Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:14:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524657.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_SRR10524657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524657.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:14:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,287,810
Mapped reads	2,124,718 / 92.87%
Unmapped reads	163,092 / 7.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,615 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	100,710 / 4.4%
Duplication rate	3.51%
Clipped reads	2,128,958 / 93.06%

2.2. ACGT Content

Number/percentage of A's	31,799,607 / 25.23%
Number/percentage of C's	25,856,398 / 20.51%
Number/percentage of T's	38,069,326 / 30.2%
Number/percentage of G's	30,312,070 / 24.05%
Number/percentage of N's	17,281 / 0.01%
GC Percentage	44.56%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.3591

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

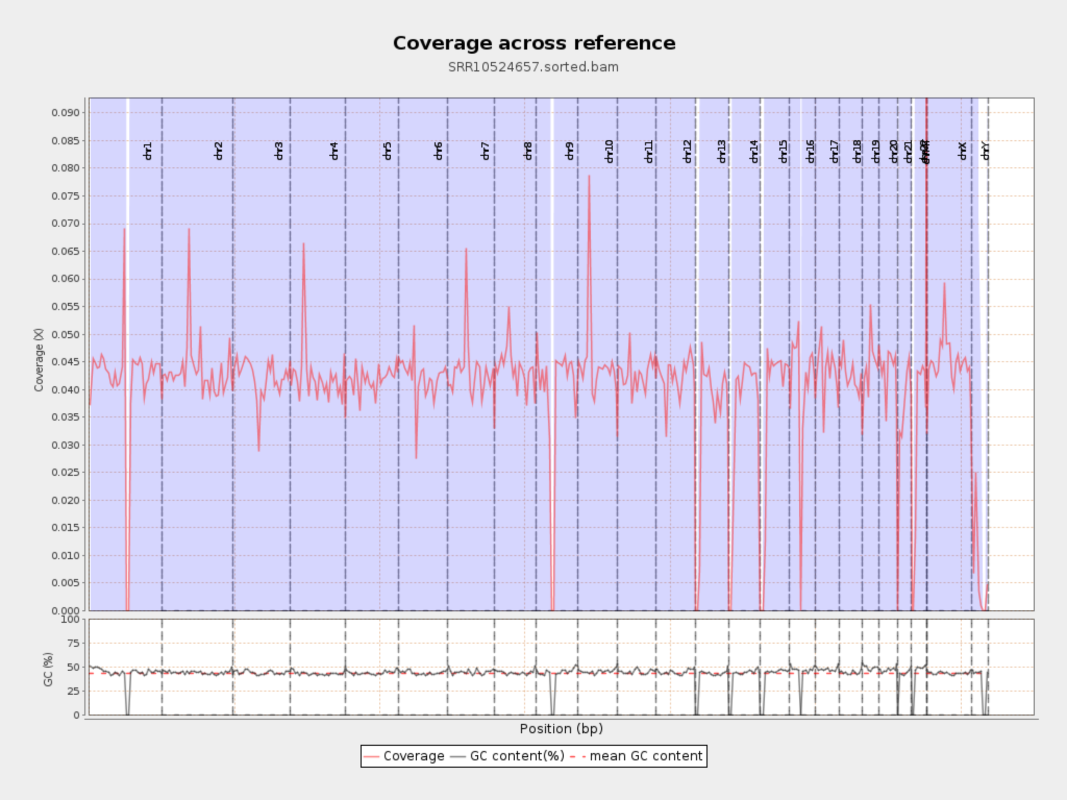
General error rate	0.51%
Mismatches	627,671
Insertions	9,312
Mapped reads with at least one insertion	0.44%
Deletions	23,449
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.23%

2.6. Chromosome stats

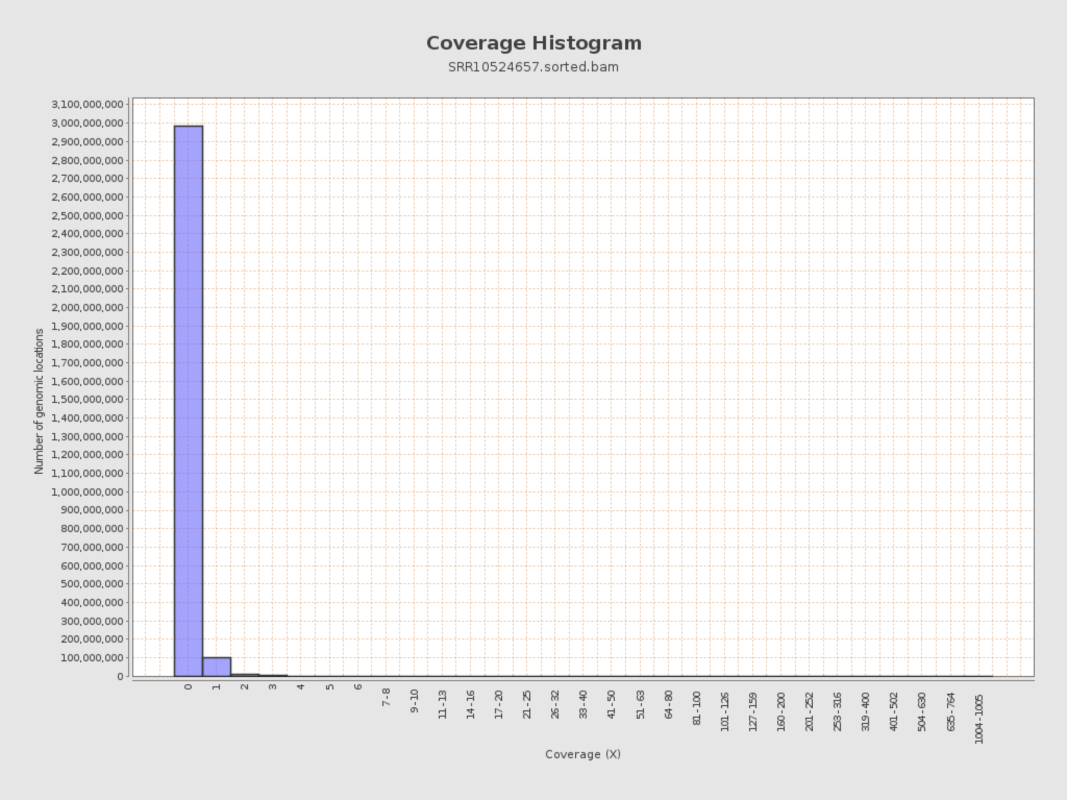
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10276002	0.0412	0.6379
chr2	243199373	10595006	0.0436	0.5047
chr3	198022430	8337637	0.0421	0.2276
chr4	191154276	8092133	0.0423	0.2615
chr5	180915260	7570483	0.0418	0.2295
chr6	171115067	7226903	0.0422	0.263
chr7	159138663	6923390	0.0435	0.4313

chr8	146364022	6418331	0.0439	0.3866
chr9	141213431	5333636	0.0378	0.3051
chr10	135534747	6114970	0.0451	0.3651
chr11	135006516	5758769	0.0427	0.3185
chr12	133851895	5684849	0.0425	0.2331
chr13	115169878	3918433	0.034	0.207
chr14	107349540	3728227	0.0347	0.2224
chr15	102531392	3657666	0.0357	0.2109
chr16	90354753	3656006	0.0405	0.2443
chr17	81195210	3504059	0.0432	0.2546
chr18	78077248	3341267	0.0428	0.5692
chr19	59128983	2640436	0.0447	0.4907
chr20	63025520	2745104	0.0436	0.2393
chr21	48129895	1654576	0.0344	0.2424
chr22	51304566	1518526	0.0296	0.1921
chrMT	16571	2593	0.1565	0.564
chrX	155270560	6992763	0.045	0.2635
chrY	59373566	400108	0.0067	0.2362

