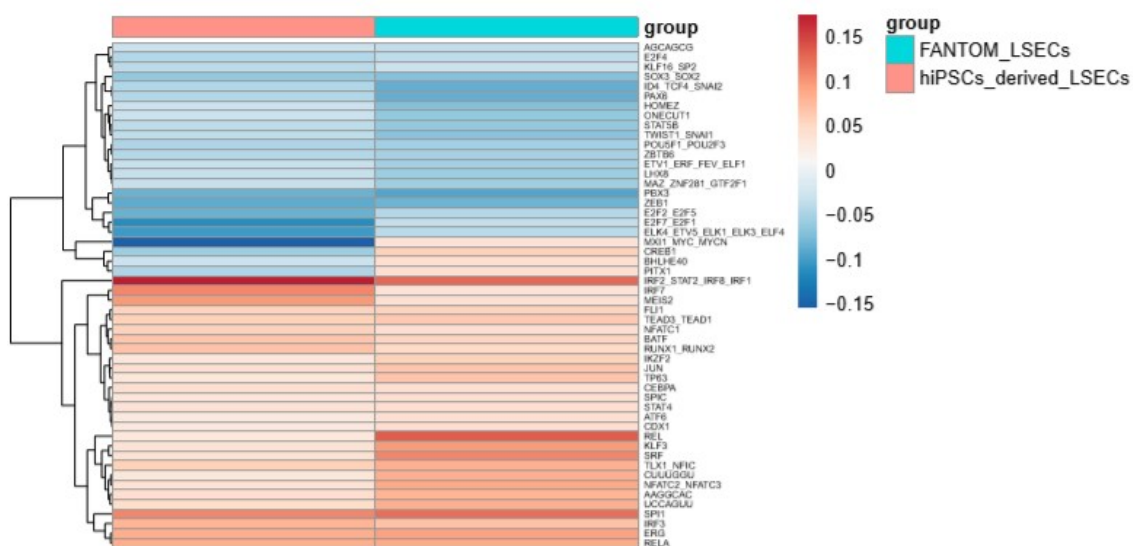
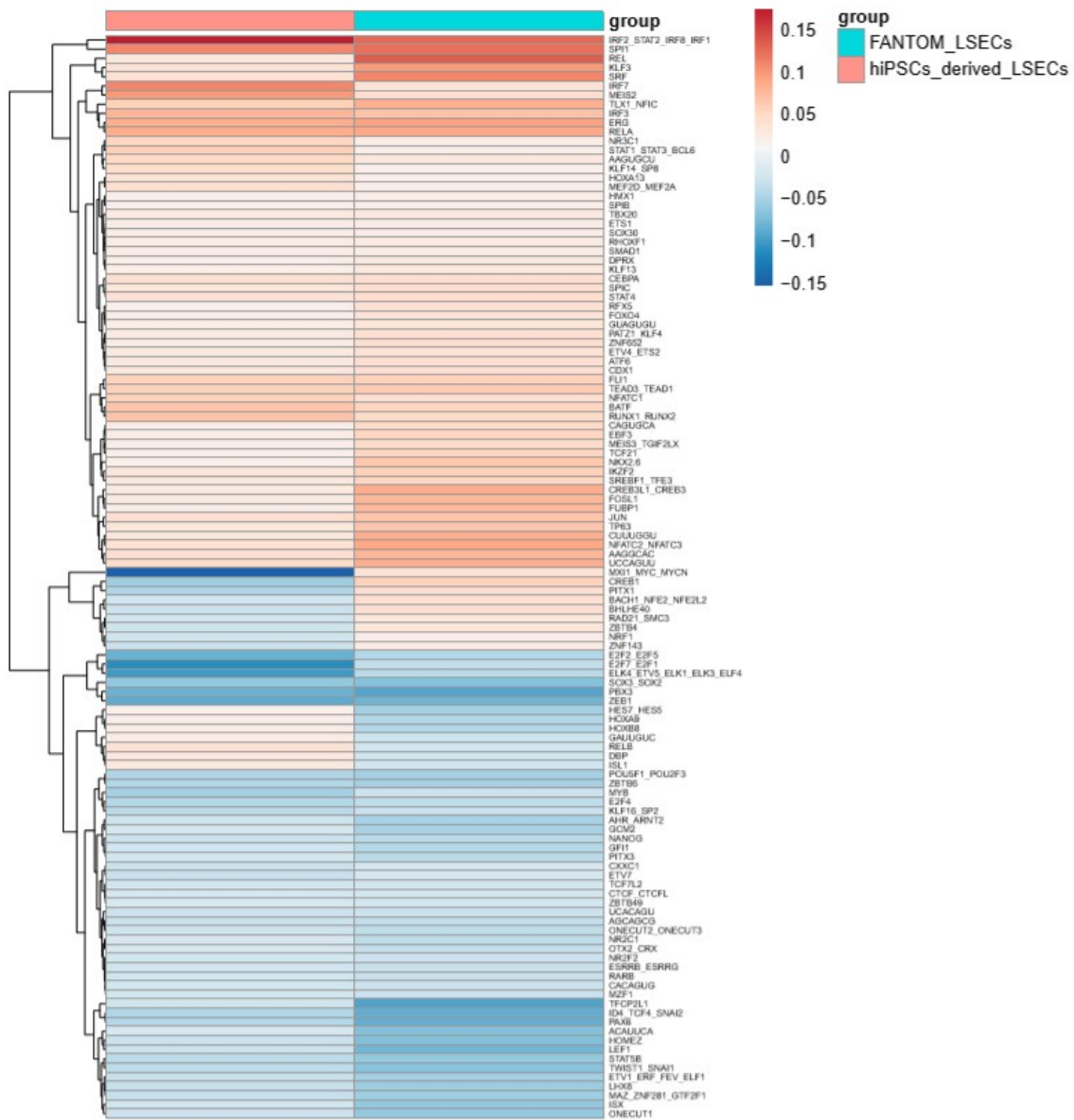


Average TF motif activities with  $\text{abs}(z\text{-values}) > 0.03$  (n=52)



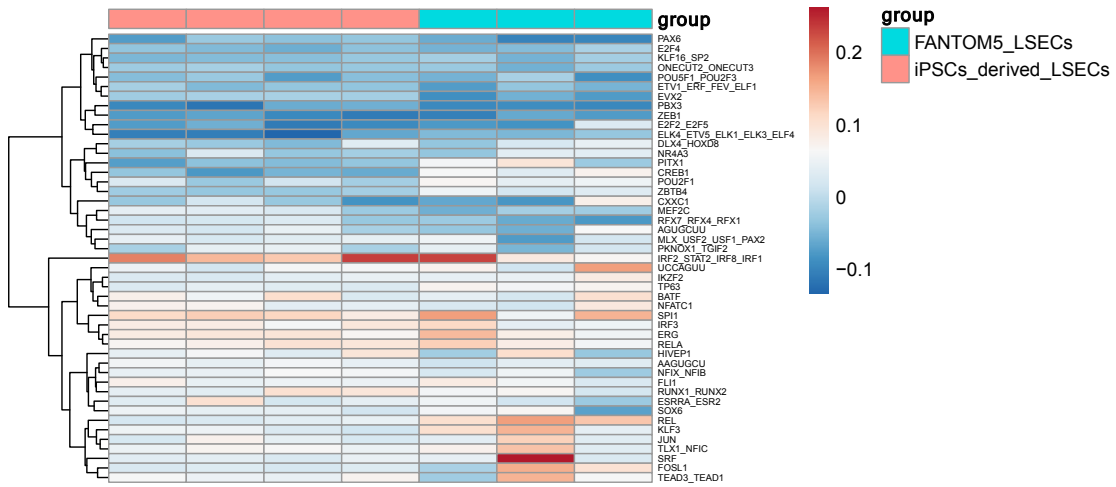
Heatmap comparison of average transcription factor motif activities (n=52) returned by applying a cutoff of  $\text{abs}(0.03)$  (z-values  $< -0.03$  and z-values  $> 0.03$ ) to ISMARA data obtained from hiPSCs-derived LSECs samples (n=4) and FANTOM5 (n=3) reference datasets.

Average TF motif activities with  $\text{abs}(z\text{-values}) > 0.02$  (n=118)



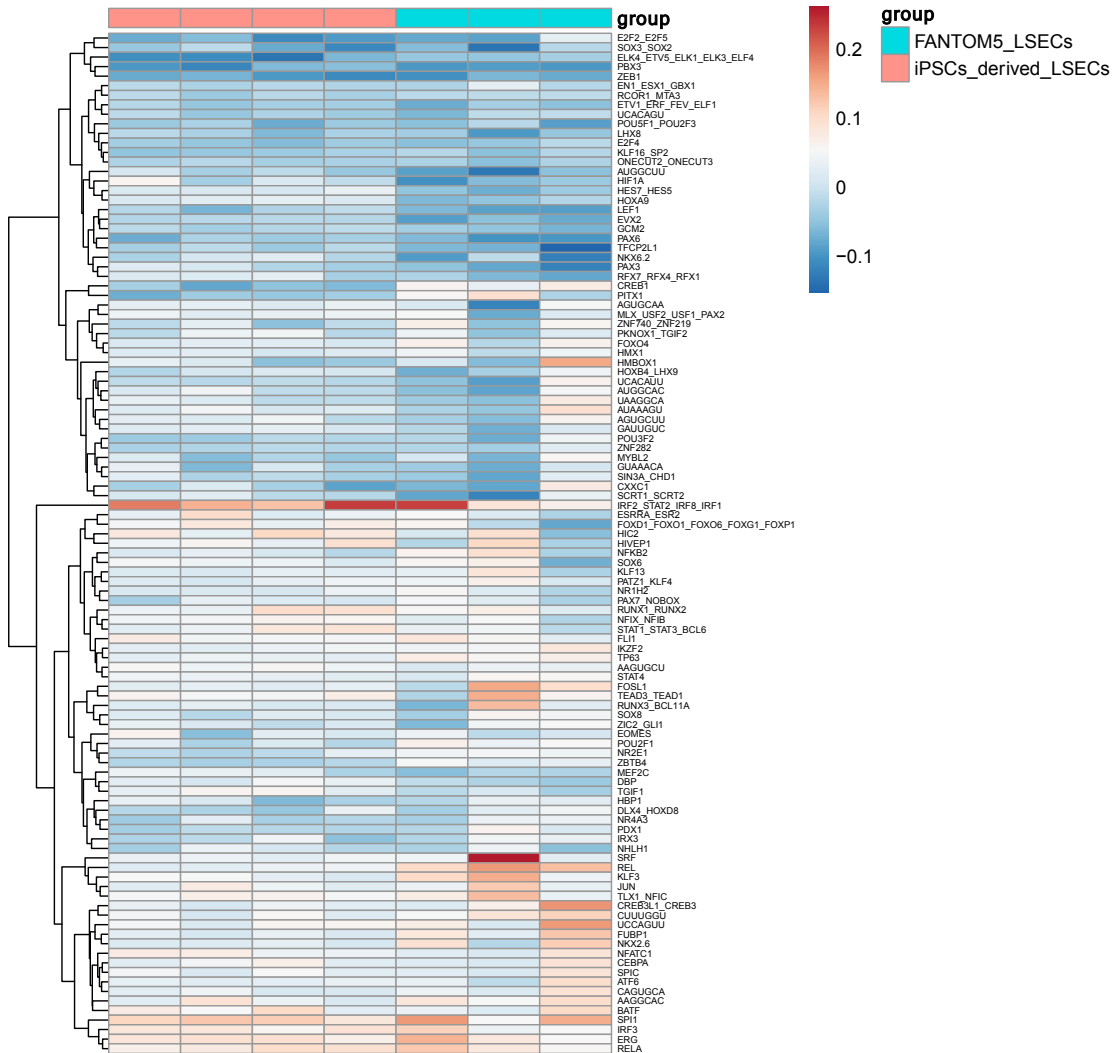
Heatmap comparison of average transcription factor motif activities (n=118) returned by applying a cutoff of  $\text{abs}(0.02)$  (z-values  $< -0.02$  and z-values  $> 0.02$ ) to ISMARA data obtained from hiPSCs-derived LSECs samples (n=4) and FANTOM5 (n=3) reference datasets.

TF motif activities with  $\text{abs}(z\text{-values}) > 0.015$  (n=47)



Heatmap comparison of transcription factor motif activities (n=47) returned by applying a cutoff of  $\text{abs}(0.015)$  (z-values  $< -0.015$  and z-values  $> 0.015$ ) to ISMARA data obtained from hiPSCs-derived LSECs samples (n=4) and FANTOM5 (n=3) reference datasets.

TF motif activities with  $\text{abs}(z\text{-values}) > 0.01$  (n=107)



Heatmap comparison of transcription factor motif activities (n=107) returned by applying a cutoff of  $\text{abs}(0.01)$  (z-values  $< -0.01$  and z-values  $> 0.01$ ) to ISMARA data obtained from hiPSCs-derived LSECs samples (n=4) and FANTOM5 (n=3) reference datasets.