BBSG503 Bioinformatics

1. Tumor suppressor gene mutations (WGS), DNA methylation (Bisulfite-Seq)
2. Estrogen receptor alpha ChIP-Seq
3. Which exons/introns of RUNX1 and ETO are translocated in t(8;21) AML?

Software setup

a. Download and RUN IGV at:
"http://pharmacology.slu.edu/zhanglab/BBSG503/igv24.jnlp" (requires java 8)
"http://pharmacology.slu.edu/zhanglab/BBSG503/igv23_work_withjava7.jnlp" (requires java 7)

b. Datasets to be loaded:

- The Cancer Genome Atlas / Ovarian Cancer (hg18 human genome build)
  - DNA Methylation
  - Somatic Mutations (BCM)
  - Somatic Mutations (Wash U)
  - Somatic Mutations (BI)
- ENCODE/NIH (MCF-7 cells, ERα ChiaPet, hg19 genome build)

1. p53 (TP53) tumor suppressor frame-shift mutation in Exon 4 (chr17:7520037-7520315)
   - Load "Somatic Mutations" tracks above
   - enter coordinates: chr17:7520037-7520315
   - identify frame-shift mutation (colored in "red")
   - "Copy Details to Clipboard"

2. Rb1 tumor suppressor methylation
   - Load "DNA Methylation" track above
   - Go to "Rb1" gene
   - Identified the regions that are methylated
   - "Copy Details to Clipboard"

3. Is PGR (Progesterone receptor) an estrogen receptor target gene?
   - Hg19, ENCODE, MCF7, ERalpha
   - Go to PGR gene
   - Does ERα bind to the gene? Does it bind to "AGGTCA"?

4. Which exons/introns of AML1/RUNX1 and ETO are fused together?
We already know the junction between AML1 and ETO in the AML1-ETO cDNA as follows

RUNX1 ETO/RUNX1T1
CATCAAAATCACAGTGGATGGGCCCCGAGAACCTCGAA ATCGTACTGAGAAGCACTCCACAAT

   - Use "Find Motif" under the "Tools" menu
   - Enter RUNX1, RUNX1T1 sequences flanking the junction
   - Identify introns/exons corresponding to junction sequences of RUNX1 and RUNX1T1 genes