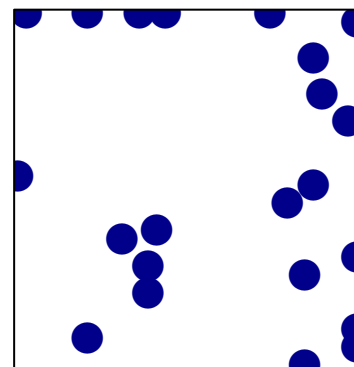
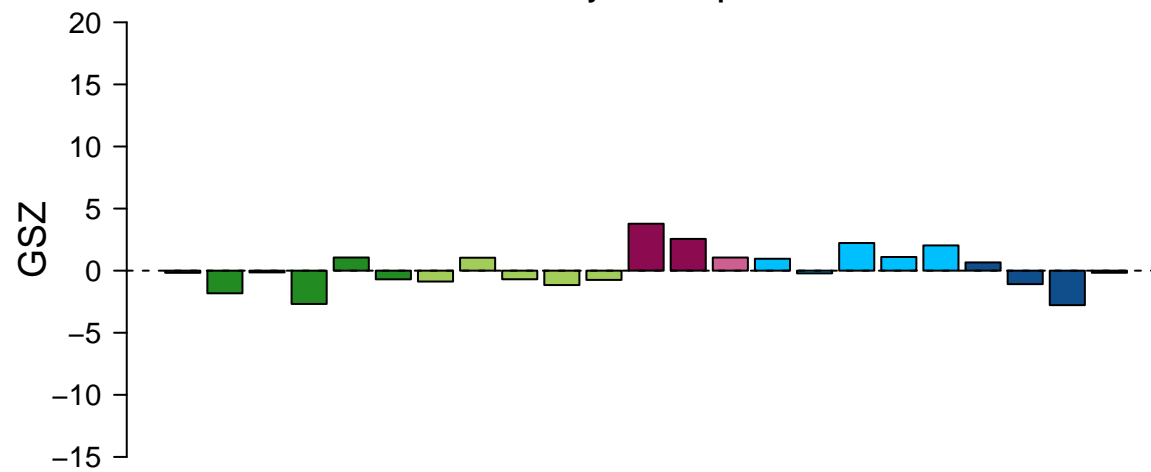
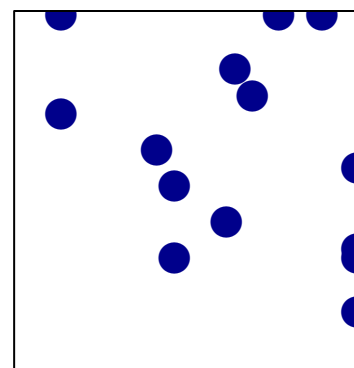


blastocyst development



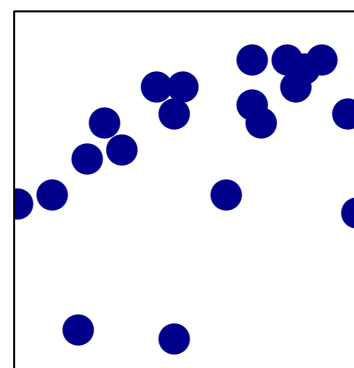
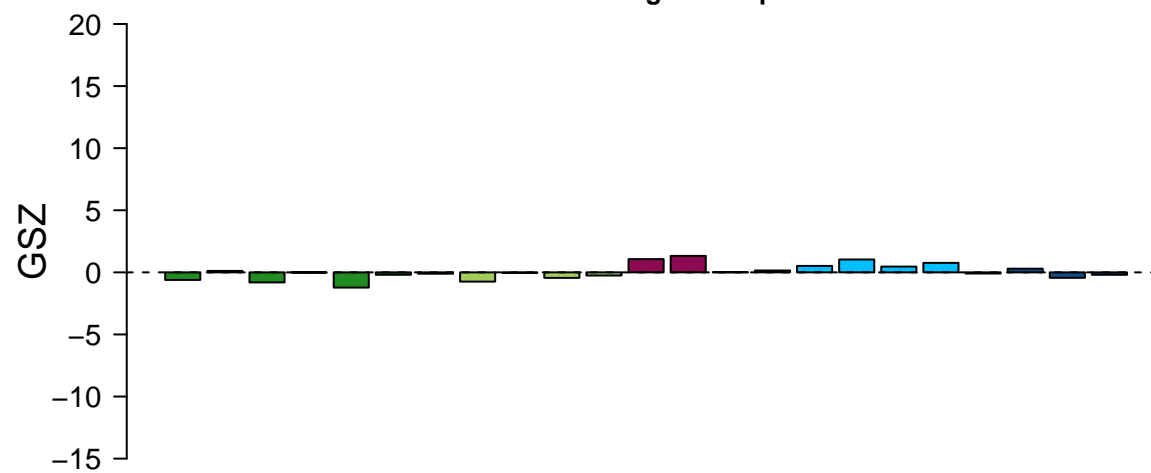
features = 22 , max = 1

cerebellar Purkinje cell layer development



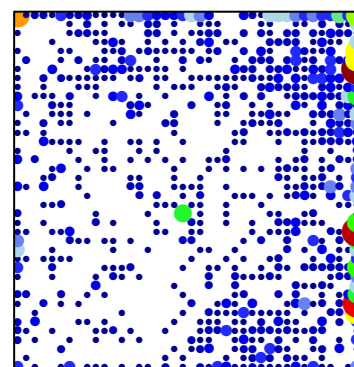
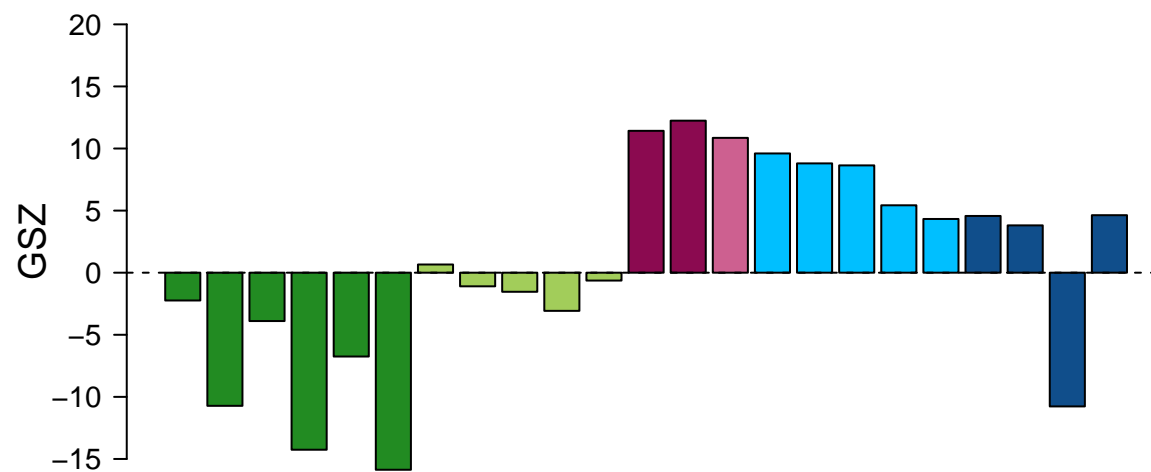
features = 14 , max = 1

G2 DNA damage checkpoint



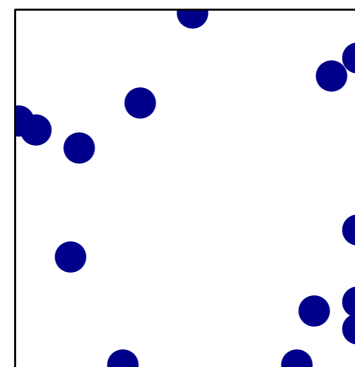
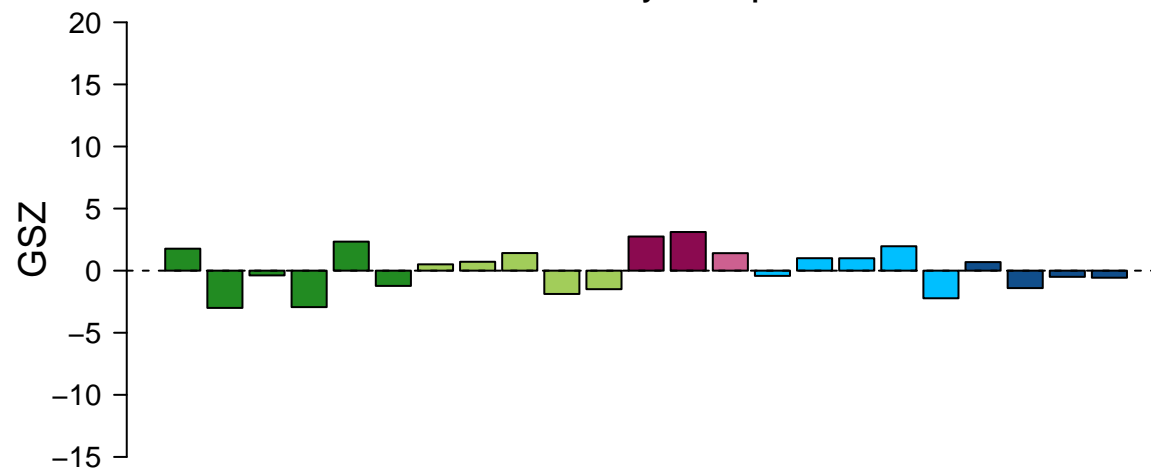
features = 20 , max = 1

mitochondrion



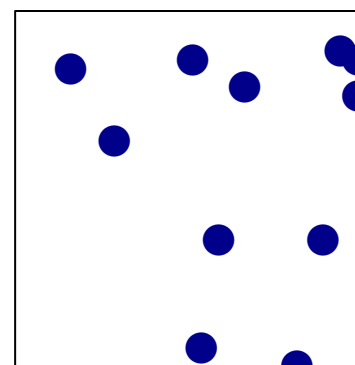
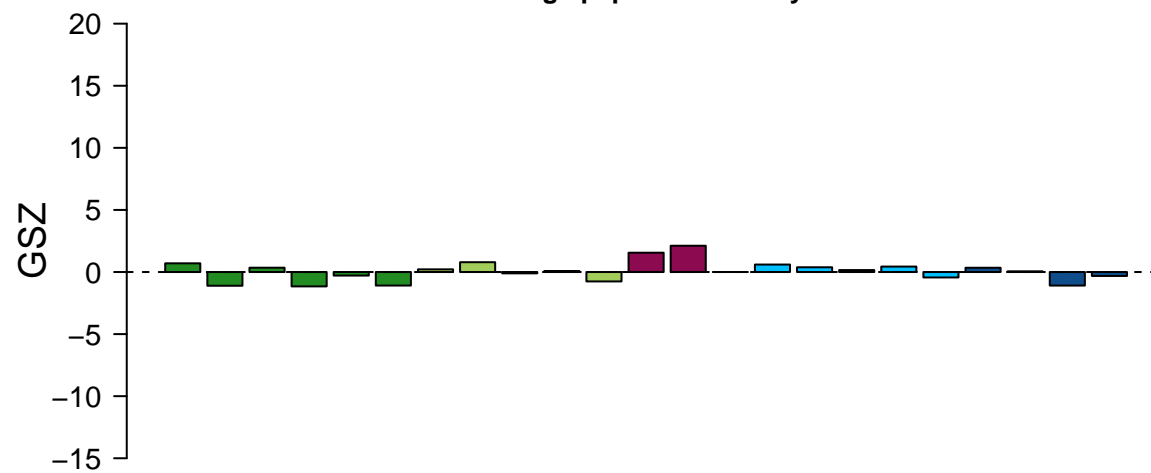
features = 1441 , max = 16

nitric oxide biosynthetic process



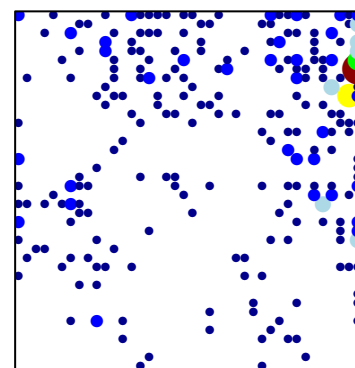
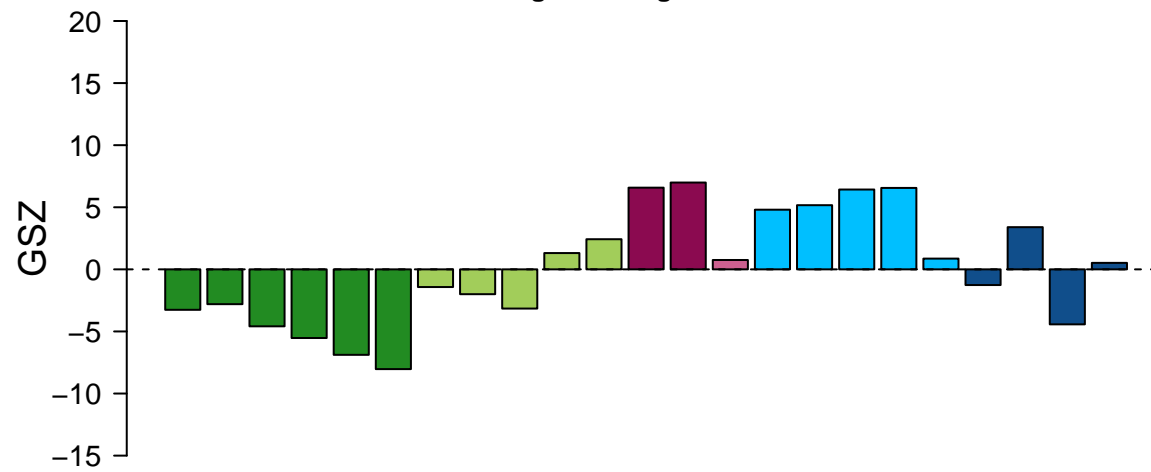
features = 14 , max = 1

omega peptidase activity



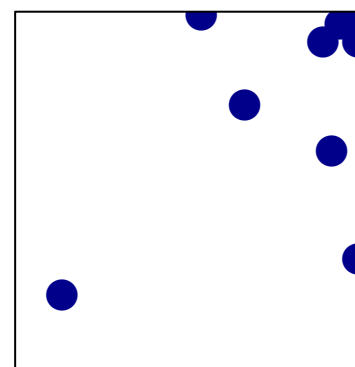
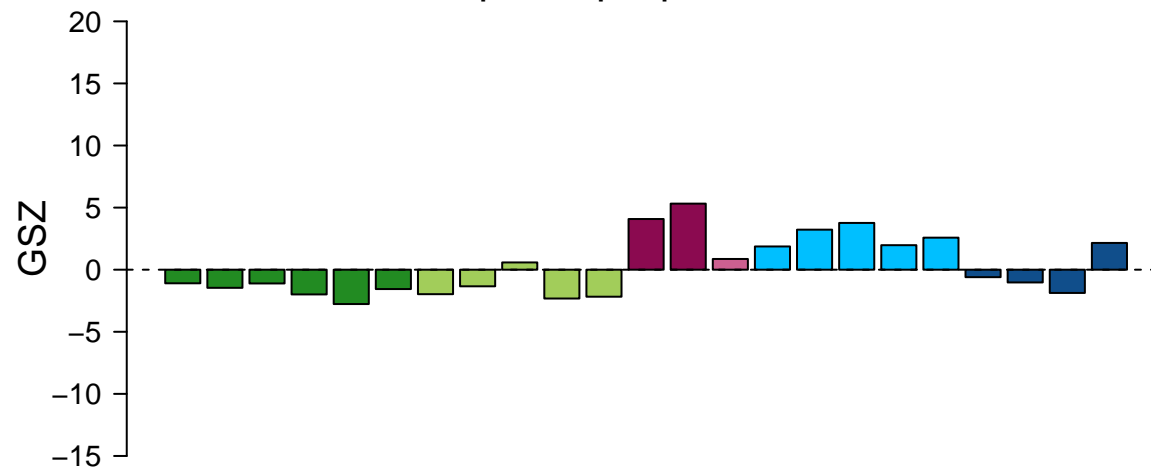
features = 11 , max = 1

organelle organization



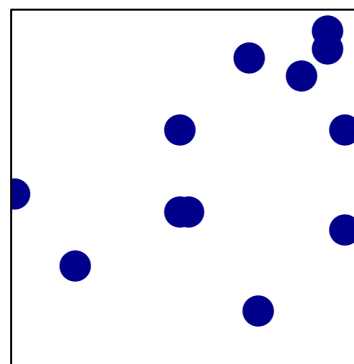
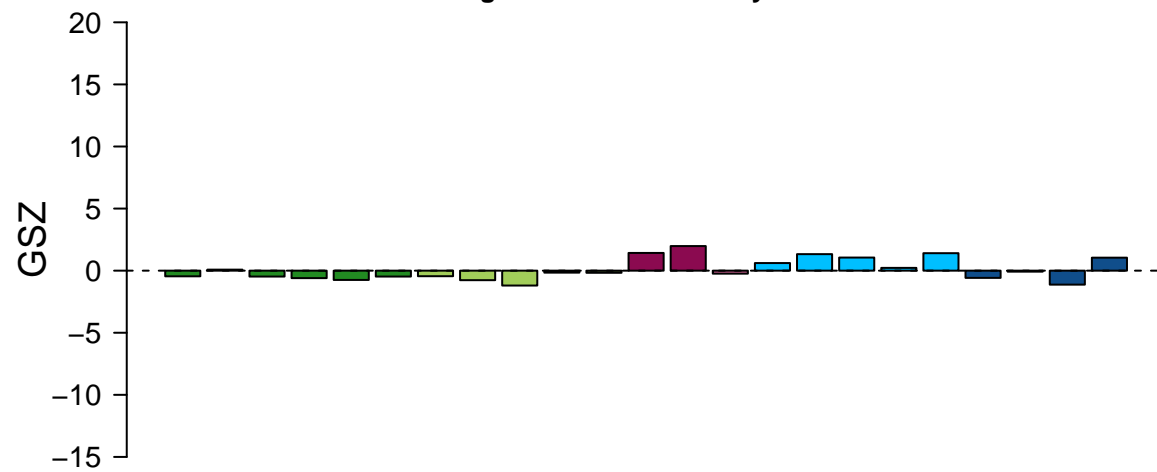
features = 291 , max = 7

pentose-phosphate shunt



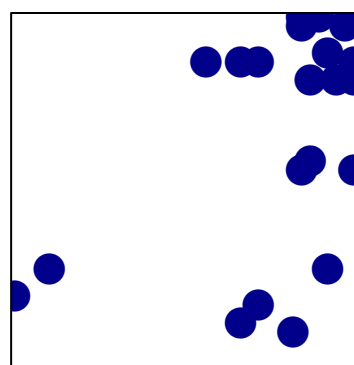
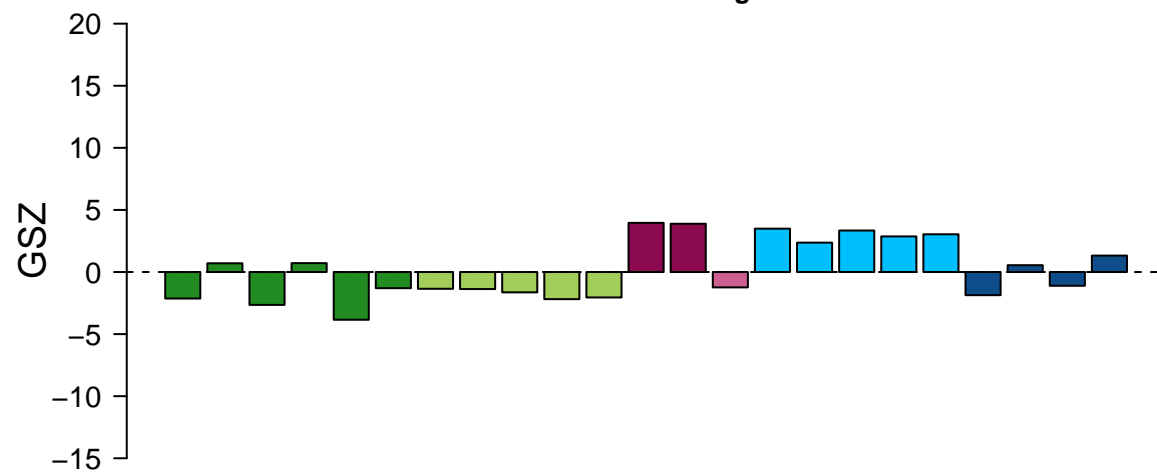
features = 10 , max = 1

regulation of DNA methylation



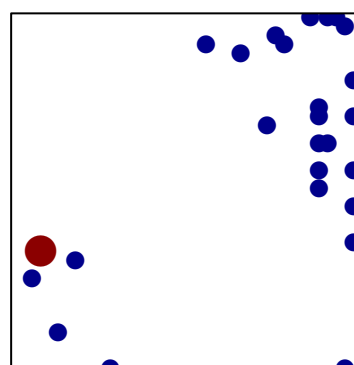
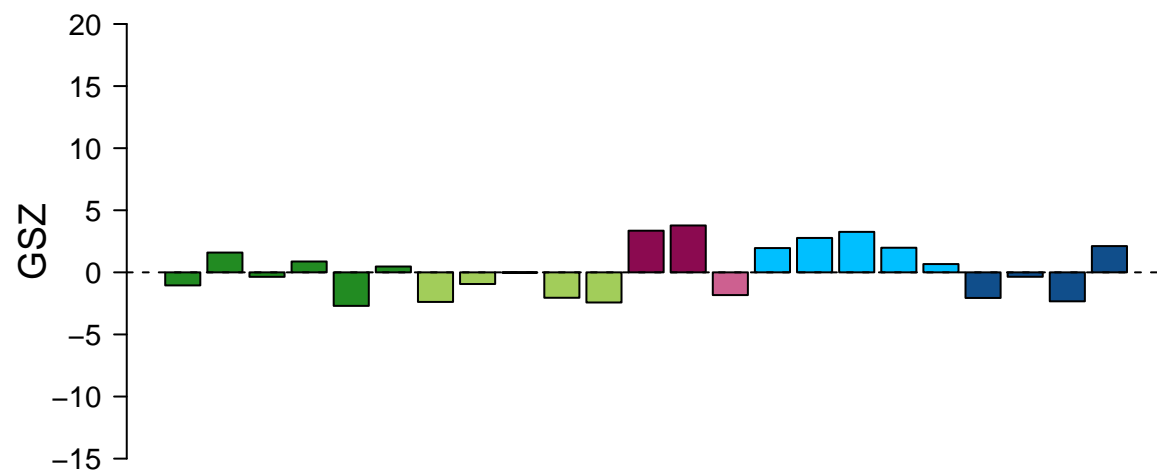
features = 12 , max = 1

snRNA binding



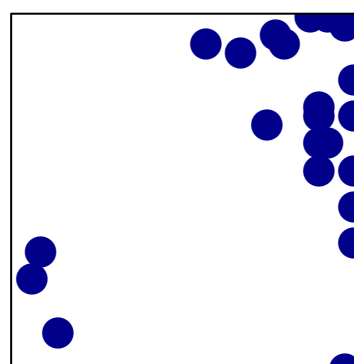
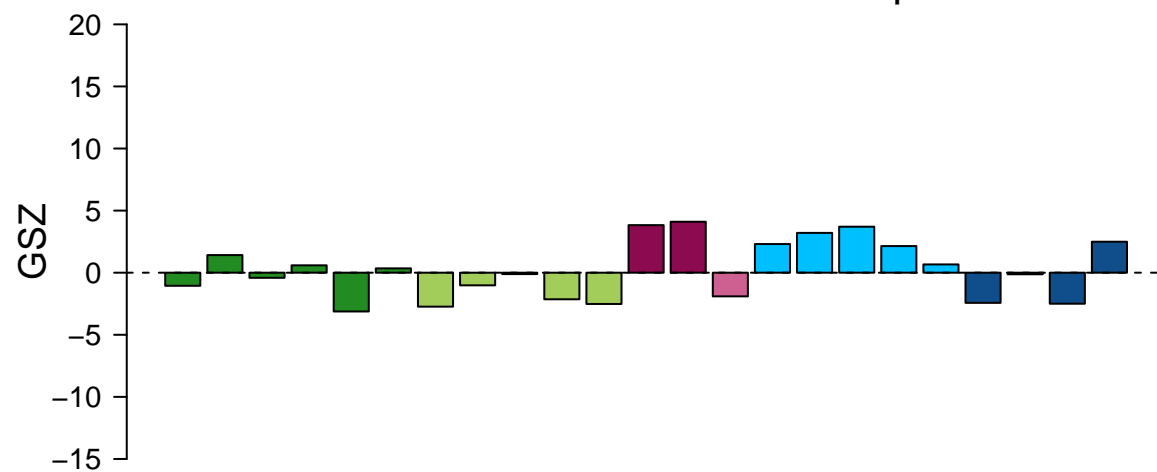
features = 22 , max = 1

telomere maintenance via recombination



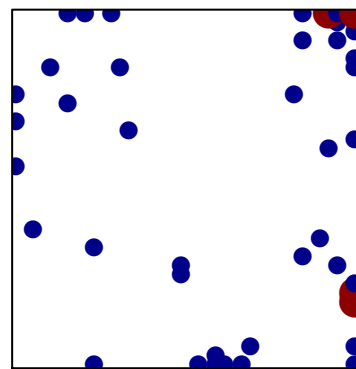
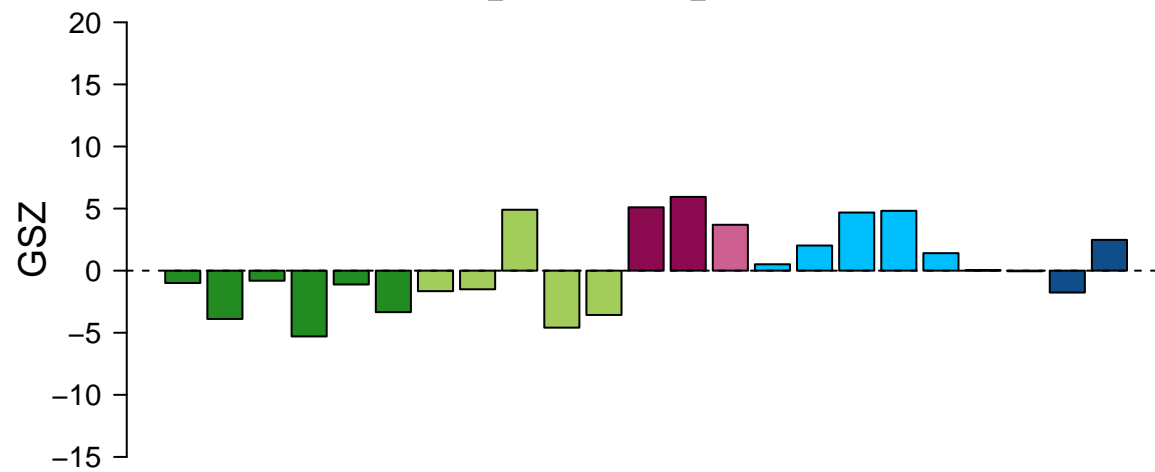
features = 27 , max = 2

telomere maintenance via semi-conservative replication



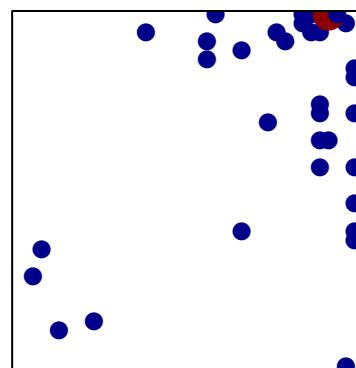
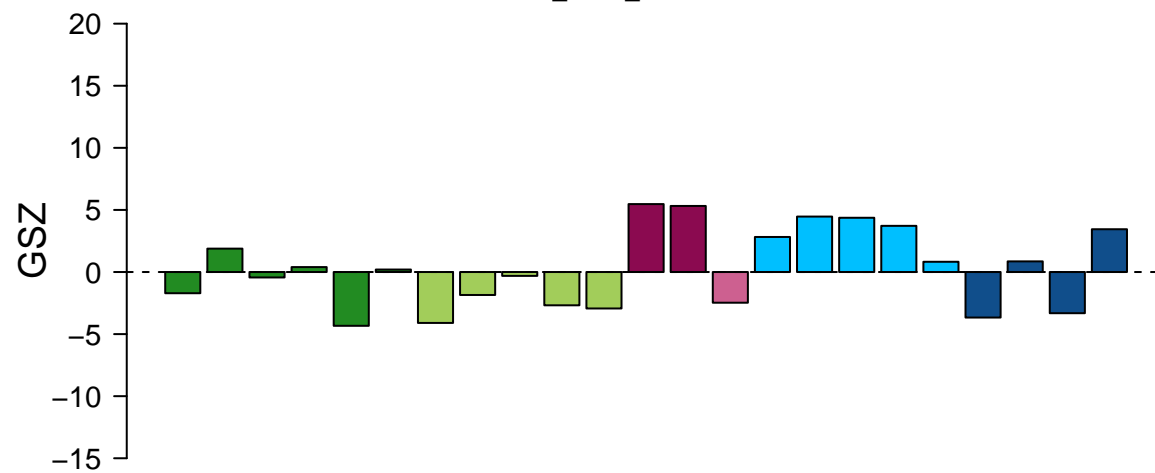
features = 23 , max = 1

KEGG_GLUTATHIONE_METABOLISM



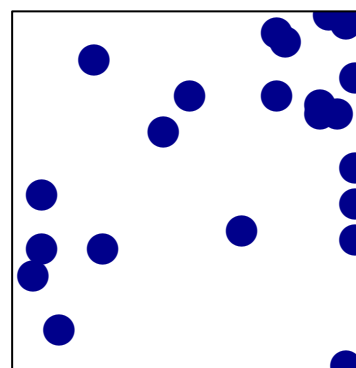
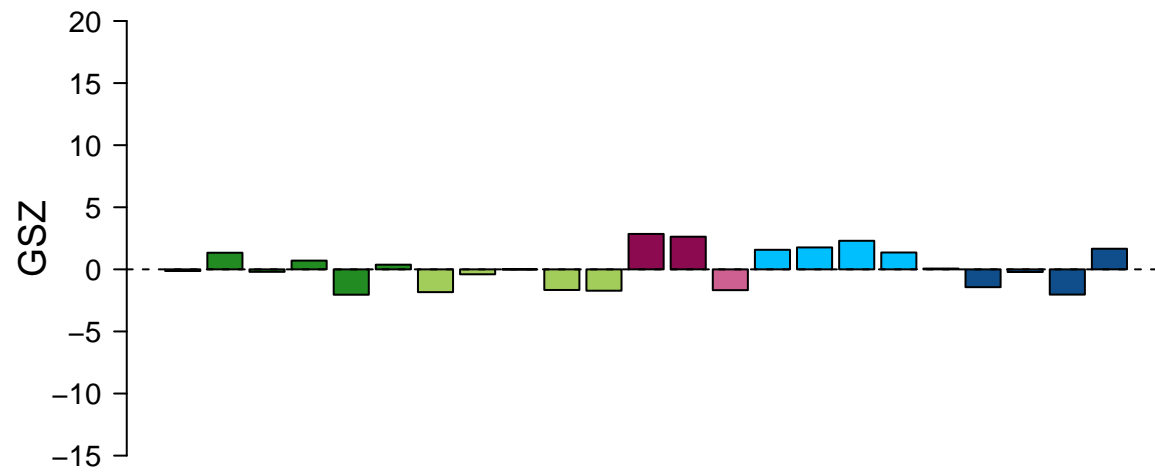
features = 47 , max = 2

KEGG_DNA_REPLICATION



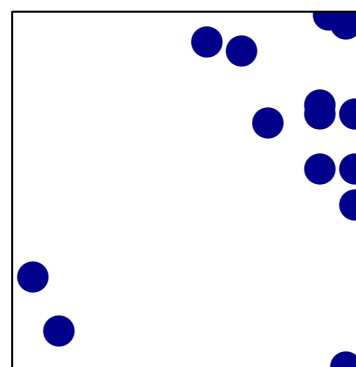
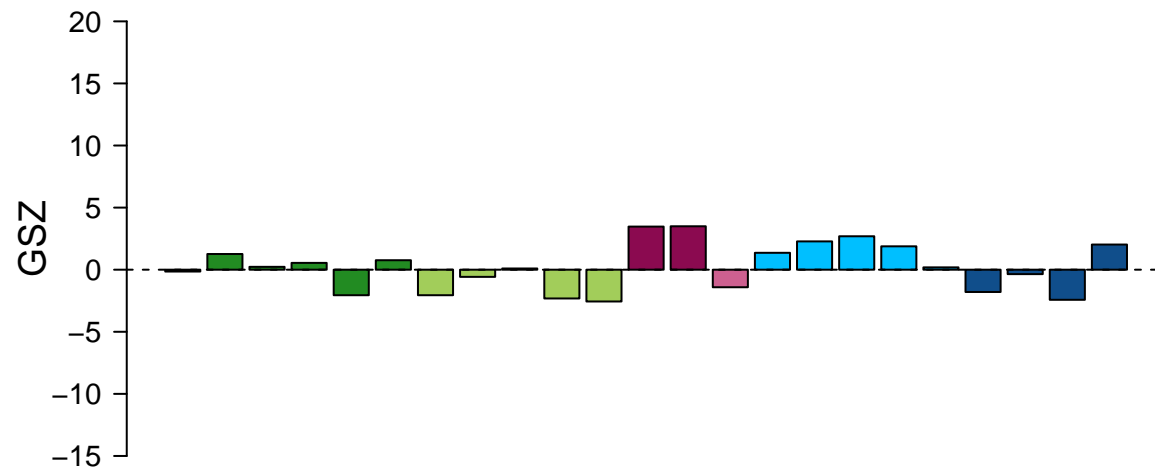
features = 35 , max = 2

KEGG_MISMATCH_REPAIR



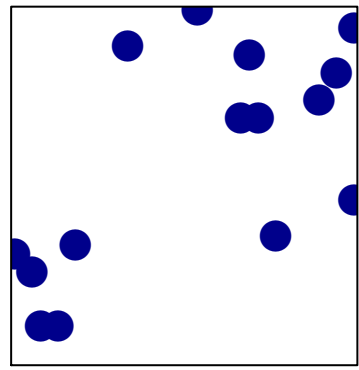
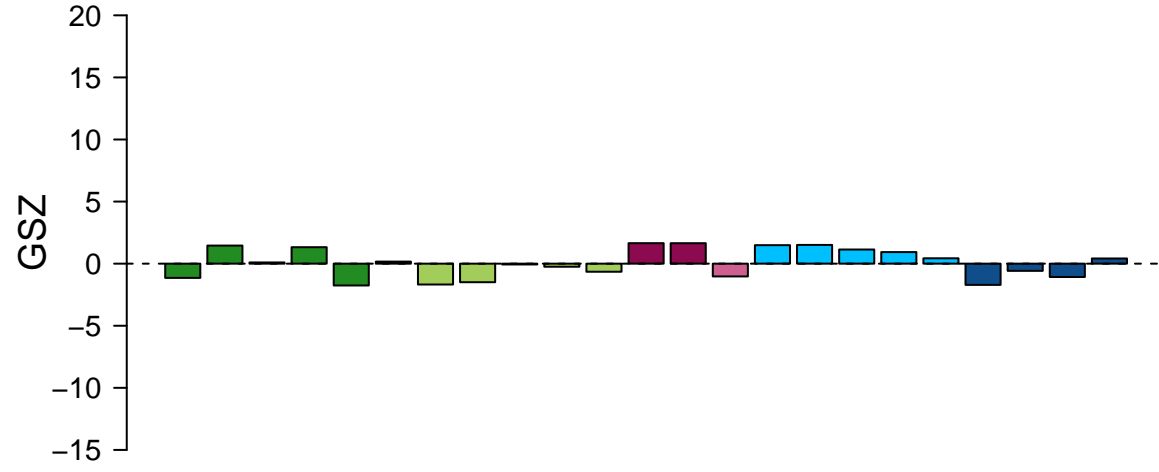
features = 22 , max = 1

REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND



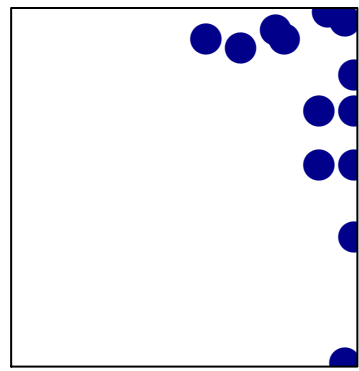
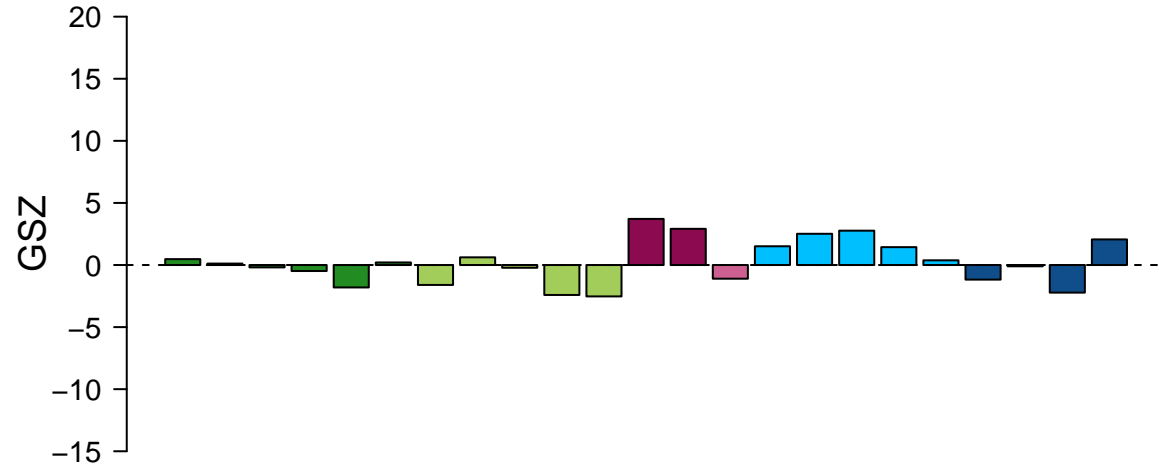
features = 15 , max = 1

REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_S



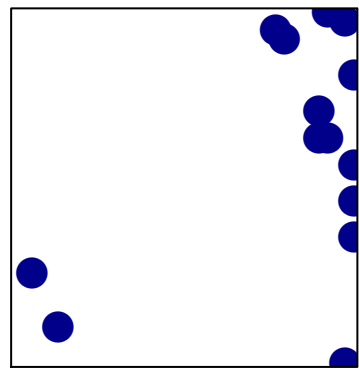
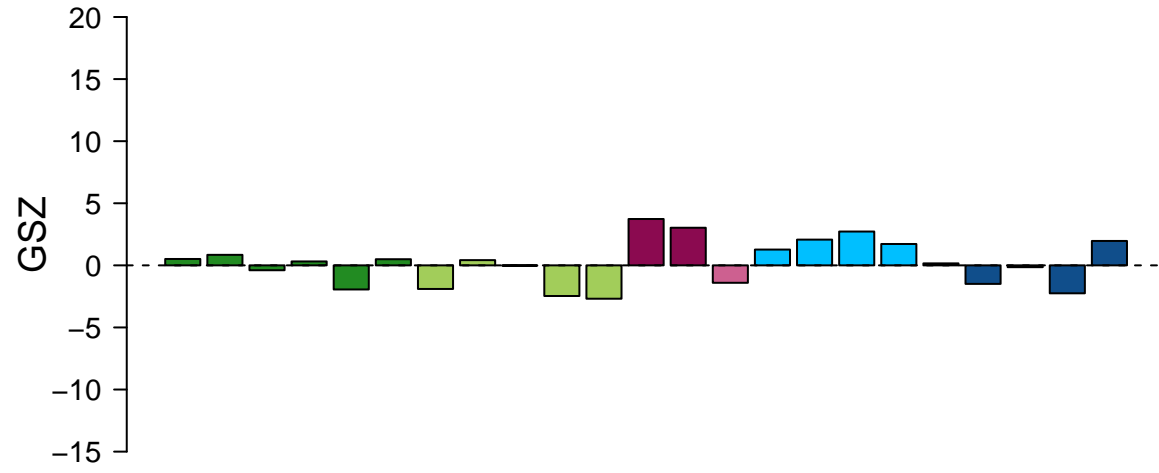
features = 15 , max = 1

REACTOME_POL_SWITCHING



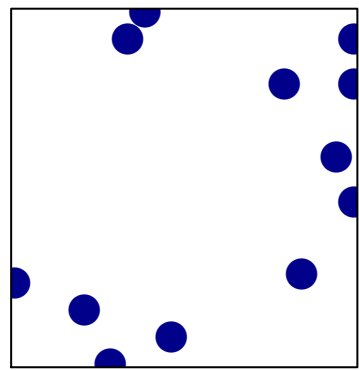
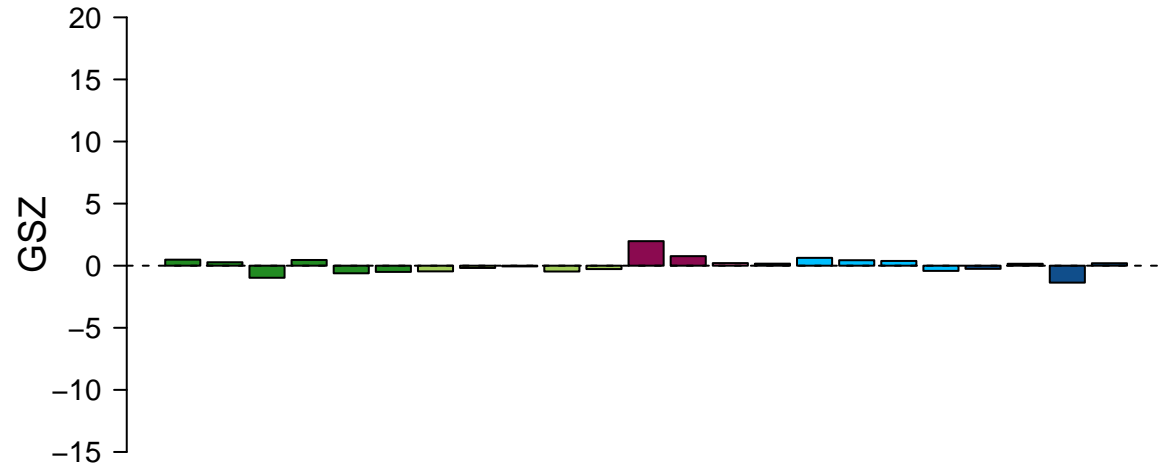
features = 13 , max = 1

REACTOME_REPAIR_SYNTHESIS_FOR_GAP_FILLING_BY_DNA_POL_IN_TC_NER



features = 14 , max = 1

REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE



features = 12 , max = 1