Table S1. Classifying Top ESC Reprogramming Candidates.

TF	Z Score	η (10^{-3})	Rank Z$*\eta$	Classification	Citation or GO Term
Pou5f1 (Oct4)	2.77	2.45	1	Reprogramming	[1]
Gm13242	1.59	3.98	2	Unknown	biological process
Nr0b1	2.44	2.59	3	Pluripotency	[2]
Nanog	2.30	2.65	4	Reprogramming	[1]
Zfp42	2.04	2.74	5	Pluripotency	[3]
Hsf2bp	1.42	3.49	6	Unknown	biological process
Esrrb	1.74	2.49	7	Reprogramming	[1]
Zscan4f	1.01	3.86	8	Reprogramming	[4]
Klf4	1.04	3.25	9	Reprogramming	[1]
Zfp459	0.83	3.98	10	Unknown	biological process
Zscan4c	0.82	3.86	11	Pluripotency	telomere lengthening
Zic3	1.17	2.65	12	Pluripotency	[5]
Zfp936	1.15	2.66	13	Unknown	biological process
Zfp229	0.76	3.84	14	Unknown	biological process
Zfp600	0.71	3.98	15	Unknown	biological process
Zfp640	1.10	2.55	16	Differentiation	skeletal system morphogenesis
Gm10324	1.09	2.55	17	Unknown	biological process
Zscan10	1.04	2.65	18	Pluripotency	[6]
Utf1	2.03	1.30	19	Reprogramming	[1]
2610305D13Rik	1.02	2.45	20	Unknown	biological process
Tfcp2l1	1.26	1.90	21	Pluripotency	[7]
Klf8	0.58	4.12	22	Differentiation	[8]
Epas1	0.70	3.18	23	Differentiation	erythrocyte differentiation
Tbx3	1.09	2.03	24	Reprogramming	[1]
Tcf15	0.89	2.37	25	Differentiation	[9]

Table has top 50 embryonic stem cell (ESC) reprogramming candidates (as ranked by z-score times predictivity, η_i^{μ}). Classification of each TF is either justified by paper citation or GO Process term. Reprogramming TFs are in a pre-existing reprogramming protocol, pluripotency TFs help maintain the ESC state but are non-essential for reprogramming, differentiation TFs are expressed in ESC but help induce cell fate change *in vivo*, and unknown TFs have no known function.

Table S1 Continued. Classifying Top ESC Reprogramming Candidates.

TF	Z Score	η (10^{-3})	Rank Z$*\eta$	Classification	Citation or GO Term
Tcfl5	0.82	2.56	26	Unknown	regulation of transcription
Sall4	1.72	1.17	27	Reprogramming	[1]
Zfp553	0.87	2.22	28	Unknown	regulation of transcription
Sox2	1.96	0.97	29	Reprogramming	[1]
Grhl3	0.61	2.75	30	Differentiation	ectoderm development
Zbtb10	0.75	2.22	31	Unknown	negative regulation of transcription
Mycn	1.90	0.85	32	Differentiation	lung development
Sap30	0.93	1.72	33	Differentiation	skeletal muscle cell differentiation
Zbtb8a	0.83	1.88	34	Unknown	regulation of transcription
Klf5	1.23	1.25	35	Differentiation	skeletal muscle cell differentiation
Sall1	1.30	1.18	36	Differentiation	neural tube development
AA987161	0.60	2.36	37	Unknown	biological process
Klf9	0.70	1.96	38	Differentiation	embryo implantation
Myc	0.73	1.86	39	Reprogramming	[1]
Rarg	0.87	1.54	40	Differentiation	bone morphogenesis
Tead2	1.03	1.15	41	Differentiation	lateral mesoderm development
Dnmt3b	1.33	0.88	42	Pluripotency	genetic imprinting
Nr5a2	0.67	1.75	43	Reprogramming	[1]
Nr1d2	0.74	1.53	44	Differentiation	regulation of skeletal muscle cell differentiation
Cbx7	1.14	0.99	45	Differentiation	chromatin modification
Bnip3	1.40	0.77	46	Differentiation	brown fat cell differentiation
Rbpms	1.63	0.64	47	Unknown	transcription, DNA-templated
Zfp7	0.91	1.15	48	Unknown	regulation of transcription, DNA-templated
Lin28a	0.78	1.31	49	Reprogramming	[1]
Zfp423	0.55	1.79	50	Differentiation	cell differentiation

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