Electronic Supplementary Material (ESI) for Molecular BioSystems. This journal is © The Royal Society of Chemistry 2014

Supplementary Data:

Table S1

Intensity Score	3	2	1	neg	Total Cores
Colon:					
Adenocarcinoma	5 (20)	17 (68)	3 (12)	0	25
Normal Colon Tissue	0	1 (25)	3 (75)	0	4
Cancer Adjacent Normal	2 (33.33)	2 (33.33)	0	2 (33.33)	6
Breast:					
Invasive ductal carcinoma	3 (12.5)	13 (54.16)	5 (20.83)	3 (12.5)	24
Normal Breast Tissue	0	4 (100)	0	0	4
Prostate:					
Adenocarcinoma	11 (45.83)	8 (33.33)	1 (4.16)	4 (16.66)	24
Normal Prostate Tissue	0	0	2 (50)	2 (50)	4
Cancer Adjacent Normal	1 (16.66)	5 (83.33)	0	0	6
Pancreas:					
Duct Adenocarcinoma	8 (32)	13 (52)	3 (12)	1 (4)	25
Normal Pancreas Tissue	0	6 (60)	2 (20)	2 (20)	10
Lung:					
Squamous	5 (50)	5 (50)	0	0	10
Adenocarcinoma	6 (40)	8 (53.33)	1 (6.66)	0	15
Normal Lung Tissue	0	1 (10)	1 (10)	8 (80)	10

Table S1: Intensity scoring for immunohistochemistry of hnRNPA2B1 on Mixed Tissue Array Slide. Scoring of 1, 2, and 3 relates to weak staining, intermediate staining, and strong staining, respectively. The percentage of total tissue cores with that particular intensity score is shown in brackets.

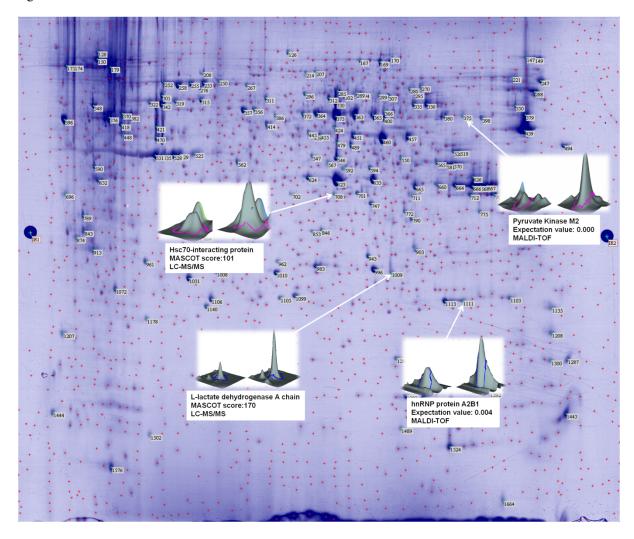


Figure S1: 2D gel (colloidal Coomassie Blue G-250 stained preparative gel) showing the positions for 4 proteins, hnRNPA2B1, Pyruvate Kinase M2, Hsc-70 Interacting protein and Lactate Dehydrogenase (A-chain) that were selected for further analysis in clinical samples. 3D images are also included for each of the 4 proteins representing the 2D-DIGE analysis for the comparison of normal human bronchial epithelial cell line (NHBE) compared to squamous cell carcinoma cell lines. Details of the mass spectrometry platform used to positively identify the proteins are included (MALDI-TOF/LC-MS/MS) together with the associated expectation value/MASCOT score.

Figure S2

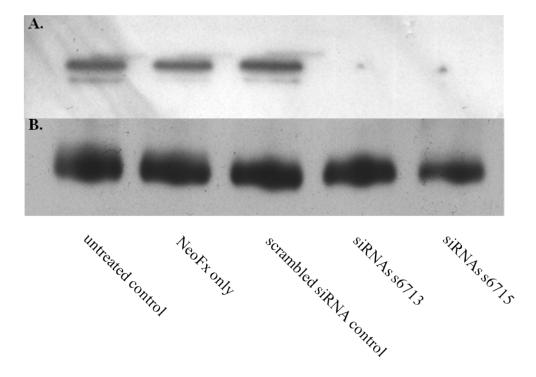


Figure S2: Western blot analysis of whole cell lysates of DLKP-M transfected cells. A reduction in the levels of hnRNPA2B1 (A) can be seen in the two knockdown siRNAs s6713 and s6715 when compared to the untreated control, NeoFx only and scrambled siRNA controls. (15 μ g protein loaded per lane). (B) α -tubulin loading control