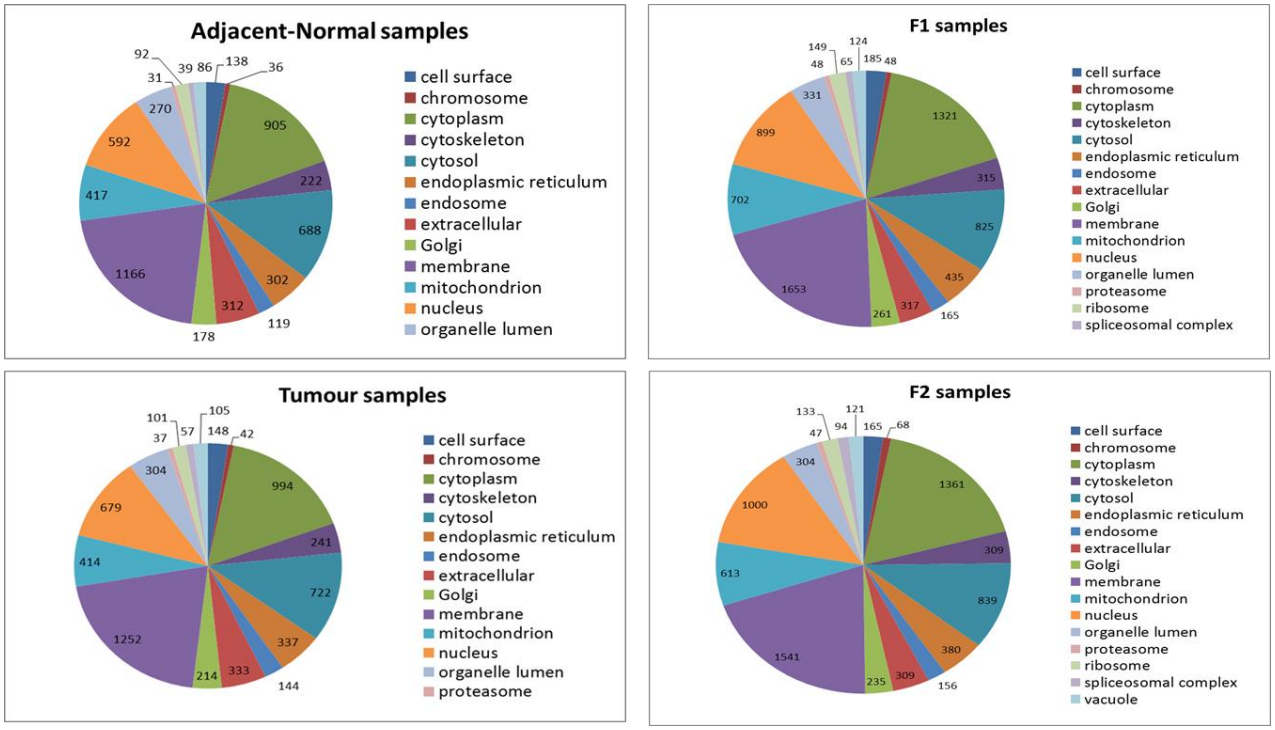
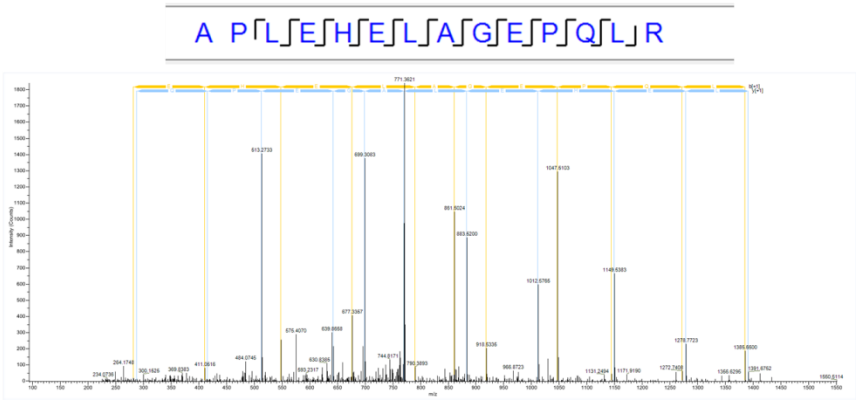
Supplementary Figure S1. Cellular component annotation using Gene Ontology analysis through the ProteinCenter node in Proteome Discoverer for each of the sample sets.

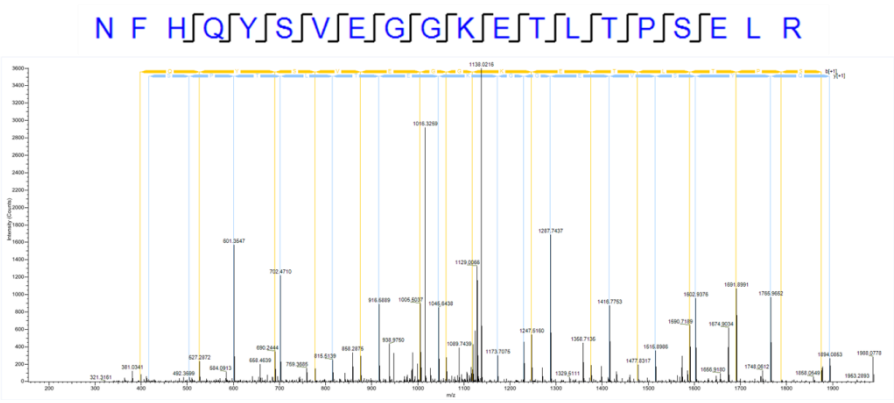


The efficiency of membrane protein enrichment was assessed using gene ontology annotation by the ProteinCenter software. Supplementary figure 1 shows the number of proteins from each sample set in relation to their cellular component annotation. Membrane-associated proteins relate to 48.8%, 66.5%, 47.8% and 59.5% of the total proteins identified for adjacent-normal, tumour, PDX F1 and PDX F2 samples.

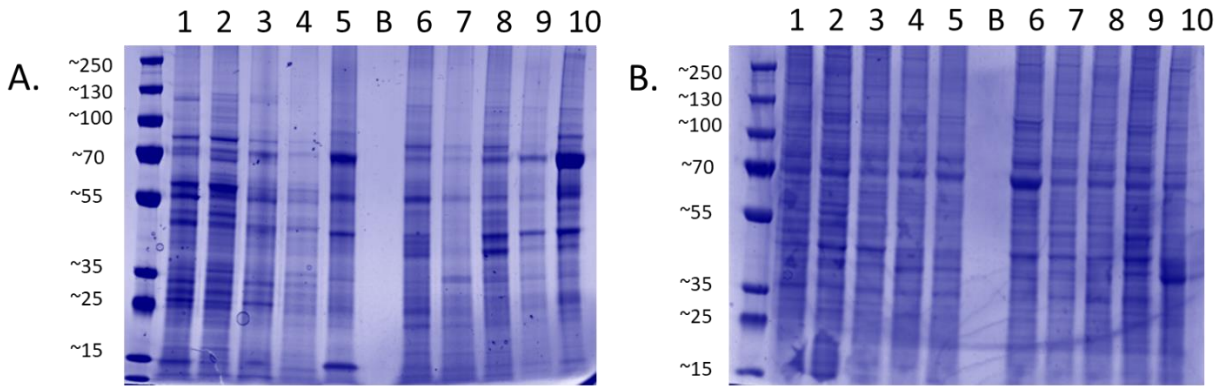
CLIC-3 (77% identity)
Human: APLEHELAGEPQL
Mouse: APLDHELAQEPHL



Protein S100-A14 (80% identity)
Human: NFHQYSVEGGKETLTPSELR
Mouse: NFHKYSVAGKKETLTPAELR



Supplementary Figure S2: MS/MS spectra of two human-specific peptides identified from the PDAC PDX F1 generation. Sequence alignments using BLASTp of the identified human peptides to their corresponding mouse peptides are shown. The protein sequence homology between the two species is indicated.



Supplementary Figure S3: Coomassie stained gels validating loading of lanes prior to the Western blot of CD55. Coomassie stained gel of (A) Five representative adjacent-normal tissues and primary PDAC tumours membrane protein enriched fractions (Lanes 1-5: 89N, 91N, 116N, 120N and 161N, Lane B is a Blank, Lanes 6-10: 65T, 120T, 140T, 160T and 161T). Coomassie stained gel of (B) 5 representative membrane-enriched fractions from PDX F1 and F2 tumours (Lane 1-5:89F1, 116F1, 141F1, 160F, 161F1, Lane B: Blank, Lanes 6-10: 65F2, 80F2, 89F2, 99F2 and 160F2).