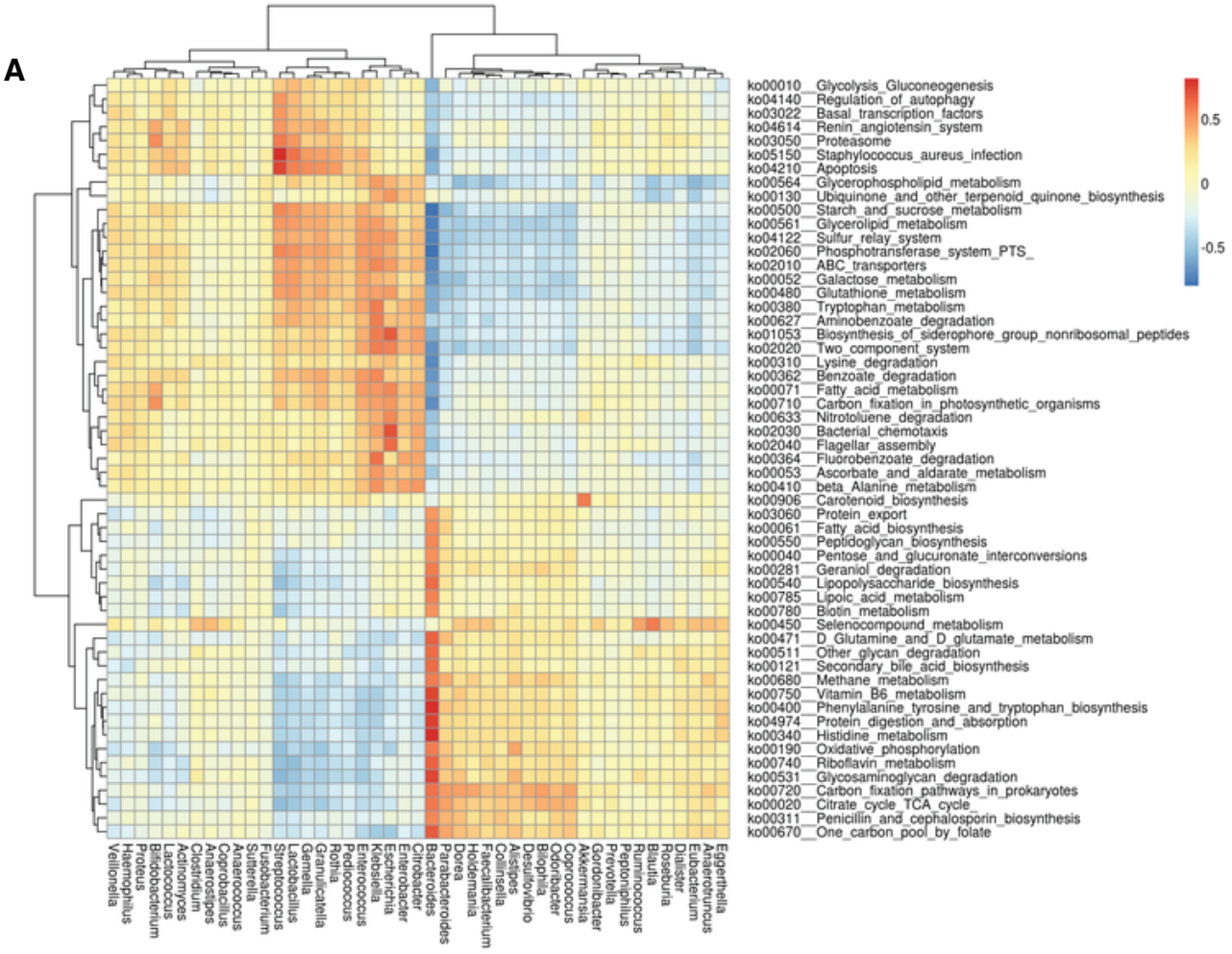
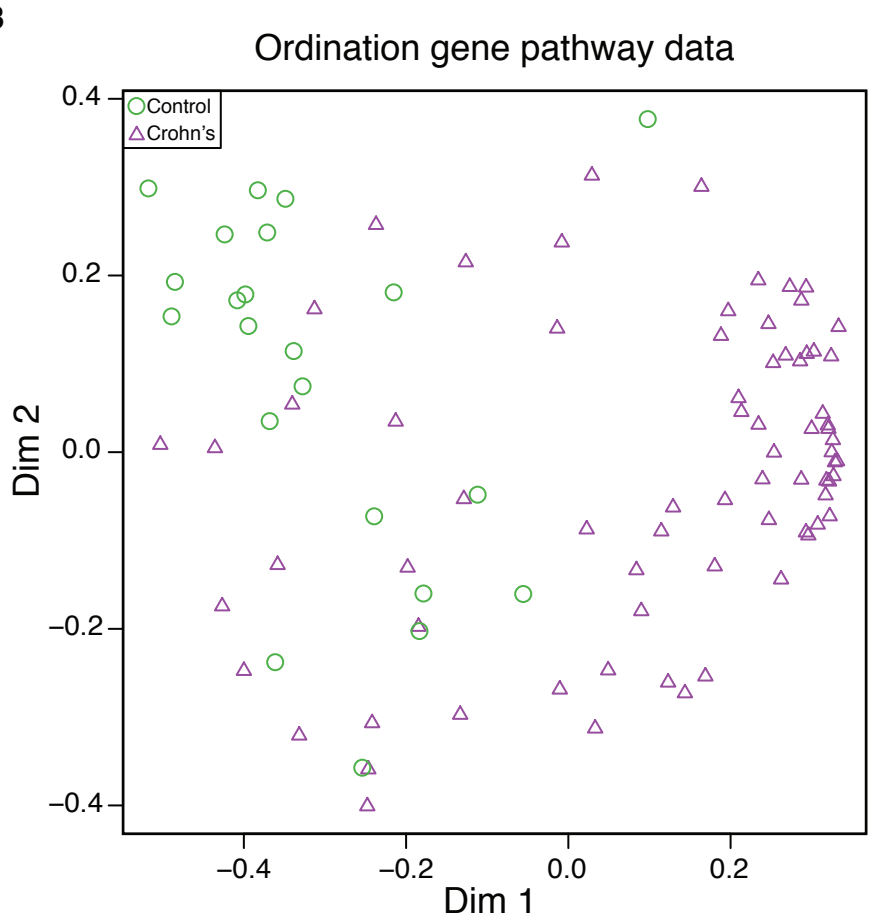

A
ko00010__Glycolysis_Gluconeogenesis
ko04140__Regulation_of_autophagy
ko03022__Basal_transcription_factors
ko04614__Renin_angiotensin_system
ko03050__Proteasome
ko05150__Staphylococcus_aureus_infection
ko04210__Apoptosis
ko00564__Glycerophospholipid_metabolism
ko00130__Ubiquinone_and_other_terpenoid_quinone_biosynthesis
ko00500__Starch_and_sucrose_metabolism
ko00561__Glycerolipid_metabolism
ko04122__Sulfur_relay_system
ko02060__Phosphotransferase_system_PTS_
ko02010__ABC_transporters
ko00052__Galactose_metabolism
ko00480__Glutathione_metabolism
ko00380__Tryptophan_metabolism
ko00627__Aminobenzoate_degradation
ko01053__Biosynthesis_of_siderophore_group_nonribosomal_peptides
ko02020__Two_component_system
ko00310__Lysine_degradation
ko00362__Benzoate_degradation
ko00071__Fatty_acid_metabolism
ko00710__Carbon_fixation_in_photosynthetic_organisms
ko00633__Nitrotoluene_degradation
ko02030__Bacterial_chemotaxis
ko02040__Flagellar_assembly
ko00364__Fluorobenzoate_degradation
ko00053__Ascorbate_and_aldarate_metabolism
ko00410__beta_Alanine_metabolism
ko00906__Carotenoid_biosynthesis
ko03060__Protein_export
ko00061__Fatty_acid_biosynthesis
ko00550__Peptidoglycan_biosynthesis
ko00040__Pentose_and_glucuronate_interconversions
ko00281__Geraniol_degradation
ko00540__Lipopolysaccharide_biosynthesis
ko00785__Lipoic_acid_metabolism
ko00780__Biotin_metabolism
ko00450__Selenocompound_metabolism
ko00471__D_Glutamine_and_D_glutamate_metabolism
ko00511__Other_glycan_degradation
ko00121__Secondary_bile_acid_biosynthesis
ko00680__Methane_metabolism
ko00750__Vitamin_B6_metabolism
ko00400__Phenylalanine_tyrosine_and_tryptophan_biosynthesis
ko04974__Protein_digestion_and_absorption
ko00340__Histidine_metabolism
ko00190__Oxidative_phosphorylation
ko00740__Riboflavin_metabolism
ko00531__Glycosaminoglycan_degradation
ko00720__Carbon_fixation_pathways_in_prokaryotes
ko00020__Citrate_cycle_TCA_cycle_
ko00311__Penicillin_and_cephalosporin_biosynthesis
ko00670__One_carbon_pool_by_folate
0.5
0
-0.5
Veillonella
Haemophilus
Proteus
Bifidobacterium
Lactococcus
Actinomyces
Clostridium
Anaerostipes
Coprobacillus
Anaerococcus
Sutterella
Fusobacterium
Streptococcus
Lactobacillus
Gemella
Granulicatella
Rothia
Pediococcus
Enterococcus
Kibdelia
Escherichia
Enterobacter
Citrobacter
Bacteroides
Parabacteroides
Dorea
Holdemania
Faecalibacterium
Collinsella
Alistipes
Desulfovibrio
Blautia
Odoribacter
Coprococcus
Akkermansia
Gordonibacter
Prevotella
Peptoniphilus
Ruminococcus
Blautia
Roseburia
Dialister
Eubacterium
Anaerotruncus
Eggerthella


B
Ordination gene pathway data
Control
Crohn's
0.4
0.2
0.0
−0.2
−0.4
Dim 2
−0.4
−0.2
0.0
0.2
Dim 1