Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 07:32:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524514.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_SRR10524514 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524514.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 07:32:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524514.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,977,288
Mapped reads	2,724,963 / 91.53%
Unmapped reads	252,325 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,128 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	293,380 / 9.85%
Duplication rate	7.91%
Clipped reads	2,734,702 / 91.85%

2.2. ACGT Content

Number/percentage of A's	37,614,994 / 23.68%
Number/percentage of C's	32,805,388 / 20.66%
Number/percentage of T's	50,722,429 / 31.94%
Number/percentage of G's	37,678,040 / 23.72%
Number/percentage of N's	2,263 / 0%
GC Percentage	44.38%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.481

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

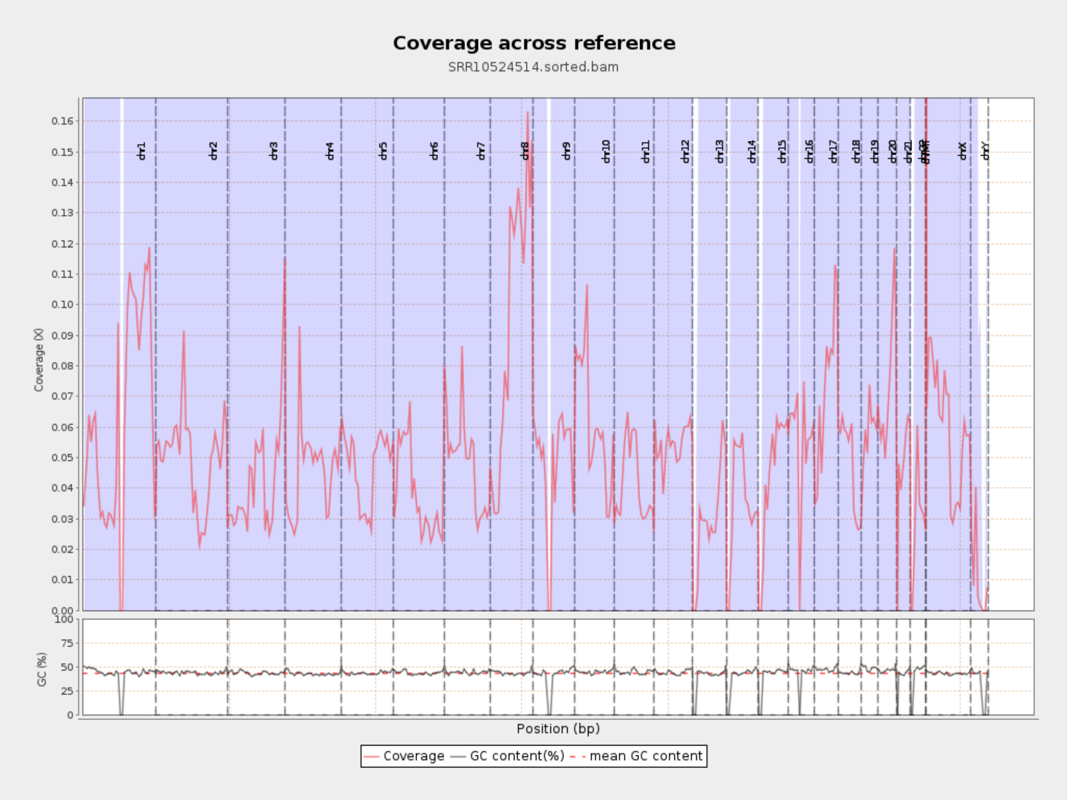
General error rate	0.53%
Mismatches	819,830
Insertions	9,643
Mapped reads with at least one insertion	0.35%
Deletions	28,230
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.39%

2.6. Chromosome stats

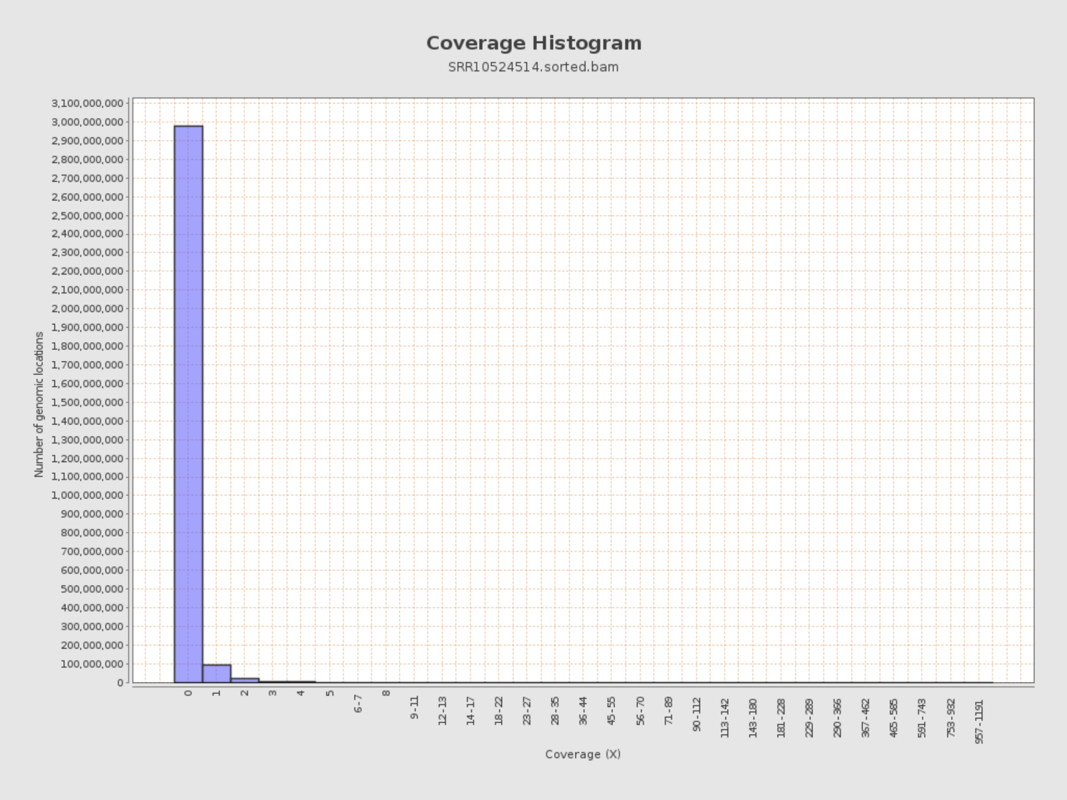
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15668916	0.0629	0.9297
chr2	243199373	12295269	0.0506	0.6059
chr3	198022430	8449349	0.0427	0.2661
chr4	191154276	8802491	0.046	0.3769
chr5	180915260	8542078	0.0472	0.2808
chr6	171115067	6520867	0.0381	0.3119
chr7	159138663	7785686	0.0489	0.5601

chr8	146364022	14317558	0.0978	0.5304
chr9	141213431	6700908	0.0475	0.3885
chr10	135534747	8336096	0.0615	0.5383
chr11	135006516	5634777	0.0417	0.4065
chr12	133851895	7345079	0.0549	0.3044
chr13	115169878	3485760	0.0303	0.2241
chr14	107349540	3849000	0.0359	0.2538
chr15	102531392	4381868	0.0427	0.2655
chr16	90354753	4923761	0.0545	0.3302
chr17	81195210	5898509	0.0726	0.3773
chr18	78077248	3775479	0.0484	0.7184
chr19	59128983	3435290	0.0581	0.6459
chr20	63025520	4757179	0.0755	0.3642
chr21	48129895	2305802	0.0479	0.3431
chr22	51304566	1435341	0.028	0.2154
chrMT	16571	192724	11.6302	7.6931
chrX	155270560	9411838	0.0606	0.3519
chrY	59373566	619131	0.0104	0.344

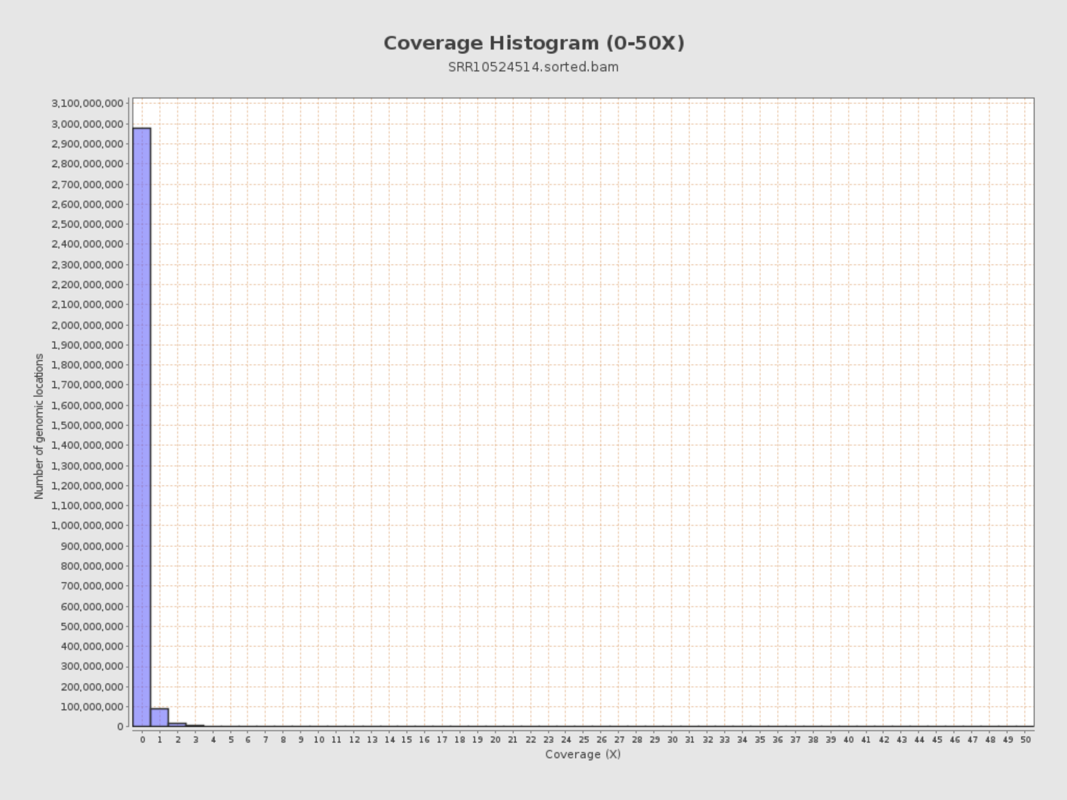
3. Results : Coverage across reference



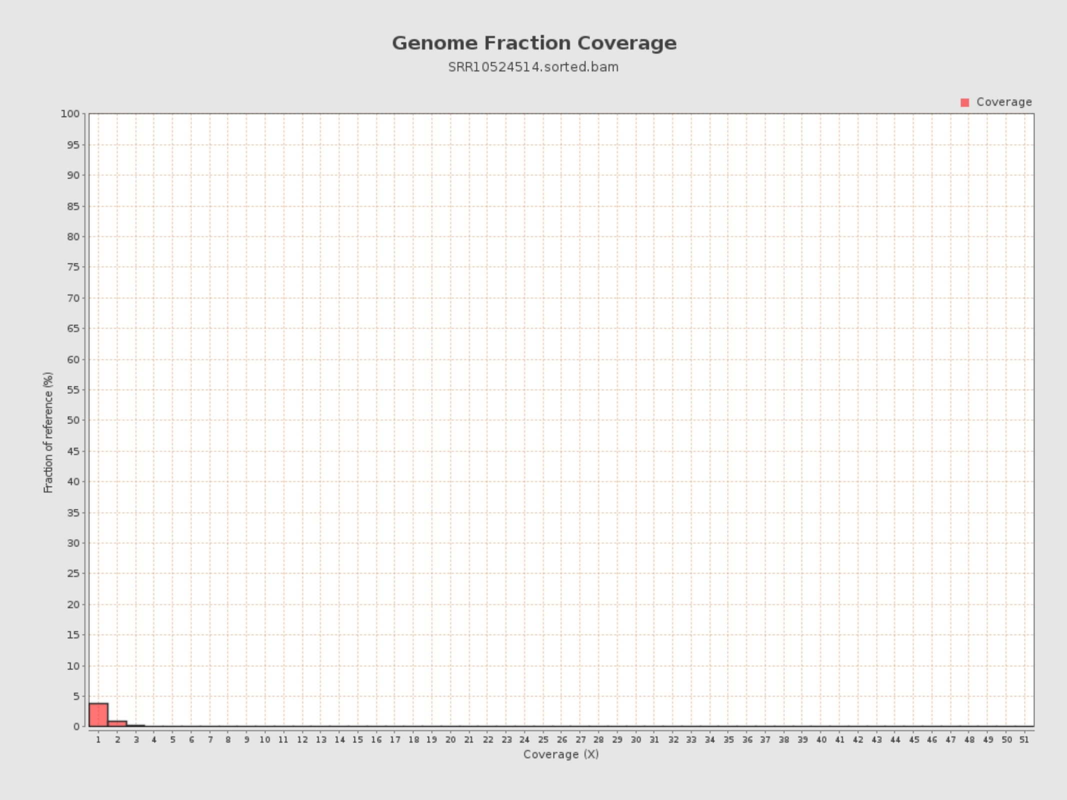
4. Results : Coverage Histogram



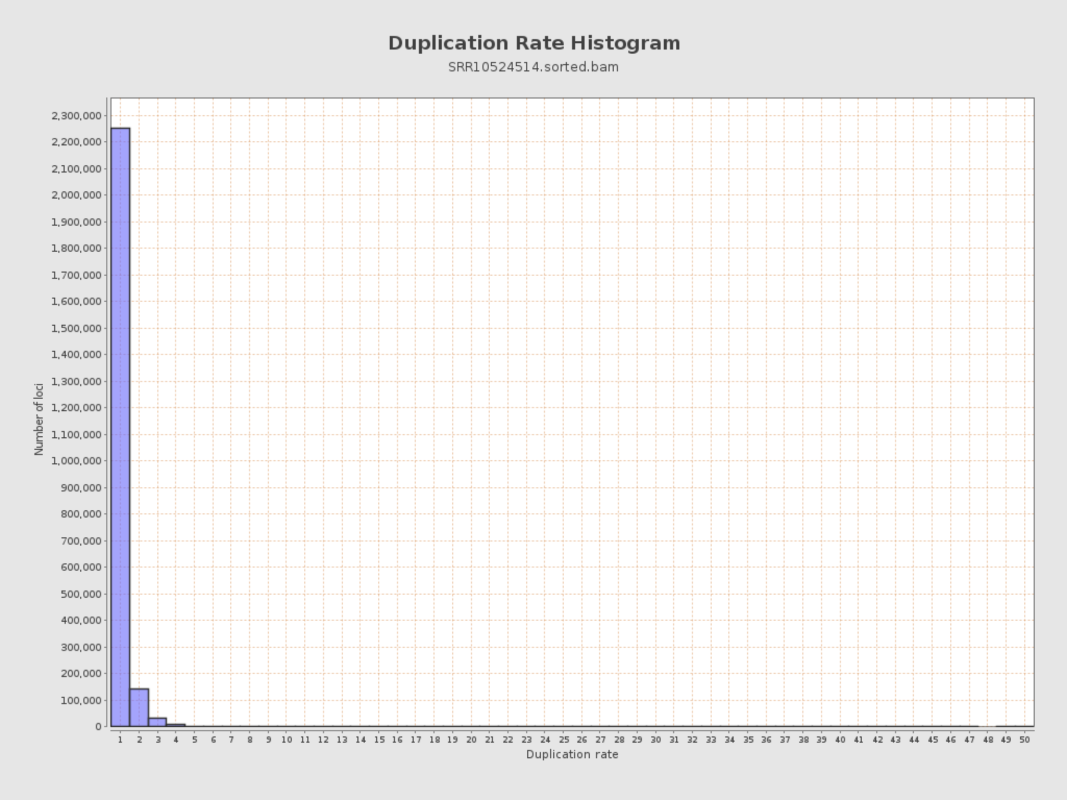
5. Results : Coverage Histogram (0-50X)



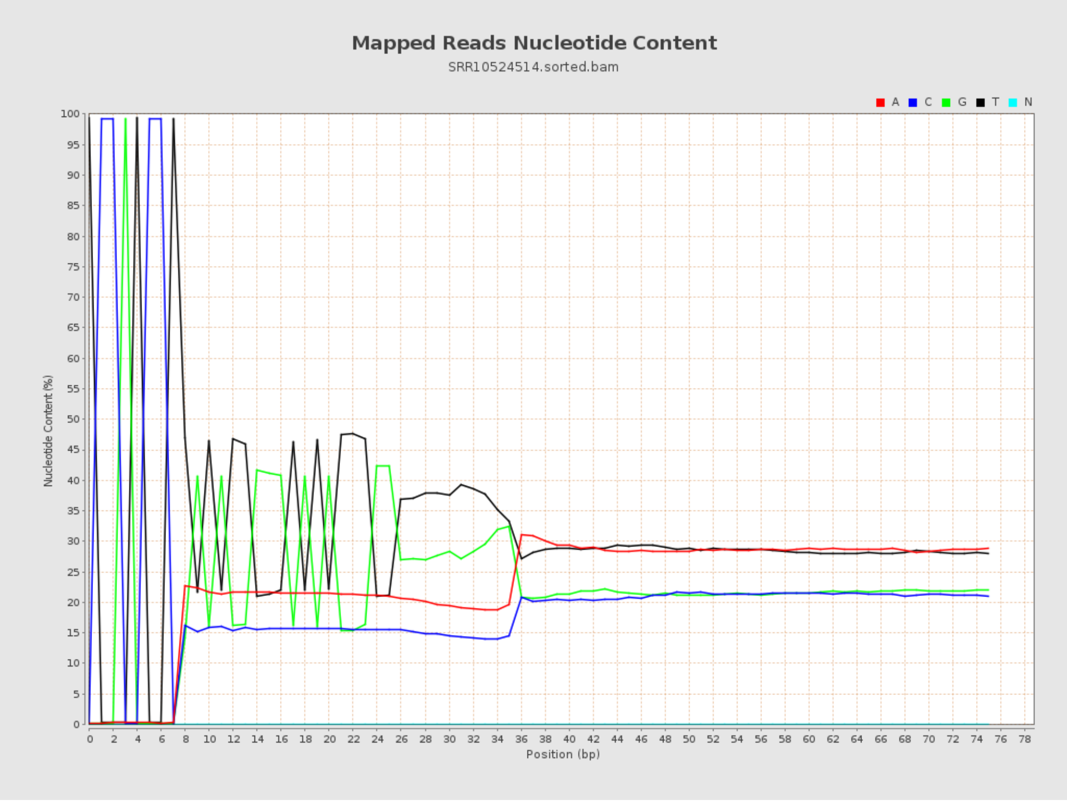
6. Results : Genome Fraction Coverage



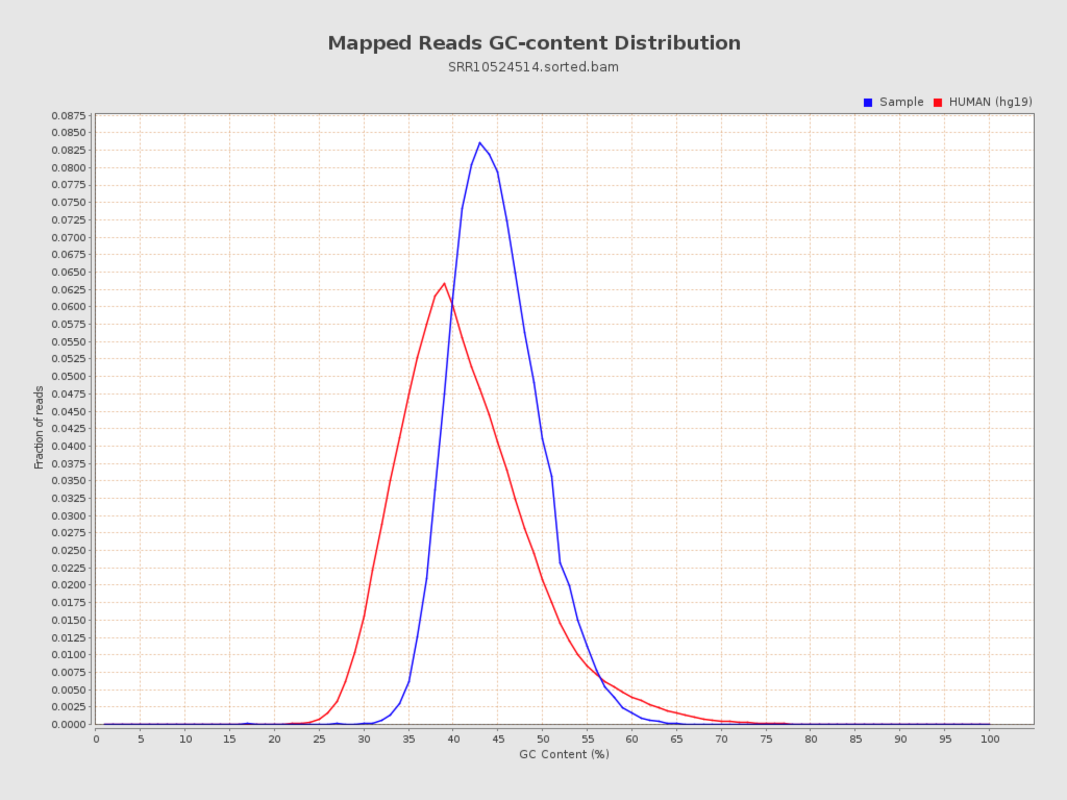
7. Results : Duplication Rate Histogram



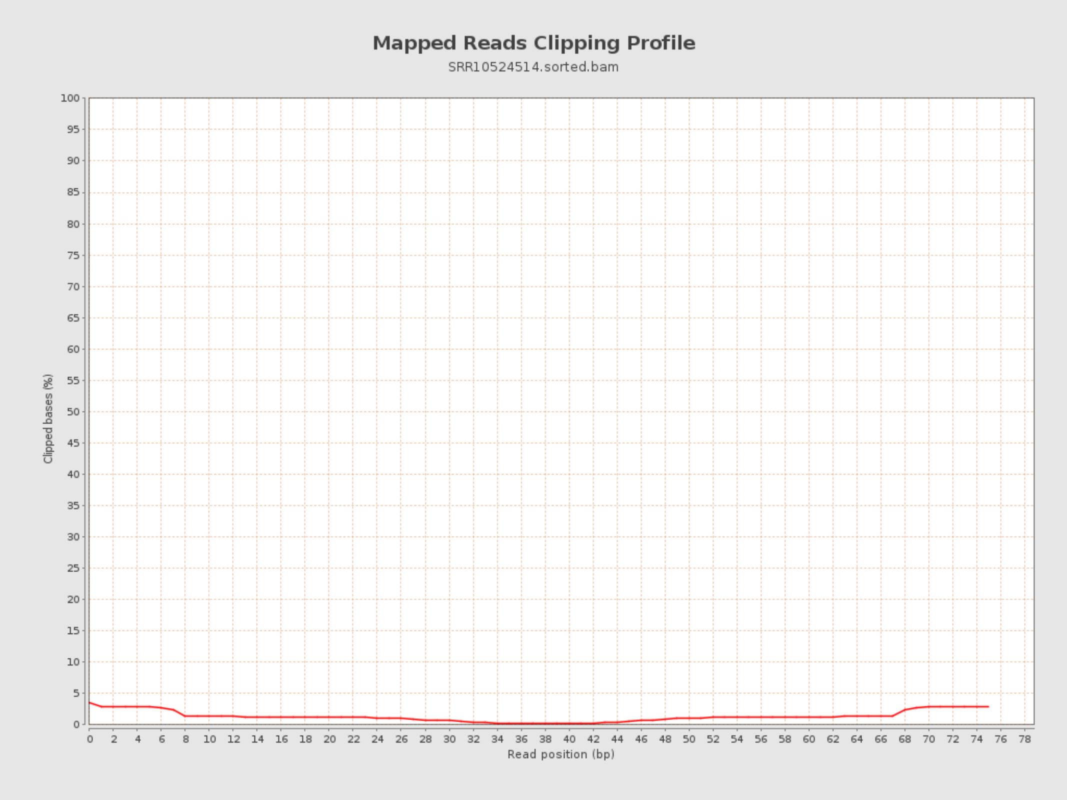
8. Results : Mapped Reads Nucleotide Content



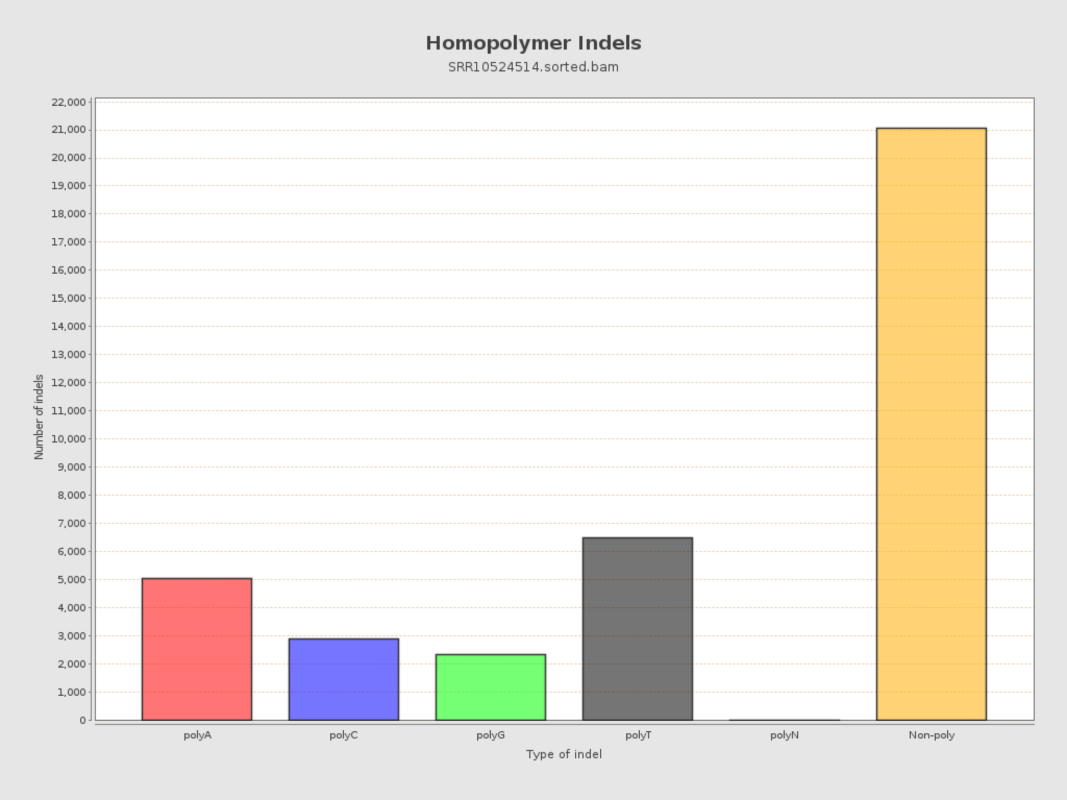
9. Results : Mapped Reads GC-content Distribution



