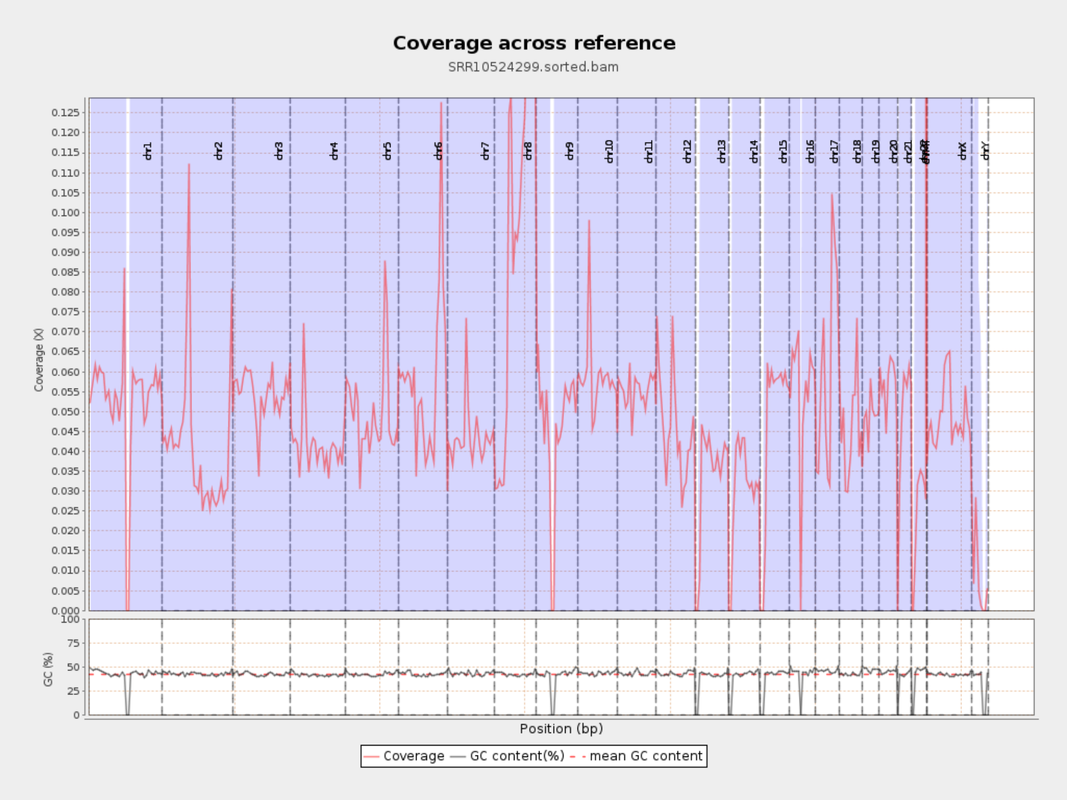
General error rate	0.52%
Mismatches	793,122
Insertions	10,632
Mapped reads with at least one insertion	0.39%
Deletions	25,858
Mapped reads with at least one deletion	0.95%
Homopolymer indels	42.15%

2.6. Chromosome stats

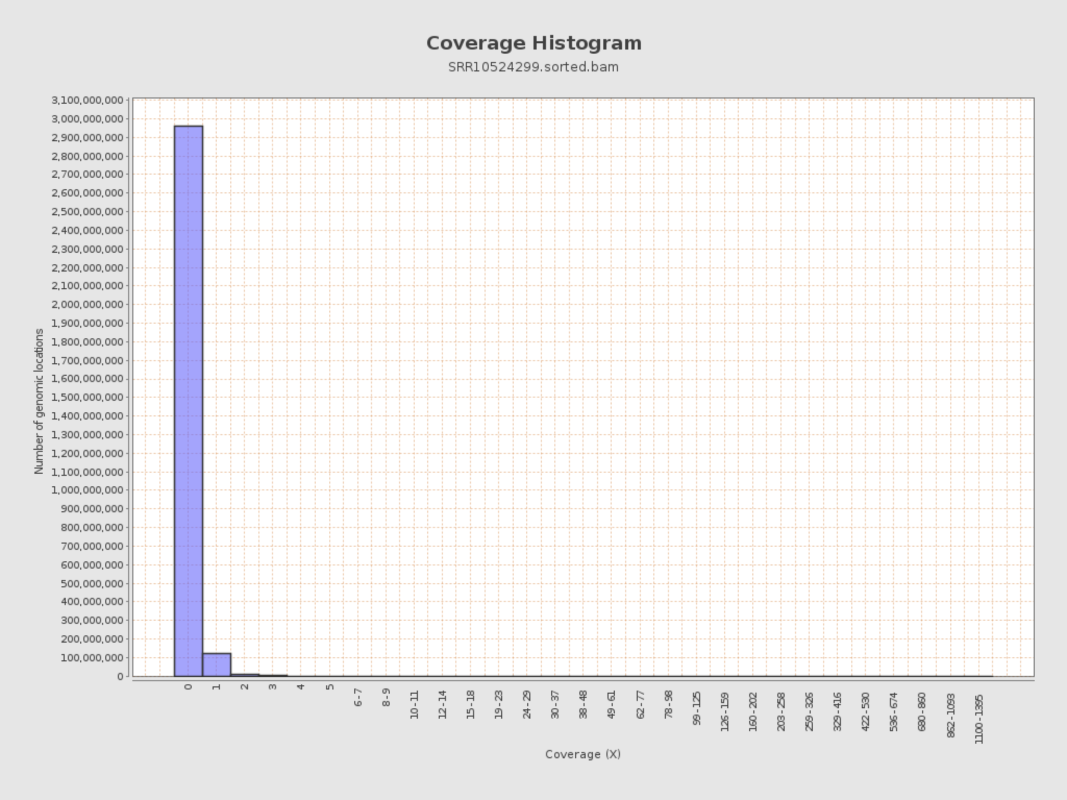
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13137864	0.0527	0.848
chr2	243199373	9988368	0.0411	0.6161
chr3	198022430	10755104	0.0543	0.2656
chr4	191154276	7917701	0.0414	0.279
chr5	180915260	9022880	0.0499	0.2545
chr6	171115067	9878423	0.0577	0.3118
