Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:12:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524776.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_SRR10524776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524776.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:12:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,934,455
Mapped reads	1,765,409 / 91.26%
Unmapped reads	169,046 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,316 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	80,598 / 4.17%
Duplication rate	3.51%
Clipped reads	1,766,651 / 91.33%

2.2. ACGT Content

Number/percentage of A's	25,128,631 / 24.81%
Number/percentage of C's	19,629,801 / 19.38%
Number/percentage of T's	31,954,706 / 31.55%
Number/percentage of G's	24,560,346 / 24.25%
Number/percentage of N's	12,219 / 0.01%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.2806

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

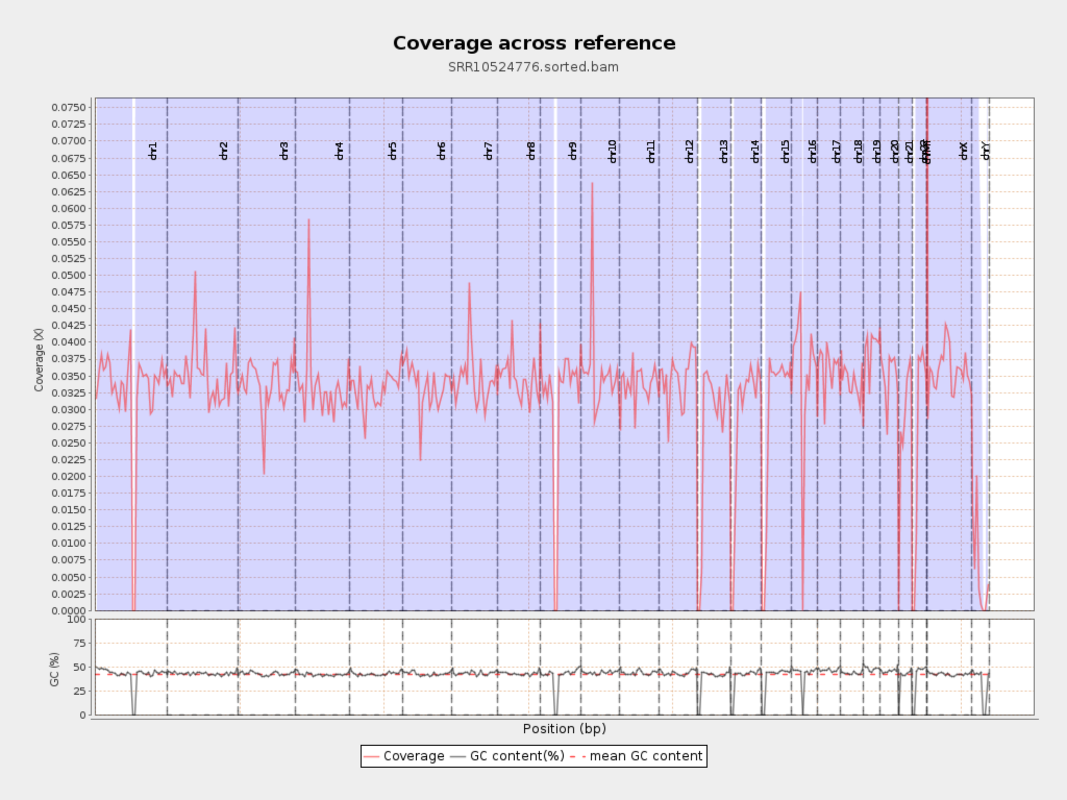
General error rate	0.52%
Mismatches	513,549
Insertions	8,197
Mapped reads with at least one insertion	0.46%
Deletions	20,324
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.78%

2.6. Chromosome stats

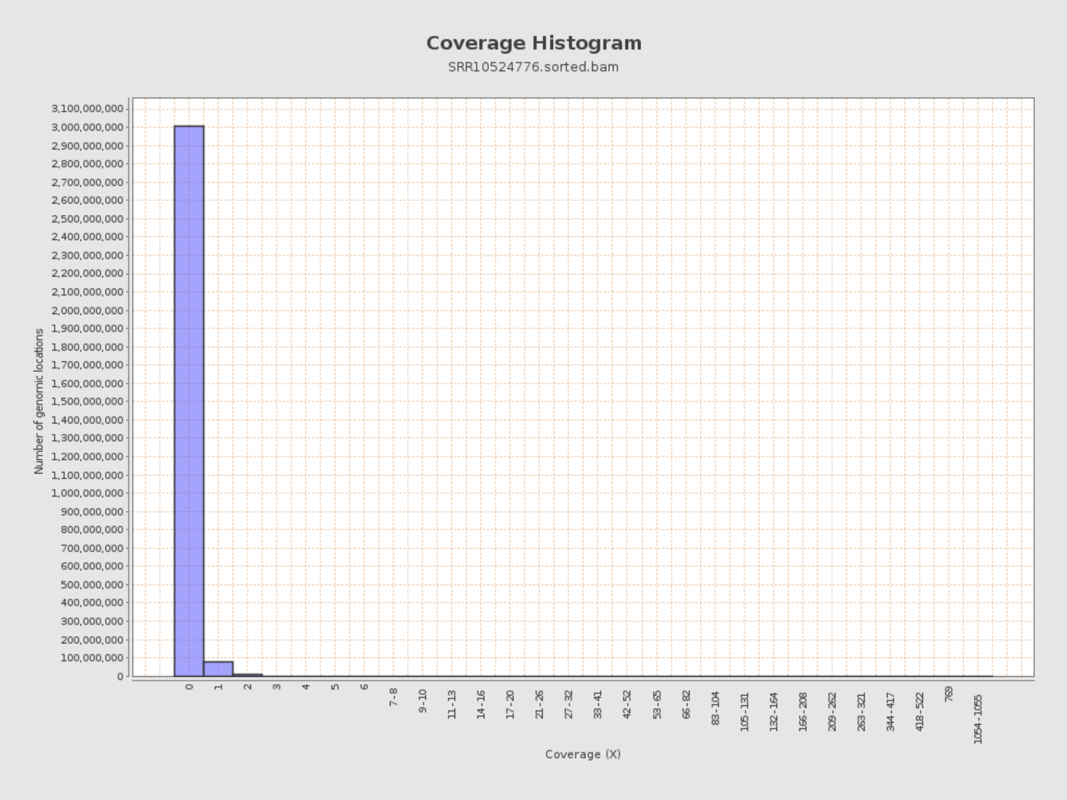
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8077224	0.0324	0.3701
chr2	243199373	8536864	0.0351	0.4848
chr3	198022430	6653500	0.0336	0.2088
chr4	191154276	6409282	0.0335	0.2333
chr5	180915260	5994809	0.0331	0.2044
chr6	171115067	5738607	0.0335	0.2291
chr7	159138663	5513388	0.0346	0.3292

chr8	146364022	5055405	0.0345	0.2569
chr9	141213431	4340292	0.0307	0.241
chr10	135534747	4850870	0.0358	0.314
chr11	135006516	4570817	0.0339	0.2521
chr12	133851895	4635991	0.0346	0.2148
chr13	115169878	3116364	0.0271	0.1857
chr14	107349540	3018743	0.0281	0.1918
chr15	102531392	2956313	0.0288	0.1937
chr16	90354753	3130938	0.0347	0.2292
chr17	81195210	2940807	0.0362	0.2243
chr18	78077248	2658806	0.0341	0.365
chr19	59128983	2294242	0.0388	0.3146
chr20	63025520	2202019	0.0349	0.2204
chr21	48129895	1353970	0.0281	0.208
chr22	51304566	1305745	0.0255	0.1817
chrMT	16571	44542	2.6879	2.2599
chrX	155270560	5574179	0.0359	0.2296
chrY	59373566	344835	0.0058	0.1602

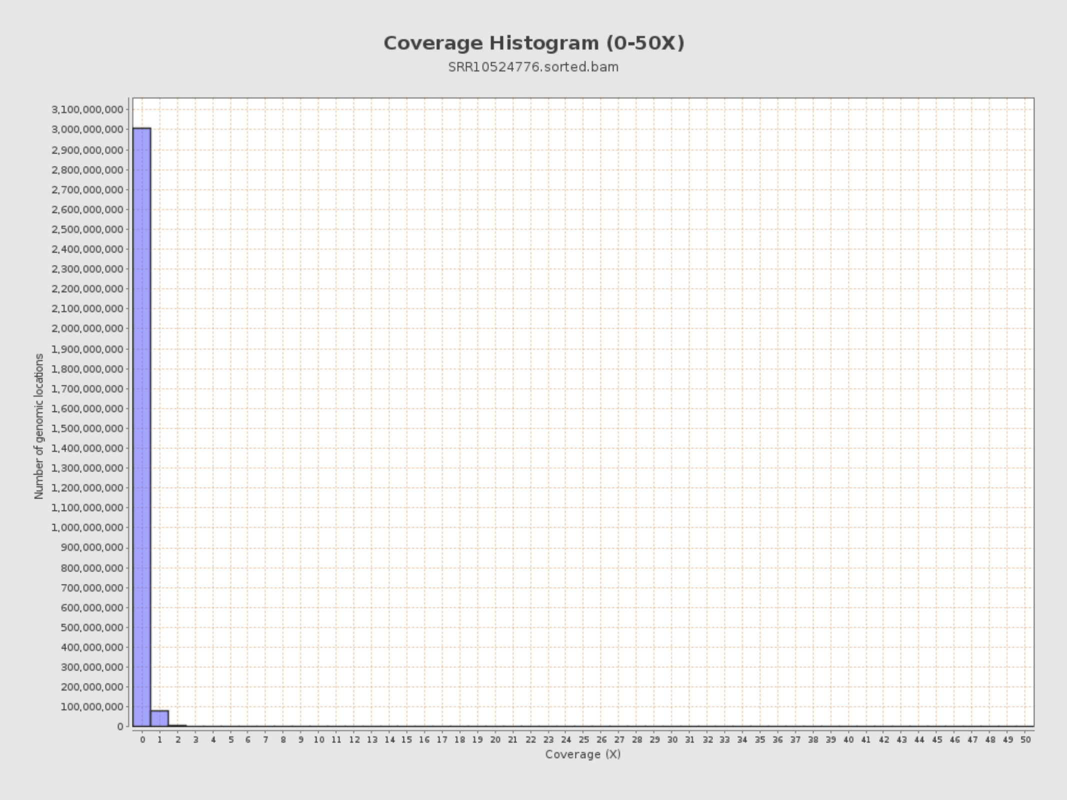
3. Results : Coverage across reference



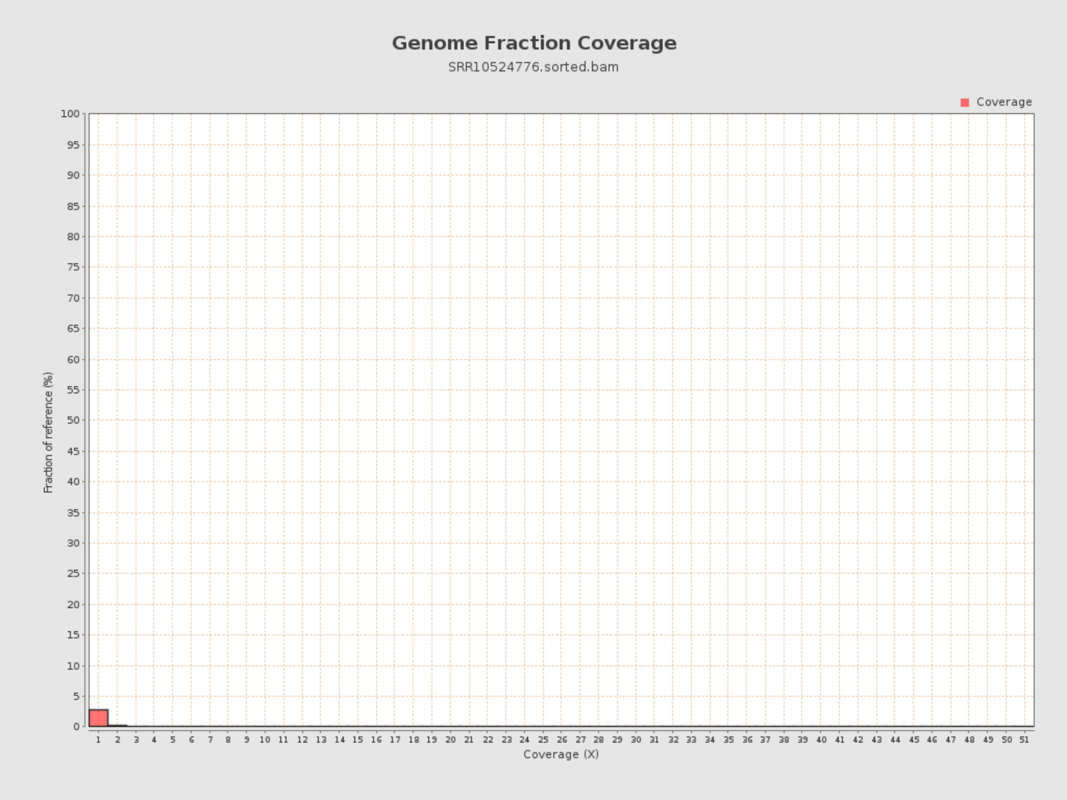
