Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:39:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524948.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_SRR10524948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:39:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,780,021
Mapped reads	1,643,377 / 92.32%
Unmapped reads	136,644 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,611 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	48,389 / 2.72%
Duplication rate	2.02%
Clipped reads	1,642,188 / 92.26%

2.2. ACGT Content

Number/percentage of A's	25,550,538 / 26.31%
Number/percentage of C's	16,596,764 / 17.09%
Number/percentage of T's	30,589,214 / 31.5%
Number/percentage of G's	24,379,984 / 25.1%
Number/percentage of N's	1,138 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.2875

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

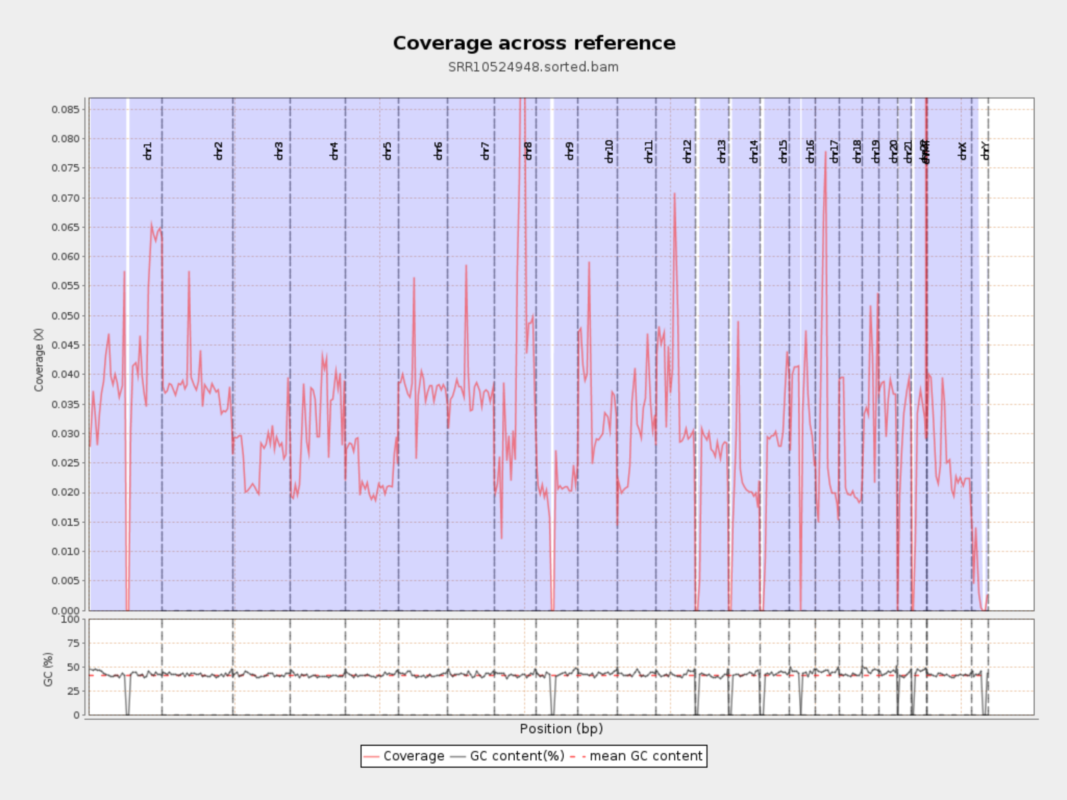
General error rate	0.49%
Mismatches	466,430
Insertions	6,742
Mapped reads with at least one insertion	0.41%
Deletions	19,069
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.54%