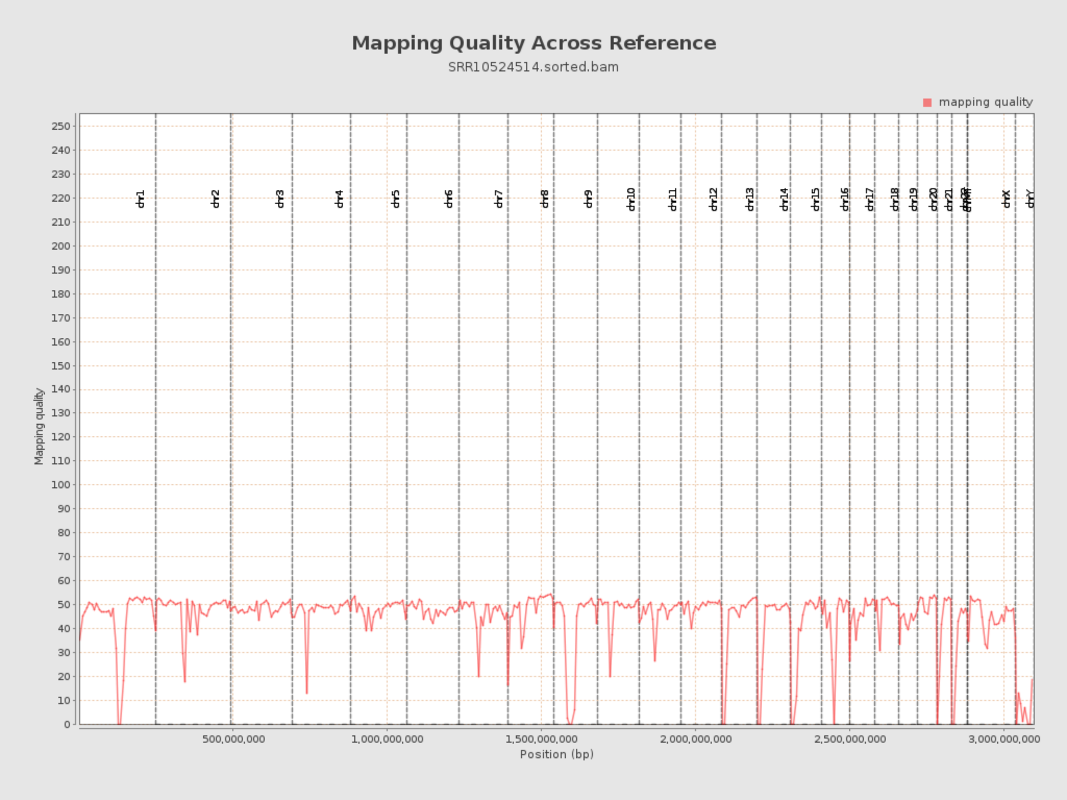
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram