

Supplementary Materials to Comprehensive Histopathology Imaging in Pancreatic Biopsies: High Definition Infrared Imaging with Machine Learning Approach

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Experimental details

In order to collect experimental data for multitude of samples within reasonable time frame, optimizations of measurement pipeline were necessary. Raw interferograms were Fourier-Transformed and stitched using separate computer, making no impact on measurement time. Combination of this approach and regular detector pumping allowed continuous measurement of large areas for 10-13.5 hours (without liquid nitrogen refill). Nonetheless, measurements of large areas come with the risk of defocusing due to sample tilt. This issue was overcome by implementation of in home-written scripts for focusing modality, which resulted in high quality data. Optimization and customization of measurement routines elevated the scanning time of single TMA (20x16 mm in size) to 2.5 days for SD and 2.5 weeks for HD.

Model validation

Two different ways for ROC and AUC calculation were applied during different stages of final model's creation. Pixel level ROC statistic was used during an iterative process of classifier training/tuning to assess its ability for a successful single pixel classification. ROC curve for each class was calculated based on biased two class model (specific class versus five other classes merged into one). Initial probability ratio of such models was always 1:5, due to classes' size imbalance and the thresholds used for ROC calculations are based on trees voting. This approach is very different from conventional way applied here to evaluated final model. Core level and patient level ROC statistic are based on summation of prediction pixels from each tissue core or patient, respectively. A statistical analysis in the form of confidence intervals was applied to obtained values of AUC. Standard error for AUC is evaluated as:

$$SE(AUC) = \sqrt{\frac{AUC(1 - AUC) + (n_1 - 1)(Q_1 - AUC^2) + (n_0 - 1)(Q_2 - AUC^2)}{n_0 n_1}},$$

where n_0 is the number of samples for positive class, n_1 is the number of other samples and:

$$Q_1 = \frac{AUC}{2 - AUC}, \quad Q_2 = \frac{2AUC^2}{1 + AUC}.$$

In general, histopathological model creation is tedious and iterative process. It consists of many rounds of annotations corrections and optimizations. In case of this study, hundredths of models were created before achieving satisfactory results.

Table S1. Description of patients with Tissue Micro Arrays (TMA) location and cores represented with BIOMAX Inc. notation (Letter – TMA row, Number – TMA column).

Patient number	PA2081b	PA2072a	PA1002a	PA961e	BBS14011	BIC14011a
1	A1,A2	-	-	B3	-	-
2	A3,A4	-	A4	D10	-	-
3	A5,A6	-	-	-	-	-
4	A7,A8	-	F4,F9	E7	-	-
5	A9,A10,I5,I6	-	A2,A7	-	-	-
6	A11,A12	B3,B4,B5	-	-	-	-
7	A13,A14	B12,B13,B14	C3,C8	A3	-	-
8	A15,A16	C8,C9,C10	C4,C9	-	-	-
9	B1,B2	-	A3	B10	-	-
10	B3,B4	-	-	C2	-	-
11	B5,B6	-	-	-	-	-
12	B7,B8	-	H2,H7	F12	-	-
13	B9,B10	G7,G8,G9	B5,B10	-	-	-
14	B11,B12	-	-	-	-	-
15	B13,B14	E12,E13,E14	E5, E10	-	-	-
16	B15,B16	-	-	-	-	-
17	C1,C2	E15,E16,F1	C2,C7	C12	-	-
18	C3,C4	-	-	-	-	-
19	C5,C6	-	-	-	-	-
20	C7,C8	G16,H1,H2	-	C8	-	-
21	C9,C10	I5,I6,I7	E3,F8	E6	-	-
22	C11,C12	D13,D14,D15	-	B9	-	-
23	C13,C14	A16,B1,B2	-	-	-	F1,F2
24	C15,C16	-	B3,B8	C10	-	-
25	D1,D2	-	B1,B6	A6	-	-
26	D3,D4	-	-	-	-	-
27	D5,D6	H9,H10,H11	-	C1	-	-
28	D7,D8	-	-	-	-	-
29	D9,D10	-	-	G1	-	-
30	D11,D12	-	-	-	-	-
31	D13,D14	G1,G2,G3	E2,E7	G2	-	-
32	D15,D16	-	-	-	-	-
33	E1,E2	-	-	-	-	-
34	E3,E4	-	-	-	-	-
35	E5,E6	-	-	-	-	-
36	E7,E8	-	-	G3	-	-
37	E9,E10	-	G4,G9	-	-	-
38	E11,E12	J7,J8,J9	G5,G10	-	-	-
39	E13,E14	-	-	G5	-	-
40	E15,E16	-	-	-	-	-
41	F1,F2	-	H1,H6	-	-	-
42	F3,F4	C2,C3,C4	-	-	-	-
43	F5,F6	-	-	-	-	-
44	F7,F8	-	-	G11	-	-
45	F10	-	-	G10	-	-

46	-	-	-	-	-	-
47	-	-	-	-	-	-
48	-	-	-	-	-	-
49	-	-	-	-	-	-
50	-	-	-	-	-	-
51	-	-	-	-	-	-
52	-	-	-	-	-	-
53	G9,G10	-	-	-	-	-
54	G11,G12	-	-	-	-	-
55	G13,G14	-	-	-	-	-
56	G15,G16	-	-	-	-	-
57	H1,H2	-	-	-	-	-
58	H3,H4	-	-	-	-	-
59	H5,H6	-	-	-	-	-
60	H7,H8	-	-	-	-	-
61	H9,H10	-	-	-	-	-
62	H11,H12	-	-	-	-	-
63	H13,H14	-	-	-	-	-
64	H15,H16	-	-	-	-	-
65	I1,I2	-	-	-	-	-
66	I3,I4	-	-	-	-	-
67	I7,I8	-	-	-	-	-
68	I9,I10	-	-	-	-	-
69	I11	-	-	-	-	-
70	I13,I14	-	-	-	-	-
71	I15,I16	-	-	-	-	-
72	J1,J2	-	-	-	-	-
73	J3,J4	-	-	-	-	-
74	J5,J6	-	-	-	-	-
75	-	-	-	-	-	-
76	J9,J10	-	-	-	-	-
77	J11,J12	-	-	-	-	-
78	J13,J14	-	-	-	-	-
79	J15,J16	-	-	-	-	-
80	K1,K2	-	-	-	-	-
81	K3,K4	-	-	-	-	-
82	K5,K6	-	-	-	-	-
83	K7,K8	-	-	-	-	-
84	K9,K10	-	-	-	-	-
85	K11,K12	-	-	C9	-	-
86	K13,K14	A13,A14,A15	-	B2	-	-
87	K15,K16	-	-	-	-	-
88	L1,L2	-	-	-	-	-
89	L3,L4	-	-	-	-	-
90	L5,L6	-	-	-	-	-
91	L7,L8	-	-	-	-	-
92	L9,L10	-	-	-	A3	-
93	L11,L12	-	-	-	-	-
94	L13,L14	-	-	-	-	-
95	L15,L15	M4,M5,M6	J1,J6	-	-	-
96	-	L5,L6,L7	J4,J9	-	-	-
97	M3,M4	-	I10	-	-	-
98	M5,M6	-	I9	-	-	-
99	M7,M8	-	J3,J8	-	-	-
100	M9,M10	M3	I6	-	-	-
101	M11,M12	L11,L12,L13	J2,J7	-	-	-
102	M13,M14	-	I8	-	-	-
103	M15,M16	M10,M11,M12	I7	-	-	-

104	-	A1,A2,A3	-	-	-	-
105	-	A4,A5,A6	-	-	-	-
106	-	A7,A8	-	-	-	-
107	-	A10,A11,A12	-	B4	-	-
108	-	B6,B7,B8	-	-	-	-
109	-	B9,B10,B11	-	-	-	-
110	-	B15,B16,C1	-	B11	-	-
111	-	C5,C6,C7	-	-	-	-
112	-	C11,C12,C13	-	-	-	-
113	-	C14,C15,C16	-	B8	-	-
114	-	D1,D2,D3	-	E9	-	-
115	-	D4,D5,D6	-	-	-	-
116	-	D7,D8,D9	-	-	-	-
117	-	D10,D11,D12	-	D8	-	-
118	-	D16,E1,E2	D4,D9	C5	-	-
119	-	E3,E4,E5	-	C3	-	F5,F6
120	-	E6,E7,E8	D2,D7	D6	-	-
121	-	E9,E10,E11	-	-	-	-
122	-	F2,F3,F4	-	E2	-	-
123	-	F5,F6,F7	-	-	-	-
124	-	F8,F9,F10	C1,C6	-	-	-
125	-	F11,F12,F13	B4,B9	C4	-	-
126	-	F14,F15,F16	-	D1	-	-
127	-	G4,G5,G6	-	-	-	-
128	-	G10,G11,G12	-	-	-	-
129	-	G13,G14,G15	-	-	-	-
130	-	H5	-	-	-	-
131	-	H6,H7,H8	-	-	-	-
132	-	H12,H13,H14	H3,H8	-	-	-
133	-	H15,H16,I1	-	-	-	-
134	-	I2,I3,I4	-	-	-	-
135	-	I8,I9,10	-	-	-	F3,F4
136	-	I11,I12,I13	-	G6	-	-
137	-	I14,I15,I16	-	-	-	-
138	-	J1,J2,J3	-	F3	-	-
139	-	J4,J5,J6	G3,G8	E11	-	-
140	-	J10,J11,J12	C5,C10	F10	-	-
141	-	J13,J14,J15	F5,F10	-	-	-
142	-	J16,K1,K2	-	-	-	F7,F8
143	-	K3,K4,K5	H5,H10	F11	-	-
144	-	K6,K7,K8	-	F7	-	-
145	-	K9,K10,K11	-	-	-	-
146	-	K12,K13,K14	-	E3	-	-
147	-	K15,K16,L1	F1,F6	D2	-	-
148	-	L2,L3,L4	-	-	E6	-
149	-	L8,L9,L10	-	H12	-	-
150	-	L14,L15,L16	-	-	-	-
151	-	M7,M8,M9	-	-	-	-
152	-	M13,M14,M15	-	D3	-	-
153	-	-	A1,B7	-	-	-
154	-	-	A5,D1	-	-	-
155	-	-	A6,D3	E5	-	-
156	-	-	A10,D5	-	-	-
157	-	-	B2,D6	-	-	-
158	-	-	D8,E6	E4	-	-
159	-	-	D10,E8	E1	-	-
160	-	-	E1,E9	-	-	-
161	-	-	E3,E2	-	-	-

162	-	-	E4,F7	-	-	-
163	-	-	G1	F1	-	-
164	-	-	G2,J5	-	-	-
165	-	-	G6,J10	F8	-	-
166	-	-	G7	F6	-	-
167	-	-	H4	-	-	-
168	-	-	-	A1	-	-
169	-	-	-	A2	-	-
170	-	-	-	A4	-	-
171	-	-	-	A5	-	-
172	-	-	-	A7	-	-
173	-	-	-	A8	-	-
174	-	-	-	A10	-	-
175	-	-	-	A11	-	-
176	-	-	-	A12	-	-
177	-	-	-	B1	-	-
178	-	-	-	B5	-	-
179	-	-	-	B6	-	-
180	-	-	-	B7	-	-
181	-	-	-	B12	-	-
182	-	-	-	C6	-	-
183	-	-	-	C7	-	-
184	-	-	-	-	-	-
185	-	-	-	D4	D2	-
186	-	-	-	D5	-	-
187	-	-	-	D7	-	-
188	-	-	-	D9	-	-
189	-	-	-	D11	-	-
190	-	-	-	D12	-	-
191	-	-	-	-	-	-
192	-	-	-	E10	-	-
193	-	-	-	F2	-	-
194	-	-	-	F4	-	-
195	-	-	-	F5	-	-
196	-	-	-	F9	-	-
197	-	-	-	G4	-	-
198	-	-	-	-	-	-
199	-	-	-	G8	-	-
200	-	-	-	G9	-	-
201	-	-	-	G12	-	-
202	-	-	-	H1	-	-
203	-	-	-	H2	-	-
204	-	-	-	H3	-	-
205	-	-	-	H4	-	-
206	-	-	-	H5	-	-
207	-	-	-	H6	-	-
208	-	-	-	-	-	-
209	-	-	-	-	-	-
210	-	-	-	-	A1	-
211	-	-	-	-	A2	-
212	-	-	-	-	A4	B7,B8
213	-	-	-	-	A5	-
214	-	-	-	-	A6	-
215	-	-	-	-	A7	-
216	-	-	-	-	A8	C3,C4
217	-	-	-	-	B1	-
218	-	-	-	-	B2	-
219	-	-	-	-	B3	-

220	-	-	-	-	B4	-
221	-	-	-	-	B5	-
222	-	-	-	-	B6	-
223	-	-	-	-	B7	B1,B2
224	-	-	-	-	B8	-
225	-	-	-	-	C1	-
226	-	-	-	-	C2	A3,A4
227	-	-	-	-	C3	-
228	-	-	-	-	C4	-
229	-	-	-	-	C5	-
230	-	-	-	-	C6	-
231	-	-	-	-	-	-
232	-	-	-	-	C8	-
233	-	-	-	-	D1	-
234	-	-	-	-	D3	-
235	-	-	-	-	D4	-
236	-	-	-	-	D5	-
237	-	-	-	-	D6	-
238	-	-	-	-	D7	A5,A6
239	-	-	-	-	D8	B3,B4
240	-	-	-	-	E1	-
241	-	-	-	-	E2	-
242	-	-	-	-	E3	-
243	-	-	-	-	E4	-
244	-	-	-	-	E5	-
245	-	-	-	-	E7	-
246	-	-	-	-	E8	-
247	-	-	-	-	F1	-
248	-	-	-	-	F2	-
249	-	-	-	-	F3	B5,B6
250	-	-	-	-	F4	E3,E4
251	-	-	-	-	F5	-
252	-	-	-	-	F6	C1,C2
253	-	-	-	-	F7	E7,E8
254	-	-	-	-	F8	-
255	-	-	-	-	-	A1,A2
256	-	-	-	-	-	A7,A8
257	-	-	-	-	-	C5,C6
258	-	-	-	-	-	C7,C8
259	-	-	-	-	-	D1,D2
260	-	-	-	-	-	D3,D4
261	-	-	-	-	-	D5,D6
262	-	-	-	-	-	D7,D8
263	-	-	-	-	-	E1,E2
264	-	-	-	-	-	E5,E6

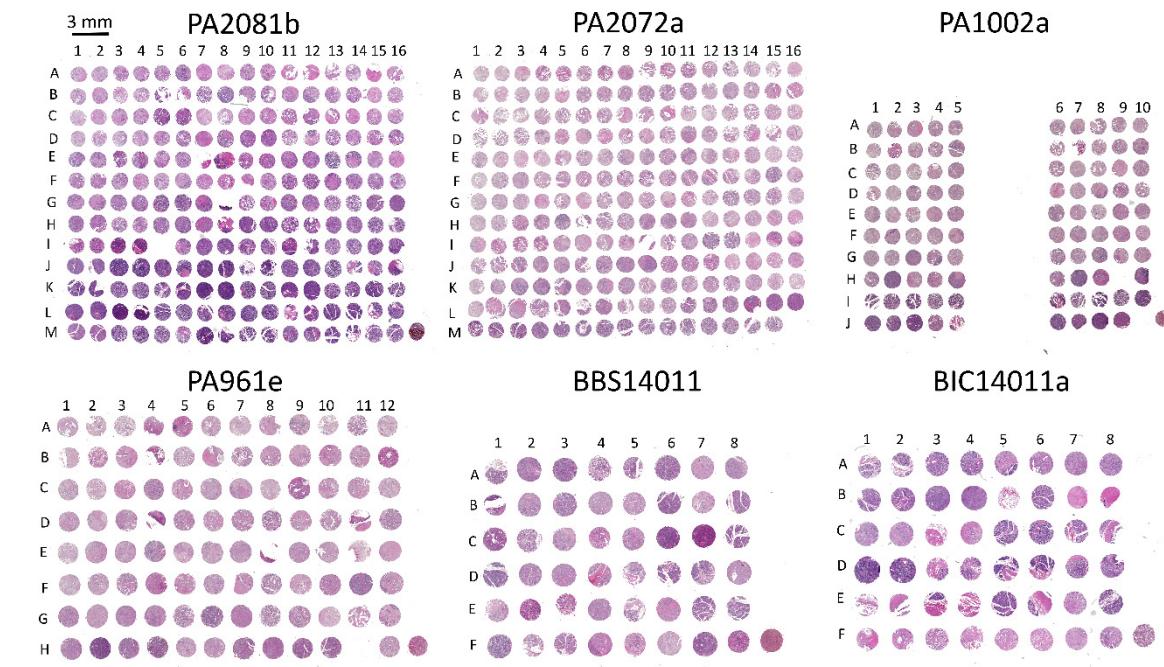


Figure S1. H&E images of pancreatic Micro Tissue Arrays used in this study. Cores in each matrix are numbered according to BIOMAX Inc. notation.

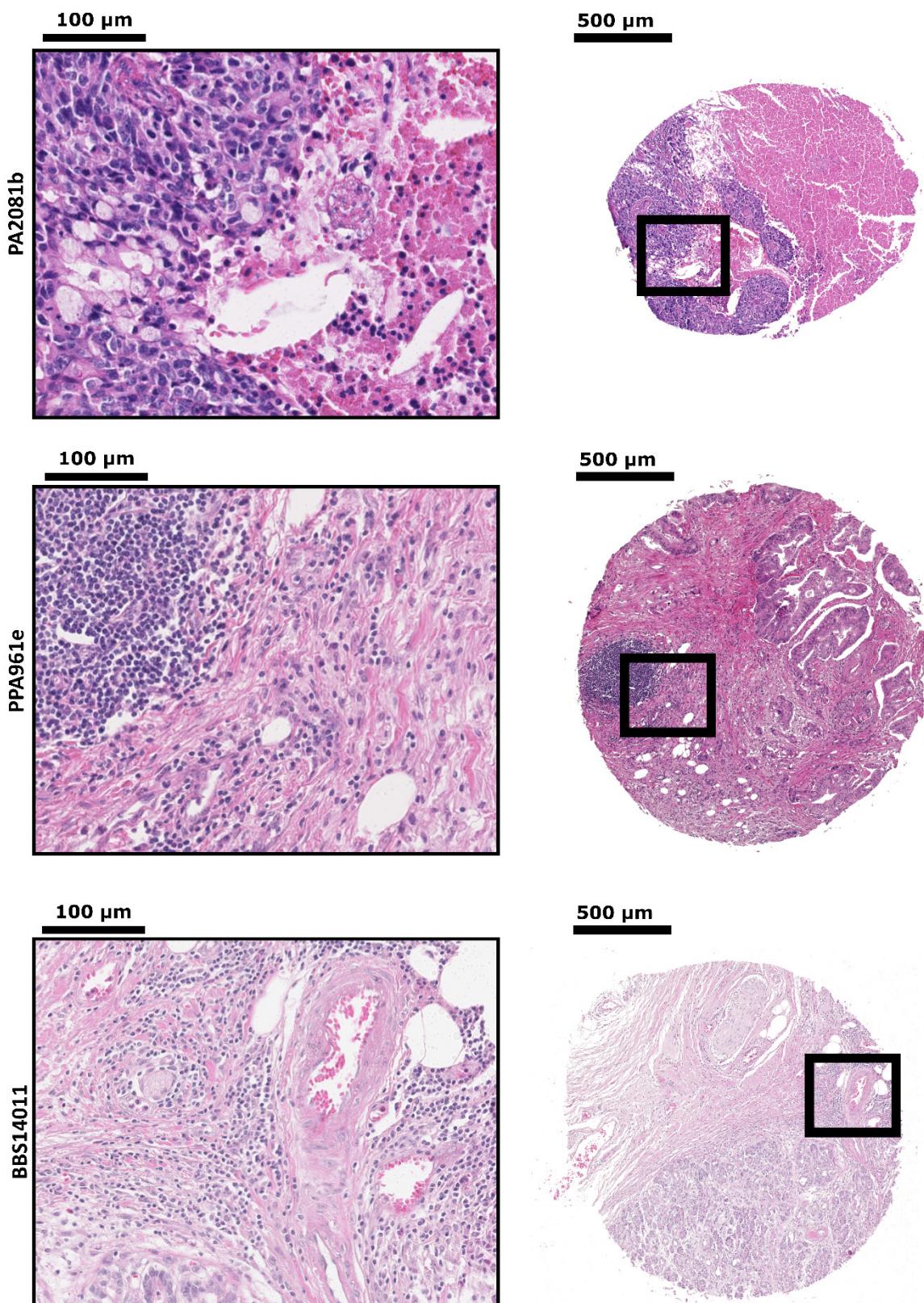


Figure S2. H&E images of zoomed biopsies (from TMAs PA2081b, PA961e, BBS14011) shown in Figures 2 and 4.

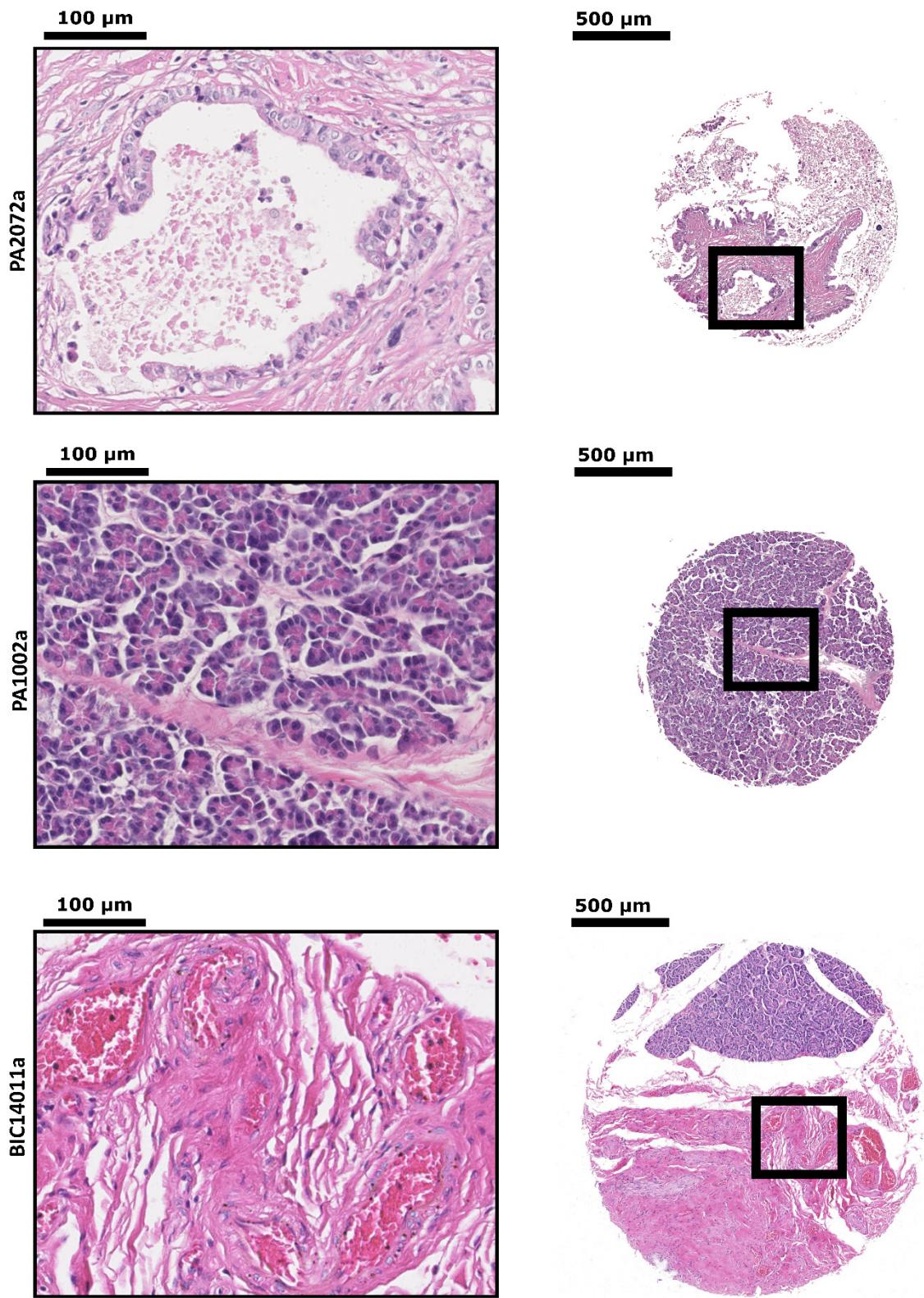


Figure S3. H&E images of zoomed biopsies (from TMAs PA2072a, PA1002a, BIC14011a) shown in Figures 2 and 4.

Spectral regions used for biochemical information extraction

Table S2. List of spectral regions used for biochemical information extraction. Additional region of 1586-1705 cm⁻¹ (Amide I), was defined for normalization purpose.

No.	Band range [cm ⁻¹]	
1	940	980
2	1015	1040
3	980	1050
4	1040	1070
5	980	1100
6	1050	1100
7	980	1140
8	1050	1140
9	1100	1140
10	1010	1155
11	1160	1180
12	1140	1180
13	1190	1210
14	1180	1210
15	1210	1280
16	1190	1290
17	1180	1290
18	1210	1290
19	1263	1296
20	1295	1320
21	1295	1325
22	1325	1346
23	1340	1360
24	1360	1390
25	1346	1420
26	1360	1425
27	1420	1478
28	1425	1480
29	1478	1586
30	1490	1590
31	1710	1760
32	2825	2860
33	2800	2880
34	2880	2940
35	2940	2980
36	2800	3025
37	3000	3025
38	2995	3095
39	3025	3100
40	2995	3570
41	3100	3600

Validation description

Cancer class includes patient annotations: Malignant. **Inflammation class** includes patient annotation Inflammation. **Healthy class** includes patient annotation: Normal, NAT, PanIN.

Table S3. FT-IR patient annotations to folds in cross validation and test sets for Random Forest classification. Patients remaining in each set were assigned to a given model set.

validation type_fold	Patient annotation		
	Cancer	Inflammation	Healthy
Cross_validation_set_1	24, 28, 29, 35, 39, 42, 44, 86, 106, 113, 114, 120, 123, 124, 126, 128, 132, 134, 139, 153, 155, 156, 162, 165, 177, 192, 193, 196, 200	185, 214, 220, 223, 239, 240, 241, 242, 243, 244, 245, 247, 248	87, 91, 95, 97, 102, 149, 262, 263
Cross_validation_set_2	2, 5, 11, 13, 15, 16, 19, 25, 36, 37, 55, 58, 59, 61, 62, 110, 121, 127, 130, 138, 141, 144, 154, 167, 171, 172, 179, 183, 186, 187, 207	64, 72, 92, 217, 219, 222, 224, 225, 228, 229, 235, 260, 261	73, 74, 78, 88, 90, 93, 100

Cross_validation_set_3	3, 7, 9, 12, 17, 22, 26, 30, 31, 32, 34, 40, 43, 53, 107, 108, 109, 111, 118, 142, 147, 157, 158, 160, 169, 176, 178, 180, 190, 194, 203	65, 69, 70, 215, 226, 227, 230, 232, 246, 249, 253, 258, 259	79, 84, 89, 99, 103, 150, 151
Cross_validation_set_4	4, 8, 14, 18, 21, 23, 41, 45, 56, 60, 104, 112, 116, 133, 137, 143, 159, 163, 164, 168, 170, 188, 189, 197, 199, 201, 202, 205, 206	66, 67, 148, 211, 212, 213, 221, 233, 234, 236, 251, 252, 255	76, 77, 82, 83, 85, 94, 96
External_test_set	1, 6, 10, 20, 27, 33, 38, 54, 57, 105, 115, 117, 119, 122, 125, 129, 131, 135, 136, 140, 145, 146, 161, 166, 173, 174, 175, 181, 182, 195, 204	63, 68, 71, 210, 216, 218, 237, 238, 250, 254, 256, 257, 264	80, 81, 98, 101, 152