S1 Table. Demographic and biological features in the two groups of initial RNA sequencing and identifying candidate gene expressions, respectively

Parameters, number of patients	Group for initial RNA	Group for candidate gene	<i>p</i> -value ^a
or mean \pm SD	sequencing, n = 18	expressions, $n = 10$	
Sex, male/female	4/14	1/9	0.626
Age, years	60 ± 10	58 ± 8	0.567
Primary tumor site, colon/rectum	10/8	7/3	0.689
CLM, single/multiple	11/7	4/6	0.433
Level of serum CEA, ng/ml	70.6 ± 163.2	47 ± 99	0.677
Metastatic lymph node+	12	6	1
Lymphovascular invasion+	8	6	0.695
Perineural invasion+	7	4	1
Differentiation of PCC, WD/MD/PD	0/18/0	9/1	0.357
MSI of PCC, MSS/MSI-L/MSI-H	17/0/1	10/0/0	1
p53 expression of PCC ^b , 0-1/2-4	7/11	4/5	1
ALDH1A1 mRNA overexpression ^b	14	9	0.626
IGFBP1 mRNA overexpression ^b	16	9	1

SD, standard deviation; PCC, primary colorectal cancer; CLM, colorectal liver metastasis; CEA, carcinoembryonic antigen; WD/MD/PD, well-/moderately-/poorly-differentiated; MSI, microsatellite instability; MSS, microsatellite stable; MSI-L, MSI with low frequency; MSI-H, MSI with high frequency; ISR, intersphincteric resection; pStage, pathological AJCC stage; n.a., not applicable. Bold prints, p < 0.05.

^aAll parameters were compared using Fisher's exact test with two-sided verification or Pearson's χ^2 test and an unpaired Student's *t*-test.

^bNuclear expression of p53: 0, no expression; 1, $0-\le 25\%$; 2, $>25-\le 50\%$; 3, $>-\le 75\%$; 4, >75%.

^cFold-changes of mRNA expression compared to that of normal colic epithelium: if greater in CLM than in PCC.