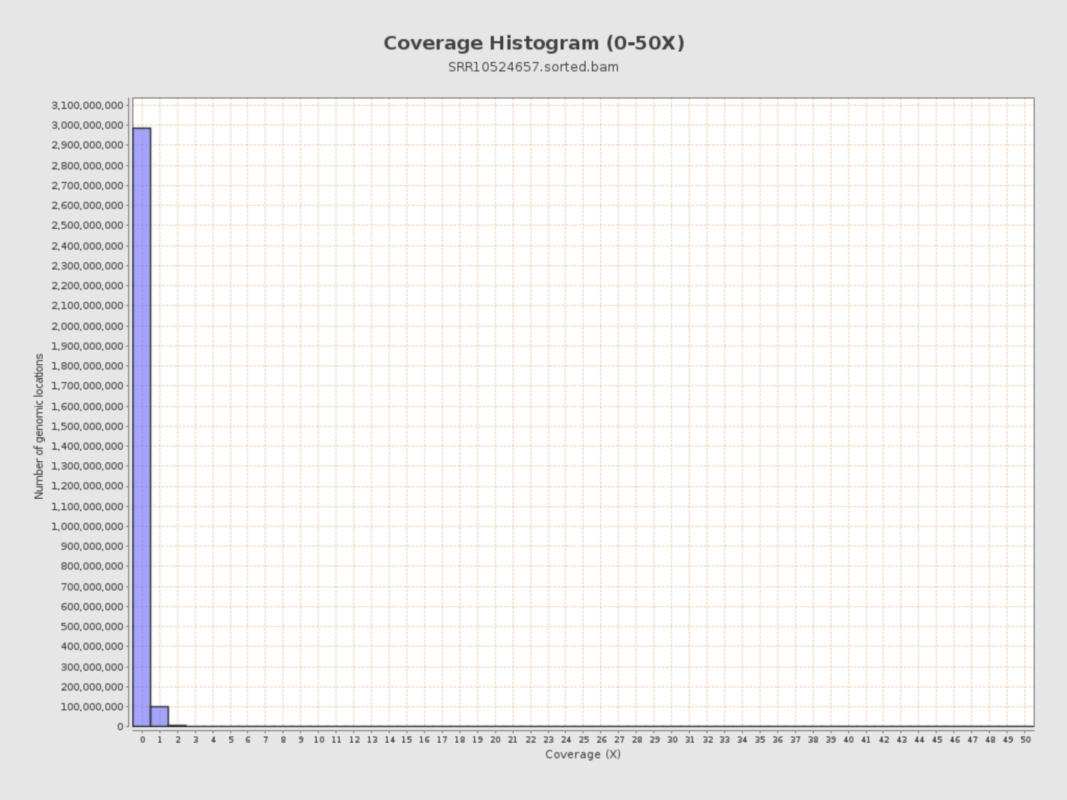
3. Results : Coverage across reference



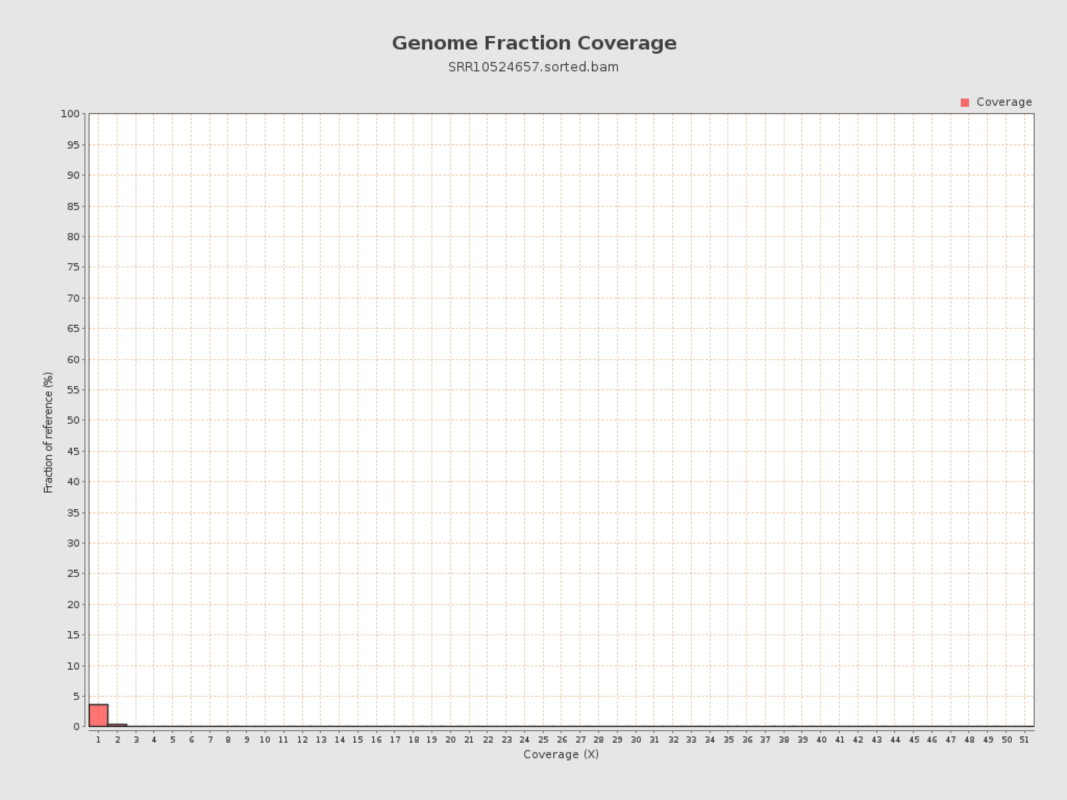
4. Results : Coverage Histogram



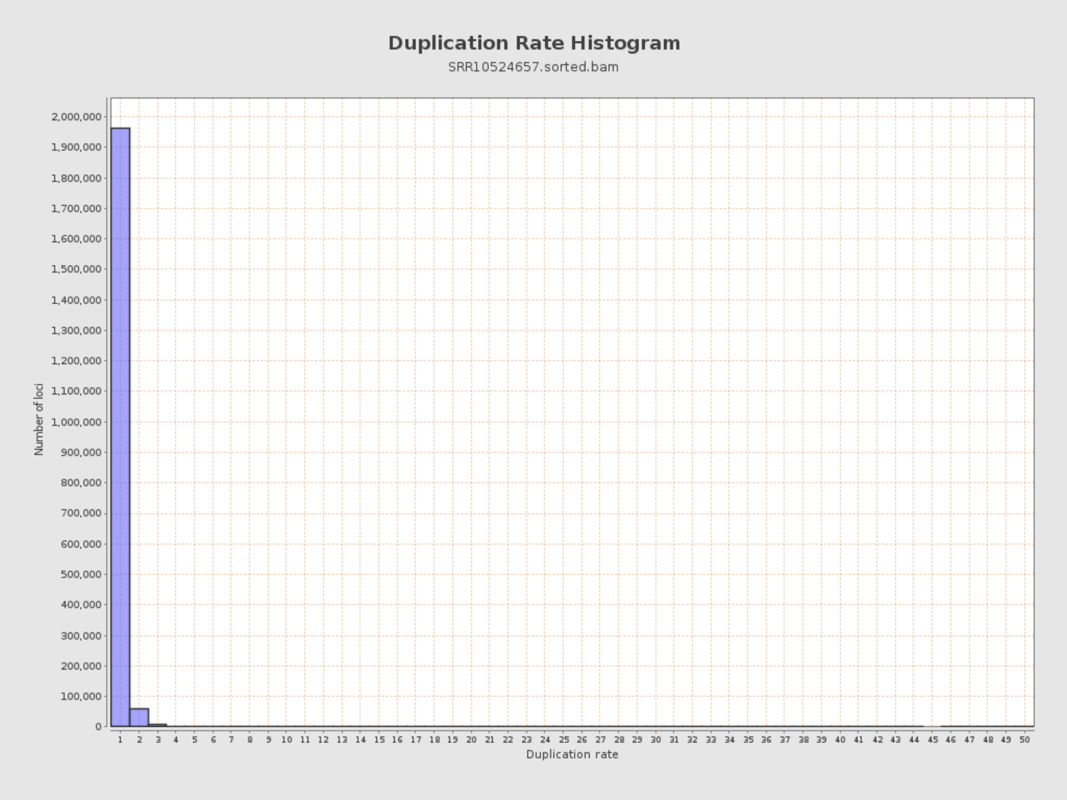
5. Results : Coverage Histogram (0-50X)



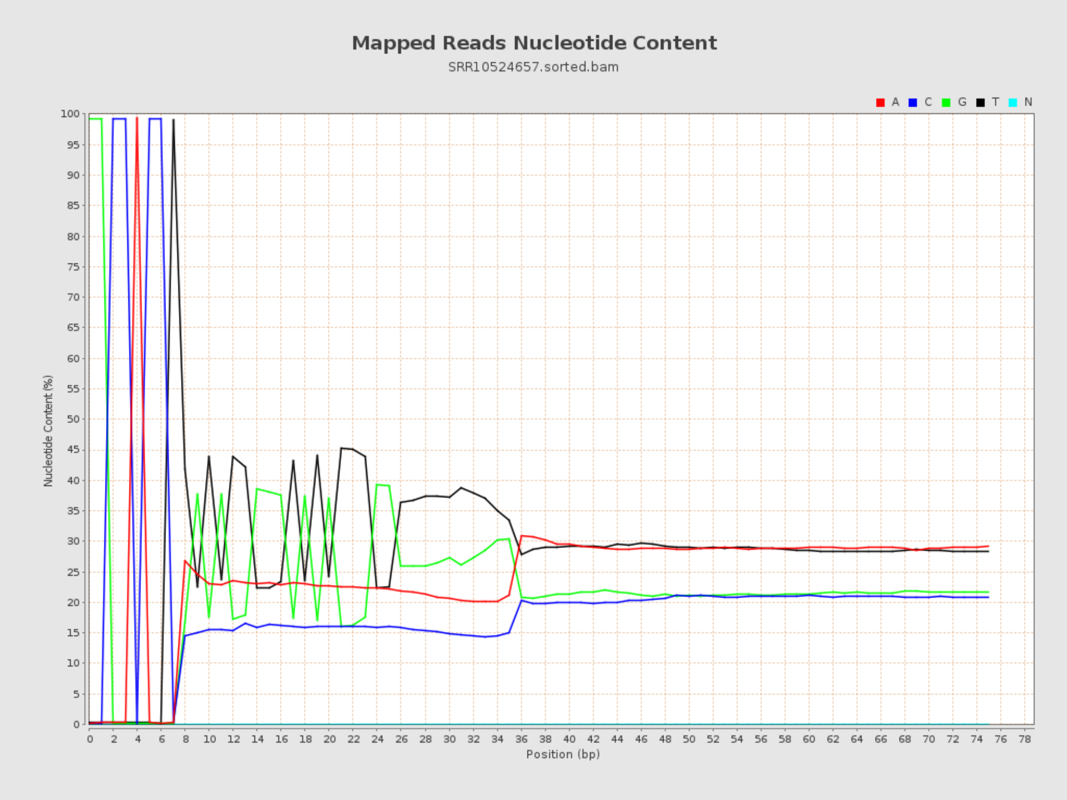
6. Results : Genome Fraction Coverage



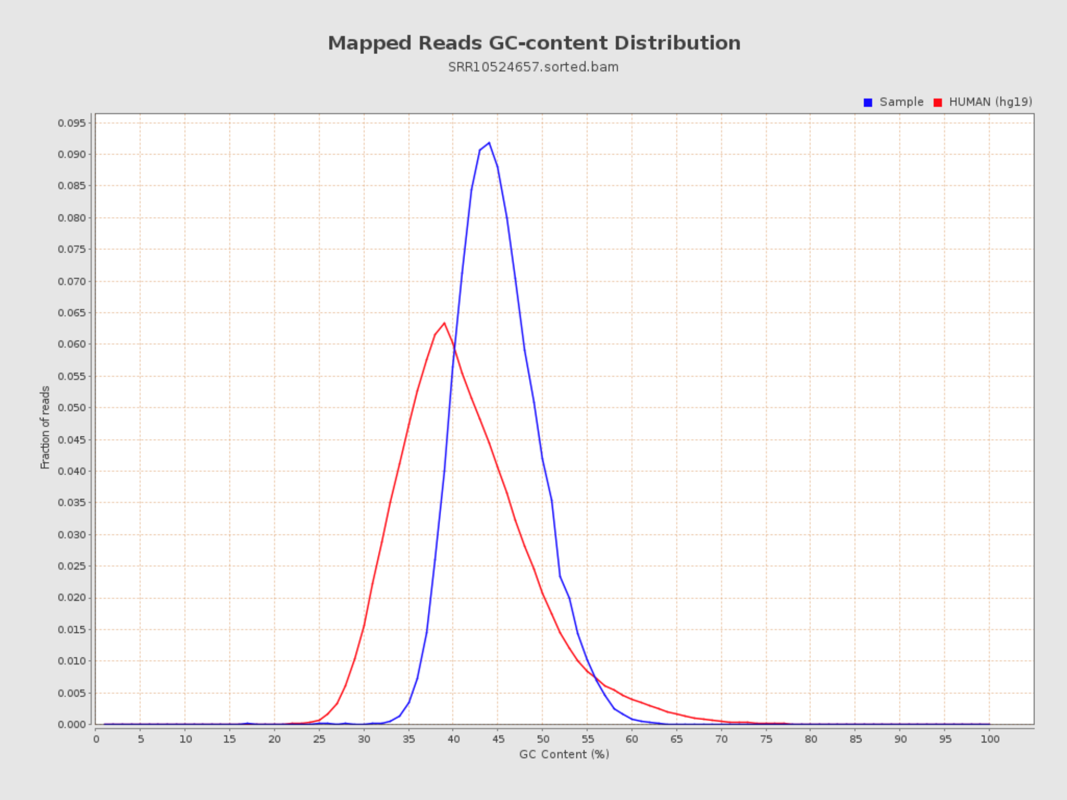
7. Results : Duplication Rate Histogram



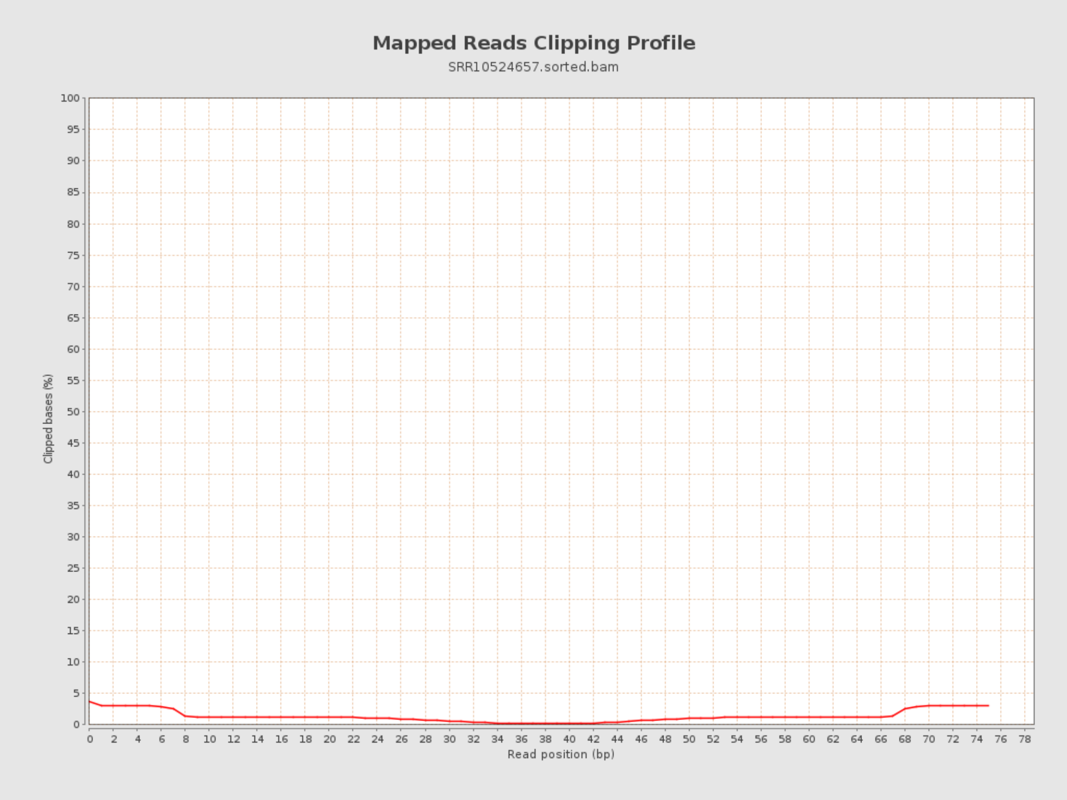
8. Results : Mapped Reads Nucleotide Content



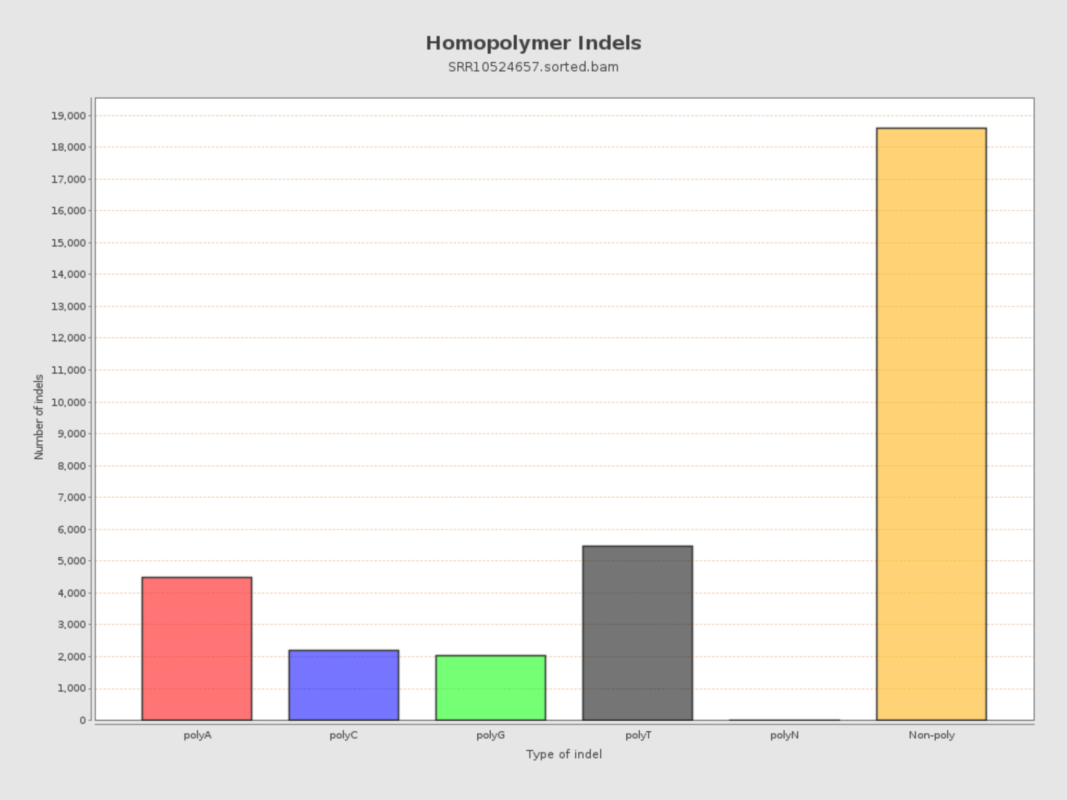
9. Results : Mapped Reads GC-content Distribution



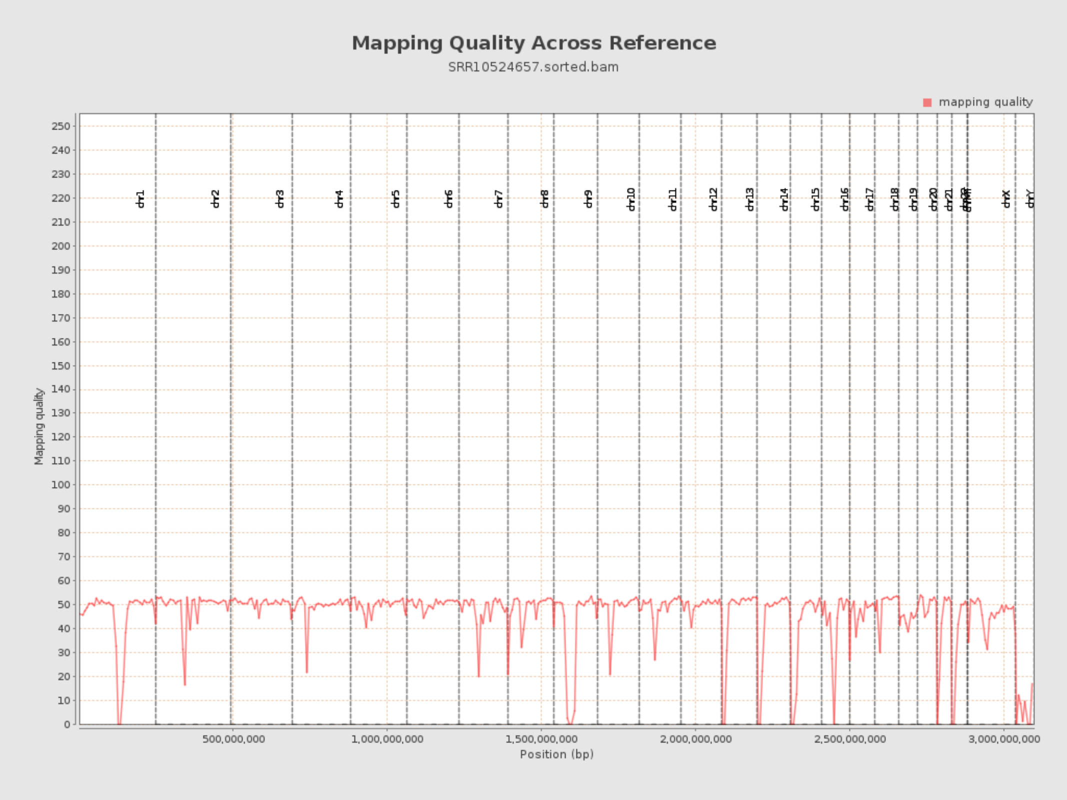
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram