A novel anti-inflammatory activity of mcIRBP from *Momordica charantia* is associated with the improvement of diabetic nephropathy

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Supplementary Figure 1

Supplementary Fig. 1. Functional classification of mcIRBP-affected genes in kidney. Pie chart shows all the functional groups affected by mcIRBP. Group name and the percentage of group gene number in the total number of gene are shown on the bottom.



2-Arachidonoylglycerol biosynthesis (0.16%) ATP synthesis (0.16%) Adrenaline and noradrenaline biosynthesis (0.49%) Amino acid metabolism (2.3%) Apoptosis signaling pathway (2.3%) Blood coagulation (3.45%) Cadherin signaling pathway (4..77%) Cortocotropin releasing factor receptor signaling pathway (0.16%) De novo pyrimidine ribonucleotides biosythesis (0.16%) EGF receptor signaling pathway (1.32%) Enkephalin release (0.49%) Formyltetrahydroformate biosynthesis (0.16%) Gamma-aminobutyric acid synthesis (0.16%) Gonadotropin-releasing hormone receptor pathway (3.45%) Histamine H1/2 receptor mediated signaling pathway (0.49%) Insulin/IGF pathway (1.81%) JAK/STAT signaling pathway (0.16%) Muscarinic acetylcholine receptor signaling pathway (1.81%) Nicotinic acetylcholine receptor signaling pathway (1.97%) Opioid proenkephalin pathway (0.33%) Oxytocin receptor mediated signaling pathway (0.16%) PI3 kinase pathway (0.49%) Pyrimidine metabolism (0.33%) Salvage pyrimidine ribonucleotides (0.33%) Thyrotropin-releasing hormone receptor signaling pathway (0.66%) VEGF signaling pathway (0.82%)

Wnt signaling pathway (6.91%)

5-Hydroxytryptamine degredation (0.49%) Acetate utilization (0.16%) Alpha adrenergic receptor signaling pathway (0.49%) Angiogenesis (3.45%) Axon guidance (1.64%) Bupropion degradation (0.16%) Cell cycle (0.33%) Cytoskeletal regulation by Rho GTPase (1.32%) DNA replication (0.33%) Endogenous cannabinoid signaling (0.33%) FAS signaling pathway (0.16%) Fructose galactose metabolism (0.16%) General transcription regulation (0.33%) Hedgehog signaling pathway (0.33%) Hypoxia response via HIF activation (0.33%) Integrin signalling pathway (2.63%) Metabotropic glutamate receptor pathway (2.63%) Nicotine degradation (0.49%) Notch signaling pathway (0.82%) Opioid proopiomelanocortin pathway (0.66%) P53 pathway (3.29%) Plasminogen activating cascade (0.99%) Ras pathway (0.66%) Synaptic vesicle trafficking (0.99%) Transcription regulation by bZIP transcription factor (0.66%) Vasopressin synthesis (0.33%)

p38 MAPK pathway (0.33%)

5HT type receptor mediated signaling pathway (1.32%) Adenine and hypoxanthine salvage pathway (0.16%) Androgen/estrogene/progesterone biosynthesis (0.49%) Angiotensin II-stimulated signaling (0.16%) Beta adrenergic receptor signaling pathway (1.32%) CCKR signaling map (2.3%) Circadian clock system (0.49%) De novo purine biosynthesis (0.33%) Dopamine receptor mediated signaling pathway (0.66%) Endothelin signaling pathway (1.48%) FGF signaling pathway (2.3%) GABA-B receptor II signaling (0.49%) Glycolysis (0.33%) Heterotrimeric G-protein signaling pathway (6.41%) Inflammation and immunity (12.5%) Ionotropic glutamate receptor pathway (1.32%) Methylcitrate cycle (0.16%) Nicotine pharmacodynamics pathway (0.49%) Opioid prodynorphin pathway (0.49%) Oxidative stress response (0.99%) PDGF signaling pathway (1.97%) Pyridoxal-5-phosphate biosynthesis (0.16%) S-adenosylmethionine biosynthesis (0.16%) TGF-beta signaling pathway (2.14%) Ubiquitin proteasome pathway (0.49%) Vitamin D metabolism and pathway (0.49%)