4. Results : Coverage Histogram



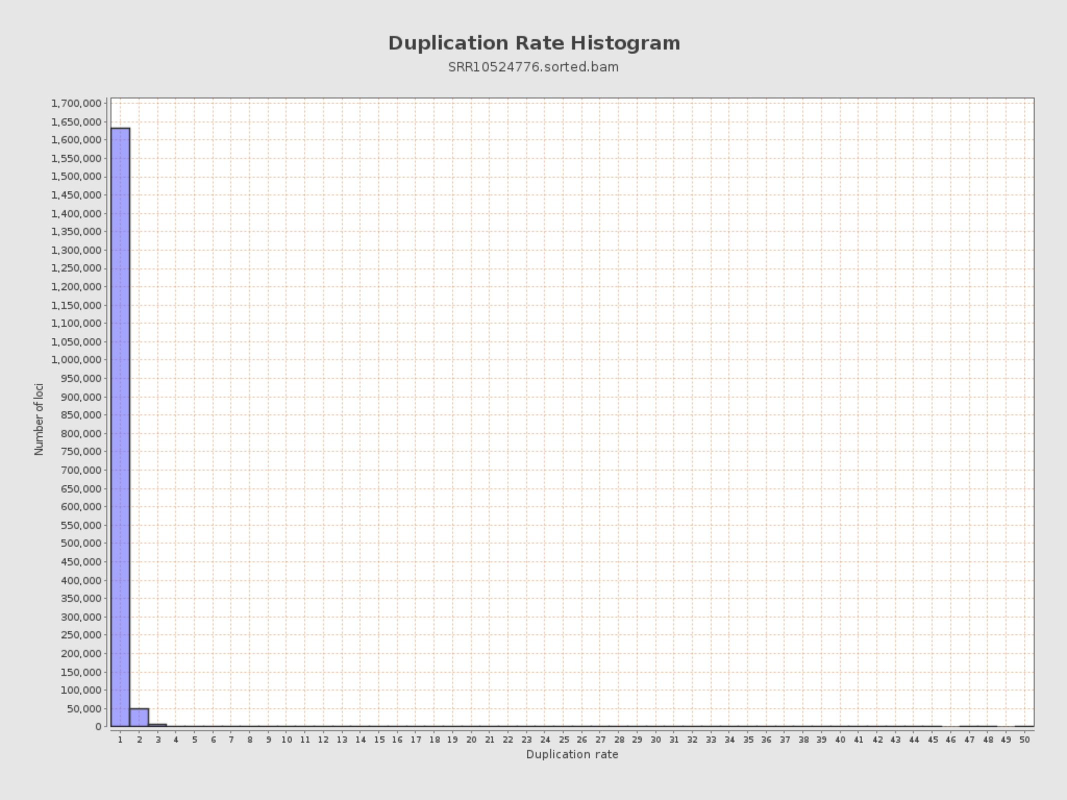
5. Results : Coverage Histogram (0-50X)



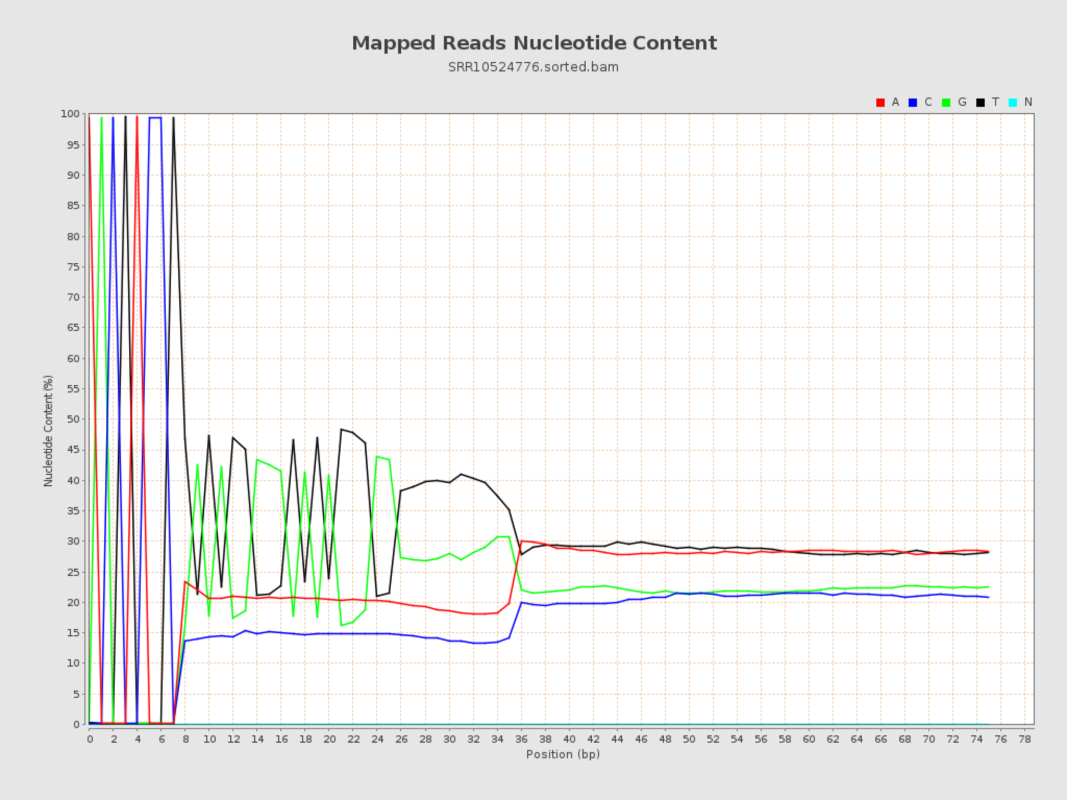
6. Results : Genome Fraction Coverage



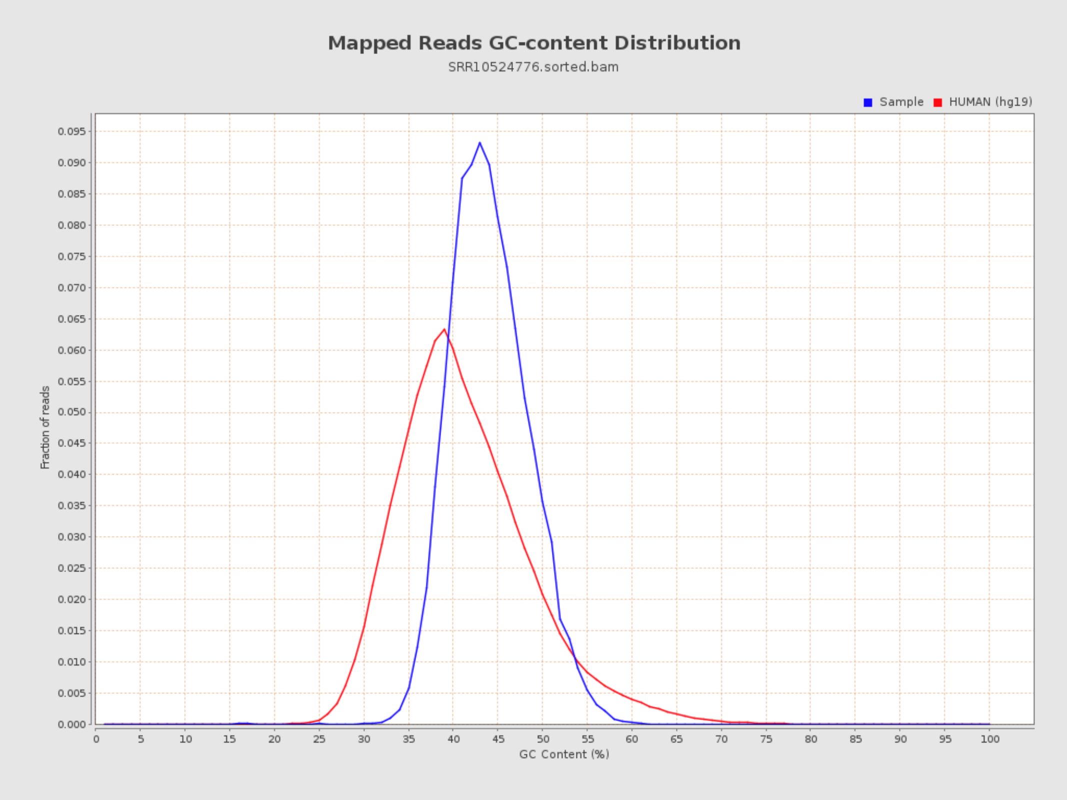
