Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:36:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524342.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_SRR10524342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:36:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,030,921
Mapped reads	1,868,833 / 92.02%
Unmapped reads	162,088 / 7.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,032 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	84,597 / 4.17%
Duplication rate	3.29%
Clipped reads	1,873,619 / 92.25%

2.2. ACGT Content

Number/percentage of A's	26,651,320 / 24.41%
Number/percentage of C's	20,814,636 / 19.06%
Number/percentage of T's	34,704,339 / 31.78%
Number/percentage of G's	27,009,548 / 24.74%
Number/percentage of N's	15,241 / 0.01%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0353

Standard Deviation	0.3333

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

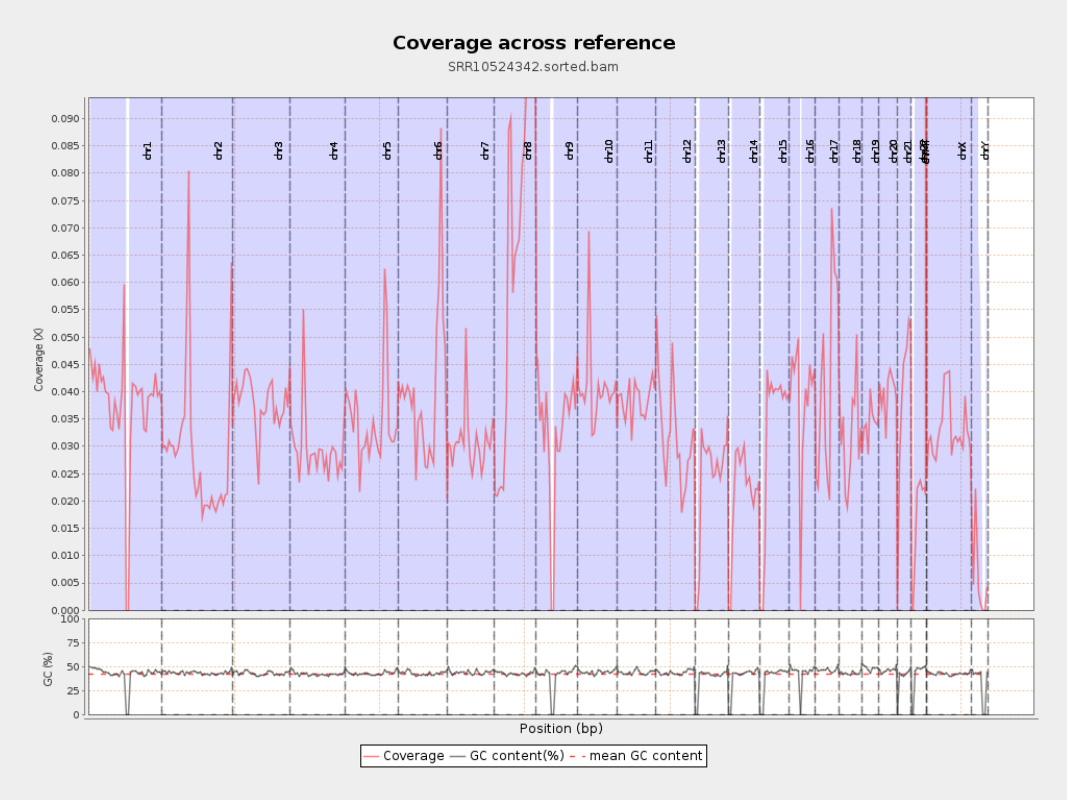
General error rate	0.52%
Mismatches	549,926
Insertions	6,793
Mapped reads with at least one insertion	0.36%
Deletions	18,410
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.42%

2.6. Chromosome stats

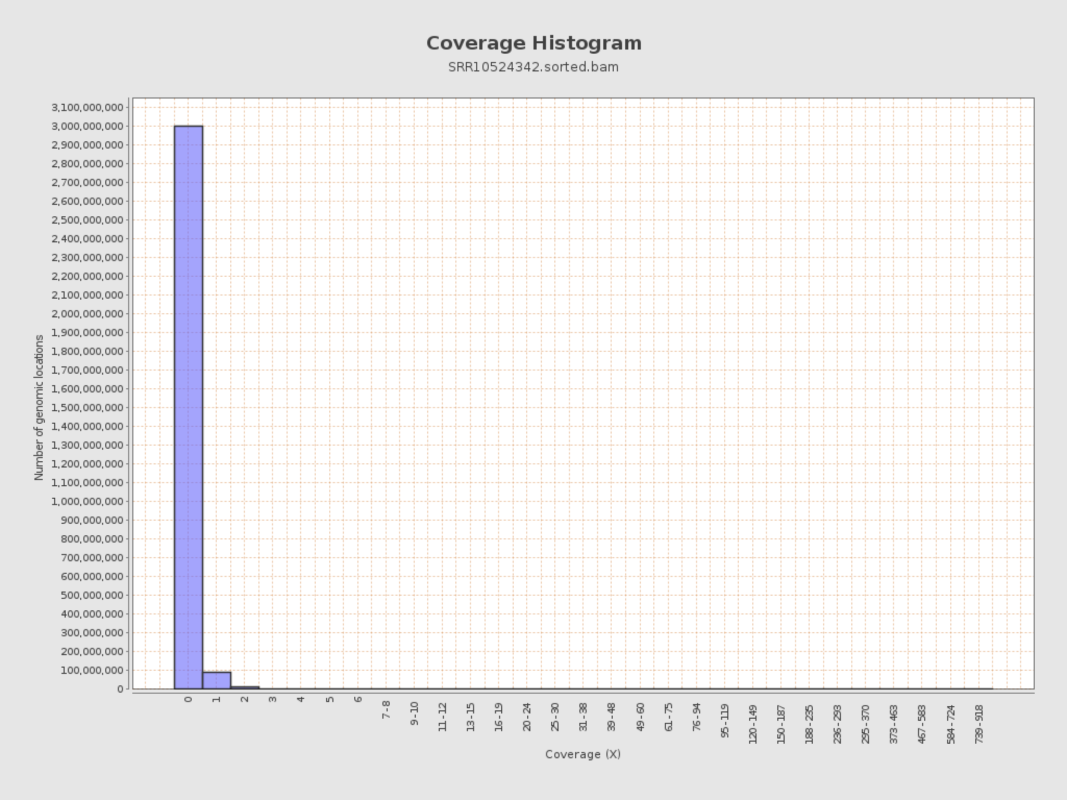
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9342253	0.0375	0.6098
chr2	243199373	7041845	0.029	0.4276
chr3	198022430	7499720	0.0379	0.2157
chr4	191154276	5607303	0.0293	0.2341
chr5	180915260	6324357	0.035	0.2083
chr6	171115067	6816584	0.0398	0.2391
chr7	159138663	4916647	0.0309	0.3703

chr8	146364022	11252843	0.0769	0.4159
chr9	141213431	4502513	0.0319	0.2566
chr10	135534747	5499006	0.0406	0.3314
chr11	135006516	5186519	0.0384	0.2673
chr12	133851895	4263586	0.0319	0.2024
chr13	115169878	2729103	0.0237	0.1706
chr14	107349540	2275024	0.0212	0.1704
chr15	102531392	3329610	0.0325	0.1986
chr16	90354753	3482236	0.0385	0.2317
chr17	81195210	3406324	0.042	0.248
chr18	78077248	2531065	0.0324	0.4438
chr19	59128983	2025462	0.0343	0.3995
chr20	63025520	2513789	0.0399	0.231
chr21	48129895	1884986	0.0392	0.2424
chr22	51304566	825149	0.0161	0.1414
chrMT	16571	501490	30.2631	17.7853
chrX	155270560	5128482	0.033	0.2218
chrY	59373566	338827	0.0057	0.1884

