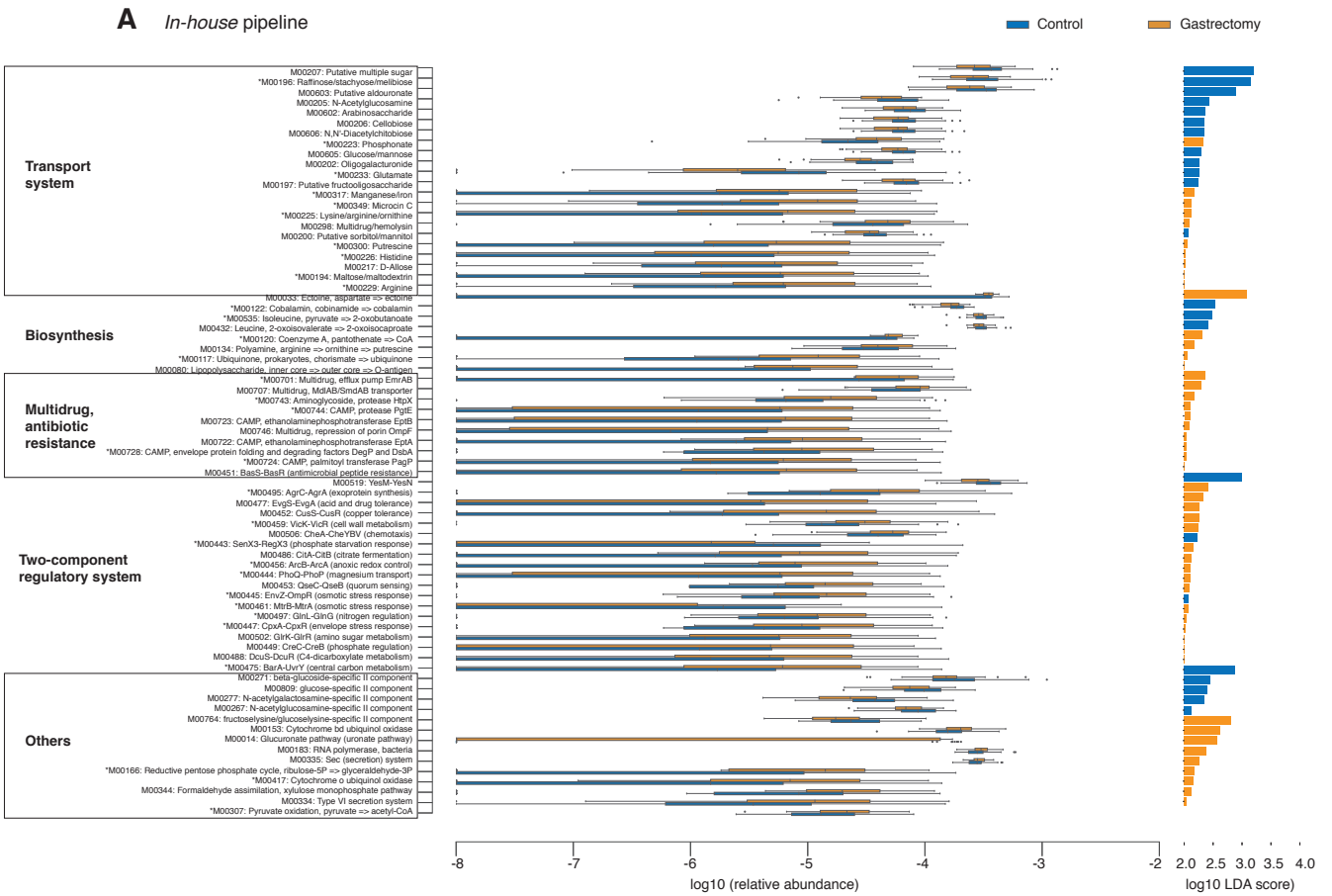
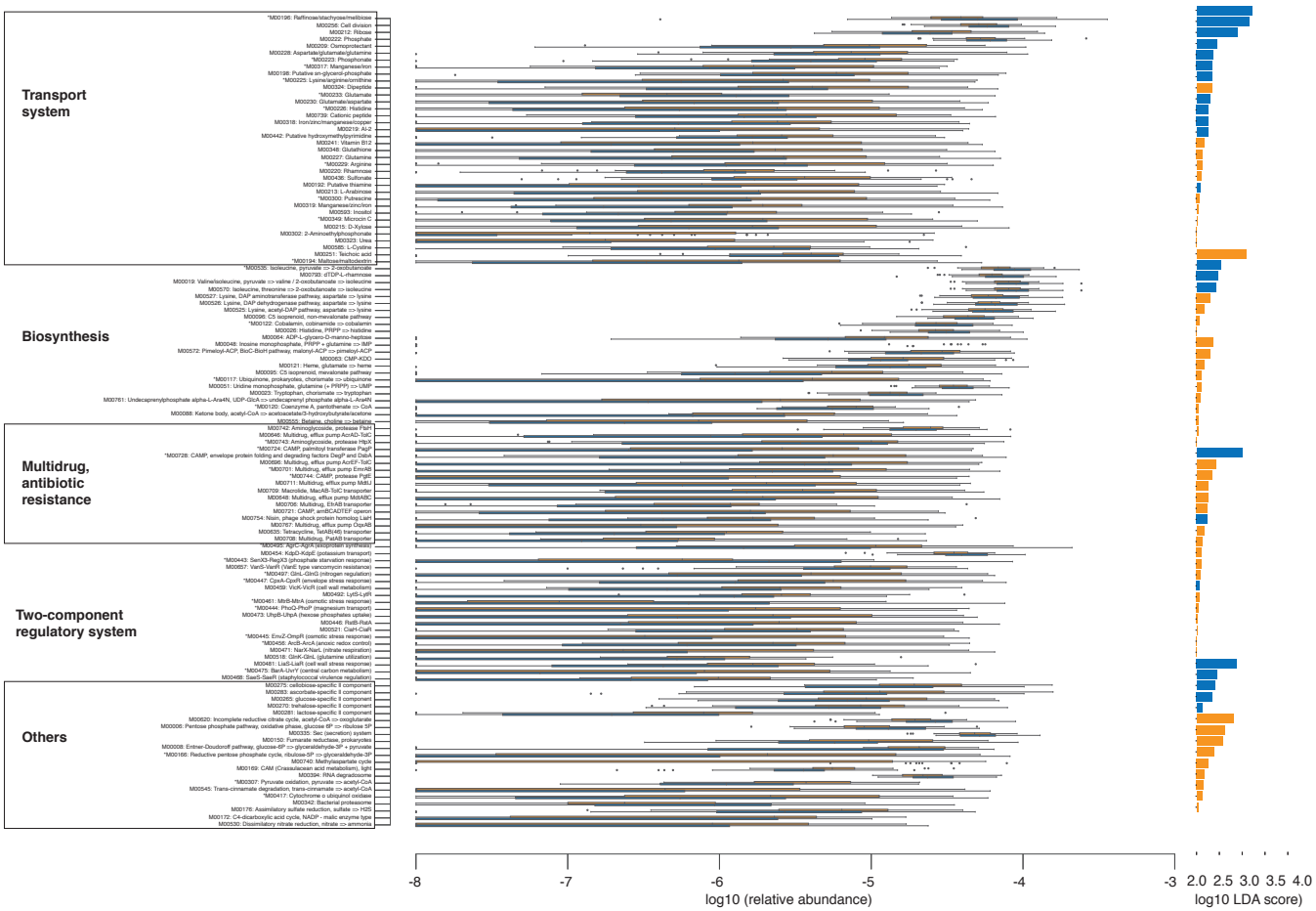

A
In-house pipeline
Control
Gastrectomy
Transport system
M00207: Putative multiple sugar
*M00196: Raffinose/stachyose/melibiose
M00603: Putative aldouronate
M00205: N-Acetylglucosamine
M00602: Arabinosaccharide
M00206: Cellobiose
M00606: N,N'-Diacetylchitobiose
*M00223: Phosphonate
M00605: Glucose/mannose
M00202: Oligogalacturonide
*M00233: Glutamate
M00197: Putative fructooligosaccharide
*M00317: Manganese/iron
*M00349: Microcin C
*M00225: Lysine/arginine/ornithine
M00298: Multidrug/hemolysin
M00200: Putative sorbitol/mannitol
*M00300: Putrescine
*M00226: Histidine
M00217: D-Allose
*M00194: Maltose/maltodextrin
*M00229: Arginine
Biosynthesis
M00033: Ectoine, aspartate => ectoine
*M00122: Cobalamin, cobinamide => cobalamin
*M00535: Isoleucine, pyruvate => 2-oxobutanoate
M00432: Leucine, 2-oxoisovalerate => 2-oxoisocaproate
*M00120: Coenzyme A, pantothenate => CoA
M00134: Polyamine, arginine => ornithine => putrescine
*M00117: Ubiquinone, prokaryotes, chorismate => ubiquinone
M00080: Lipopolysaccharide, inner core => outer core => O-antigen
Multidrug, antibiotic resistance
*M00701: Multidrug, efflux pump EmrAB
M00707: Multidrug, MdlAB/SmdAB transporter
*M00743: Aminoglycoside, protease HtpX
*M00744: CAMP, protease PgtE
M00723: CAMP, ethanolaminephosphotransferase EptB
M00746: Multidrug, repression of porin OmpF
M00722: CAMP, ethanolaminephosphotransferase EptA
*M00728: CAMP, envelope protein folding and degrading factors DegP and DsbA
*M00724: CAMP, palmitoyl transferase PagP
M00451: BasS-BasR (antimicrobial peptide resistance)
Two-component regulatory system
M00519: YesM-YesN
*M00495: AgrC-AgrA (exoprotein synthesis)
M00477: EvgS-EvgA (acid and drug tolerance)
M00452: CusS-CusR (copper tolerance)
*M00459: VicK-VicR (cell wall metabolism)
M00506: CheA-CheYBV (chemotaxis)
*M00443: SenX3-RegX3 (phosphate starvation response)
M00486: CitA-CitB (citrate fermentation)
*M00456: ArcB-ArcA (anoxic redox control)
*M00444: PhoQ-PhoP (magnesium transport)
M00453: QseC-QseB (quorum sensing)
*M00445: EnvZ-OmpR (osmotic stress response)
*M00461: MtrB-MtrA (osmotic stress response)
*M00497: GlnL-GlnG (nitrogen regulation)
*M00447: CpxA-CpxR (envelope stress response)
M00502: GlrK-GlrR (amino sugar metabolism)
M00449: CreC-CreB (phosphate regulation)
M00488: DcuS-DcuR (C4-dicarboxylate metabolism)
*M00475: BarA-UvrY (central carbon metabolism)
Others
M00271: beta-glucoside-specific II component
M00809: glucose-specific II component
M00277: N-acetylgalactosamine-specific II component
M00267: N-acetylglucosamine-specific II component
M00764: fructoselysine/glucoselysine-specific II component
M00153: Cytochrome bd ubiquinol oxidase
M00014: Glucuronate pathway (uronate pathway)
M00183: RNA polymerase, bacteria
M00335: Sec (secretion) system
*M00166: Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P
*M00417: Cytochrome o ubiquinol oxidase
M00344: Formaldehyde assimilation, xylulose monophosphate pathway
M00334: Type VI secretion system
*M00307: Pyruvate oxidation, pyruvate => acetyl-CoA
-8 -7 -6 -5 -4 -3 -2
log10 (relative abundance)
2.0 2.5 3.0 3.5 4.0
log10 LDA score)


B HUMAnN2 pipeline
Transport system
*M00196: Raffinose/stachyose/melibiose
M00256: Cell division
M00212: Ribose
M00222: Phosphate
M00209: Osmoprotectant
M00228: Aspartate/glutamate/glutamine
*M00223: Phosphonate
*M00317: Manganese/iron
M00198: Putative sn-glycerol-phosphate
*M00225: Lysine/arginine/ornithine
M00324: Dipeptide
*M00233: Glutamate
M00230: Glutamate/aspartate
*M00238: Histidine
M00739: Cationic peptide
M00318: Iron/zinc/manganese/copper
M00219: Al-2
M00442: Putative hydroxymethylpyrimidine
M00241: Vitamin B12
M00346: Glutathione
M00227: Glutamine
*M00229: Arginine
M00220: Rhamnose
M00436: Sulfonate
M00192: Putative thiamine
M00213: L-Arabinose
*M00300: Putrescine
M00319: Manganese/zinc/iron
M00593: Inositol
*M00349: Microcin C
M00215: D-Xylose
M00302: 2-Aminoethylphosphonate
M00320: Urea
M00585: L-Cystine
M00251: Teichoic acid
*M00194: Maltose/maltodextrin
Biosynthesis
*M00535: Isoleucine, pyruvate => 2-oxobutanoate
M00793: dTDP-L-rhamnose
M00019: Valine/isoleucine, pyruvate => valine / 2-oxobutanoate => isoleucine
M00570: Isoleucine, threonine => 2-oxobutanoate => isoleucine
M00527: Lysine, DAP aminotransferase pathway, aspartate => lysine
M00526: Lysine, DAP dehydrogenase pathway, aspartate => lysine
M00525: Lysine, acetyl-DAP pathway, aspartate => lysine
M00096: C5 isoprenoid, non-mevalonate pathway
*M00122: Cobalamin, cobinamide => cobalamin
M00026: Histidine, PRPP => histidine
M00064: ADP-L-glycero-D-manno-heptose
M00048: Inosine monophosphate, PRPP + glutamine => IMP
M00572: Pimeloyl-ACP, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP
M00063: CMP-KDO
M00121: Heme, glutamate => heme
M00095: C5 isoprenoid, mevalonate pathway
*M00117: Ubiquinone, prokaryotes, chorismate => ubiquinone
M00051: Uridine monophosphate, glutamine (+ PRPP) => UMP
M00023: Tryptophan, chorismate => tryptophan
M00761: Undecaprenylphosphate alpha-L-Ara4N, UDP-GlcA => undecaprenyl phosphate alpha-L-Ara4N
*M00120: Coenzyme A, pantothenate => CoA
M00088: Ketone body, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone
M00555: Betaine, choline => betaine
Multidrug, antibiotic resistance
M00742: Aminoglycoside, protease FtsH
M00946: Multidrug, efflux pump AcrAD-TolC
*M00743: Aminoglycoside, protease HtpX
*M00724: CAMP, palmitoyl transferase PagP
*M00728: CAMP, envelope protein folding and degrading factors DegP and DsbA
M00998: Multidrug, efflux pump AcrEF-TolC
*M00701: Multidrug, efflux pump EmrAB
*M00744: CAMP, protease PgtE
M00711: Multidrug, efflux pump MdtJ
M00709: Macrolide, MacAB-TolC transporter
M00648: Multidrug, efflux pump MdtABC
M00706: Multidrug, EmrAB transporter
M00721: CAMP, arnBCADTEF operon
M00754: Nisin, phage shock protein homolog LiaH
M00767: Multidrug, efflux pump OqxAB
M00835: Tetracycline, TetA(B/46) transporter
M00708: Multidrug, PatAB transporter
*M00495: AgrC-AgrA (exoprotein synthesis)
M00454: KdpD-KdpE (potassium transport)
*M00443: SenX3-RegX3 (phosphate starvation response)
M00657: VanS-VanR (VanE type vancomycin resistance)
*M00497: GlnL-GlnG (nitrogen regulation)
*M00447: CpxA-CpxR (envelope stress response)
M00459: VicK-VicR (cell wall metabolism)
M00492: LytS-LytR
Two-component regulatory system
*M00461: MtrB-MtrA (osmotic stress response)
*M00444: PhoQ-PhoP (magnesium transport)
M00473: UhpB-UhpA (hexose phosphates uptake)
M00446: RstB-RstA
M00521: CiaH-CiaR
*M00445: EnvZ-OmpR (osmotic stress response)
*M00456: ArcB-ArcA (anoxic redox control)
M00471: NarX-NarL (nitrate respiration)
M00518: GlnK-GlnL (glutamine utilization)
M00481: LiaS-LiaR (cell wall stress response)
*M00475: BarA-UvrY (central carbon metabolism)
M00468: SaeS-SaeR (staphylococcal virulence regulation)
Others
M00275: cellobiose-specific II component
M00283: ascorbate-specific II component
M00265: glucose-specific II component
M00270: trehalose-specific II component
M00281: lactose-specific II component
M00620: Incomplete reductive citrate cycle, acetyl-CoA => oxoglutarate
M00006: Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P
M00335: Sec (secretion) system
M00150: Fumarate reductase, prokaryotes
M00008: Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate
*M00166: Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P
M00740: Methylaspartate cycle
M00169: CAM (Crassulacean acid metabolism), light
M00394: RNA degradosome
*M00307: Pyruvate oxidation, pyruvate => acetyl-CoA
M00545: Trans-cinnamate degradation, trans-cinnamate => acetyl-CoA
*M00417: Cytochrome o ubiquinol oxidase
M00342: Bacterial proteasome
M00176: Assimilatory sulfate reduction, sulfate => H2S
M00172: C4-dicarboxylic acid cycle, NADP - malic enzyme type
M00530: Dissimilatory nitrate reduction, nitrate => ammonia
-8 -7 -6 -5 -4 -3
log10 (relative abundance)
2.0 2.5 3.0 3.5 4.0
log10 LDA score)