Form-Vessel Classification of Cholangioscopy Findings to Diagnose Biliary Tract Carcinoma's Superficial Spread

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Supplementary Material

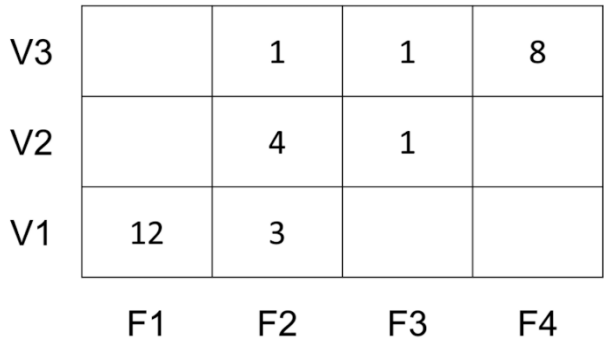

Figure S1. Association between pathology and F–V factors. The 30 biopsy specimens are summarized in the Table in which F and V factors are combined. The numbers in the squares represent the number of biopsied specimens in each F–V evaluations. A positive correlation was observed between F- and V-factor scores (correlation coefficient: 0.91).

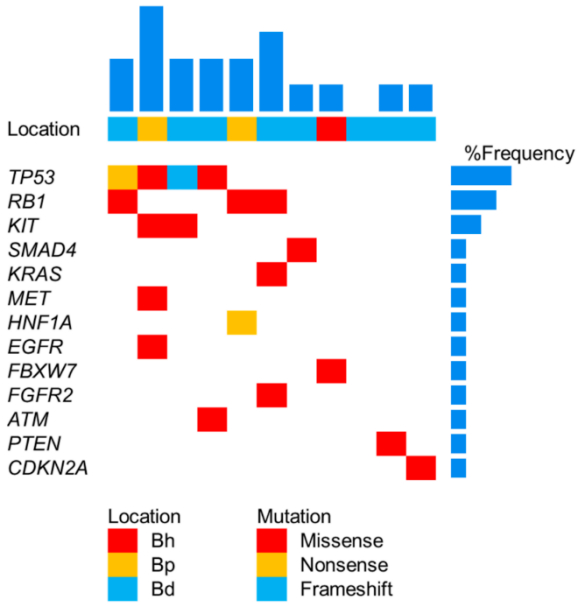

Figure S2. Genetic mutations detected in biopsied samples of the main tumor. The upper panel shows the tumor location and the number of mutations in each case as a bar graph. The squares in the main panel show the mutations detected in the tumor samples divided by mutation type. The histogram on the right shows the percentage of cases with a mutation in each gene, detected by screening for 50 cancer-related genes. Bh, intrahepatic bile duct; Bp, perihilar bile duct; Bd, distal bile duct.

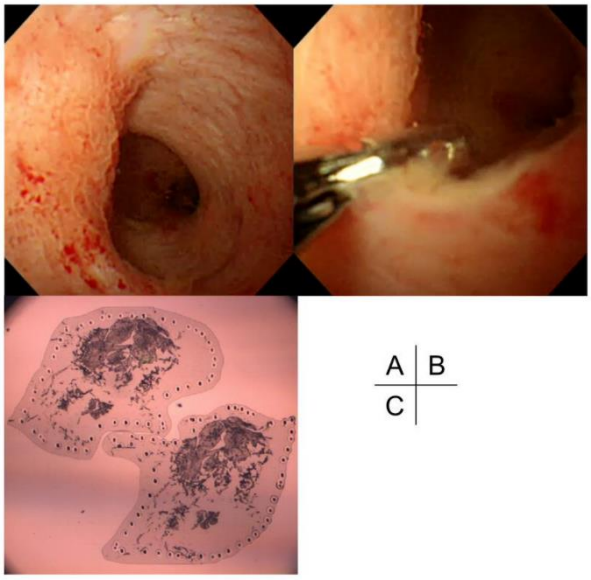

Figure S3. Bile duct biopsies conducted via peroral cholangioscope (POCS)**.** (**A**) POCS findings of the bile duct were determined as F2V3. (**B**) Bile duct epithelium with F2V3 findings biopsied via POCS. (**C**) Formalin-fixed, paraffin-embedded biopsied specimens were laser-capture microdissected and used for DNA extraction.

Table S1. DNA status of all biopsy specimens.

Number	Case	DNA extracted (ng)	Mean read depth
1	1	23.2	4025
2	2	< 2.0	6835
3	2	< 2.0	3697
4	3	< 2.0	9630
5	3	< 2.0	4364
6	3	< 2.0	8974
7	3	25.8	2298
8	4	13	7500
9	4	26	4166
10	4	7.9	7759
11	4	14.1	12761
12	5	4.6	261
13	6	34	7640
14	6	2.7	2322
15	6	< 2.0	5721
16	6	7.2	12055
17	7	< 2.0	11024
18	7	14.8	9870
19	7	13	6738
20	7	29.6	1996
21	8	< 2.0	8018
22	9	< 2.0	13359
23	9	3.8	9232
24	9	22.4	6671
25	10	< 2.0	16055
26	10	< 2.0	12821
27	11	< 2.0	12766
28	11	2.5	12480
29	11	7.4	6325
30	11	7.7	3666

Table S2. Evaluation of F–V classification and genetic mutation for each biopsy specimen.

Number	Case	Main-tumor location	F factor	V factor	Pathology	Genes with mutation (VAF, %)
1	1	Bd	4	3	malignant	*TP53* (68.7), *RB1* (17.7)
2	2	Bp	2	3	malignant	*TP53* (40.2), *KIT* (7.8), *MET* (4.7), *EGFR* (3.8)
3	2	Bp	1	1	benign	
4	3	Bd	2	2	malignant	*KIT* (2.4), *TP53* (2.2)
5	3	Bd	2	2	benign	*TP53* (7.5)
6	3	Bd	1	1	benign	
7	3	Bd	4	3	malignant	
8	4	Bd	3	2	benign	*ATM* (15.4)
9	4	Bd	3	3	malignant	*TP53* (24.3), *ATM* (23.3)
10	4	Bd	1	1	benign	
11	4	Bd	1	1	benign	
12	5	Bp	4	3	malignant	*HNF1A* (18.1), *RB1* (12.7)
13	6	Bd	2	2	benign	*RB1* (17.4), *KRAS* (5.3), *FGFR2* (4.7)
14	6	Bd	2	2	benign	*RB1* (19.8), *FGFR2* (4.0)
15	6	Bd	1	1	benign	
16	6	Bd	4	3	benign	
17	7	Bd	4	3	malignant	*SMAD4* (30.4)
18	7	Bd	1	1	benign	
19	7	Bd	2	1	benign	
20	7	Bd	2	1	benign	
21	8	Bh	4	3	benign	*FBXW7* (21.4)
22	9	Bd	1	1	benign	
23	9	Bd	2	1	benign	
24	9	Bd	4	3	malignant	
25	10	Bd	1	1	benign	*PTEN* (2.2)
26	10	Bd	1	1	benign	
27	11	Bd	1	1	benign	*CDKN2A* (2.2)
28	11	Bd	1	1	benign	
29	11	Bd	1	1	benign	
30	11	Bd	4	3	benign	