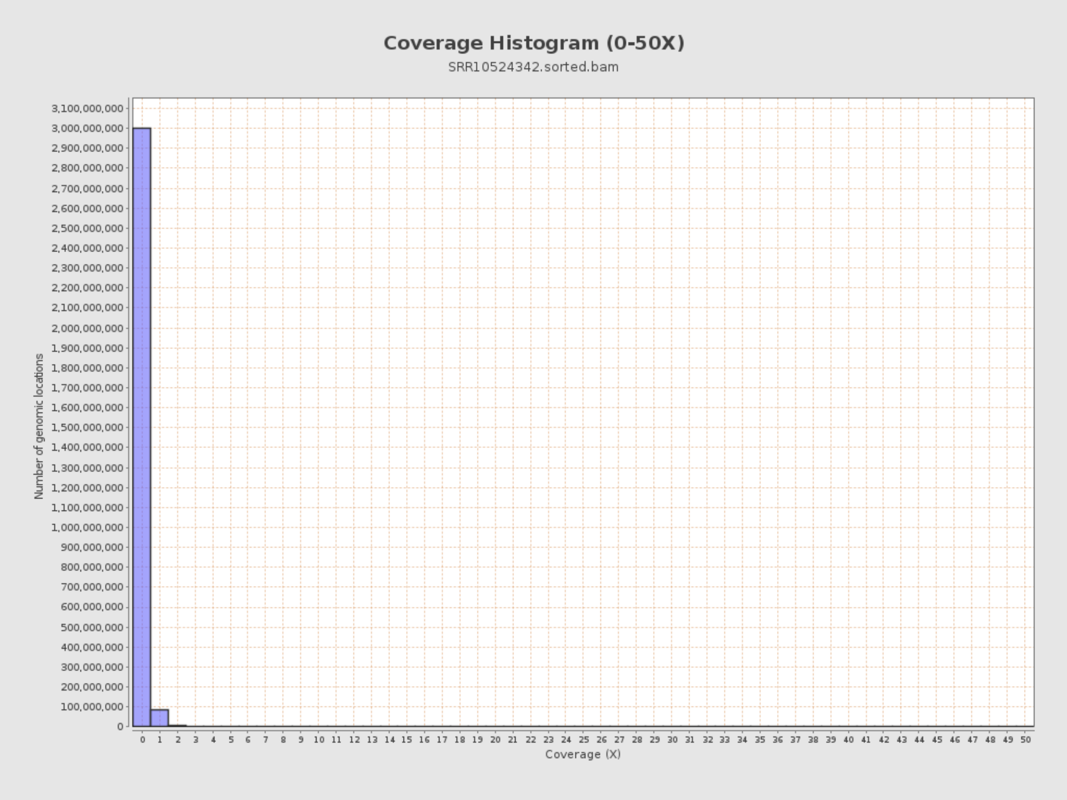
3. Results : Coverage across reference



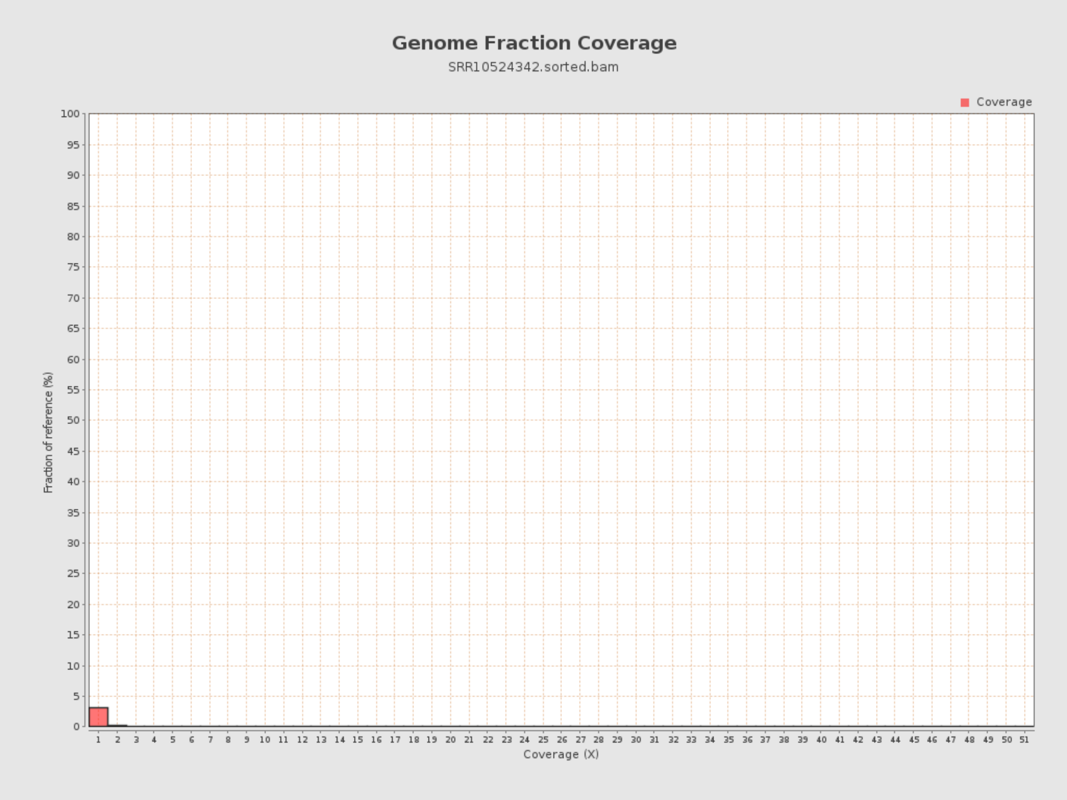
4. Results : Coverage Histogram



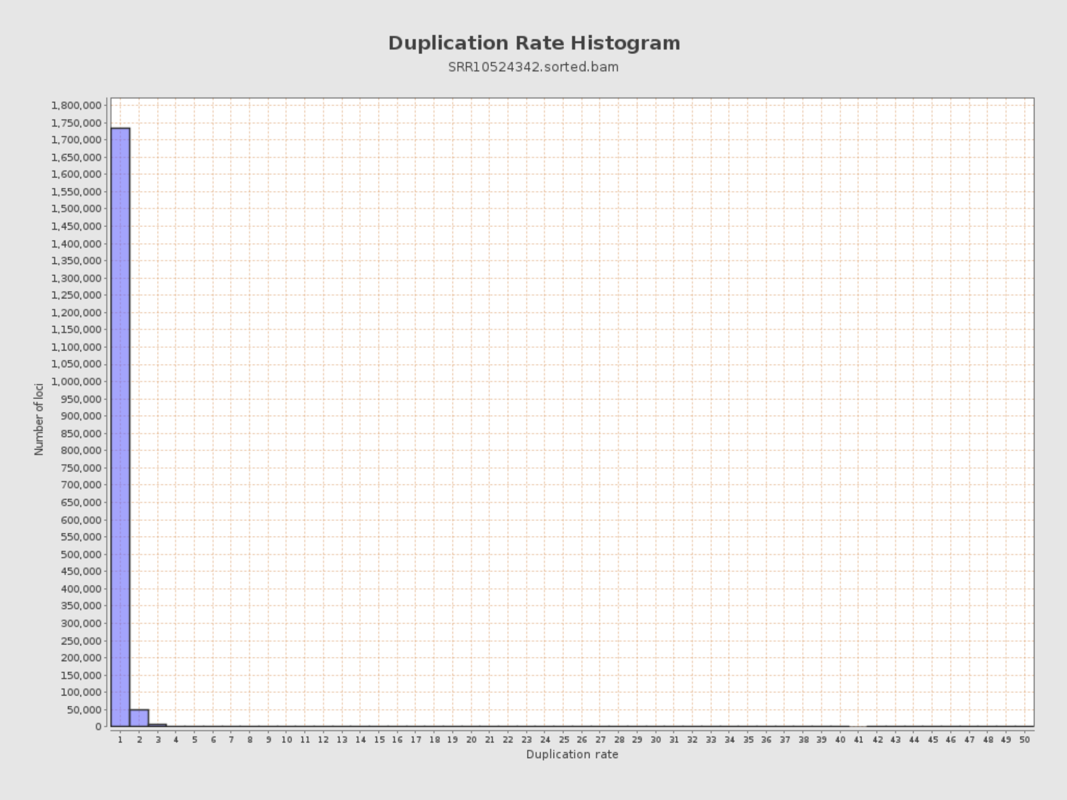
5. Results : Coverage Histogram (0-50X)



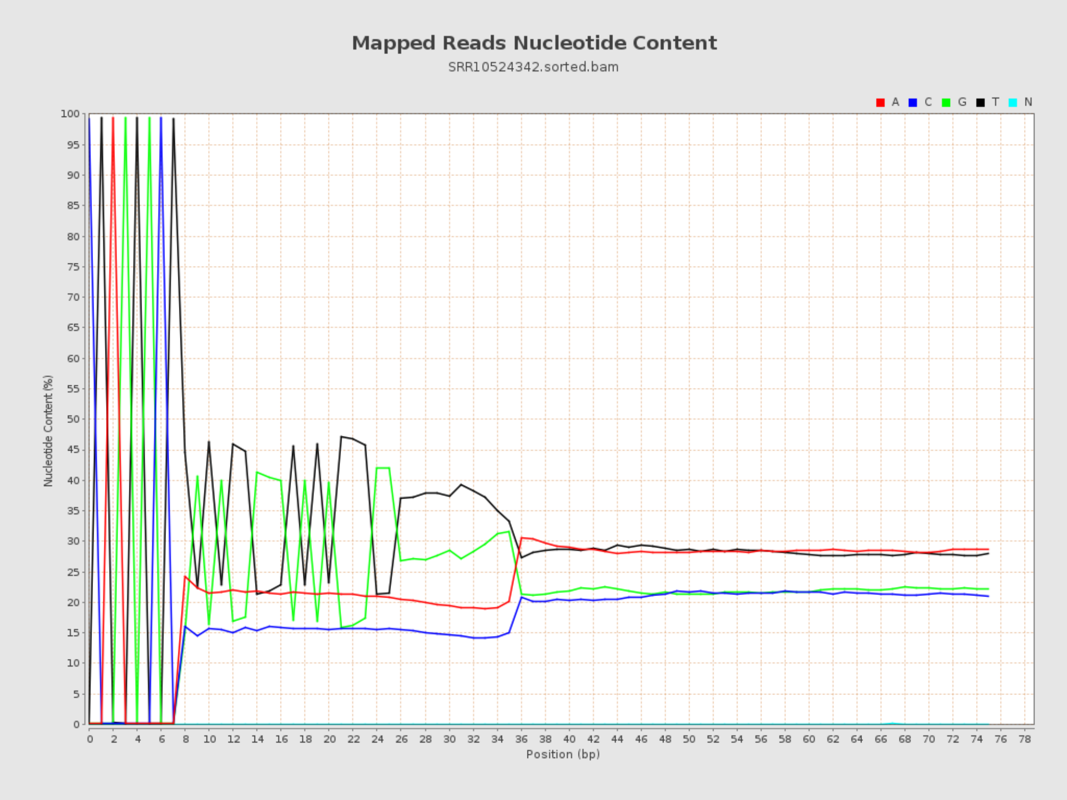
6. Results : Genome Fraction Coverage



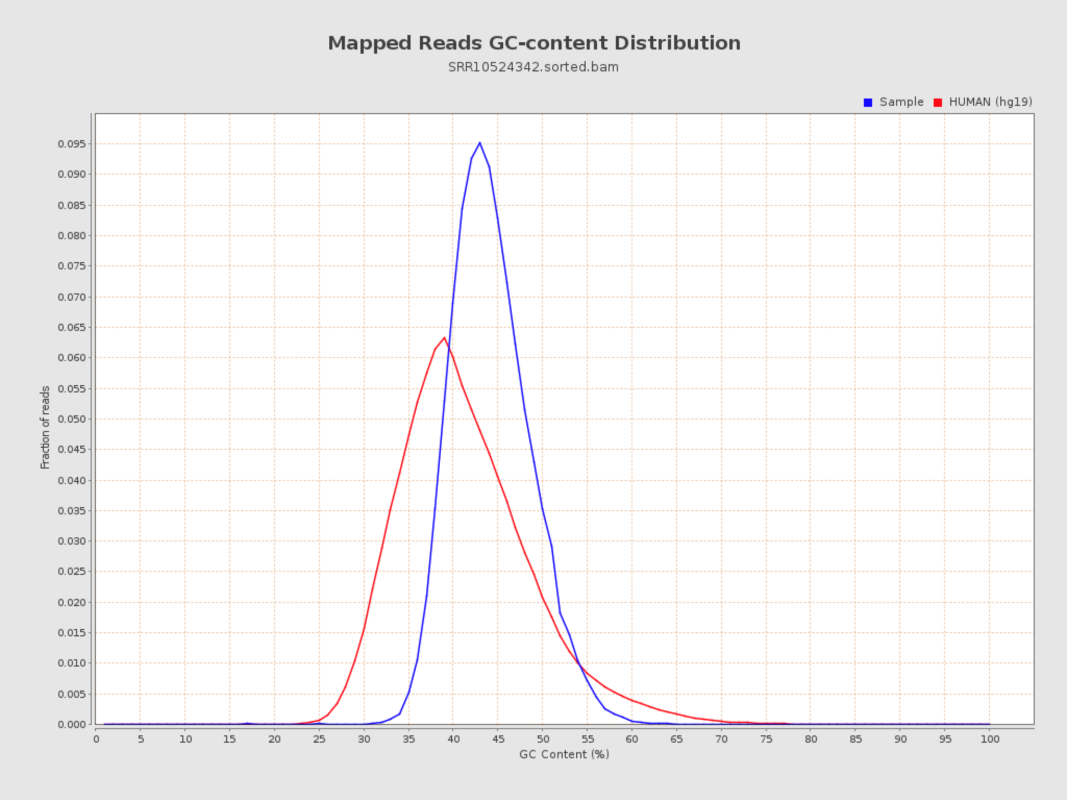
7. Results : Duplication Rate Histogram



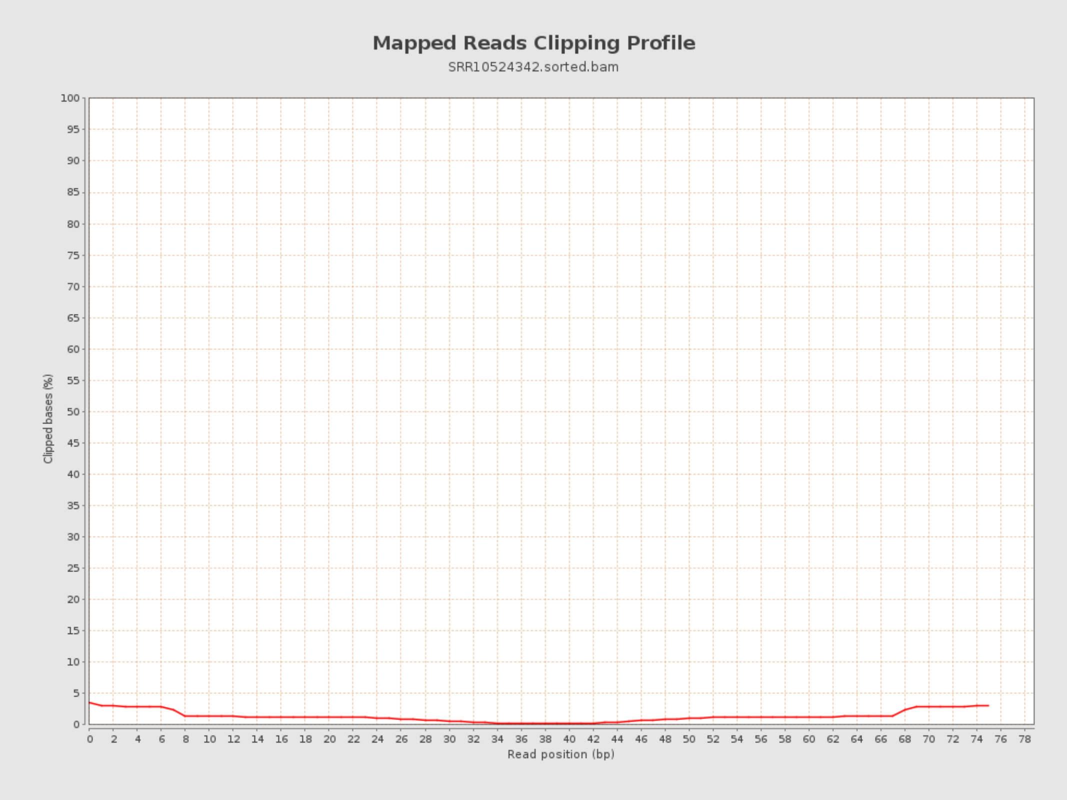
8. Results : Mapped Reads Nucleotide Content



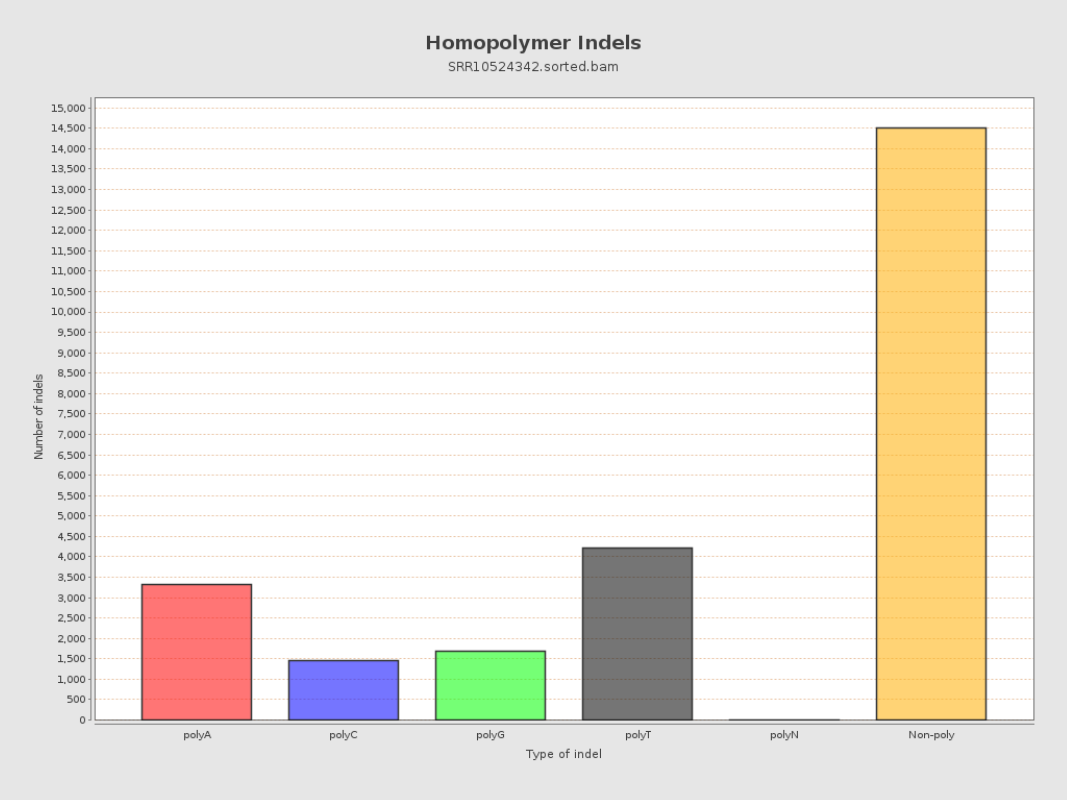
9. Results : Mapped Reads GC-content Distribution



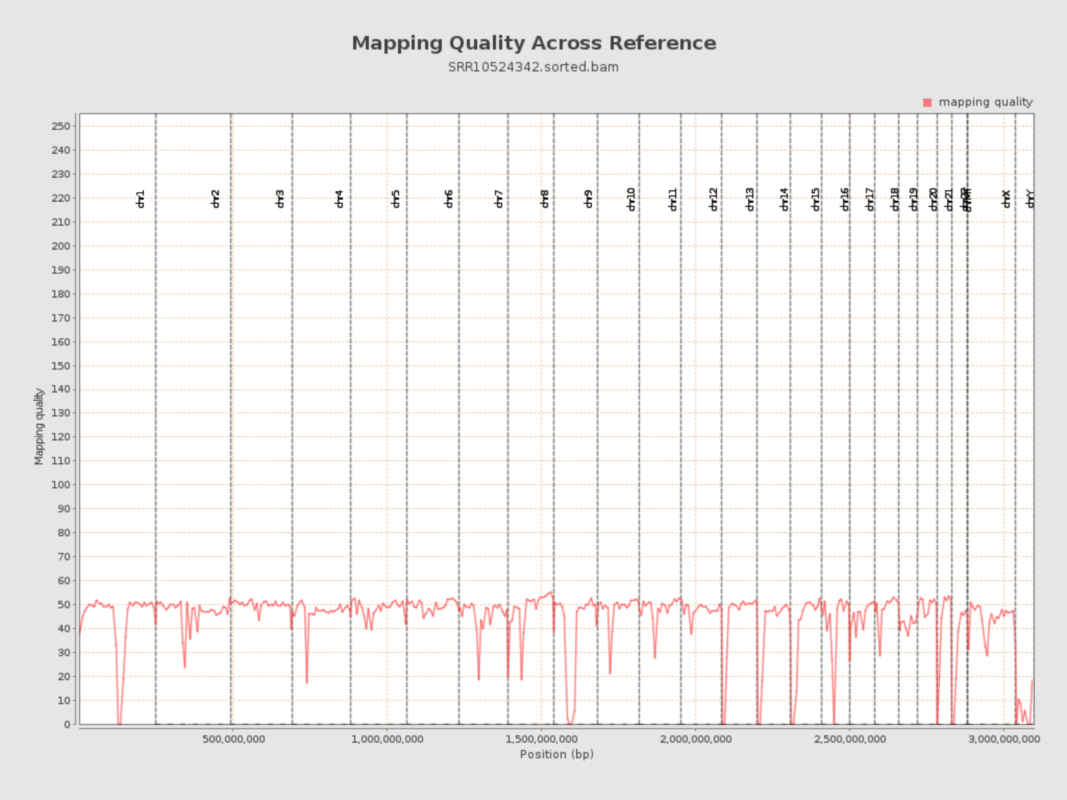
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram