Validation of SFRP1 Promoter Hypermethylation in Plasma as a Prognostic Marker for Survival and Gemcitabine Effectiveness in Patients with Stage IV Pancreatic Adenocarcinoma

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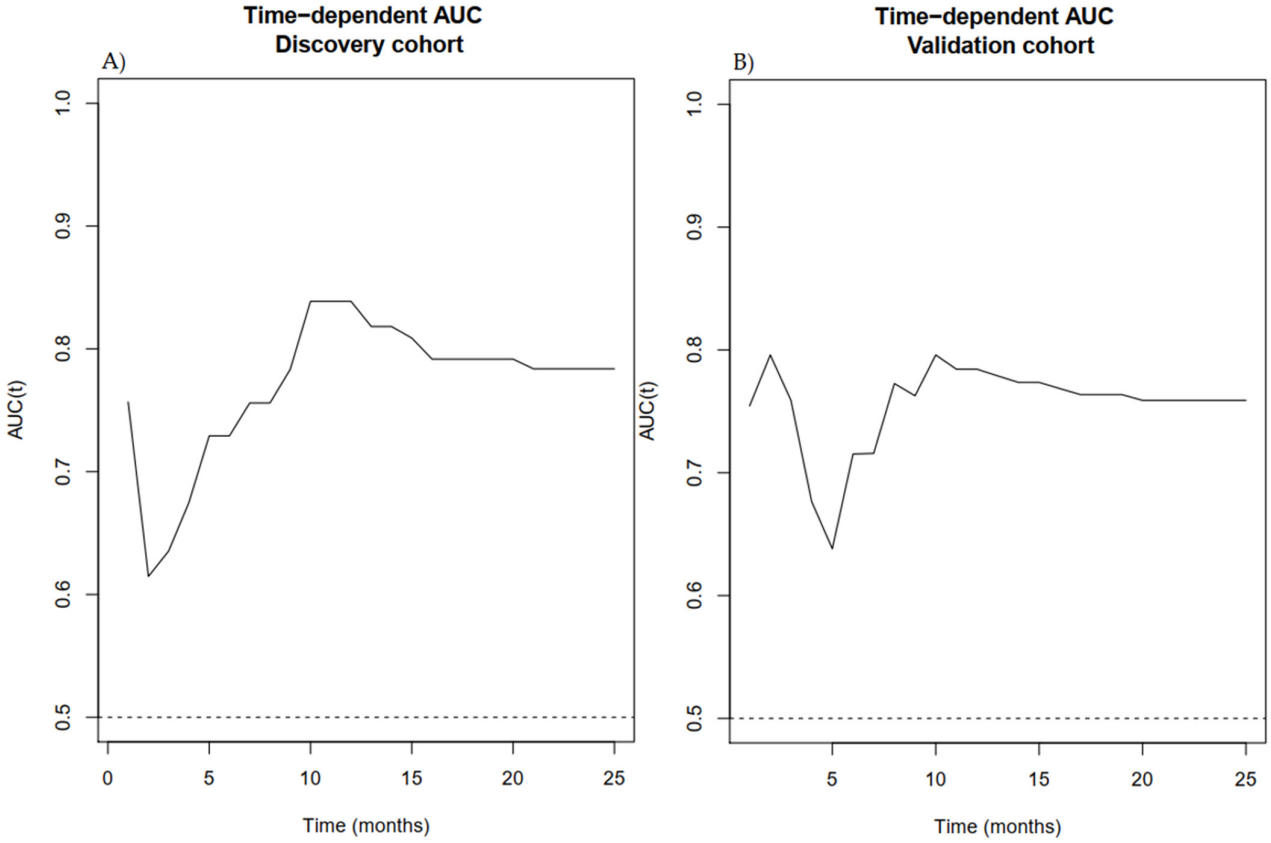

Figure S1. (**A**) IPCW estimation of cumulative/dynamic time-dependent AUC plots for patients in the discovery cohort. Accuracy of promoter hypermethylation of SFRP1 under assumption of proportional hazards. IPCW estimates of AUC(t) versus time. Estimated one-year concordance was C = 0.64 (standard error = 0.04). (**B**) IPCW estimation of cumulative/dynamic time-dependent AUC plots for patients in the validation cohort. Accuracy of promoter hypermethylation of SFRP1 under assumption of proportional hazards. IPCW estimates of AUC(t) versus time. Estimated one-year concordance was C = 0.64 (standard error = 0.04).

Table S1. DNA sequences for probes and primers.

Primer/Probe	DNA Sequence	Amplicon size
SFRP1 M1	GGA GTT GAT TGG TTG CGC	
SFRP1 M2	CGC GAC ACT AAC TCC G	90
SFRP1 M beacon	(HEX)CGC GAT G + GT T + CG + GTC G + TA ATC GCG(Dabcyl)	
SFRP1 Am	GAG GCG ATT GGT TTT CGC	
SFRP1 Bm	CGC GAC ACT AAC TCC G	121
M1; inner methylation specific forward primer for the array		
M2; inner methylation specific reverse primer for the array		
M beacon; methylation specific probe		
Am; outer methylation specific forward primer for the nested/semi-nested PCR (Round one of PCR)		
Bm; outer methylation specific reverse primer for the nested/semi-nested PCR (Round one of PCR)		

+; Locked nucleic acid