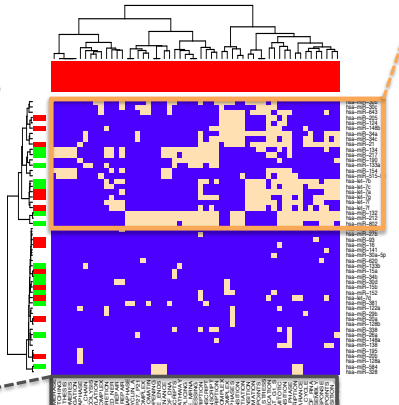
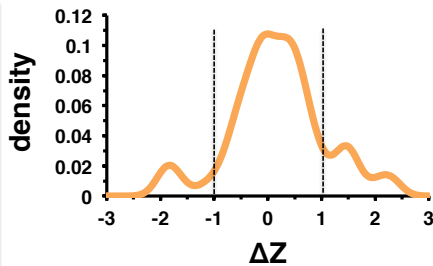


A

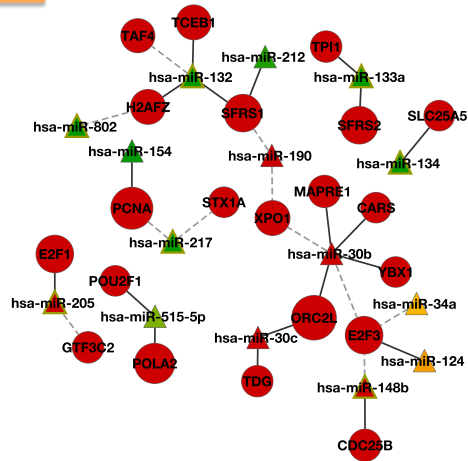
diff. expr.
pathways,
miRsdownregulated
upregulated

hsa-miR-30b
hsa-miR-30c
hsa-miR-643
hsa-miR-205
hsa-miR-124
hsa-miR-148b
hsa-miR-34a
hsa-miR-34c
hsa-miR-21
hsa-miR-134
hsa-miR-217
hsa-miR-190
hsa-miR-133a
hsa-miR-154
hsa-miR-515-5p
hsa-let-7b
hsa-let-7c
hsa-let-7a
hsa-let-7f
hsa-let-7i
hsa-miR-132
hsa-miR-212
hsa-miR-802

B



C



REPAIR_SYNTHESIS_OF_PATCH_27_30_BASES_LONG_BY_DNA_POLYMERASE
POLYMERASE_SWITCHING
LAGGING_STRAND_SYNTHESIS
EXTENSION_OF_TELOMERES
DNA_STRAND_ELONGATION
DNA_OTTER_PERSISTENCE
ELECTRON_TRANSPORT_CHAIN
GLYCOLYSIS
ACTIVATION_OF_THE_PFK_F3_4_KINASE
TRANSCRIPTION_COUPLING_NEAR
GLUCOSE_REGULATION_OF_INSULIN_SECRETION
BASE_EXCISION_DNA_REPAIR
REGULATION_OF_APC_ACTIVATORS
CD220_PHOSPHORYLATION
CDT1_ASSOCIATION_WITH_THE_CD28_ORC_ORIGIN_COMPLEX
RNA_POLYMERASE_I_PROMOTER_OPENING
TELOMERASE_MAINTENANCE
PACKAGING_OF_TELOMERES_ENDS
ELONGATION_AND_PROCESSING_OF_CAPPED_TRANSCRIPTS
MRNA_SPLICING_MINOR_PATHWAY
MRNA_3_END_PROCESSING
TRANSPORT_OF_MATURE_MRNA
DERIVED_FROM_AN_INTRON_CONTAINING_TRANSCRIPT
FORMATION_AND_MATURATION_OF_MRNA_TRANSCRIPT
ASSOCIATION_OF_LICENSING_FACTORS_WITH_THE_PREFERENTIAL_COMPLEX
CD28_ASSOCIATION_WITH_THE_ORC_ORIGIN_COMPLEX
MITOTIC_M.M.G1_PHASES
DNA_REPLICATION_PRE-INITIATION
CYCLIN_A1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION
E2F_ENABLED_INHIBITION_OF_PRE-REPLICATION_G2_M_CHECKPOINTS
ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS
E2F_MEDIATED_TRANSITION_FROM_G1_S_TO_S
E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
CELL_CYCLE_MITOTIC
G1_S_THRUS_PHASE
RNA_POLYMERASE_I_III_AND_MITOCHONDRIAL_TRANSCRIPTION
RNA_POLYMERASE_I_III_OTTER_CLEARANCE
LIFE_PHASE_OF_RNA
METABOLISM_OF_RNA
SNRP_ASSEMBLY
CELL_CYCLE_CHECKPOINTS
CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION
HV_LIFE_CYCLE

(diff. exp.) miR
gene

expr.

increasing number
of pathwaysgain $\Delta Z > 1$
loss $\Delta Z < -1$