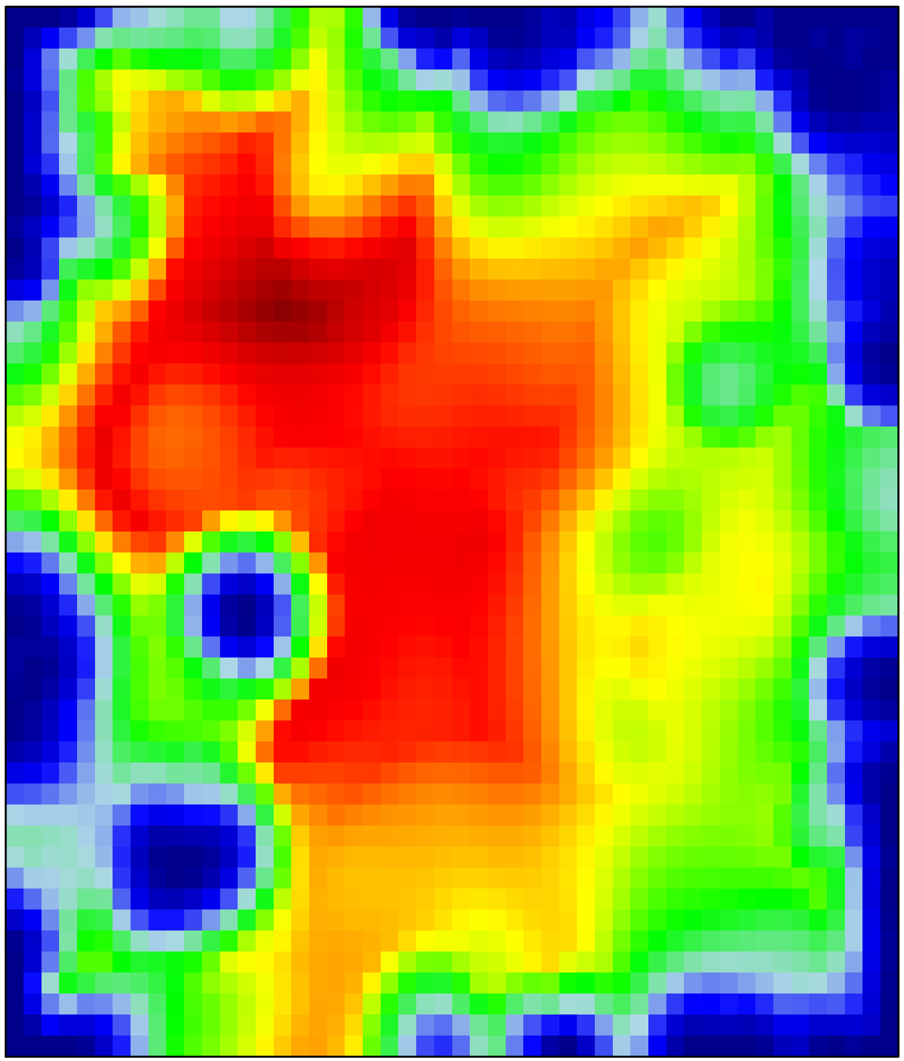
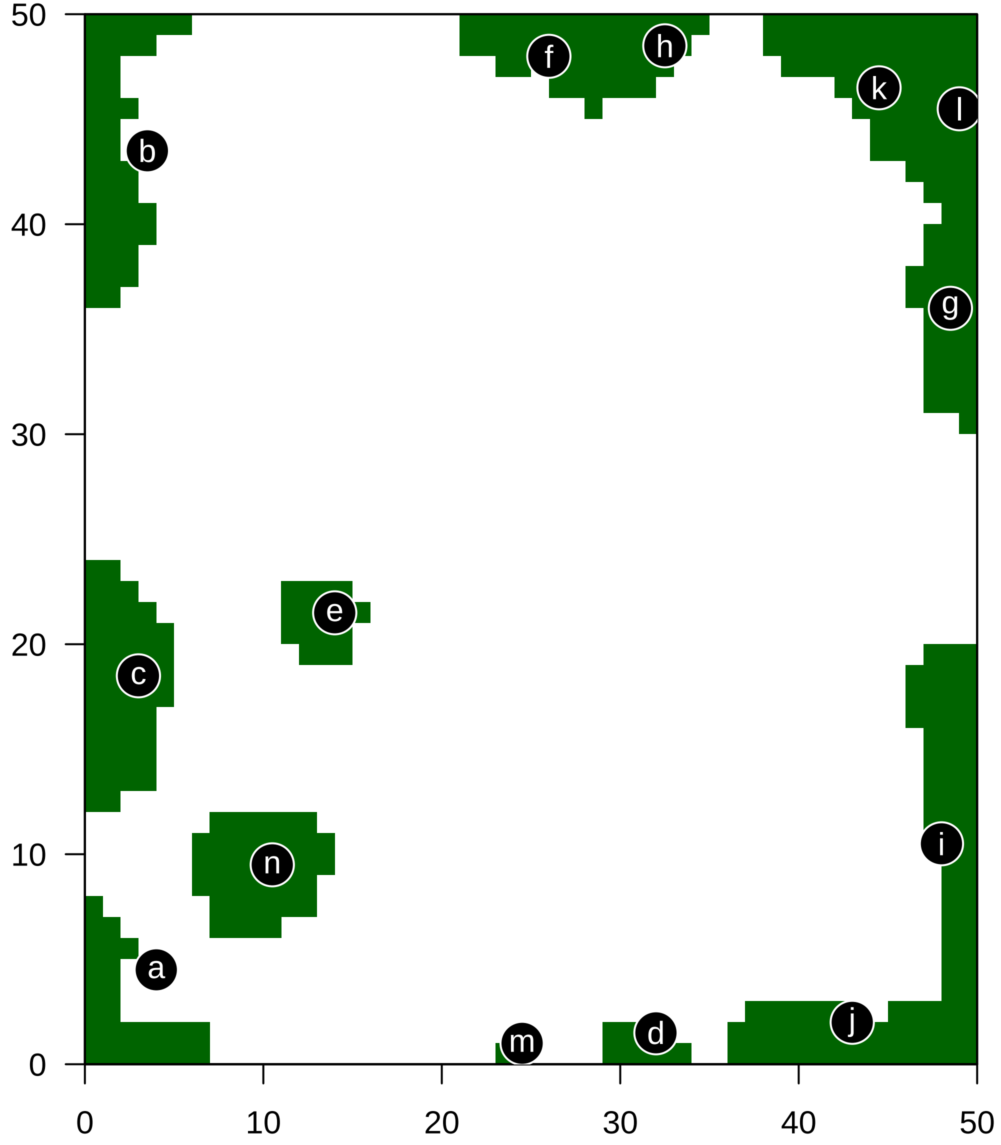
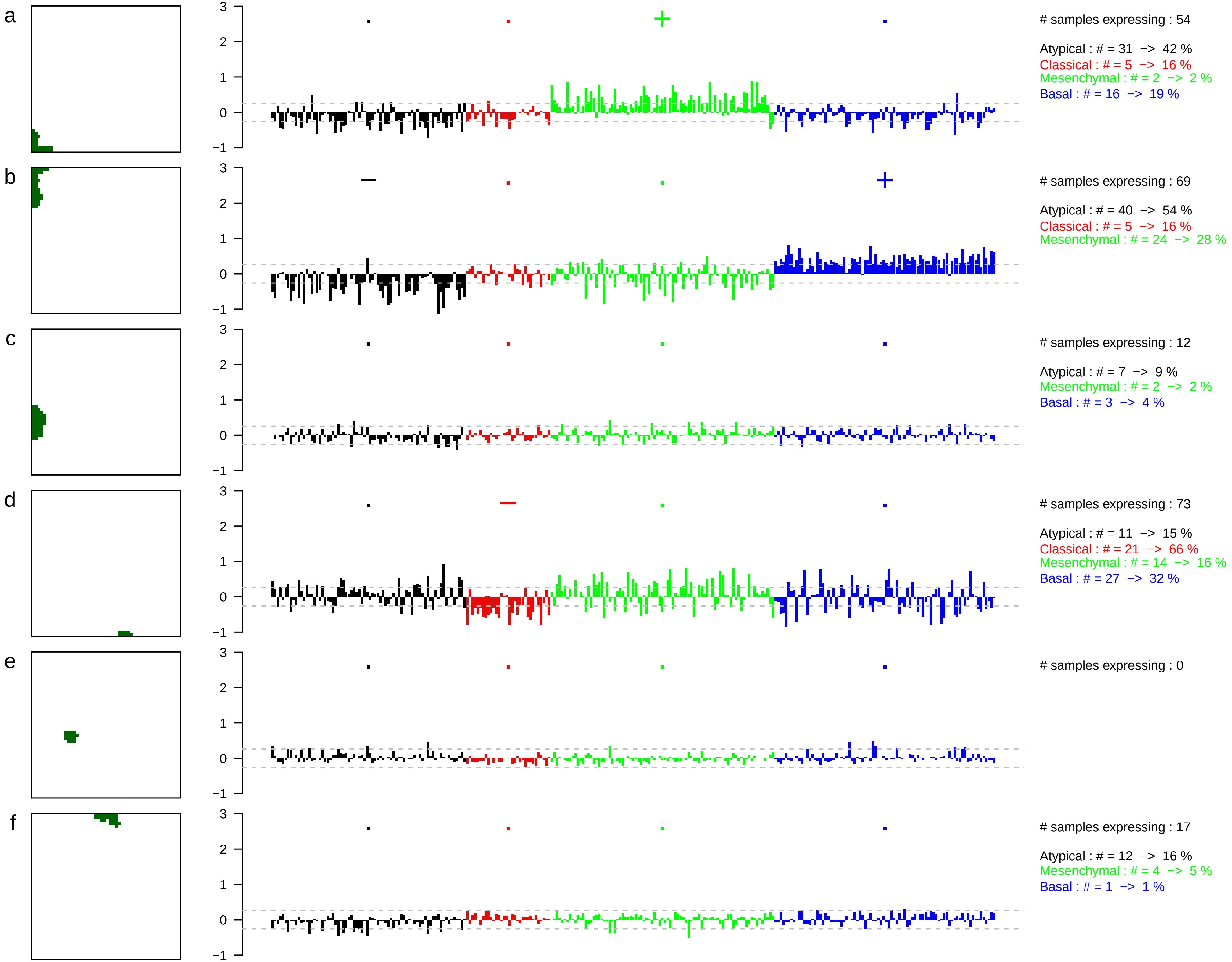
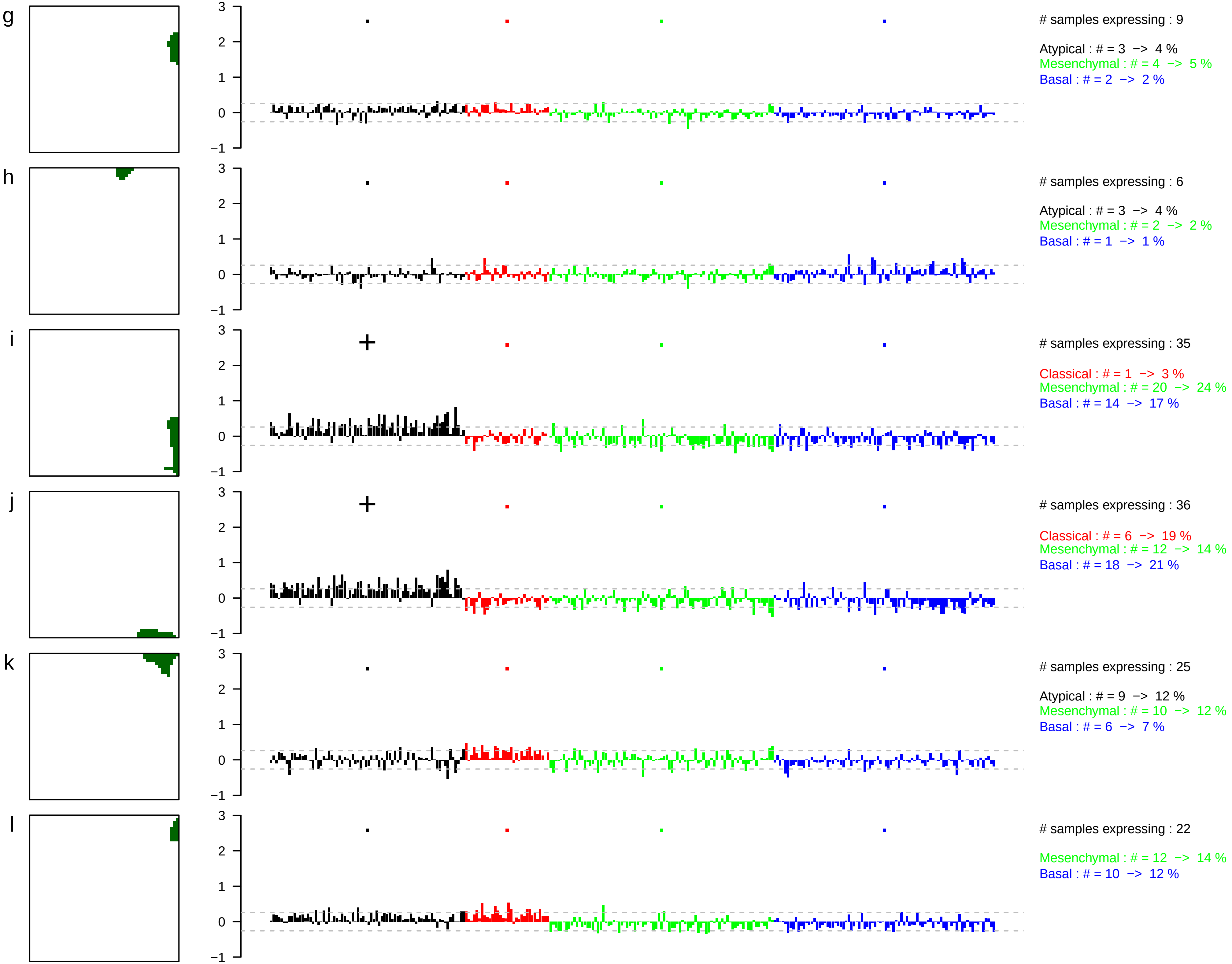


Sample−Underexpression

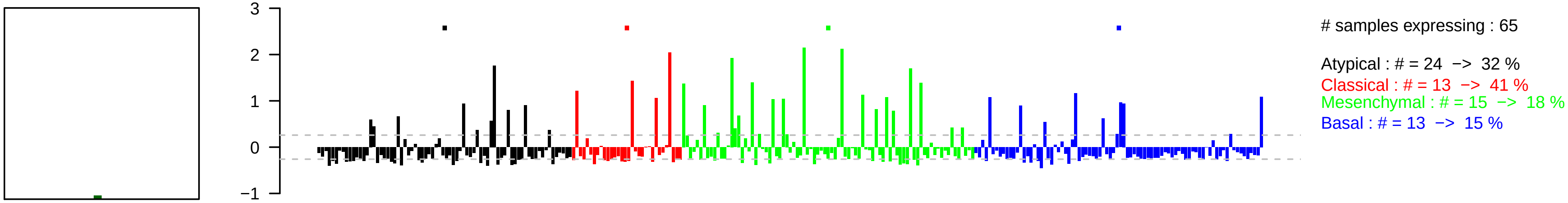


Spots


a
3
2
1
0
−1
samples expressing : 54
Atypical : # = 31 -> 42 %
Classical : # = 5 -> 16 %
Mesenchymal : # = 2 -> 2 %
Basal : # = 16 -> 19 %
b
3
2
1
0
−1
samples expressing : 69
Atypical : # = 40 -> 54 %
Classical : # = 5 -> 16 %
Mesenchymal : # = 24 -> 28 %
c
3
2
1
0
−1
samples expressing : 12
Atypical : # = 7 -> 9 %
Mesenchymal : # = 2 -> 2 %
Basal : # = 3 -> 4 %
d
3
2
1
0
−1
samples expressing : 73
Atypical : # = 11 -> 15 %
Classical : # = 21 -> 66 %
Mesenchymal : # = 14 -> 16 %
Basal : # = 27 -> 32 %
e
3
2
1
0
−1
samples expressing : 0
f
3
2
1
0
−1
samples expressing : 17
Atypical : # = 12 -> 16 %
Mesenchymal : # = 4 -> 5 %
Basal : # = 1 -> 1 %

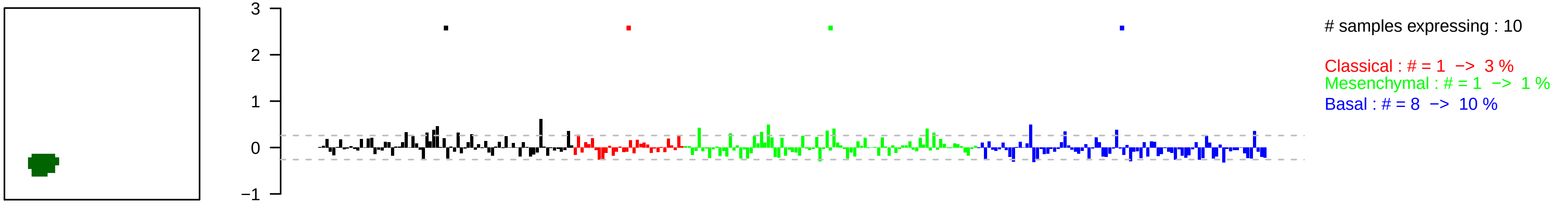

g
3
2
1
0
−1
samples expressing : 9
Atypical : # = 3 –> 4 %
Mesenchymal : # = 4 –> 5 %
Basal : # = 2 –> 2 %
h
samples expressing : 6
Atypical : # = 3 –> 4 %
Mesenchymal : # = 2 –> 2 %
Basal : # = 1 –> 1 %
i
+
samples expressing : 35
Classical : # = 1 –> 3 %
Mesenchymal : # = 20 –> 24 %
Basal : # = 14 –> 17 %
j
+
samples expressing : 36
Classical : # = 6 –> 19 %
Mesenchymal : # = 12 –> 14 %
Basal : # = 18 –> 21 %
k
samples expressing : 25
Atypical : # = 9 –> 12 %
Mesenchymal : # = 10 –> 12 %
Basal : # = 6 –> 7 %
l
samples expressing : 22
Mesenchymal : # = 12 –> 14 %
Basal : # = 10 –> 12 %

m

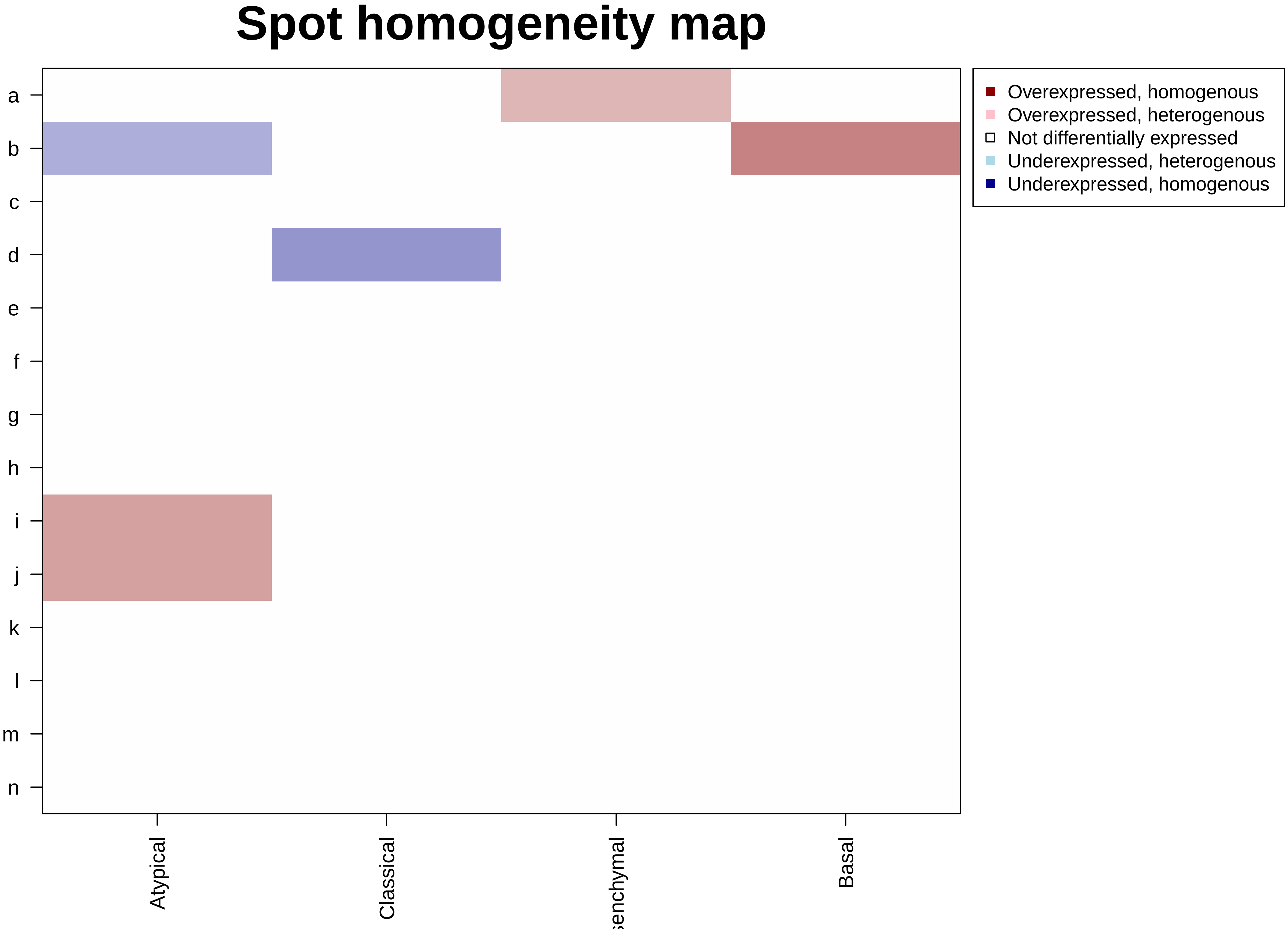


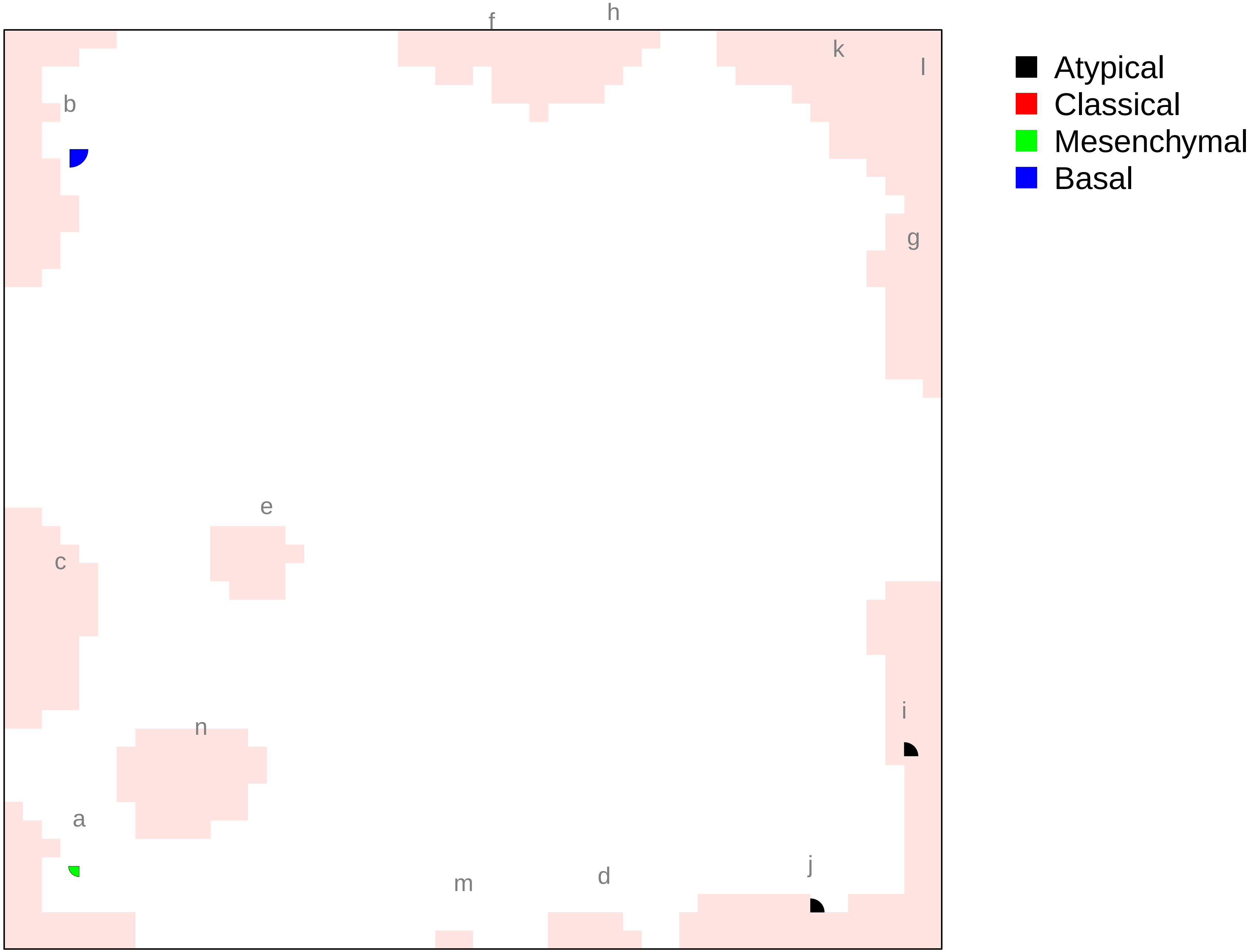
3
2
1
0
−1
samples expressing : 65
Atypical : # = 24 –> 32 %
Classical : # = 13 –> 41 %
Mesenchymal : # = 15 –> 18 %
Basal : # = 13 –> 15 %

n

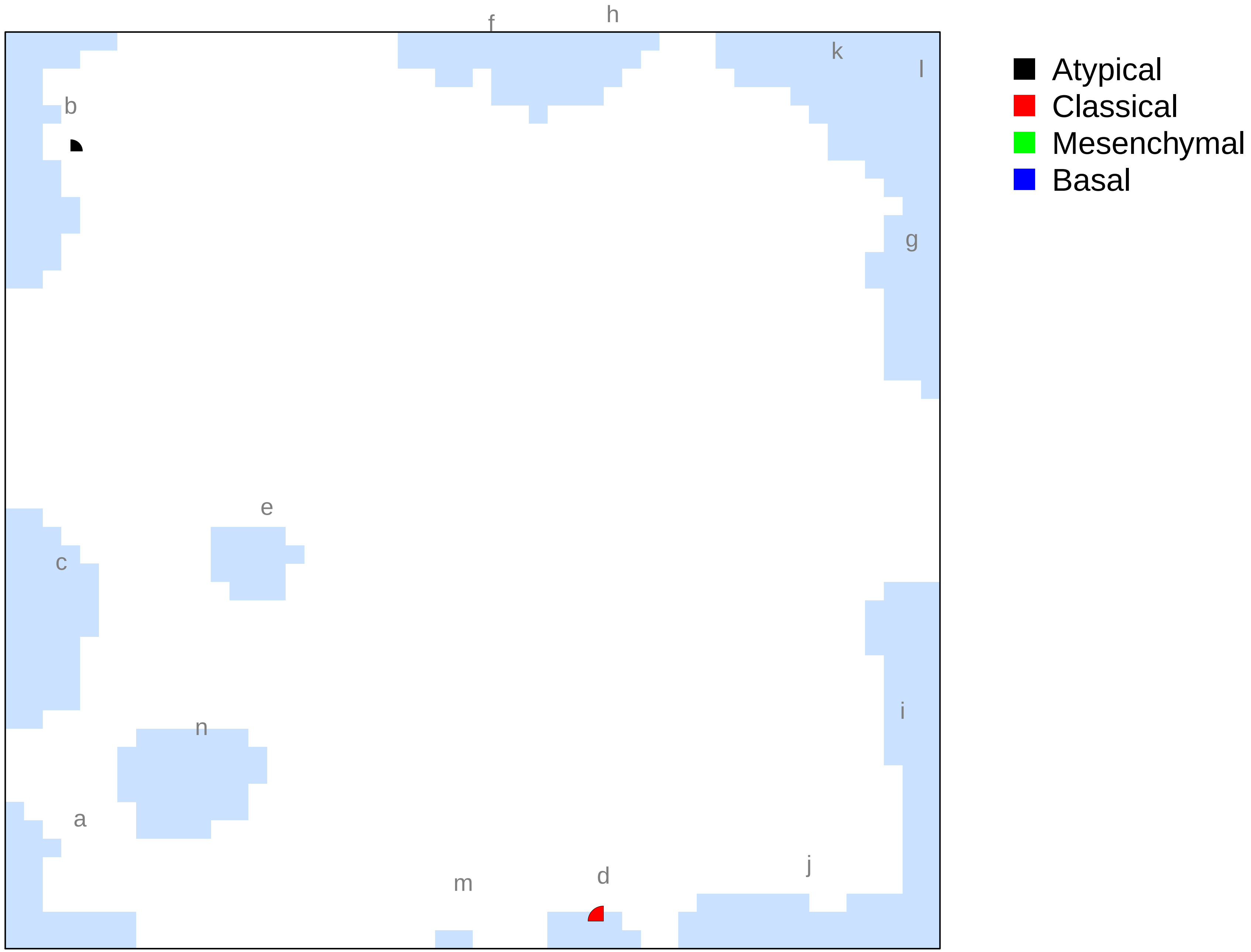


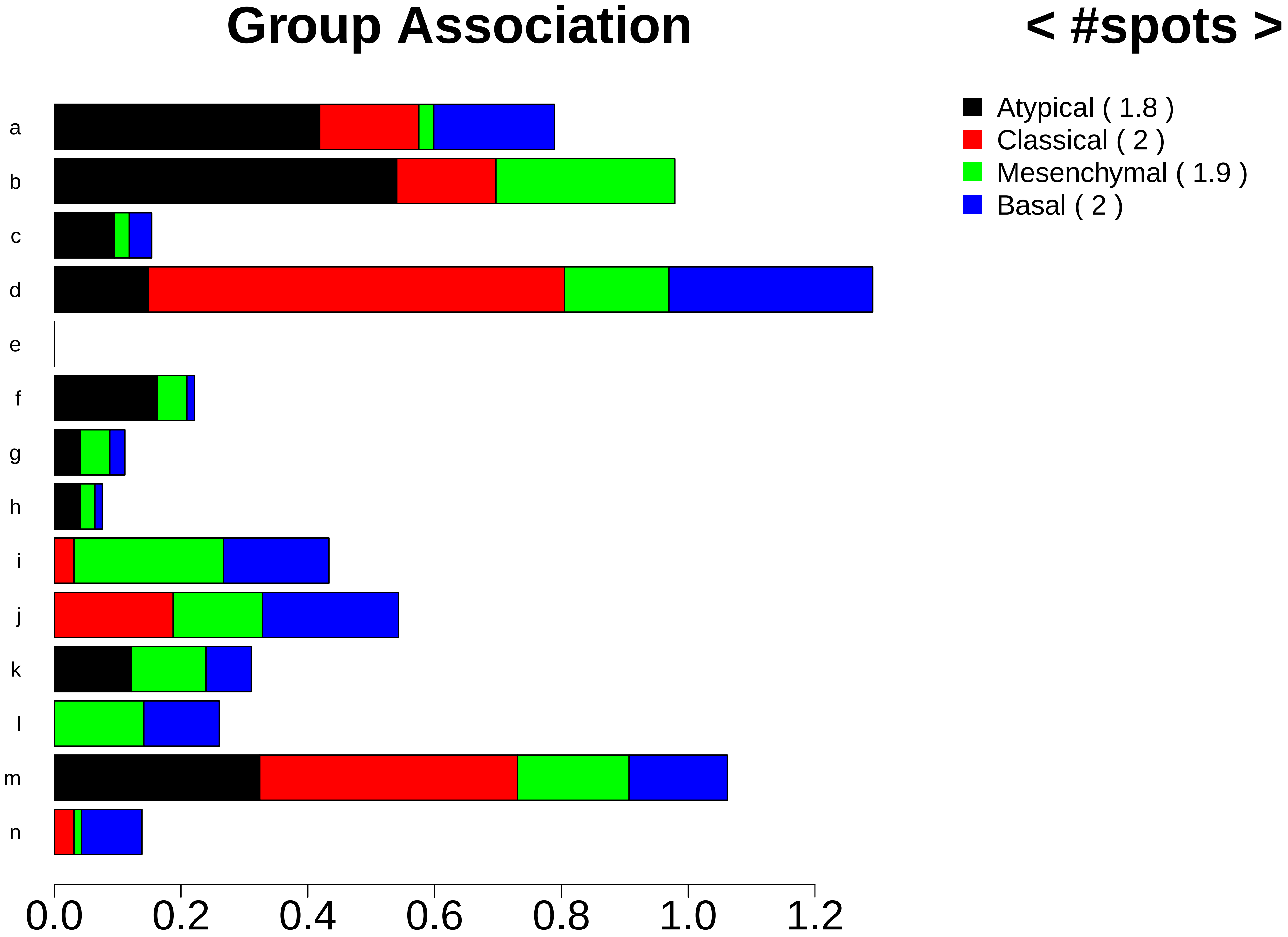
3
2
1
0
−1
samples expressing : 10
Classical : # = 1 –> 3 %
Mesenchymal : # = 1 –> 1 %
Basal : # = 8 –> 10 %

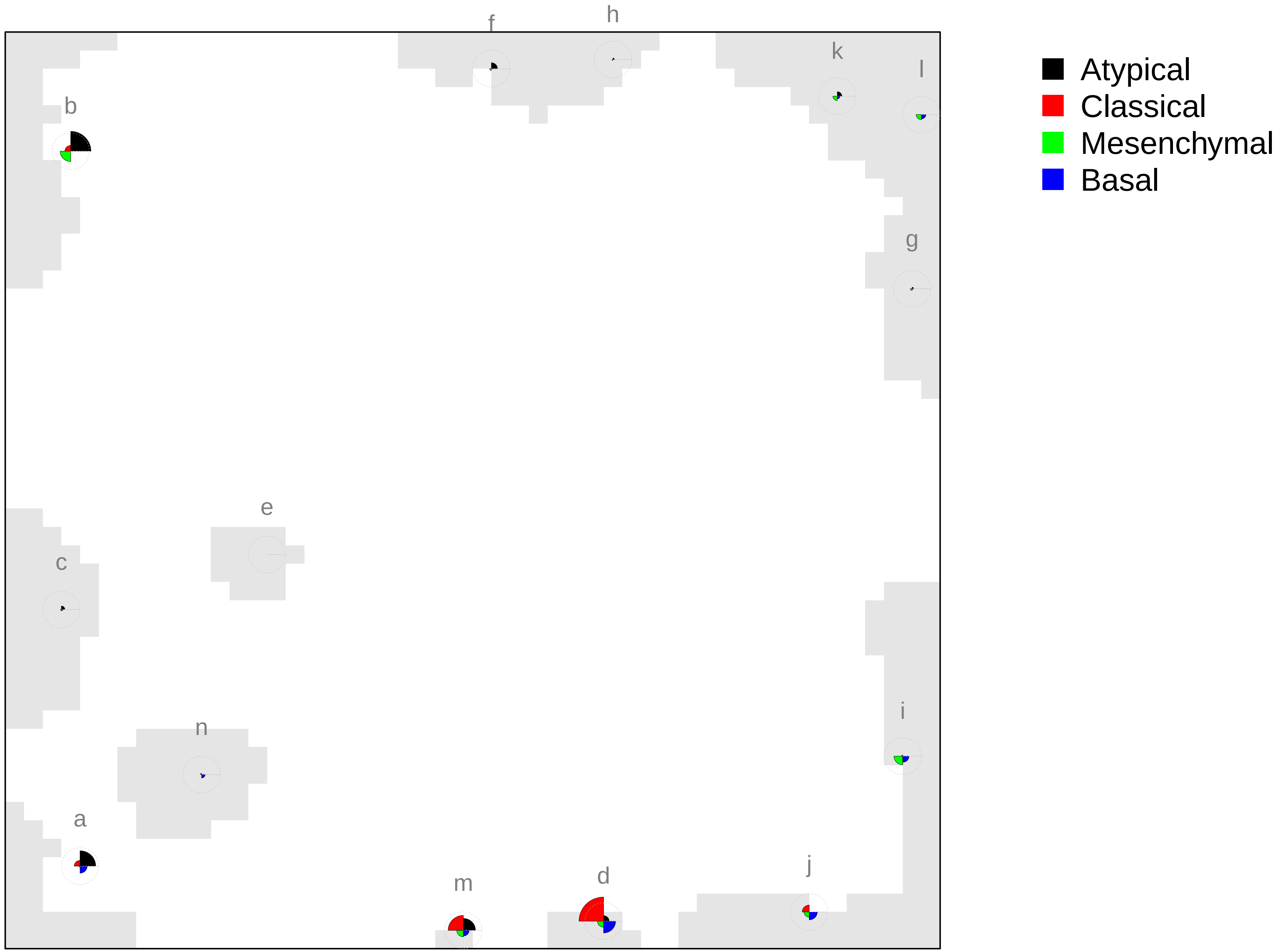

Spot homogeneity map
a
b
c
d
e
f
g
h
i
j
k
l
m
n
Atypical
Classical
senchymal
Basal
Overexpressed, homogenous
Overexpressed, heterogenous
Not differentially expressed
Underexpressed, heterogenous
Underexpressed, homogenous

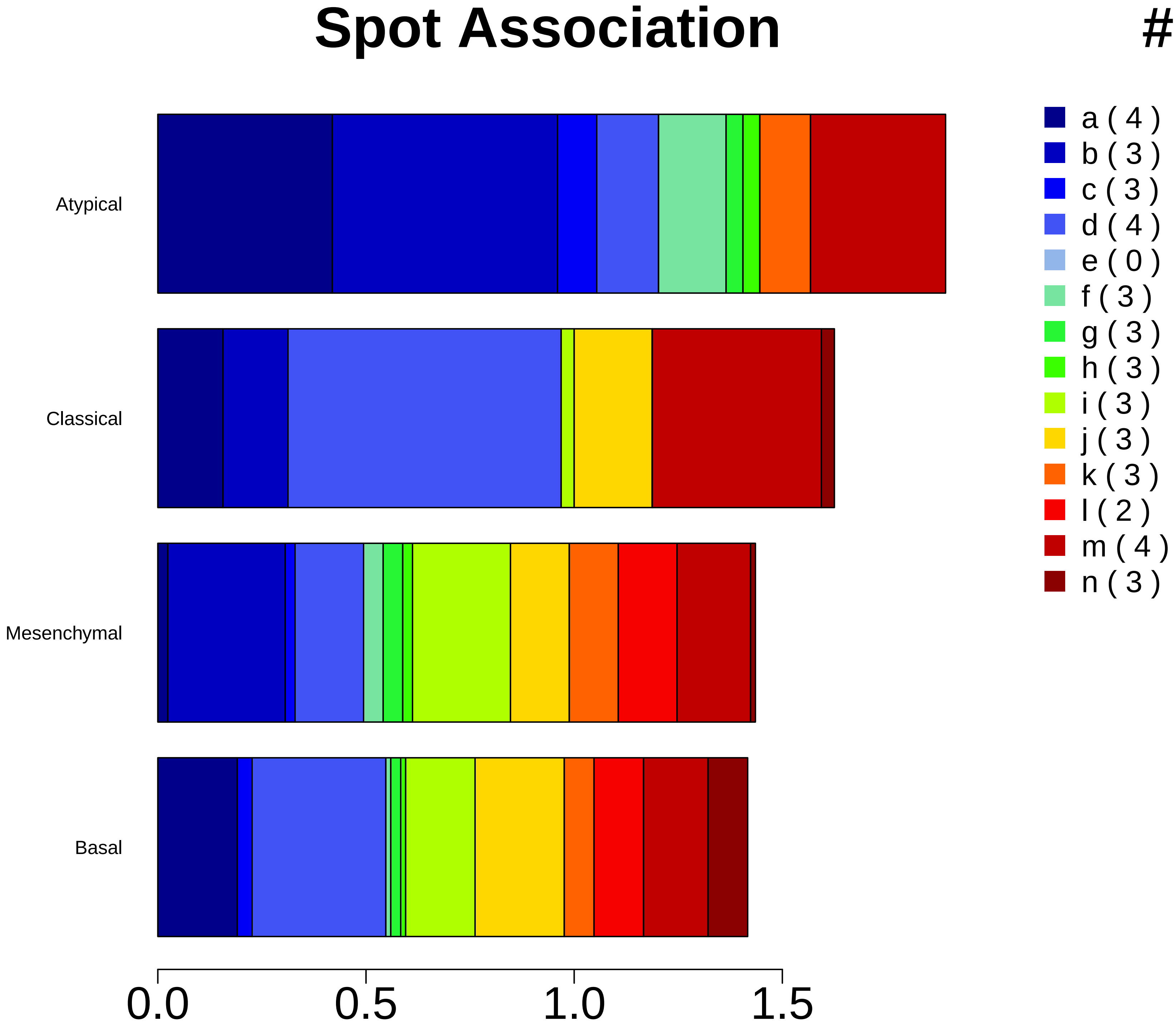


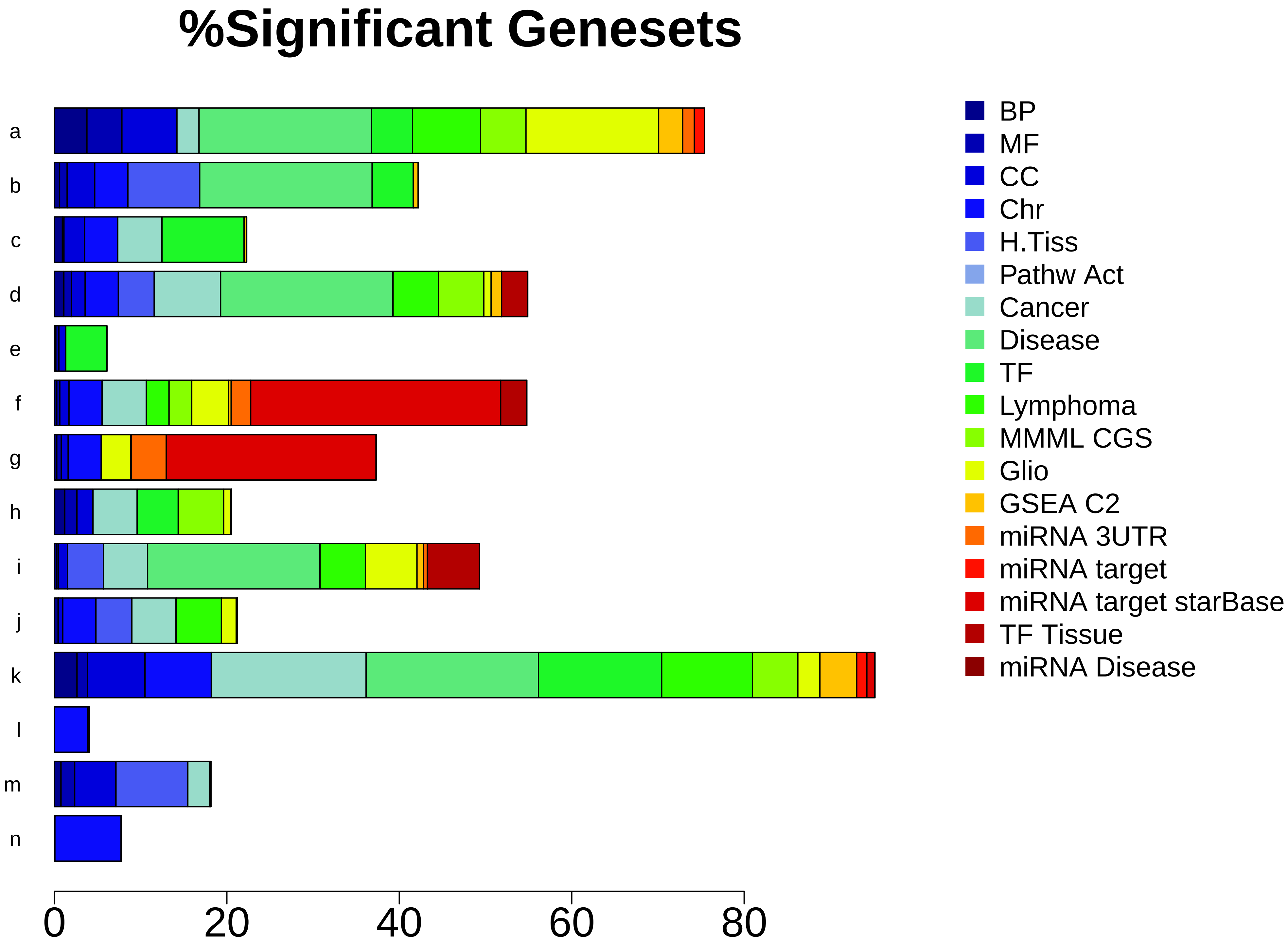
f
h
k
l
b
g
e
c
n
i
a
j
m
d
Atypical
Classical
Mesenchymal
Basal

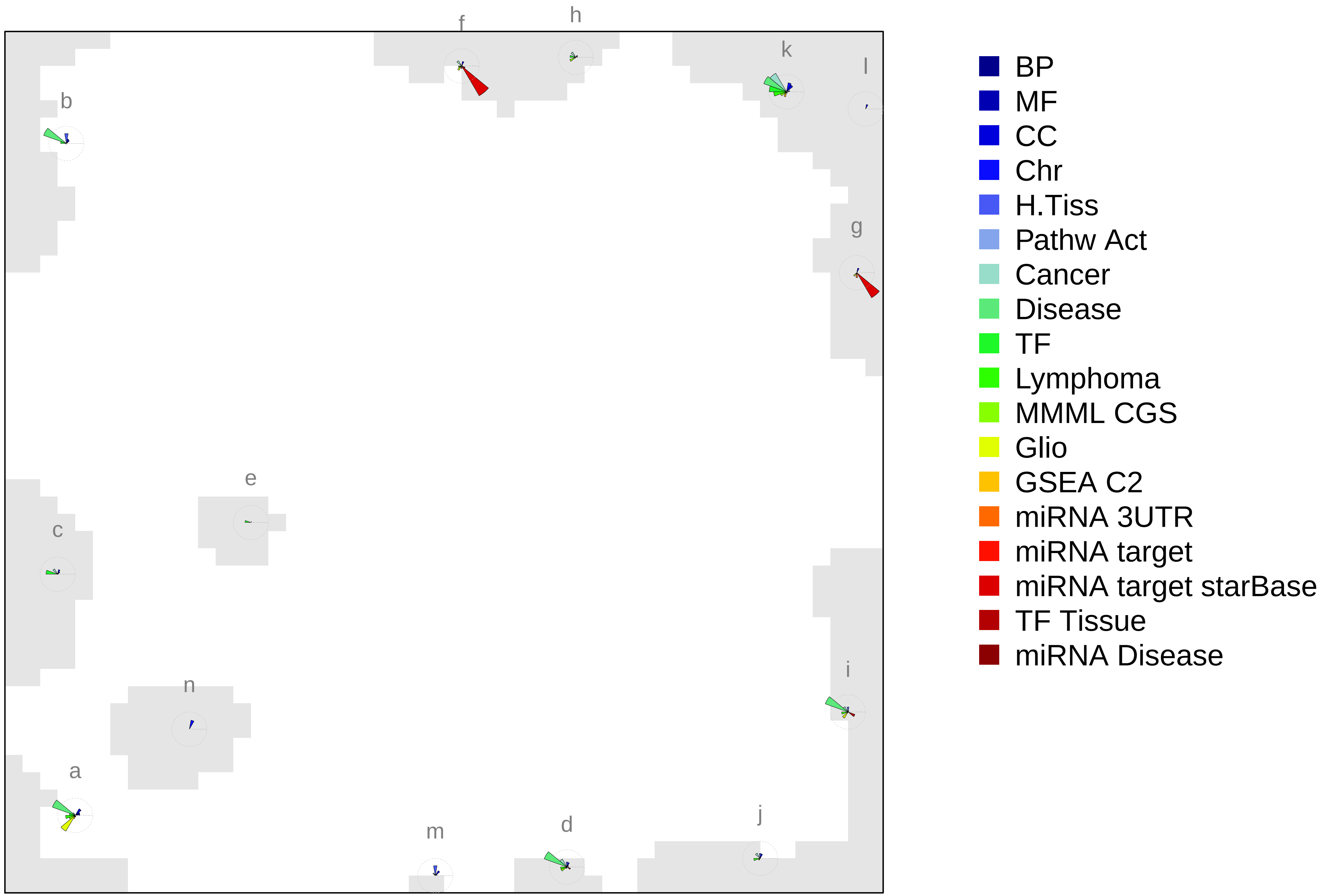

f
h
k
l
b
g
e
c
i
n
a
j
m
d
Atypical
Classical
Mesenchymal
Basal


Group Association
< #spots >
Atypical (1.8)
Classical (2)
Mesenchymal (1.9)
Basal (2)
a
b
c
d
e
f
g
h
i
j
k
l
m
n
0.0
0.2
0.4
0.6
0.8
1.0
1.2


f
h
k
l
b
g
e
c
i
n
a
m
d
j
Atypical
Classical
Mesenchymal
Basal


Spot Association
#groups
Atypical
Classical
Mesenchymal
Basal
0.0
0.5
1.0
1.5
a (4)
b (3)
c (3)
d (4)
e (0)
f (3)
g (3)
h (3)
i (3)
j (3)
k (3)
l (2)
m (4)
n (3)


%Significant Genesets
a
b
c
d
e
f
g
h
i
j
k
l
m
n
0
20
40
60
80
BP
MF
CC
Chr
H.Tiss
Pathw Act
Cancer
Disease
TF
Lymphoma
MMML CGS
Glio
GSEA C2
miRNA 3UTR
miRNA target
miRNA target starBase
TF Tissue
miRNA Disease


f
h
k
l
b
g
e
c
i
n
a
j
m
d
BP
MF
CC
Chr
H.Tiss
Pathw Act
Cancer
Disease
TF
Lymphoma
MMML CGS
Glio
GSEA C2
miRNA 3UTR
miRNA target
miRNA target starBase
TF Tissue
miRNA Disease