Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:27:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524635.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_SRR10524635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524635.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:27:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,639,719
Mapped reads	1,518,916 / 92.63%
Unmapped reads	120,803 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,364 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	80,375 / 4.9%
Duplication rate	4.27%
Clipped reads	1,519,479 / 92.67%

2.2. ACGT Content

Number/percentage of A's	21,650,192 / 24.53%
Number/percentage of C's	16,338,942 / 18.51%
Number/percentage of T's	28,459,869 / 32.25%
Number/percentage of G's	21,807,212 / 24.71%
Number/percentage of N's	522 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2485

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

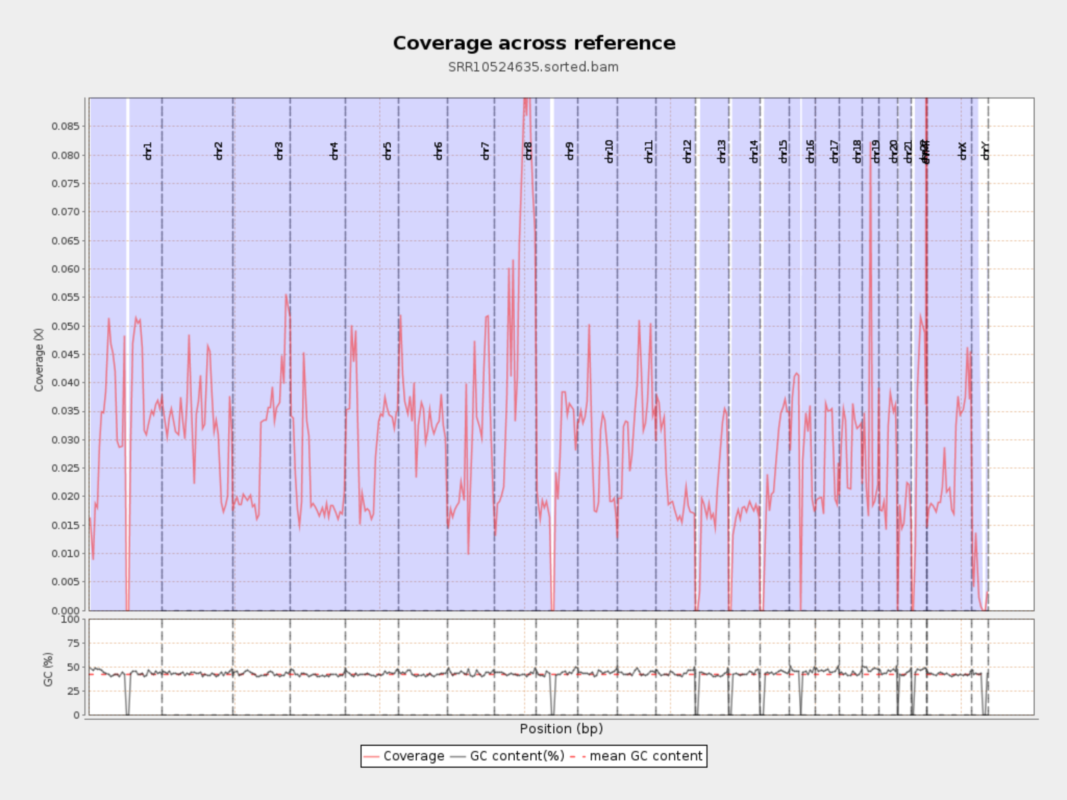
General error rate	0.48%
Mismatches	411,301
Insertions	5,672
Mapped reads with at least one insertion	0.37%
Deletions	16,461
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.12%

2.6. Chromosome stats

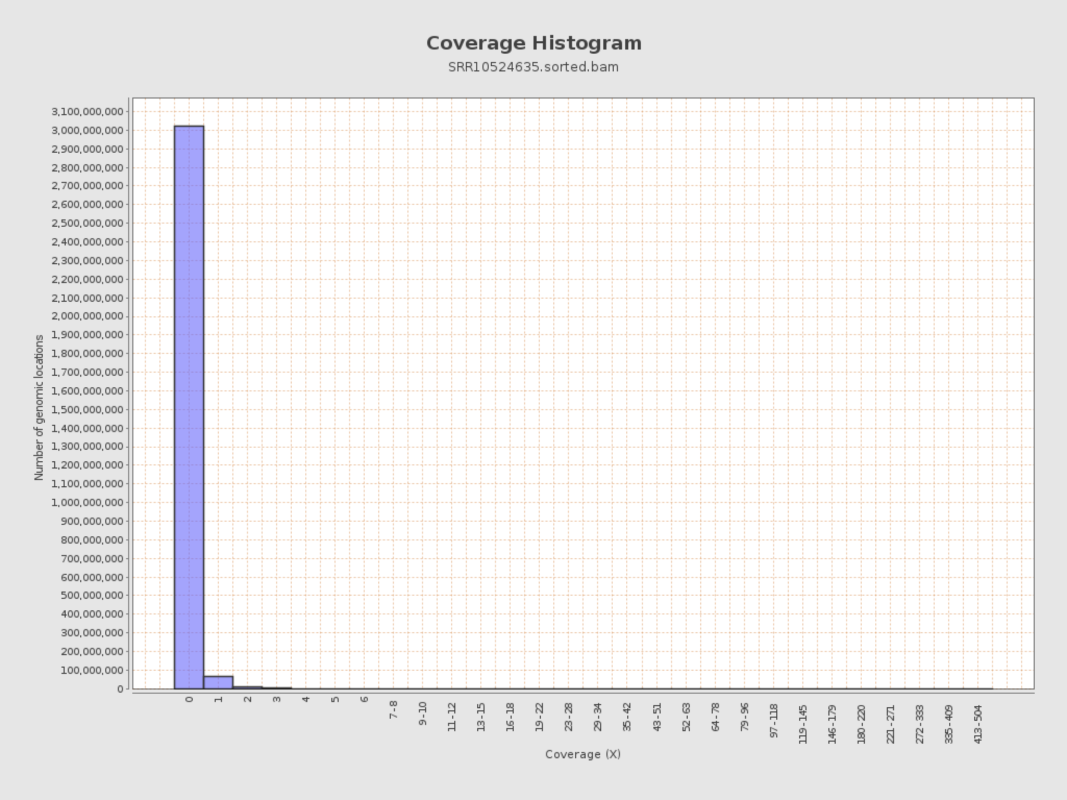
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8334862	0.0334	0.4021
chr2	243199373	8027636	0.033	0.291
chr3	198022430	5826716	0.0294	0.1958
chr4	191154276	4089620	0.0214	0.1938
chr5	180915260	5550345	0.0307	0.1995
chr6	171115067	5925261	0.0346	0.2263
chr7	159138663	4544085	0.0286	0.297

chr8	146364022	7786403	0.0532	0.3389
chr9	141213431	3345308	0.0237	0.2136
chr10	135534747	3829223	0.0283	0.253
chr11	135006516	4538921	0.0336	0.2465
chr12	133851895	2961839	0.0221	0.1735
chr13	115169878	2199432	0.0191	0.1571
chr14	107349540	1629510	0.0152	0.1455
chr15	102531392	2385650	0.0233	0.1823
chr16	90354753	2673760	0.0296	0.2028
chr17	81195210	2083600	0.0257	0.1883
chr18	78077248	2364478	0.0303	0.3268
chr19	59128983	1806817	0.0306	0.2874
chr20	63025520	1679071	0.0266	0.1887
chr21	48129895	794430	0.0165	0.1614
chr22	51304566	1620709	0.0316	0.2037
chrMT	16571	4471	0.2698	0.5718
chrX	155270560	4057420	0.0261	0.2022
chrY	59373566	225917	0.0038	0.1114

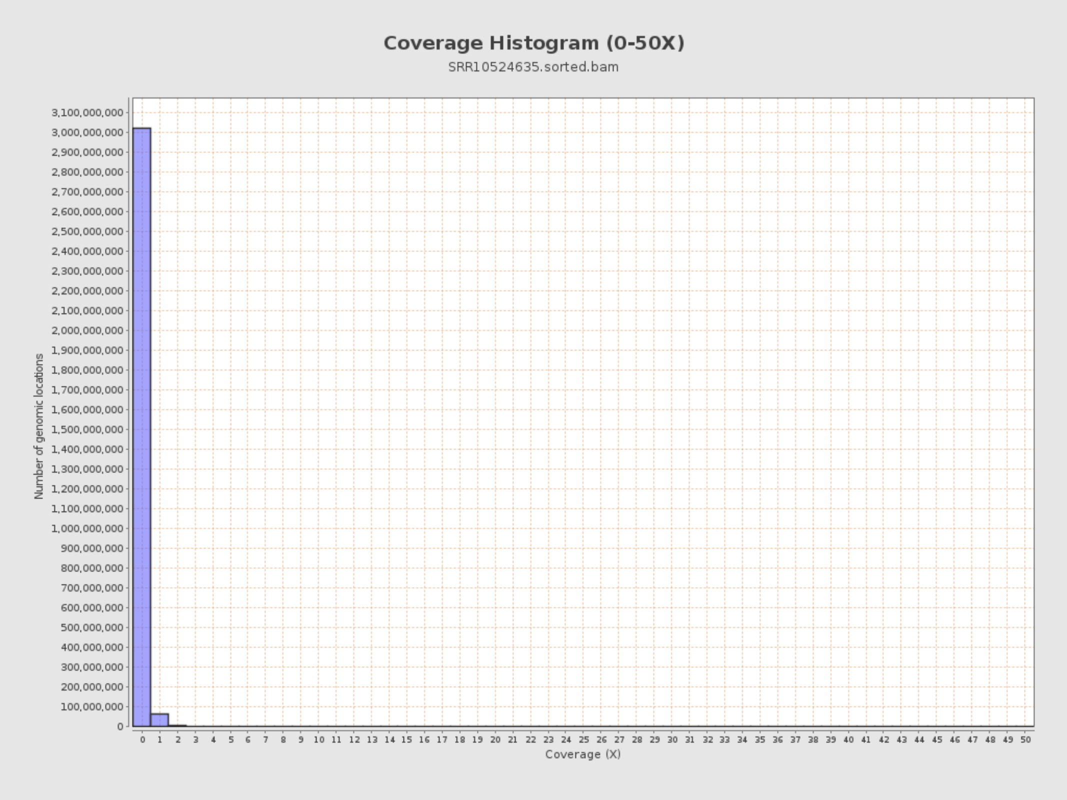
3. Results : Coverage across reference



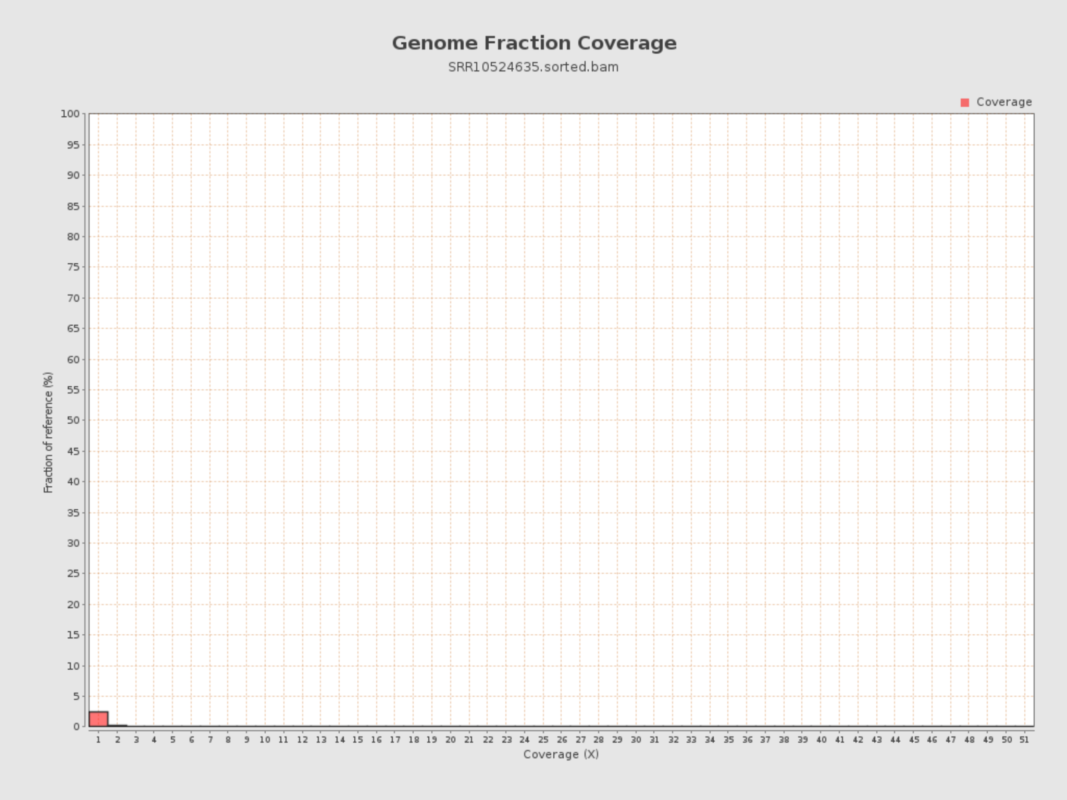
4. Results : Coverage Histogram



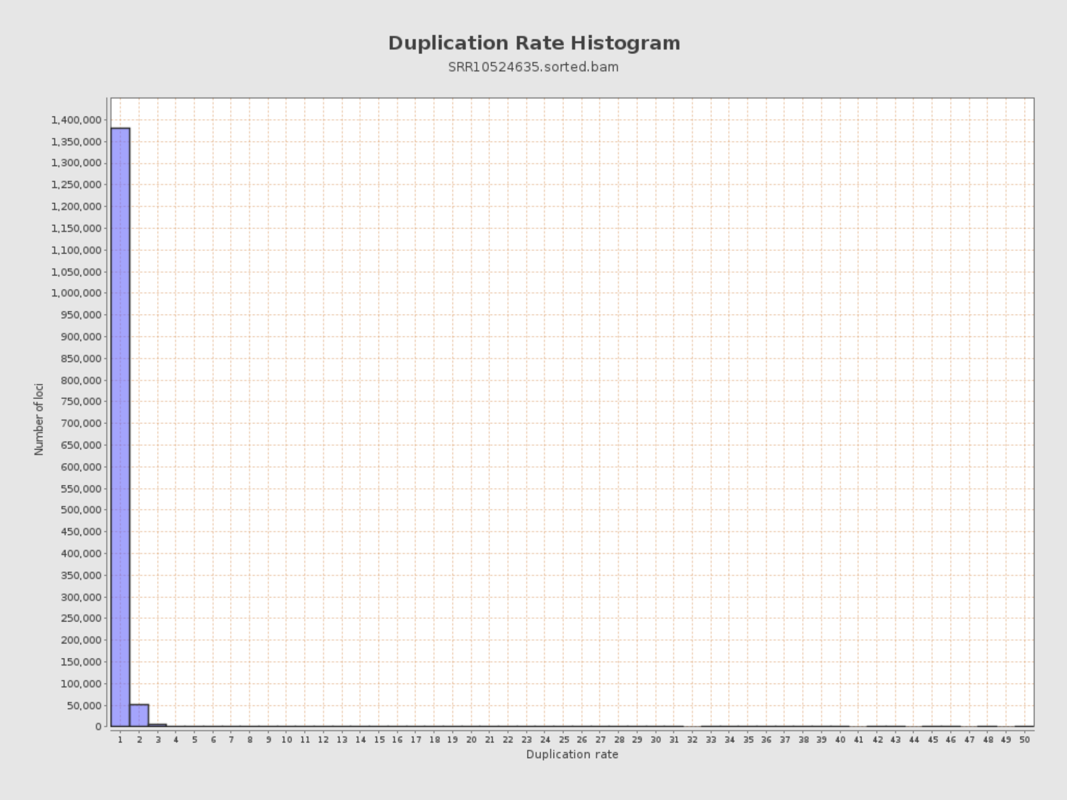
5. Results : Coverage Histogram (0-50X)



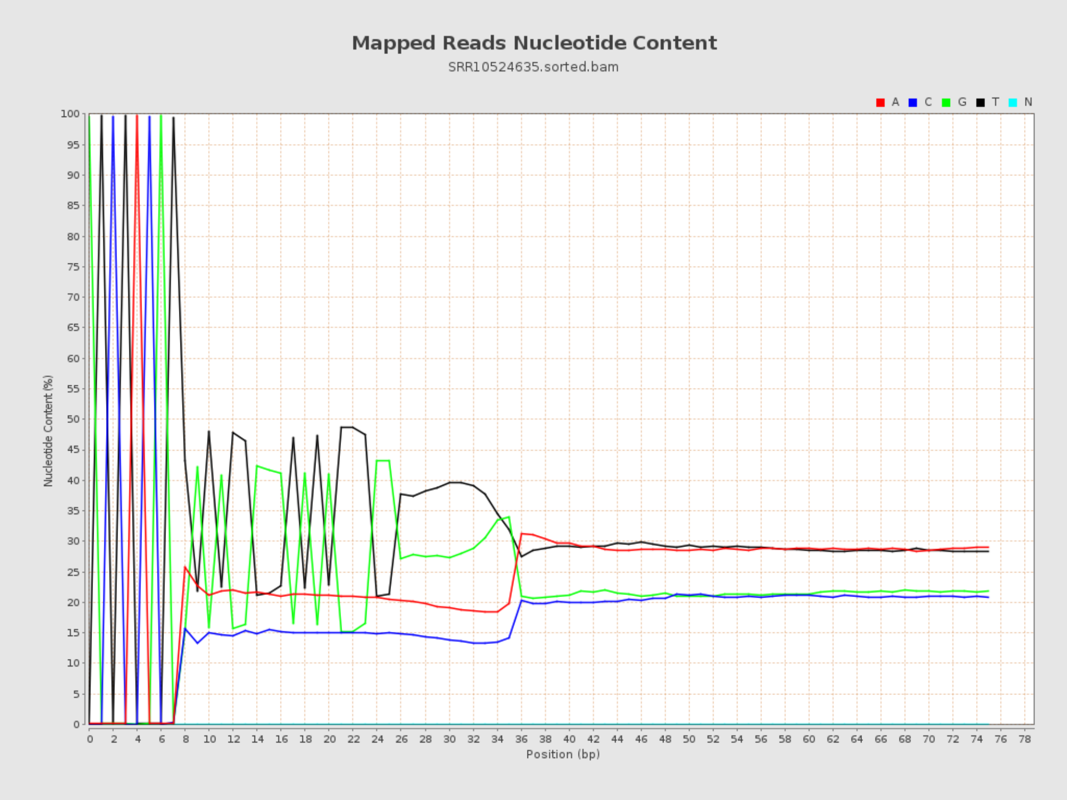
6. Results : Genome Fraction Coverage



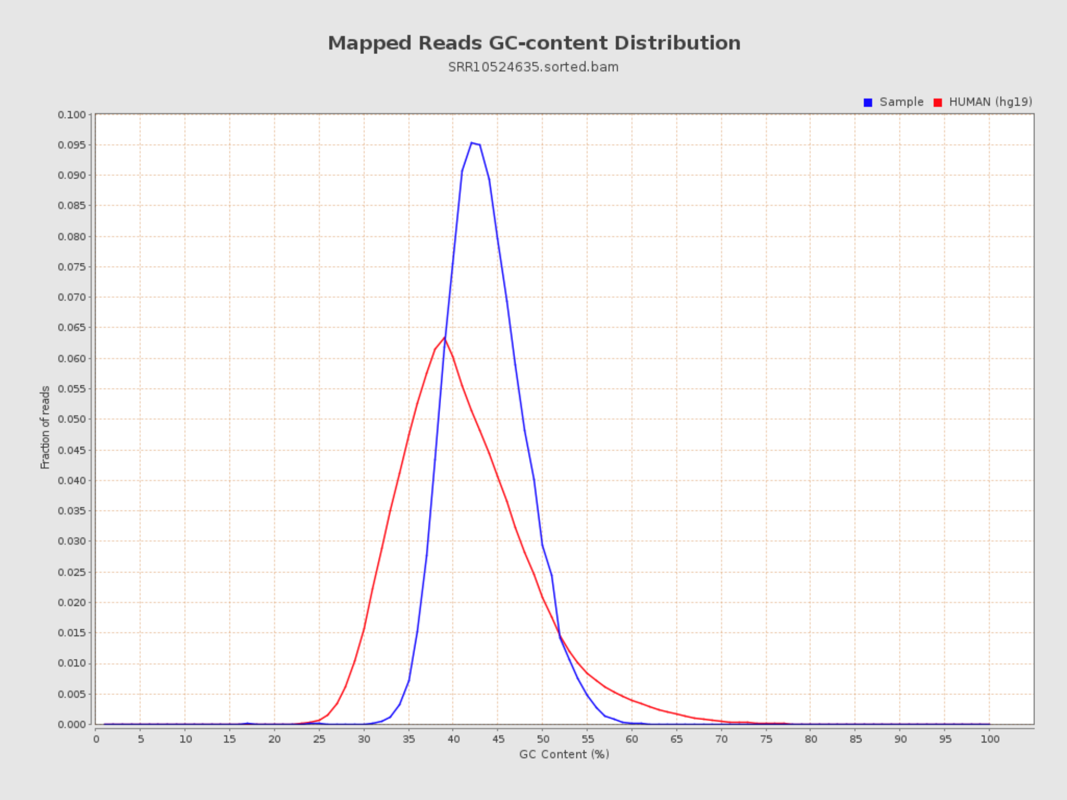
7. Results : Duplication Rate Histogram



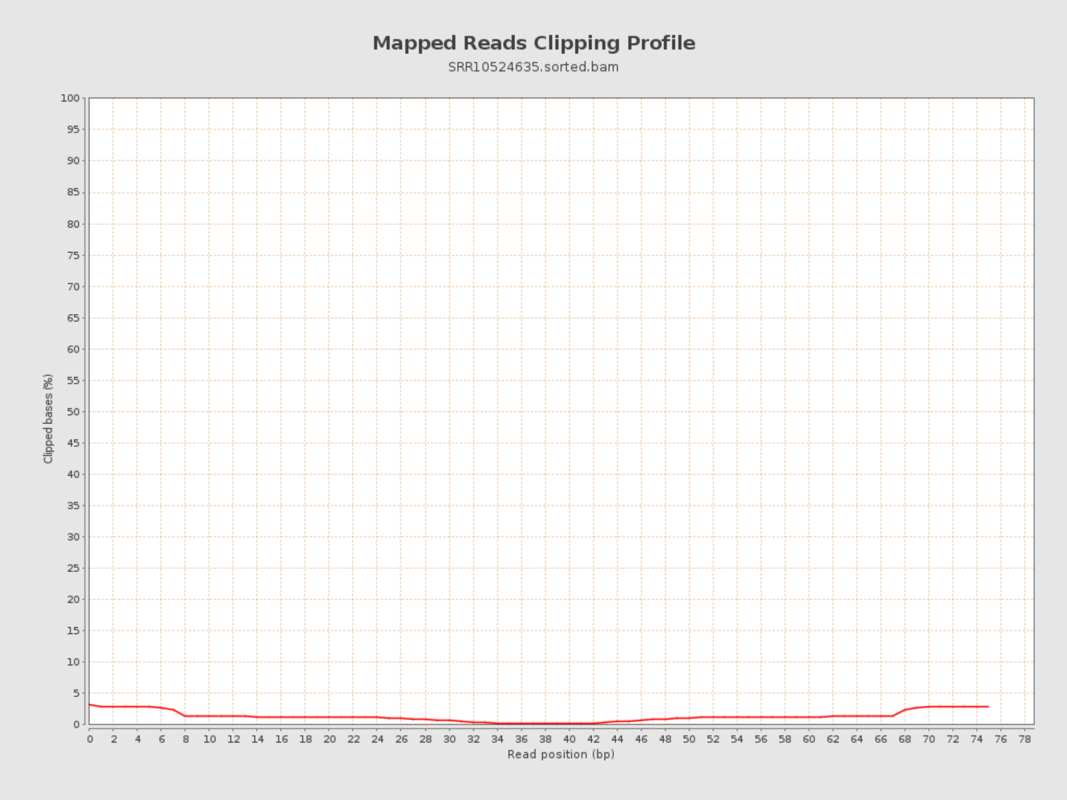
8. Results : Mapped Reads Nucleotide Content



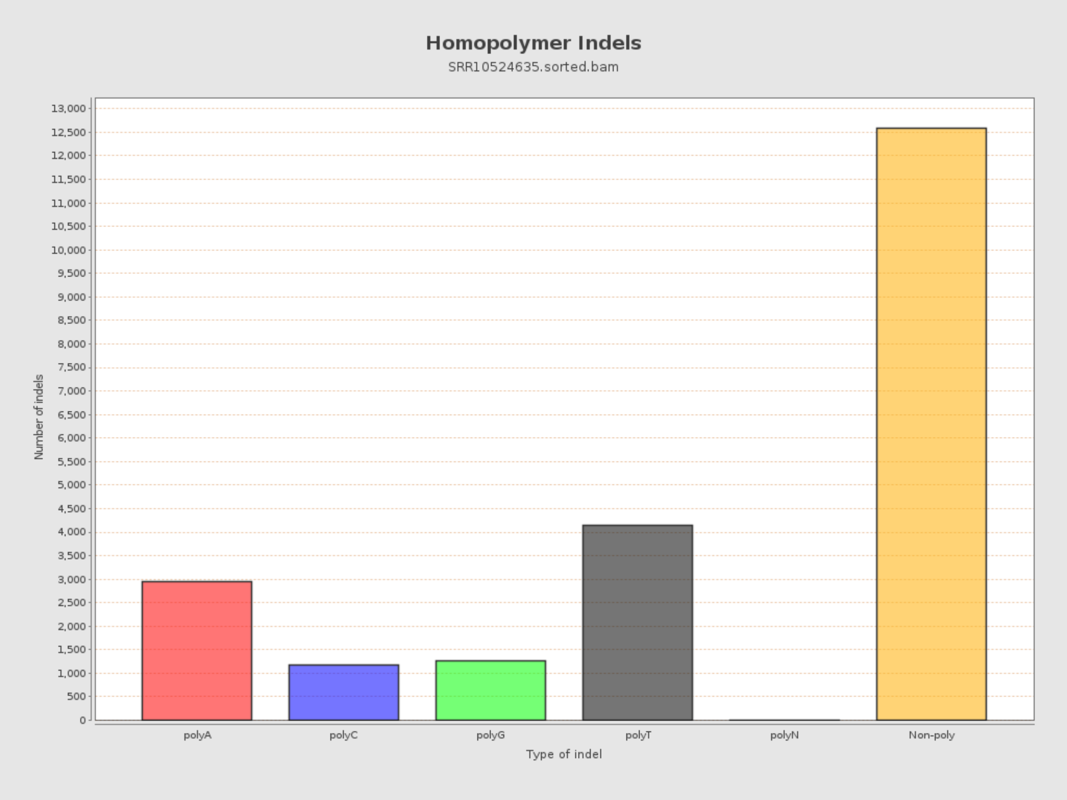
9. Results : Mapped Reads GC-content Distribution



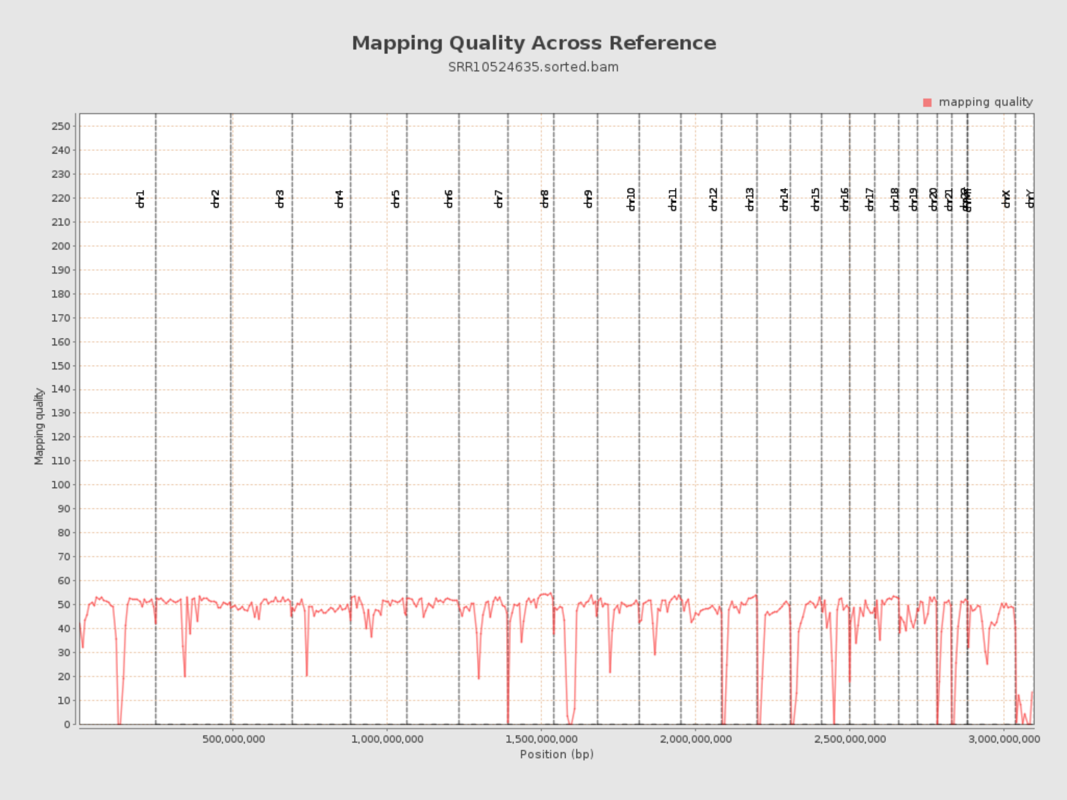
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram