

Supplementary Table S1

	<i>Reference</i>	<i>Article</i>	<i>Specie</i>	<i>Platform</i>	<i>Approach</i>	<i>Database</i>	<i>Accession Number</i>
<i>ES cells and reprogramming process</i>	48	Proteome adaptation in cell reprogramming proceeds via distinct transcriptional networks	Mus musculus	Agilent 1200 HPLC (nanoLC) coupled to a Thermo LTQ-Orbitrap Velos (MS)	Proteomics	proteomeXchange (consortium)	PXD000413
<i>ES cells-derived differentiation</i>	49	Reconstitution of the mouse germ cell specification pathway in culture by pluripotent stem cells	Mus musculus	Affymetrix Mouse430_2 (GPL1261 and A-AFFY-45)	Expression Array	GEO (NCBI)	GSE30056
<i>ES cells and reprogramming process</i>	50	Genome-wide characterization of the routes to pluripotency	Mus musculus	Life Technologies SOLiD 5500xl NCBIM37 Gene + Transcript	RNA-Seq	Sequence Read Archive (NCBI)	SRP046744
<i>Cells from developing embryo</i>	51	Temporal Transcriptional Profiling of Somatic and Germ Cells Reveals Biased Lineage Priming of Sexual Fate in the Fetal Mouse Gonad	Mus musculus	Affymetrix MoGene-1_0-ST V1	Expression Array	GEO (NCBI)	GSE27715
<i>Cells from developing embryo, ES cells /MEF/iPS cells</i>	52	The Transcriptional and Functional Properties of Mouse Epiblast Stem Cells Resemble the Anterior Primitive Streak	Mus musculus	Illumina MouseWG-6 v2	Expression Array	GEO (NCBI)	GSE46227
<i>ES cells-derived differentiation</i>	53	SOX2 co-occupies distal enhancer elements with distinct POU factors in ESCs and NPCs to specify cell state	Mus musculus	Affimetric Mouse430_2	Expression Array	GEO (NCBI)	GSE38850
<i>Different stem cell types</i>	54	Comparative transcriptome analysis of embryonic and adult stem cells with extended and limited differentiation capacity	Mus musculus	Affymetrix Mouse430_2	Expression Array	GEO (NCBI)	GSE6933
<i>ES cells-derived differentiation</i>	55	Dynamic and coordinated epigenetic regulation of developmental transitions in the cardiac lineage	Mus musculus	Illumina Genome Analyzer IIx RNASeq mm9 Gene TMM-RPKM (GPL11002)	RNA-Seq	GnomEx (Utah)	7R2

Supplementary Table S1. Related to Supplementary Fig. S2. Meta-analysis of microarray, RNA-seq and proteomic datasets analyzed in this work. Studies were selected from the Stemformatics web tool.