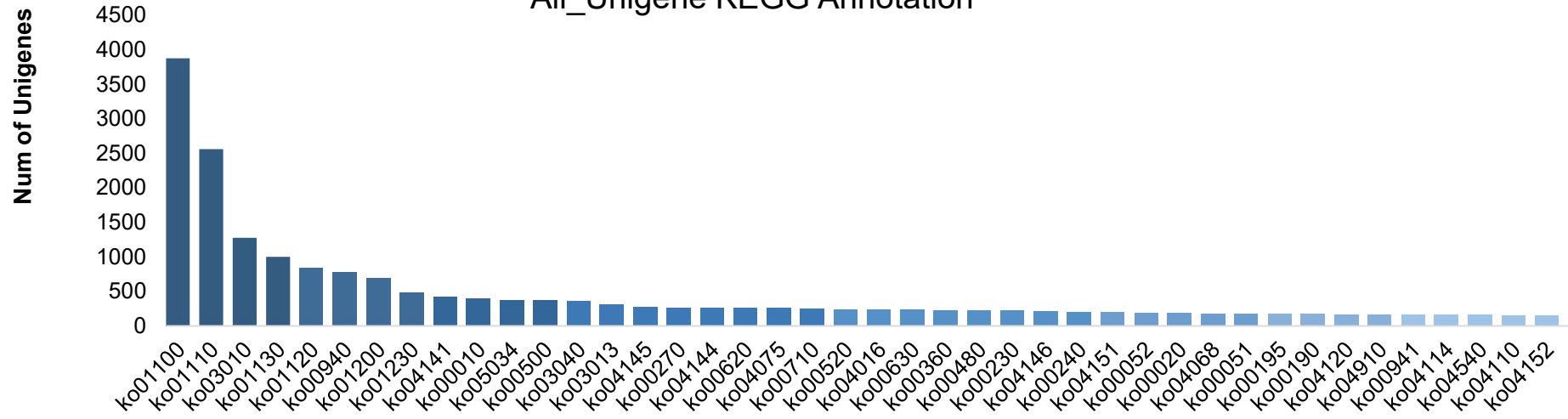


# All\_Unigene KEGG Annotation



- ko01100 Metabolic pathways
- ko01110 Biosynthesis of secondary metabolites
- ko03010 Ribosome
- ko01130 Biosynthesis of antibiotics
- ko01120 Microbial metabolism in diverse environments
- ko00940 Phenylpropanoid biosynthesis
- ko01200 Carbon metabolism
- ko01230 Biosynthesis of amino acids
- ko04141 Protein processing in endoplasmic reticulum
- ko00010 Glycolysis / Gluconeogenesis
- ko05034 Alcoholism
- ko00500 Starch and sucrose metabolism
- ko03040 Spliceosome
- ko03013 RNA transport
- ko04145 Phagosome
- ko00270 Cysteine and methionine metabolism
- ko04144 Endocytosis
- ko00620 Pyruvate metabolism
- ko04075 Plant hormone signal transduction
- ko00710 Carbon fixation in photosynthetic organisms
- ko00520 Amino sugar and nucleotide sugar metabolism
- ko04016 MAPK signaling pathway - plant
- ko00630 Glyoxylate and dicarboxylate metabolism
- ko00360 Phenylalanine metabolism
- ko00480 Glutathione metabolism
- ko00230 Purine metabolism
- ko00240 Pyrimidine metabolism
- ko00240 Pyrimidine metabolism
- ko04151 PI3K-Akt signaling pathway
- ko00052 Galactose metabolism
- ko00020 Citrate cycle
- ko04068 FoxO signaling pathway
- ko00051 Fructose and mannose metabolism
- ko00195 Photosynthesis
- ko00190 Oxidative phosphorylation
- ko04120 Ubiquitin mediated proteolysis
- ko04910 Insulin signaling pathway
- ko00941 Flavonoid biosynthesis
- ko04540 Gap junction
- ko04110 Cell cycle
- ko04152 AMPK signaling pathway