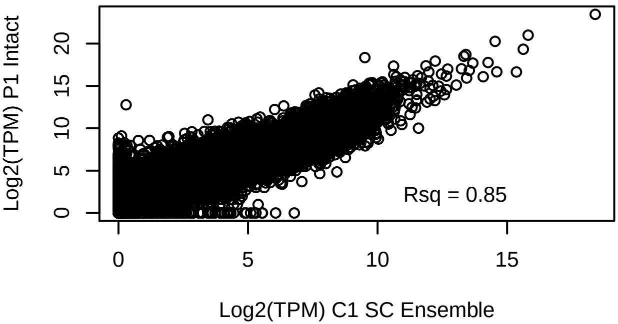
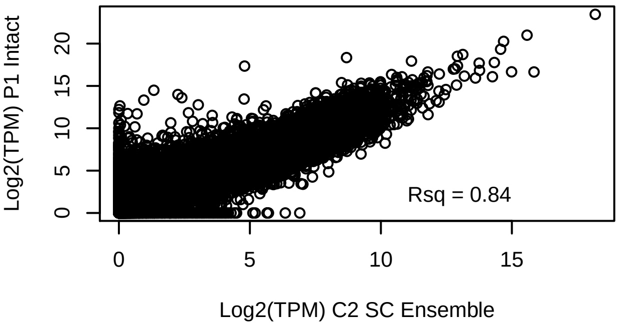
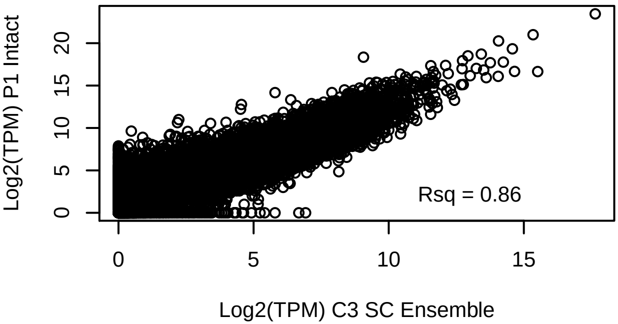
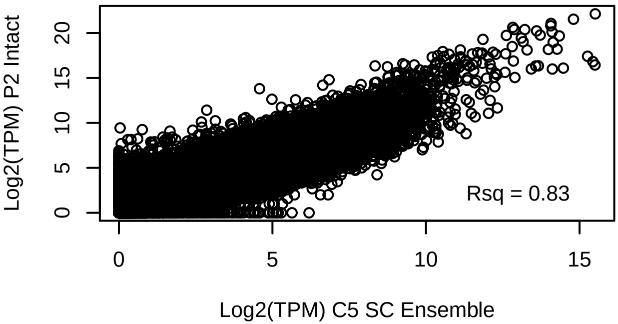
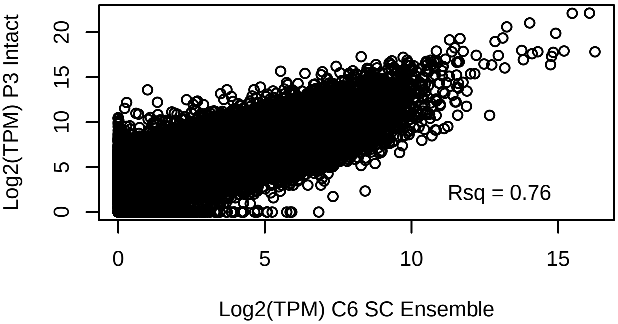
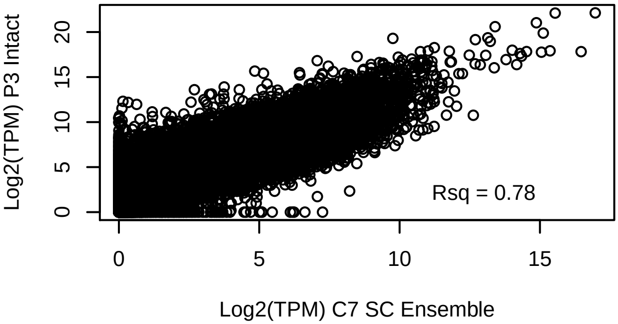

Log2(TPM) P1 Intact
0
5
10
15
20
Rsq = 0.85
0
5
10
15
Log2(TPM) C1 SC Ensemble

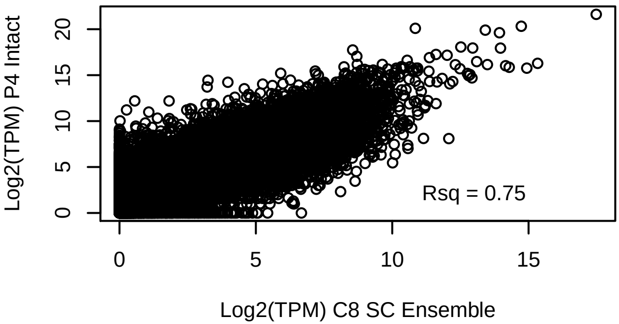

Log2(TPM) P1 Intact
0
5
10
15
20
Rsq = 0.84
0
5
10
15
Log2(TPM) C2 SC Ensemble

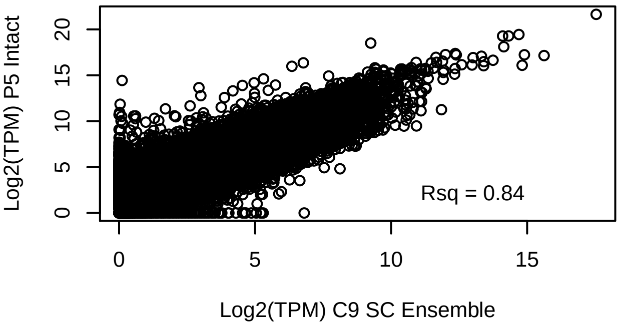

Log2(TPM) P1 Intact
0
5
10
15
20
Rsq = 0.86
0
5
10
15
Log2(TPM) C3 SC Ensemble

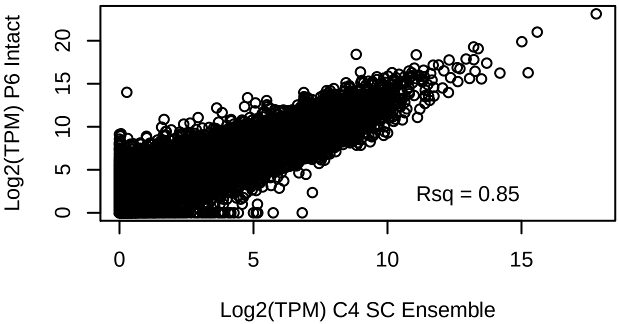

Log2(TPM) P2 Intact
0
5
10
15
20
Rsq = 0.83
0
5
10
15
Log2(TPM) C5 SC Ensemble

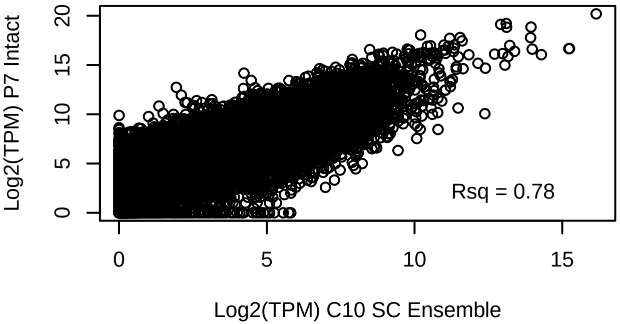

Log2(TPM) P3 Intact
0
5
10
15
20
Rsq = 0.76
0
5
10
15
Log2(TPM) C6 SC Ensemble

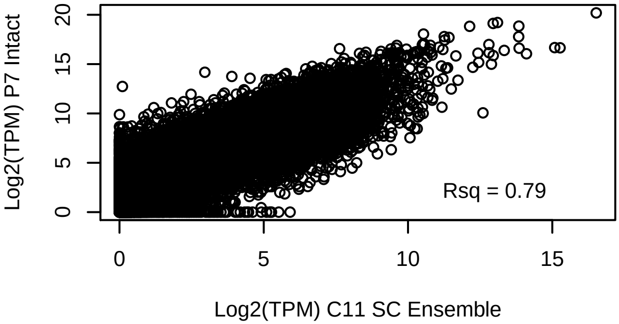

Log2(TPM) P3 Intact
0
5
10
15
20
Rsq = 0.78
0
5
10
15
Log2(TPM) C7 SC Ensemble

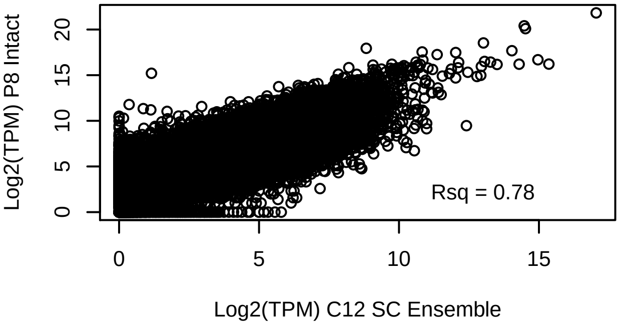

Log2(TPM) P4 Intact
0
5
10
15
20
0
5
10
15
Rsq = 0.75
Log2(TPM) C8 SC Ensemble

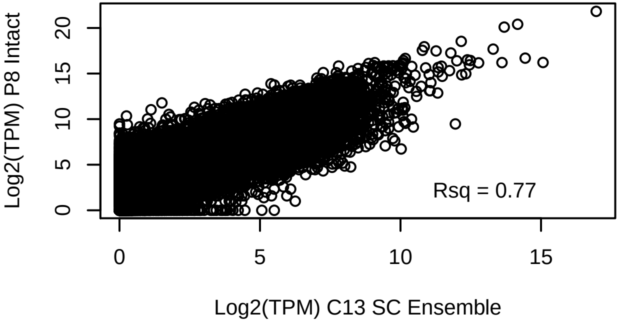

Log2(TPM) P5 Intact
0
5
10
15
20
0
5
10
15
Rsq = 0.84
Log2(TPM) C9 SC Ensemble


Log2(TPM) P6 Intact
0
5
10
15
20
0
5
10
15
Rsq = 0.85
Log2(TPM) C4 SC Ensemble


Log2(TPM) P7 Intact
0
5
10
15
20
0
5
10
15
Rsq = 0.78
Log2(TPM) C10 SC Ensemble


Log2(TPM) P7 Intact
0
5
10
15
20
0
5
10
15
Rsq = 0.79
Log2(TPM) C11 SC Ensemble


Log2(TPM) P8 Intact
0
5
10
15
20
0
5
10
15
Rsq = 0.78
Log2(TPM) C12 SC Ensemble


Log2(TPM) P8 Intact
0
5
10
15
20
Rsq = 0.77
0
5
10
15
Log2(TPM) C13 SC Ensemble

Supplemental_Fig_S4: Pairwise comparisons of patient bulk intact and ensemble single cell transcriptomes are highly correlated regardless of microfluidic chip preparation.

Scatter plots of average $\log_2$(TPM) expression of bulk intact and ensemble single cell transcriptomes for each patient islet. The C1, C2, etc, labels correspond to the single cell microfluidic chip preparation(s). Pearson's R-square values range from 0.75 to 0.86. TPM = Transcripts per million, Rsq = Pearson's R-squared, SC = Single cell ensemble, P = Patient Donor.