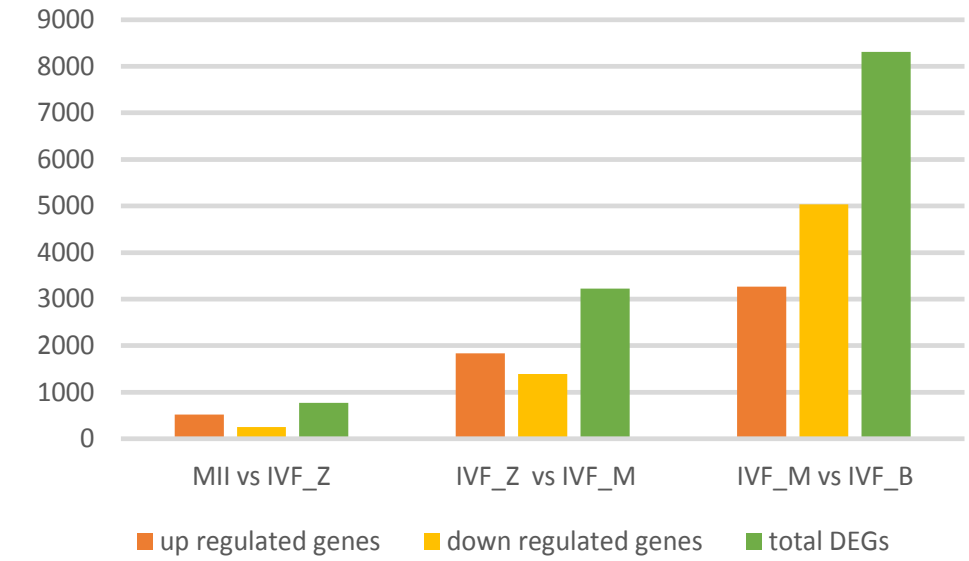
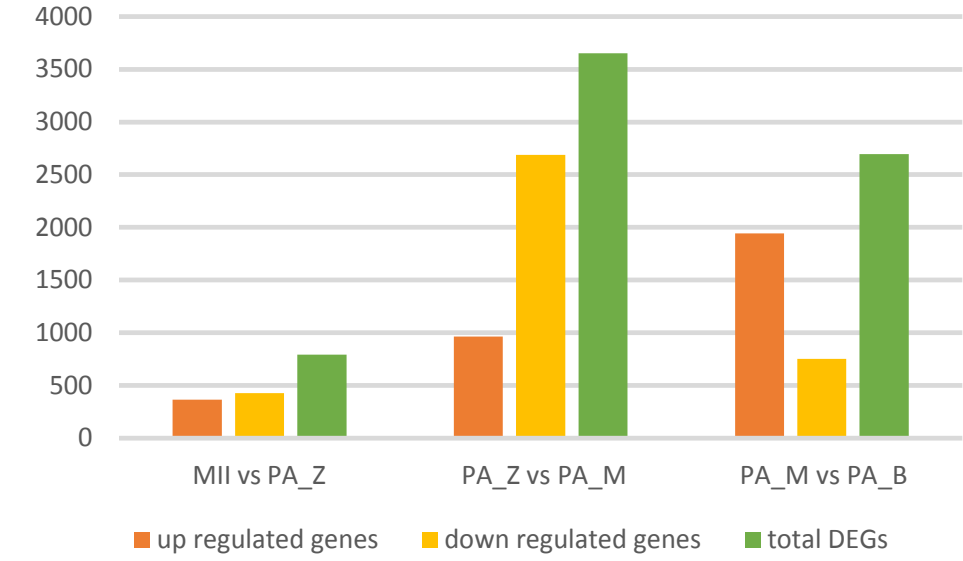
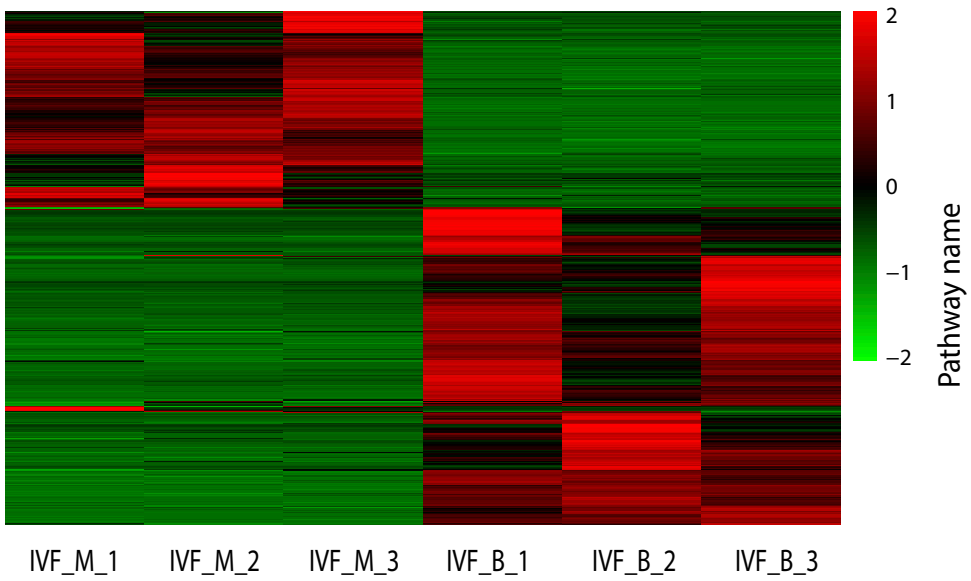
A


9000
8000
7000
6000
5000
4000
3000
2000
1000
0
MII vs IVF_Z
IVF_Z vs IVF_M
IVF_M vs IVF_B
up regulated genes
down regulated genes
total DEGs

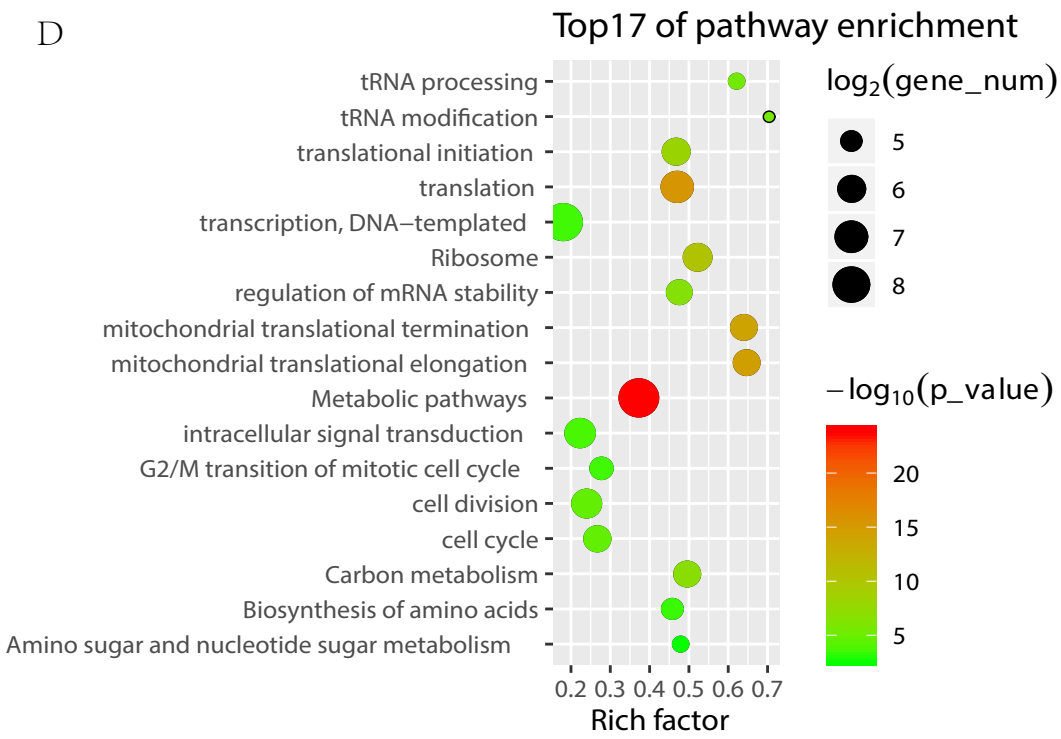
B


4000
3500
3000
2500
2000
1500
1000
500
0
MII vs PA_Z
PA_Z vs PA_M
PA_M vs PA_B
up regulated genes
down regulated genes
total DEGs