2.6. Chromosome stats

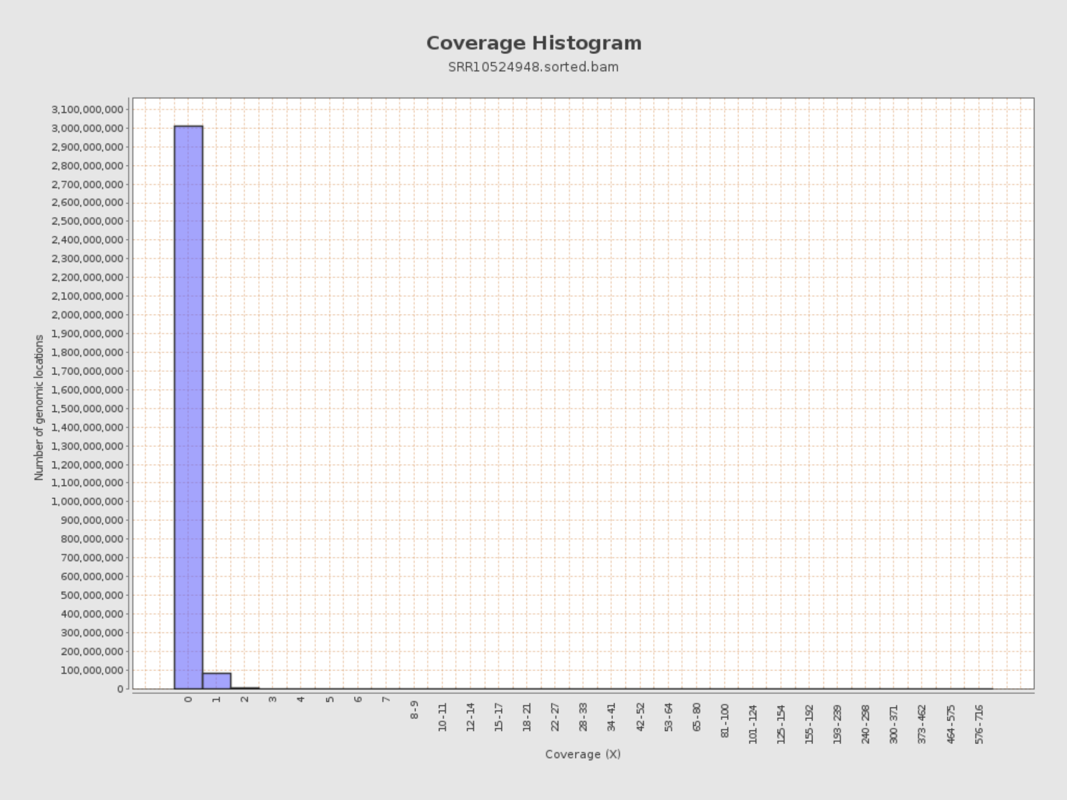
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10171516	0.0408	0.5562
chr2	243199373	9232260	0.038	0.3152
chr3	198022430	5284897	0.0267	0.177
chr4	191154276	6161849	0.0322	0.2097
chr5	180915260	4186966	0.0231	0.1668
chr6	171115067	6520237	0.0381	0.2929
chr7	159138663	6025029	0.0379	0.3924

chr8	146364022	6334100	0.0433	0.3031
chr9	141213431	2647153	0.0187	0.2155
chr10	135534747	4881432	0.036	0.2785
chr11	135006516	4024052	0.0298	0.2571
chr12	133851895	5206044	0.0389	0.2138
chr13	115169878	2708891	0.0235	0.1666
chr14	107349540	2168458	0.0202	0.1602
chr15	102531392	2624269	0.0256	0.1889
chr16	90354753	2990580	0.0331	0.2052
chr17	81195210	2605962	0.0321	0.2715
chr18	78077248	1902510	0.0244	0.3693
chr19	59128983	2241633	0.0379	0.3388
chr20	63025520	2272790	0.0361	0.2073
chr21	48129895	1374067	0.0285	0.1938
chr22	51304566	1221316	0.0238	0.165
chrMT	16571	8743	0.5276	0.7835
chrX	155270560	4101011	0.0264	0.2063
chrY	59373566	254406	0.0043	0.1019

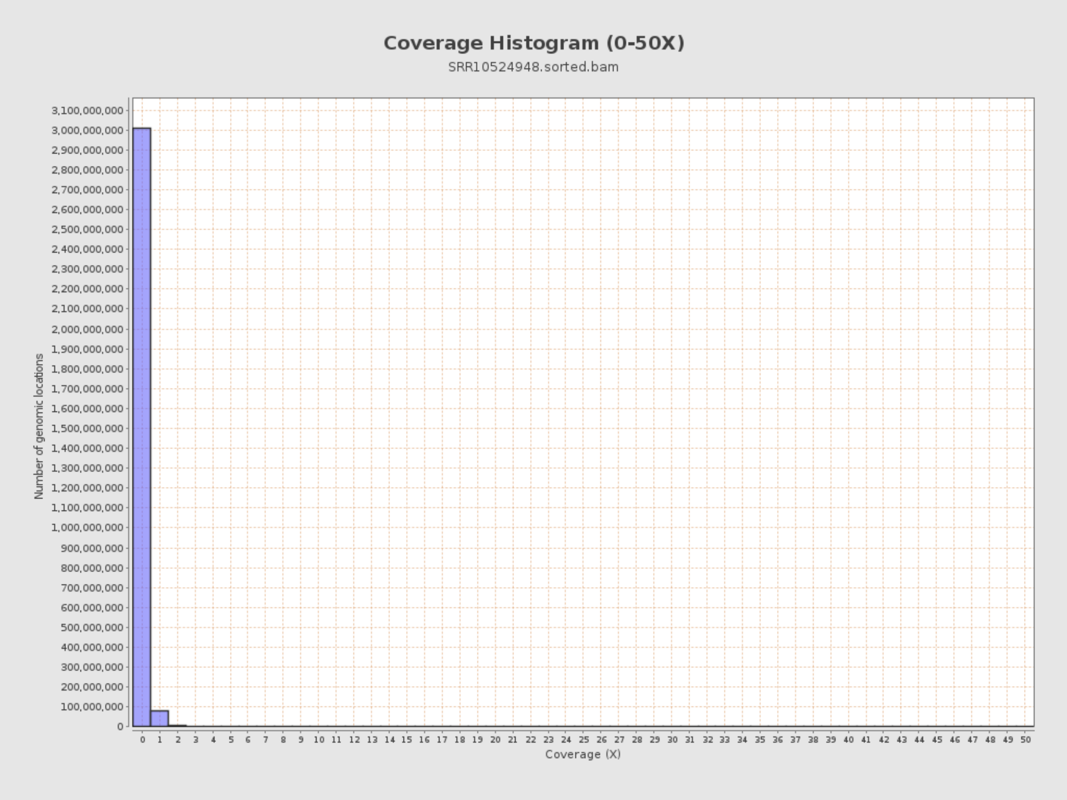
3. Results : Coverage across reference



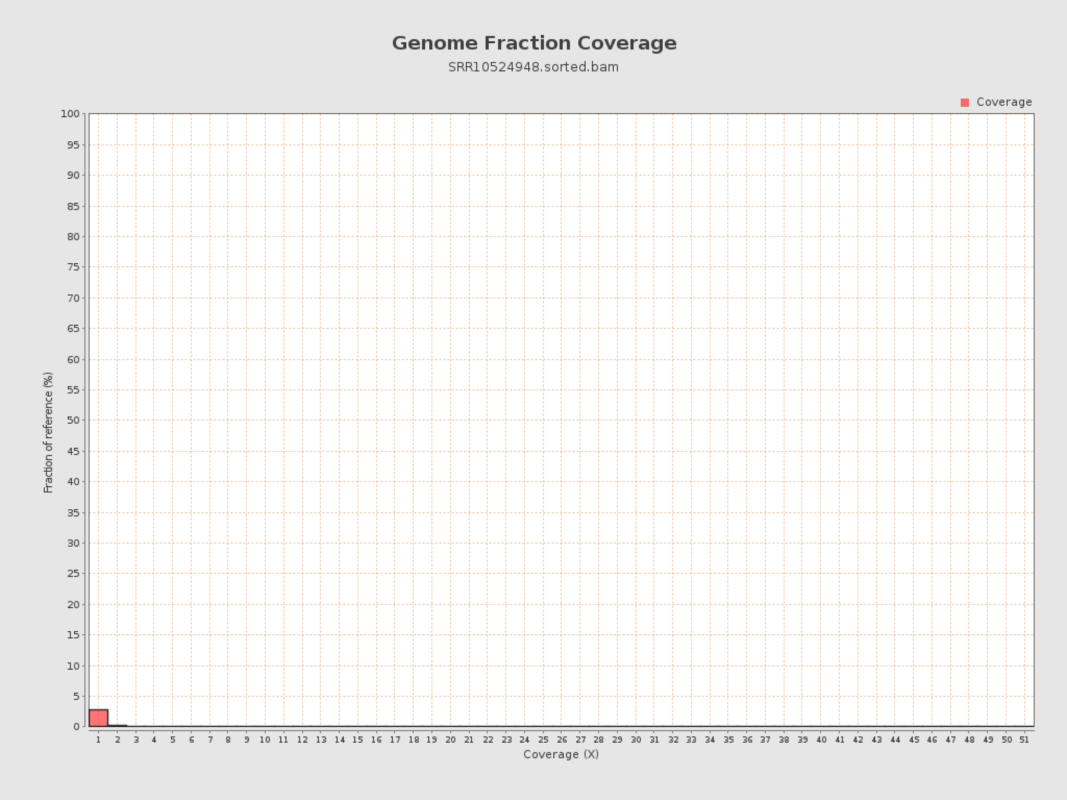
4. Results : Coverage Histogram



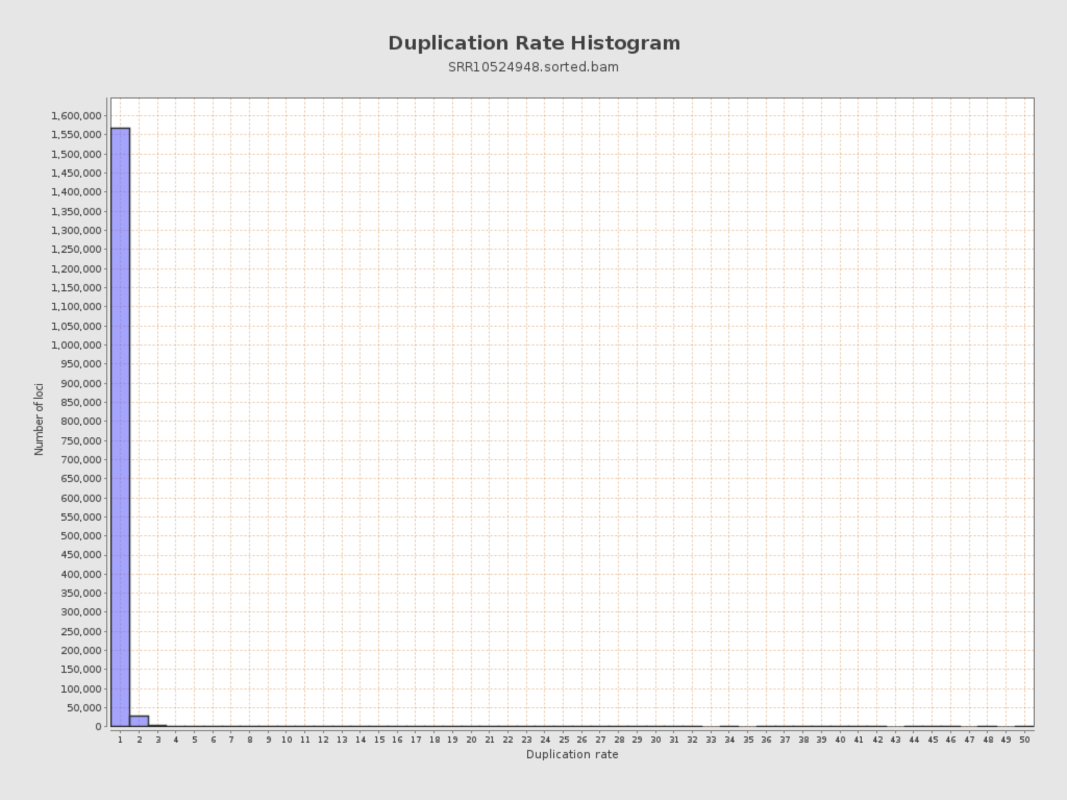
5. Results : Coverage Histogram (0-50X)



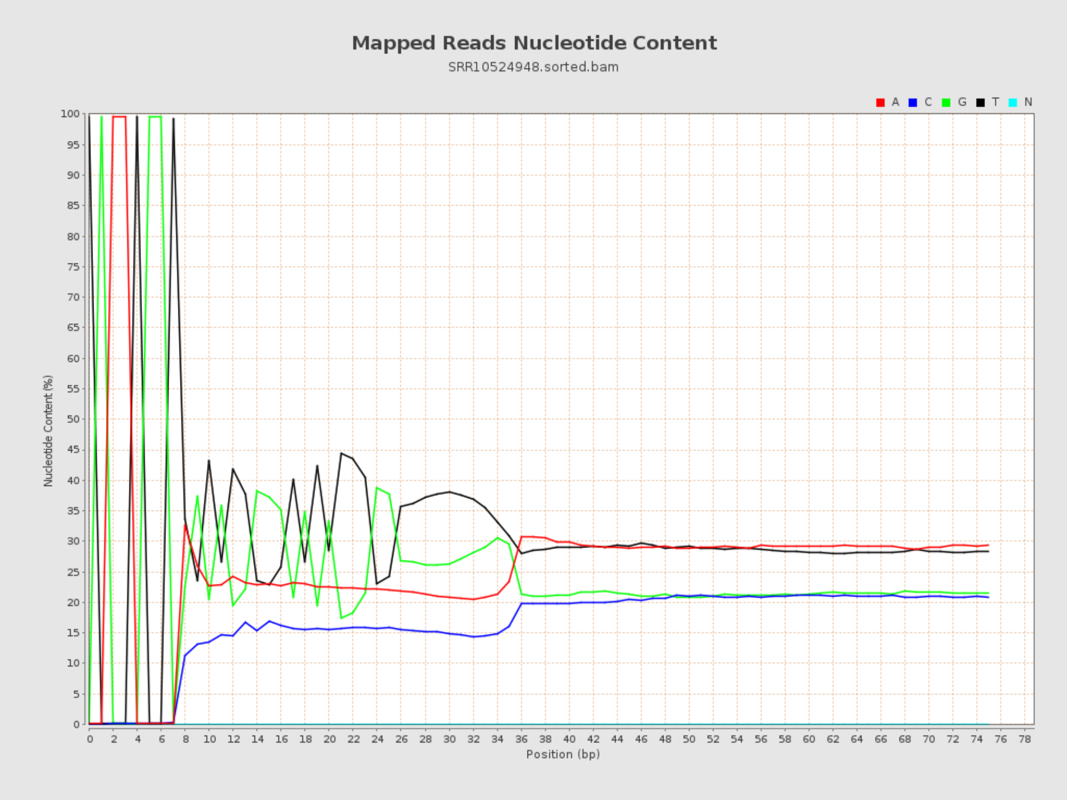
6. Results : Genome Fraction Coverage



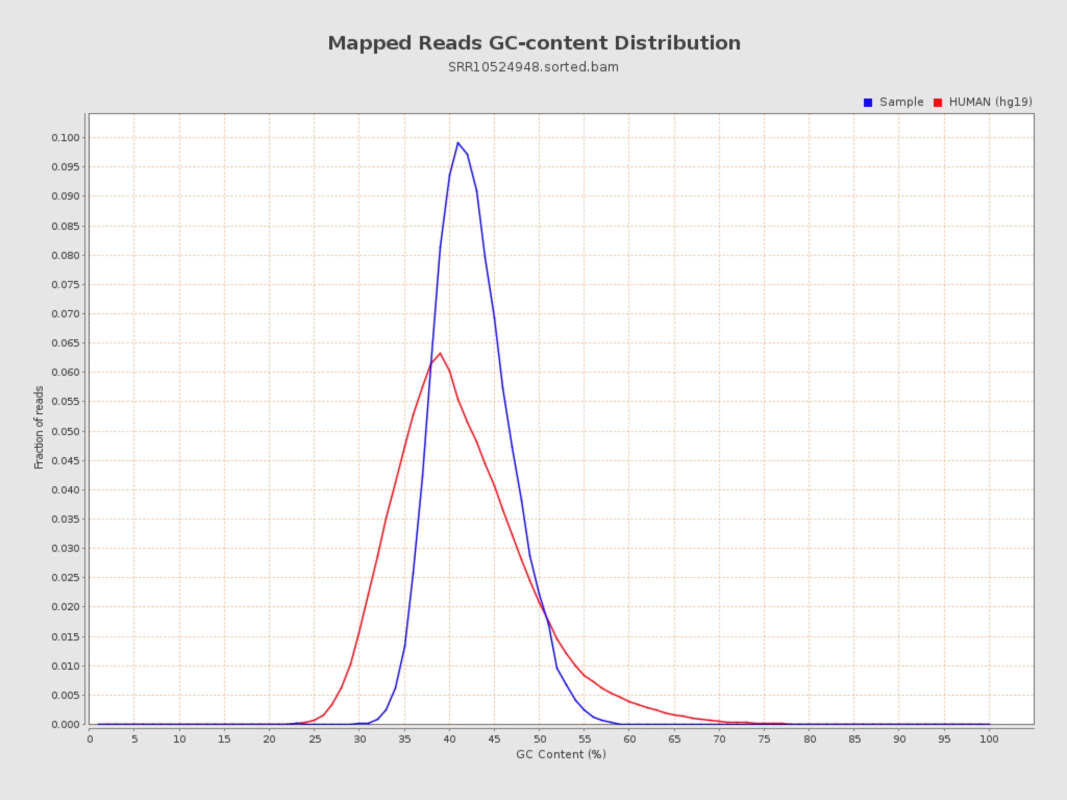
7. Results : Duplication Rate Histogram



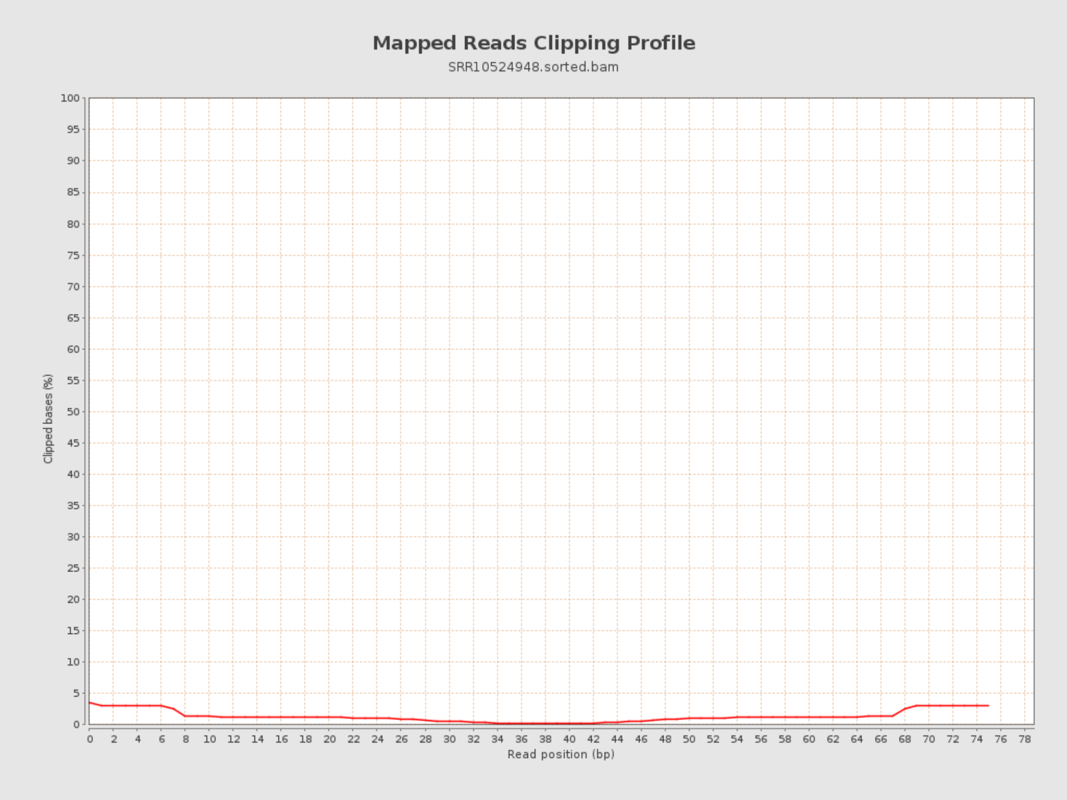
8. Results : Mapped Reads Nucleotide Content



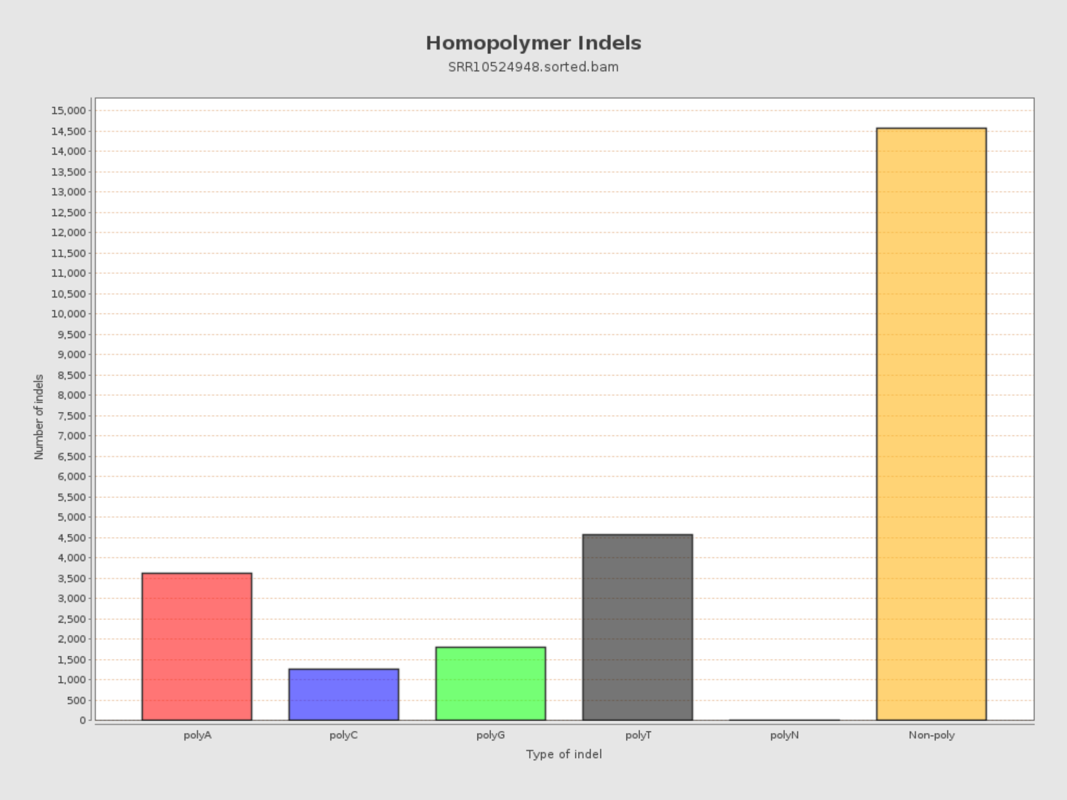
9. Results : Mapped Reads GC-content Distribution



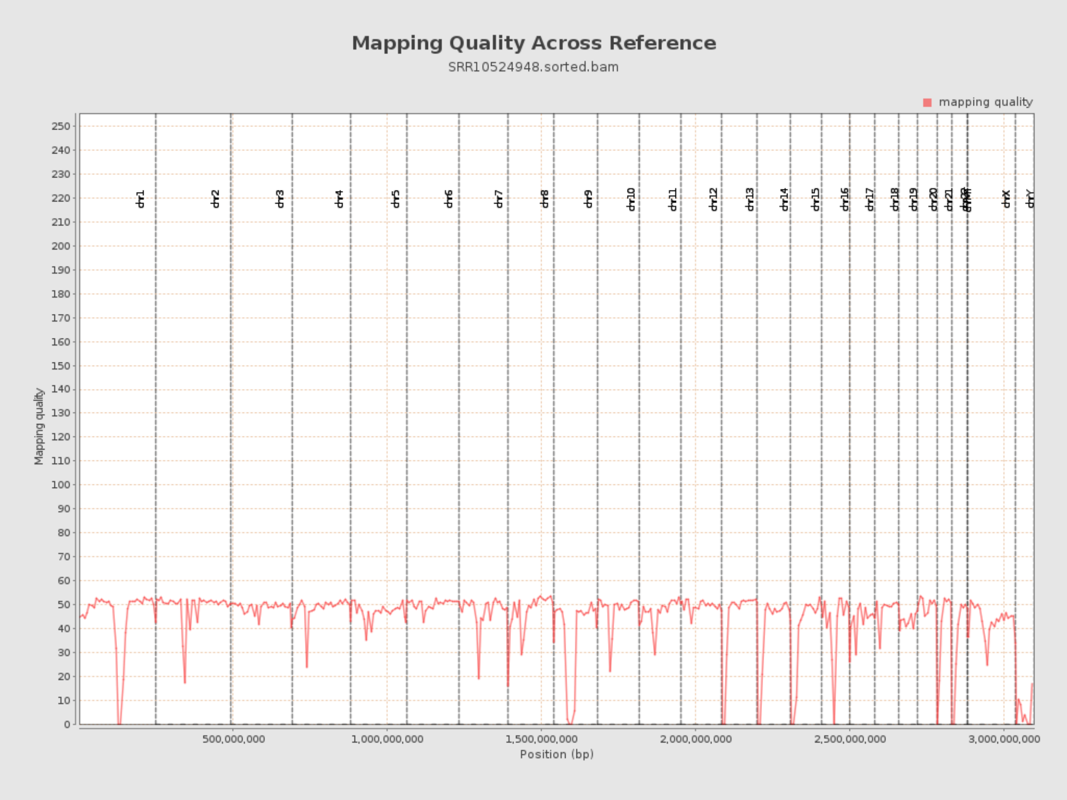
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram