Procedure I RNA-seq Re-analysis on bladder cancer cell lines with Galaxy

1. Register account: <https://usegalaxy.org>
2. Download raw sequence data of 8x bladder cancer cells from Xinqiao’s Galaxy Account
3. Upload these raw data to your Galaxy Account
4. Run “hisat2” each cell line
5. Run “htseq-count” for each cell line
6. Download “htseq-count” result and combined to one file
7. Run “DESeq2” or “edgeR” or “limma” for 8x cell lines with two group: PEM sensitive and PEM resistant
8. Run pathway analysis (or gene set analysis, or function analysis)
   1. Run “EnrichmentBrowser” for pathway analysis
   2. Go to MSigDB ([www.gsea-msigdb.org](http://www.gsea-msigdb.org)), using ranked gene list.
9. Ref