Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:12:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524492.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_SRR10524492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524492.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:12:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,090,059
Mapped reads	1,864,553 / 89.21%
Unmapped reads	225,506 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,552 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	147,420 / 7.05%
Duplication rate	6.17%
Clipped reads	1,862,519 / 89.11%

2.2. ACGT Content

Number/percentage of A's	26,019,223 / 24.27%
Number/percentage of C's	21,520,243 / 20.07%
Number/percentage of T's	34,731,103 / 32.39%
Number/percentage of G's	24,950,432 / 23.27%
Number/percentage of N's	2,046 / 0%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3282

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

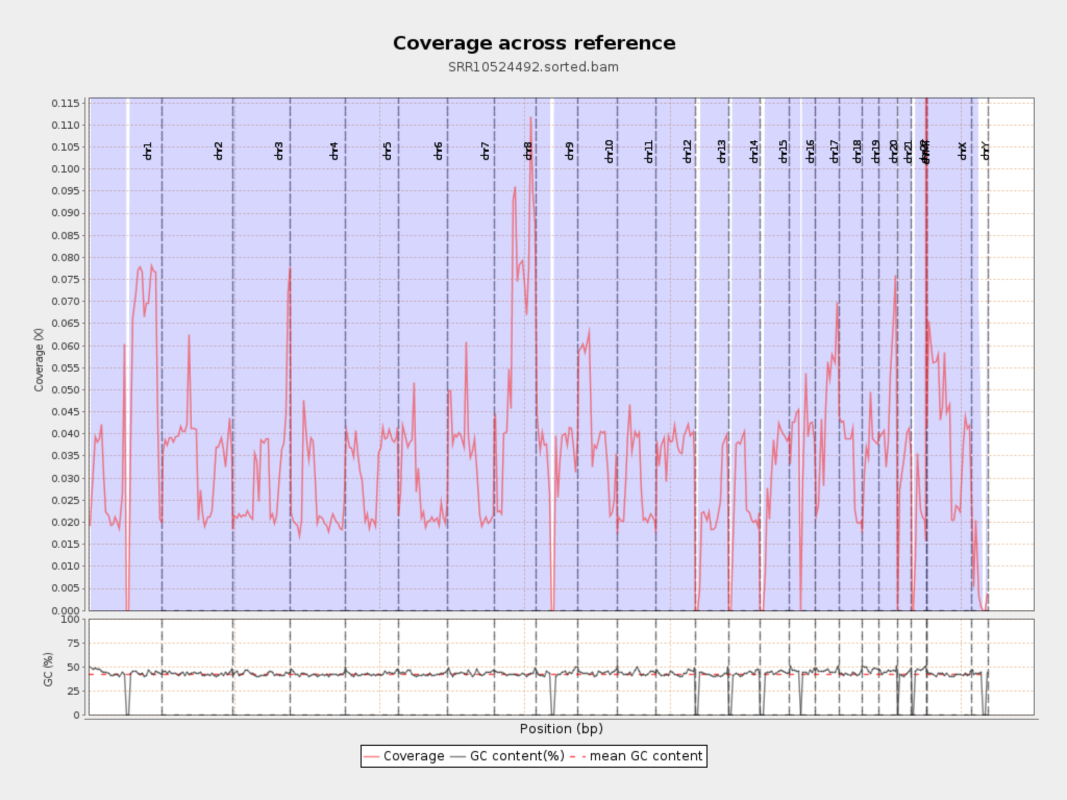
General error rate	0.5%
Mismatches	520,818
Insertions	8,188
Mapped reads with at least one insertion	0.44%
Deletions	21,788
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.17%

