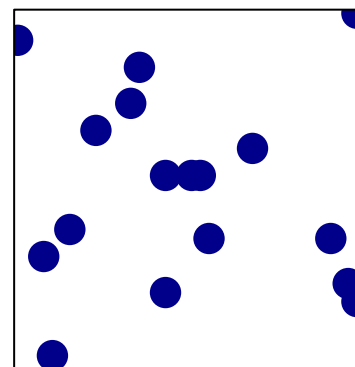
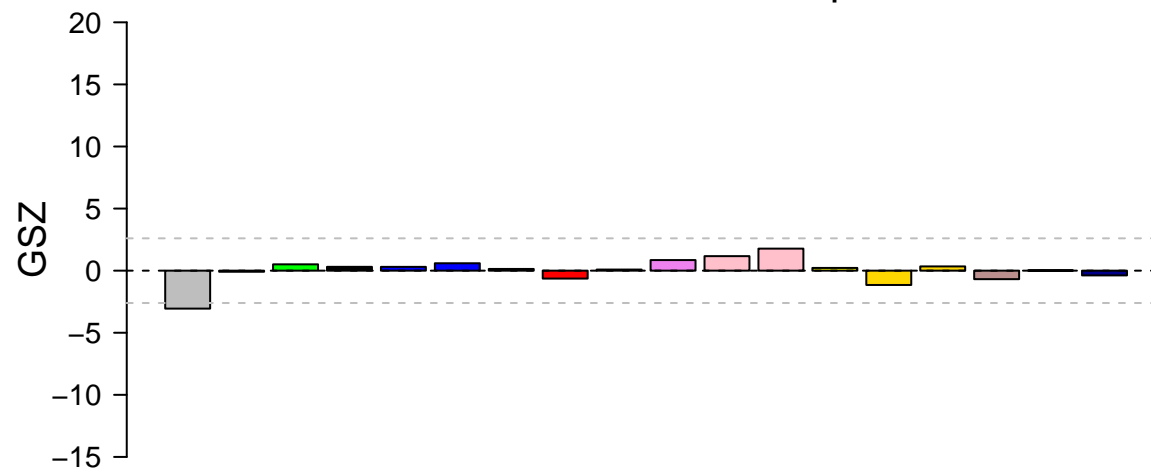
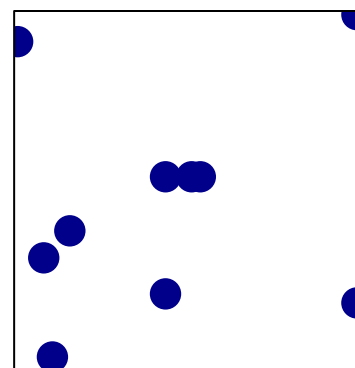
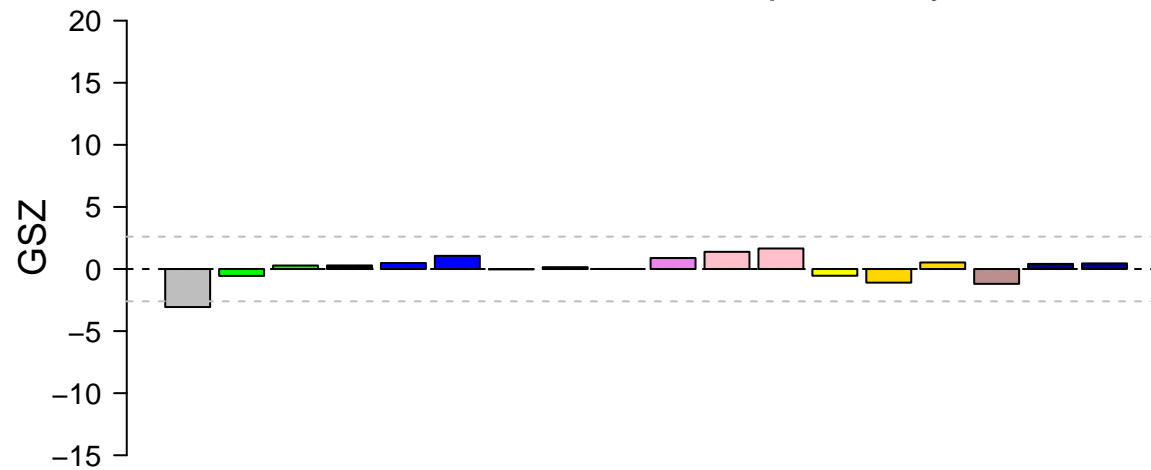


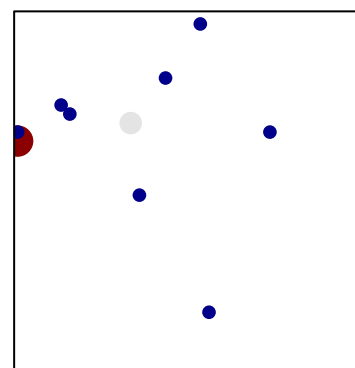
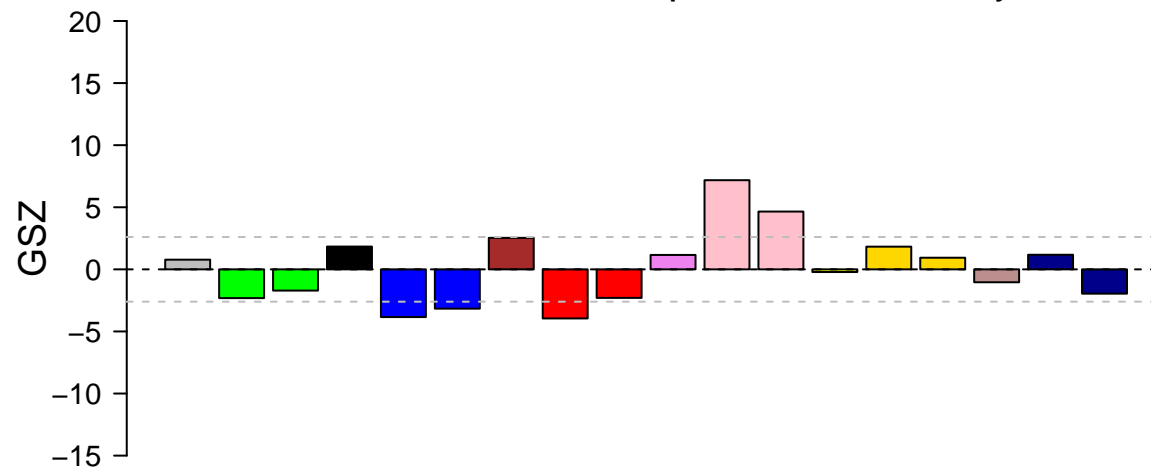
ammonium transmembrane transport



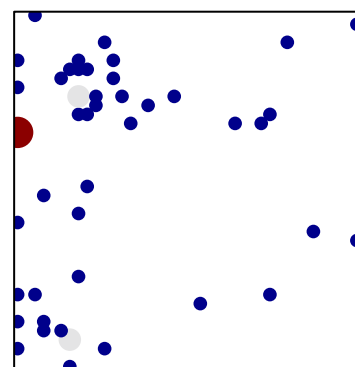
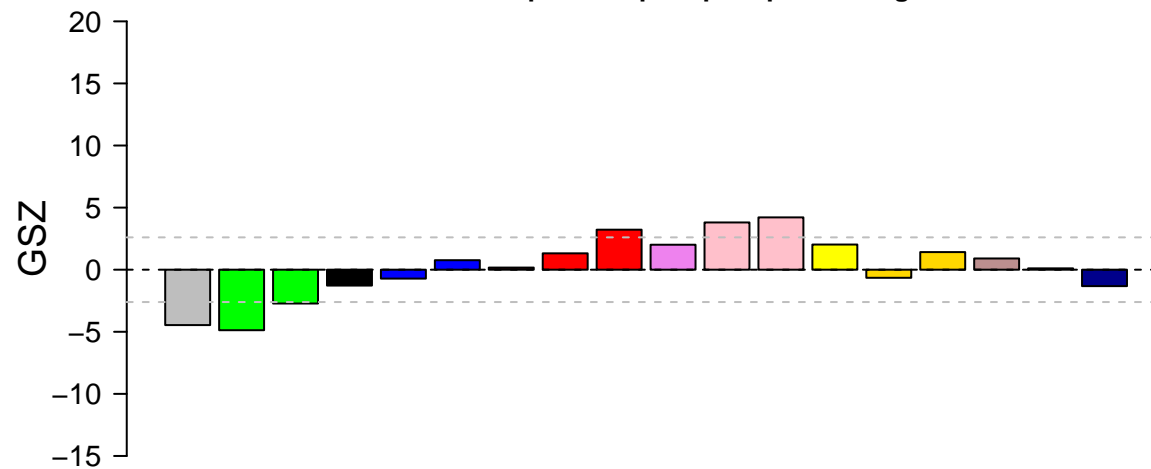
ammonium transmembrane transporter activity



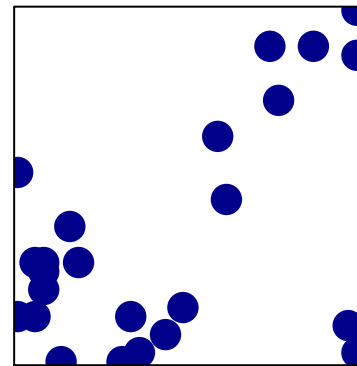
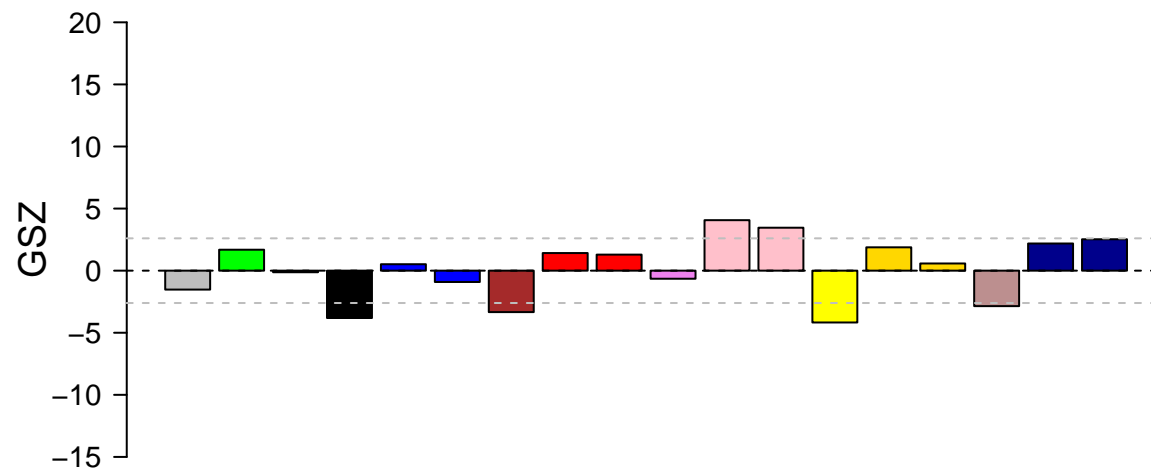
ATP-activated inward rectifier potassium channel activity



calcium-dependent phospholipid binding

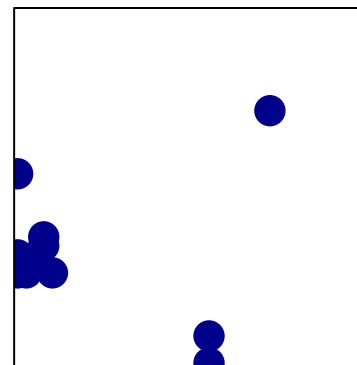
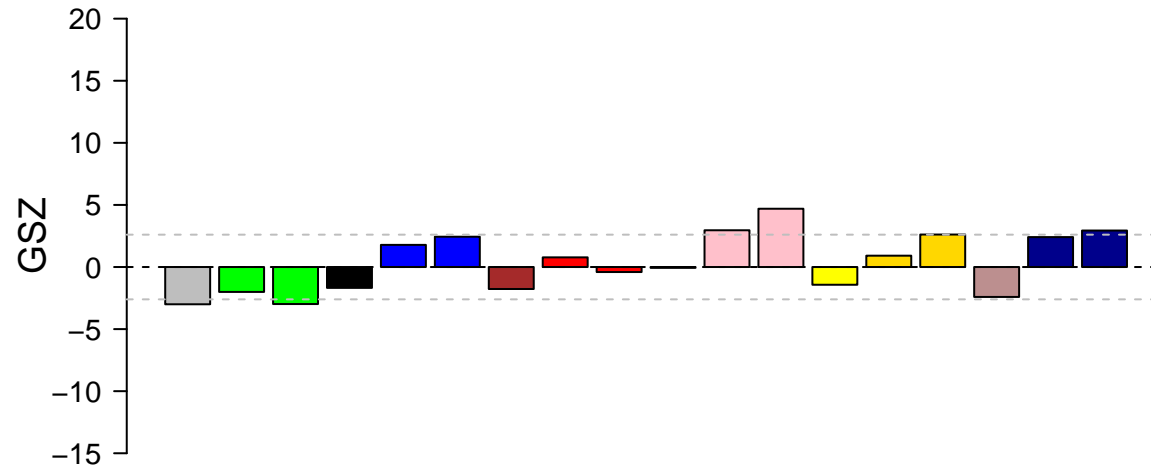


cellular iron ion homeostasis



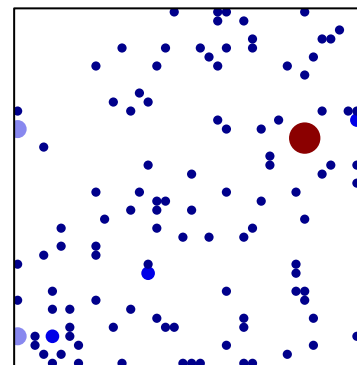
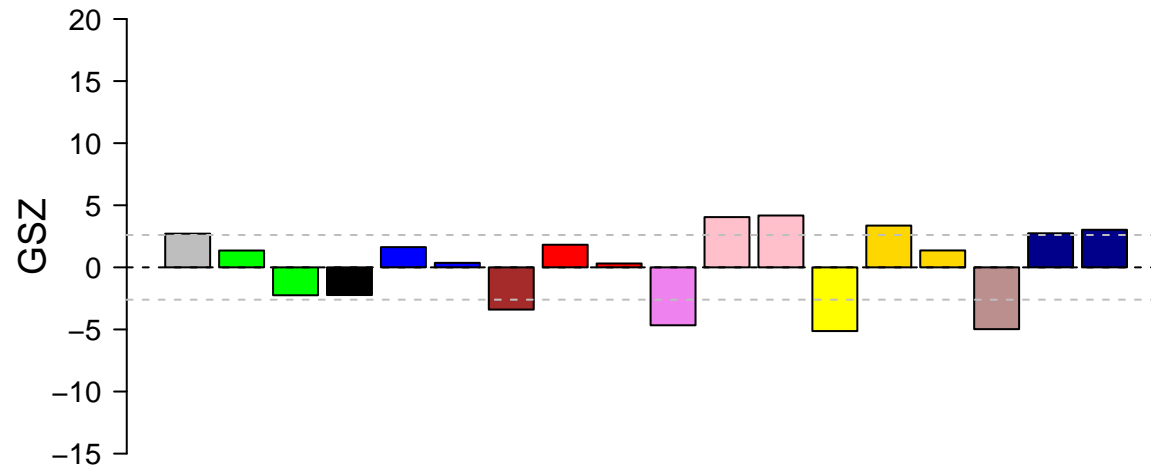
features = 24 , max = 1

cellular response to nitrogen starvation



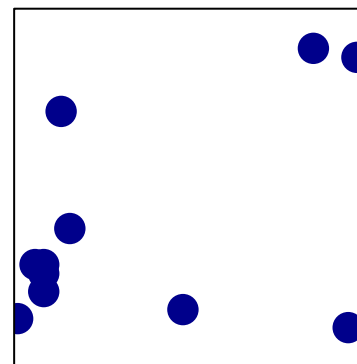
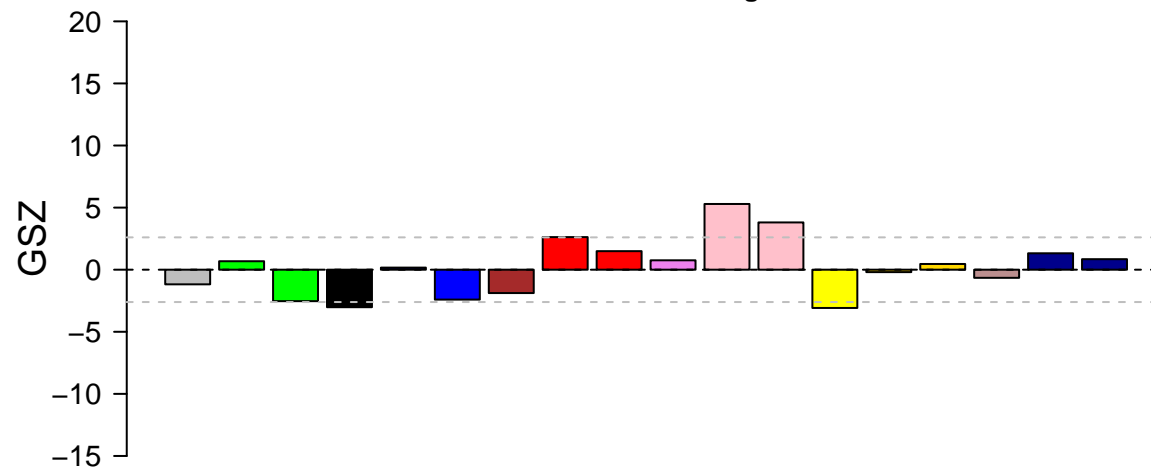
features = 11 , max = 1

cysteine-type peptidase activity



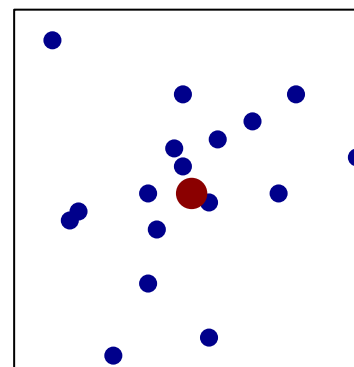
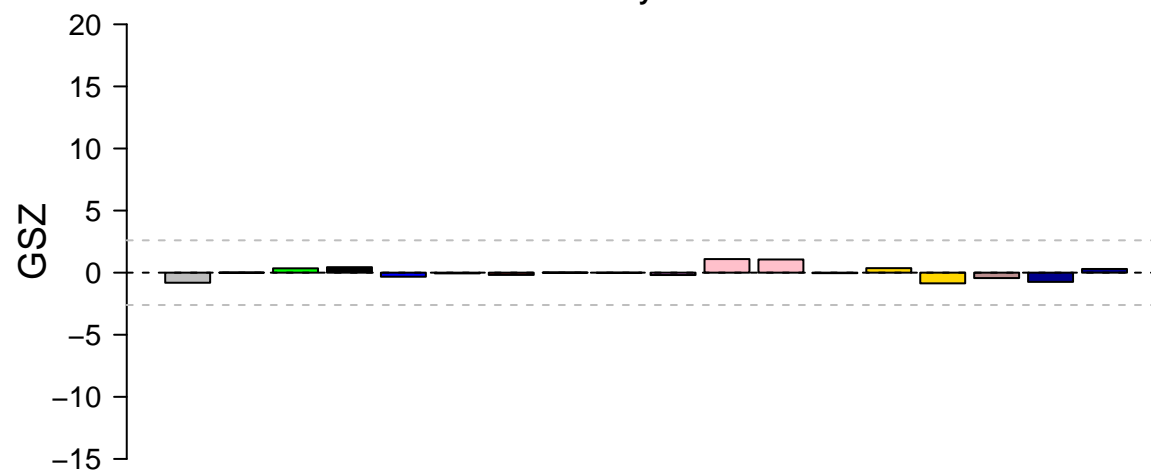
features = 123 , max = 6

ferric iron binding



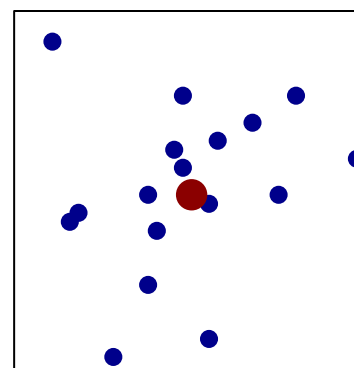
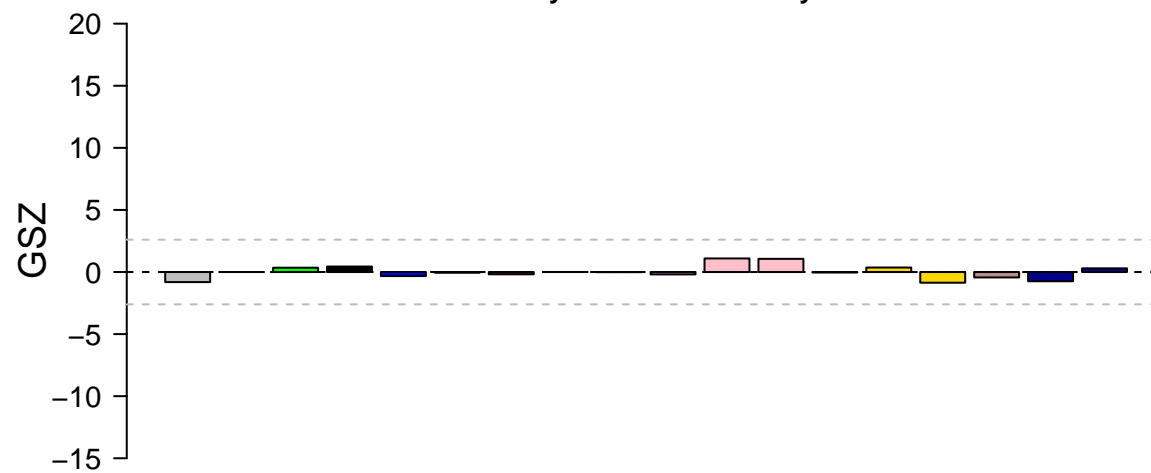
features = 11 , max = 1

fucosylation



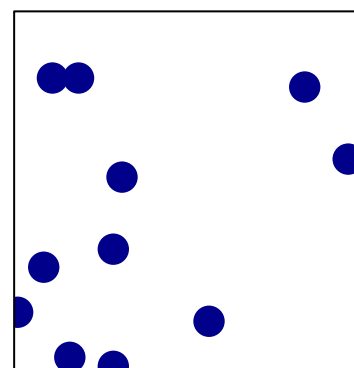
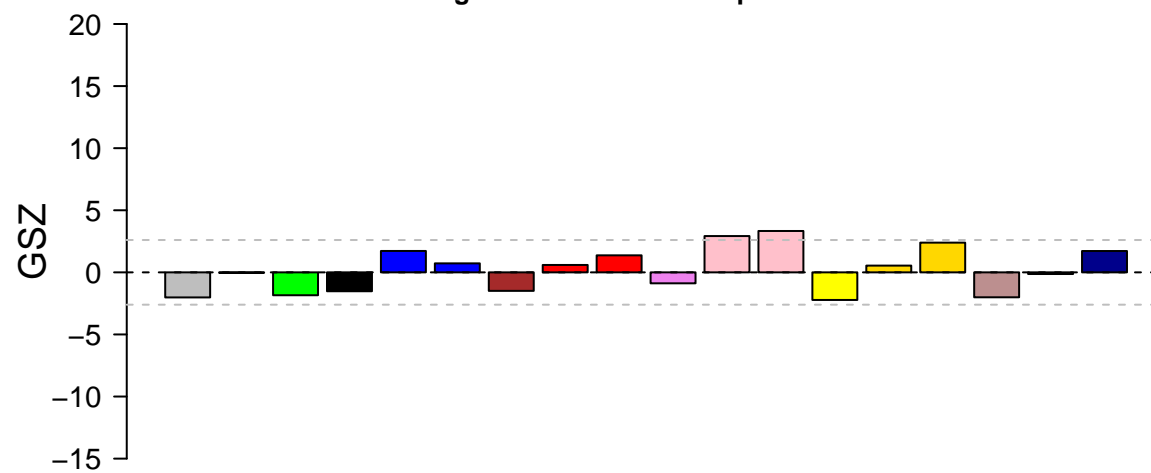
features = 19 , max = 2

fucosyltransferase activity



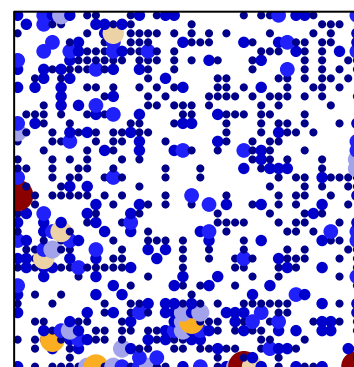
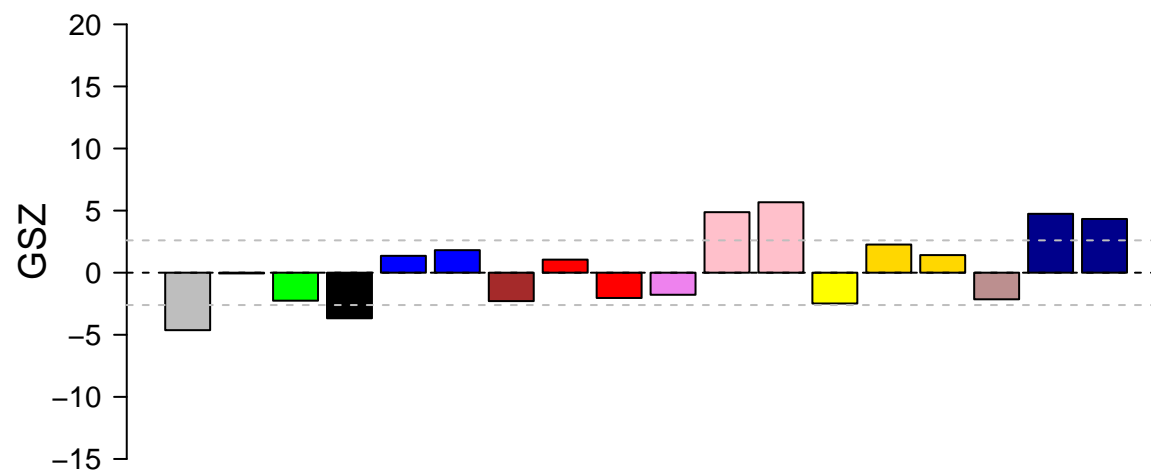
features = 19 , max = 2

glutathione metabolic process



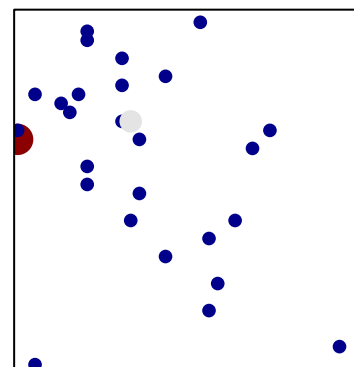
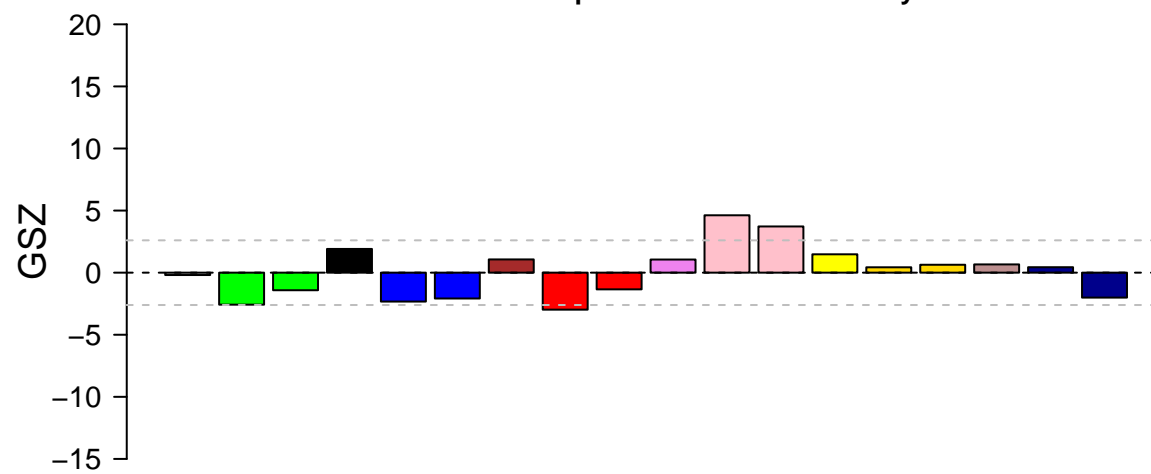
features = 11 , max = 1

intracellular



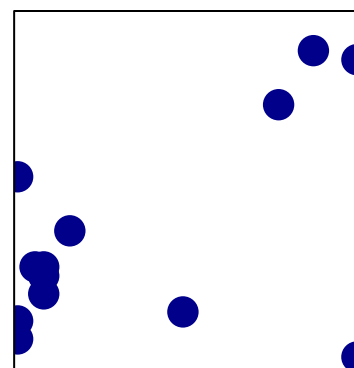
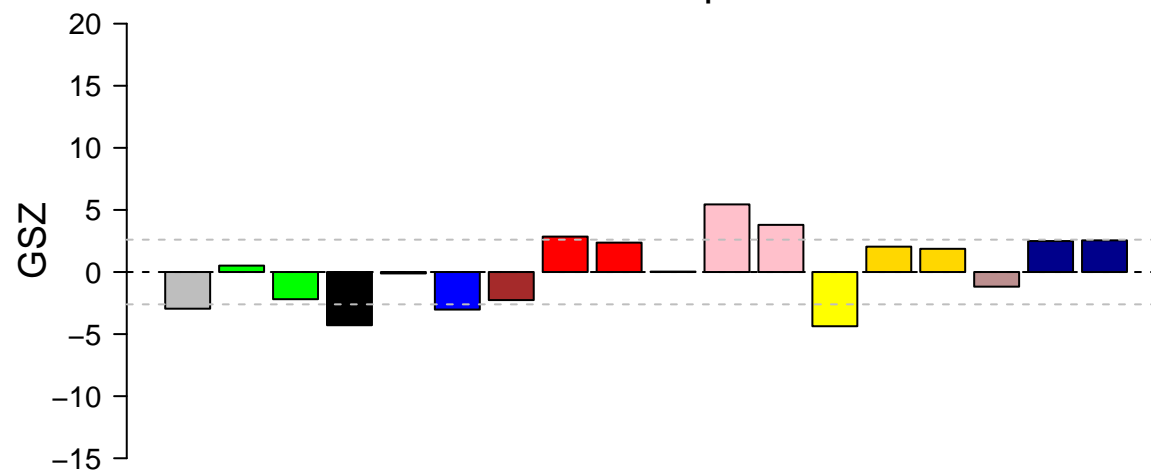
features = 1066 , max = 8

inward rectifier potassium channel activity



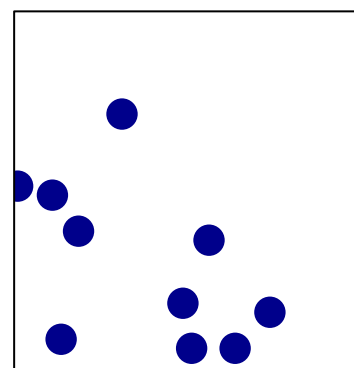
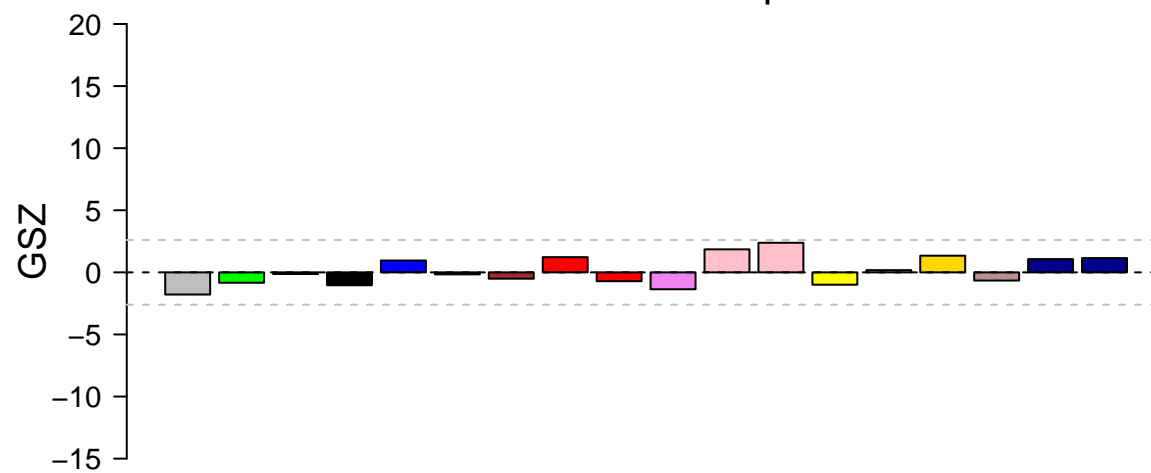
features = 31 , max = 3

iron ion transport



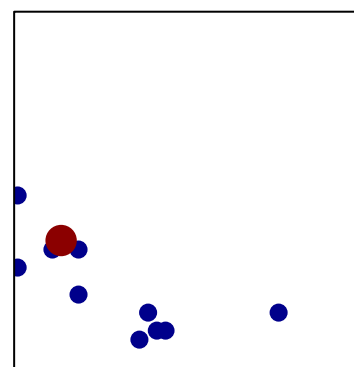
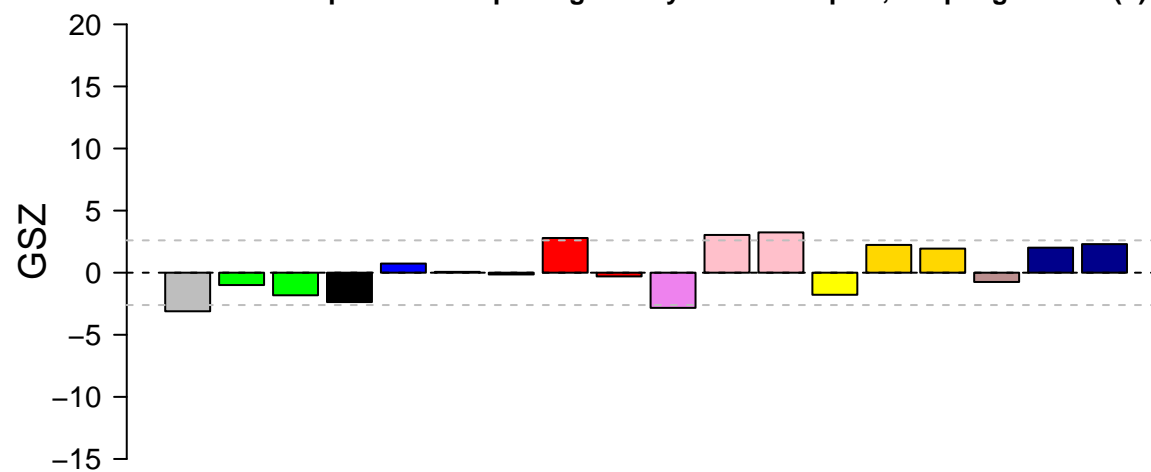
features = 13 , max = 1

mitochondrial envelope



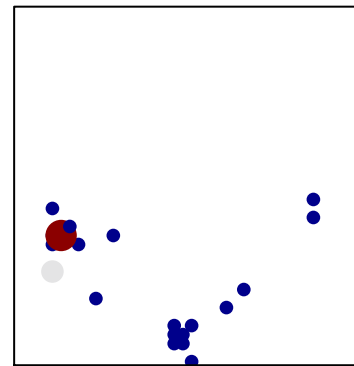
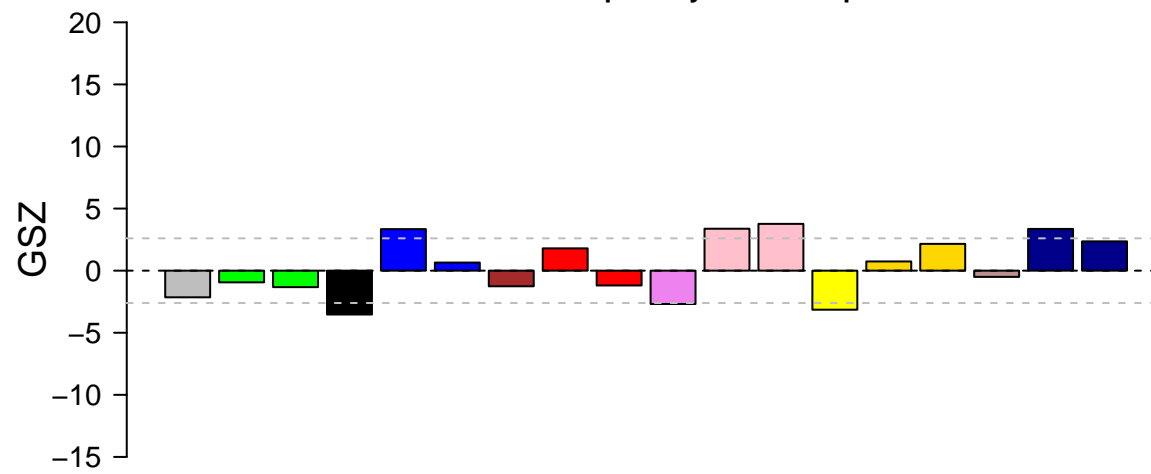
features = 10 , max = 1

mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)



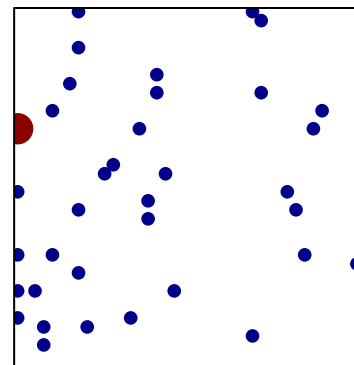
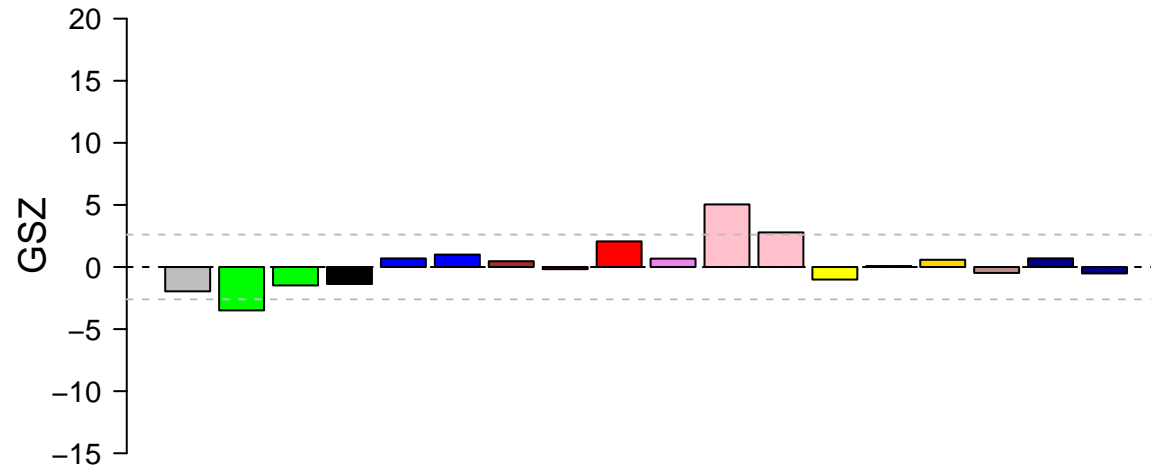
features = 12 , max = 2

mitochondrial respiratory chain complex I



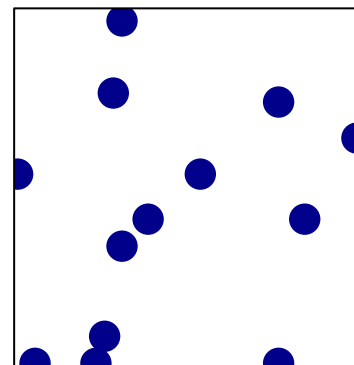
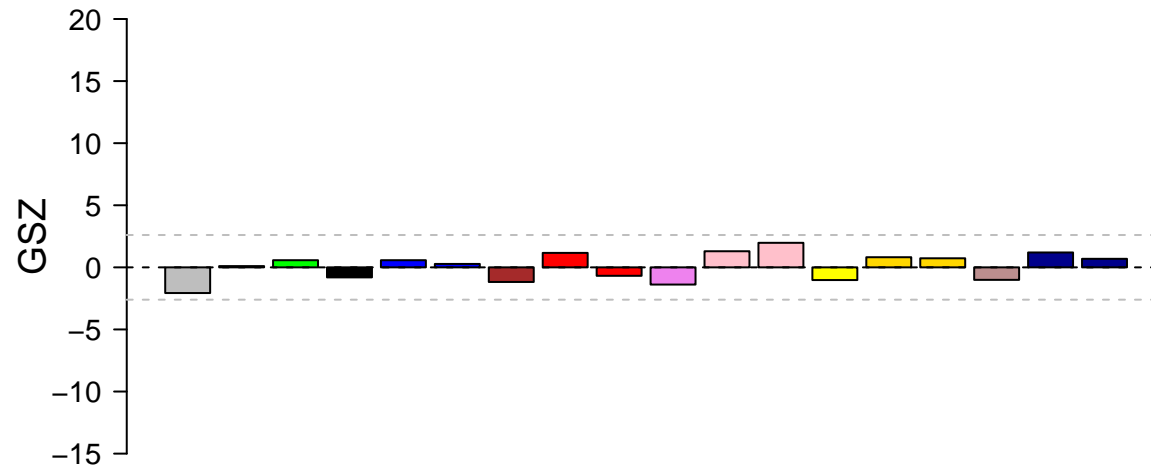
features = 23 , max = 3

negative regulation of catalytic activity



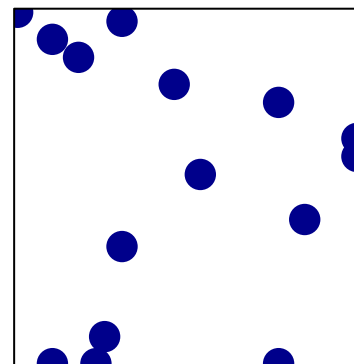
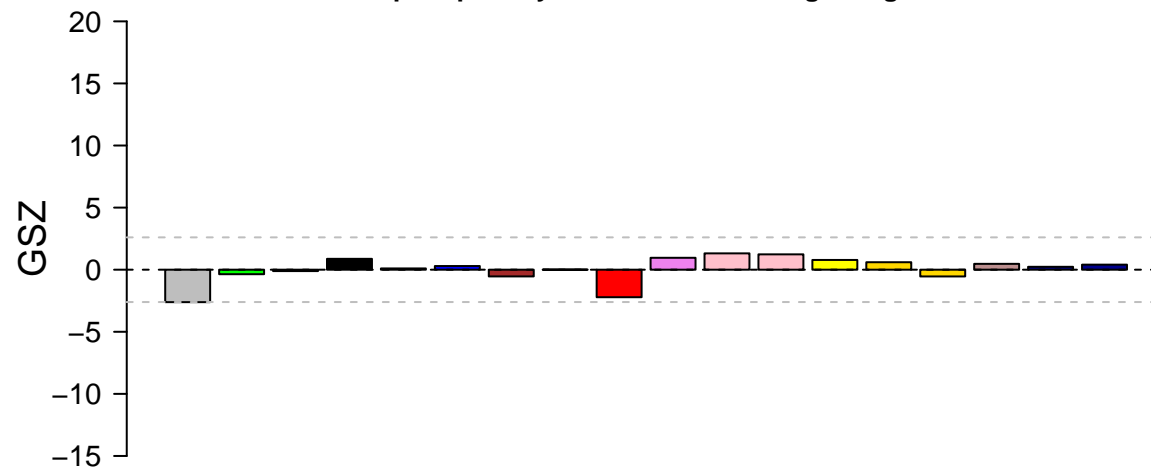
features = 38 , max = 3

phosphatidylinositol-3-phosphate biosynthetic process



features = 13 , max = 1

phosphatidylinositol 3-kinase signaling



features = 15 , max = 1