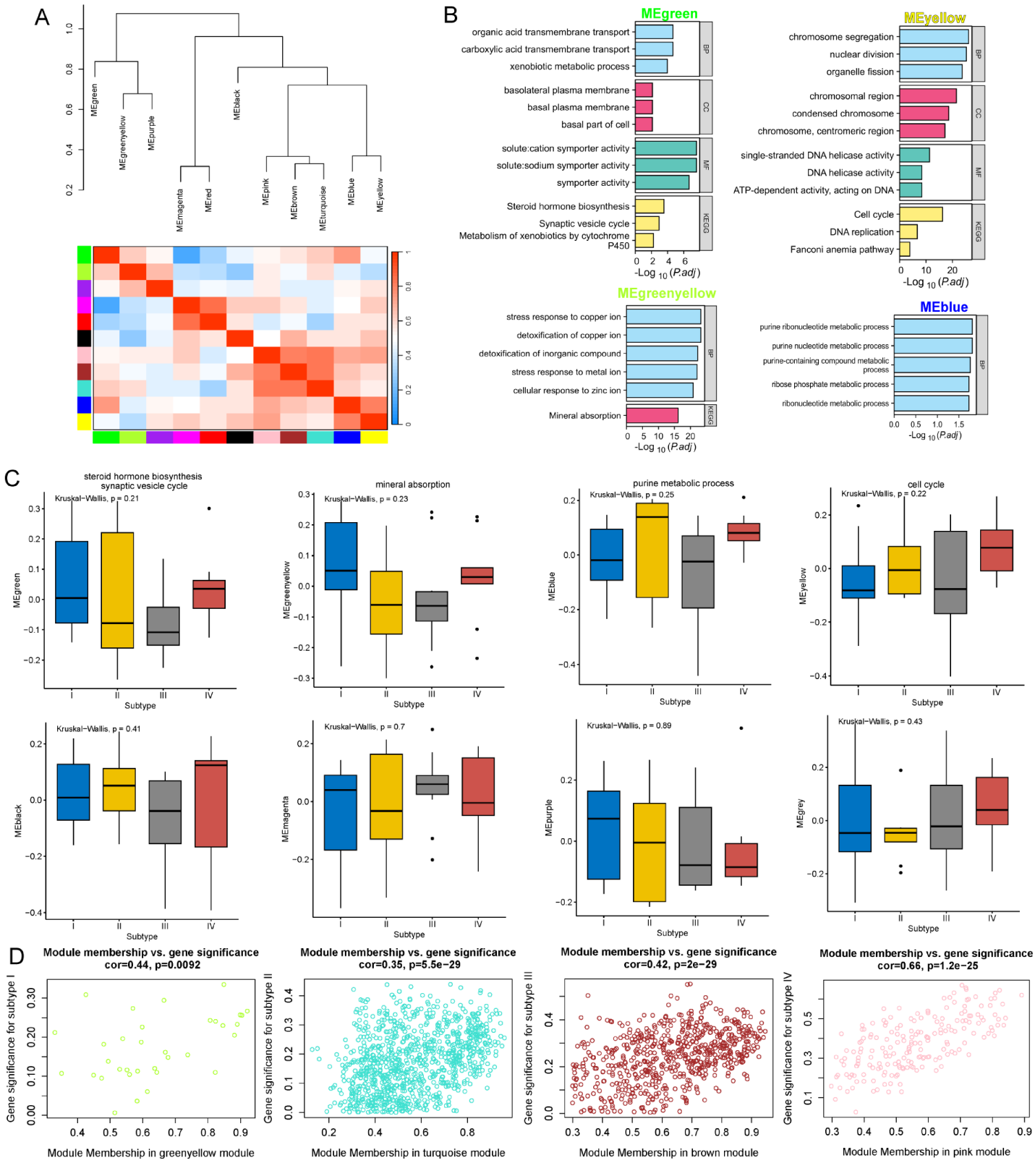
A
MEgreen
MEgreenyellow
MEpurple
MEblack
MEmagenta
MEred
MEpink
MEbrown
MEturquoise
MEblue
MEyellow
B
MEgreen
organic acid transmembrane transport
carboxylic acid transmembrane transport
xenobiotic metabolic process
basolateral plasma membrane
basal plasma membrane
basal part of cell
solute:cation symporter activity
solute:sodium symporter activity
symporter activity
Steroid hormone biosynthesis
Synaptic vesicle cycle
Metabolism of xenobiotics by cytochrome P450
BP
CC
MF
KEGG
-Log 10 (P.adj)
MEyellow
chromosome segregation
nuclear division
organelle fission
chromosomal region
condensed chromosome
chromosome, centromeric region
single-stranded DNA helicase activity
DNA helicase activity
ATP-dependent activity, acting on DNA
Cell cycle
DNA replication
Fanconi anemia pathway
MEgreenyellow
stress response to copper ion
detoxification of copper ion
detoxification of inorganic compound
stress response to metal ion
cellular response to zinc ion
Mineral absorption
MEblue
purine ribonucleotide metabolic process
purine nucleotide metabolic process
purine-containing compound metabolic process
ribose phosphate metabolic process
ribonucleotide metabolic process
C
steroid hormone biosynthesis
synaptic vesicle cycle
Kruskal–Wallis, p = 0.21
mineral absorption
Kruskal–Wallis, p = 0.23
purine metabolic process
Kruskal–Wallis, p = 0.25
cell cycle
Kruskal–Wallis, p = 0.22
Kruskal–Wallis, p = 0.41
Kruskal–Wallis, p = 0.7
Kruskal–Wallis, p = 0.89
Kruskal–Wallis, p = 0.43
MEgreen
MEgreenyellow
MEblue
MEyellow
MEblack
MEmagenta
MEpurple
MEgrey
Subtype
D
Module membership vs. gene significance
cor=0.44, p=0.0092
cor=0.35, p=5.5e−29
cor=0.42, p=2e−29
cor=0.66, p=1.2e−25
Gene significance for subtype I
Gene significance for subtype II
Gene significance for subtype III
Gene significance for subtype IV
Module Membership in greenyellow module
Module Membership in turquoise module
Module Membership in brown module
Module Membership in pink module