7. Results : Duplication Rate Histogram



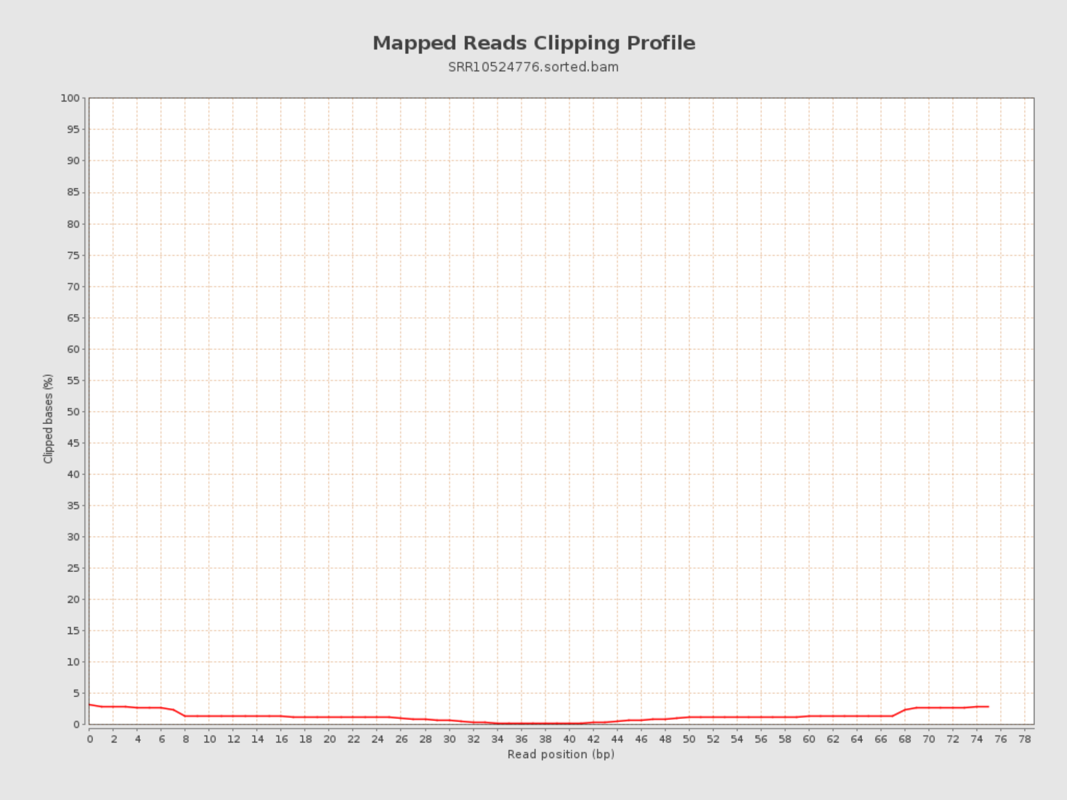
8. Results : Mapped Reads Nucleotide Content



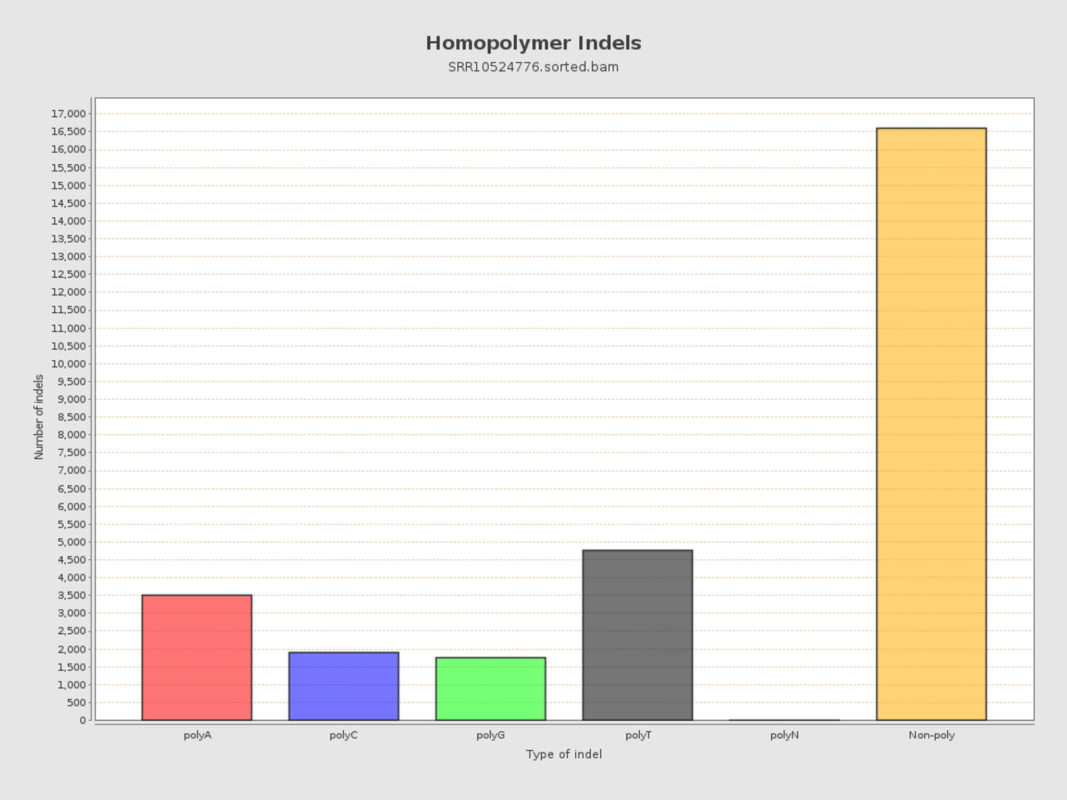
9. Results : Mapped Reads GC-content Distribution



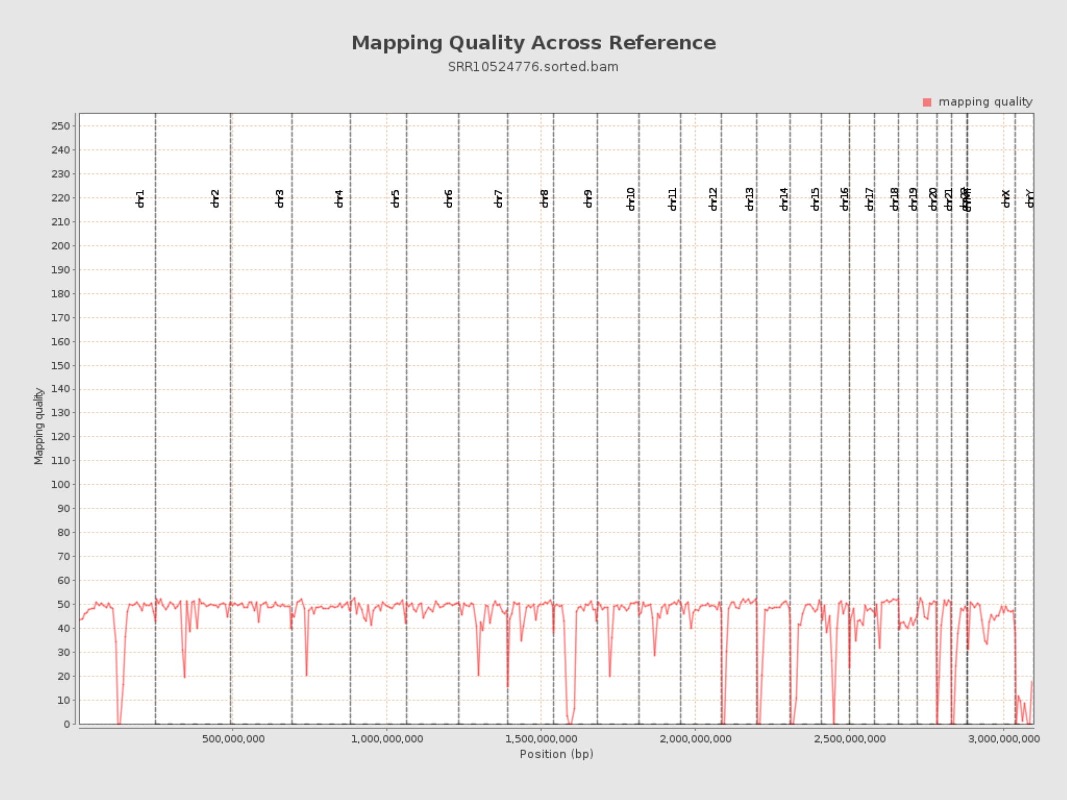
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram