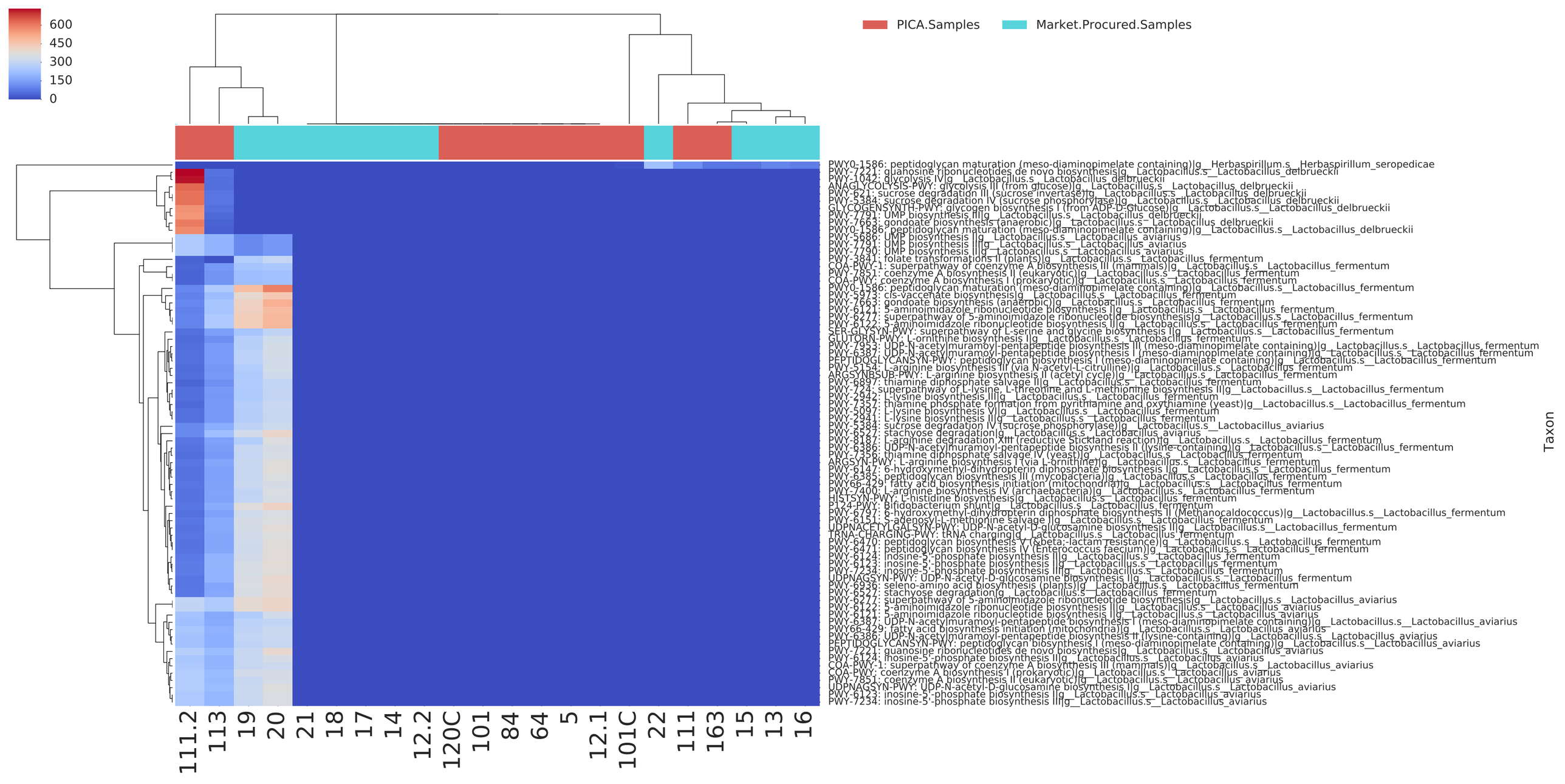
600
450
300
150
0
PICA.Samples
Market.Procured.Samples
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g__Herbaspirillum.s__Herbaspirillum_seropedicae
PWY-7221: guanosine ribonucleotides de novo biosynthesis|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY-1042: glycolysis IV|g__Lactobacillus.s__Lactobacillus_delbrueckii
ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY-621: sucrose degradation III (sucrose invertase)|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY-5384: sucrose degradation IV (sucrose phosphorylase)|g__Lactobacillus.s__Lactobacillus_delbrueckii
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY-7791: UMP biosynthesis III|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY-7663: gondoate biosynthesis (anaerobic)|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_delbrueckii
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-7791: UMP biosynthesis III|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-7790: UMP biosynthesis II|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-3841: folate transformations II (plants)|g__Lactobacillus.s__Lactobacillus_fermentum
COA-PWY-1: superpathway of coenzyme A biosynthesis III (mammals)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7851: coehzyme A biosynthesis II (eukaryotic)|g__Lactobacillus.s__Lactobacillus_fermentum
COA-PWY: coenzyme A biosynthesis I (prokaryotic)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-5973: cis-vaccenate biosynthesis|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7663: gondoate biosynthesis (anaerobic)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis I|g__Lactobacillus.s__Lactobacillus_fermentum
GLUTORN-PWY: L-ornithine biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7953: UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_fermentum
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-5154: L-arginine biosynthesis III (via N-acetyl-L-citrulline)|g__Lactobacillus.s__Lactobacillus_fermentum
ARGSYNBSUB-PWY: L-arginine biosynthesis II (acetyl cycle)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6897: thiamine diphosphate salvage II|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-724: superpathway of L-lysine, L-threonine and L-methionine biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-2942: L-lysine biosynthesis III|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7357: thiamine phosphate formation from pyrithiamine and oxythiamine (yeast)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-5097: L-lysine biosynthesis VI|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-2941: L-lysine biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-5384: sucrose degradation IV (sucrose phosphorylase)|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6527: stachyose degradation|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6187: L-arginine degradation XIII (reductive Stickland reaction)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7356: thiamine diphosphate salvage IV (yeast)|g__Lactobacillus.s__Lactobacillus_fermentum
ARGSYN-PWY: L-arginine biosynthesis I (via L-ornithine)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6385: peptidoglycan biosynthesis III (mycobacteria)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6429: fatty acid biosynthesis initiation (mitochondria)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7400: L-arginine biosynthesis IV (archaebacteria)|g__Lactobacillus.s__Lactobacillus_fermentum
HISTSYN-PWY: L-histidine biosynthesis|g__Lactobacillus.s__Lactobacillus_fermentum
P124-PWY: Bifidobacterium shunt|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6707: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (Methanocaldococcus)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6151: S-adenosyl-L-methionine salvage II|g__Lactobacillus.s__Lactobacillus_fermentum
UDPNACETYLGALSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
TRNA-CHARGING-PWY: tRNA charging|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6470: peptidoglycan biosynthesis V (beta-lactam resistance)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6471: peptidoglycan biosynthesis IV (Enterococcus faecium)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6124: inosine-5'-phosphate biosynthesis II|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6123: inosine-5'-phosphate biosynthesis I|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-7234: inosine-5'-phosphate biosynthesis III|g__Lactobacillus.s__Lactobacillus_fermentum
UDPNAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis I|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6936: seleno-amino acid biosynthesis (plants)|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6527: stachyose degradation|g__Lactobacillus.s__Lactobacillus_fermentum
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6429: fatty acid biosynthesis initiation (mitochondria)|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)|g__Lactobacillus.s__Lactobacillus_aviarius
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-7221: guanosine ribonucleotides de novo biosynthesis|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6124: inosine-5'-phosphate biosynthesis II|g__Lactobacillus.s__Lactobacillus_aviarius
COA-PWY-1: superpathway of coenzyme A biosynthesis III (mammals)|g__Lactobacillus.s__Lactobacillus_aviarius
COA-PWY: coenzyme A biosynthesis I (prokaryotic)|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-7851: coehzyme A biosynthesis II (eukaryotic)|g__Lactobacillus.s__Lactobacillus_aviarius
UDPNAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis I|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-6123: inosine-5'-phosphate biosynthesis I|g__Lactobacillus.s__Lactobacillus_aviarius
PWY-7234: inosine-5'-phosphate biosynthesis III|g__Lactobacillus.s__Lactobacillus_aviarius
111.2
113
19
20
21
18
17
14
12.2
120C
101
84
64
5
12.1
101C
22
111
163
15
13
16
Taxon