chr7	159138663	6960840	0.0437	0.5105

chr8	146364022	15996636	0.1093	0.5143
chr9	141213431	6410387	0.0454	0.3235
chr10	135534747	7974720	0.0588	0.4303
chr11	135006516	7445637	0.0552	0.3495
chr12	133851895	6136216	0.0458	0.2489
chr13	115169878	3847713	0.0334	0.2105
chr14	107349540	3269962	0.0305	0.2225
chr15	102531392	4820659	0.047	0.2536
chr16	90354753	4990800	0.0552	0.2901
chr17	81195210	4905068	0.0604	0.3125
chr18	78077248	3625226	0.0464	0.6479
chr19	59128983	2876653	0.0487	0.5652
chr20	63025520	3599951	0.0571	0.2791
chr21	48129895	2277447	0.0473	0.2764
chr22	51304566	1192941	0.0233	0.1724
chrMT	16571	127971	7.7226	5.2302
chrX	155270560	7510288	0.0484	0.2961
chrY	59373566	452220	0.0076	0.2168

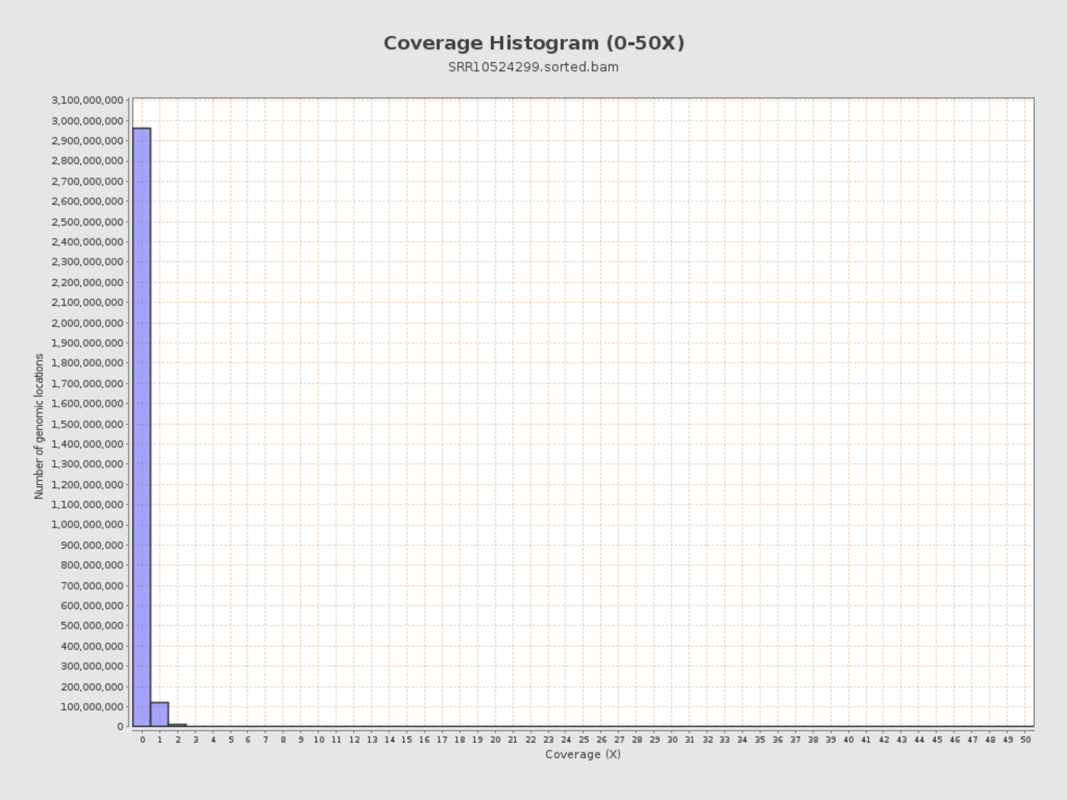
3. Results : Coverage across reference



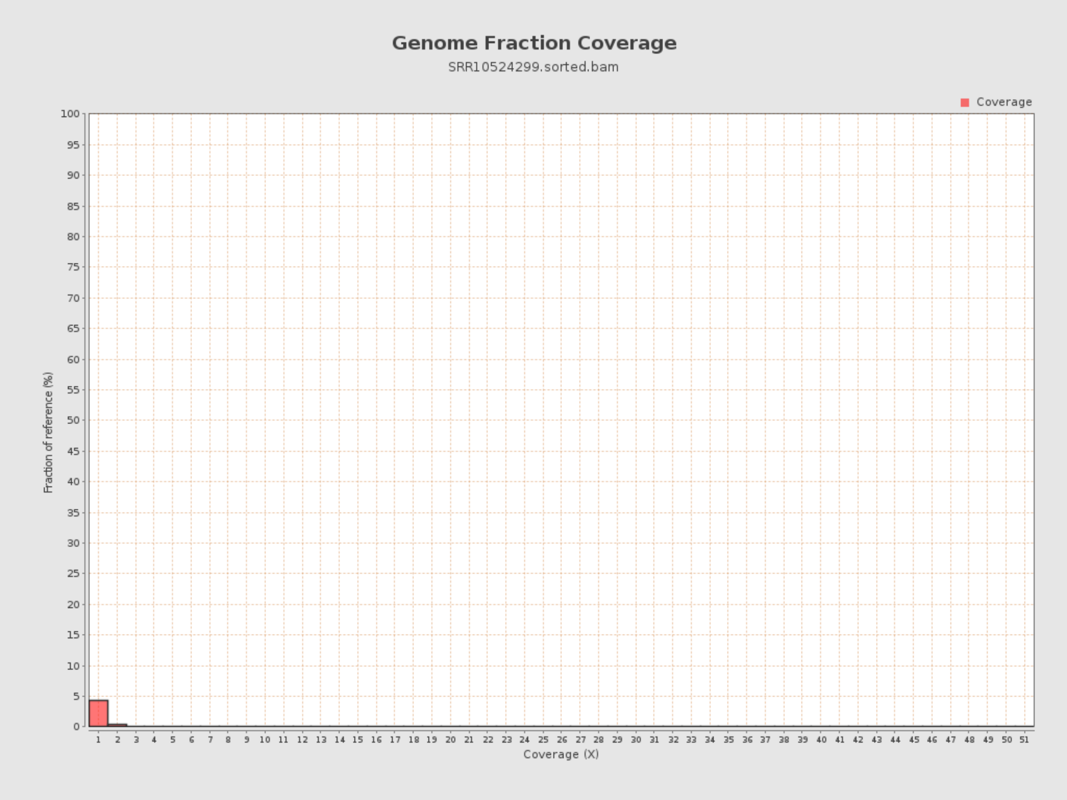
