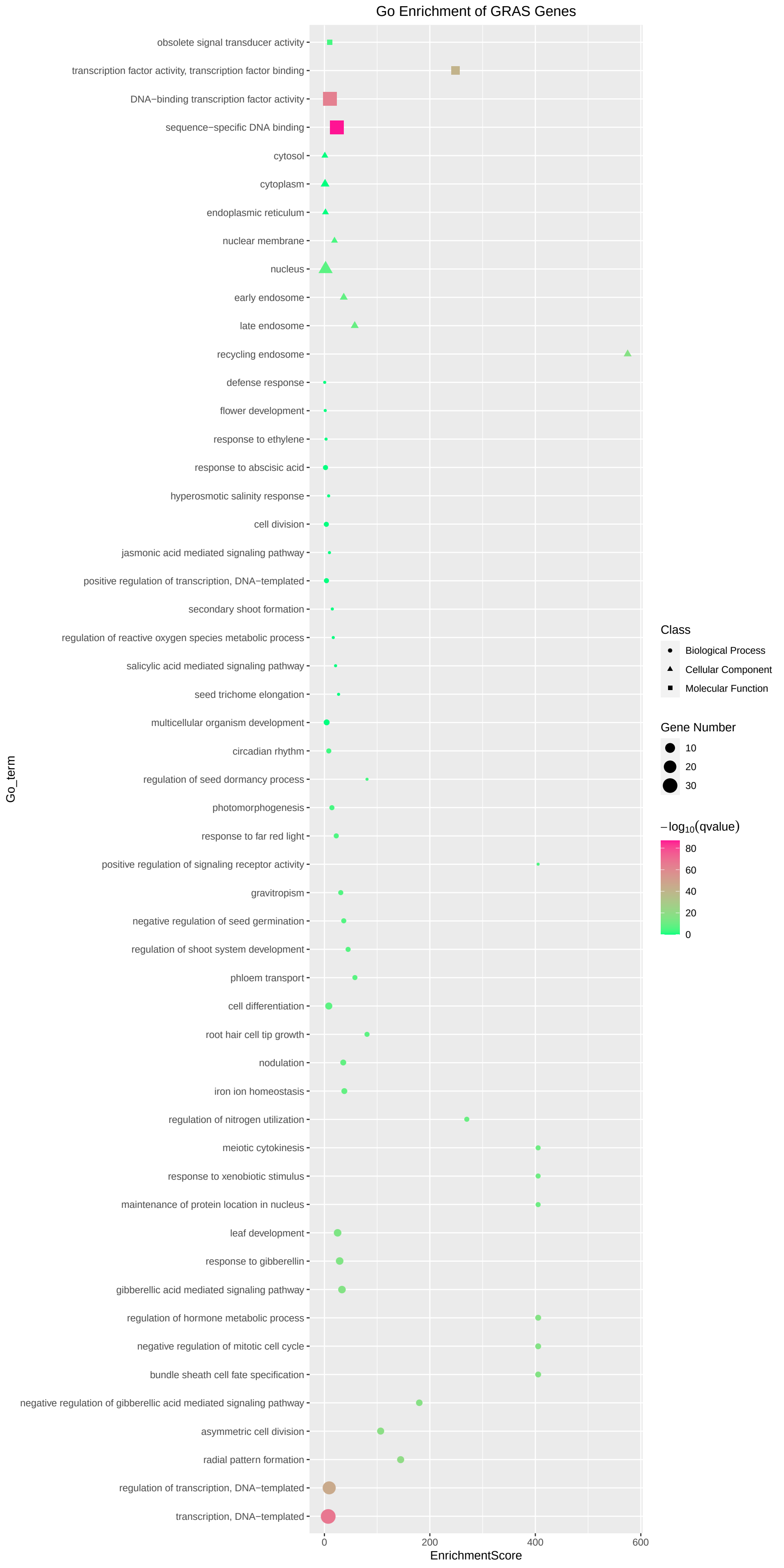
Go Enrichment of GRAS Genes
obsolete signal transducer activity
transcription factor activity, transcription factor binding
DNA−binding transcription factor activity
sequence−specific DNA binding
cytosol
cytoplasm
endoplasmic reticulum
nuclear membrane
nucleus
early endosome
late endosome
recycling endosome
defense response
flower development
response to ethylene
response to abscisic acid
hyperosmotic salinity response
cell division
jasmonic acid mediated signaling pathway
positive regulation of transcription, DNA−templated
secondary shoot formation
regulation of reactive oxygen species metabolic process
salicylic acid mediated signaling pathway
seed trichome elongation
multicellular organism development
circadian rhythm
regulation of seed dormancy process
photomorphogenesis
response to far red light
positive regulation of signaling receptor activity
gravitropism
negative regulation of seed germination
regulation of shoot system development
phloem transport
cell differentiation
root hair cell tip growth
nodulation
iron ion homeostasis
regulation of nitrogen utilization
meiotic cytokinesis
response to xenobiotic stimulus
maintenance of protein location in nucleus
leaf development
response to gibberellin
gibberellic acid mediated signaling pathway
regulation of hormone metabolic process
negative regulation of mitotic cell cycle
bundle sheath cell fate specification
negative regulation of gibberellic acid mediated signaling pathway
asymmetric cell division
radial pattern formation
regulation of transcription, DNA−templated
transcription, DNA−templated
Go_term
0
200
400
600
EnrichmentScore
Class
Biological Process
Cellular Component
Molecular Function
Gene Number
10
20
30
−log10(qvalue)
80
60
40
20
0