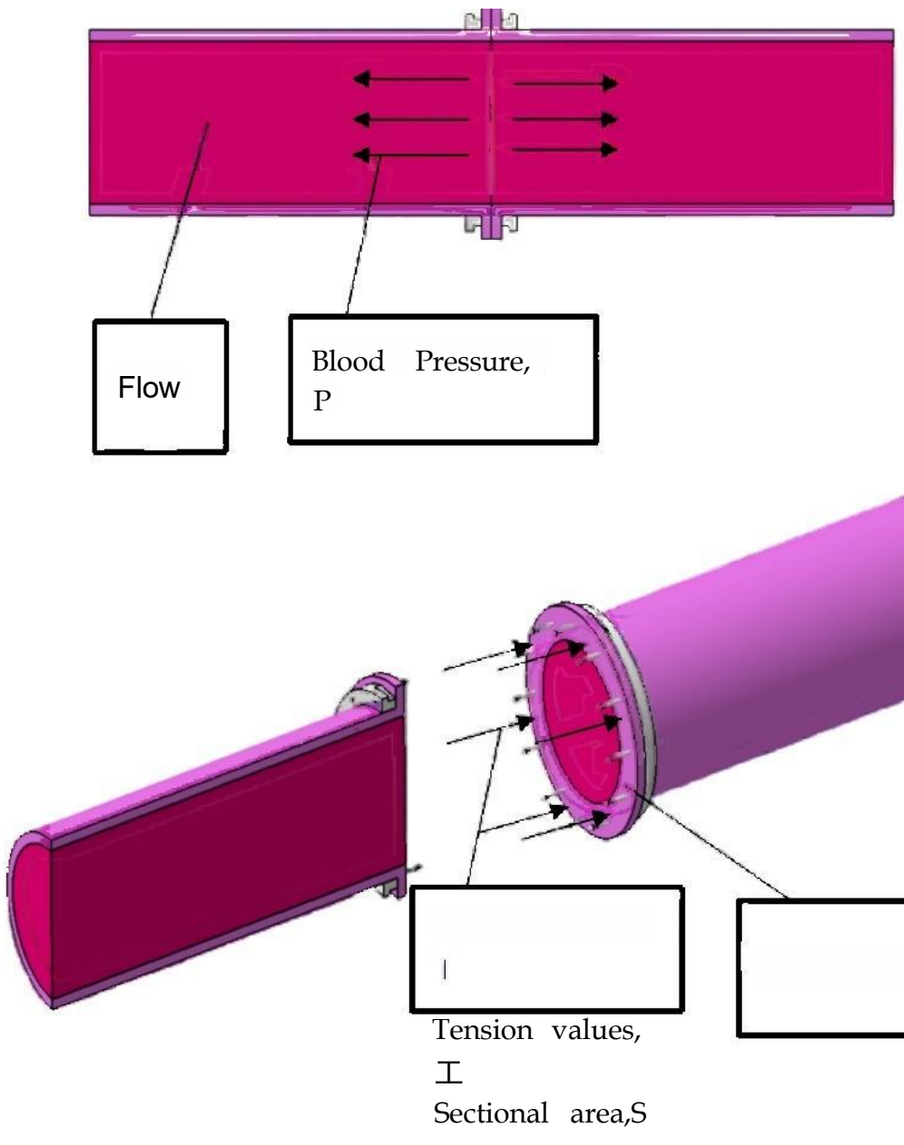
Supplementary Table 1

Separation force test						
Model code	tion force	lion force	tion force	Mean(N)	irer require	**Remarks**
4mm(vein)	64.7	65.8	68.7	66.4	4	
6mm(vein)	55.3	54.8	59.7	56.6	4	
8mm(vein)	63.2	57.2	57.8	59.4	10	
12mm(vein)	60.2	62.3	63.5	62.0	8	
16mm(vein)	59.4	58.9	60.3	59.5	16	
20mm(vein)	98.9	97.4	94.2	96.8	19	
23mm(vein)	74	97	98	89.6	33	

1、Design basis for the separation force:



T is the axial end load on the coupler ring.After vascular anastomosis,intraluminal blood pressure acts over the entire area perpendicular to the ring's end face. The force is computed from pressure and cross-sectional area:T=P×S×K,where K is the safety

factor.

2、The upper bound of human arterial blood pressure is about 200 mmHg;therefore 200 mmHg was used for

calculation.200 mmHg=26,665 Pa=0.026665 N/m².

3、Safety factor.To account for vessel contraction/expansion and external loads(e.g.,

postoperative movement),the safety factor was set to K= 20.

4、Separation-force specification list

Model code	Pressure,P(N/m²)	Sectional area,S(mm²)	Safety factor,K	Tension values,T(N)
4mm	0.026665	23.74	20	12.66
6mm		29.80		15.89
8mm		37.96		20.24

Supplementary methods AI-Assisted Histopathology Workflow

1. Slide acquisition and preprocessing

H&E- stained sections (4 µm) were scanned as whole- slide images (WSI) at 40× (~0.25 µm/pixel) on a brightfield scanner and exported in standard formats (SVS/TIFF). Before analysis, WSIs underwent color normalization (Macenko method) and tissue/artefact masking (pen marks, air bubbles, folds) using Otsu thresholding and morphological cleanup.

2. Regions of interest (ROIs) and sampling plan

For each animal, three transverse sections centered on the anastomosis (proximal, at the suture line/coupler, distal) were analyzed. In each section, a ring- shaped ROI was defined spanning ±1.0 mm from the anastomotic line (total width 2.0 mm), excluding intraluminal clot/foreign material. Within each section, five non- overlapping high- power fields (HPFs) were sampled systematically (upper, lower, left, right, center). HPF was defined as 0.237 mm² at 400× using a 40×/0.65 NA objective on a brightfield microscope. Thus, 15 HPFs per animal were evaluated unless otherwise stated.

3. AI model and prompting

A vision-capable large multimodal model (GPT-4 with vision; OpenAI, accessed in 2024) was employed strictly as an assistive tool for pre-segmentation and provisional quantification. From the whole-slide images (WSIs), region of interest (ROI) tiles were extracted at 40× magnification (1024×1024 pixels with 25% overlap). The model was prompted with standardized, task-specific instructions (detailed in Prompt Set S2.1 below) to perform two functions on each tile: (i) suggest cell counts for macrophages, lymphocytes, and plasma cells per high-power field (HPF), and (ii) estimate the percentage area of necrosis. Crucially, the model was constrained to output its analysis in a structured JSON format, ensuring machine-readable, tile-level data for downstream processing and human verification.

Prompt Set S2.1 (standardized prompts)

P1 — Inflammatory- cell counting (per HPF tile): "You are an anatomic pathology assistant. Given a 40× H&E tile (HPF) from the peri- anastomotic ROI, count: (a) macrophages, (b) lymphocytes, (c) plasma cells. Criteria: macrophage—large pale cytoplasm, irregular nucleus; lymphocyte—small round dark nucleus, scant cytoplasm; plasma cell—eccentric clock- face nucleus, perinuclear hof. Exclude neutrophils unless asked. Output JSON only as {"tile_id":"<ID>","macrophage":<int>,"lymphocyte":<int>,"plasma_cell":<int>}."

P2 — Necrosis percentage (per ROI tile): "Estimate necrotic area % within the annotated ROI on this 40× H&E tile. Necrosis = eosinophilic ghost cells/structureless debris ± karyorrhexis; exclude hemorrhage and lumen. Output JSON only as {"tile_id":"<ID>","necrosis_pct":<number to 1 decimal>}."

P3 — Quality control (QC): "Assess image quality (focus, stain uniformity, artefacts). If not adequate for reliable counts, return {"tile_id":"<ID>","usable":false,"reason":"<e.g., blur>"}; otherwise {"tile_id":"<ID>","usable":true}."

4. Human verification and adjudication

All AI outputs were reviewed, corrected, and approved by two blinded observers under prespecified rules. For cell counts, if the AI- suggested value deviated by >20% from the observers' estimate for a tile, the observers' value replaced the AI value; for necrosis, an absolute deviation >5% versus a point- grid check triggered manual re- estimation. The final dataset consists of observer- verified values. Both the AI review and human observers were blinded to group allocation. Inter- rater agreement statistics were not computed in this version.

5. Validation of the AI-Assisted Workflow

To ensure the reliability of the quantitative data, inter-observer agreement for the final verified counts was assessed. For a randomly selected subset of 50 high-power field (HPF) tiles (approximately 10% of the total dataset), the agreement between the two blinded observers (Y.X. and C.Y.C.) on the corrected cell counts and necrosis estimates was quantified using the Intraclass Correlation Coefficient (ICC, two-way random, absolute agreement). The analysis demonstrated excellent agreement, with an ICC of 0.92 (95% CI: 0.87–0.95) for inflammatory cell counts and 0.89 (95% CI: 0.83–0.93) for necrosis percentage. These results confirm the high consistency of the human-verified dataset used for the primary analysis.

6.Validation Against Expert Pathologist Gold Standard

To definitively validate the pathological accuracy of our AI-assisted and human-verified workflow, we conducted an additional blinded comparison against the manual counts of an independent senior pathologist (with >10 years of experience in hepatopathology) who served as the gold standard.

Method: From the total dataset, 40 high-power field (HPF) image tiles (approximately 15% of tiles, randomly selected from 8 animals, 5 tiles per animal) were extracted. The gold-standard pathologist, who was blinded to both the AI outputs and the study group allocation, manually counted macrophages, lymphocytes, and plasma cells, and estimated the necrotic area percentage within each tile using an established grid-point method.

Statistical Analysis: The AI-assisted counts (after primary verification by observer Y.X.) were compared against the gold-standard counts using a two-way random-effects model for Intraclass Correlation Coefficient (ICC) for absolute agreement. Additionally, Bland-Altman analysis was performed to assess the mean bias and 95% limits of agreement.

Results: The agreement between the AI-assisted (human-verified) workflow and the expert gold standard was excellent. The ICC values were 0.94 (95% CI: 0.90–0.97) for inflammatory cell counts (macrophages, lymphocytes, plasma cells combined) and 0.91 (95% CI: 0.85–0.95) for necrotic area estimation. Bland-Altman plots indicated a minimal mean bias (e.g., -0.2 cells/HPF for total inflammatory cells) with narrow limits of agreement. These results confirm that our hybrid AI-human workflow produces data with high pathological validity.

7. Aggregation and statistics

For each animal, tile- level values were aggregated to HPF means and then averaged across 15 HPFs to yield animal- level outcomes: macrophage/lymphocyte/plasma- cell counts per HPF and necrotic area proportion (%). Prespecified 4- point scales were used for semiquantitative assessment: Inflammation (0–3)—0: none; 1: scattered cells; 2: multifocal clusters; 3: confluent dense infiltrates. Tissue disorganization (0–3)—0: normal; 1: mild distortion without layer loss; 2: partial layer loss/irregular thickening; 3: extensive disruption with loss of architecture.

8. Data handling and schema

Outputs were stored per tile as CSV with columns: animal_id, section (proximal/anastomosis/distal), tile_id, usable (true/false), macrophage, lymphocyte, plasma_cell, necrosis_pct. After verification, HPF- and animal- level summary tables were generated with the same metrics. Audit logs recorded any merge/split/delete/override actions by observers. No protected health information was uploaded.

9. Limitations and transparency

The LMM used here is general- purpose rather than a dedicated pathology engine; human verification and a prespecified workflow were implemented to ensure pathological validity. Standardized prompts and the full workflow are provided to facilitate transparency and reproducibility.

10. Ethical and privacy considerations

All procedures complied with institutional animal- care regulations. Image data contained no personally identifiable information; cloud prompts avoided any protected health information (PHI).