Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:41:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524839.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_SRR10524839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524839.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:41:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	935,738
Mapped reads	865,860 / 92.53%
Unmapped reads	69,878 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,927 / 0.63%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	19,116 / 2.04%
Duplication rate	1.51%
Clipped reads	867,844 / 92.74%

2.2. ACGT Content

Number/percentage of A's	13,943,039 / 27.49%
Number/percentage of C's	8,705,782 / 17.17%
Number/percentage of T's	16,168,203 / 31.88%
Number/percentage of G's	11,890,688 / 23.45%
Number/percentage of N's	6,329 / 0.01%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.1817

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

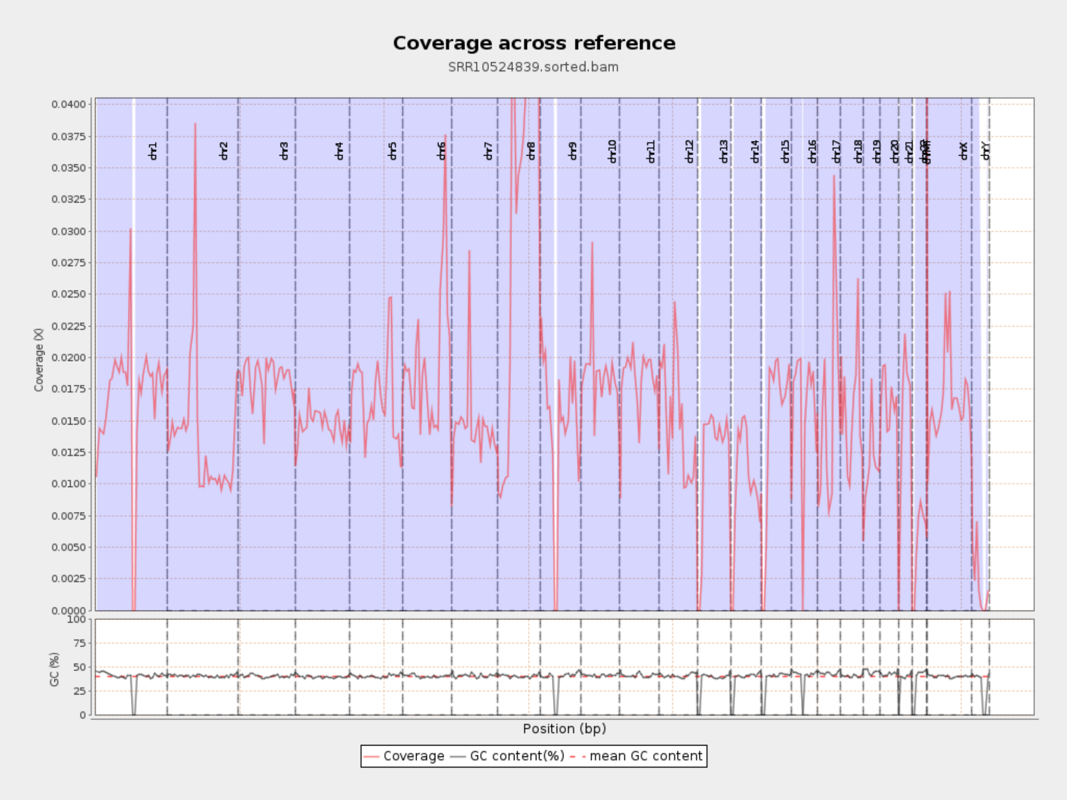
General error rate	0.5%
Mismatches	243,028
Insertions	4,636
Mapped reads with at least one insertion	0.53%
Deletions	9,491
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.99%

2.6. Chromosome stats

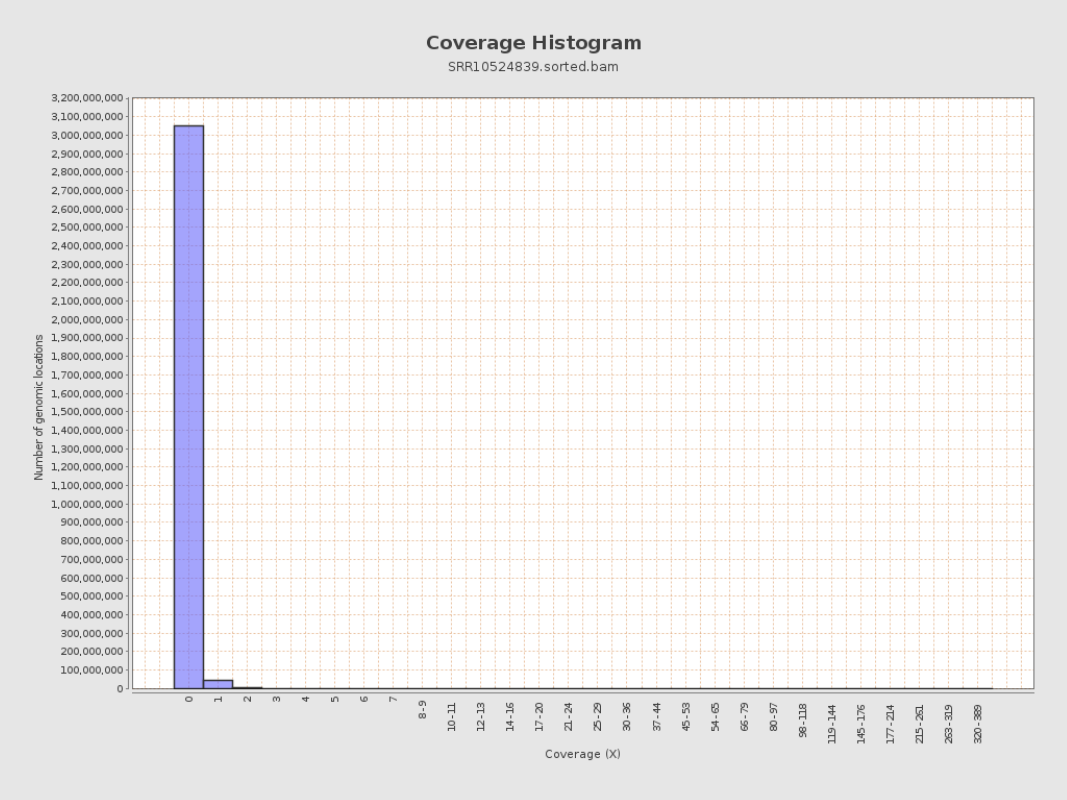
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4190882	0.0168	0.3152
chr2	243199373	3313831	0.0136	0.174
chr3	198022430	3645627	0.0184	0.1413
chr4	191154276	2803658	0.0147	0.1317
chr5	180915260	3079934	0.017	0.1361
chr6	171115067	3318566	0.0194	0.1549
chr7	159138663	2340049	0.0147	0.2385

chr8	146364022	5535872	0.0378	0.2593
chr9	141213431	2096803	0.0148	0.1622
chr10	135534747	2531530	0.0187	0.1797
chr11	135006516	2482754	0.0184	0.1711
chr12	133851895	2004473	0.015	0.1286
chr13	115169878	1371012	0.0119	0.1144
chr14	107349540	1064202	0.0099	0.1085
chr15	102531392	1519851	0.0148	0.1277
chr16	90354753	1423084	0.0157	0.1375
chr17	81195210	1310770	0.0161	0.1402
chr18	78077248	1237288	0.0158	0.2689
chr19	59128983	687862	0.0116	0.2167
chr20	63025520	1029766	0.0163	0.1345
chr21	48129895	724424	0.0151	0.1329
chr22	51304566	282538	0.0055	0.0771
chrMT	16571	800	0.0483	0.2144
chrX	155270560	2607393	0.0168	0.1477
chrY	59373566	125891	0.0021	0.062

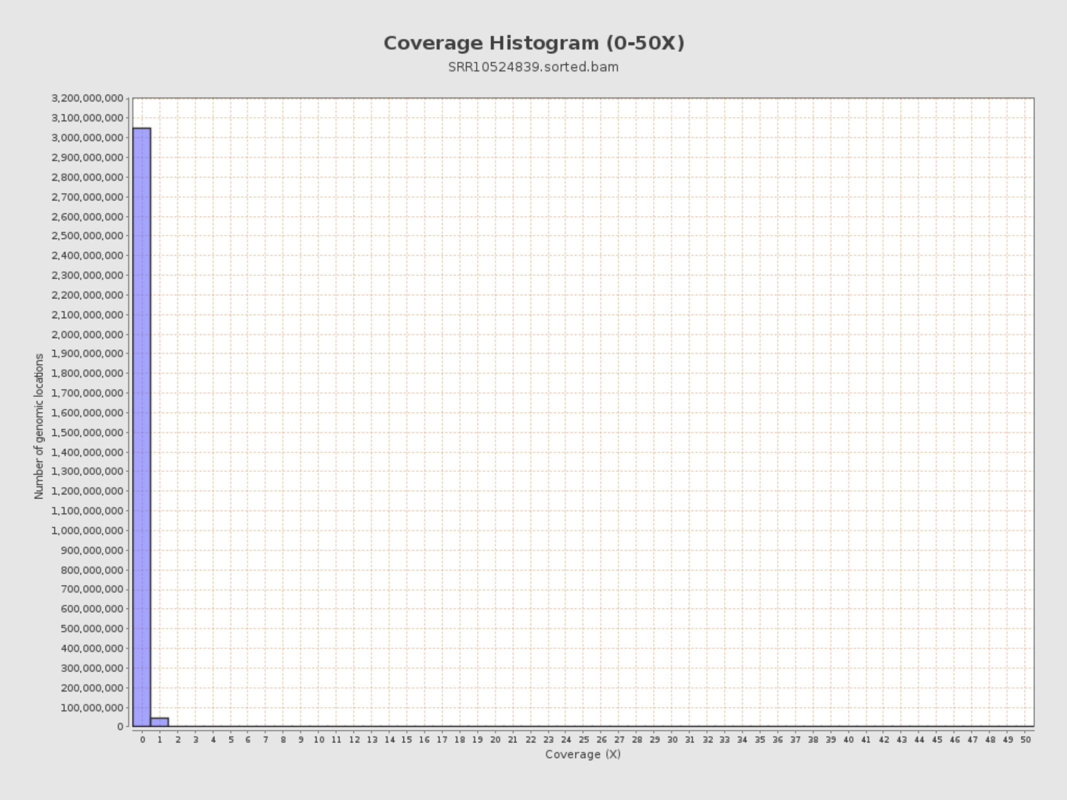
3. Results : Coverage across reference



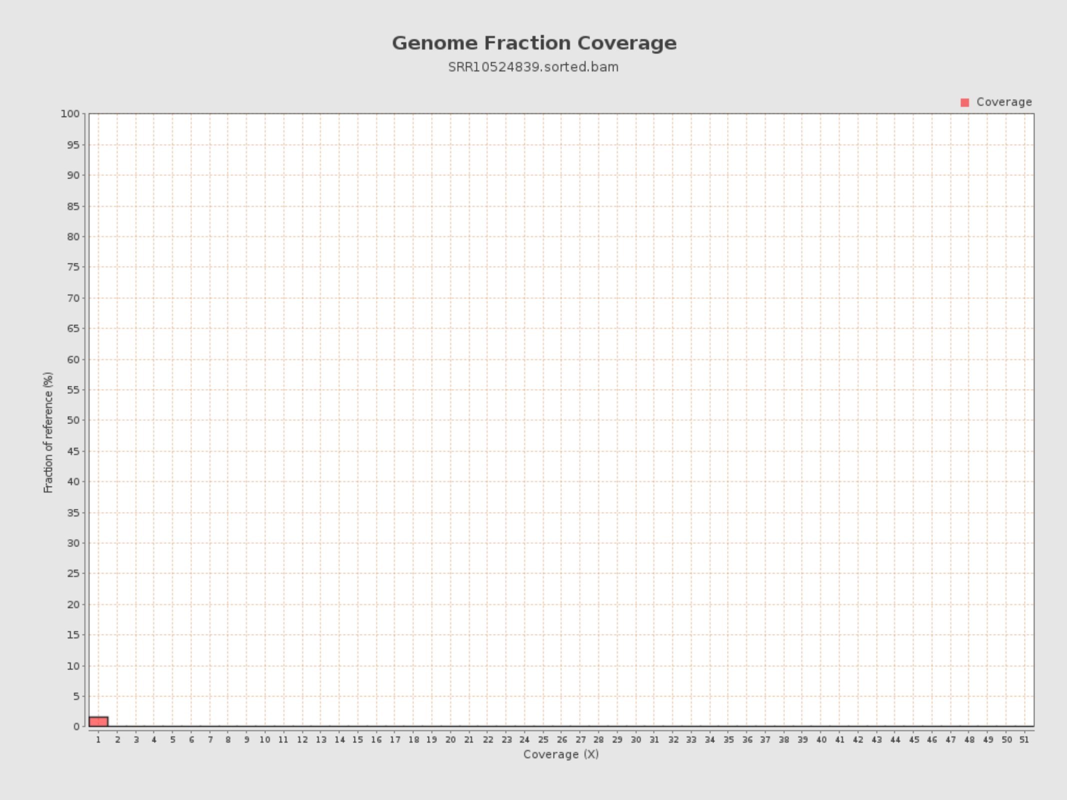
4. Results : Coverage Histogram



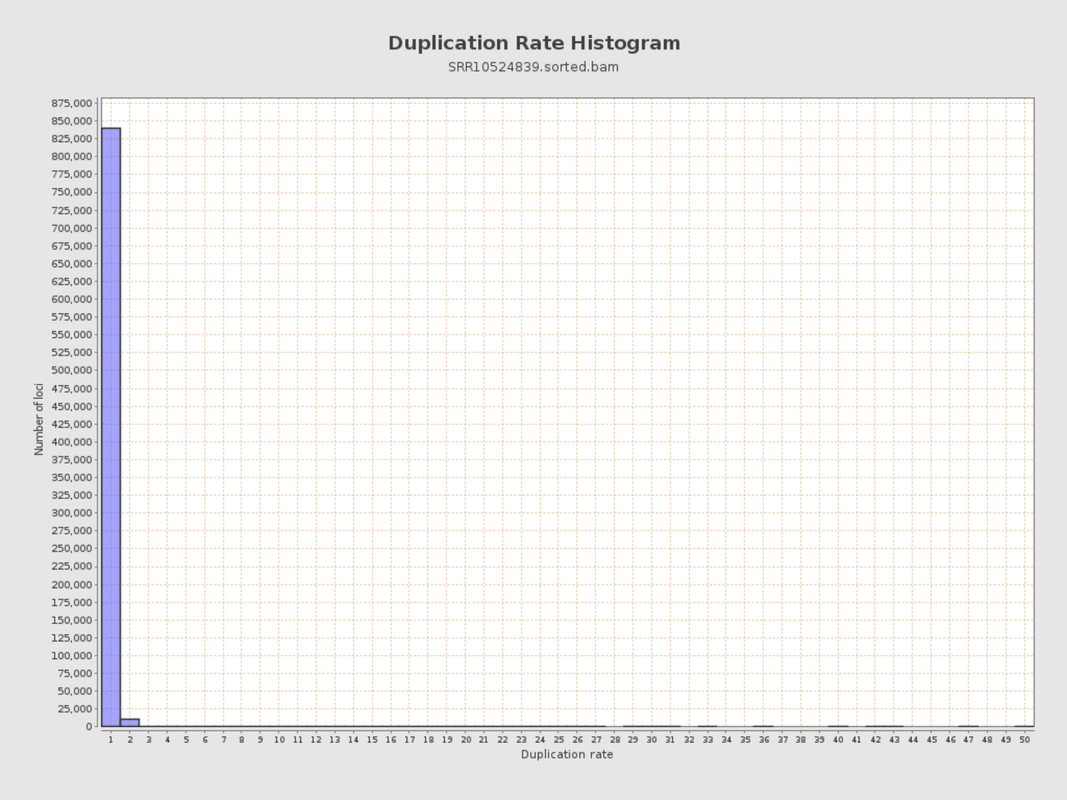
5. Results : Coverage Histogram (0-50X)



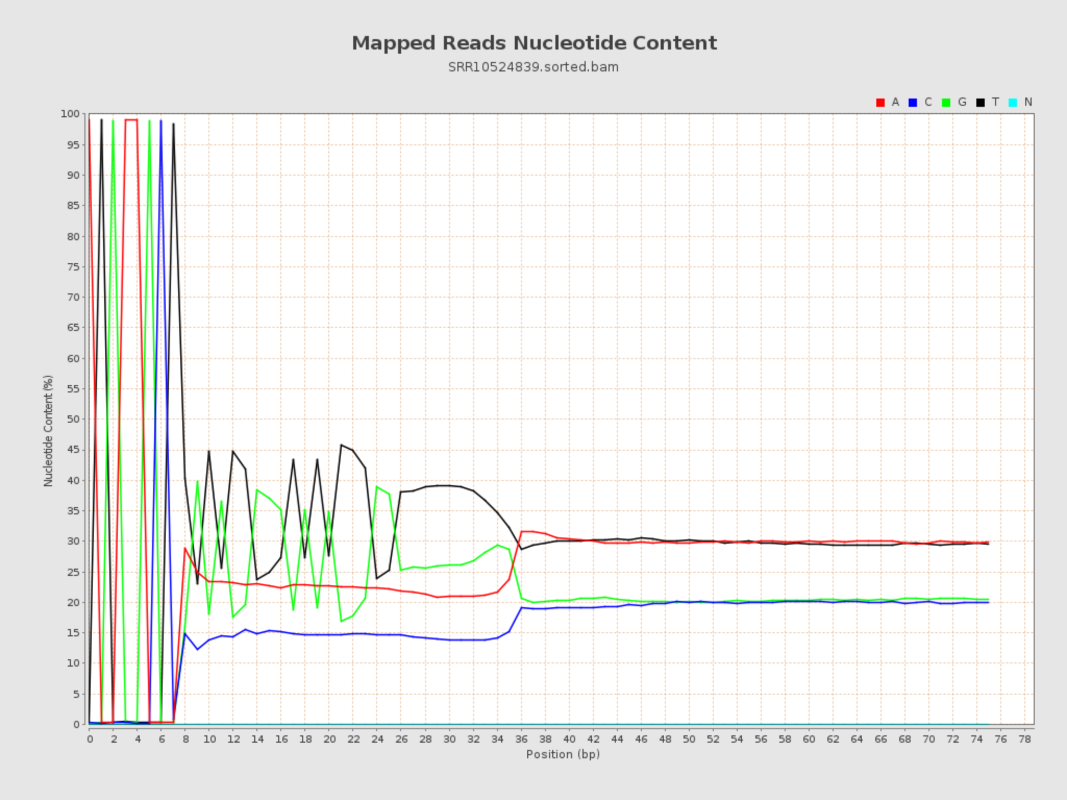
6. Results : Genome Fraction Coverage



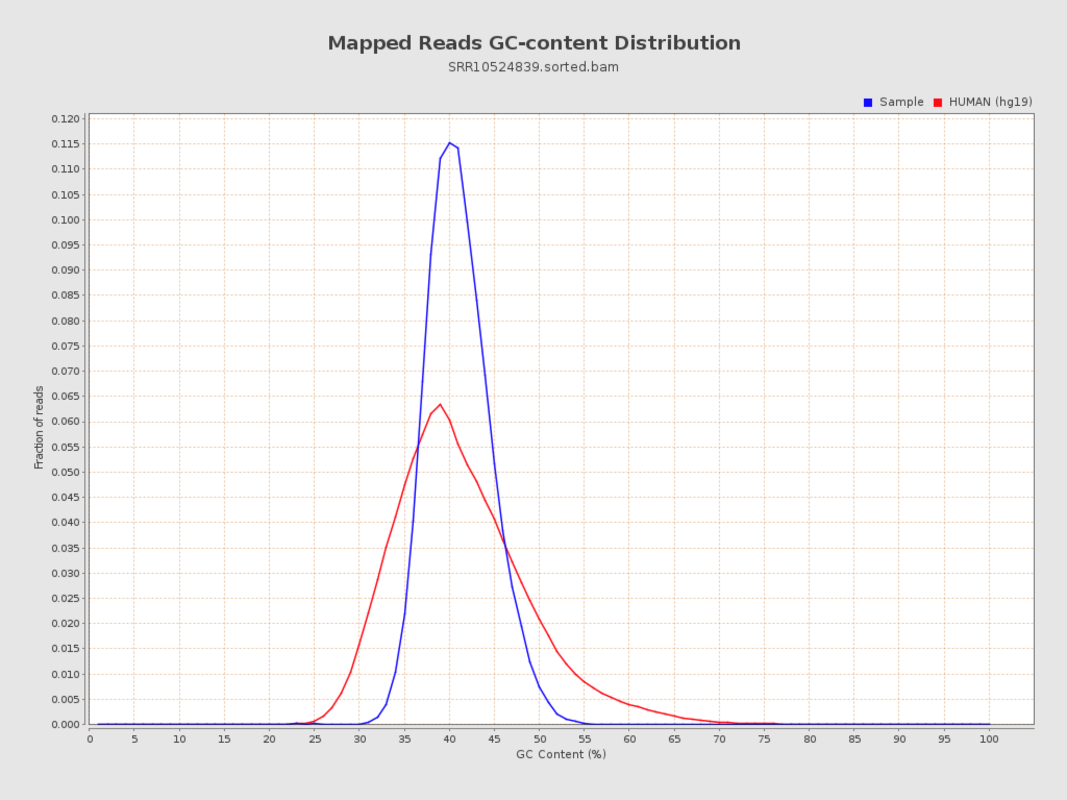
7. Results : Duplication Rate Histogram



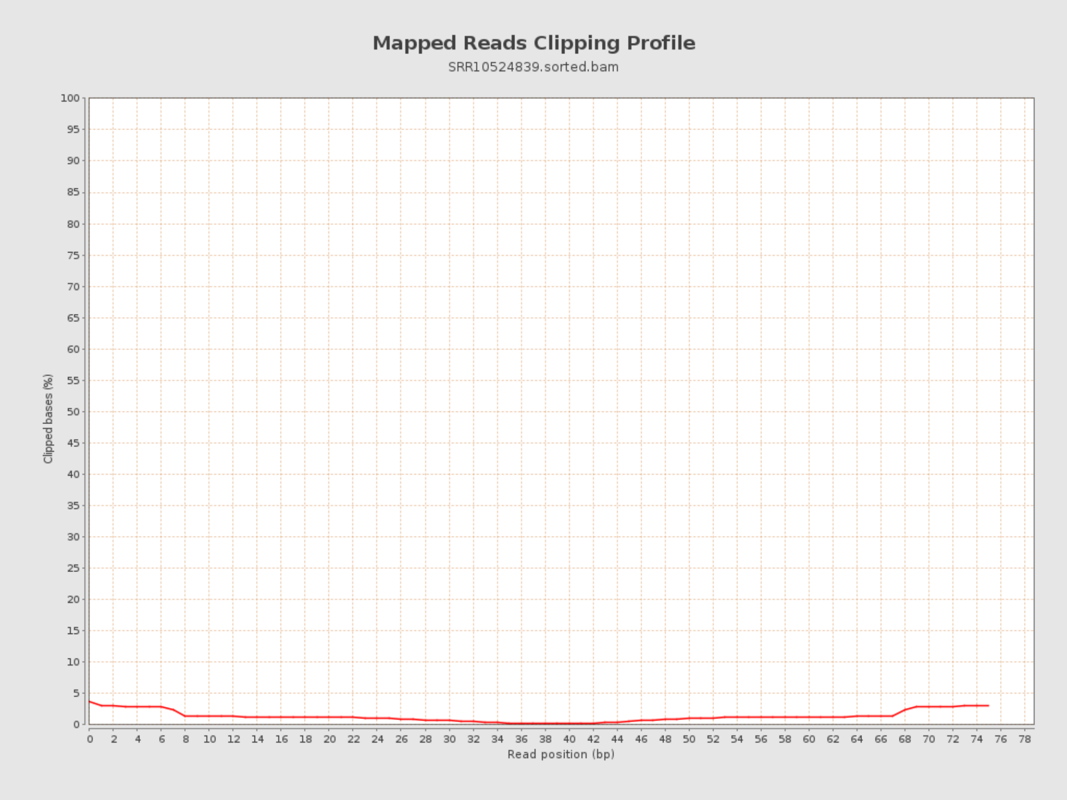
8. Results : Mapped Reads Nucleotide Content



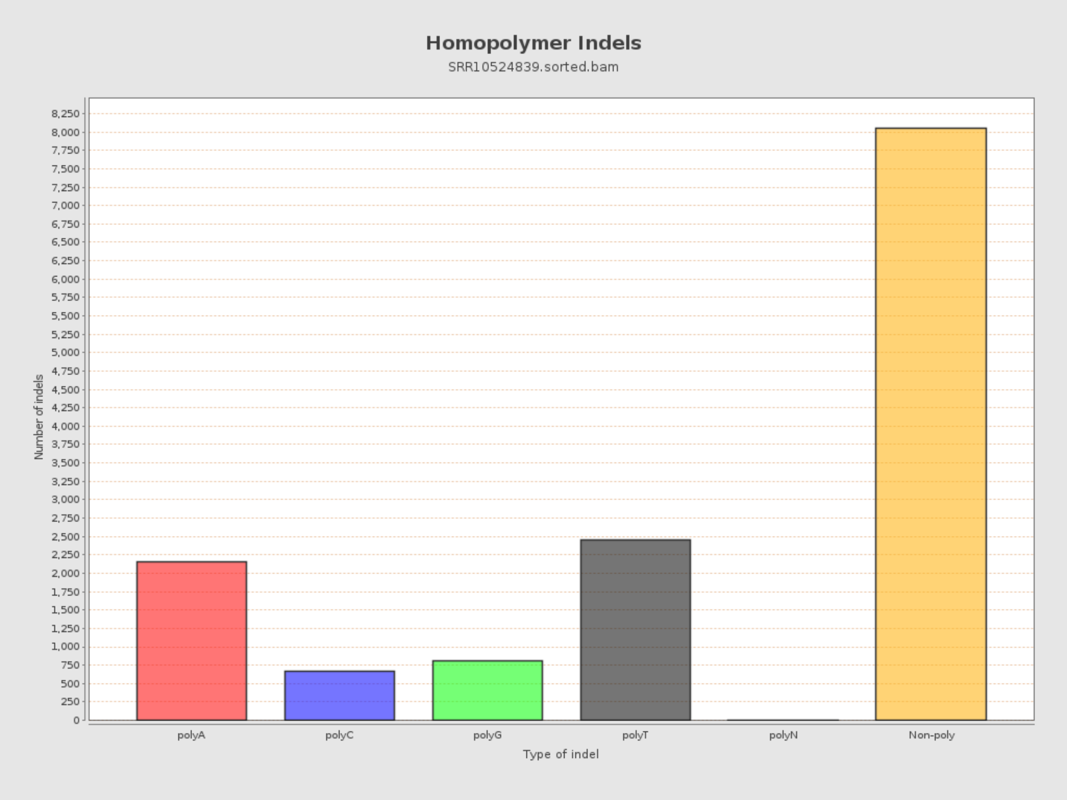
9. Results : Mapped Reads GC-content Distribution



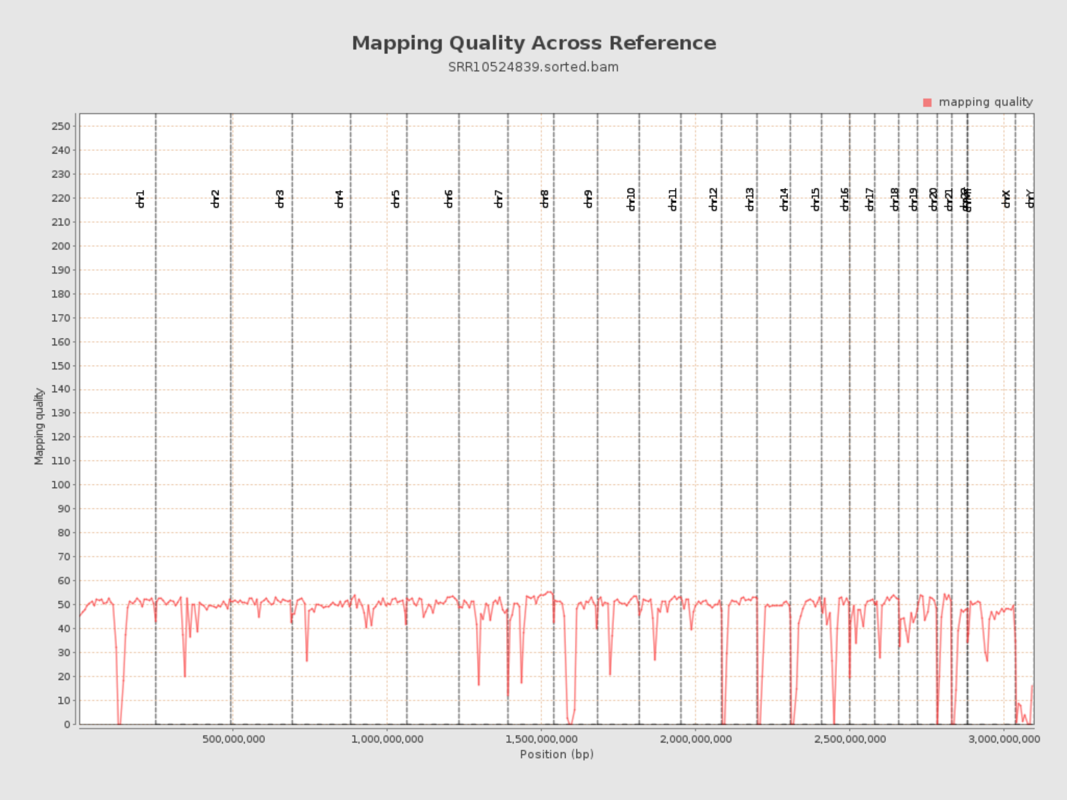
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram