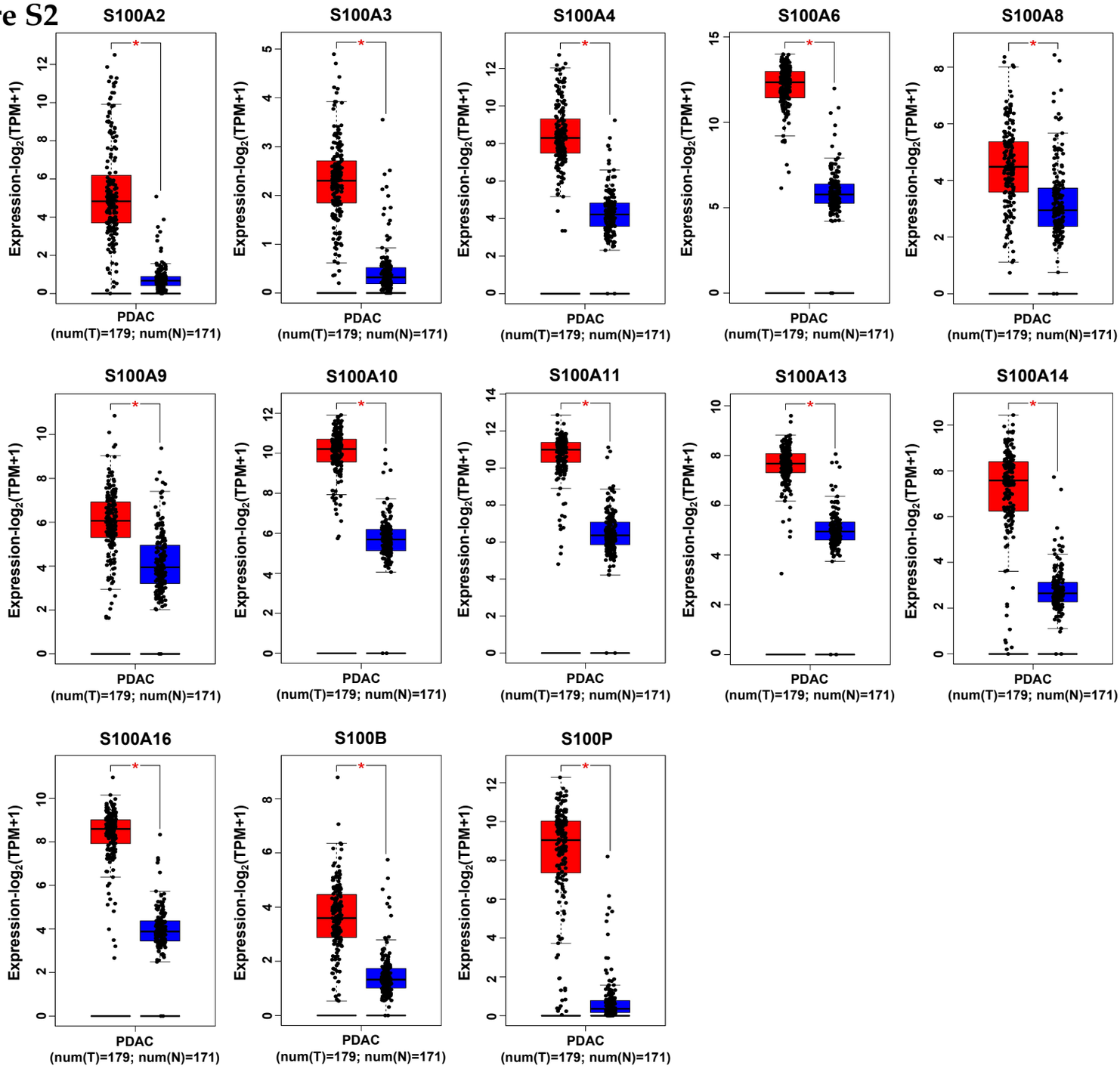
Figure S1

S100	A1		A2		A3		A4		A5		A6		A7		A7A		A7B		A8		A9		A10		A11		A12		A13		A14		A16		B		G		P		Z	
Analysis Type by Cancer	Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal	
Bladder cancer			2								1										1				3						2				1				1			
Brain and CNS Cancer		7					2				2								1				7		5				2				1								
Breast Cancer		2						1				3	2						2				1	1	2	1	1		1		6		1			7			13			
Cervical Cancer																					1							1				2							1			
Colorectal Cancer			16		3								1		1				4		4			2	15		1					7		2		2			11	1	1	
Esophageal Cancer				2		1														1		2		4		3		3		2		3		2				1	2		
Gastric Cancer			1				1									1							3		1															4		
Head and Neck Cancer	1	3	2		1			1		1		1	4		3					1		2	2	1	1							3						1	1		
Kidney Cancer		1		6	1						2										3		4		6						1		1							
Leukemia				1			3	3			1	4	2						3	6	3	9	2	2	1	10		12	5				2						9		
Liver Cancer											3									3			3		2						1								1		
Lung Cancer		1	7			8		12				1								8		3		6				2		1								3		
Lymphoma							4	1			5												3	2	6				8				1						3		
Melanoma	1			1																											1			2				1		
Myeloma																				1		1						1													
Other Cancer			1				4	1			1				2					1	1	1	2		6		2	1			1	1			1						
Ovarian Cancer	2		3								1													1	1				1		2							1			
Pancreatic Cancer			1				3				2												4		4				2		1		2					5			
Prostate Cancer								1				2																		1		1		1		1					
Sarcoma		5			1		1	2			1	1								8		2	1	2	1	1				1		4				7				4		
Significant Unique Analyses	4	19	33	10	6	9	17	22		1	18	12	9		6	1			10	29	12	21	29	21	54	15	4	20	17	7	13	22	7	6	2	18			38	25	1	
Total Unique Analyses	349		335		342		309		300		243		320		153		22		344		326		352		314		344		343		248		171		362		296		344		147	



Box color is determined by the best gene rank percentile for the analyses within the box.
The numbers listed in each box represent the number of datasets that meet the filter criteria.

Figure S2


S100A2
S100A3
S100A4
S100A6
S100A8
S100A9
S100A10
S100A11
S100A13
S100A14
S100A16
S100B
S100P
Expression-log2(TPM+1)
PDAC
(num(T)=179; num(N)=171)

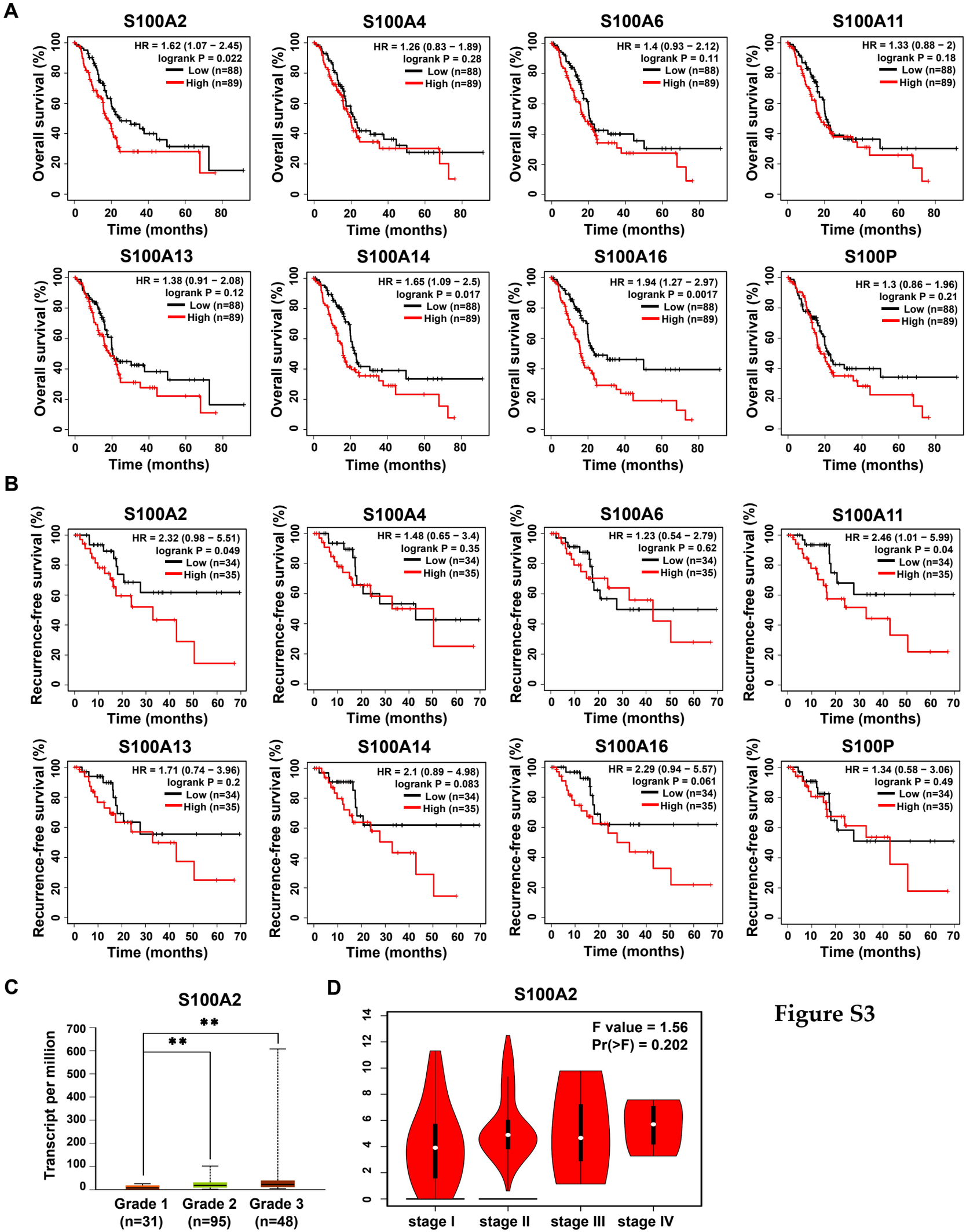
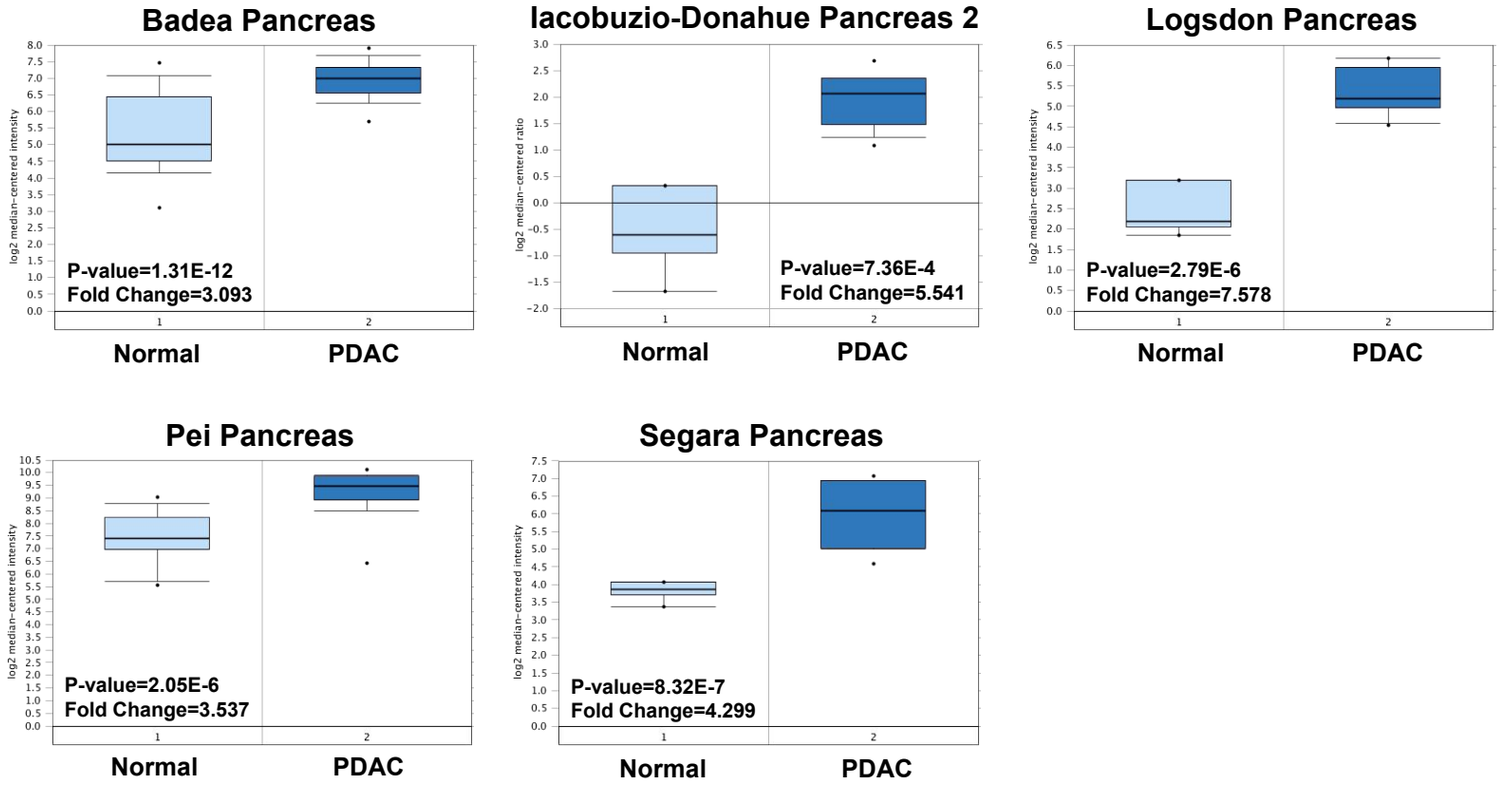

A
S100A2
HR = 1.62 (1.07 − 2.45)
logrank P = 0.022
Low (n=88)
High (n=89)
S100A4
HR = 1.26 (0.83 − 1.89)
logrank P = 0.28
Low (n=88)
High (n=89)
S100A6
HR = 1.4 (0.93 − 2.12)
logrank P = 0.11
Low (n=88)
High (n=89)
S100A11
HR = 1.33 (0.88 − 2)
logrank P = 0.18
Low (n=88)
High (n=89)
S100A13
HR = 1.38 (0.91 − 2.08)
logrank P = 0.12
Low (n=88)
High (n=89)
S100A14
HR = 1.65 (1.09 − 2.5)
logrank P = 0.017
Low (n=88)
High (n=89)
S100A16
HR = 1.94 (1.27 − 2.97)
logrank P = 0.0017
Low (n=88)
High (n=89)
S100P
HR = 1.3 (0.86 − 1.96)
logrank P = 0.21
Low (n=88)
High (n=89)
Overall survival (%)
Time (months)
B
S100A2
HR = 2.32 (0.98 − 5.51)
logrank P = 0.049
Low (n=34)
High (n=35)
S100A4
HR = 1.48 (0.65 − 3.4)
logrank P = 0.35
Low (n=34)
High (n=35)
S100A6
HR = 1.23 (0.54 − 2.79)
logrank P = 0.62
Low (n=34)
High (n=35)
S100A11
HR = 2.46 (1.01 − 5.99)
logrank P = 0.04
Low (n=34)
High (n=35)
S100A13
HR = 1.71 (0.74 − 3.96)
logrank P = 0.2
Low (n=34)
High (n=35)
S100A14
HR = 2.1 (0.89 − 4.98)
logrank P = 0.083
Low (n=34)
High (n=35)
S100A16
HR = 2.29 (0.94 − 5.57)
logrank P = 0.061
Low (n=34)
High (n=35)
S100P
HR = 1.34 (0.58 − 3.06)
logrank P = 0.49
Low (n=34)
High (n=35)
Recurrence-free survival (%)
Time (months)
C
S100A2
Transcript per million
**
**
Grade 1 (n=31)
Grade 2 (n=95)
Grade 3 (n=48)
D
S100A2
F value = 1.56
Pr(>F) = 0.202
stage I
stage II
stage III
stage IV

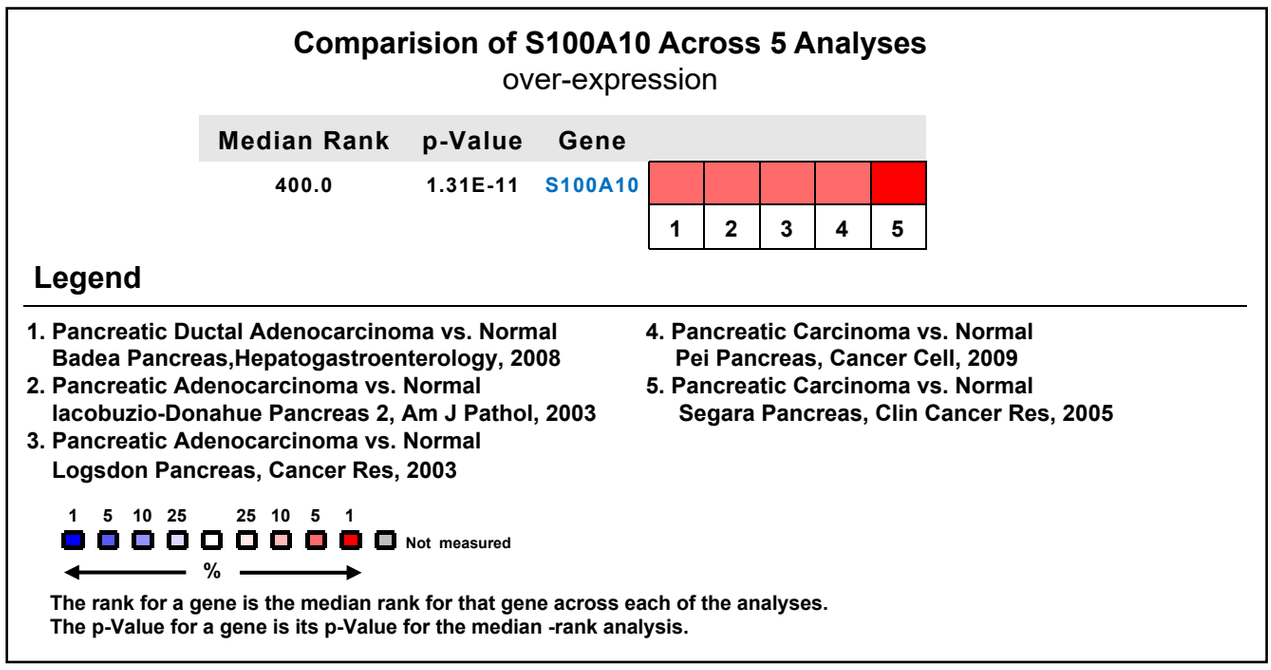
Figure S3

Figure S4

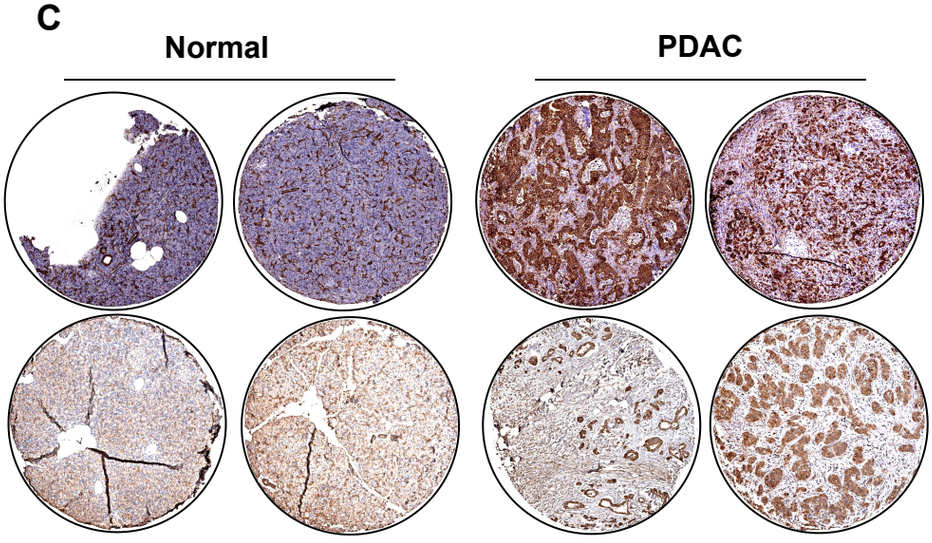
A



B



C



D

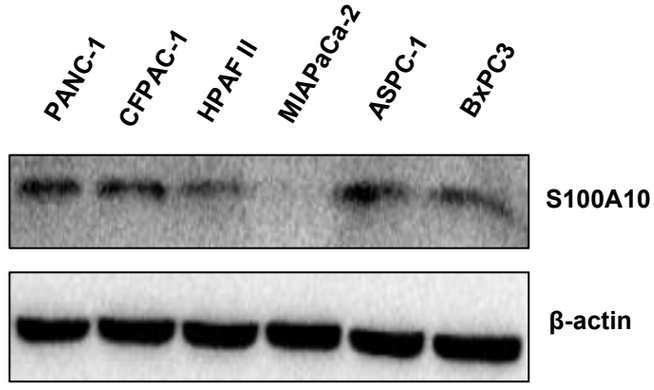
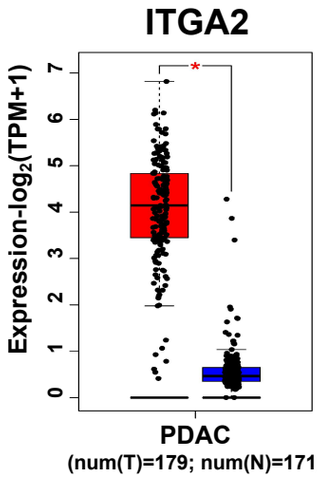
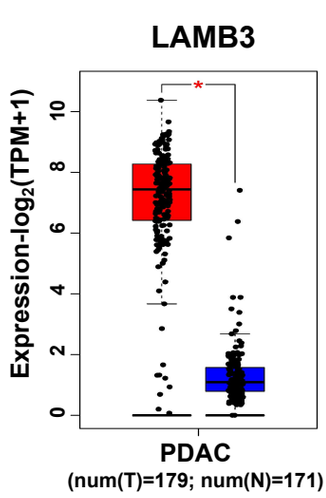
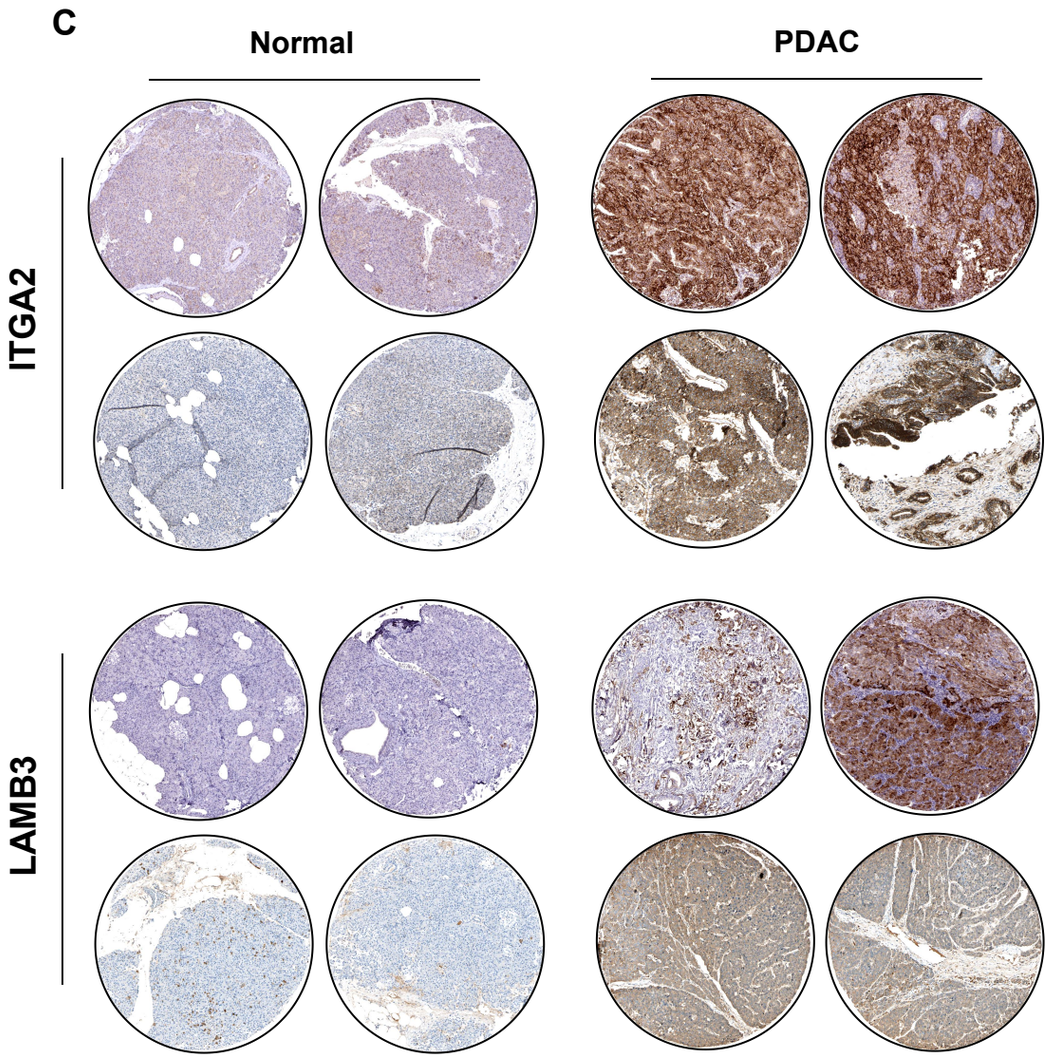
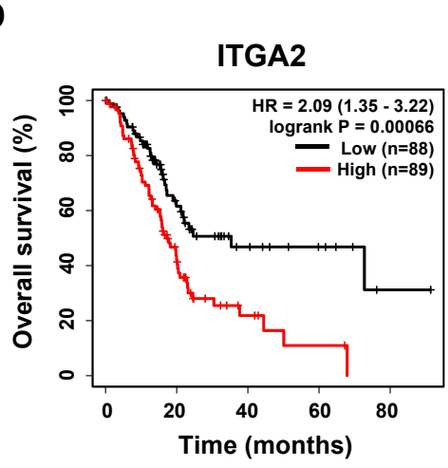


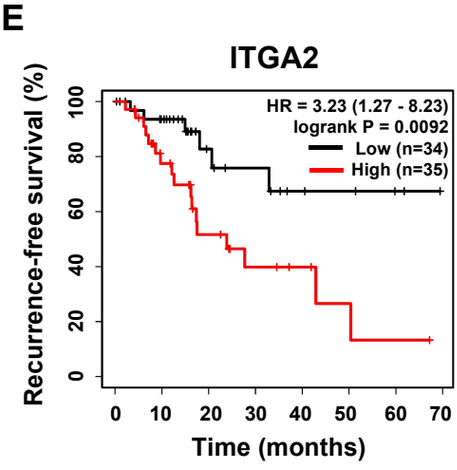
Figure S5

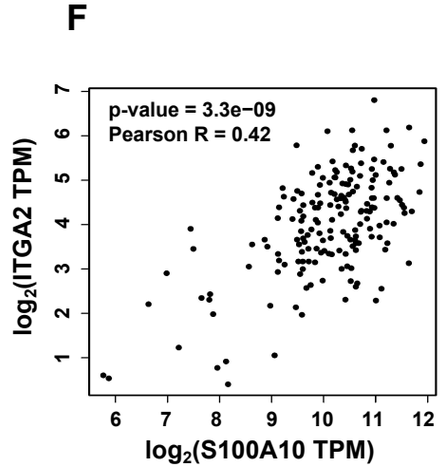

A
ITGA2
Expression-log2(TPM+1)
PDAC
(num(T)=179; num(N)=171)

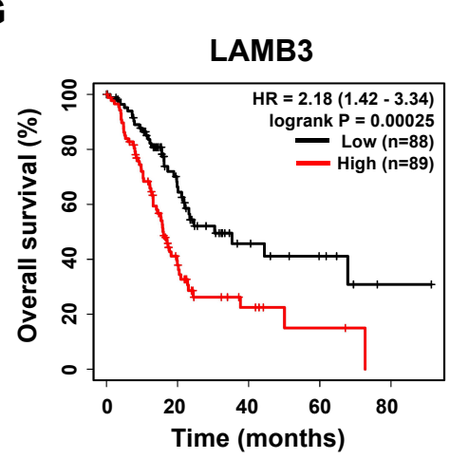

B
LAMB3
Expression-log2(TPM+1)
PDAC
(num(T)=179; num(N)=171)

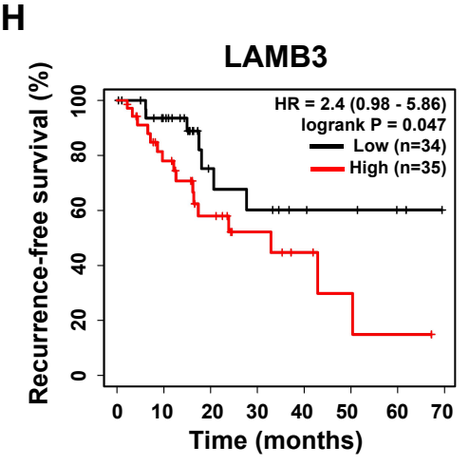

C
Normal
PDAC
ITGA2
LAMB3


D
ITGA2
HR = 2.09 (1.35 - 3.22)
logrank P = 0.00066
Low (n=88)
High (n=89)
Overall survival (%)
Time (months)


E
ITGA2
HR = 3.23 (1.27 - 8.23)
logrank P = 0.0092
Low (n=34)
High (n=35)
Recurrence-free survival (%)
Time (months)


F
p-value = 3.3e−09
Pearson R = 0.42
log2(ITGA2 TPM)
log2(S100A10 TPM)


G
LAMB3
HR = 2.18 (1.42 - 3.34)
logrank P = 0.00025
Low (n=88)
High (n=89)
Overall survival (%)
Time (months)


H
LAMB3
HR = 2.4 (0.98 - 5.86)
logrank P = 0.047
Low (n=34)
High (n=35)
Recurrence-free survival (%)
Time (months)

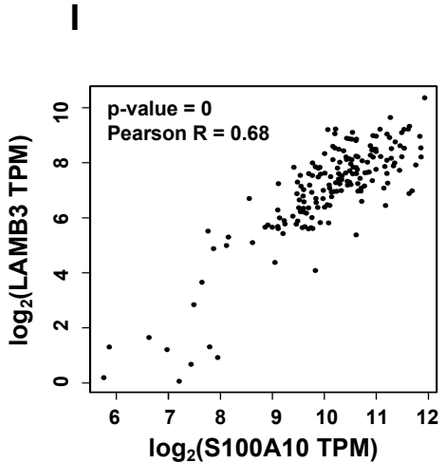

I
p-value = 0
Pearson R = 0.68
log2(LAMB3 TPM)
log2(S100A10 TPM)

Figure S6

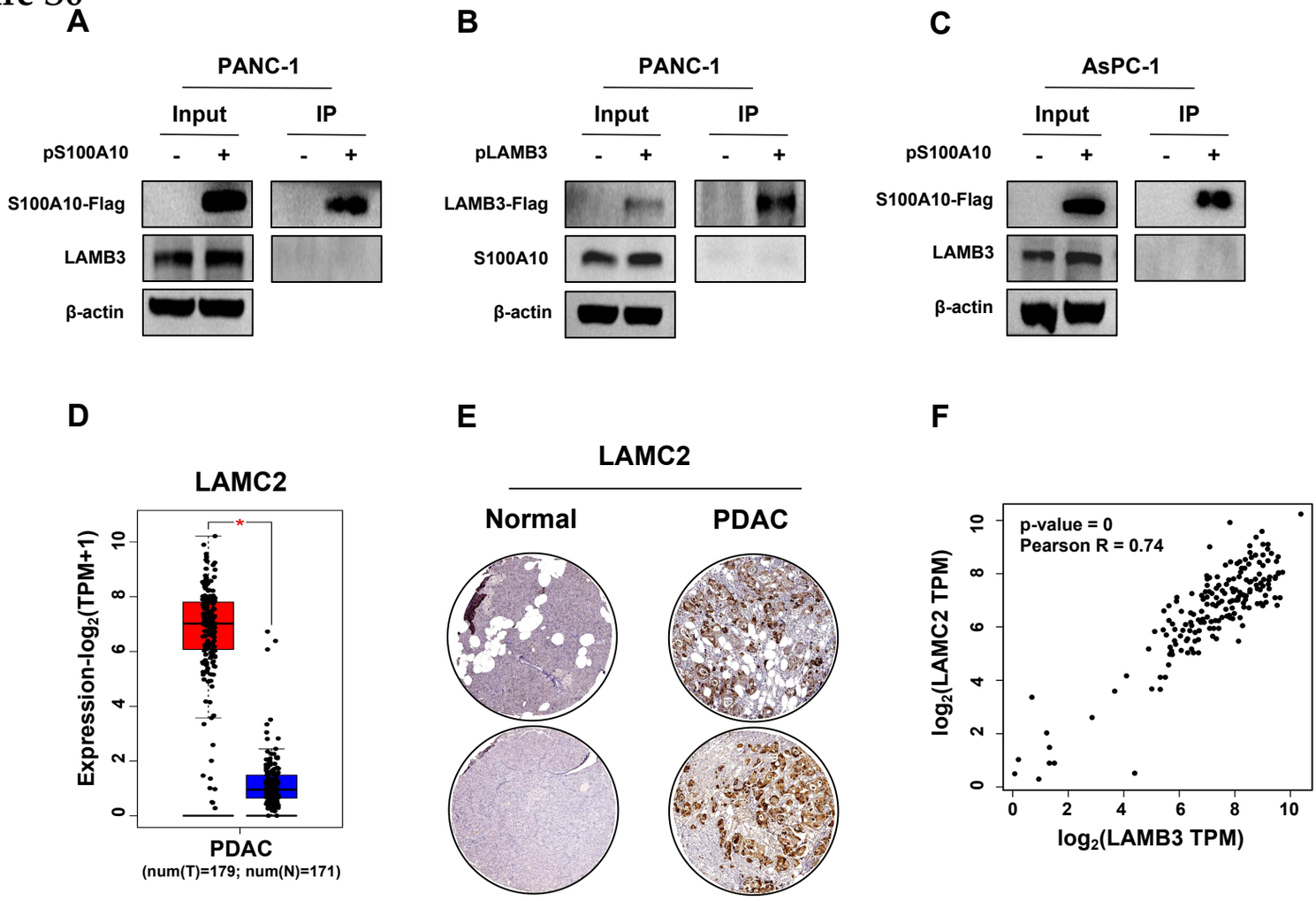

A
PANC-1
Input
IP
pS100A10
- + - +
S100A10-Flag
LAMB3
β-actin
B
PANC-1
Input
IP
pLAMB3
- + - +
LAMB3-Flag
S100A10
β-actin
C
AsPC-1
Input
IP
pS100A10
- + - +
S100A10-Flag
LAMB3
β-actin
D
LAMC2
Expression-log2(TPM+1)
0 2 4 6 8 10
*
PDAC
(num(T)=179; num(N)=171)
E
LAMC2
Normal
PDAC
F
p-value = 0
Pearson R = 0.74
log2(LAMC2 TPM)
0 2 4 6 8 10
log2(LAMB3 TPM)
0 2 4 6 8 10

Figure 2B

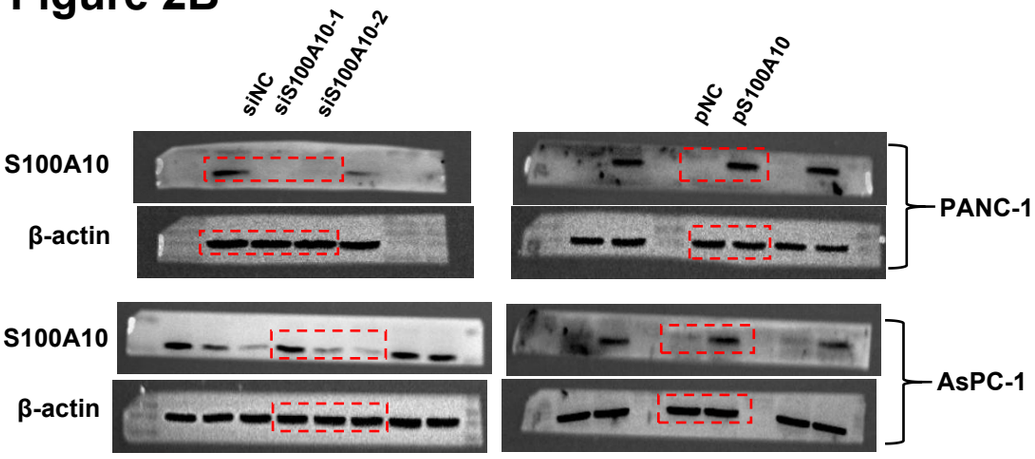


Figure 3B

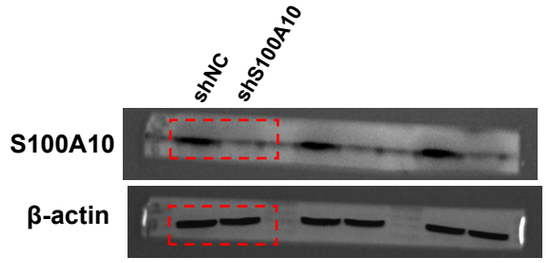


Figure 5A

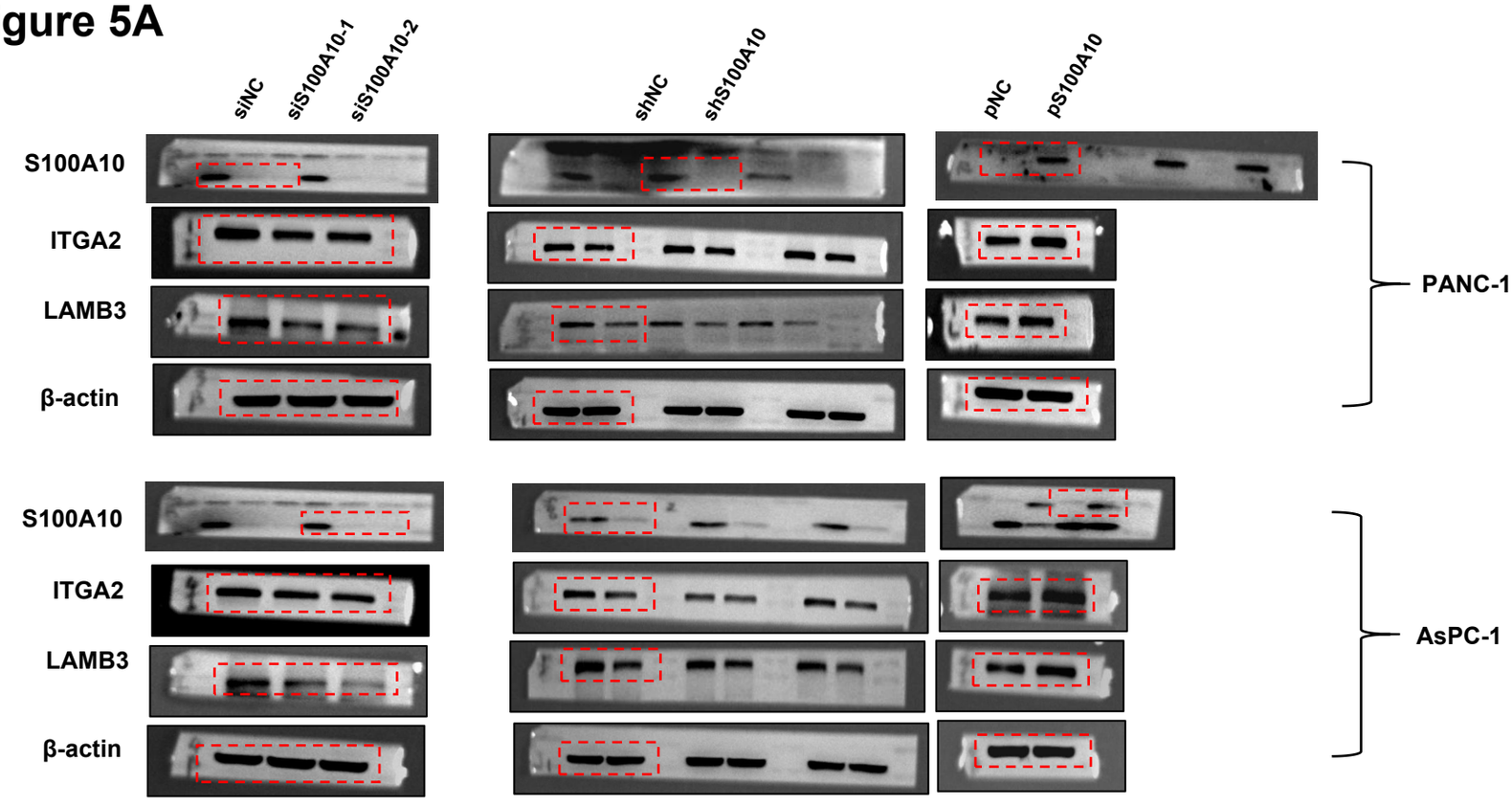


Figure 6B

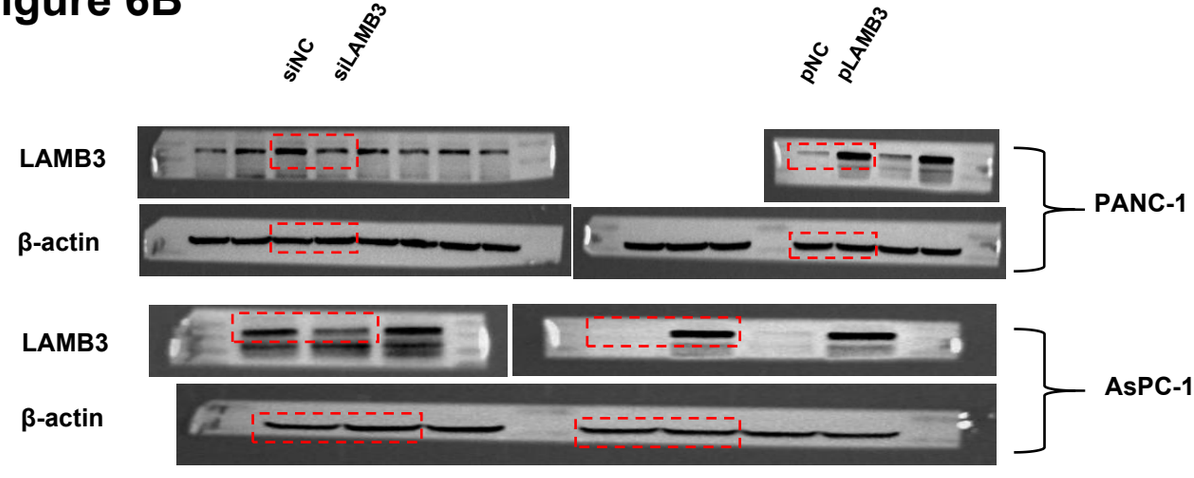


Figure 7A

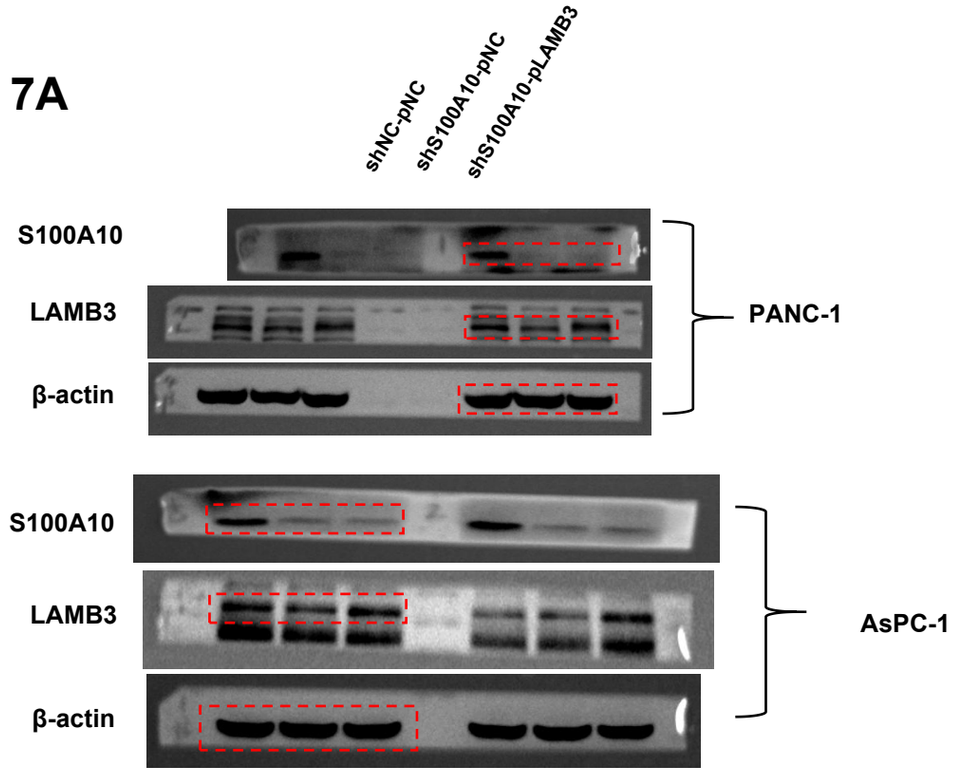


Figure 8A

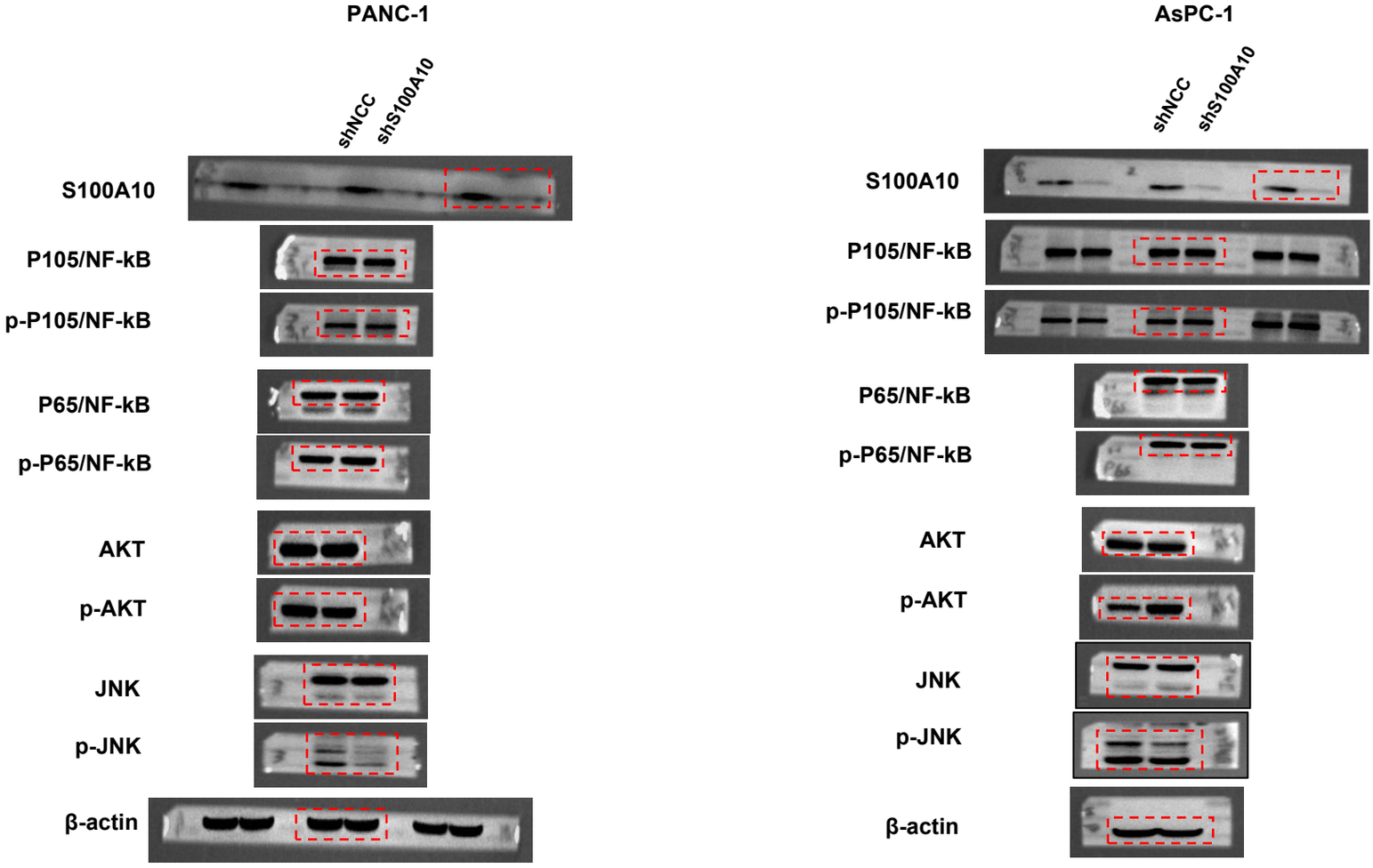


Figure 8B

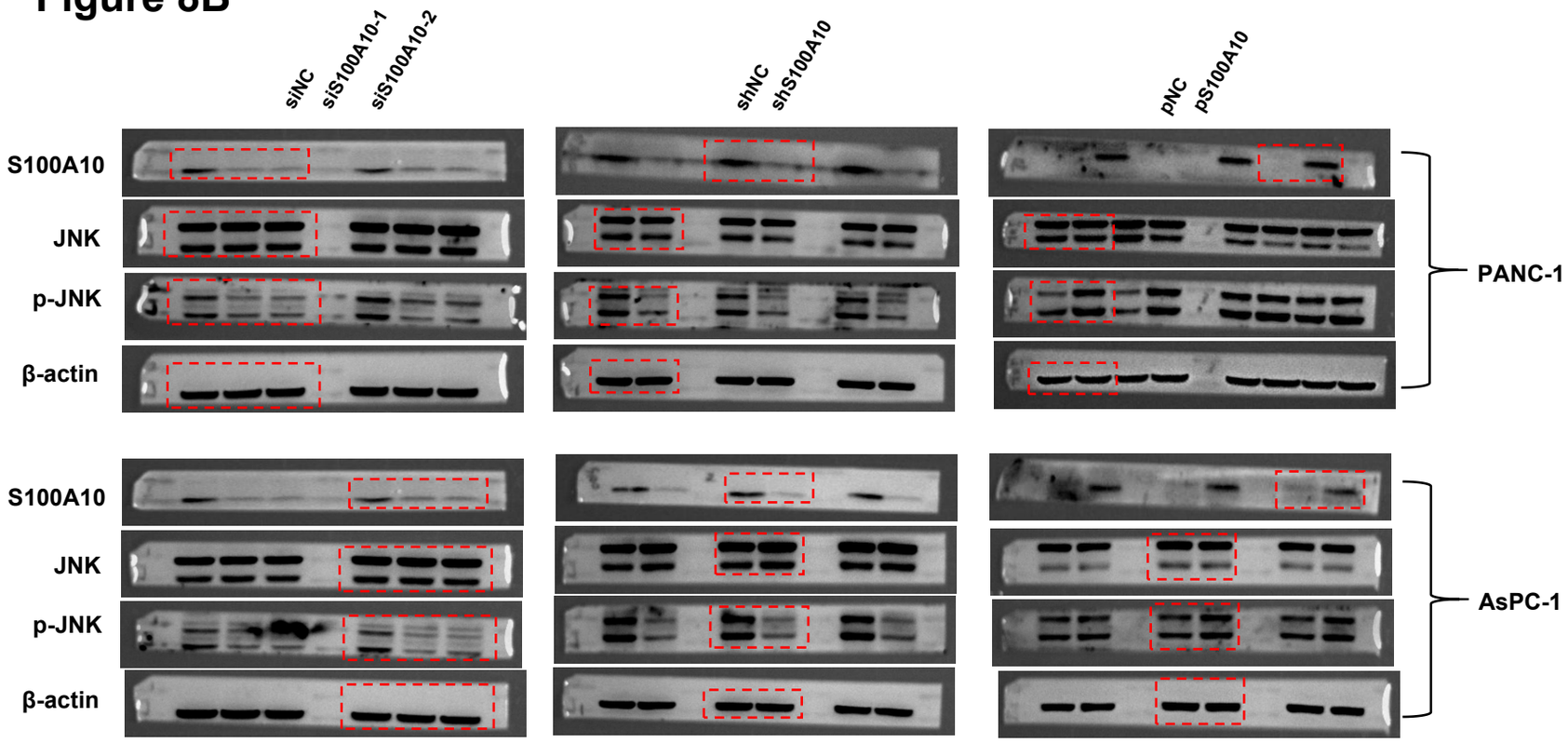


Figure 8C

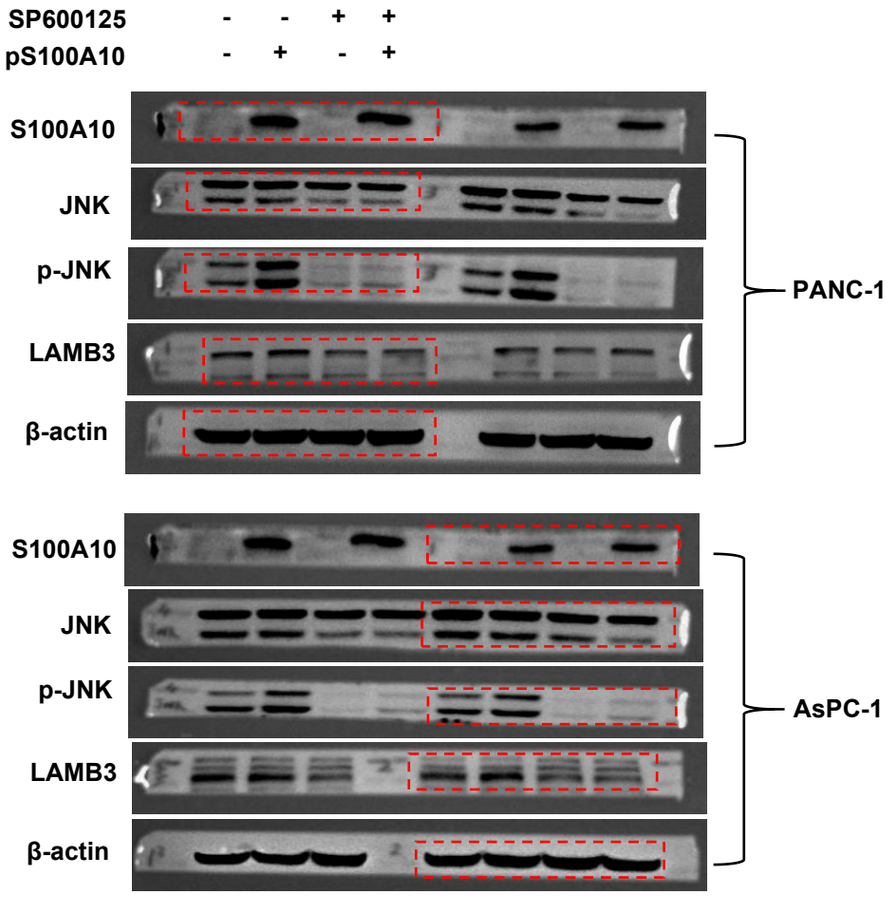


Figure 8D

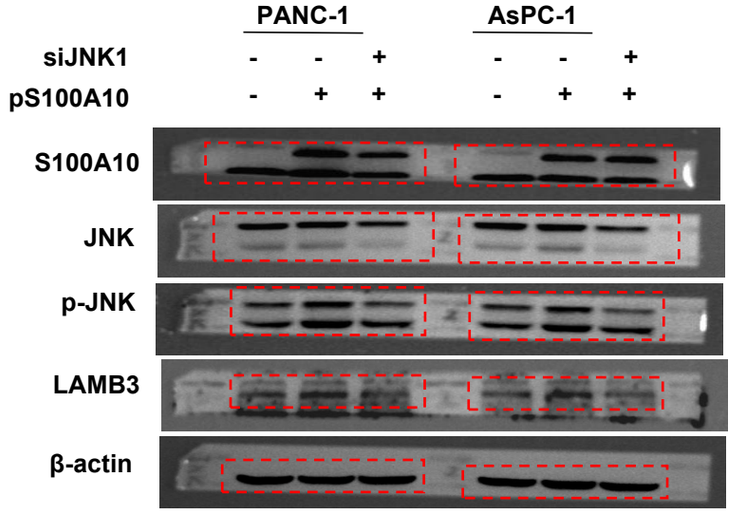


Figure 8H

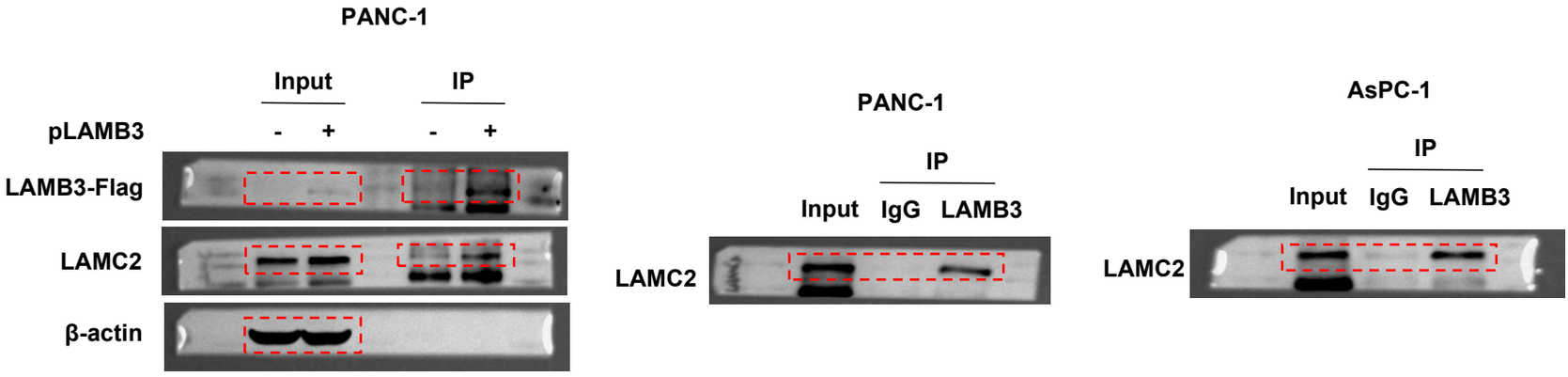


Figure S4H

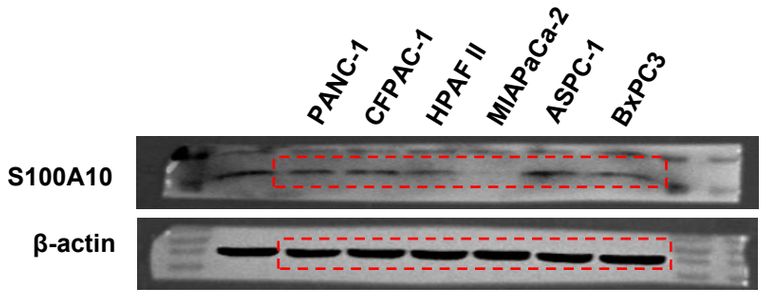


Figure S6A-C

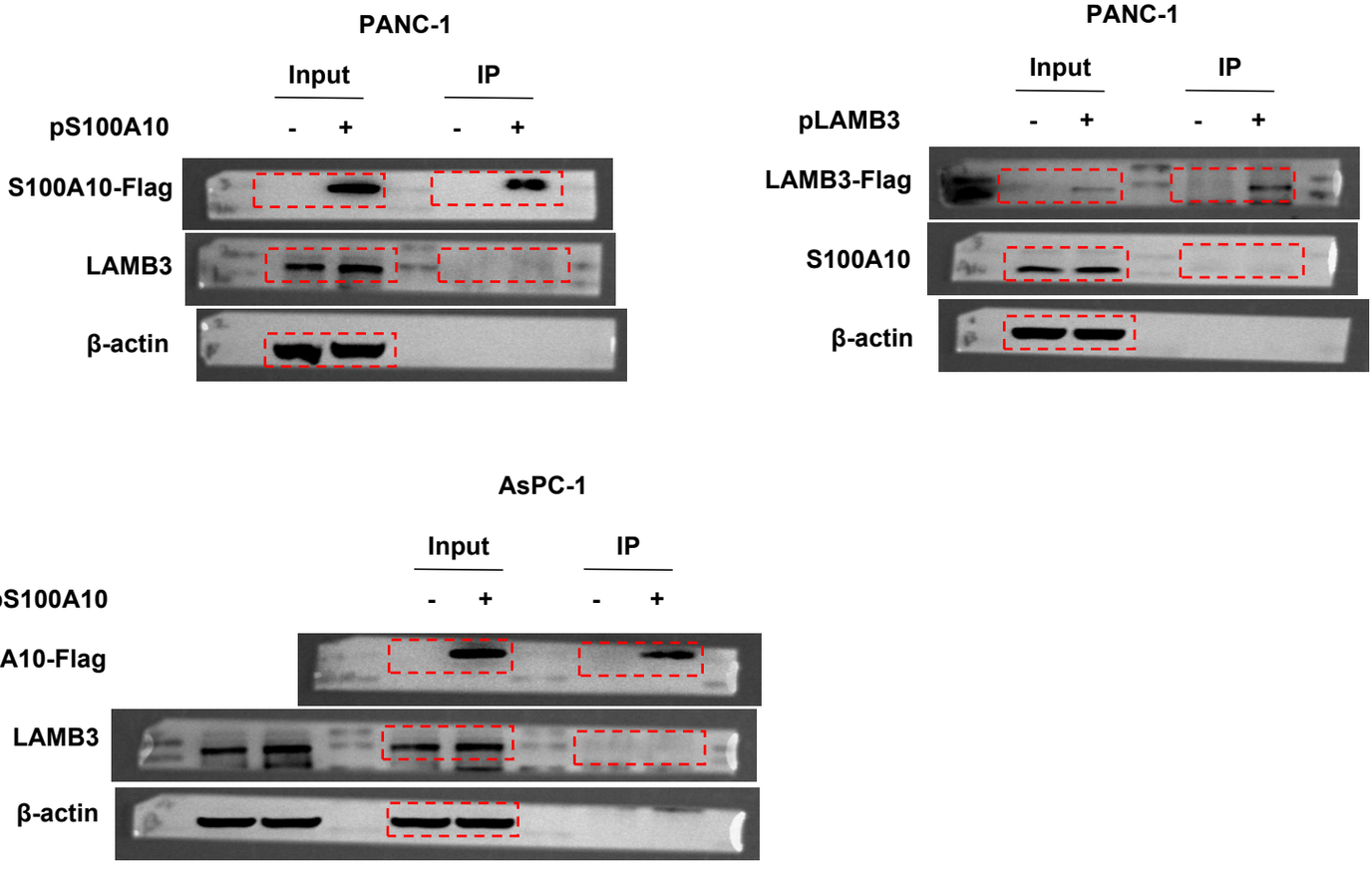


Figure S7. Whole western blot images.