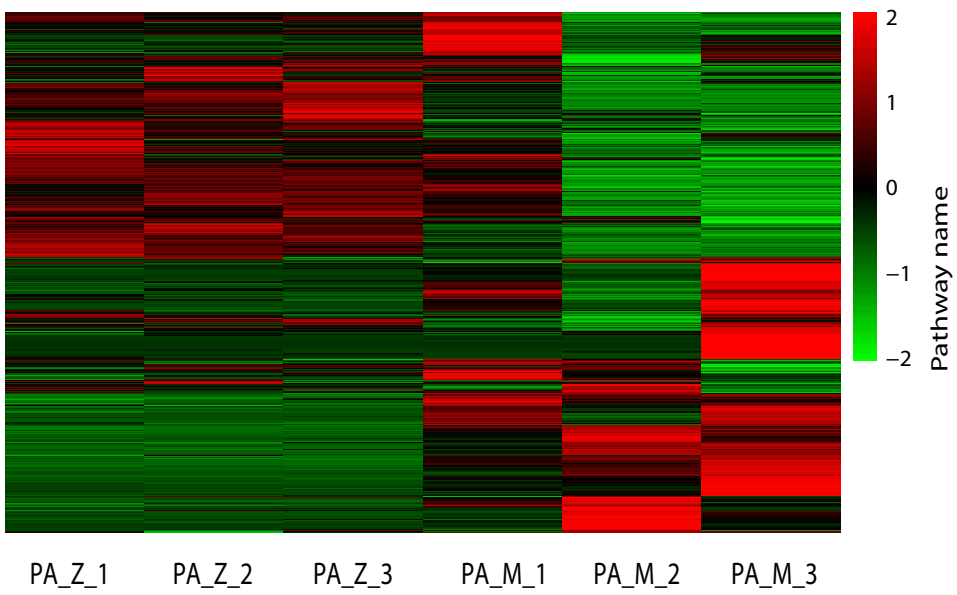
C


2
1
0
−1
−2
Pathway name
IVF_M_1
IVF_M_2
IVF_M_3
IVF_B_1
IVF_B_2
IVF_B_3

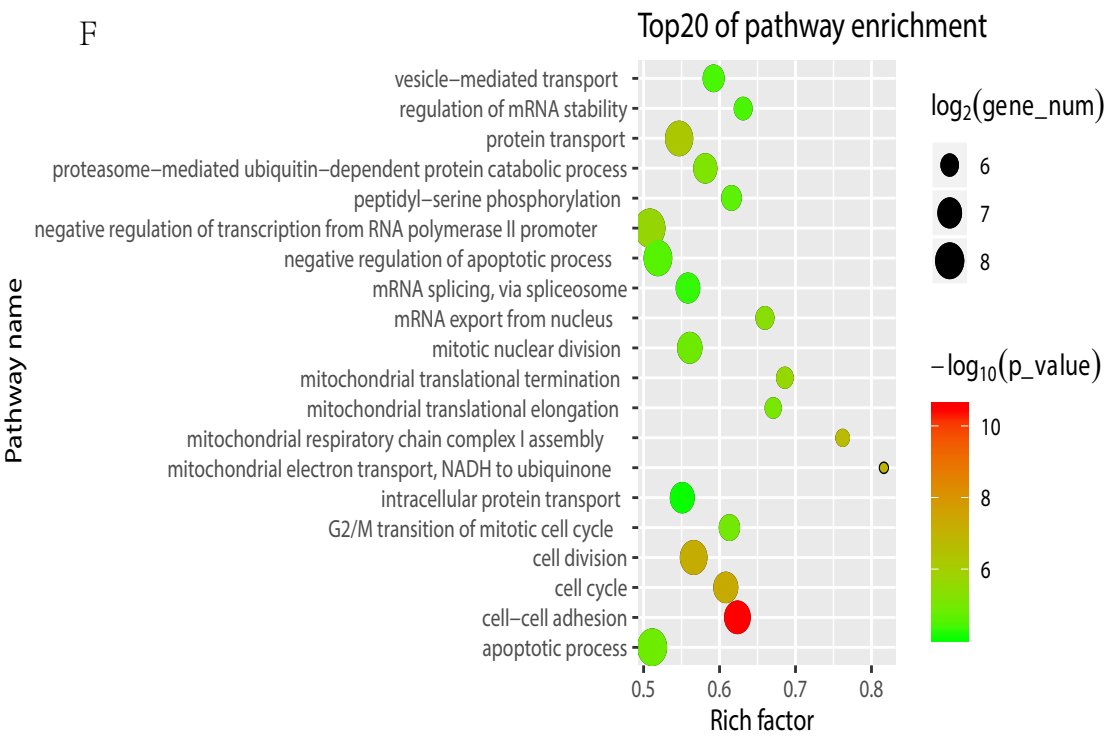
D


Top17 of pathway enrichment
tRNA processing
tRNA modification
translational initiation
translation
transcription, DNA−templated
Ribosome
regulation of mRNA stability
mitochondrial translational termination
mitochondrial translational elongation
Metabolic pathways
intracellular signal transduction
G2/M transition of mitotic cell cycle
cell division
cell cycle
Carbon metabolism
Biosynthesis of amino acids
Amino sugar and nucleotide sugar metabolism
log2(gene_num)
5
6
7
8
−log10(p_value)
20
15
10
5
0.2 0.3 0.4 0.5 0.6 0.7
Rich factor

E


2
1
0
−1
−2
Pathway name
PA_Z_1
PA_Z_2
PA_Z_3
PA_M_1
PA_M_2
PA_M_3

F


Top20 of pathway enrichment
vesicle−mediated transport
regulation of mRNA stability
protein transport
proteasome−mediated ubiquitin−dependent protein catabolic process
peptidyl−serine phosphorylation
negative regulation of transcription from RNA polymerase II promoter
negative regulation of apoptotic process
mRNA splicing, via spliceosome
mRNA export from nucleus
mitotic nuclear division
mitochondrial translational termination
mitochondrial translational elongation
mitochondrial respiratory chain complex I assembly
mitochondrial electron transport, NADH to ubiquinone
intracellular protein transport
G2/M transition of mitotic cell cycle
cell division
cell cycle
cell−cell adhesion
apoptotic process
log2(gene_num)
6
7
8
−log10(p_value)
10
8
6
0.5
0.6
0.7
0.8
Rich factor