Supplementary Figure 1. Immunohistochemistry (IHC) methods as follows: spares were dewaxed, hydrated, blocked, followed by incubation with primary antibody 4°C overnight (Both antibodies were diluted 1:200, Proteintech, Chicago, USA), and further incubation with the streptavidin-biotin complex (Maixin, Fuzhou, China). After diaminobenzidine and hematoxylin (Beyotime, Shanghai, China) staining, tissue was quantified using a composite score obtained by multiplying the staining intensity level (0, no staining; 1, weak staining; 2, moderate staining; 3, strong staining) with the percentage of positive cells (0, 0%; 1, 1-10%; 2, 10-50%; 3, > 50%). A. C-MYC without expression; B. C-MYC with lower expression; C. C-MYC with High expression; D. HMGA2 without expression; E. HMGA2 with lower expression; F. HMGA2 with high expression.
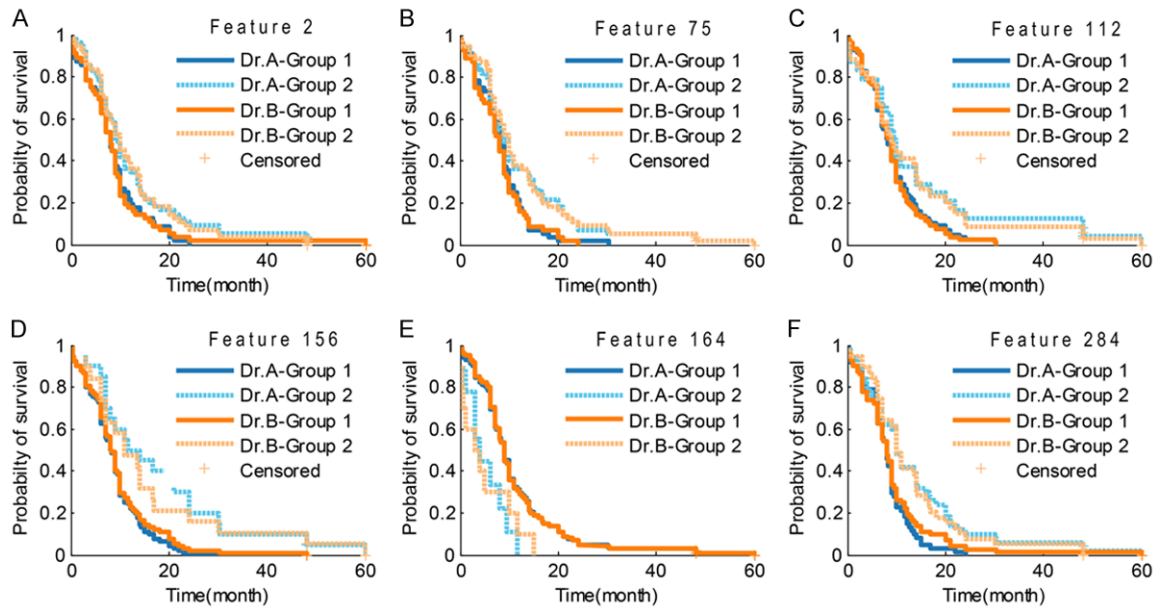
Supplementary Figure 2. Kaplan-Meier curves for Features in patients with pancreatic ductal adenocarcinoma. We compute feature value of the tumor region by two experienced doctors' segmentation and split into two groups by feature median: (A) Feature 2, (B) Feature 75, (C) Feature 112, (D) Feature 156, (E) Feature 164, and (F) Feature 284.
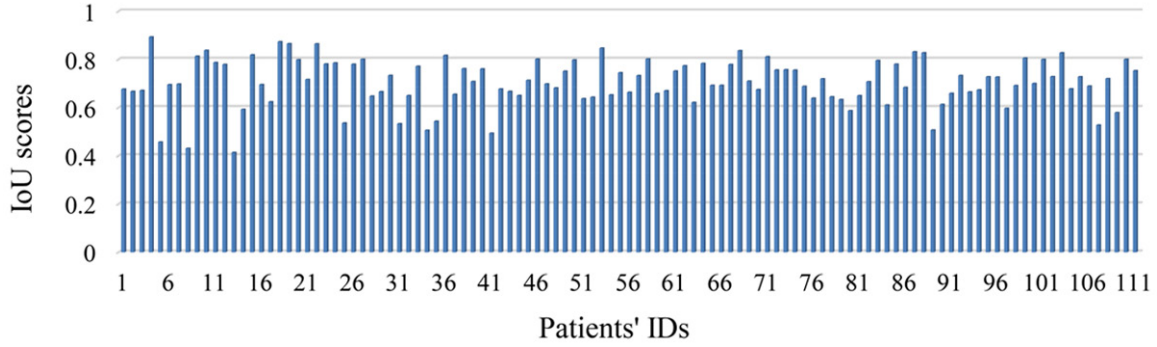
Supplementary Figure 3. Intersection-over-union scores of the corresponding patients from the segmented images between two doctors.

Supplementary Table 1. Multivariate Cox regression analysis of survival rate in patients with pancreatic ductal adenocarcinoma

| Factors	Groups	Survival time range (month)	95% CI		P
			Lower	Upper	
Age (year)	< 59	10.367 ± 1.243	7.113	10.887	0.787
Age (year)	≥ 59	9.064 ± 1.605	6.833	9.767	
Gender	Male	12.419 ± 1.752	7.725	10.275	0.326
Gender	Female	8.943 ± 0.986	6.153	10.447	

Note: CI, confidence level.
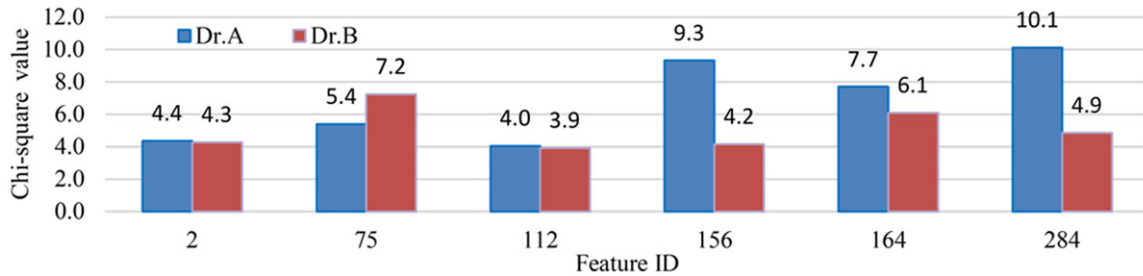
Supplementary Figure 4. Six features whose chi-square values are greater than 3.8 in two doctors' log-rank tests for patients' survival time prediction. Higher value identifies a stronger distinguishing power. Blue bars indicate chi-square values computed from the ROIs that are segmented by Dr. A, and red bars indicate chi-square values computed from the ROIs that are segmented by Dr. B.
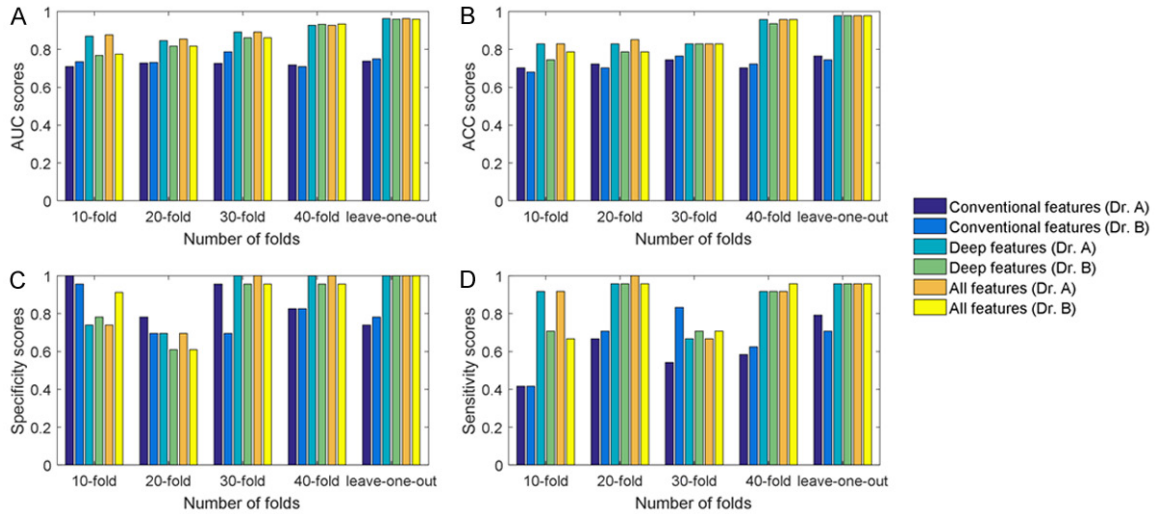
Supplementary Figure 5. C-MYC expression classification using selected conventional features, deep convolutional features and all features extracted from the ROIs segmented by Dr. A and Dr. B in different k-folds cross validation tests (Scores V.S. N-folds). A. AUC scores; B. Accuracy scores; C. Specificity scores; D. Sensitivity scores.
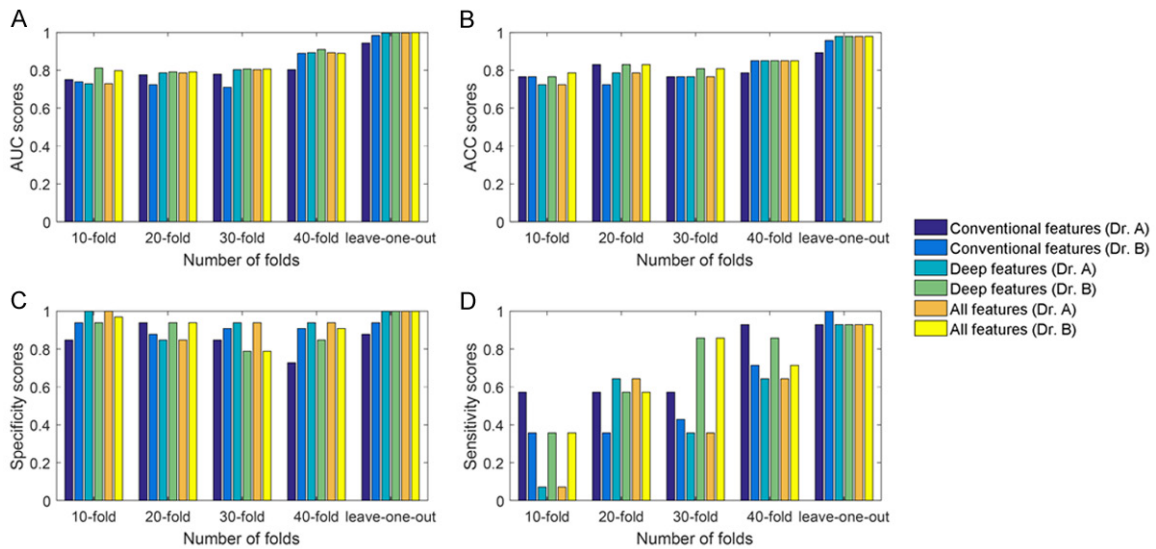
Supplementary Figure 6. HMGA2 expression classification using selected conventional features, deep convolutional features and all features extracted from the ROIs segmented by Dr. A and Dr. B in different k-folds cross validation tests (Scores V.S. N-folds). A. AUC scores; B. Accuracy scores; C. Specificity scores; D. Sensitivity scores.

Supplementary Table 2. Correlations of C-MYC and HGMA2 protein expression with the age and gender of pancreatic ductal adenocarcinoma

Variables	C-MYC			HMGA2		
	High expression	Low expression	P	High expression	Low expression	P
Sample size	24	23		14	33	
Gender (male/female)	17/7	18/5	0.5594[a]	11/3	24/9	0.6743[a]
Age(years)	57.96 ± 9.93	55.52 ± 10.15	0.5776[b]	55.50 ± 11.96	57.30 ± 9.20	0.4098[b]

Note: [a]Pearson Chi-square test, [b]Two-sample t-test. C-MYC: C-MYC protein; HMGA2: high-motility group AT-hook2 protein.