Do engineered iPS and ES cells have similar molecular signatures?

Comparing expression and epigenetics in stem cells

http://jura.wi.mit.edu/bio/education/HS2012/

Exercises:

1. Open Java TreeView to visualize the expression data.
   Double click on the TreeView shortcut on the Desktop
   Menu -> File -> Open
   Select Desktop -> HS_Program_2012 -> Expression ->Expression_log2_values_HS_2012.cdt

   You can use the menu “Analysis-> Find genes” to search for specific genes. Each row corresponds to a gene and each column corresponds to a cell sample. The samples are clustered based on their similarities of gene expression. When you click on a tree branch the area selected will show on the middle panel. Green represents low or no expression. Red represents high expression. Black represents middle expression levels.

2. Open IGV to visualize the epigenetic (histone modification) data.
   Double click on the IGV shortcut in the Desktop.
   Menu -> File -> Open Session
   Select Desktop -> HS_Program_2012 -> IGVsession -> igv_session.all.xml

   Zoom in a chromosome until you see the alignments. To zoom in a specific gene, write the gene name (ex: Nanog) in the white search box (to the left of the “Go” button) and click on “Go”. The histone modification and cell type are written on the left panel (ex: H3K27me3 (Fibroblasts)). If any of these labels are missing in a panel, you may need to scroll with the scroll bar at the right side of the panel.

3. Using Java TreeView, find the expression pattern of the genes used to reprogram fibroblasts into iPS cells. To zoom in on a specific gene, go to Analysis -> Find Genes, enter a gene symbol, and click on “Search”. If the gene is found, click on a row of the table of the pop-up box. The genes used to turn fibroblasts into iPS cells are POU5F1, SOX2, MYC, NANOG. In which cells are they being expressed? In which cells are they shut down?

4. Find the histone marks of the genes used to reprogram fibroblasts into iPS cells: POU5F1, SOX2, MYC, NANOG. In which cells is the histone mark H3K4me3 associated with these genes? Use Java TreeView to look at expression and IGV browser to look at H3K4me3.

5. Using Java TreeView find other genes that are OFF (green) in fibroblasts and consistently ON (red or black) in ES and iPS cells. Then look at the histone marks associated with those genes using IGV. Complete a table like this:

Gene name	**Fibroblast expression**	**ES, iPS expression**	**H3K27me3 in Fibroblast**	**H3K27me3 in ES and iPS**	**H3K4me3 in Fibroblast**	**H3 K4me3 in ES and iPS**
EGLN3	OFF	ON	NO (just a few reads)	NO	NO (just a few reads)	YES

6. Using Java TreeView find other genes that are ON (red) in fibroblasts and consistently OFF (green or black) in ES and iPS cells. Then look at the histone marks associated with those genes using IGV. Complete a table like this:

Gene name	**Fibroblast expression**	**ES, iPS expression**	**H3K27me3 in Fibroblast**	**H3K27me3 in ES and iPS**	**H3K4me3 in Fibroblast**	**H3 K4me3 in ES and iPS**
PLP2	ON	OFF	NO	YES	?	YES

7. Based on what you wrote in the tables of questions 5 and 6, is the histone modification H3K4me3 associated with genes being turned ON or OFF? You can look at any cell type.

8. Based on what you wrote in the tables of questions 5 and 6, is the histone modification H3K27me3 associated with genes being turned ON or OFF? You can look at any cell type.

9. In ES and iPS cells there are genes that have both K4me3 and K27me3 marks. Are those turned ON or OFF?

10. Are H3K4m3 and H3K27me3 histone marks more often found at the beginning or end of a gene?

11. Zoom in on the H3K4me3 histone marks at a position like chr19:41,257,141-41,257,210 and note that in the middle of the browser, the reads all show a "C" (cytosine) while the genome sequence at the bottom shows a "G" (guanine). How could this difference in DNA sequences happen? Other examples:
    - chr19:40,789,891-40,789,960
    - chr19:40,697,026-40,697,095

12. Are engineered iPS cells and embryonic stem cells the same?