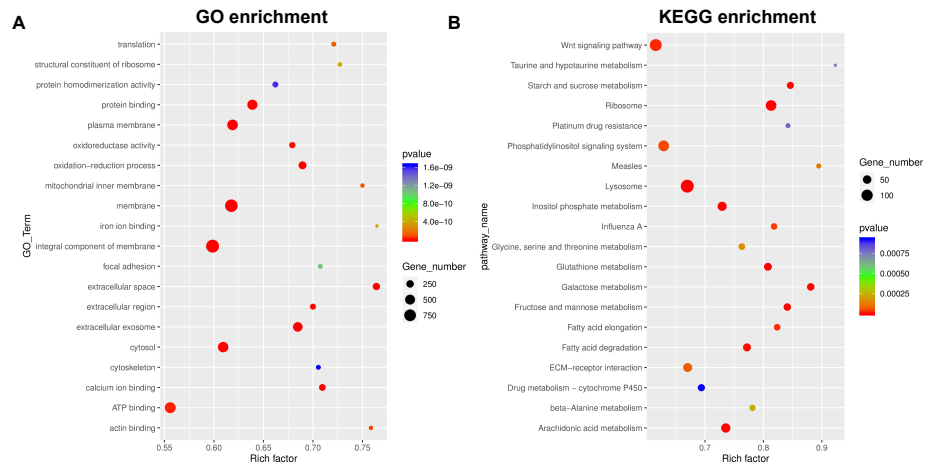
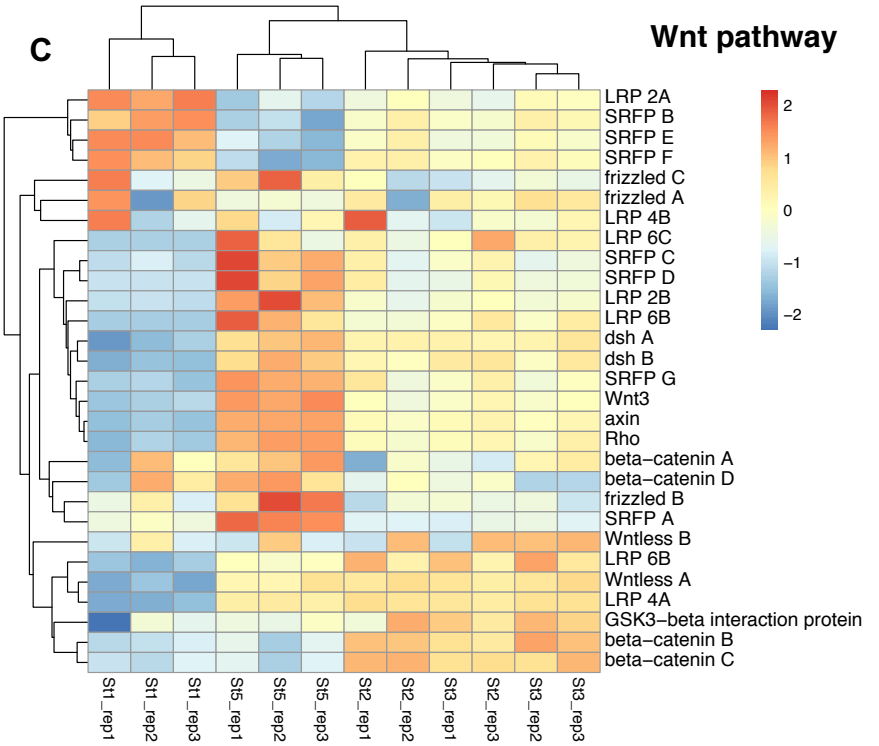
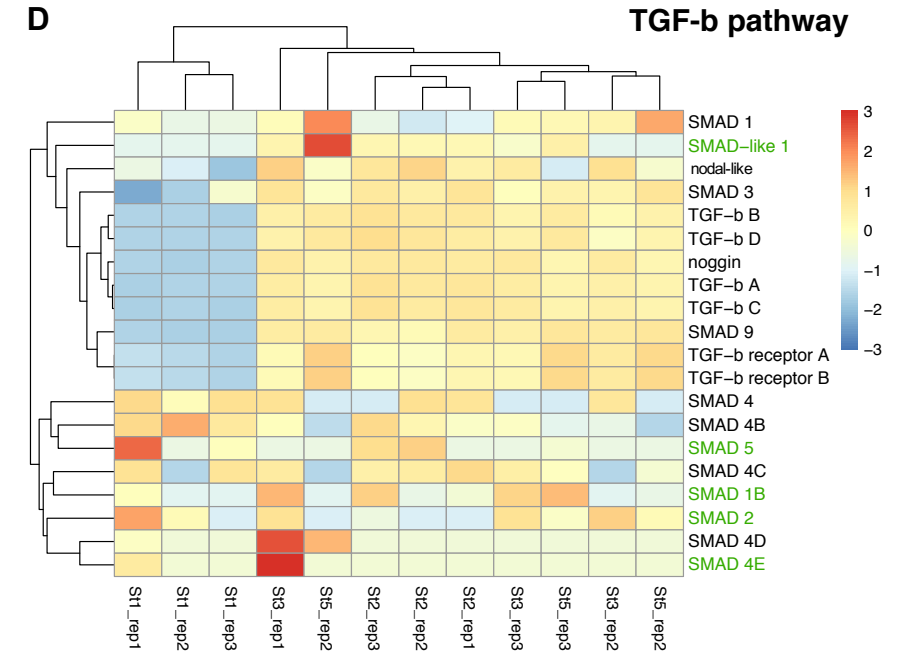

A
GO enrichment
translation
structural constituent of ribosome
protein homodimerization activity
protein binding
plasma membrane
oxidoreductase activity
oxidation−reduction process
mitochondrial inner membrane
membrane
iron ion binding
integral component of membrane
focal adhesion
extracellular space
extracellular region
extracellular exosome
cytosol
cytoskeleton
calcium ion binding
ATP binding
actin binding
GO_Term
0.55
0.60
0.65
0.70
0.75
Rich factor
pvalue
1.6e−09
1.2e−09
8.0e−10
4.0e−10
Gene_number
250
500
750
B
KEGG enrichment
Wnt signaling pathway
Taurine and hypotaurine metabolism
Starch and sucrose metabolism
Ribosome
Platinum drug resistance
Phosphatidylinositol signaling system
Measles
Lysosome
Inositol phosphate metabolism
Influenza A
Glycine, serine and threonine metabolism
Glutathione metabolism
Galactose metabolism
Fructose and mannose metabolism
Fatty acid elongation
Fatty acid degradation
ECM−receptor interaction
Drug metabolism − cytochrome P450
beta−Alanine metabolism
Arachidonic acid metabolism
pathway_name
0.7
0.8
0.9
Rich factor
Gene_number
50
100
pvalue
0.00075
0.00050
0.00025


C
Wnt pathway
LRP 2A
SRFP B
SRFP E
SRFP F
frizzled C
frizzled A
LRP 4B
LRP 6C
SRFP C
SRFP D
LRP 2B
LRP 6B
dsh A
dsh B
SRFP G
Wnt3
axin
Rho
beta−catenin A
beta−catenin D
frizzled B
SRFP A
Wntless B
LRP 6B
Wntless A
LRP 4A
GSK3−beta interaction protein
beta−catenin B
beta−catenin C
St1_rep1
St1_rep2
St1_rep3
St5_rep1
St5_rep2
St5_rep3
St2_rep1
St2_rep2
St3_rep1
St2_rep3
St3_rep2
St3_rep3
2
1
0
−1
−2


D
TGF-b pathway
SMAD 1
SMAD−like 1
nodal-like
SMAD 3
TGF−b B
TGF−b D
noggin
TGF−b A
TGF−b C
SMAD 9
TGF−b receptor A
TGF−b receptor B
SMAD 4
SMAD 4B
SMAD 5
SMAD 4C
SMAD 1B
SMAD 2
SMAD 4D
SMAD 4E
St1_rep1
St1_rep2
St1_rep3
St3_rep1
St5_rep2
St2_rep3
St2_rep2
St2_rep1
St3_rep3
St5_rep3
St3_rep2
St5_rep2
3
2
1
0
−1
−2
−3