Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:20:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524974.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_SRR10524974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524974.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:20:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,537,912
Mapped reads	2,344,871 / 92.39%
Unmapped reads	193,041 / 7.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,301 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	124,223 / 4.89%
Duplication rate	4.01%
Clipped reads	2,342,978 / 92.32%

2.2. ACGT Content

Number/percentage of A's	35,100,721 / 25.73%
Number/percentage of C's	25,124,145 / 18.42%
Number/percentage of T's	43,924,858 / 32.2%
Number/percentage of G's	32,266,662 / 23.65%
Number/percentage of N's	1,653 / 0%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.3644

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

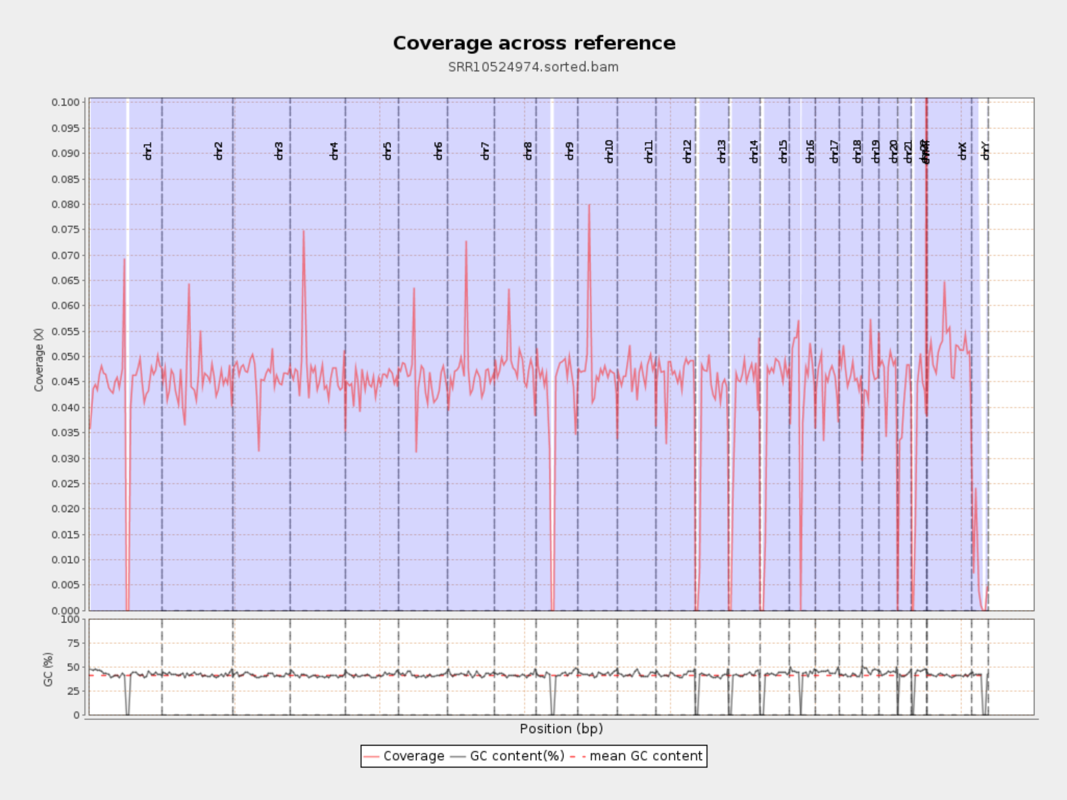
General error rate	0.5%
Mismatches	661,940
Insertions	8,721
Mapped reads with at least one insertion	0.37%
Deletions	25,530
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.07%

2.6. Chromosome stats

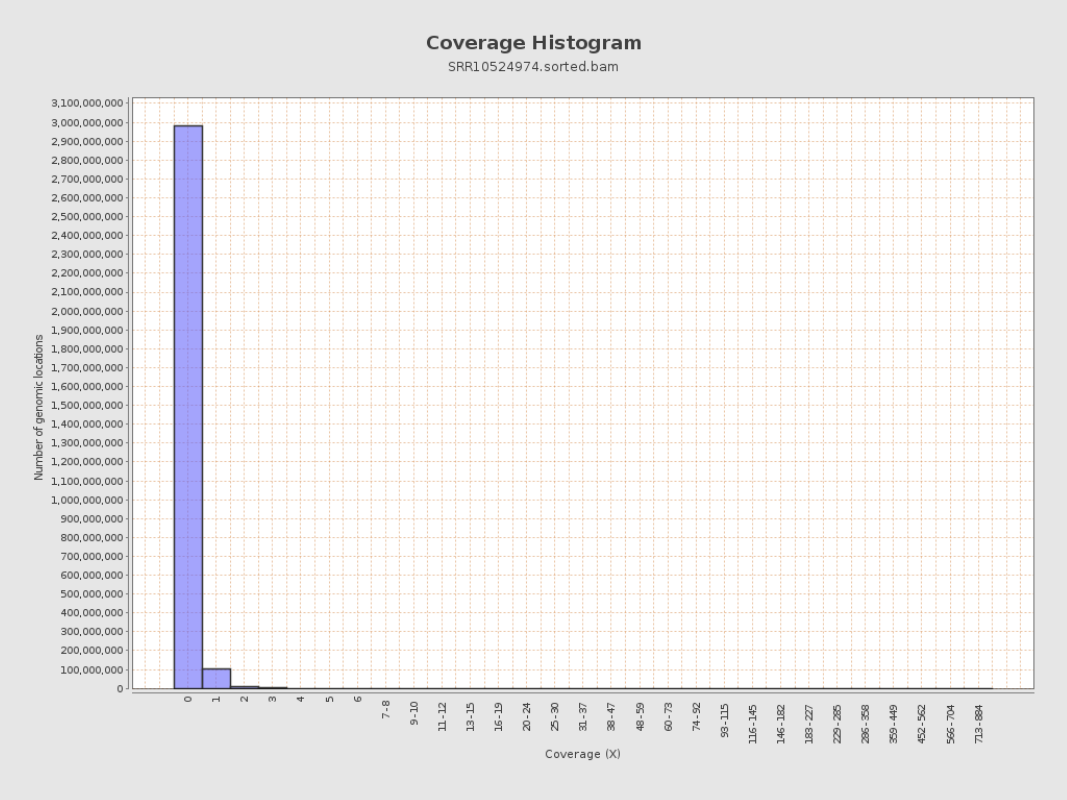
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10749445	0.0431	0.6675
chr2	243199373	11094645	0.0456	0.4007
chr3	198022430	9181538	0.0464	0.2491
chr4	191154276	9001688	0.0471	0.2941
chr5	180915260	8135096	0.045	0.2448
chr6	171115067	7831222	0.0458	0.3211
chr7	159138663	7481235	0.047	0.4548

chr8	146364022	7064724	0.0483	0.3928
chr9	141213431	5717121	0.0405	0.3147
chr10	135534747	6531966	0.0482	0.3842
chr11	135006516	6287781	0.0466	0.34
chr12	133851895	6230445	0.0465	0.2507
chr13	115169878	4340557	0.0377	0.2237
chr14	107349540	4168963	0.0388	0.2357
chr15	102531392	3925000	0.0383	0.2401
chr16	90354753	4014181	0.0444	0.2641
chr17	81195210	3620685	0.0446	0.2729
chr18	78077248	3672351	0.047	0.5495
chr19	59128983	2706658	0.0458	0.4425
chr20	63025520	2928900	0.0465	0.2571
chr21	48129895	1794453	0.0373	0.253
chr22	51304566	1624445	0.0317	0.2022
chrMT	16571	6262	0.3779	0.6602
chrX	155270560	7941321	0.0511	0.2928
chrY	59373566	410952	0.0069	0.194

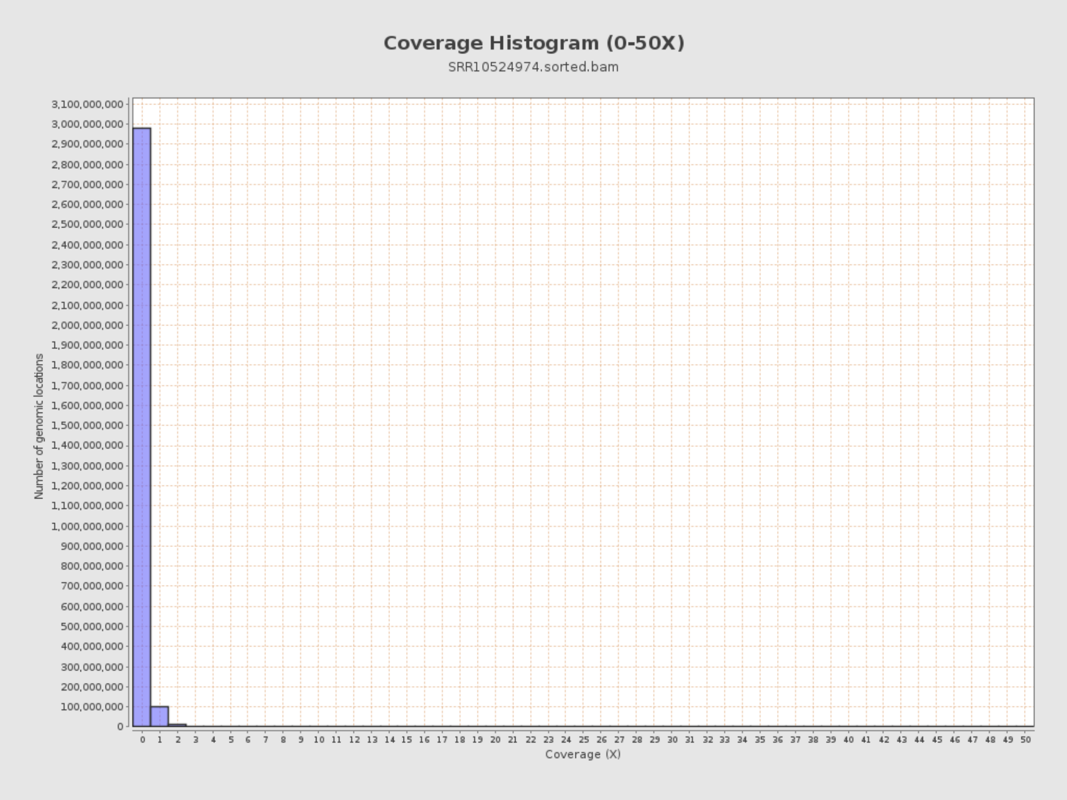
3. Results : Coverage across reference



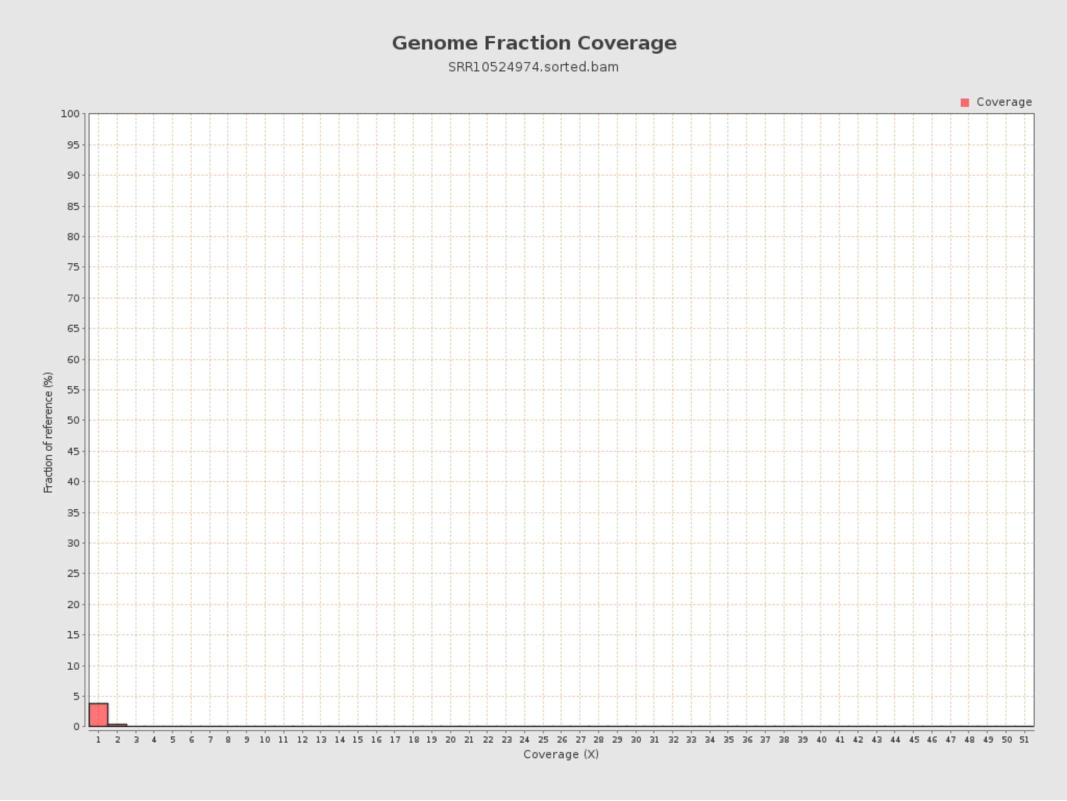
4. Results : Coverage Histogram



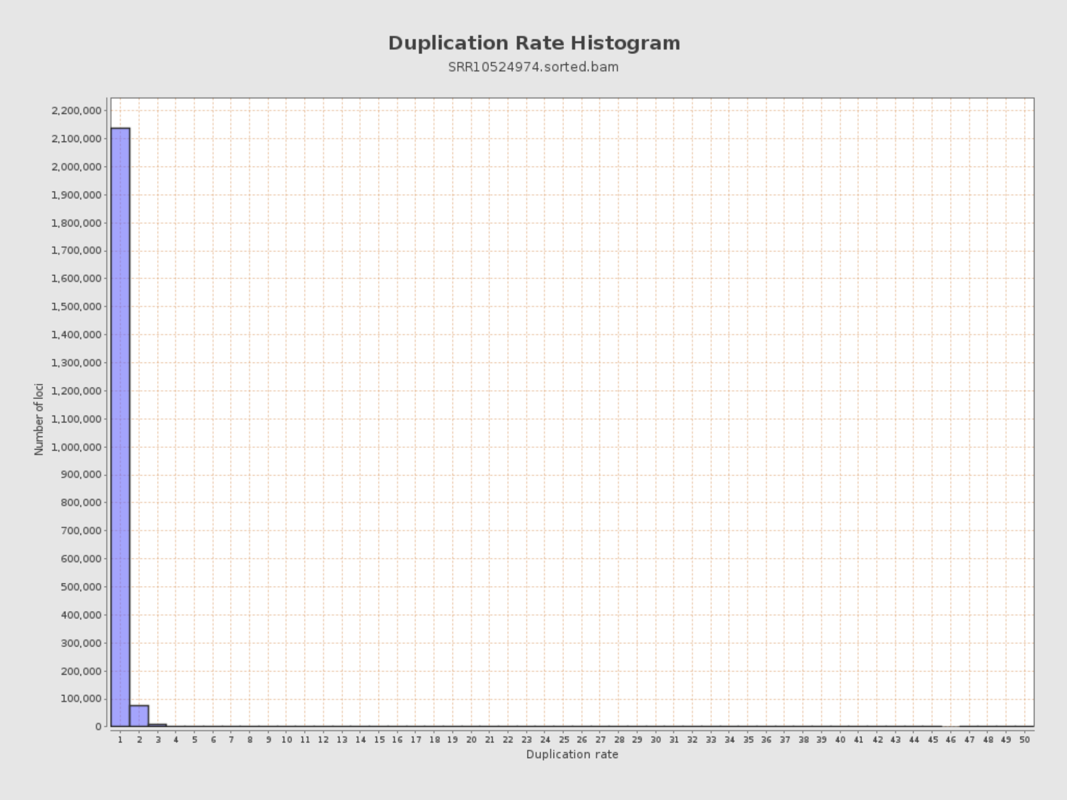
5. Results : Coverage Histogram (0-50X)



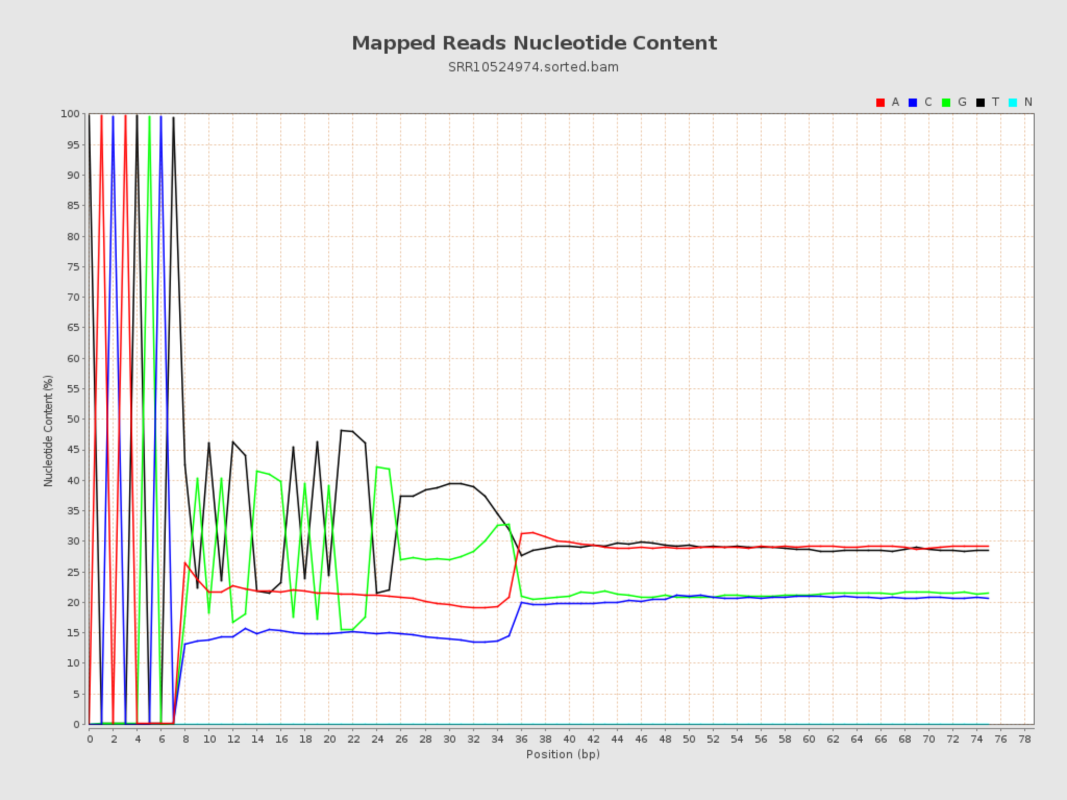
6. Results : Genome Fraction Coverage



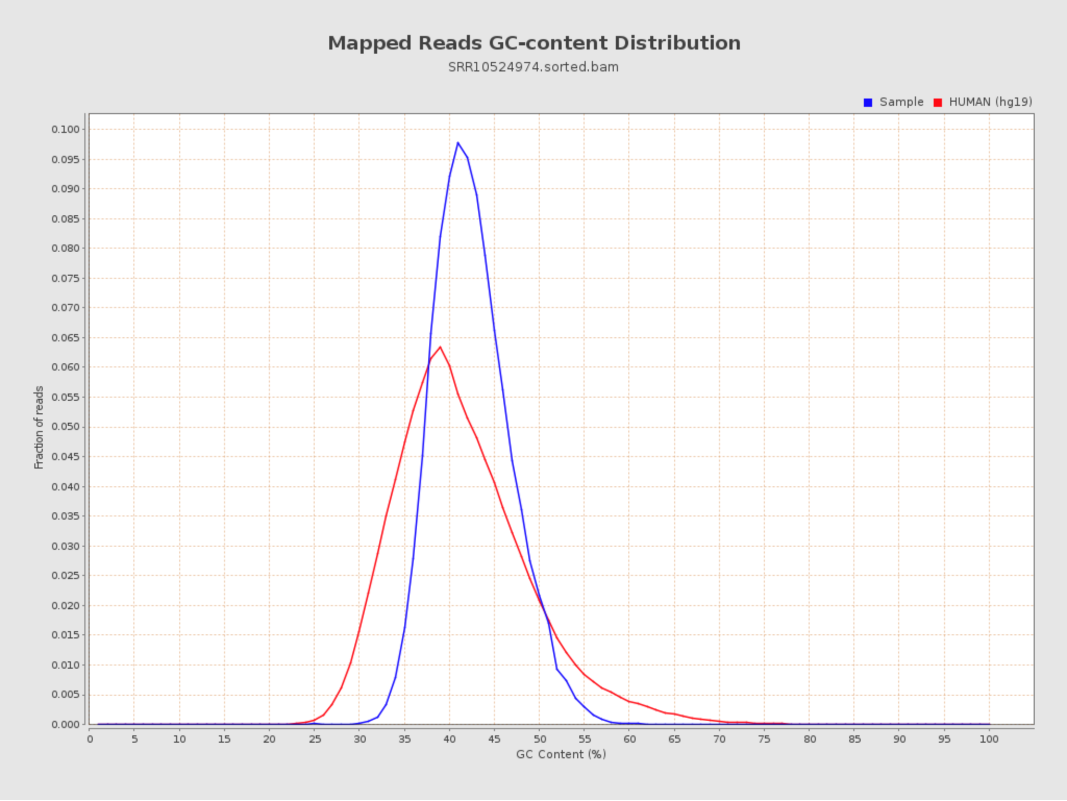
7. Results : Duplication Rate Histogram



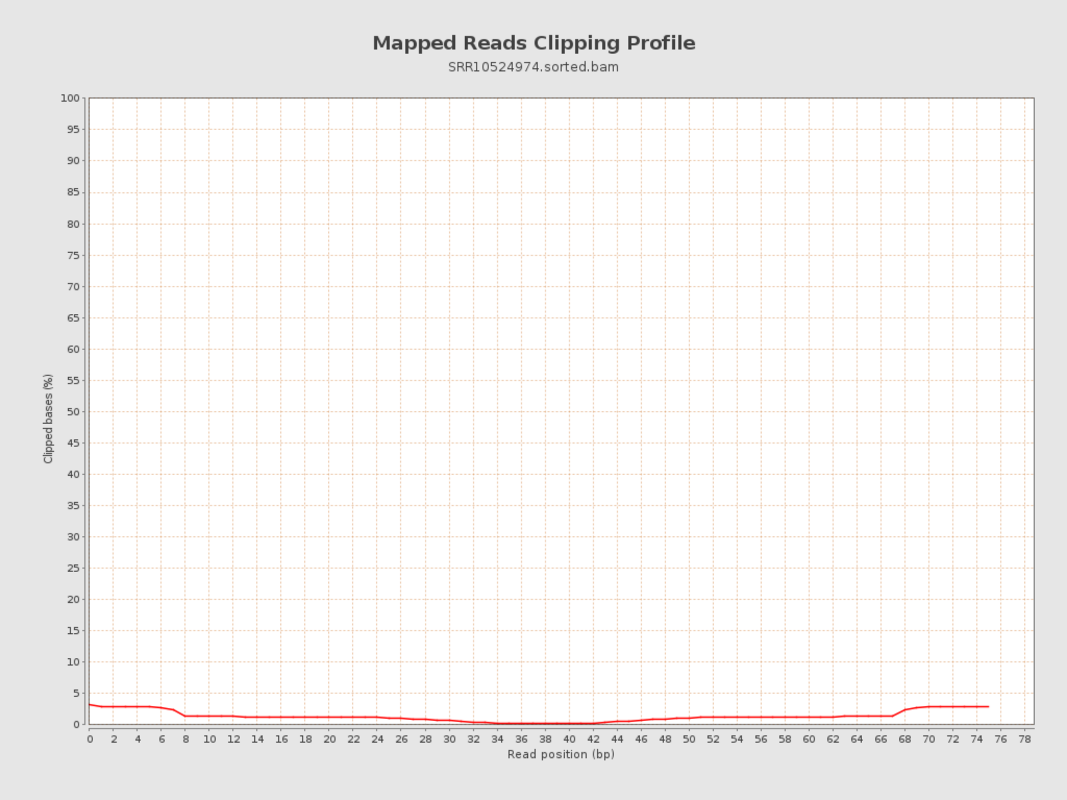
8. Results : Mapped Reads Nucleotide Content



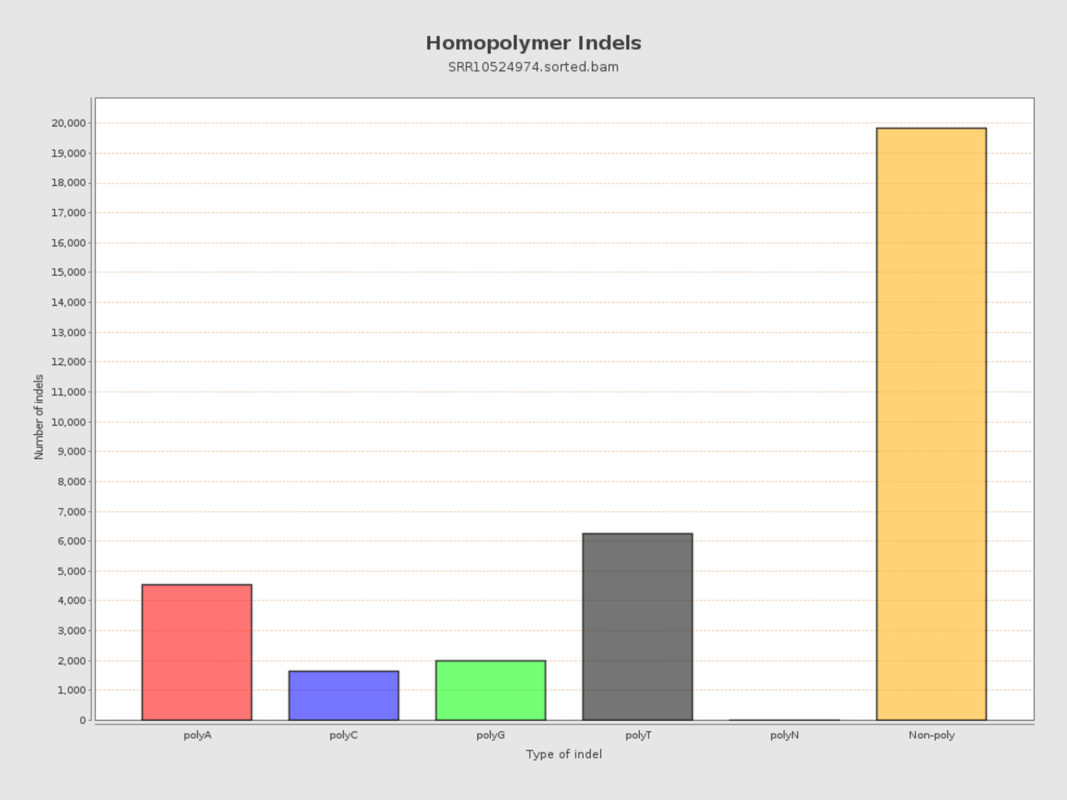
9. Results : Mapped Reads GC-content Distribution



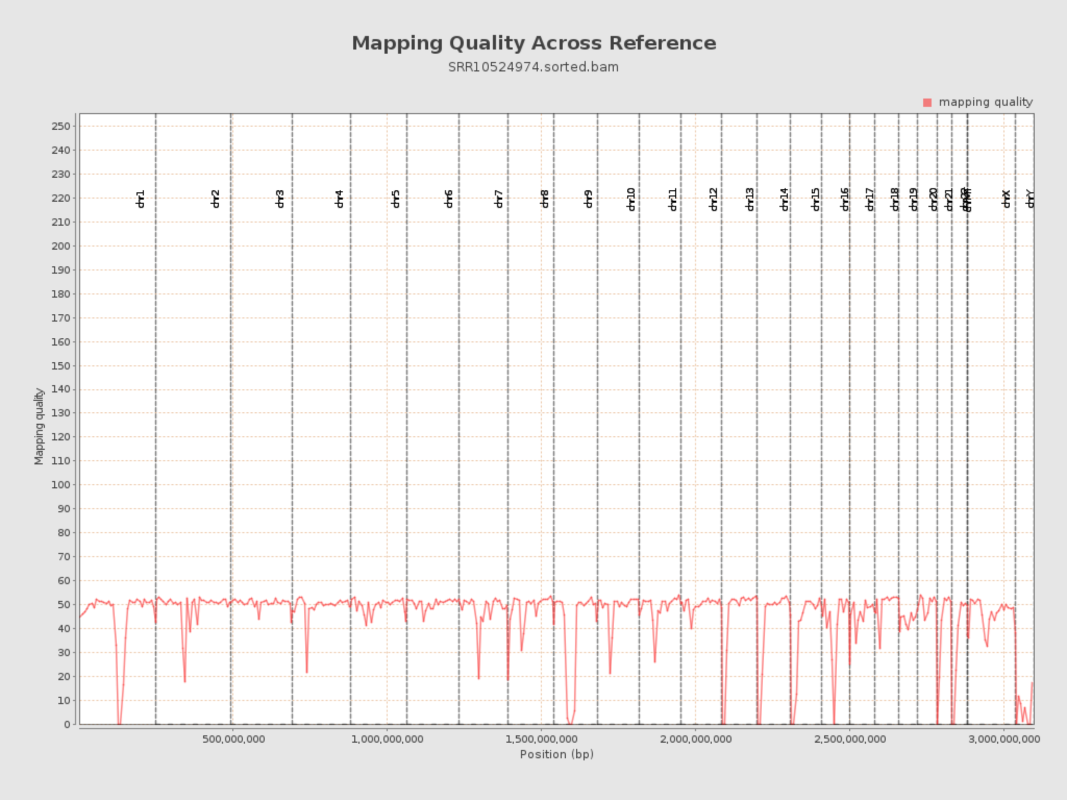
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram