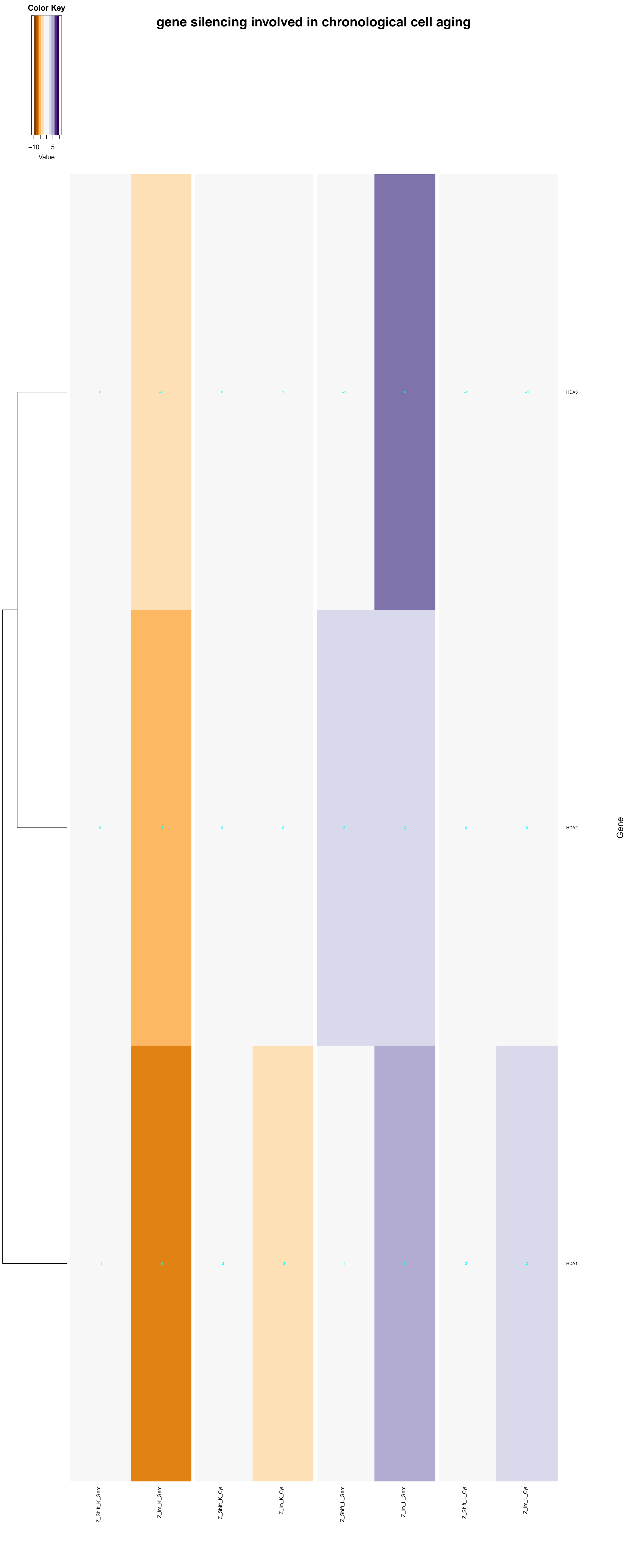
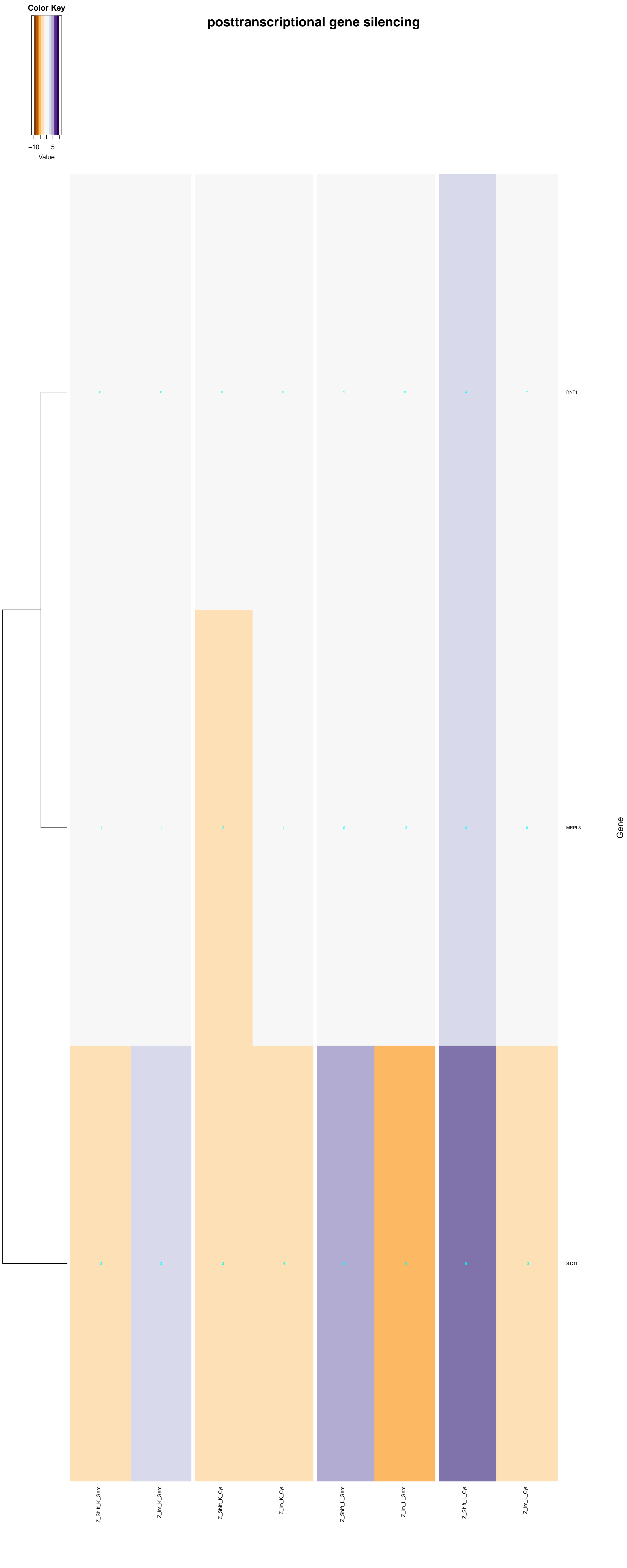
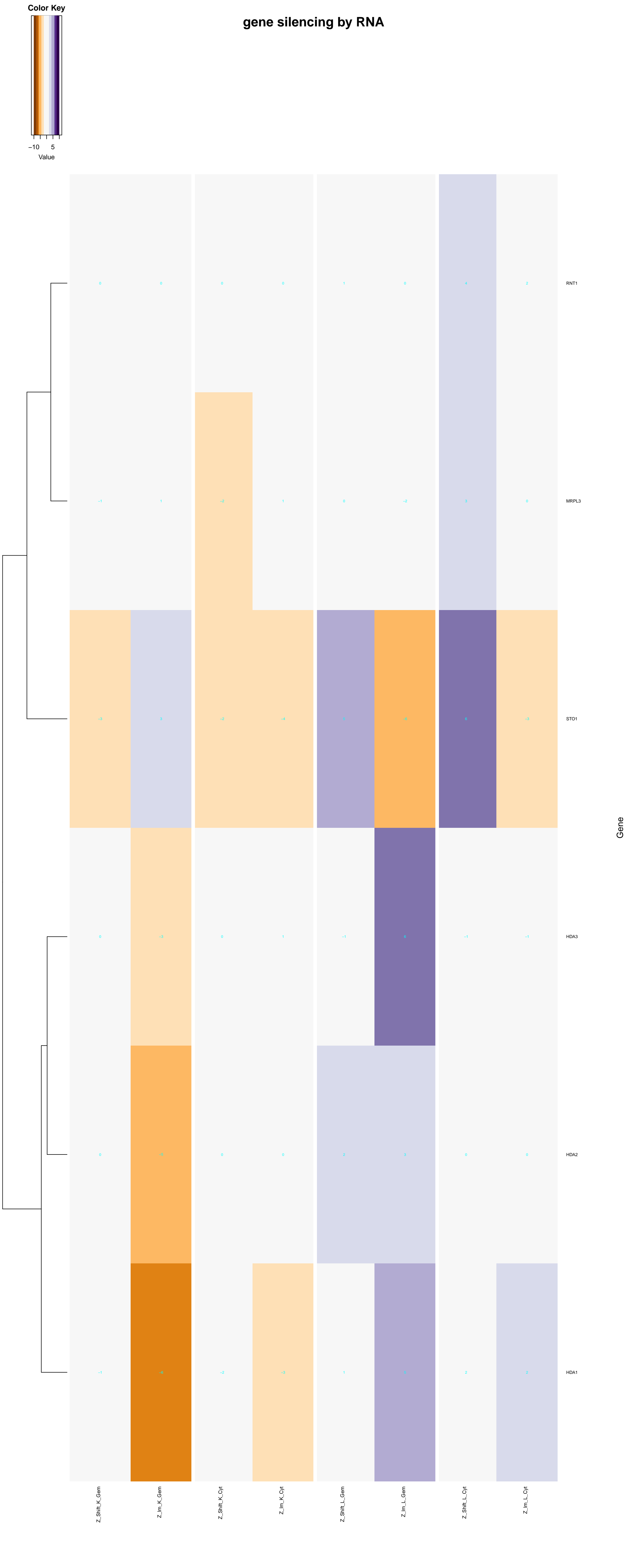
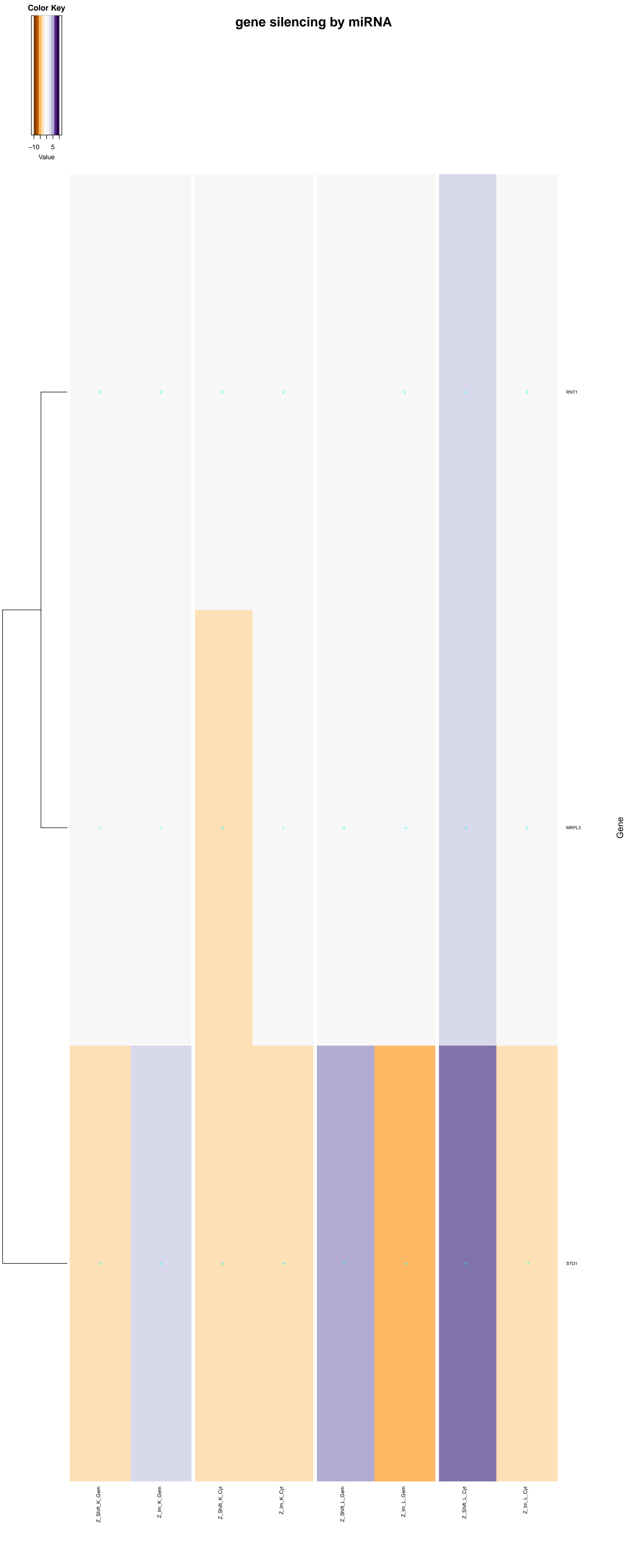


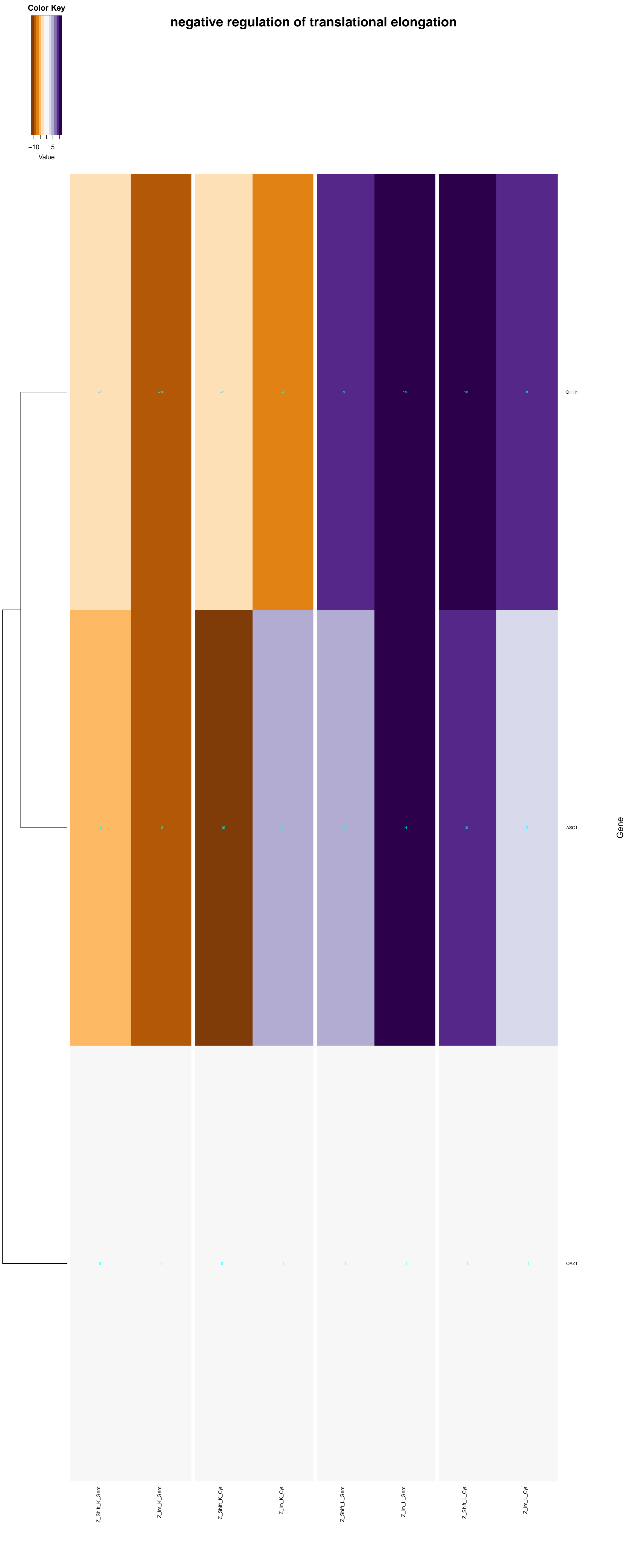
gene silencing involved in chronological cell aging

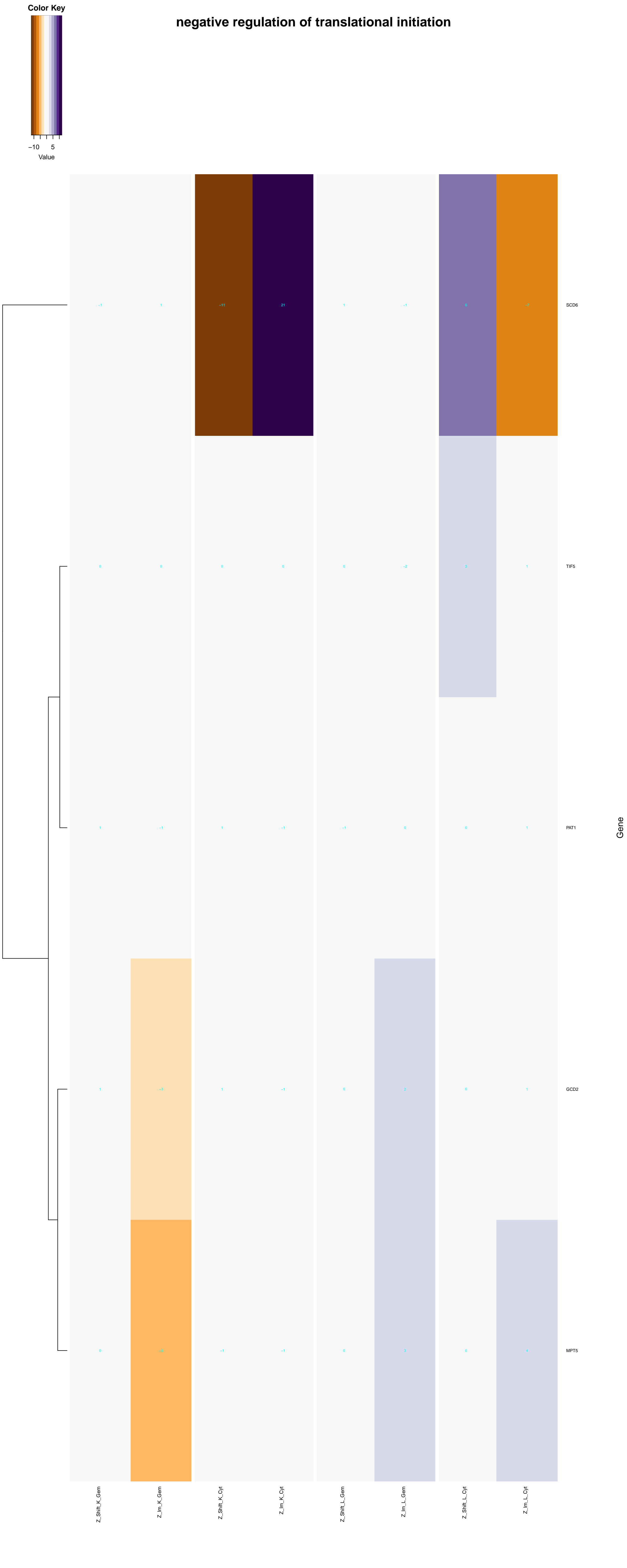


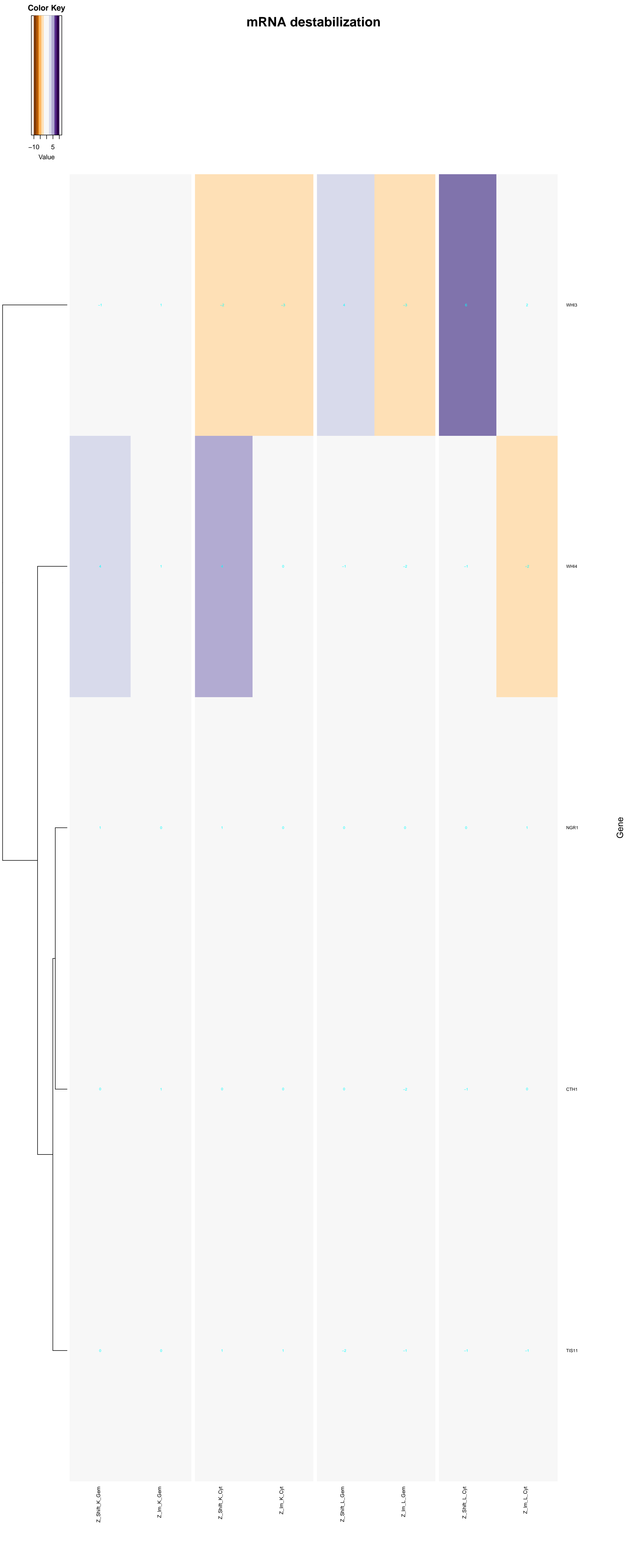


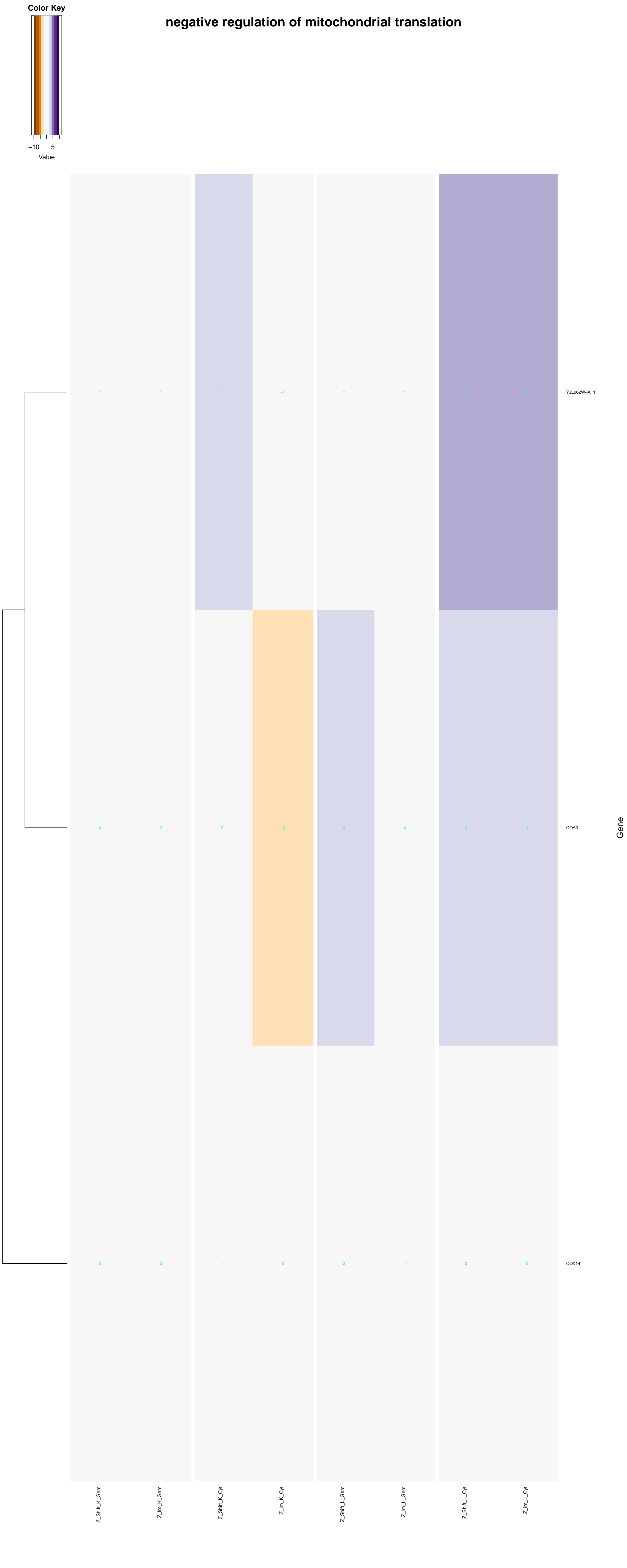


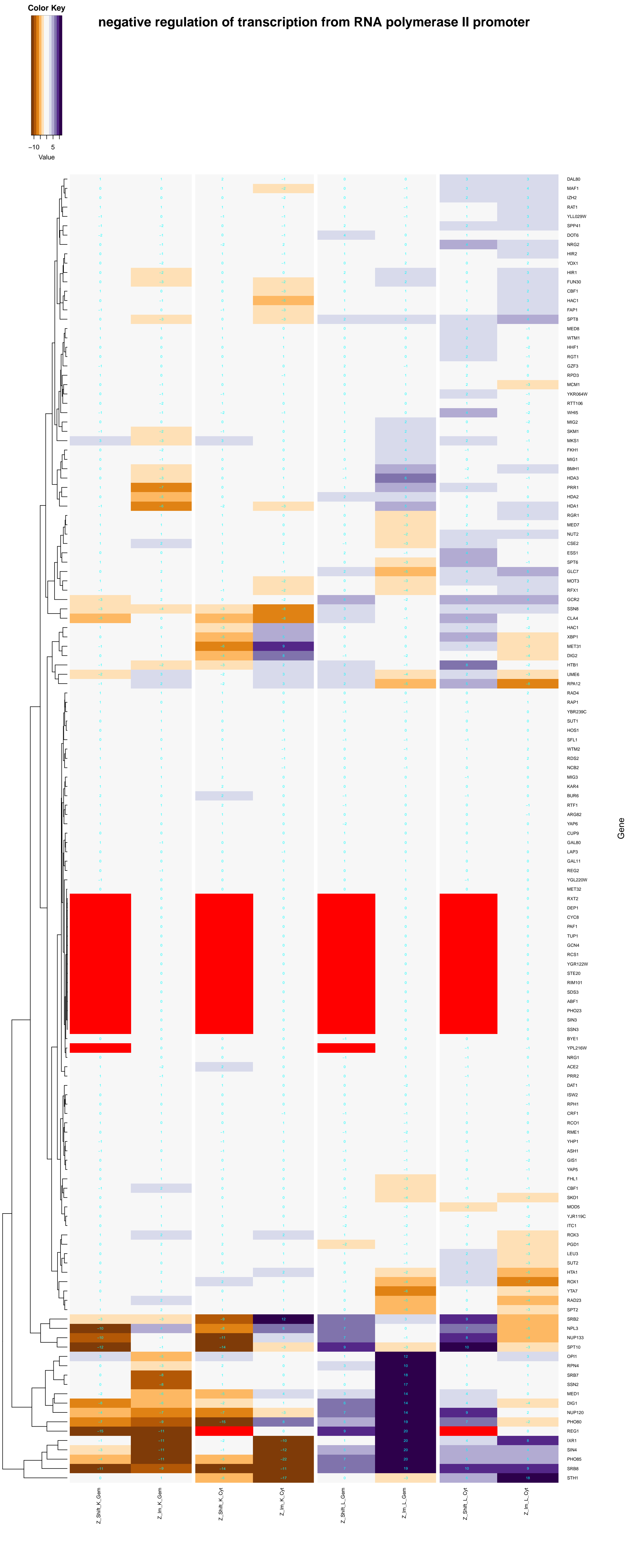


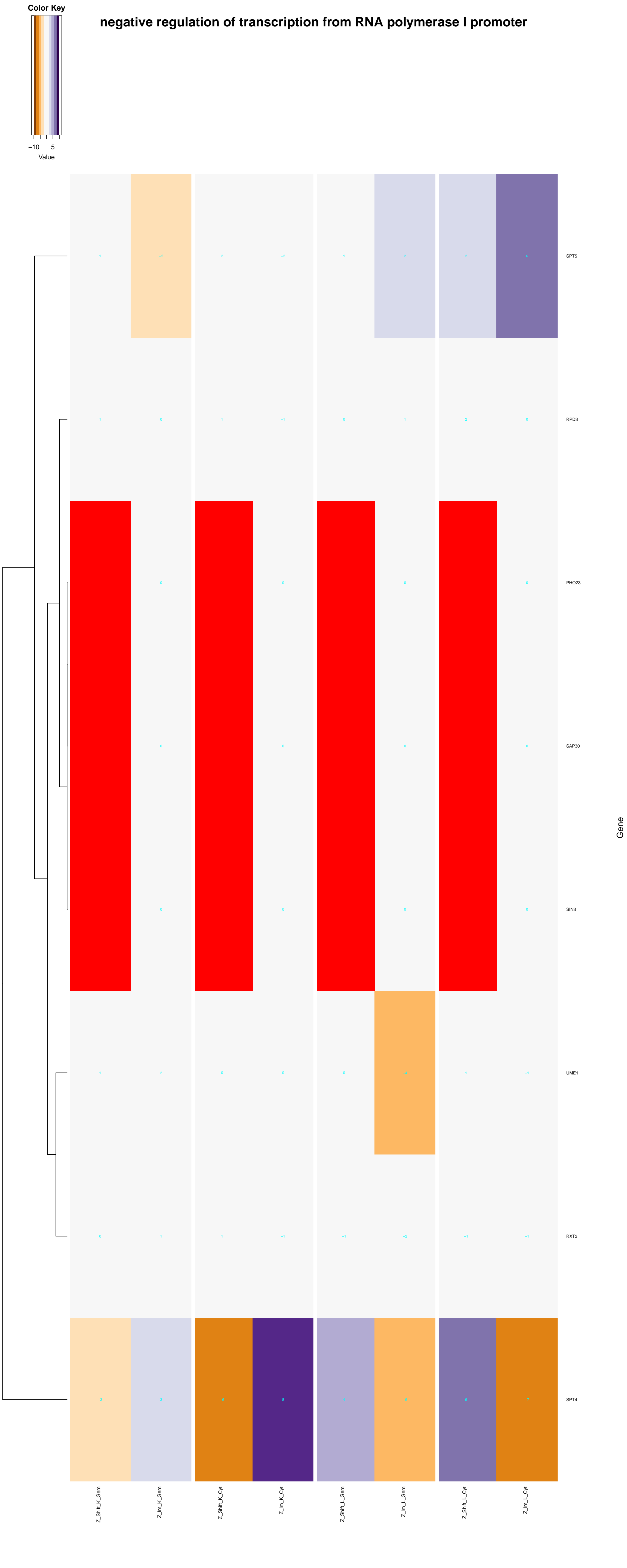


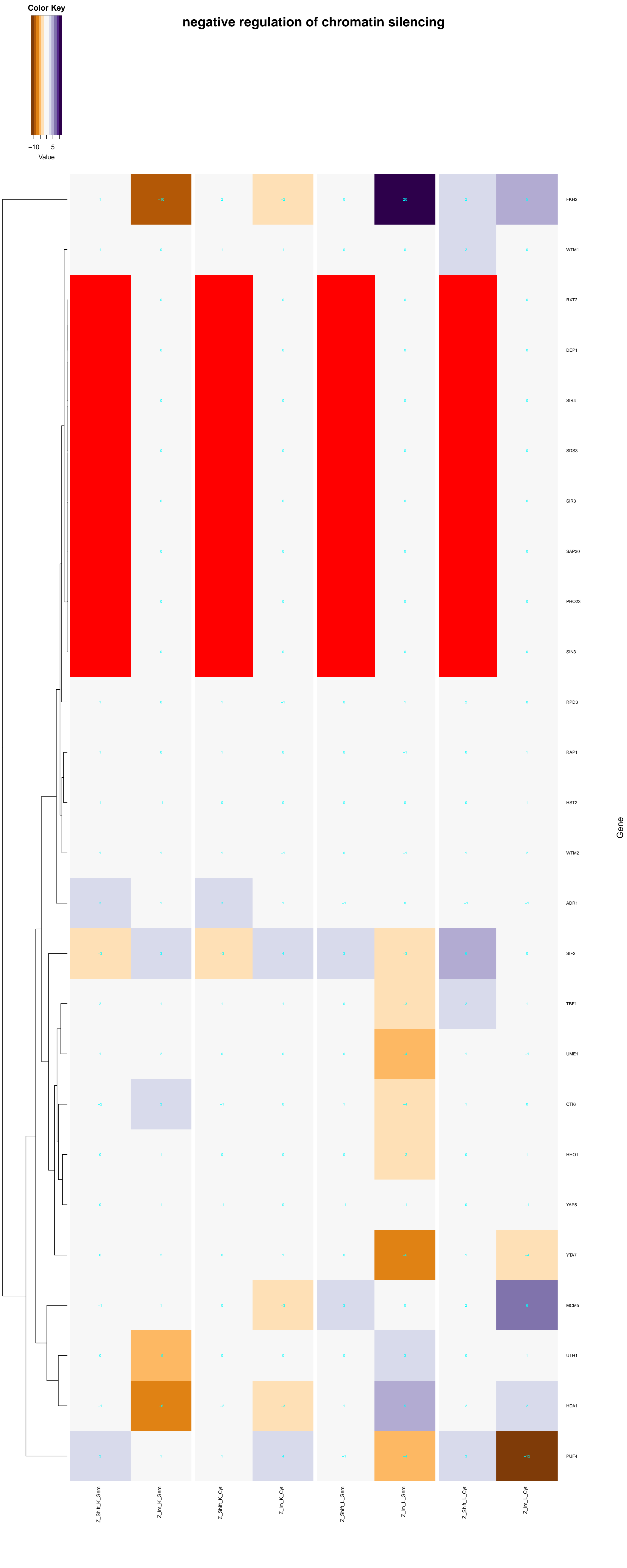


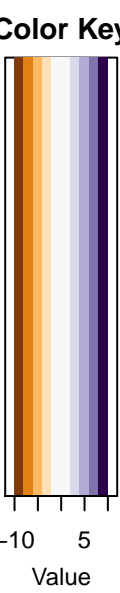




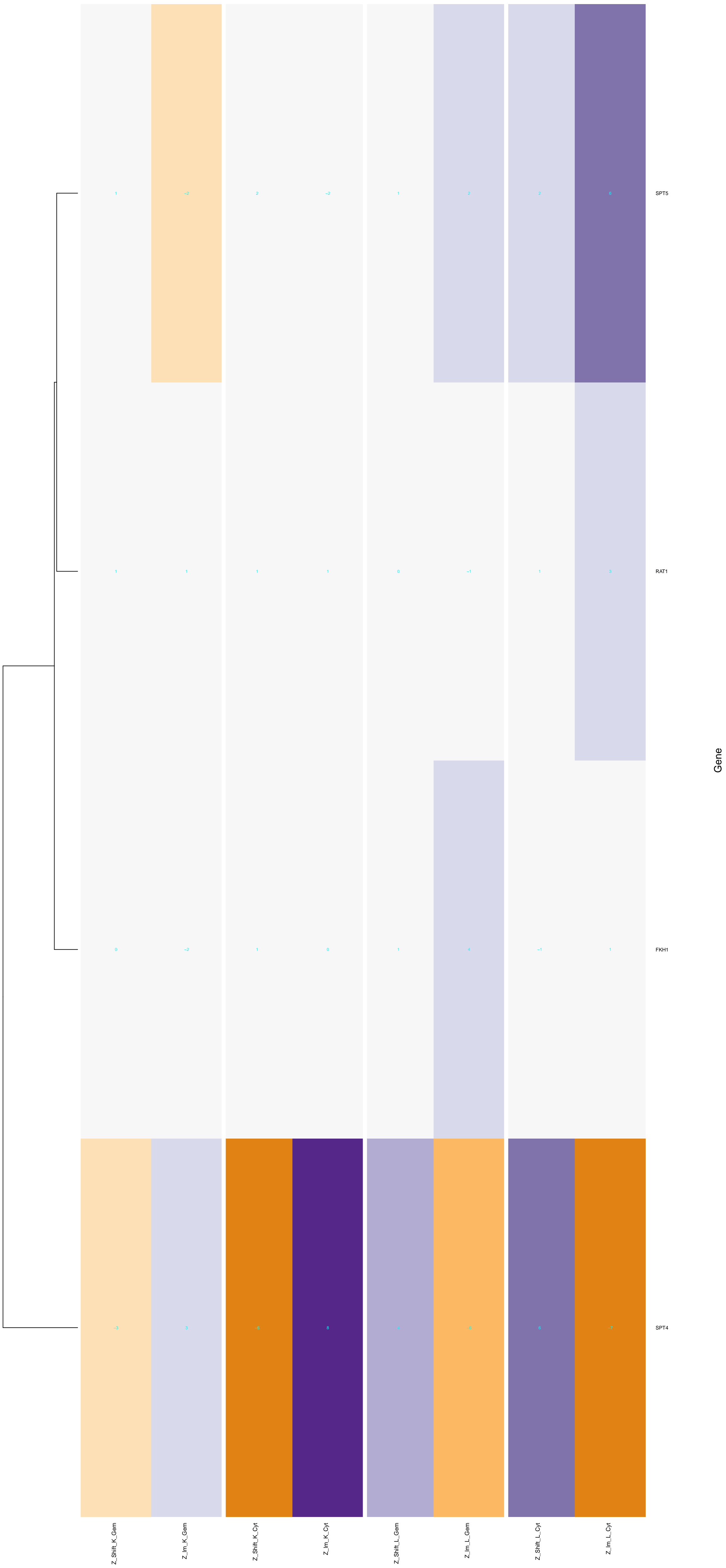


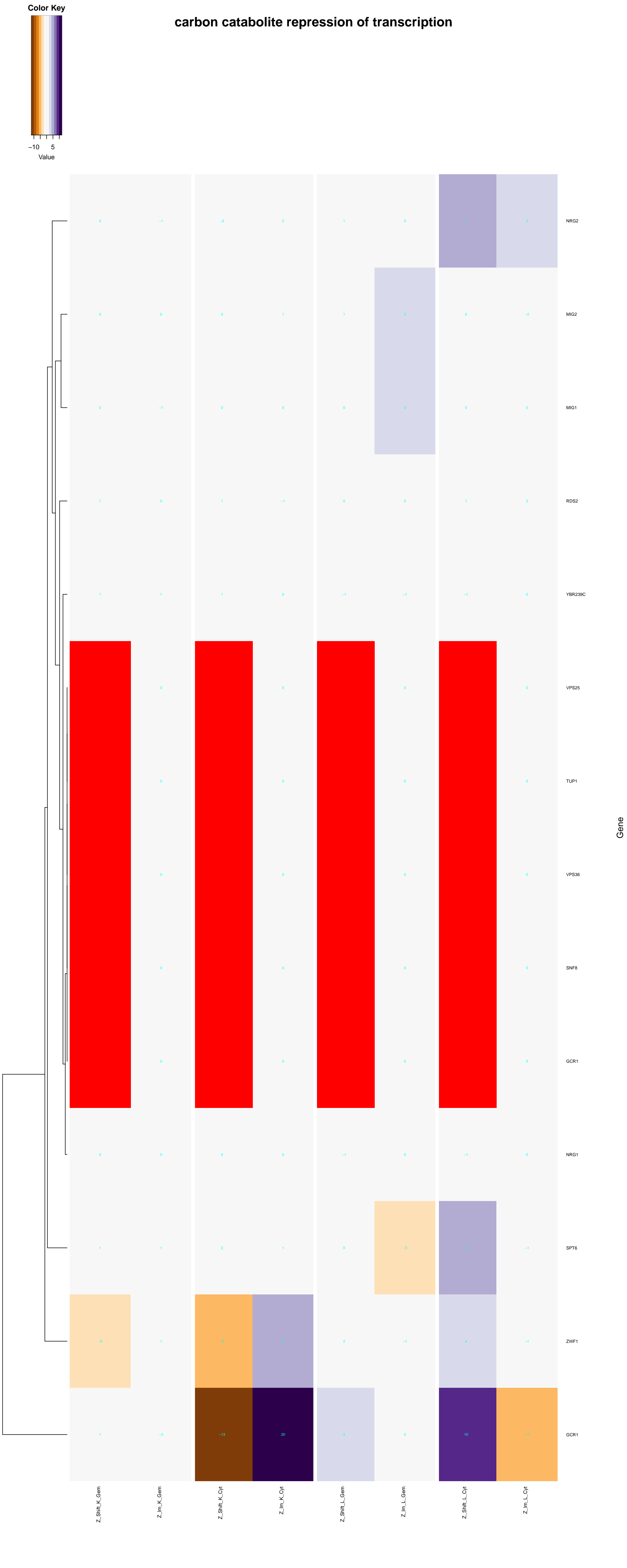


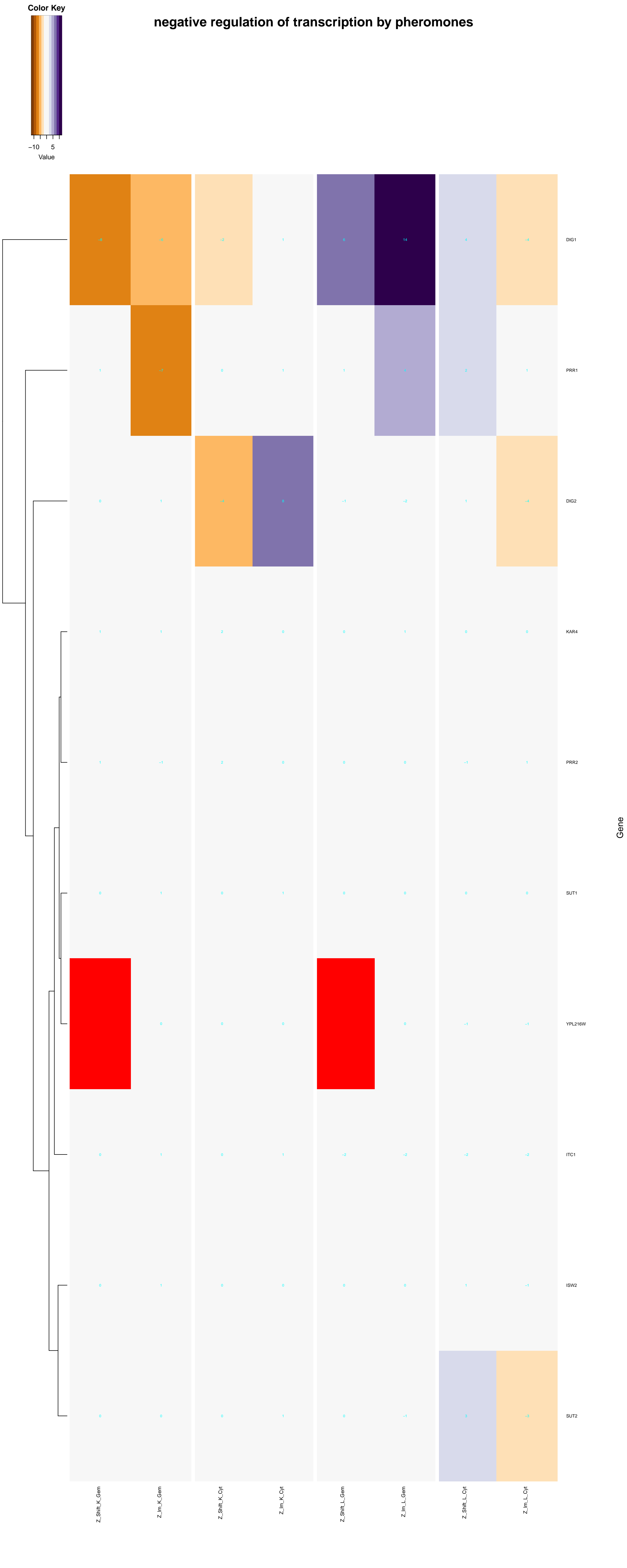


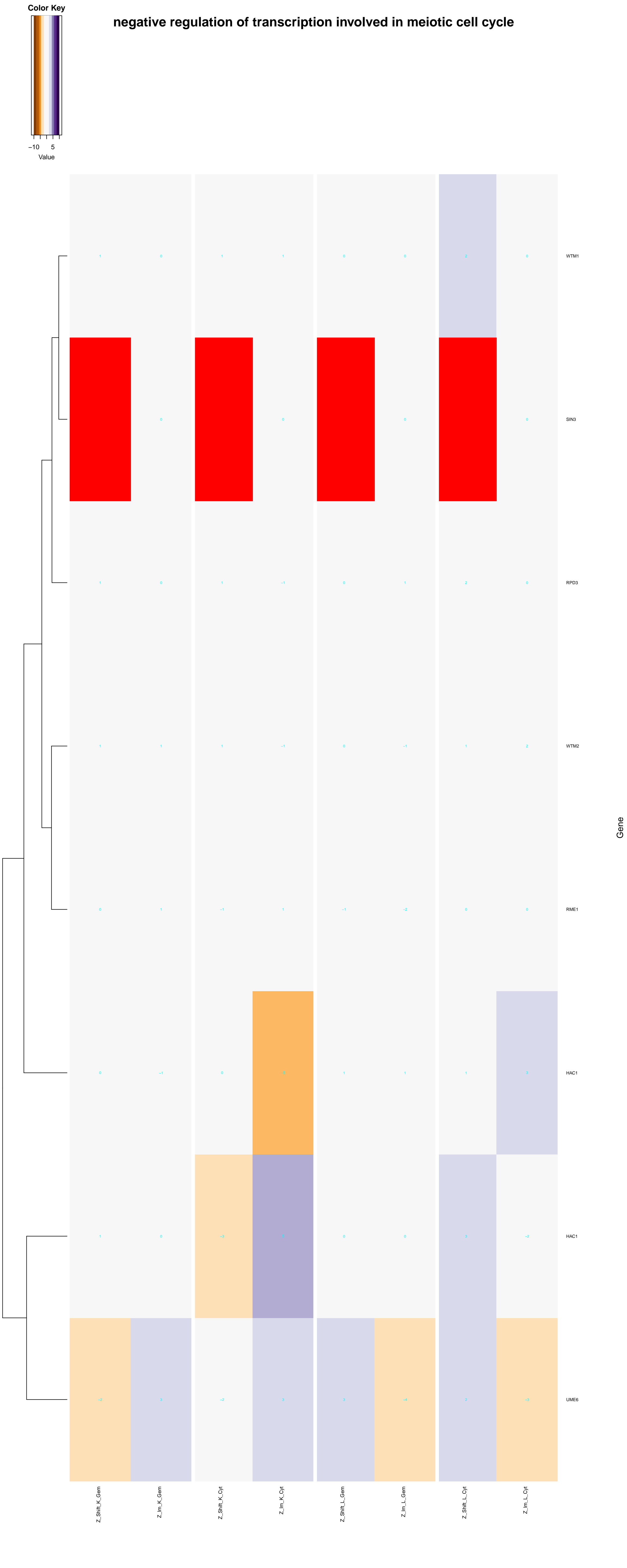


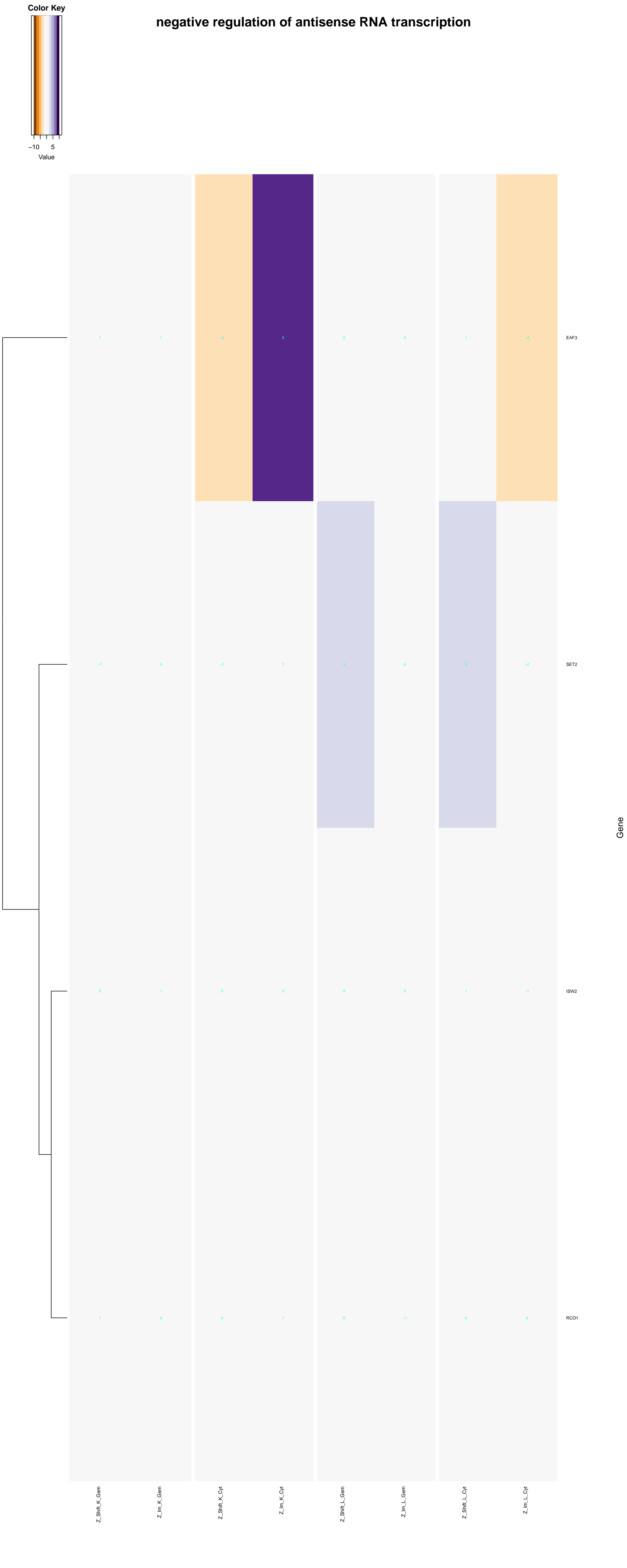
negative regulation of DNA-templated transcription, elongation





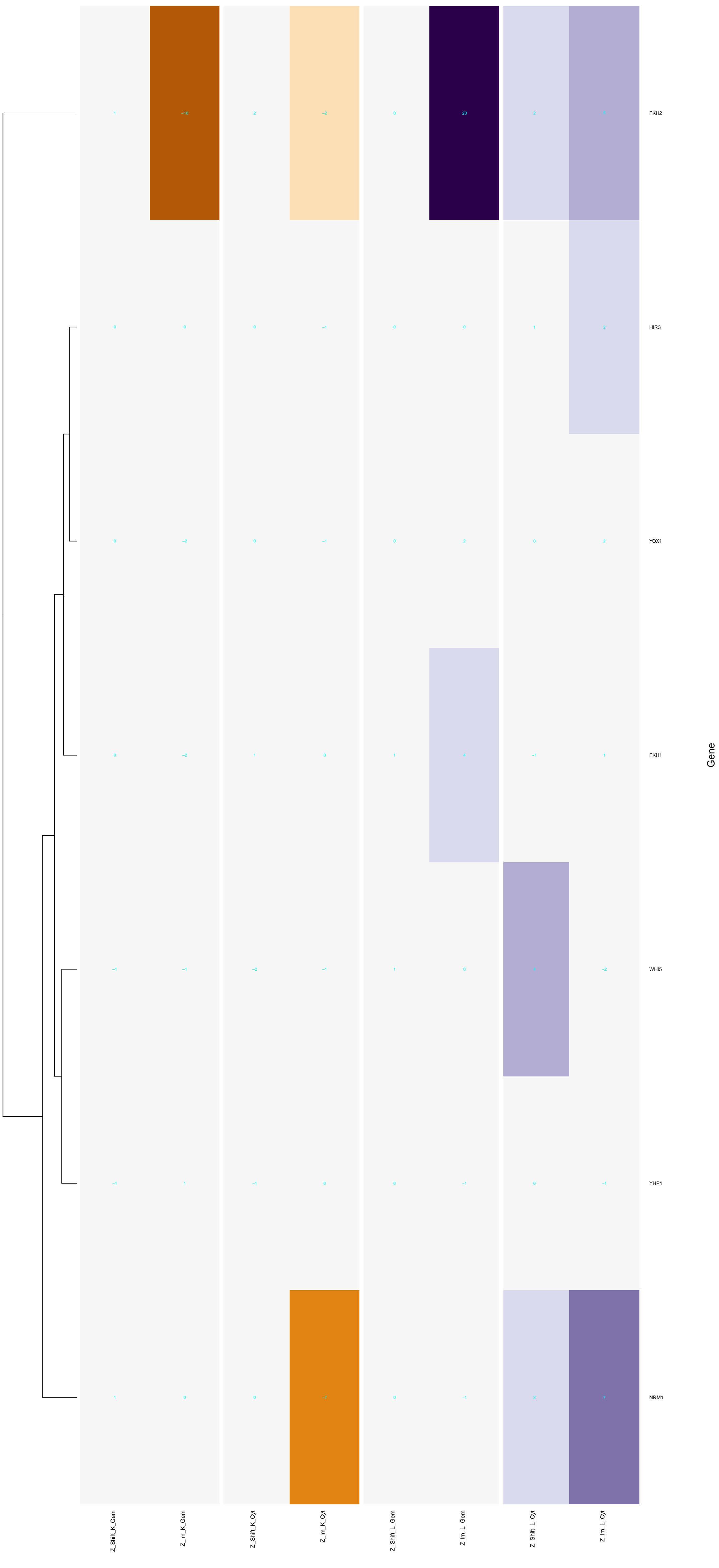


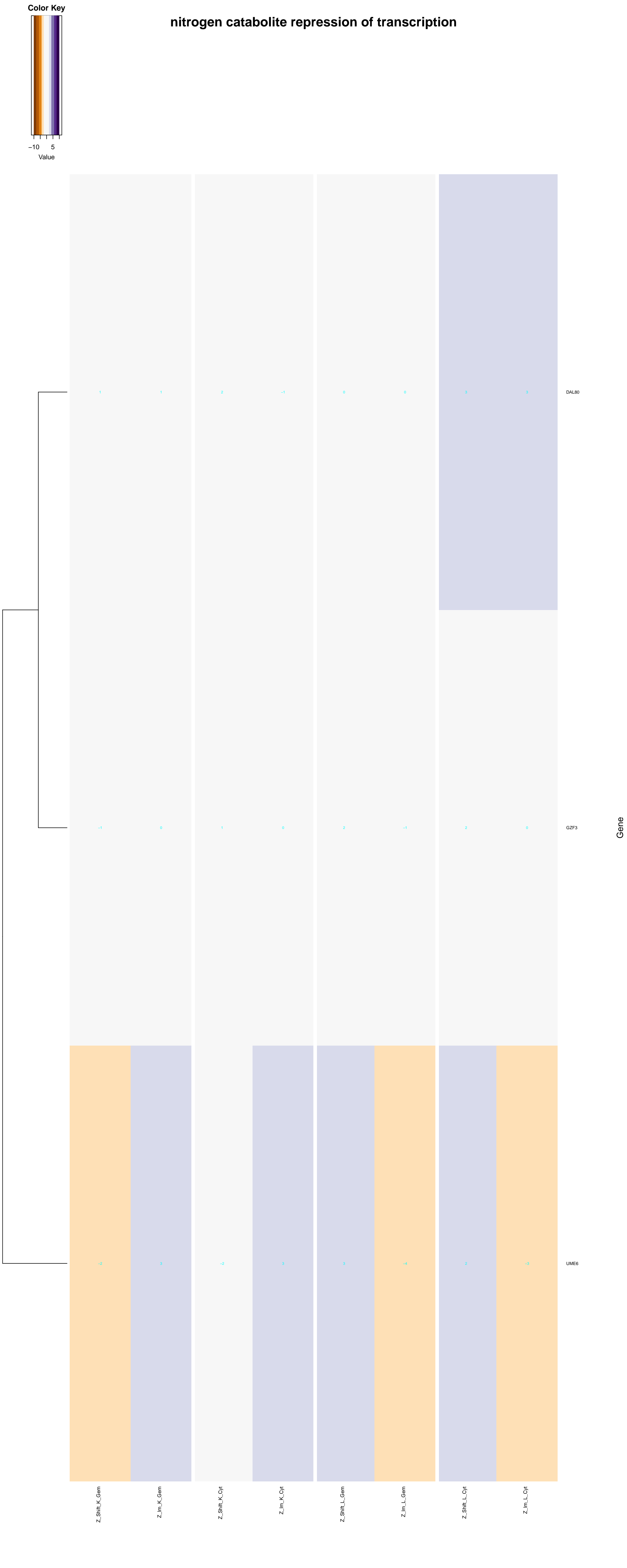


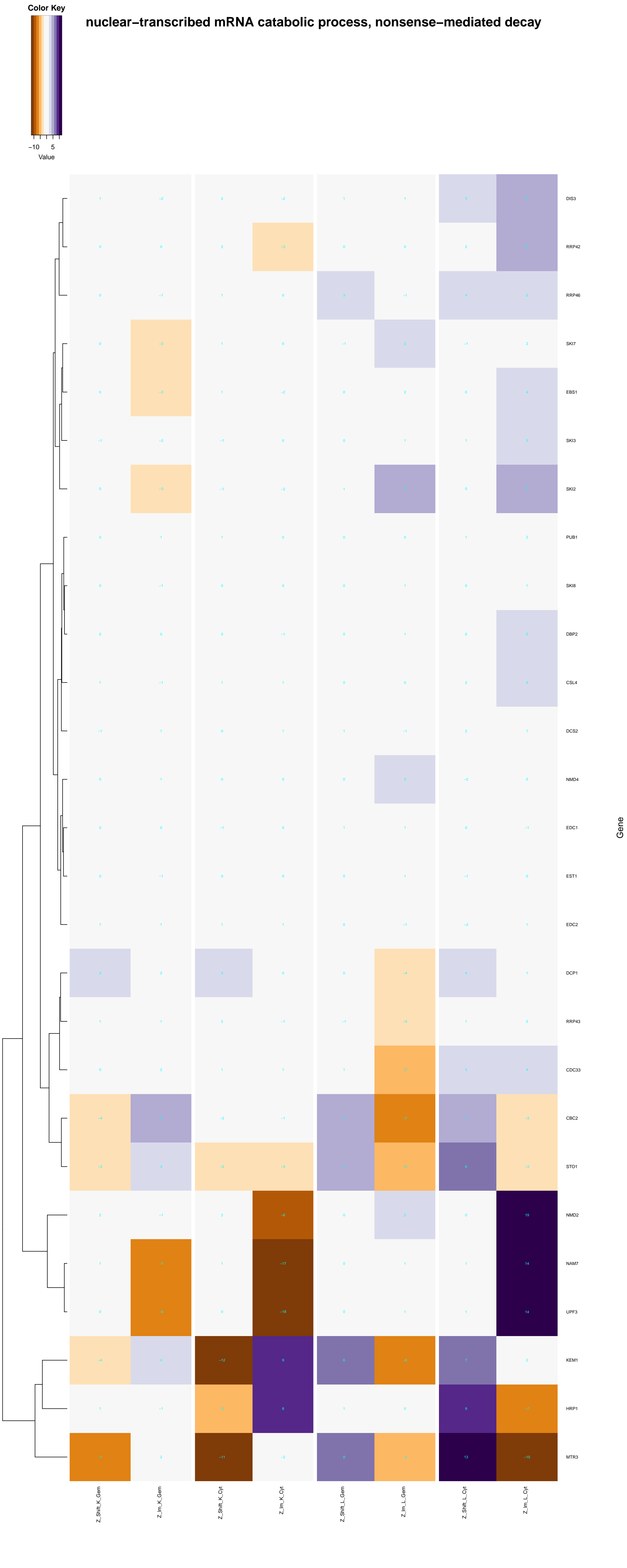


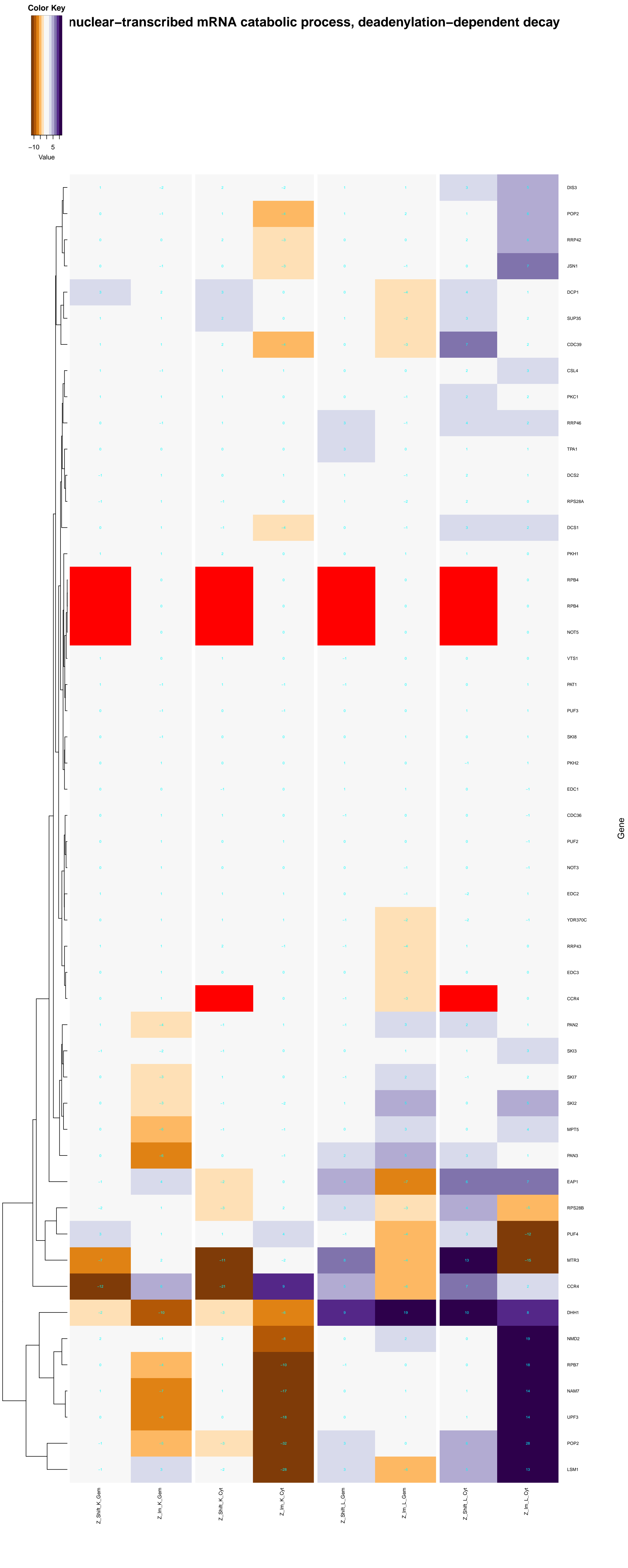


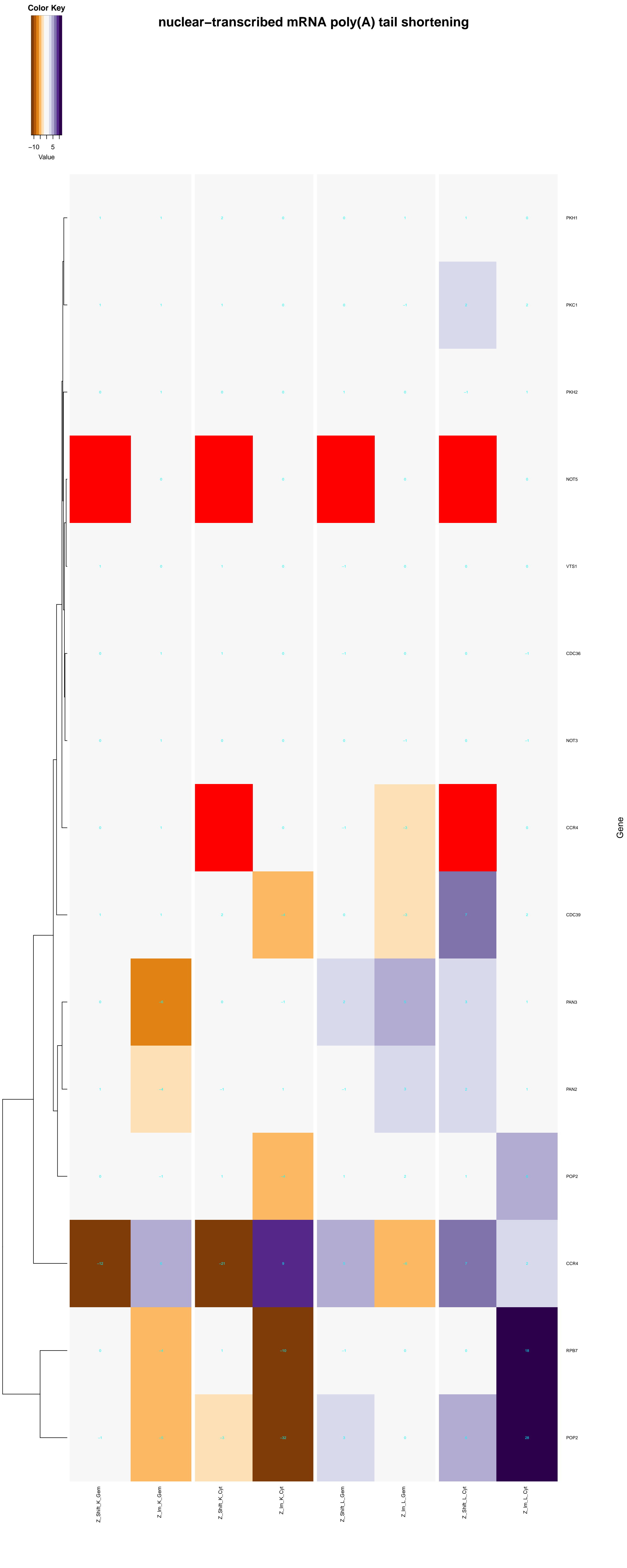
egative regulation of transcription involved in G1/S transition of mitotic cell cycle

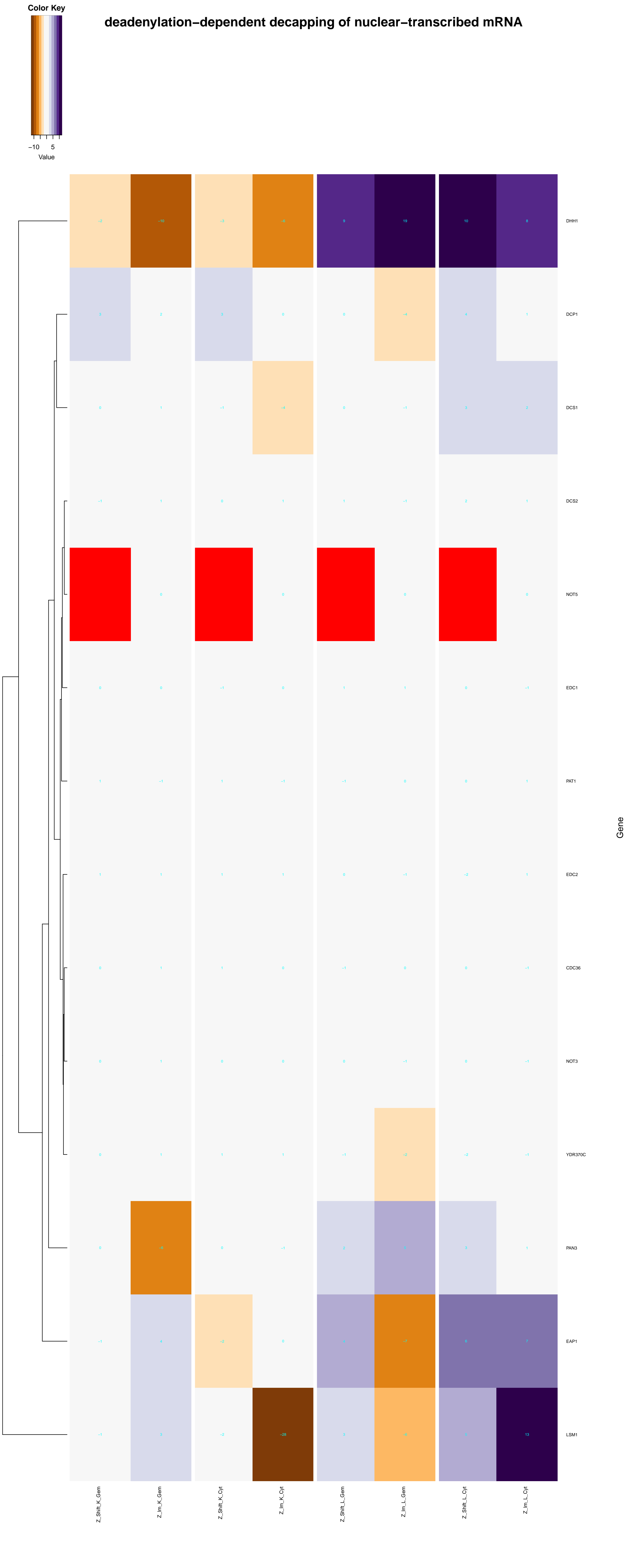


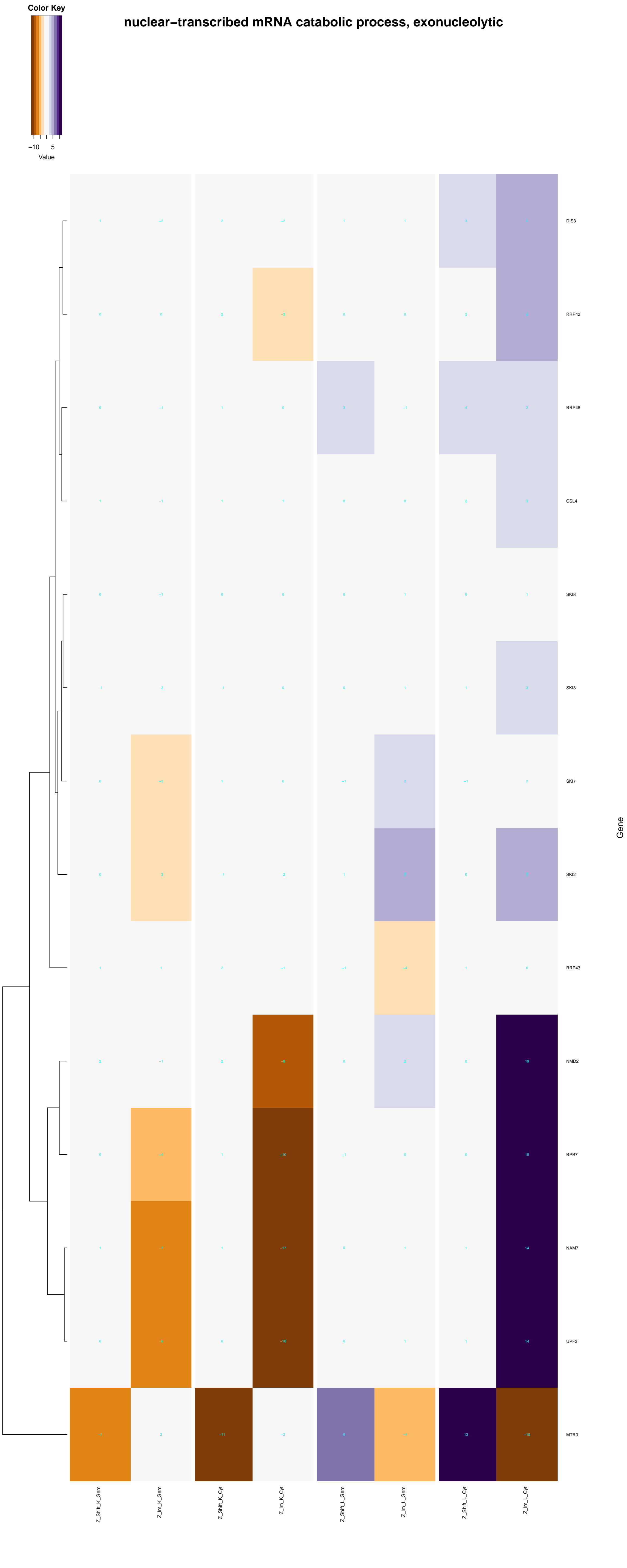








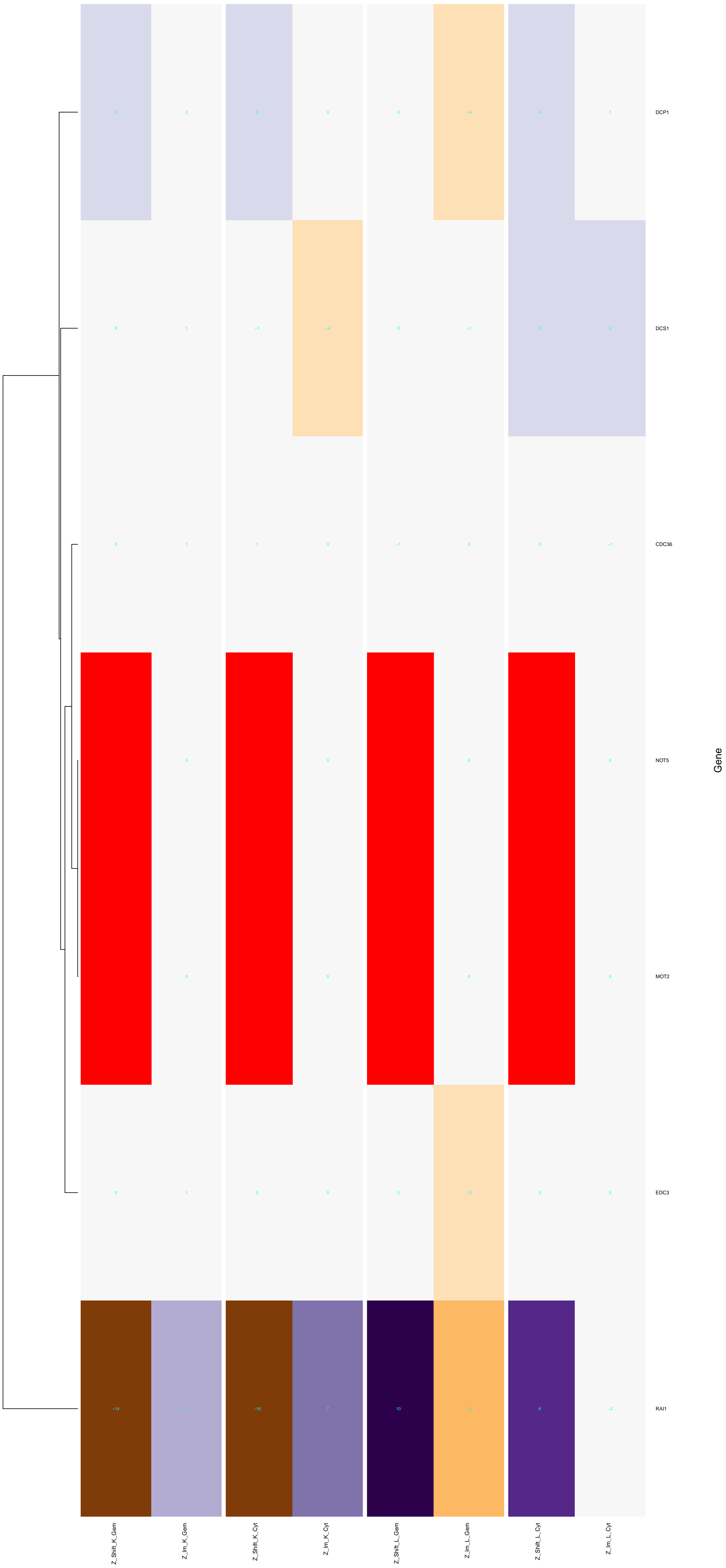


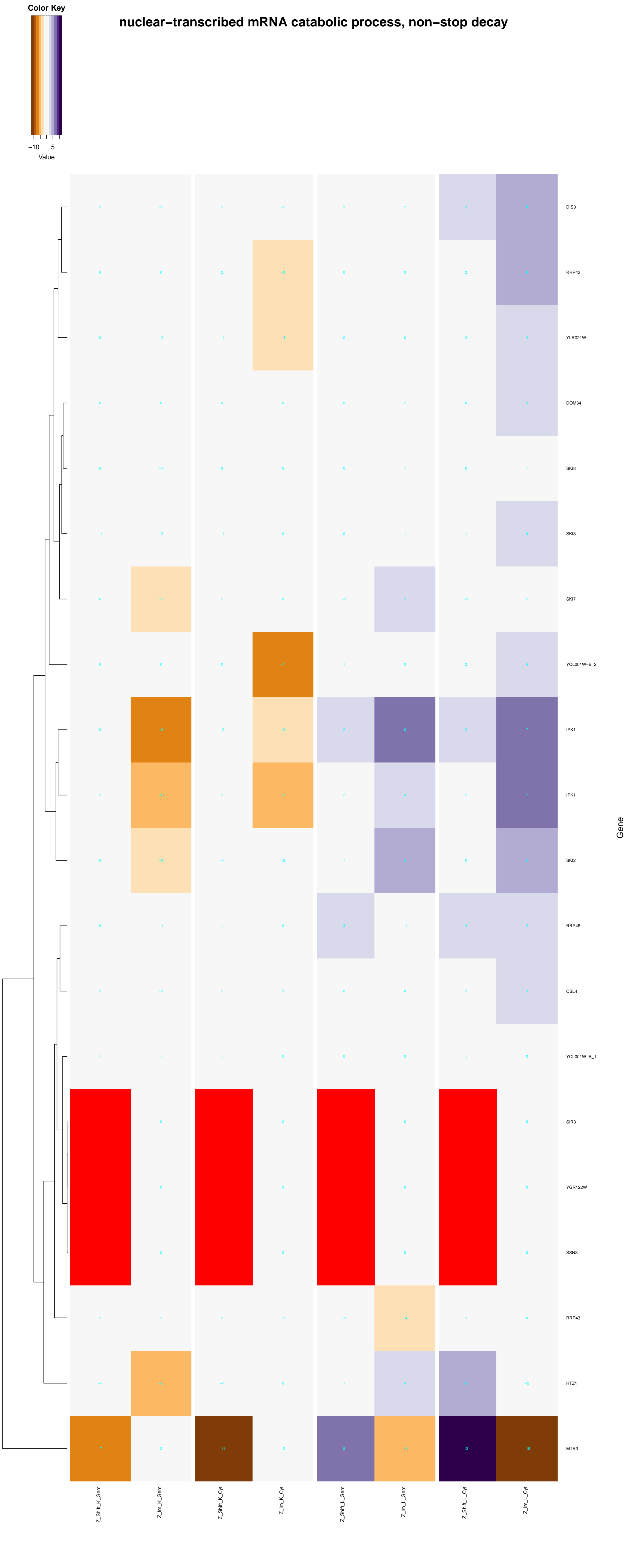


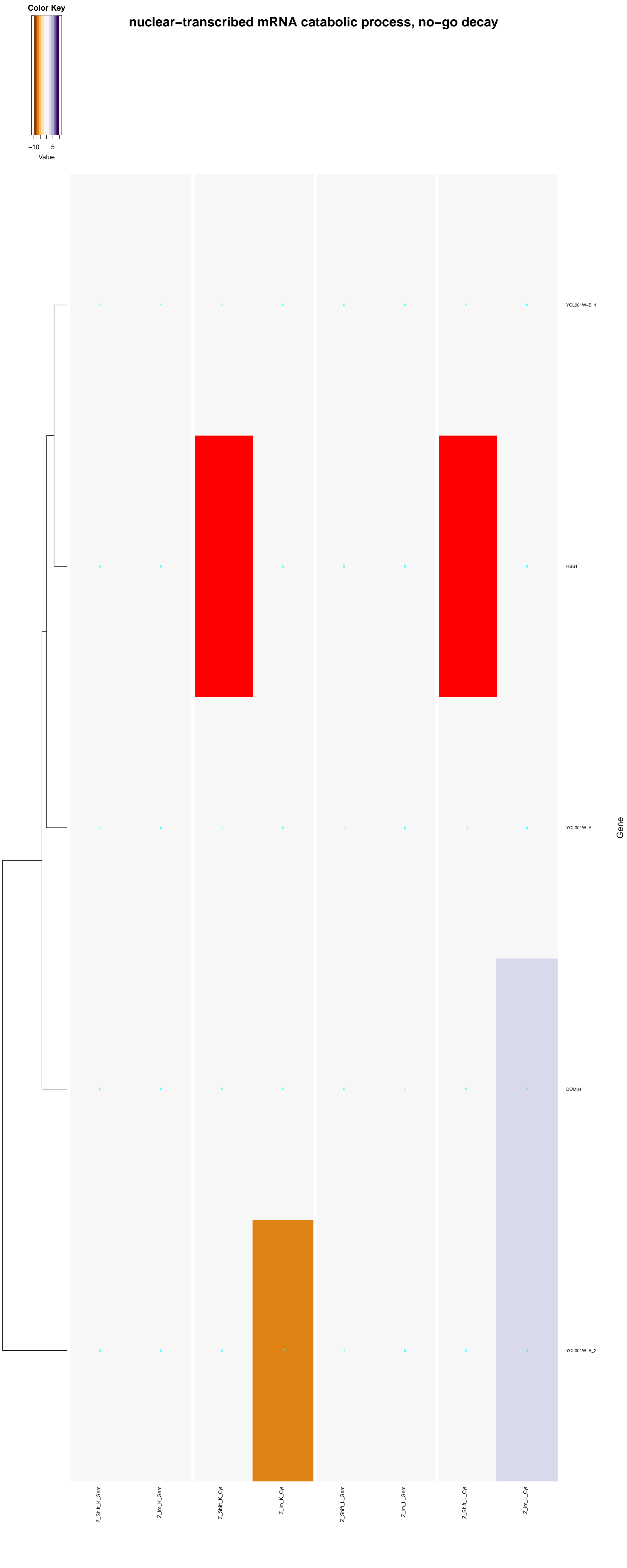


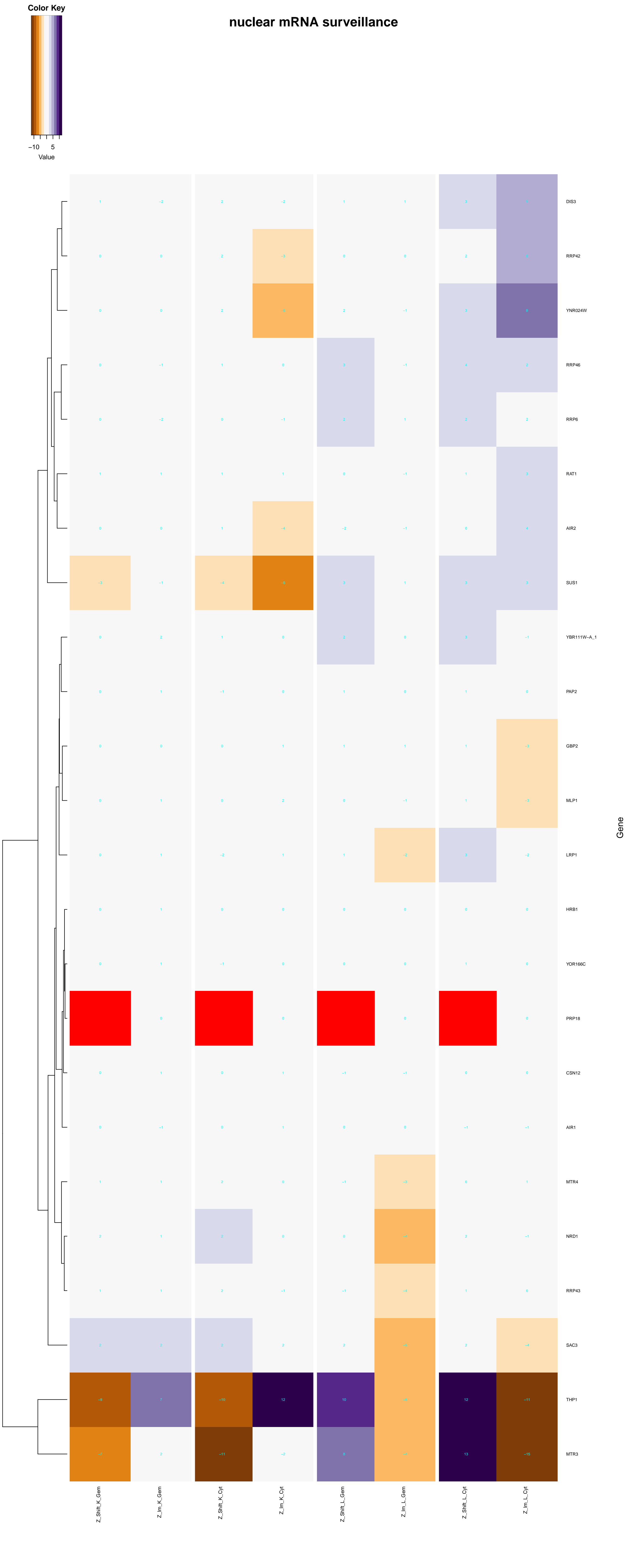


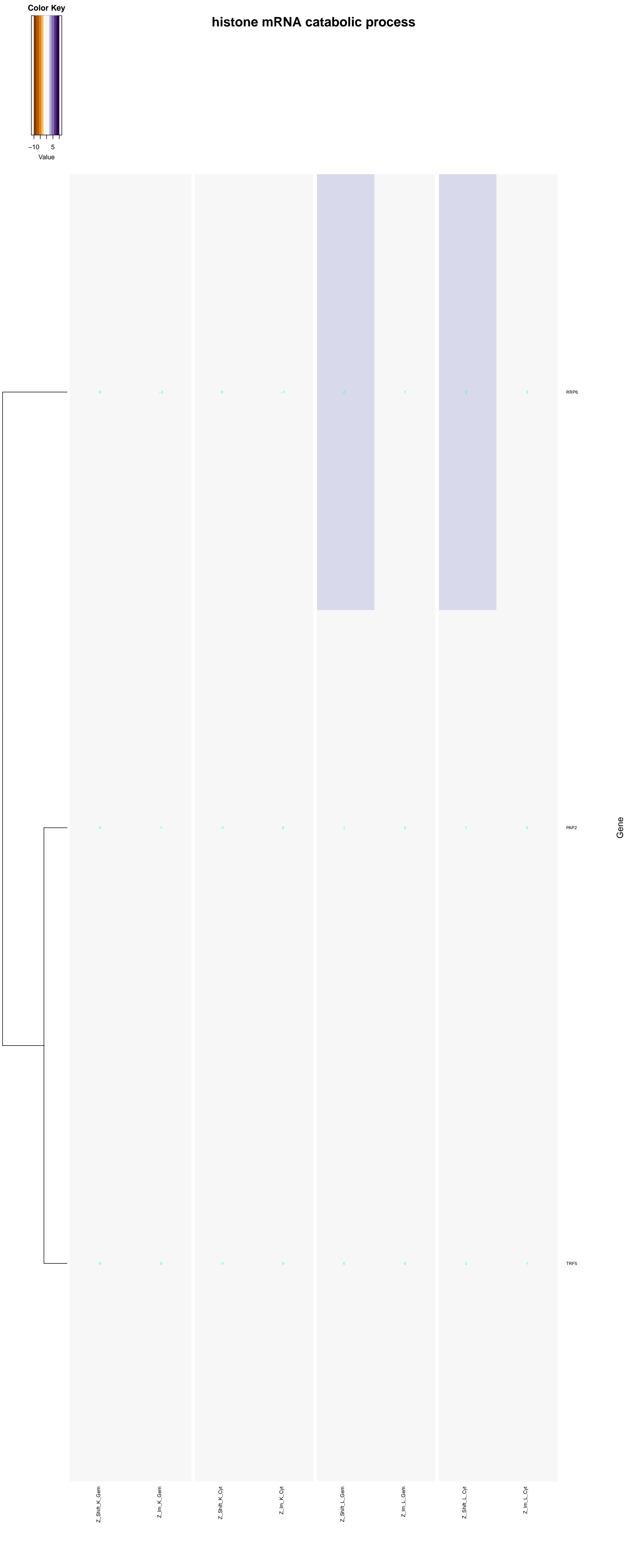
uclear-transcribed mRNA catabolic process, deadenylation-independent decay



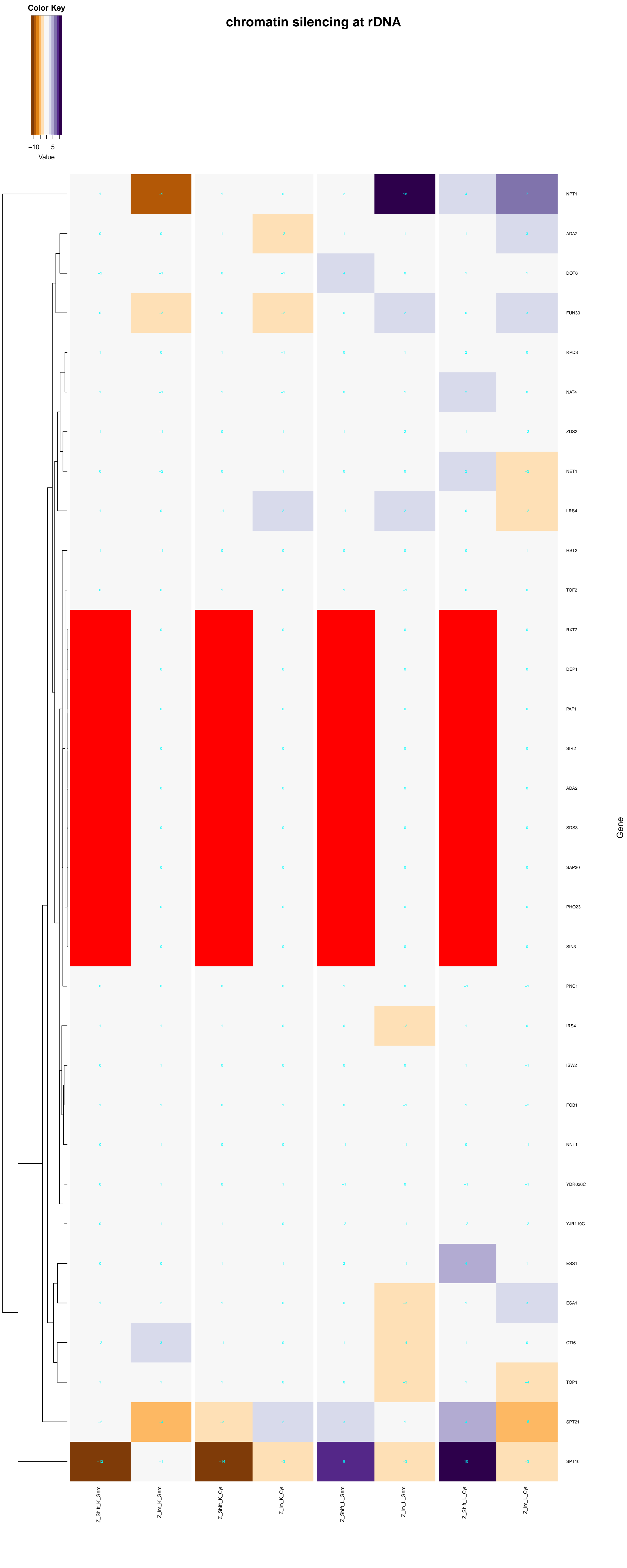


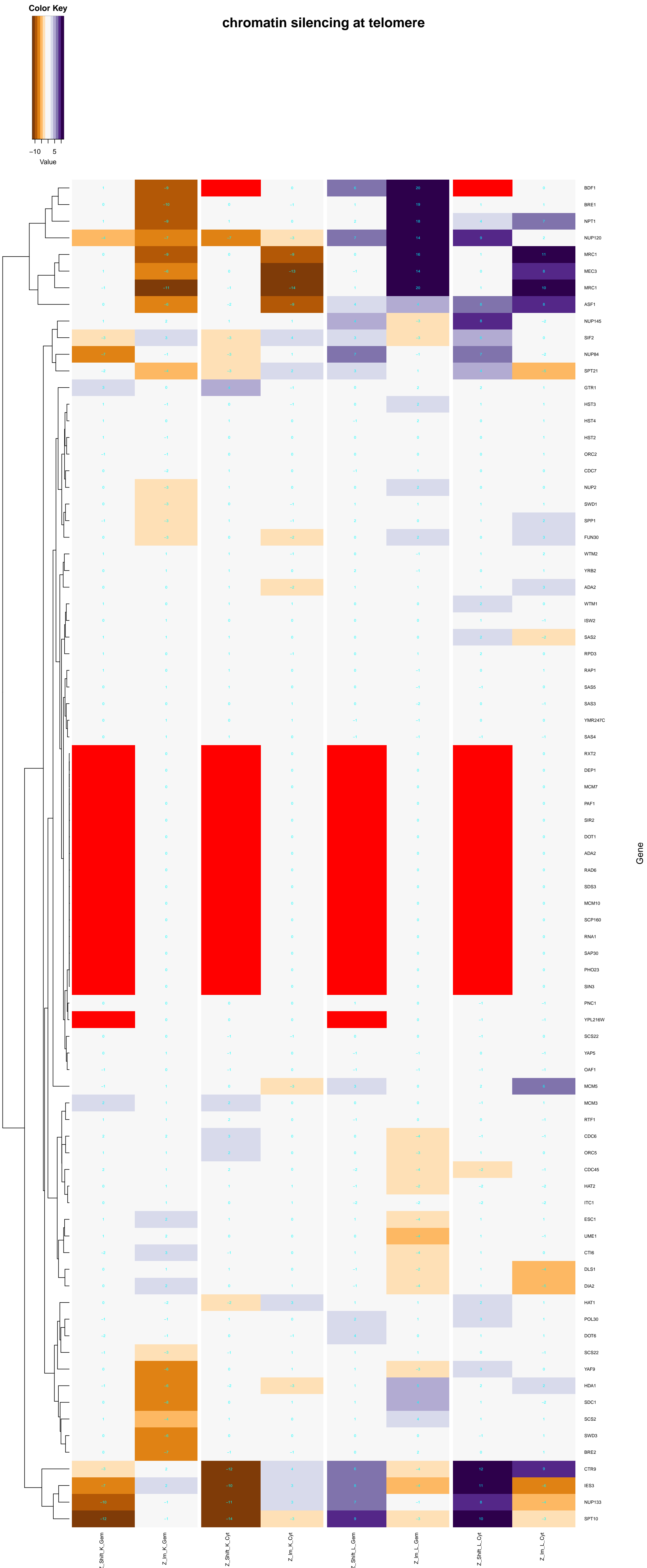


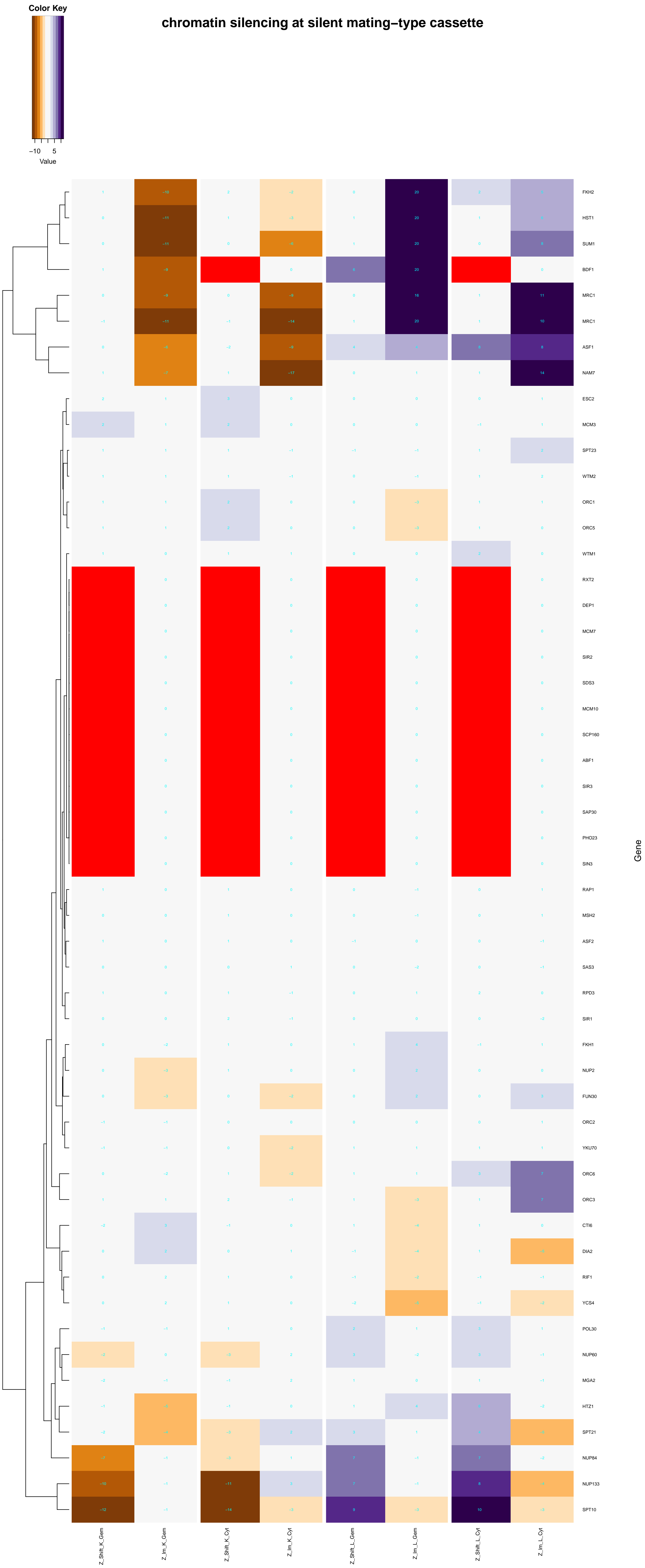


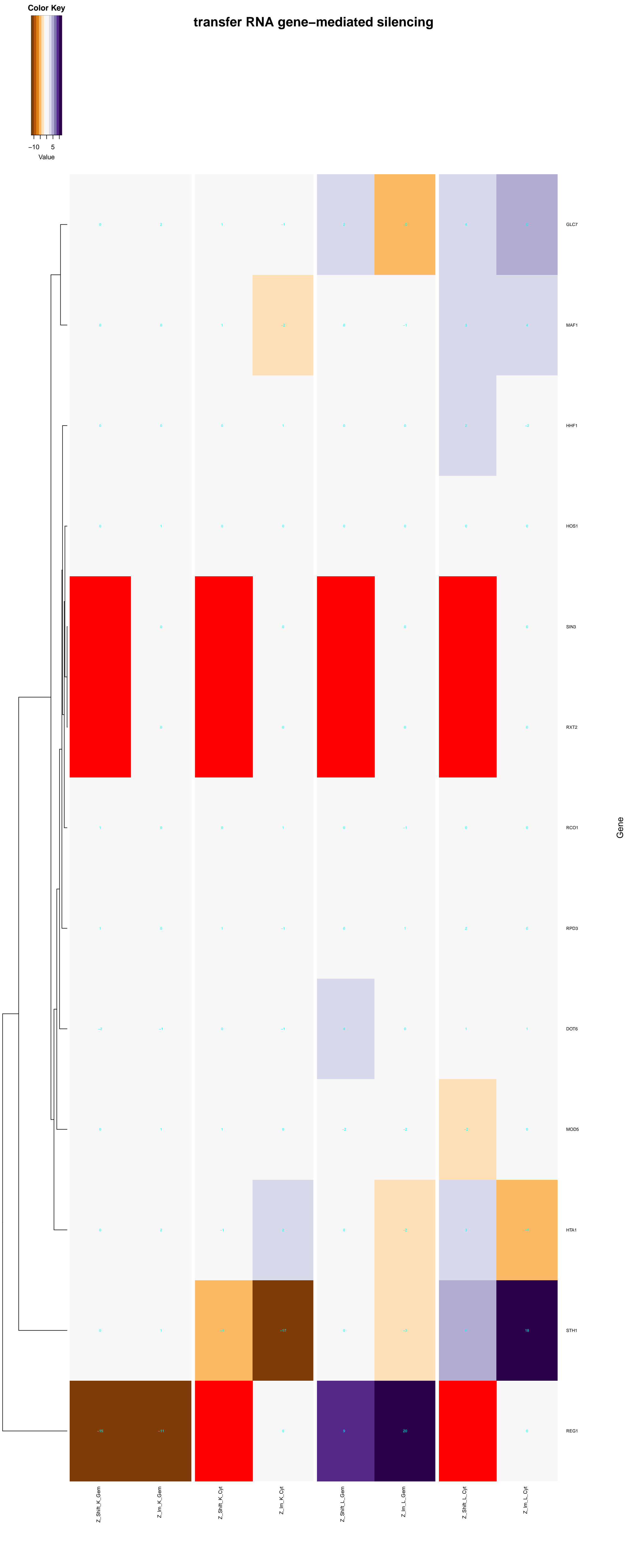


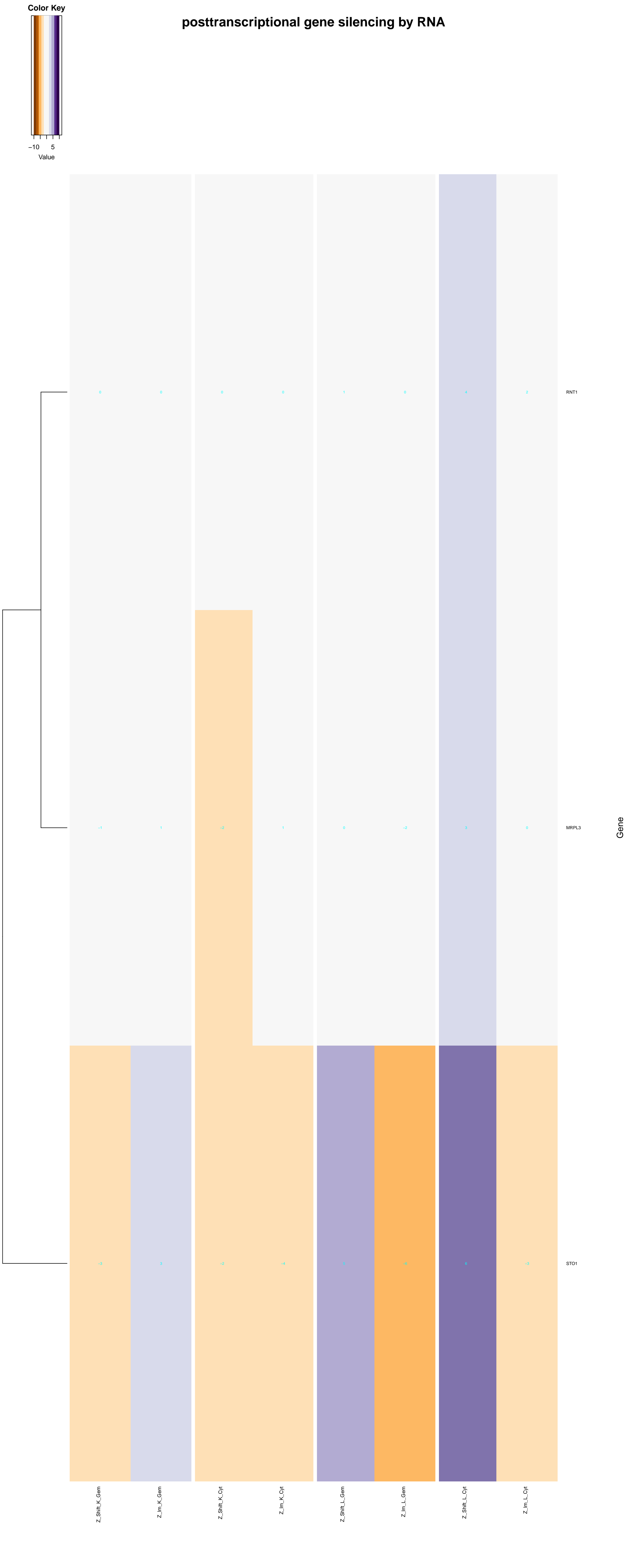


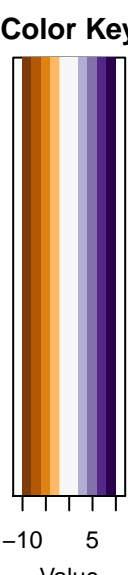




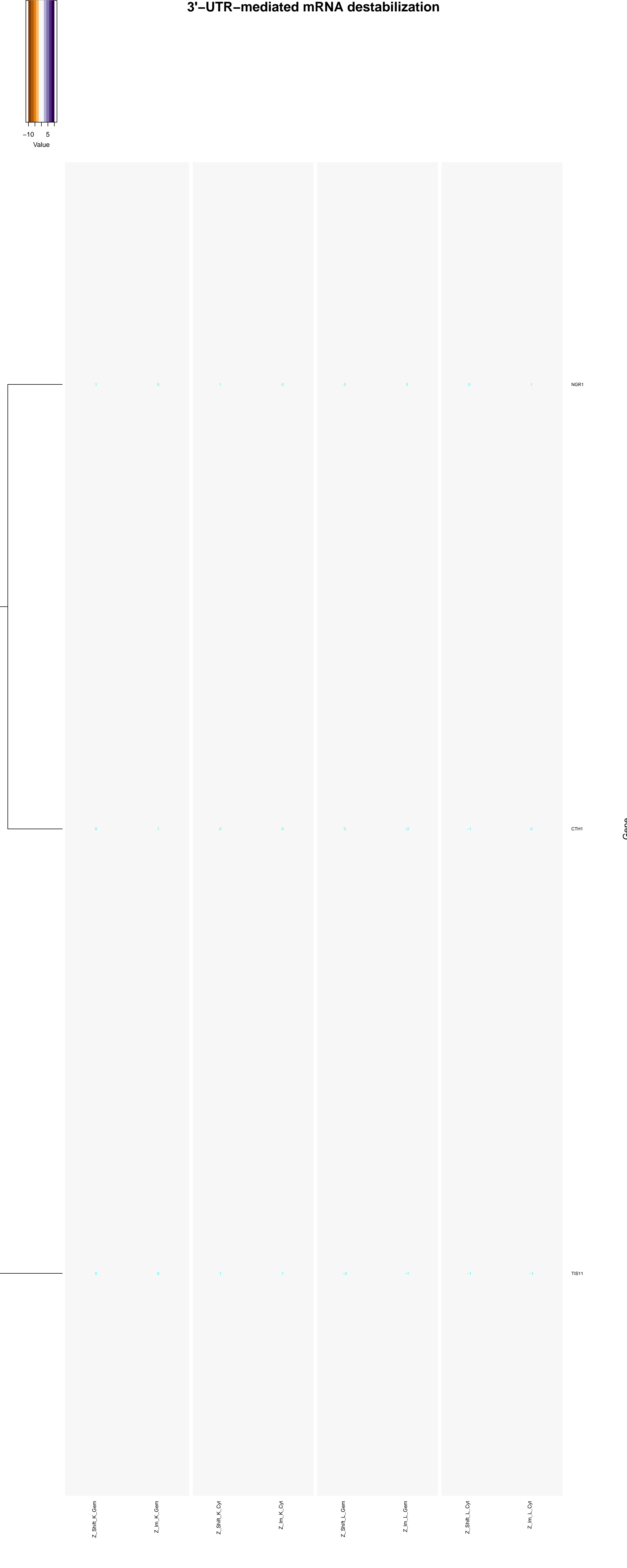


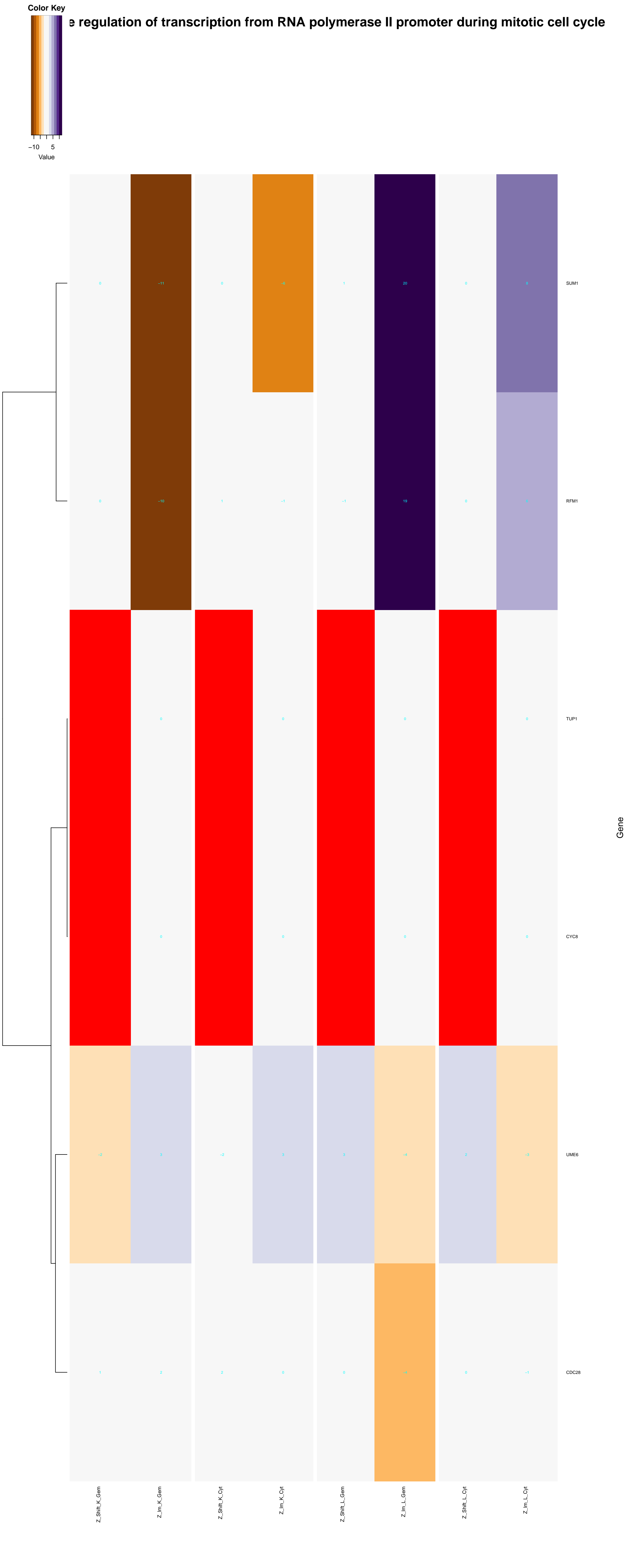


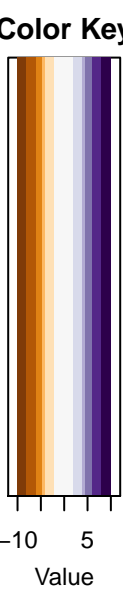




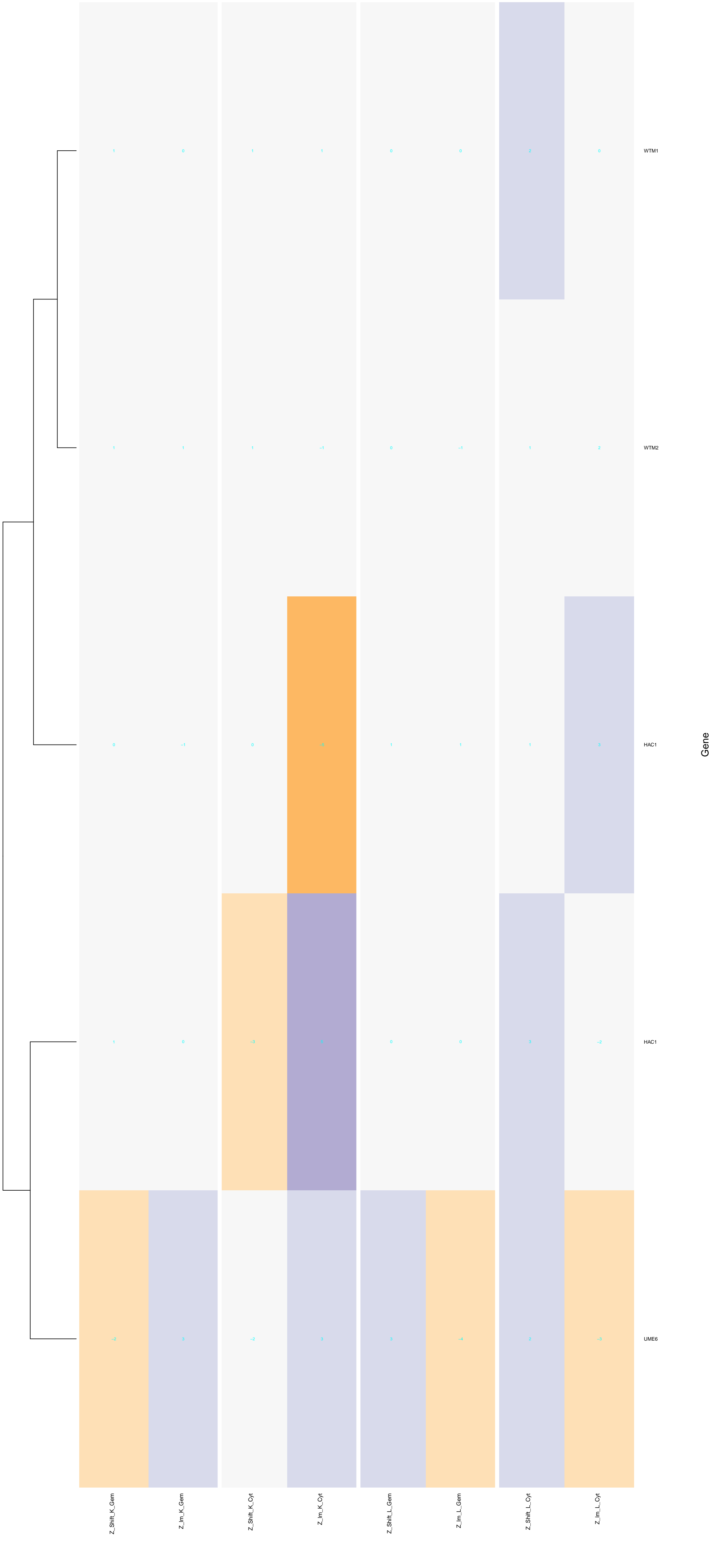
3'-UTR-mediated mRNA destabilization

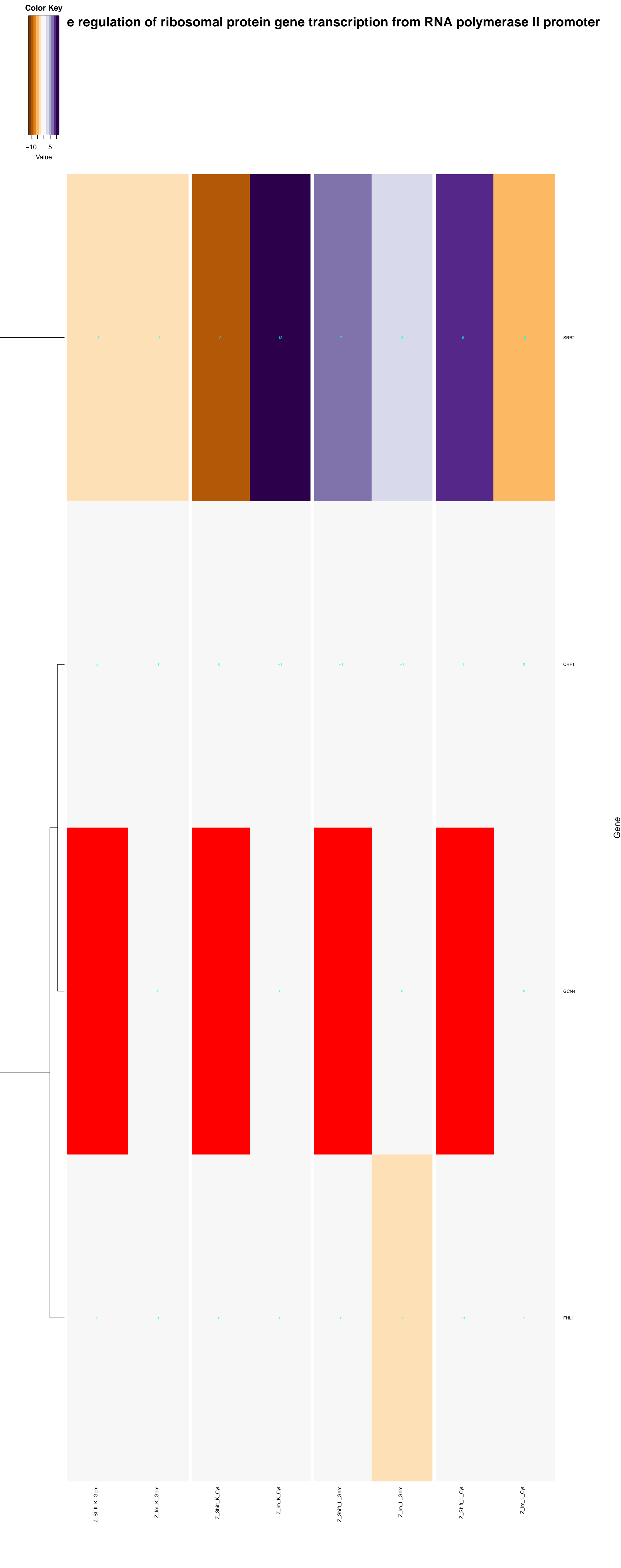


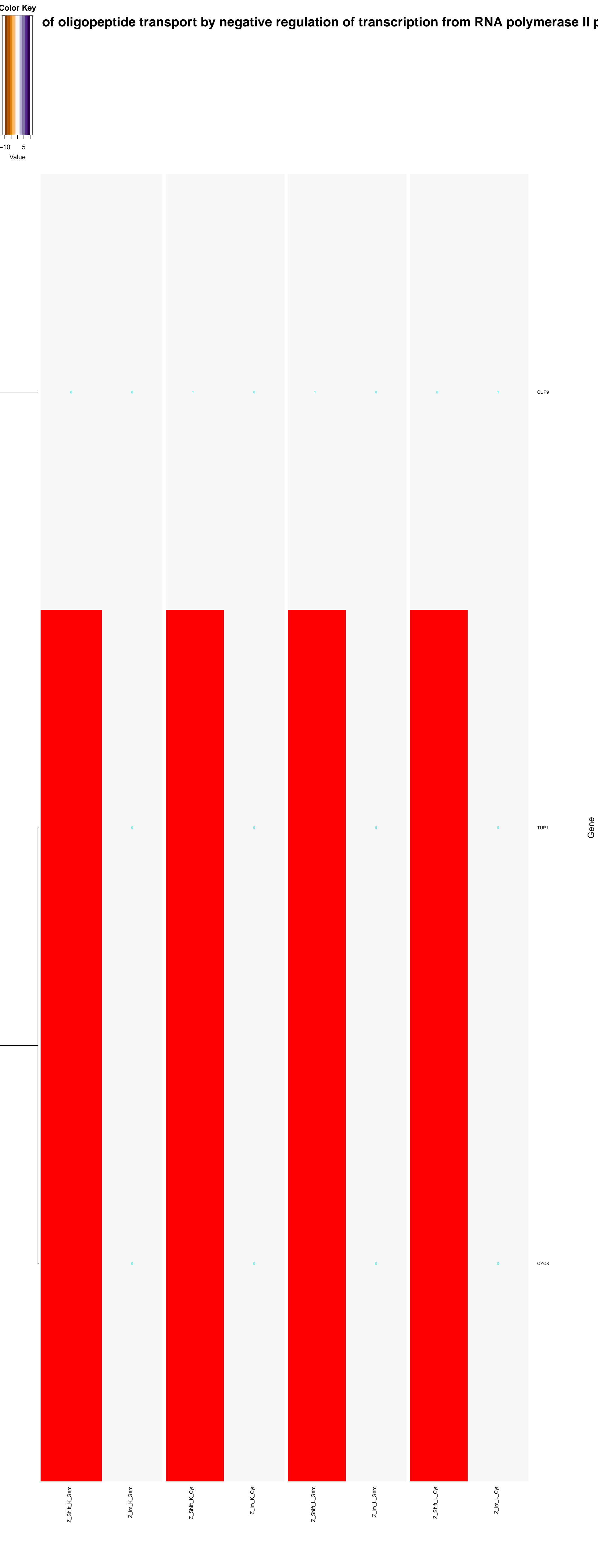


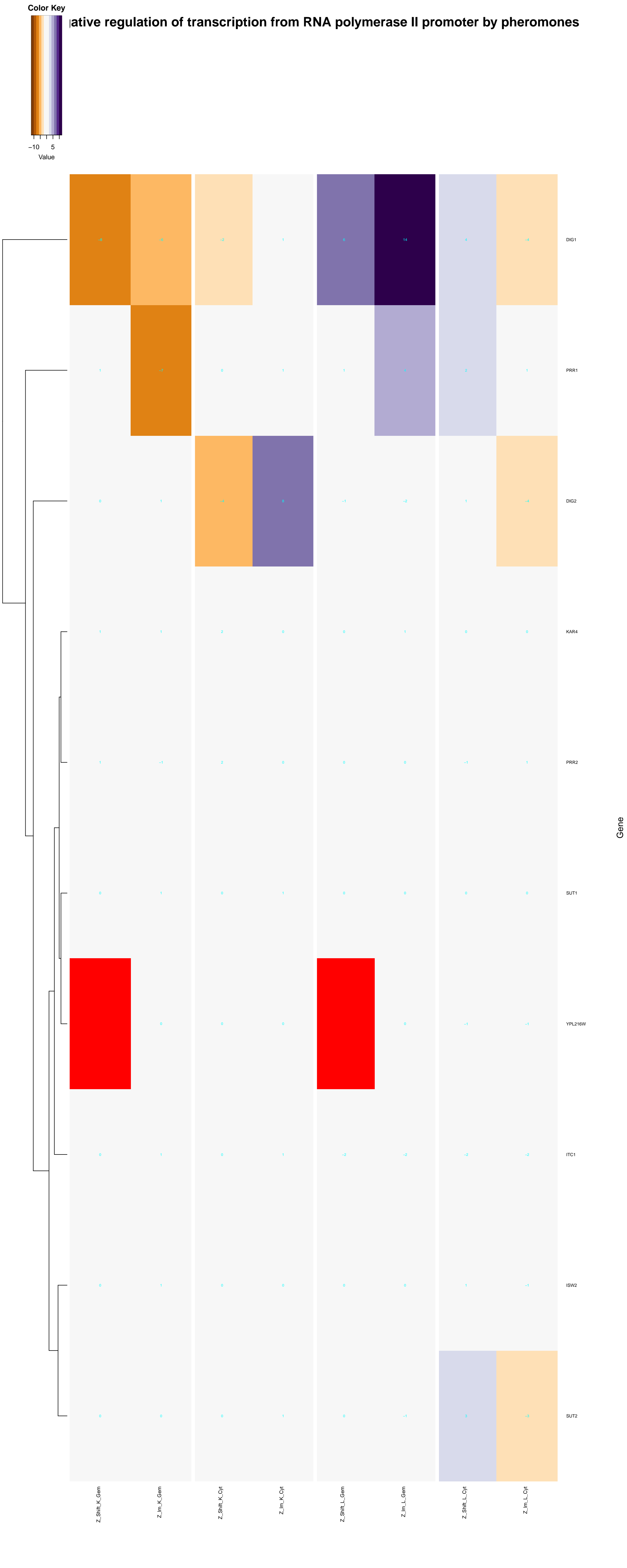


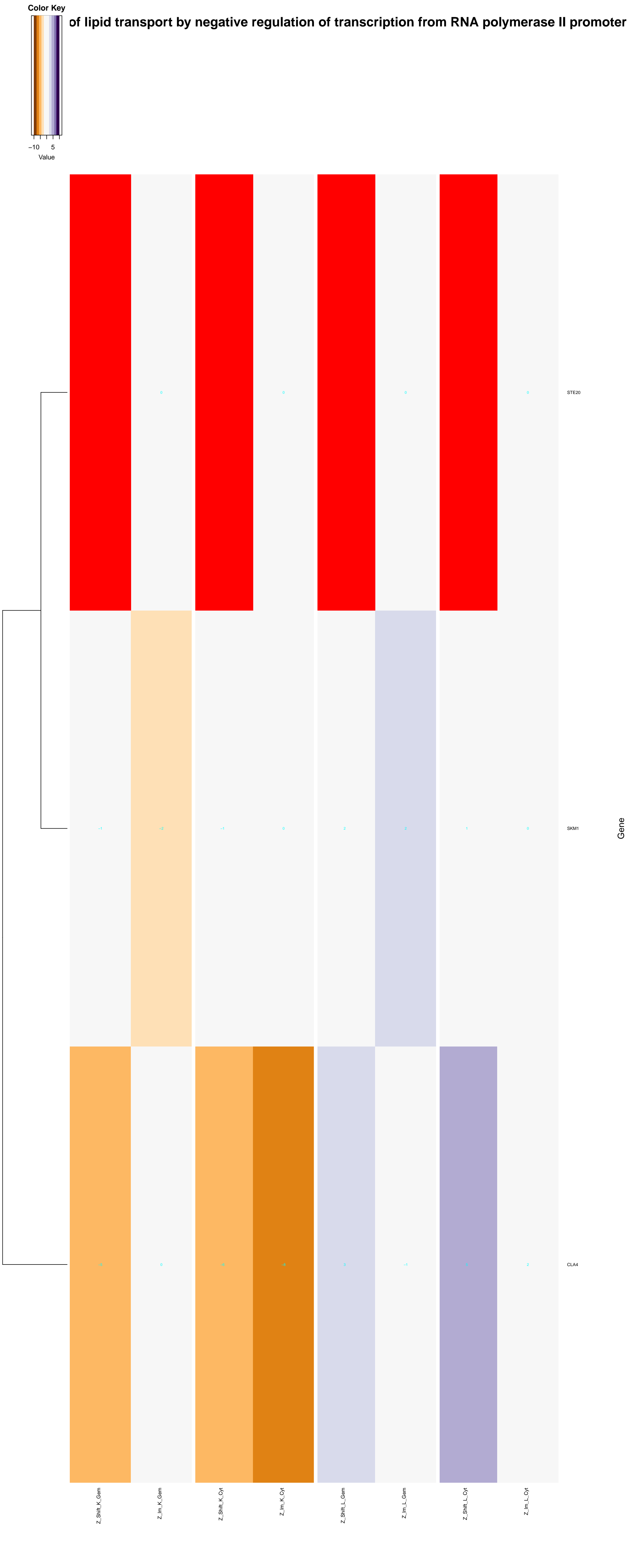
egulation of transcription from RNA polymerase II promoter involved in meiotic cell cycle

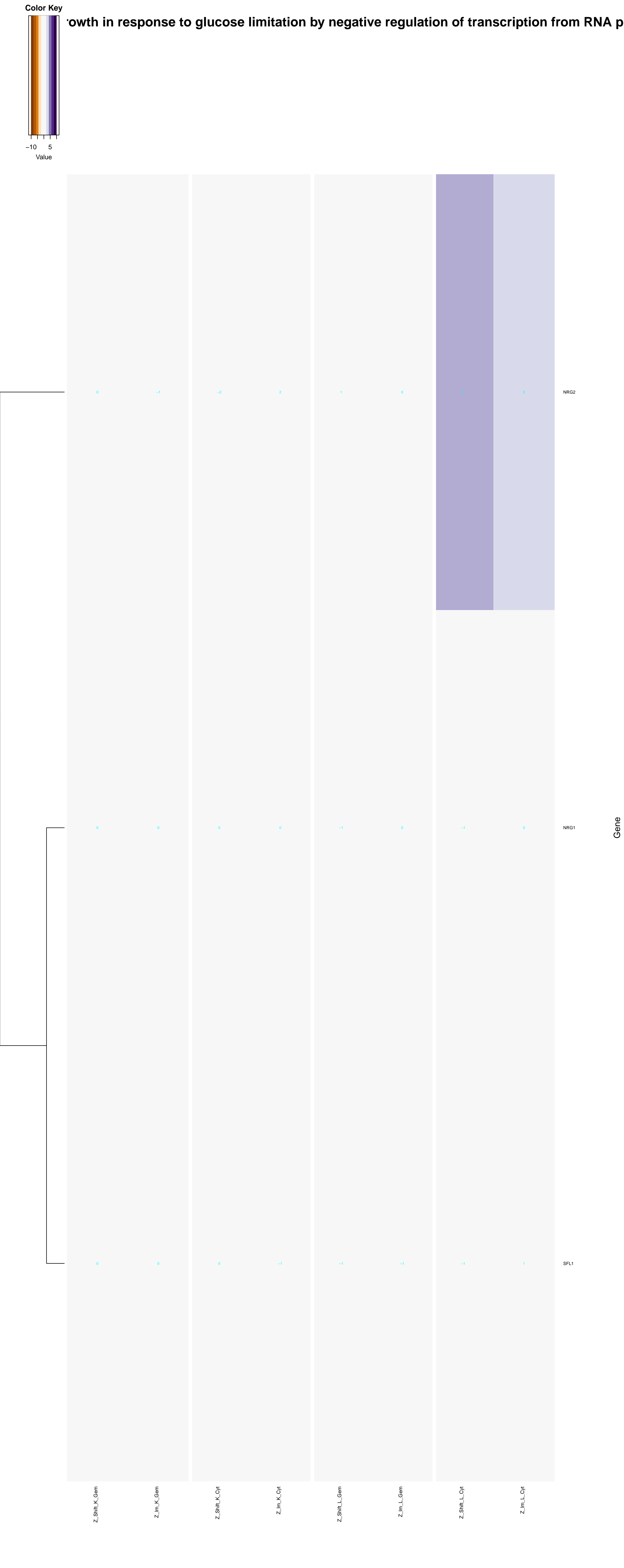




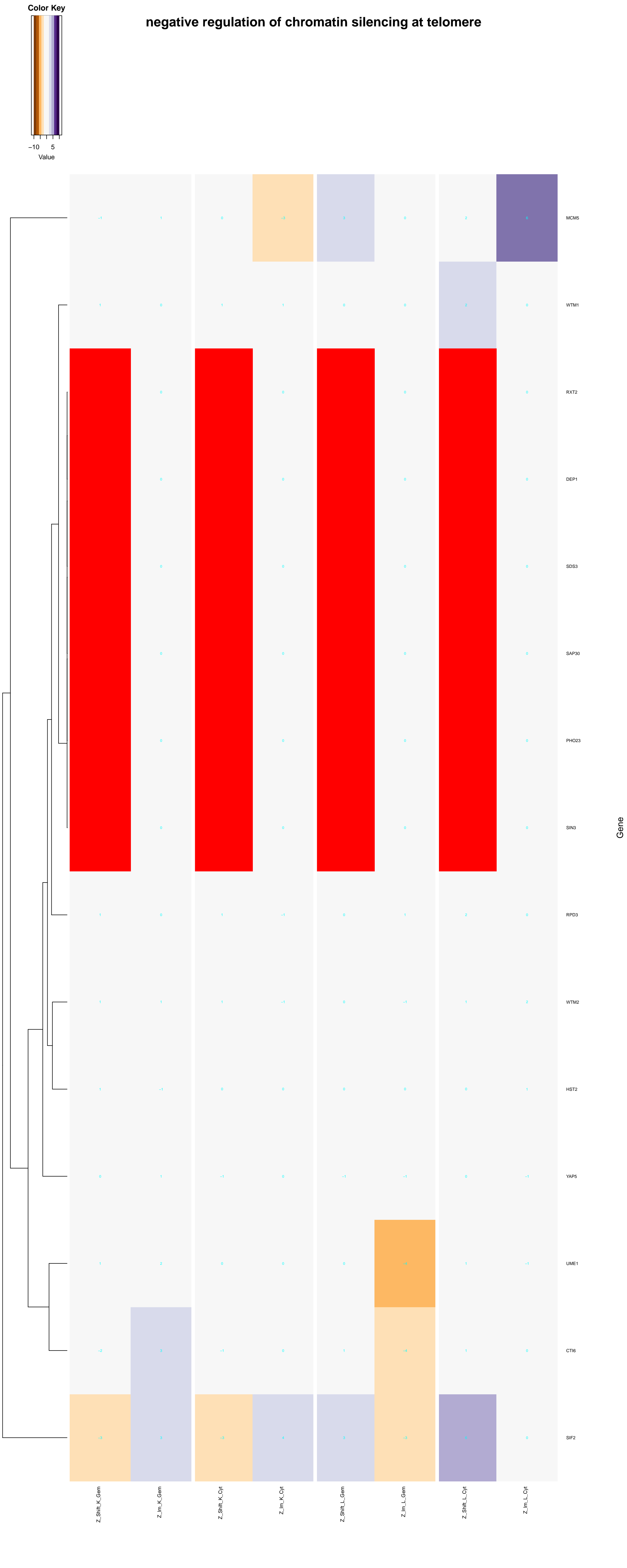


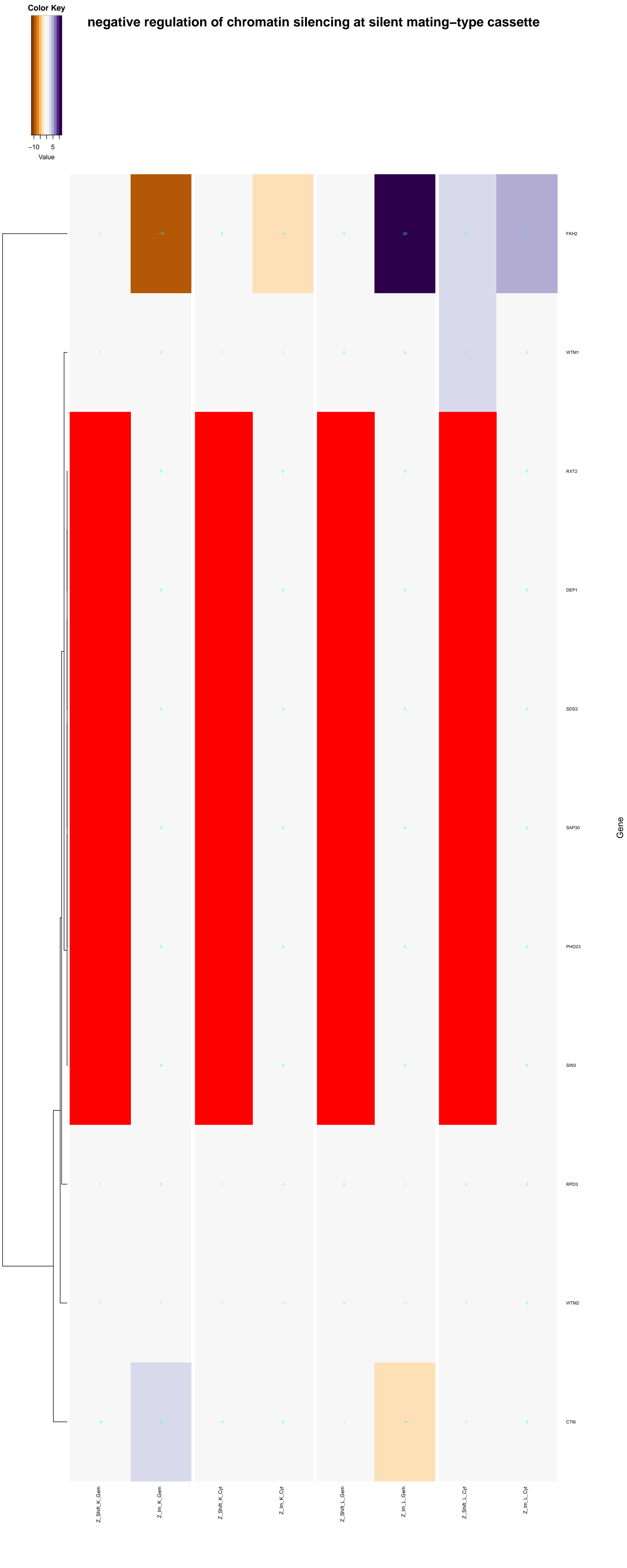


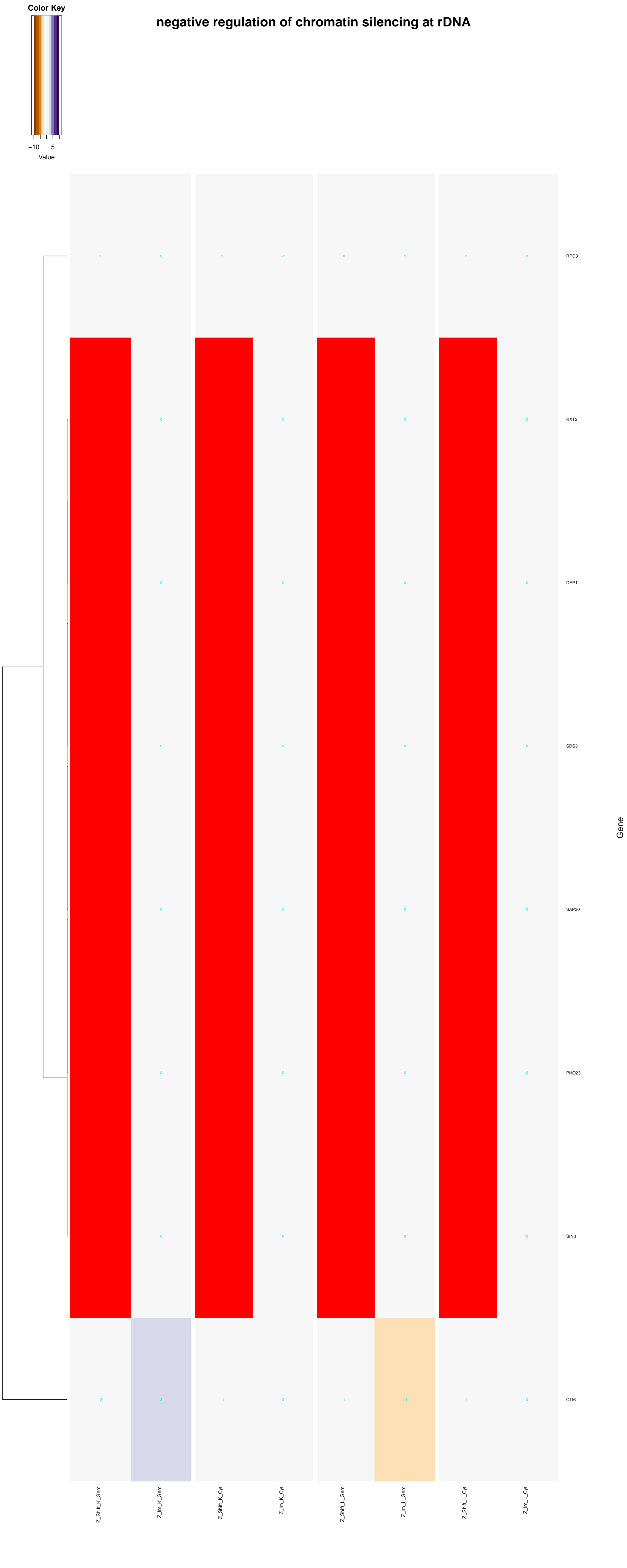


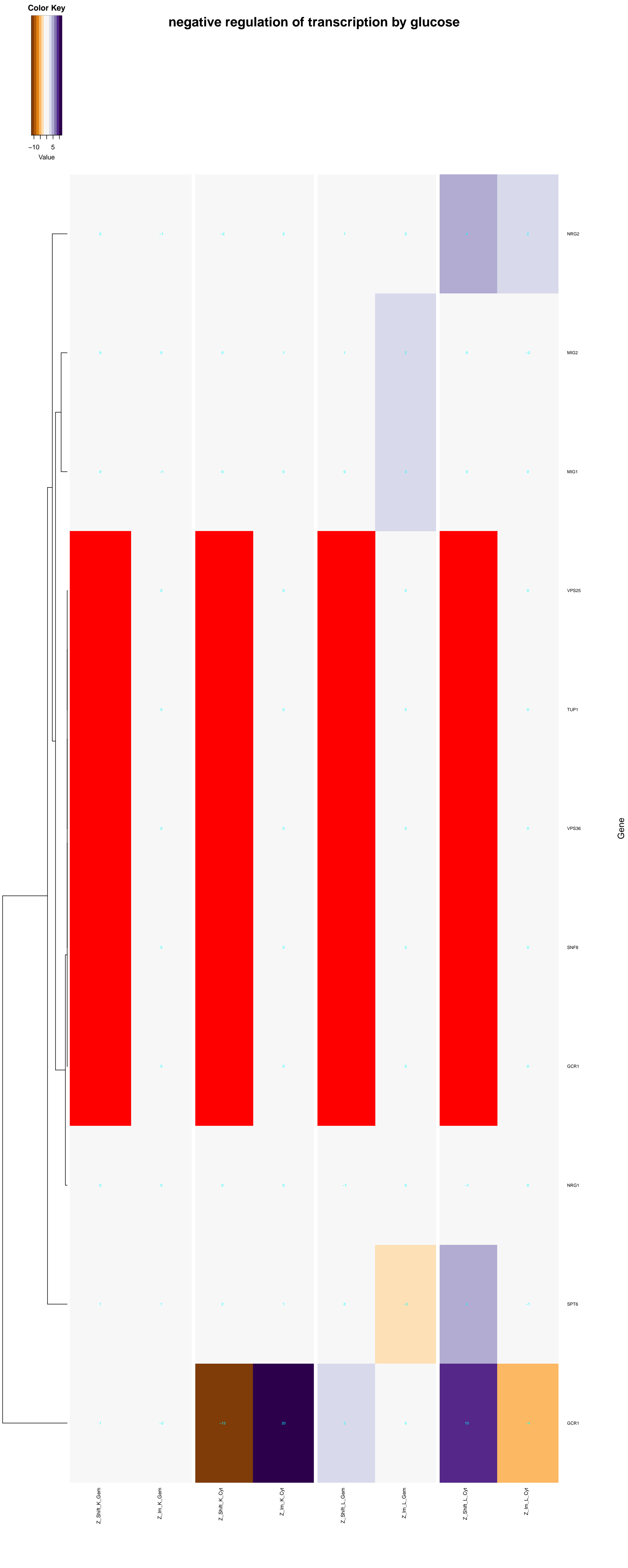


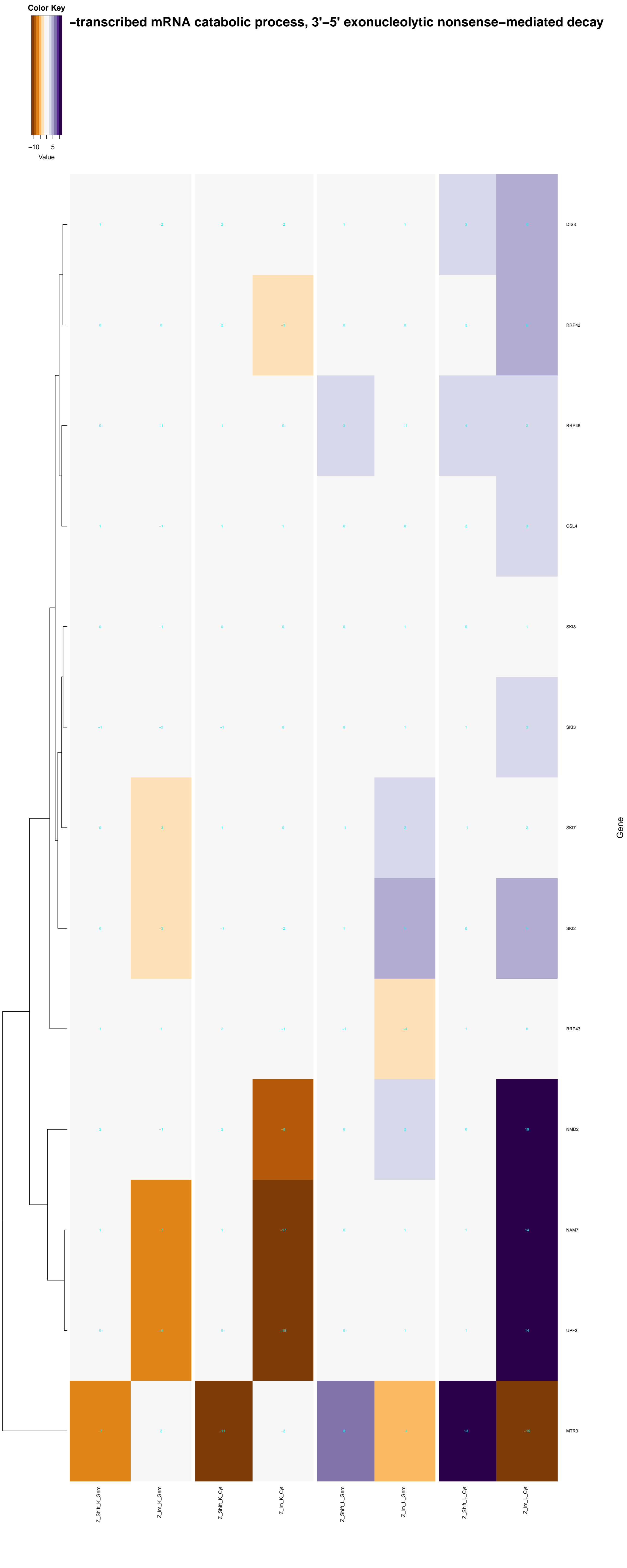


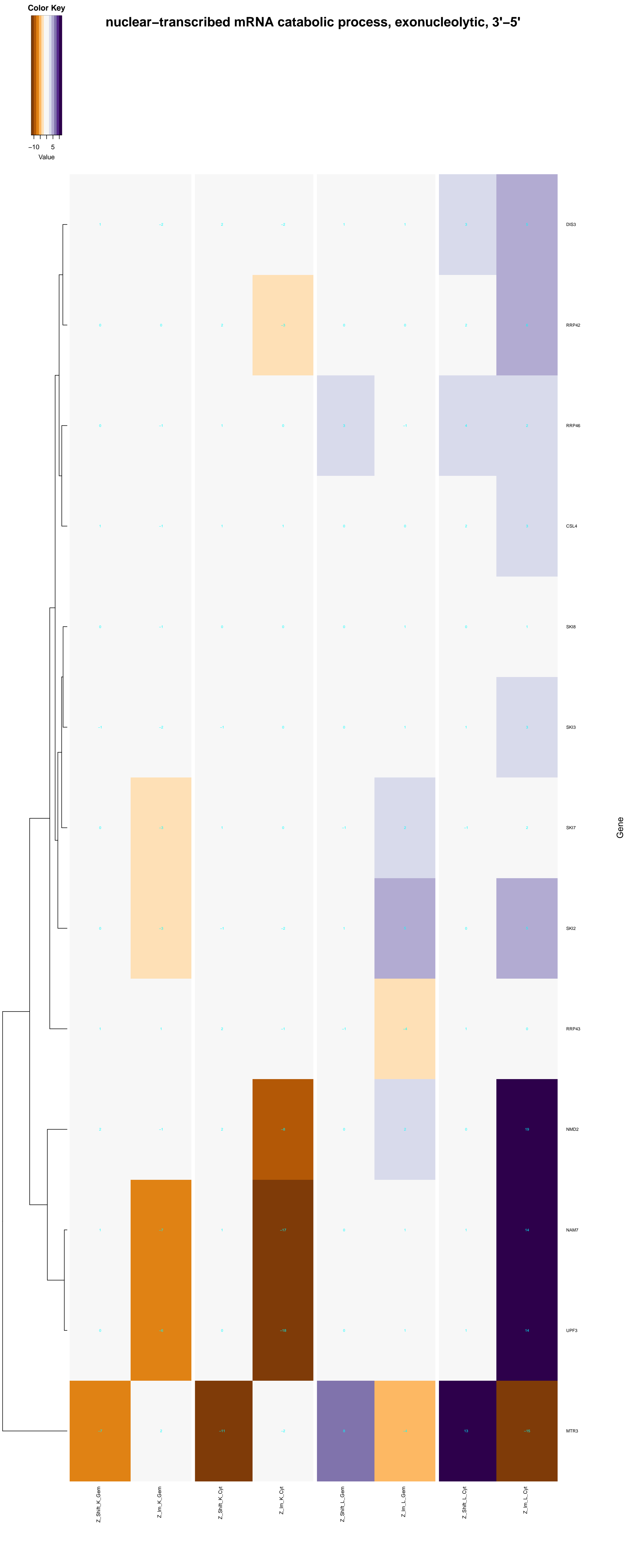


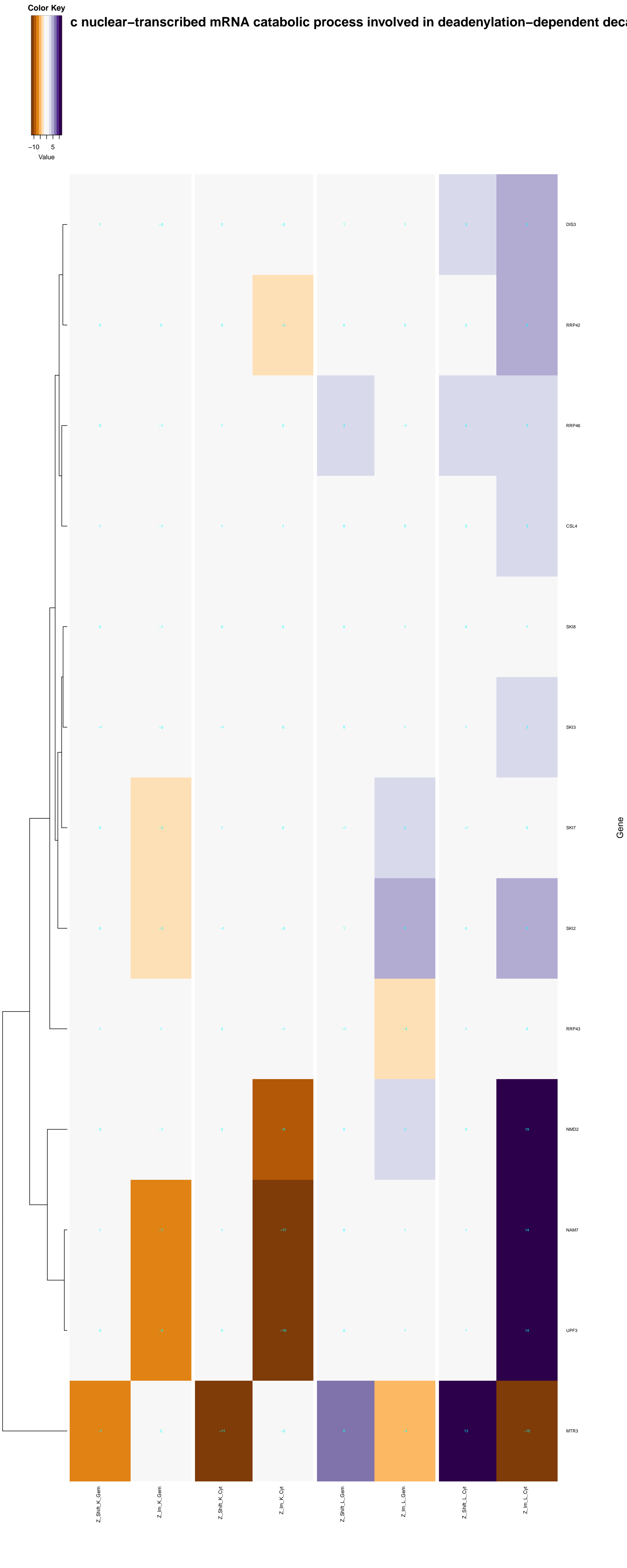


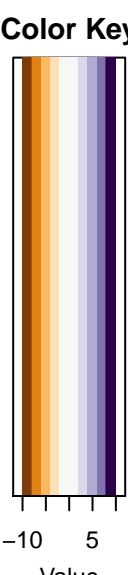




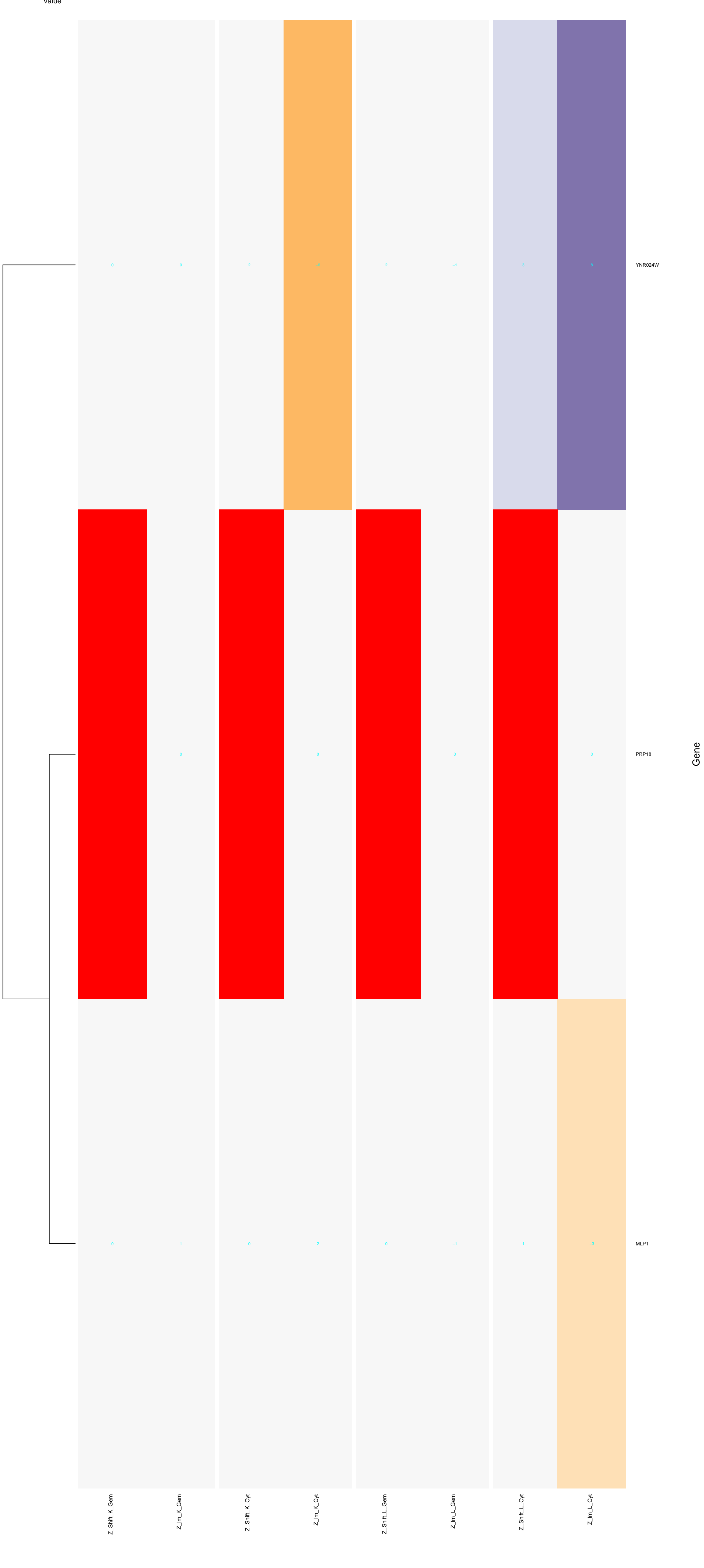


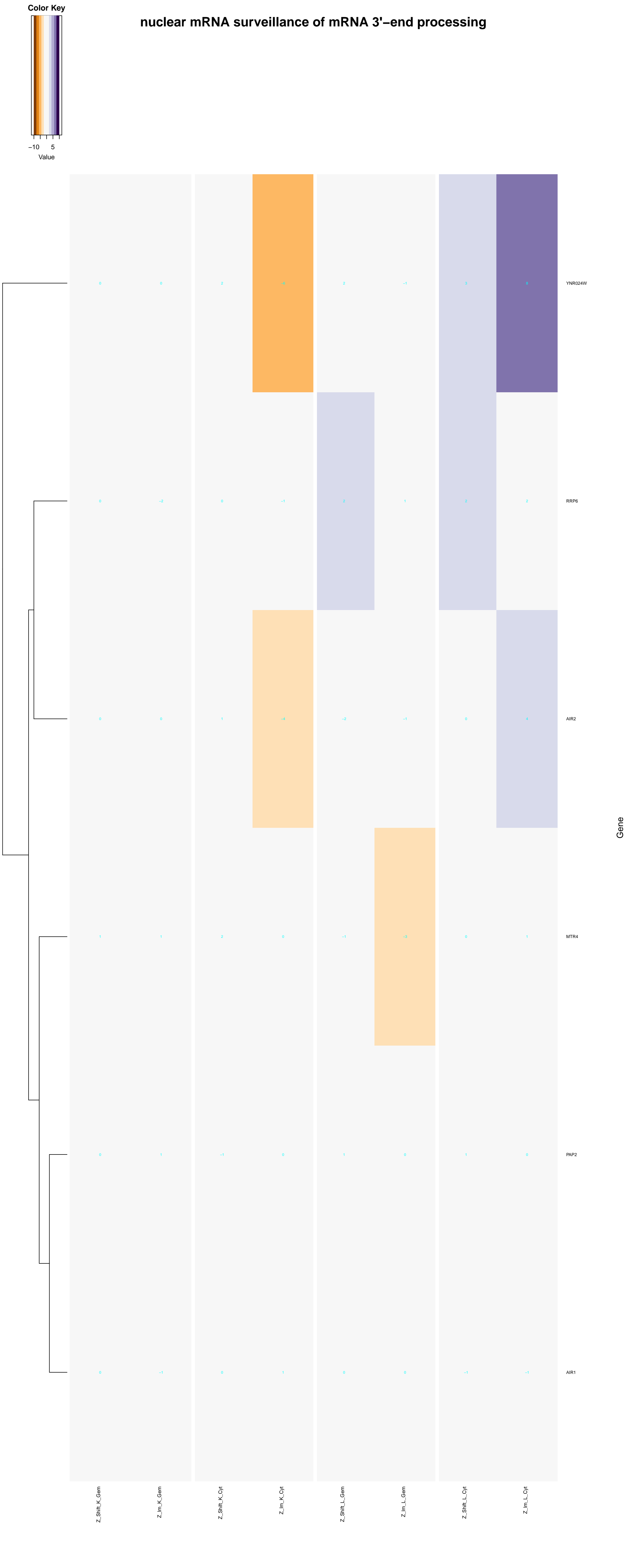


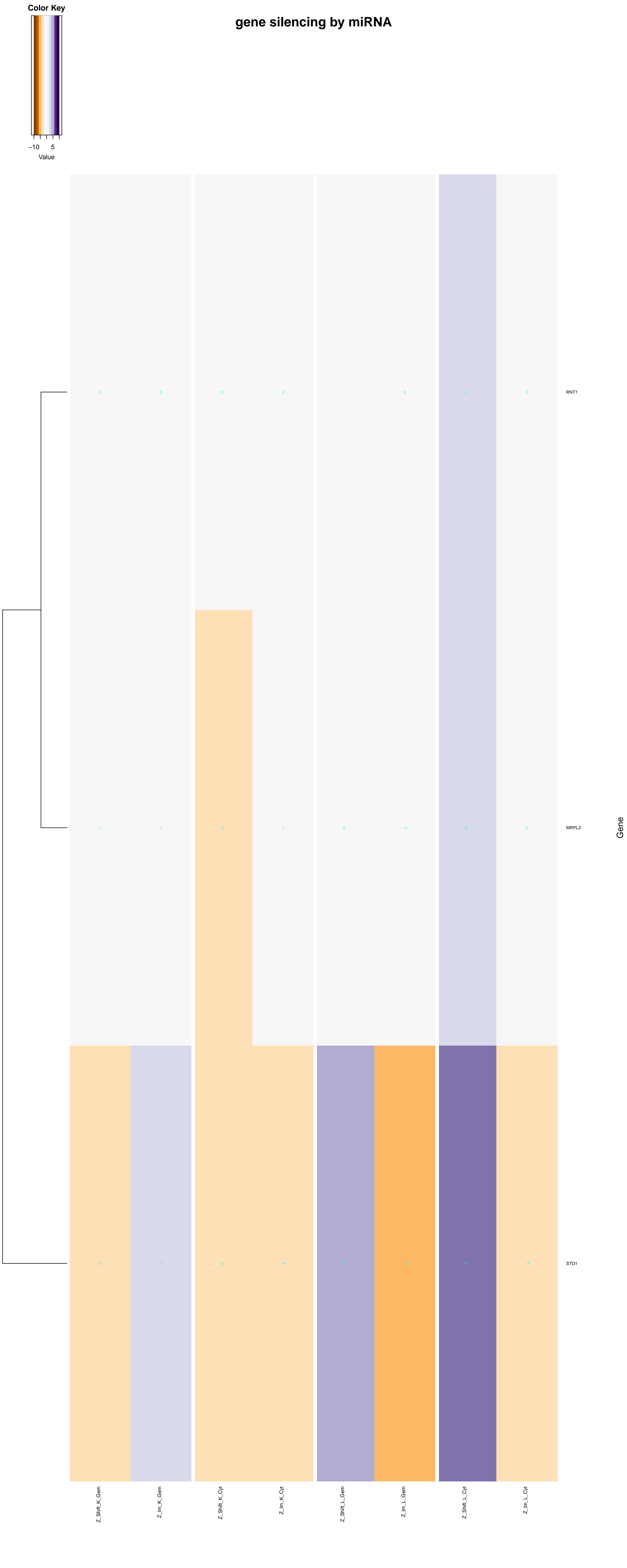




nuclear mRNA surveillance of spliceosomal pre-mRNA splicing









egative regulation of transcription from RNA polymerase II promoter by glucose

