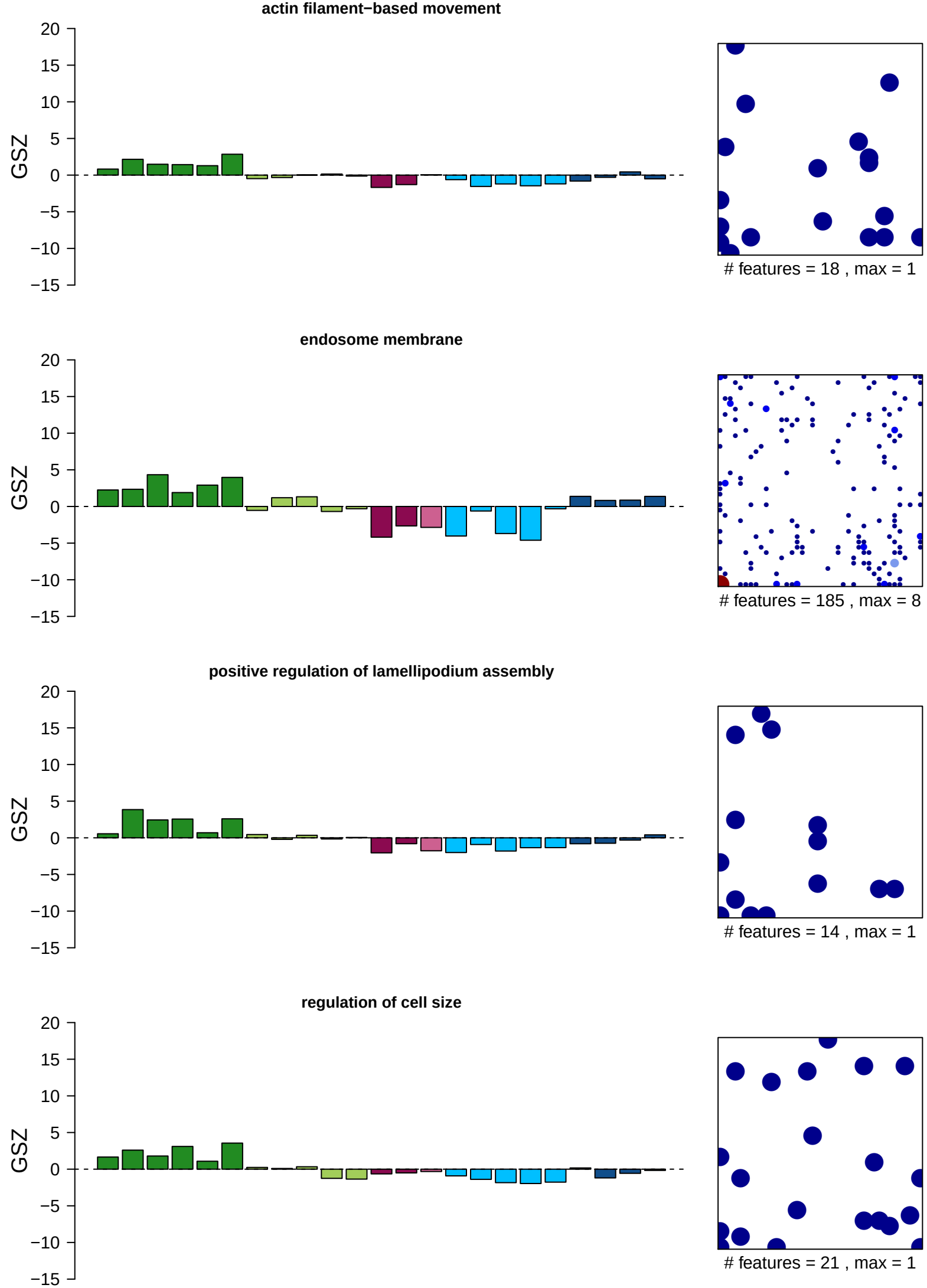
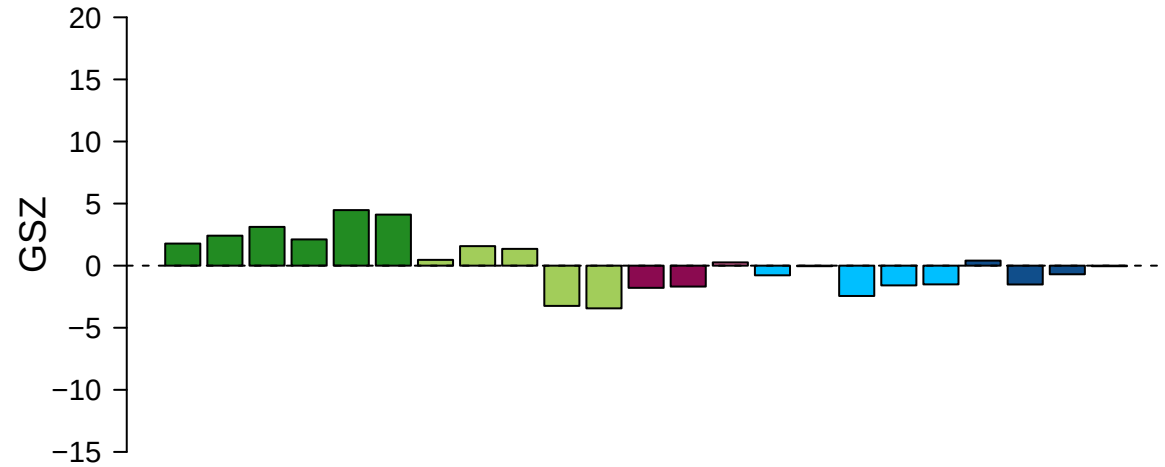
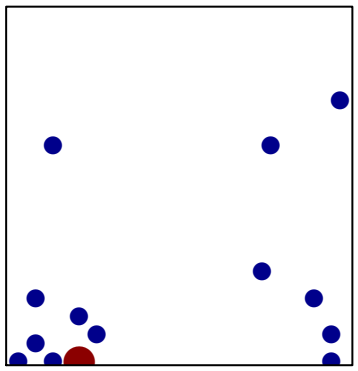

actin filament−based movement
GSZ
20
15
10
5
0
−5
−10
−15
features = 18 , max = 1
endosome membrane
GSZ
20
15
10
5
0
−5
−10
−15
features = 185 , max = 8
positive regulation of lamellipodium assembly
GSZ
20
15
10
5
0
−5
−10
−15
features = 14 , max = 1
regulation of cell size
GSZ
20
15
10
5
0
−5
−10
−15
features = 21 , max = 1

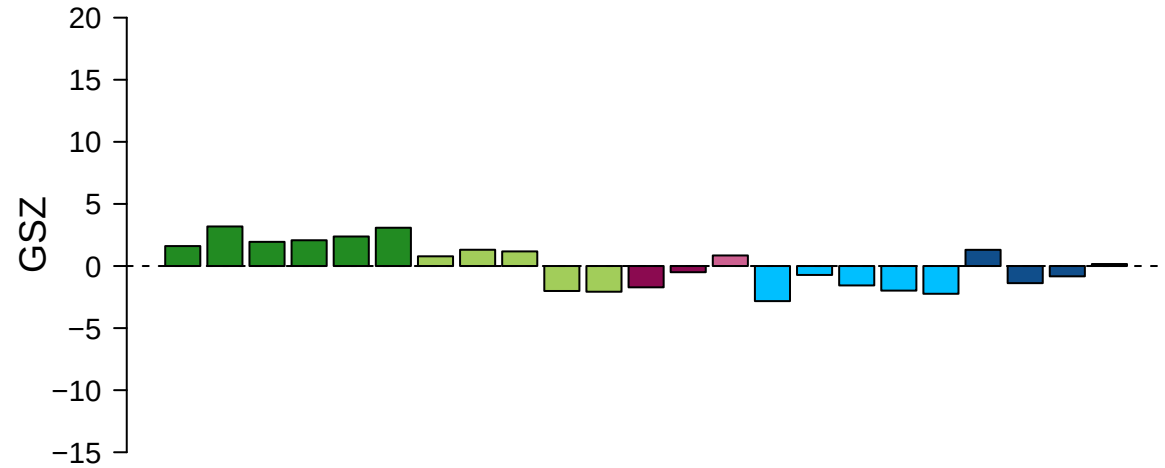
regulatory region DNA binding

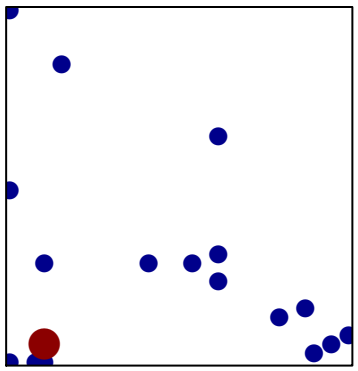




features = 15 , max = 2

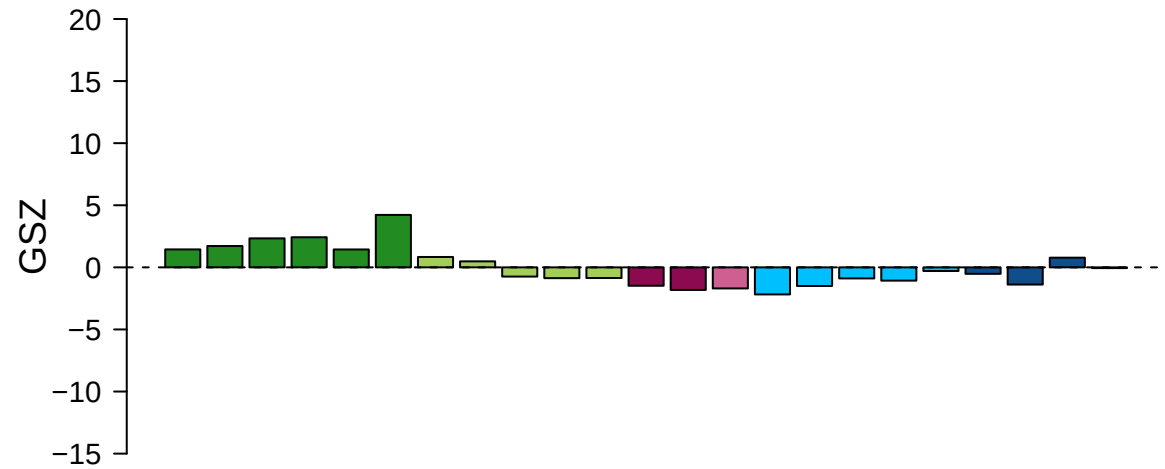
BIOCARTA_NKCELLS_PATHWAY

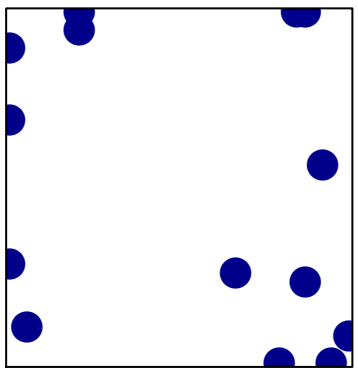




features = 19 , max = 2

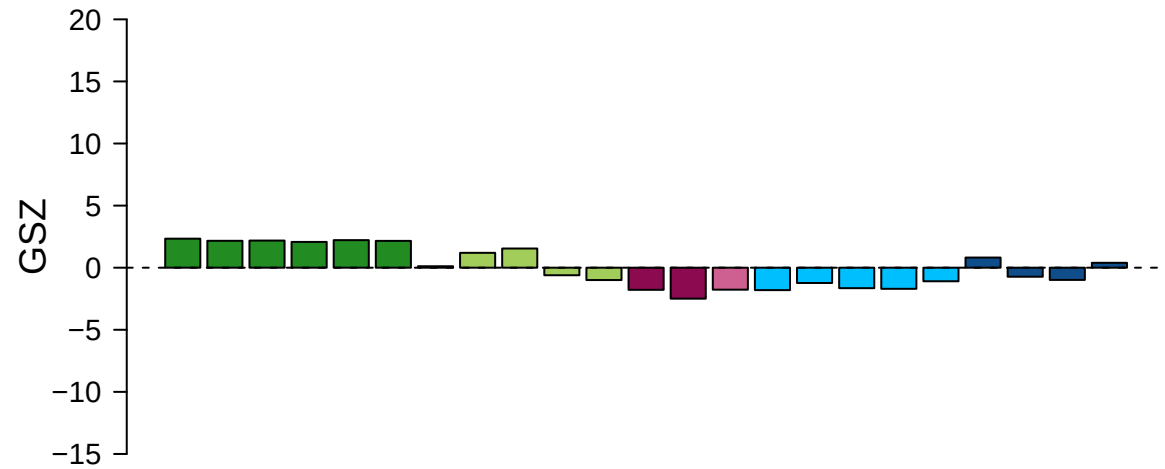
ACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TF

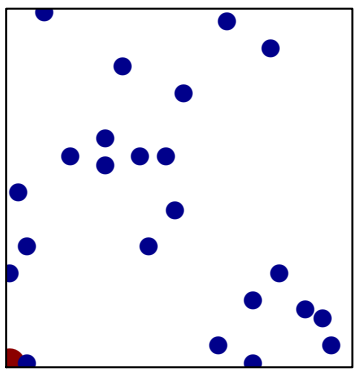




features = 14 , max = 1

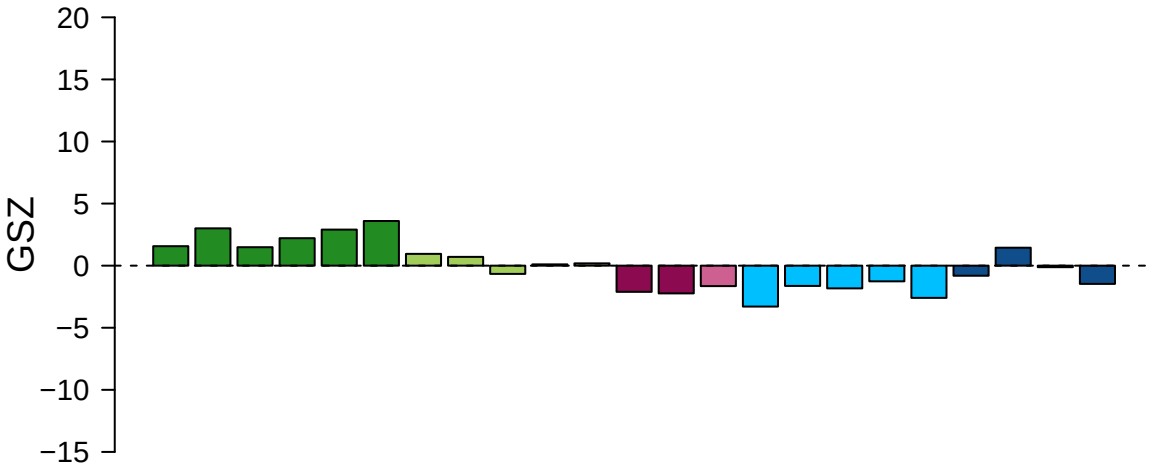
GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP

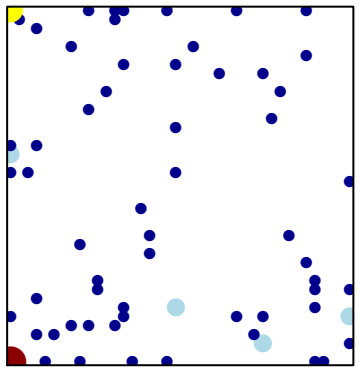




features = 25 , max = 2

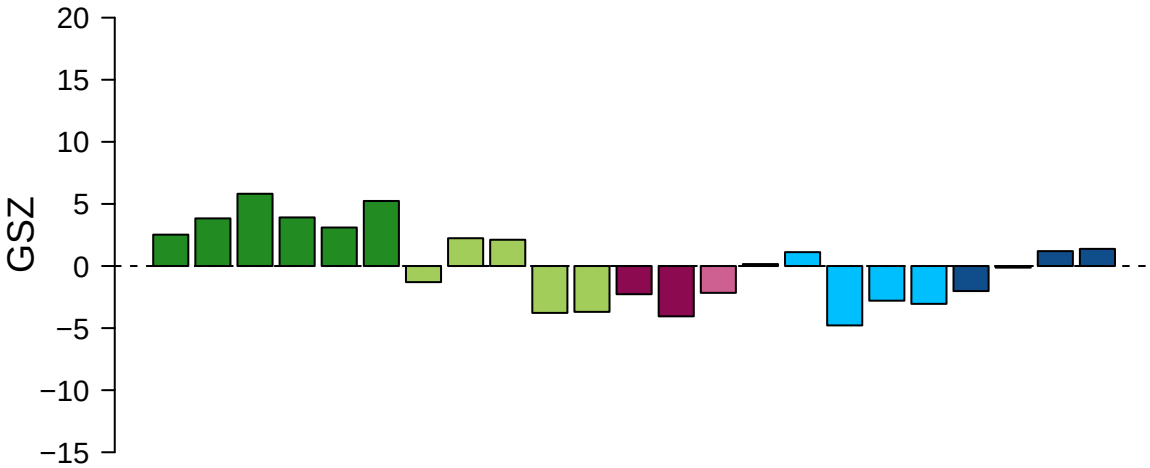
BOYLAN_MULTIPLE_MYELOMA_D_DN

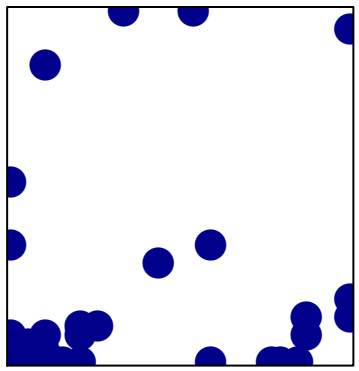




features = 73 , max = 4

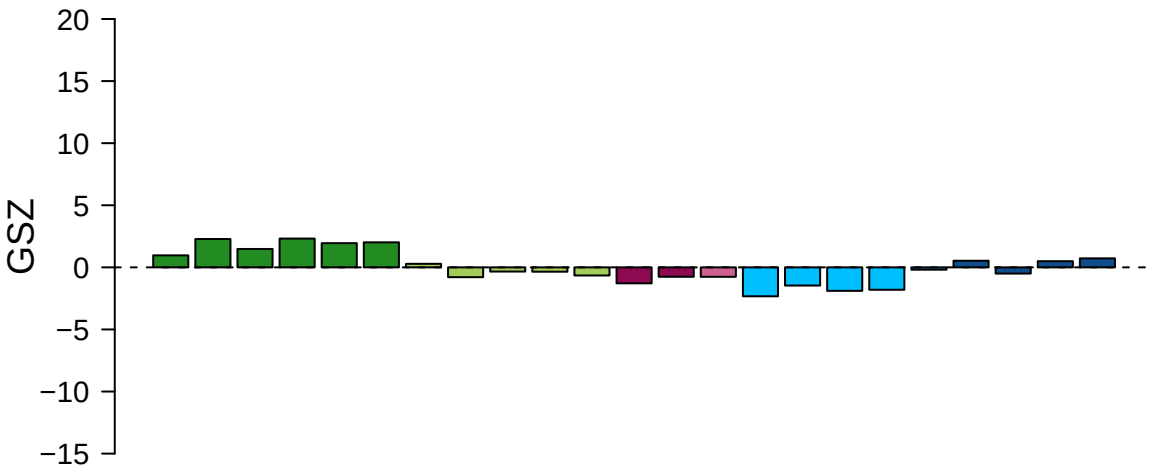
PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION

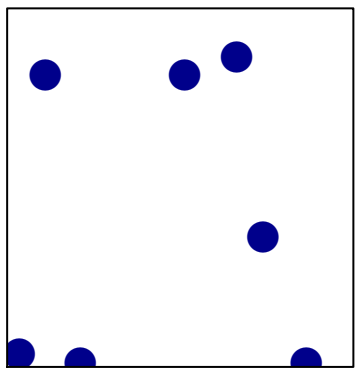




features = 29 , max = 1

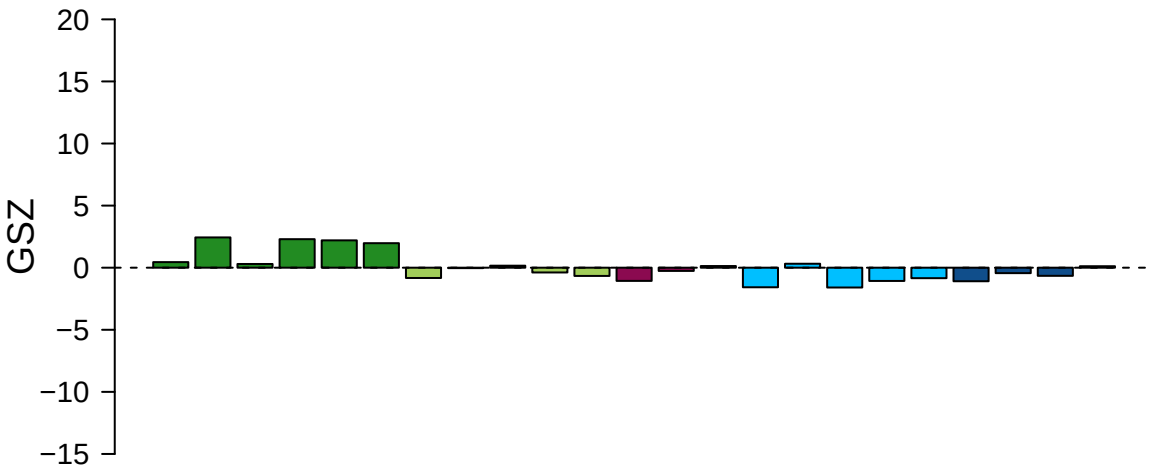
YAMANAKA_GLIOBLASTOMA_SURVIVAL_DN

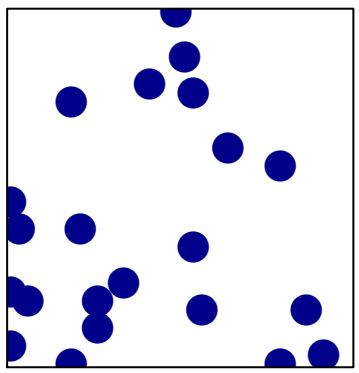




features = 7 , max = 1

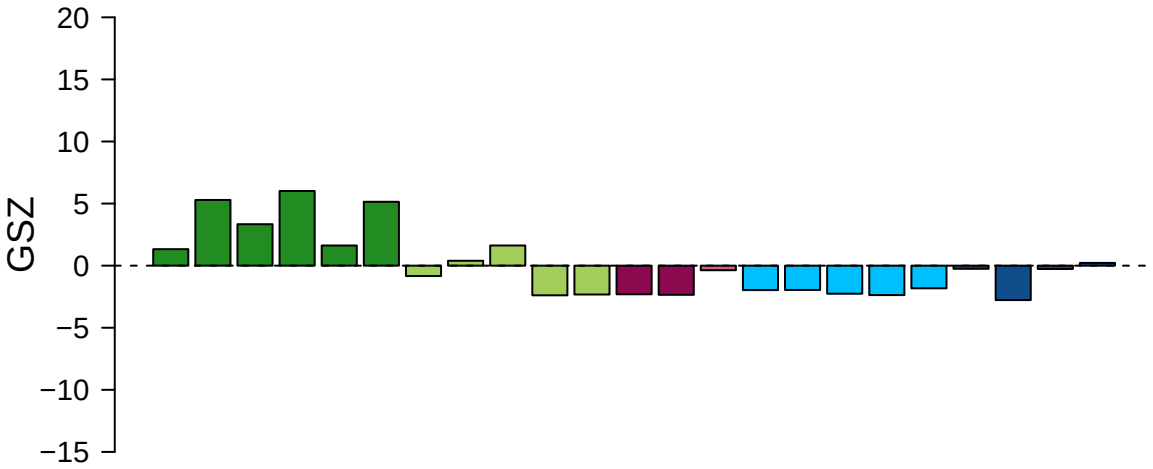
NAD+ ADP−ribosyltransferase activity

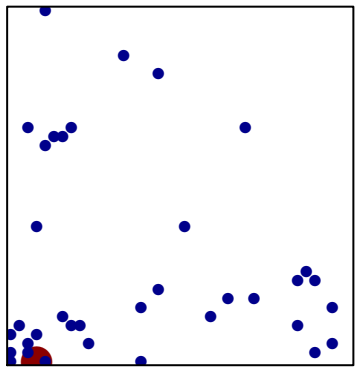




features = 22 , max = 1

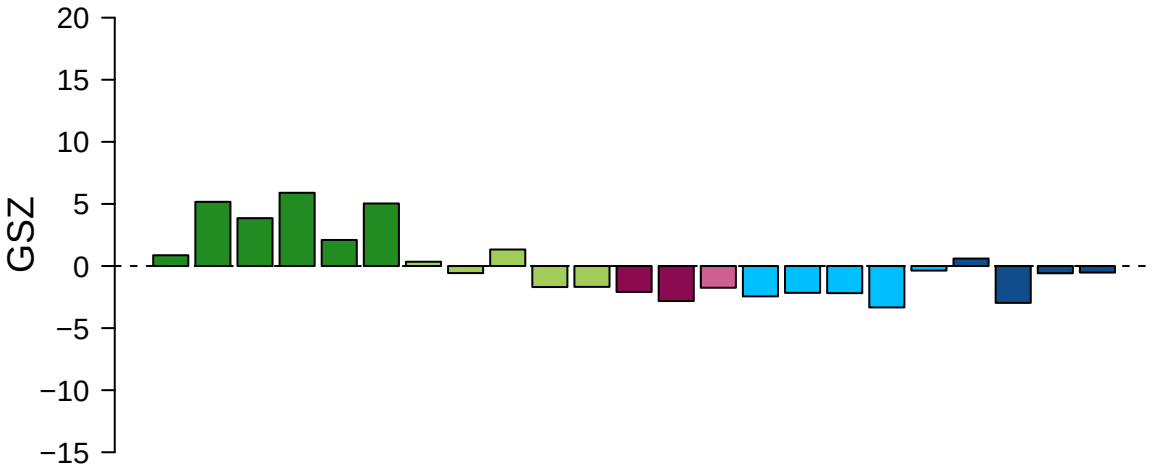
peptidyl−tyrosine autophosphorylation

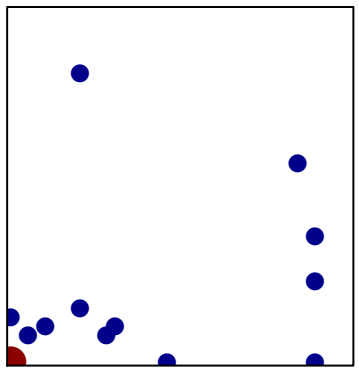




features = 40 , max = 4

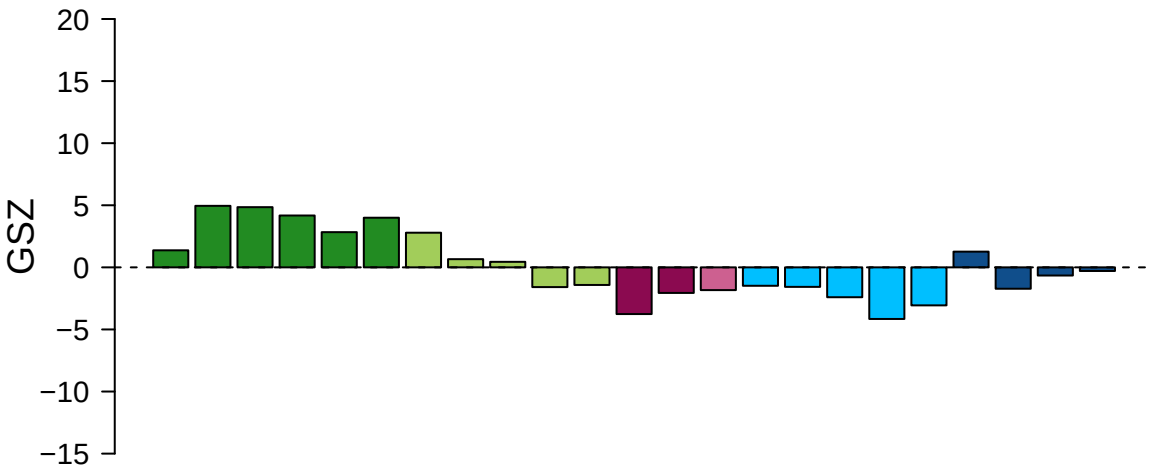
GENTLES_modul12

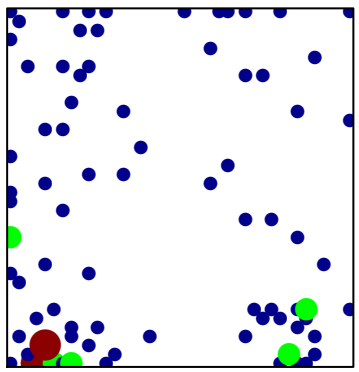




features = 14 , max = 2

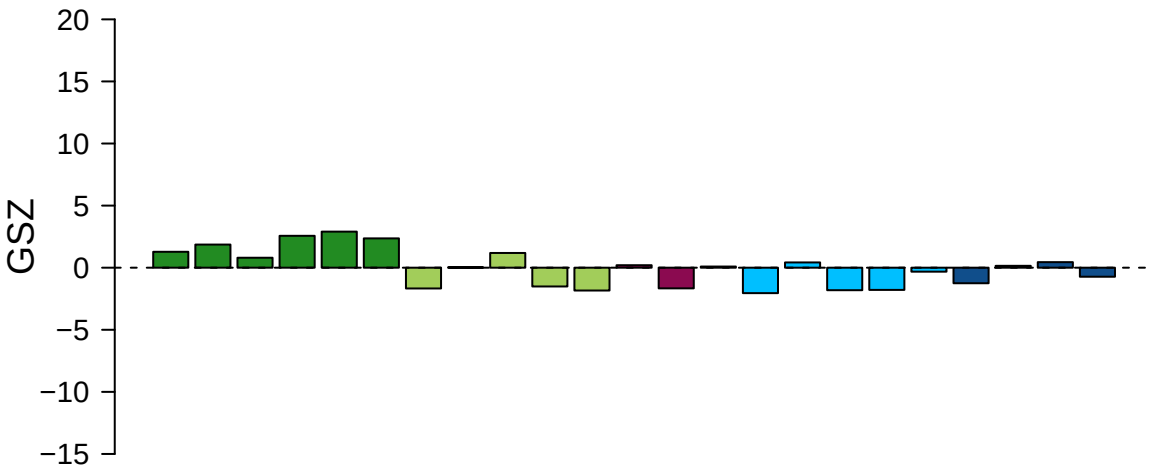
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS

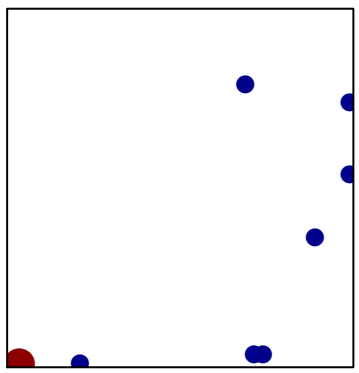




features = 90 , max = 3

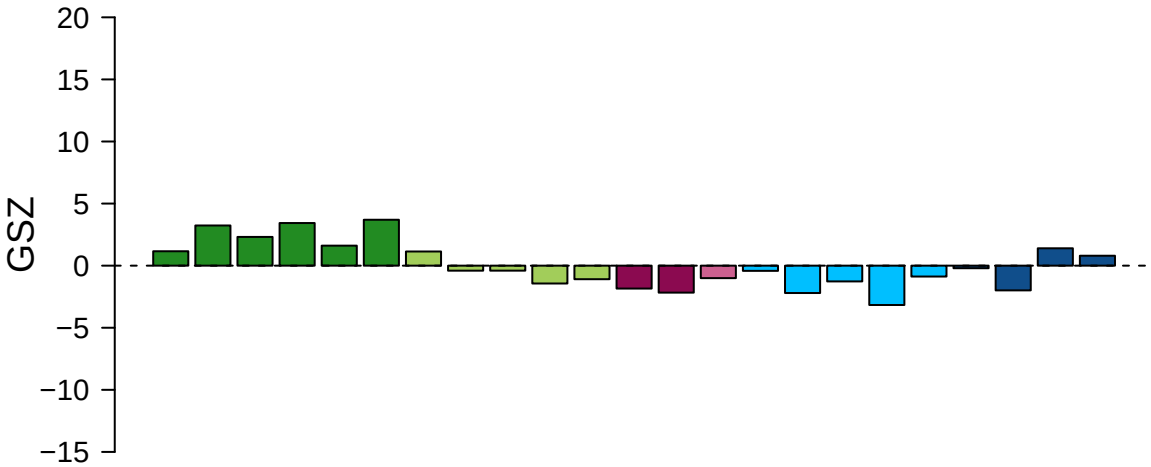
BIOCARTA_SODD_PATHWAY

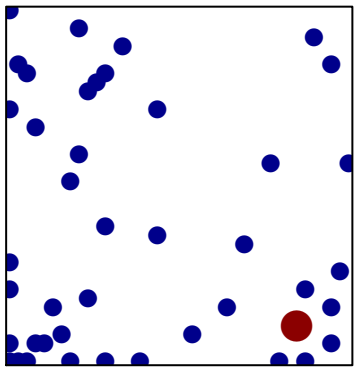




features = 9 , max = 2

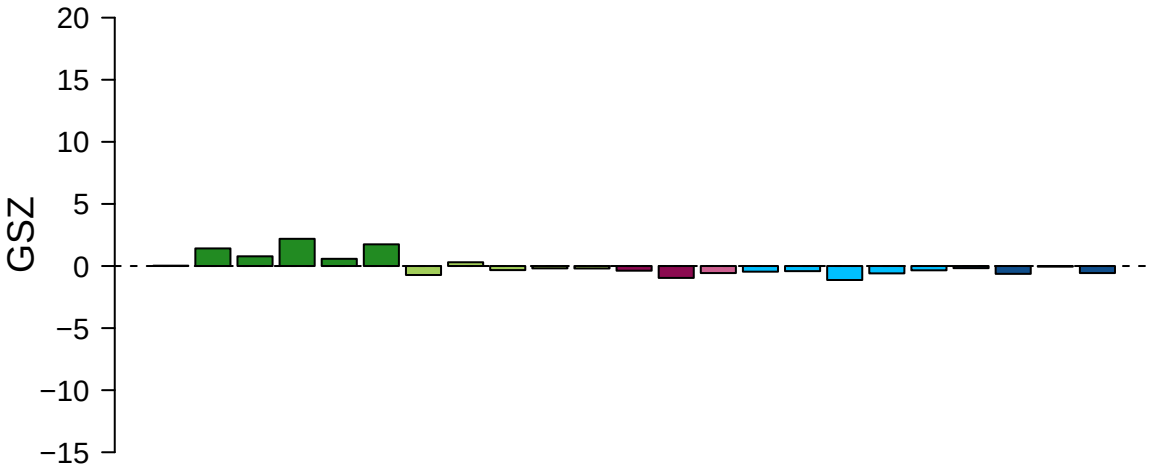
PID_RHOA_REG_PATHWAY

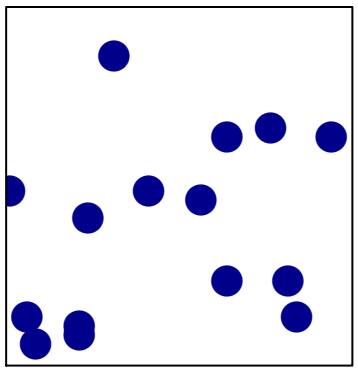




features = 44 , max = 2

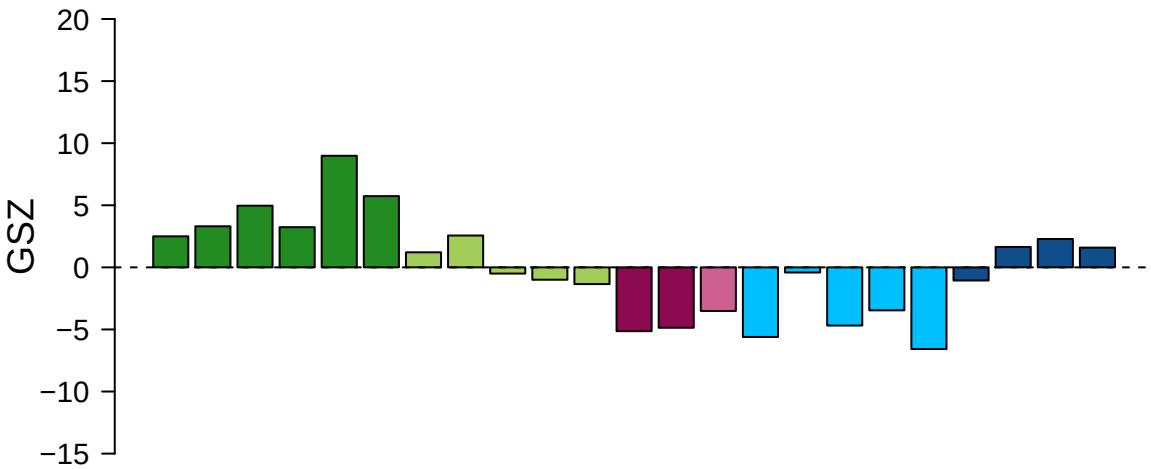
REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS

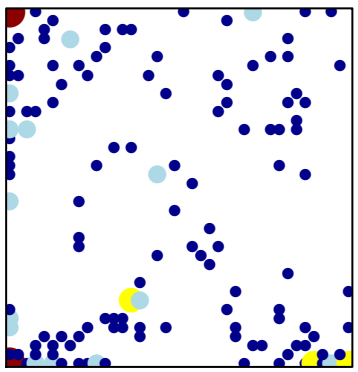




features = 15 , max = 1

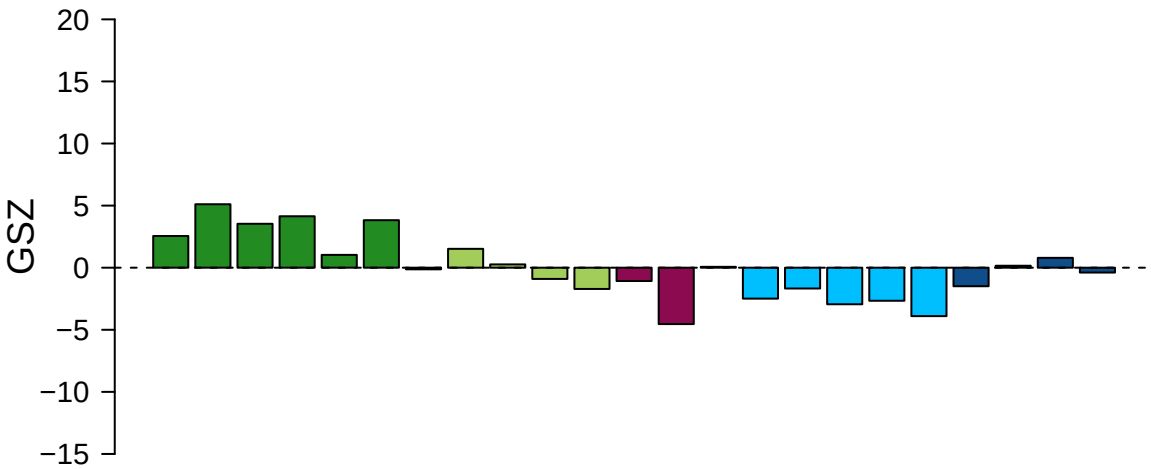
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP

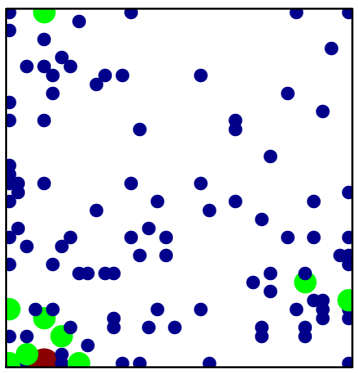




features = 160 , max = 4

SCHLOSSER_SERUM_RESPONSE_UP





features = 121 , max = 3