Genomic data for chromatin states

	F1	F2	F3	F4	F5	B1	B2	B3	B4	B5
R1	Enh	Enh	Enh	Enh	Enh	TSS	TSS	TSS	TSS	TSS
R2	Enh	Het	Het	Het	Het	Enh	Enh	Enh	Enh	Enh
R3	Enh	Enh	Enh	Tx	Enh	Tx	Tx	Tx	Tx	Tx
R4	Quies	Quies	Quies	Quies	Quies	Enh	Enh	Enh	Enh	Enh

Is enhancer (1) or not (0)?

Enhancer feature table

	F1	F2	F3	F4	F5	B1	B2	B3	B4	B5
R1	1	1	1	1	1	0	0	0	0	0
R2	1	0	0	0	0	1	1	1	0	1
R3	1	1	1	0	1	0	0	0	0	0
R4	0	0	0	0	0	1	1	1	1	1

Frequency cutoff

1. Calculate feature ratio in foreground and background

	F	B
R1	1	0
R2	0.2	0.8
R3	1	0
R4	0	1

2. Filter regions by requiring foreground ratio >= cutoff (default 0.8), background ratio <= cutoff (default 0.2)

R1
R3

Fisher's exact test

1. Use Fisher's exact test to calculate p-value

	#1 in F	#0 in F	#1 in B	#0 in B	q-value
R1	5	0	0	5	0.004
R2	1	4	4	1	0.996
R3	4	1	0	5	0.02
R4	0	5	5	0	1

2. Filter regions by requiring q-value <= cutoff (default 0.01)

R1

K-means clustering

1. Perform k-means clustering

		F1	F2	F3	F4	F5	B1	B2	B3	B4	B5
C1	R1	1	1	1	1	1	0	0	0	0	0
C1	R3	1	1	1	0	1	0	0	0	0	0
C2	R2	1	0	0	0	0	1	1	1	0	1
C2	R4	0	0	0	0	0	1	1	1	1	1

2. Calculate feature density in each cluster

	F1	F2	F3	F4	F5	B1	B2	B3	B4	B5
C1	1	1	1	0.5	1	0	0	0	0	0
C2	0.5	0	0	0	0	1	1	1	0.5	1

3. Obtain median density in foreground and the highest density (default) in background

	F	B
C1	1	0
C2	0	1

4. Filter clusters by requiring foreground density >= cutoff (default the highest feature density of background), and foreground density >= cutoff (default 0.4)

R1
R3