2.6. Chromosome stats

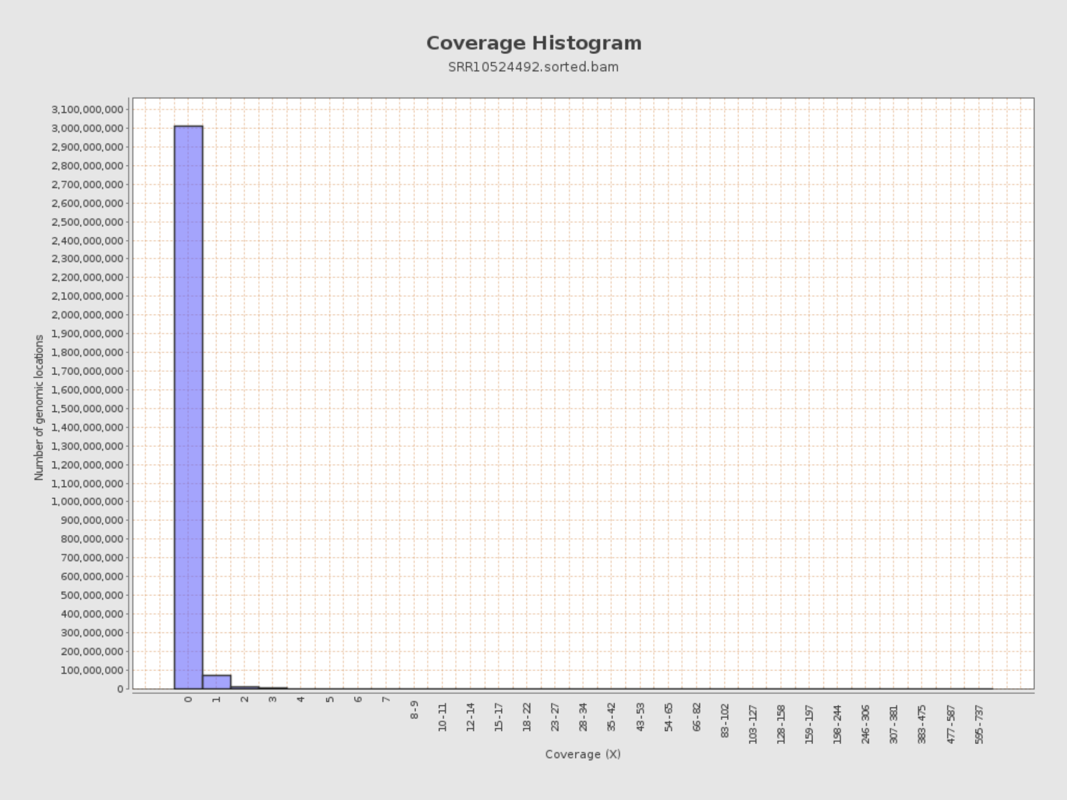
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10704241	0.0429	0.5795
chr2	243199373	8671892	0.0357	0.4002
chr3	198022430	5967109	0.0301	0.2102
chr4	191154276	4667863	0.0244	0.2279
chr5	180915260	5976792	0.033	0.2186
chr6	171115067	4707587	0.0275	0.2574
chr7	159138663	5411899	0.034	0.425

chr8	146364022	9412815	0.0643	0.3627
chr9	141213431	4620651	0.0327	0.2934
chr10	135534747	5748587	0.0424	0.3255
chr11	135006516	3819736	0.0283	0.3205
chr12	133851895	5075057	0.0379	0.2369
chr13	115169878	2455580	0.0213	0.1782
chr14	107349540	2608417	0.0243	0.1935
chr15	102531392	2910831	0.0284	0.2164
chr16	90354753	3442284	0.0381	0.2499
chr17	81195210	3786890	0.0466	0.2765
chr18	78077248	2623318	0.0336	0.4922
chr19	59128983	2201139	0.0372	0.4154
chr20	63025520	3082808	0.0489	0.272
chr21	48129895	1516039	0.0315	0.233
chr22	51304566	895281	0.0175	0.1586
chrMT	16571	14414	0.8698	1.1114
chrX	155270560	6593023	0.0425	0.2812
chrY	59373566	345562	0.0058	0.1613

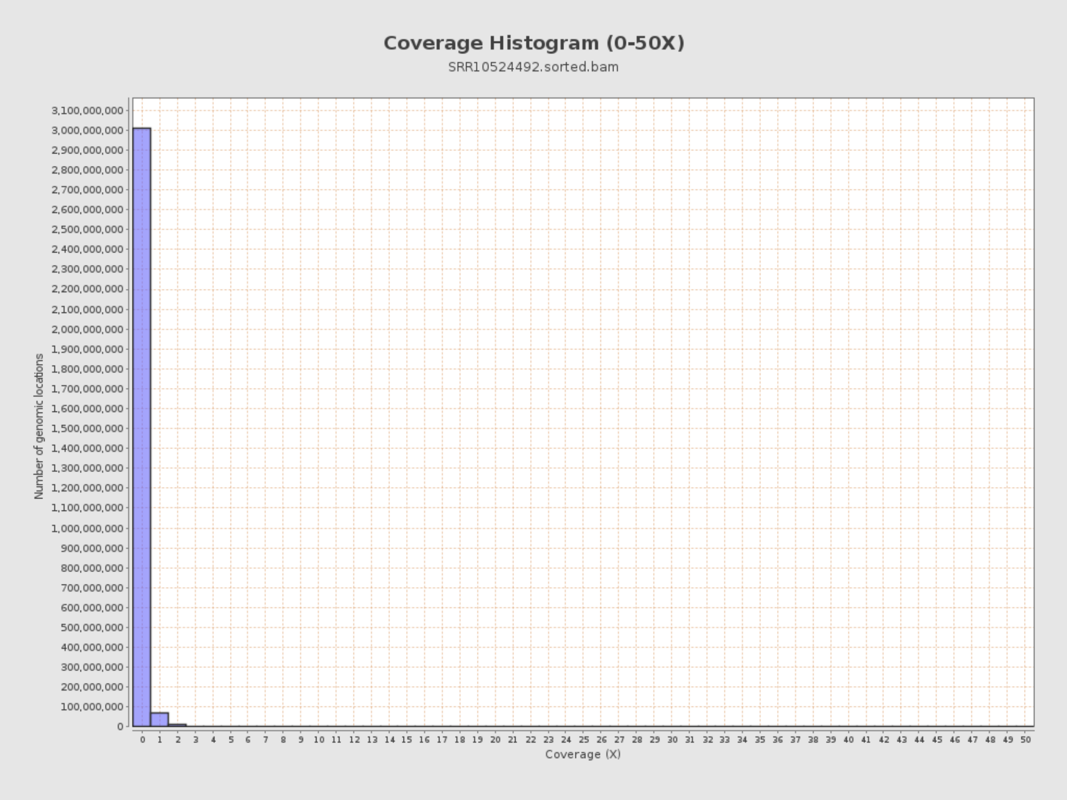
3. Results : Coverage across reference



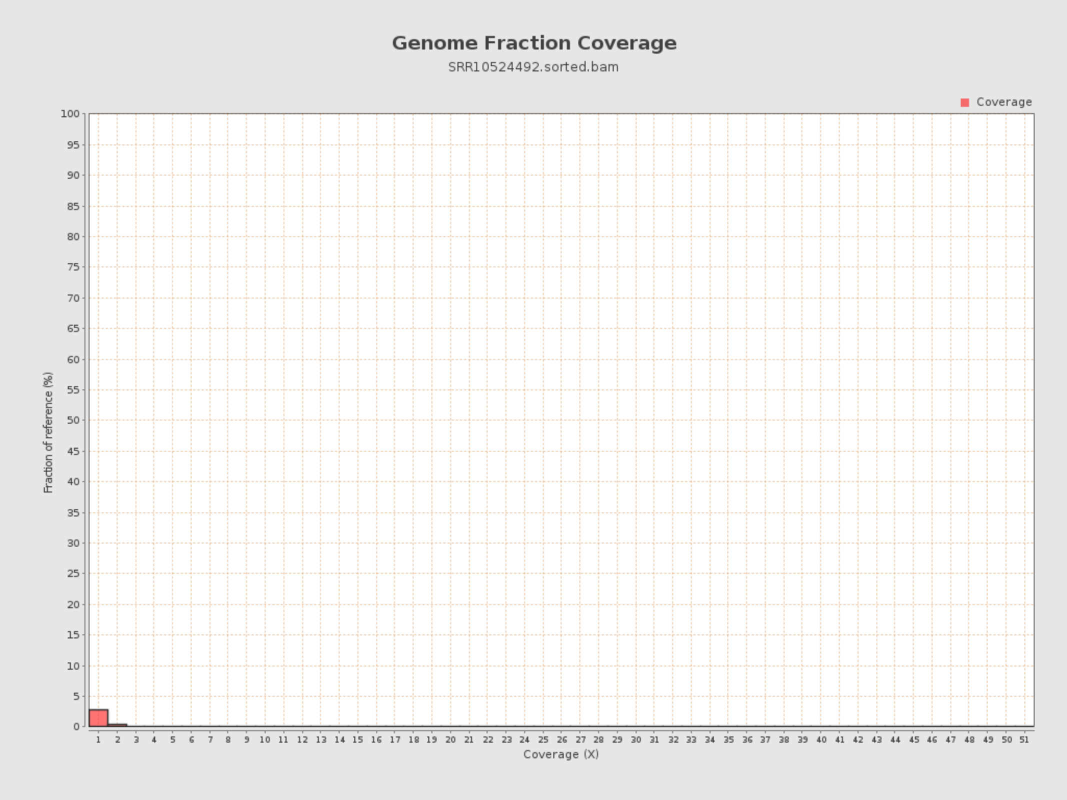
4. Results : Coverage Histogram



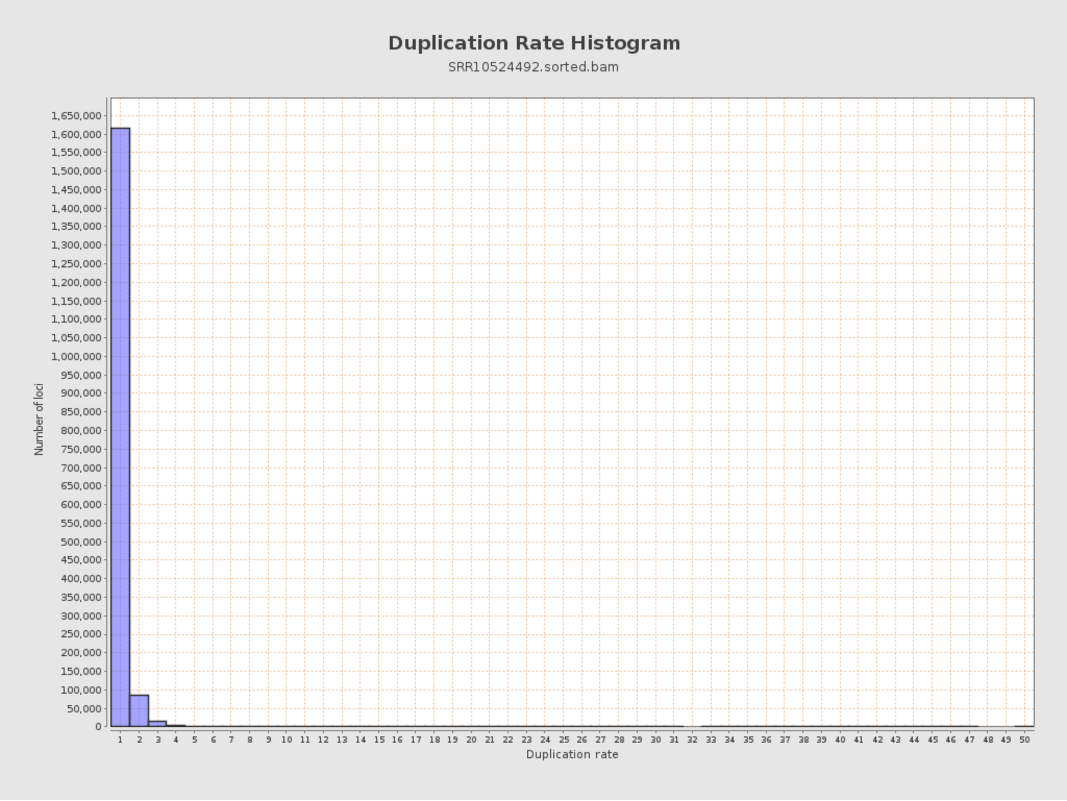
5. Results : Coverage Histogram (0-50X)



