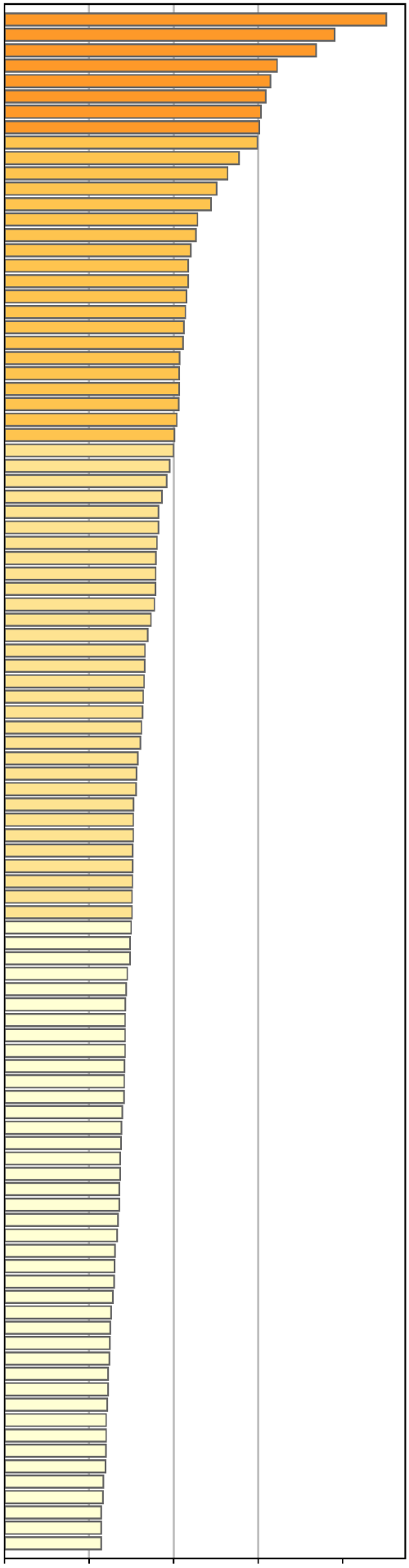
Fig. S3:Gene ontology enrichment analysis of differentially expressed genes



R-HSA-1474244: Extracellular matrix organization
M5884: NABA CORE MATRISOME
R-HSA-381426: Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Bi
GO:0048729: tissue morphogenesis
GO:0042476: odontogenesis
GO:0030855: epithelial cell differentiation
GO:0007423: sensory organ development
GO:0042303: molting cycle
GO:0060021: roof of mouth development
GO:0050900: leukocyte migration
GO:0010817: regulation of hormone levels
GO:0051384: response to glucocorticoid
GO:0001568: blood vessel development
GO:0034754: cellular hormone metabolic process
GO:0007178: transmembrane receptor protein serine/threonine kinase signaling pathway
GO:0008015: blood circulation
GO:0098742: cell-cell adhesion via plasma-membrane adhesion molecules
GO:0009612: response to mechanical stimulus
GO:0009611: response to wounding
GO:0060584: regulation of prostaglandin-endoperoxide synthase activity
GO:0001822: kidney development
hsa05410: Hypertrophic cardiomyopathy (HCM)
hsa03320: PPAR signaling pathway
GO:0045602: negative regulation of endothelial cell differentiation
M5885: NABA MATRISOME ASSOCIATED
GO:0048589: developmental growth
GO:0006575: cellular modified amino acid metabolic process
GO:0060349: bone morphogenesis
GO:0044706: multi-multicellular organism process
GO:0055123: digestive system development
GO:0050890: cognition
GO:0008285: negative regulation of cell proliferation
R-HSA-9006934: Signaling by Receptor Tyrosine Kinases
hsa04390: Hippo signaling pathway
GO:0048732: gland development
GO:0030325: adrenal gland development
hsa04010: MAPK signaling pathway
GO:0043408: regulation of MAPK cascade
GO:0061061: muscle structure development
R-HSA-419812: Calcitonin-like ligand receptors
GO:0060070: canonical Wnt signaling pathway
GO:0009064: glutamine family amino acid metabolic process
GO:0072593: reactive oxygen species metabolic process
GO:0060541: respiratory system development
GO:0046113: nucleobase catabolic process
hsa04974: Protein digestion and absorption
GO:0045664: regulation of neuron differentiation
GO:0001101: response to acid chemical
GO:0048762: mesenchymal cell differentiation
R-HSA-3000157: Laminin interactions
M255: PID HIF1 TFPATHWAY
GO:0019216: regulation of lipid metabolic process
GO:0042594: response to starvation
R-HSA-445095: Interaction between L1 and Ankyrins
GO:0030155: regulation of cell adhesion
hsa05146: Amoebiasis
hsa04360: Axon guidance
R-HSA-5339717: Misspliced LRP5 mutants have enhanced beta-catenin-dependent signaling
R-HSA-1566977: Fibronectin matrix formation
GO:0045746: negative regulation of Notch signaling pathway
GO:0060712: spongiotrophoblast layer development
GO:0045745: positive regulation of G protein-coupled receptor signaling pathway
GO:0010876: lipid localization
GO:0035987: endodermal cell differentiation
GO:0030837: negative regulation of actin filament polymerization
hsa04964: Proximal tubule bicarbonate reclamation
GO:0045109: intermediate filament organization
GO:0042552: myelination
GO:0010935: regulation of macrophage cytokine production
GO:0042063: gliogenesis
GO:0015711: organic anion transport
GO:0045650: negative regulation of macrophage differentiation
R-HSA-977068: Termination of O-glycan biosynthesis
GO:0032787: monocarboxylic acid metabolic process
GO:0032602: chemokine production
R-HSA-449147: Signaling by Interleukins
GO:0050651: dermatan sulfate proteoglycan biosynthetic process
GO:0050961: detection of temperature stimulus involved in sensory perception
R-HSA-210991: Basigin interactions
R-HSA-446728: Cell junction organization
R-HSA-6785807: Interleukin-4 and Interleukin-13 signaling
GO:0010566: regulation of ketone biosynthetic process
GO:2000465: regulation of glycogen (starch) synthase activity
GO:0060322: head development
M223: PID BETA CATENIN NUC PATHWAY
GO:0050665: hydrogen peroxide biosynthetic process
GO:0042326: negative regulation of phosphorylation
GO:0007264: small GTPase mediated signal transduction
hsa00260: Glycine, serine and threonine metabolism
GO:0045124: regulation of bone resorption
GO:2000096: positive regulation of Wnt signaling pathway, planar cell polarity pathway
R-HSA-2022377: Metabolism of Angiotensinogen to Angiotensins
GO:1903019: negative regulation of glycoprotein metabolic process
GO:0050873: brown fat cell differentiation
hsa04068: FoxO signaling pathway
M167: PID AP1 PATHWAY
GO:0051272: positive regulation of cellular component movement
GO:0071233: cellular response to leucine
R-HSA-1483115: Hydrolysis of LPC
R-HSA-975578: Reactions specific to the complex N-glycan synthesis pathway