TABLE I: Supplementary table, five best three-gene trans-differentiation recipes for PN source clusters as ranked by RMSD. Taken from DBN inference results for all 518,592 possible combinations. Metrics summed over all $74 - 3 = 71$ unperturbed genes.

S-I → T-II (ref. RMSD = 0.3358 / Pearson R = 0.5853)		
Three-gene recipe	RMSD	Pearson R
TESPA1 ↑ POU6F2 ↓ SATB2 ↑	0.1252	0.9666
TESPA1 ↑ POU6F2 ↓ SLC6A1 ↓	0.1272	0.9699
GAD1 ↓ TESPA1 ↑ POU6F2 ↓	0.1281	0.9670
CUX2 ↑ POU6F2 ↓ SATB2 ↑	0.1307	0.9619
GAD1 ↓ CUX2 ↑ POU6F2 ↓	0.1338	0.9637
S-I → T-III (ref. RMSD = 0.4884 / Pearson R = -0.2805)		
Three-gene recipe	RMSD	Pearson R
ADARB2 ↓ GAD1 ↑ SATB2 ↓	0.0775	0.9596
ADARB2 ↓ SLC6A1 ↑ SATB2 ↓	0.0825	0.9591
ADARB2 ↓ GRIK3 ↑ SATB2 ↓	0.0894	0.9639
ERBB4 ↑ ADARB2 ↓ SATB2 ↓	0.0915	0.9547
ADARB2 ↓ GRIP1 ↑ SATB2 ↓	0.0958	0.9483
S-I → T-IV (ref. RMSD = 0.5704 / Pearson R = -0.5077)		
Three-gene recipe	RMSD	Pearson R
ERBB4 ↑ ADARB2 ↑ SATB2 ↓	0.1165	0.9589
ADARB2 ↑ SLC6A1 ↑ SATB2 ↓	0.1179	0.9513
ADARB2 ↑ GAD1 ↑ SATB2 ↓	0.1183	0.9446
KIAA12117 ↓ ADARB2 ↑ SATB2 ↓	0.1289	0.9556
ADARB2 ↑ GRIP1 ↑ SATB2 ↓	0.1295	0.9491
S-II → T-I (ref. RMSD = 0.3358 / Pearson R = 0.5853)		
Three-gene recipe	RMSD	Pearson R
GAD1 ↓ TESPA1 ↓ POU6F2 ↑	0.0723	0.9812
GAD1 ↓ CUX2 ↓ POU6F2 ↑	0.0751	0.9824
CUX2 ↓ SLIT3 ↓ POU6F2 ↑	0.0761	0.9878
PDZD2 ↓ CUX2 ↓ POU6F2 ↑	0.0765	0.9864
ERBB4 ↓ TESPA1 ↓ POU6F2 ↑	0.0768	0.9802
S-II → T-III (ref. RMSD = 0.5655 / Pearson R = -0.4221)		
Three-gene recipe	RMSD	Pearson R
ADARB2 ↓ GAD1 ↑ SATB2 ↓	0.0794	0.9581
ADARB2 ↓ SLC6A1 ↑ SATB2 ↓	0.0891	0.9551
ADARB2 ↓ GRIP1 ↑ SATB2 ↓	0.0994	0.9450
ERBB4 ↑ ADARB2 ↓ SATB2 ↓	0.1033	0.9471
GRIK3 ↑ SLC6A1 ↑ SATB2 ↓	0.1047	0.9383
S-II → T-IV (ref. RMSD = 0.6125 / Pearson R = -0.5156)		
Three-gene recipe	RMSD	Pearson R
ADARB2 ↑ GAD1 ↑ SATB2 ↓	0.1230	0.9405
ADARB2 ↑ SLC6A1 ↑ SATB2 ↓	0.1249	0.9482
ERBB4 ↑ ADARB2 ↑ SATB2 ↓	0.1286	0.9541
ADARB2 ↑ GRIP1 ↑ SATB2 ↓	0.1327	0.9477
KIAA1211L ↓ ADARB2 ↑ SATB2 ↓	0.1422	0.9503

TABLE II: Supplementary table, five best three-gene trans-differentiation recipes as ranked by RMSD. Taken from DBN inference results for all 518,592 possible combinations. Metrics summed over all $74 - 3 = 71$ unperturbed genes.

S-III → T-I (ref. RMSD = 0.4884 / Pearson R = -0.2805)		
Three-gene recipe	RMSD	Pearson R
GAD1 ↓ POU6F2 ↑ SATB2 ↑	0.0986	0.9643
ERBB4 ↓ POU6F2 ↑ SATB2 ↑	0.1072	0.9610
GAD1 ↓ CUX2 ↓ SATB2 ↑	0.1072	0.9598
GAD1 ↓ TESPA1 ↓ SATB2 ↑	0.1080	0.9556
POU6F2 ↑ SLC6A1 ↓ SATB2 ↑	0.1122	0.9580
S-III → T-II (ref. RMSD = 0.5655 / Pearson R = -0.4221)		
Three-gene recipe	RMSD	Pearson R
GAD1 ↓ POU6F2 ↓ SATB2 ↑	0.1564	0.9381
GRIP1 ↓ POU6F2 ↓ SATB2 ↑	0.1571	0.9443
POU6F2 ↓ SLC6A1 ↓ SATB2 ↑	0.1611	0.9353
ERBB4 ↓ POU6F2 ↓ SATB2 ↑	0.1630	0.9319
TESPA1 ↑ POU6F2 ↓ SATB2 ↑	0.1635	0.9446
S-III → T-IV (ref. RMSD = 0.3832 / Pearson R = 0.2390)		
Three-gene recipe	RMSD	Pearson R
NFIB ↑ ADARB2 ↑ SATB2 ↓	0.0981	0.9742
ADARB2 ↑ GRIK3 ↓ SATB2 ↓	0.0987	0.9750
ADARB2 ↑ GRIK3 ↓ SATB2 ↓	0.0993	0.9812
ERBB4 ↑ ADARB2 ↑ GRIK3 ↓	0.1013	0.9776
ERBB4 ↑ ADARB2 ↑ GAD1 ↑	0.1013	0.9610
S-IV → T-I (ref. RMSD = 0.5704 / Pearson R = -0.5077)		
Three-gene recipe	RMSD	Pearson R
GAD1 ↓ POU6F2 ↑ SATB2 ↑	0.1014	0.9635
ERBB4 ↓ POU6F2 ↑ SATB2 ↑	0.1100	0.9600
GAD1 ↓ CUX2 ↓ SATB2 ↑	0.1113	0.9578
GAD1 ↓ TESPA1 ↓ SATB2 ↑	0.1124	0.9532
ERBB4 ↓ CUX2 ↓ SATB2 ↑	0.1140	0.9602
S-IV → T-II (ref. RMSD = 0.6125 / Pearson R = -0.5156)		
Three-gene recipe	RMSD	Pearson R
GAD1 ↓ POU6F2 ↓ SATB2 ↑	0.1610	0.9351
GRIP1 ↓ POU6F2 ↓ SATB2 ↑	0.1624	0.9412
ERBB4 ↓ POU6F2 ↓ SATB2 ↑	0.1664	0.9291
POU6F2 ↓ CBLN2 ↓ SATB2 ↑	0.1666	0.9310
KIAA1211L ↑ POU6F2 ↓ SATB2 ↑	0.1684	0.9293
S-IV → T-III (ref. RMSD = 0.3832 / Pearson R = 0.2390)		
Three-gene recipe	RMSD	Pearson R
ADARB2 ↓ GRIK3 ↑ SATB2 ↓	0.0581	0.9784
NFIB ↓ ADARB2 ↓ SLC6A1 ↑	0.0592	0.9781
NFIB ↓ ADARB2 ↓ GAD1 ↑	0.0595	0.9772
ADARB2 ↓ GRIK3 ↑ SLC6A1 ↑	0.0605	0.9795
ADARB2 ↓ GAD1 ↑ GRIK3 ↑	0.0618	0.9788