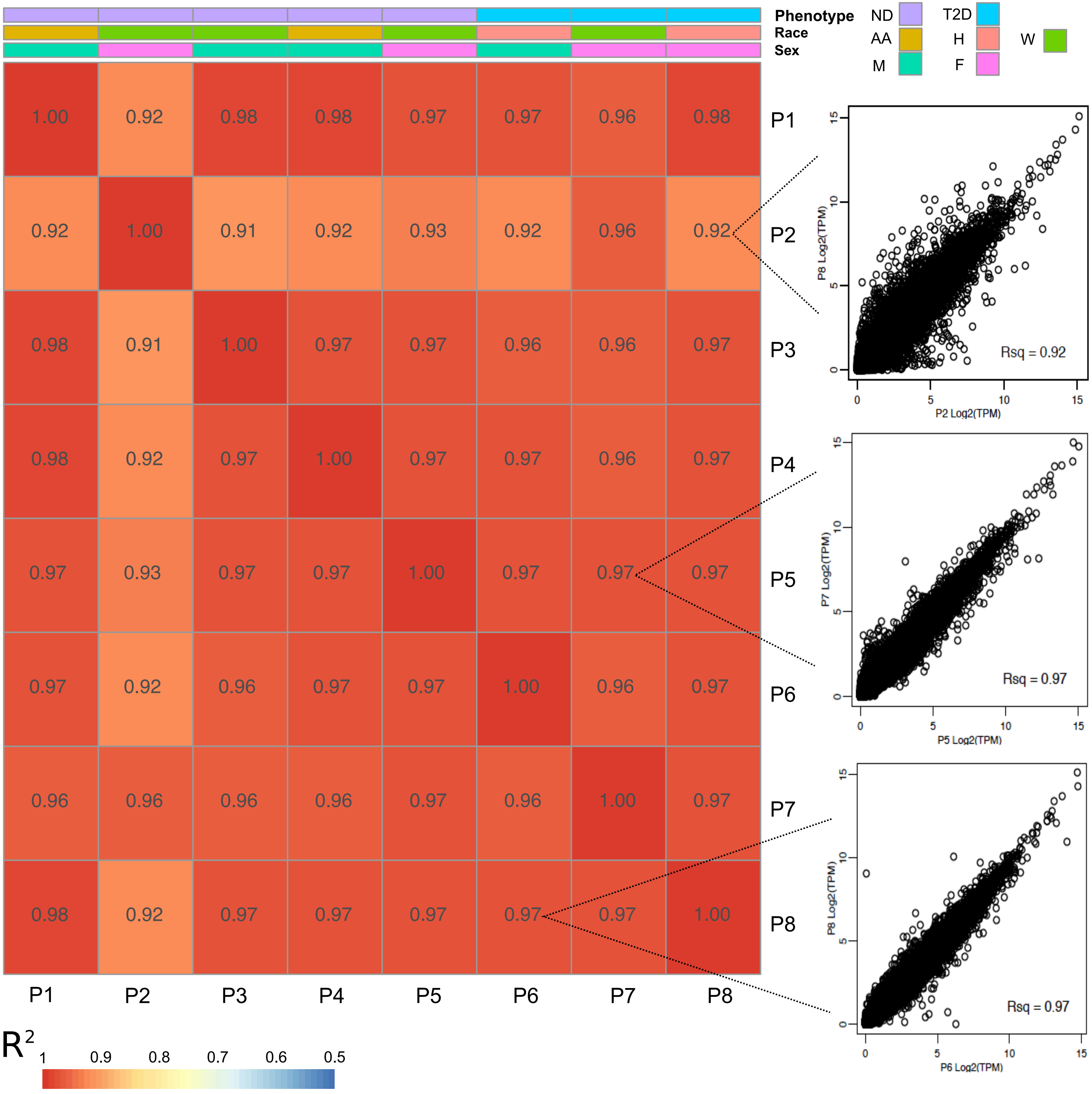

	P1	P2	P3	P4	P5	P6	P7	P8
Phenotype	ND	ND	ND	ND	ND	T2D	T2D	T2D
Race	AA	W	W	AA	W	H	W	H
Sex	M	F	M	M	F	M	F	F
P1	1.00	0.92	0.98	0.98	0.97	0.97	0.96	0.98
P2	0.92	1.00	0.91	0.92	0.93	0.92	0.96	0.92
P3	0.98	0.91	1.00	0.97	0.97	0.96	0.96	0.97
P4	0.98	0.92	0.97	1.00	0.97	0.97	0.96	0.97
P5	0.97	0.93	0.97	0.97	1.00	0.97	0.97	0.97
P6	0.97	0.92	0.96	0.97	0.97	1.00	0.96	0.97
P7	0.96	0.96	0.96	0.96	0.97	0.96	1.00	0.97
P8	0.98	0.92	0.97	0.97	0.97	0.97	0.97	1.00

Supplemental_Fig_S3: Ensemble single cell transcriptomes from each patient islet are highly correlated.

Heatmap of Pearson's R-squared values between patient ensemble single cell transcriptomes. R-squared values ranged from 0.91 to 0.98 implying minimal batch effects across patient samples. Also shown are inset scatter plots for specific correlations providing further evidence that the single cell transcriptomes are well correlated between patients. TPM = Transcripts per million, R^2 = Pearson's R-squared, P = Patient Donor, ND = non-diabetic, T2D = Type 2 diabetic, H = Hispanic, W = White, AA = African American, M = Male, F = Female.