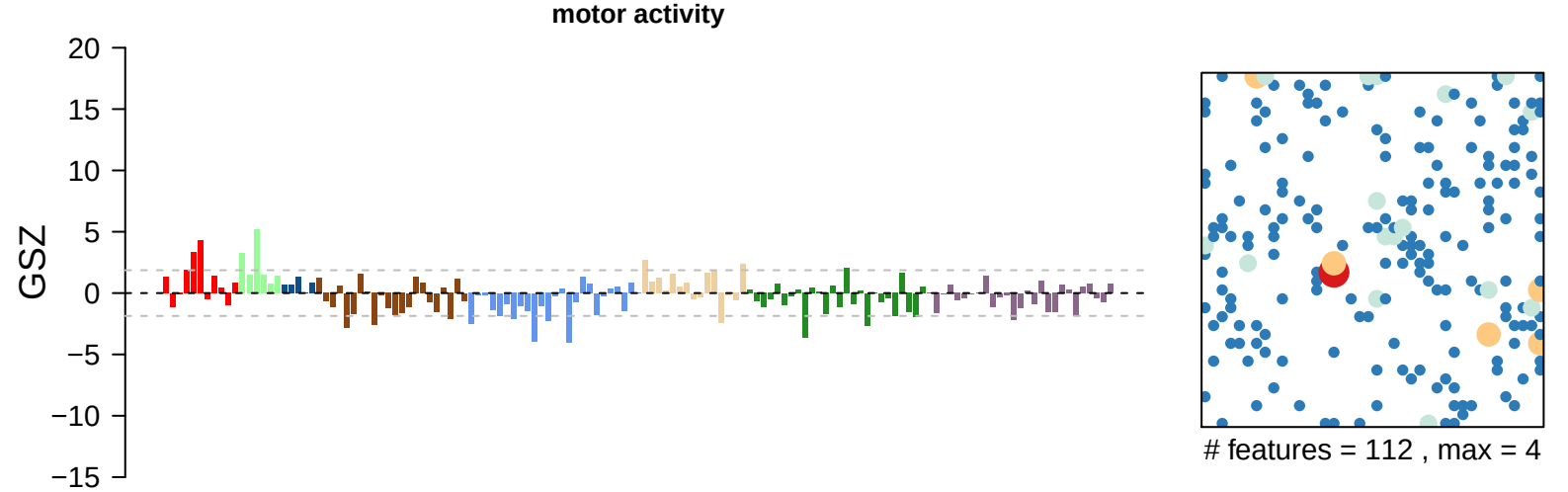
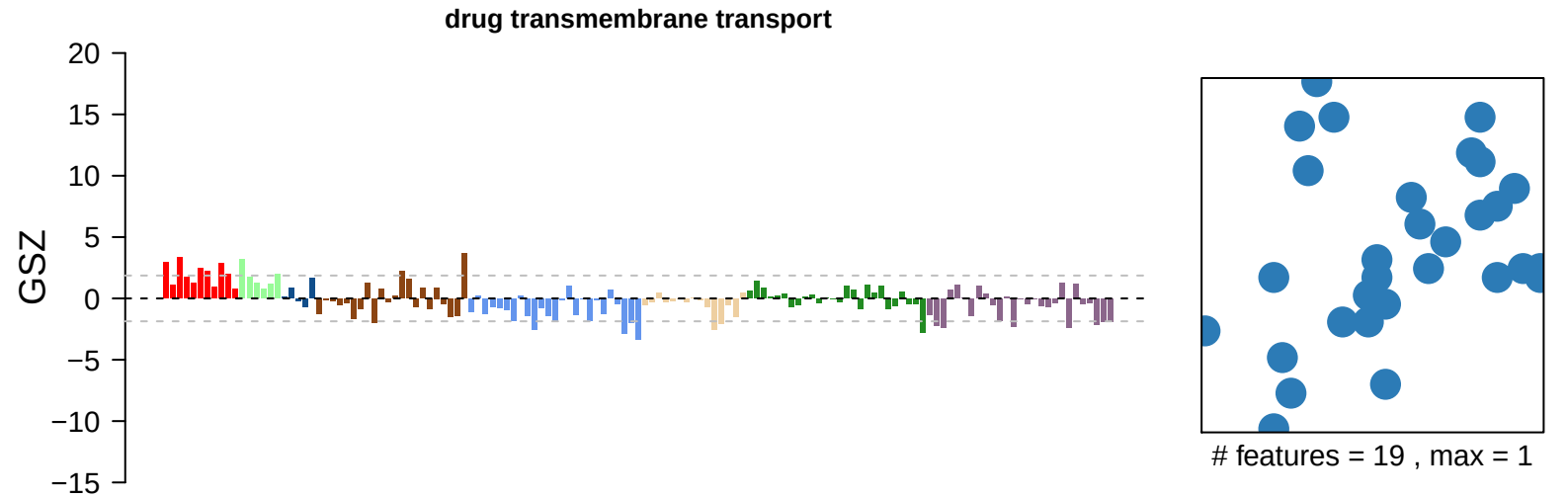
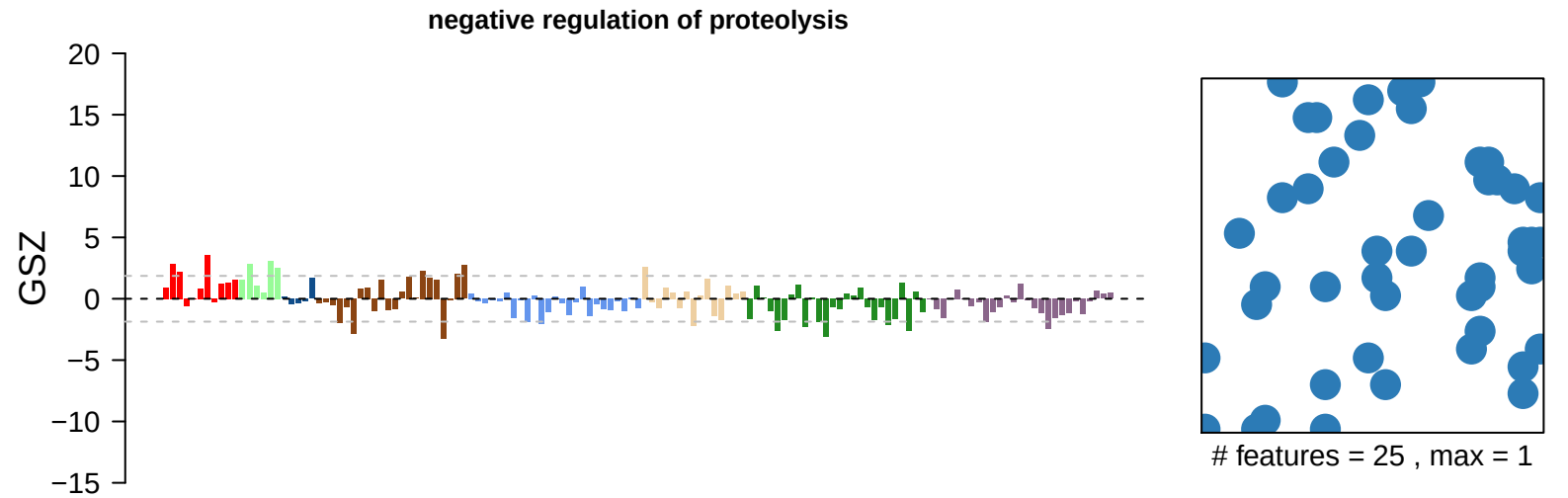
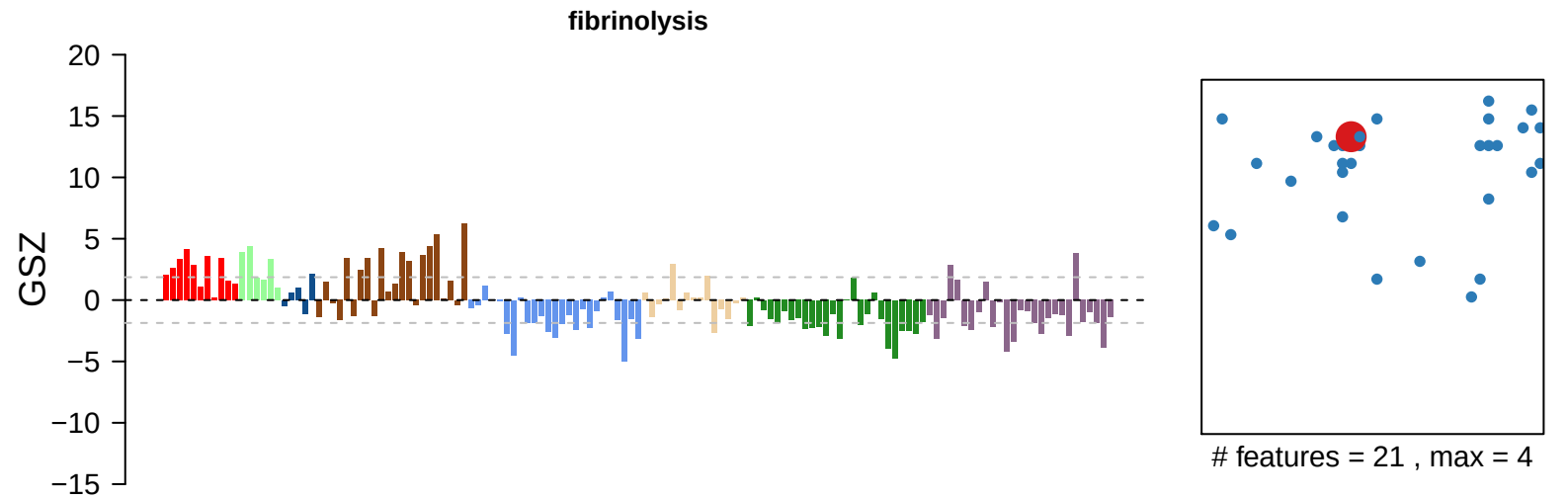
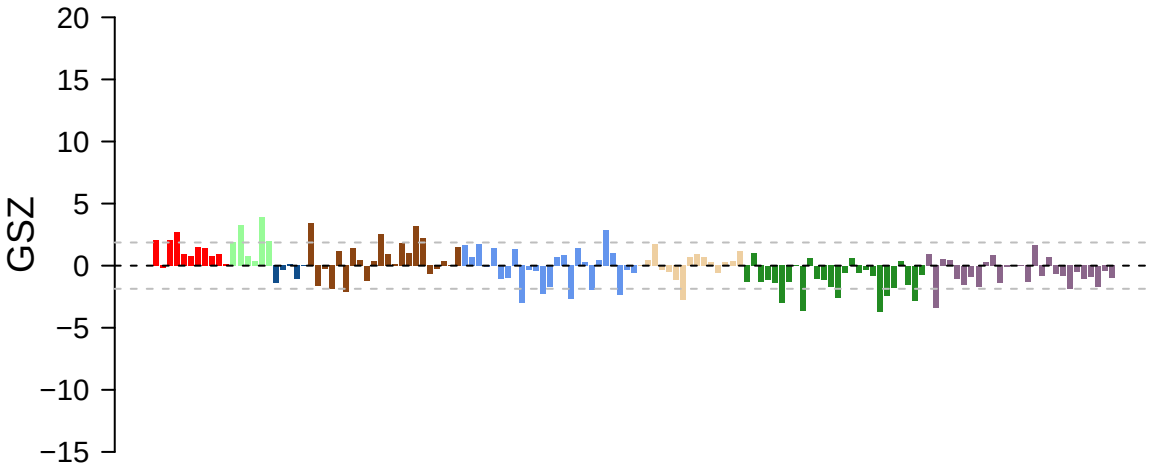

motor activity
GSZ
20
15
10
5
0
−5
−10
−15
features = 112 , max = 4

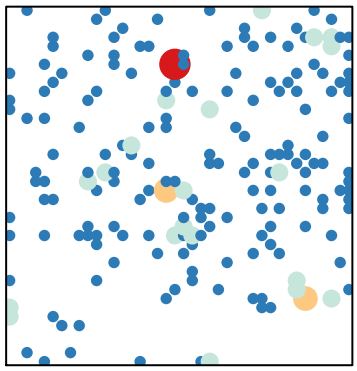

drug transmembrane transport
GSZ
20
15
10
5
0
−5
−10
−15
features = 19 , max = 1


negative regulation of proteolysis
GSZ
20
15
10
5
0
−5
−10
−15
features = 25 , max = 1


fibrinolysis
GSZ
20
15
10
5
0
−5
−10
−15
features = 21 , max = 4

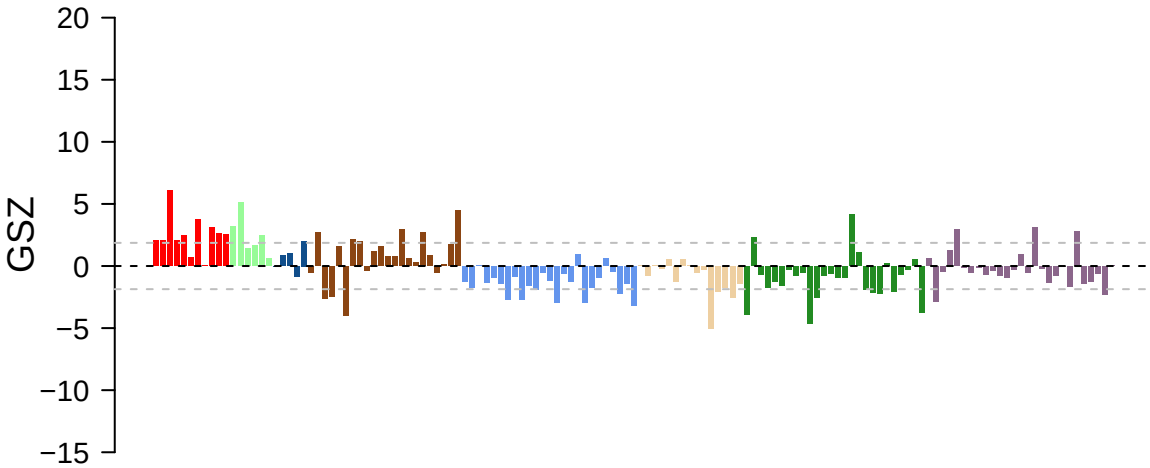
anatomical structure morphogenesis

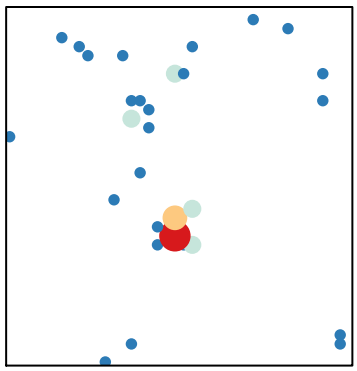




features = 106 , max = 4

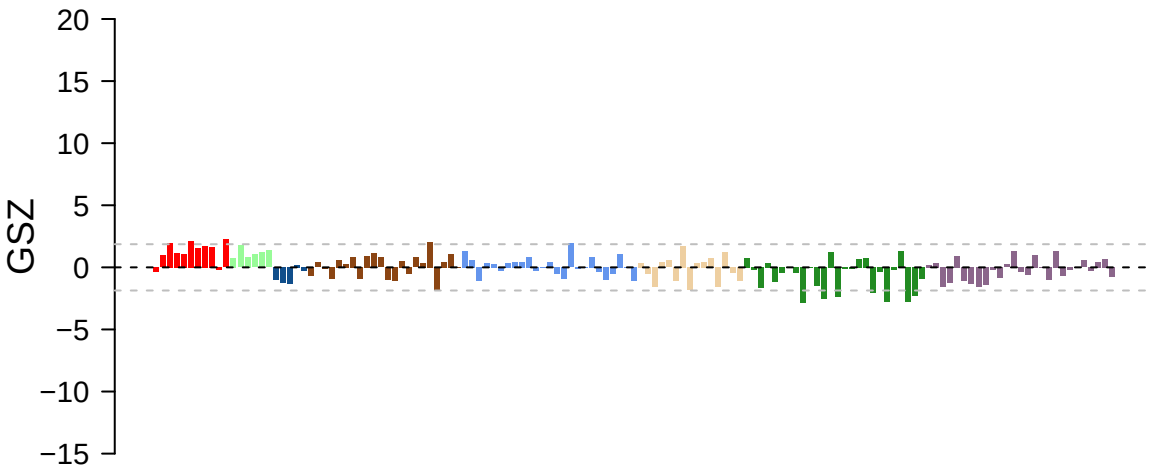
proteoglycan binding

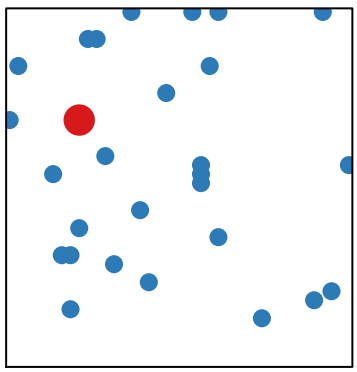




features = 15 , max = 4

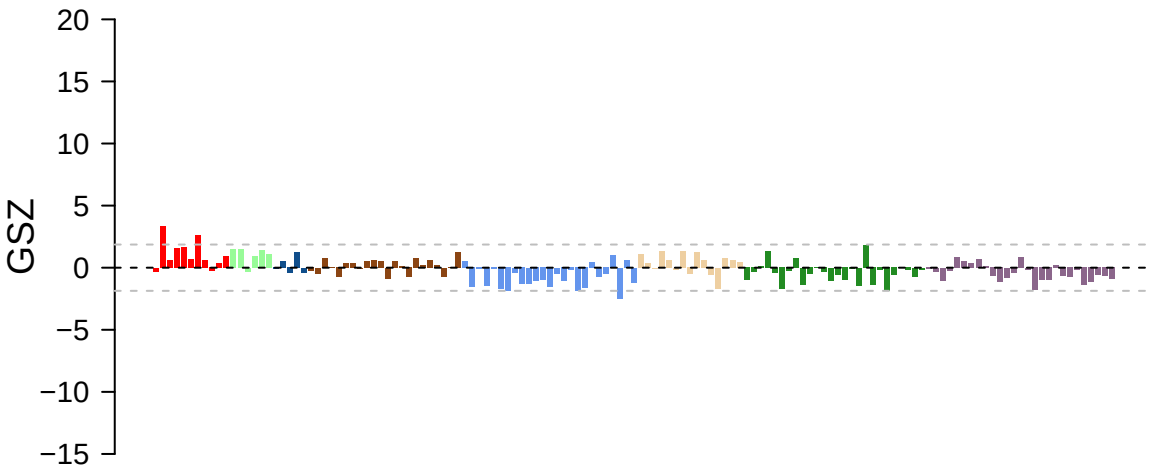
regulation of nucleic acid−templated transcription

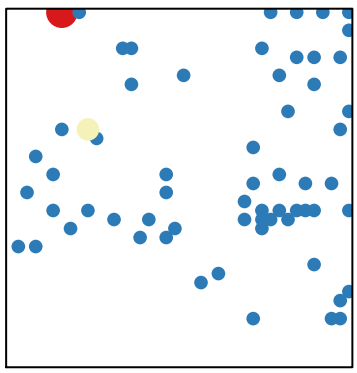




features = 16 , max = 2

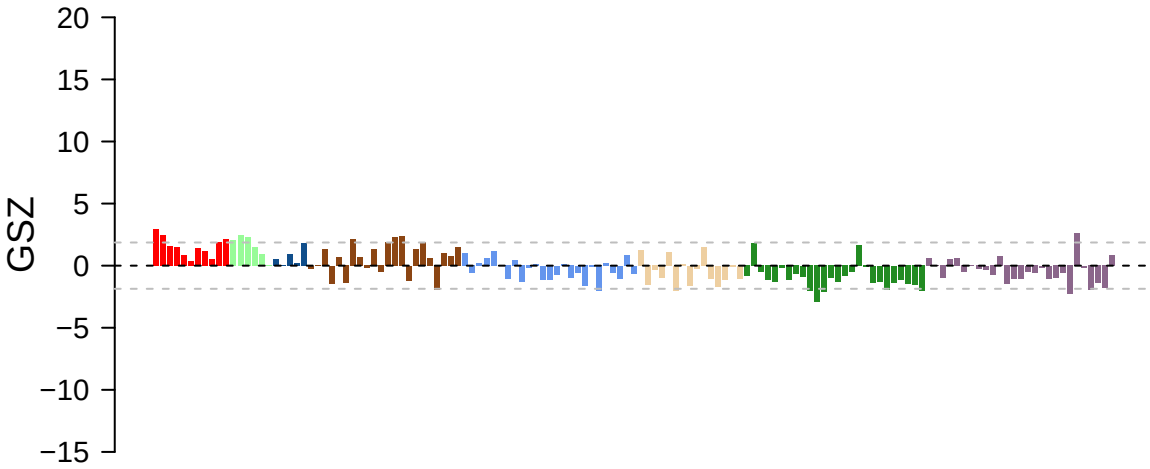
excretion

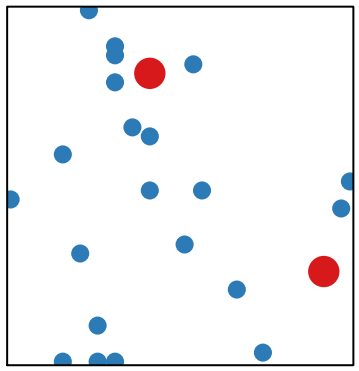




features = 34 , max = 3

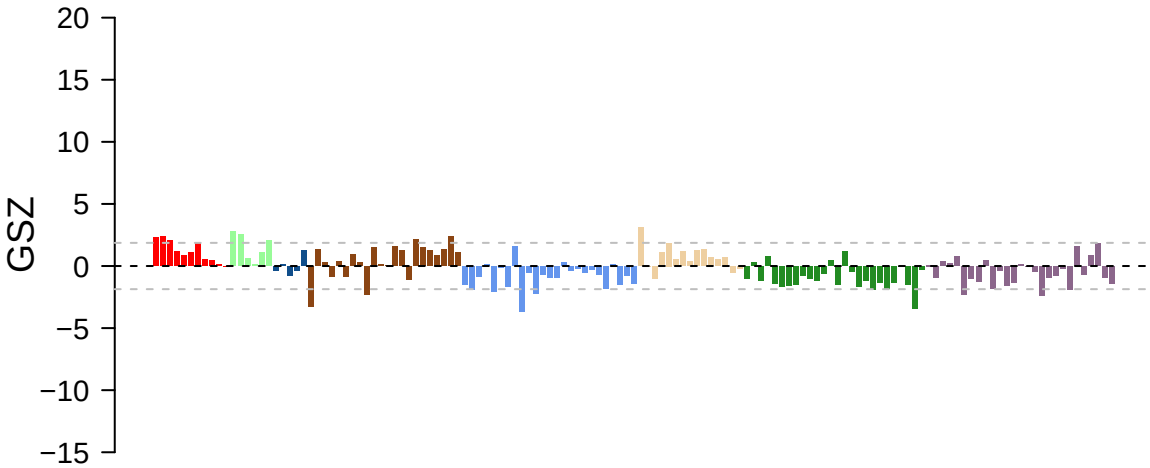
negative regulation of nitric oxide biosynthetic process

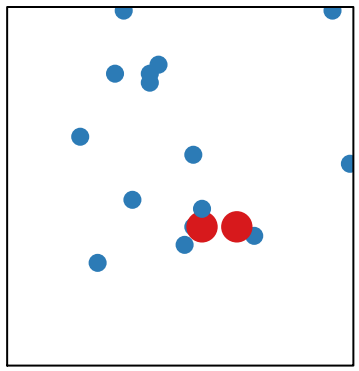




features = 14 , max = 2

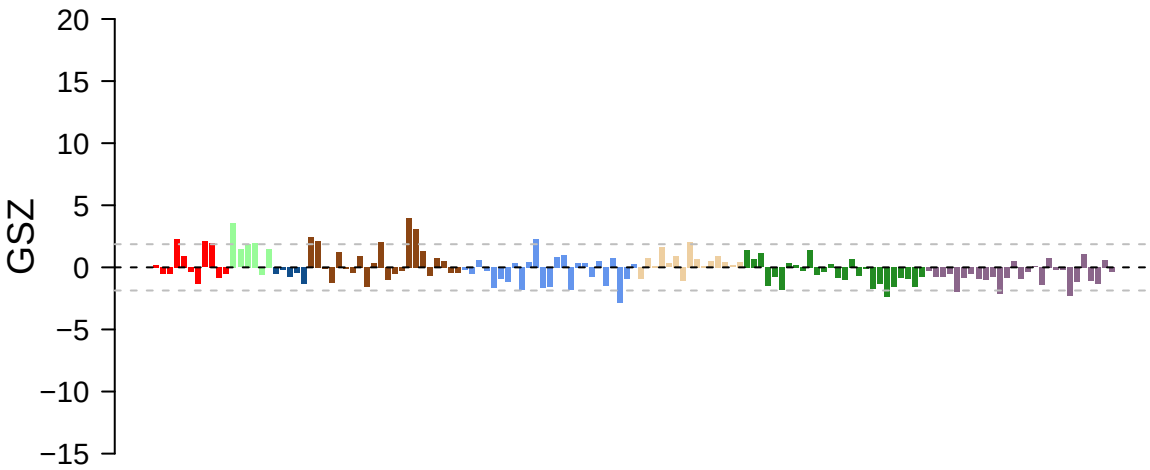
removal of superoxide radicals

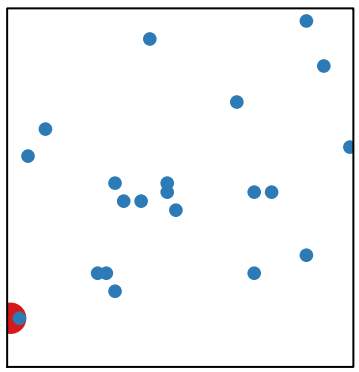




features = 12 , max = 2

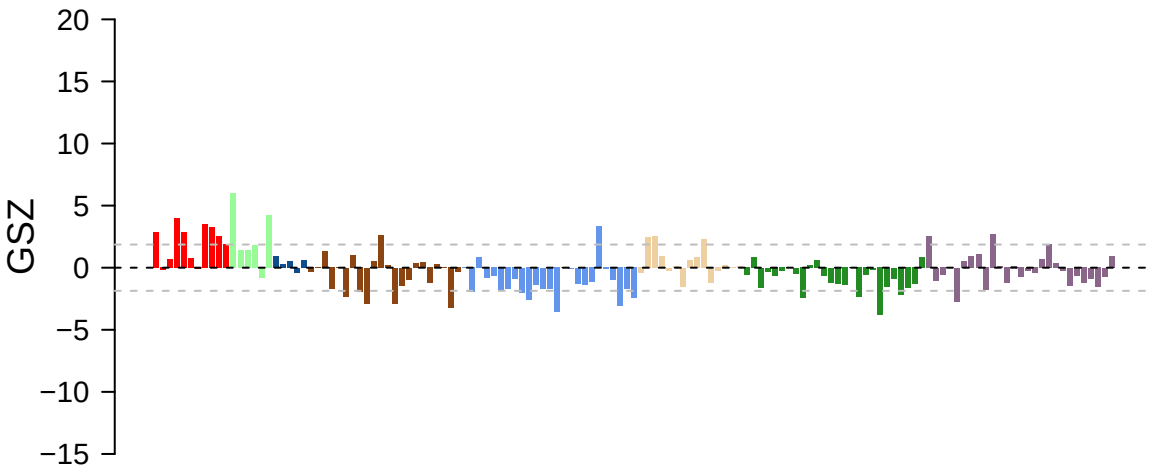
hindlimb morphogenesis

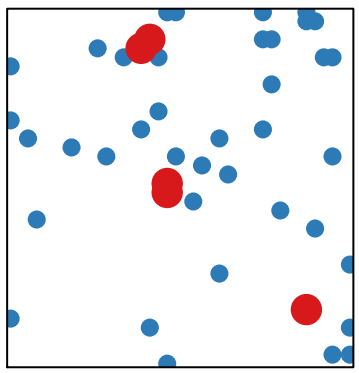




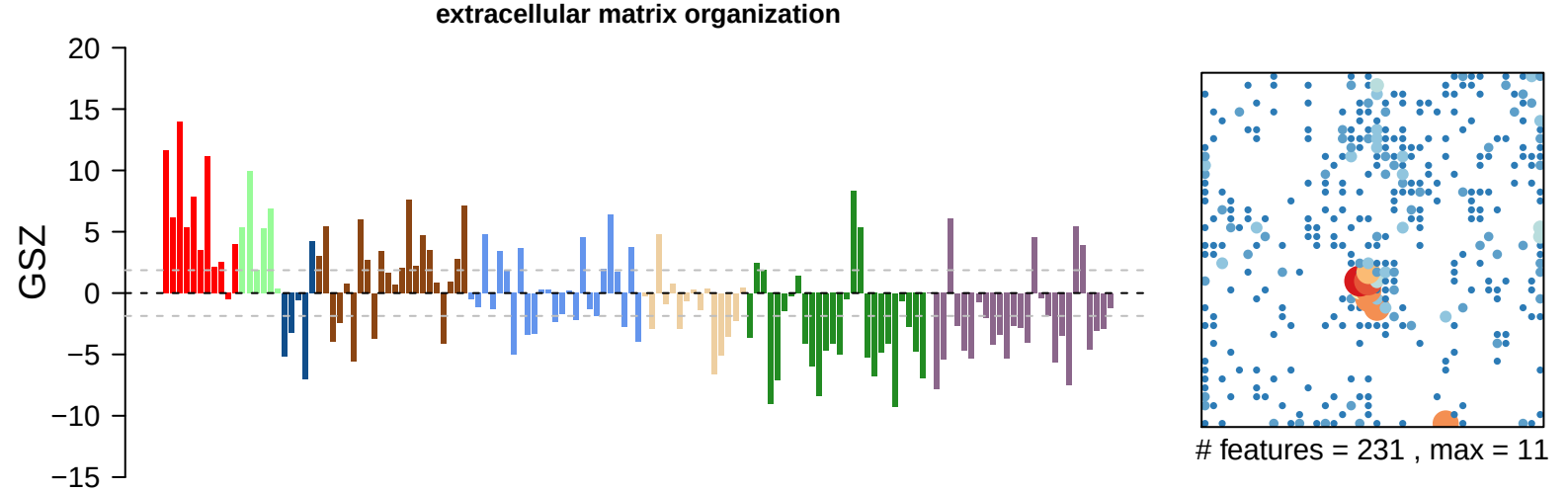
features = 10 , max = 3

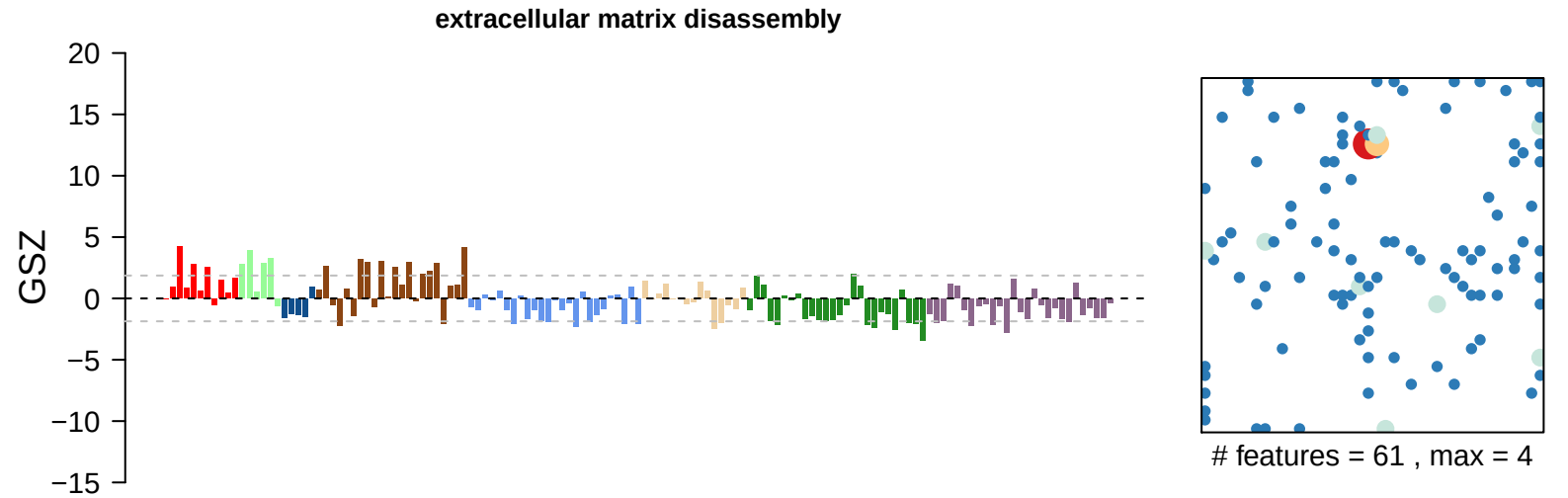
proximal/distal pattern formation

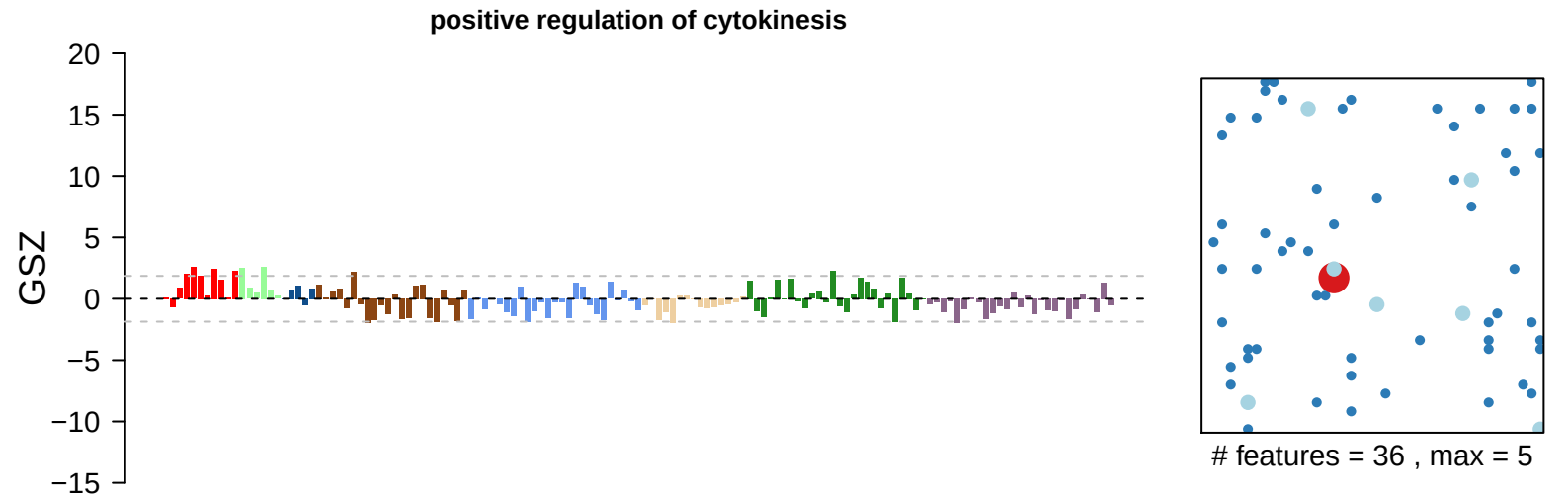


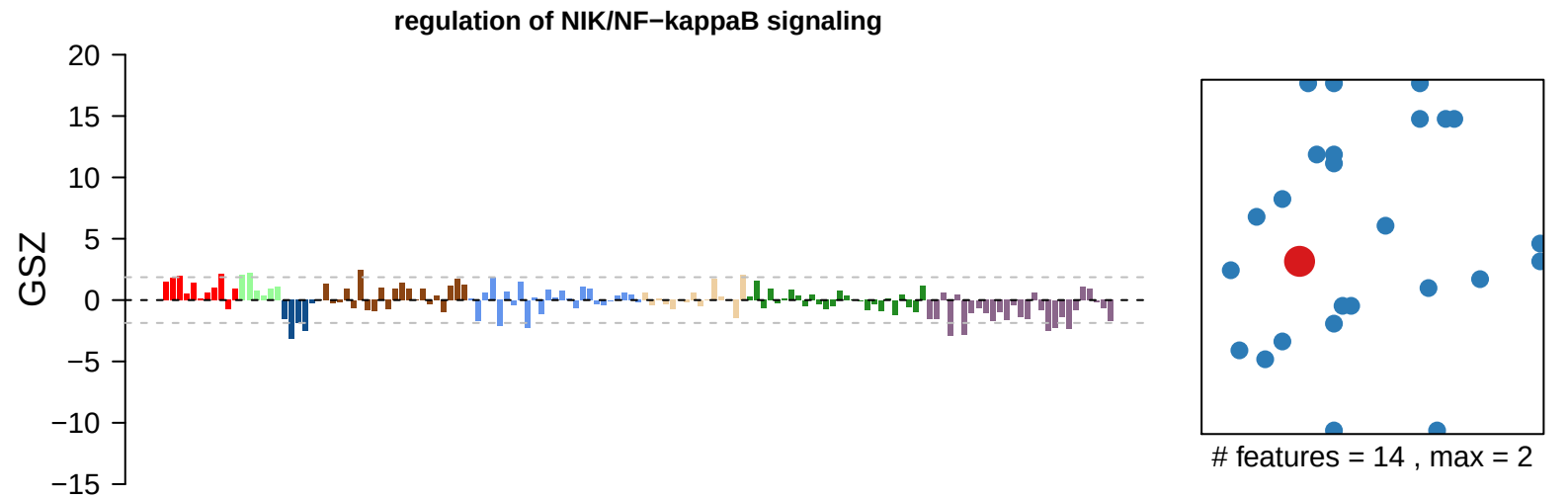


features = 23 , max = 2

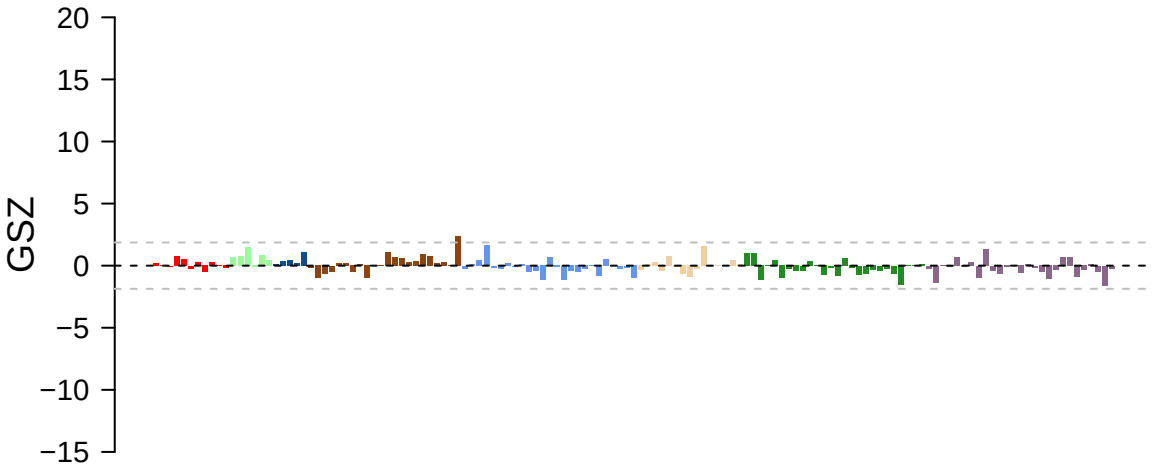

extracellular matrix organization
GSZ
20
15
10
5
0
−5
−10
−15
features = 231 , max = 11

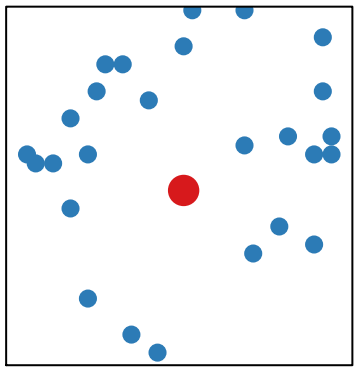

extracellular matrix disassembly
GSZ
20
15
10
5
0
−5
−10
−15
features = 61 , max = 4


positive regulation of cytokinesis
GSZ
20
15
10
5
0
−5
−10
−15
features = 36 , max = 5


regulation of NIK/NF−kappaB signaling
GSZ
20
15
10
5
0
−5
−10
−15
features = 14 , max = 2

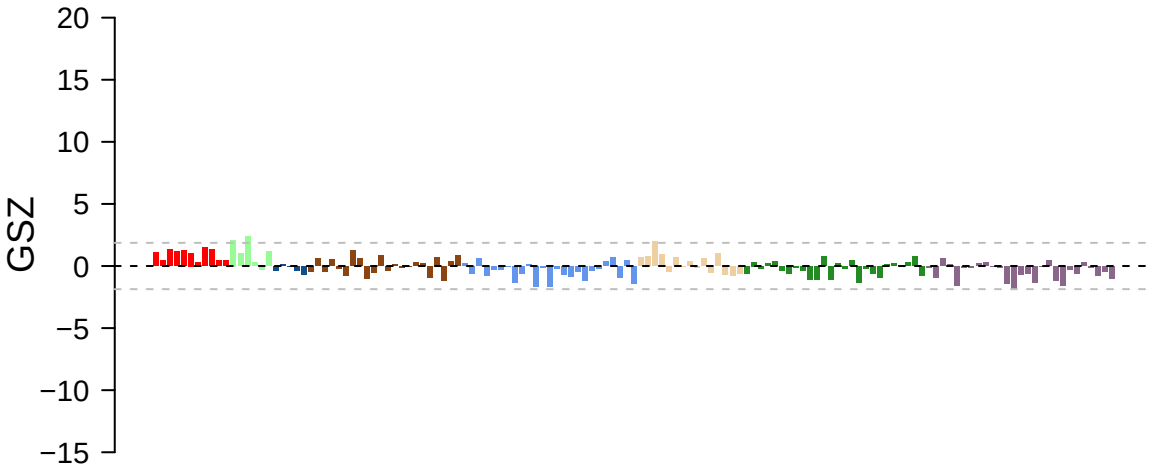
regulation of proteolysis

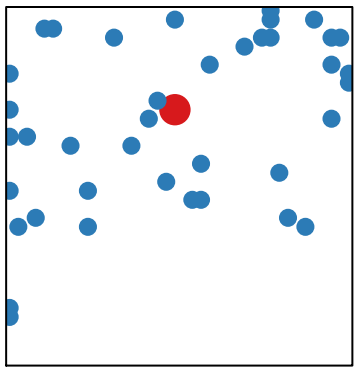




features = 12 , max = 2

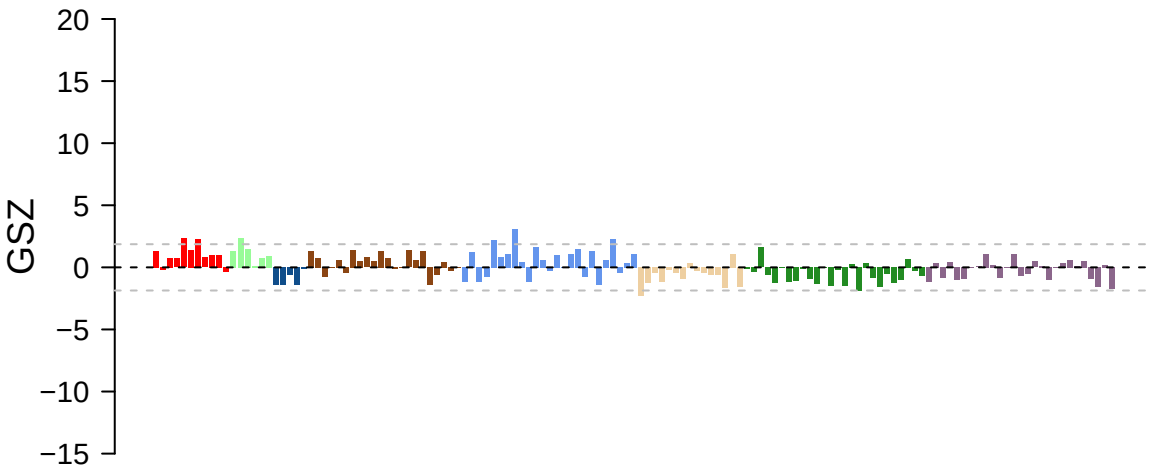
epithelial cell development

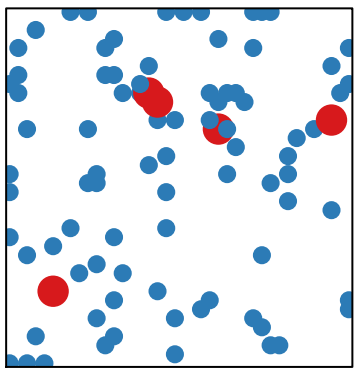




features = 11 , max = 2

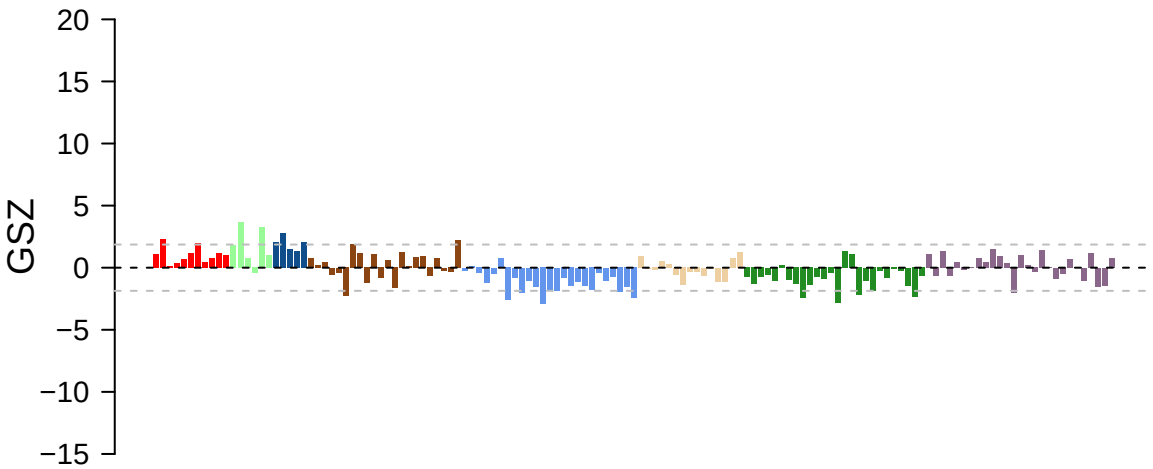
pigmentation

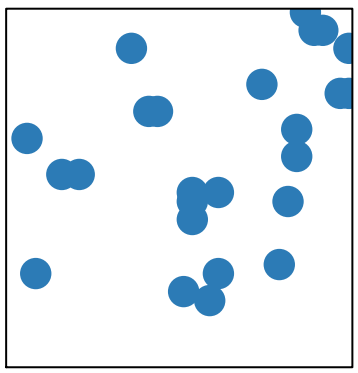




features = 38 , max = 2

retinoic acid metabolic process





features = 13 , max = 1