Software and algorithms used in this study for genomic data analysis

Tool & Version	Purpose	Input data	Output results	Source
Strelka (2.9.4 for Genomics England WGS data, 2.0.15 for other WGS data)	Call somatic mutations and indels	Aligned sequencing data (.bam files)	Somatic SNVs and indels	https://github.com/Illumina/strelka
ASCAT 2.1	Call copy number for data data not from Genomics England	Aligned .bam files	Allele-specific copy number profiles	https://github.com/VanLoo-lab/ascat
Manta	Call structural variants	Aligned .bam files	Structural variant calls (SVs)	https://github.com/Illumina/manta
Canvas 1.38.0.1554	Infer copy number for Genomics England data	Aligned .bam files	Allele-specific copy number profiles	https://github.com/Illumina/canvas
Picard 3.1.1 (LiftoverVcf)	Convert VCF files from hg38 to hg19 coordinates	VCF files (hg38)	Lifted VCF files (hg19)	https://broadinstitute.github.io/picard/
GISTIC2.0	Identify recurrent amplifications/deletions across the Barrett's cohort	Copy number segmentation files	G-scores, peak regions, significant genes	https://github.com/broadinstitute/gistic2
dNdScv 0.1.0	Identify positively selected (driver) genes	SNV/indel mutation table	List of significant driver genes	https://github.com/im3sanger/dndscv
SigProfilerExtractor & deconstructSigs	Identify and quantify mutational signatures	VCF files with SNVs and indels	Sample-specific mutational signatures and contributions	https://github.com/AlexandrovLab/SigProfilerExtractor https://github.com/raerose01/deconstructSigs
Amplicon Architect 1.2 & Amplicon Classifier 0.4.13	Reconstruct and classify amplified genomic regions (e.g., ecDNA, BFB)	Aligned .bam files	Amplicon structures and classifications	https://github.com/virajbdeshpande/AmpliconArchitect https://github.com/AmpliconSuite/AmpliconClassifier

ShatterSeek 1.1	To identify chromothripsis events	Structural variants + copy number profiles	Predicted chromothripsis events	https://github.com/parklab/ShatterSeek
GATK Mutect2 4.1.7.0	Call somatic mutations in WES samples	Aligned .bam files	Somatic SNV and indel calls	https://gatk.broadinstitute.org/hc/en-us/articles/360036485152-Mutect2
PyClone 0.13.1	Infer subclonal populations from SNV data	Somatic mutation table	Subclonal clusters with VAF and CCF estimates	https://github.com/Roth-Lab/pyclone
ClonEvol 0.99.11	Construct phylogenetic trees of tumour evolution	Subclonal populations data	Reconstructed clonal phylogenies	https://github.com/hdng/clonevol
REVOLVER 1.0.0	Infer evolutionary trajectories across patients	Subclonal mutation profiles from multiple regions	Evolutionary trees, clusters, and recurrent trajectories	https://github.com/caravagnalab/revolver
Space Ranger 3.1.3	Process 10x Genomics Visium HD spatial transcriptomics data	Raw FASTQ and image data	Aligned gene expression matrices and spatial metadata	http://github.com/10XGenomics/spaceranger
Loupe Browser 8.1.2	Visualize and analyze spatial transcriptomics data	Space Ranger output files	Interactive spatial gene expression plots	https://www.10xgenomics.com/support/software/loupe-browser/latest
Scanpy 1.11.1	Analyze spatial gene expression matrices	Gene expression matrix	Cluster annotations, spatial plots	https://github.com/scverse/scanpy