

Supplementary Materials for

Fractal circuit sensors enable rapid quantification of biomarkers for donor lung assessment for transplantation

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This PDF file includes:

- Fig. S1. Validation of LTx probes and FraCS approach with DNA targets.
- Fig. S2. GAPDH validation with RNA.
- Fig. S3. qPCR validation.
- Fig. S4. Bland-Altman analysis of FraCS versus qPCR.
- Table S1. Bland-Altman results of FraCS versus qPCR.

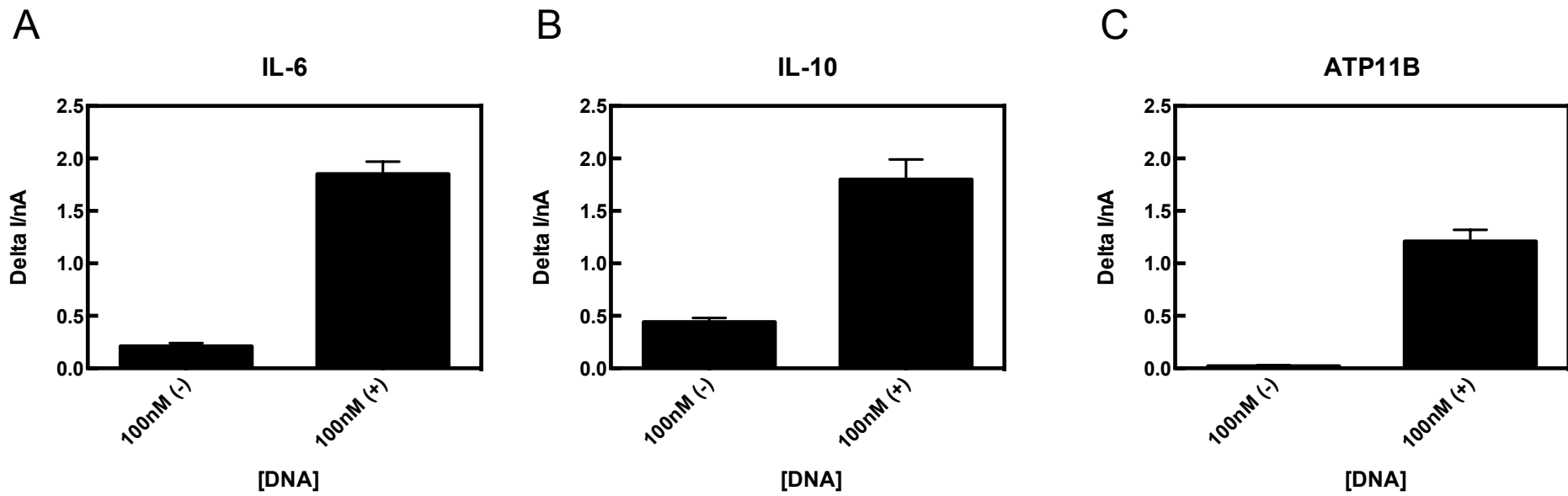


Figure S1. Validation of LTx Probes and FraCS approach with DNA targets. Hybridization signals for FraCS challenged with 100nM complementary (+) or non-complementary (-) DNA for (A) IL-6, (B) IL-10, and (C) ATP11B sensors. Data represented are of n=15 different sensors. Columns represent mean and error-bars indicate s.e.m.

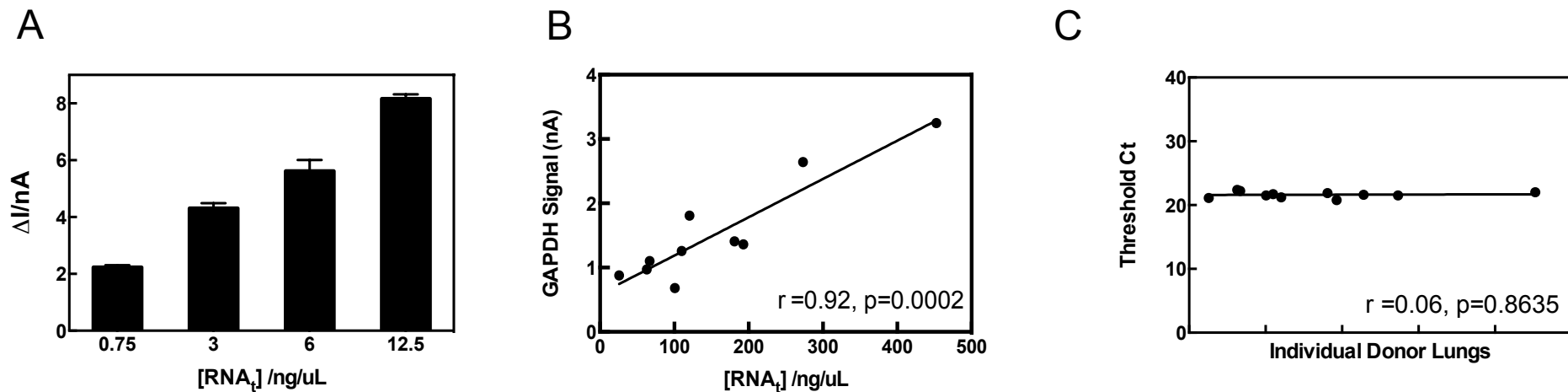


Figure S2. GAPDH Validation with RNA. (A) Total RNA titration profile for GAPDH sensors. Data represented are of $n=15$ different sensors. Columns represent mean and error-bars indicate s.e.m. (B) Correlation of GAPDH signals obtained from FraCS versus total RNA concentration (Data were analyzed by two-tailed, Pearson correlation) ($n=10$ different donor lungs). (C) Correlation of GAPDH signals obtained from qPCR expression levels (Threshold Ct) for $n=11$ different donor lungs (Data were analyzed by two-tailed, Pearson correlation).

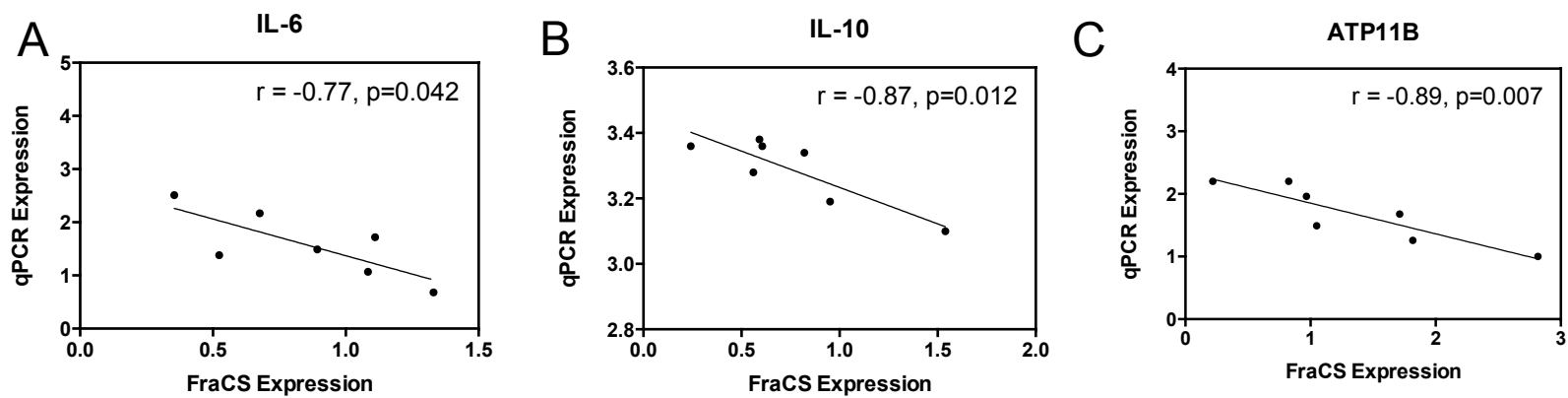


Figure S3. qPCR Validation. Correlation of signals obtained from qPCR versus FraCS in individual donor lungs (n=7) for (A) IL-6, (B) IL-10, and (C) ATP11B sensors. Data were analyzed by two-tailed, Pearson correlation.

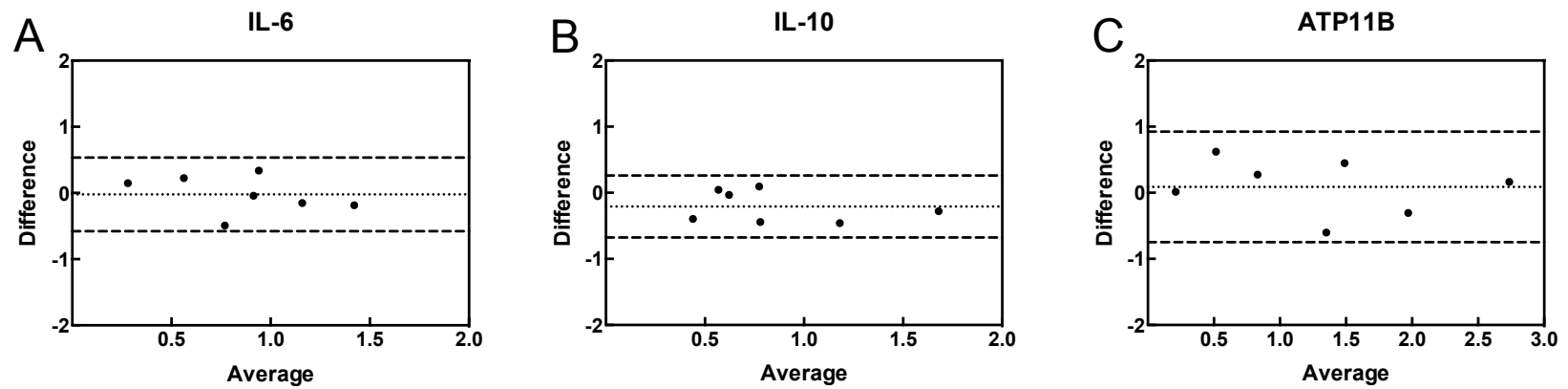


Figure S4. Bland-Altman Analysis of FraCS vs. qPCR. Bland-Altman comparison (difference versus average) of signals obtained from individual donor lungs (n=7) run on both the FraCS and qPCR platforms for (A) IL-6, (B) IL-10, and (C) ATP11B.

Table S1. Bland-Altman Results of FraCS vs. qPCR.

Biomarker	Mean Difference	Mean Difference Significantly Different From 0 ?	95% Limits of Agreement	Slope Significant ?
IL-6	-0.02	No (p=0.84)	-0.58 to 0.53	No (p=0.42)
IL-10	-0.21	No (p=0.06)	-0.68 to 0.26	No (p=0.52)
ATP11B	0.088	No (p=0.61)	-0.75 to 0.92	No (p=0.60)