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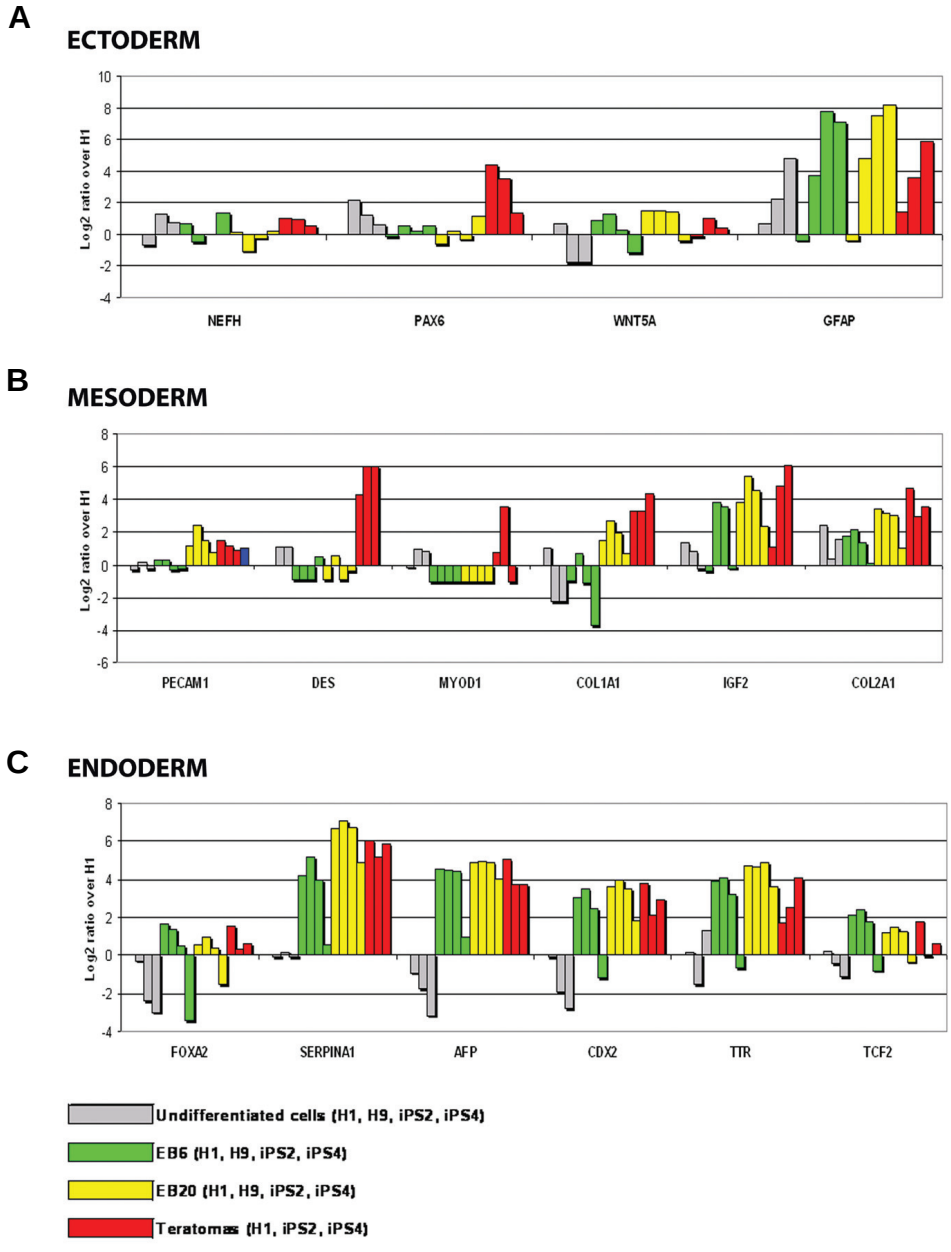
SUPPLEMENTARY MATERIAL

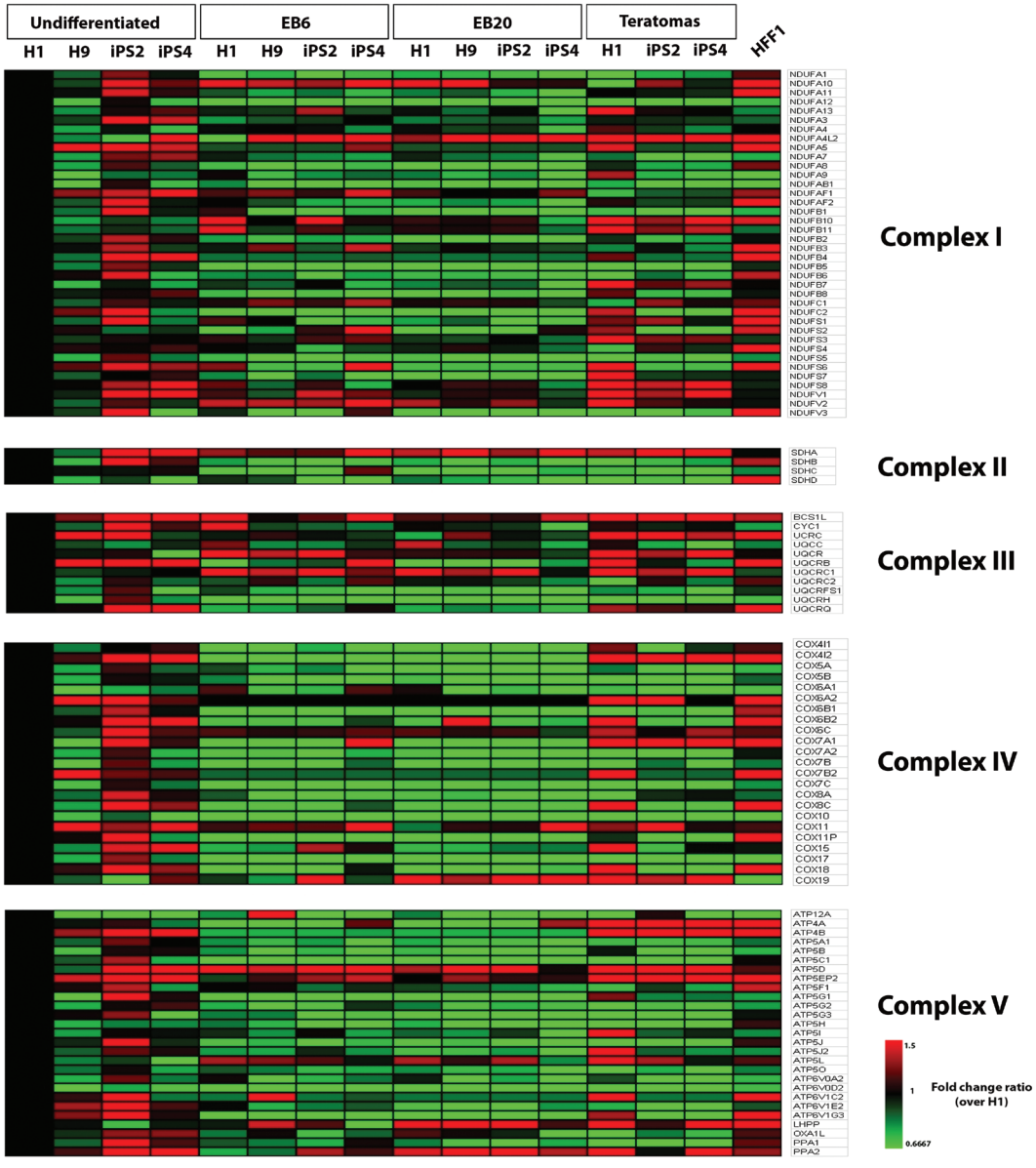
corresponding to:

Modulation of mitochondrial biogenesis and bioenergetic metabolism upon *in vitro* and *in vivo* differentiation of human ES and iPS cells

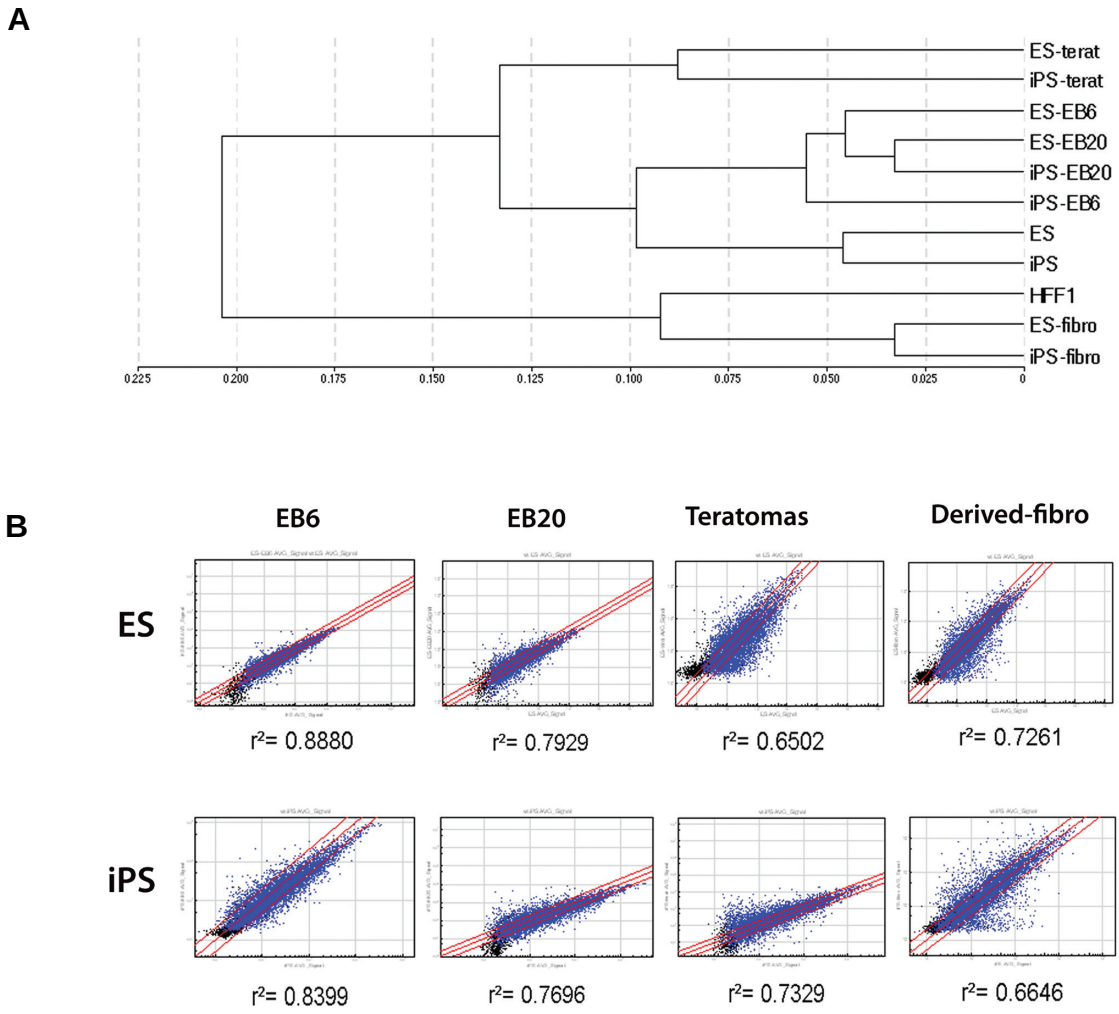
ALESSANDRO PRIGIONE and JAMES ADJAYE



Supplementary Fig. 1. Expression of markers of germ layer specification upon differentiation of human ES and iPS cells. *The microarray data were analyzed in relation to the expression of markers of differentiation and germ layer commitment. Results are shown as log2 ratio values in comparison to H1 expression.* **(A)** *Similar transcriptional response of ectodermal markers was observed upon differentiation of ES and iPS cells. Analyzed genes include* NEFH, PAX6, WNT5A, *and* GFAP. **(B)** *Mesoderm-related transcripts were similarly regulated in differentiated ES and iPS cells. Genes include* PECAM1, DES, MYOD1, COL1A1, IGF2, *and* COL2A1. **(C)** *Expression of endodermal markers during ES and iPS differentiation appeared mainly comparable. Transcripts comprise* FOXA2, SERPIKNA1, AFP, CDX2, TTR, *and* TCF2.



Supplementary Fig. 2. Transcriptional analysis of nuclear-encoded mitochondrial complexes. *Heatmap figure focusing on a panel of genes involved in mitochondrial energy metabolism. Genes were divided accordingly to the respective mitochondrial complex (Complex I, II, III, IV, and V). Results represent fold change values compared to H1 expression (fold change 1.5, p value ≤0.01, and differential p value ≤0.01); up- and down-regulated transcripts are depicted in red and green respectively.*



Supplementary Fig. 3. Transcriptional profiling of spontaneously differentiated cells and selectively differentiated cells. *Microarray data were re-analyzed by including also expression data of previously obtained human ES cell-derived and human iPS cell-derived fibroblasts (DFs) (Prigione* et al. *2010).* **(A)** *Hierarchical clustering of the samples showing how both ES and iPS cell derived-fibroblasts clustered together with somatic HFF1 fibroblasts and are distinct from undifferentiated and spontaneously differentiated ES and iPS cells.* **(B)** *Scatter plot graphs showing the degree of correlation between undifferentiated ES cells and differentiated cells (upper raw of graphs), and the degree of correlation between undifferentiated iPS cells and differentiated cells (lower raw of graphs). The values of the correlation coefficient (r square) decreased with differentiation both in ES and iPS cells.*

SUPPLEMENTARY TABLE 1

PRIMER SETS USED FOR Q-PCR ANALYSIS

Gene	Forward sequence (5'-3')	Reverse sequence (5'-3')
ACTB	TCAAGATCATTGCTCCTCCTGAG	ACATCTGCTGGAAGGTGGACA
GAPDH	CTGGTAAAGTGGATATTGTTGCCAT	TGGAATCATATTGGAACATGTAAACC
OCT4	GTGGAGGAAGCTGACAACAA	ATTCTCCAGGTTGCCTCTCA
POLG	GCTGGTGGAAGAGCGTTACTC	GAAGCTGCTTAGCCCTGAGAT
POLG2	GGTTTGGGGGTCGAGTAGATG	TTCCACTTAGGAAATGCCTTCTC
NRF1	AACAAAATTGGGCCACGTTACA	TCTGGACCAGGCCATTAGCA
TFAM	ATGGCGTTTCTCCGAAGCAT	CAGATGAAAACCACCTCGGTAA
PGC1A	GCTTTCTGGGTGGACTCAAGT	TCTAGTGTCTCTGTGAGGACTG
PGC1B	CCACATCCTACCCAACATCAAG	CACAAGGCCGTTGACTTTTAGA
SNAI1	CCACTTCTGGCCACATCAGC	GCCCTCCCTCCACAGAAATG
SLUG	ATCTGCCAGACGCGAACTCA	CAACAATGGCAACCAGACAACC