1. cellranger pipeline

Include cellranger.sh pipeline along with mkref.sh

2. workspace

2.1 Preprocssing

Preprocessing\_and\_QC.Rmd

2.2 Neural Subset

Neural\_subsets/HB10/13/16/deab\_hpf\_neural\_RNA-seq.Rmd -- just the portions of this to subset and reprocess.

2.3 Figures 1-3

Neural\_subsets/ClusterNaming\_and\_plots\_HB10/13/16.Rmd

Be sure to include extra plots from figures.

Be sure this has differential gene determination and write table.

2.3.1 Questions for Charles

1. Do you want me to generate these figures completely in R (except for umap labelling and leaving space for zebrafish images of rhomobomere staining)? If so, do you want me to add A, B, C, etc... labels?
2. Fig1E and Fig3D -- the expression umaps and violin plots are redundant. Should we choose one or the other? If we choose violin plots, I can consolidate these into one stacked plot to conserve space. Or if we choose expression umaps, these umaps along with Fig1C and F or Fig3E could be consolidated with ordering according to order mentioned in results.

2.4 Figures 4 and 6

What notebooks did these come from?

Need to include generation of DA motifs and plots of interest.

2.4.1 Questions for Charles

1. Do you know which .nb.html files you got these chromVar expression umaps from?
2. Do you want me to generate these figures completely in R (except for umap labelling and leaving space for zebrafish images of rhomobomere staining)? If so, do you want me to add A, B, C, etc... labels?
3. Do you want to include enriched or chromVar DA motifs for the supplemental table that goes with these figures? The umaps are chromVar activity

2.5 Figure 5

Neural\_subsets/HB10/13/16hpf\_clustertree.Rmd (these are HB10/13/16hpf\_clustertree\_unrooted.png)

2.6 Figure 7

IntegrationOfIndependentNeuralSubsets/Integration\_3WT\_neural\_subsets.Rmd -- add correct resolution clustering and save umap without labels and w/ legend at end

IntegrationOfIndependentNeuralSubsets/int3WT\_clustertree.Rmd

2.6.1 new Fig 7 notebook

Once have final gene list for E and F (comparing gene expression per cell) generate new notebook that has:

\* D: labelling of HB.1, HB.2 and HB.3 in integrated dataset

\* E: Coexpression of sets of genes in umap (may only need third umap and simple legend for colors w/out color threshold)

\* F: Barplots of sets of genes

2.7 Supplemental Fig S1

2.7.1 Question for Charles

1. What should be in this figure?

2.8. Supplemental Figs S2, S3, S4

InitialExploration/ClusterNaming\_and\_plots\_HB10/13/16.Rmd these are HB10/13/16hpf\_combined2Plot.png

2.8.1 Question for Charles

1. Do you want these still as combined plots?
2. Do you want me to add A, B, C labels to them?