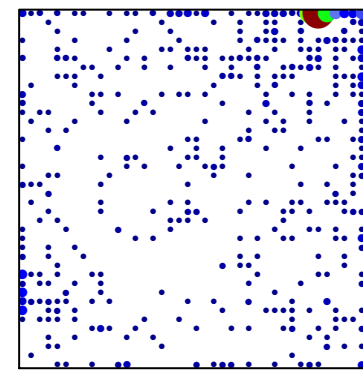
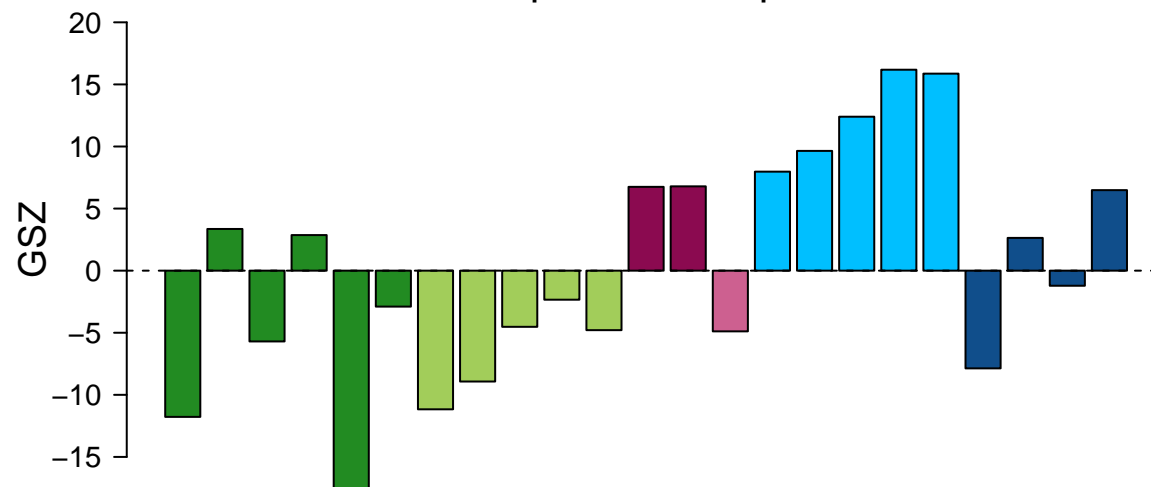
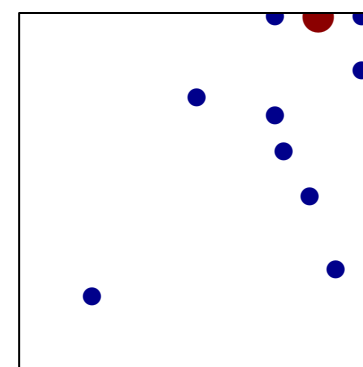
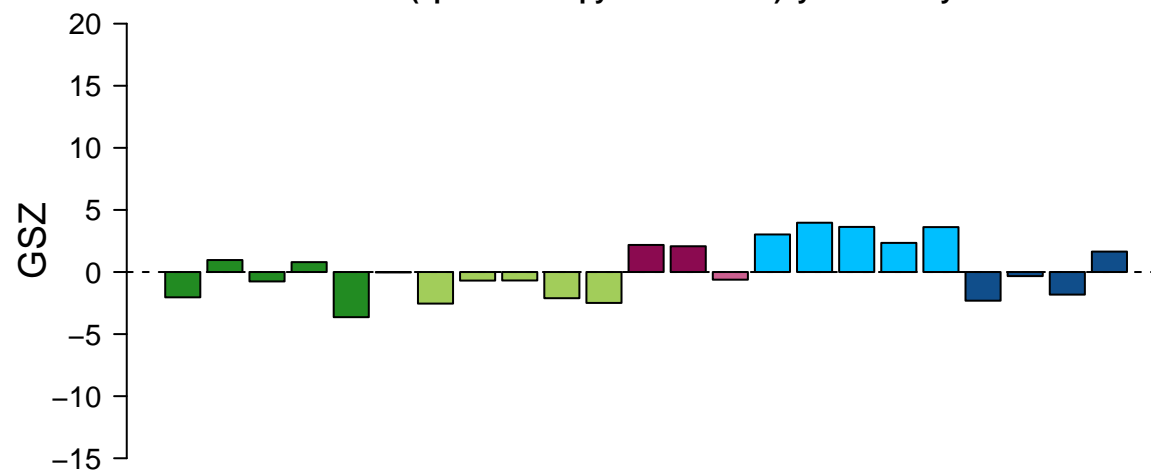


cellular protein metabolic process



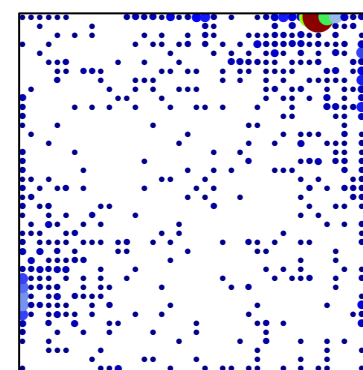
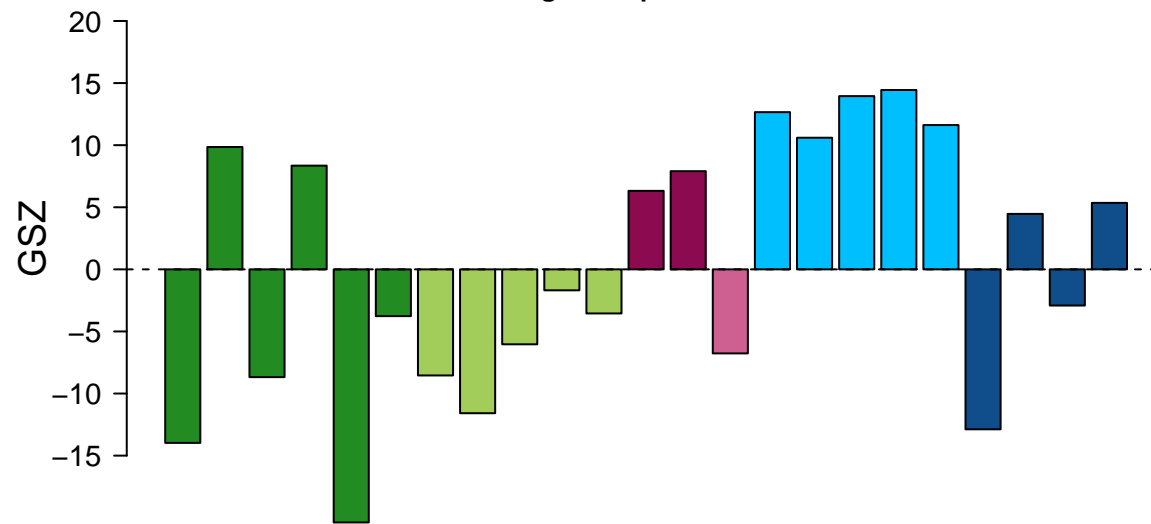
features = 633 , max = 32

DNA-(apurinic or apyrimidinic site) lyase activity



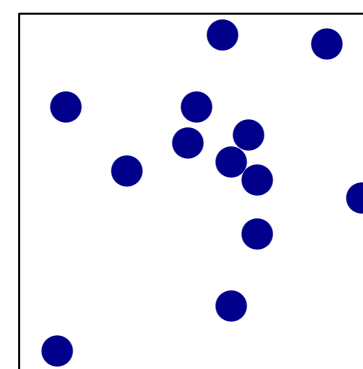
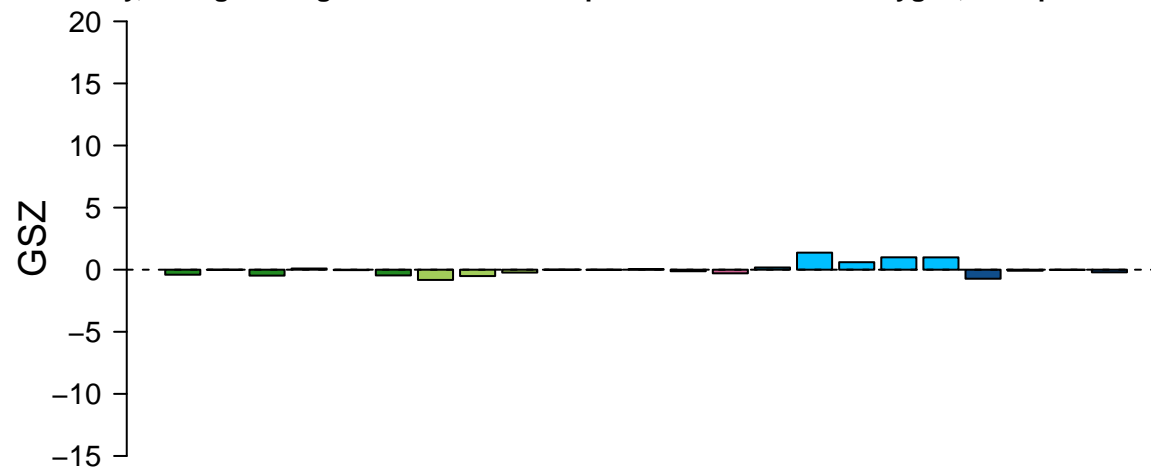
features = 11 , max = 2

gene expression



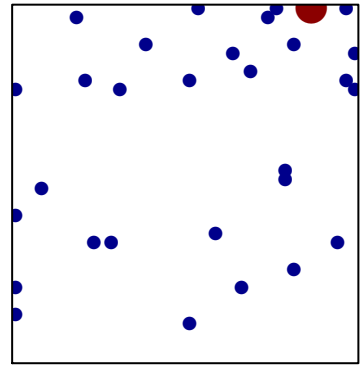
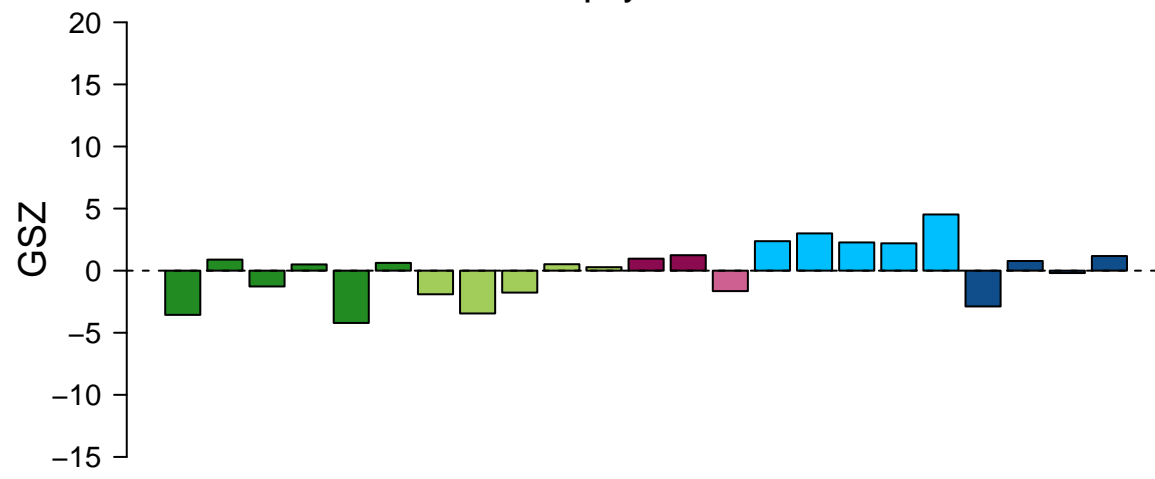
features = 820 , max = 33

ase activity, acting on single donors with incorporation of molecular oxygen, incorporation of t



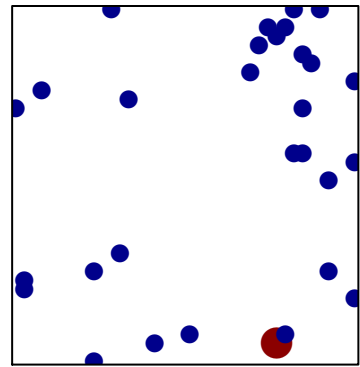
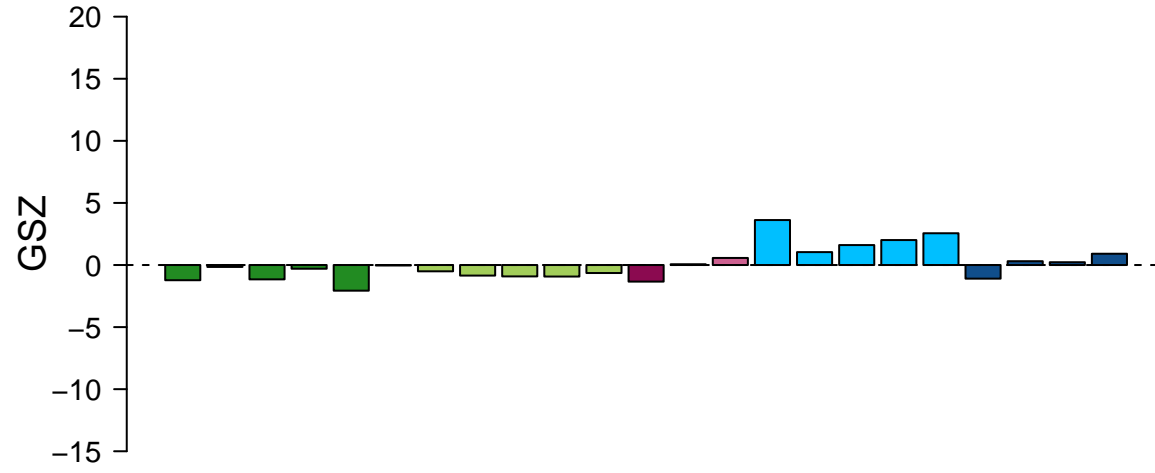
features = 13 , max = 1

polysome



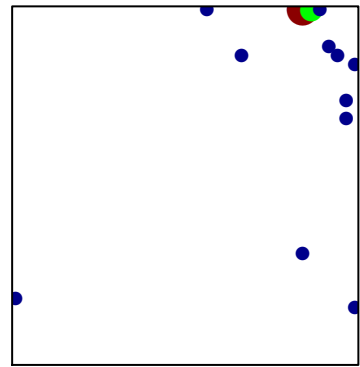
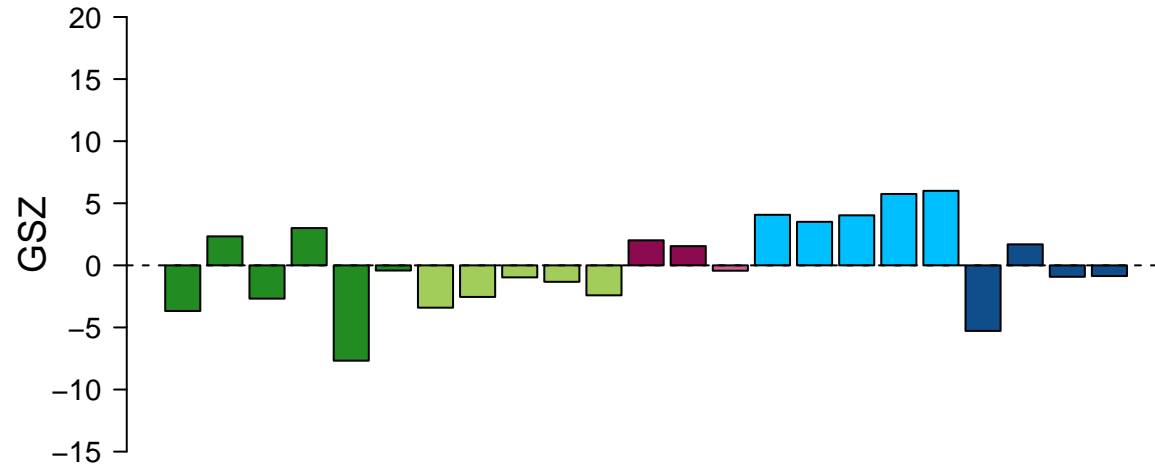
features = 32 , max = 3

regulation of mitophagy



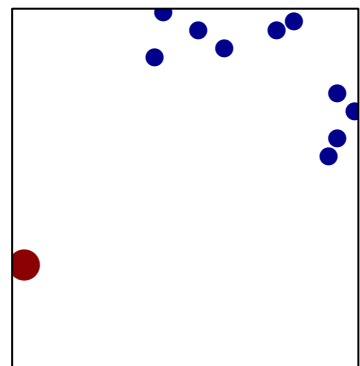
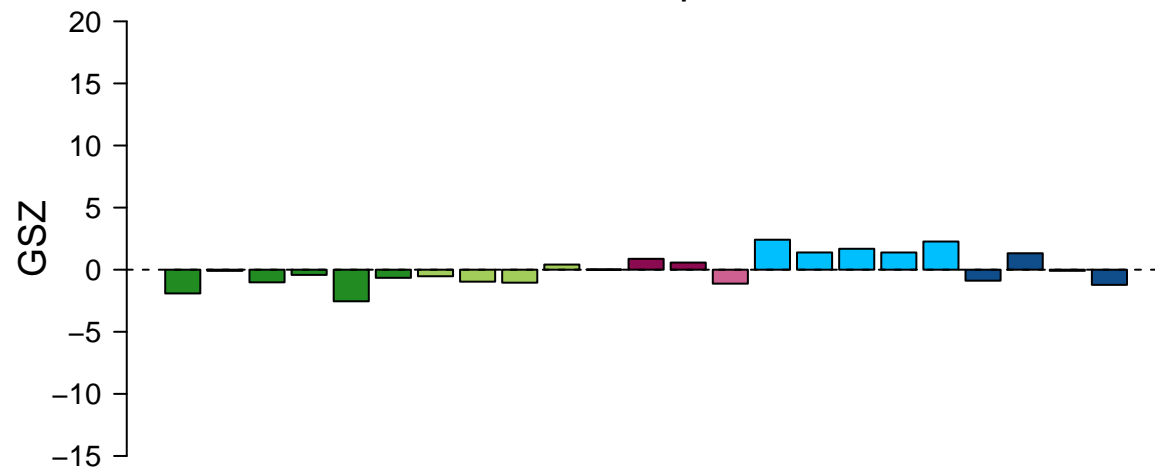
features = 31 , max = 2

ribosomal large subunit biogenesis



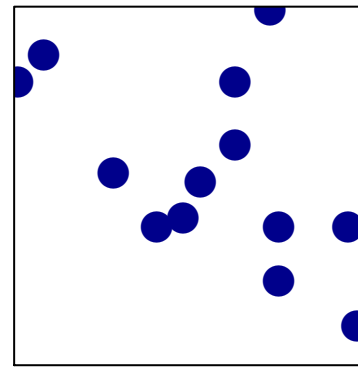
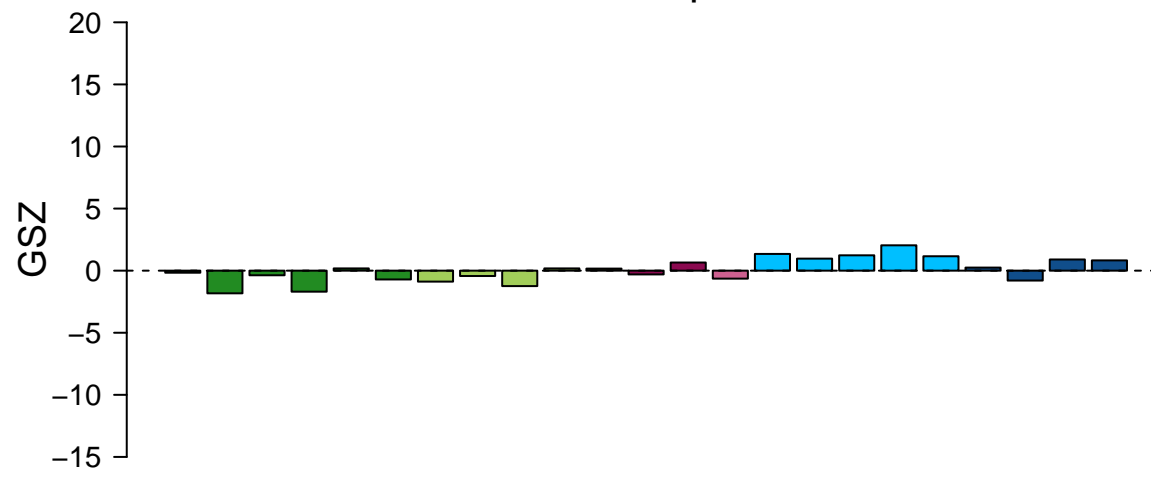
features = 17 , max = 3

SMN complex



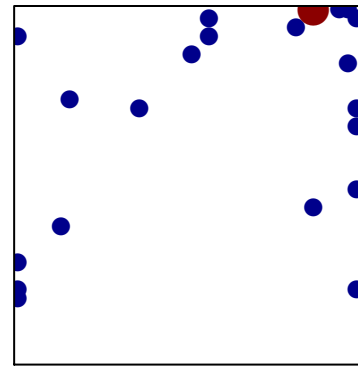
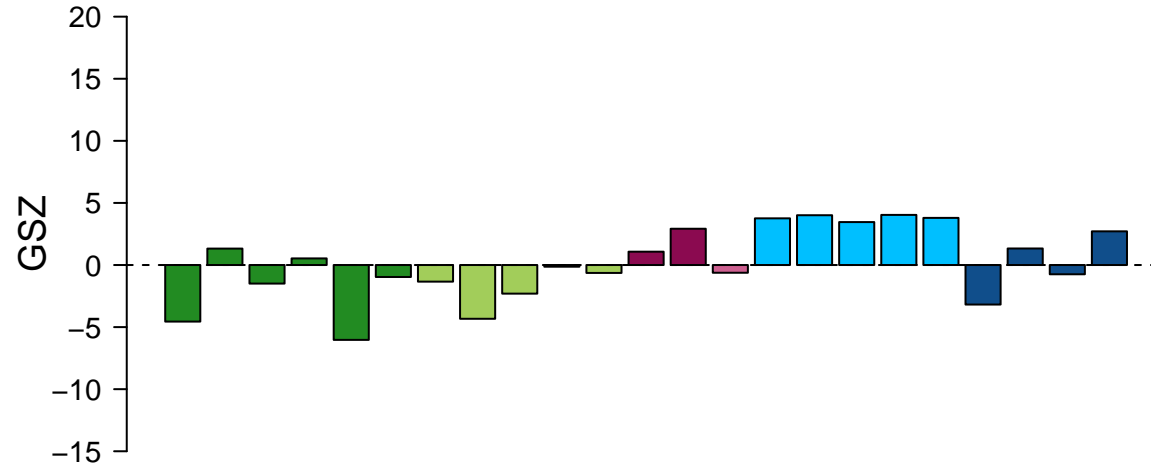
features = 12 , max = 2

tissue development



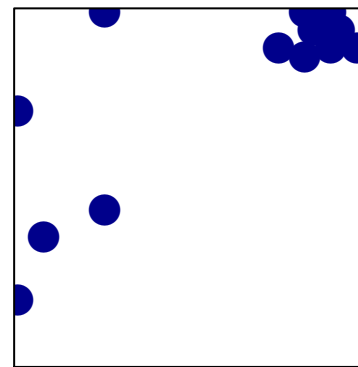
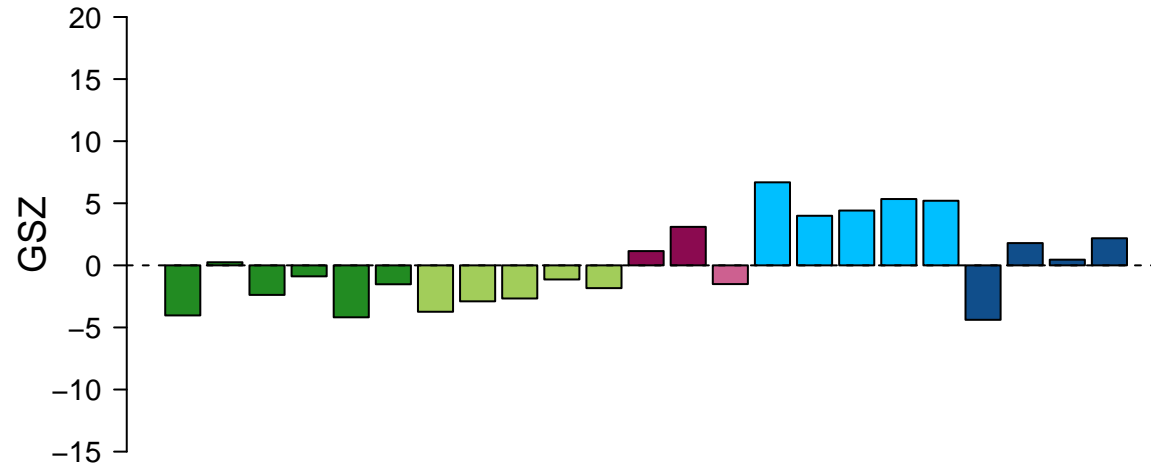
features = 13 , max = 1

translation elongation factor activity



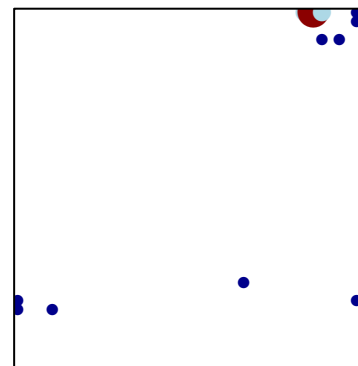
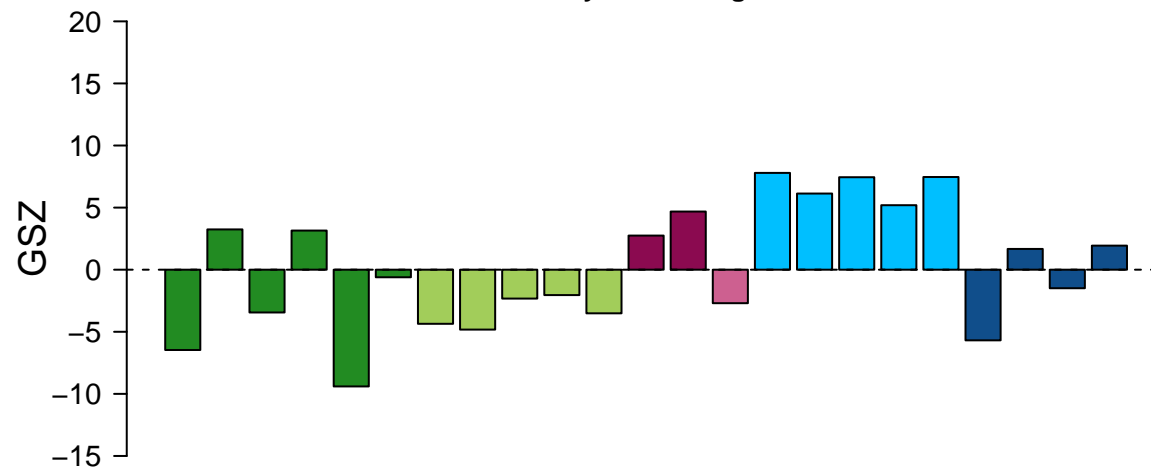
features = 22 , max = 2

BENTINK_myc.1



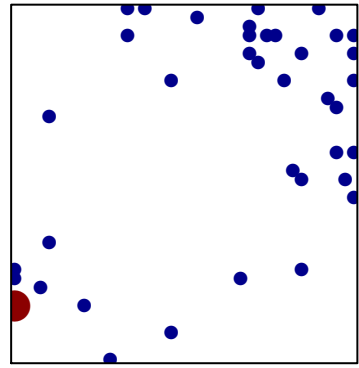
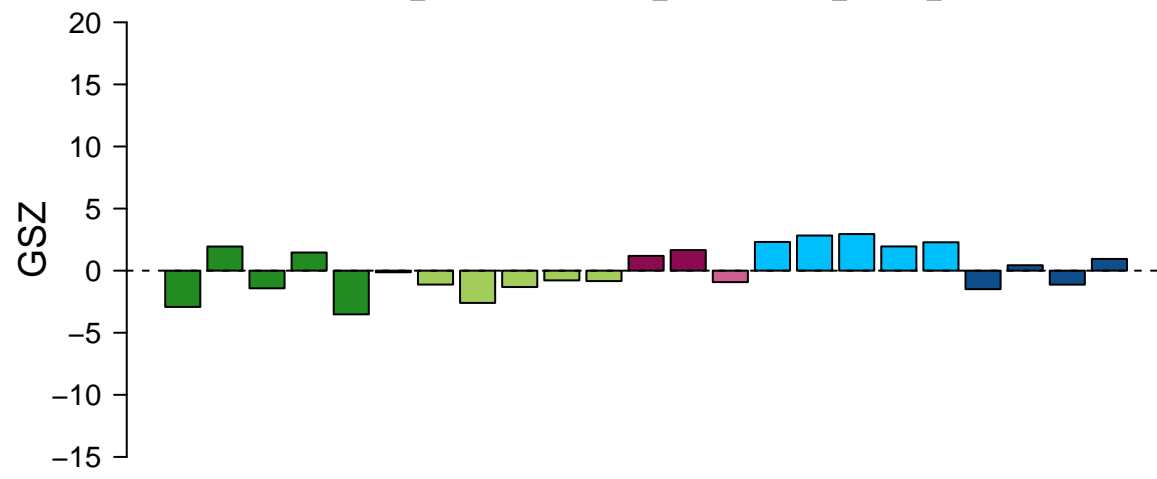
features = 14 , max = 1

MYC_Protein synthesis degradation UP



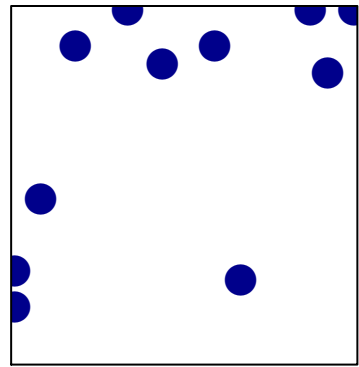
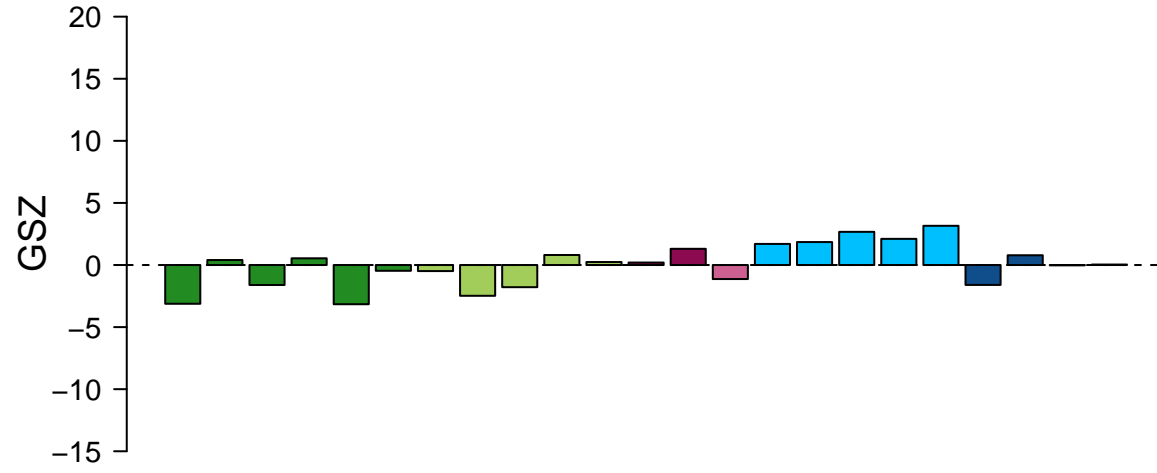
features = 17 , max = 4

REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY



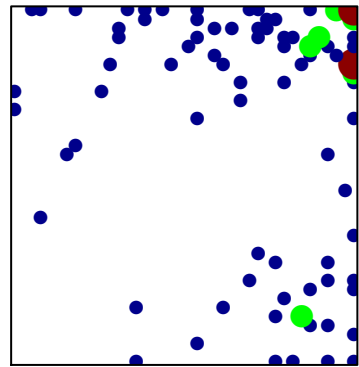
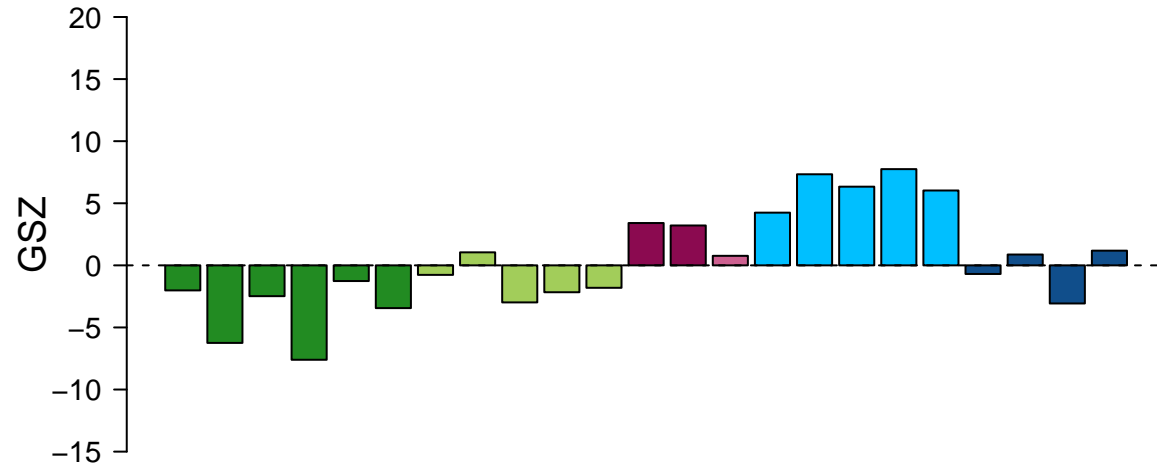
features = 40 , max = 3

REACTOME_MTORC1_MEDIATED_SIGNALLING



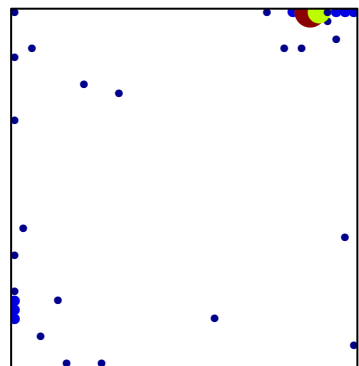
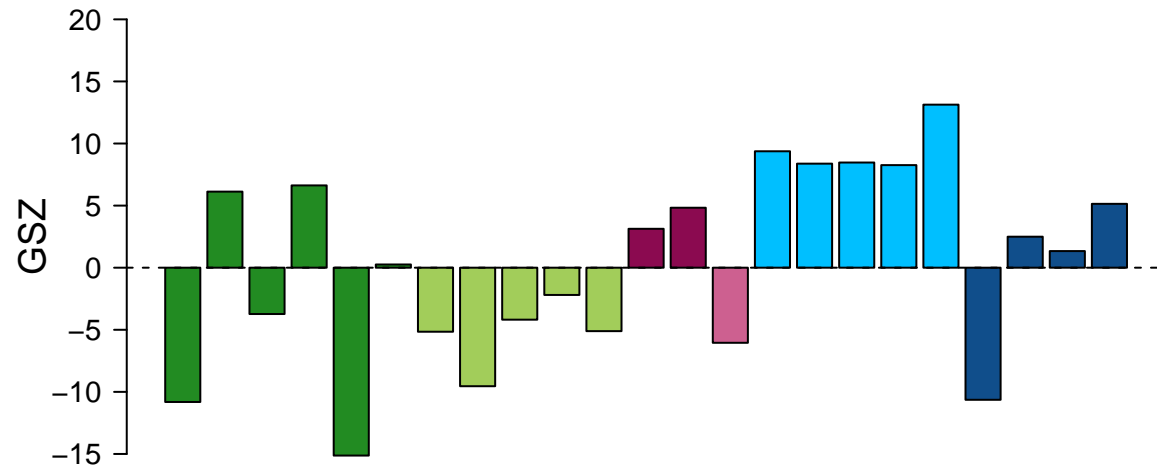
features = 11 , max = 1

WINTER_HYPOXIA_UP



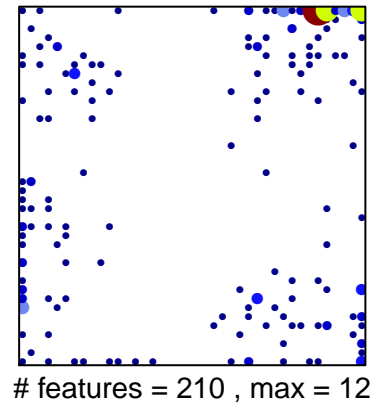
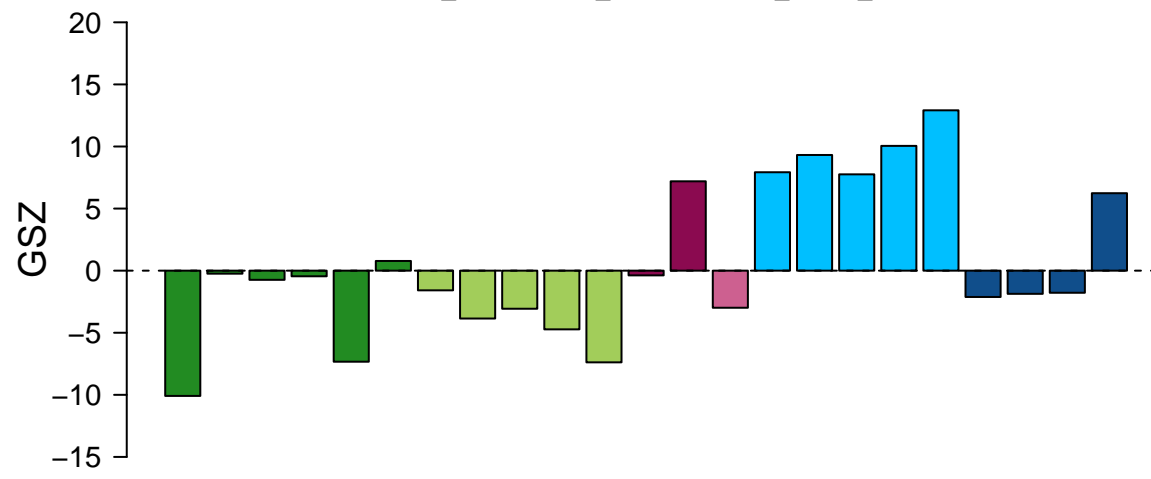
features = 90 , max = 3

TIEN_INTESTINE_PROBIOTICS_6HR_UP

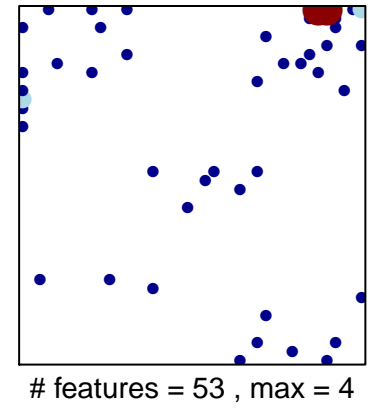
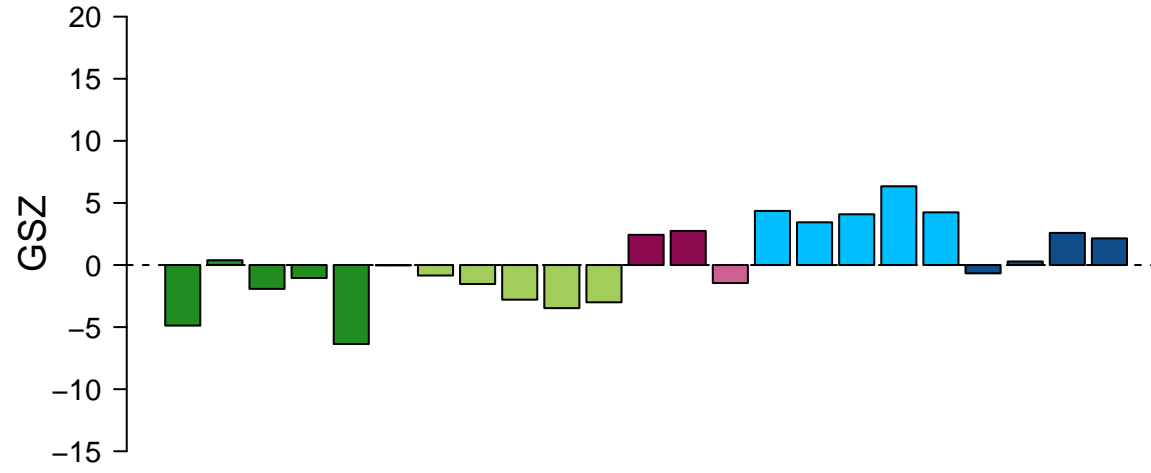


features = 54 , max = 9

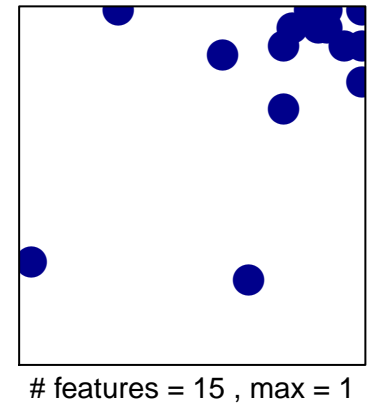
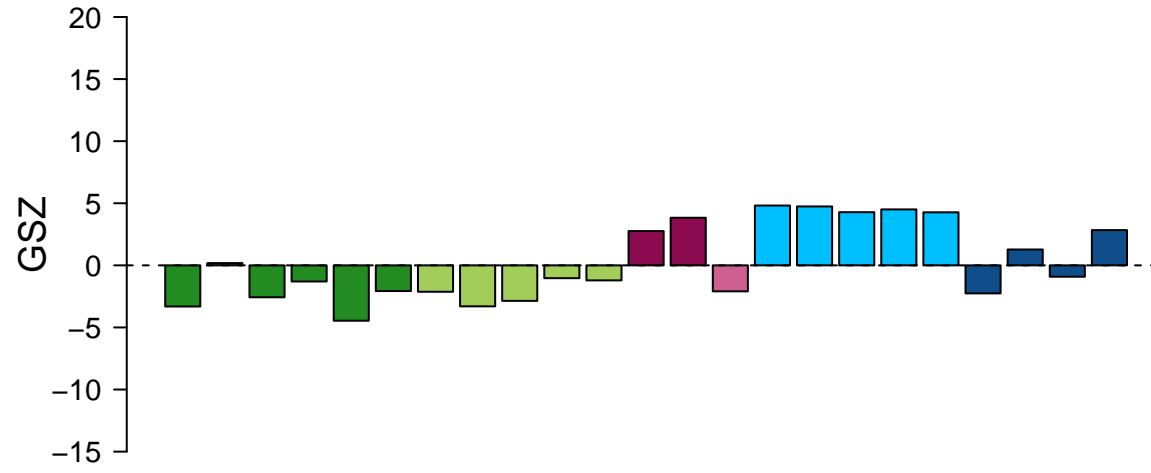
TIEN_INTESTINE_PROBIOTICS_24HR_DN



LEE_LIVER_CANCER_MYC_UP



XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN



MODY_HIPPOCAMPUS_PRENATAL

