Table S1. Data sets used in this study.

Data Set ID	Species	Name	Cell Origin	Number of expressed genes[a]	Number of APA genes surveyed	T-test *P*-value[b]	Ref
GSE10871	Mouse	B lymph.	B lymphocyte	16,104	687	1.80E-02	[1]
GSE14012	Mouse	MEF.a	Mouse embryonic fibroblast	14,373	703	4.60E-02	[2]
GSE15267	Mouse	MEF.b	Mouse embryonic fibroblast	15,993	755	2.00E-02	-
GSE12499	Mouse	NSC.a	Adult neural stem cells	14,817	754	5.60E-06	[3]
GSE10806	Mouse	NSC.b	Adult neural stem cells	14,708	721	4.91E-04	[4]
GSE12390	Human	BJ	Neonatal foreskin fibroblast	14,755	1,078	8.56E-07	[5]
GSE9832	Human	MRC5	Fetal lung fibroblast	15,274	1,556	1.20E-02	[6]
GSE9709	Human	NFF	Neonatal foreskin fibroblast	14,903	1,036	4.10E-02	[7]
GSE9865	Human	NHDF	Neonatal foreskin fibroblast	14,280	974	2.93E-05	[8]
GSE11350	Human	SC	Spermatogonial cells from adult human testis	16,079	1,032	5.20E-06	[9]

[a]Expressed genes are those with detectable signals in at least half of samples in a set, using the MAS5 present and absent call. All mouse data sets used Affymetrix GeneChip Mouse Genome 430 v2.0, and all human data sets used Affymetrix GeneChip Human Genome U133 Plus v2.0.

[b]T-test was used to compare sample nRUD values before vs. after reprogramming, as shown in Figure 2.

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