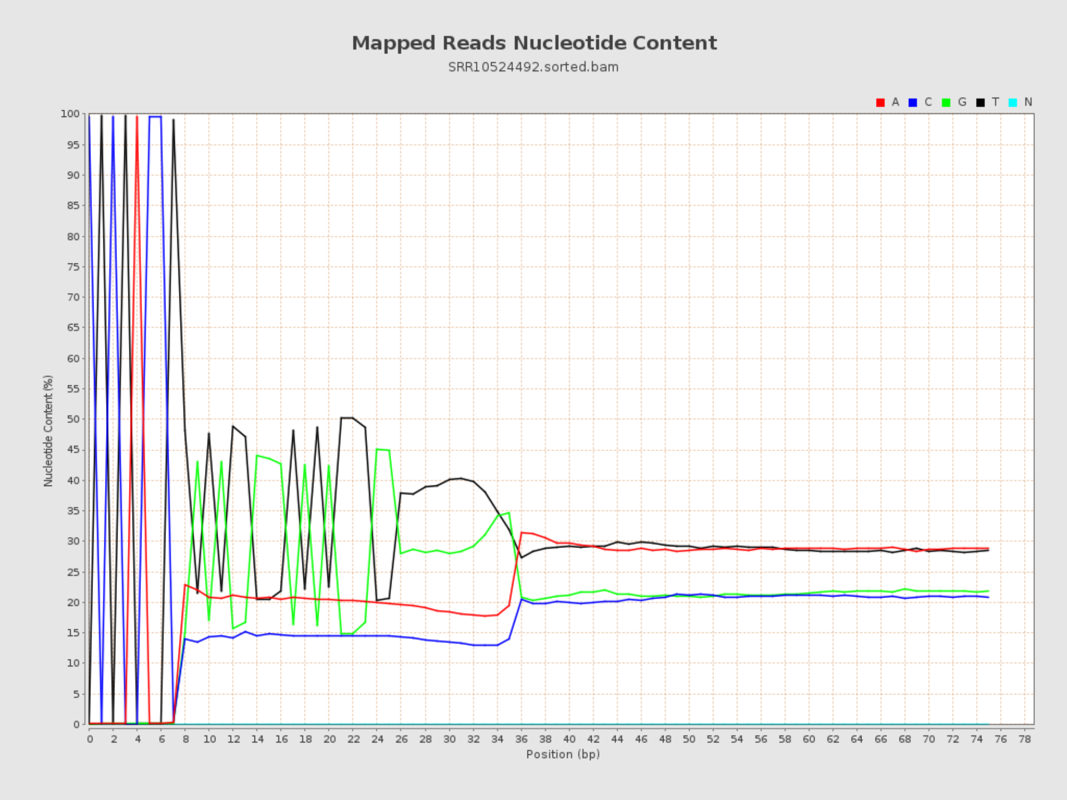
6. Results : Genome Fraction Coverage



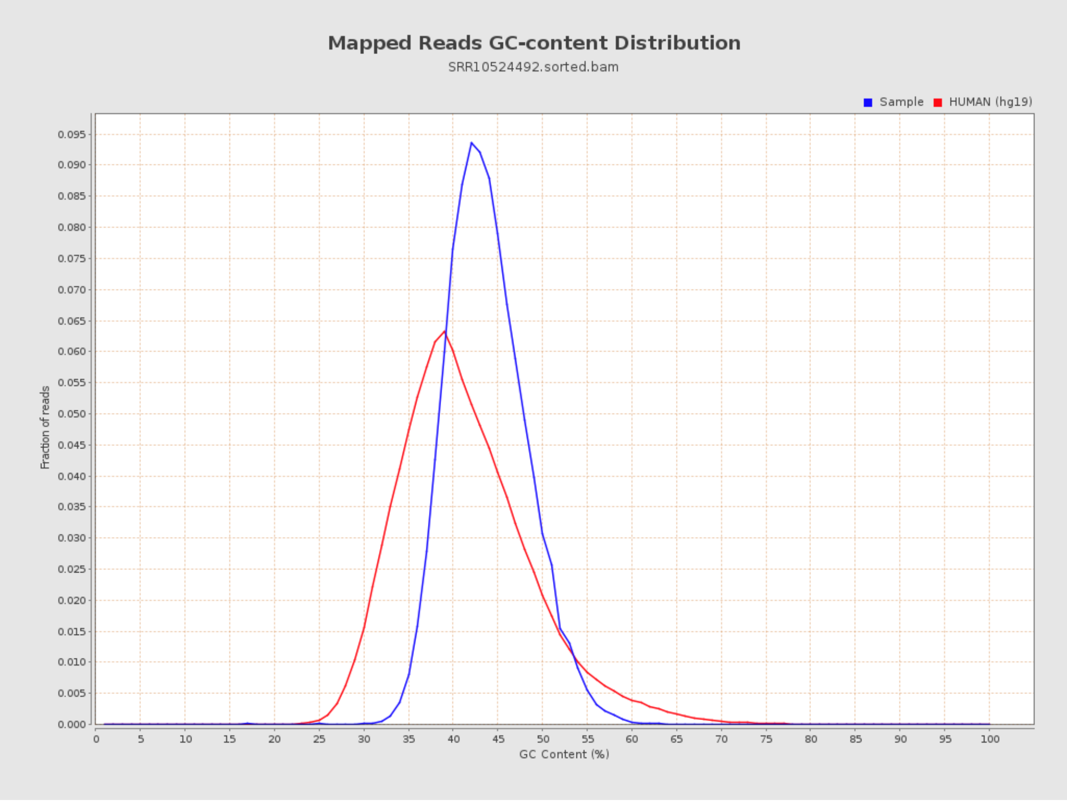
7. Results : Duplication Rate Histogram



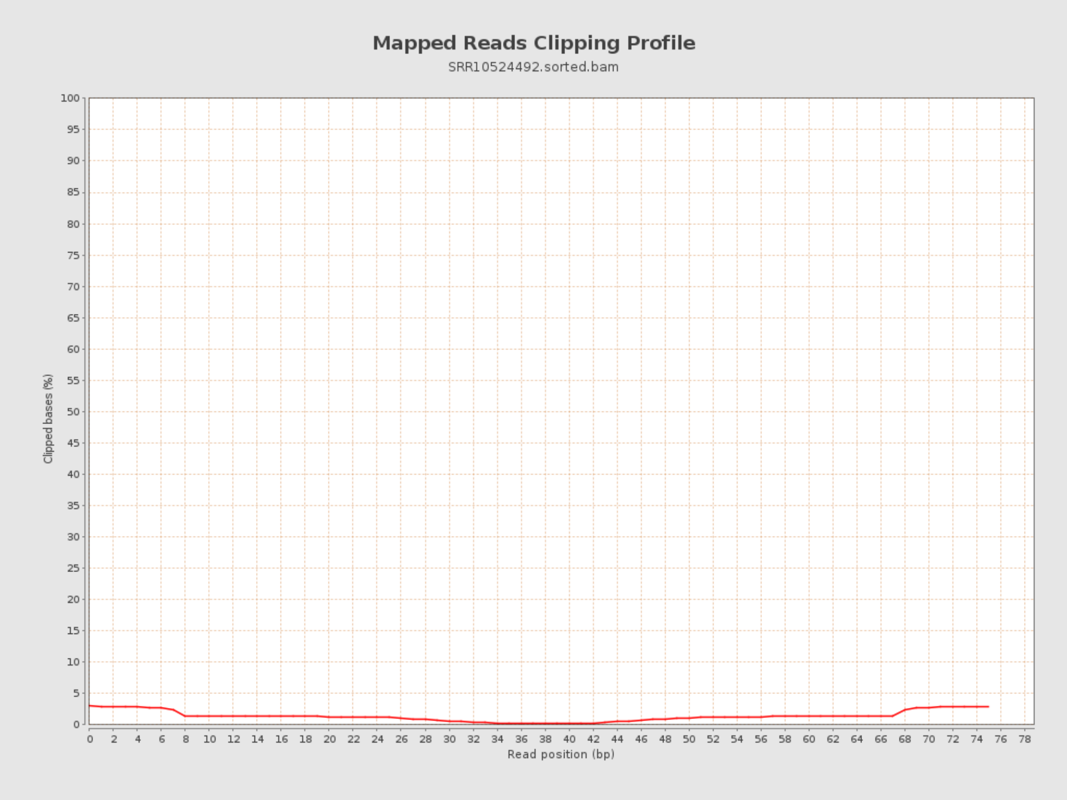
8. Results : Mapped Reads Nucleotide Content



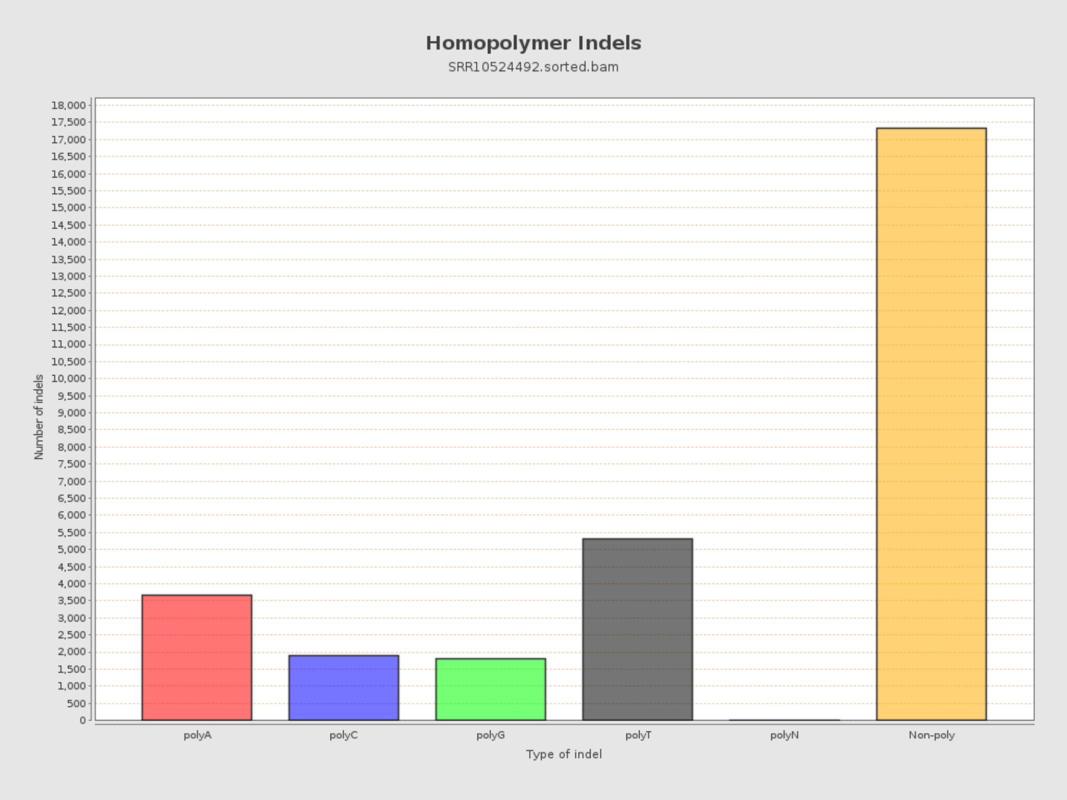
9. Results : Mapped Reads GC-content Distribution



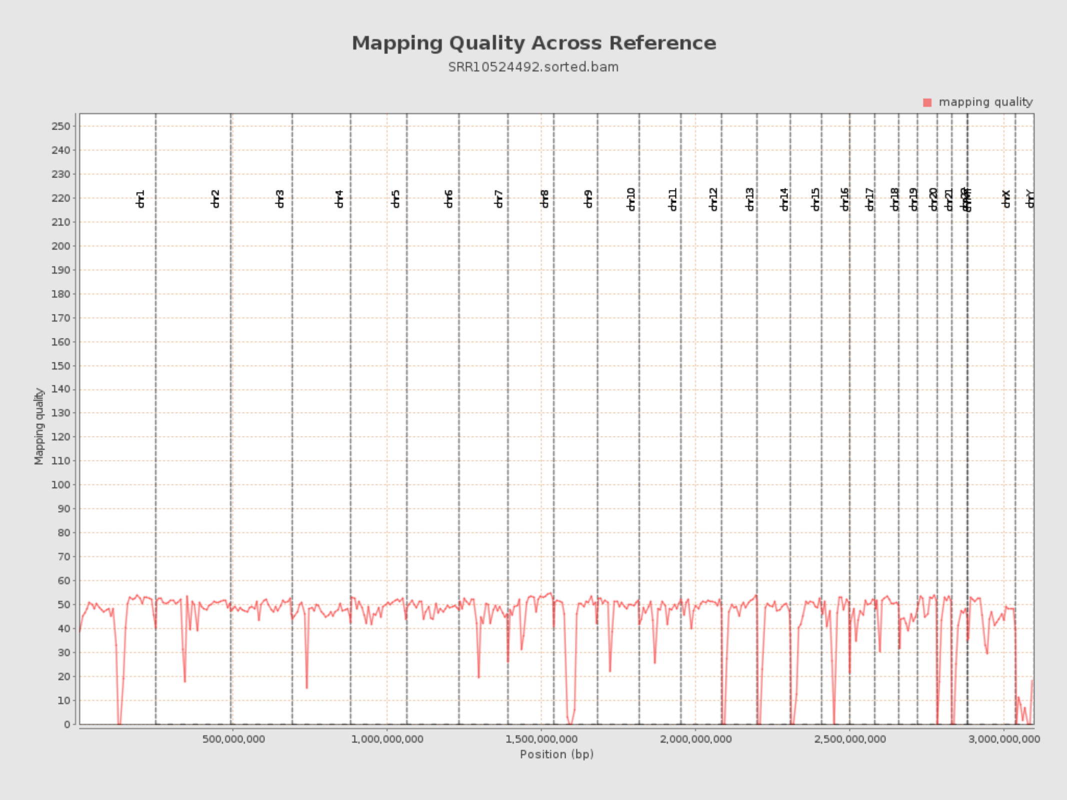
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram