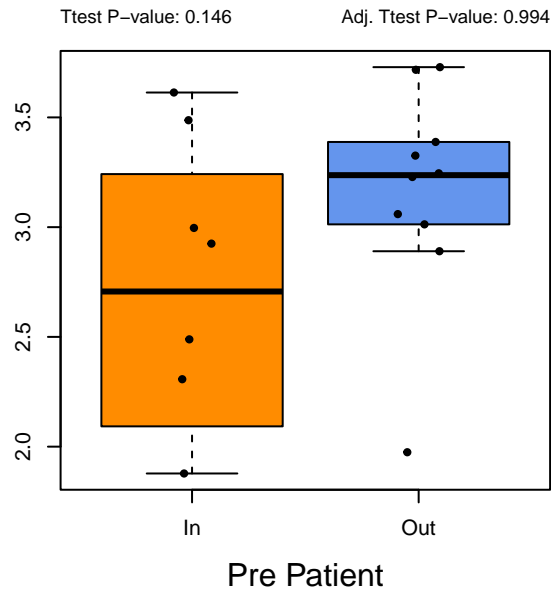
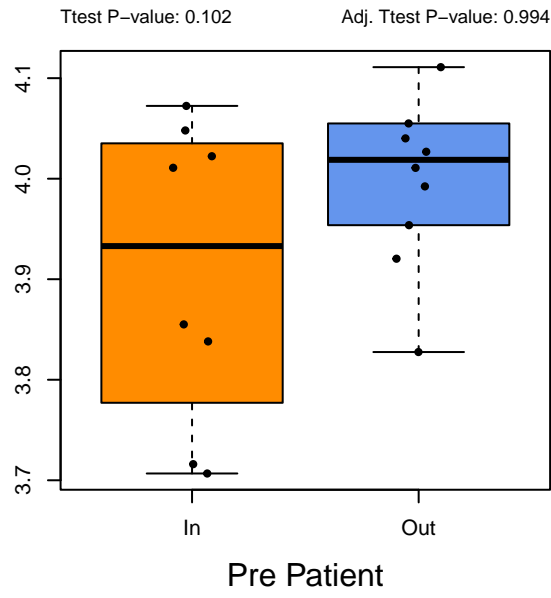


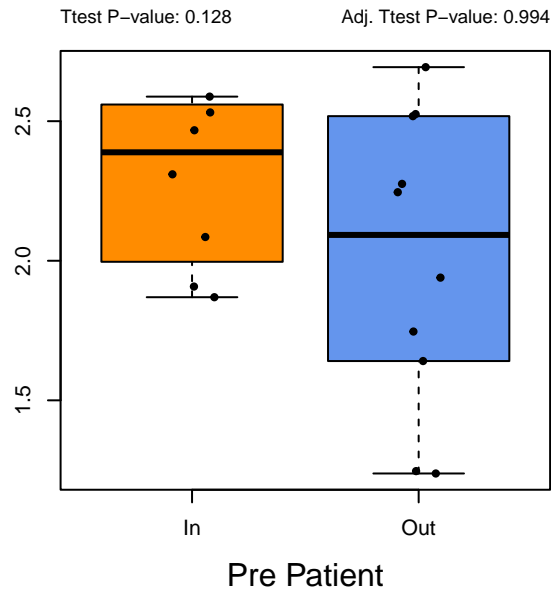
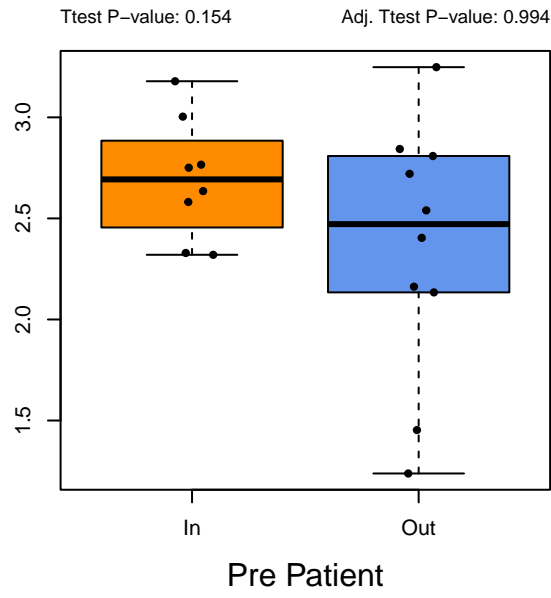
PWY-4984: urea cycle



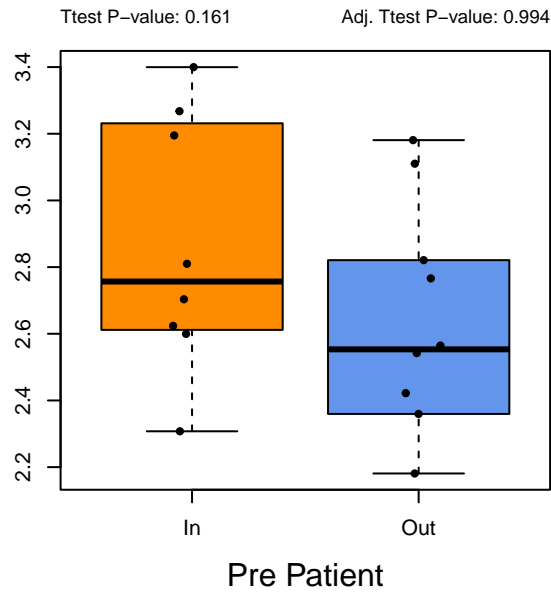
PWY-5695: inosine 5'-phosphate degradation



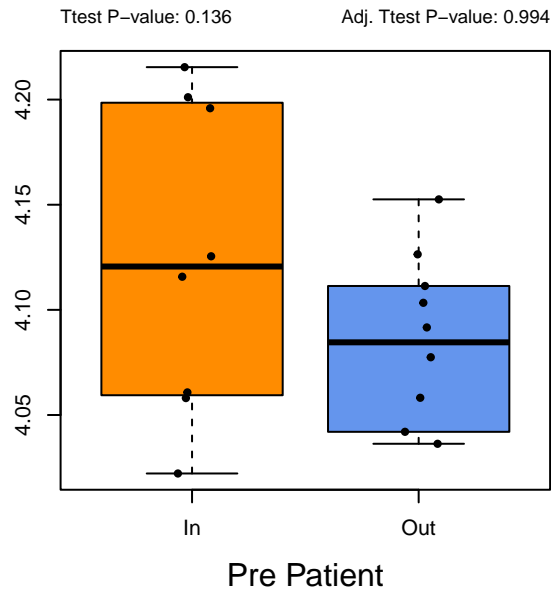
PWY-5837: 2-carboxy-1,4-naphthoquinol biosynt-PWY: superpathway of (R,R)-butanediol biosy



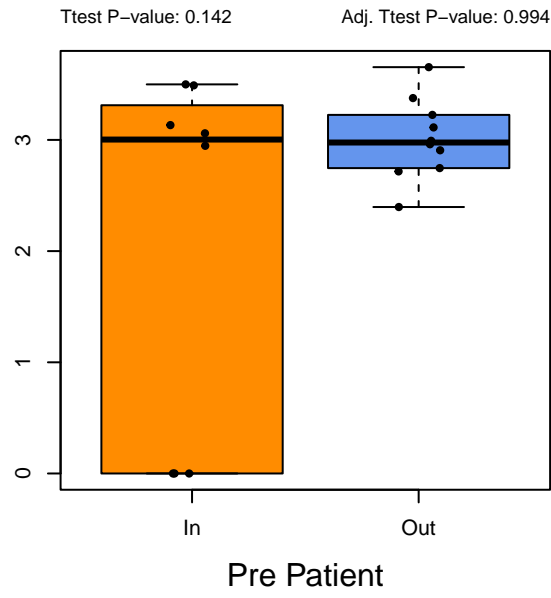
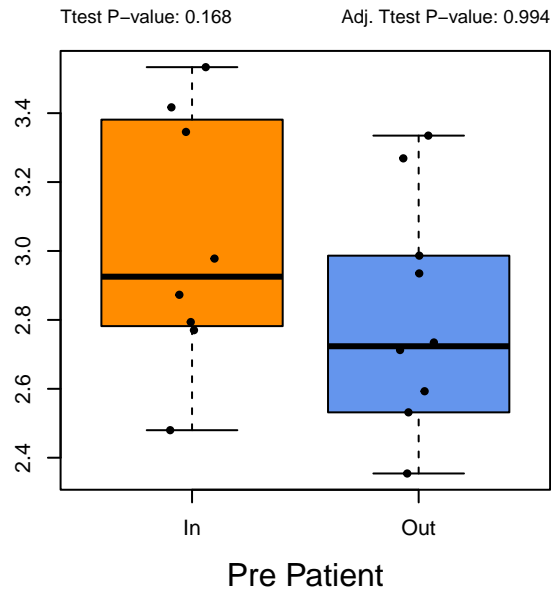
PWY-6612: superpathway of tetrahydrofolate biosyr



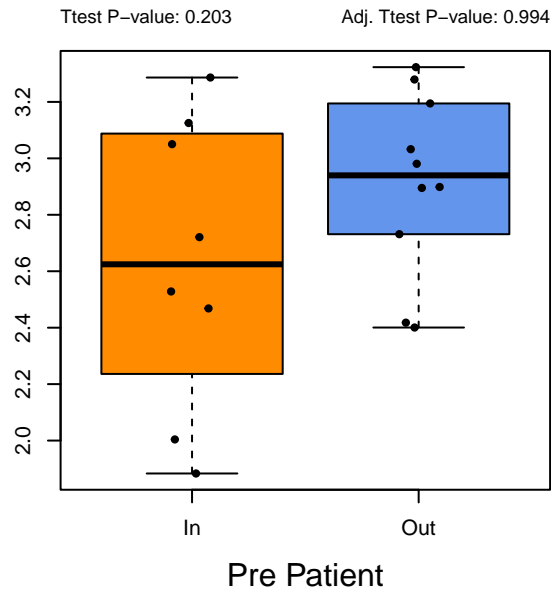
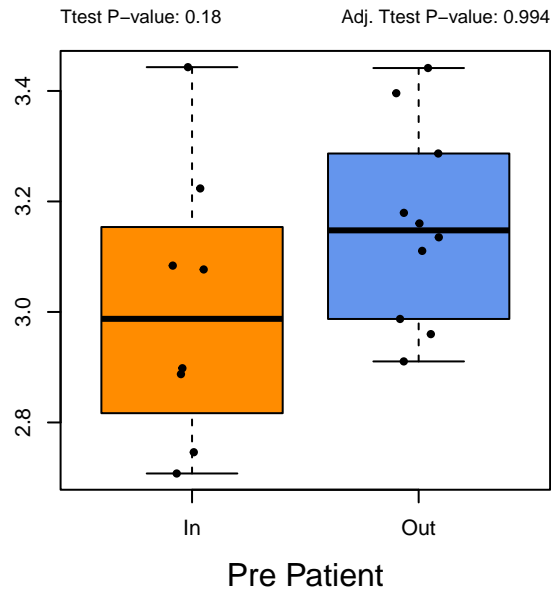
PWY-5103: L-isoleucine biosynthesis III



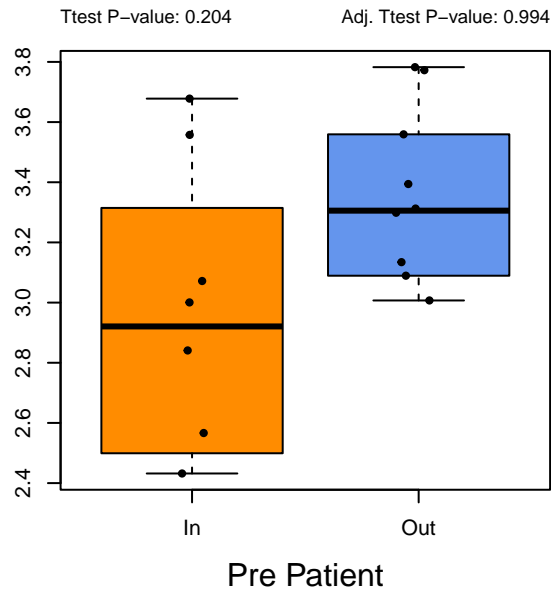
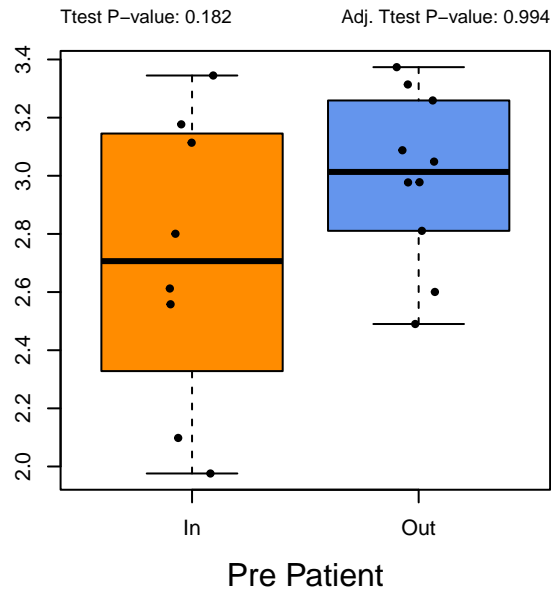
PWY: superpathway of tetrahydrofolate biosynthes5971: palmitate biosynthesis (type II fatty acid s



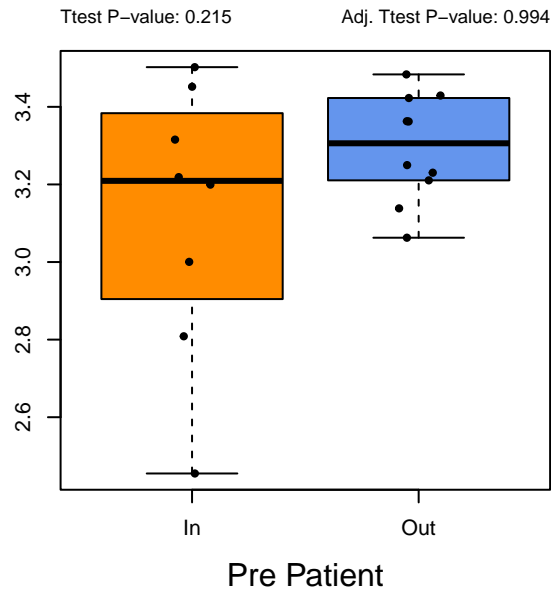
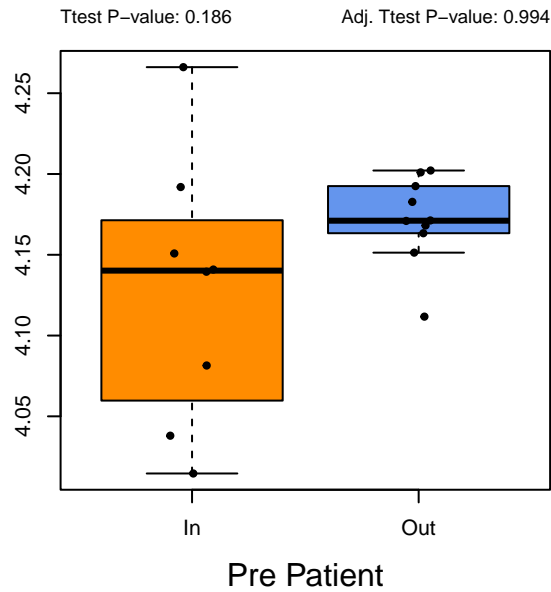
P161-PWY: acetylene degradation (anaerobicPWY-6606: guanosine nucleotides degradation



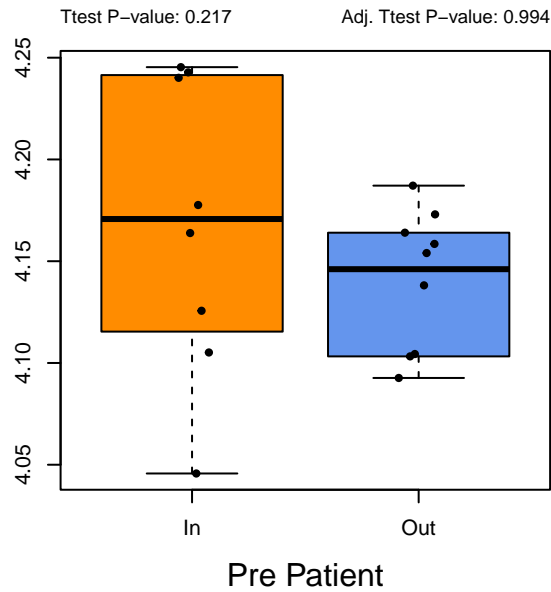
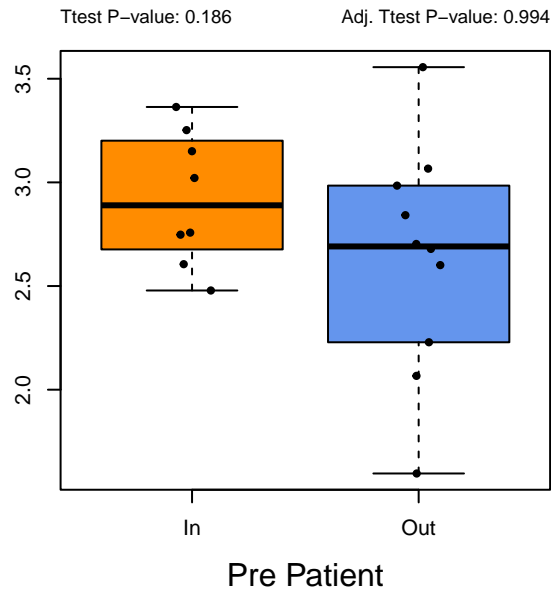
CITRULBIO-PWY: L-citrulline biosynthesis 7: superpathway of fermentation (Chlamydomo

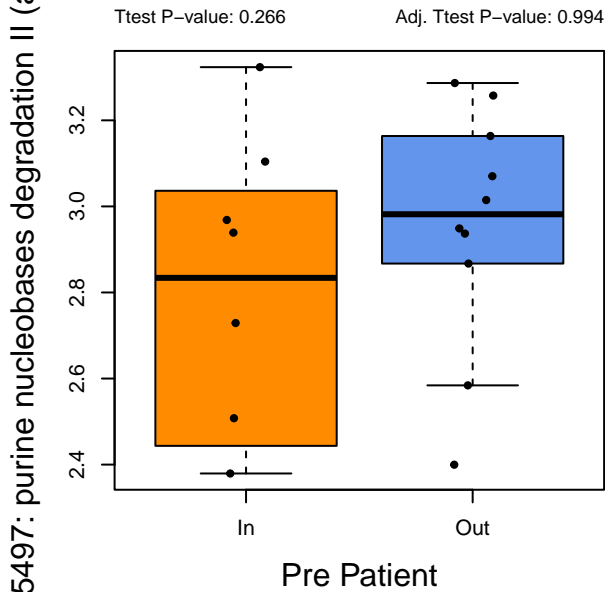
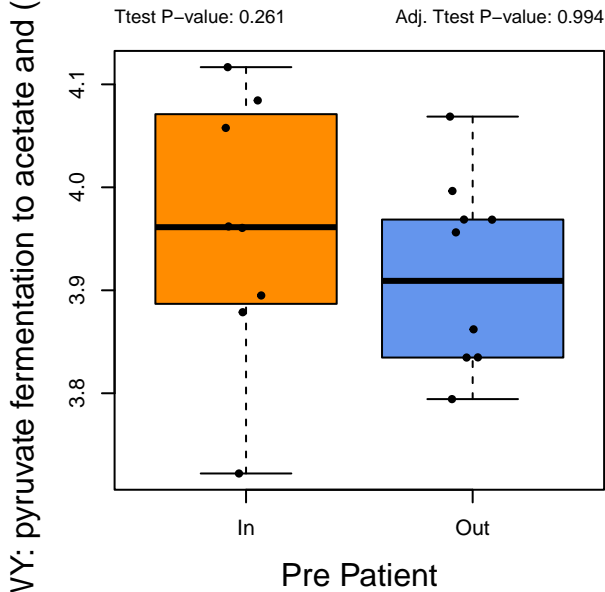
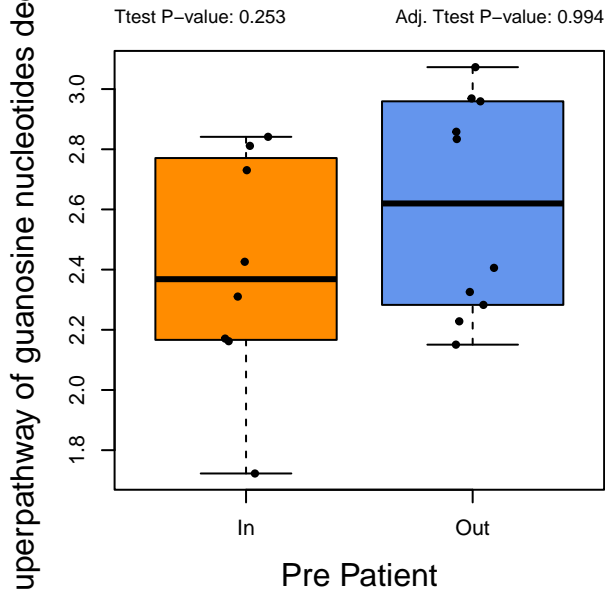
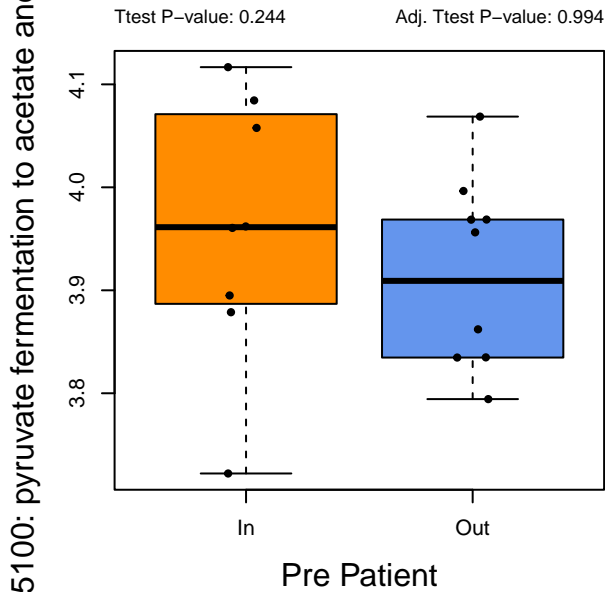
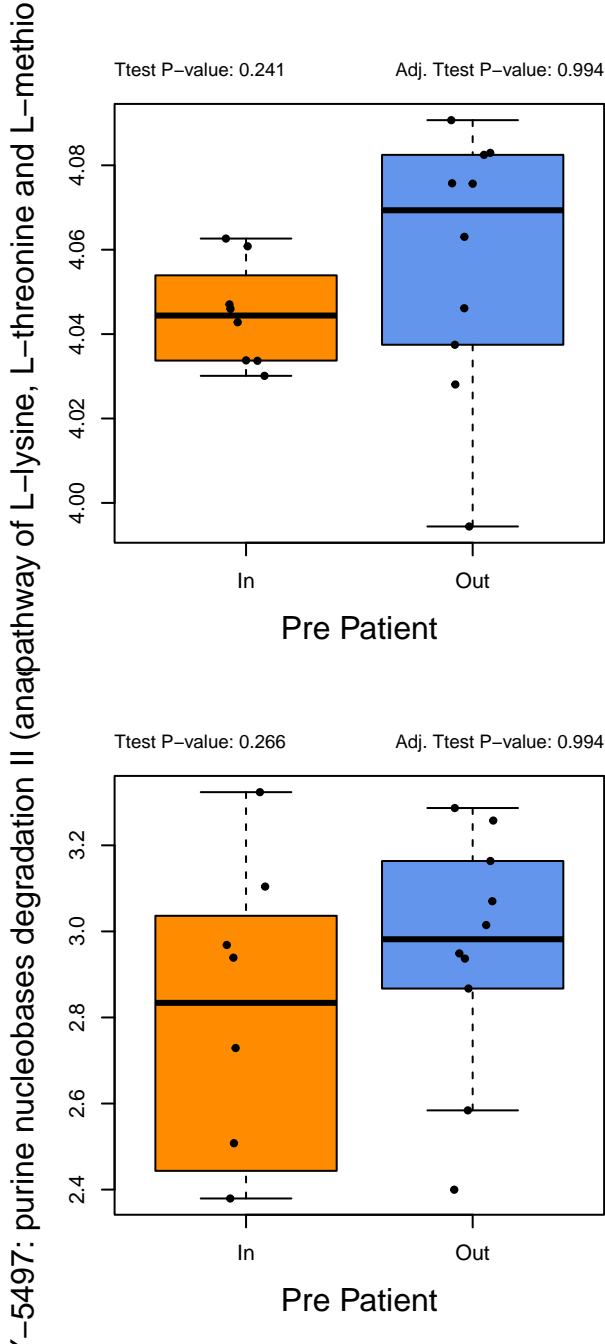
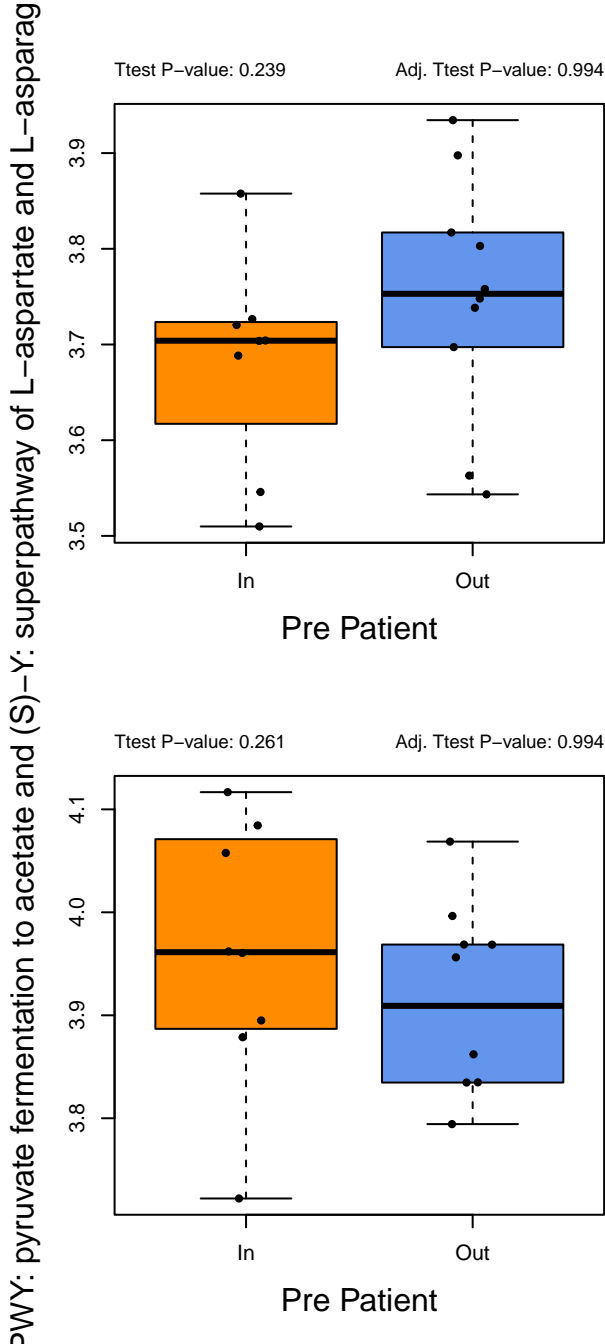
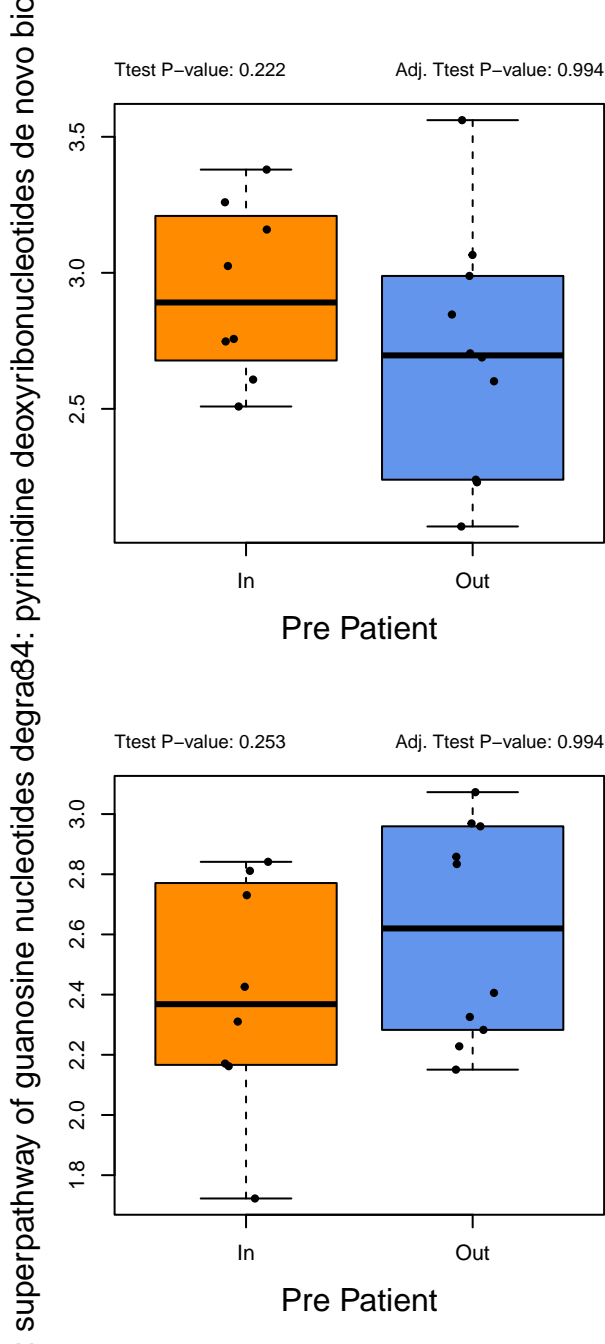
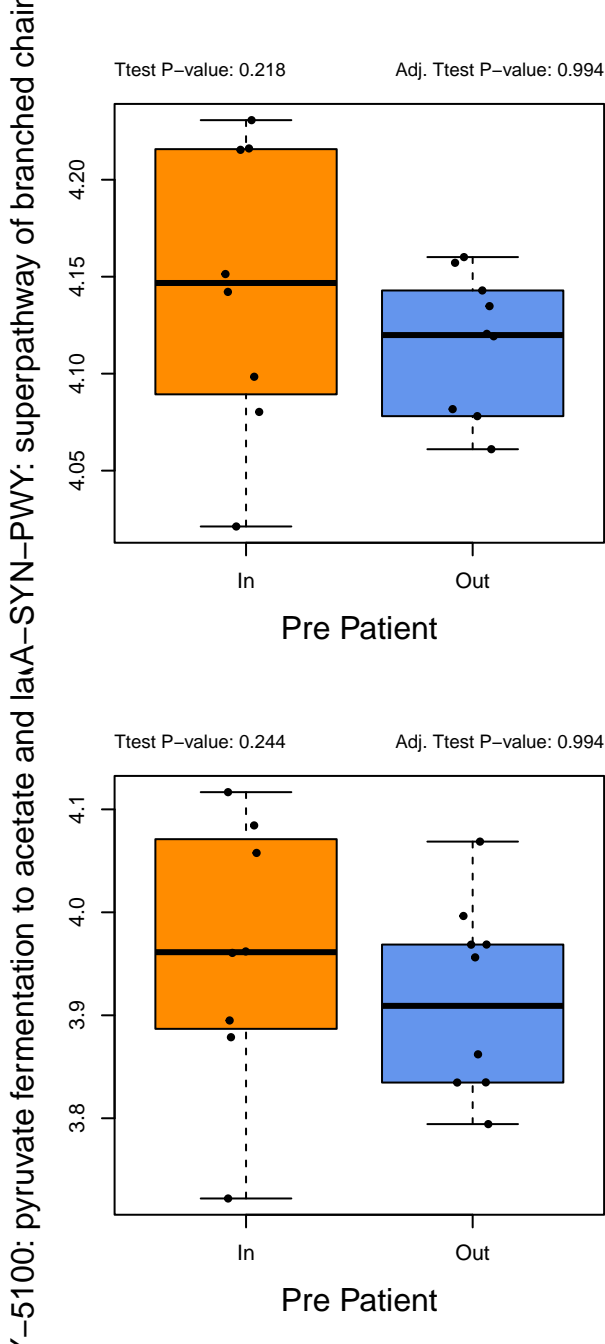


WY-7761: NAD salvage pathway II (PNC IV cy66-429: fatty acid biosynthesis initiation (mitoch

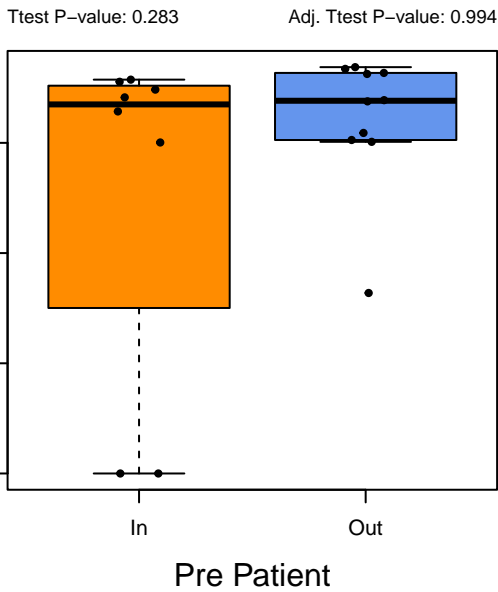


SYN-PWY: L-isoleucine biosynthesis I (from thr5: pyrimidine deoxyribonucleotides de novo bio

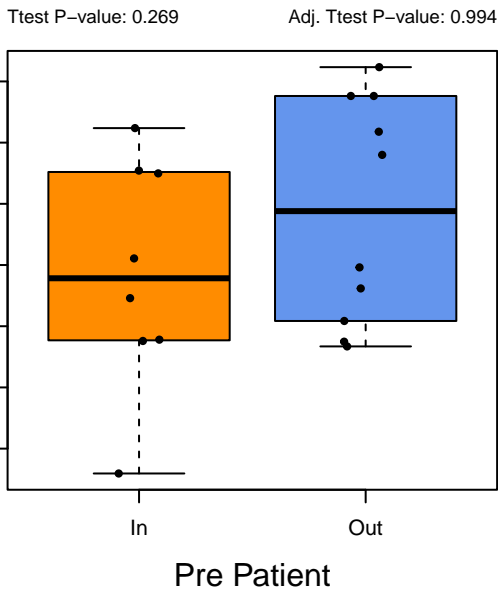




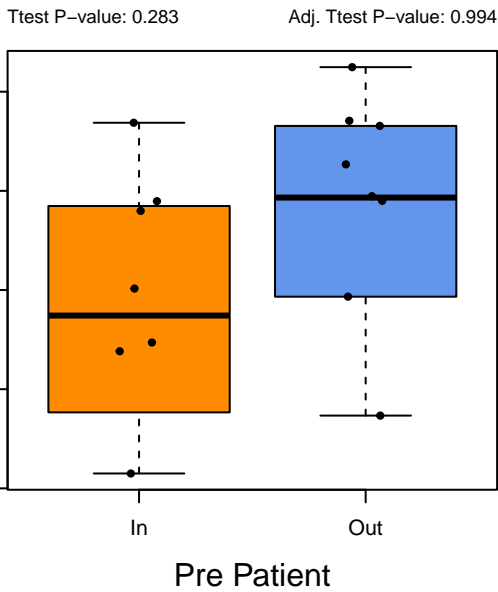
PWY-5030: L-histidine degradation III



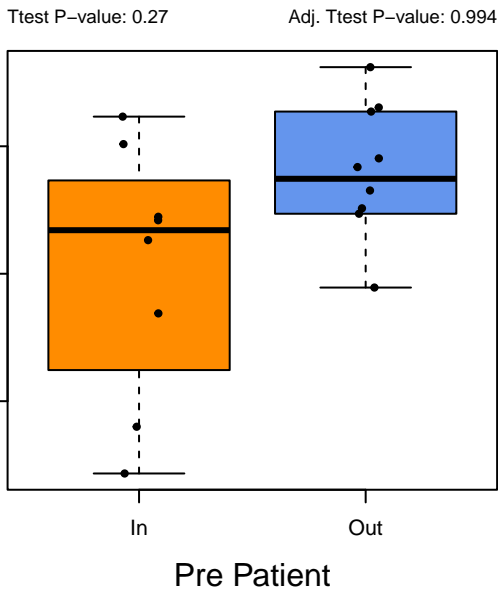
PWY-6607: guanosine nucleotides degradation



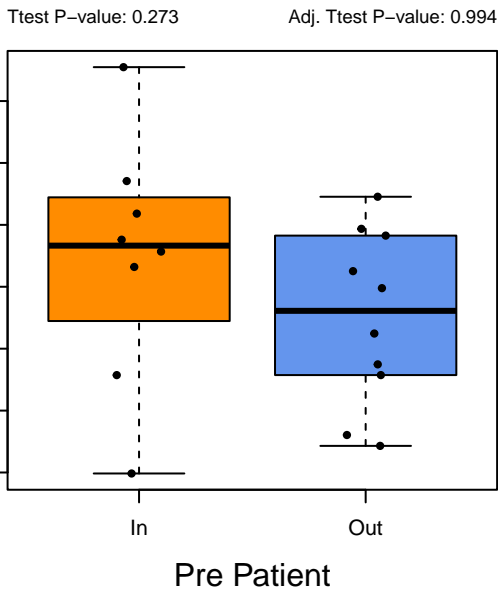
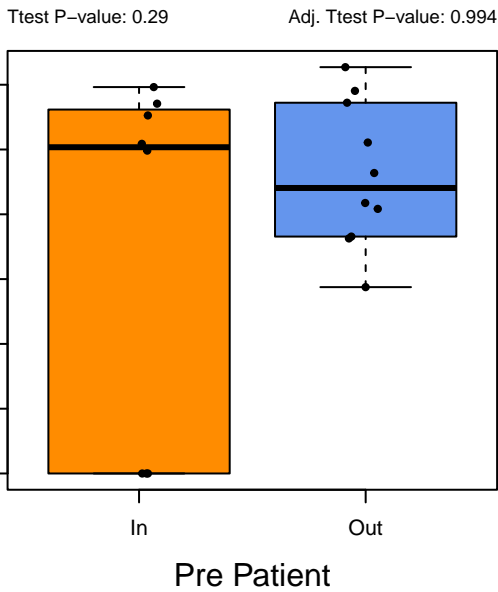
PWY66-399: gluconeogenesis III



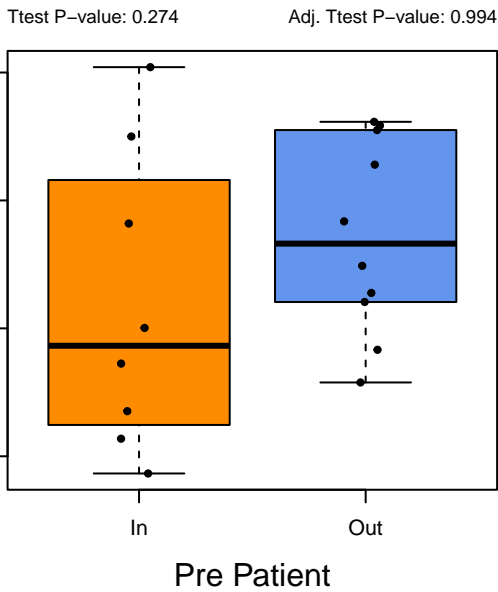
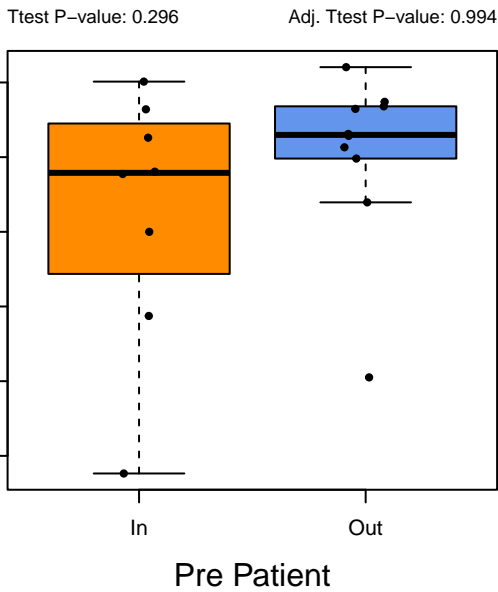
PWY-1042: glycolysis IV|unclassified



pathway of sulfur amino acid biosynthesis (Sacch

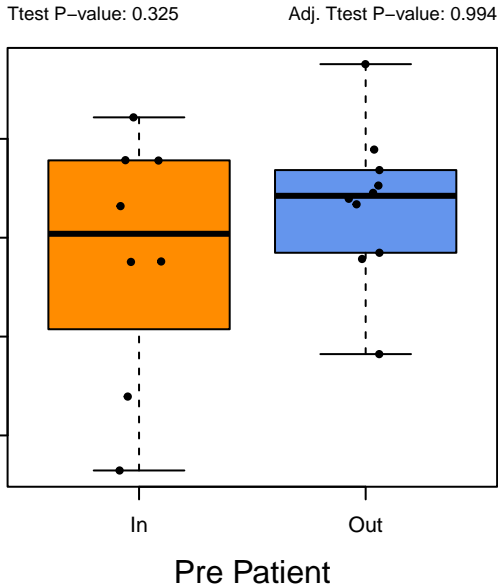
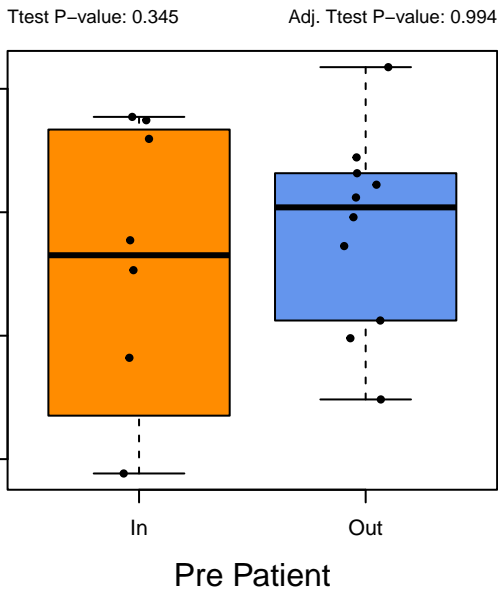


WY: coenzyme A biosynthesis I (prokaryotic)|un-7221: guanosine ribonucleotides de novo biosyn

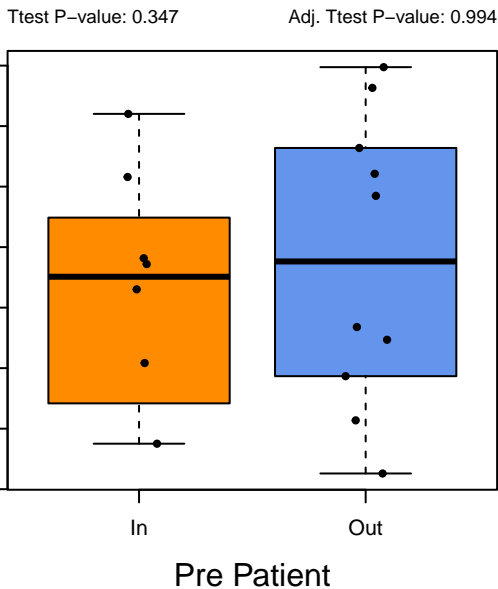




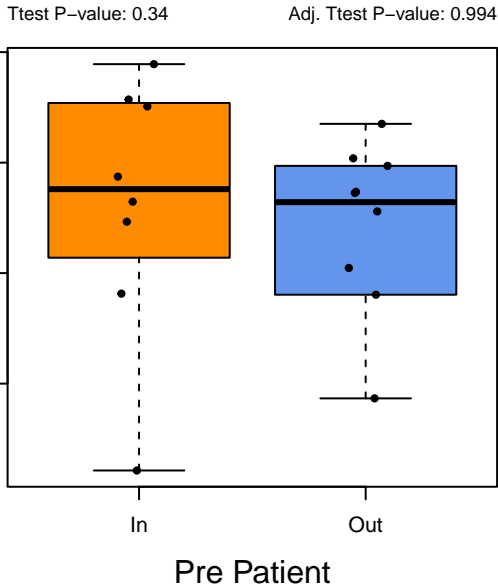
PWY-8073: lipid IVA biosynthesis (P. putida) -6609: adenine and adenosine salvage III



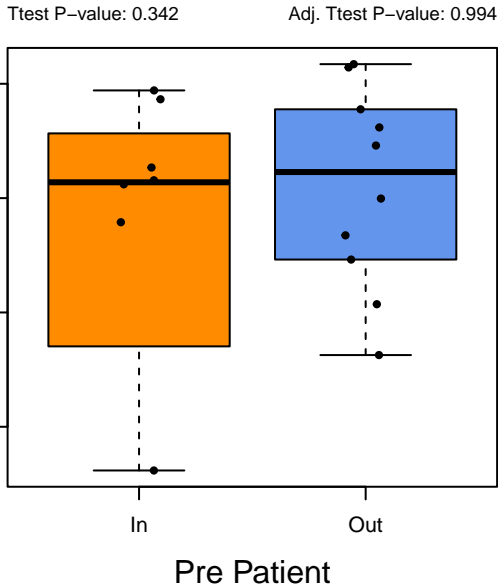
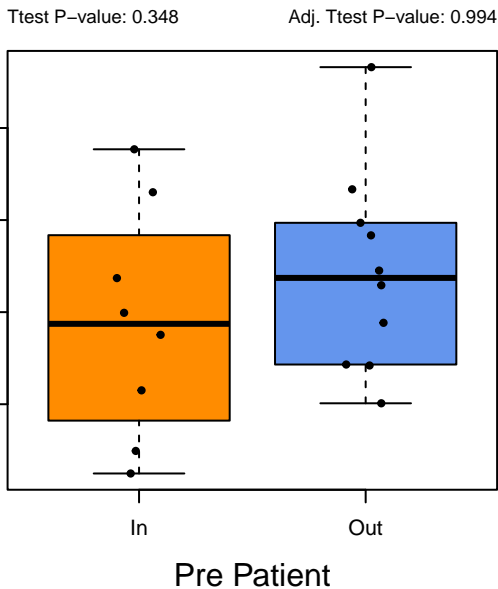
PWY-8004: Entner-Doudoroff pathway I



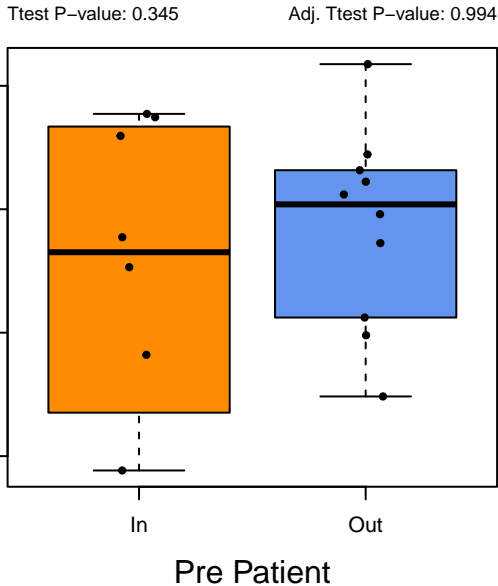
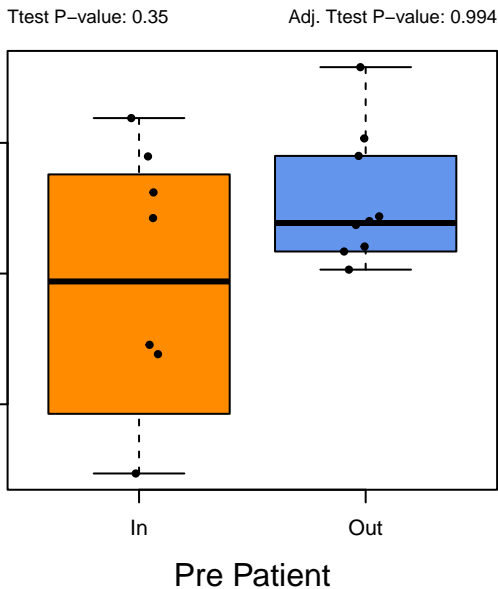
PWY-8004: Entner-Doudoroff pathway I



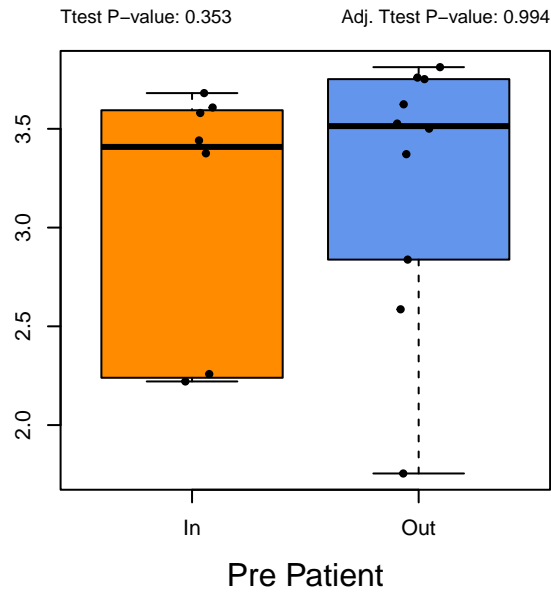
PWY-862: (5Z)-dodecanoate biosynthesis I



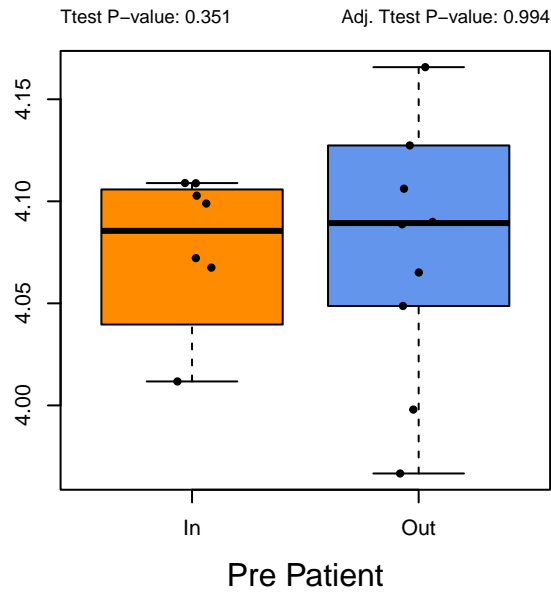
PWY-862: (5Z)-dodecanoate biosynthesis I



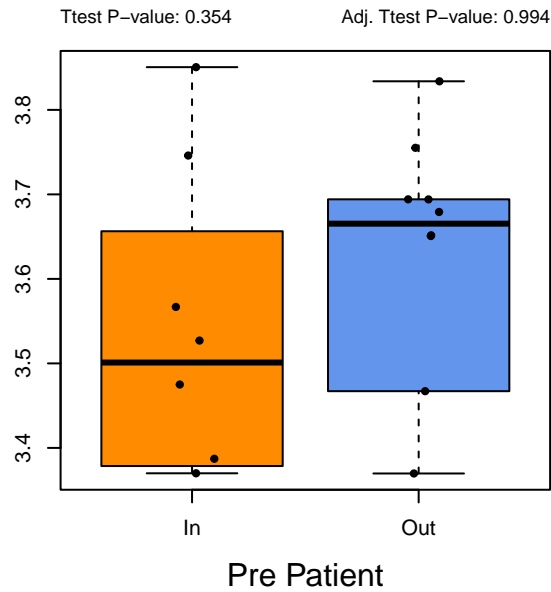
ARGININE-SYN4-PWY: L-ornithine biosynthesis



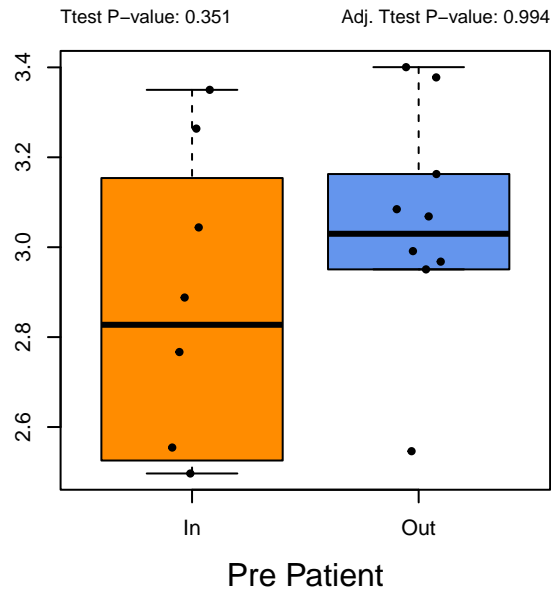
HISTSYN-PWY: L-histidine biosynthesis



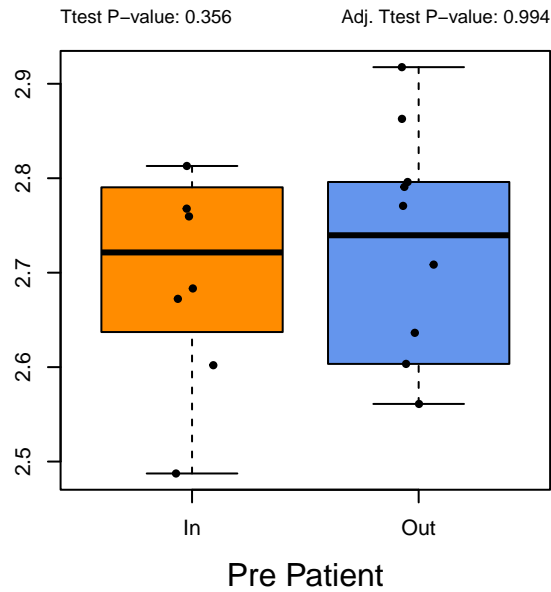
PWY-6731: starch degradation III



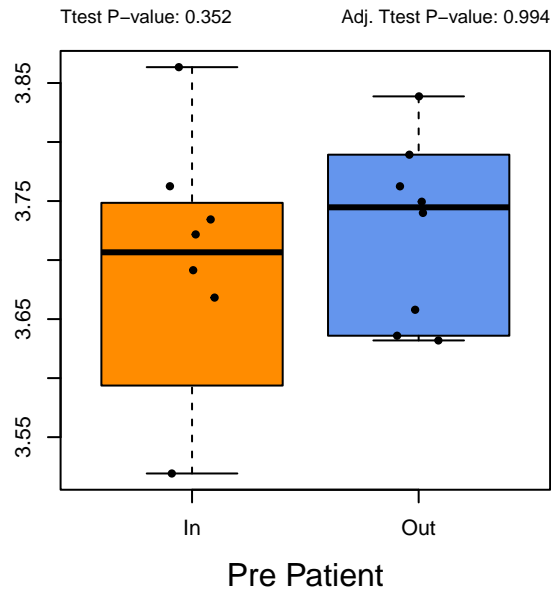
WY-6969: TCA cycle V (2-oxoglutarate synth



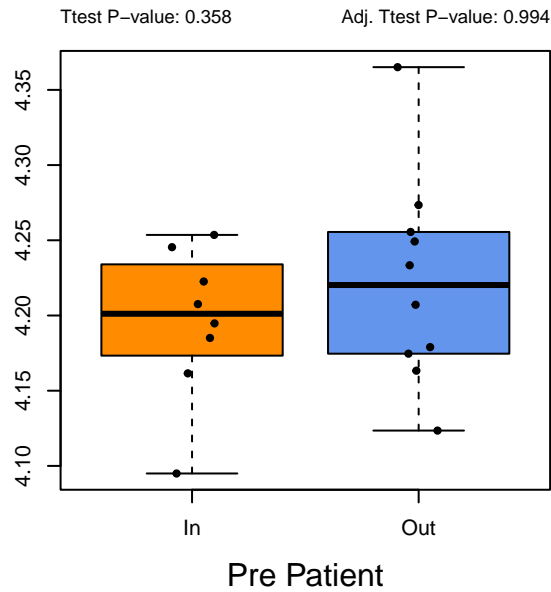
YN2-PWY: heme b biosynthesis II (oxygen-ind



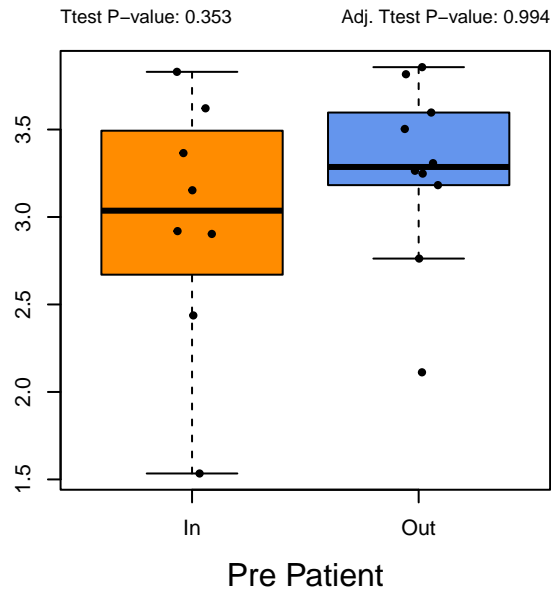
RHAMCAT-PWY: L-rhamnose degradation I



PWY-6609: adenine and adenosine salvage



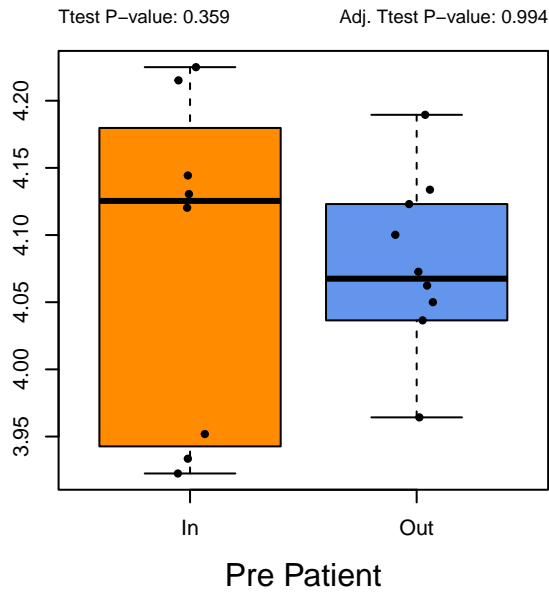
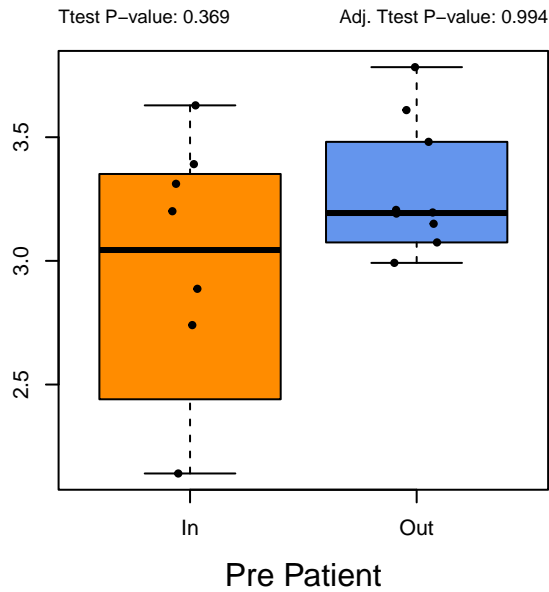
PWY-6609: adenine and adenosine salvage I



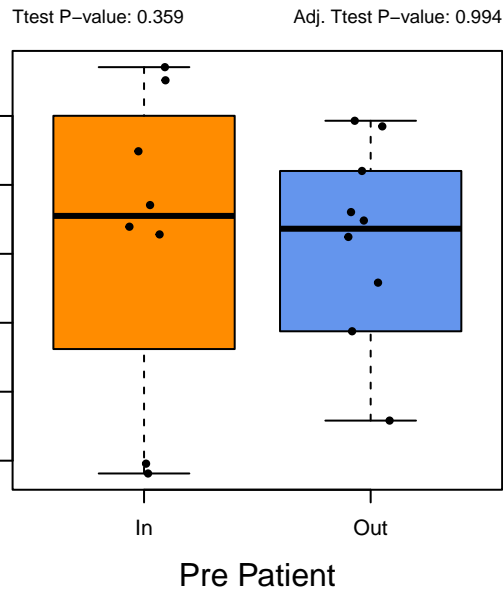
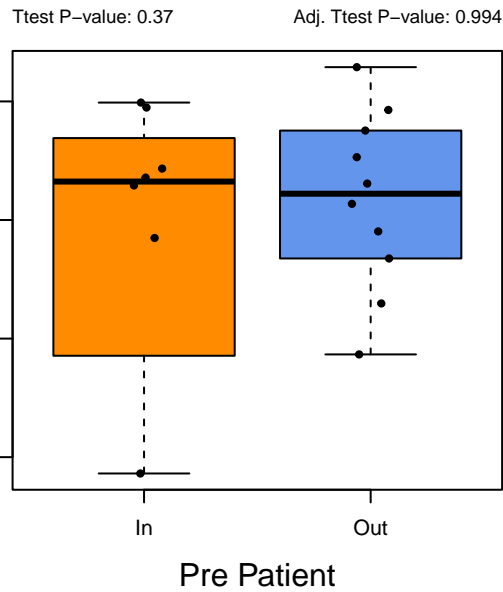


peptidoglycan biosynthesis I (meso-diaminop

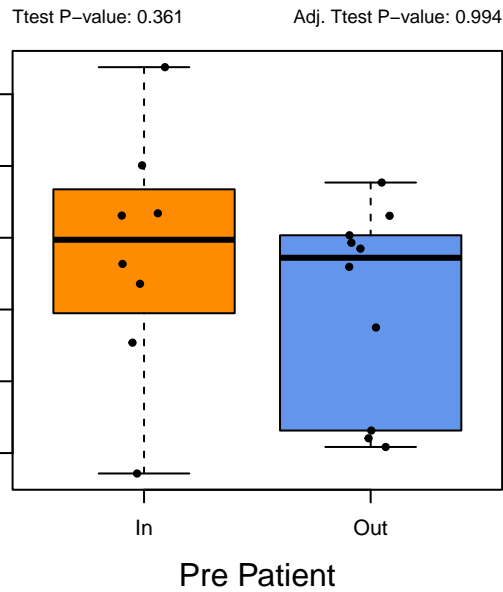
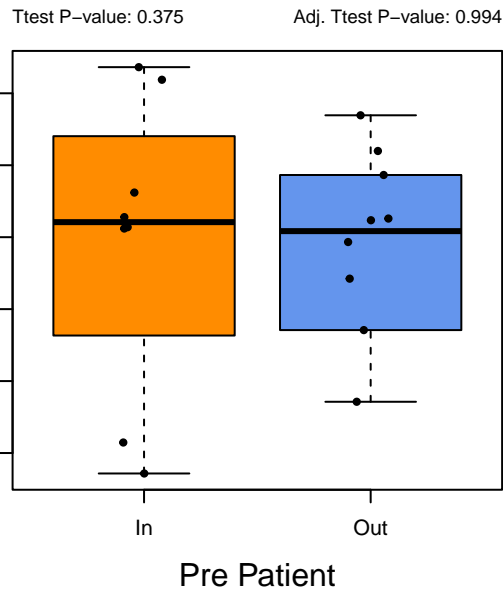
GLUTORN-PWY: L-ornithine biosynthesis



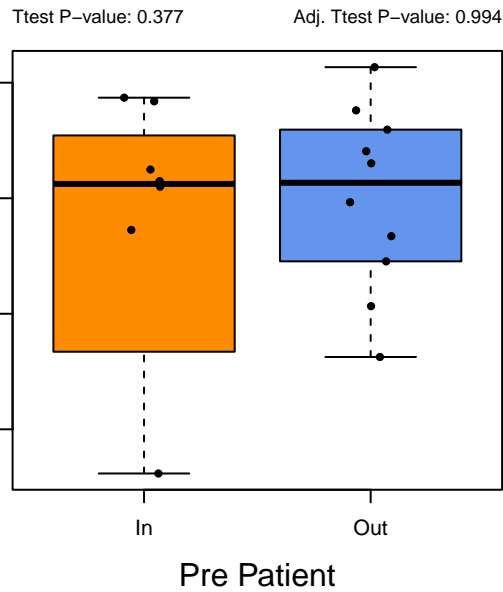
YN-ELONG-PWY: fatty acid elongation --- satYNBSUB-PWY: L-arginine biosynthesis II (ace



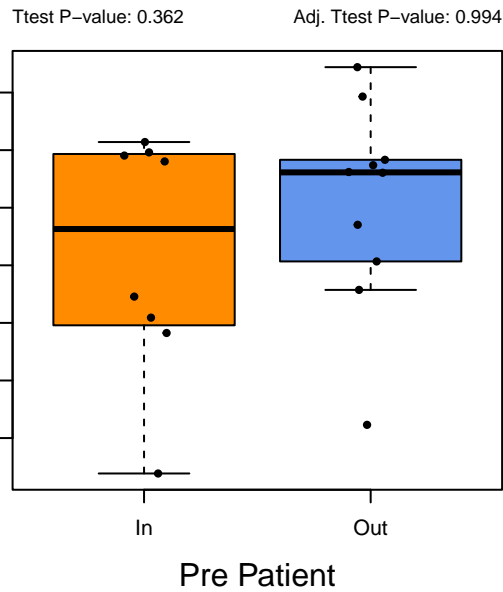
SYN-PWY: L-arginine biosynthesis I (via L-orr-6628: superpathway of L-phenylalanine biosy



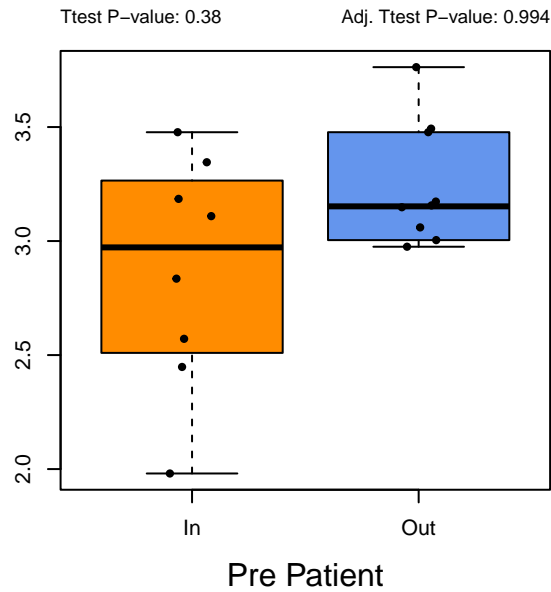
2: palmitoleate biosynthesis I (from (5Z)-dodec



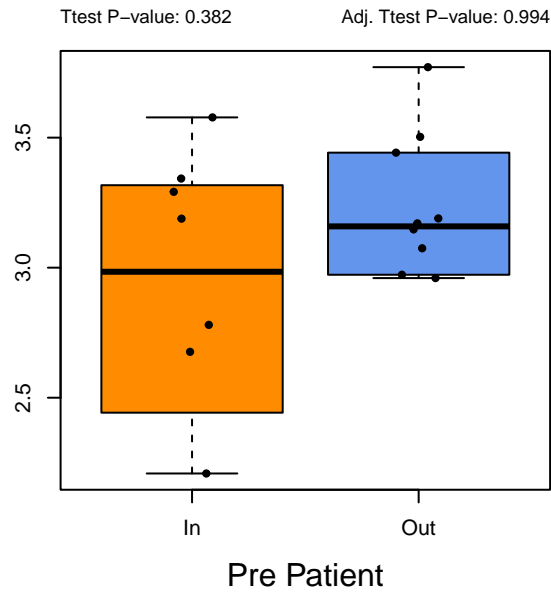
GLYCOCAT-PWY: glycogen degradation I



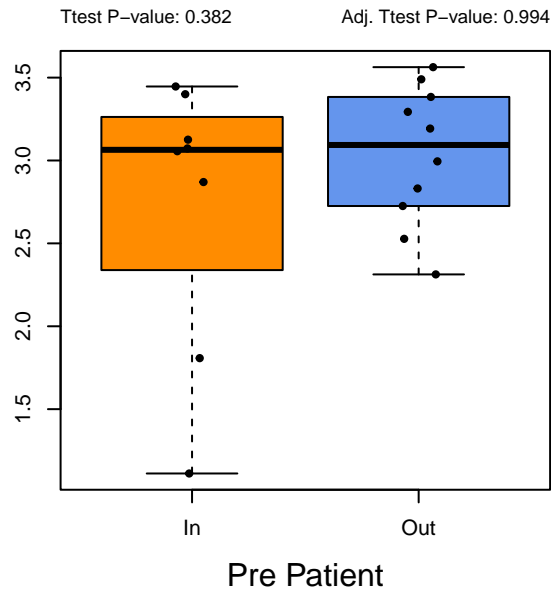
PWY-6151: S-adenosyl-L-methionine salvage guanosine ribonucleotides de novo biosynthes



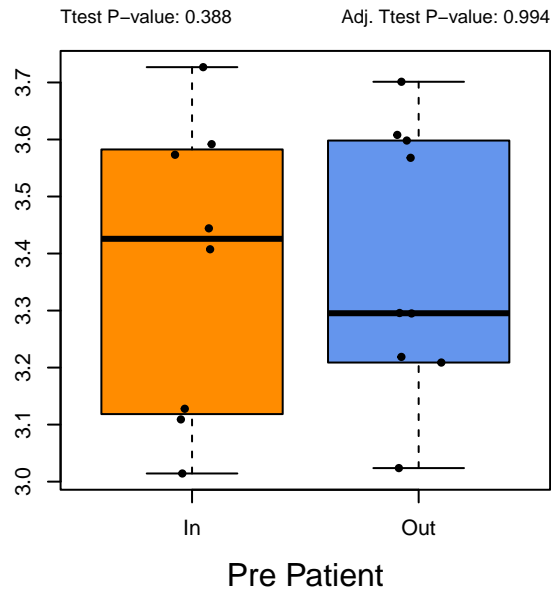
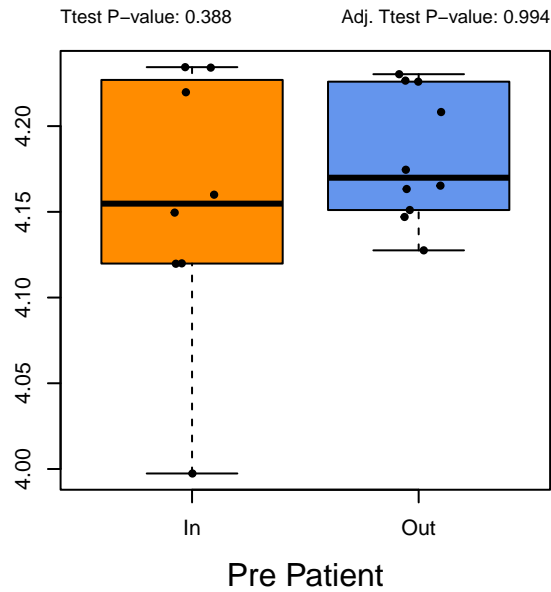
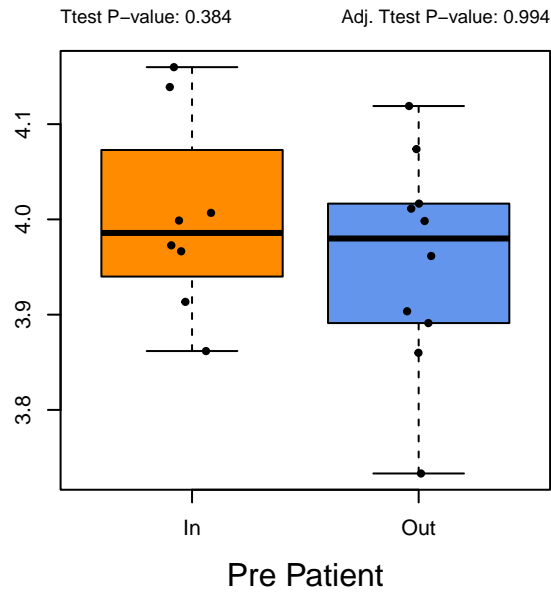
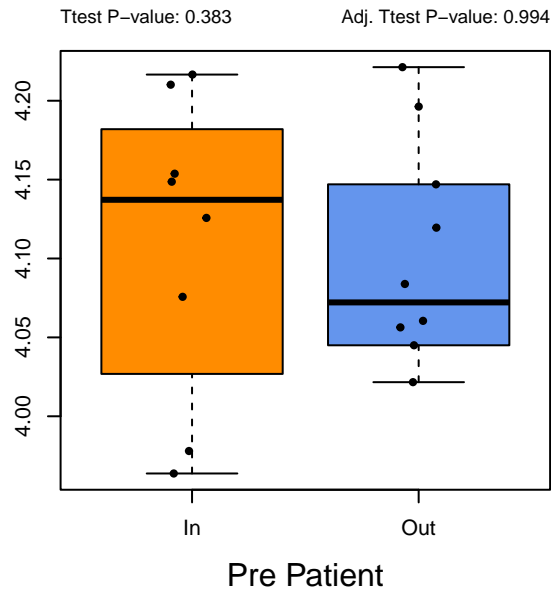
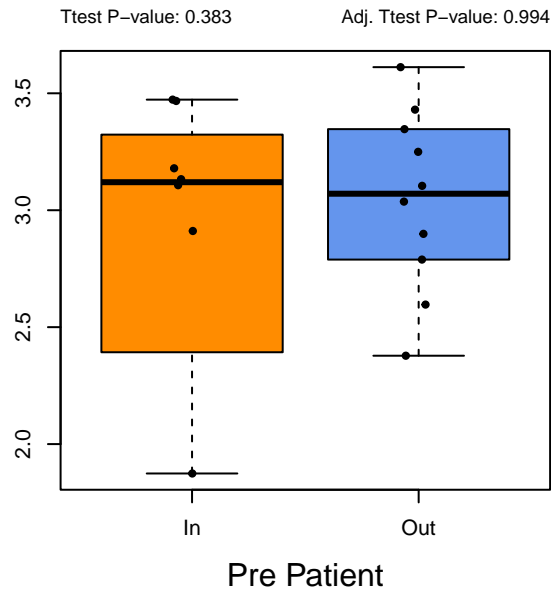
ine phosphate formation from pyriithamine and5: peptidoglycan biosynthesis III (mycobacteria)



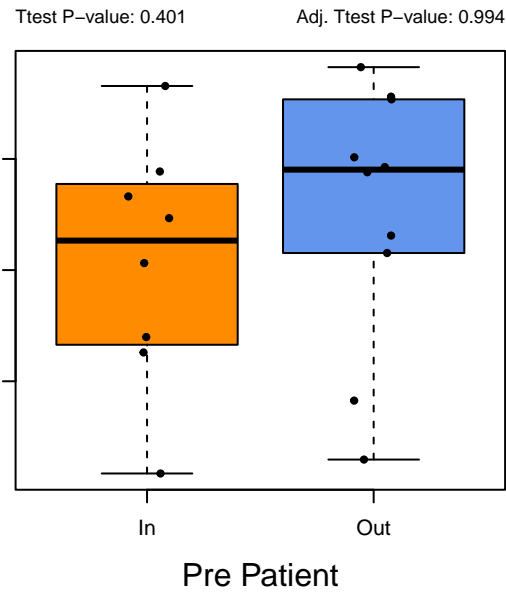
Imuramoyl-pentapeptide biosynthesis III (mesoY-5989: stearate biosynthesis II (bacteria and p



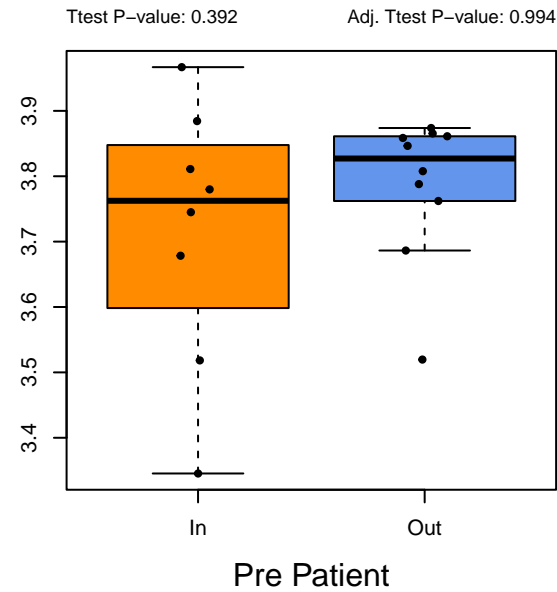
erpathway of geranylgeranyl diphosphate biosyr PWY-7664: oleate biosynthesis IV (anaerobic



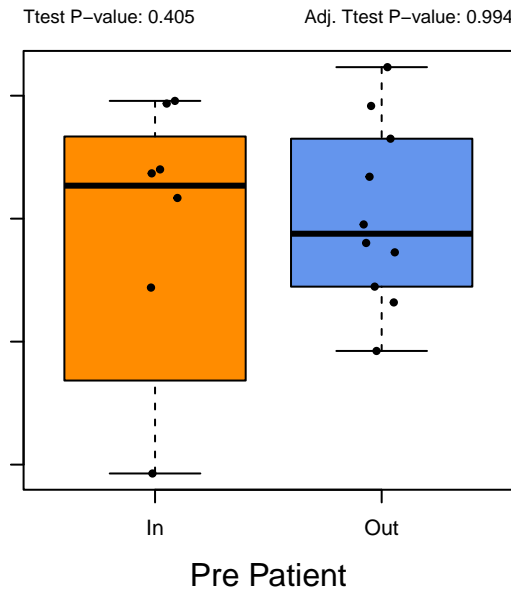
PWY-6270: isoprene biosynthesis I



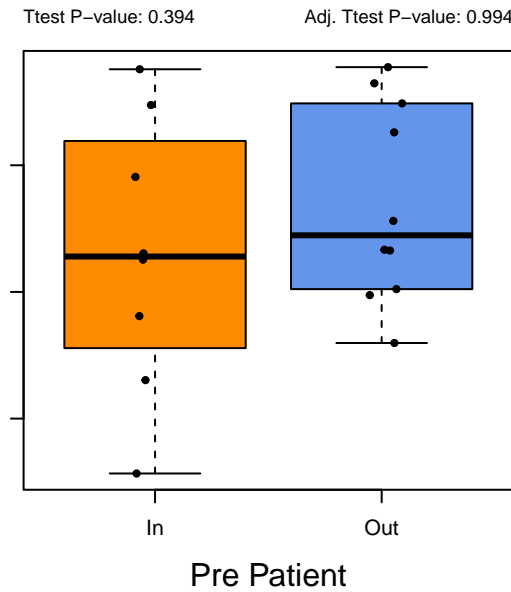
.6901: superpathway of glucose and xylose degradation



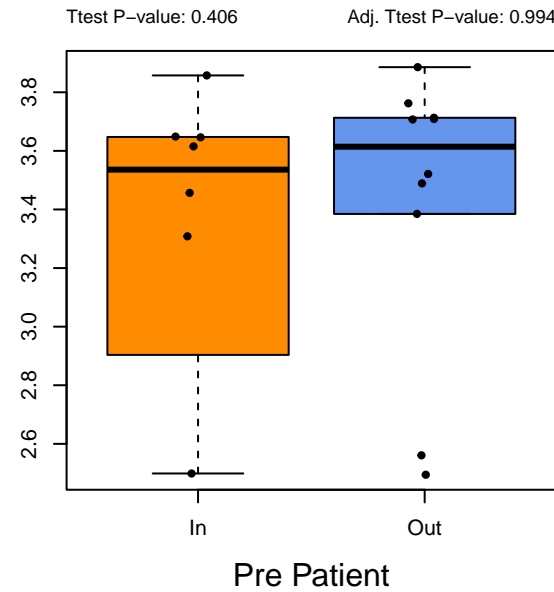
BIOSYNTHESIS-PWY: biotin biosynthesis



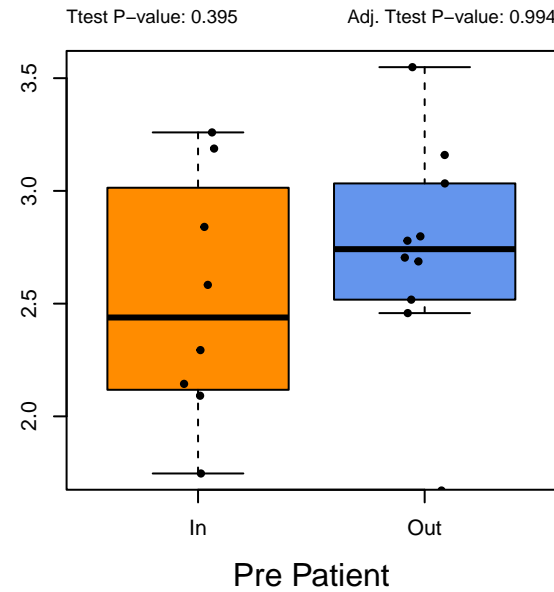
BIOSYNTHESIS-PWY: biotin biosynthesis



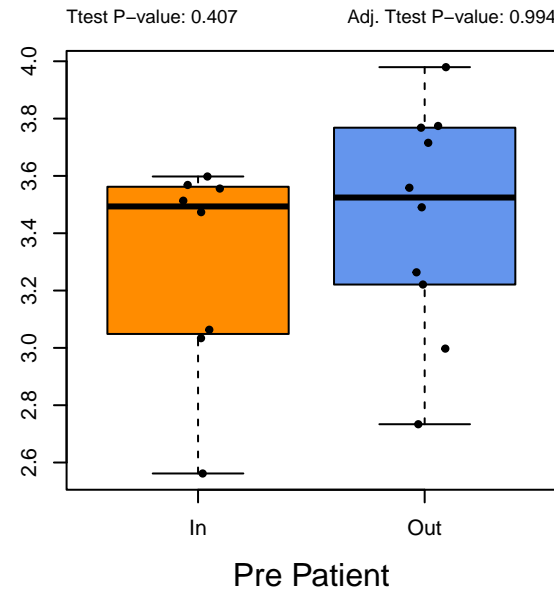
perpathway of pyridoxal 5'-phosphate biosynthesis



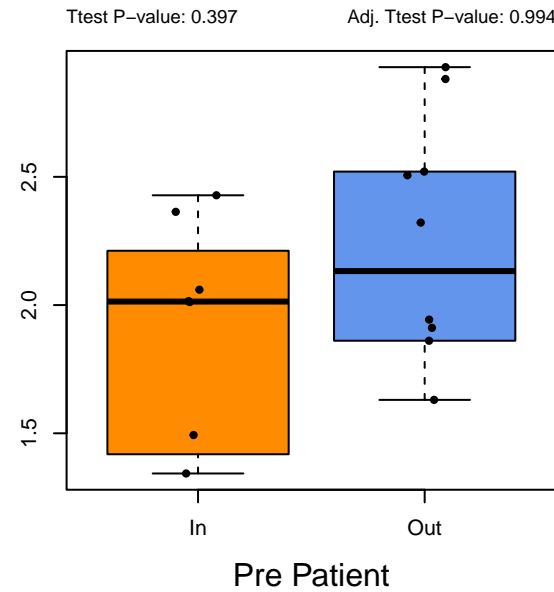
perpathway of pyridoxal 5'-phosphate biosynthesis



7: 6-hydroxymethyl-dihydropterin diphosphate pathway of geranylgeranyldiphosphate biosynthesis

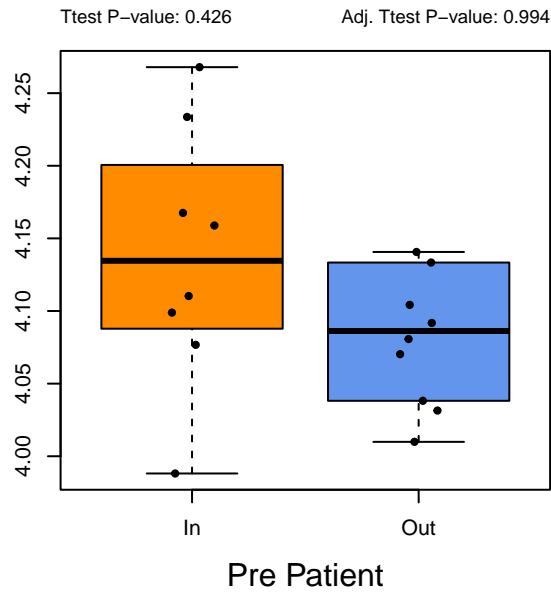


7: 6-hydroxymethyl-dihydropterin diphosphate pathway of geranylgeranyldiphosphate biosynthesis

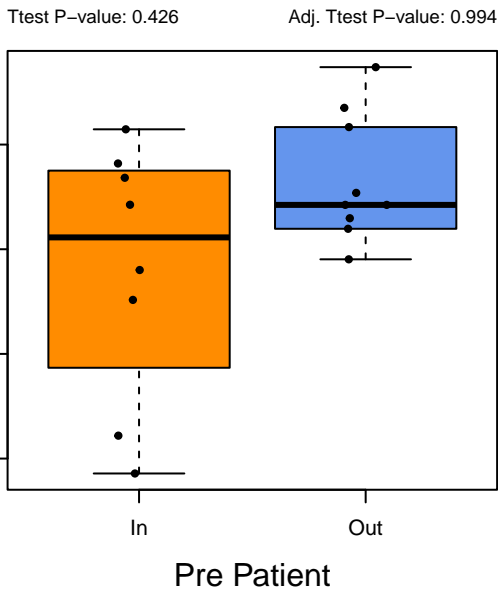




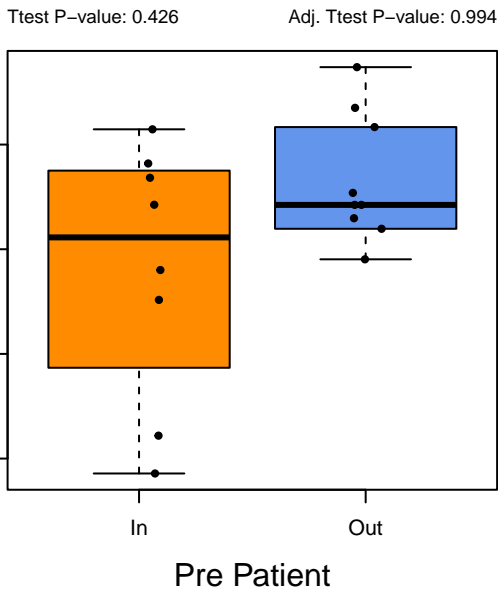
Y-7400: L-arginine biosynthesis IV (archaeabT-PWY: pentose phosphate pathway (non-oxi



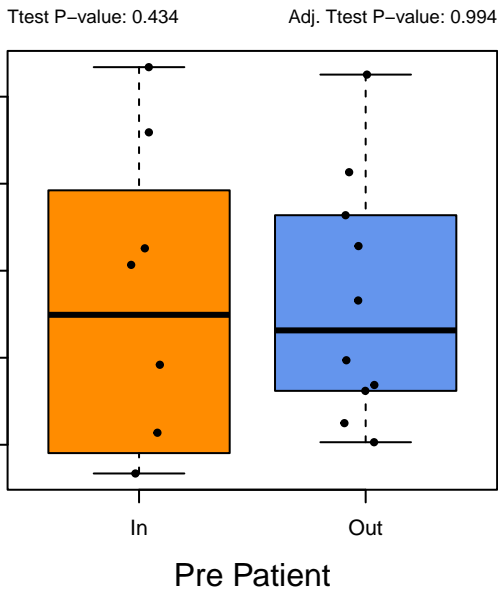
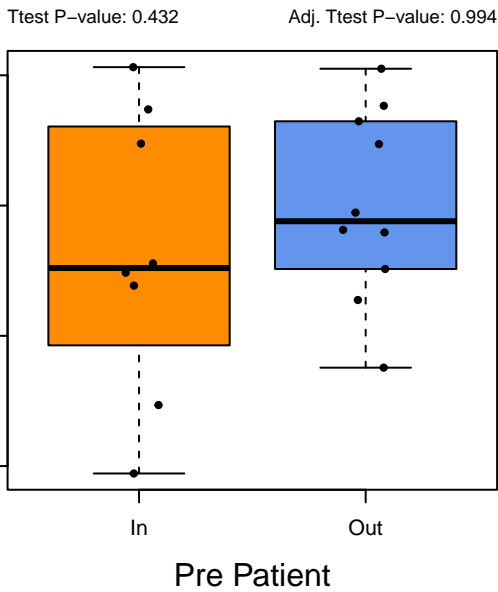
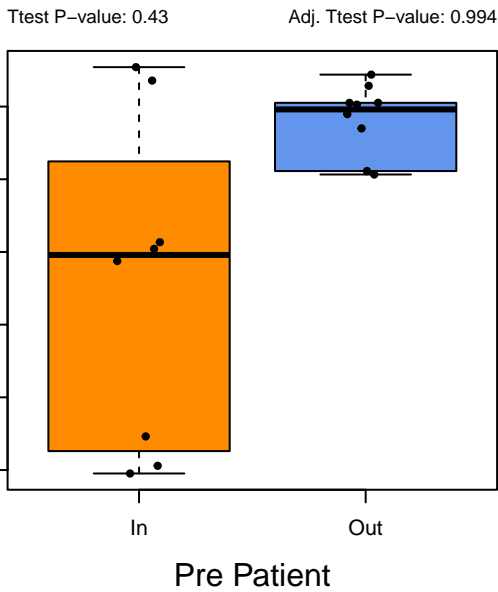
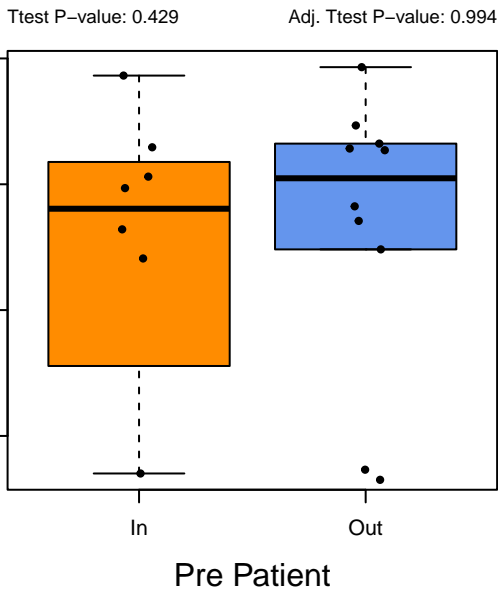
L-PWY: peptidoglycan biosynthesis I (meso-dia 5-aminoimidazole ribonucleotide biosynthesis



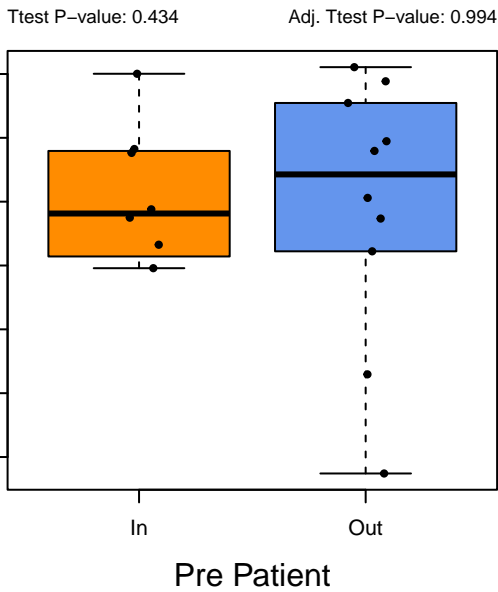
-7345: superpathway of anaerobic sucrose degradation of 5-aminoimidazole ribonucleotide bios



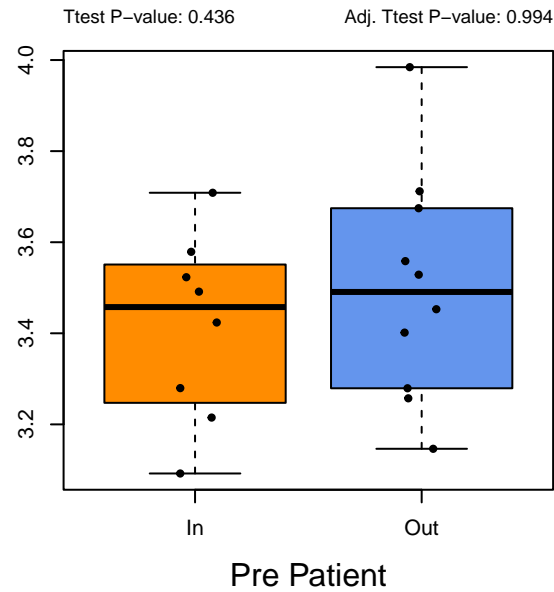
DOXSYN-PWY: pyridoxal 5'-phosphate biosyn



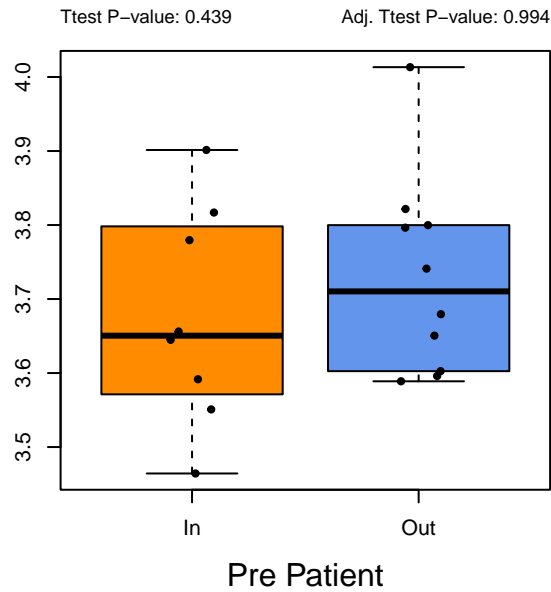
GLUCONEO-PWY: gluconeogenesis I



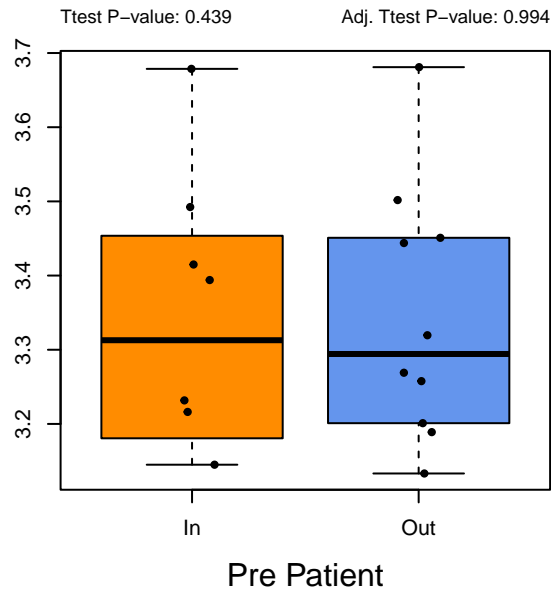
PWY0-1319: CDP-diacylglycerol biosynthesis4-PWY: purine nucleobases degradation I (ana



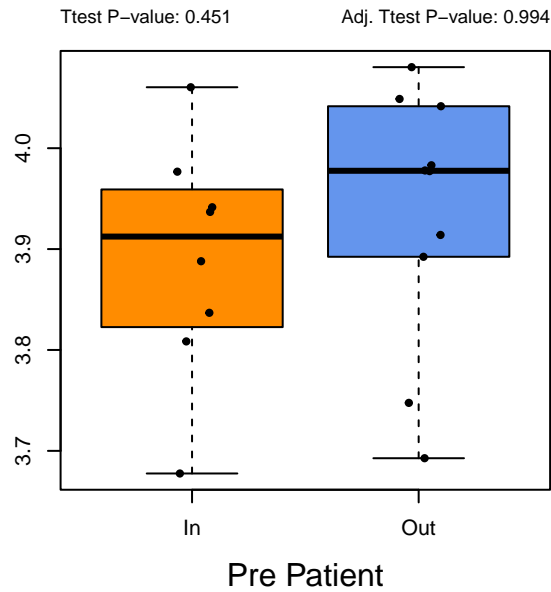
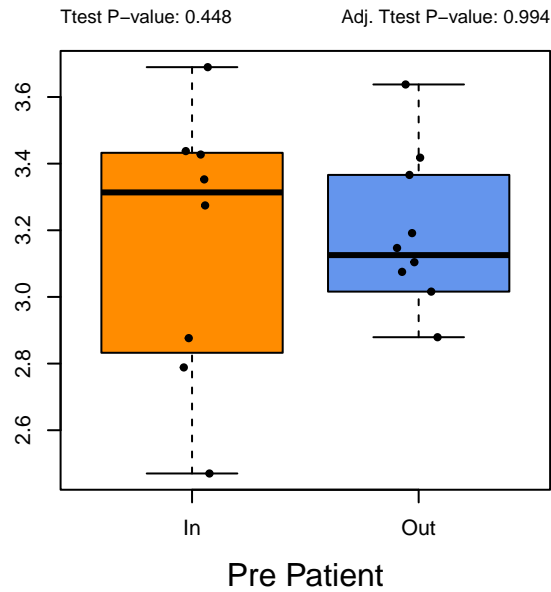
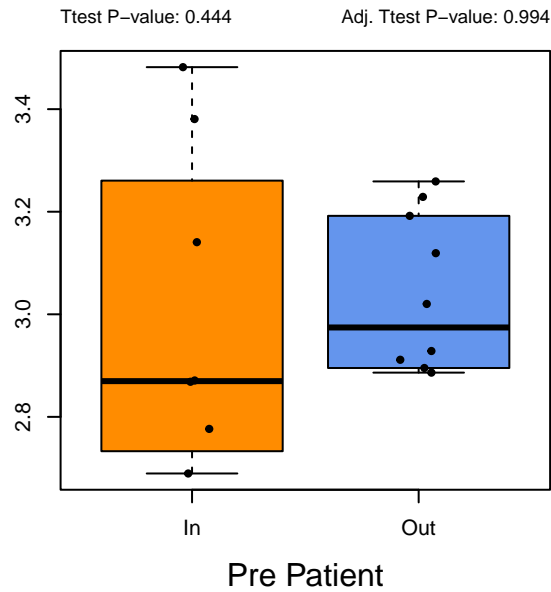
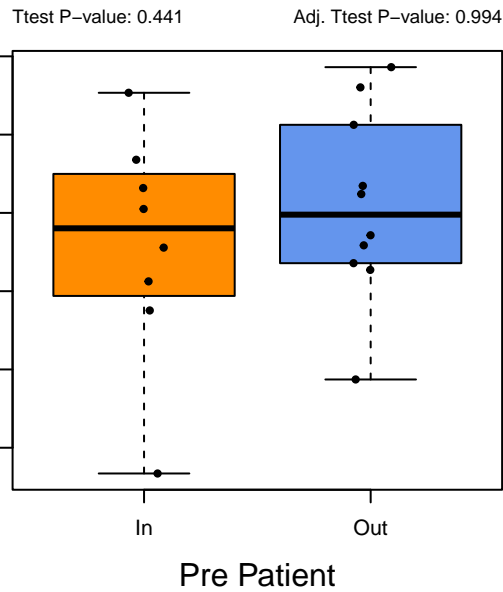
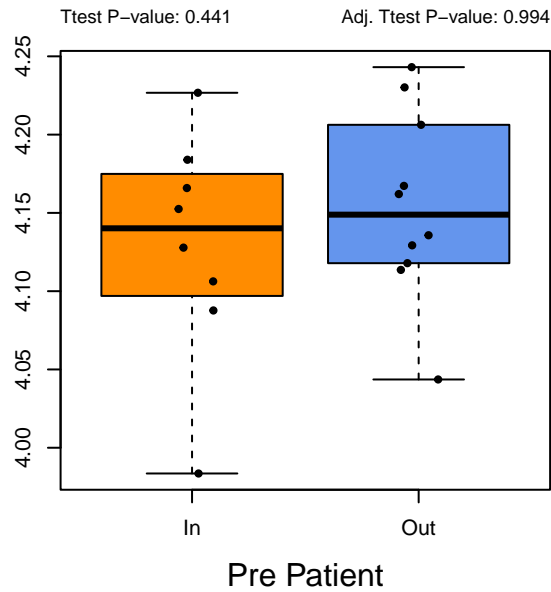
PWY-6305: superpathway of putrescine biosynth.YCOLYSIS: glycolysis I (from glucose 6-phosph



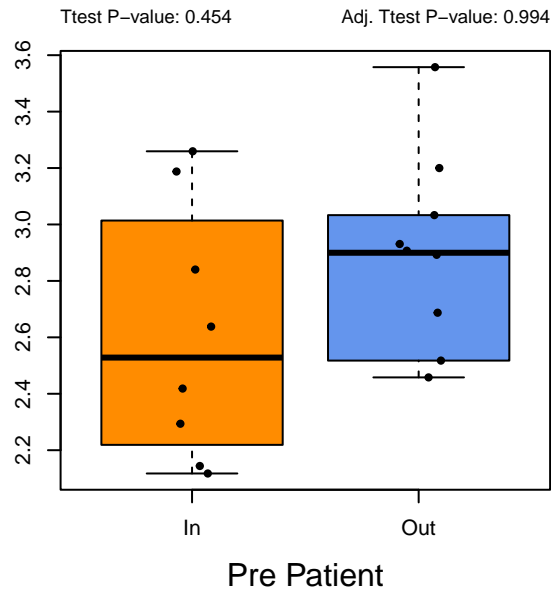
PWY-7392: taxadiene biosynthesis (engineere-D: superpathway of glycolysis and the Entner



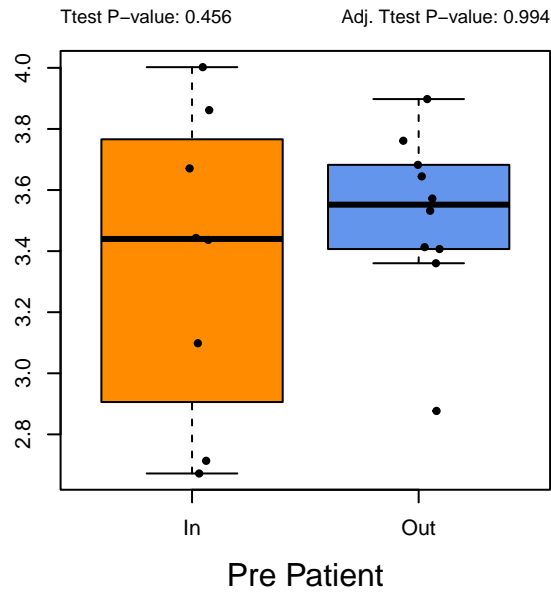
PWY-7560: methylerythritol phosphate pathway PWY-5667: CDP-diacylglycerol biosynthesis



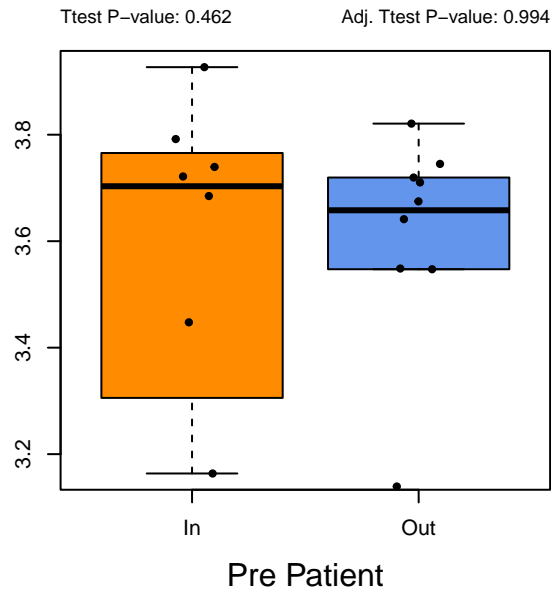
—1296: purine ribonucleosides degradation[unc]: pyruvate fermentation to acetate and lactate



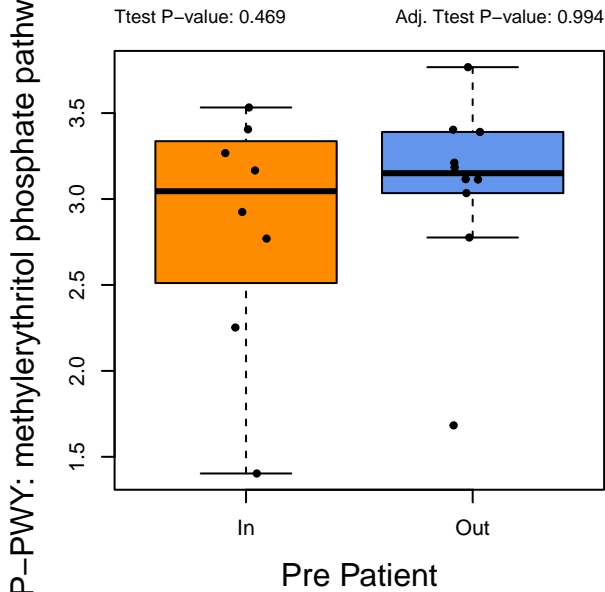
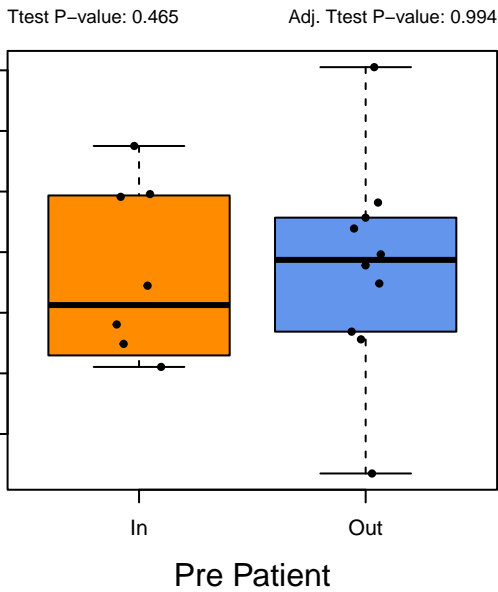
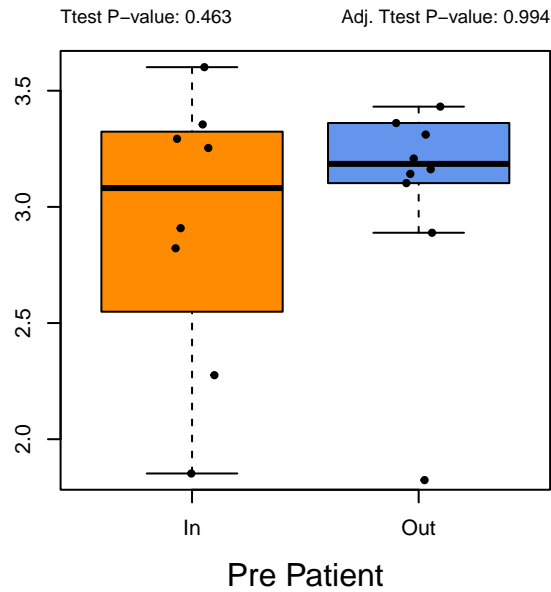
PP-PWY: methylerythritol phosphate pathway 17: L-arginine degradation XIII (reductive Stickla



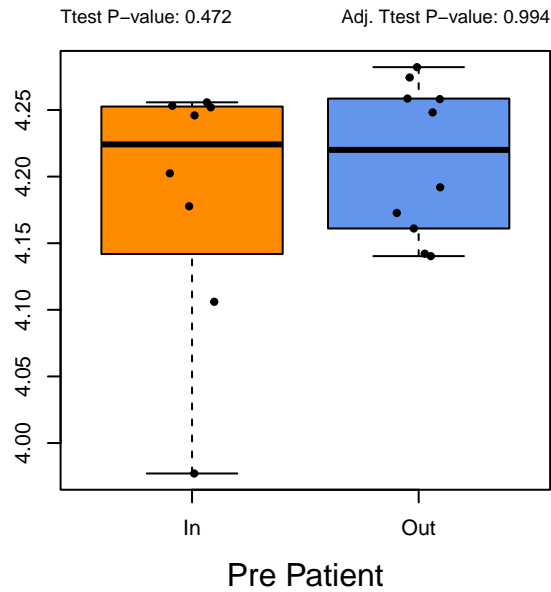
↓-PWY: superpathway of phospholipid biosynth



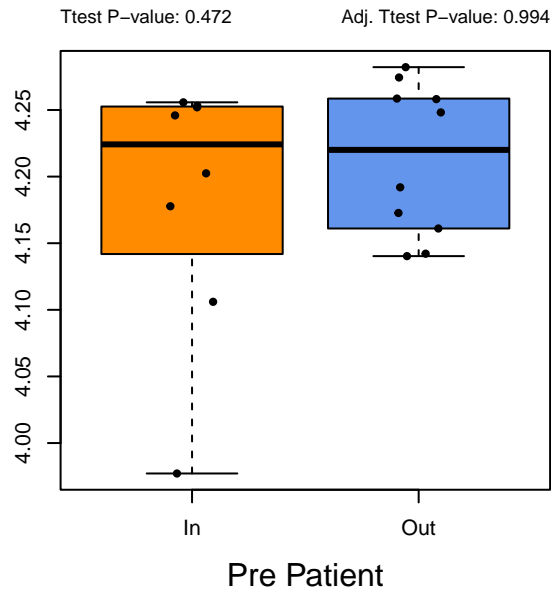
chorismate biosynthesis from 3-dehydroquinate



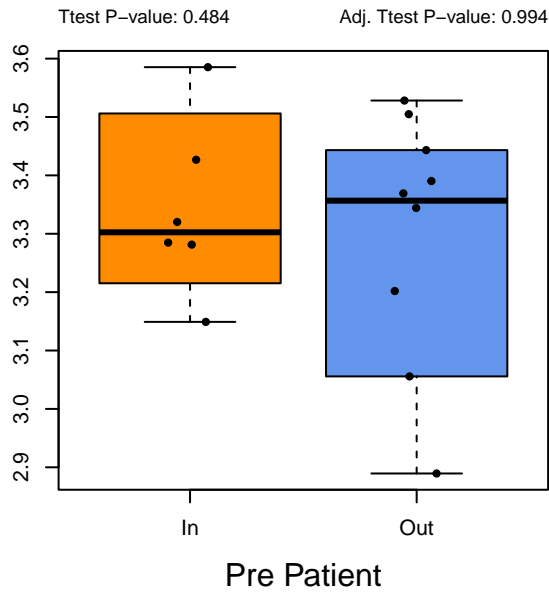
PWY-7791: UMP biosynthesis III



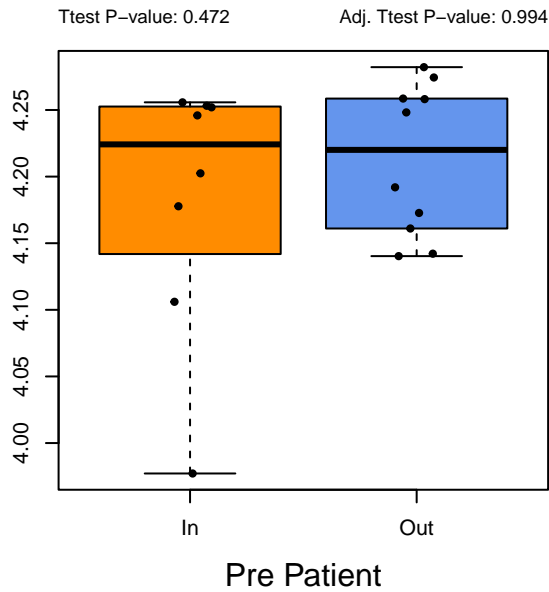
PWY-7790: UMP biosynthesis II



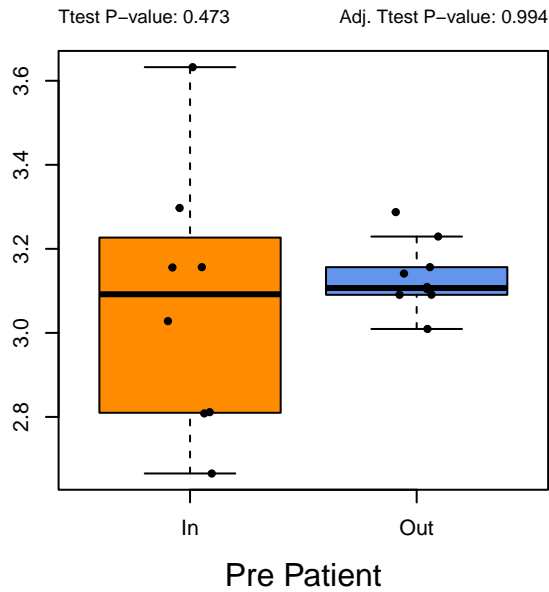
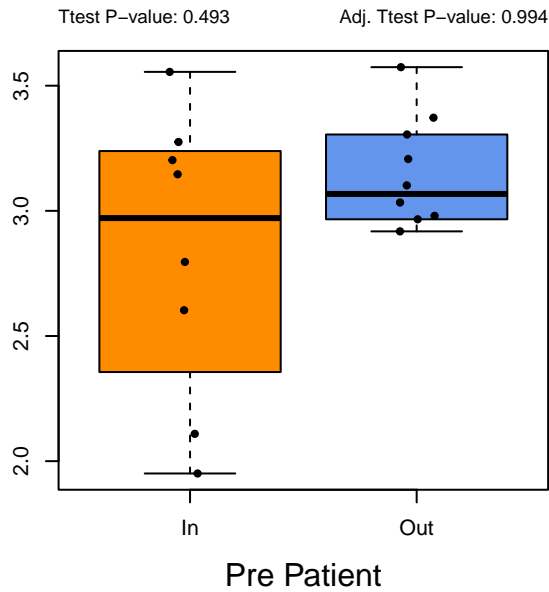
0: peptidoglycan biosynthesis V (&beta;-lactam



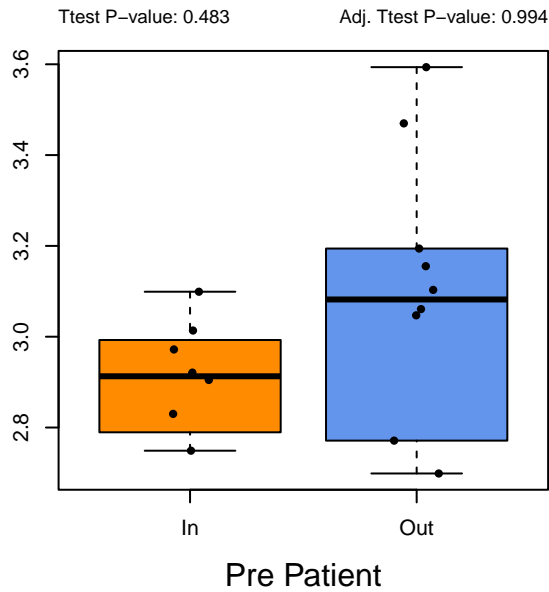
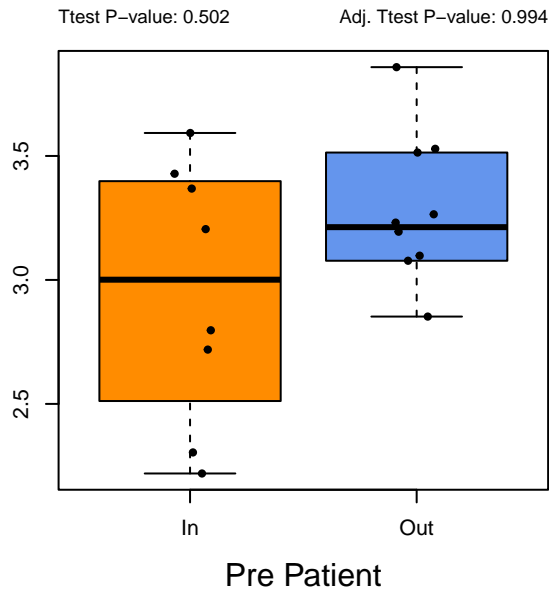
PWY-5686: UMP biosynthesis I



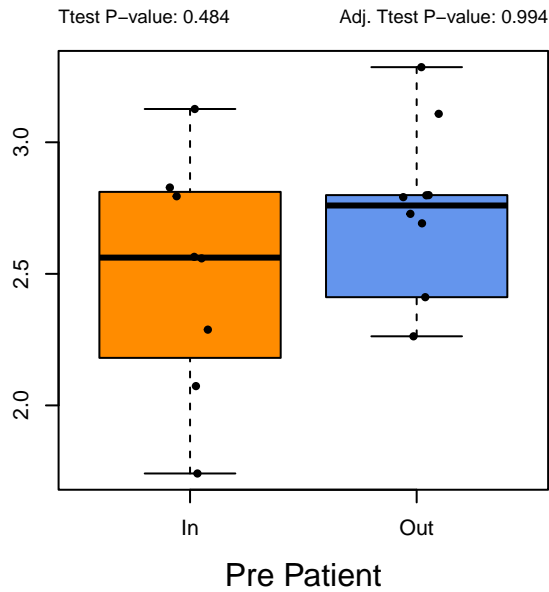
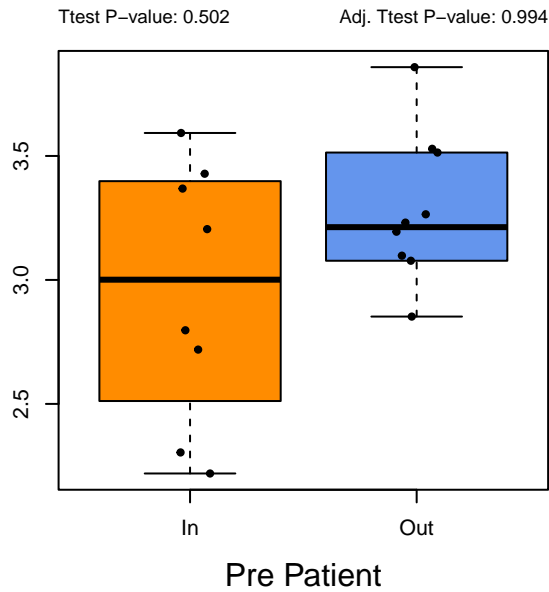
17: D-galactose degradation I (Leloir pathway)|L-PWY: superpathway of glycerol degradation to



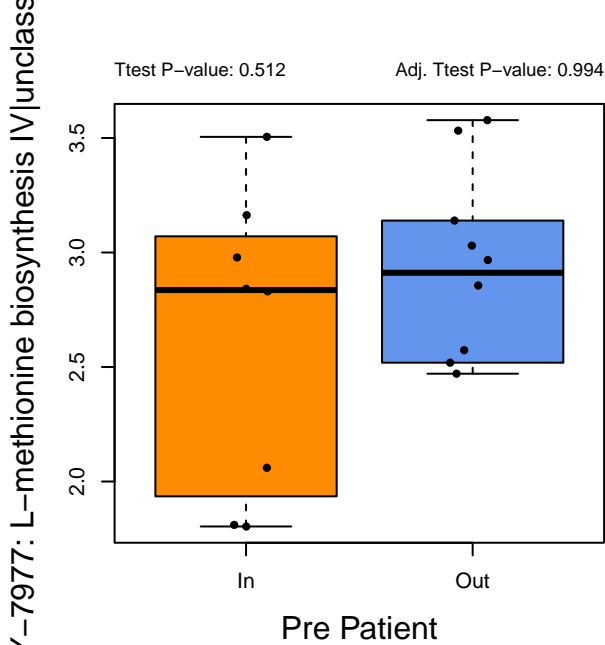
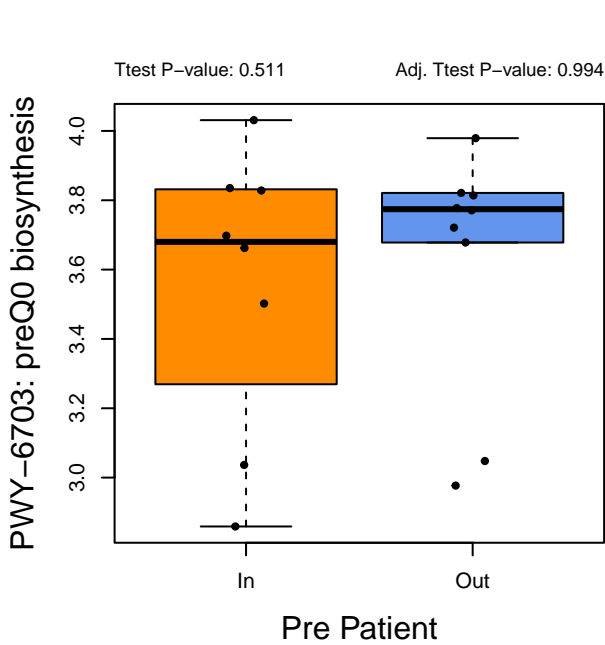
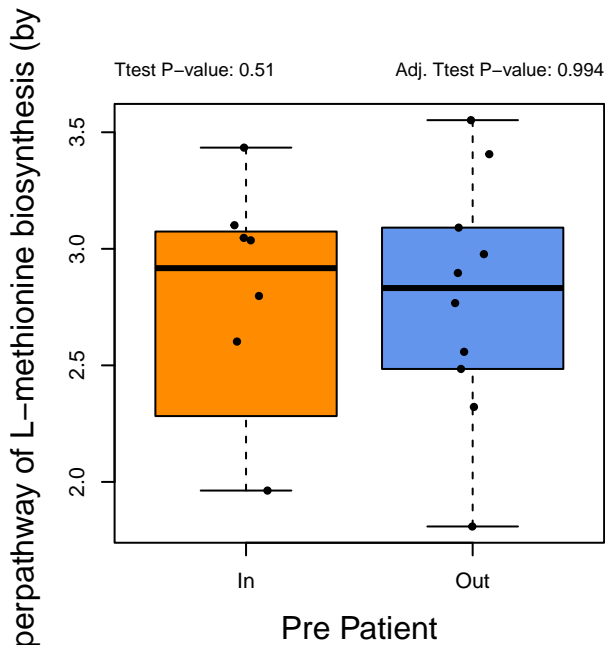
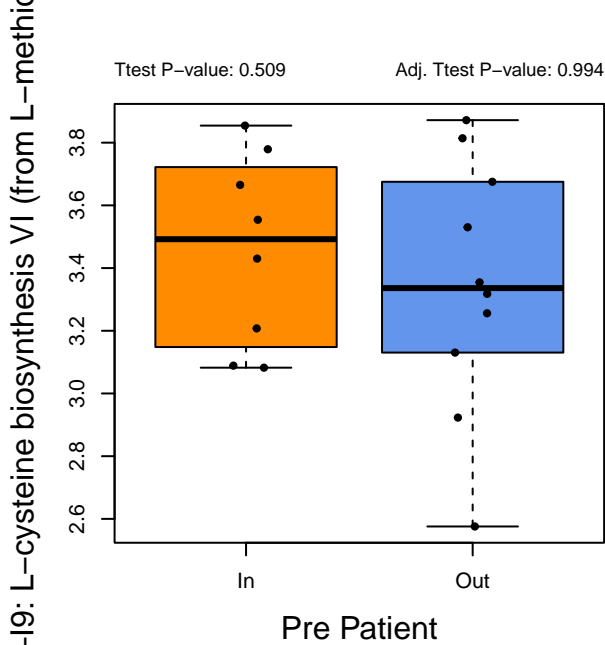
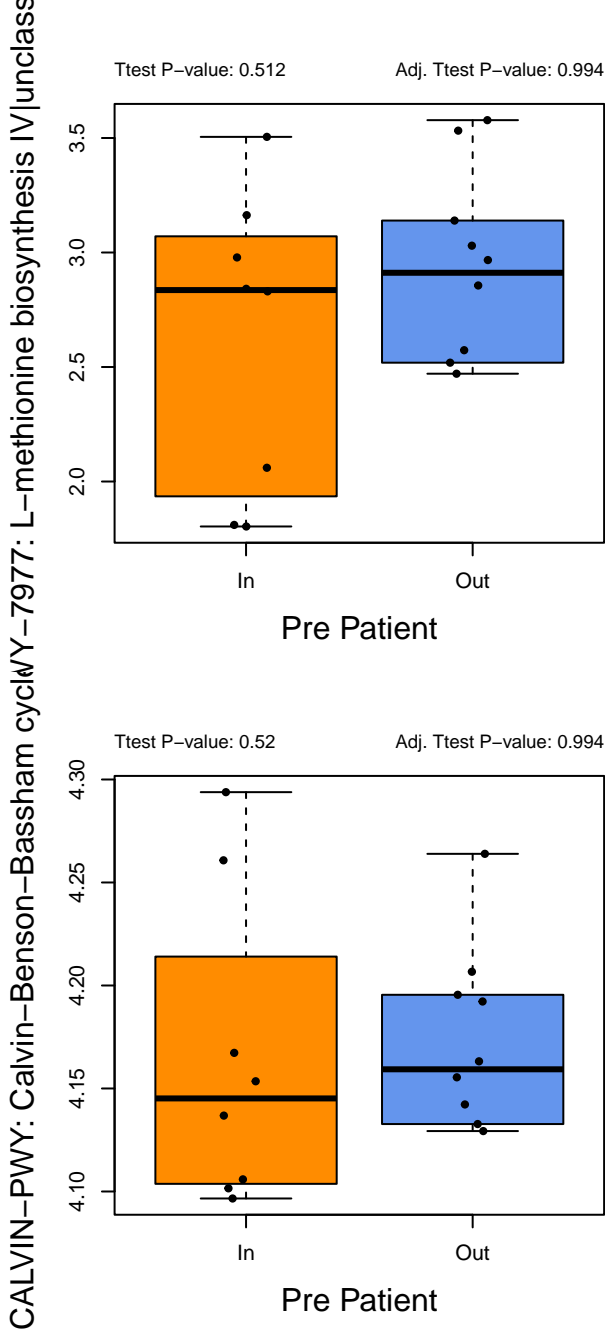
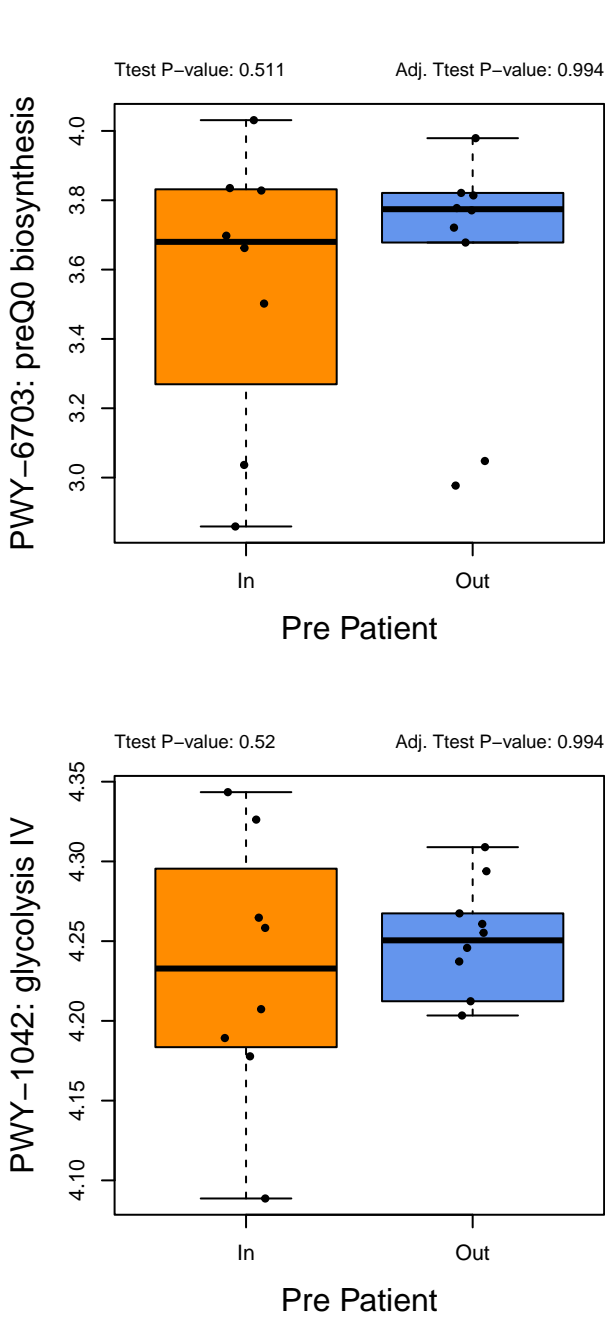
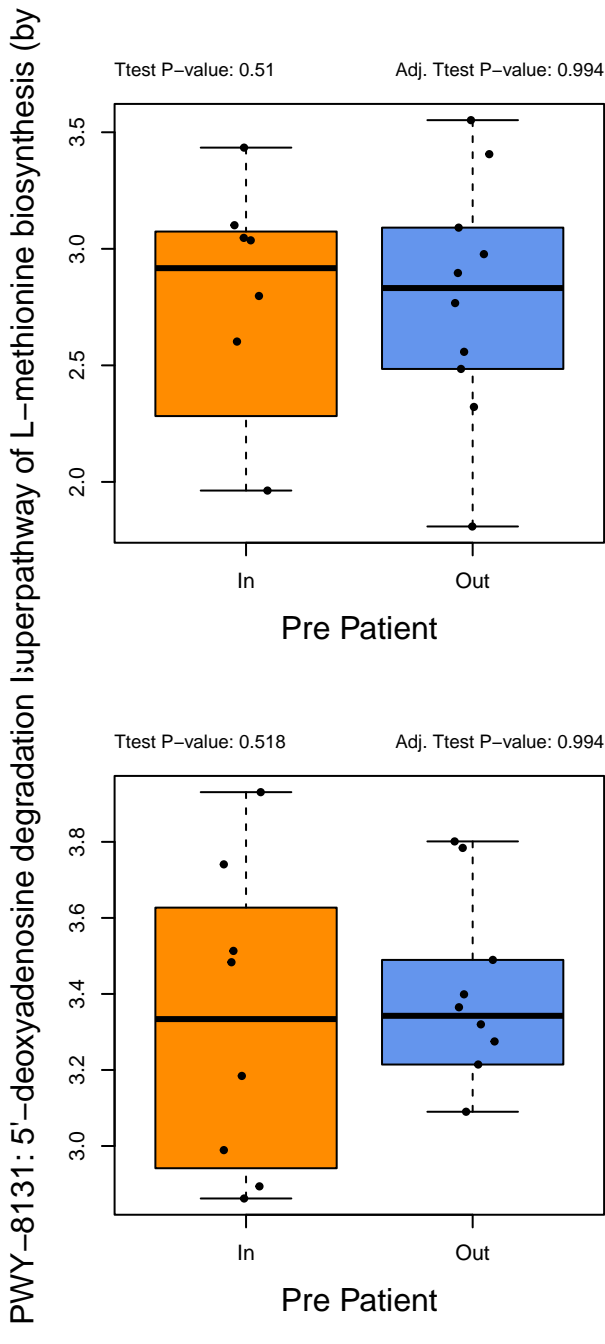
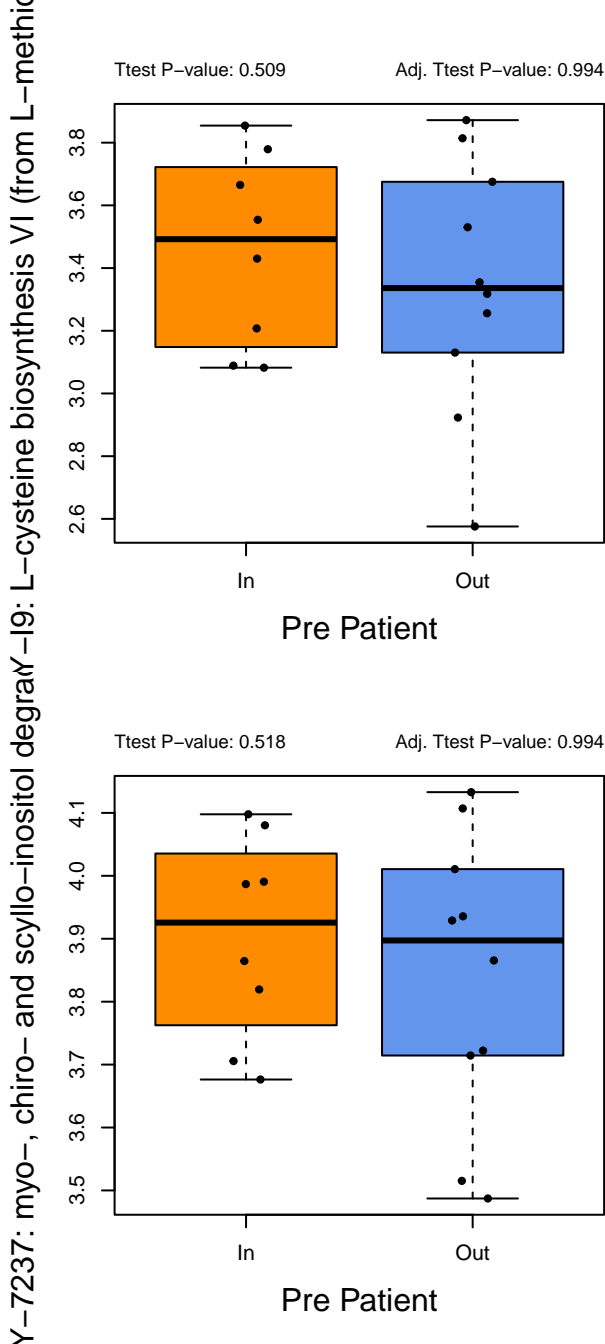
PWY-7791: UMP biosynthesis III|unclassifiedWY-5676: acetyl-CoA fermentation to butanoate



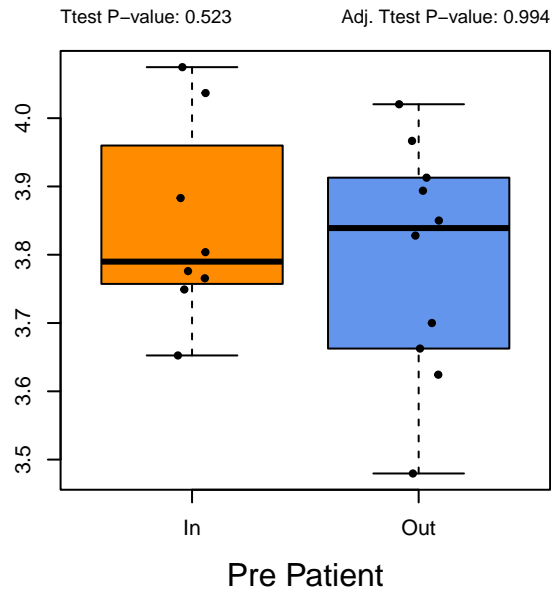
PWY-7790: UMP biosynthesis II|unclassified-PWY: phosphopantothenate biosynthesis I|un



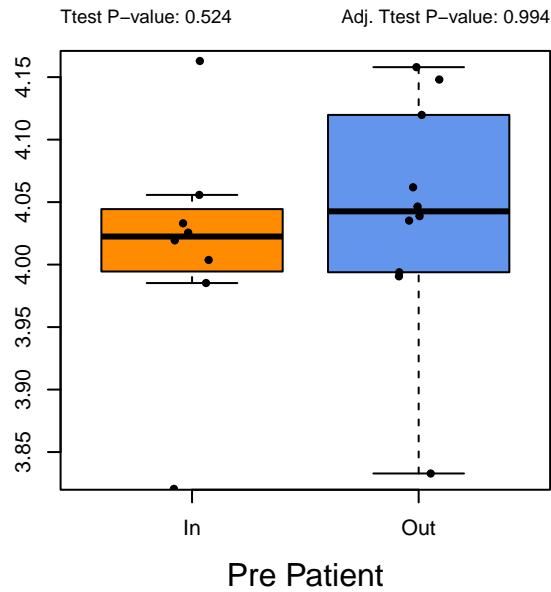




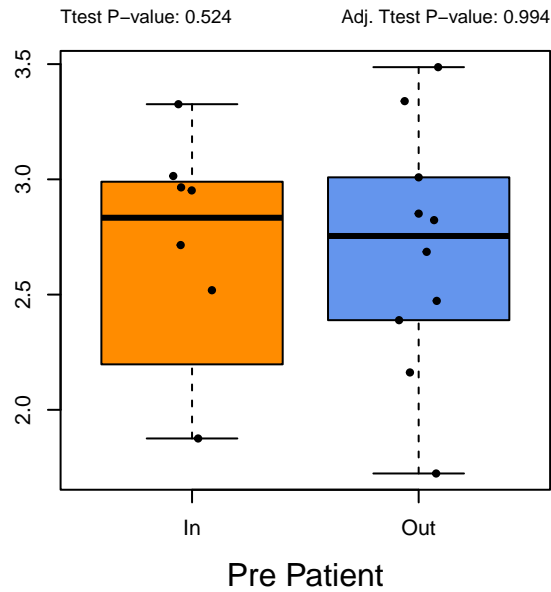
Y-6317: D-galactose degradation I (Leloir pathY-5188: tetrapyrrole biosynthesis I (from glut



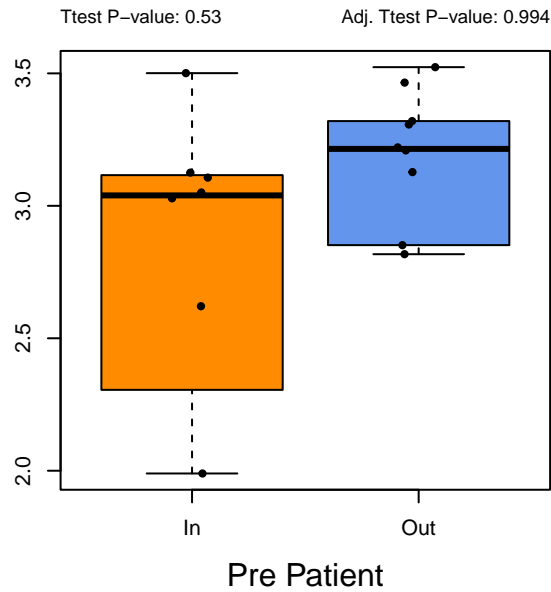
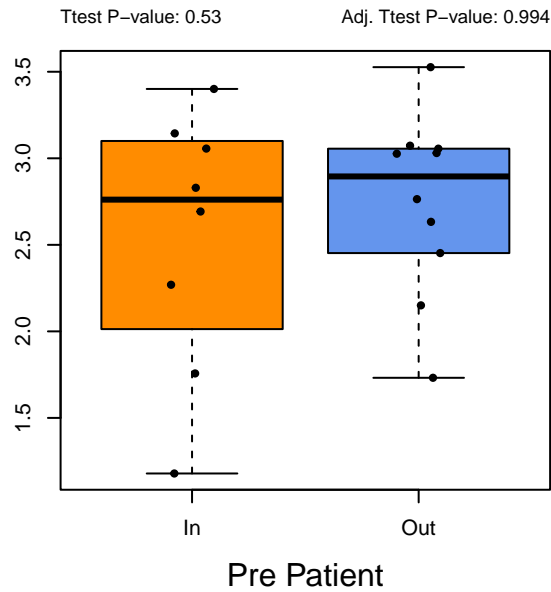
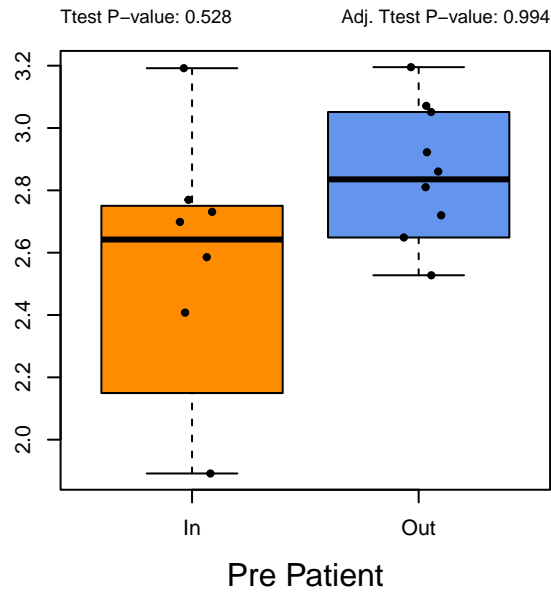
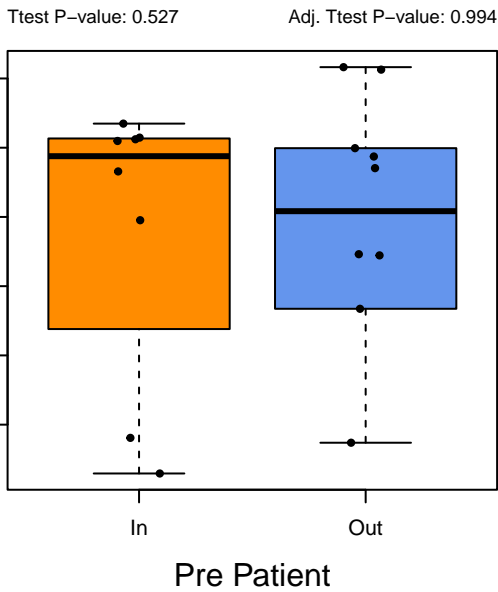
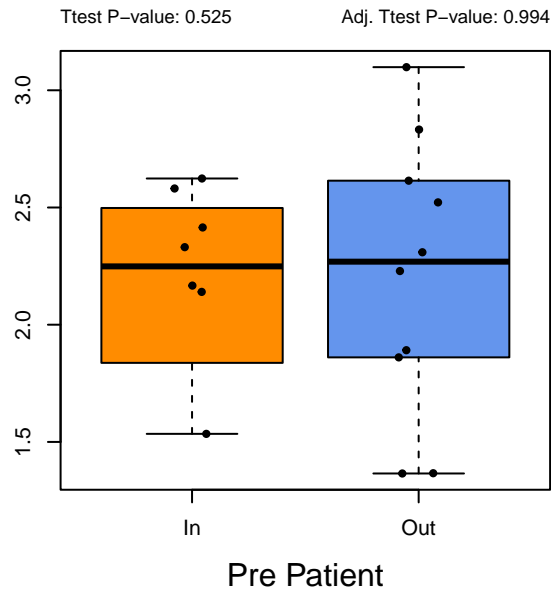
Y-5136: fatty acid &beta;-oxidation II (plant peroPWY-6123: inosine-5'-phosphate biosynthesis

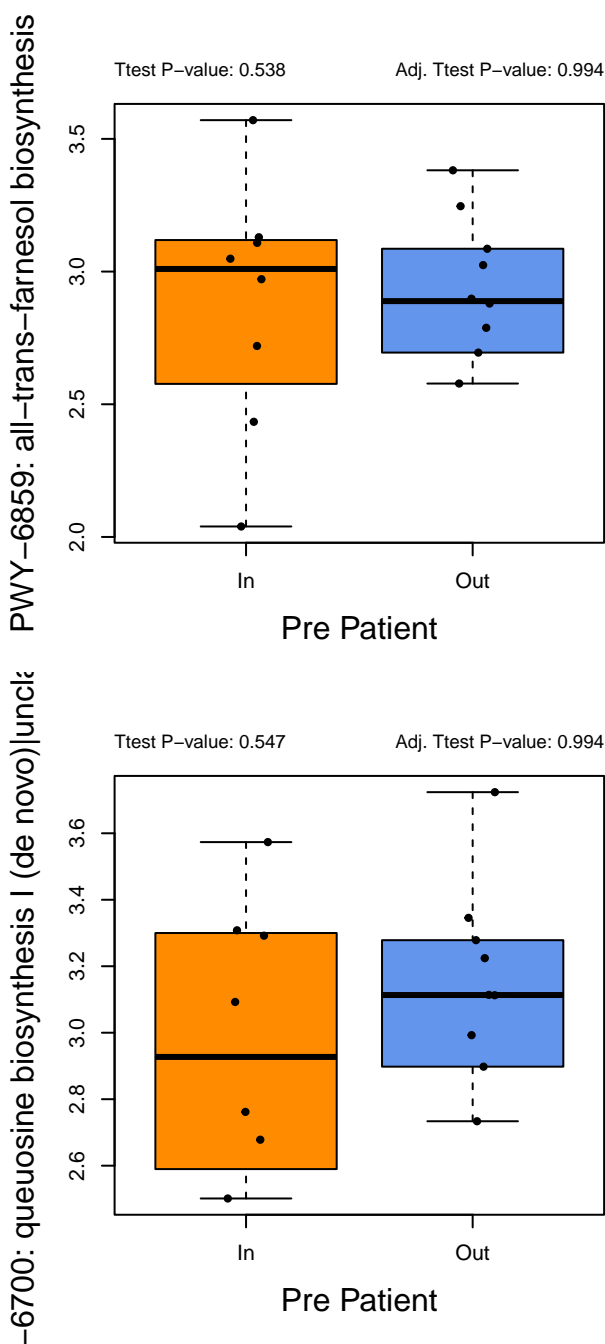
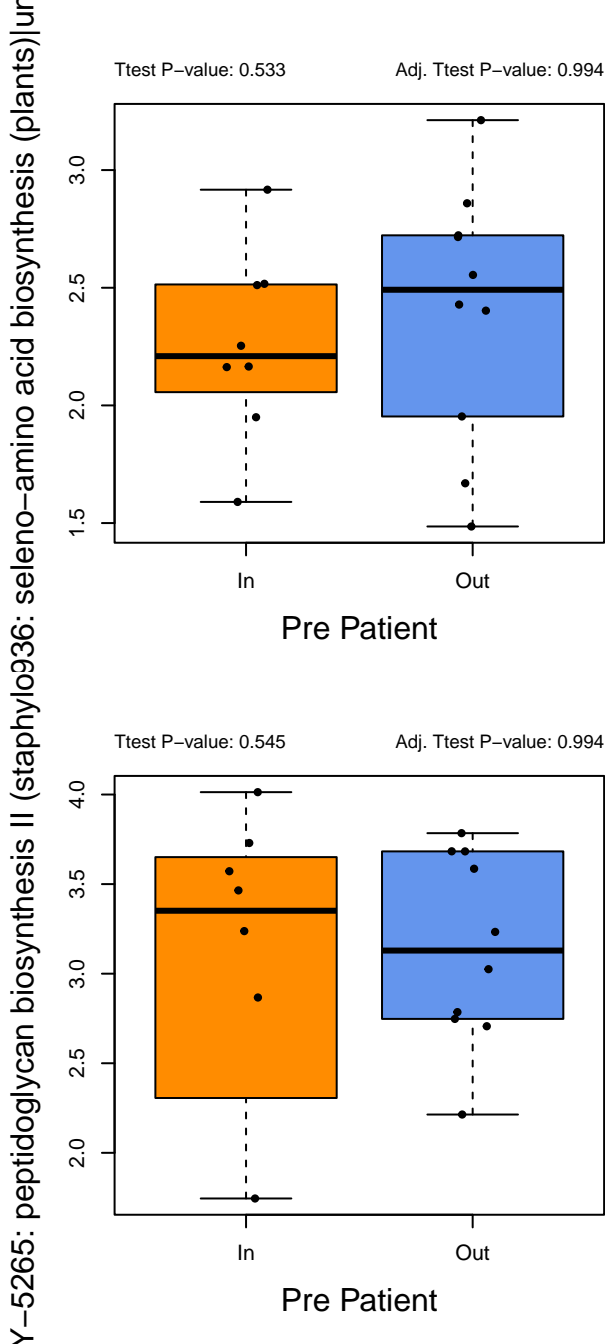
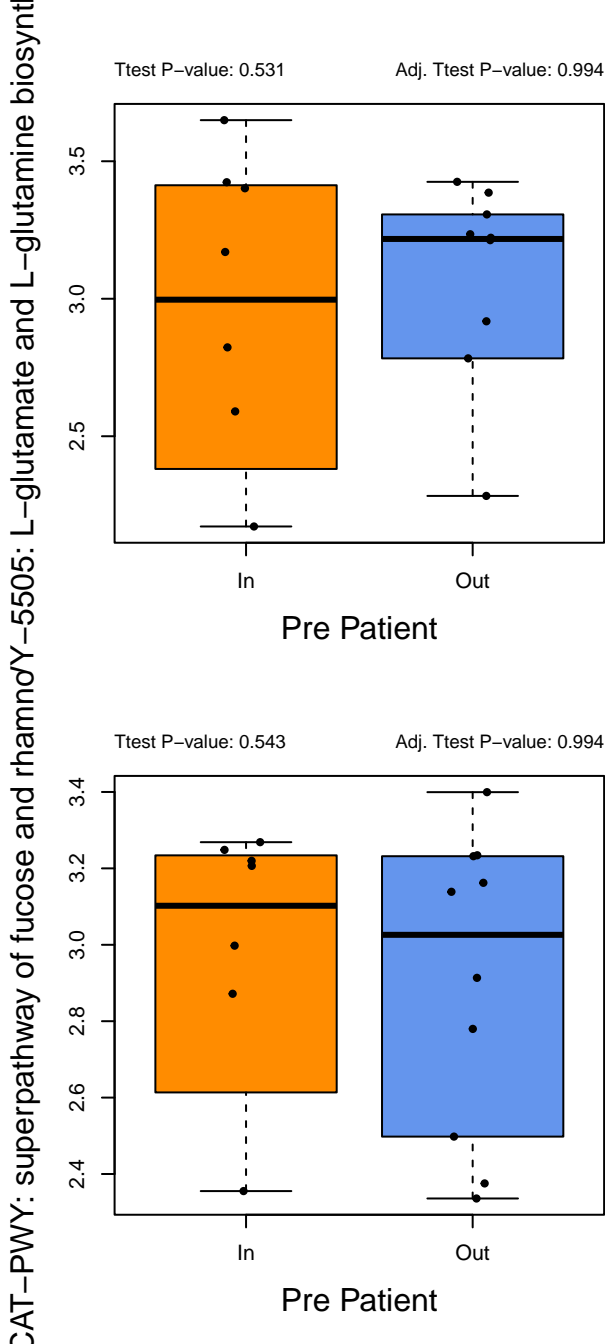
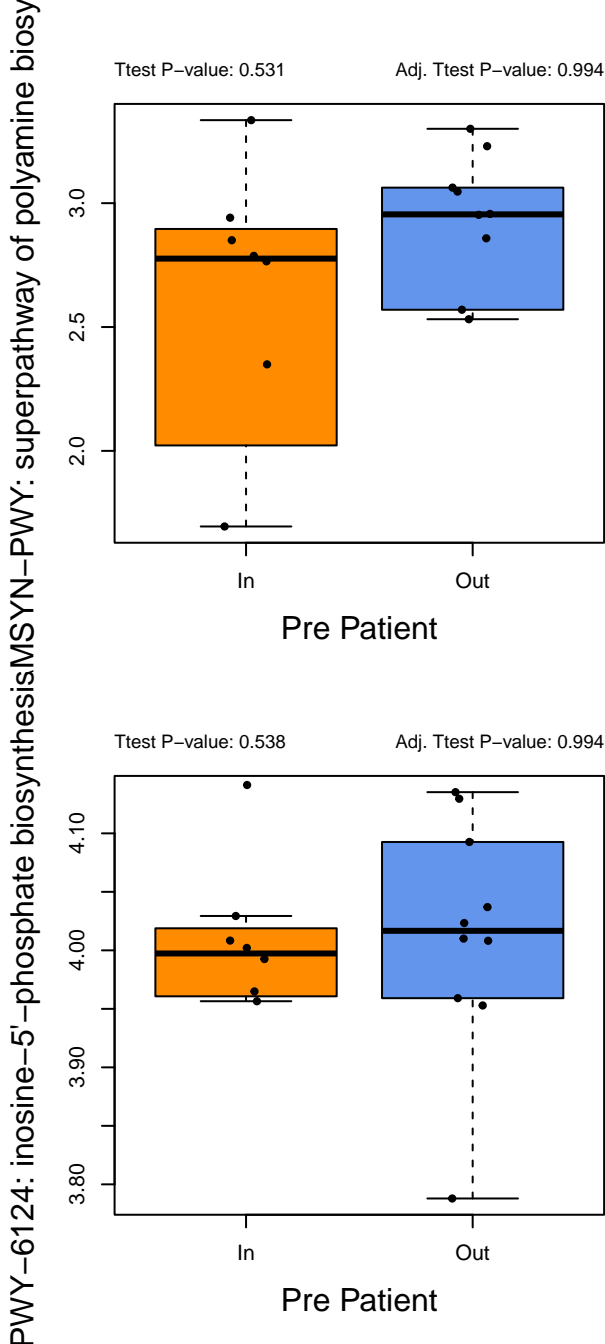


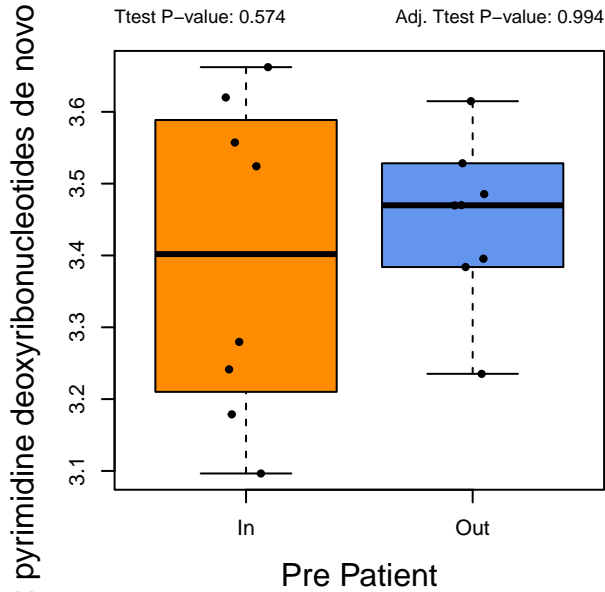
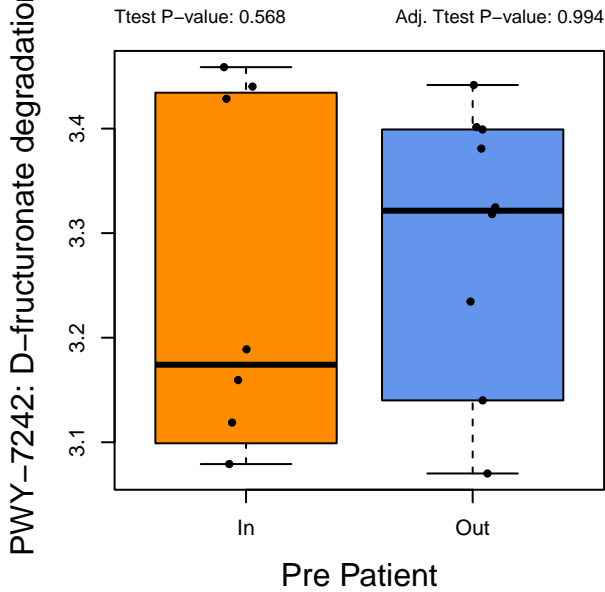
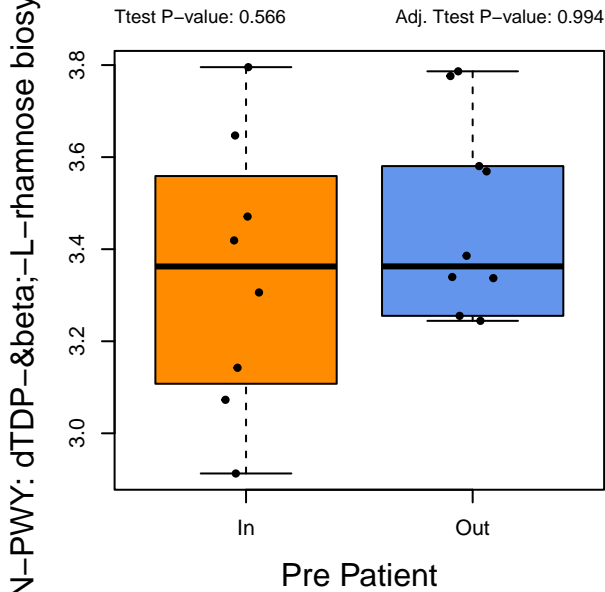
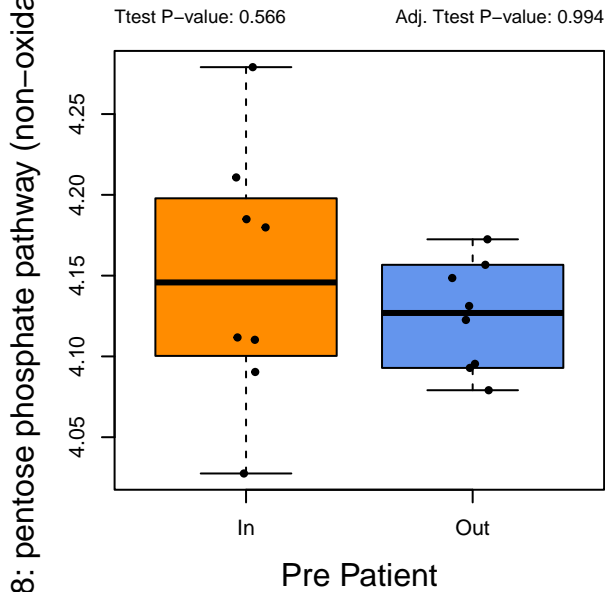
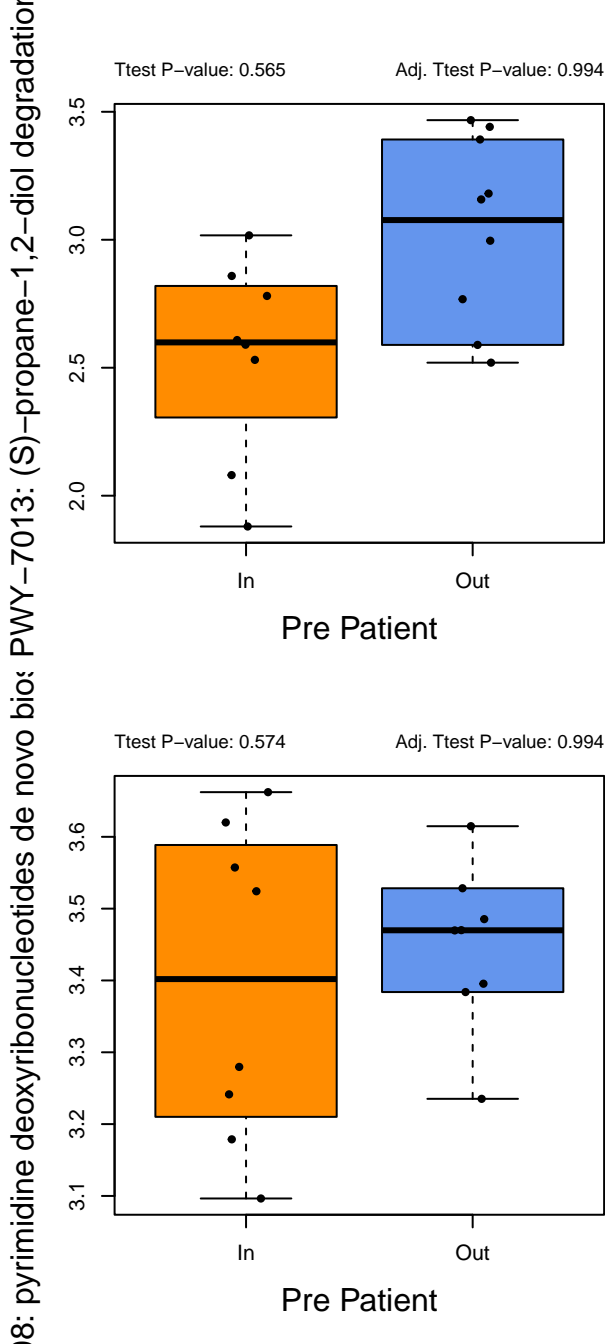
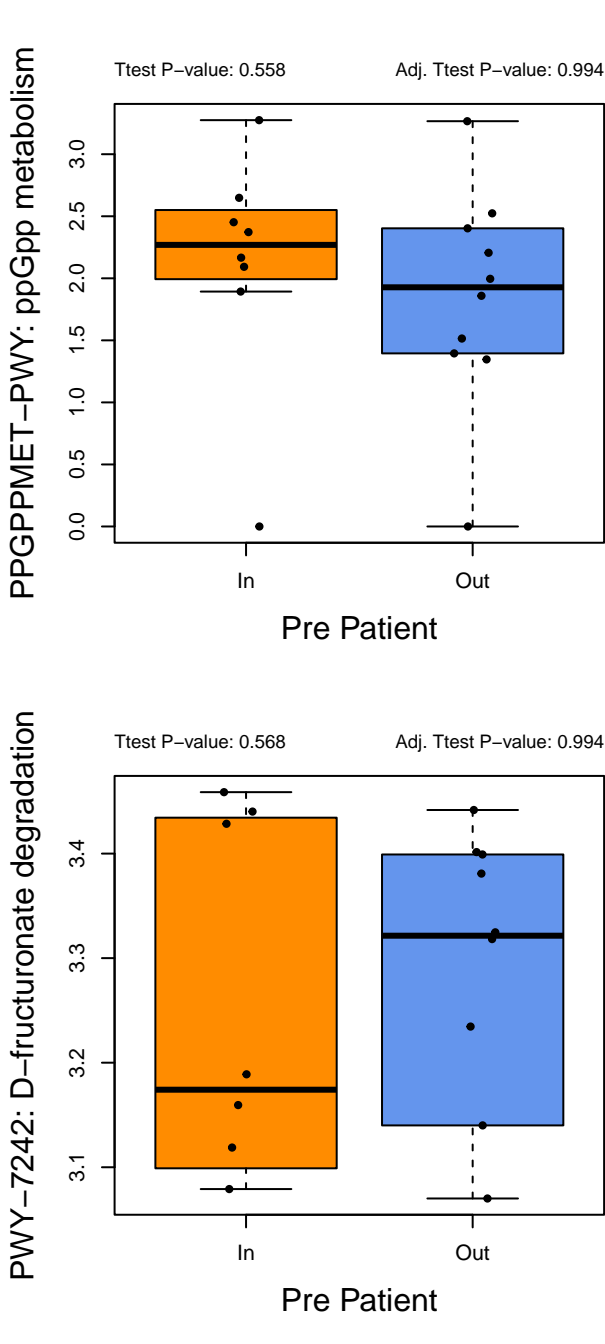
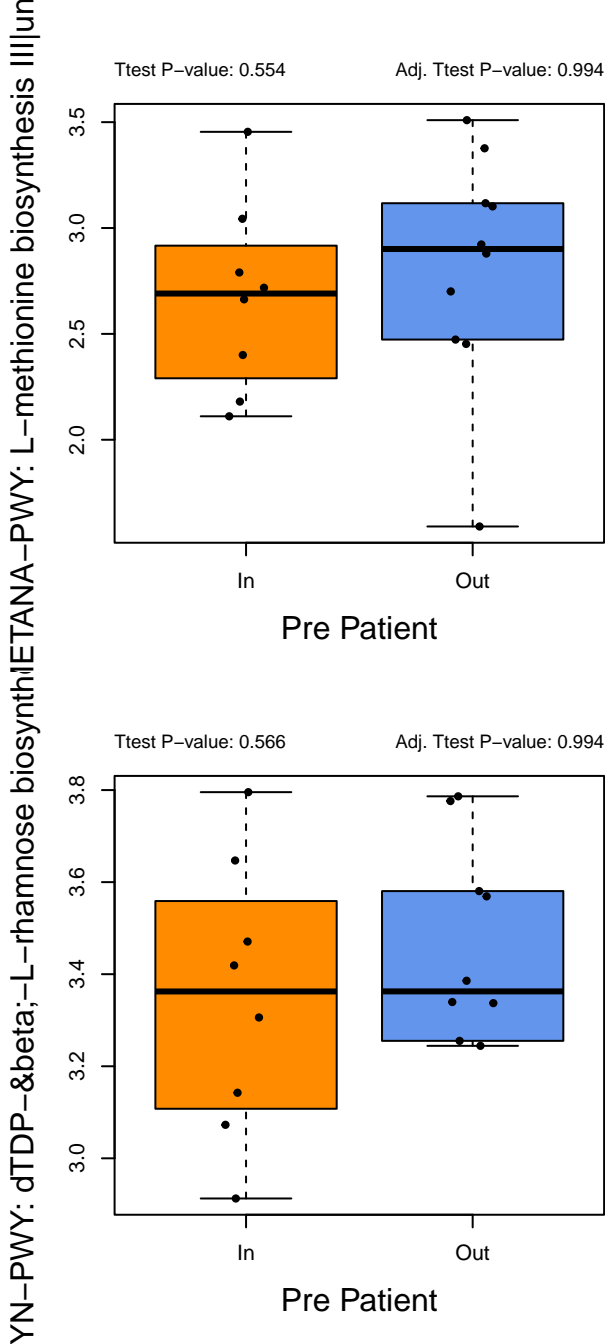
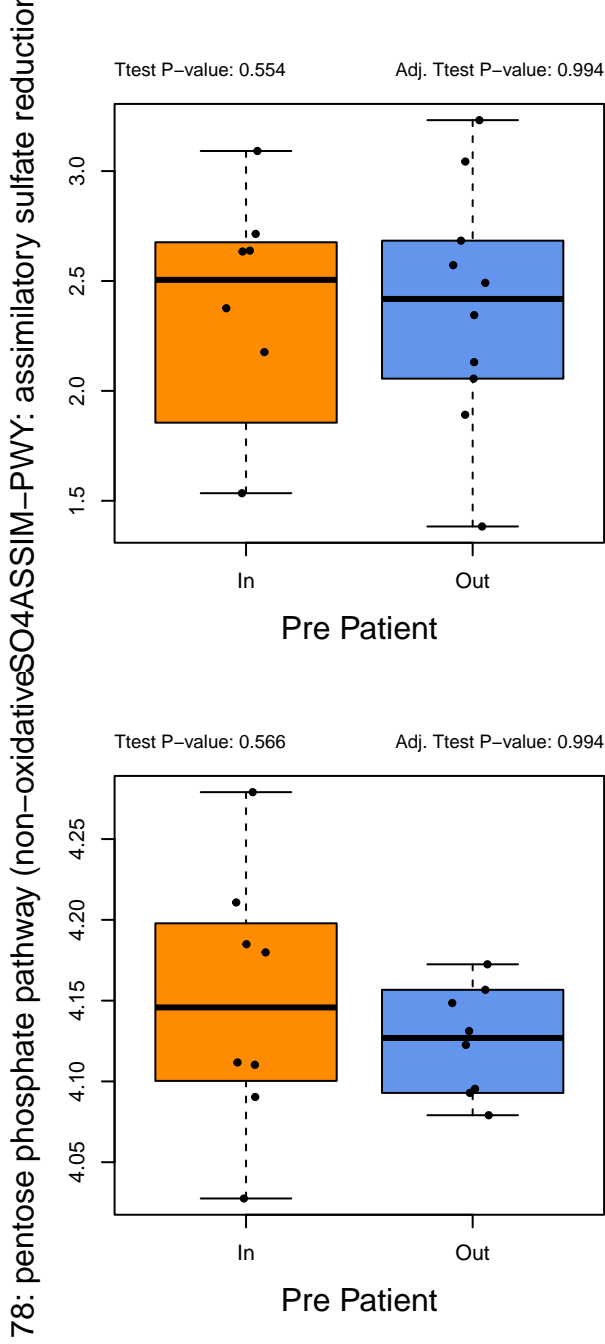
99: pyrimidine deoxyribonucleosides salvageWY: superpathway of sulfate assimilation and c

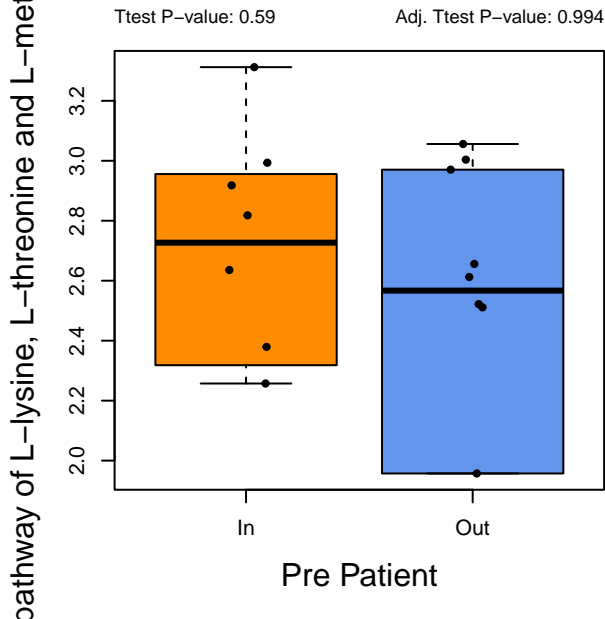
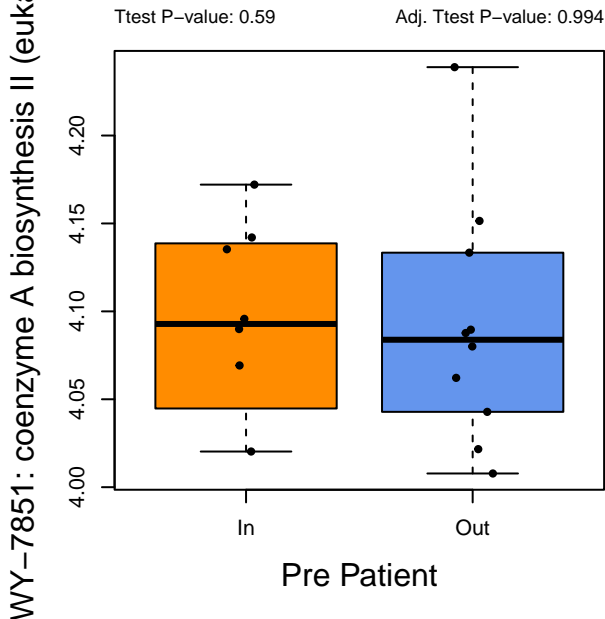
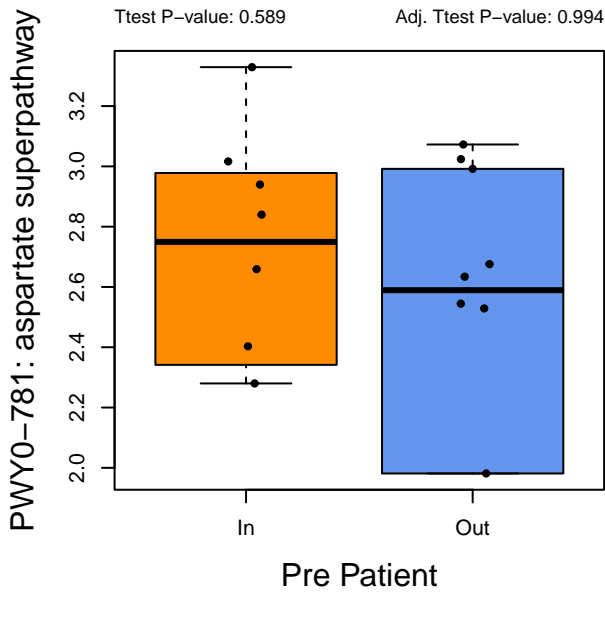
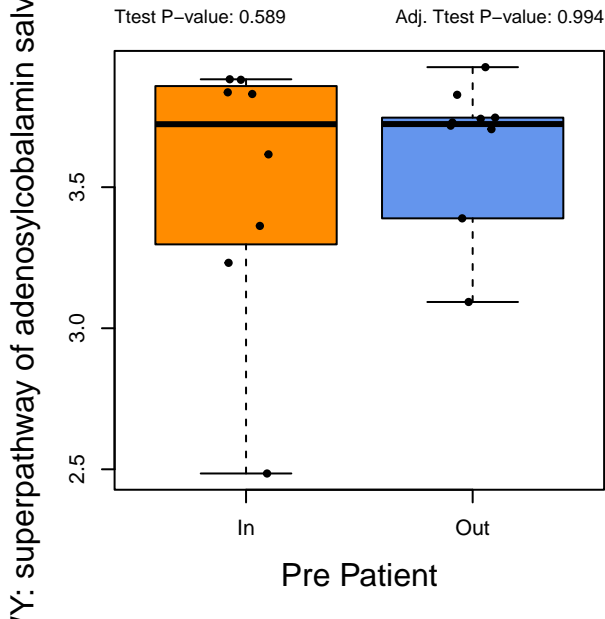
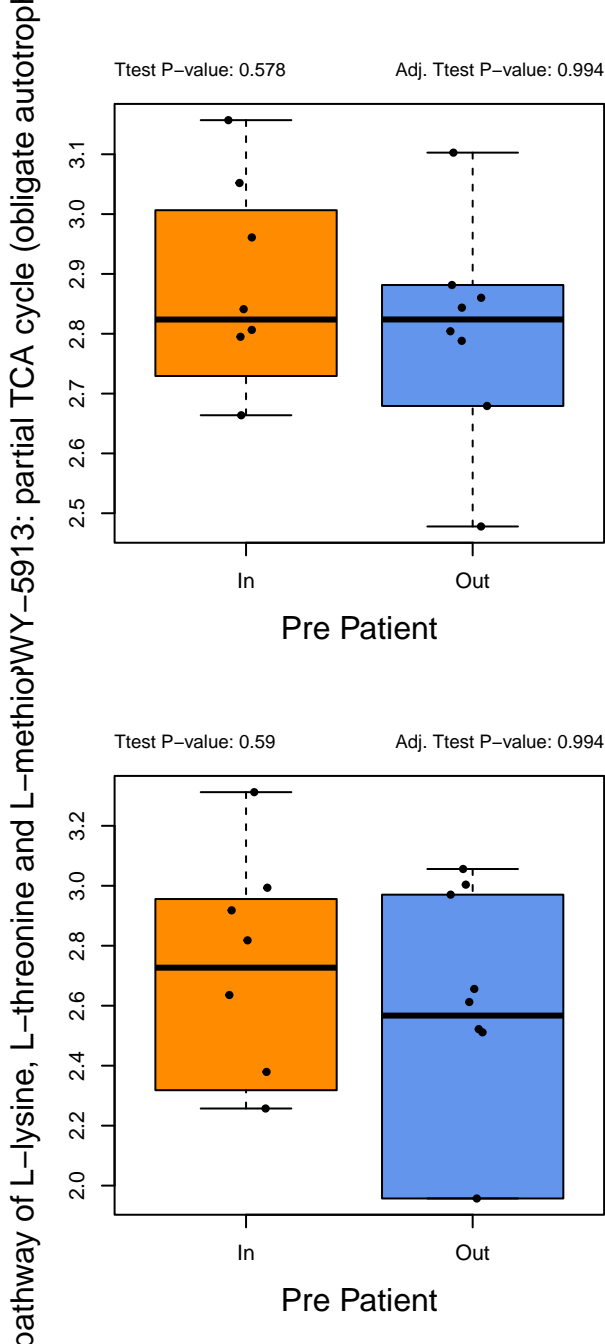
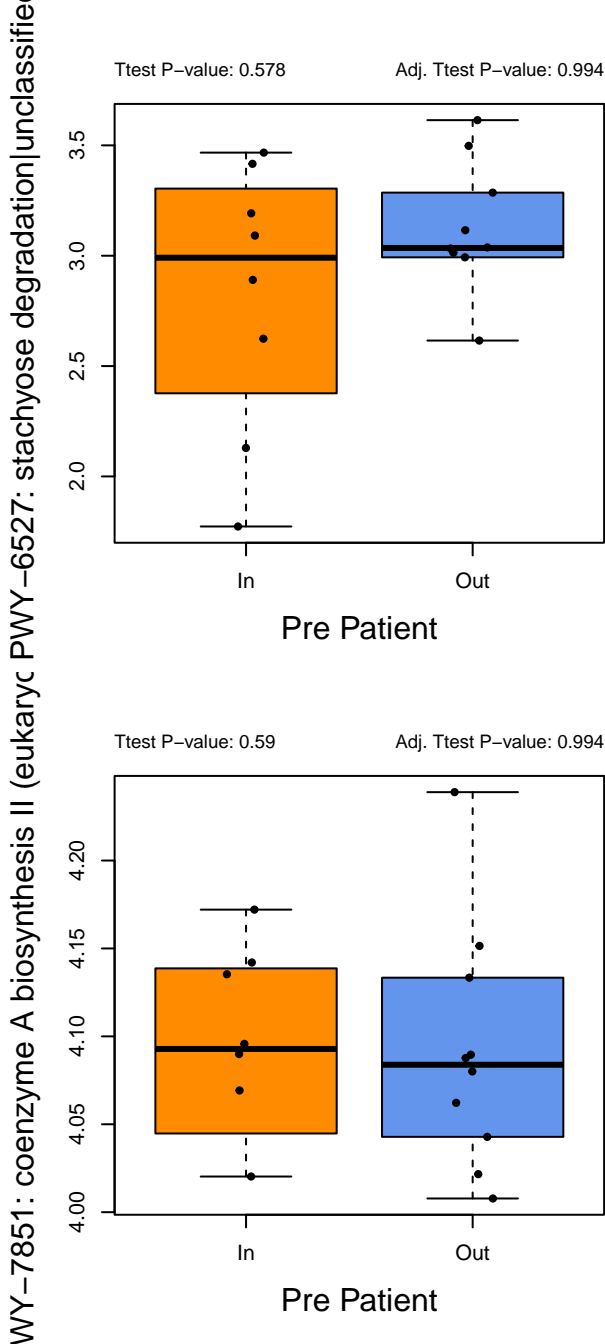
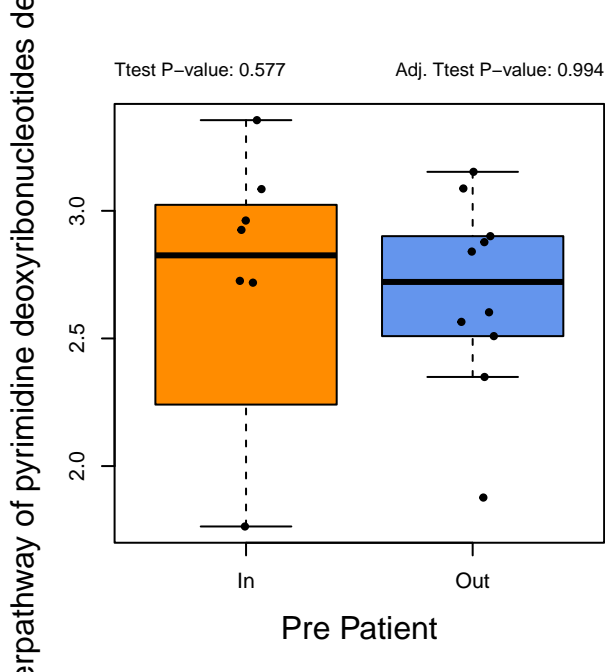
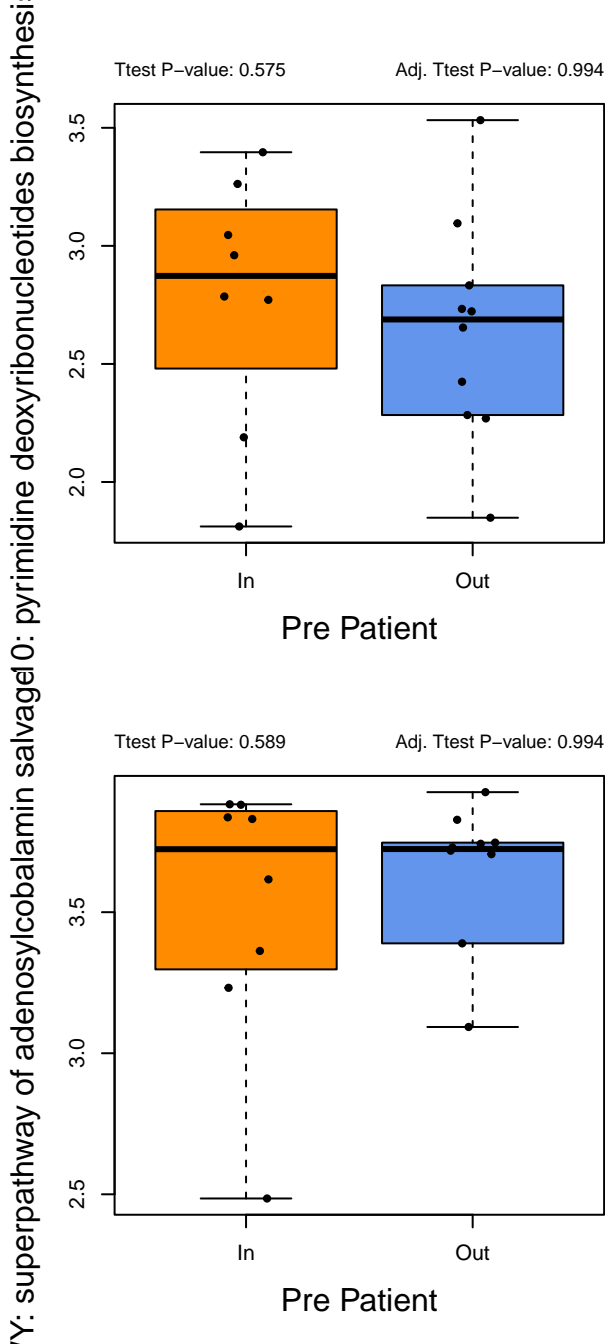


INE-SYN: superpathway of arginine and polyan PWY1ZNC-1: assimilatory sulfate reduction IV

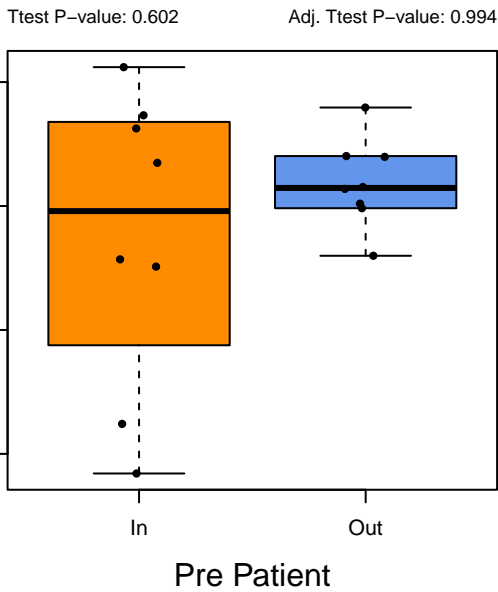




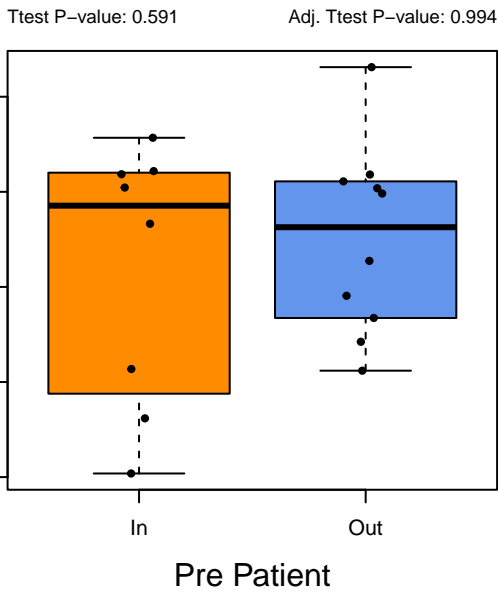




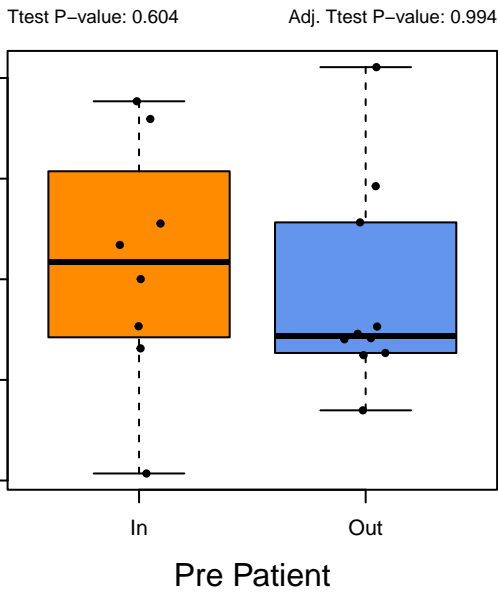
PWY: superpathway of aromatic amino acid bio



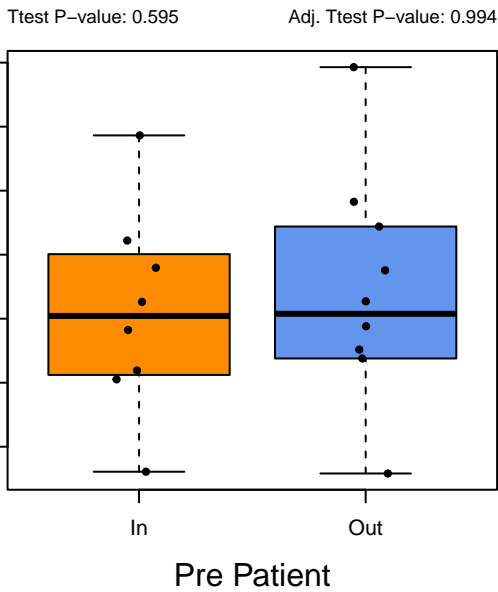
PWY-5941: glycogen degradation II



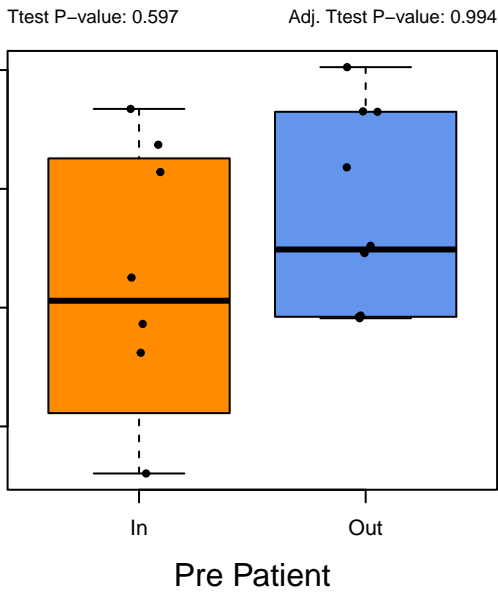
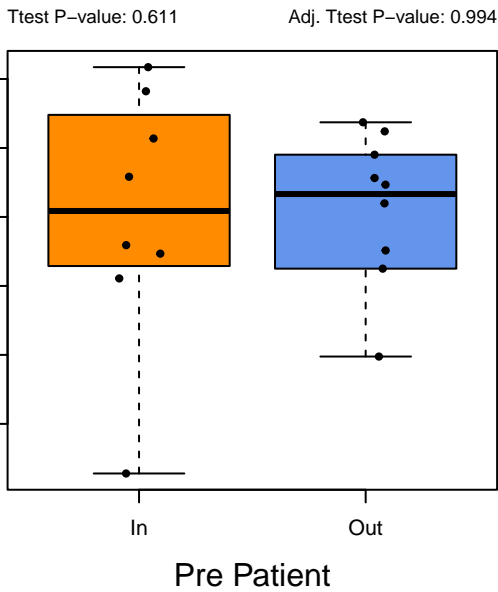
ARO-PWY: chorismate biosynthesis I



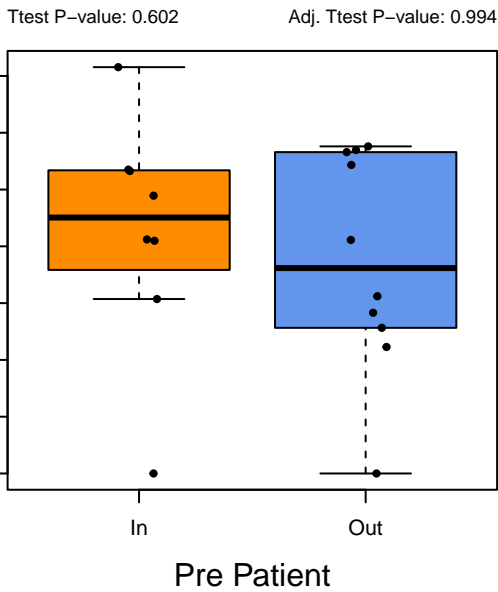
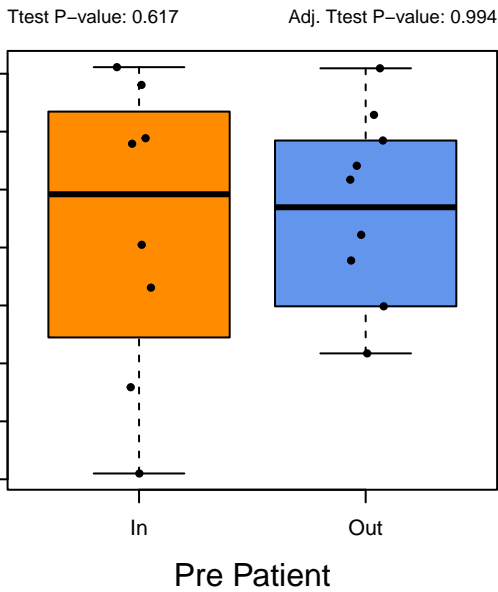
y of N-acetylglucosamine, N-acetylmannosami



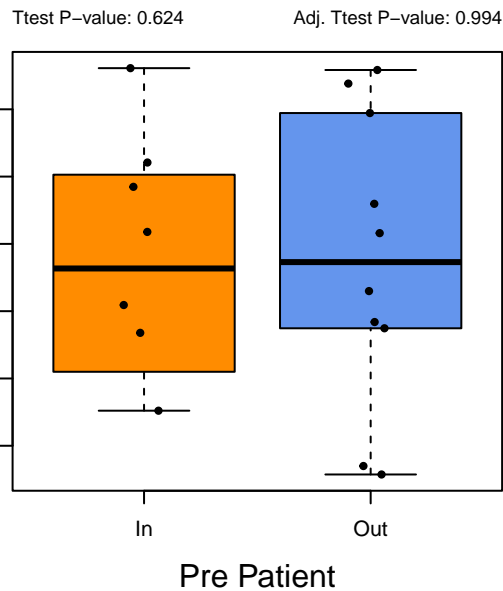
-7111: pyruvate fermentation to isobutanol (engi/Y: superpathway of L-serine and glycine biosy



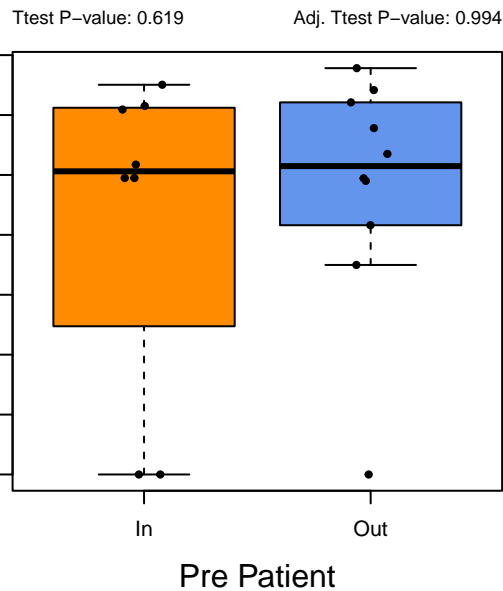
Y30-4107: NAD salvage pathway V (PNC V c)-301: L-ascorbate degradation I (bacterial, ana



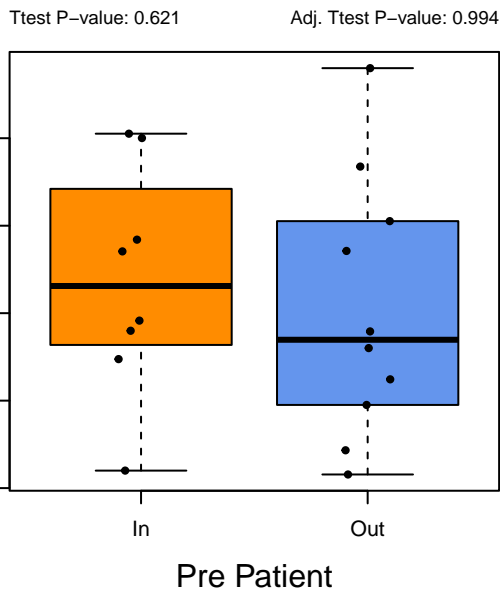
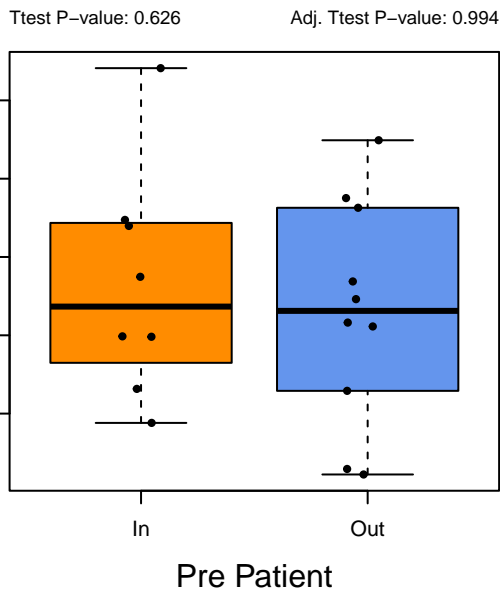
PWY-5973: cis-vaccenate biosynthesis



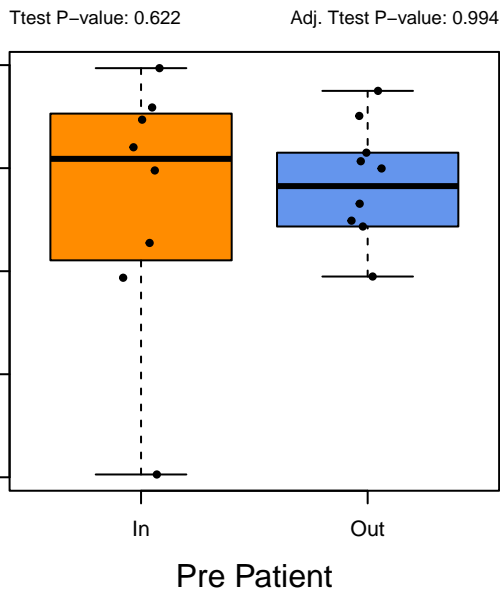
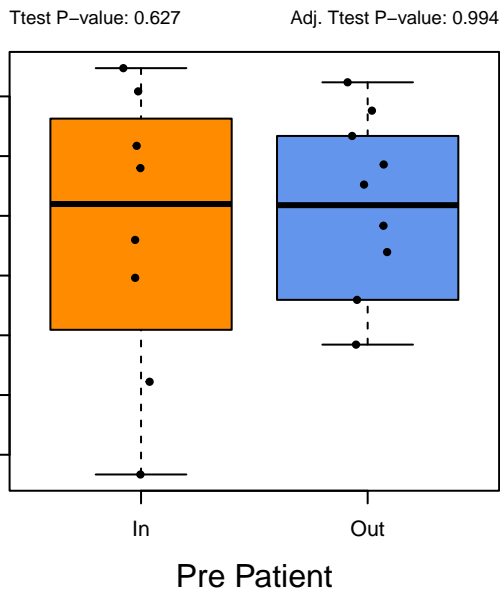
Y-5845: superpathway of menaquinol-9 biosynthesis



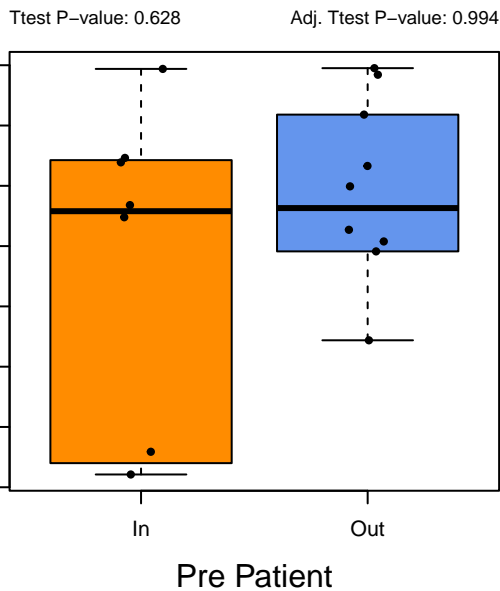
PWY-7234: inosine-5'-phosphate biosynthesis OA-PWY: coenzyme A biosynthesis I (prokaryote)



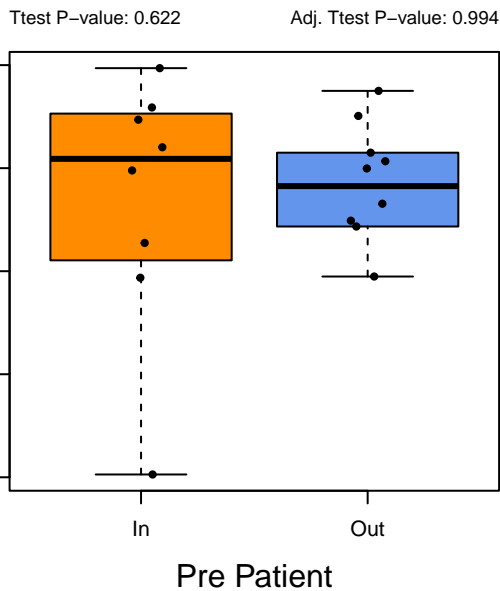
NUCSAL-PWY: NAD salvage pathway I (PNC)ALACTARDEG-PWY: D-galactarate degradation

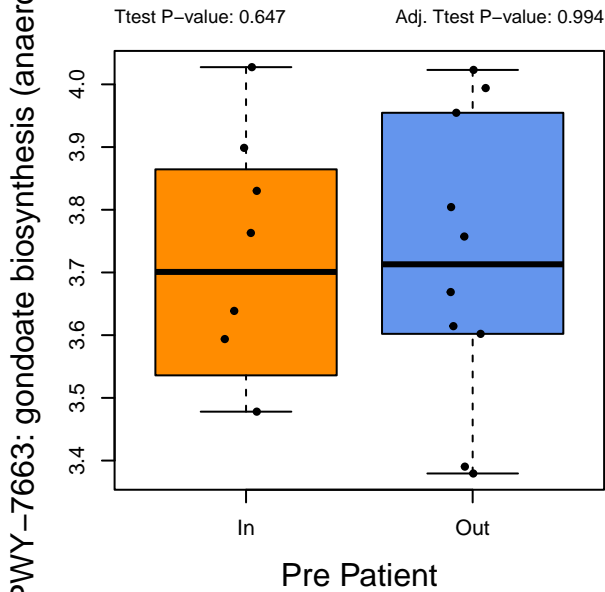
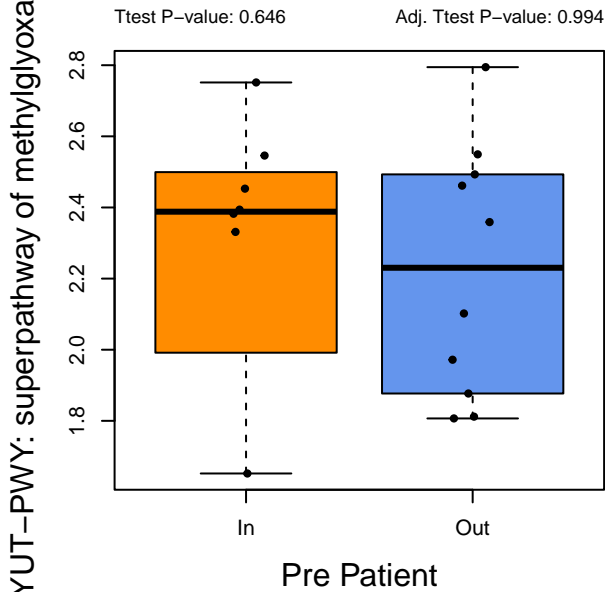
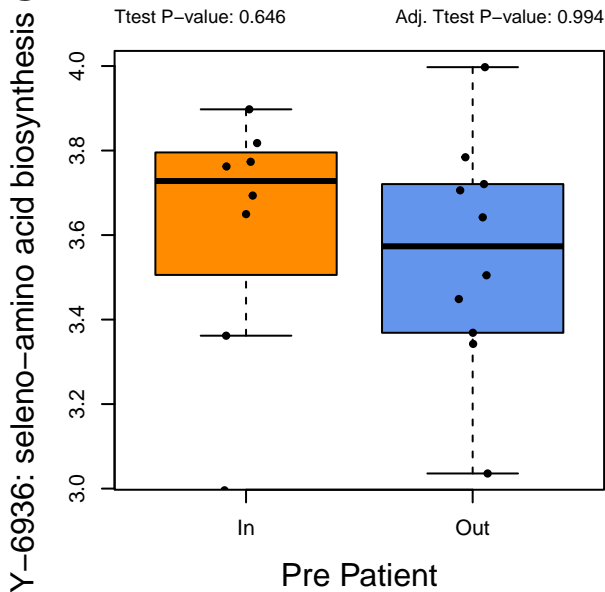
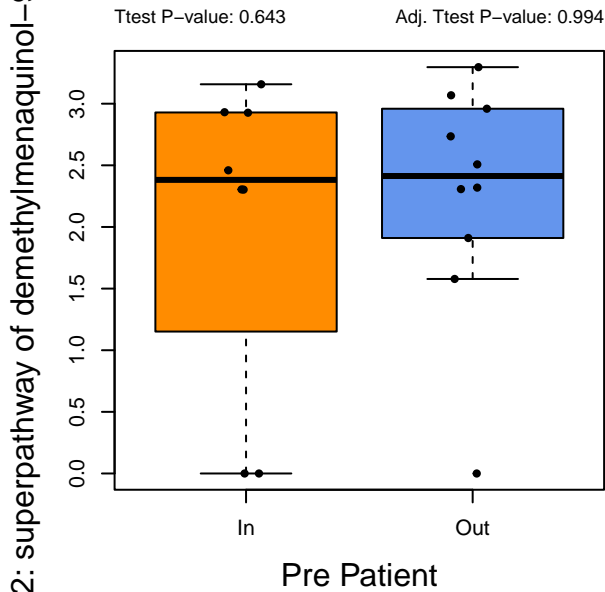
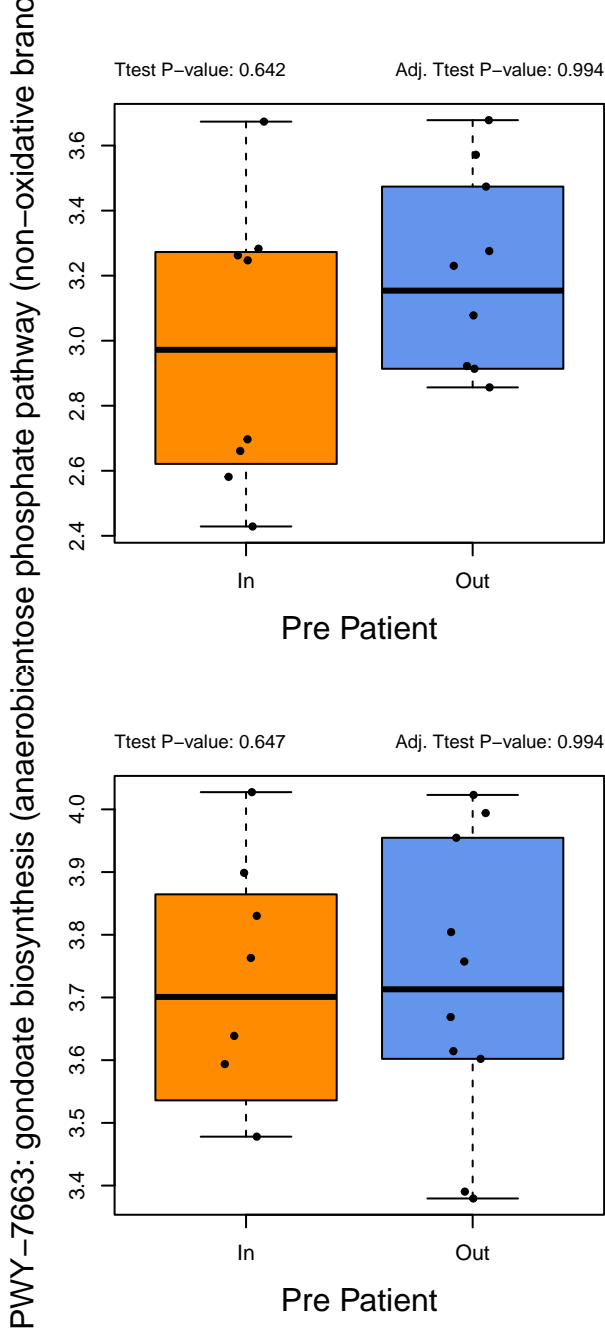
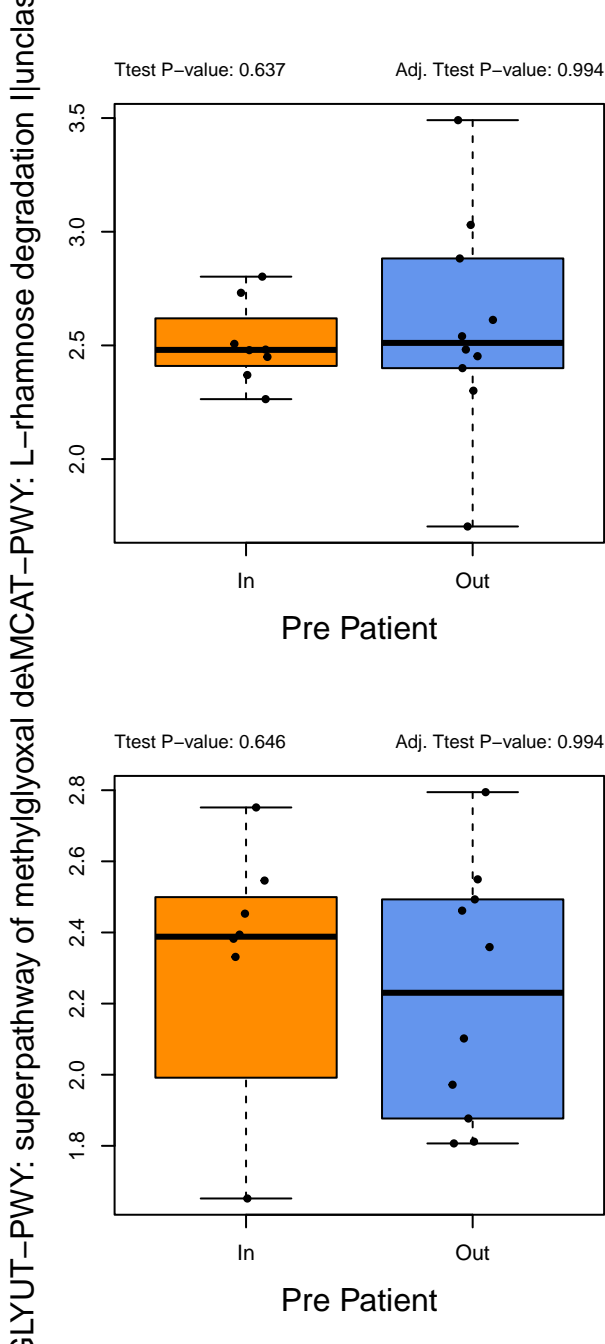
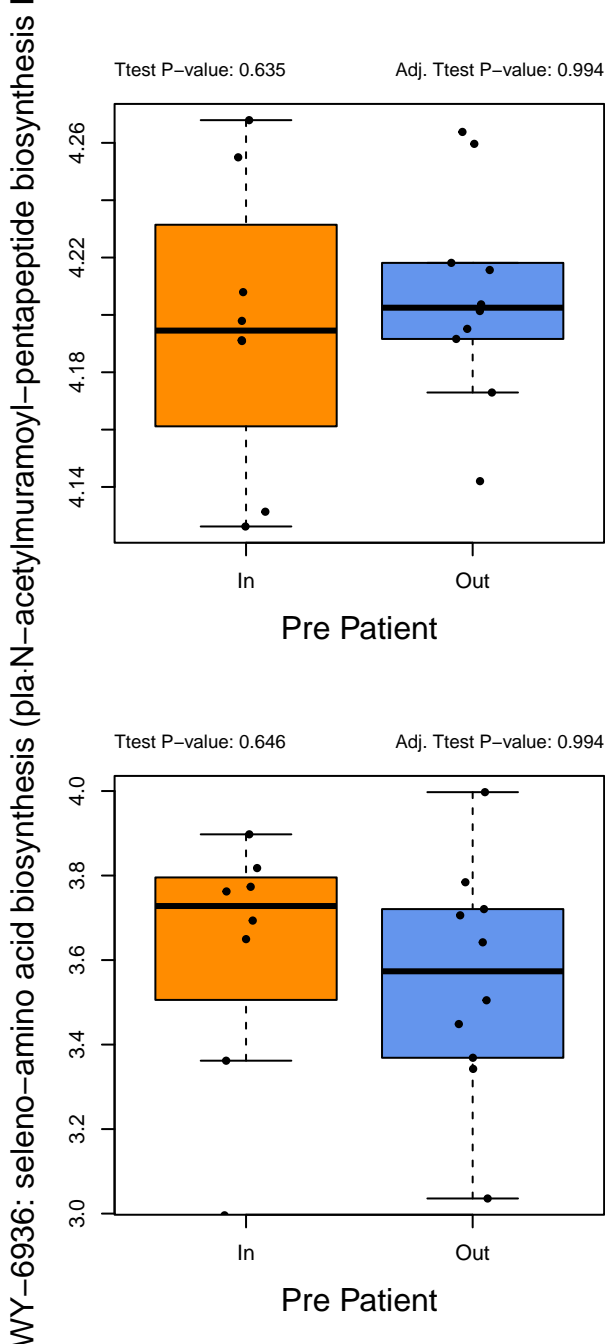
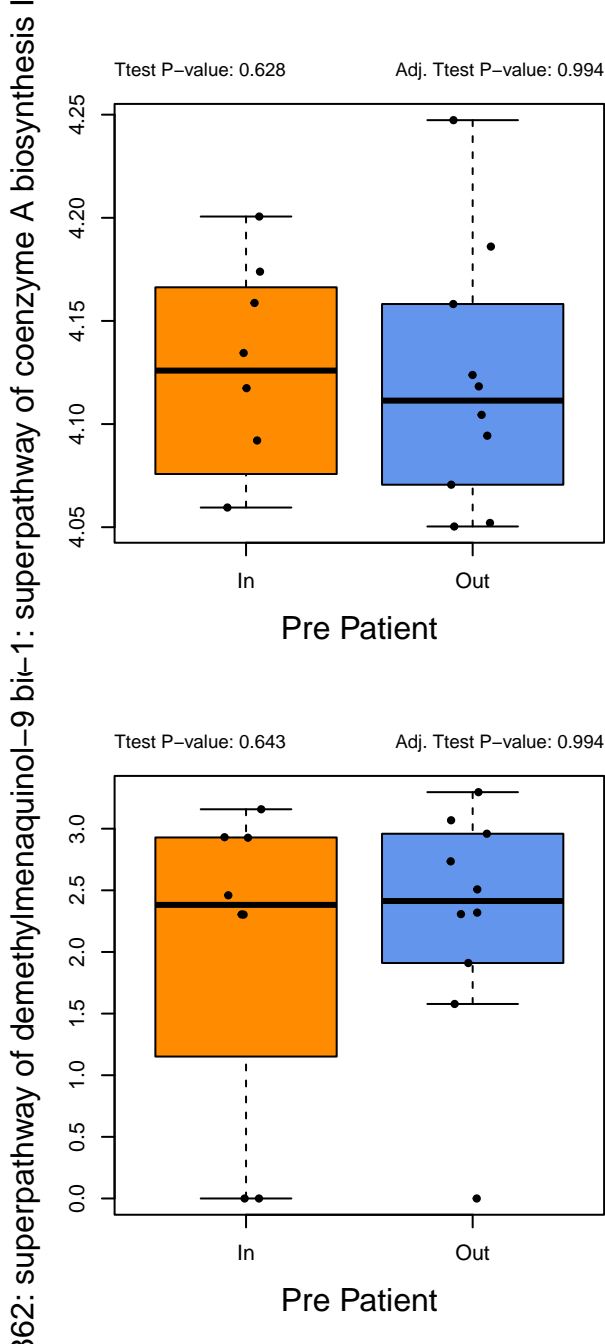


PWY-6902: chitin degradation II (Vibrio)

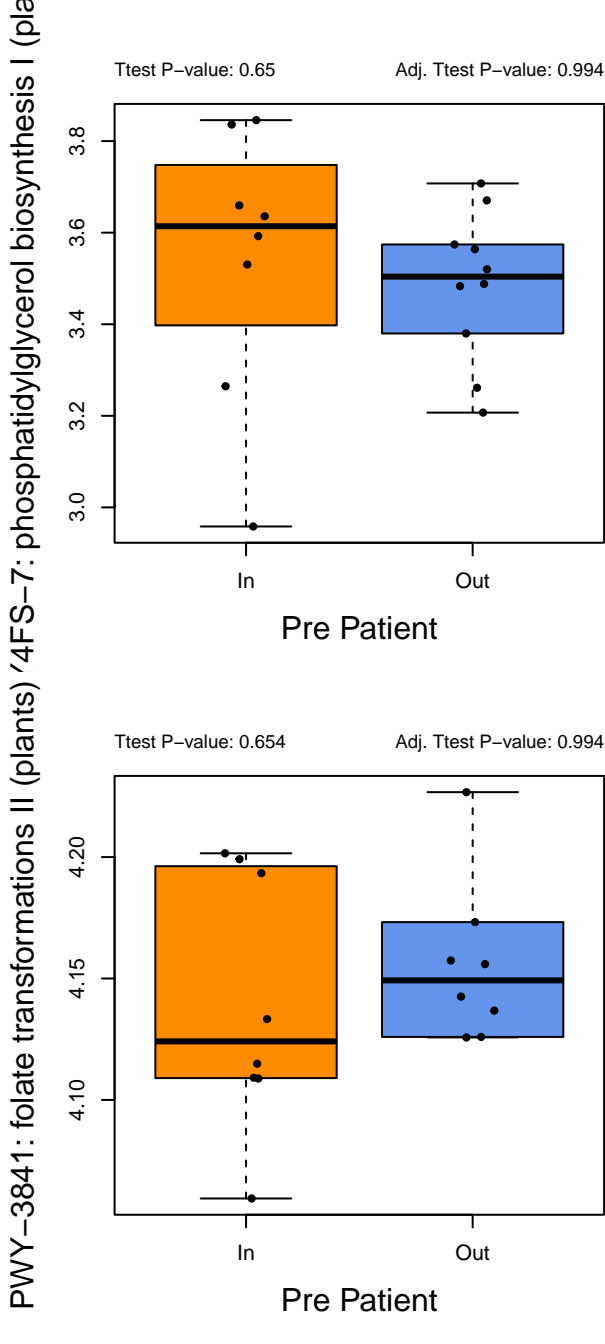
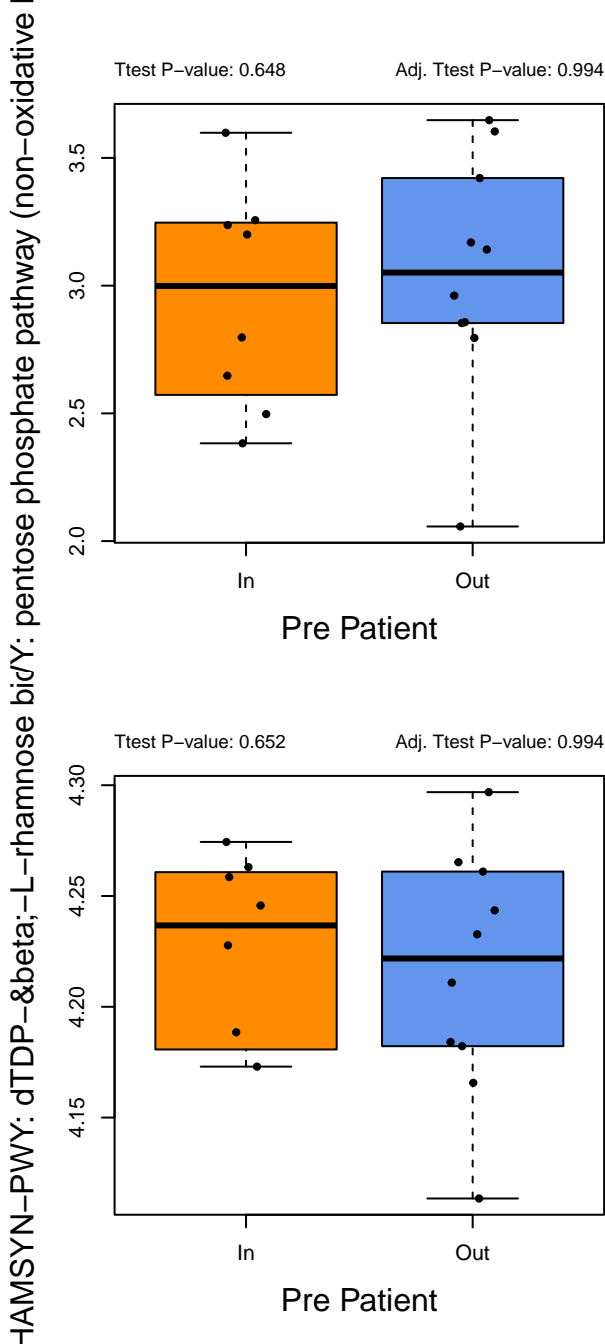
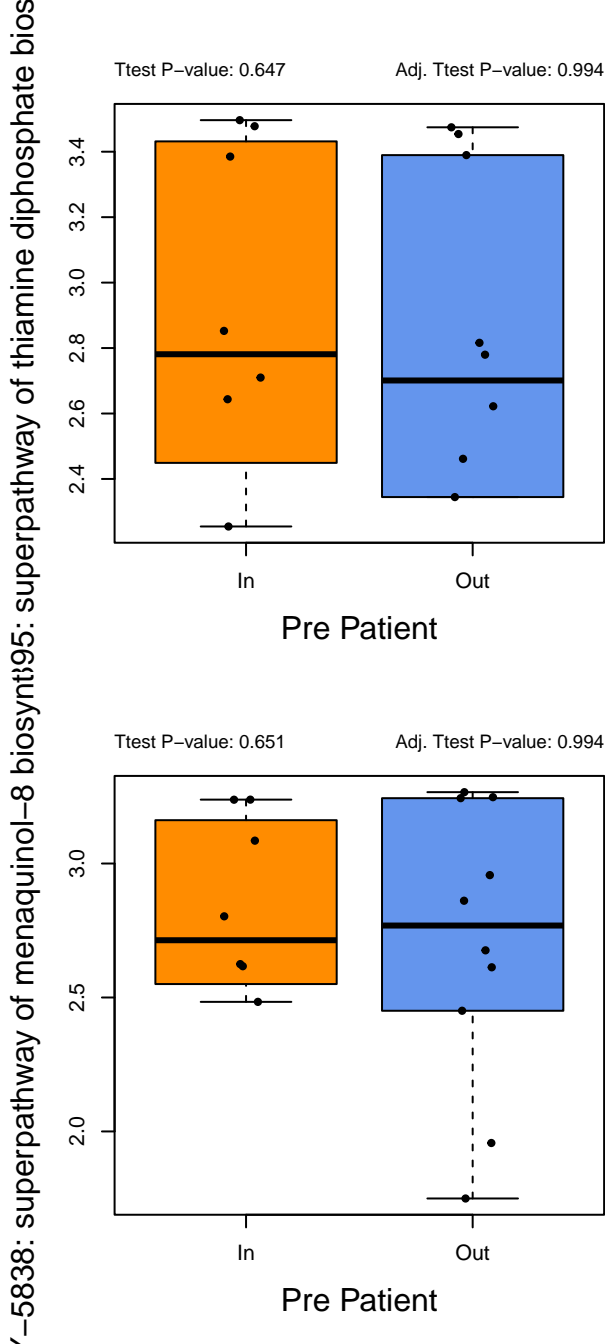
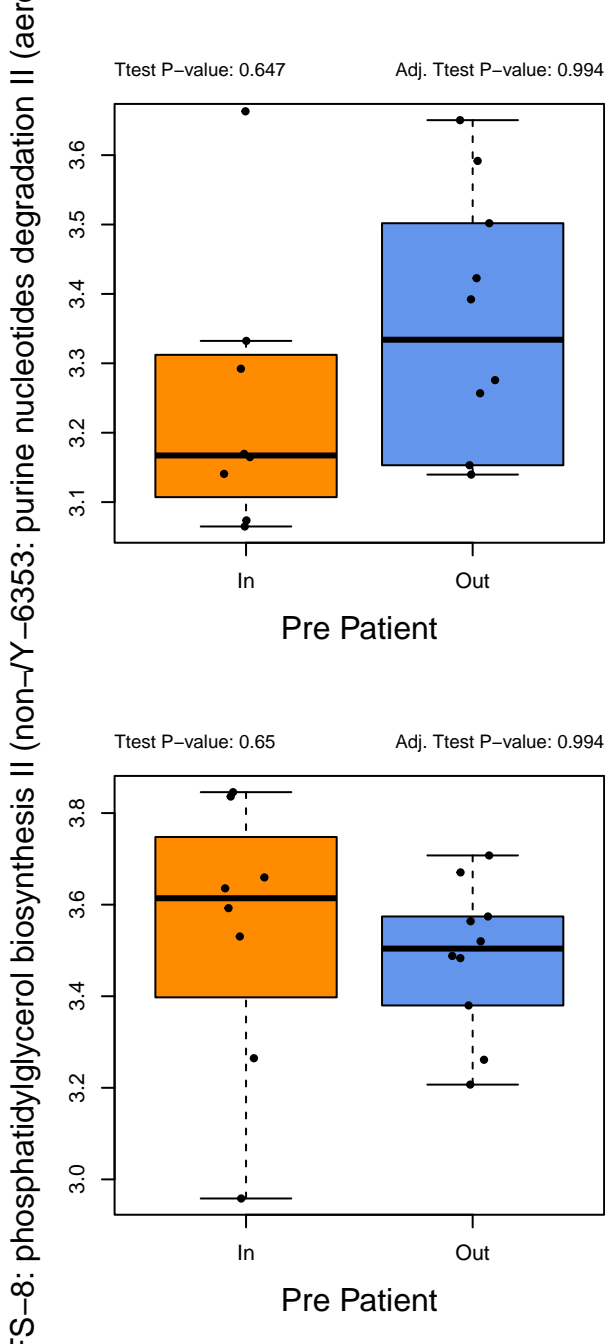


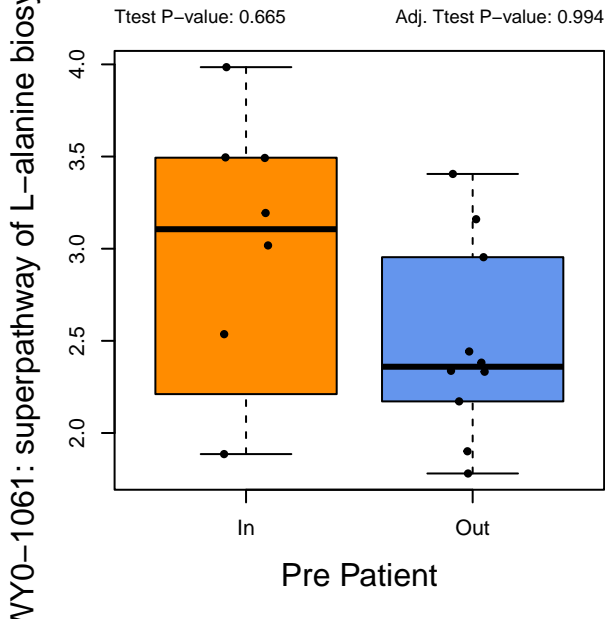
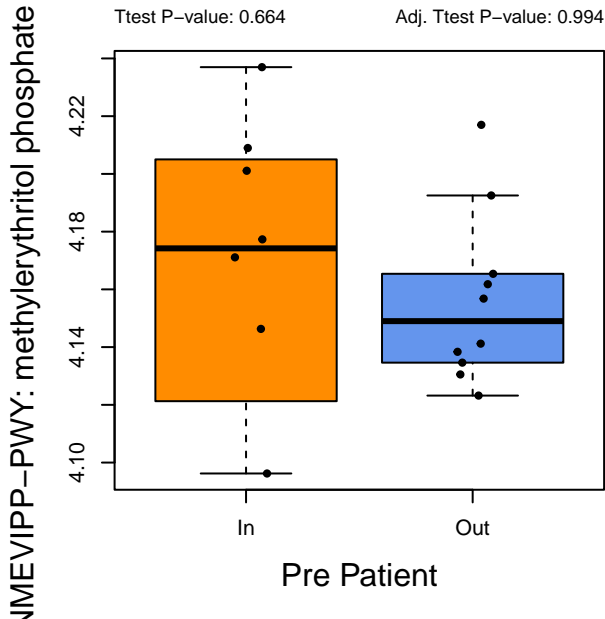
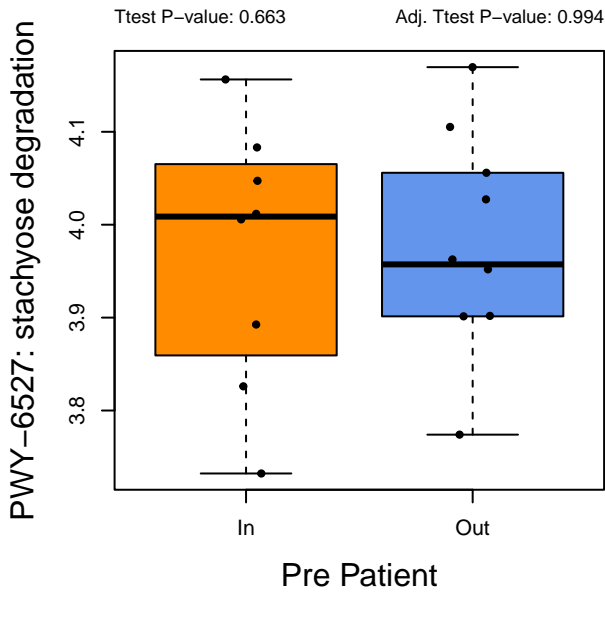
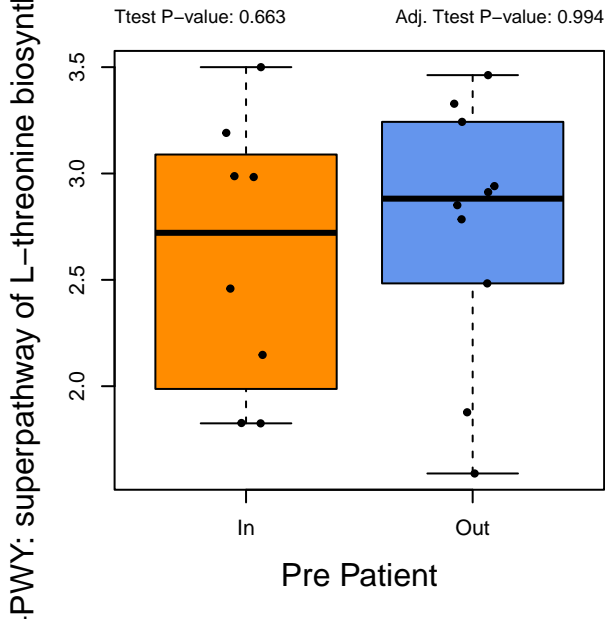
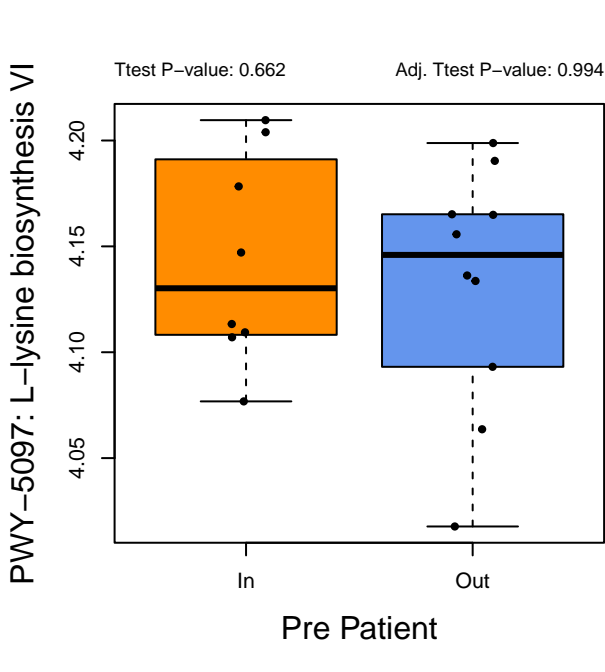
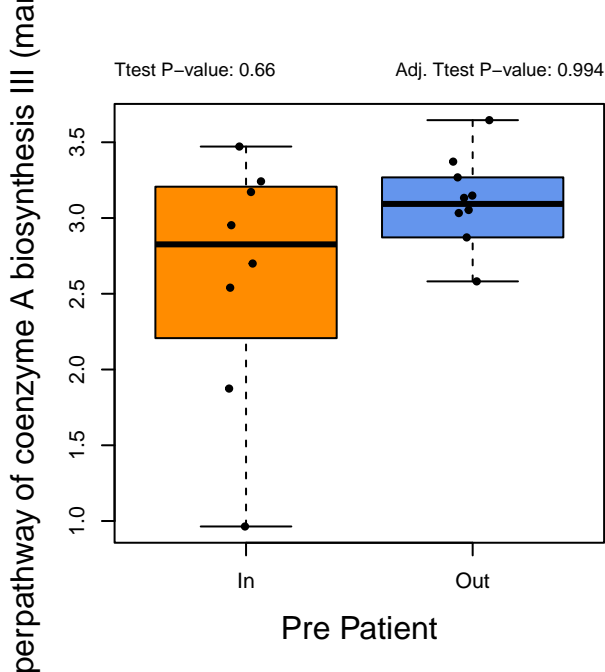
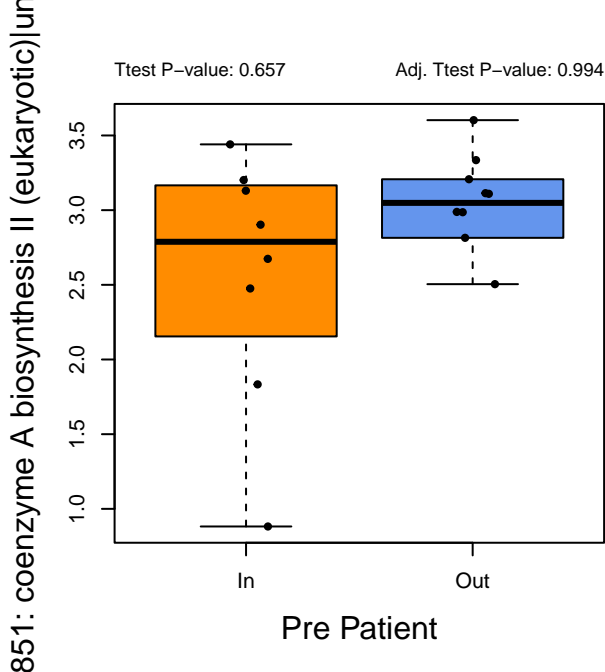
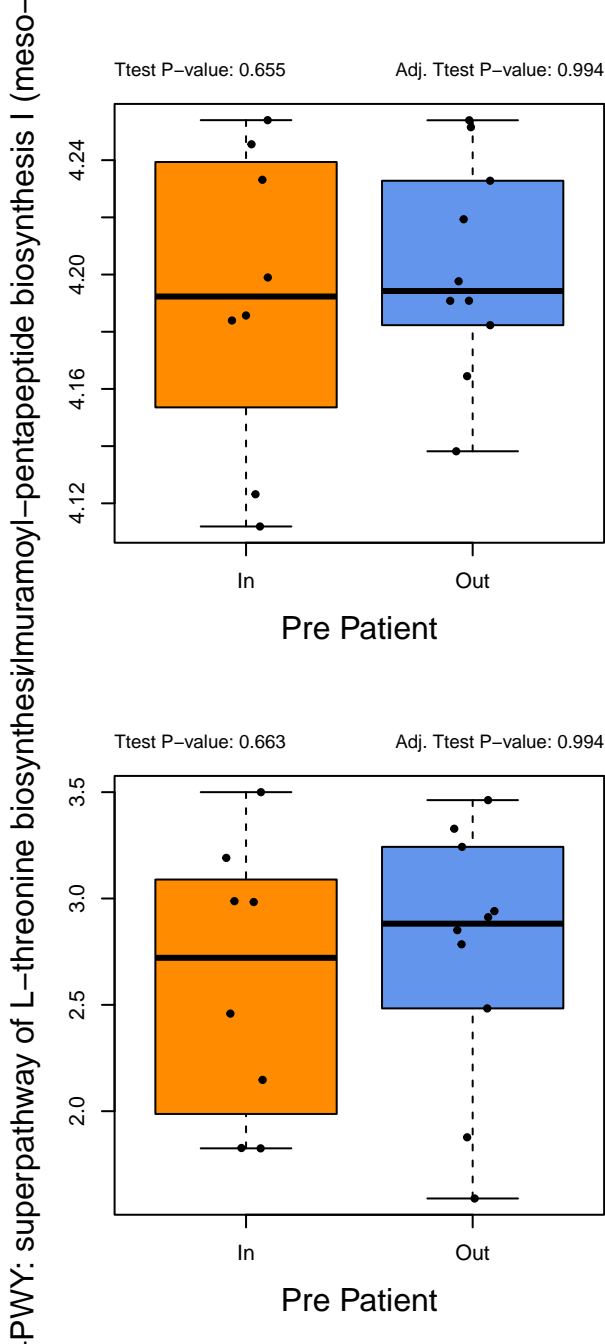
ER-PWY: superpathway of D-glucarate and D

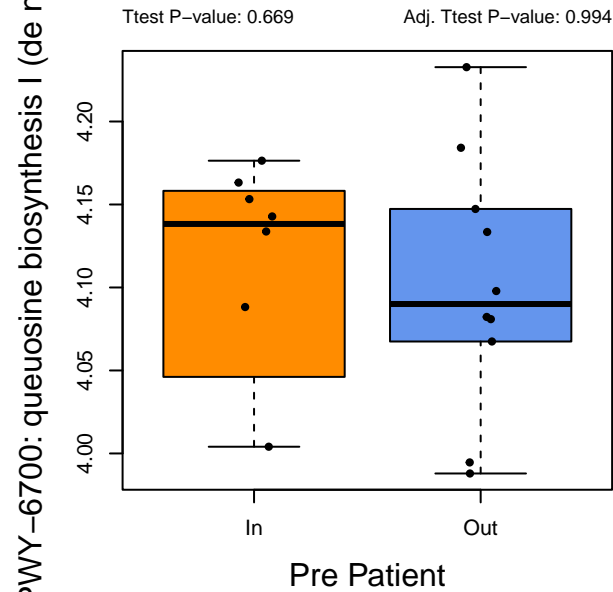
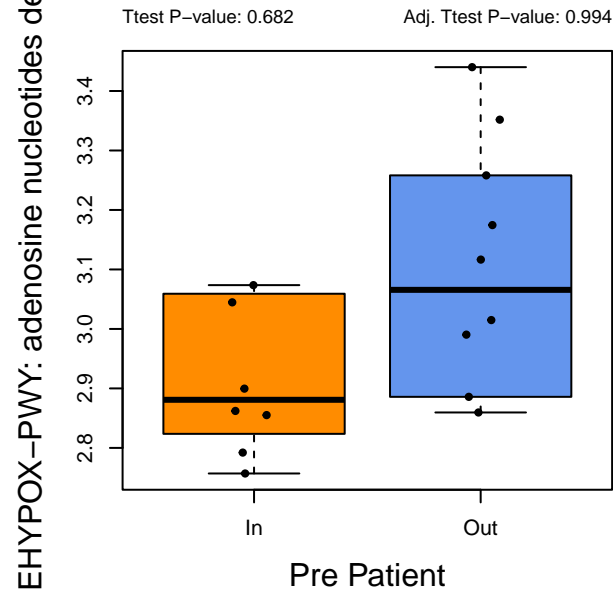
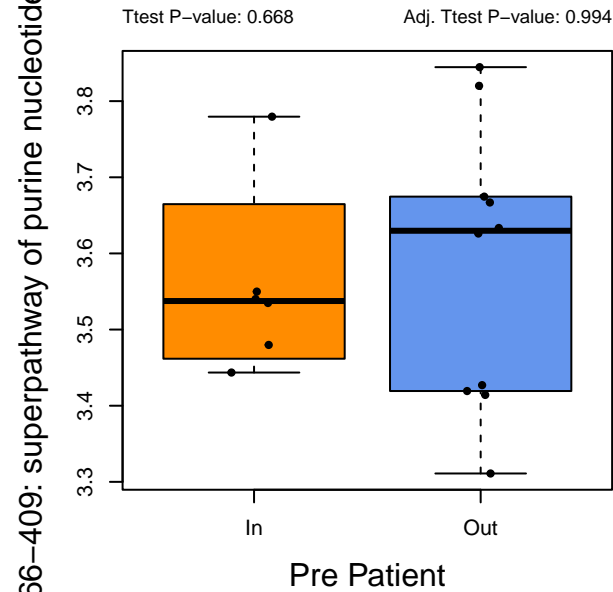
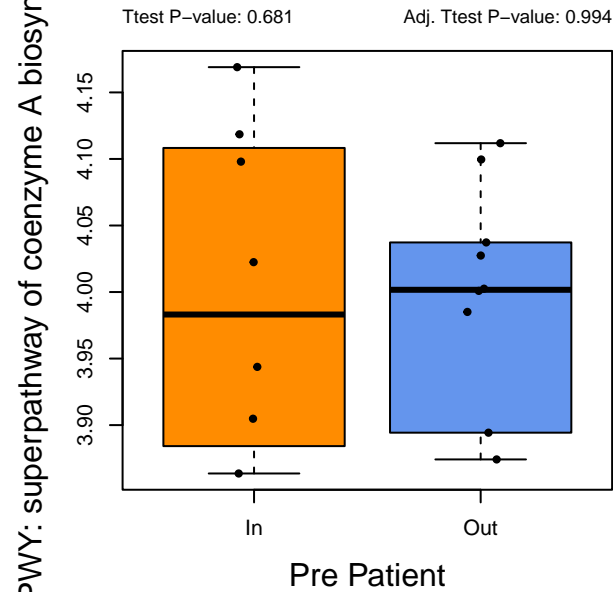
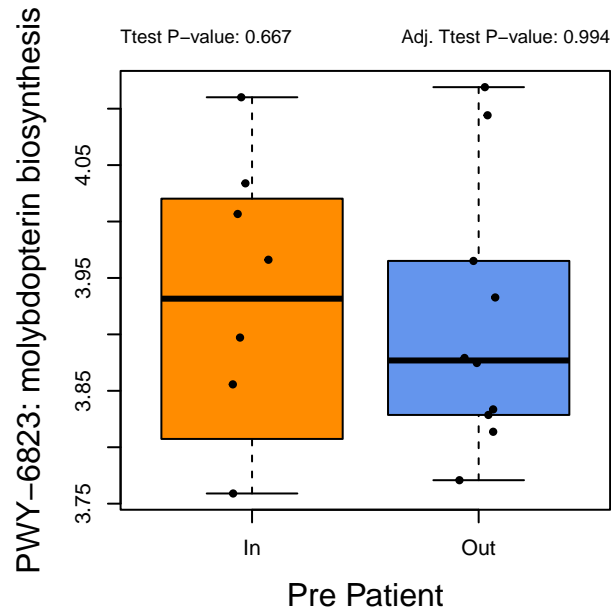
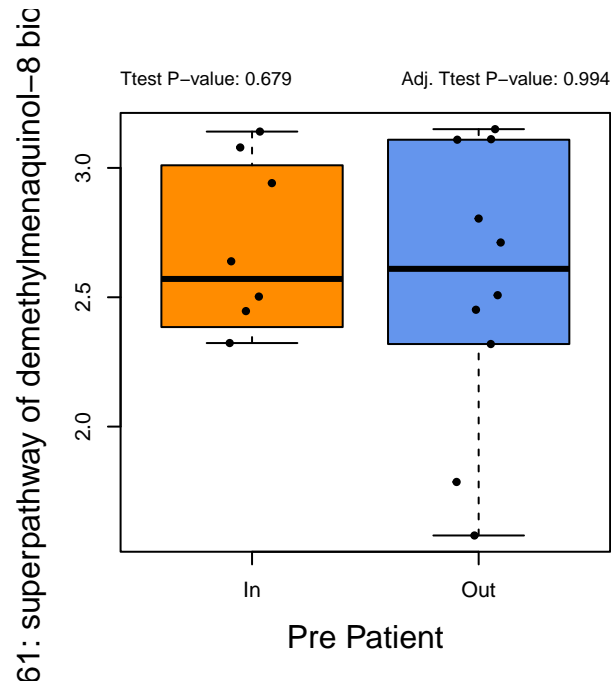
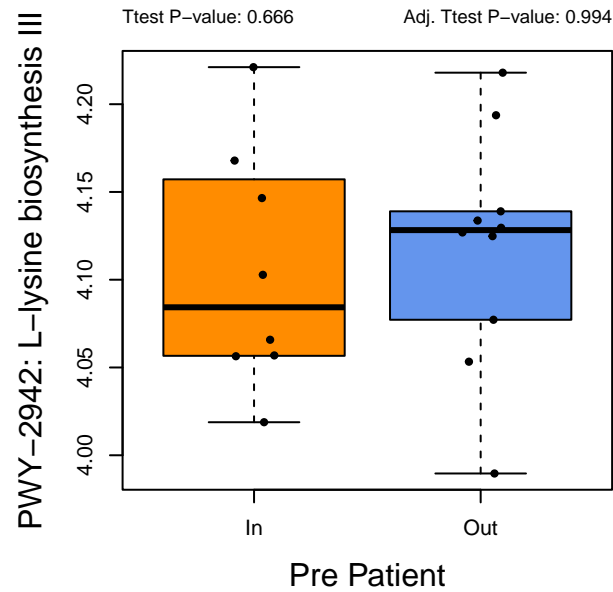
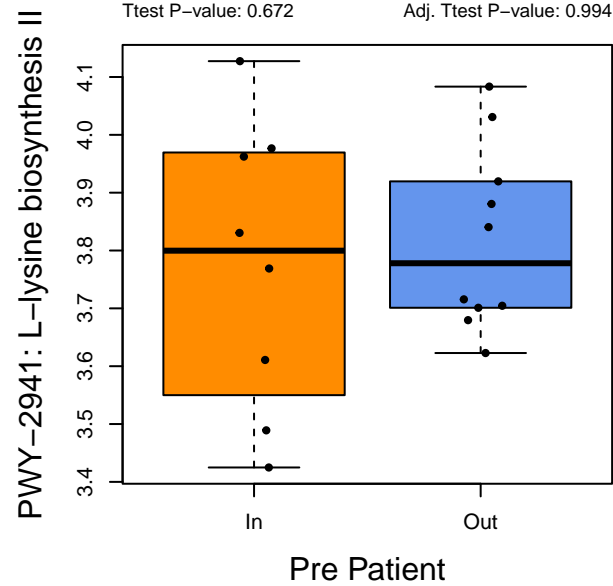




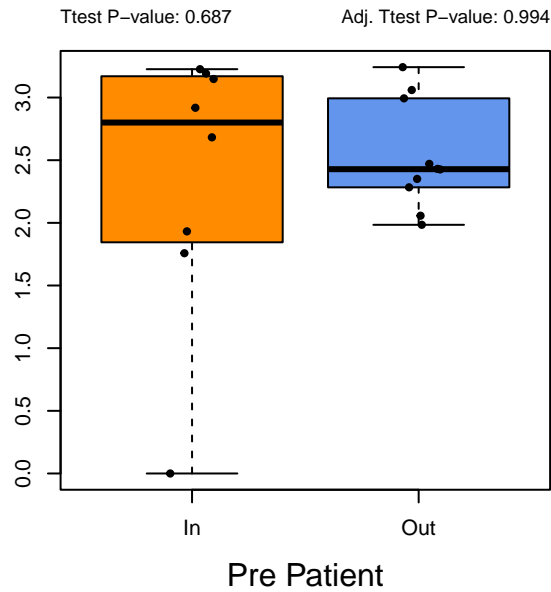




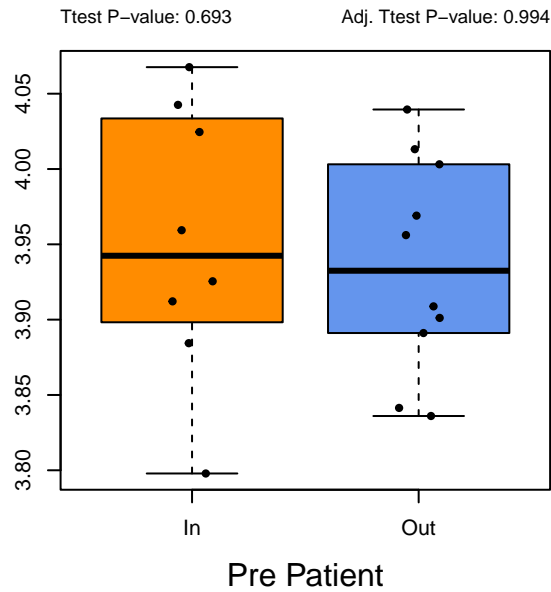




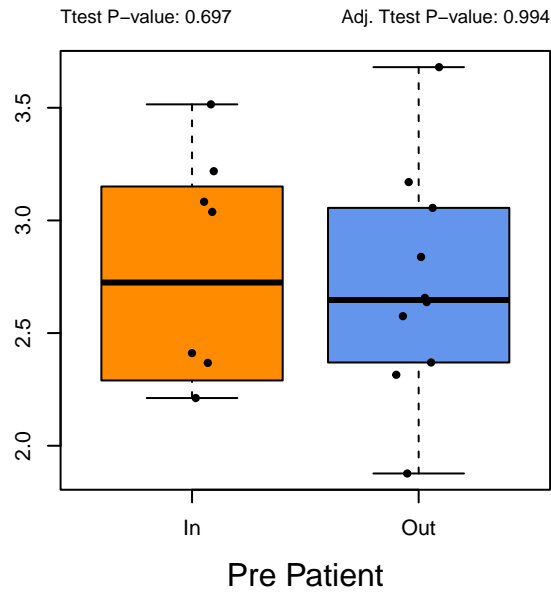
ISOPREN SYN-PWY: polyisoprenoid biosynthesis: C4 photosynthetic carbon assimilation cycle,



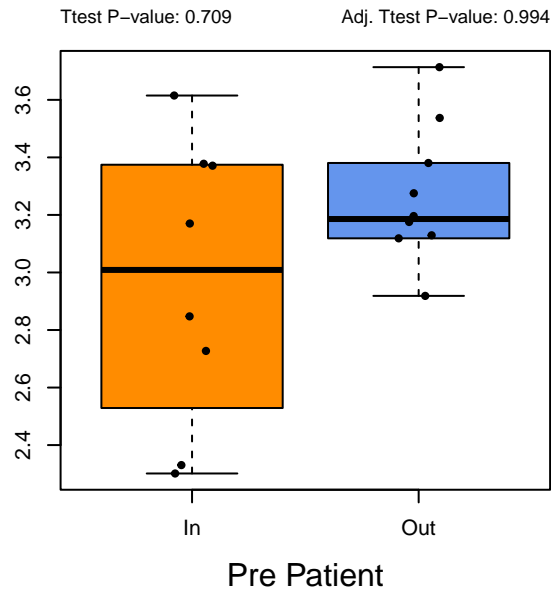
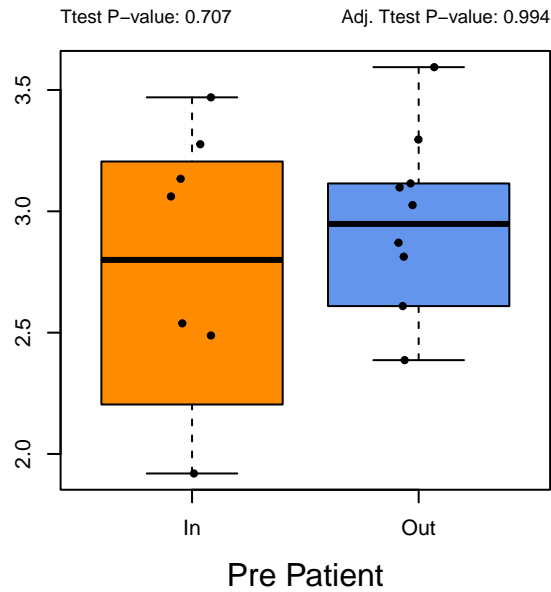
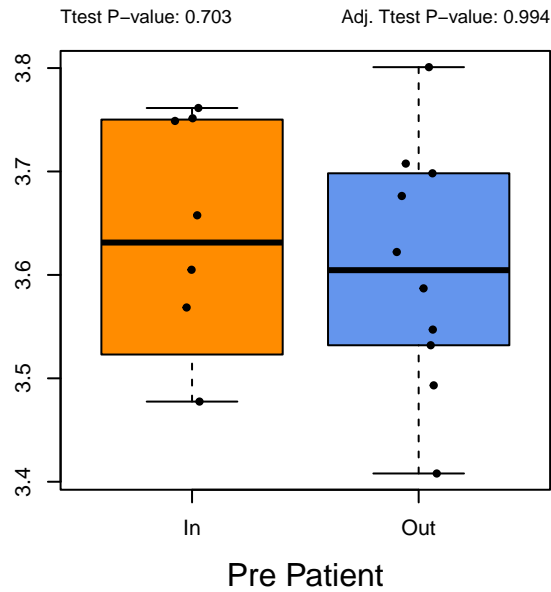
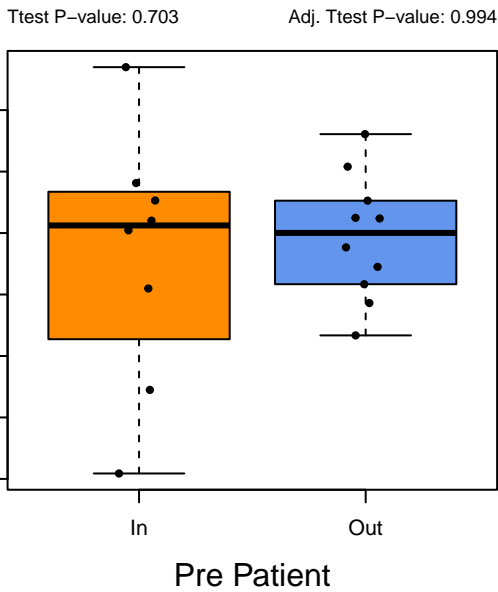
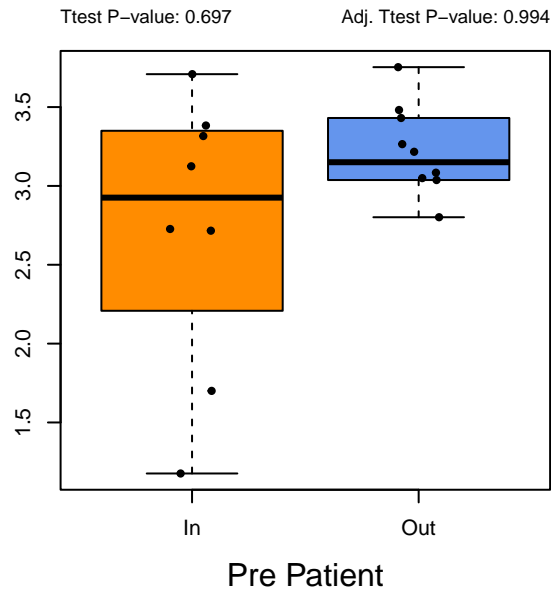
ANS SYN-PWY: colanic acid building blocks biosy



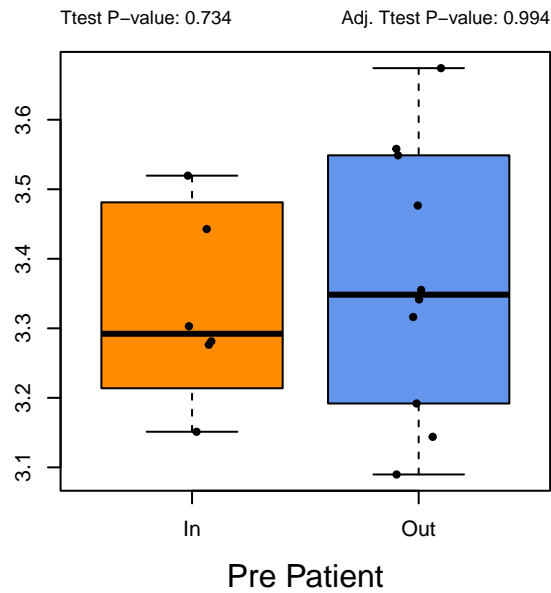
STS SYN-PWY: L-histidine biosynthesis|unclass' -5695: inosine 5'-phosphate degradation|unclass



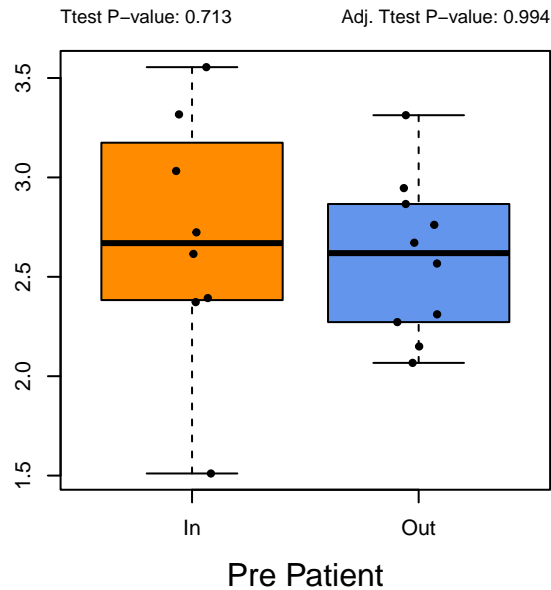
6151: S-adenosyl-L-methionine salvage |unc9: fatty acid biosynthesis initiation (mitochondria



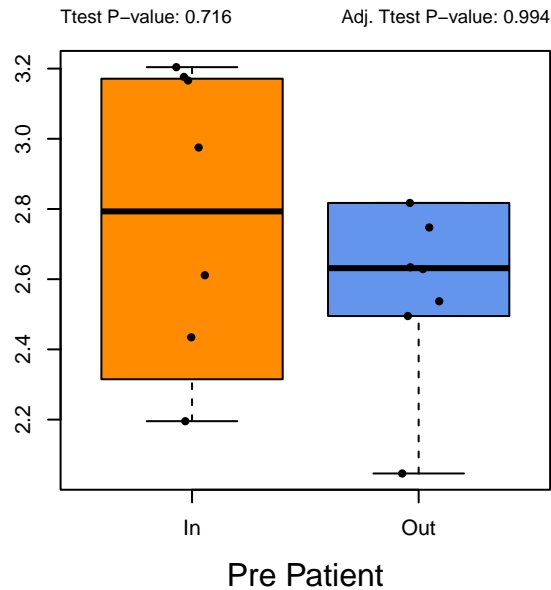
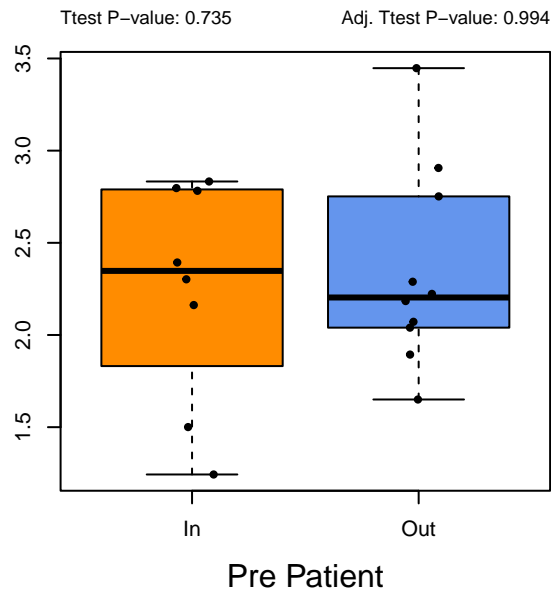
7: superpathway of purine deoxyribonucleoside:



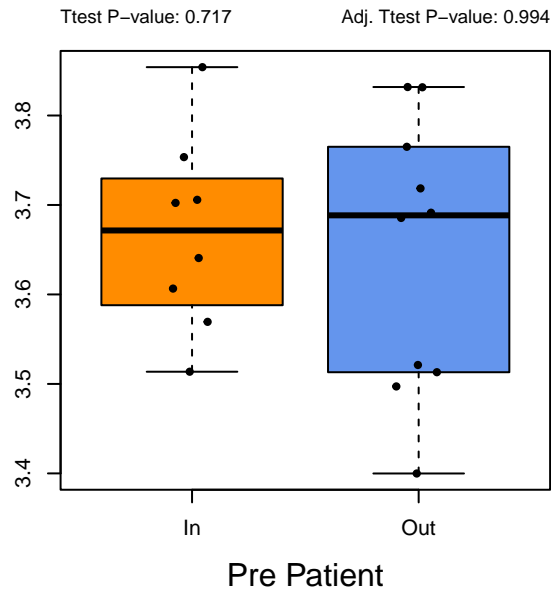
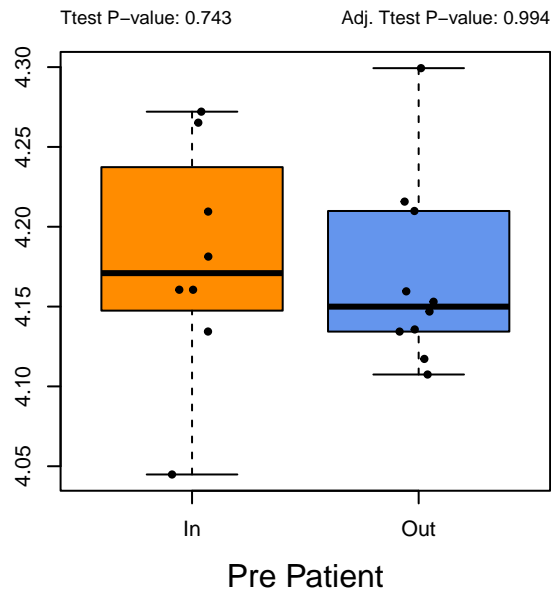
PWY-6531: mannitol cycle



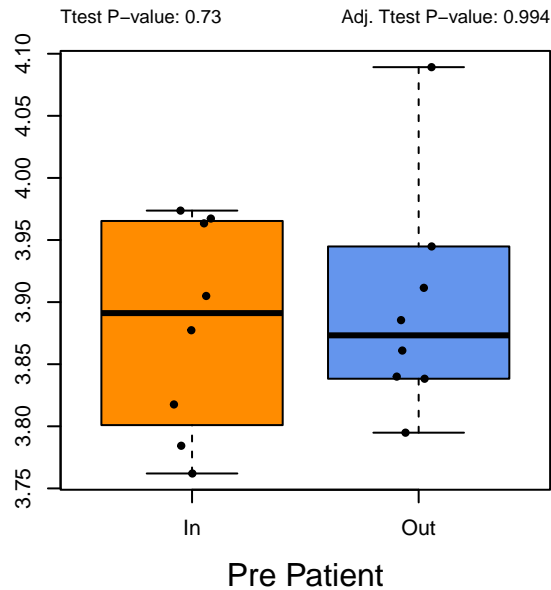
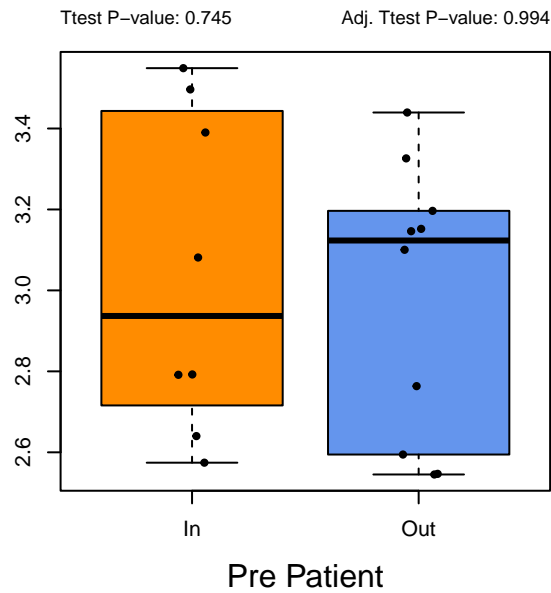
PWY: UDP-N-acetyl-D-glucosamine biosynthesophosphate formation from pyriithiamine and oxythi

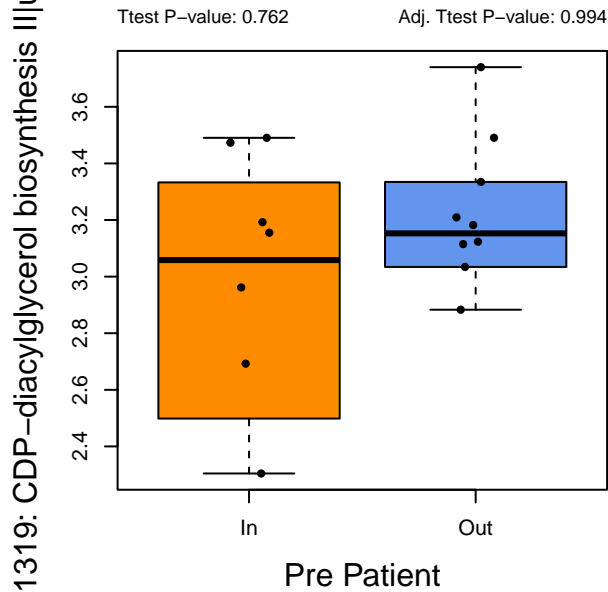
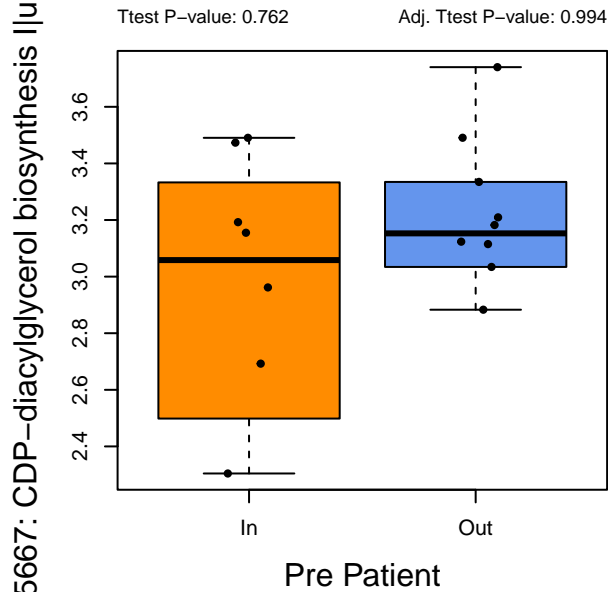
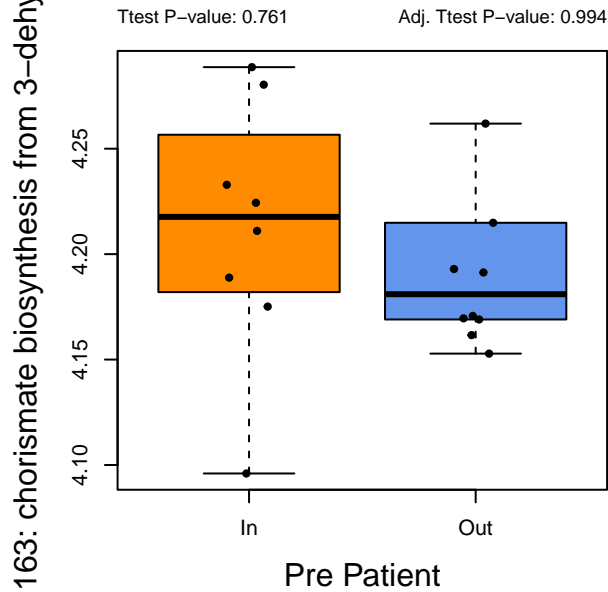
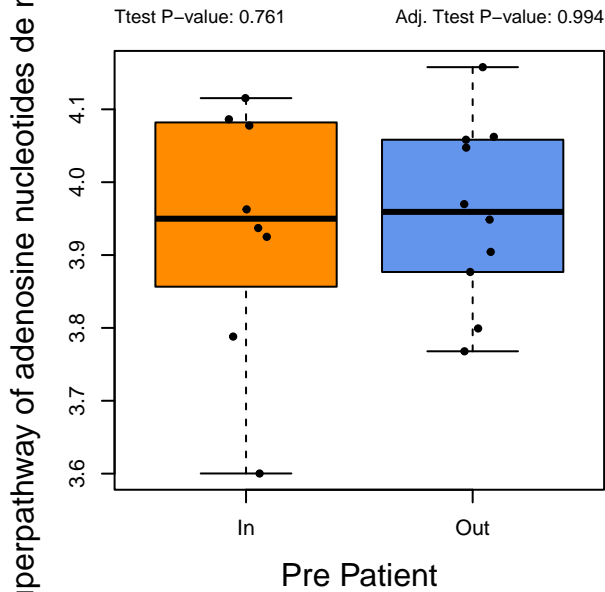
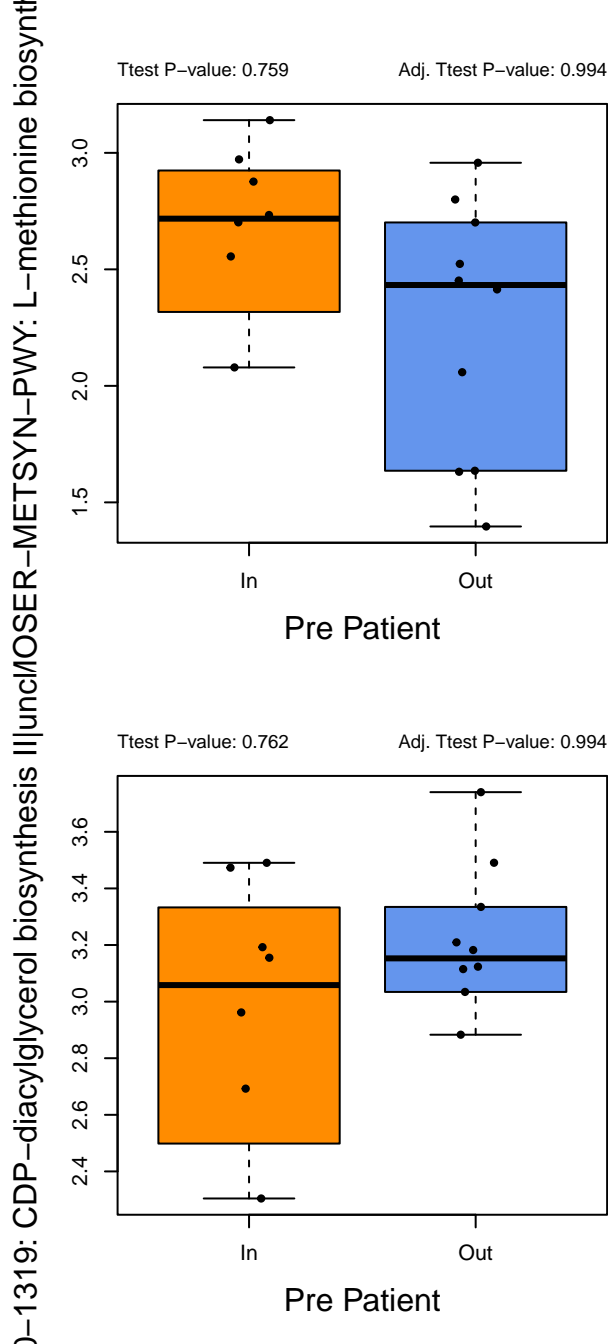
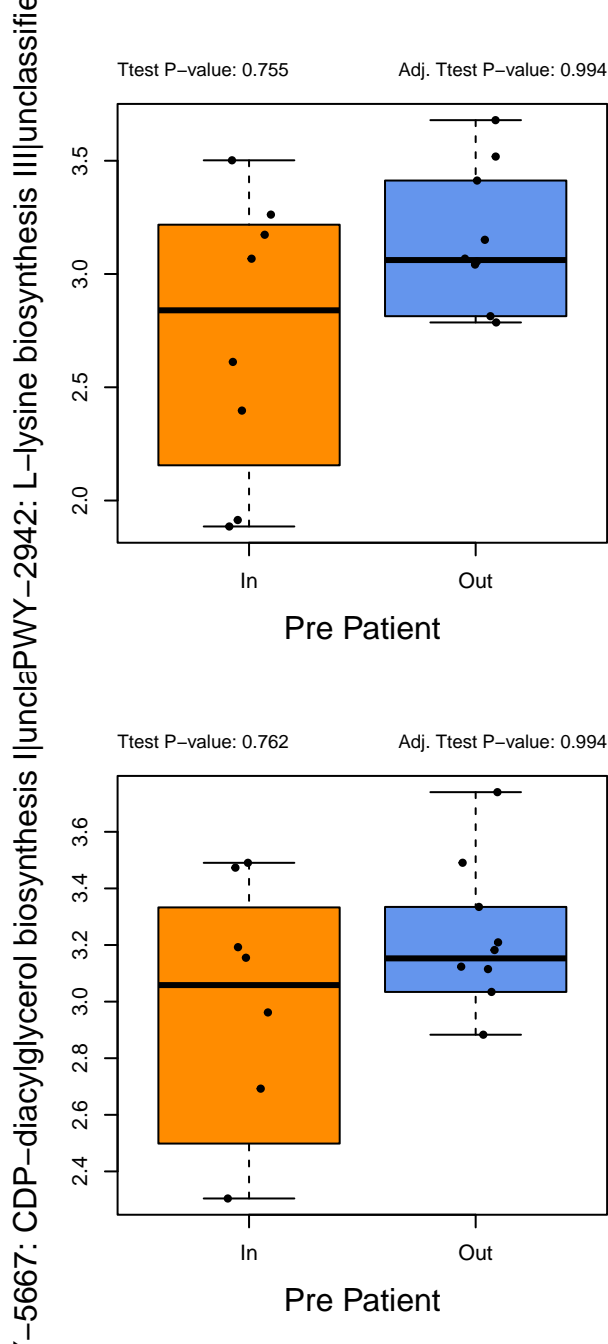
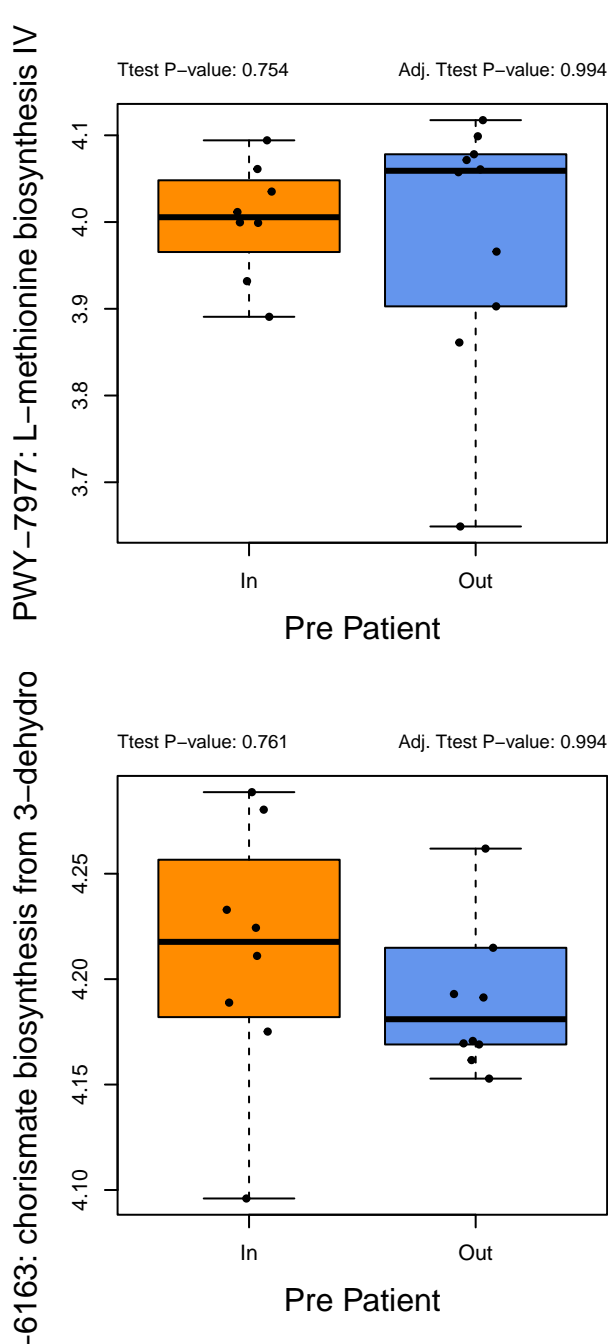
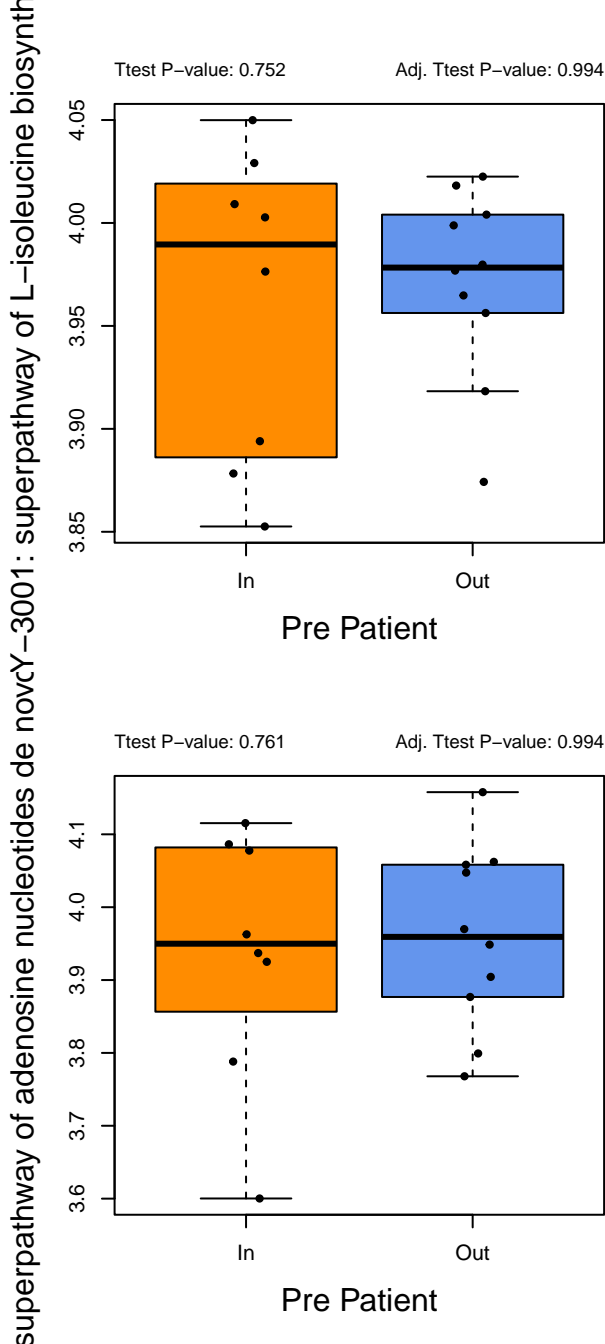


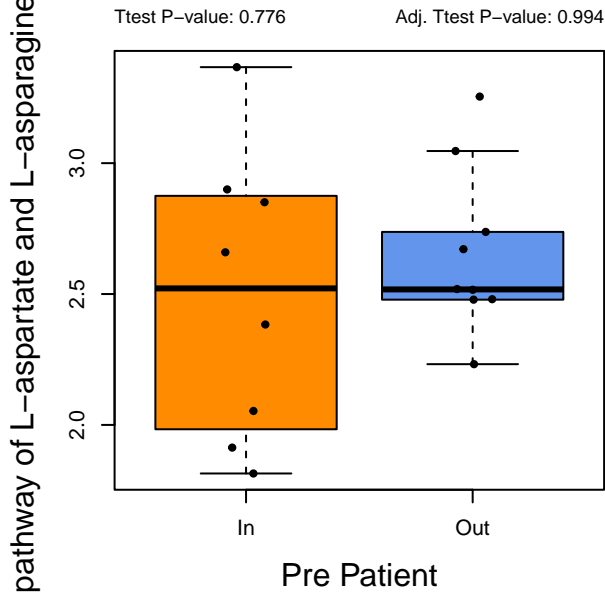
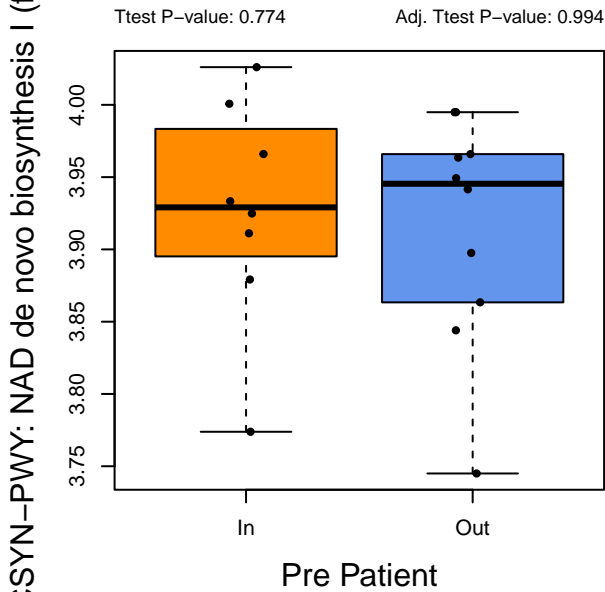
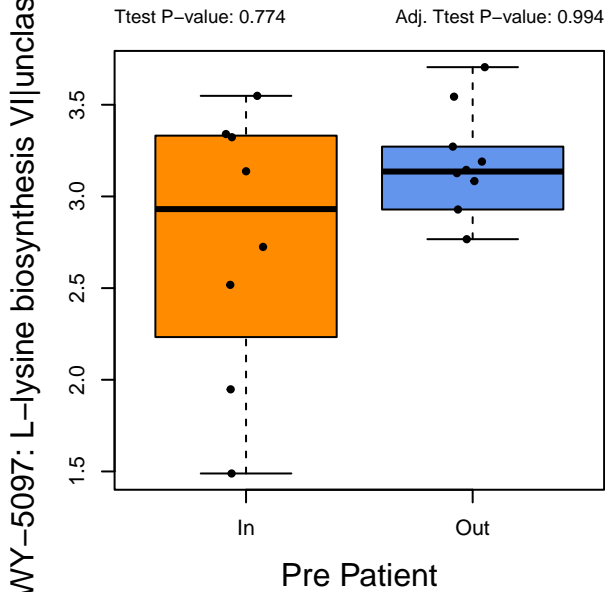
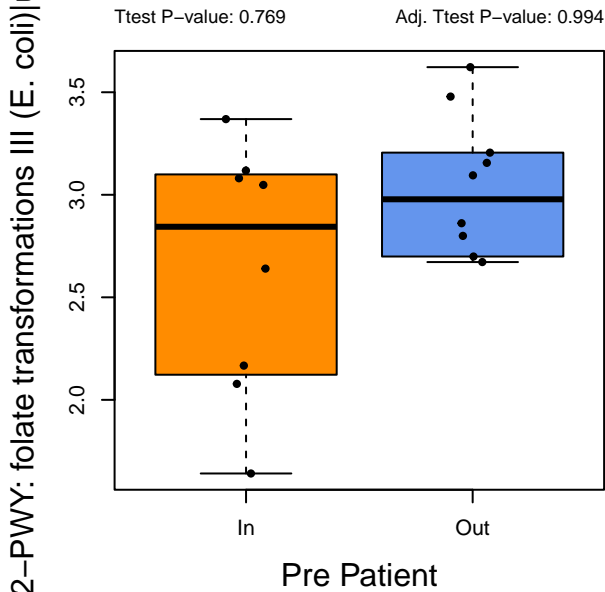
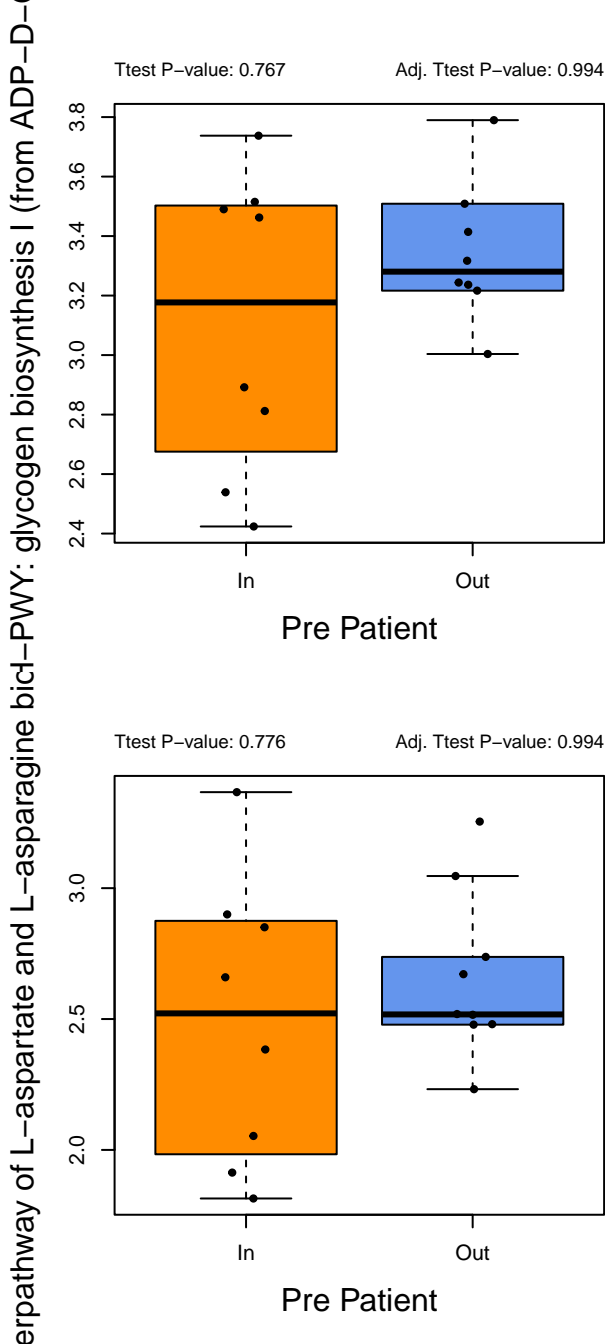
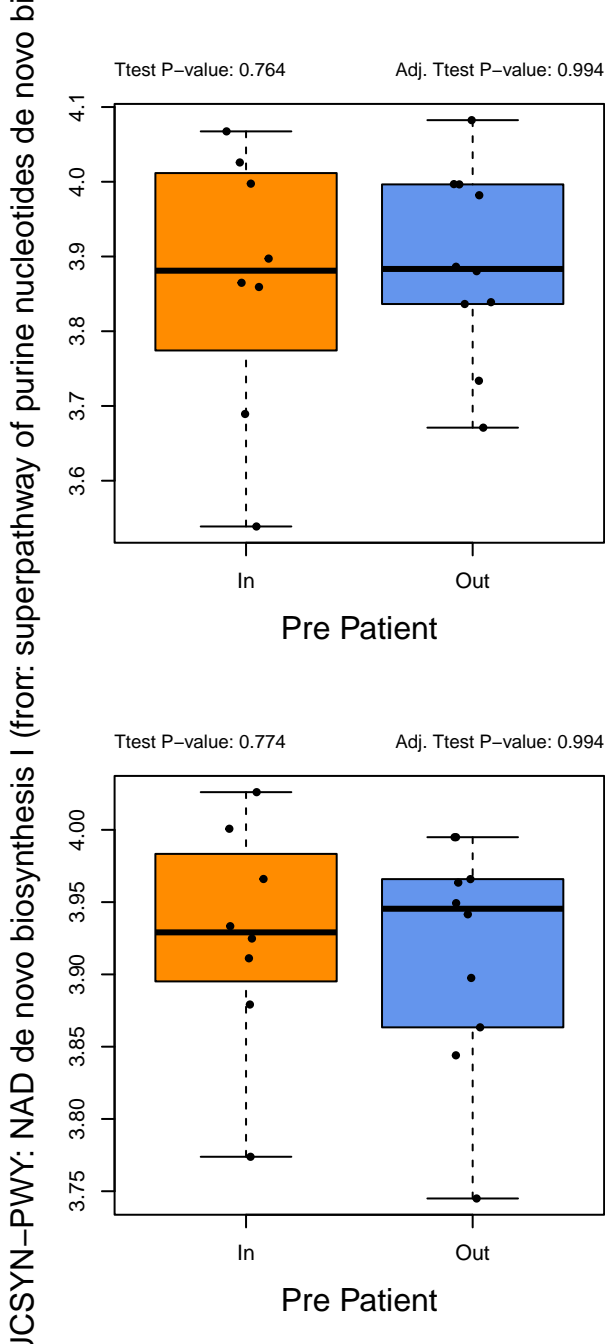
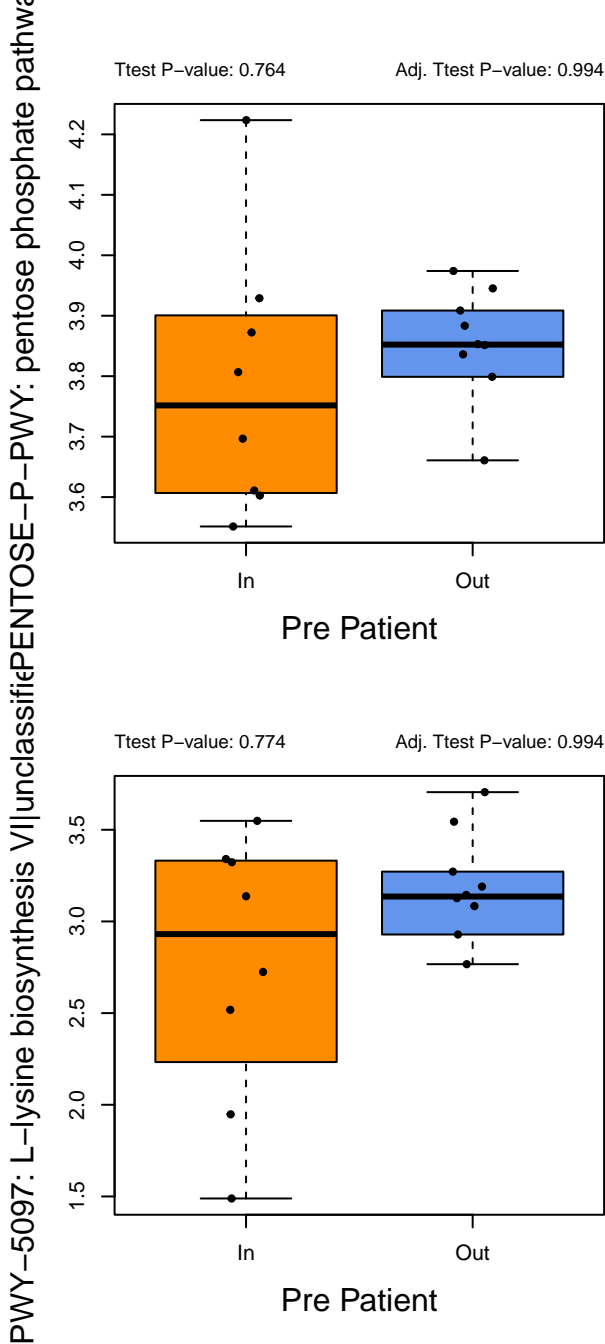
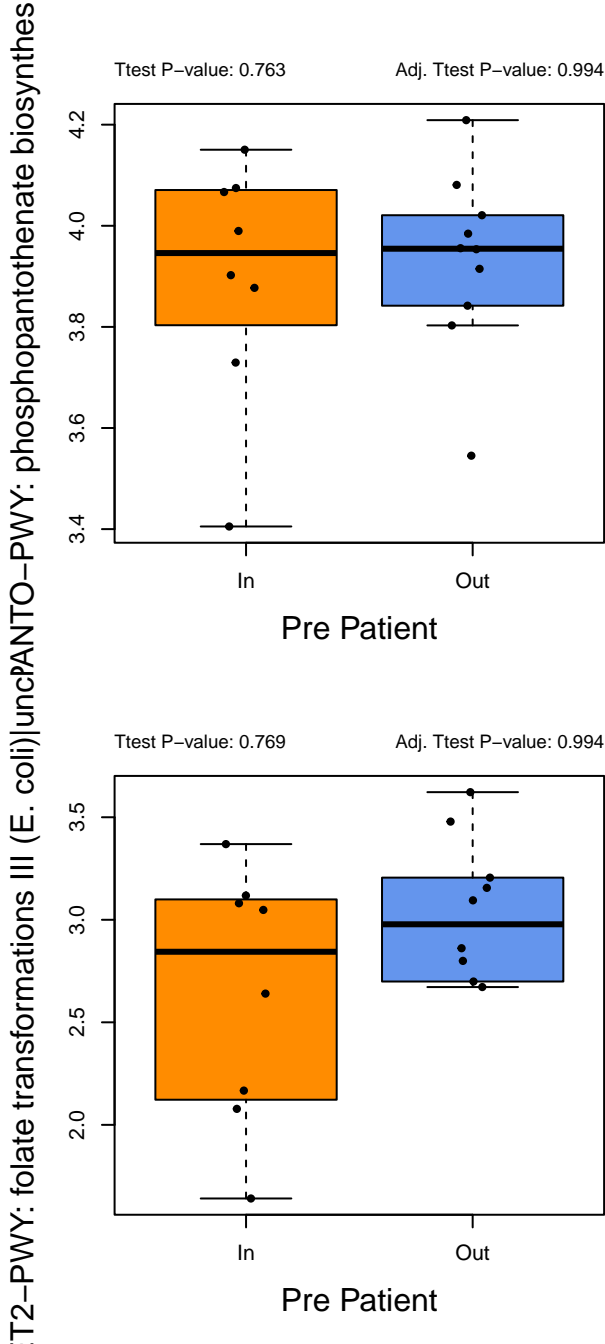
ARO-PWY: superpathway of aromatic amino achway of UDP-glucose-derived O-antigen build

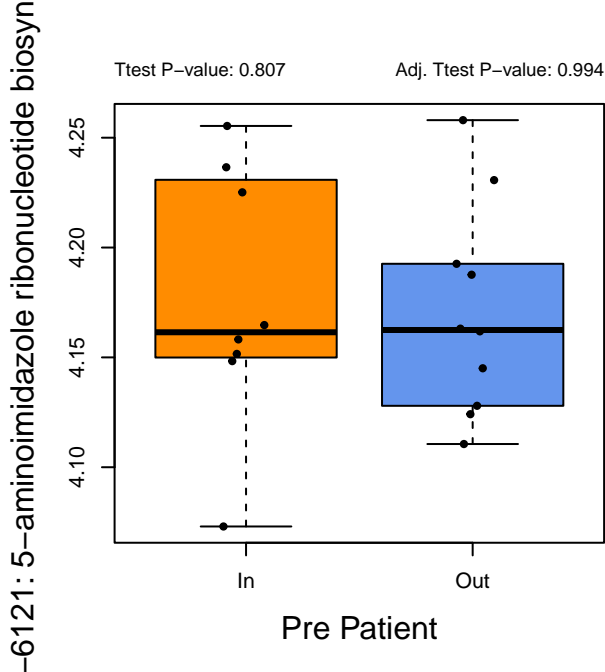
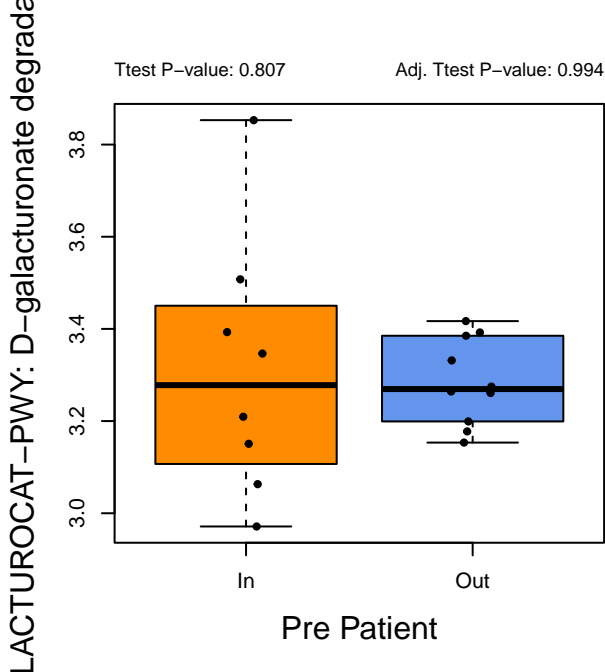
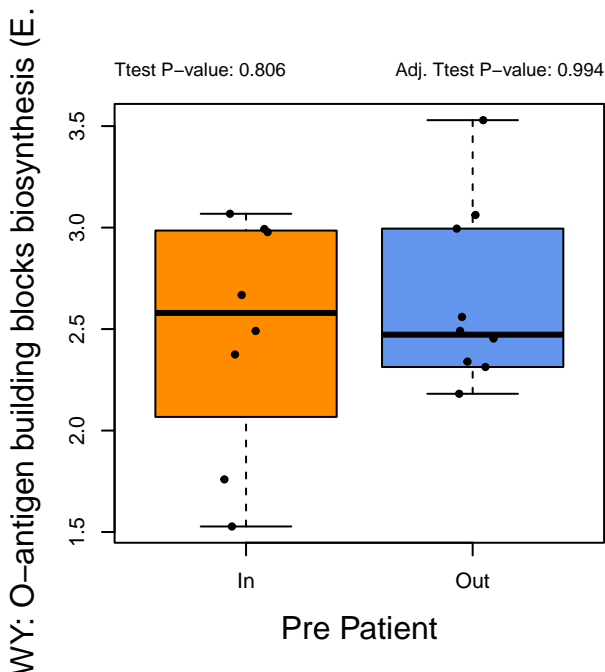
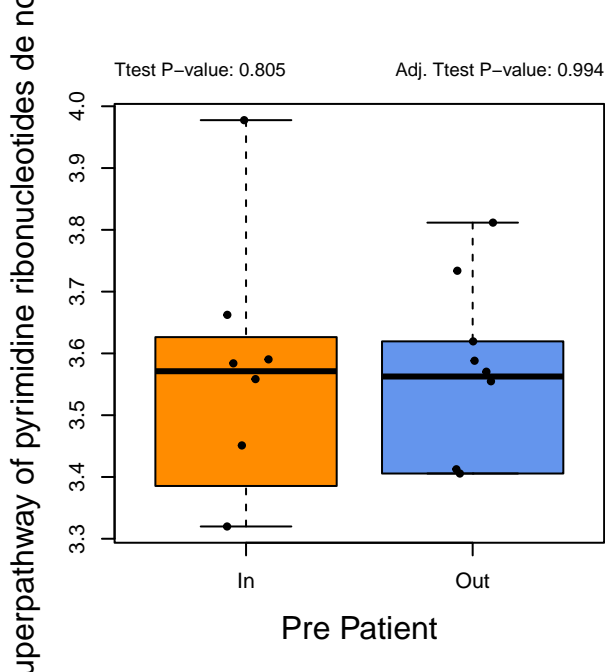
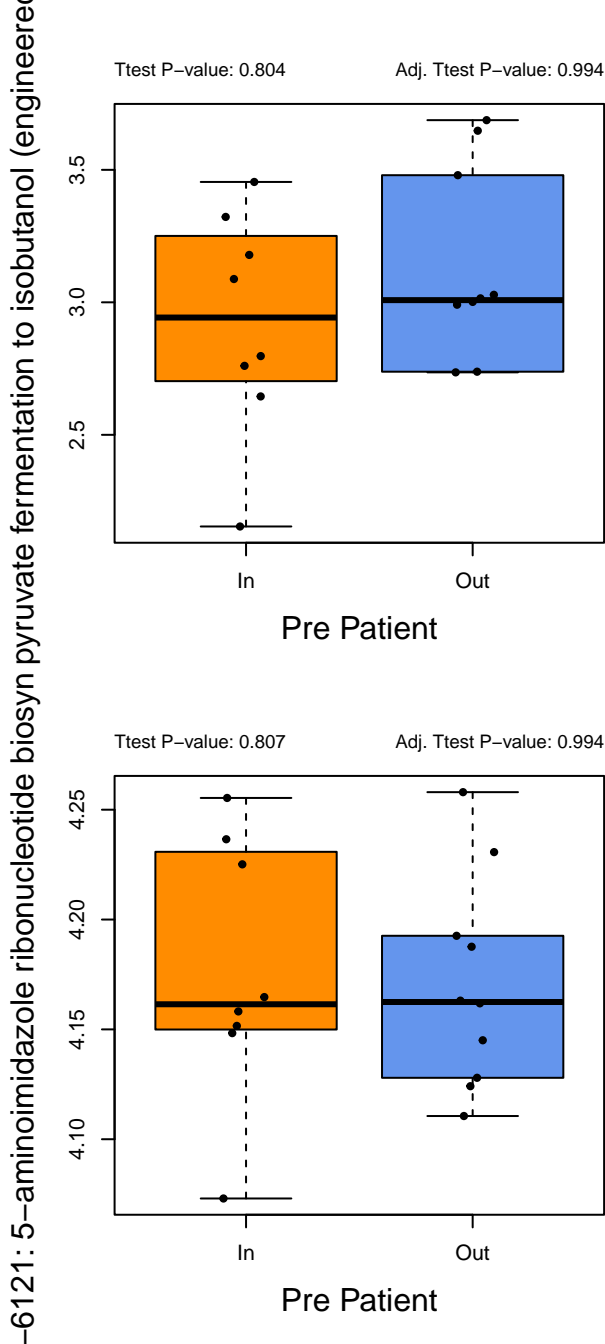
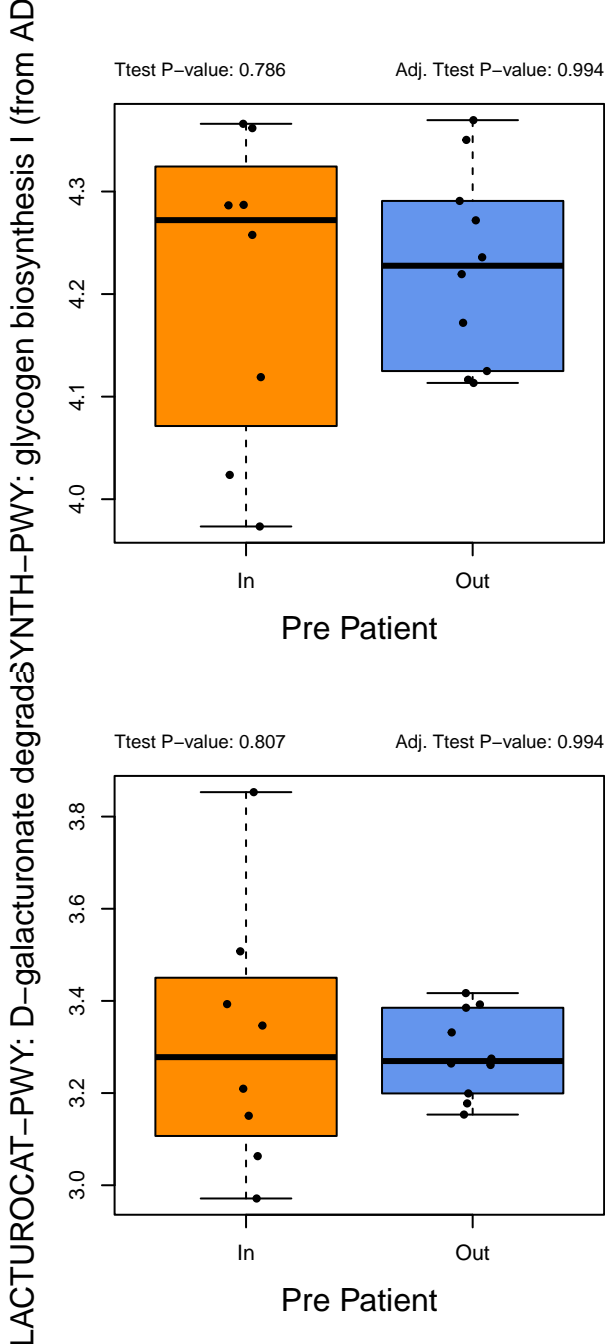
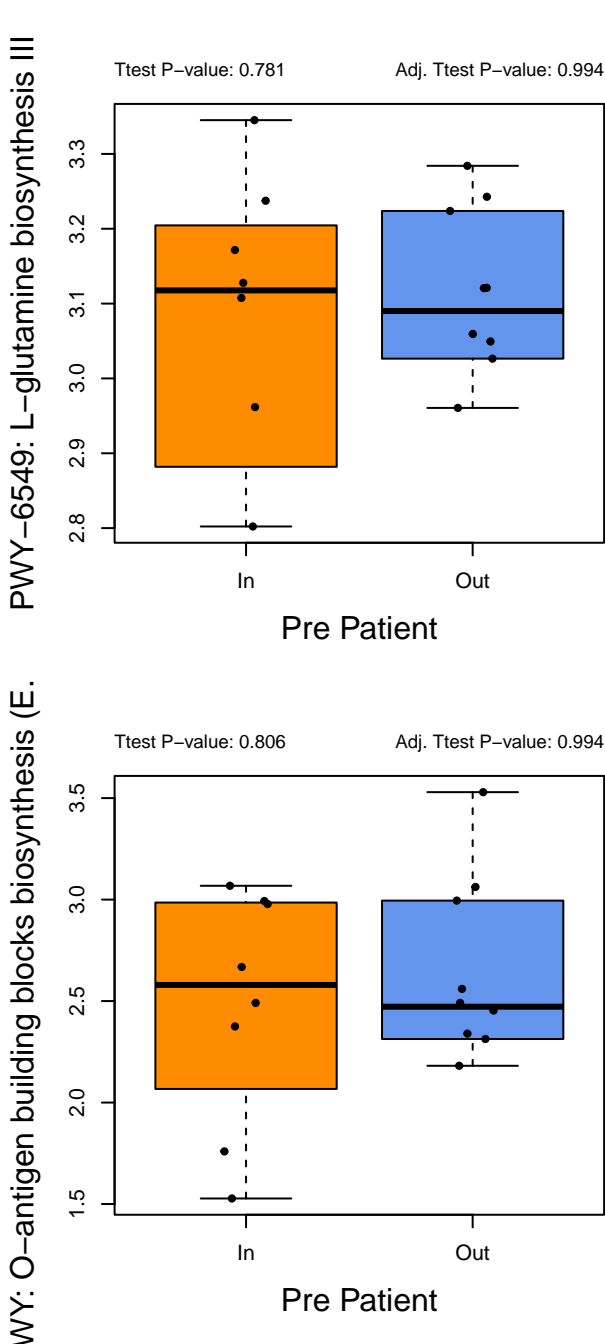
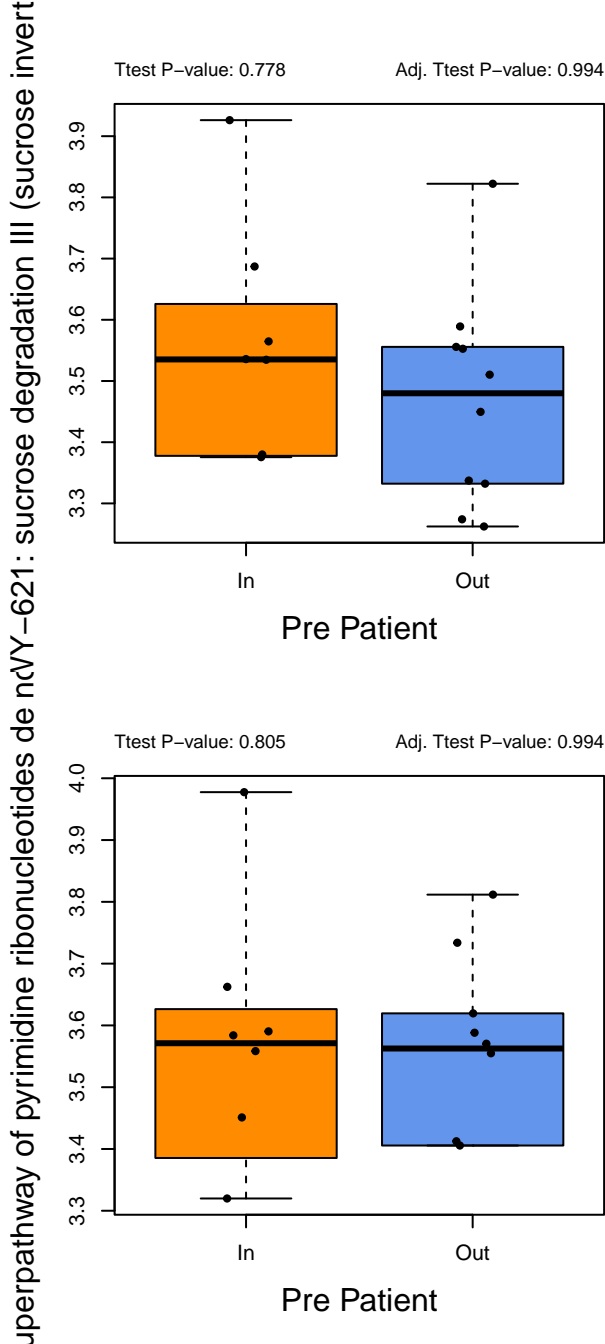


92: superpathway of L-cysteine biosynthesis (rEN-PWY: O-antigen building blocks biosynthes

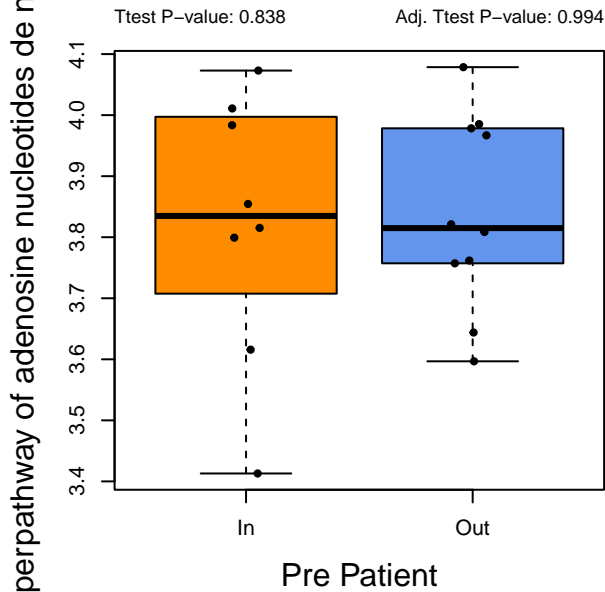
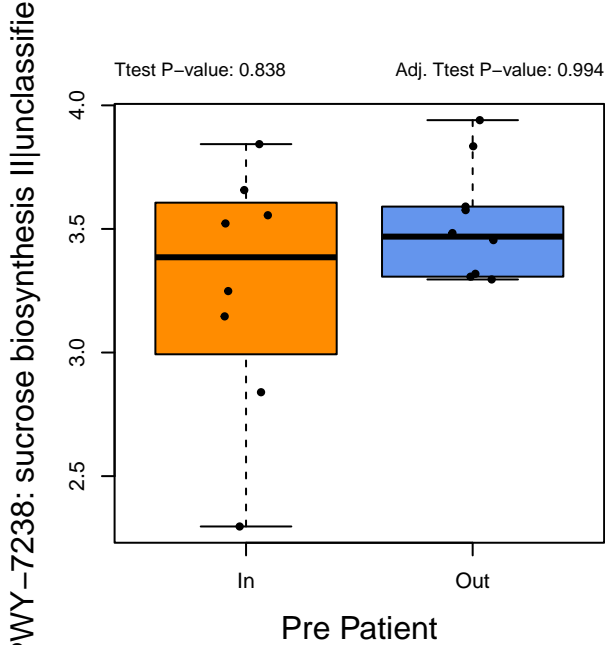
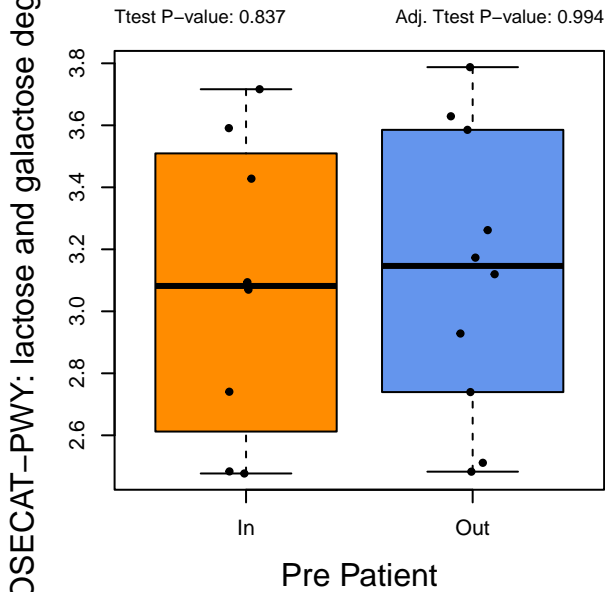
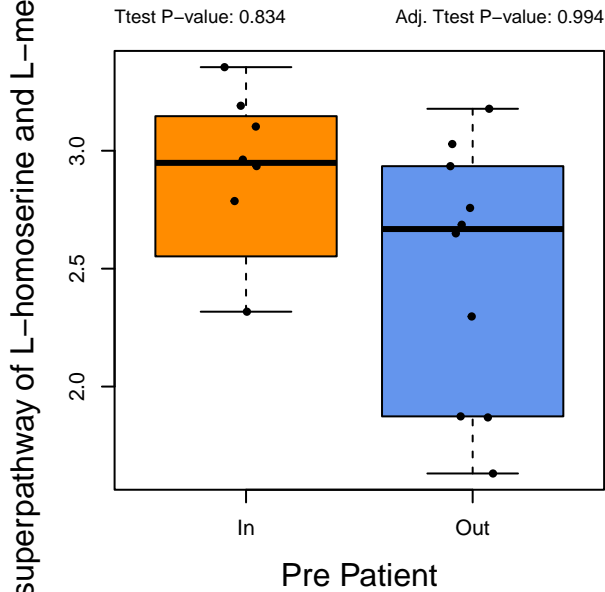
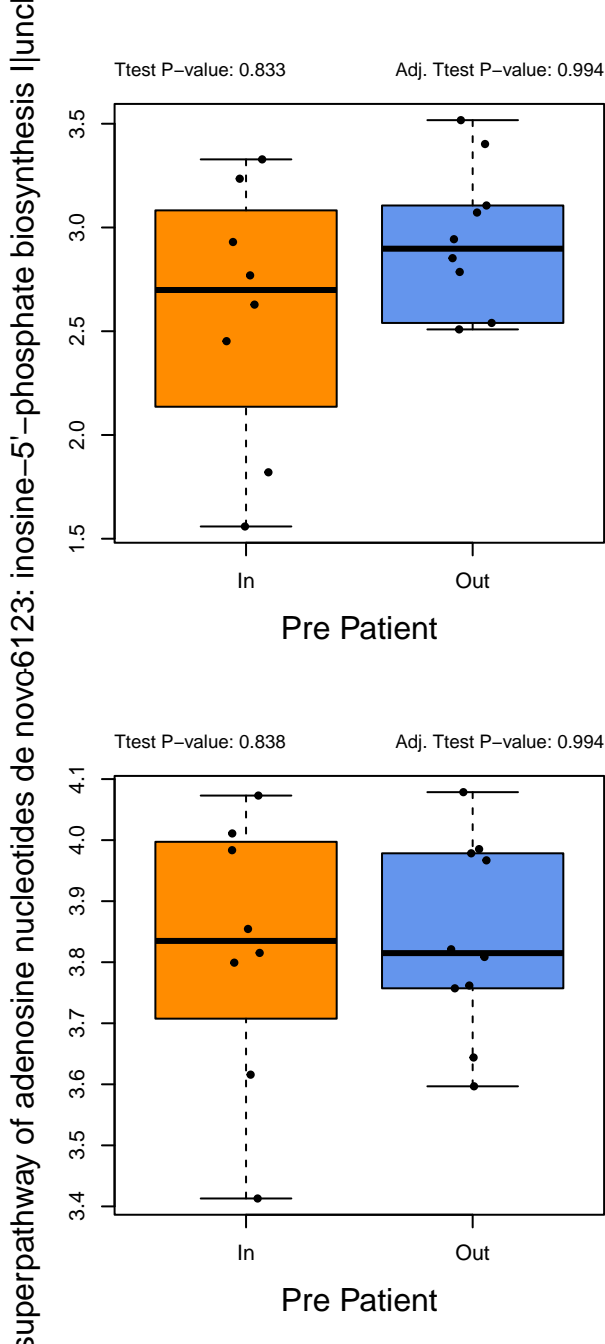
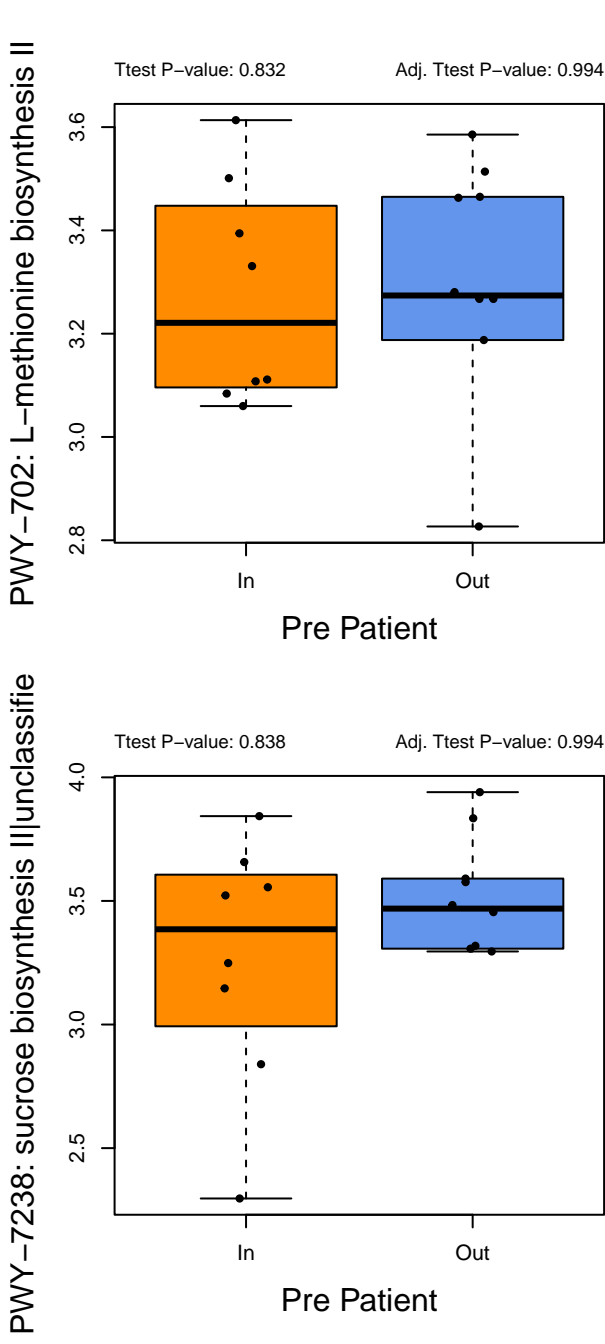
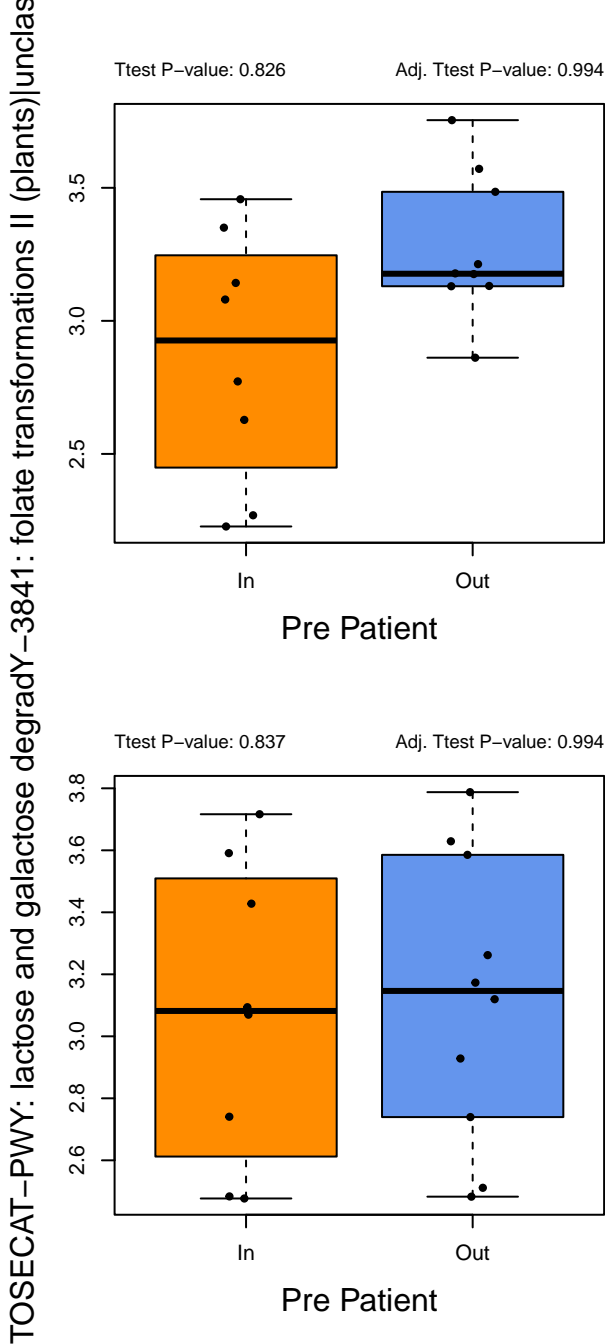
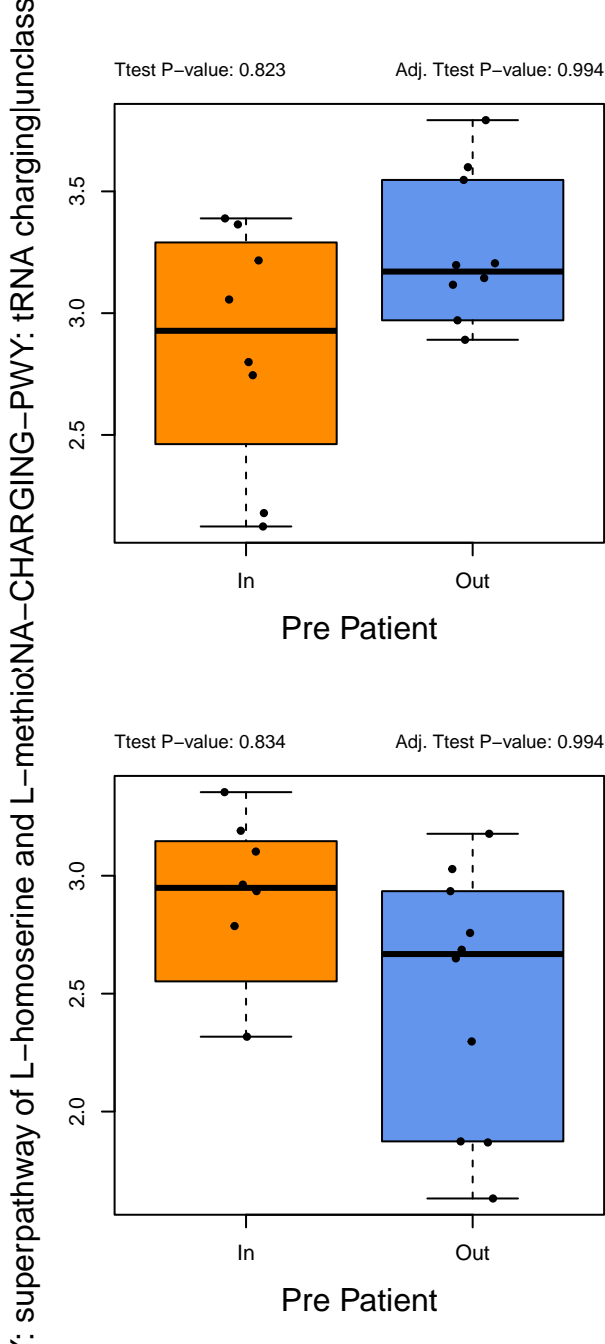




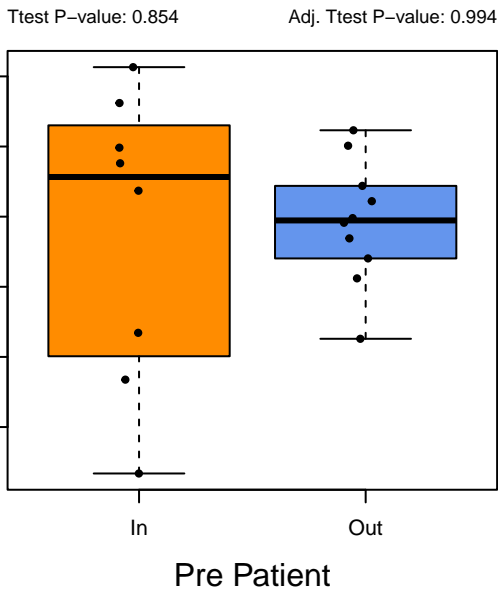




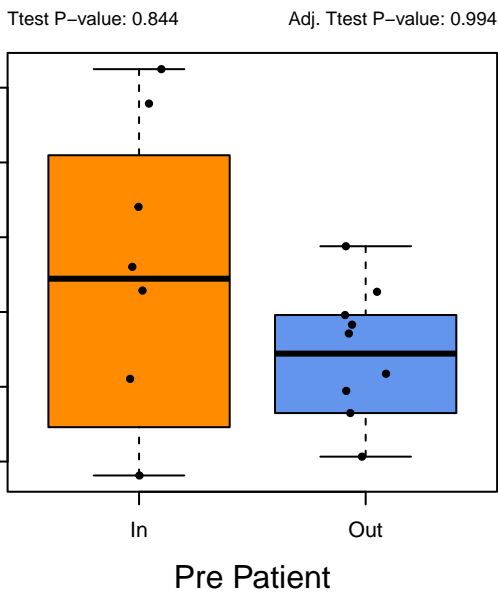




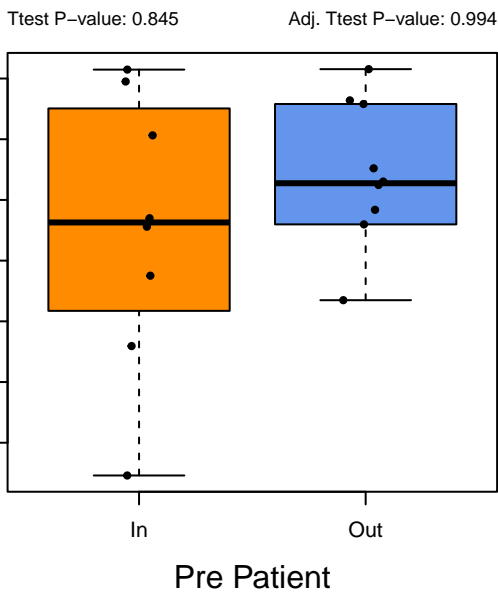
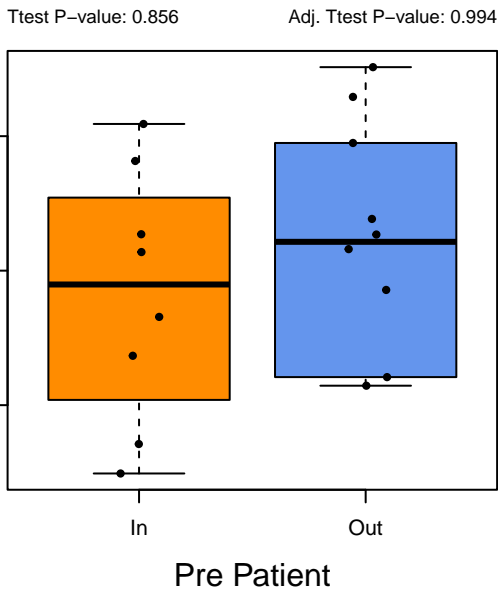
PWY-7238: sucrose biosynthesis II



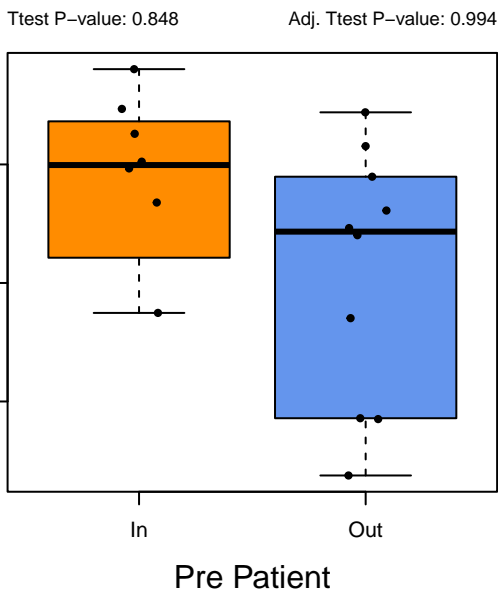
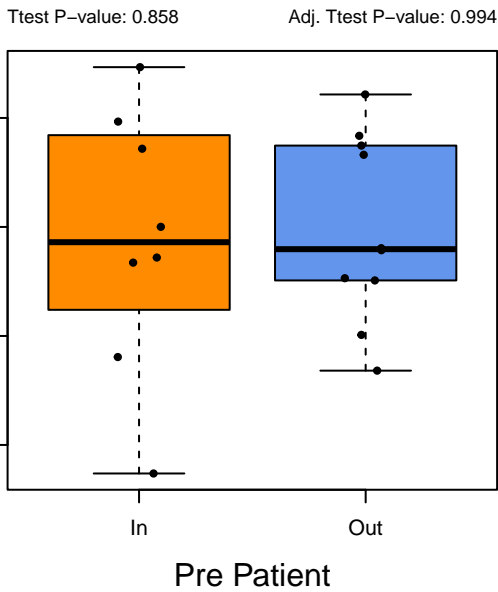
PWY-4041: &gamma;-glutamyl cycle



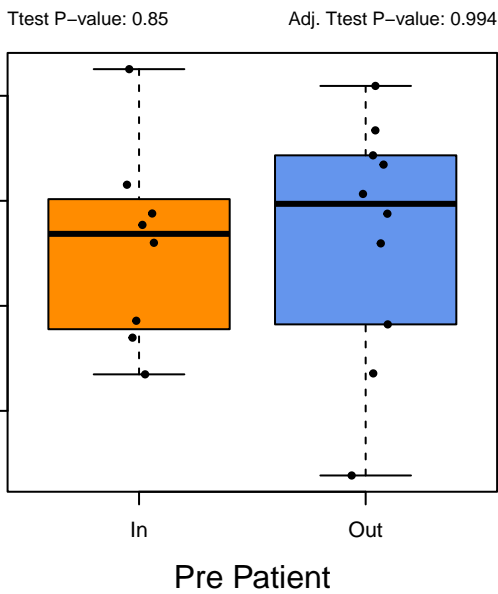
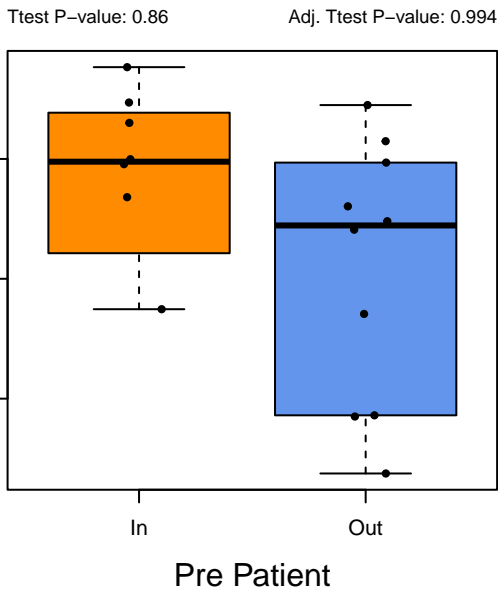
N-PWY: superpathway of branched chain amin<sup>3</sup>WY: superpathway of N-acetylneuraminate de



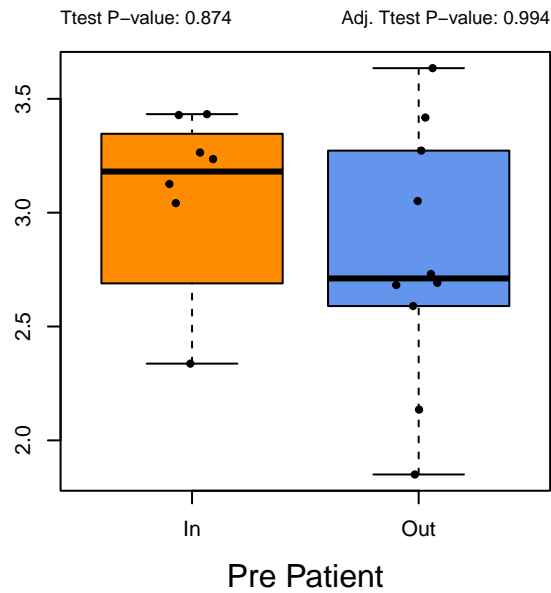
superpathway of guanosine nucleotides de nov<sup>3</sup>WY: superpathway of S-adenosyl-L-methionin



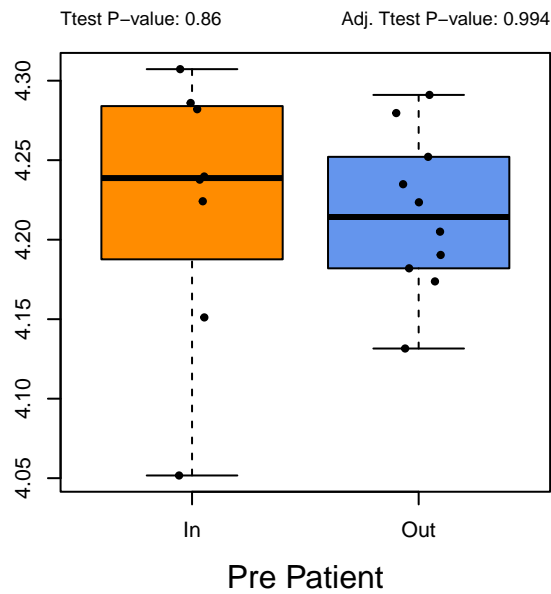
superpathway of L-methionine biosynthesis (tr<sup>3</sup>WY-7199: pyrimidine deoxyribonucleosides salv



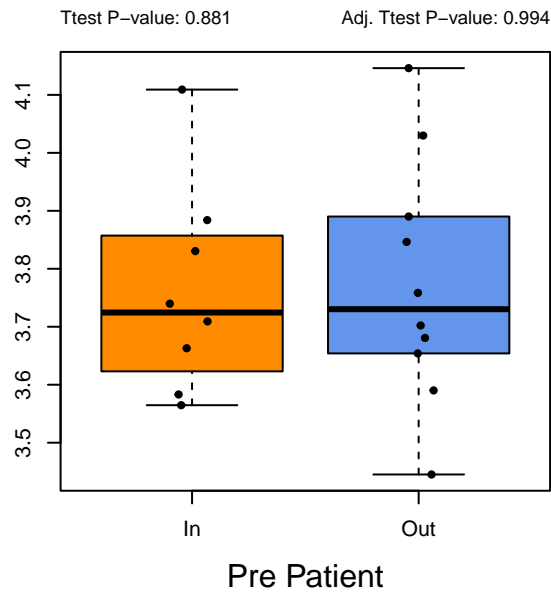
DAPLYSINESYN-PWY: L-lysine biosynthesis



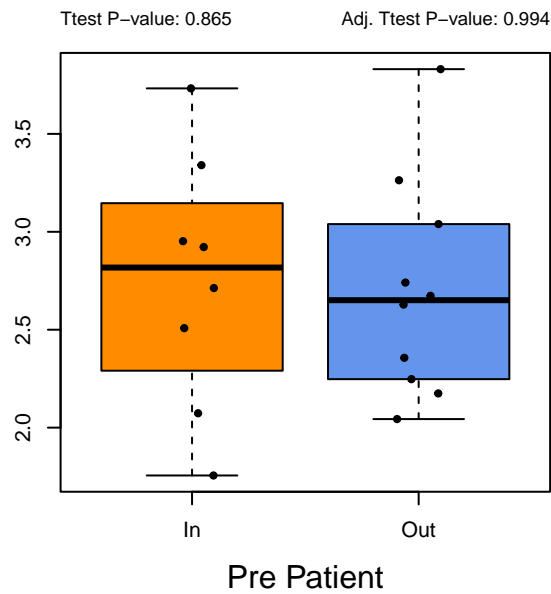
VALSYN-PWY: L-valine biosynthesis



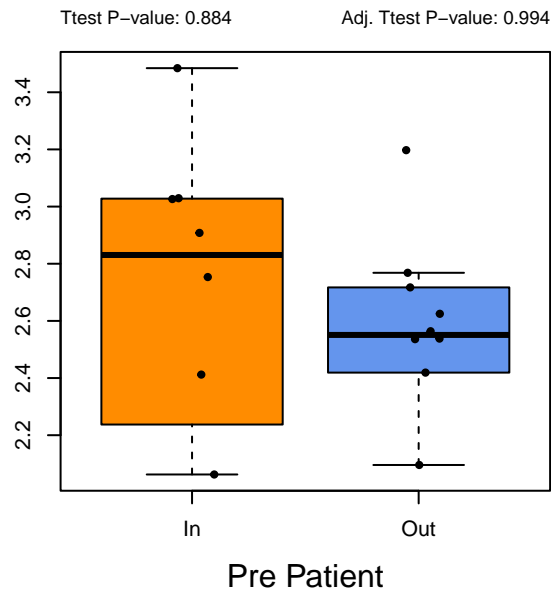
SYN-PWY: UDP-N-acetyl-D-glucosamine bic



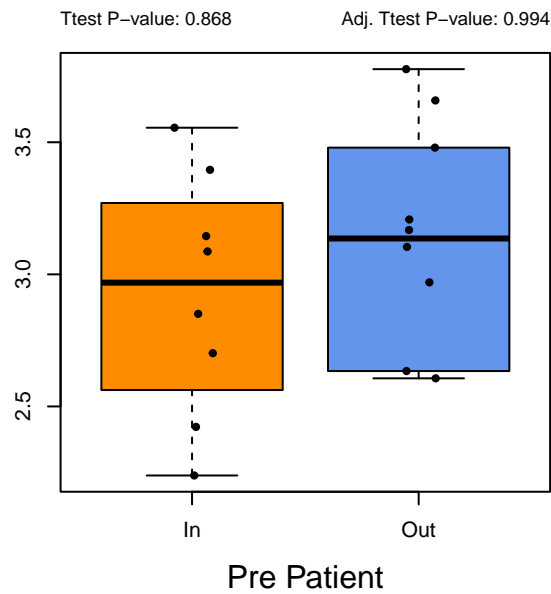
RUMP-PWY: formaldehyde oxidation I



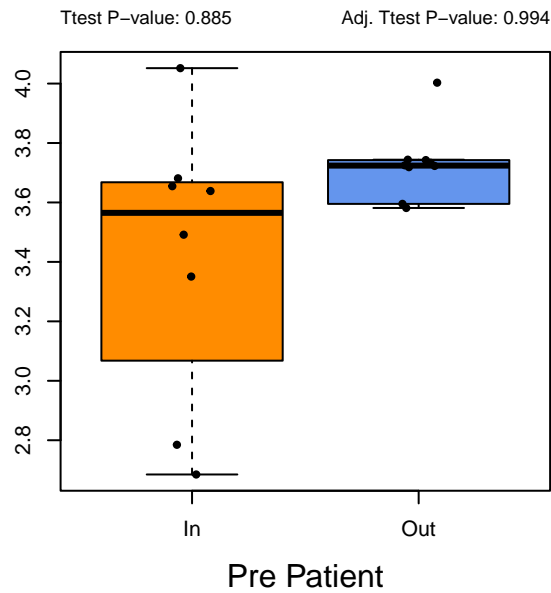
doglycan maturation (meso-diaminopimelate co'WY: L-isoleucine biosynthesis I (from threonine



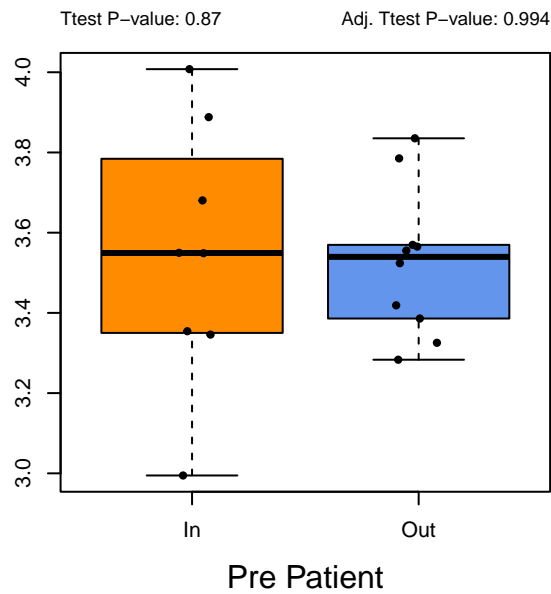
doglycan maturation (meso-diaminopimelate co'WY: L-isoleucine biosynthesis I (from threonine

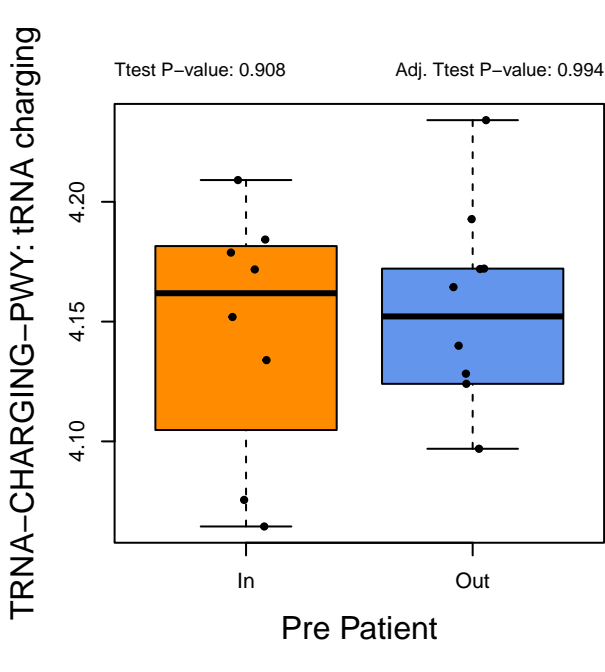
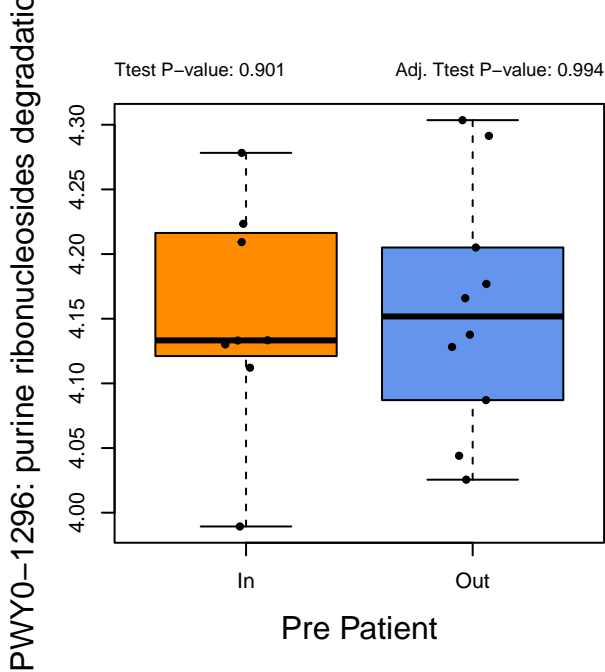
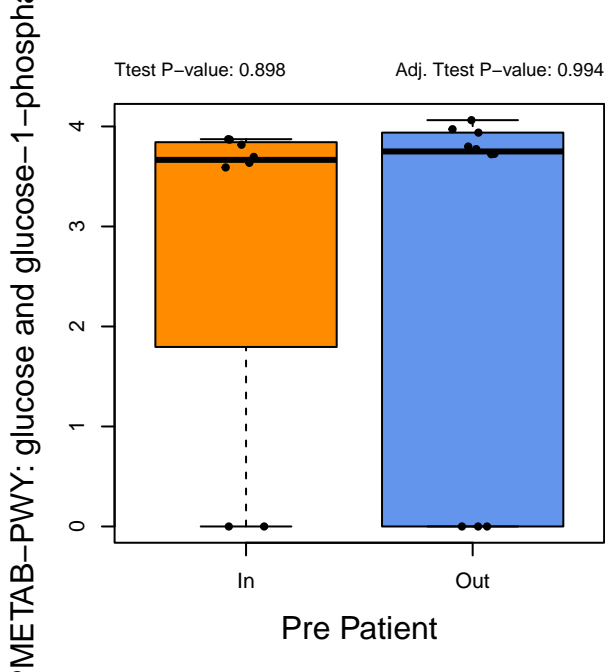
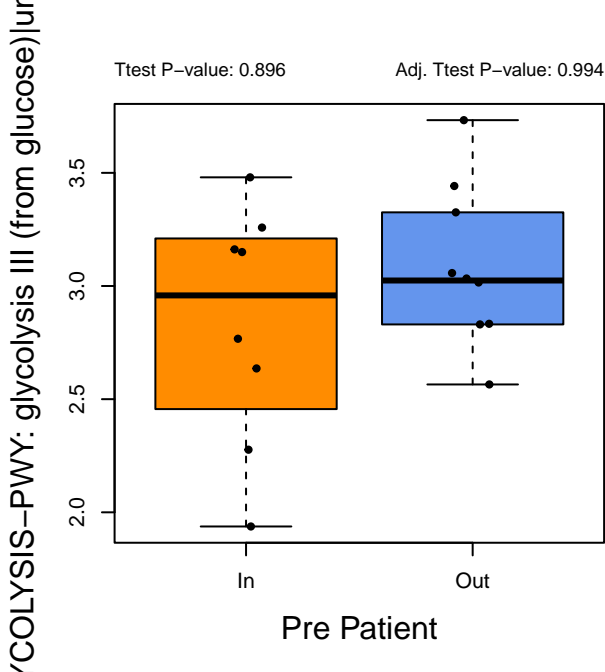
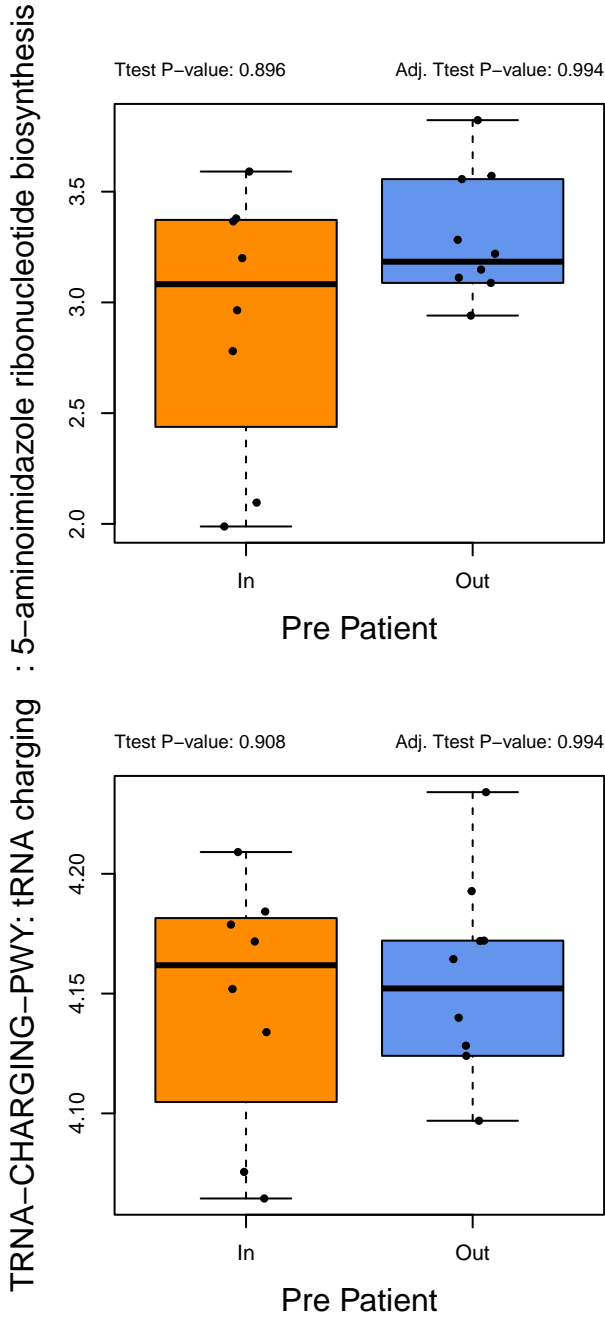
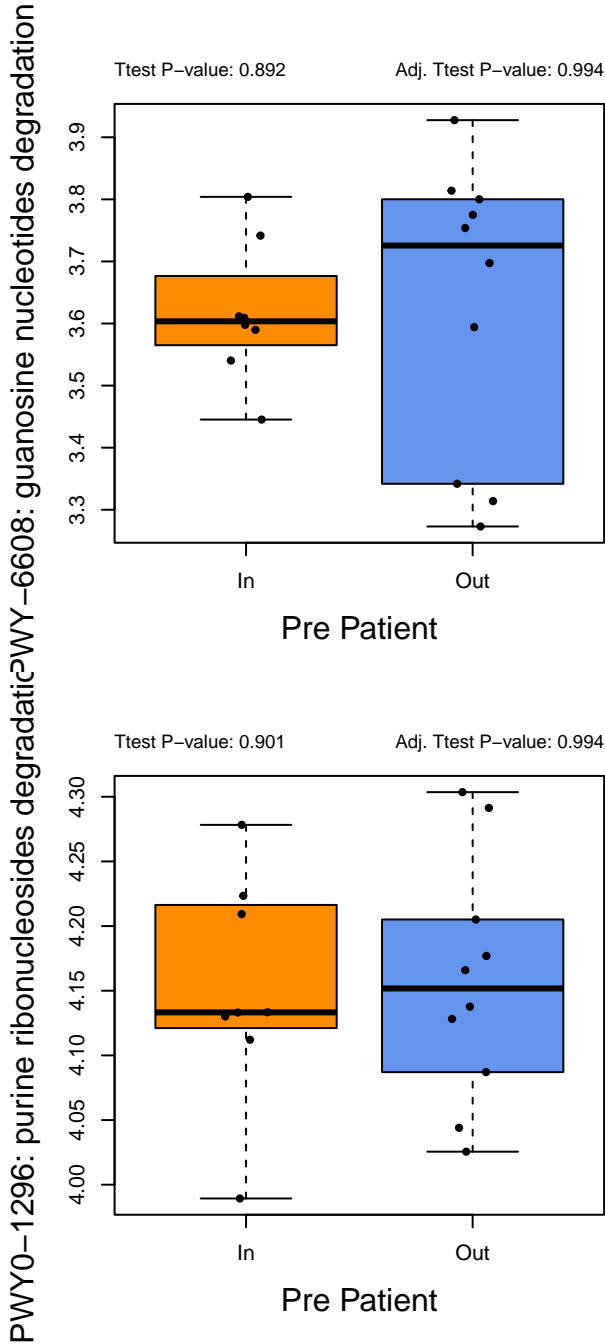
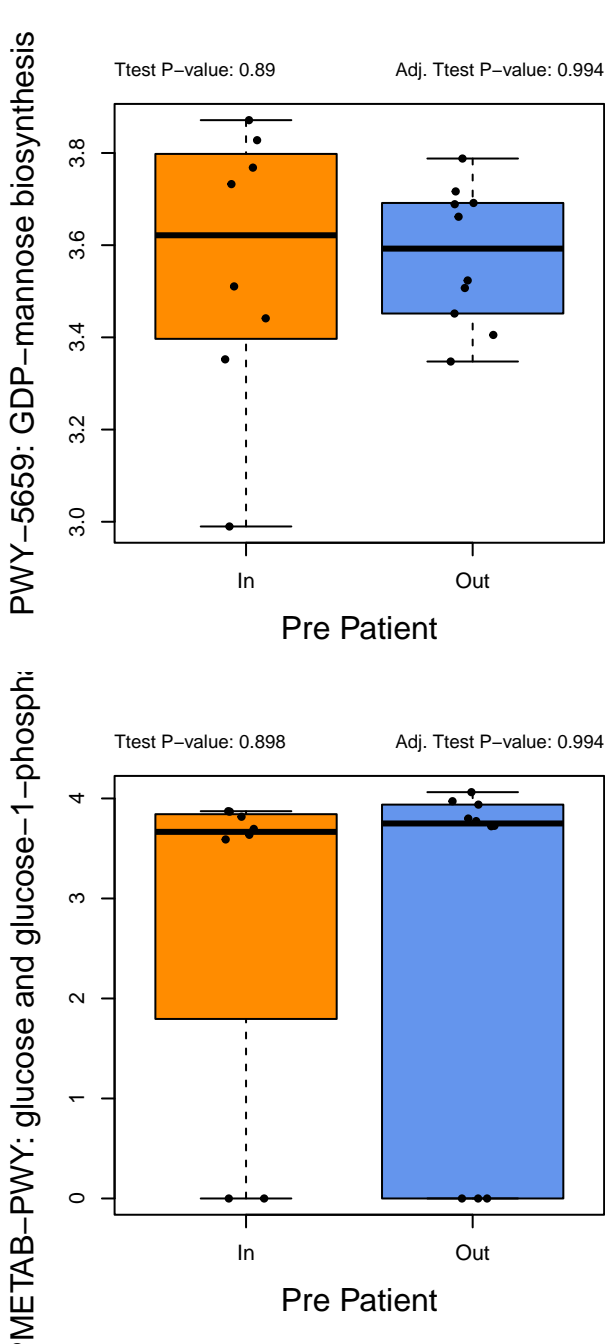
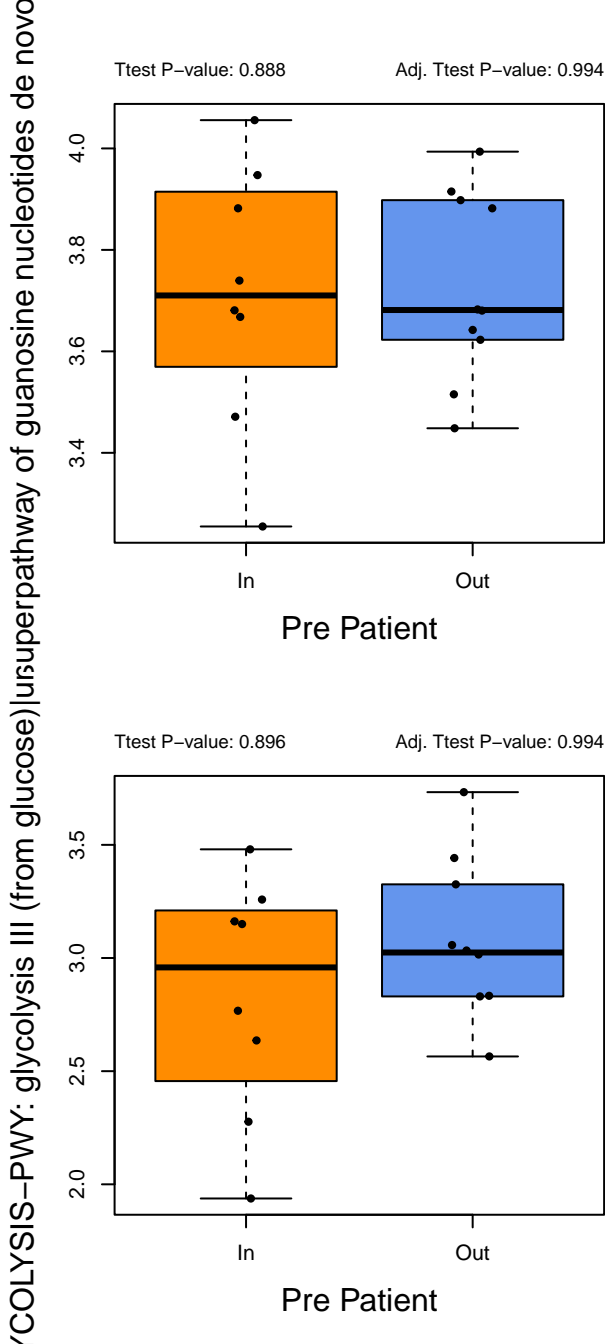


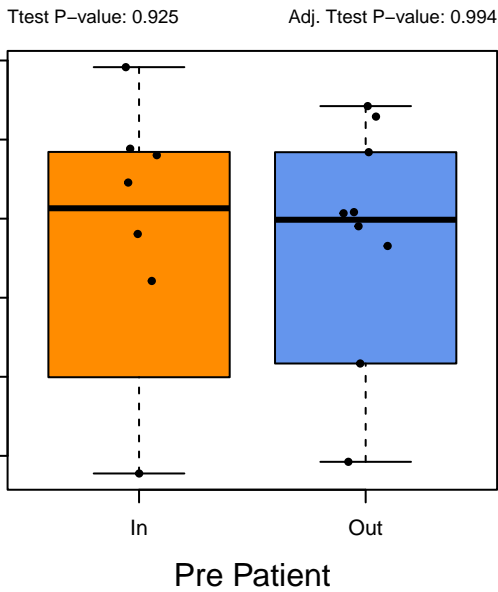
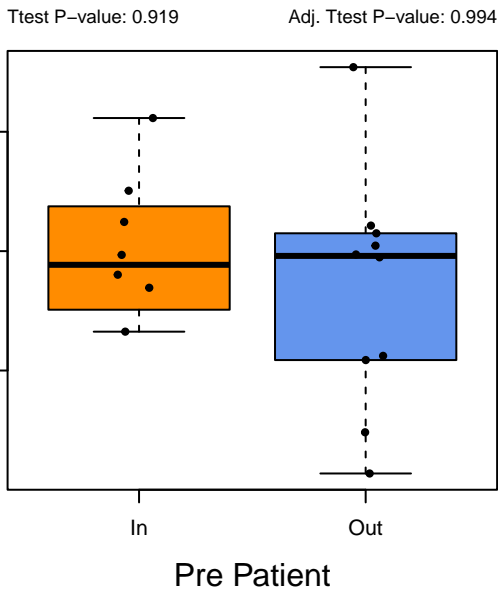
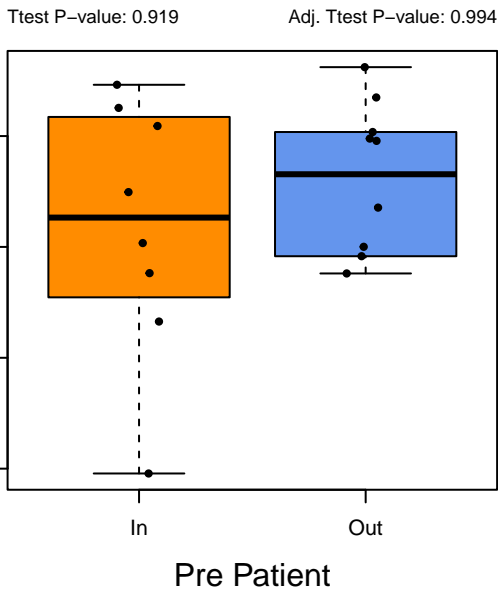
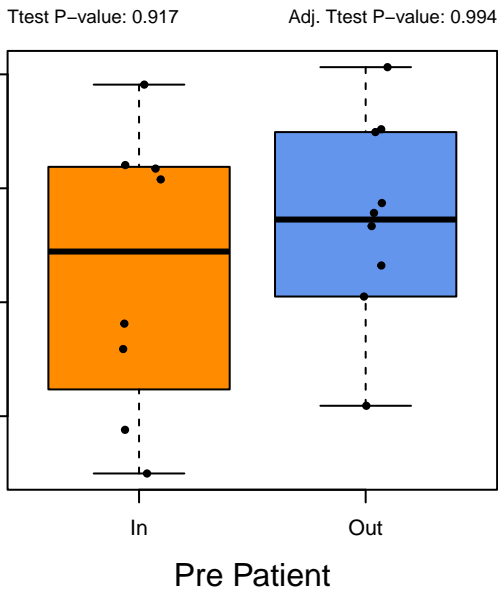
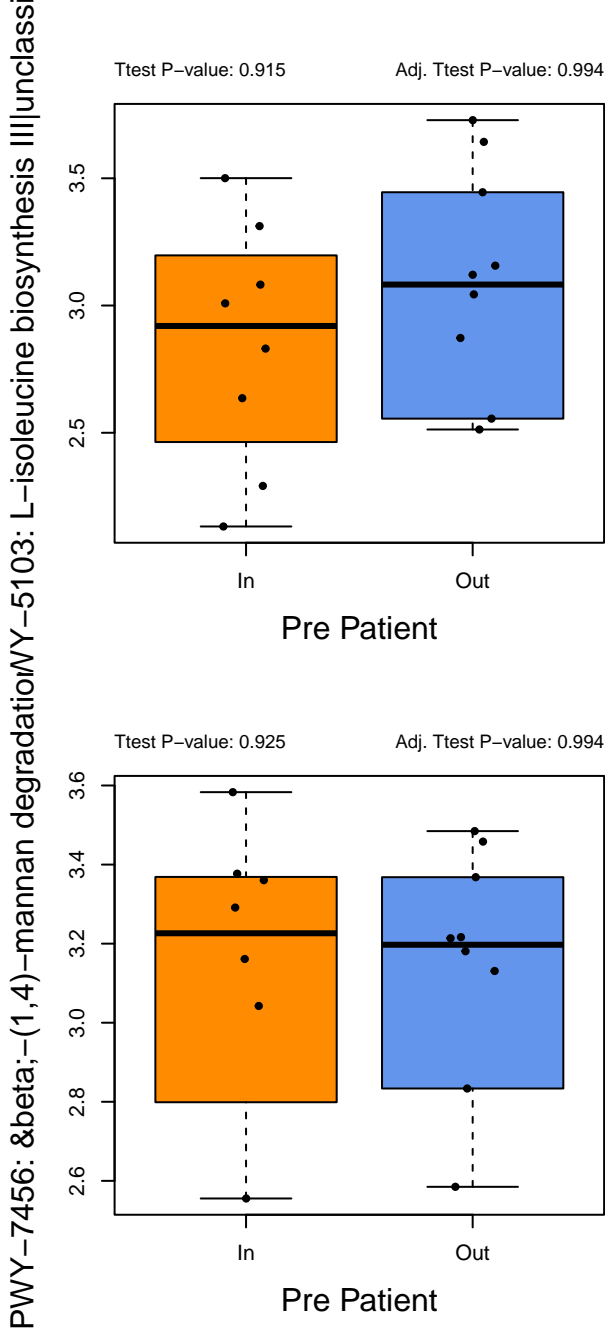
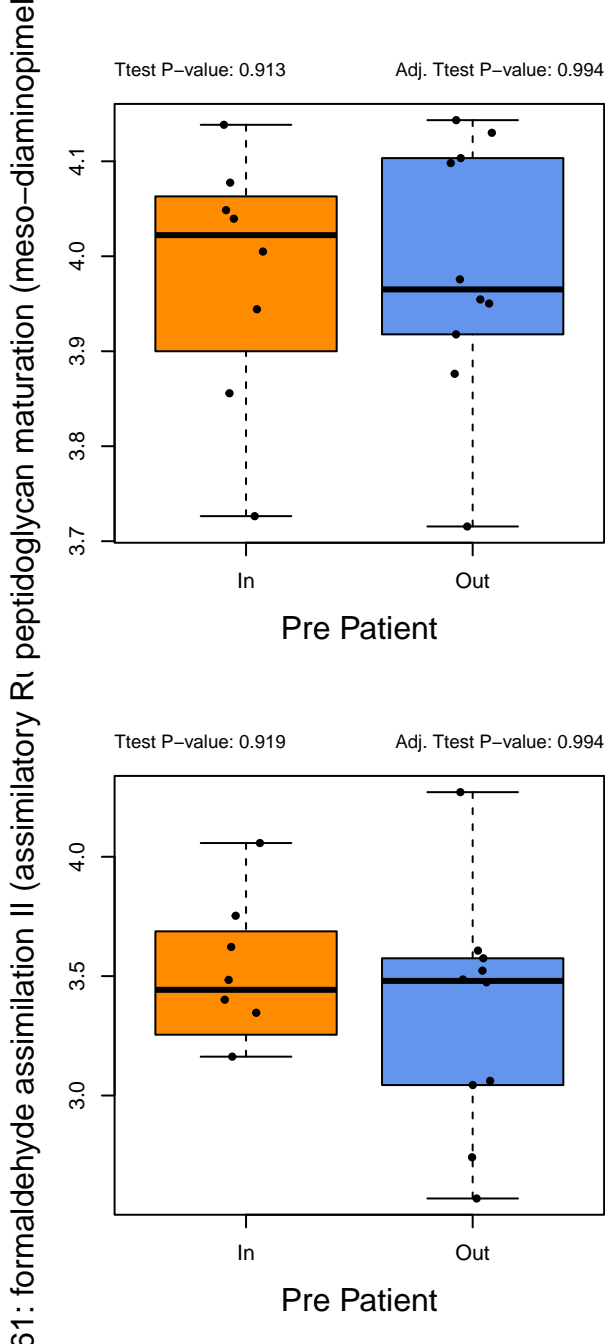
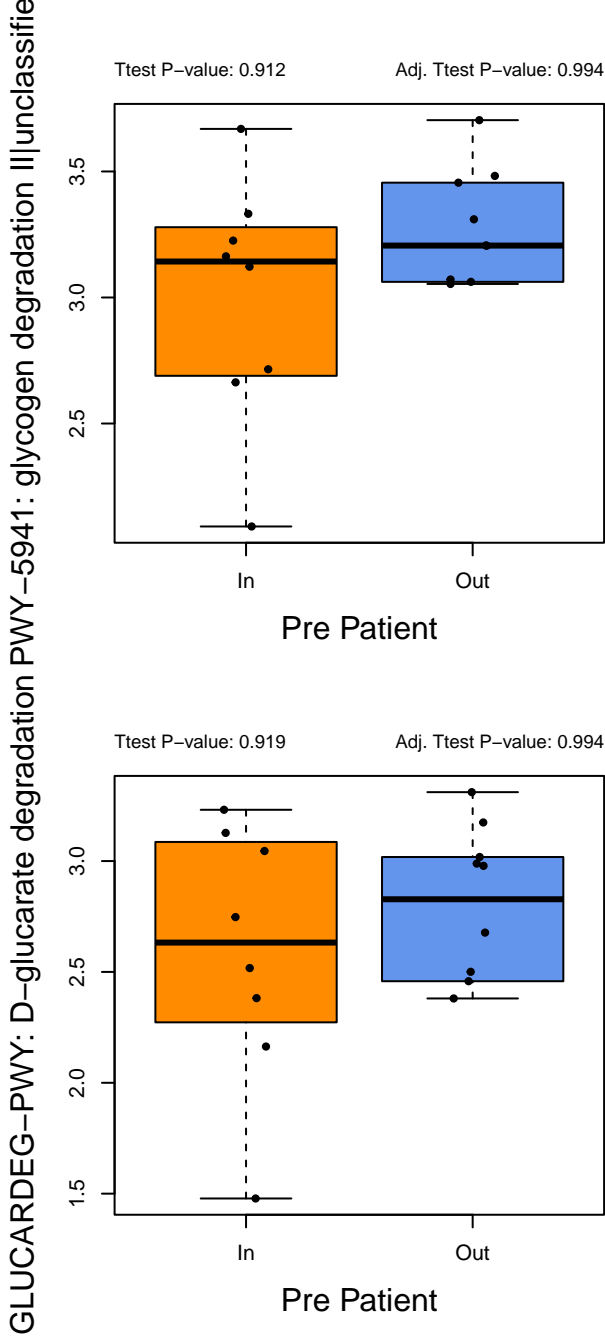
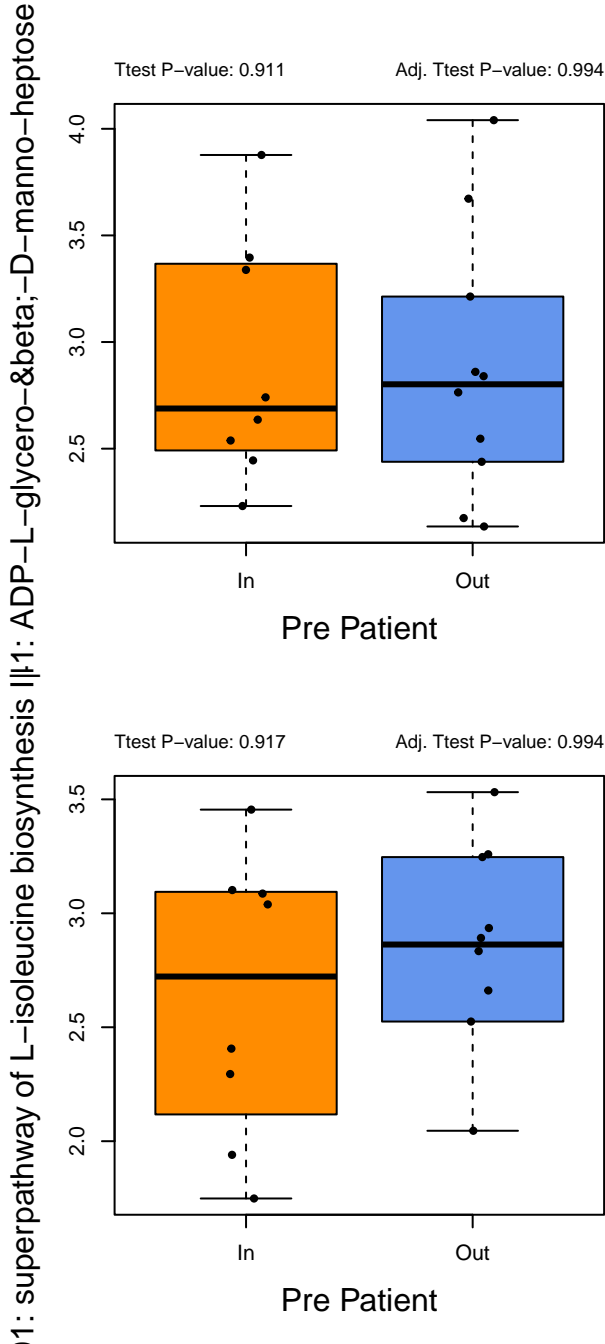
ETH-ACETATE-PWY: methanogenesis from act5384: sucrose degradation IV (sucrose phosph

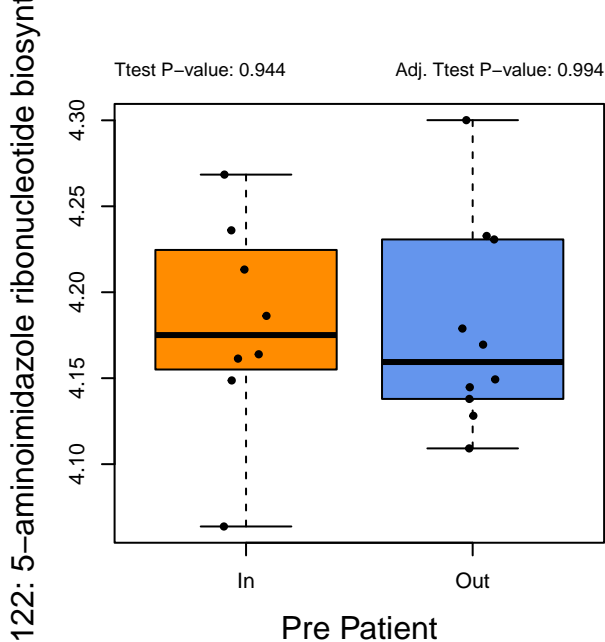
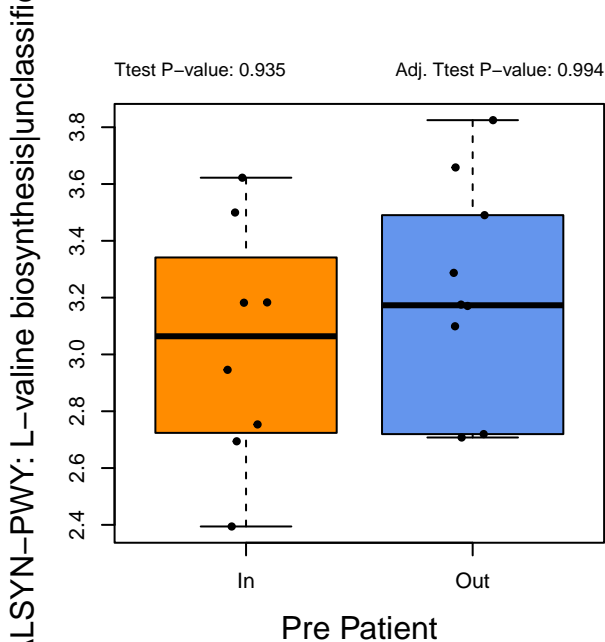
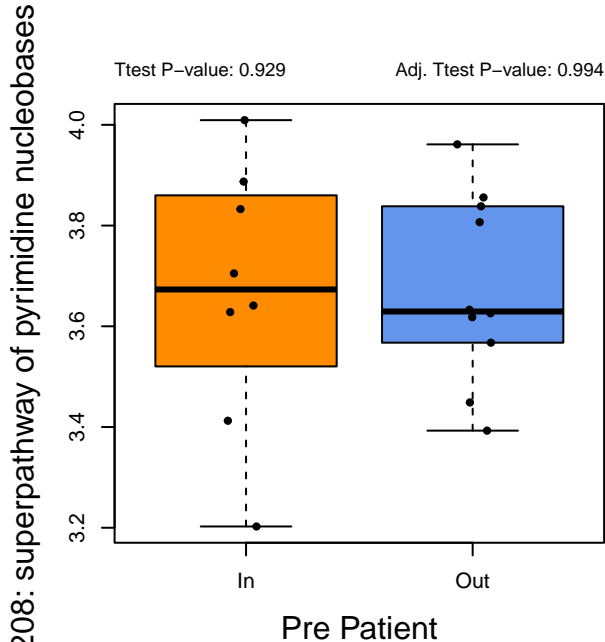
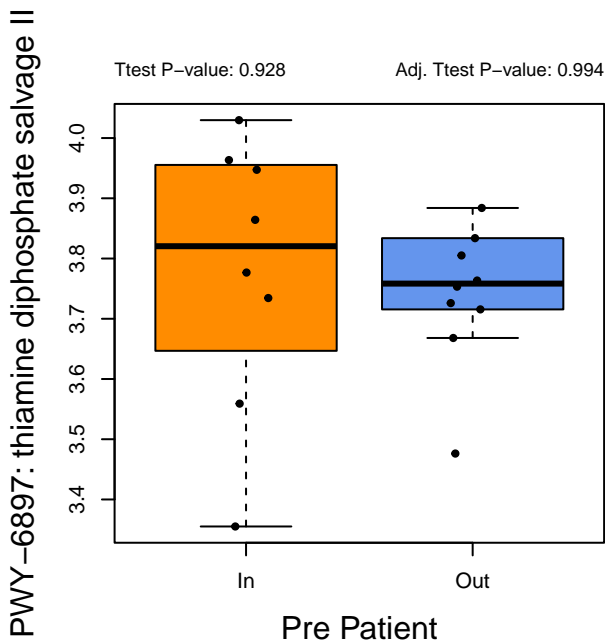
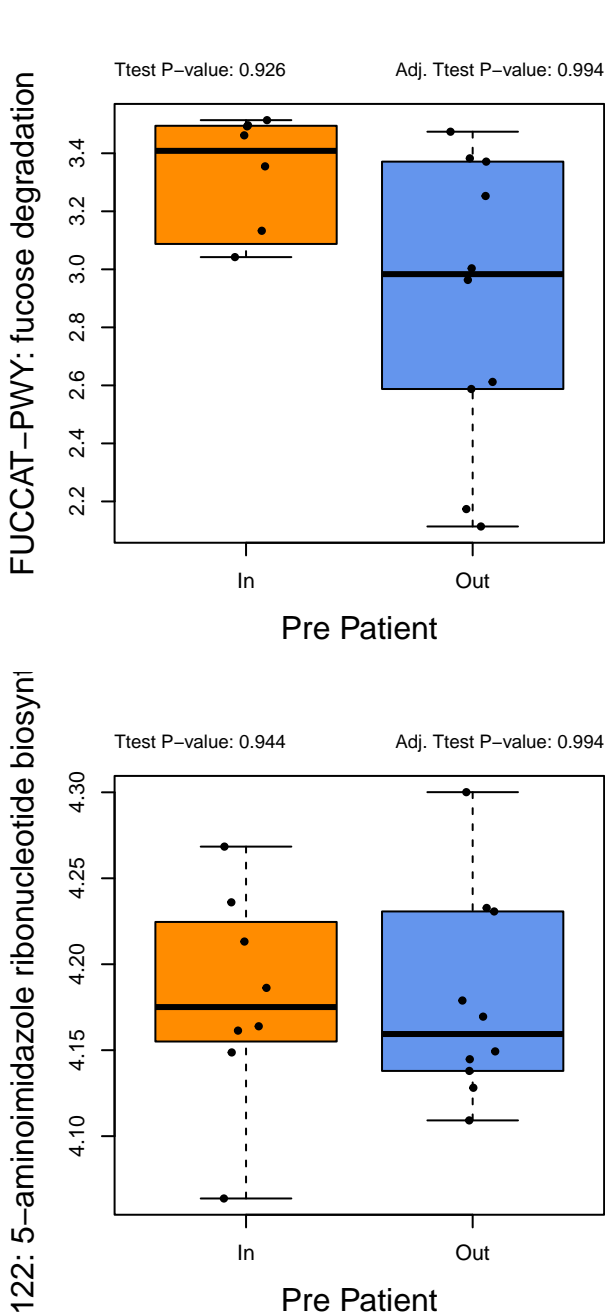
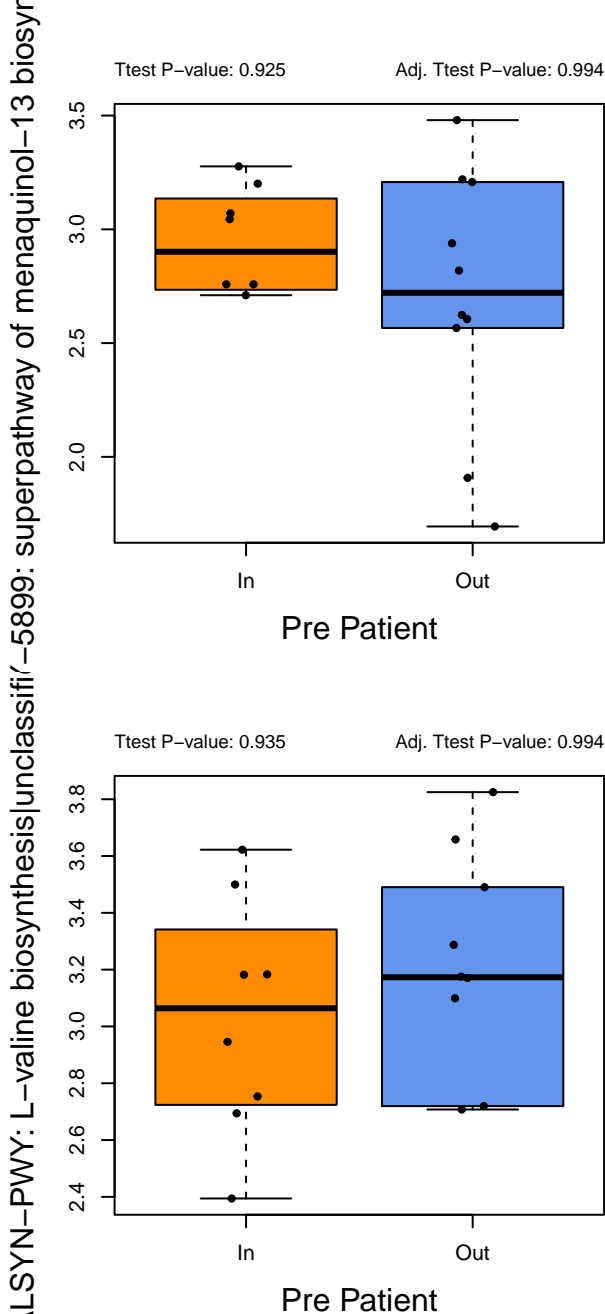
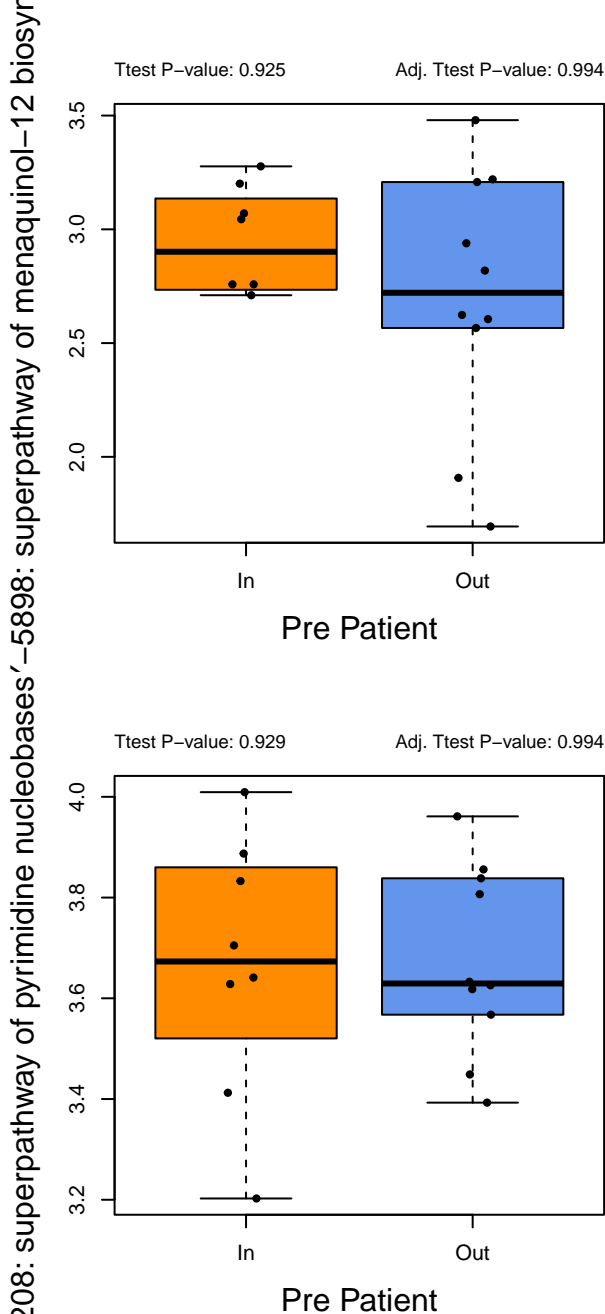
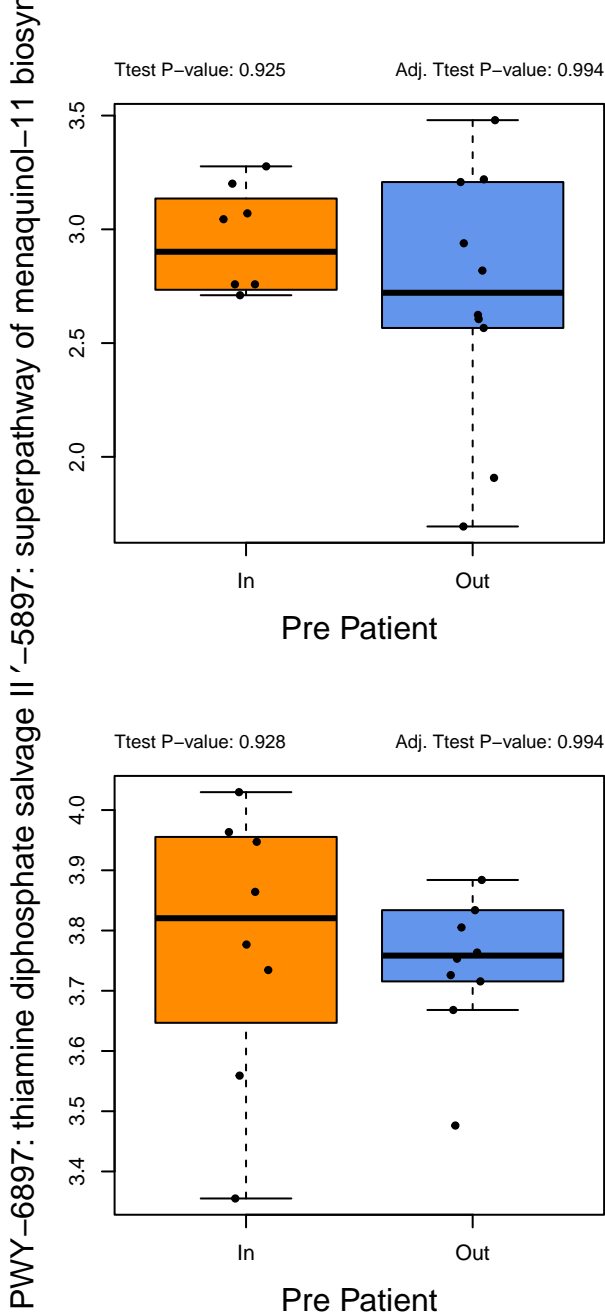


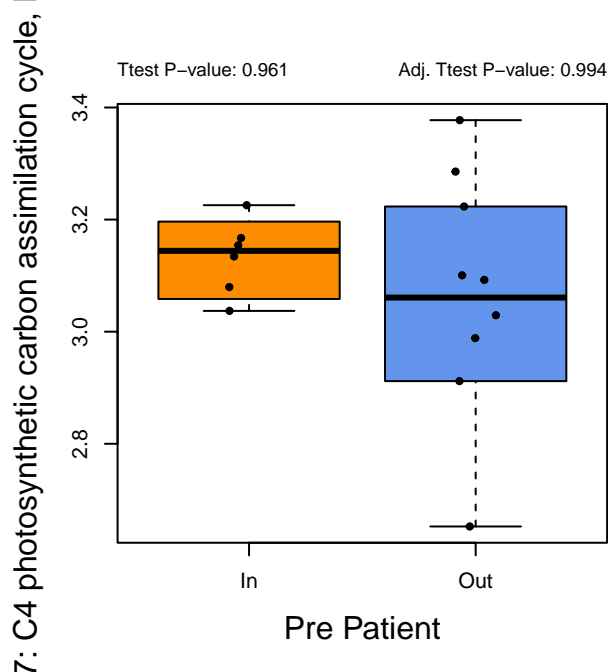
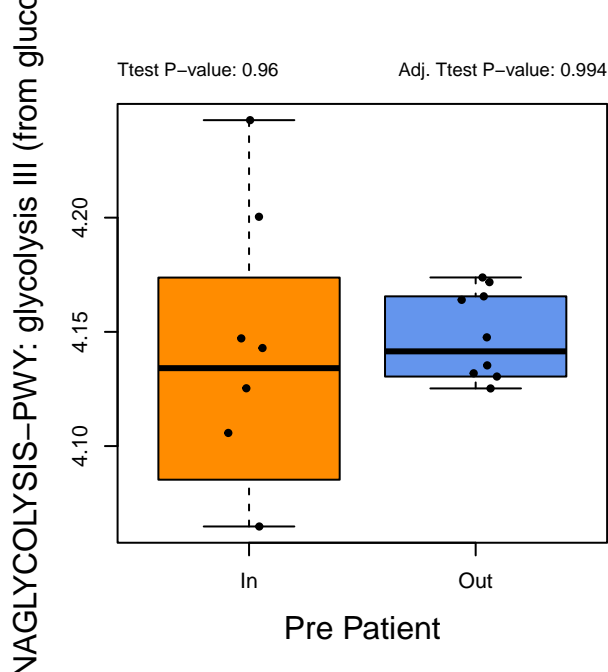
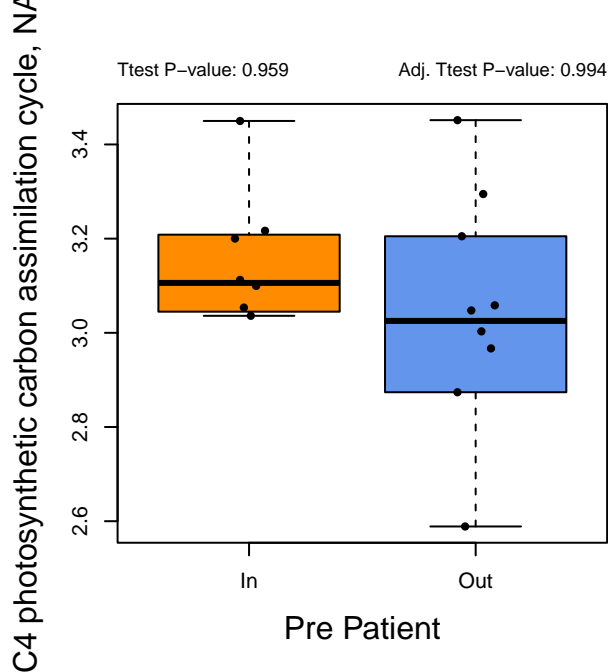
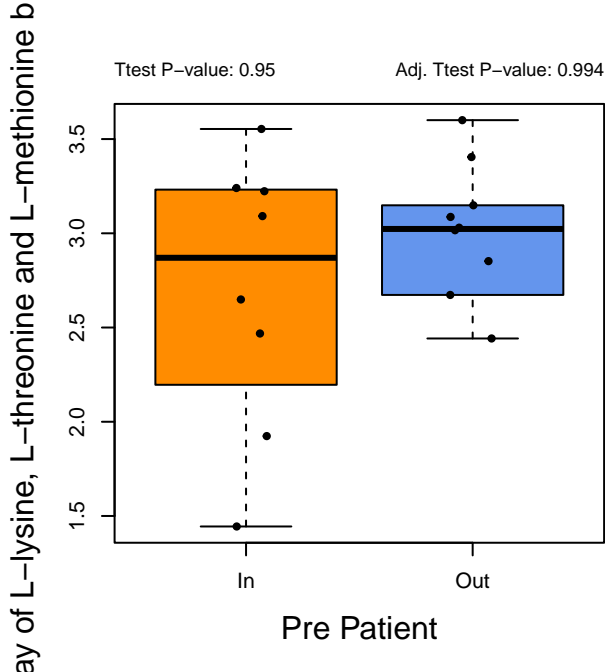
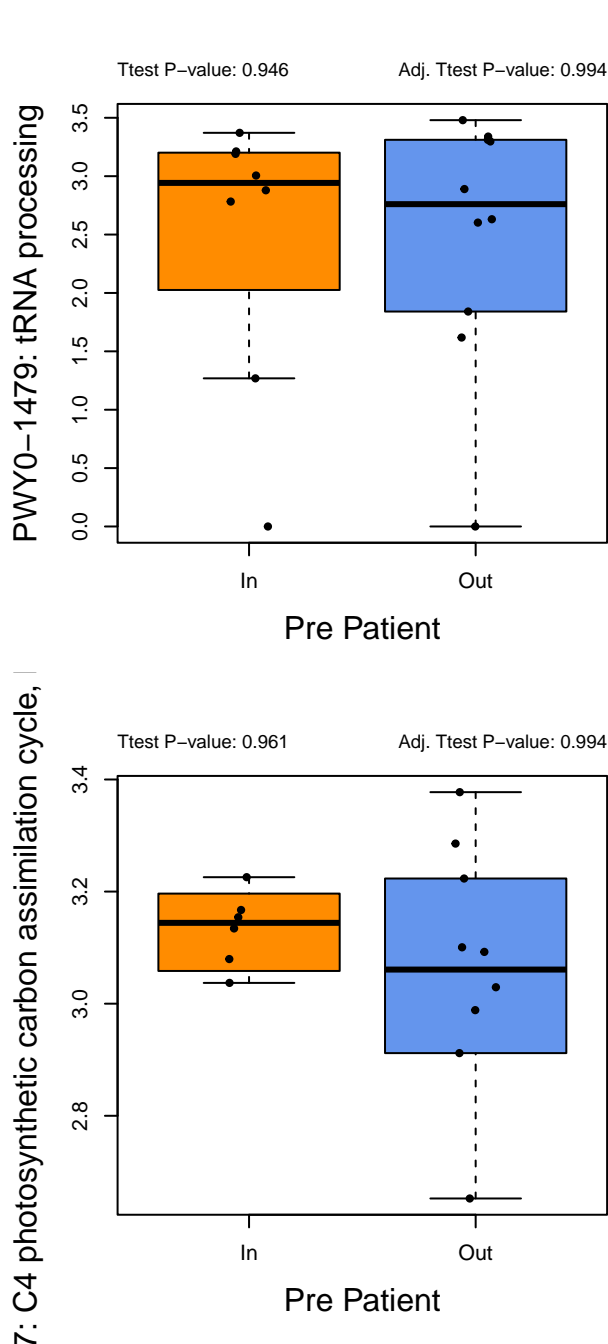
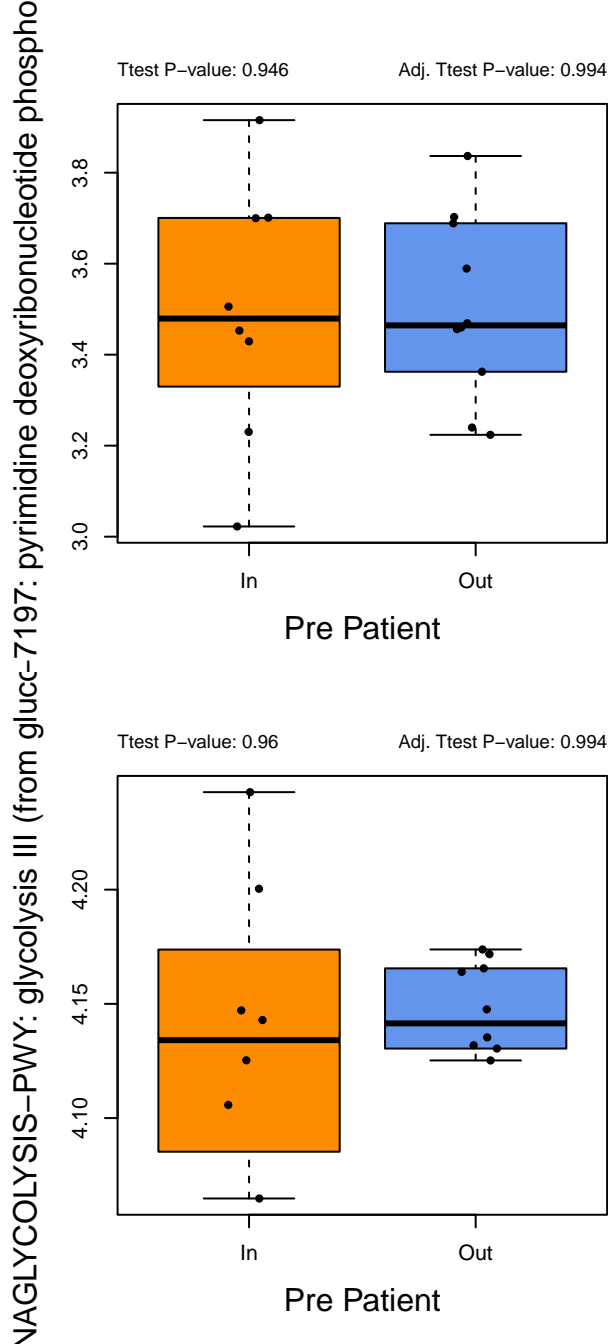
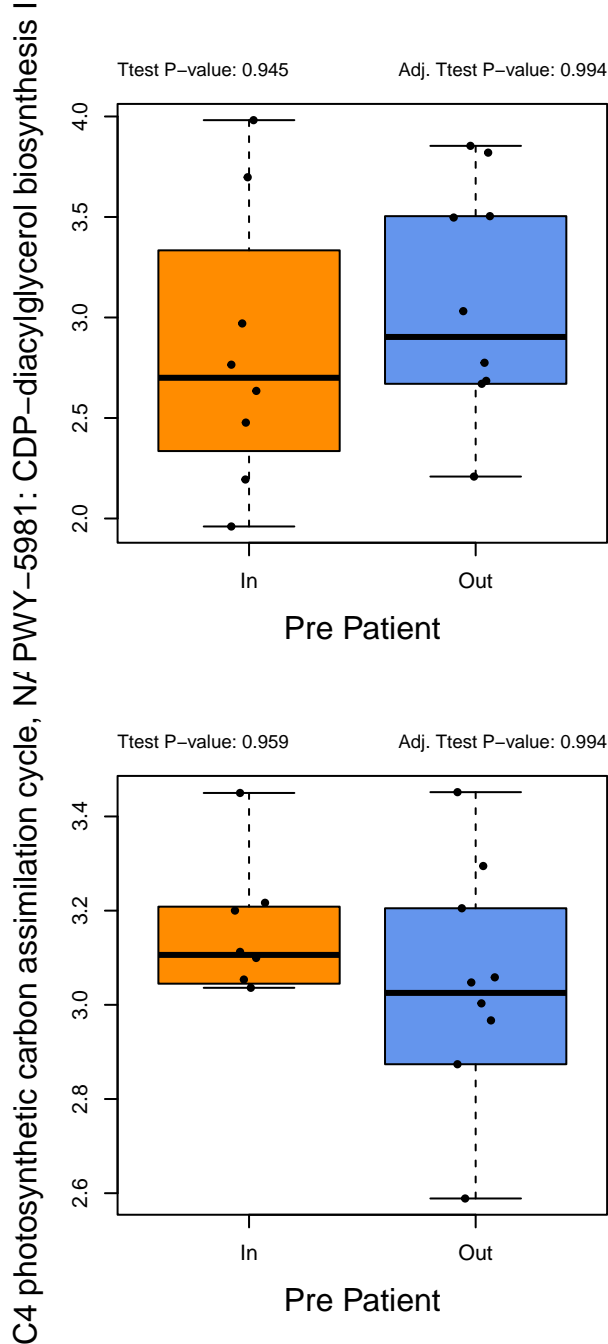
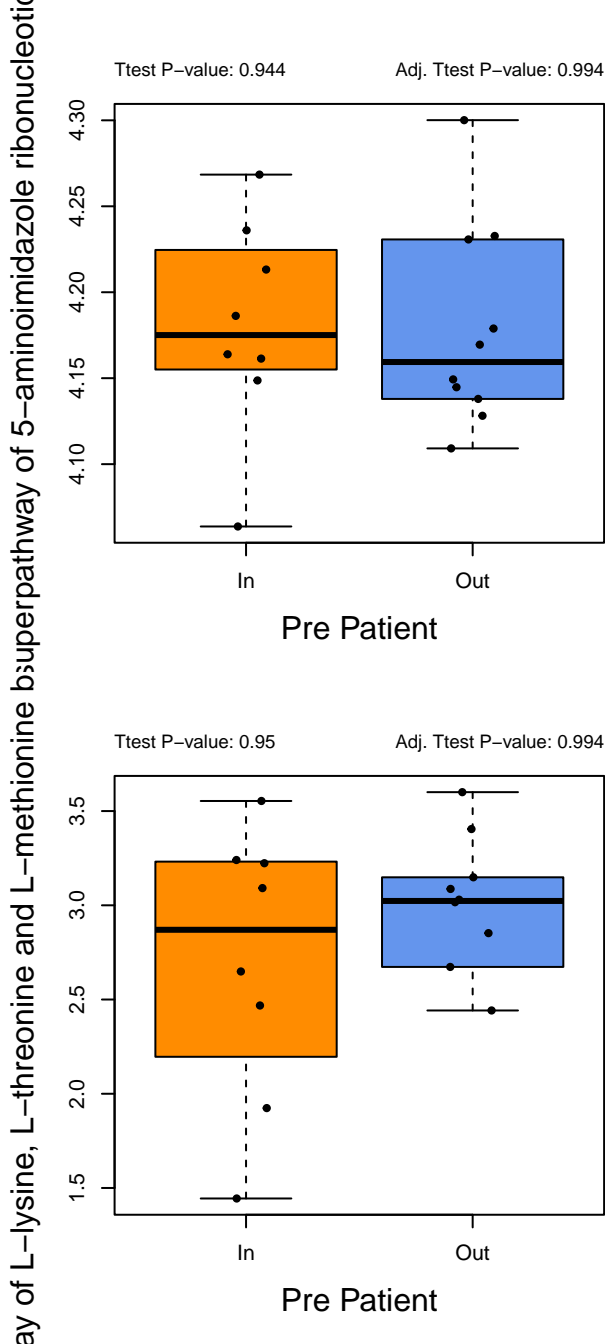
ETH-ACETATE-PWY: methanogenesis from act5384: sucrose degradation IV (sucrose phosph

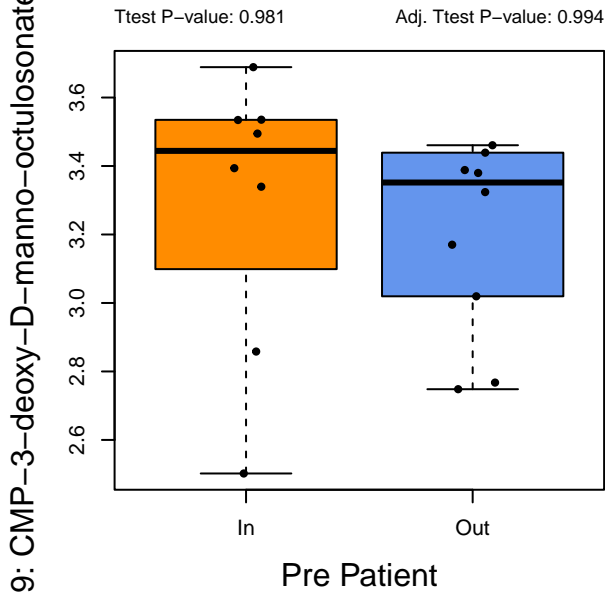
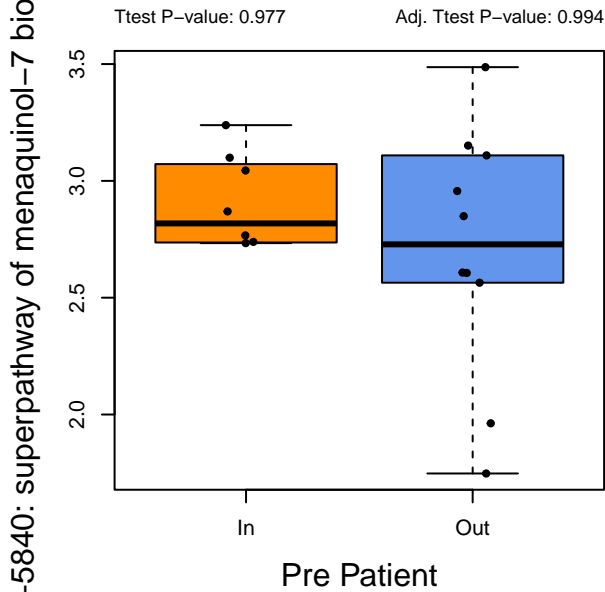
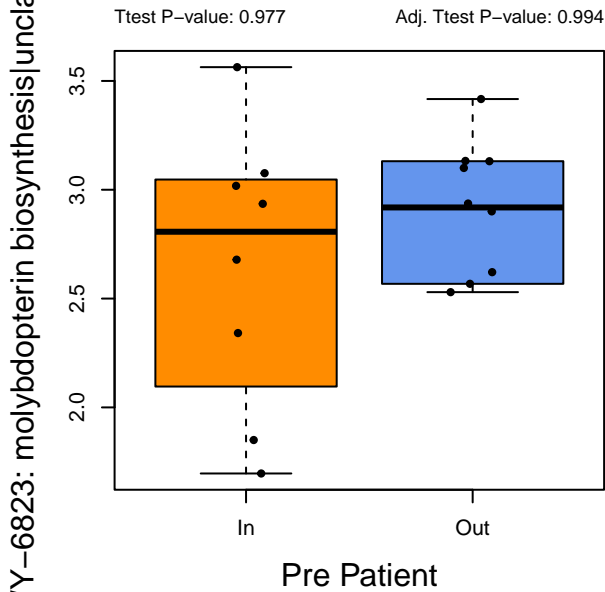
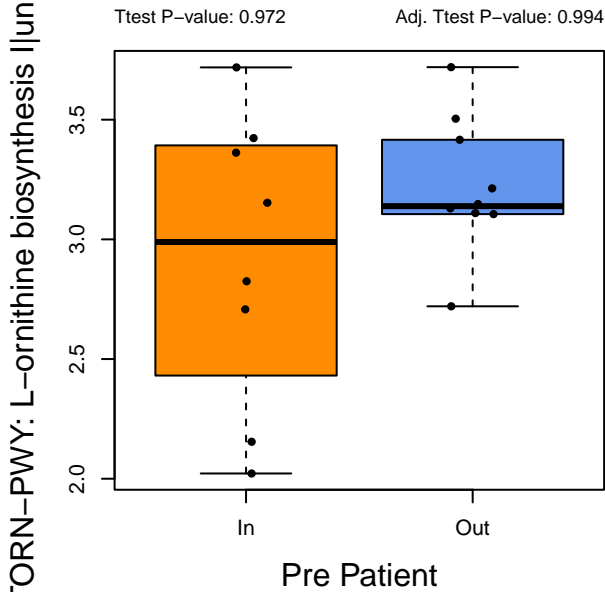
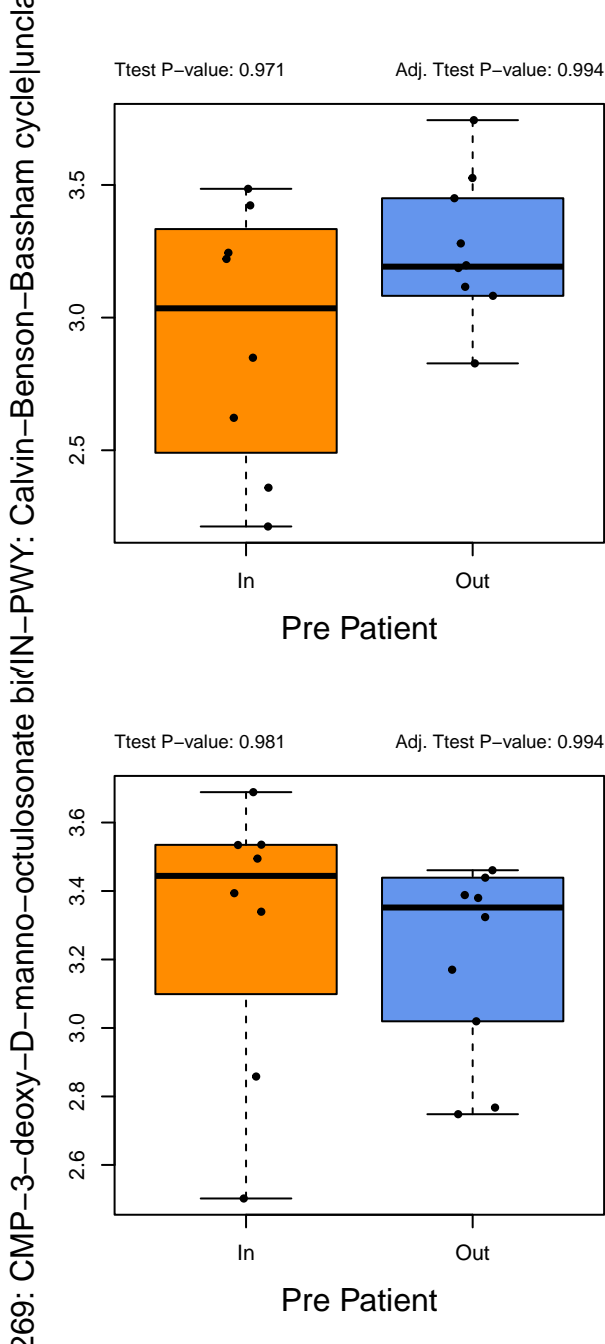
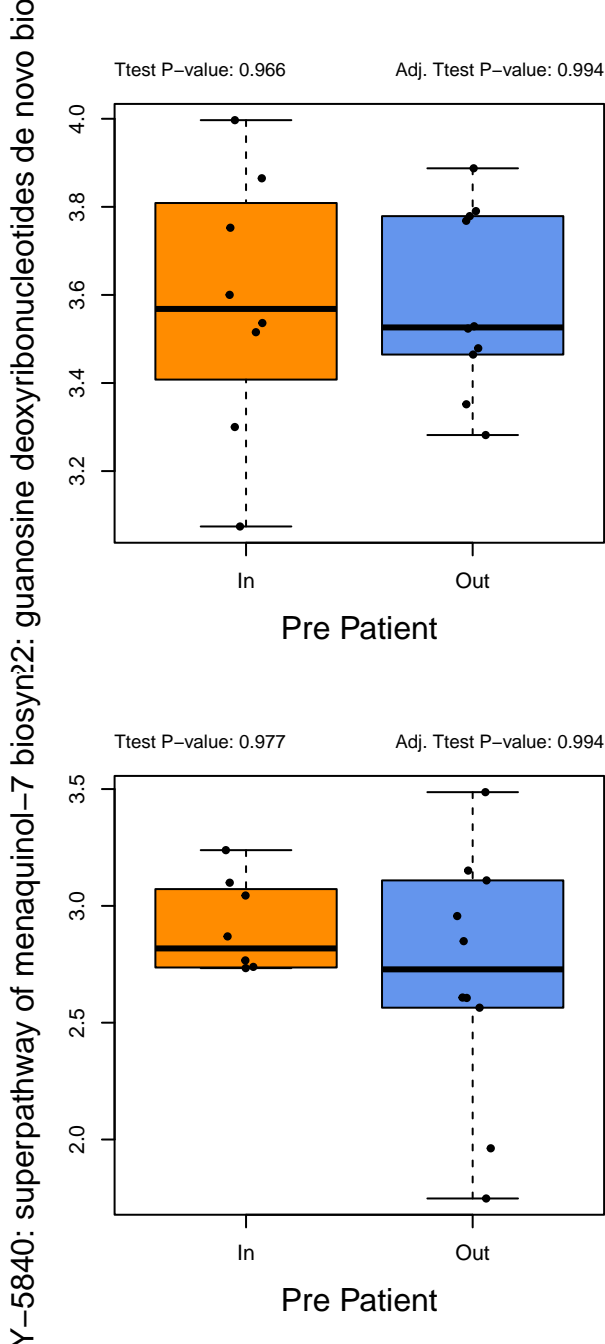
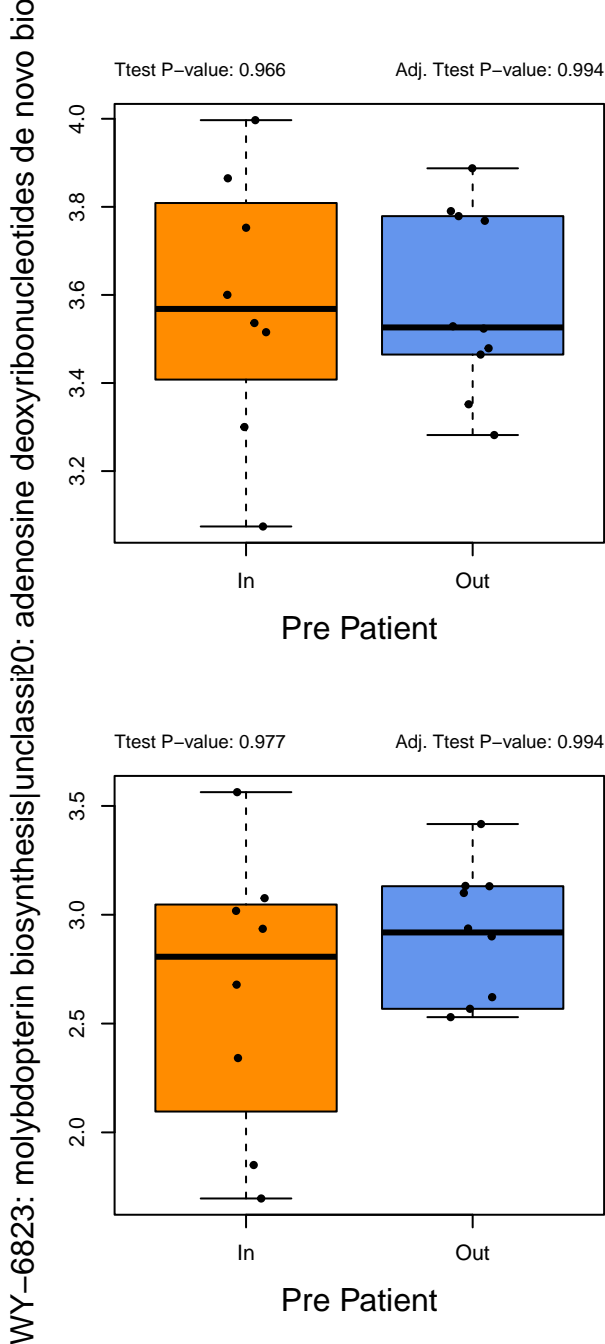
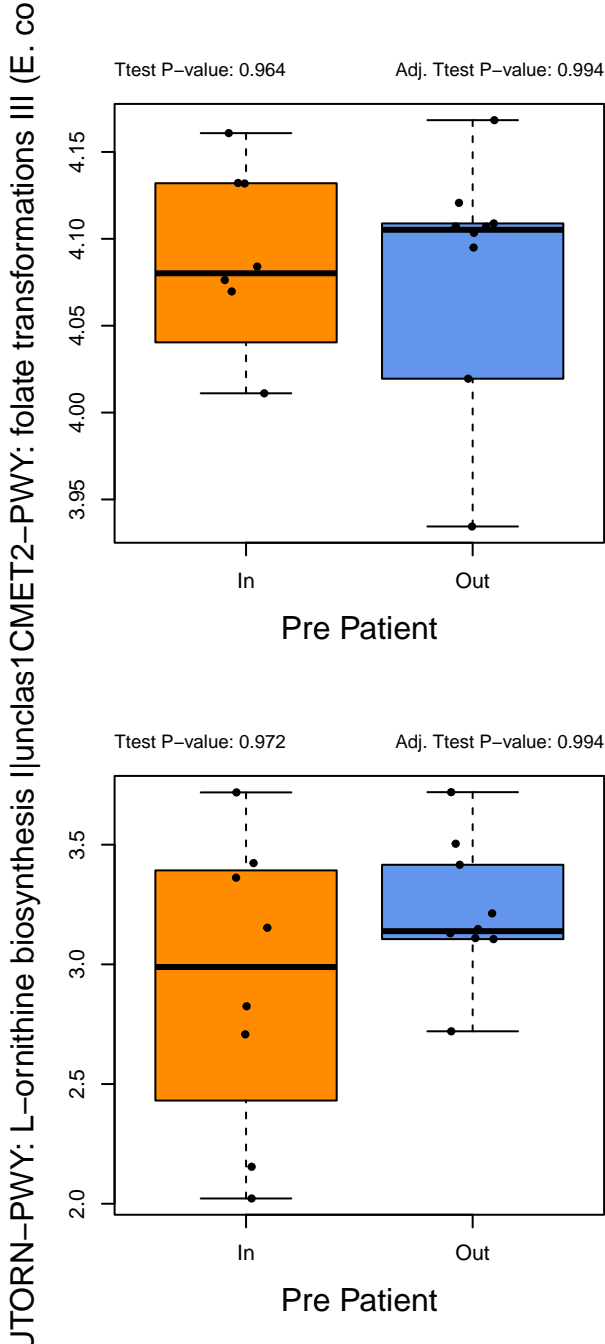






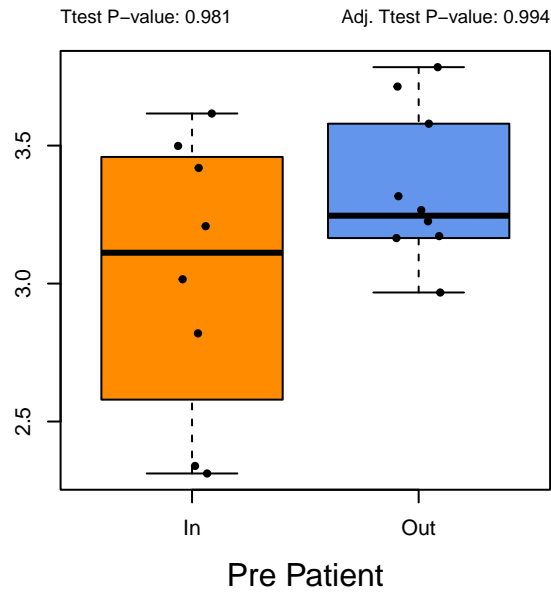




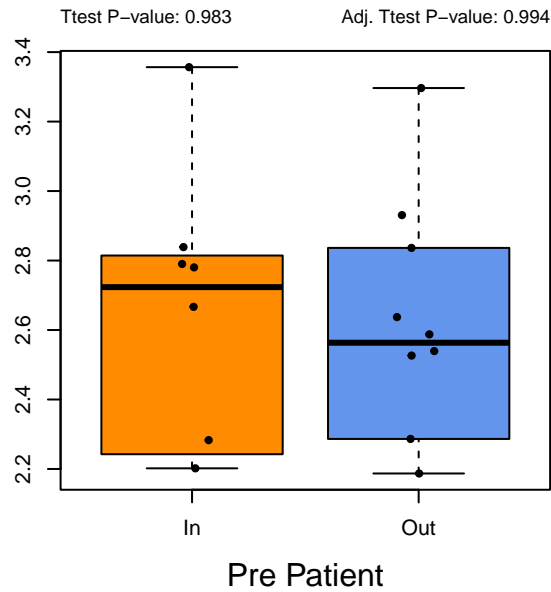




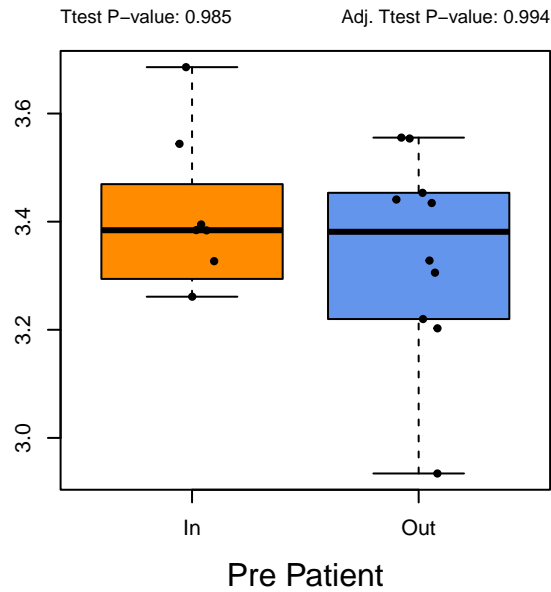
PWY0-1261: anhydromuropeptides recycling UB-PWY: L-arginine biosynthesis II (acetyl cy



PWY: L-arginine biosynthesis I (via L-ornithine of UDP-glucose-derived O-antigen building



HISDEG-PWY: L-histidine degradation I way of GDP-mannose-derived O-antigen buil



PWY-5686: UMP biosynthesis II unclassified

