

**Supplementary Table 1.** Gene Ontology Categories and Pathways for Cluster of Genes Upregulated in Differentiated SF-1-ES cells Treated with cAMP

Category	Term	P Value	Genes
SP_PIR_KEYWORDS	Secreted	0.0003	Prl2c3, Prl2c4, CCK, prsS12, Prl3b1, GHRH, S100A8, lipH, Mmp2, clpS, Wfdc1
SP_PIR_KEYWORDS	Signal	0.0003	ctsR, lipH, Wfdc1, Prl2c3, Prl2c4, SEMA6D, Ctsq, Ctsj, CCK, prsS12, Prl3b1, GHRH, Mmp2, Tmem41a, clpS
SP_PIR_KEYWORDS	Hormone	0.0006	Prl2c3, Prl2c4, CCK, Prl2c5, Prl3b1
PIR_SUPERFAMILY	PIRSF001825:Prolactin/Lactogen/ Growth hormone	0.0015	Prl2c3, Prl2c4, Prl2c5, Prl3b1
GOTERM_BP_FAT	Steroid biosynthetic process	0.0063	1600014K23Rik, Tecr, Gm4948, CYP17A1, HSD17B2
GOTERM_BP_FAT	Lipid biosynthetic process	0.0119	1600014K23Rik, Tecr, Gm4948, CDS1, CYP17A1, HSD17B2
SP_PIR_KEYWORDS	Disulfide bond	0.0135	Prl2c3, Prl2c4, Ctsj, prsS12, Prl3b1, ctsR, lipH, Mmp2, clpS, Wfdc1, SEMA6D
GOTERM_BP_FAT	Steroid metabolic process	0.0300	1600014K23Rik, Tecr, Gm4948, CYP17A1, HSD17B2
SP_PIR_KEYWORDS	Homodimer	0.0352	CDX2, S100A8
PIR_SUPERFAMILY	PIRSF001182:Papain	0.0368	Ctsj, ctsR
SP_PIR_KEYWORDS	Zymogen	0.0412	Ctsj, ctsR, Mmp2
SP_PIR_KEYWORDS	Protease	0.0486	Ctsj, prsS12, ctsR, Mmp2
<p><i>P</i> value represents the EASE score, a modified Fisher Exact <i>P</i>-Value, for gene-enrichment analysis. All categories with <i>P</i> &lt;0.05 are shown.</p>			