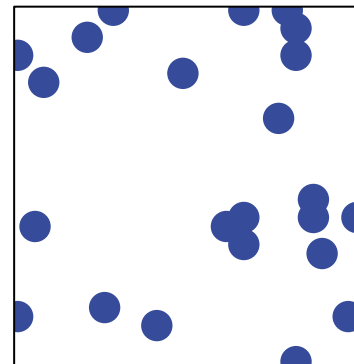
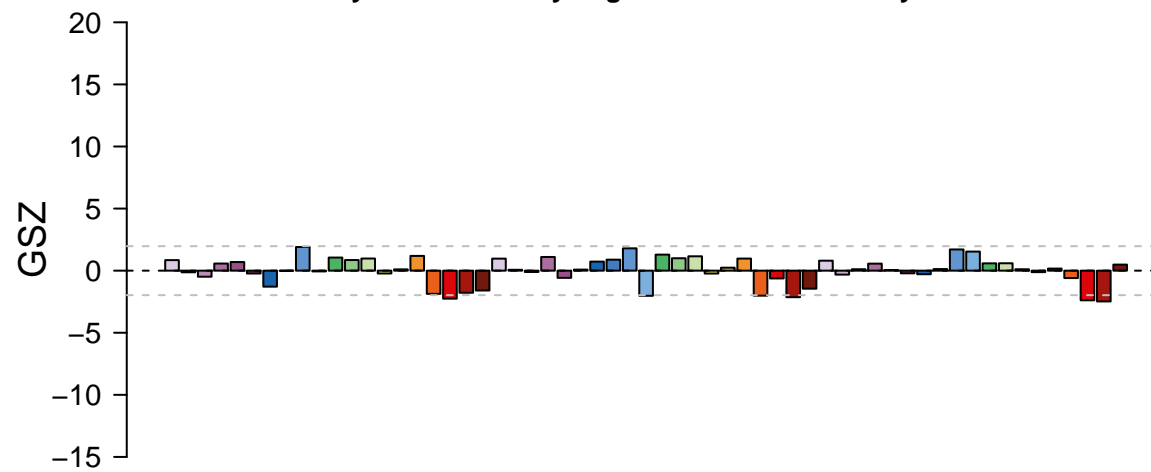
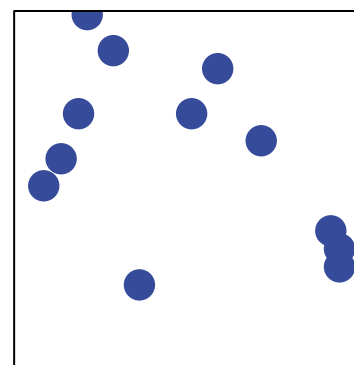
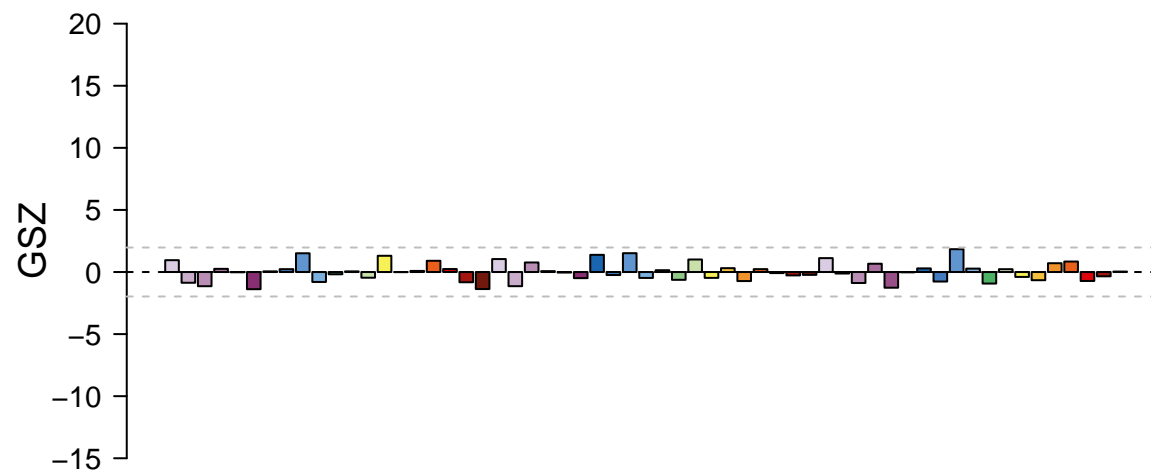


Enzyme – 7.1 Catalysing the translocation of hydrons



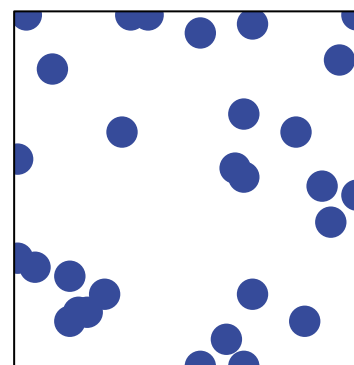
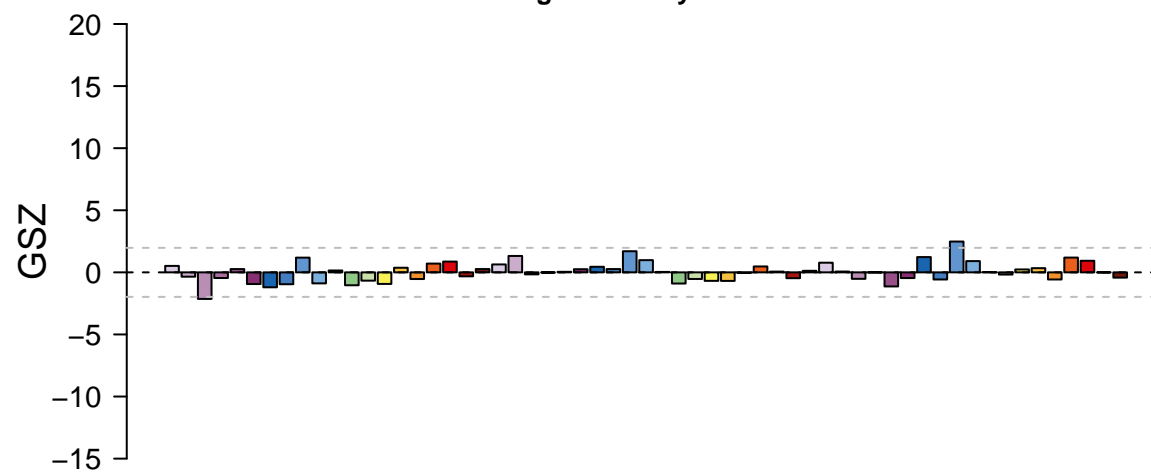
features = 24 , max = 1

Translation factors – Release factors



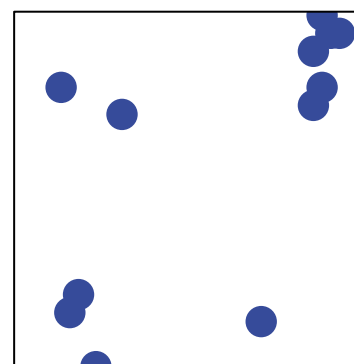
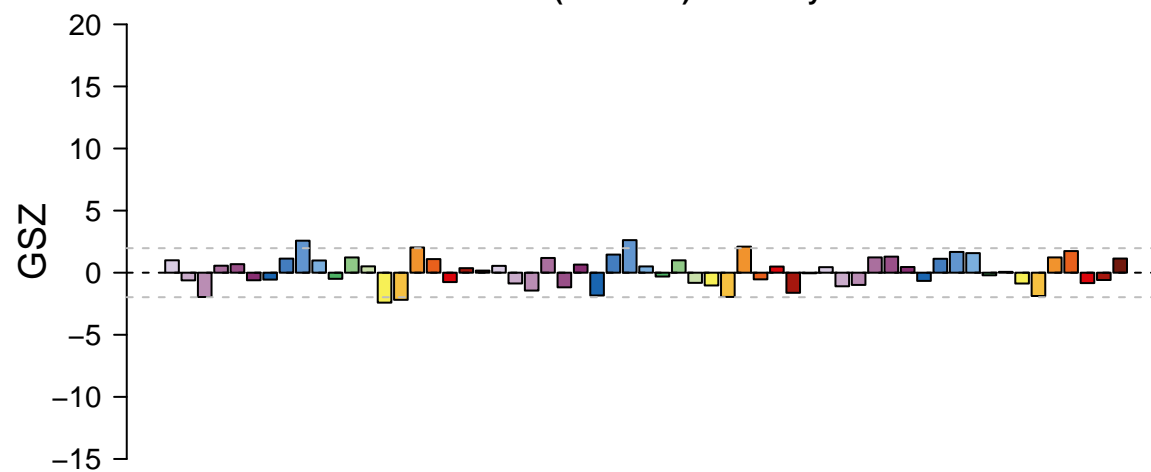
features = 12 , max = 1

Arginine biosynthesis



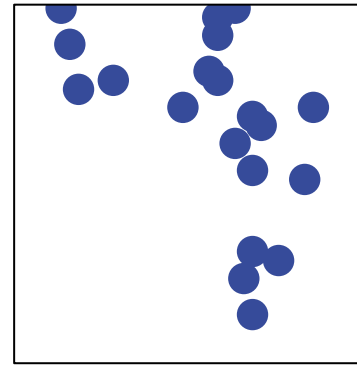
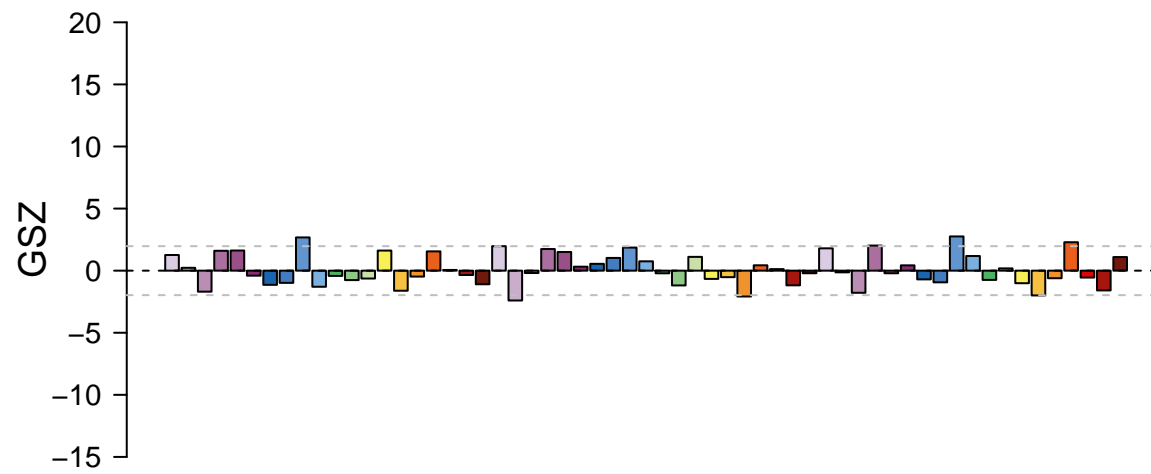
features = 29 , max = 1

ABCB (MDR/TAP) subfamily



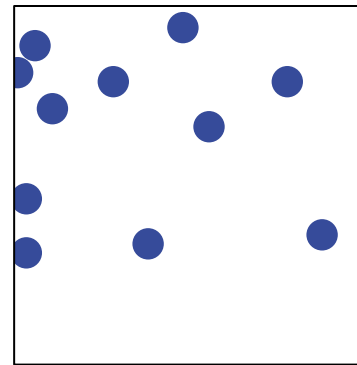
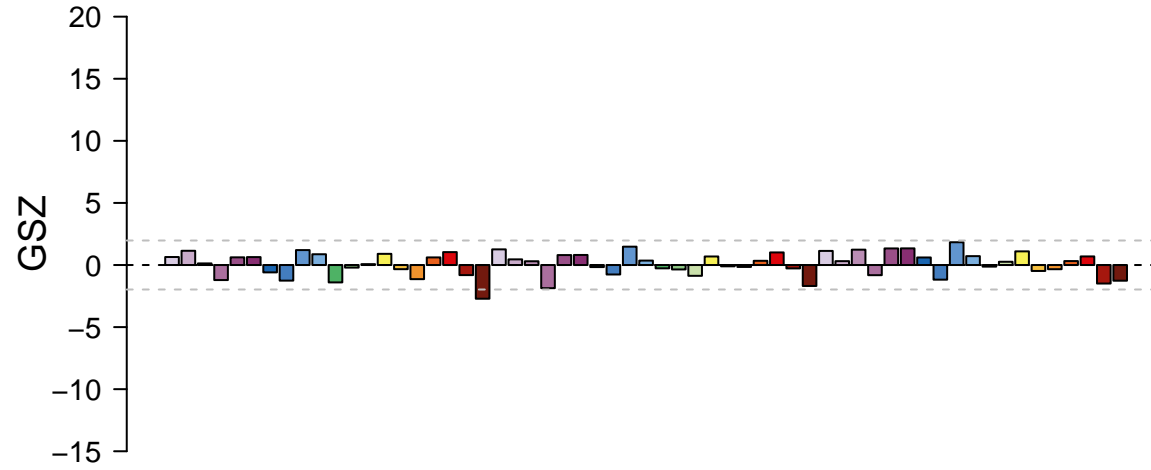
features = 12 , max = 1

tRNA modification factors



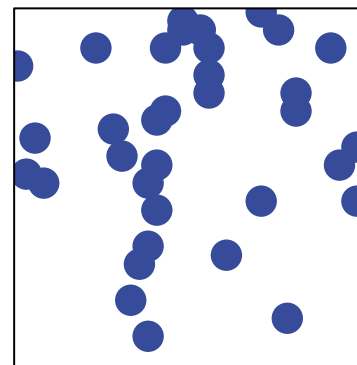
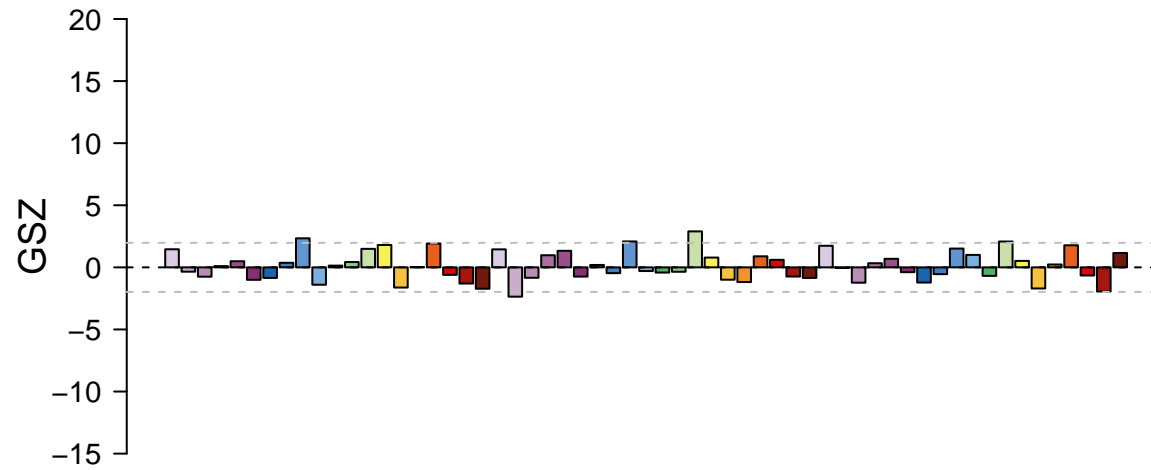
features = 20 , max = 1

Transcription factors – MADS



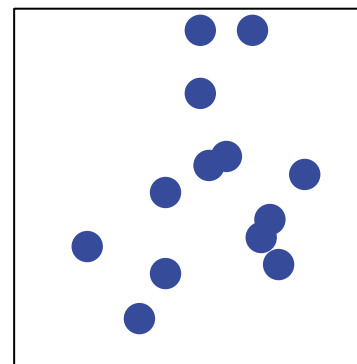
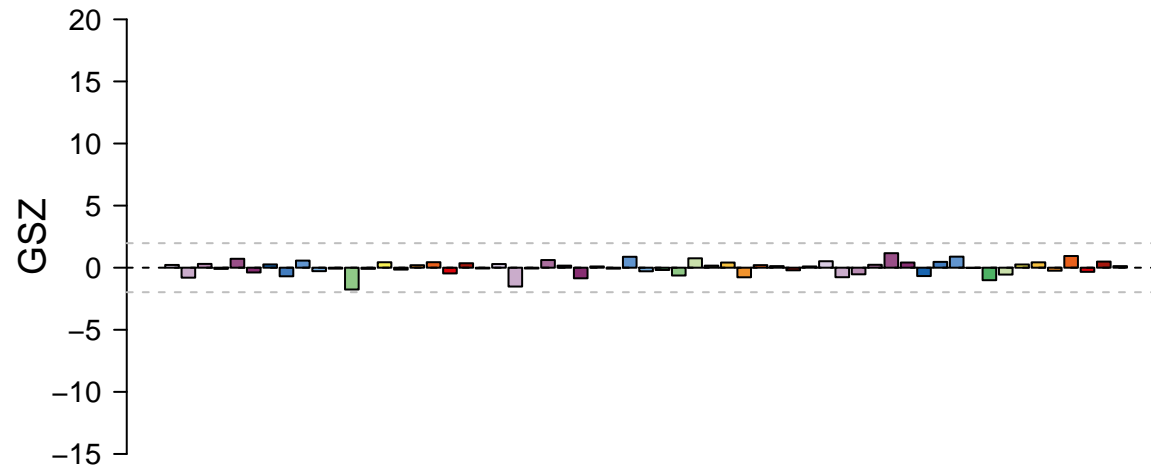
features = 11 , max = 1

Transcription factors – SET PCG



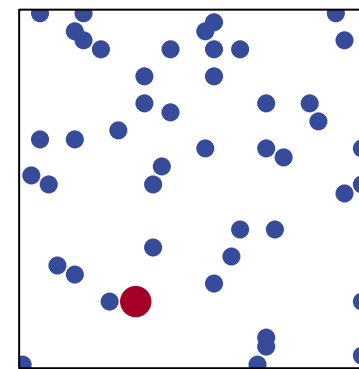
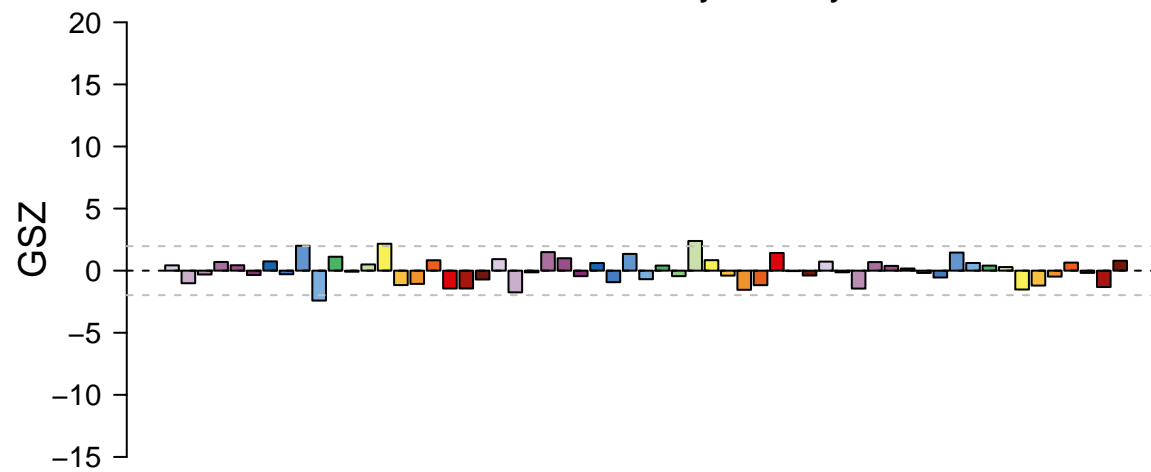
features = 34 , max = 1

Enzyme – 2.8 Transferring sulfur-containing groups



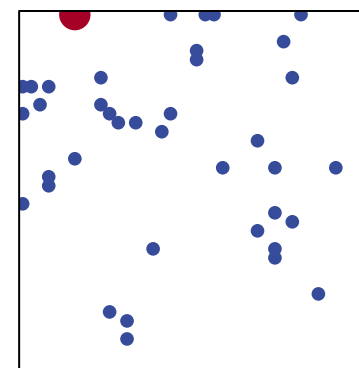
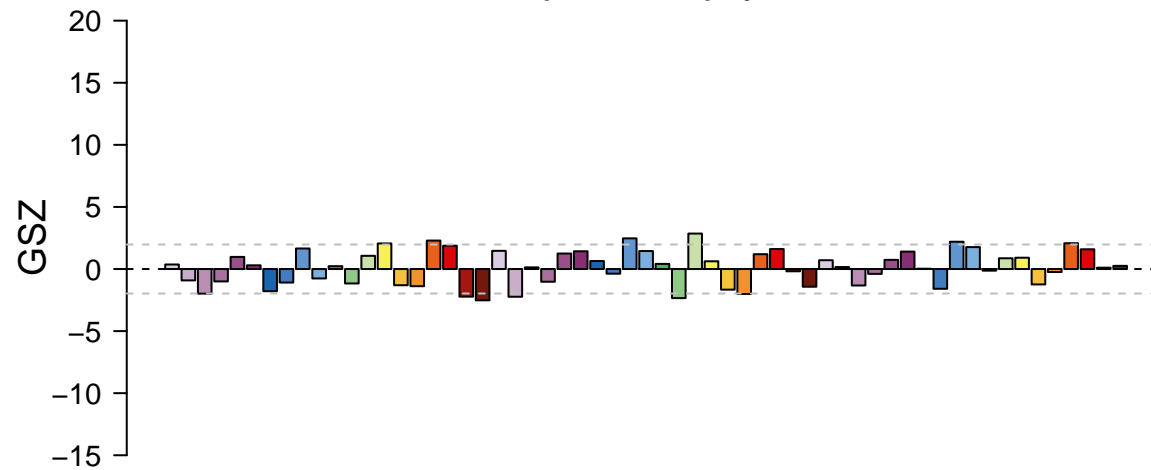
features = 13 , max = 1

Amino acid metabolism – Lysine biosynthesis



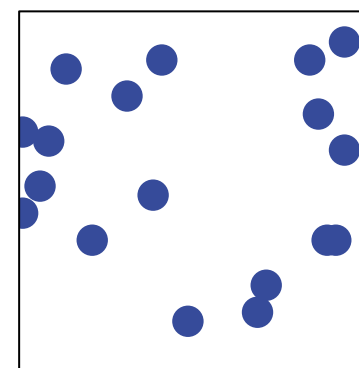
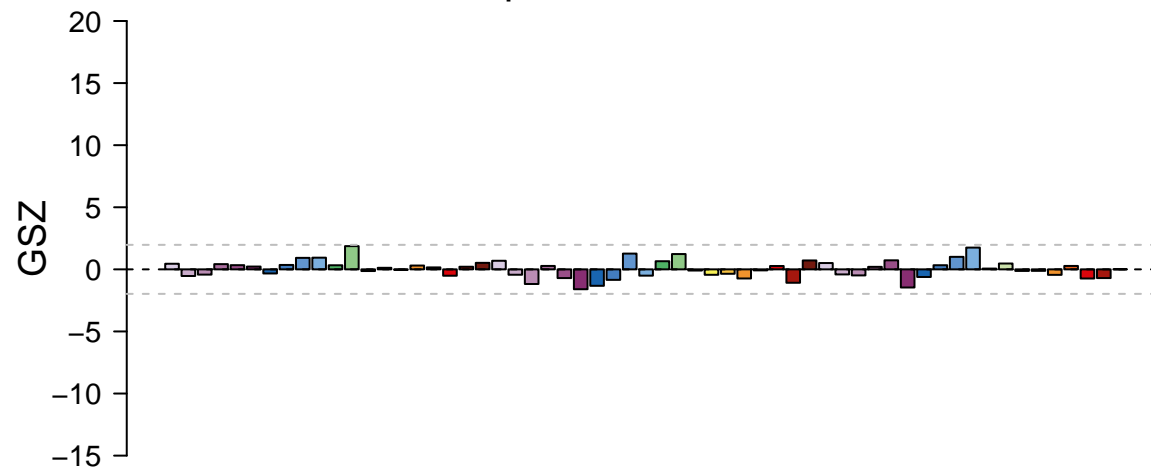
features = 48 , max = 2

Transcription – RNA polymerase



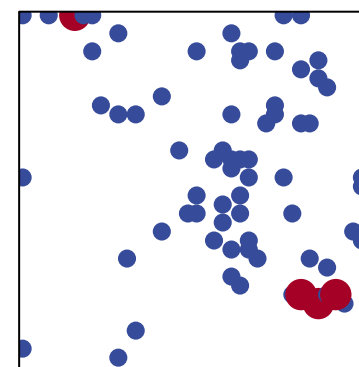
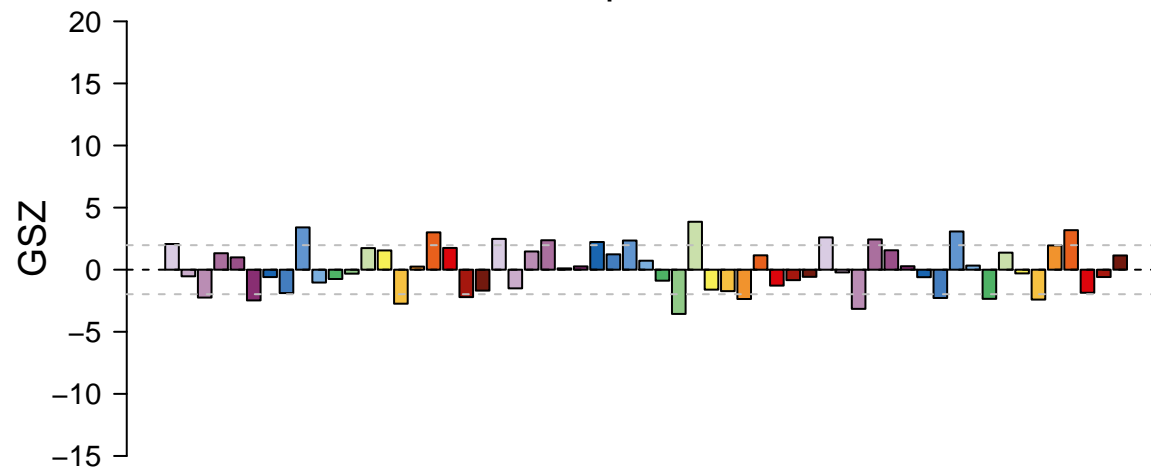
features = 41 , max = 3

Transcription factors – Other zf-DHHC



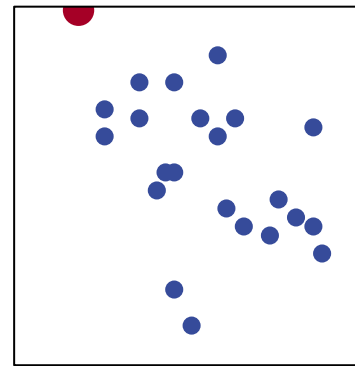
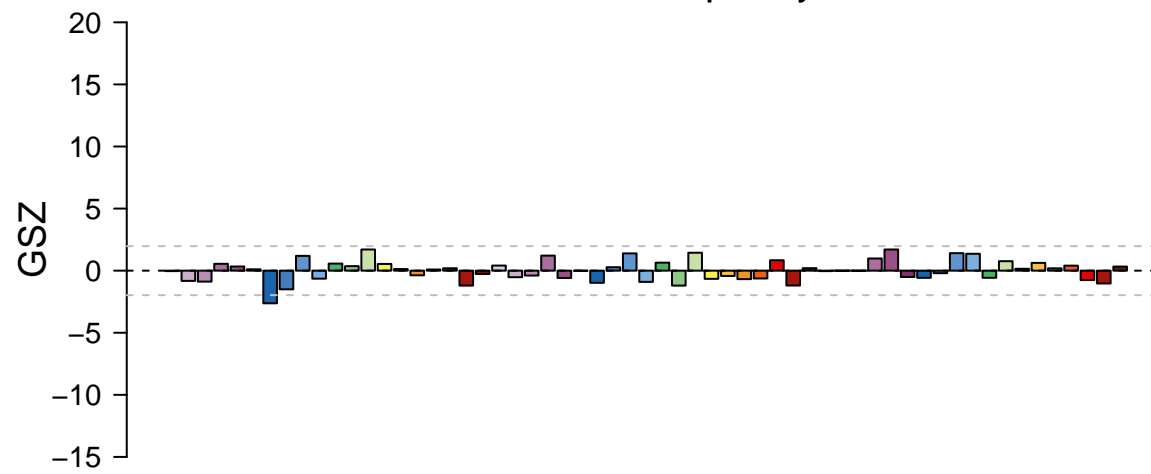
features = 18 , max = 1

Mitochondrial transcription and translation factors



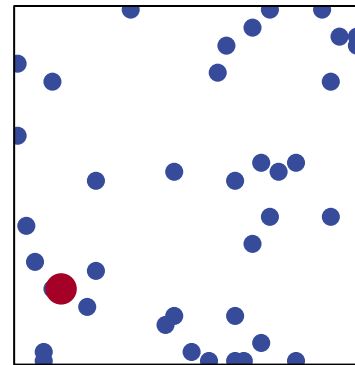
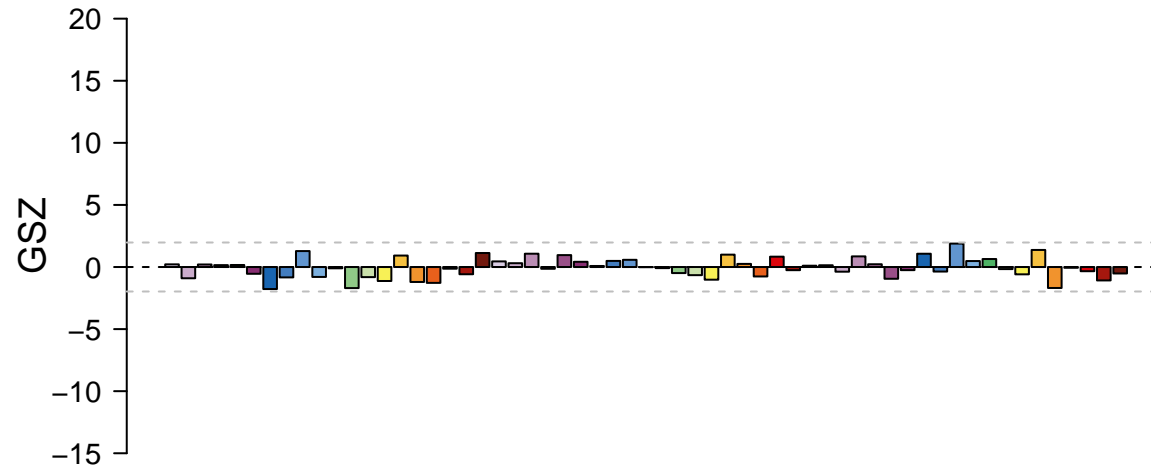
features = 75 , max = 2

Protein – Retrieval pathways



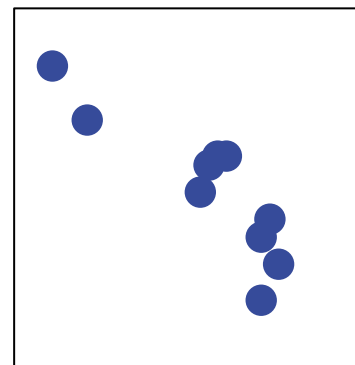
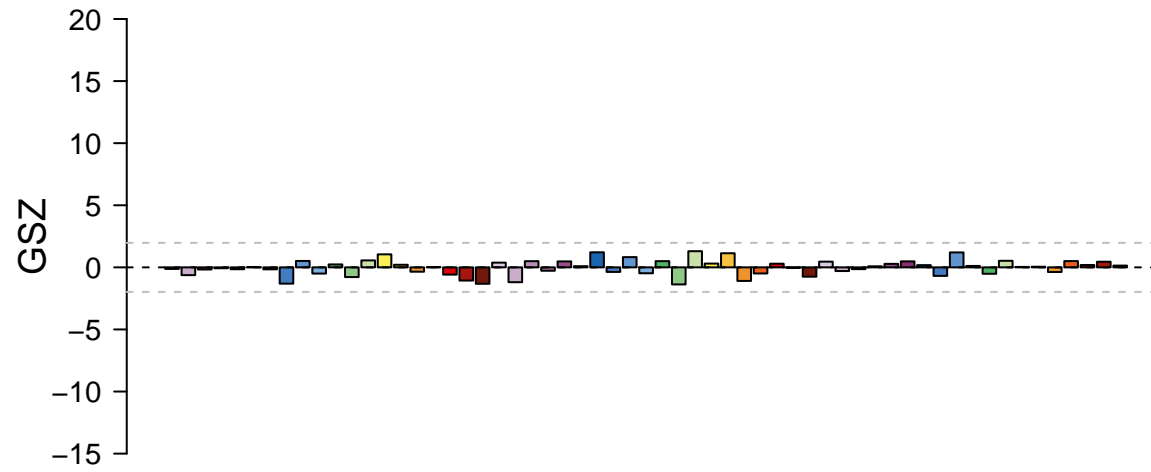
features = 24 , max = 2

Amino acid metabolism – Cysteine metabolism



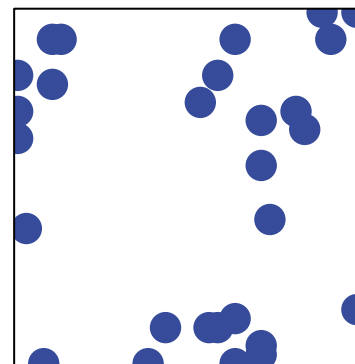
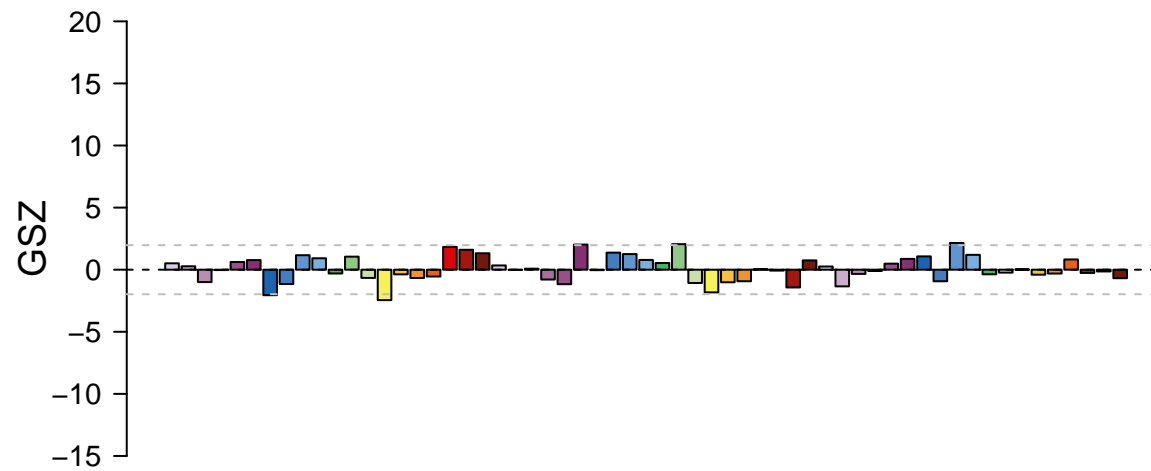
features = 40 , max = 2

Replication and repair – Sulfur relay system



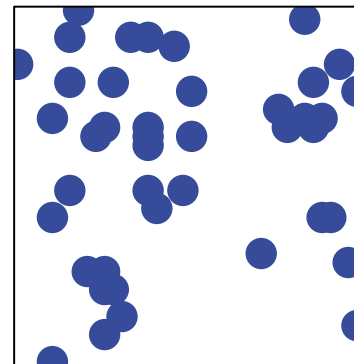
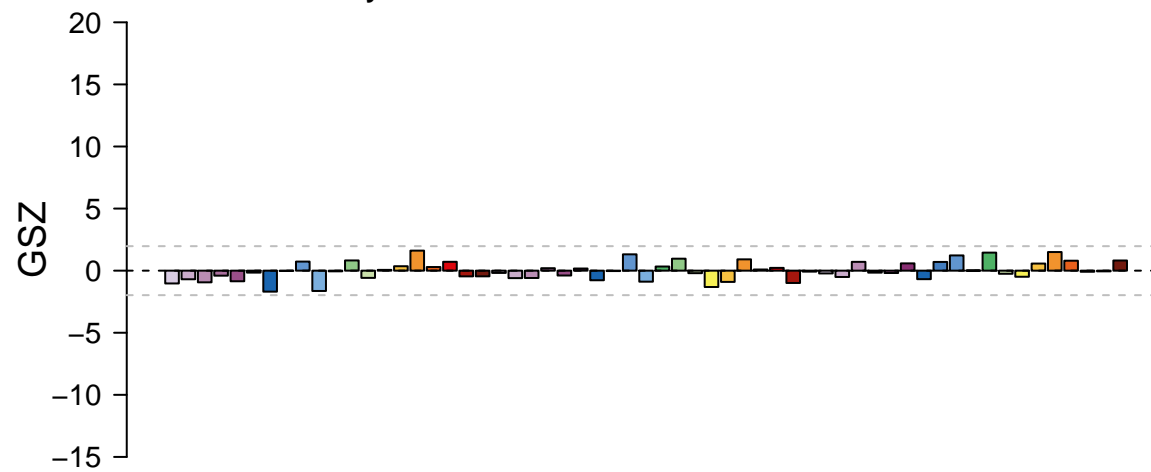
features = 10 , max = 1

Sulfur metabolism



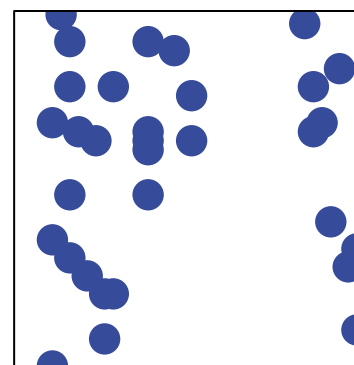
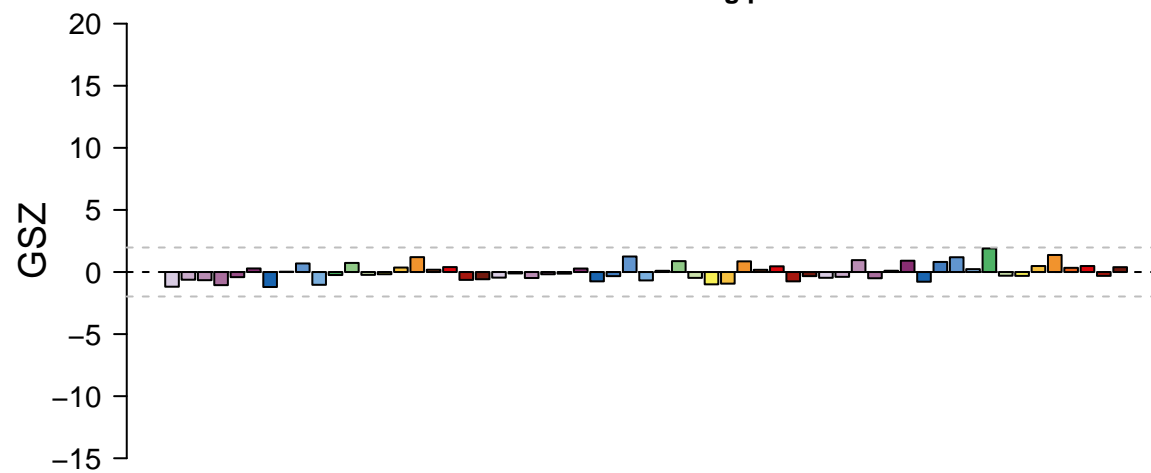
features = 28 , max = 1

Cytoskeleton – Actin filaments / Microfilaments



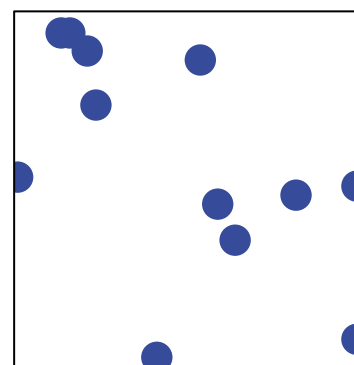
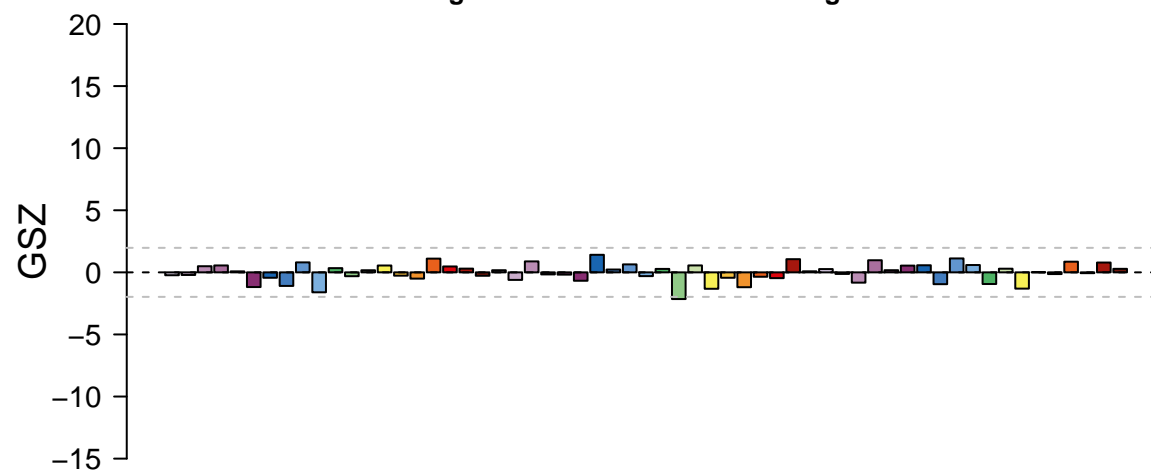
features = 42 , max = 1

Protein – Actin-binding proteins



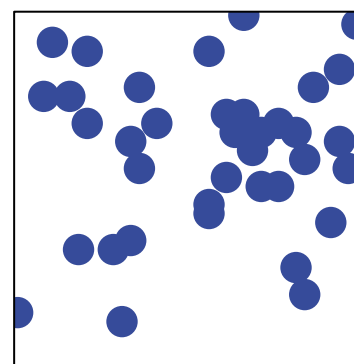
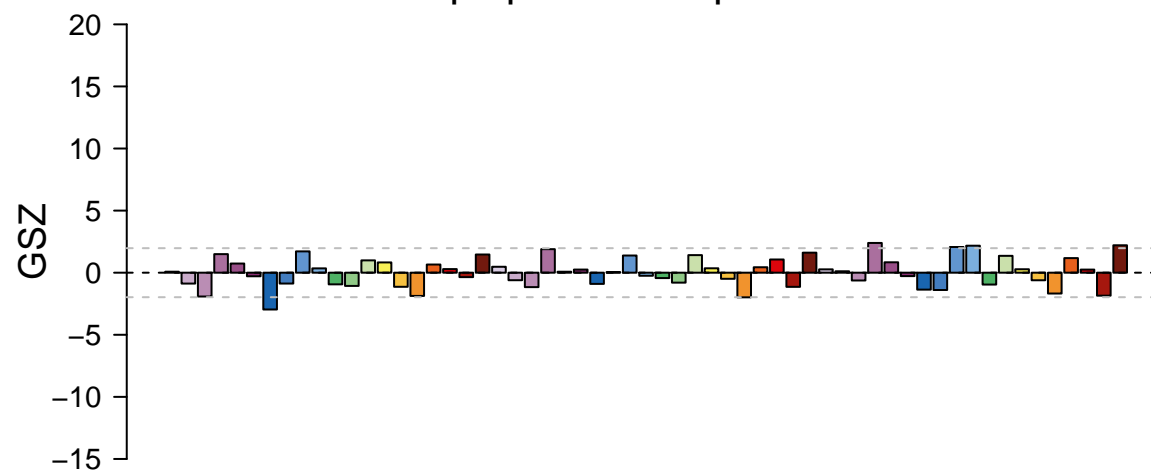
features = 32 , max = 1

Ribosome biogenesis – Other ribosome biogenesis factors



features = 12 , max = 1

Repair protein – Check point factors



features = 37 , max = 1