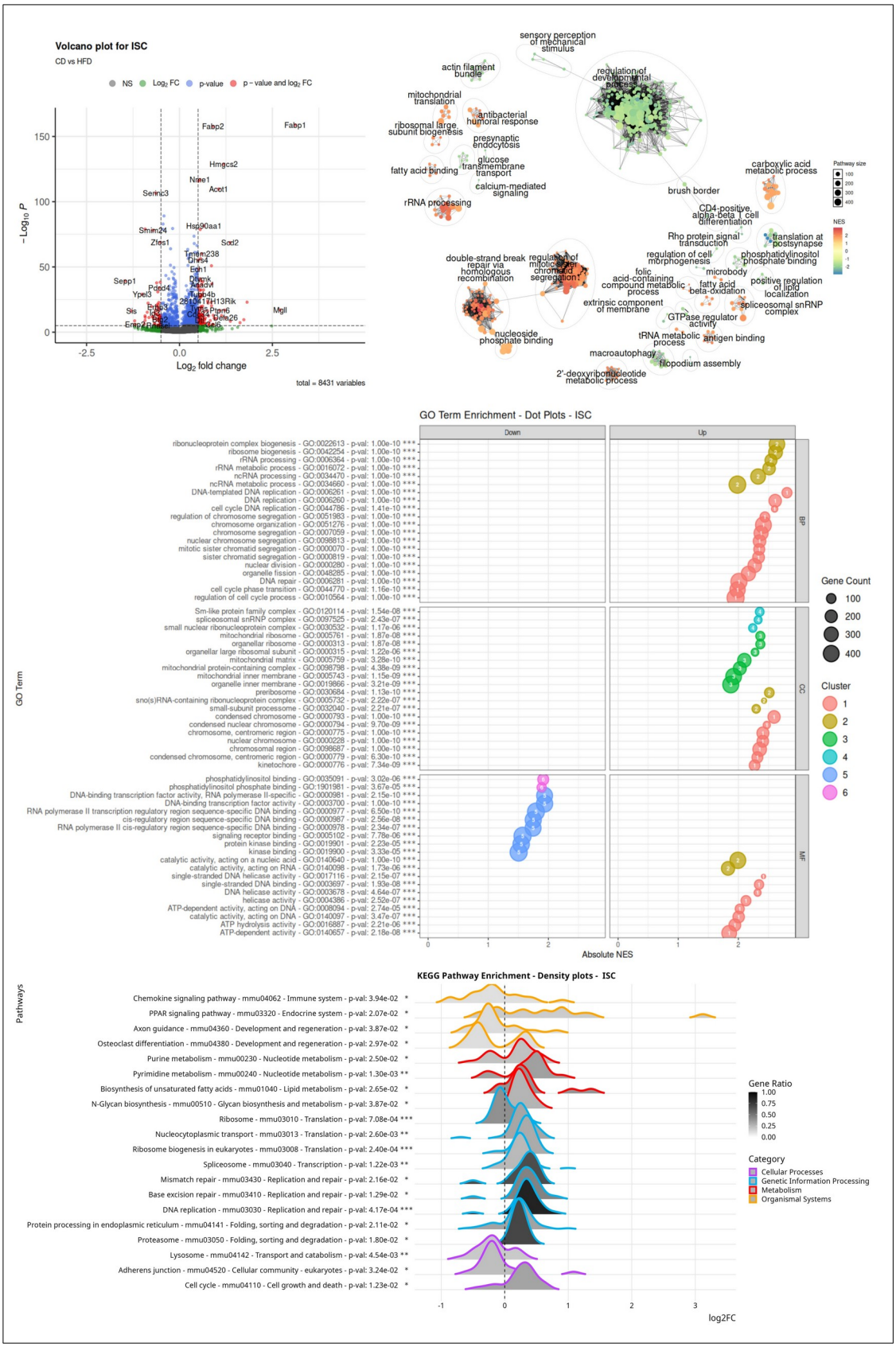
Volcano plot for ISC
CD vs HFD
NS
Log2 FC
p-value
p – value and log2 FC
Fabp2
Fabp1
Hmgcs2
Nme1
Acot1
Serinc3
Hsp90aa1
Sod2
Sepp1
Mgll
Log2 fold change
total = 8431 variables
sensory perception of mechanical stimulus
actin filament bundle
regulation of developmental process
mitochondrial translation
antibacterial humoral response
ribosomal large subunit biogenesis
presynaptic endocytosis
glucose transmembrane transport
fatty acid binding
calcium-mediated signaling
rRNA processing
carboxylic acid metabolic process
brush border
CD4-positive, alpha-beta T cell differentiation
Rho protein signal transduction
translation at postsynapse
regulation of cell morphogenesis
phosphatidylinositol phosphate binding
double-strand break repair via homologous recombination
regulation of mitotic cell cycle, chromatid segregation
microbody
positive regulation of lipid localization
extrinsic component of membrane
spliceosomal snRNP complex
GTPase regulator activity
nucleoside phosphate binding
tRNA metabolic process
antigen binding
macroautophagy
filopodium assembly
2'-deoxyribonucleotide metabolic process
Pathway size
NES
GO Term Enrichment - Dot Plots - ISC
Down
Up
BP
CC
MF
GO Term
Absolute NES
Gene Count
Cluster
KEGG Pathway Enrichment - Density plots - ISC
Pathways
Chemokine signaling pathway - mmu04062 - Immune system - p-val: 3.94e-02 *
PPAR signaling pathway - mmu03320 - Endocrine system - p-val: 2.07e-02 *
Axon guidance - mmu04360 - Development and regeneration - p-val: 3.87e-02 *
Osteoclast differentiation - mmu04380 - Development and regeneration - p-val: 2.97e-02 *
Purine metabolism - mmu00230 - Nucleotide metabolism - p-val: 2.50e-02 *
Pyrimidine metabolism - mmu00240 - Nucleotide metabolism - p-val: 1.30e-03 **
Biosynthesis of unsaturated fatty acids - mmu01040 - Lipid metabolism - p-val: 2.65e-02 *
N-Glycan biosynthesis - mmu00510 - Glycan biosynthesis and metabolism - p-val: 3.87e-02 *
Ribosome - mmu03010 - Translation - p-val: 7.08e-04 ***
Nucleocytoplasmic transport - mmu03013 - Translation - p-val: 2.60e-03 **
Ribosome biogenesis in eukaryotes - mmu03008 - Translation - p-val: 2.40e-04 ***
Spliceosome - mmu03040 - Transcription - p-val: 1.22e-03 **
Mismatch repair - mmu03430 - Replication and repair - p-val: 2.16e-02 *
Base excision repair - mmu03410 - Replication and repair - p-val: 1.29e-02 *
DNA replication - mmu03030 - Replication and repair - p-val: 4.17e-04 ***
Protein processing in endoplasmic reticulum - mmu04141 - Folding, sorting and degradation - p-val: 2.11e-02 *
Proteasome - mmu03050 - Folding, sorting and degradation - p-val: 1.80e-02 *
Lysosome - mmu04142 - Transport and catabolism - p-val: 4.54e-03 **
Adherens junction - mmu04520 - Cellular community - eukaryotes - p-val: 3.24e-02 *
Cell cycle - mmu04110 - Cell growth and death - p-val: 1.23e-02 *
Gene Ratio
Category
Cellular Processes
Genetic Information Processing
Metabolism
Organismal Systems
log2FC