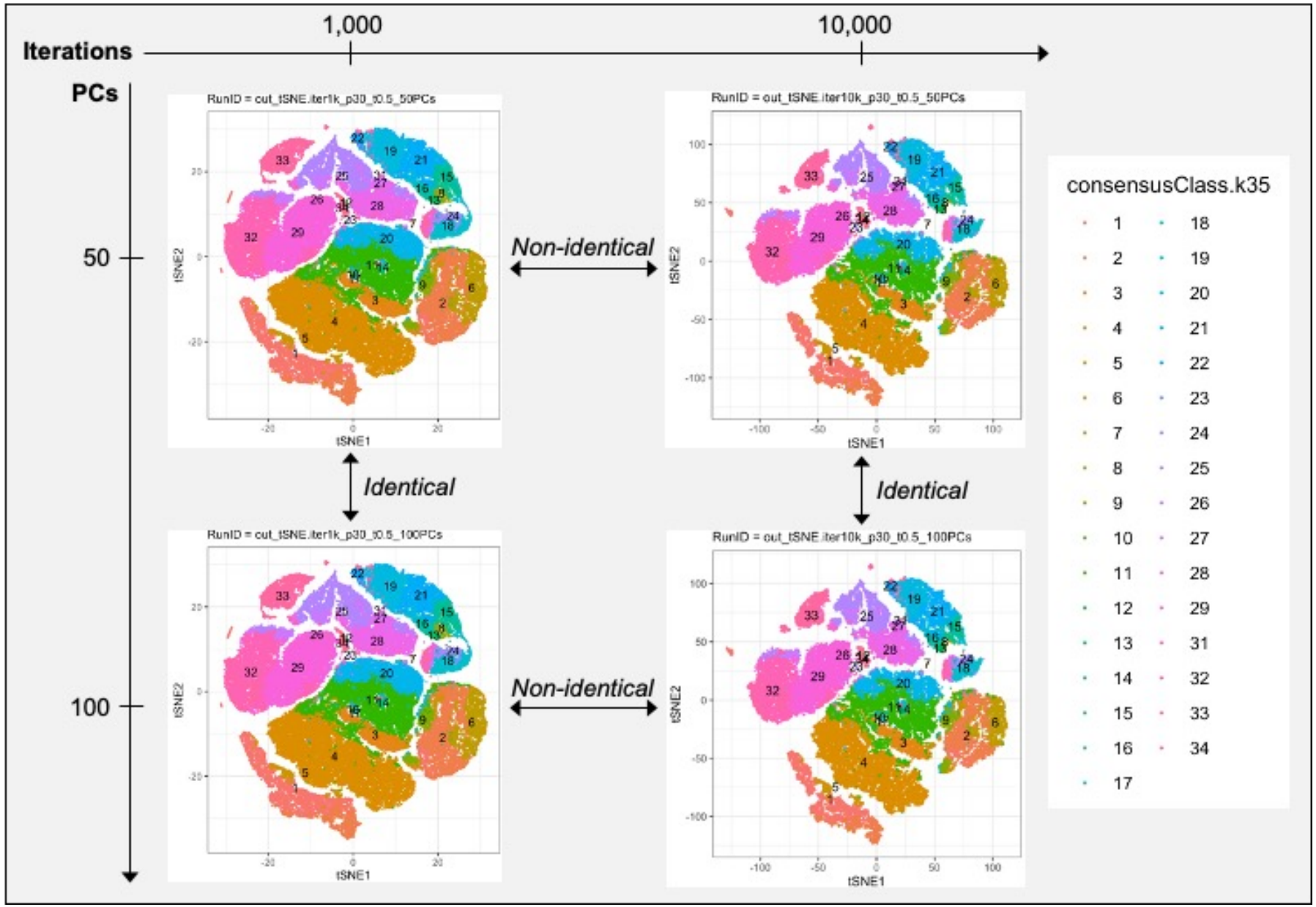
Effect of number of PCs and number of iterations

Shared parameters:
- 50k events/karyotype
- perplexity = 30
- theta = 0.5

Varying parameters:
- max_iter
- initial_dims



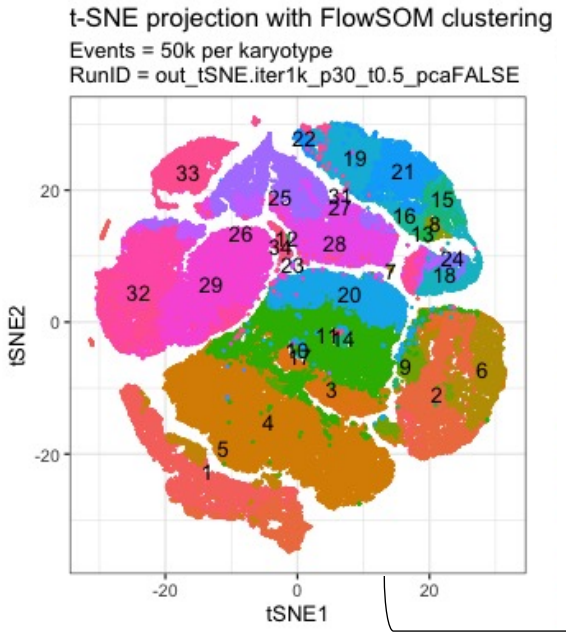
Effect of PCA and initial dimensions of PCA

Common parameters:

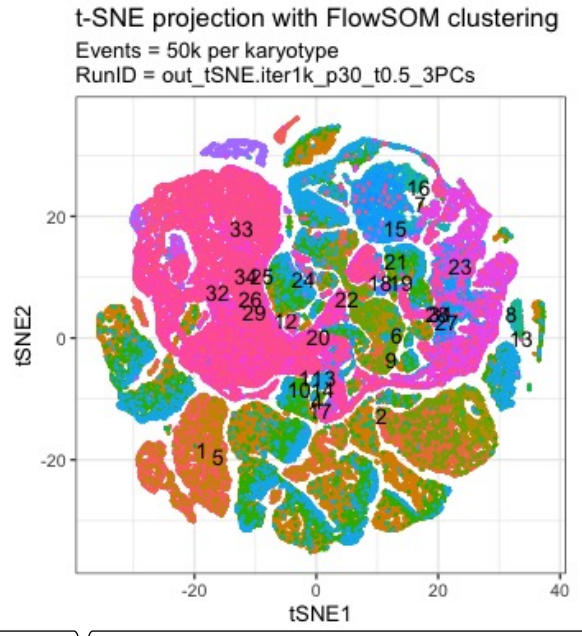
- 50,000 events per karyotype
- 1,000 iterations
- perplexity = 30
- theta = 0.5

Distinct parameters:

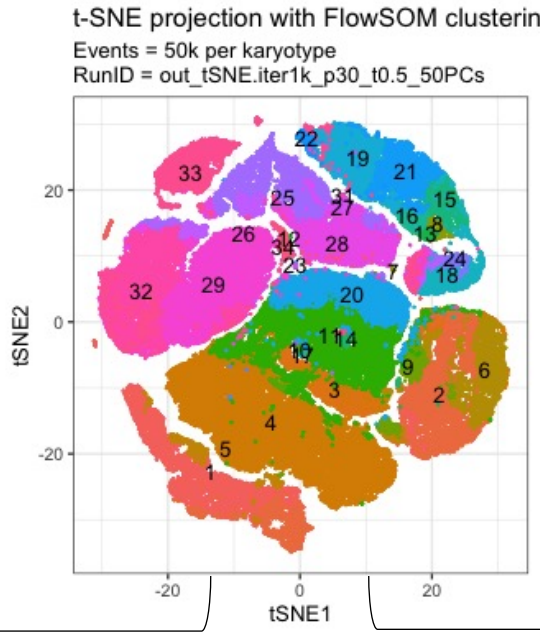
pca = FALSE



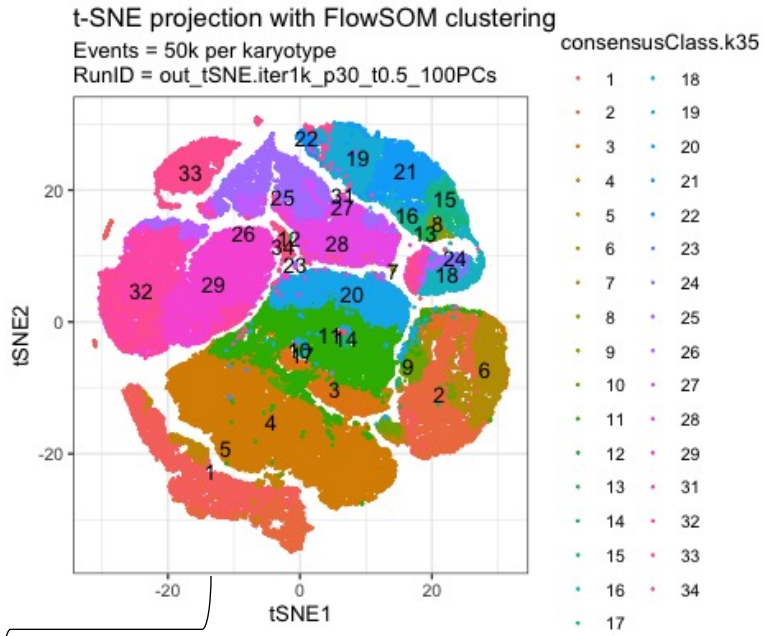
pca = TRUE
initial_dims = 3



pca = TRUE
initial_dims = 50



pca = TRUE
initial_dims = 100



*Non-identical coordinates

*Identical coordinates

*See next slide

Effect of PCA and initial dimensions of PCA

````
```{r}
setwd("/Users/shawjes/Dropbox/EspinosaGroup/P4C_CyTOF/tSNE/102821_Out")
load("CyTOF_P4C_102821_out_tSNE.iter1k_p30_t0.5_pcaFALSE_v0.2_JRS.rda")
load("CyTOF_P4C_102821_out_tSNE.iter1k_p30_t0.5_50PCs_v0.1_JRS.rda")
load("CyTOF_P4C_102821_out_tSNE.iter1k_p30_t0.5_100PCs_v0.1_JRS.rda")
```

```{r}
identical(out_tSNE.iter1k_p30_t0.5_pcaFALSE$Y, out_tSNE.iter1k_p30_t0.5_50PCs$Y)
```

[1] FALSE

```{r}
identical(out_tSNE.iter1k_p30_t0.5_50PCs$Y, out_tSNE.iter1k_p30_t0.5_100PCs$Y)
```

[1] TRUE
````

- While the tSNE plots with and without PCA are visually indistinguishable, their estimated tSNE dimensions differ numerically.

- tSNE dimensions are numerically identical whether estimated with 50 PCs or 100 PCs
- This is consistent with the maximum # of possible PCs being equal to the # of features (markers).

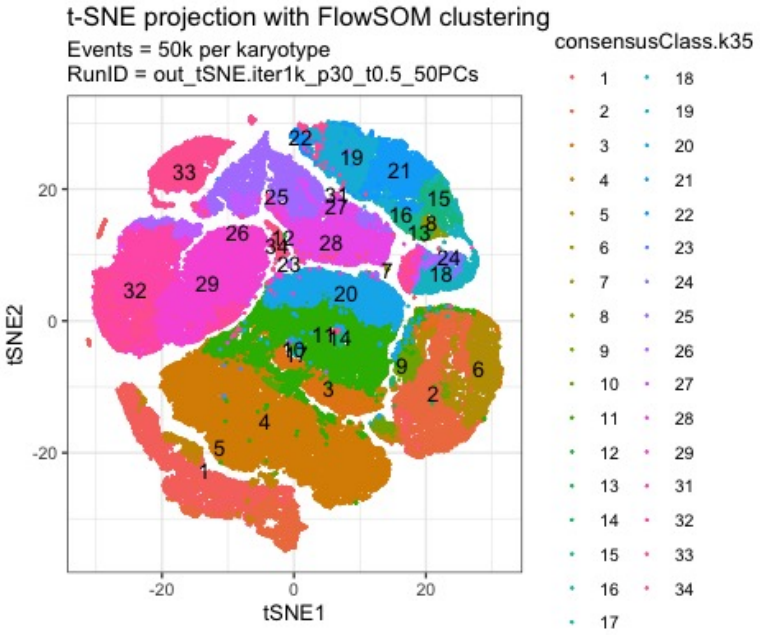
Effect of maximum number of iterations

Common parameters:

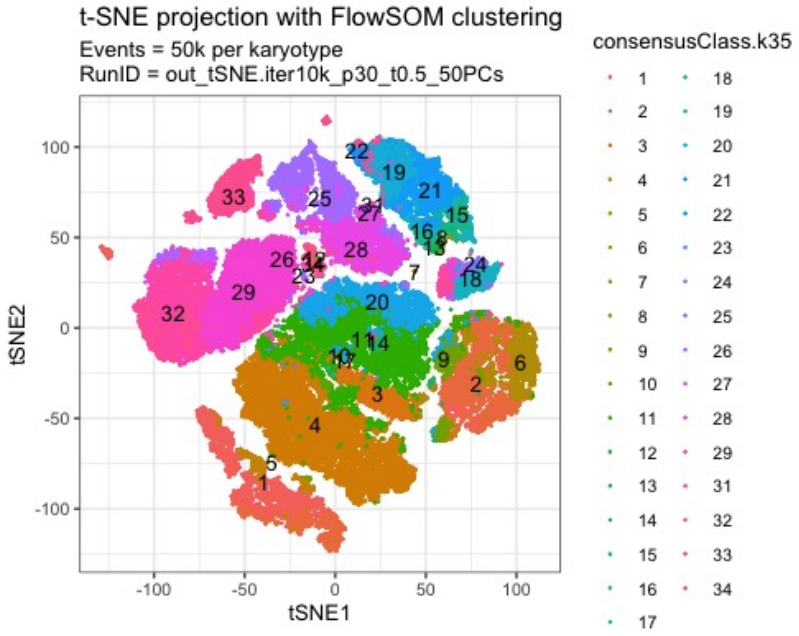
- 50,000 events per karyotype
- initial_dims = 50
- perplexity = 30
- theta = 0.5

Distinct parameters:

max_iter = 1,000



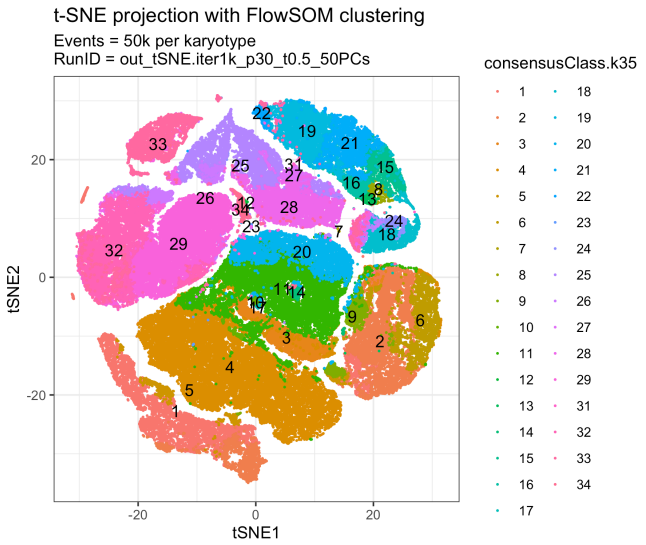
max_iter = 10,000

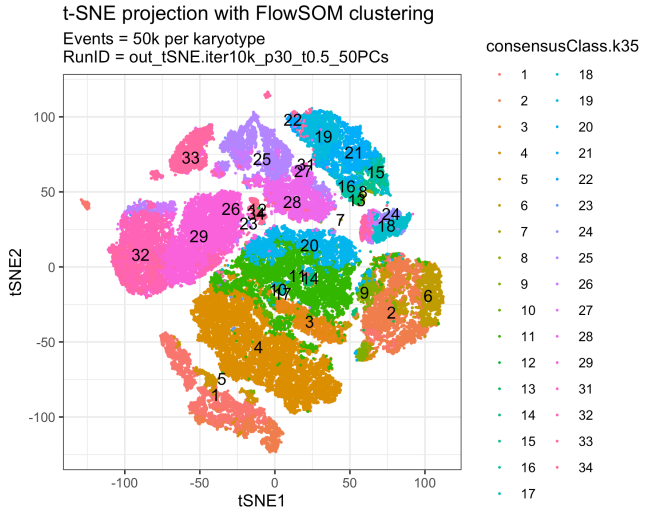


Increasing iterations

Increasing PCs

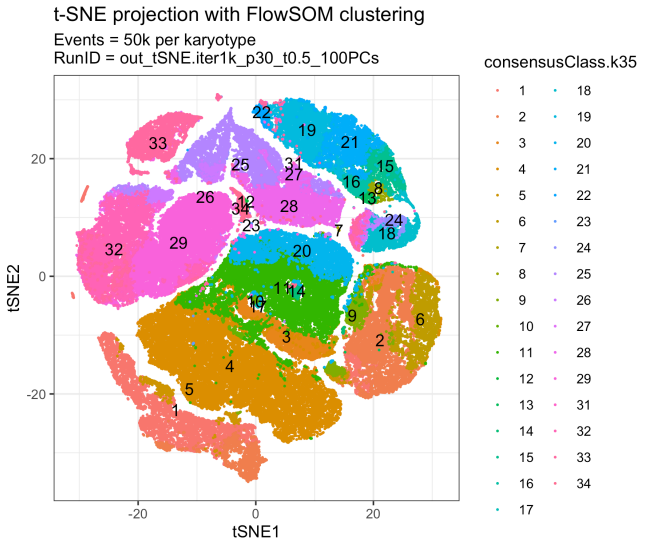
Non-identical

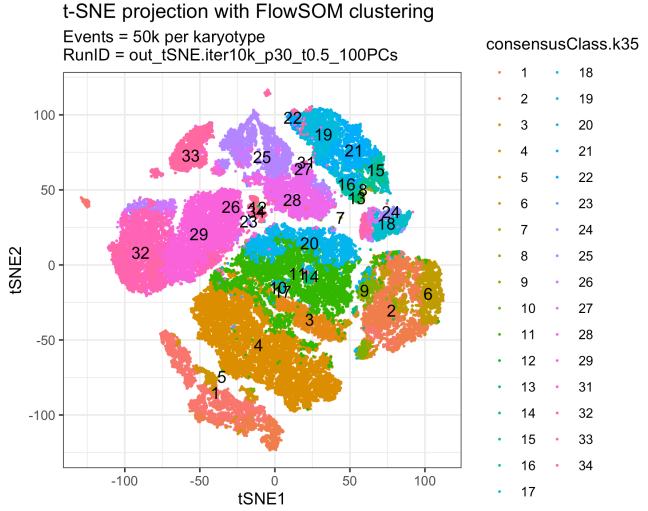




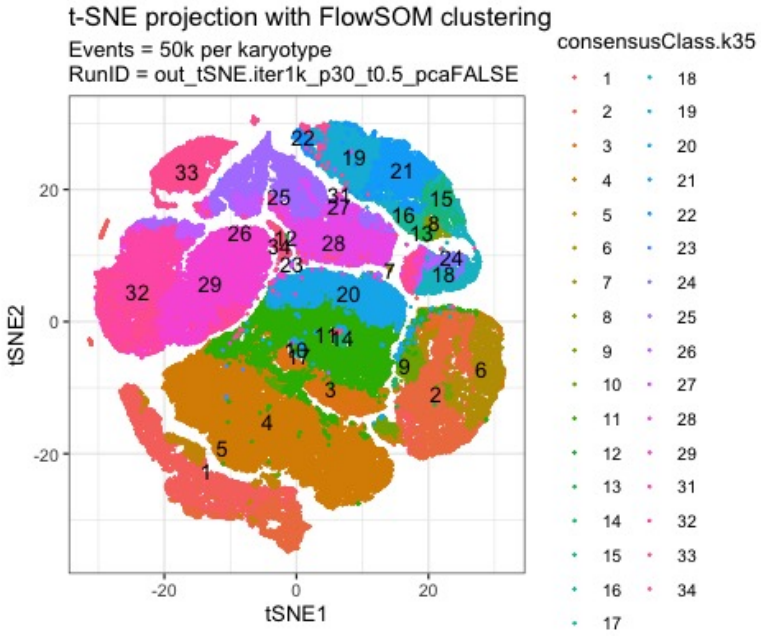
Identical

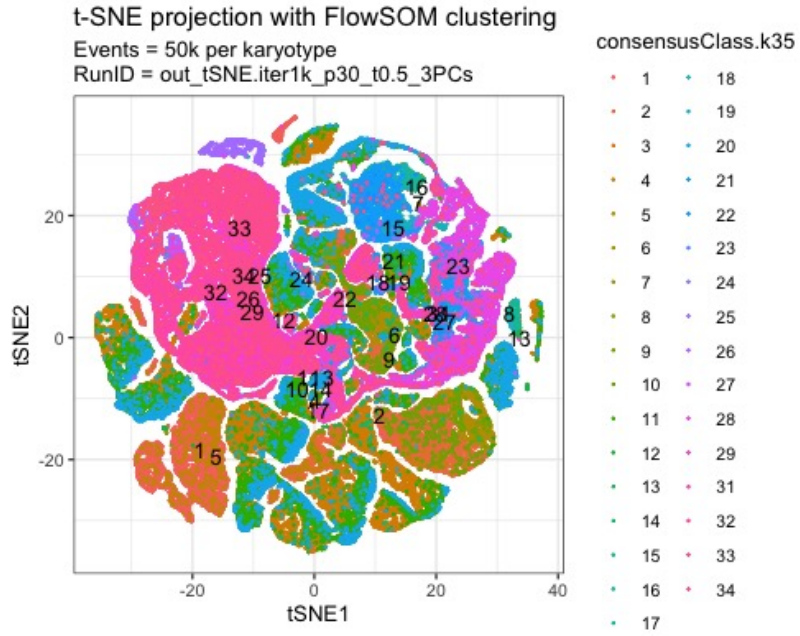
Non-identical

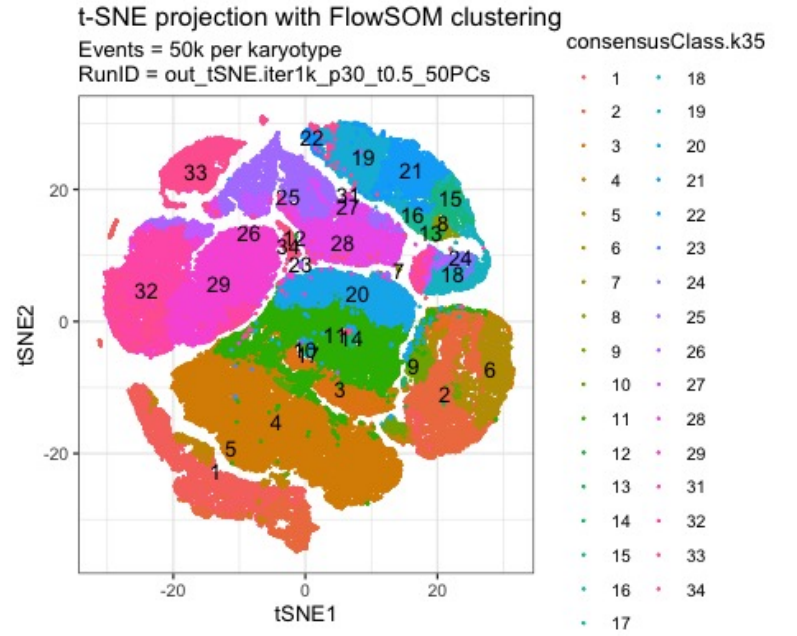


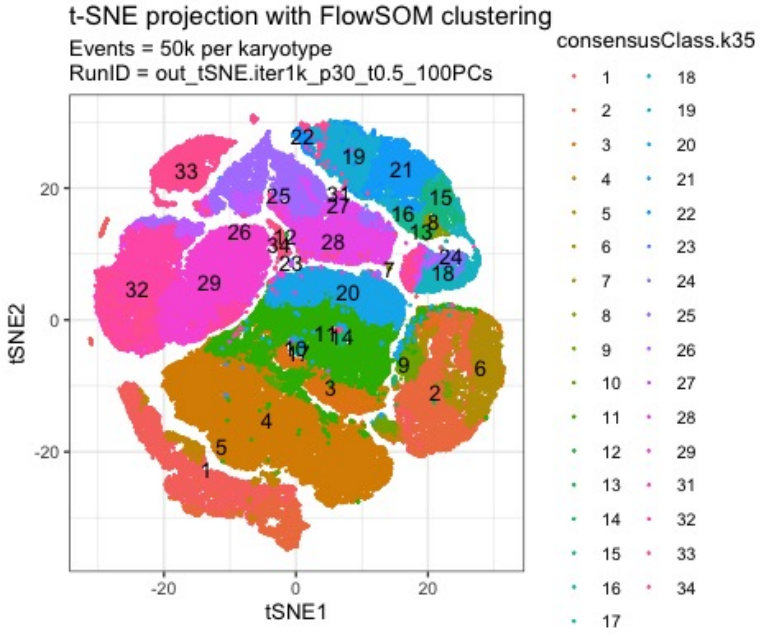


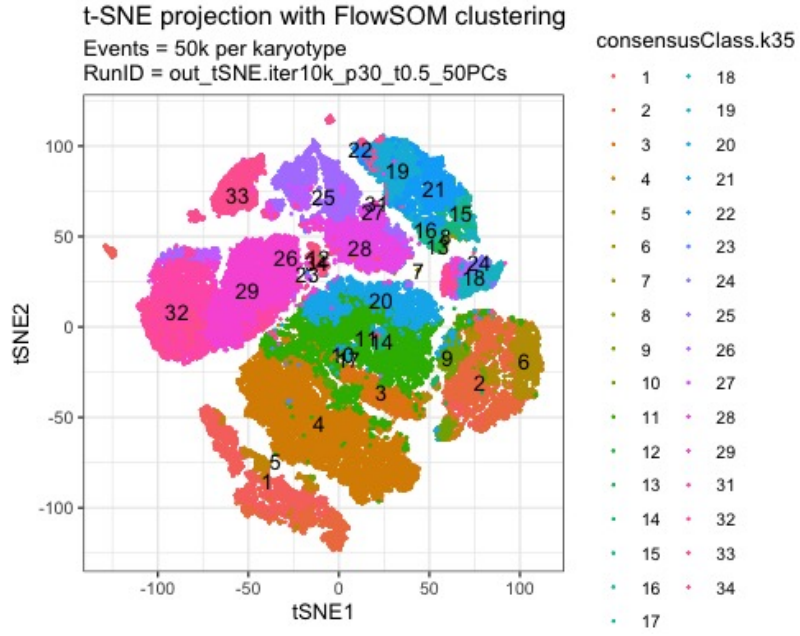
Identical

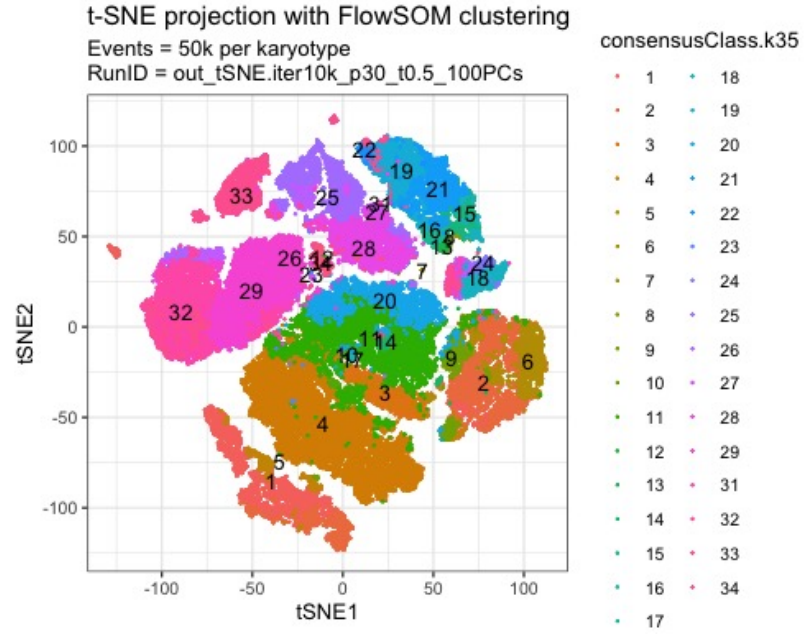

t-SNE projection with FlowSOM clustering
Events = 50k per karyotype
RunID = out_tSNE.iter1k_p30_t0.5_pcaFALSE
consensusClass.k35
tSNE1
tSNE2


t-SNE projection with FlowSOM clustering
Events = 50k per karyotype
RunID = out_tSNE.iter1k_p30_t0.5_3PCs
consensusClass.k35
tSNE1
tSNE2


t-SNE projection with FlowSOM clustering
Events = 50k per karyotype
RunID = out_tSNE.iter1k_p30_t0.5_50PCs
consensusClass.k35
tSNE1
tSNE2


t-SNE projection with FlowSOM clustering
Events = 50k per karyotype
RunID = out_tSNE.iter1k_p30_t0.5_100PCs
consensusClass.k35
tSNE1
tSNE2


t-SNE projection with FlowSOM clustering
Events = 50k per karyotype
RunID = out_tSNE.iter10k_p30_t0.5_50PCs
consensusClass.k35
tSNE1
tSNE2


t-SNE projection with FlowSOM clustering
Events = 50k per karyotype
RunID = out_tSNE.iter10k_p30_t0.5_100PCs
consensusClass.k35
tSNE1
tSNE2