4. Results : Coverage Histogram



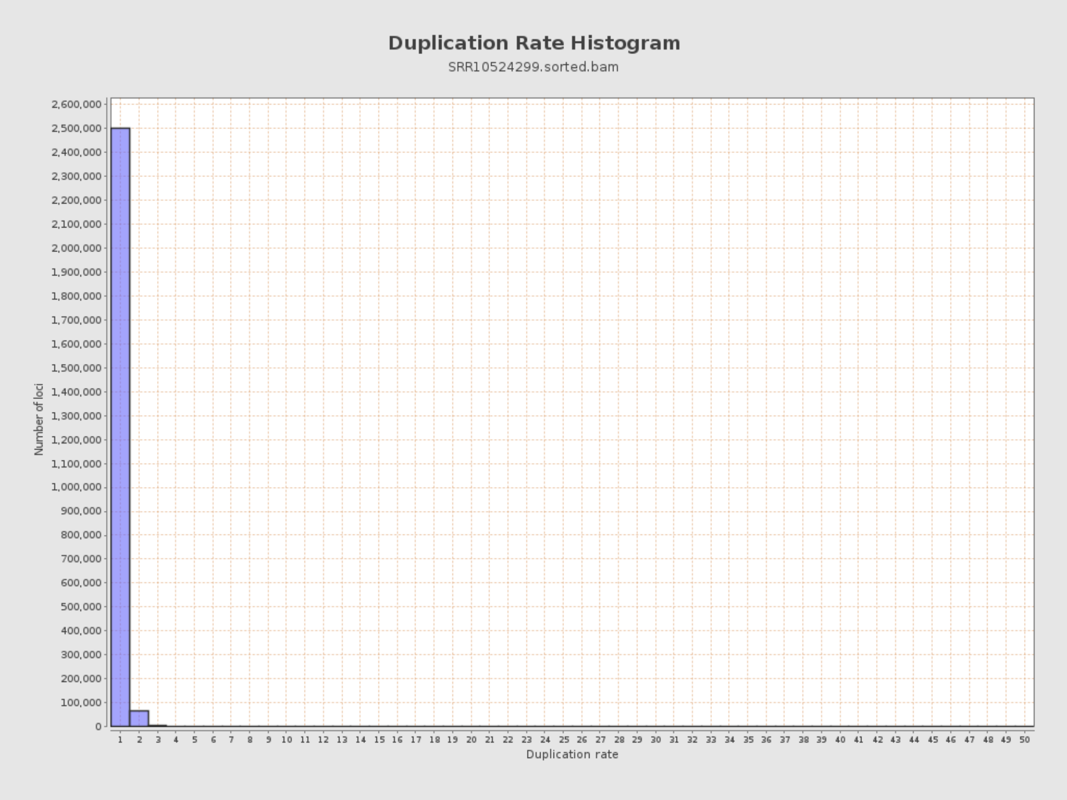
5. Results : Coverage Histogram (0-50X)



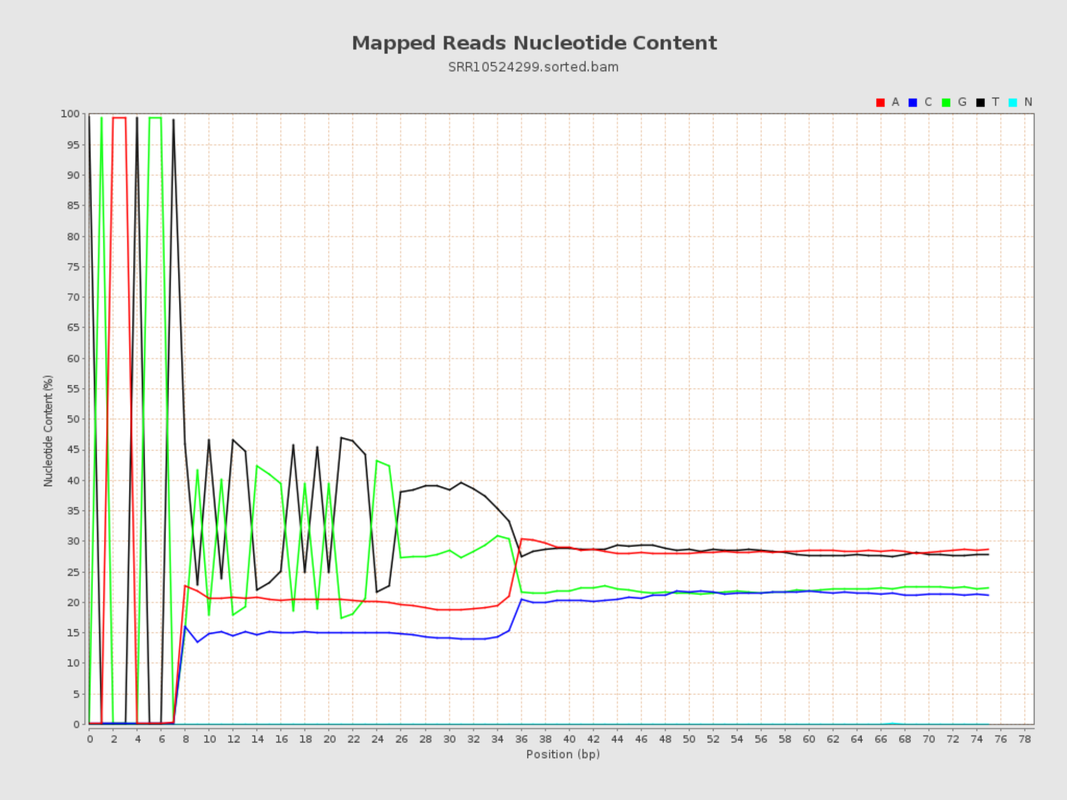
6. Results : Genome Fraction Coverage



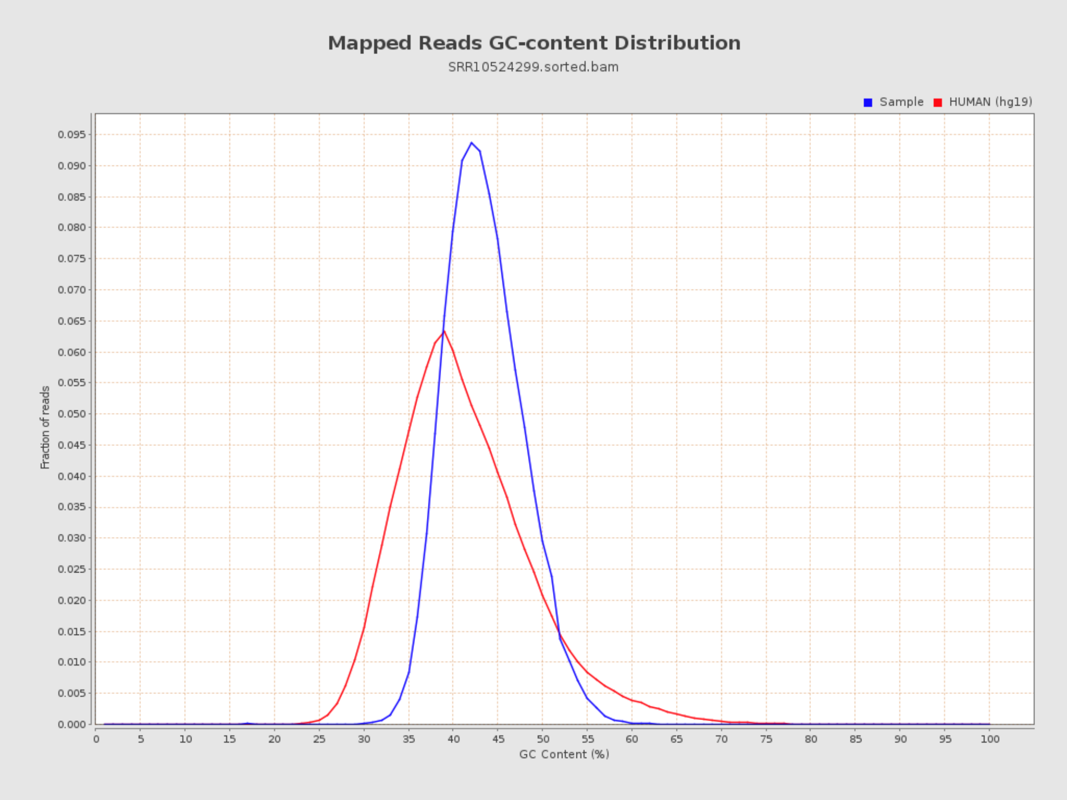
7. Results : Duplication Rate Histogram



