**Main Figures:**

Figure 1:

1. Illustrator – grab from .ai image
2. SKMEL5\_numUniqueBC\_byCondition.pdf
   1. In bcSamplingPlot.R
3. SKMEL5\_propShared\_byReplicate.pdf
   1. In bcSamplingPlot.R
4. SKMEL5\_barcode\_RPM\_rankByUTmean.pdf
   1. In bcSamplingPlot.R
5. SKMEL5\_barcode\_propRankAbundance\_comparison.pdf
   1. In bcSamplingPlot.R
6. SKMEL5\_barcode\_FCdensity\_bcOverlay.pdf
   1. In bcSamplingPlot.R

Figure 2:

1. UMAP\_combined\_SKMEL5\_hg38\_qcCCReg\_treatmentPoint.svg
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
2. ECDF\_UT-I\_withEMD.pdf
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
3. UMAP\_combined\_SKMEL5\_hg38\_qcCCReg\_treatmentDensity\_CCStatePoint.svg
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
4. SKMEL5\_allClusters\_CellCycleState\_proportion.pdf
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R

Figure 3:

1. umap\_combined\_lineageID\_tinted\_legendSpecial\_top25\_Barcode2/5/9/13.svg
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
2. SKMEL5\_I\_CellCycleState\_onlyDividing\_proportionWAverage.pdf
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
3. Idling\_bcFC\_correlation.pdf
   1. In MetaCluster\_bcCycling.R

Figure 4:

1. VennOverlap\_idlingSub25.pdf
   1. In ATAC\_analysis\_subsample.R
2. ATAC\_sub25\_annotationDistribution\_UniqueShared.pdf
   1. In ATAC\_analysis\_subsample.R
3. GOenrichment\_sub25\_I\_MF.svg
   1. In ATAC\_analysis\_subsample.R
4. SKMEL5\_sublines\_timeSeriesRNA\_rld\_Fig.svg
   1. In analysis\_subclones.R
5. Couldn’t find this on first pass. I think it is in analysis\_subclones.R, but if not just do some sort of differential expression and GO term overenrichment analysis between the untreated and idling data points, and these similar terms should pop up.
6. GO-RNA-ATACsub25\_pvalComparison\_MF.pdf
   1. In SKMEL5\_RNA-ATAC\_logq-q.R

Figure 5:

1. caFlux\_high\_Iono-Thap\_UTvI\_2021vis.pdf
   1. In caFlux\_untreatedIdling.R
2. caFlux\_high\_Iono-Thap\_UTvI\_2021vis.pdf
   1. In caFlux\_untreatedIdling.R
3. Ferroptosis\_FCHM\_selected\_wide.pdf
   1. In Ferroptosis\_heatmaps.R
4. RSL3-all\_DRC\_UTvI\_2021vis.pdf
   1. In RSL3\_plots\_2021vis.R
5. RSL3-all\_DRC\_UTvI\_2021vis.pdf
   1. In RSL3\_plots\_2021vis.R

**Supplementary Figures:**

Supplementary Figure S1:

1. Untreated\_smallClusterGO\_BP.pdf
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
2. Idling\_smallClusterGO\_BP.pdf
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
3. combined\_clustersSKMEL5.svg
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R
4. From allHallmarks\_acrossSKMEL5clusters.svg
   1. In VISION\_SKMEL5.R
5. From allHallmarks\_acrossSKMEL5clusters.svg
   1. In VISION\_SKMEL5.R

Supplementary Figure S2:

1. ClusterSizeRepresentation\_Treatment\_byBarcode\_5by5.pdf
   1. In MetaCluster\_bcCycling.R

Supplementary Figure S3:

1. umap\_combined\_lineageID\_tinted\_legendSpecial\_top25\_Barcode**ALLOTHERS**.svg
   1. In Seurat\_v3\_SKMEL5\_combined\_hg38.R

Supplementary Figure S4:

1. cCurve\_colors\_SKMEL5.pdf
   1. In preseq\_subsample.R
2. ISM\_colors\_SKMEL5.pdf
   1. In preseq\_subsample.R
3. ATAC\_sub25\_distanceToTSS\_UniqueShared.pdf
   1. In ATAC\_analysis\_subsample.R
4. GO-RNA-ATACsub25\_pvalComparison\_BP.pdf
   1. In SKMEL5\_RNA-ATAC\_logq-q.R
5. GO-RNA-ATACsub25\_pvalComparison\_CC.pdf
   1. In ATACseq/SKMEL5\_RNA-ATAC\_logq-q.R

Supplementary Figure S5: KEGG Ferroptosis pathway screenshot (<https://www.genome.jp/pathway/hsa04216>) manually boxed by me in illustrator