Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:40:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524690.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_SRR10524690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524690.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:40:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524690.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,209,671
Mapped reads	1,112,030 / 91.93%
Unmapped reads	97,641 / 8.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,551 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	35,261 / 2.91%
Duplication rate	2.29%
Clipped reads	1,113,310 / 92.03%

2.2. ACGT Content

Number/percentage of A's	17,328,976 / 26.32%
Number/percentage of C's	12,822,531 / 19.48%
Number/percentage of T's	20,566,683 / 31.24%
Number/percentage of G's	15,104,764 / 22.94%
Number/percentage of N's	8,331 / 0.01%
GC Percentage	42.42%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2199

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

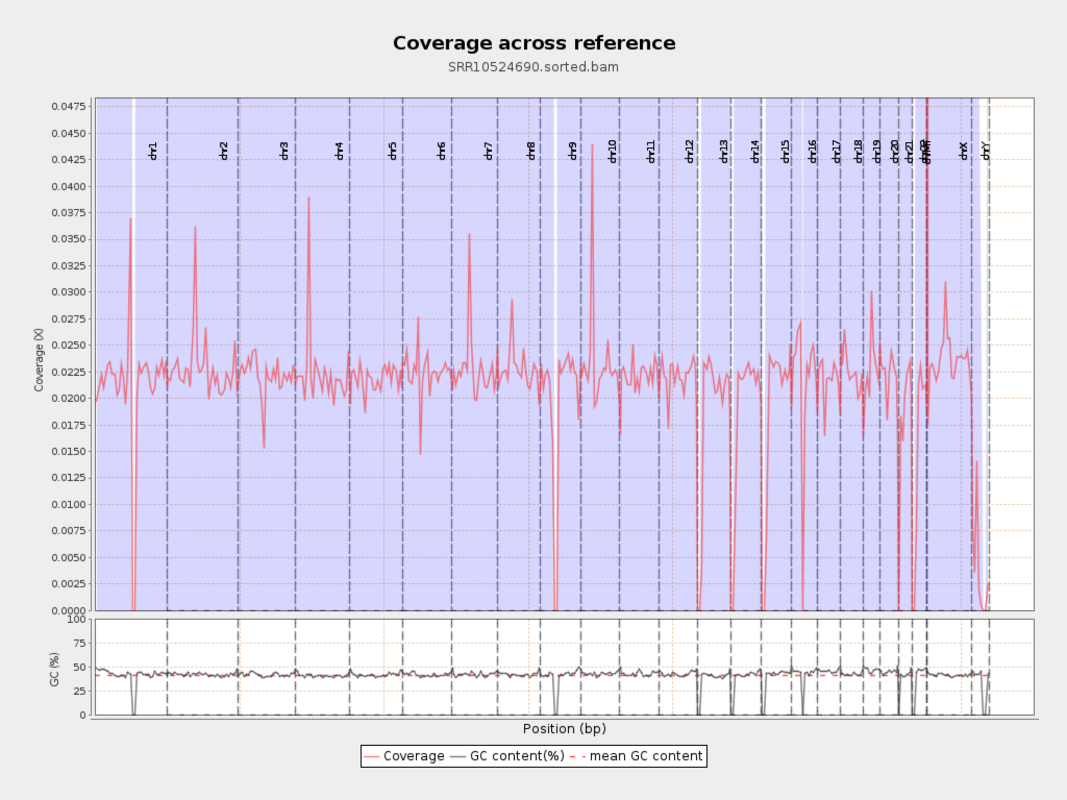
General error rate	0.52%
Mismatches	332,070
Insertions	5,137
Mapped reads with at least one insertion	0.46%
Deletions	12,481
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.57%

2.6. Chromosome stats

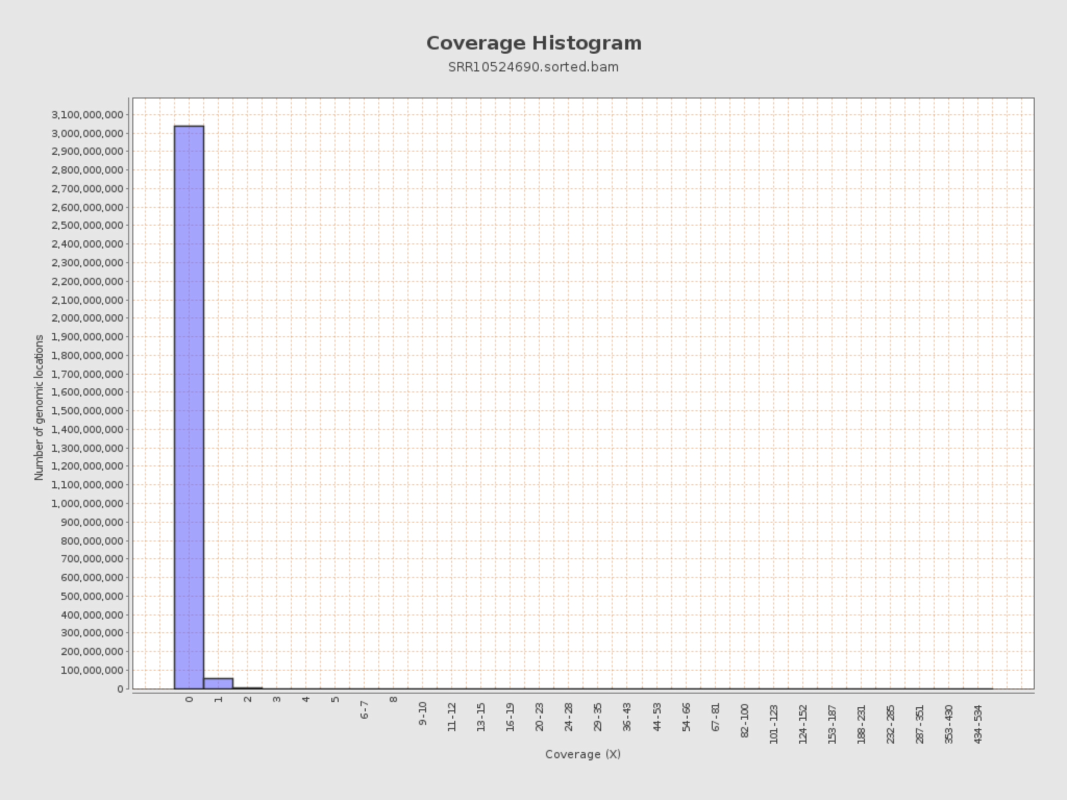
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5250190	0.0211	0.3715
chr2	243199373	5554145	0.0228	0.29
chr3	198022430	4376876	0.0221	0.1586
chr4	191154276	4273223	0.0224	0.1769
chr5	180915260	3972468	0.022	0.1584
chr6	171115067	3839639	0.0224	0.1755
chr7	159138663	3629327	0.0228	0.2559

chr8	146364022	3332815	0.0228	0.2382
chr9	141213431	2766605	0.0196	0.1901
chr10	135534747	3184798	0.0235	0.2329
chr11	135006516	2996781	0.0222	0.191
chr12	133851895	2957246	0.0221	0.16
chr13	115169878	2104969	0.0183	0.143
chr14	107349540	1973274	0.0184	0.1469
chr15	102531392	1892411	0.0185	0.1454
chr16	90354753	1926794	0.0213	0.1649
chr17	81195210	1765622	0.0217	0.1626
chr18	78077248	1758283	0.0225	0.3231
chr19	59128983	1357947	0.023	0.2908
chr20	63025520	1385166	0.022	0.1598
chr21	48129895	878406	0.0183	0.1634
chr22	51304566	766583	0.0149	0.13
chrMT	16571	12996	0.7843	0.9634
chrX	155270560	3675986	0.0237	0.1775
chrY	59373566	218770	0.0037	0.1407

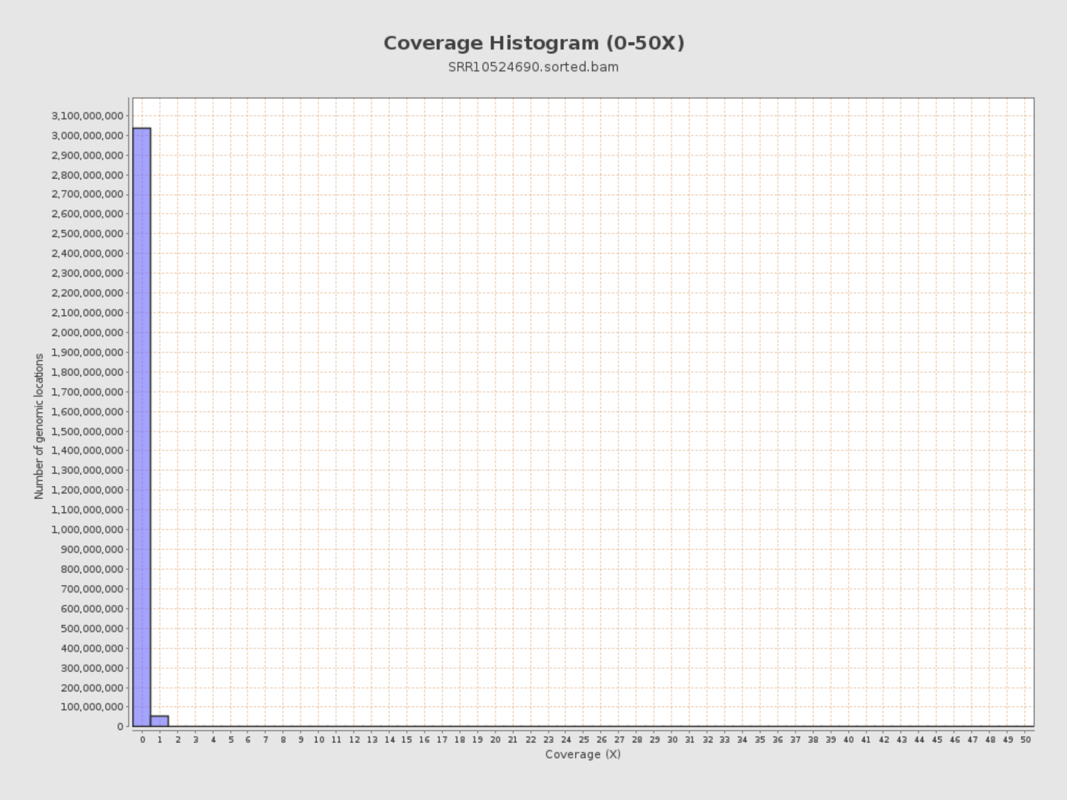
3. Results : Coverage across reference



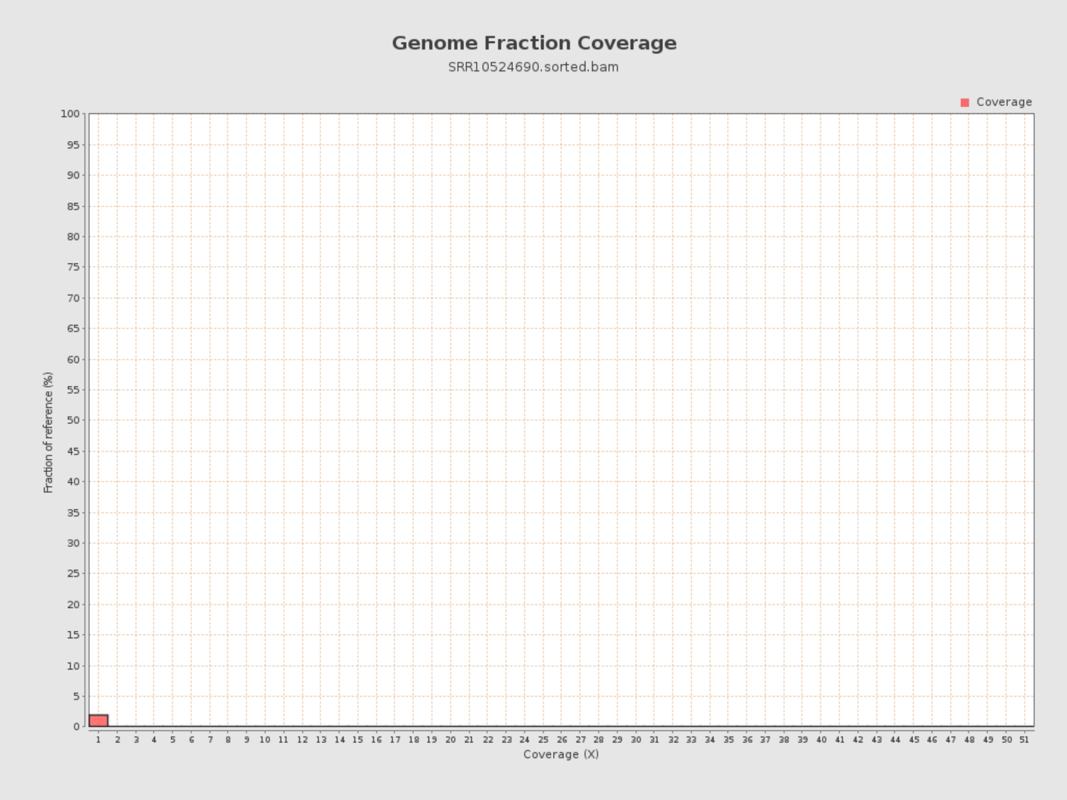
4. Results : Coverage Histogram



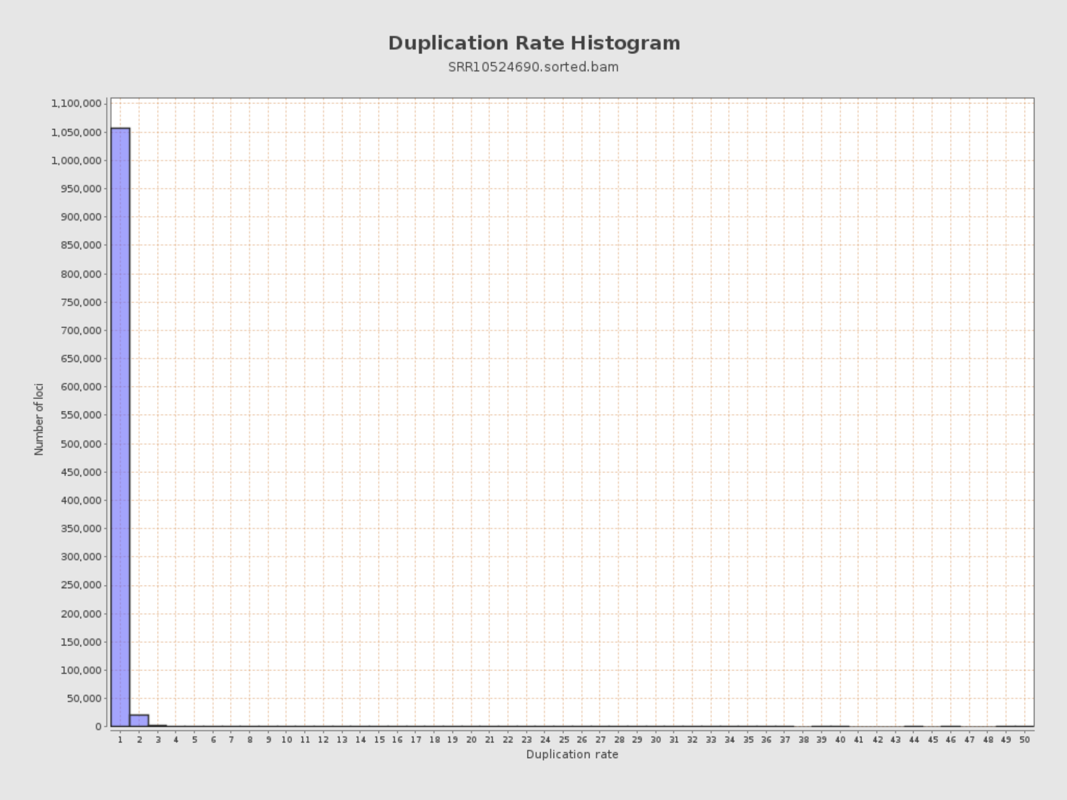
5. Results : Coverage Histogram (0-50X)



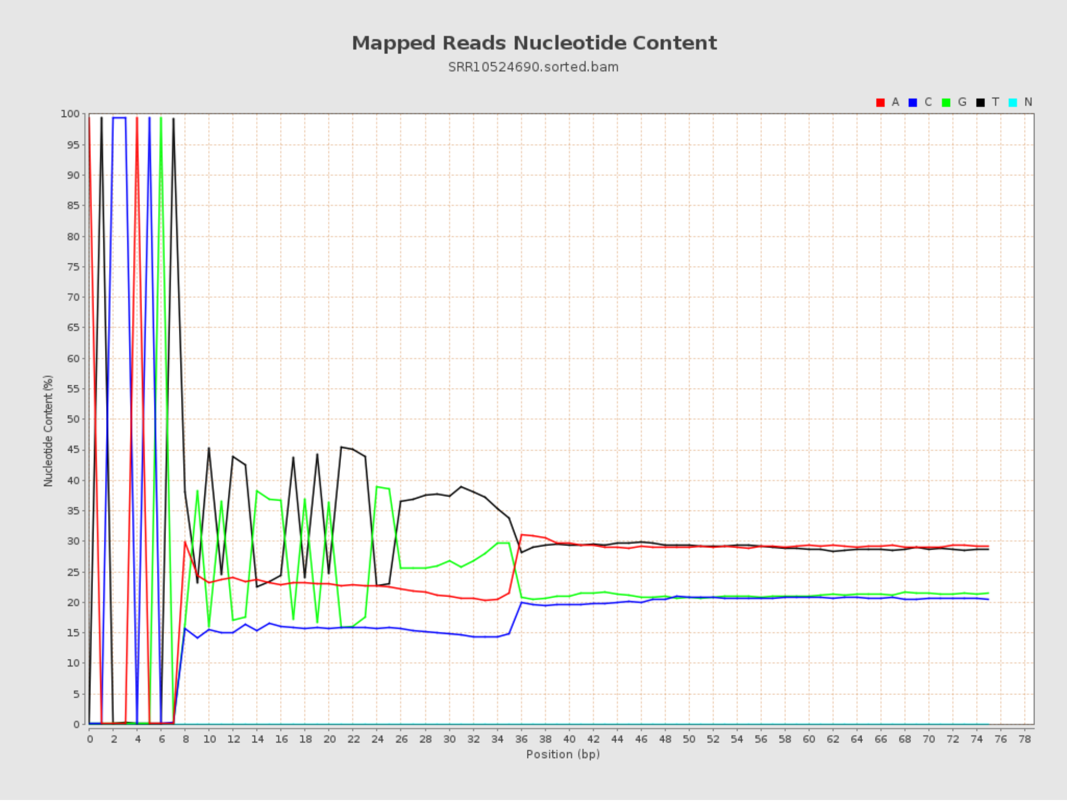
6. Results : Genome Fraction Coverage



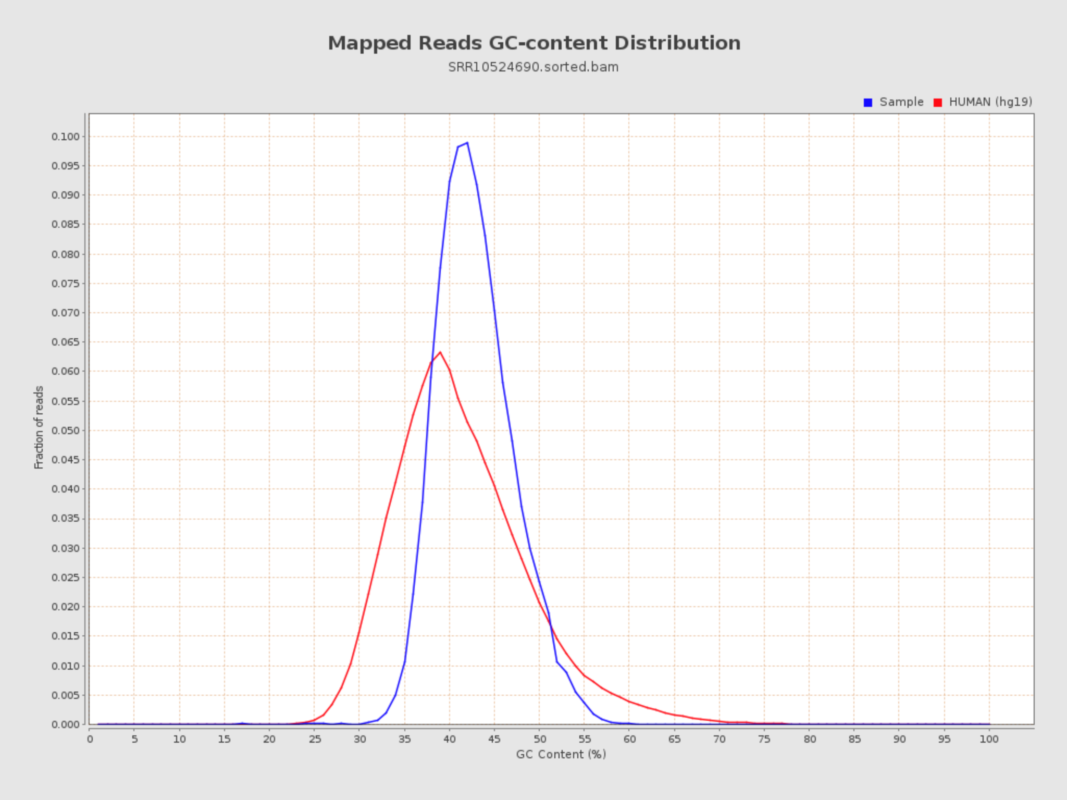
7. Results : Duplication Rate Histogram



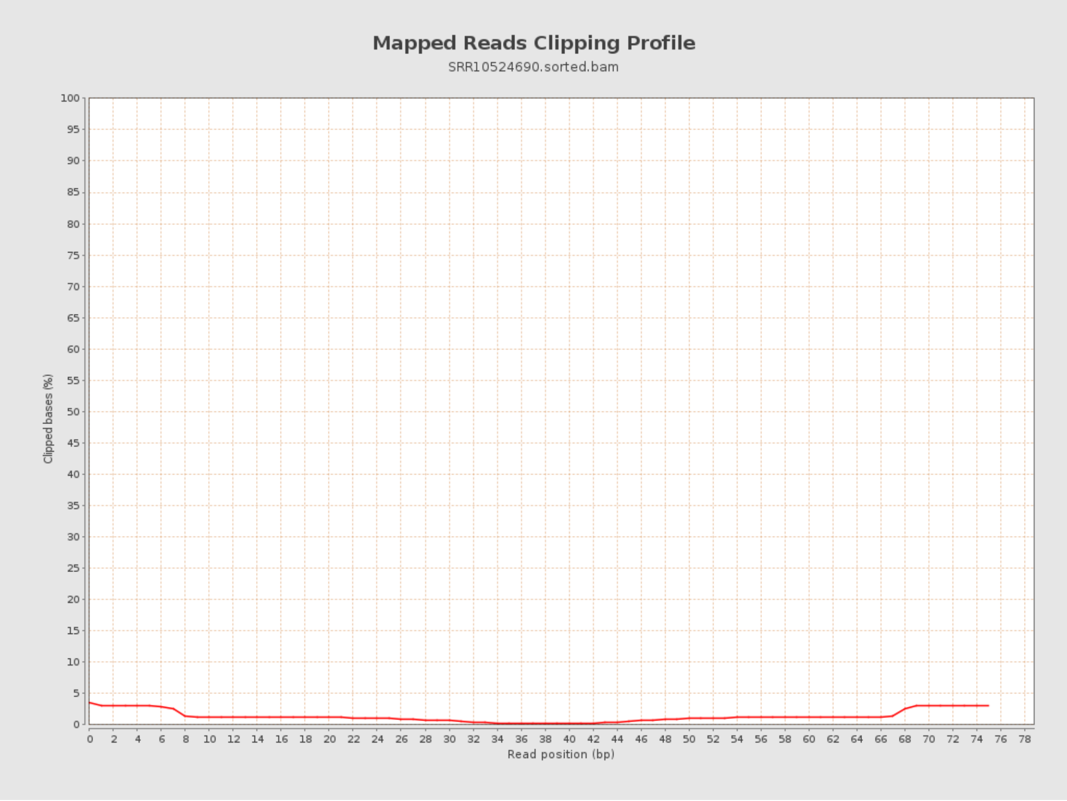
8. Results : Mapped Reads Nucleotide Content



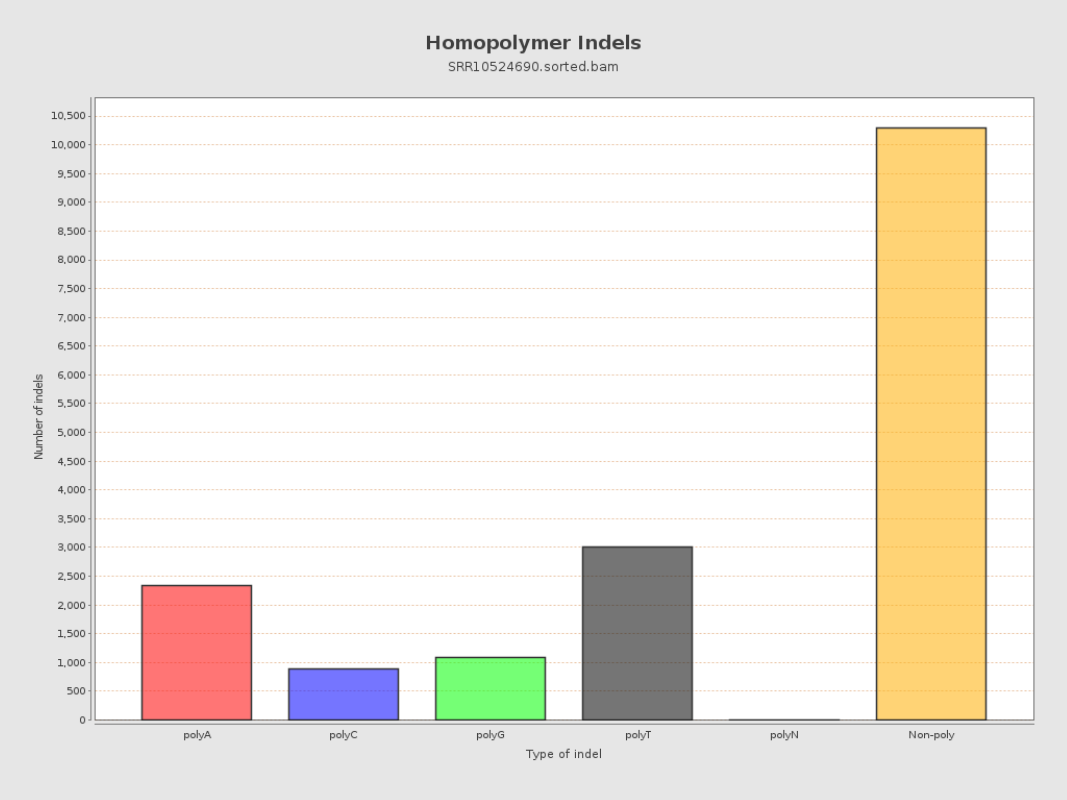
9. Results : Mapped Reads GC-content Distribution



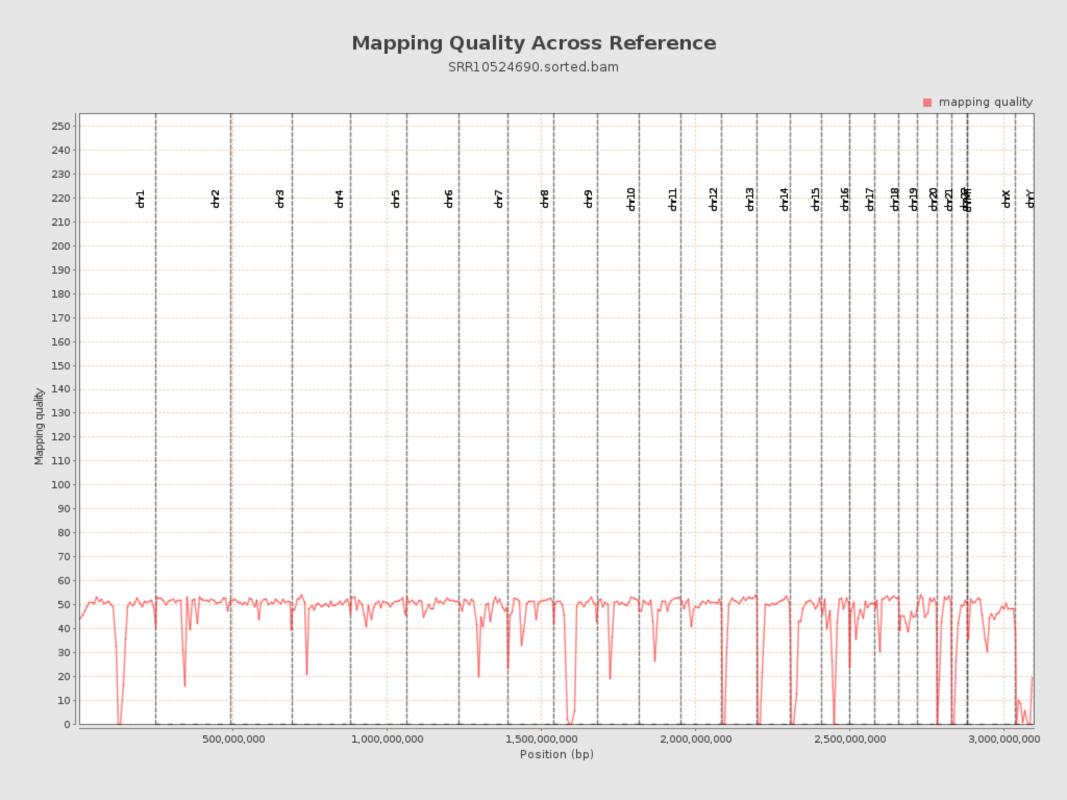
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram