

Supplementary Data

Supplementary Table: List of total miRNAs found upregulated or downregulated in pancreatic cancer patients in comparison to healthy individuals as determined by miRNA expression profile analysis on ExoChip bound exosomes.

CASE # 1		CASE # 2	
Upregulated miRNA (Fold change >1.5)	Downregulated miRNA (Fold change ≤0.67)	Upregulated miRNA (Fold change >1.5)	Downregulated miRNA (Fold change ≤0.67)
hsa-miR-1208	hsa-miR-10b*	hsa-miR-130a	hsa-miR-601
hsa-miR -1225-3P	hsa-miR-601	hsa-miR -1274B	hsa-miR-106b
hsa-miR -1290	hsa-miR-106b	hsa-miR-548a	hsa-miR-29c
hsa-miR-130a	hsa-miR-92a	hsa-miR -1208	hsa-miR-520c-3p
hsa-miR-147	hsa-miR-181c	hsa-miR-509-5p	hsa-miR -320B
hsa-miR-150	hsa-miR-328	hsa-miR-191	hsa-miR-92a
hsa-miR-151-3p	mmu-miR-374-5p	hsa-miR-520f	hsa-miR -1275
hsa-miR-184	hsa-miR-190b	mmu-miR-374-5p	hsa-miR-302c*
hsa-miR-191	hsa-miR-551b*	hsa-miR-29b	hsa-miR-205
hsa-miR-192	hsa-miR-202	hsa-miR-636	hsa-miR-222
hsa-miR-194	hsa-miR-367	hsa-miR-190b	hsa-miR-192
hsa-miR-203	hsa-miR-302a	hsa-miR-30b	hsa-miR-409-3p
hsa-miR-20a	hsa-miR-648	hsa-miR-597	hsa-miR-197
hsa-miR-212	hsa-miR -1260	hsa-miR-302d	hsa-miR-328
hsa-miR-215	hsa-miR-432*	hsa-miR-520e	hsa-miR -1290
hsa-miR-222	hsa-miR -1275	hsa-miR-331-5p	hsa-miR-135b*
hsa-miR-29b	hsa-miR -720	hsa-miR-548c	hsa-miR-376a
hsa-miR-29c	hsa-miR-302c*	hsa-miR-203	hsa-miR-27b
hsa-miR-302c	hsa-miR-573	hsa-miR-518d	hsa-miR-367
hsa-miR-302d	hsa-miR-625*	hsa-miR-150	hsa-miR -1260
hsa-miR-30b	hsa-miR-135b*	hsa-miR-551b	hsa-miR-302a
hsa-miR-30c	hsa-miR -1183	hsa-miR-571	hsa-miR-648
hsa-miR-30e-3p	hsa-miR-638	rno-miR-7*	hsa-miR-30c
hsa-miR-323-3p	hsa-miR -1274B	hsa-miR-645	hsa-miR-580
hsa-miR-346	hsa-miR-208	hsa-miR-378	hsa-miR-147
hsa-miR-34a		hsa-miR-646	hsa-miR-202
hsa-miR-34c		hsa-miR-381	hsa-miR-624
hsa-miR-375		hsa-miR-758	hsa-miR-99b*
hsa-miR-381		hsa-miR-302b	hsa-miR-659
hsa-miR-409-3p		hsa-miR-708	hsa-miR-208
hsa-miR-411		hsa-miR-657	hsa-miR-181c
hsa-miR-483-5p			hsa-miR-302c
hsa-miR-509-5p			hsa-miR-410
hsa-miR-518d			hsa-miR-661
hsa-miR-520c-3p			hsa-miR-184
hsa-miR-520e			hsa-miR-211
hsa-miR-551b			hsa-miR-324-3p
hsa-miR-571			hsa-miR-34c
hsa-miR-597			hsa-miR-551b*
hsa-miR-624			hsa-miR-212
hsa-miR-640			hsa-miR-34a
hsa-miR-646			hsa-miR-638
hsa-miR-657			
hsa-miR-659			
hsa-miR-662			
hsa-miR-708			
hsa-miR-872			
hsa-miR-888			

Figure S1

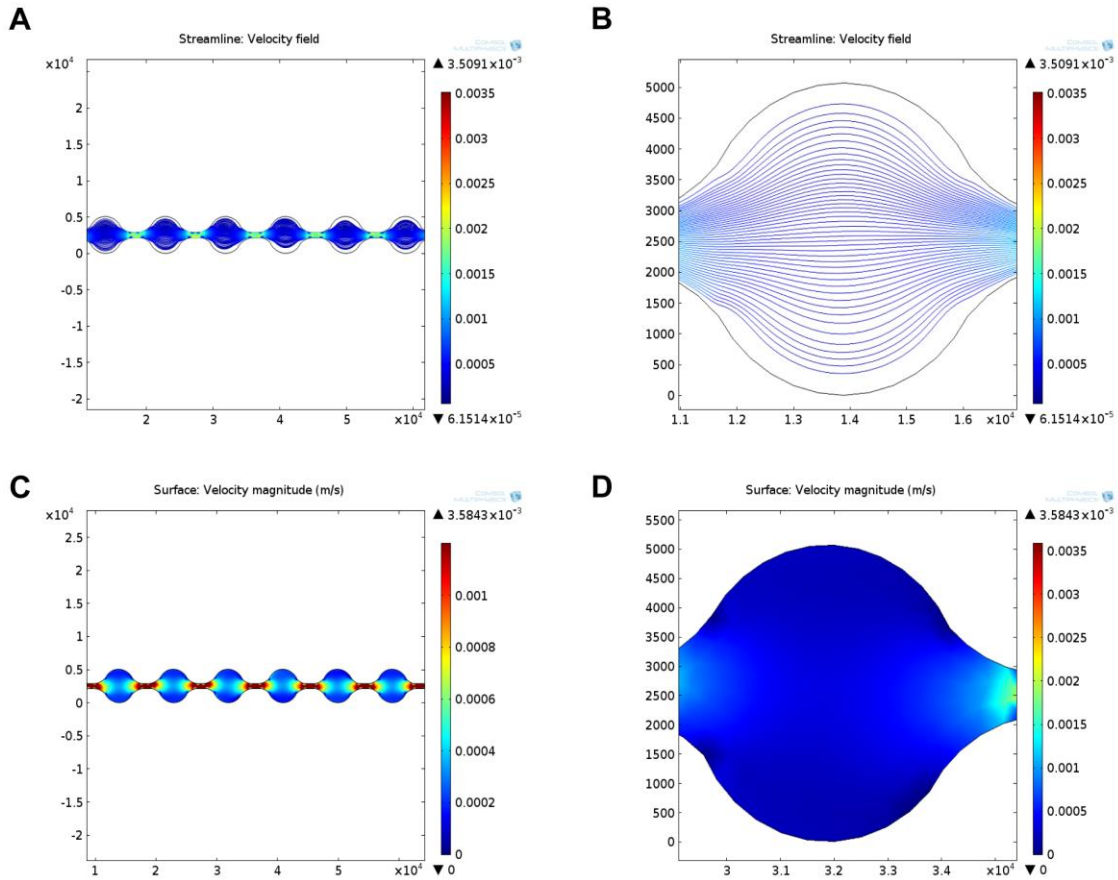


Fig. S1: Fluid dynamics studies using *Comsol Multiphysics* package. Fluid flow analysis through the newly designed ExoChip was simulated using COMSOL Multiphysics 4.3 software (COMSOL, Inc., Burlington, MA, USA) to generate velocity profile of the serum infusion. The simulation was done using inlet velocity of 0.001034 m/s (8 μ l/min) for 100 μ m channel height, and using blood density and viscosity with symmetry boundary condition and no-slip on the walls. The streamline flow analysis showed an overall consistency in the streamlined laminar flow of the fluid through the ExoChip chambers (Fig S1A,B). Further, the velocity profile showed the low velocity of the fluid in the circular region of the chambers whereas higher velocity was observed in the narrower interconnecting regions of the channels (Fig S1: C,D).

Figure:S2

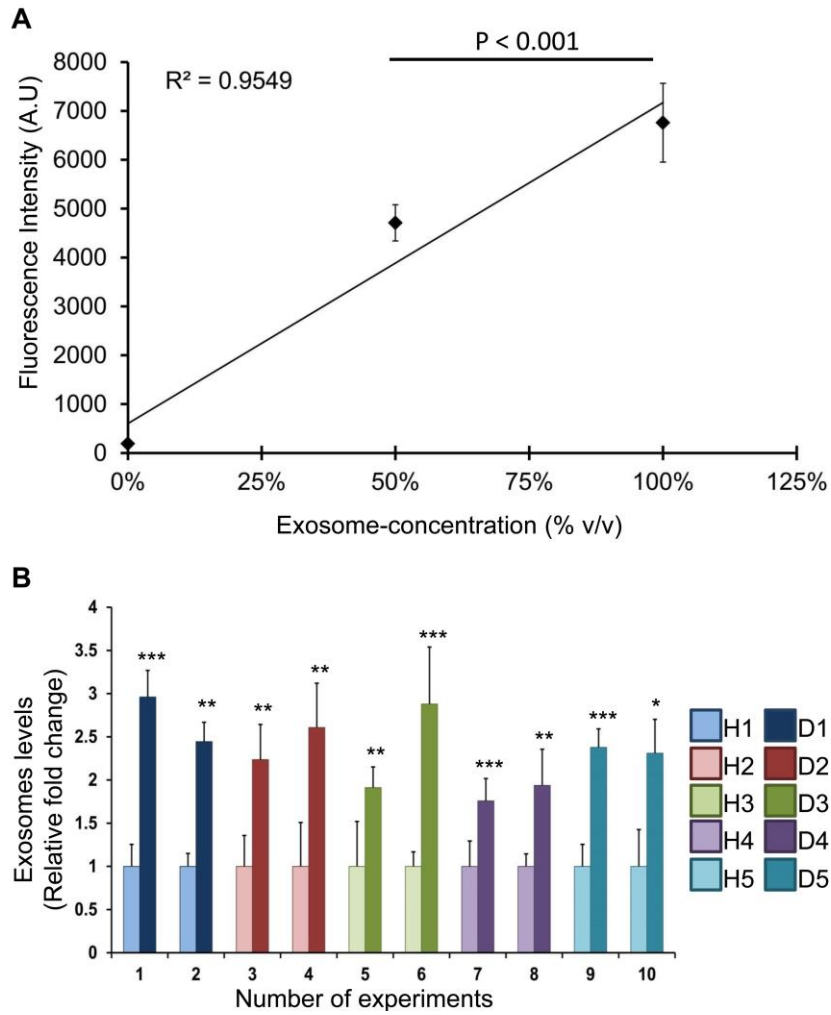


Fig. S2: A: Experimental validation for quantification of ExoChip immobilized exosomes.

To determine the sensitivity of capture and quantification of relative abundance of exosomes, a plot of the exosomes amount infused vs fluorescence intensity was generated. Exosome-free serum was prepared from 0.2 μ m filtered healthy serum using exoquick precipitation solution (SBI System Biosciences) following instructions provided by manufacturer. Samples containing increasing concentration (% volume/volume) of normal healthy serum (exosome-serum) were prepared, namely 0% exosome-serum (exosome-free serum), 50% exosome-serum (1:1, exosome-free serum/exosome-serum) and 100% exosome-serum samples, and infused through

ExoChip. Immobilized exosomes were stained with DiO and fluorescence intensity recorded as described in material and methods section. Plot shows a linear trend of exosome capture with increasing exosome concentration in the serum with *R-square* very close to 1. **B: Relative abundance of Exosome in clinical samples.** Relative fold change in exosomes levels calculated for experiments performed in duplicates, analyzing serum obtained from pancreatic cancer patients (n=5) and healthy individuals (n=5) using ExoChip. Means of the duplicate experiments for each sample is shown in Fig. 4B. ***P<0.001, **P<0.01