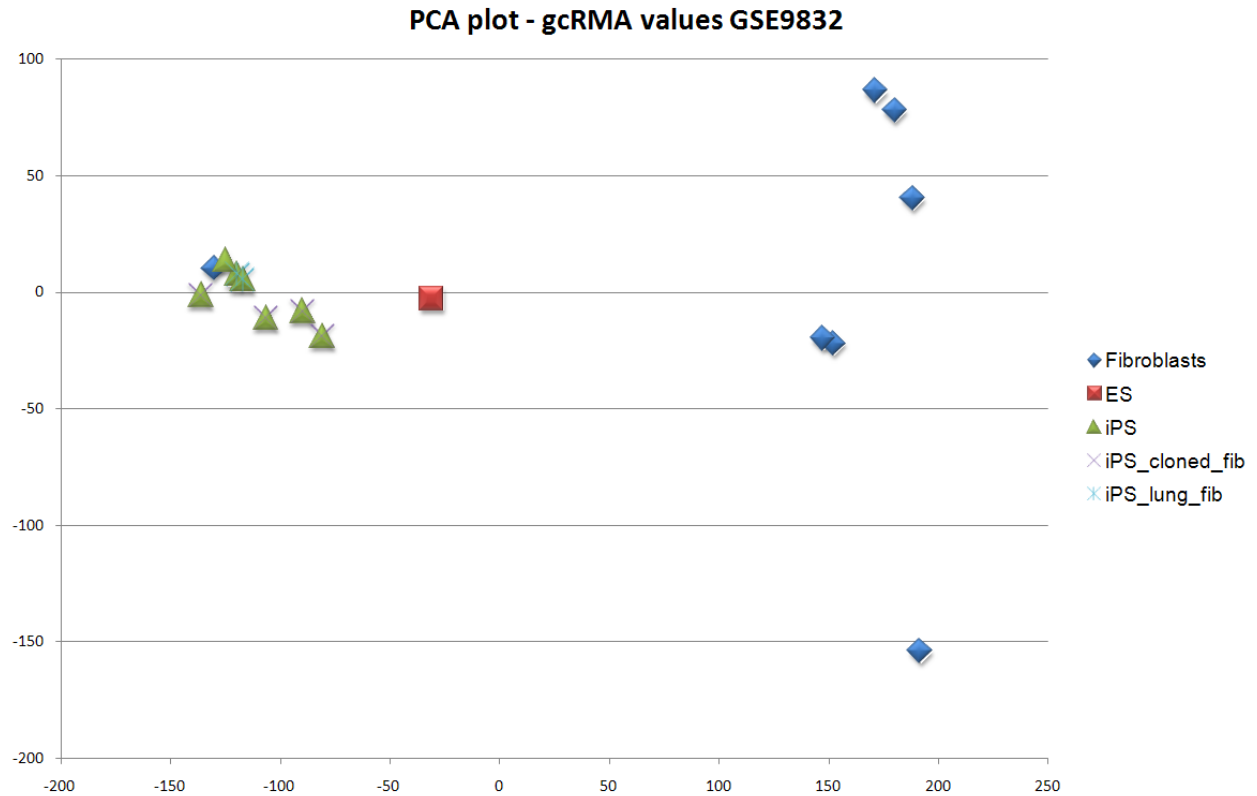
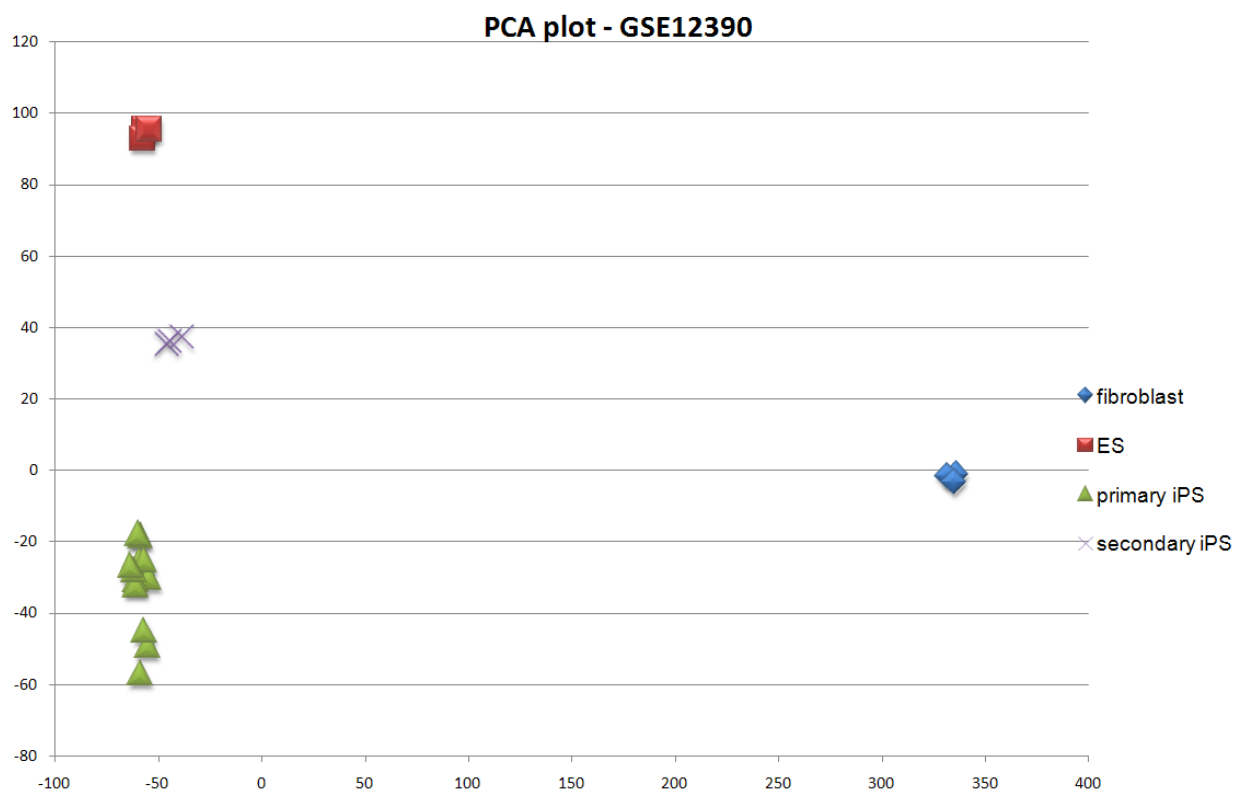
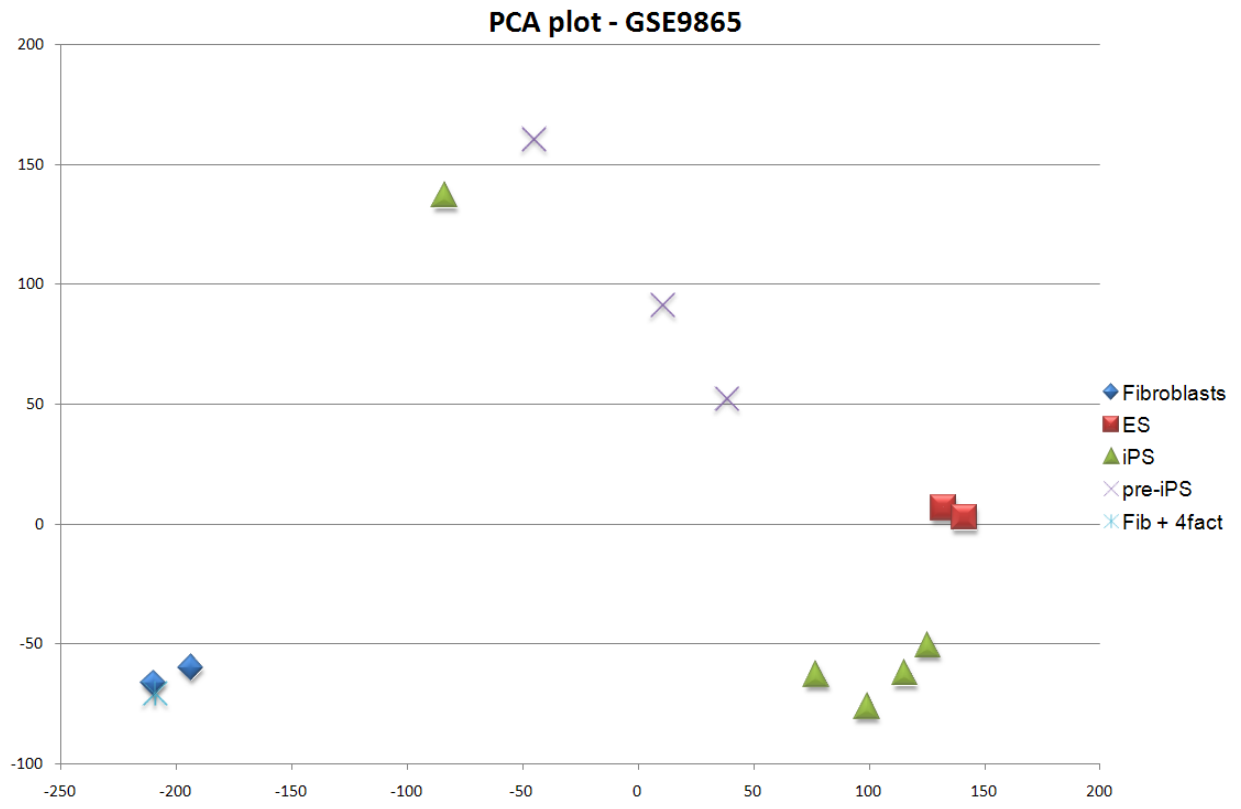


**Figure S4. Principal component analyses of Human and Mouse reprogramming datasets show that ESCs and iPSCs usually cluster together, far from the starting somatic cell population.**

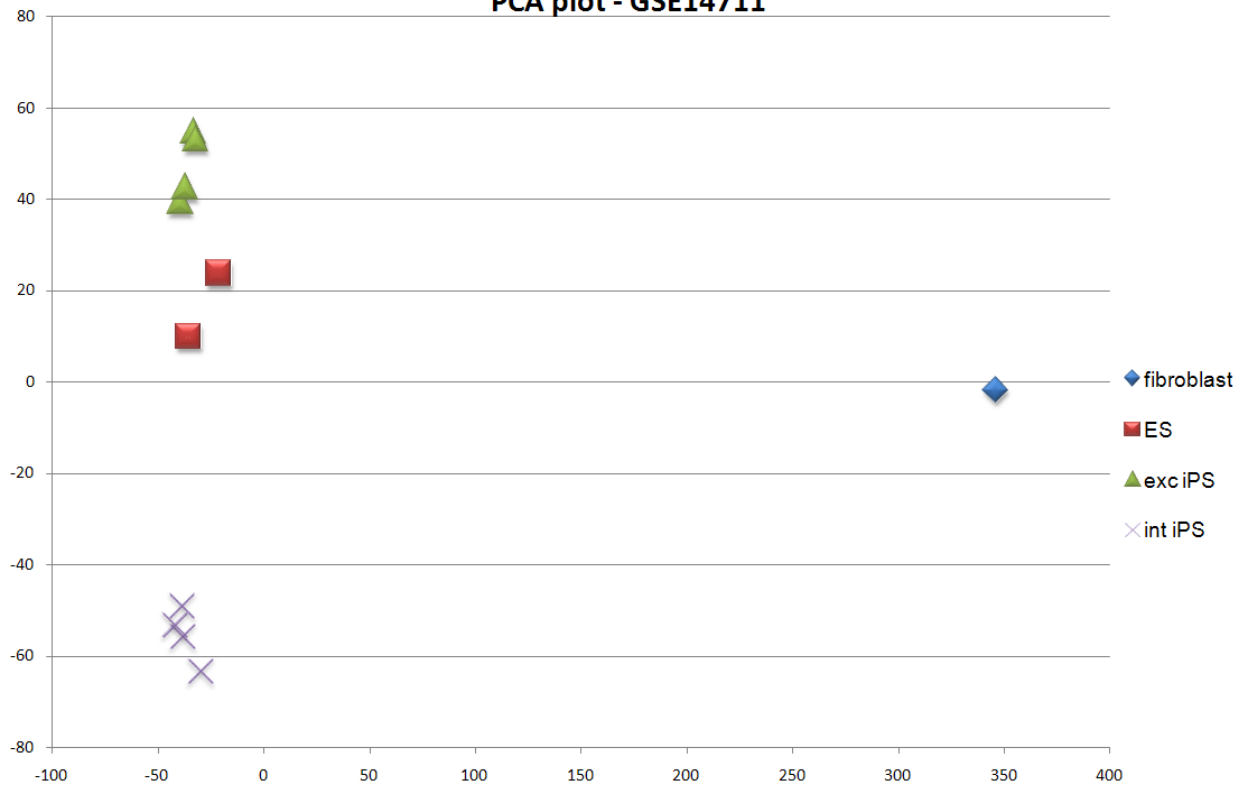
Principal component analysis of genome-wide intensity values (or log of intensity gcRNA-normalized) (A) Human datasets (B) Mouse datasets

**A- Human datasets**





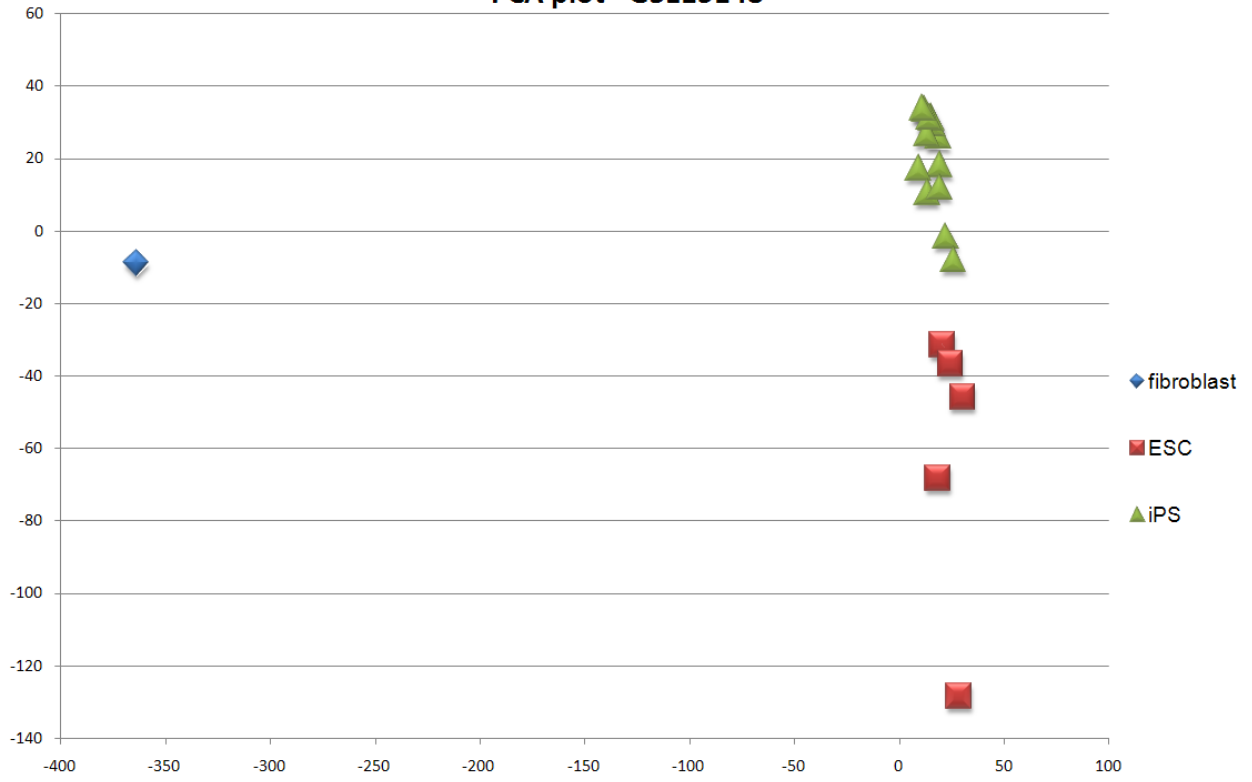
PCA plot - GSE14711



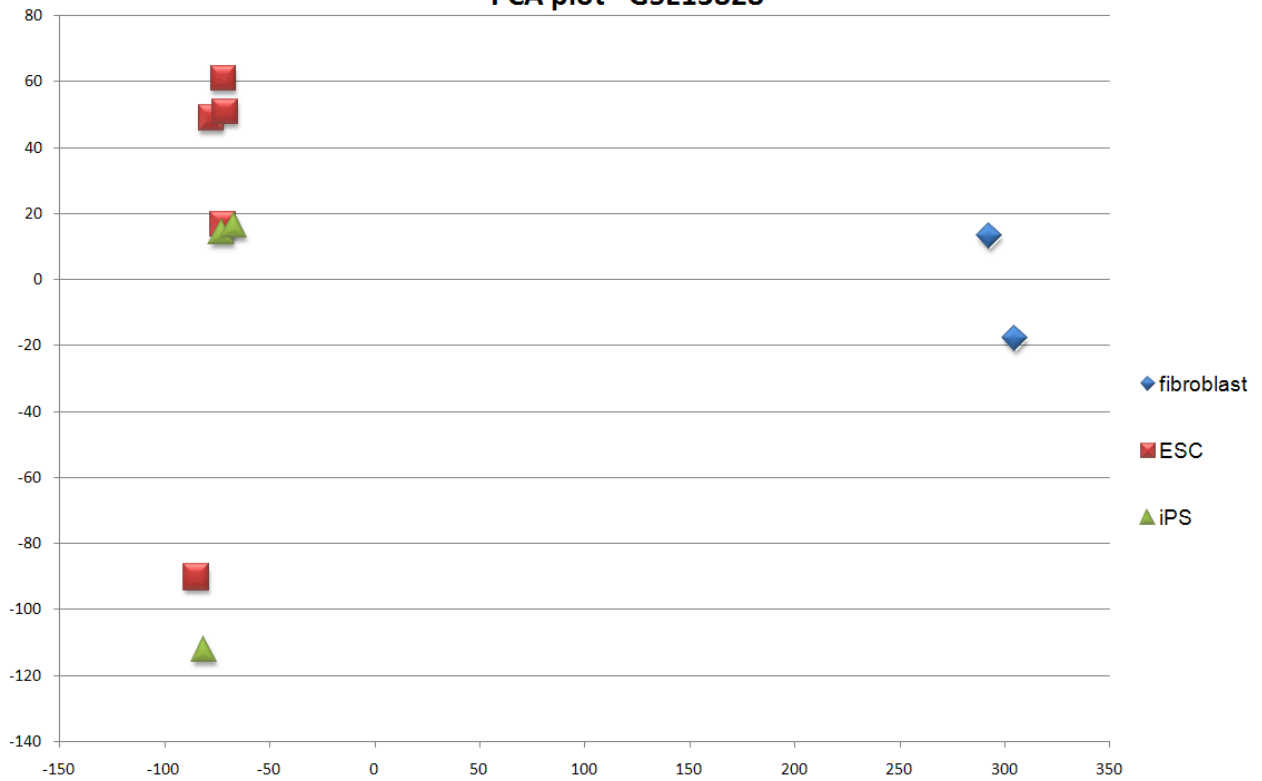
PCA plot - Melton (Huangfu et al.)



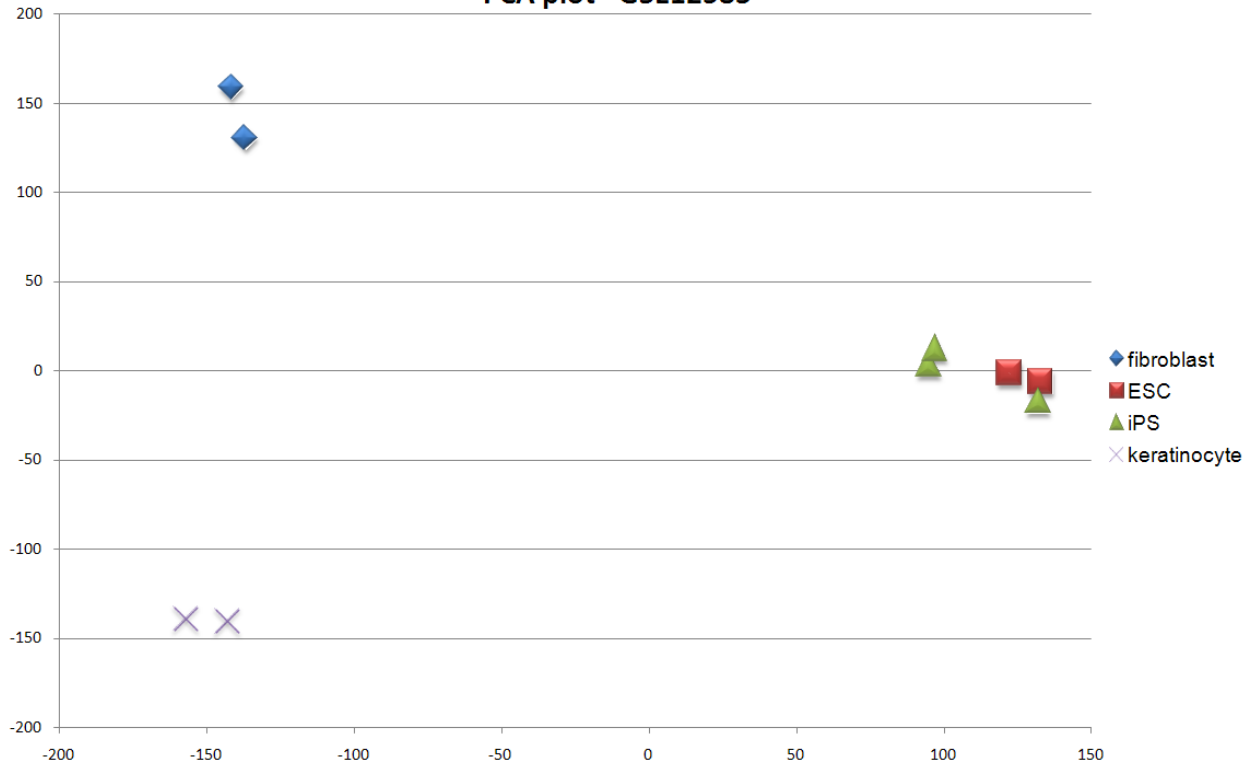
PCA plot - GSE15148



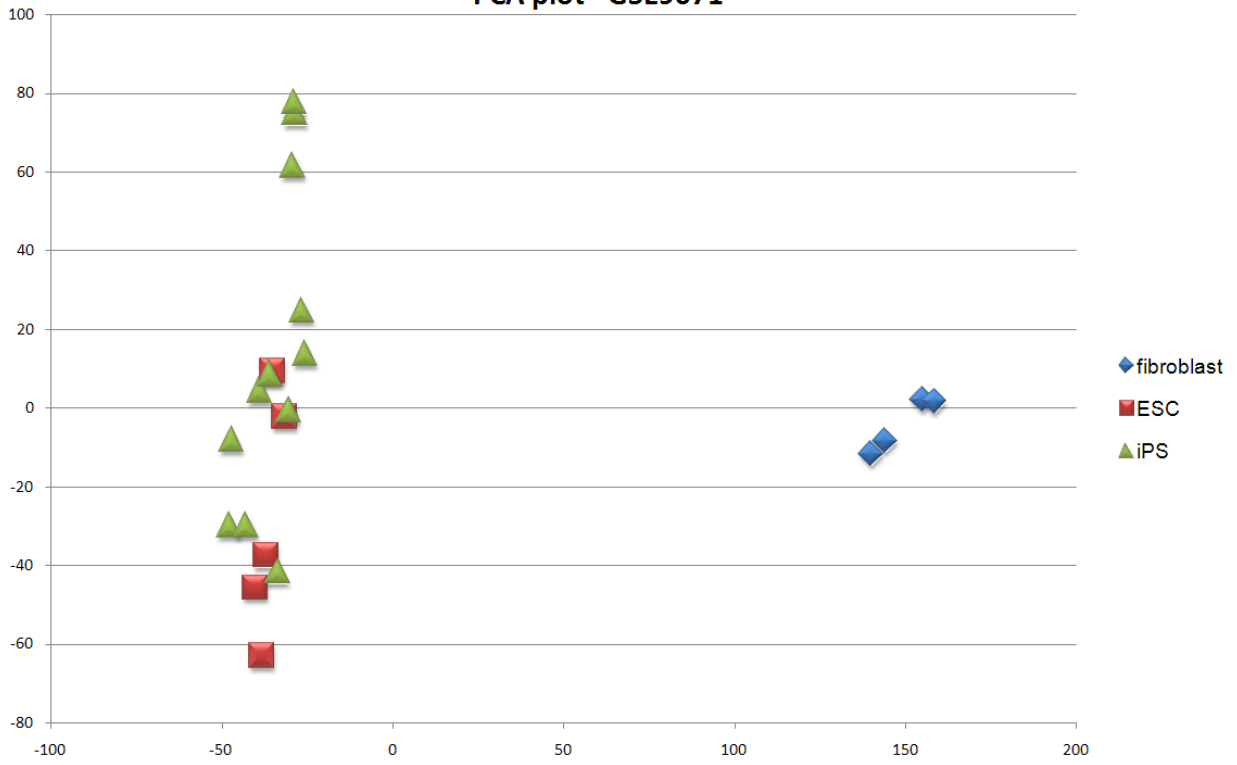
PCA plot - GSE13828



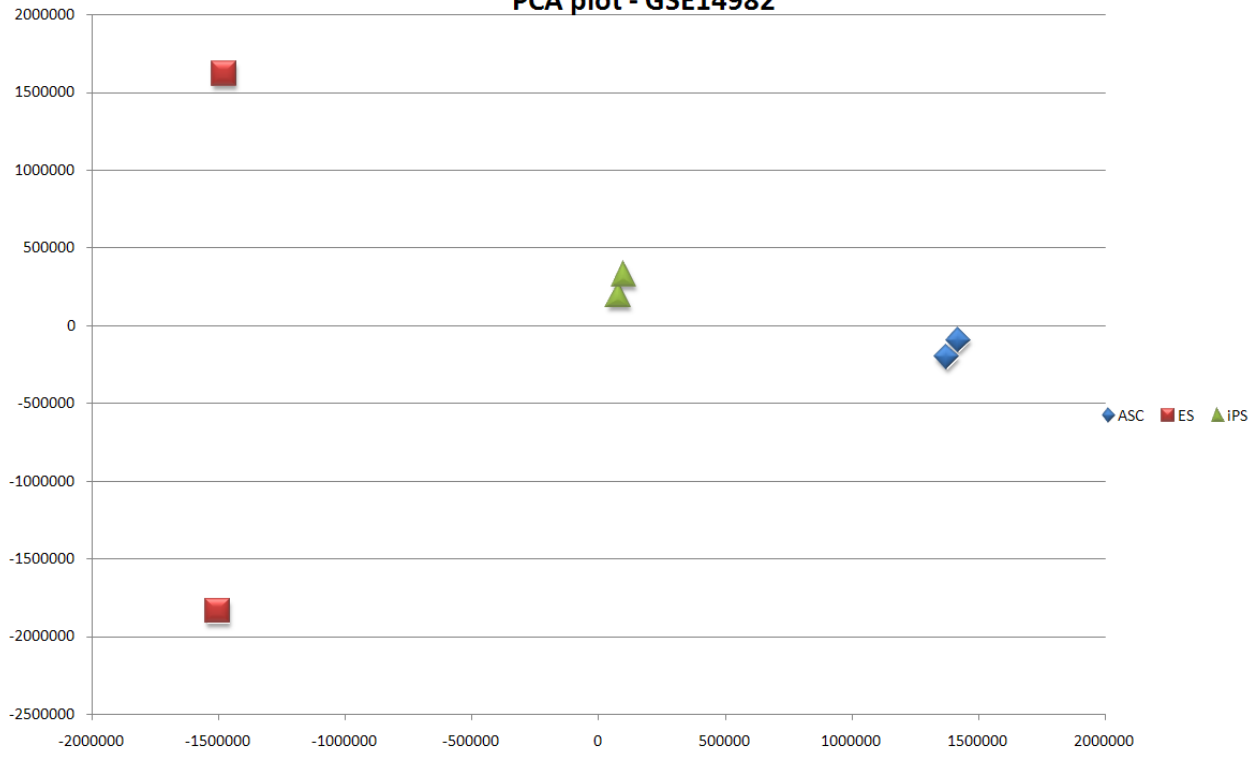
PCA plot - GSE12583



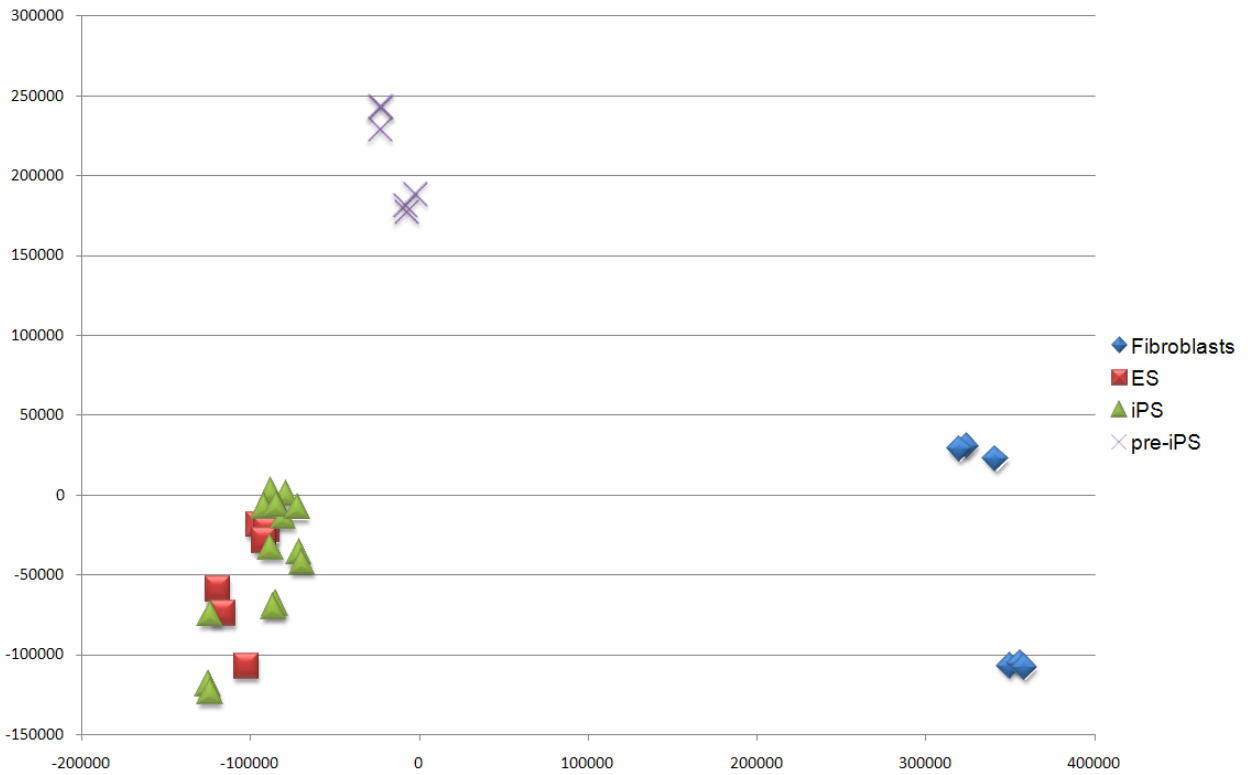
PCA plot - GSE9071



PCA plot - GSE14982

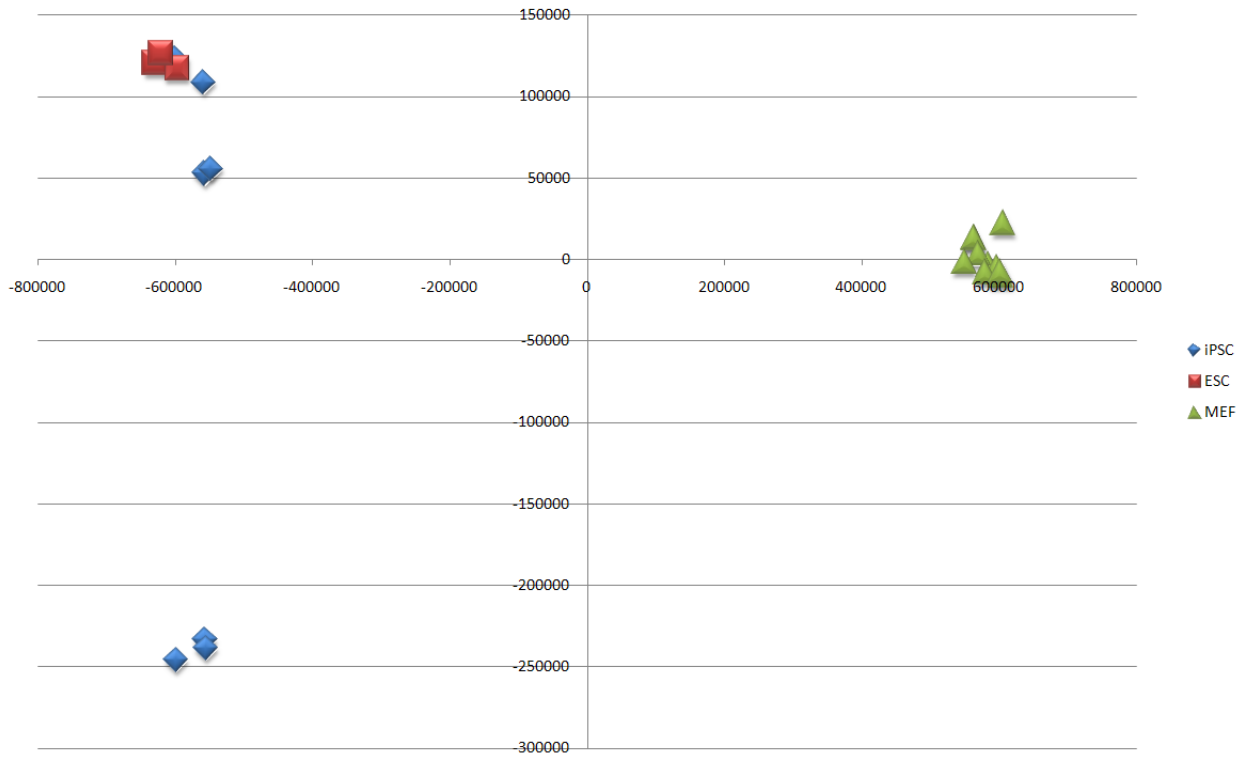


PCA plot - GSE12922

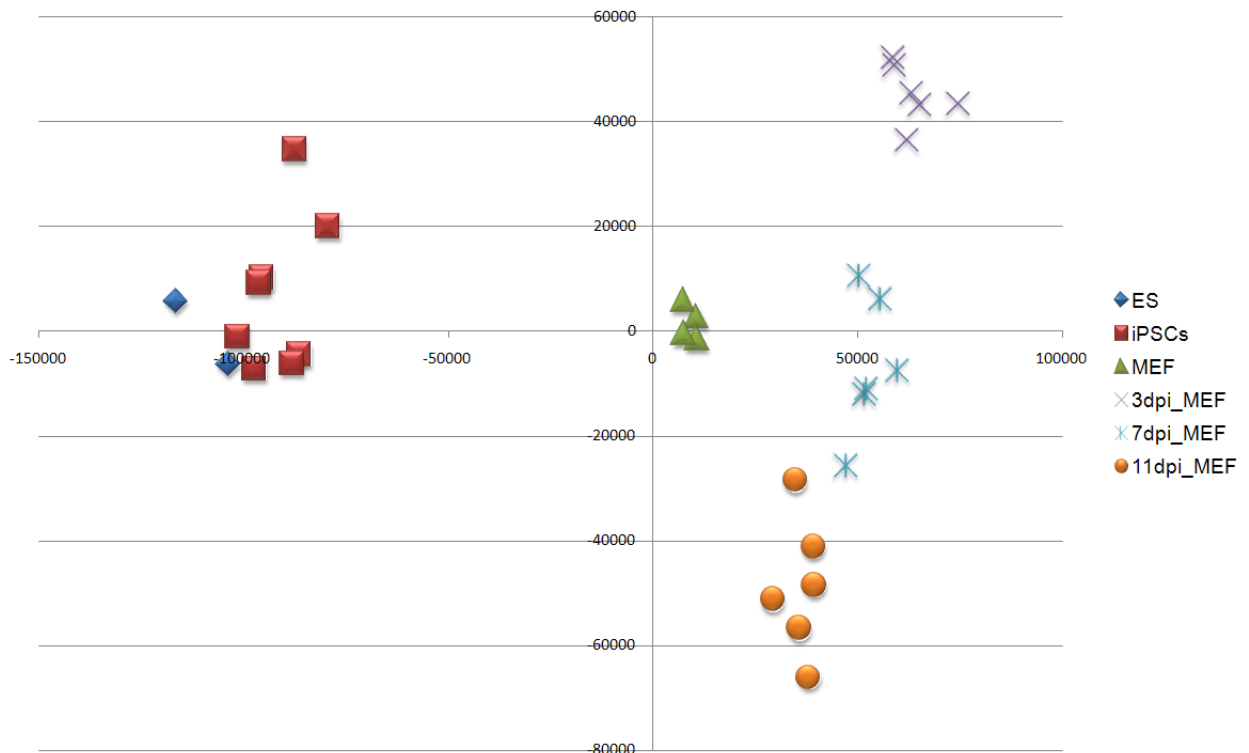


## B- Mouse datasets

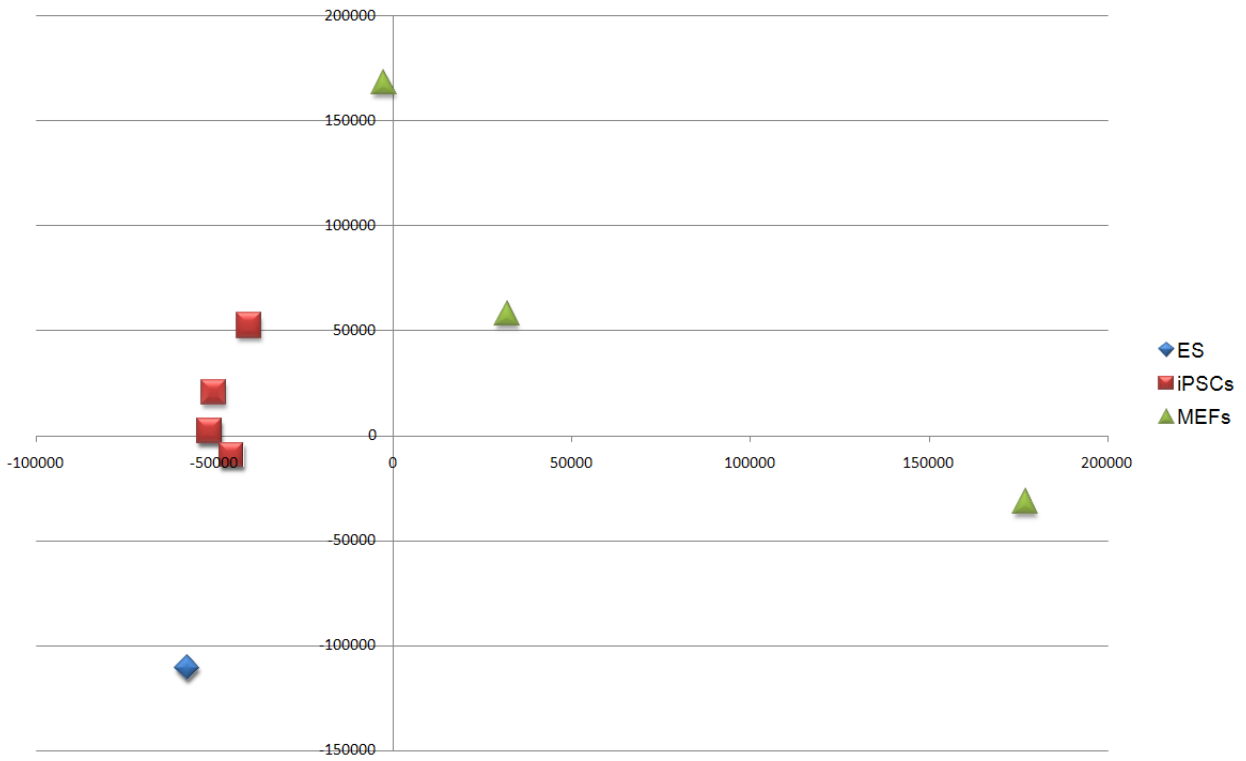
### PCA plot - E-MEXP 1037



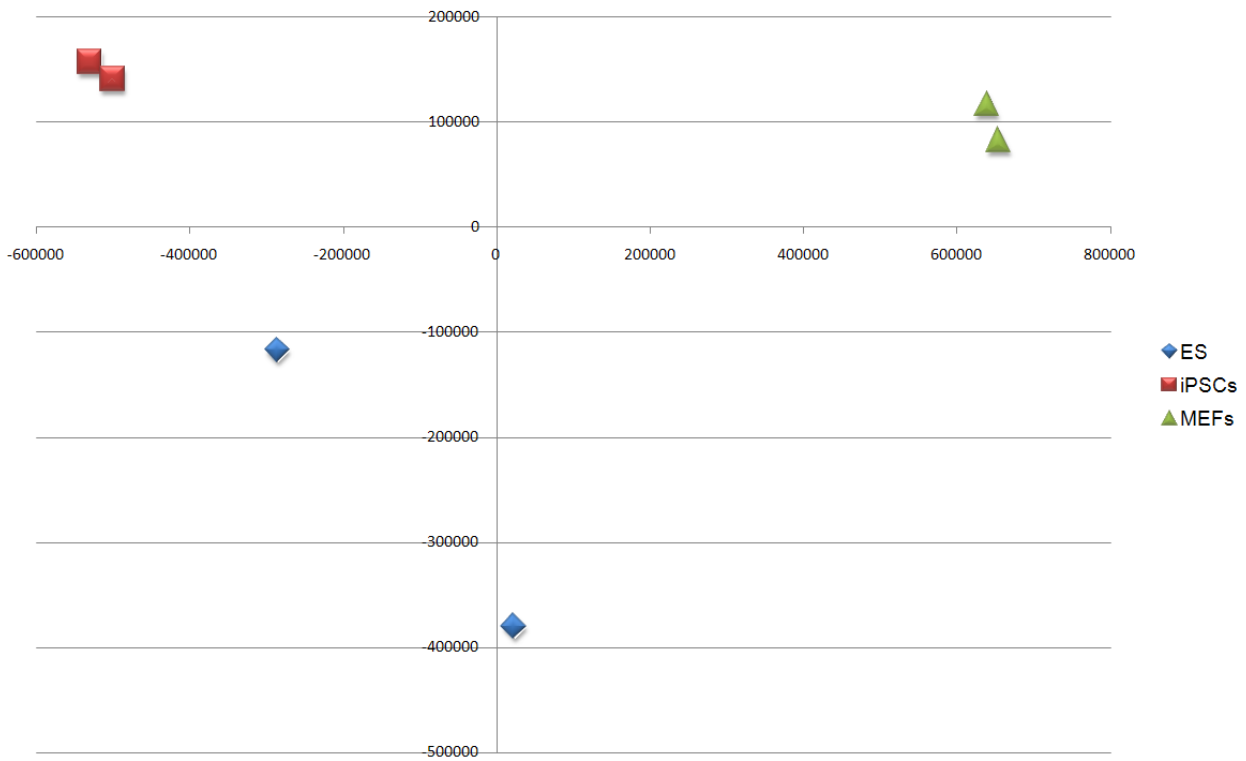
### PCA plot - GSE19023



PCA plot - GSE5259

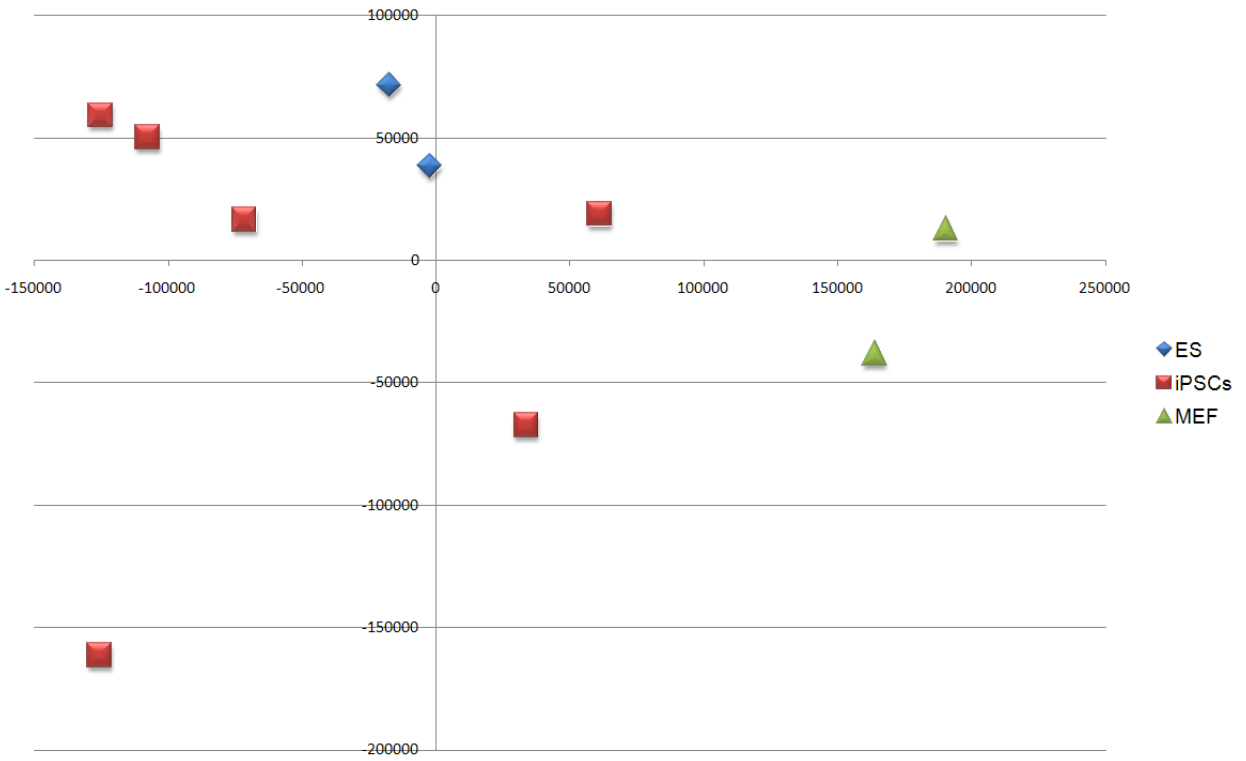


PCA plot - GSE7815

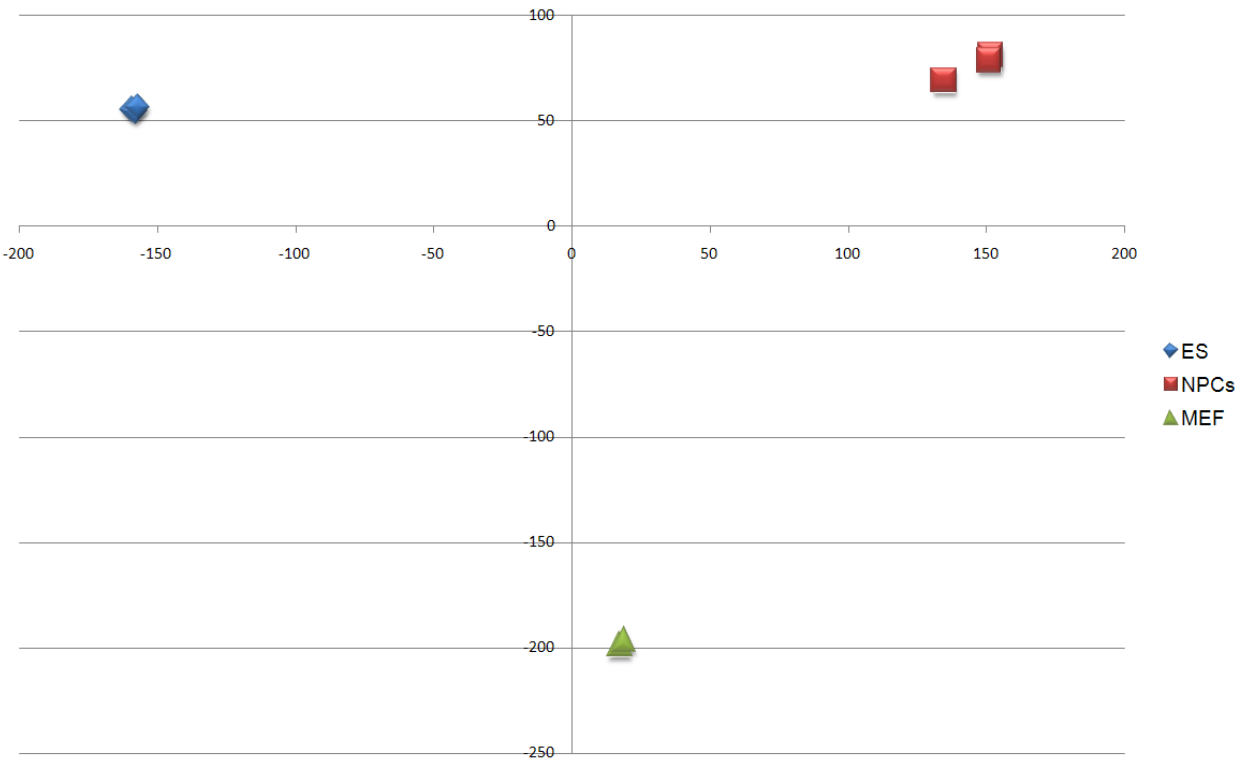




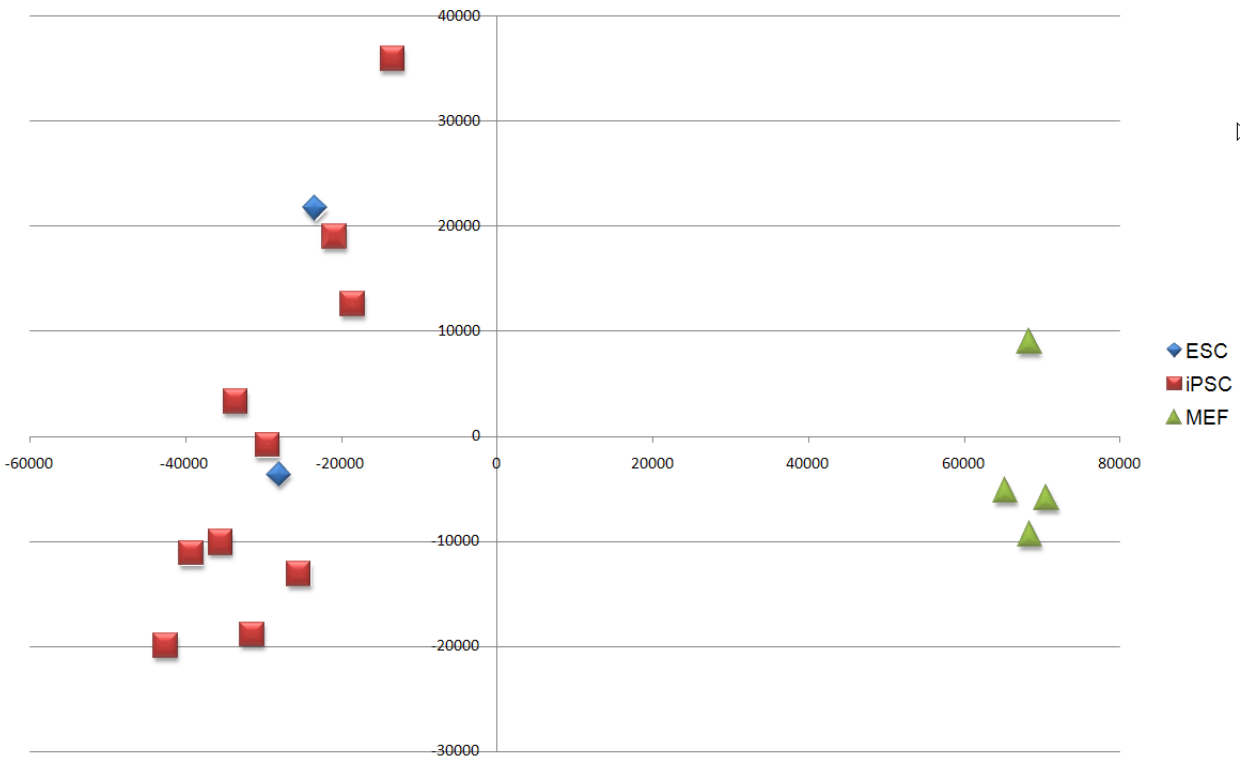
PCA plot - GSE7841



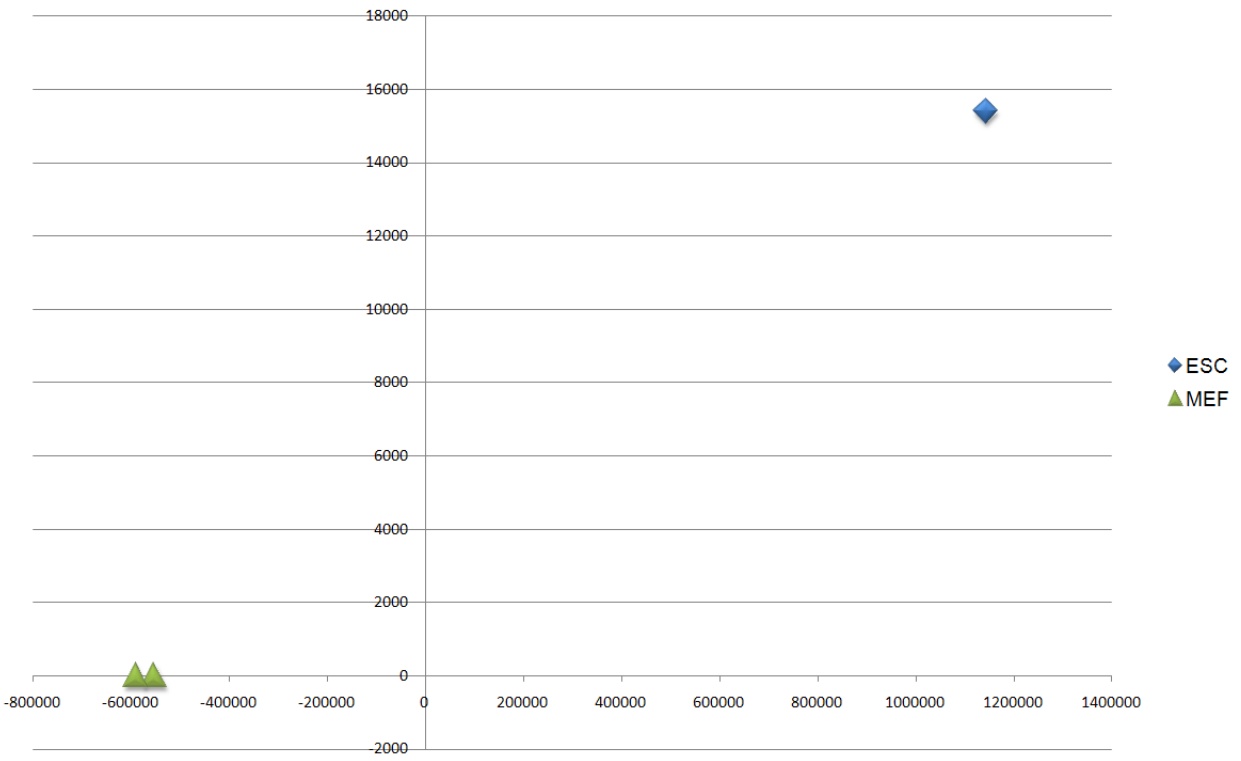
PCA plot - GSE8024



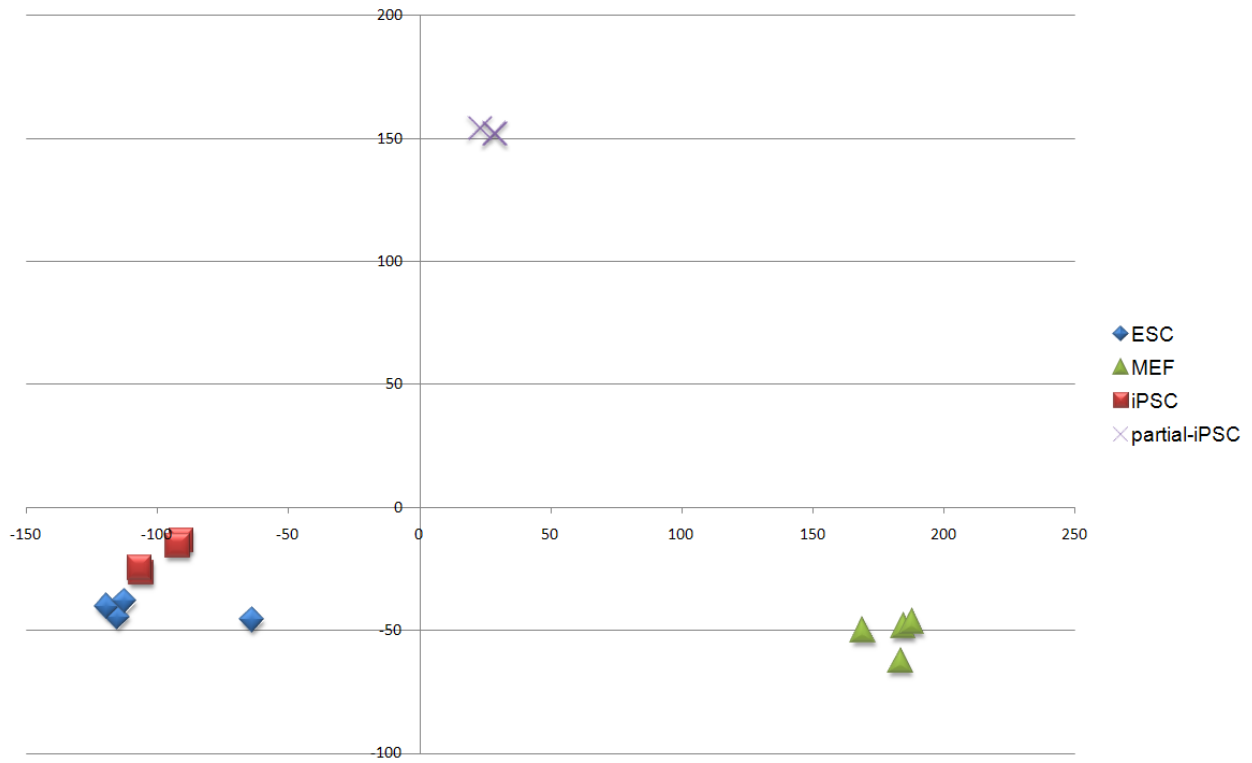
PCA plot - GSE13211



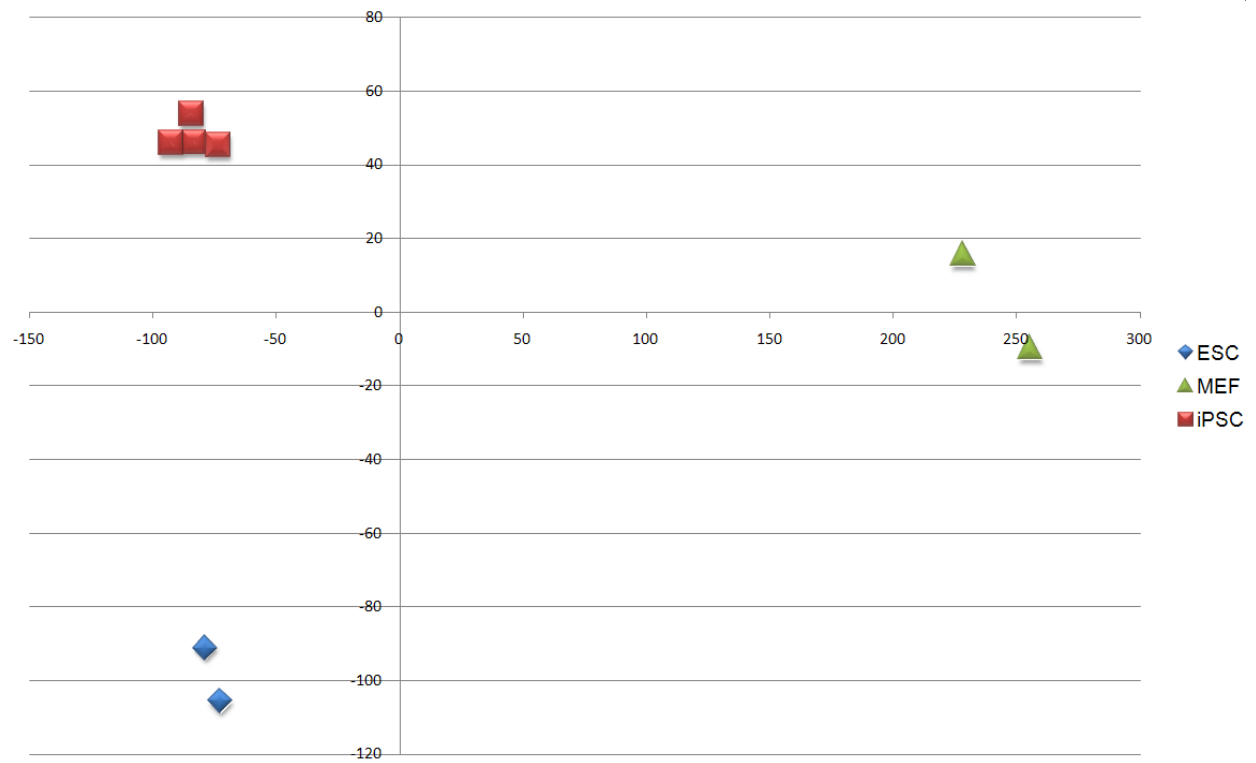
PCA plot - GSE13312



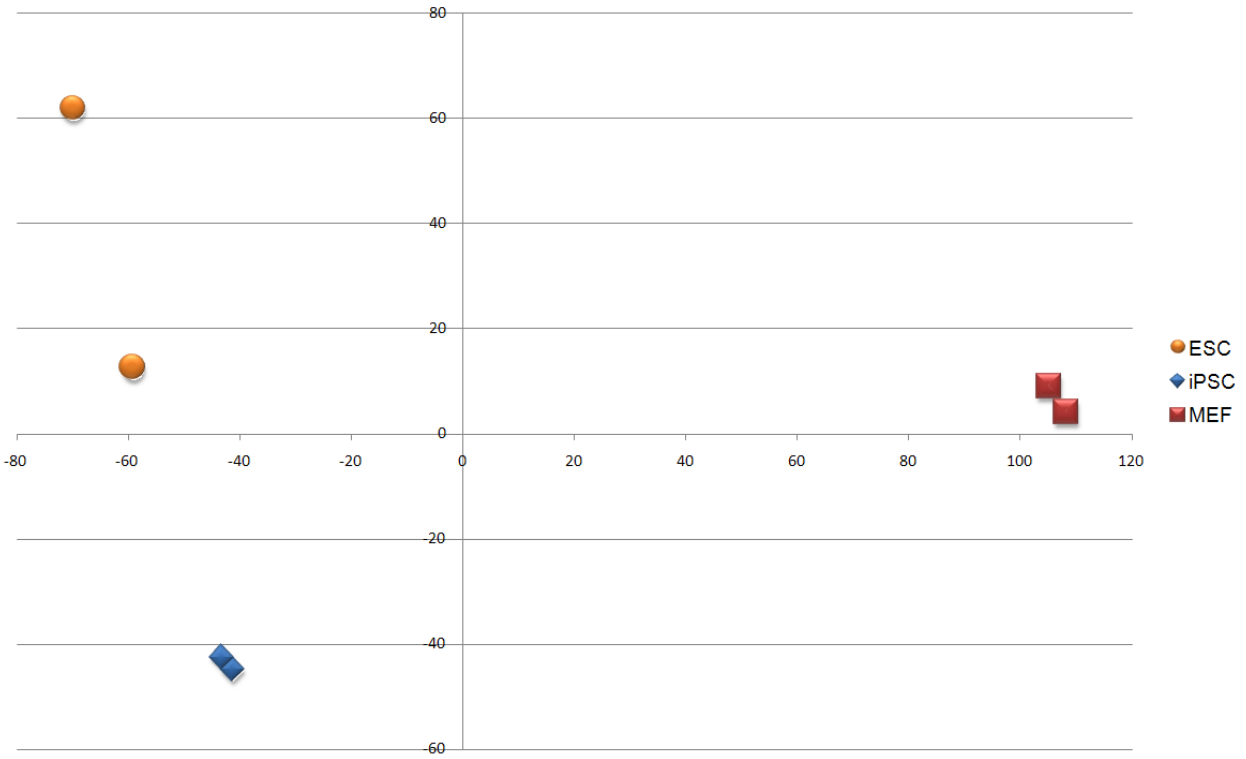
PCA plot - GSE14012



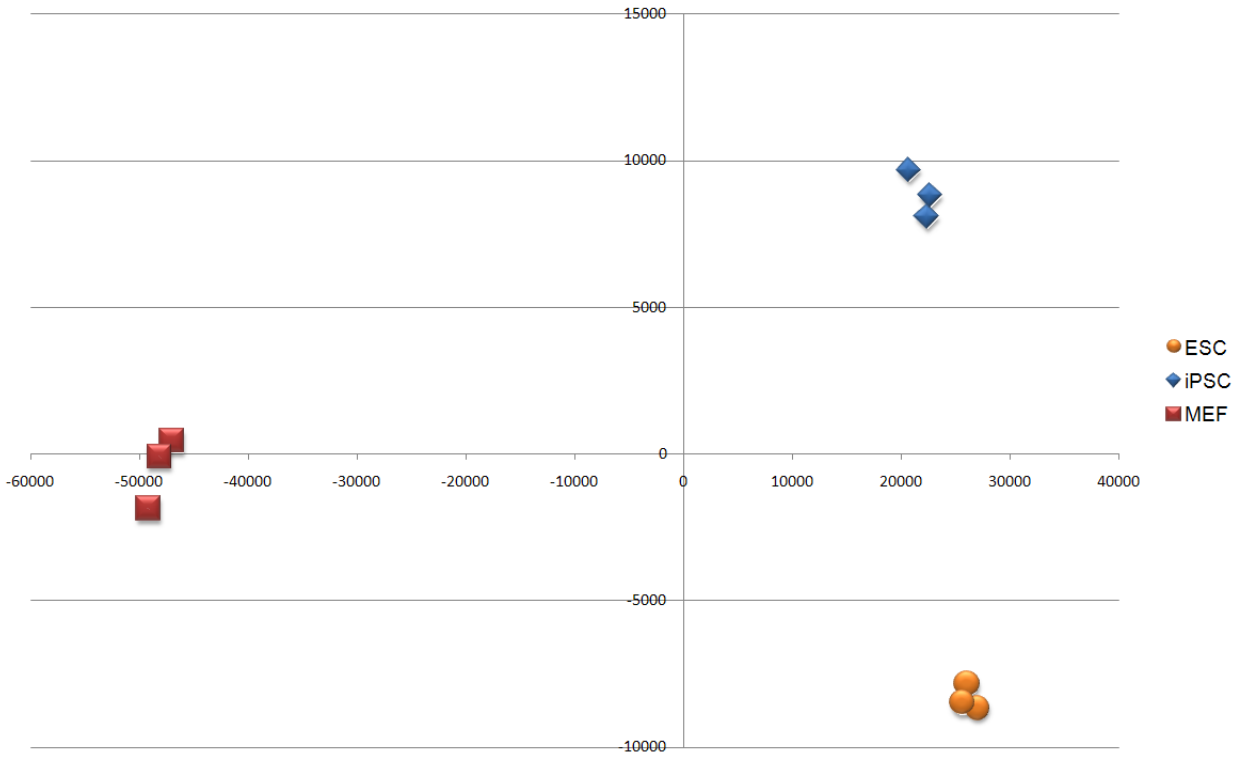
PCA plot - GSE15267



PCA plot - GSE16062



PCA plot - GSE17004



PCA plot - GSE18286

