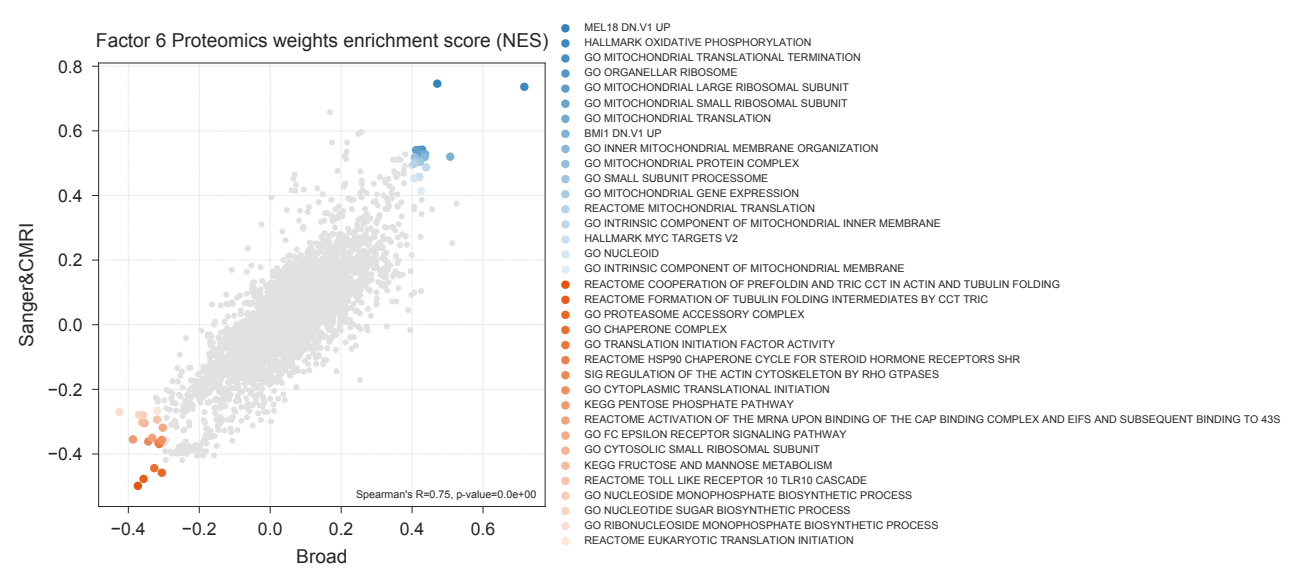
Factor 6 Proteomics weights enrichment score (NES)
Sanger&CMRI
Broad
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.4
−0.2
0.0
0.2
0.4
0.6
Spearman's R=0.75, p-value=0.0e+00
MEL18 DN.V1 UP
HALLMARK OXIDATIVE PHOSPHORYLATION
GO MITOCHONDRIAL TRANSLATIONAL TERMINATION
GO ORGANELLAR RIBOSOME
GO MITOCHONDRIAL LARGE RIBOSOMAL SUBUNIT
GO MITOCHONDRIAL SMALL RIBOSOMAL SUBUNIT
GO MITOCHONDRIAL TRANSLATION
BMI1 DN.V1 UP
GO INNER MITOCHONDRIAL MEMBRANE ORGANIZATION
GO MITOCHONDRIAL PROTEIN COMPLEX
GO SMALL SUBUNIT PROCESSOME
GO MITOCHONDRIAL GENE EXPRESSION
REACTOME MITOCHONDRIAL TRANSLATION
GO INTRINSIC COMPONENT OF MITOCHONDRIAL INNER MEMBRANE
HALLMARK MYC TARGETS V2
GO NUCLEOID
GO INTRINSIC COMPONENT OF MITOCHONDRIAL MEMBRANE
REACTOME COOPERATION OF PREFOLDIN AND TRIC CCT IN ACTIN AND TUBULIN FOLDING
REACTOME FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC
GO PROTEASOME ACCESSORY COMPLEX
GO CHAPERONE COMPLEX
GO TRANSLATION INITIATION FACTOR ACTIVITY
REACTOME HSP90 CHAPERONE CYCLE FOR STEROID HORMONE RECEPTORS SHR
SIG REGULATION OF THE ACTIN CYTOSKELETON BY RHO GTPASES
GO CYTOPLASMIC TRANSLATIONAL INITIATION
KEGG PENTOSE PHOSPHATE PATHWAY
REACTOME ACTIVATION OF THE MRNA UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS AND SUBSEQUENT BINDING TO 43S
GO FC EPSILON RECEPTOR SIGNALING PATHWAY
GO CYTOSOLIC SMALL RIBOSOMAL SUBUNIT
KEGG FRUCTOSE AND MANNOSE METABOLISM
REACTOME TOLL LIKE RECEPTOR 10 TLR10 CASCADE
GO NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS
GO NUCLEOTIDE SUGAR BIOSYNTHETIC PROCESS
GO RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS
REACTOME EUKARYOTIC TRANSLATION INITIATION