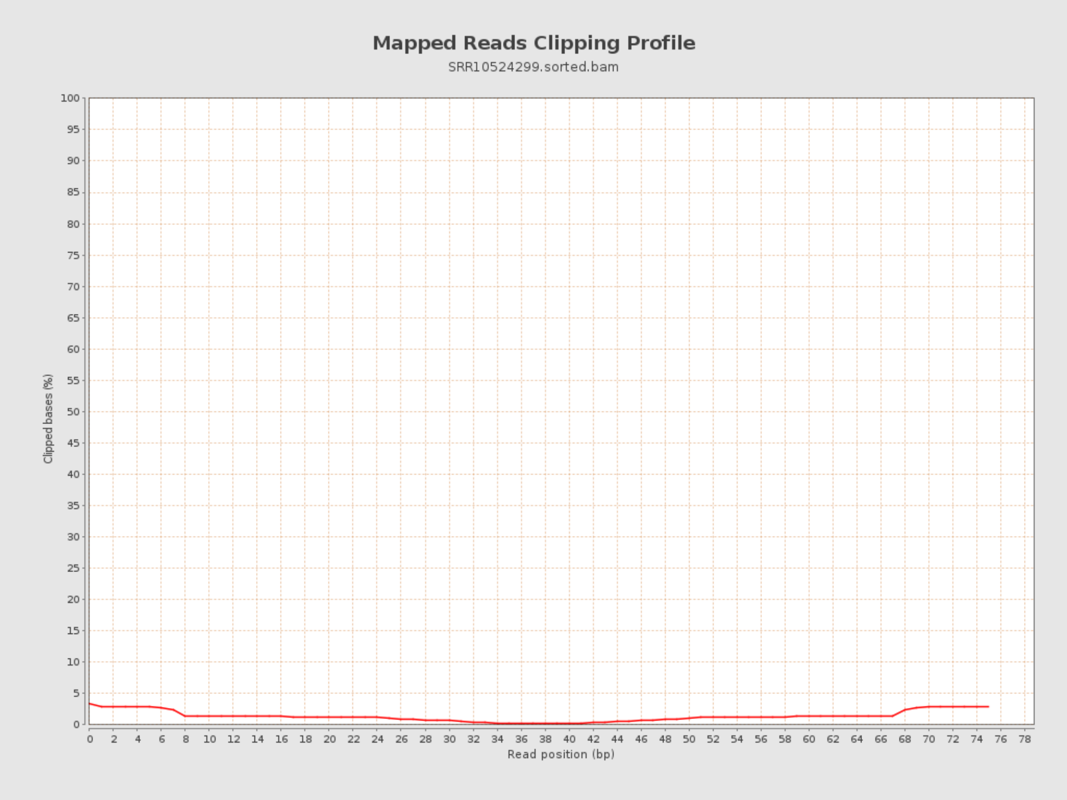
8. Results : Mapped Reads Nucleotide Content



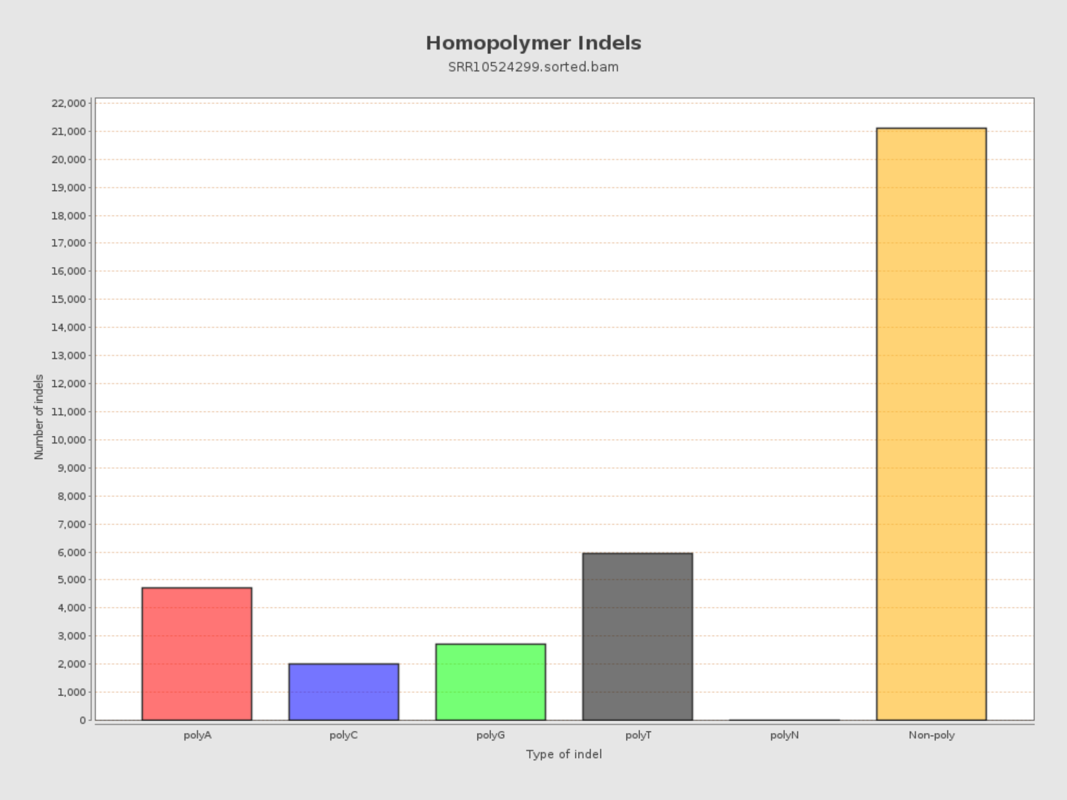
9. Results : Mapped Reads GC-content Distribution



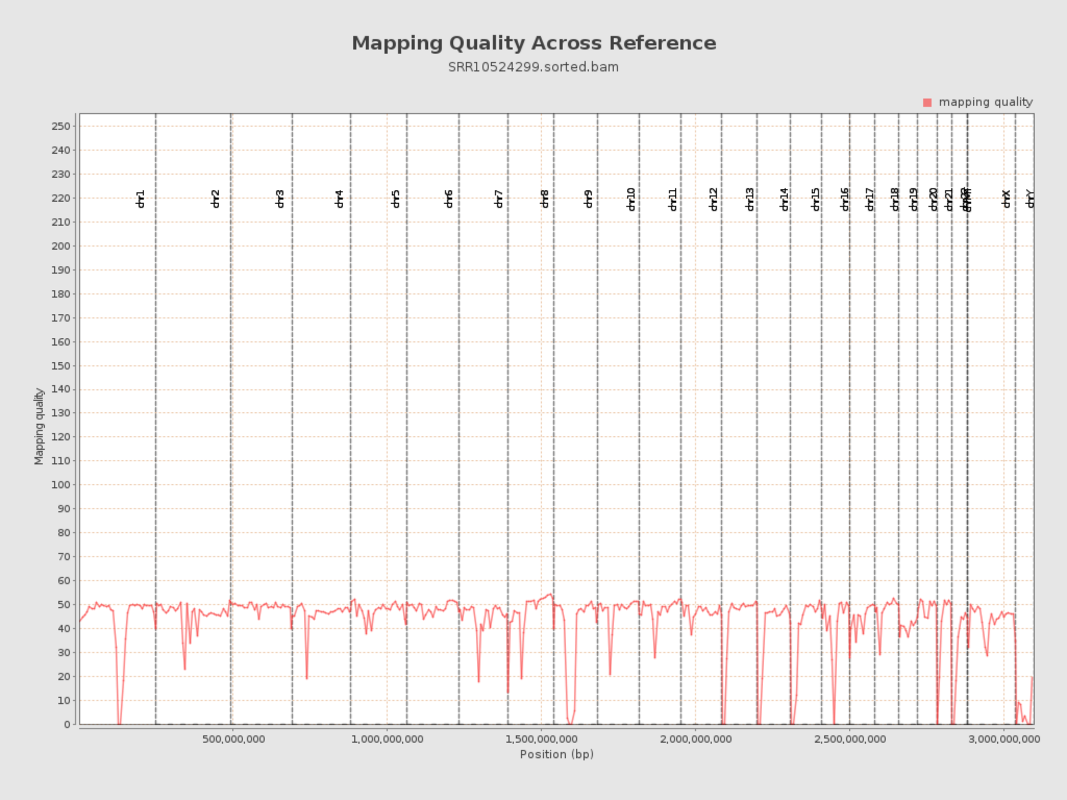
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram