



Sample Tags Zip & Download Files

	x cytofkit: an Integrated Analysis Pipeline for Mass Cytometry Data	
Raw FCS Directory :	/Users/esimonds/Downloads/experiment_12114_files Choo	se
FCS File(s):	/Users/esimonds/Downloads/experiment_12114_files/171128 Batch 11 tit Selec	ct
Markers :	Lu175 (v)>}{Yb176Di <cd90_yb176 (v)="">}{Bi209Di<i-a-i-e_bi209 (v)=""> Selec</i-a-i-e_bi209></cd90_yb176>	ct
Result Directory :	/Users/esimonds/Downloads/experiment_12114_files Choo	se
Project Name :	cytofkit_test	
Merge Method :	all min ceil fixed Fixed Number: 9999999 🕖	
Transformation Method :	autoLgcl • cytofAsinh • Fixedlogicle • none	
Cluster Method(s):	Rphenograph □ ClusterX □ DensVM □ NULL	
Visualization Method(s) :	pca □ isomap ▼ tsne □ NULL	
Cellular Progression :	⑦ diffusionmap ⓒ isomap ◉ NULL	
Reset	Submit	

```
> cytofkit_GUI()
Input arguments:
* Project Name: cytofkit_test
* Input FCS files for analysis:
   -171128 Batch 11 titration debar1_Pop09_TH-MYCN_SPL_ViableSinglets_ViableCD45_viSNE.fcs
   -171128 Batch 11 titration debar1_Pop10_TH-MYCN_Tumor_ViableSinglets_ViableCD45_viSNE.fcs
* Markers:
   -Y89Di<CD45_Y89 (v)>
   -In113Di<B220_In113 (v)>
   -In115Di<CD11a_In115 (v)>
   -La139Di < Ly - 6G_La139 (v) >
   -Nd142Di<CD49b_Nd142 (v)>
   -Nd143Di<CD11c_Nd143 (v)>
   -Nd145Di<CD27_Nd145 (v)>
   -Nd146Di<CD206_Nd146 (v)>
   -Sm147Di<CD274_Sm147 (v)>
   -Nd148Di<CD103_Nd148 (v)>
   -Sm149Di<CD152_Sm149 (v)>
   -Sm150Di<CD317_Sm150 (v)>
   -Eu151Di<Ly-6C_Eu151 (v)>
   -Eu153Di<CD11b_Eu153 (v)>
   -Gd155Di<CD8a_Gd155 (v)>
   -Gd156Di<CD4_Gd156 (v)>
   -Gd157Di<CD3e_Gd157 (v)>
   -Dy162Di<CD135_Dy162 (v)>
   -Dy163Di<CD62L_Dy163 (v)>
   -Dy164Di<CD278_Dy164 (v)>
   -Ho165Di<CD69_Ho165 (v)>
   -Er166Di<CD49d_Er166 (v)>
   -Er168Di<CD25_Er168 (v)>
   -Tm169Di < F4-80_Tm169 (v) >
   -Er170Di<CD115_Er170 (v)>
   -Yb172Di<KLRG1_Yb172 (v)>
   -Yb174Di<CD197_Yb174 (v)>
   -Lu175Di<CD44_Lu175 (v)>
   -Yb176Di<CD90_Yb176 (v)>
   -Bi209Di<I-A-I-E_Bi209 (v)>
* Data merging method: ceil
* Data transformation method: cytofAsinh
* Dimensionality reduction method: tsne
* Data clustering method(s): Rphenograph
* Data visualization method(s): tsne
* Subset progression analysis method: NULL
Extract expression data...
   19929 x 61 data was extracted!
```

Dimension reduction...

Running t-SNE...with seed 42

Interactive Exploration of cytofkit Analysis Results







