

Supplementary Table S3. Summary of *Mus musculus* microarray data

Set	Accession Number	Description	Number of Samples	Reference
1	GSE3653	Differentiation of mouse ESCs by DOX-induction of Ngn3	16	[1]
2	GSE4189	siRNA knockdown of Pou5f1 and Nanog in mouse ESCs	14	[2]
3	GSE13235	mESCs grown in low concentration of Nitric oxide	9	-
4	GSE10210	Endothelial differentiation of mESCs	16	[3]
5	GSE10806	Reprogramming mouse neural stem cells	11	[4]
6	GSE9563	Differentiation of mESCs into embryoid bodies	30	[5]
7	GSE11044	Differentiation of hematopoietic stem cells	6	[6]
8	GSE10574	Eed knockdown in mESCs	2	[7]
9	GSE10477	Conditional Pou5f1 Knockout in mESCs	3	[7]
10	GSE10476	Ring1A\B double Knockout in mESCs	4	[7]
11	GSE10534	Gata6 overexpression in mESCs	3	[7]
12	GSE7528	CYP26A1 Knockout mESCs	18	[8]
13	GSE8503	Dicer deficient mESCs	6	[9]
14	GSE9760	Expanded CAG repeats augment differentiation of mESCs	12	[10]
15	GSE6933	Unique Signature of Multipotent Adult Progenitor Cells	15	[11]
16	GSE5671	mESCs-derived cardiac precursor cells	18	[12]
17	GSE8128	Modeling insertional mutagenesis in mESCs	9	[13]
18	GSE7688	Genome wide mapping of active promoters in mESCs	5	[14]
19	GSE10871	Dissecting reprogramming through genomic analysis	32	[15]
20	GSE4307	Single cell expression data from mouse ICM	20	[16]

1. Treff NR, Vincent RK, Budde ML, Browning VL, Magliocca JF, et al. (2006) Differentiation of embryonic stem cells conditionally expressing neurogenin 3. *Stem Cells* 24: 2529-2537.
2. Loh YH, Wu Q, Chew JL, Vega VB, Zhang W, et al. (2006) The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. *Nat Genet* 38: 431-440.
3. Nikolova-Krstevski V, Bhasin M, Otu HH, Libermann T, Oettgen P (2008) Gene expression analysis of embryonic stem cells expressing VE-cadherin (CD144) during endothelial differentiation. *BMC Genomics* 9: 240.
4. Kim JB, Zaehres H, Wu G, Gentile L, Ko K, et al. (2008) Pluripotent stem cells induced from adult neural stem cells by reprogramming with two factors. *Nature* 454: 646-650.
5. Sampath P, Pritchard DK, Pabon L, Reinecke H, Schwartz SM, et al. (2008) A hierarchical network controls protein translation during murine embryonic stem cell self-renewal and differentiation. *Cell Stem Cell* 2: 448-460.
6. Orford K, Kharchenko P, Lai W, Dao MC, Worhunsky DJ, et al. (2008) Differential H3K4 methylation identifies developmentally poised hematopoietic genes. *Dev Cell* 14: 798-809.
7. Endoh M, Endo TA, Endoh T, Fujimura Y, Ohara O, et al. (2008) Polycomb group proteins Ring1A/B are functionally linked to the core transcriptional regulatory circuitry to maintain ES cell identity. *Development* 135: 1513-1524.
8. Langton S, Gudas LJ (2008) CYP26A1 knockout embryonic stem cells exhibit reduced differentiation and growth arrest in response to retinoic acid. *Dev Biol* 315: 331-354.
9. Sinkkonen L, Hugenschmidt T, Berninger P, Gaidatzis D, Mohn F, et al. (2008) MicroRNAs control de novo DNA methylation through regulation of transcriptional repressors in mouse embryonic stem cells. *Nat Struct Mol Biol* 15: 259-267.
10. Lorincz MT, Zawistowski VA (2009) Expanded CAG repeats in the murine Huntington's disease gene increases neuronal differentiation of embryonic and neural stem cells. *Mol Cell Neurosci* 40: 1-13.
11. Ulloa-Montoya F, Kidder BL, Pauwelyn KA, Chase LG, Luttun A, et al. (2007) Comparative transcriptome analysis of embryonic and adult stem cells with extended and limited differentiation capacity. *Genome Biol* 8: R163.
12. Christoforou N, Miller RA, Hill CM, Jie CC, McCallion AS, et al. (2008) Mouse ES cell-derived cardiac precursor cells are multipotent and facilitate identification of novel cardiac genes. *J Clin Invest* 118: 894-903.
13. Nord AS, Vranizan K, Tingley W, Zamboni AC, Hanspers K, et al. (2007) Modeling insertional mutagenesis using gene length and expression in murine embryonic stem cells. *PLoS One* 2: e617.
14. Barrera LO, Li Z, Smith AD, Arden KC, Cavenee WK, et al. (2008) Genome-wide mapping and analysis of active promoters in mouse embryonic stem cells and adult organs. *Genome Res* 18: 46-59.
15. Mikkelsen TS, Hanna J, Zhang X, Ku M, Wernig M, et al. (2008) Dissecting direct reprogramming through integrative genomic analysis. *Nature* 454: 49-55.
16. Kurimoto K, Yabuta Y, Ohinata Y, Ono Y, Uno KD, et al. (2006) An improved single-cell cDNA amplification method for efficient high-density oligonucleotide microarray analysis. *Nucleic Acids Res* 34: e42.