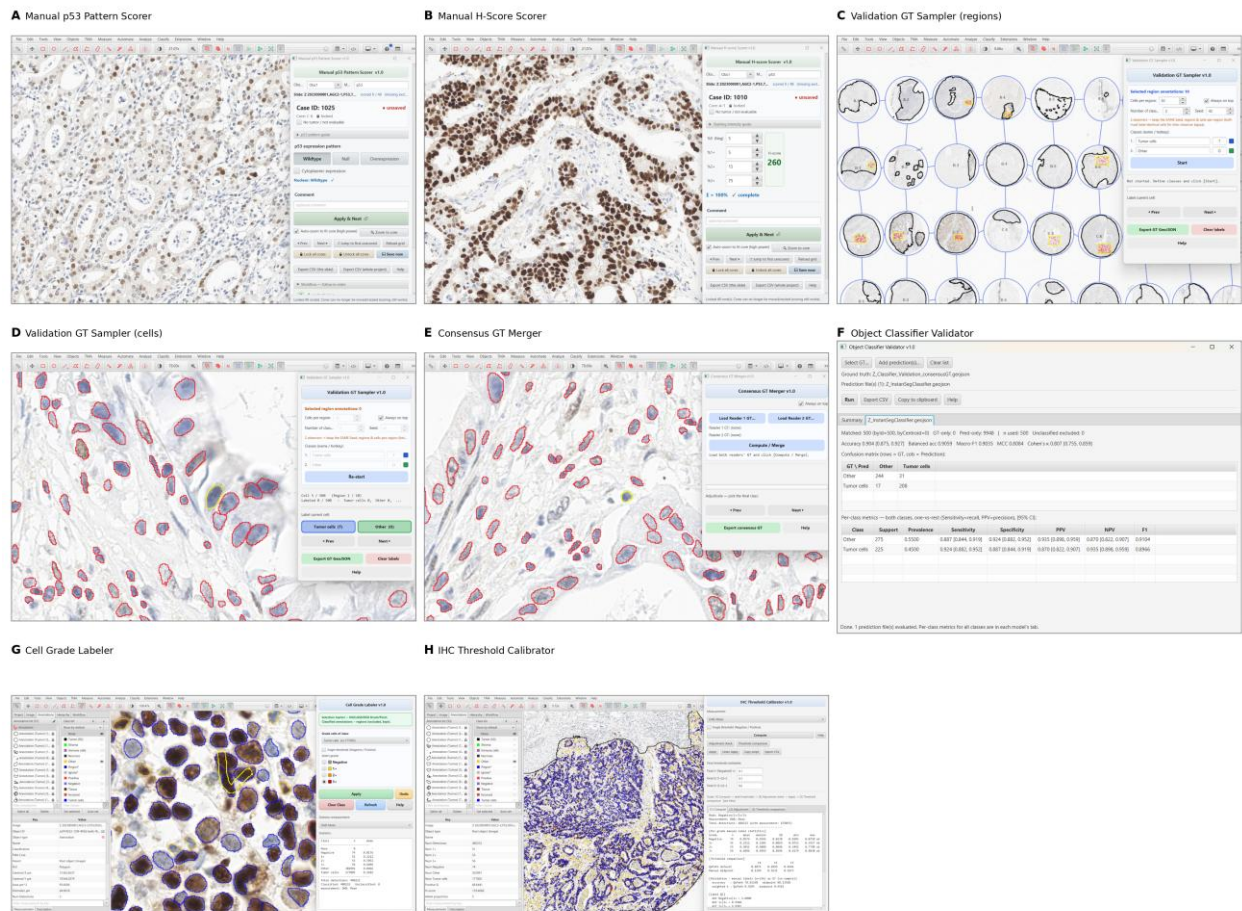




Supplementary Fig. S2. In-house QuPath tools used in the workflow. (A) Manual p53 Pattern Scorer: records the nuclear three-tier pattern (wild-type/null/overexpression) and cytoplasmic expression as independent axes for each core. (B) Manual H-Score Scorer: the percentage of tumor cells at each intensity grade is entered in 5% increments and the H-score is computed automatically. (C, D) Validation GT Sampler: cells are drawn at random with a fixed seed from selected core regions (C) and labeled by hotkey (D), so that both readers are presented with the identical cells. (E) Consensus GT Merger: matches the two readers' labels by cell object identifier, accepting concordant labels automatically and adjudicating discordant ones to build the consensus ground truth. (F) Object Classifier Validator: matches classifier predictions to the consensus ground truth cell by cell and computes the confusion matrix and performance metrics with 95% confidence intervals (Supplementary Table S2). (G) Cell Grade Labeler: labels representative tumor cells by intensity grade to generate the reference labels for threshold calibration. (H) IHC Threshold Calibrator: derives the DAB optical-density cutoffs as the midpoints of adjacent-grade means and supports quality control and application of the resulting thresholds (Supplementary Table S4). All tools are provided as Supplementary Software.