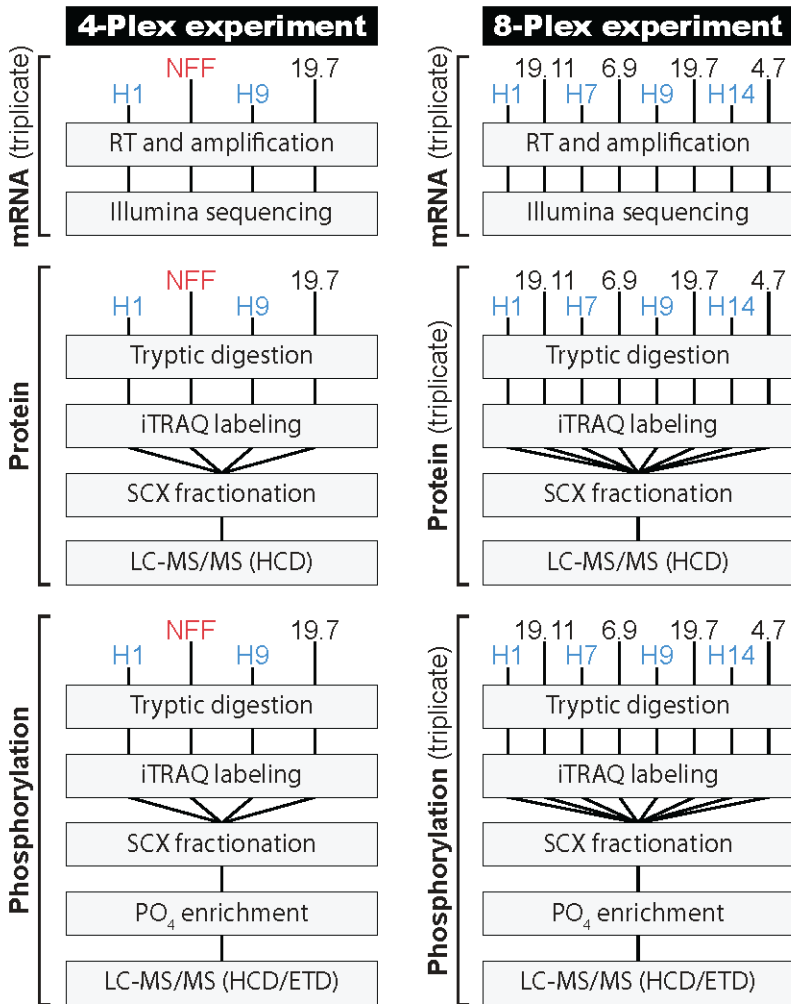
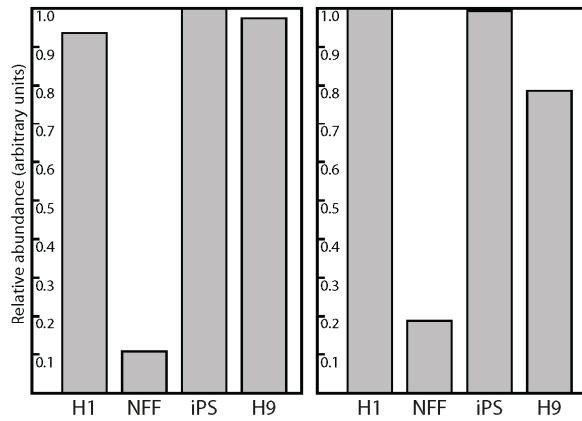
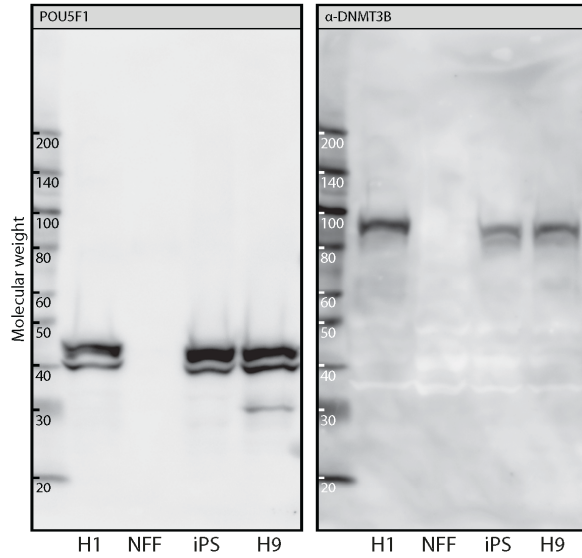


Supplementary Figure 1 - Experimental Workflow for both 4-plex and 8-plex experiments

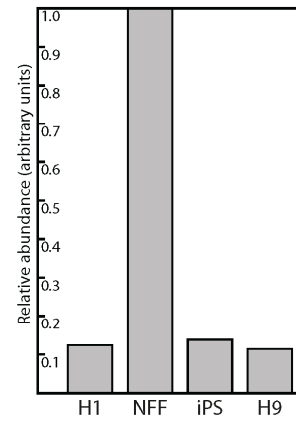
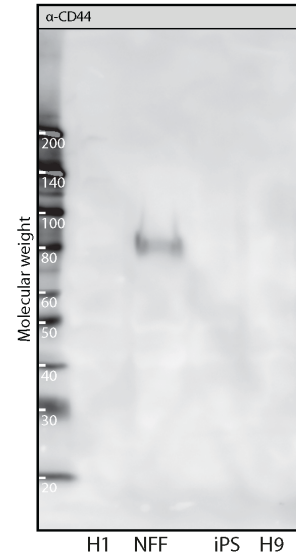


Graphical depiction of the 4-plex and 8-plex experiments.

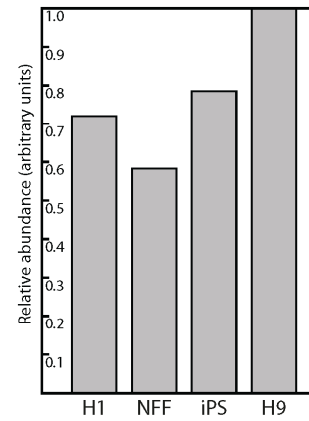
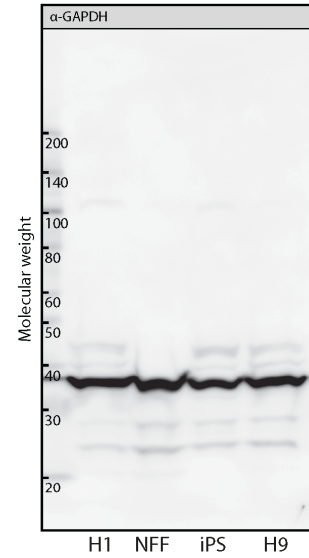
a. Pluripotent-specific



b. NFF-specific

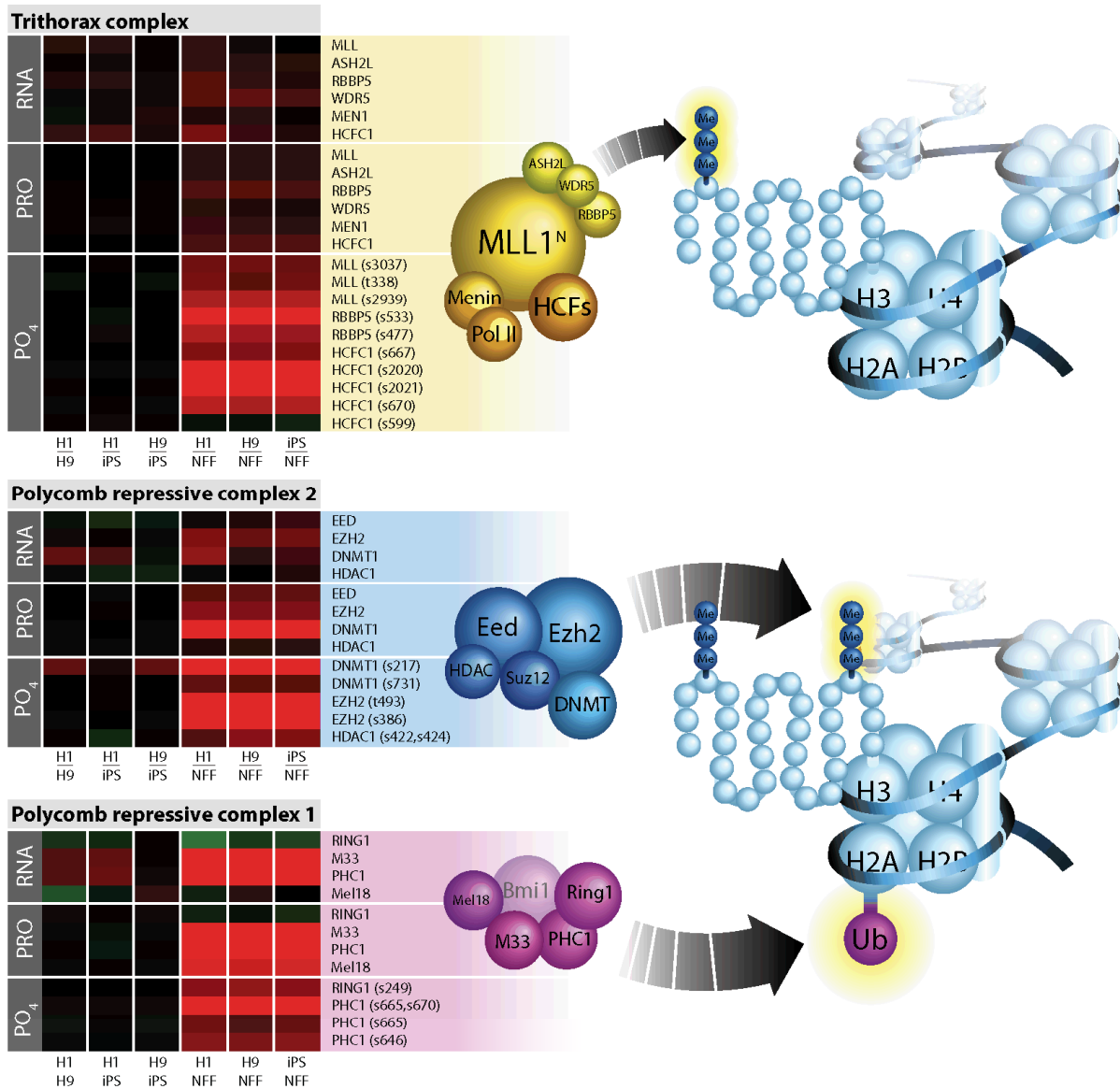


c. Loading control



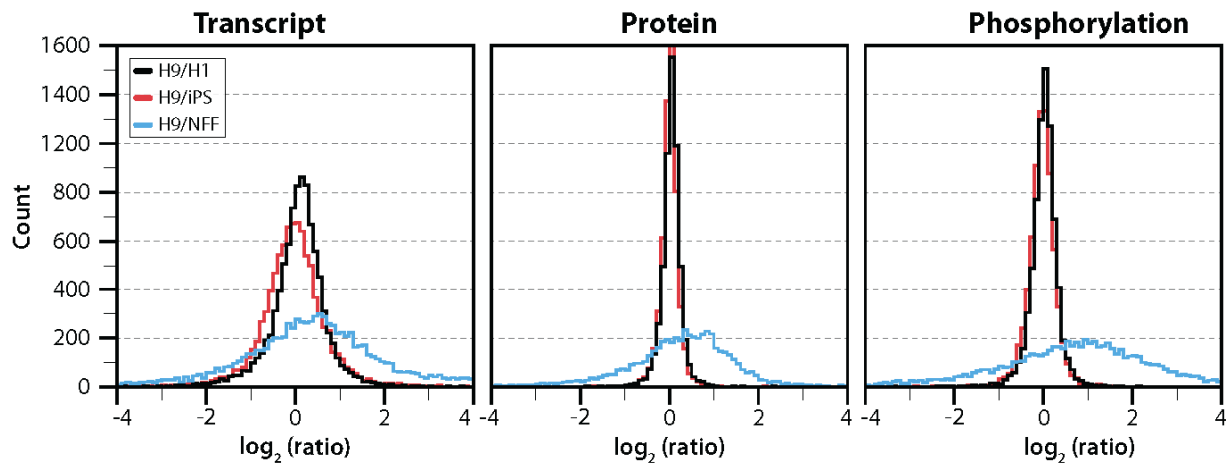
Western blot analysis and corresponding iTRAQ quantitation for POU5F1/OCT4, DNMT3B, CD44, and GAPDH.

Supplementary Figure 3 - Polycomb and trithorax transcripts, proteins, and phosphorylation sites in 4-plex experiment



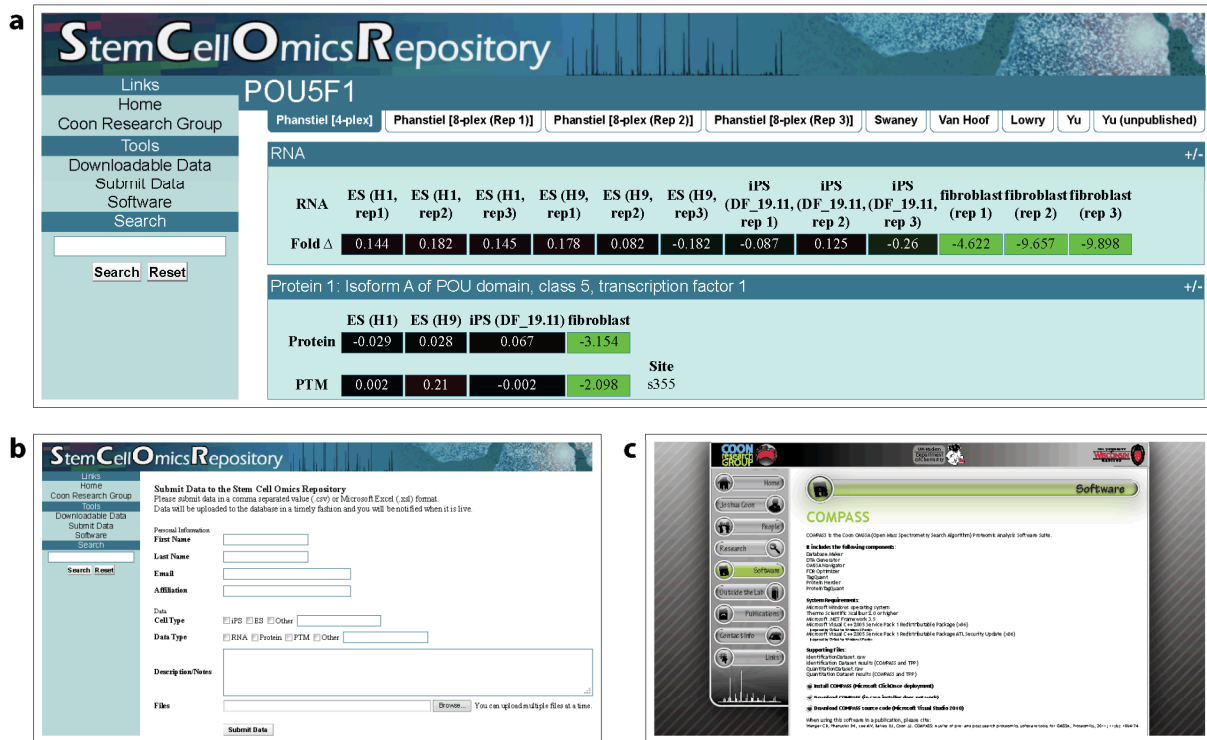
Polycomb and trithorax complexes. Quantitation of mRNA, protein, and phosphorylation site abundances for major components of the polycomb and trithorax complexes that coordinate methylation of key residues on histone H3. Our proteomic analysis identified nearly every major component of both protein groups, most of which were enriched in pluripotent lines relative to NFF cells on the mRNA, protein, and PTM level. We note that phosphorylation of several sites on both polycomb group and trithorax proteins were either unchanged or decreased in pluripotent lines. For example, phosphorylation of s249 on RING1 is lower in pluripotent lines, even though the protein is enriched in ES and iPS cells. These sites may point to important targets of post-translational regulation during differentiation.

Supplementary Figure 4 - Distribution of ratios for ES vs. ES, ES vs. iPS, and ES vs. NFF comparisons.



Distribution of \log_2 ratios for ES vs. ES, ES vs. iPS, and ES vs. NFF comparisons. Transcript, protein, and phosphorylation site comparisons are shown. Note that ES vs. iPS distributions are nearly identical to ES vs. ES distributions.

Supplementary Figure 5 - Selected screen shots from the SCOR website



Selected screen shots from the SCOR website. (a) SCOR provides quantitative information at the transcript, protein, and PTM levels. Tabs at the top of the site enable viewers to toggle through various experiments, including those from other laboratories. Quantitative values are shown as log₂ ratios compared to the median. (b) Data from large-scale analyses is submitted to SCOR through the “Submit Data” function. (c) The tools tab provides software for large-scale data processing.

Supplementary Table 4 - Distribution of ratios for ES vs. ES, ES vs. iPS, and ES vs. NFF comparisons.

Higher in this cell type	Motif	# of isoforms at least 2 fold higher in specified cell type	# of isoforms with this motif	P-value	P-value adjusted
ESsP.K...	312	415	7.41x10 ⁻³³	6.81x10 ⁻³¹
ESsP.....	1765	3194	2.81x10 ⁻³²	1.29x10 ⁻³⁰
ESsP..K..	215	318	4.91x10 ⁻¹⁴	1.51x10 ⁻¹²
ES	K.....sP.....	183	265	2.01x10 ⁻¹³	4.62x10 ⁻¹²
ESsP...K.	188	286	9.07x10 ⁻¹¹	1.67x10 ⁻⁹
ESsP...K	194	303	1.29x10 ⁻⁹	1.98x10 ⁻⁸
ESDsE.E...	60	74	1.66x10 ⁻⁹	2.18x10 ⁻⁸
ESsP.R...	184	287	2.99x10 ⁻⁹	3.44x10 ⁻⁸
EStP.K...	83	112	4.76x10 ⁻⁹	4.87x10 ⁻⁸
ES	..K...sP.....	144	230	1.26x10 ⁻⁶	1.06x10 ⁻⁵
NFF	...R.s.....	277	1407	1.76x10 ⁻⁹	1.62x10 ⁻⁷
NFFRt.S....	13	34	5.38x10 ⁻⁴	2.48x10 ⁻²

We used Fishers Exact test with Benjamini-Hochberg correction to identify motifs that were significantly enriched ($P < 0.05$) in sets of phosphorylation sites that were at least two fold more abundant in either ES or NFF cells.

Supplementary Table 8 - Selected GO terms that were enriched in sets of proteins and transcripts that were higher in iPS compared to ES cells.

GO biological process (selected terms)	Up in iPS vs ES			Up in NFF vs ES		
	RNA	Protein	Phospho-isoforms	RNA	Protein	Phospho-isoforms
Muscle system process	7.56x10 ⁻⁵	1.09x10 ⁻³	4.62x10 ⁻²	2.50x10 ⁻²	9.67x10 ⁻⁷	2.26x10 ⁻⁷
Muscle contraction	3.93x10 ⁻⁵	5.15x10 ⁻⁴	4.62x10 ⁻²	2.50x10 ⁻²	3.99x10 ⁻⁷	8.39x10 ⁻⁸
Response to wounding	4.37x10 ⁻²	5.05x10 ⁻³	4.62x10 ⁻²	6.88x10 ⁻²⁰	1.47x10 ⁻⁹	7.53x10 ⁻⁴
Circulatory system process	6.36x10 ⁻³	1.42x10 ⁻³	NA	9.02x10 ⁻⁵	3.38x10 ⁻³	NA
Tissue development	1.19x10 ⁻²	8.82x10 ⁻³	NA	2.13x10 ⁻¹⁹	1.45x10 ⁻⁵	1.54x10 ⁻²
Regulation of apoptosis	1.34x10 ⁻²	3.27x10 ⁻²	NA	4.19x10 ⁻⁸	1.11x10 ⁻²	NA
Organ development	1.01x10 ⁻⁷	1.36x10 ⁻³	NA	5.13x10 ⁻¹⁶	2.96x10 ⁻³	NA
System development	2.43x10 ⁻⁶	4.24x10 ⁻³	NA	5.95x10 ⁻¹⁶	2.49x10 ⁻⁵	9.15x10 ⁻³

Selected GO terms, and associated p-values (Fisher's Exact Test with BH correction), that were enriched in sets of proteins and transcripts that were higher in iPS compared to ES cells. P-values of the same GO terms enriched in NFF compared to ES cells are also shown. Values of "NA" indicate that p-values were greater than 0.05.

Supplementary Table 9 - Transcripts that consistently differ between ES and iPS cells.

Increased in ES cells

Gene	RNA-Seq	Chin et al.
TCERG1L	X	X
DPP6		X
FAM19A5	X	X
IRX2	X	

Increased in iPS cells

Gene	RNA-Seq	Chin et al.
CR1L	X	
ZNF208		
CTSF	X	X
GREM1		
LY6K		
ZNF560		
ZNF662		