Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:32:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524835.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_SRR10524835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:32:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,402,571
Mapped reads	1,288,138 / 91.84%
Unmapped reads	114,433 / 8.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,113 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	35,515 / 2.53%
Duplication rate	1.86%
Clipped reads	1,295,798 / 92.39%

2.2. ACGT Content

Number/percentage of A's	18,309,991 / 24.46%
Number/percentage of C's	14,935,256 / 19.95%
Number/percentage of T's	24,278,109 / 32.43%
Number/percentage of G's	17,322,251 / 23.14%
Number/percentage of N's	9,242 / 0.01%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2516

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

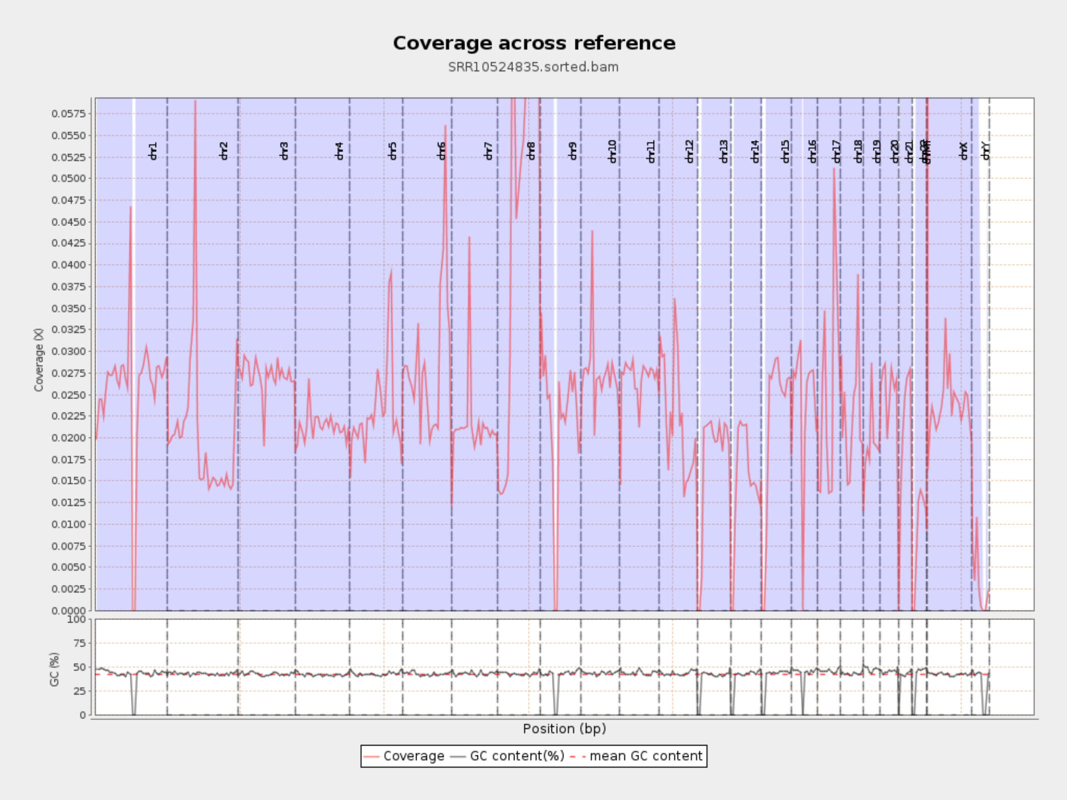
General error rate	0.5%
Mismatches	363,456
Insertions	4,409
Mapped reads with at least one insertion	0.34%
Deletions	13,854
Mapped reads with at least one deletion	1.07%
Homopolymer indels	45.28%

2.6. Chromosome stats

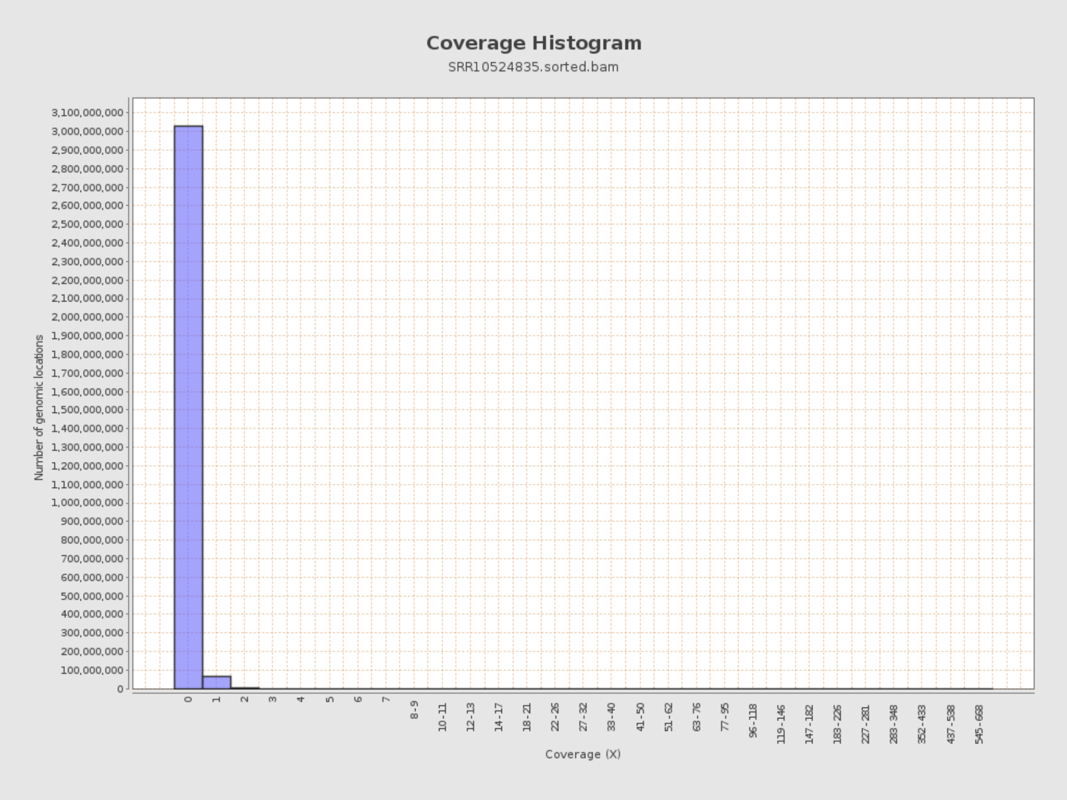
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6364081	0.0255	0.4906
chr2	243199373	4897797	0.0201	0.2434
chr3	198022430	5378632	0.0272	0.1746
chr4	191154276	4069098	0.0213	0.1639
chr5	180915260	4242460	0.0234	0.1627
chr6	171115067	4852947	0.0284	0.1924
chr7	159138663	3460558	0.0217	0.3542

chr8	146364022	8097087	0.0553	0.3367
chr9	141213431	3131006	0.0222	0.2135
chr10	135534747	3737796	0.0276	0.2351
chr11	135006516	3631308	0.0269	0.2204
chr12	133851895	2962940	0.0221	0.1608
chr13	115169878	1977813	0.0172	0.1392
chr14	107349540	1591747	0.0148	0.1352
chr15	102531392	2234652	0.0218	0.1583
chr16	90354753	2153068	0.0238	0.1756
chr17	81195210	2124981	0.0262	0.1902
chr18	78077248	1785979	0.0229	0.3473
chr19	59128983	1152972	0.0195	0.3323
chr20	63025520	1592429	0.0253	0.1692
chr21	48129895	984076	0.0204	0.1605
chr22	51304566	468549	0.0091	0.1001
chrMT	16571	79498	4.7974	3.4138
chrX	155270560	3717173	0.0239	0.1884
chrY	59373566	187858	0.0032	0.0886

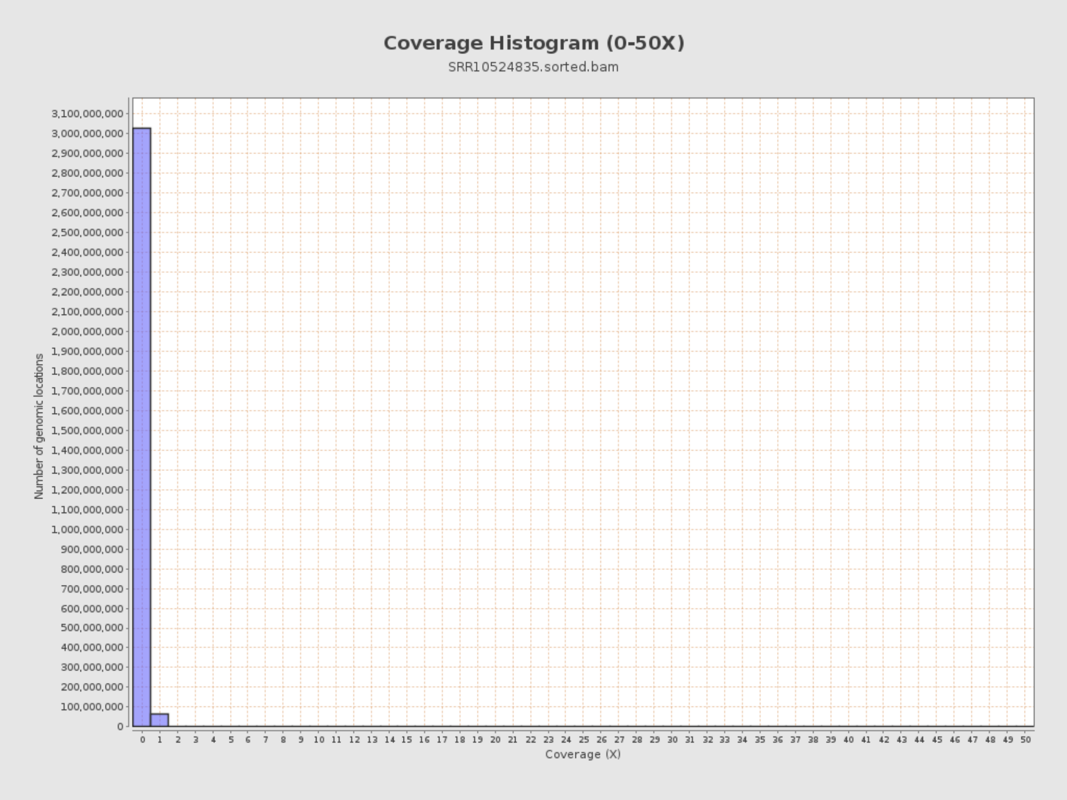
3. Results : Coverage across reference



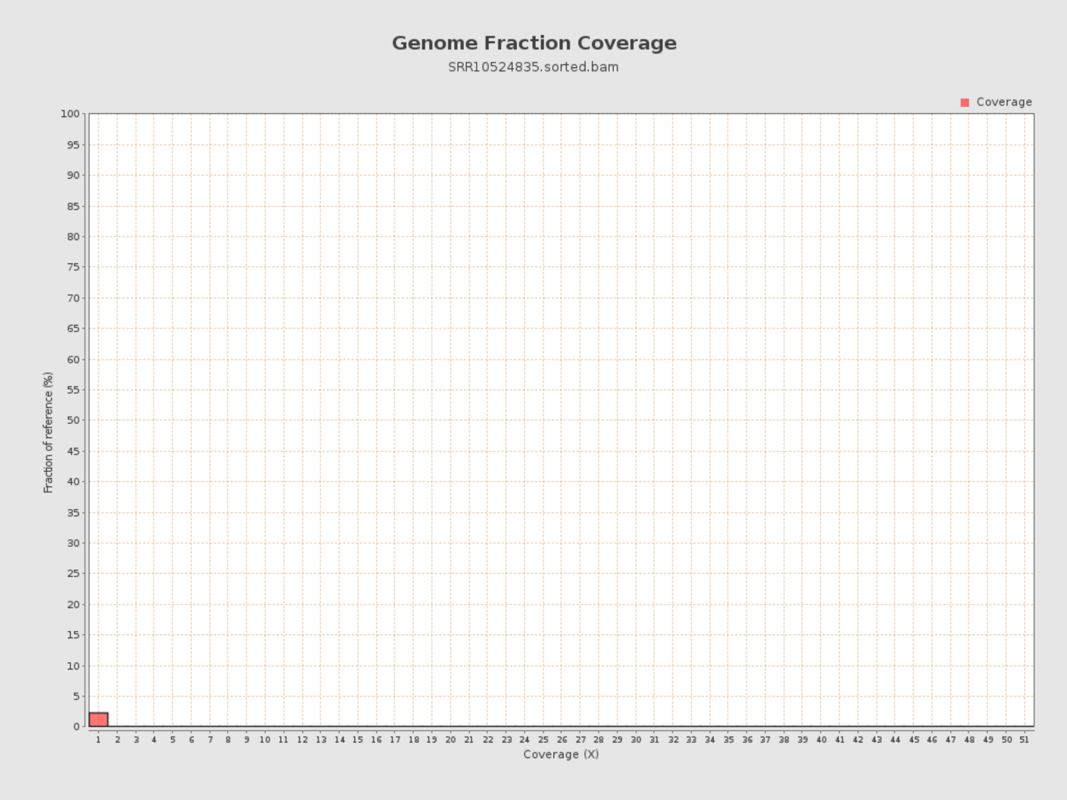
4. Results : Coverage Histogram



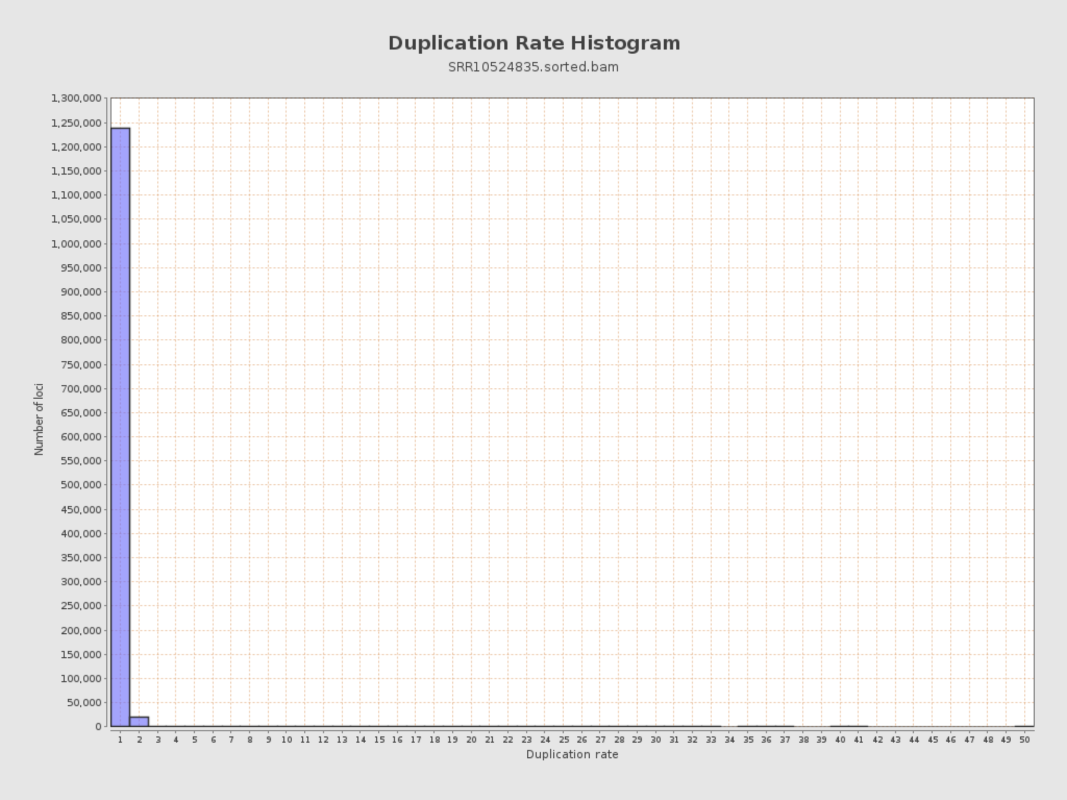
5. Results : Coverage Histogram (0-50X)



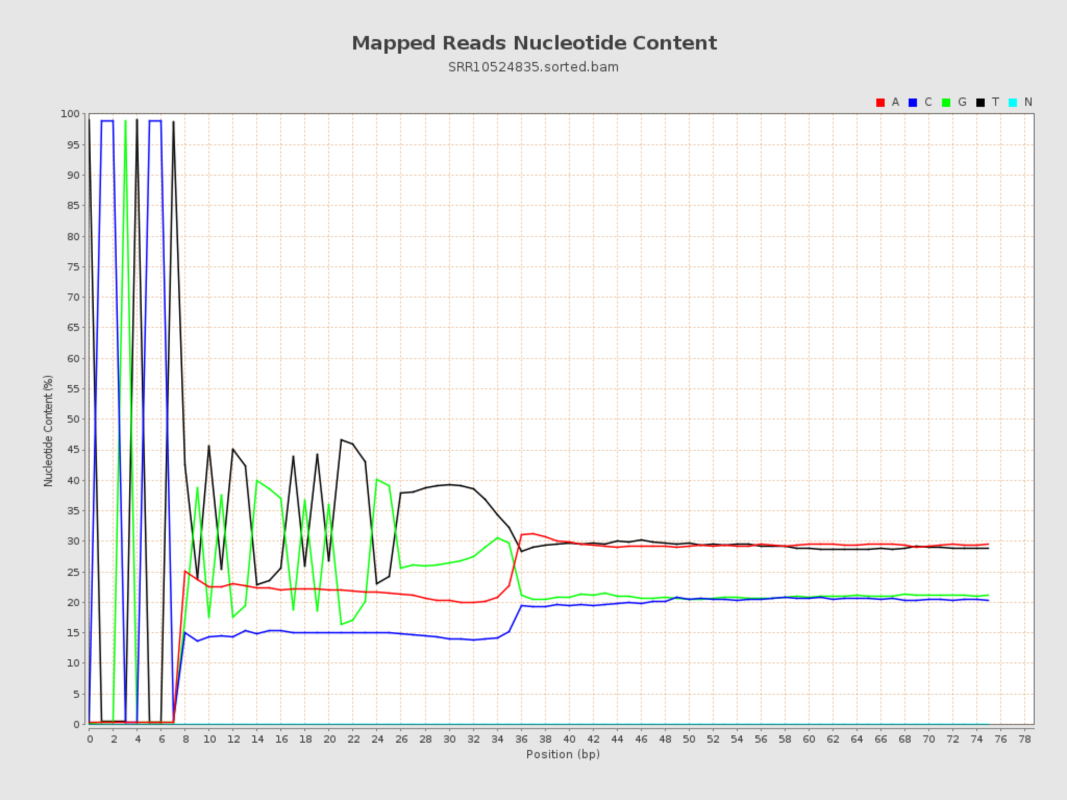
6. Results : Genome Fraction Coverage



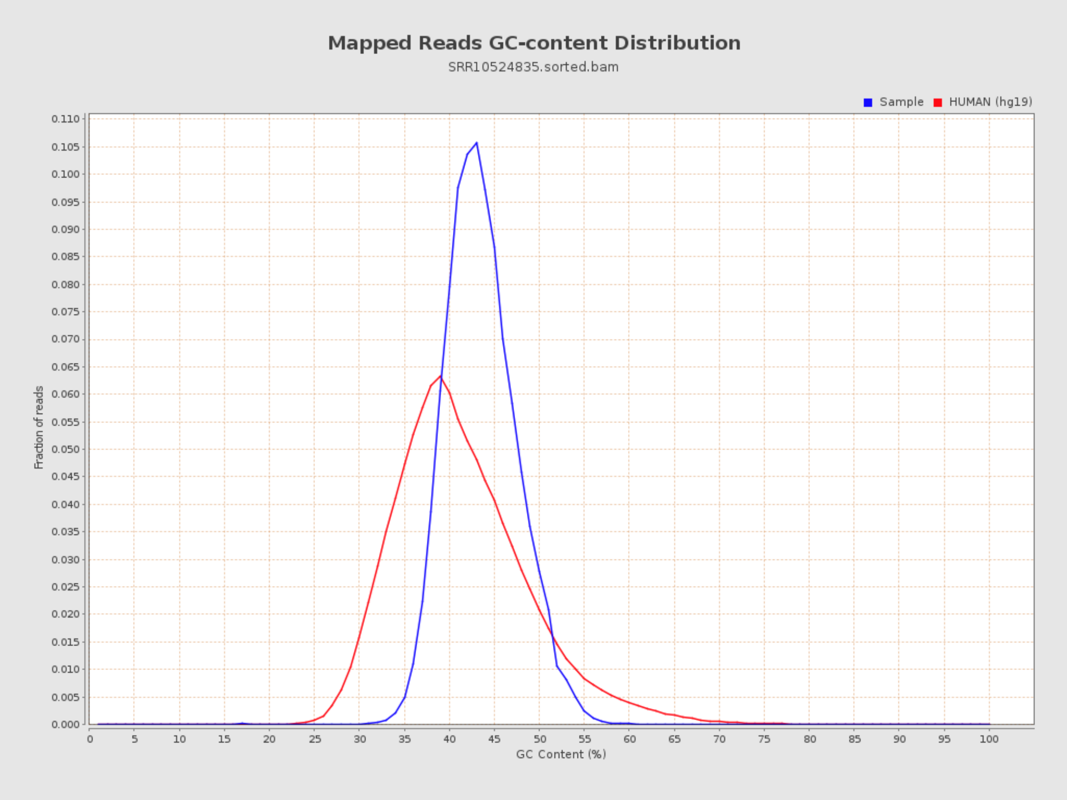
7. Results : Duplication Rate Histogram



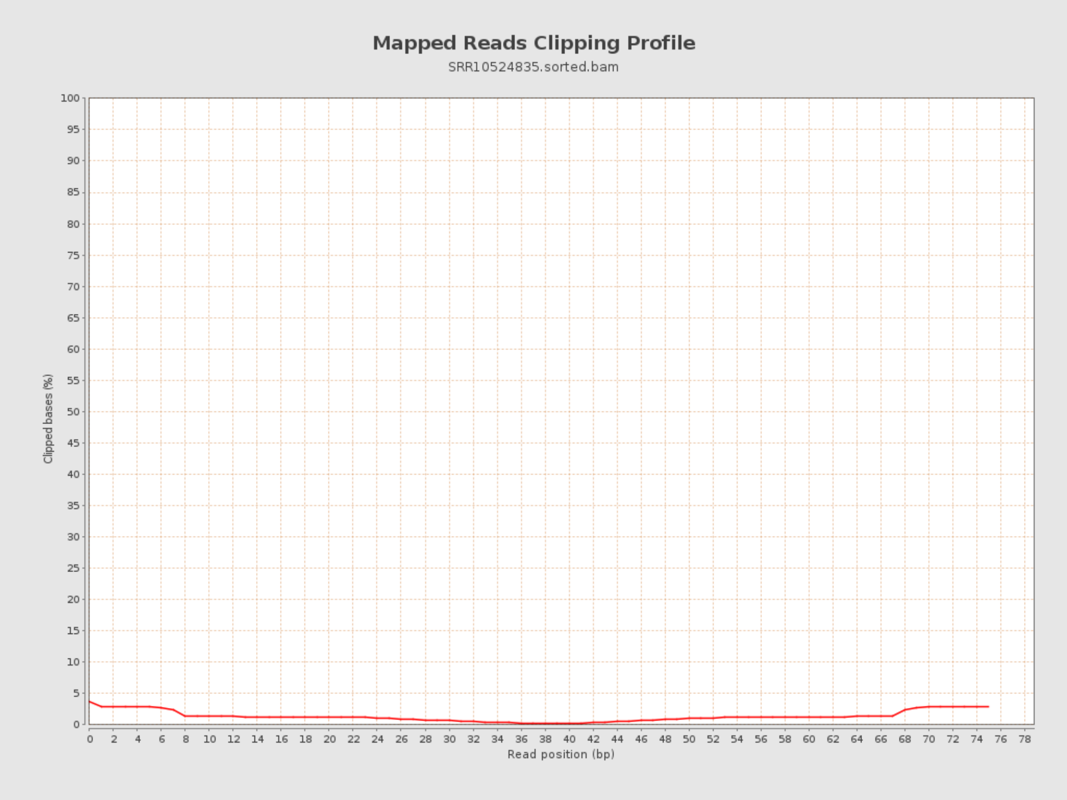
8. Results : Mapped Reads Nucleotide Content



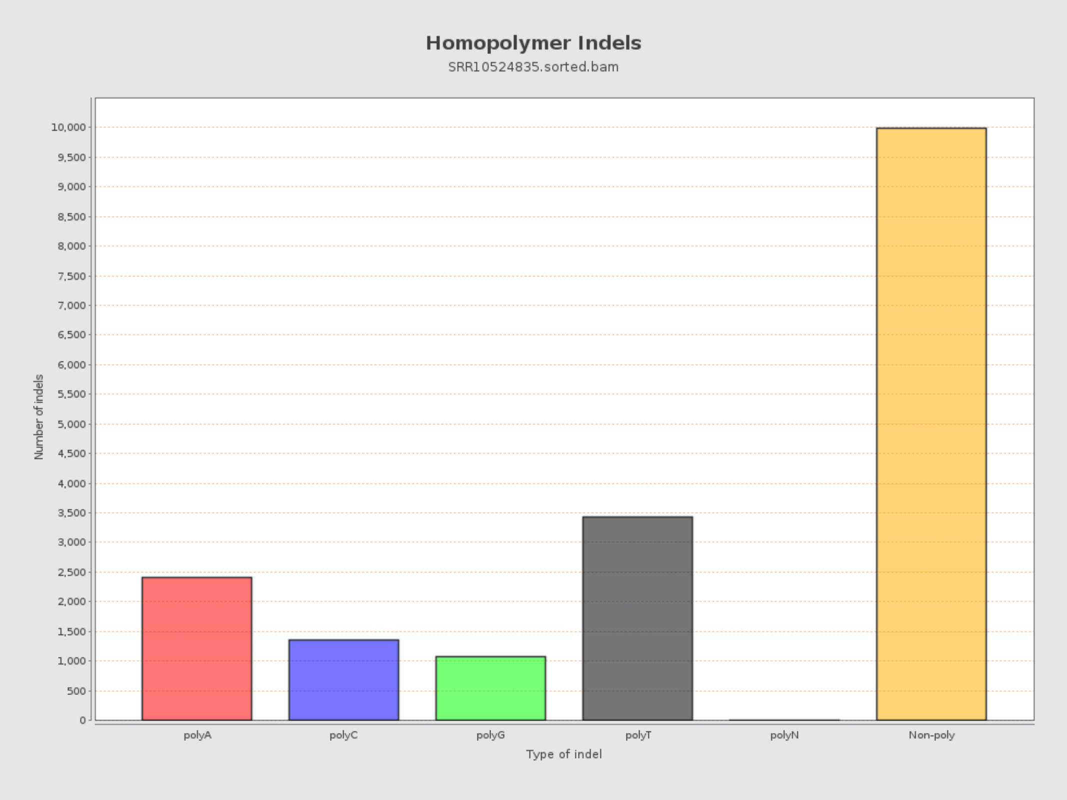
9. Results : Mapped Reads GC-content Distribution



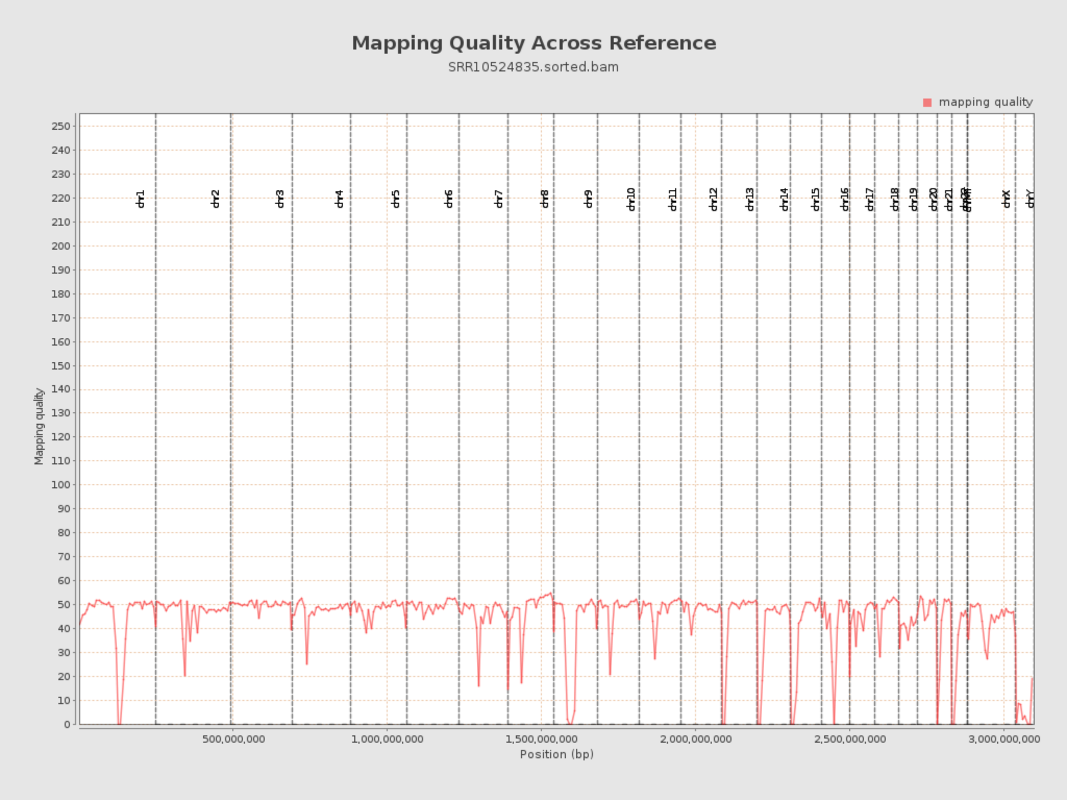
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram