Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:44:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524949.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_SRR10524949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:44:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,678,464
Mapped reads	1,529,909 / 91.15%
Unmapped reads	148,555 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,026 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	45,466 / 2.71%
Duplication rate	2.06%
Clipped reads	1,529,139 / 91.1%

2.2. ACGT Content

Number/percentage of A's	23,846,061 / 26.69%
Number/percentage of C's	15,767,205 / 17.65%
Number/percentage of T's	27,714,643 / 31.02%
Number/percentage of G's	22,003,725 / 24.63%
Number/percentage of N's	1,048 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2694

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

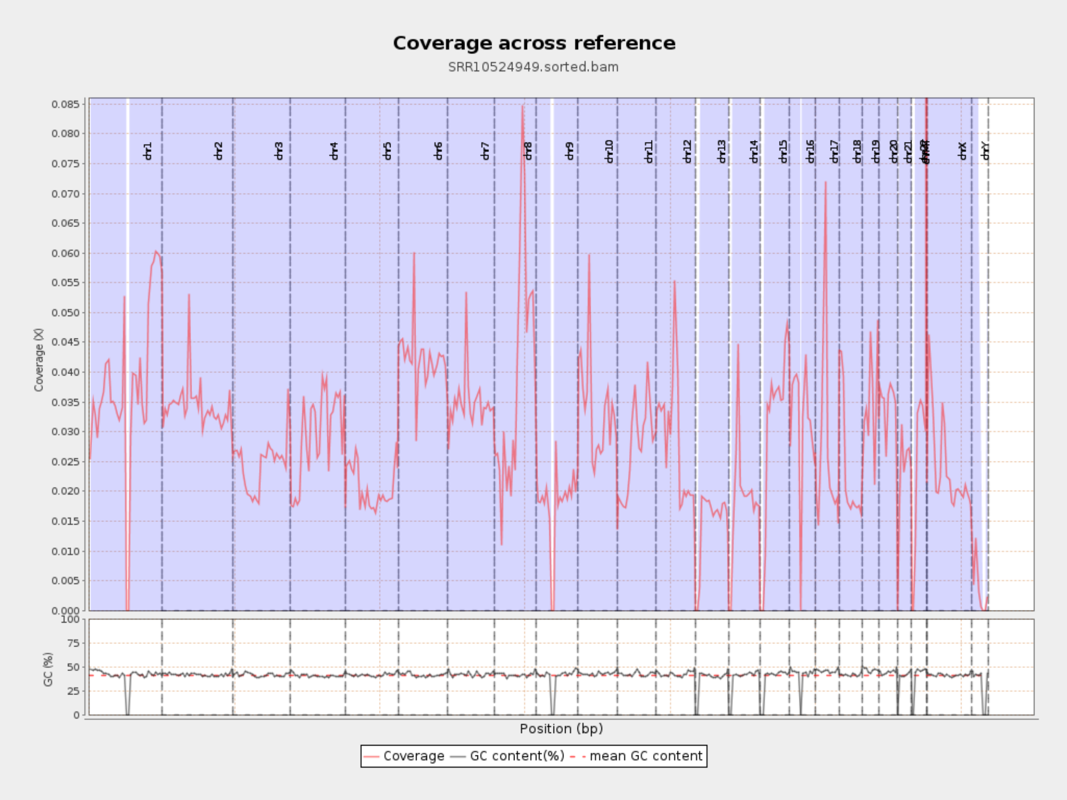
General error rate	0.5%
Mismatches	436,888
Insertions	6,357
Mapped reads with at least one insertion	0.41%
Deletions	17,214
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.99%

2.6. Chromosome stats

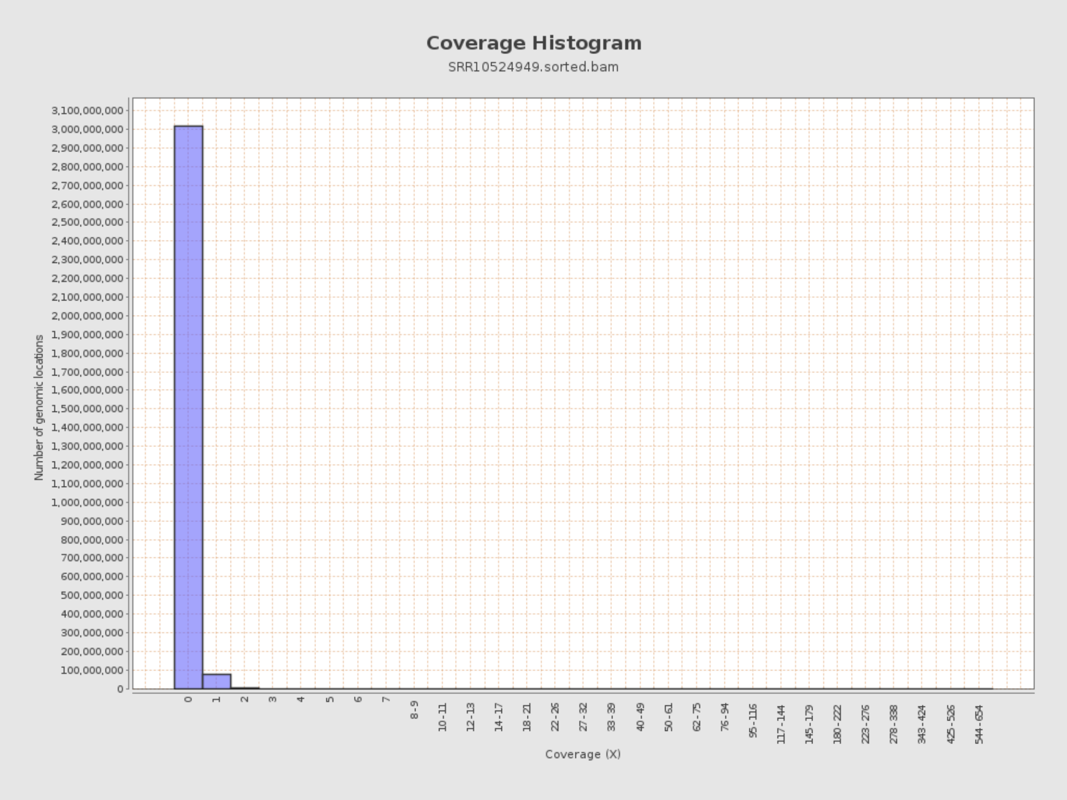
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9377472	0.0376	0.5024
chr2	243199373	8372633	0.0344	0.3177
chr3	198022430	4868733	0.0246	0.1695
chr4	191154276	5636176	0.0295	0.2011
chr5	180915260	3748898	0.0207	0.1577
chr6	171115067	7237281	0.0423	0.3078
chr7	159138663	5569660	0.035	0.3592

chr8	146364022	5669813	0.0387	0.2734
chr9	141213431	2484170	0.0176	0.2138
chr10	135534747	4563519	0.0337	0.2514
chr11	135006516	3664691	0.0271	0.2306
chr12	133851895	3810029	0.0285	0.1837
chr13	115169878	1679451	0.0146	0.132
chr14	107349540	1995293	0.0186	0.1526
chr15	102531392	3140471	0.0306	0.201
chr16	90354753	2843285	0.0315	0.2011
chr17	81195210	2294796	0.0283	0.2354
chr18	78077248	1850838	0.0237	0.3543
chr19	59128983	2068694	0.035	0.3193
chr20	63025520	2172302	0.0345	0.2024
chr21	48129895	1104196	0.0229	0.171
chr22	51304566	1180356	0.023	0.1617
chrMT	16571	16901	1.0199	1.293
chrX	155270560	3787098	0.0244	0.1981
chrY	59373566	225373	0.0038	0.095

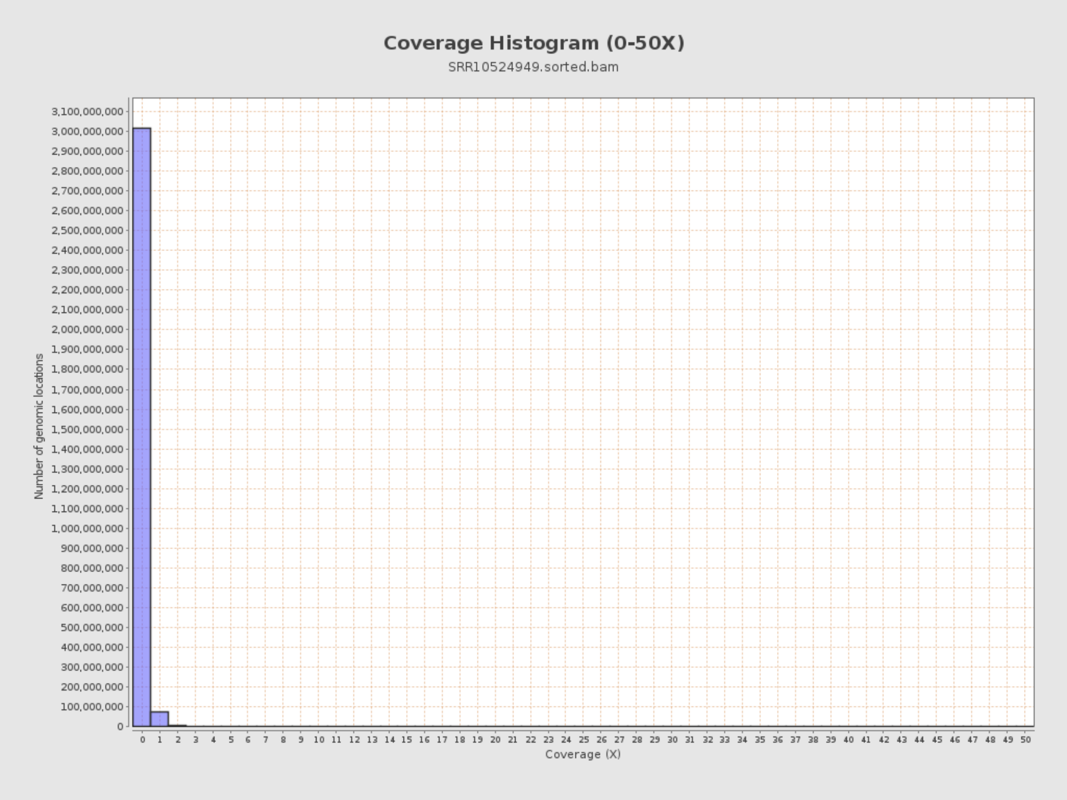
3. Results : Coverage across reference



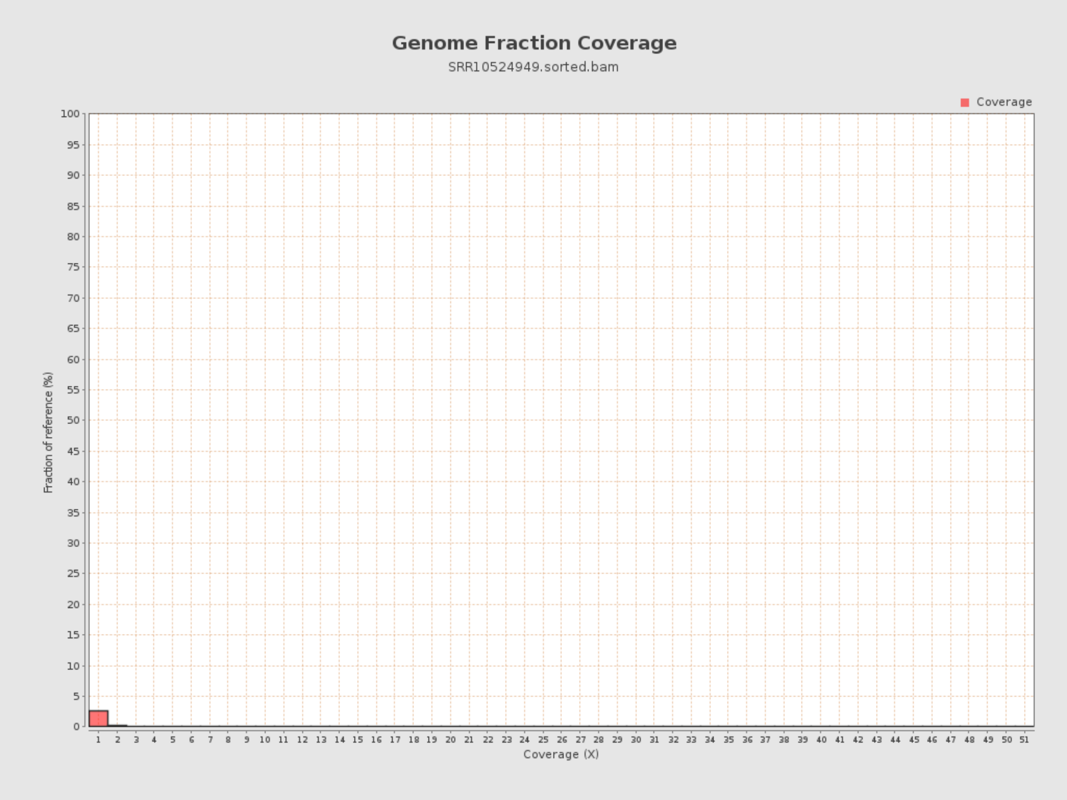
4. Results : Coverage Histogram



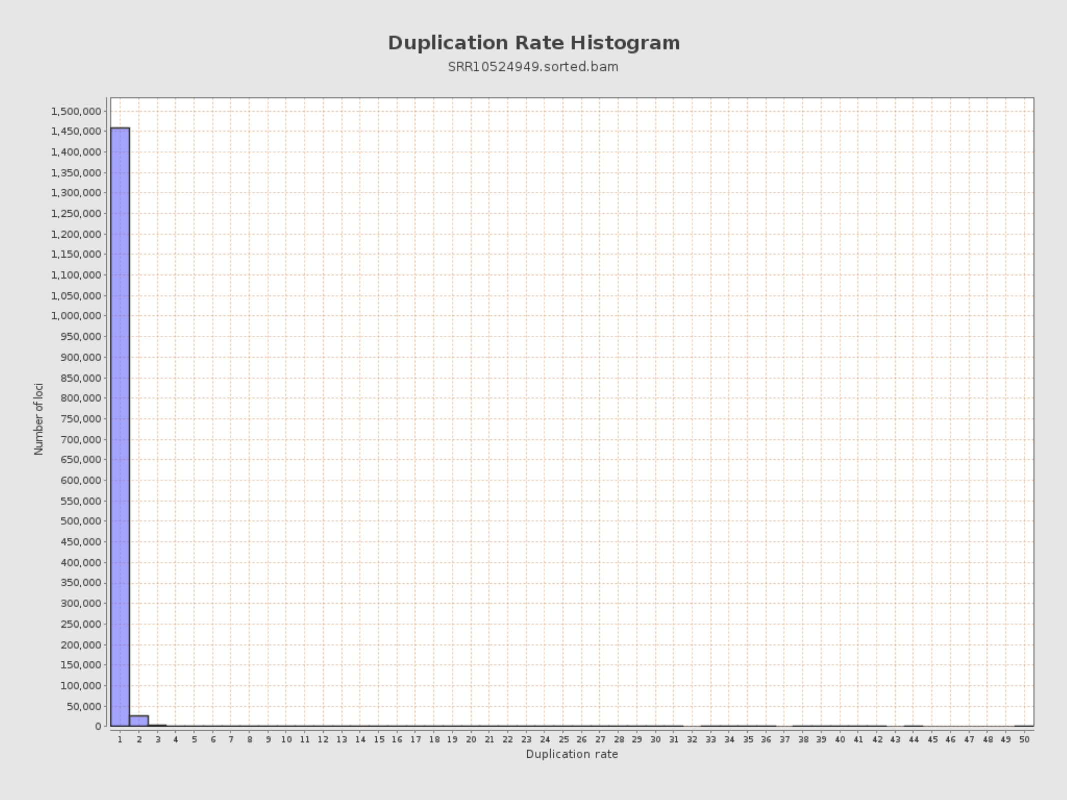
5. Results : Coverage Histogram (0-50X)



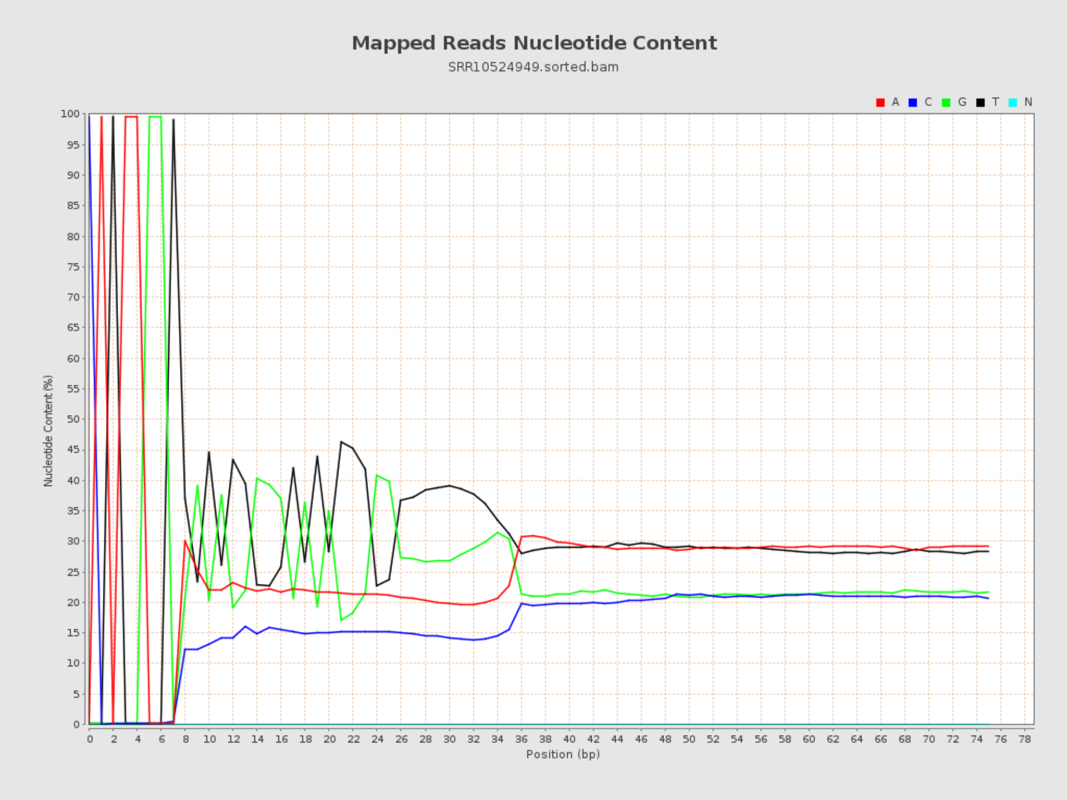
6. Results : Genome Fraction Coverage



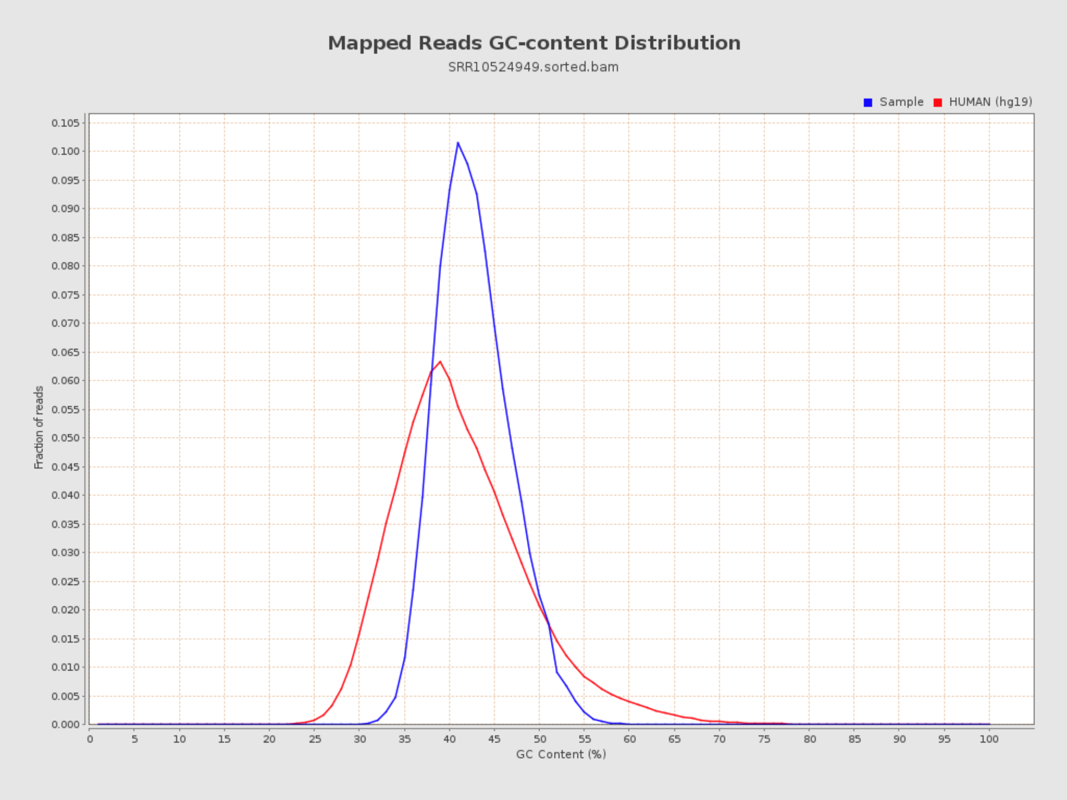
7. Results : Duplication Rate Histogram



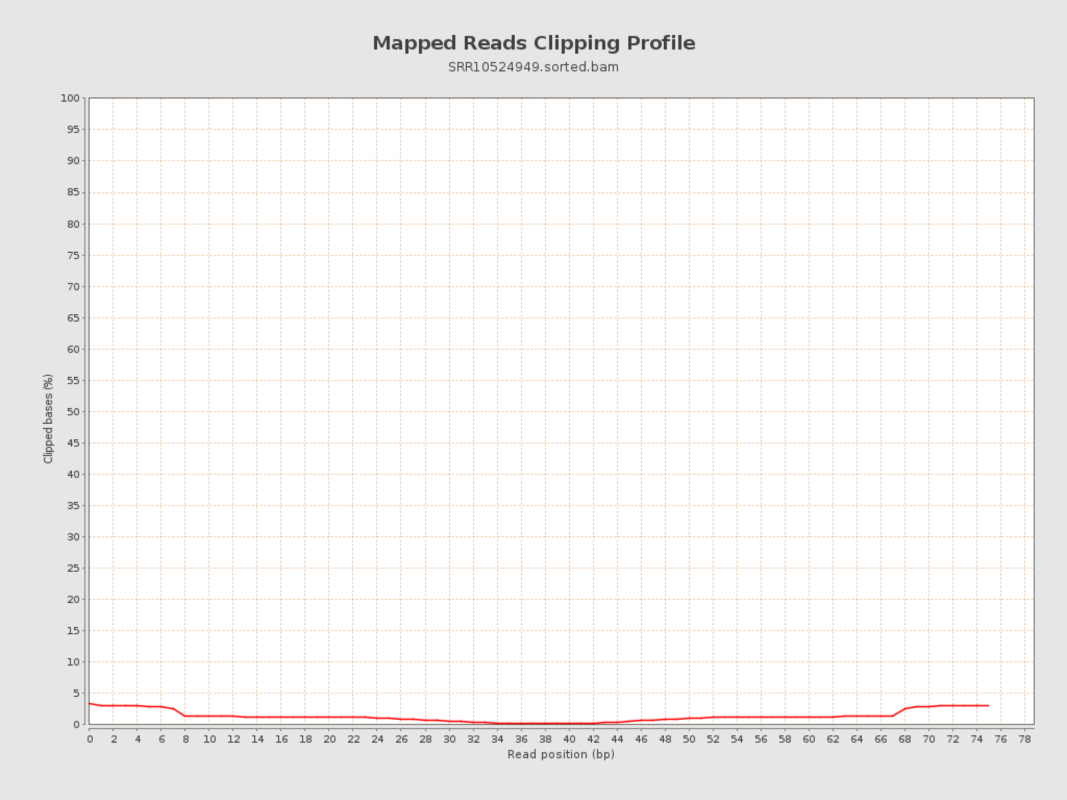
8. Results : Mapped Reads Nucleotide Content



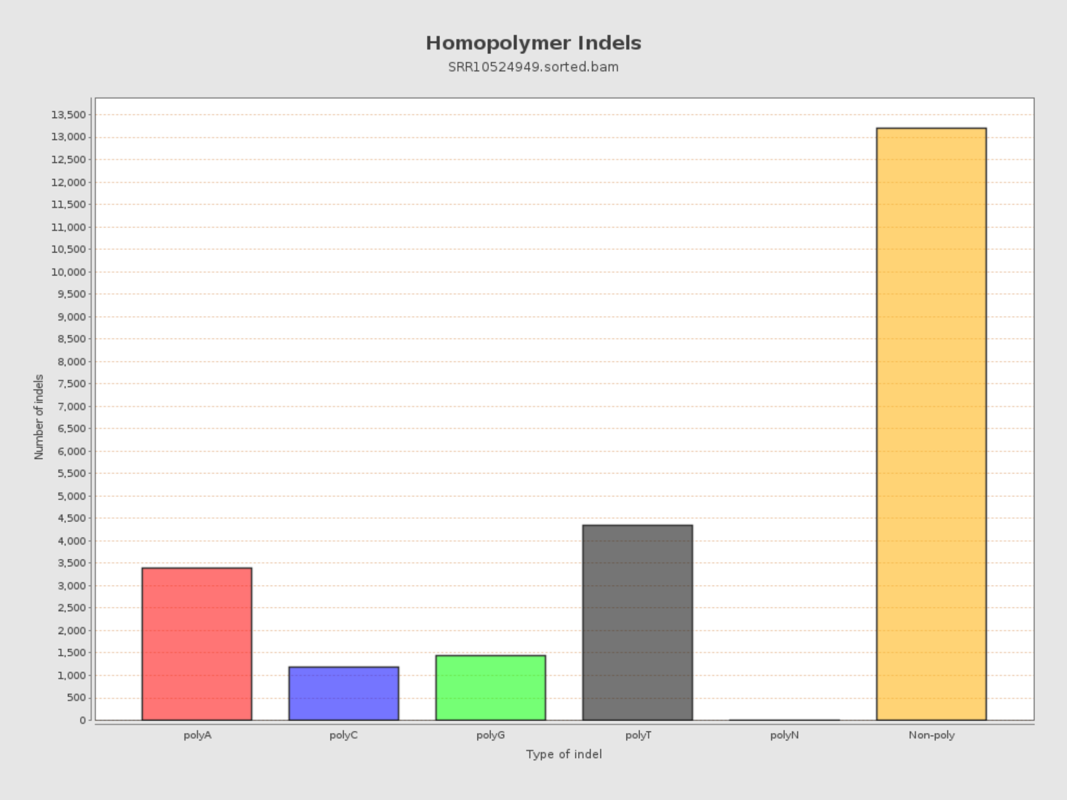
9. Results : Mapped Reads GC-content Distribution



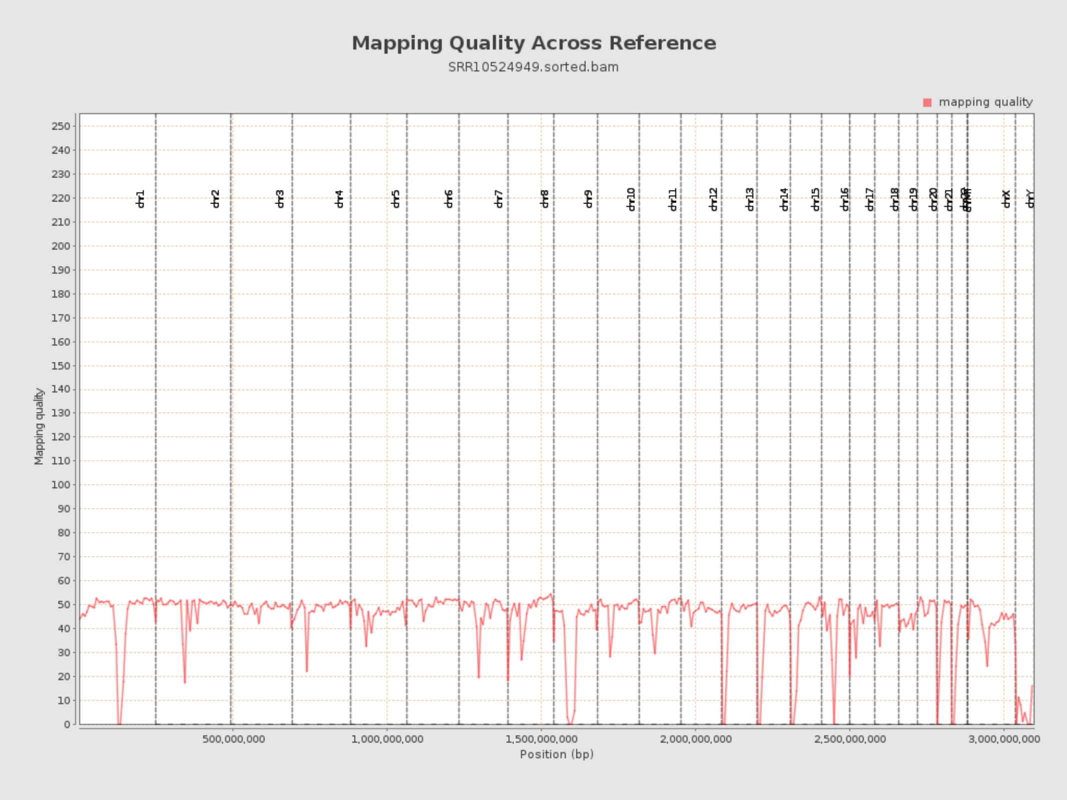
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram