A
up−regulated (79)
down−regulated (34)
−log₁₀ (P value)
log₂FC
B
Cis
GO_CC:extracellular matrix
PI3K−Akt signaling pathway
GO_BP:response to insulin
GO_BP:cell−cell adhesion
GO_BP:MAPK cascade
GO_BP:regulation of mRNA stability
GO_MF:isomerase activity
GO_MF:transporter activity
−log₁₀ (P value)
C
5 kb
CYGB
TCONS_00019024
W1
W2
W3
B1
B2
B3
D
Trans
−log₁₀ (P value)
KEGG Pathway
GO Term
Oxidative phosphorylation
GO_CC:mitochondrial inner membrane
Metabolic pathways
GO_BP:angiogenesis
GO_BP:extracellular matrix organization
GO_CC:extracellular space
GO_CC:mitochondrion
GO_BP:response to oxidative stress
GO_BP:response to hypoxia
GO_BP:inflammatory response
GO_CC:cell surface
GO_BP:negative regulation of cell migration
GO_MF:arylesterase activity
GO_CC:integral component of membrane
GO_BP:hair follicle development
GO_BP:cAMP−mediated signaling
GO_CC:cytoskeleton
GO_BP:epithelial cell−cell adhesion
GO_BP:cell adhesion
GO_CC:plasma membrane
GO_MF:fatty−acyl−CoA binding
cGMP−PKG signaling pathway