ne Set Enrichment Analysis cell cycle cell cycle checkpoints r-hsa-69620 ∠ cell cýcle r–hsa–1640170 - cell cycle, mitotic r-hsa-69278 cellular macromolecule biosynthetic process (go:0034645) copi-dependent golgi-to-er retrograde traffic r-hsa-6811434 cytoskeleton-dependent cytokinesis (go:0061640) dna metabolic process (go:0006259) dna replication (go:0006260) double-strand break repair via homologous recombination (go:0000724) eml4 and nudc in mitotic spindle formation r-hsa-9648025 g1/s transition r-hsa-69206 g2/m checkpoints r-hsa-69481 **Database** ∑g2/m transition r–hsa–69275 Gene Ontology BP KEGG Reactome matrix\_17 m phase r-hsa-68886 - microtubule cytoskeleton organization involved in mitosis (go:1902850) 2 //- mitotic anapháse r–hsa–68882 0  $_{\Gamma}$  mitotic g1 phase and g1/s transition r-hsa-453279 mitotic ğ2-g2/m phases r-hsa-453274  $\frac{1}{2}$  mitotic metaphase and anaphase r-hsa-2555396 mitotic metaphase plate congression (go:0007080) mitotic nuclear division (go:0140014) mitotic prometaphase r-hsa-68877 mitotic sister chromatid segregation (go:0000070) mitotic spindle checkpoint r-hsa-69618 mitotic spindle organization (go:0007052) oocyte meiosis positive regulation of cell cycle process (go:0090068) progesterone-mediated oocyte maturation regulation of cell cycle process (go:0010564) regulation of cyclin-dependent protein serine/threonine kinase activity (go:0000079) regulation of cytokinesis (go:0032465) regulation of mitotic cell cycle phase transition (go:1901990) resolution of sister chromatid cohesion r-hsa-2500257 rho gtpase effectors r-hsa-195258 -rho gtpases activate formins r–hsa–5663220 separation of sister chromatids r-hsa-2467813 signaling by rho gtpases r-hsa-194315 sister chromatid segregation (go:0000819) unattached kinetochores signal amplification via a mad2 inhibitory signal r-hsa-141444