

III List of DBN nodes

diagnosis: CD		
Metagenomics	Metatranscriptomics	metabolites
[1] "s__Alistipes_putredinis"	[1] "g__ASPASN-PWY: superpathway of L-aspartate and L-asparagine biosynthesis g__Bacteroides.s__Bacteroides_finegoldii"	[1] "m__Arg - Cholate"
[2] "s__Alistipes_sp_HGB5"	[2] "g__COA-PWY-1: coenzyme A biosynthesis II (mammalian) g__Bacteroides.s__Bacteroides_salyersiae"	[2] "m__C10 carnitine"
[3] "s__Anaerococcus_obesiensis"	[3] "g__COA-PWY-1: coenzyme A biosynthesis II (mammalian) g__Dysgonomonas.s__Dysgonomonas_mossii"	[3] "m__C12 carnitine"
[4] "s__Anaerococcus_vaginalis"	[4] "g__COA-PWY-1: coenzyme A biosynthesis II (mammalian) g__Ruminococcus.s__Ruminococcus_calidus"	[4] "m__C12:1 carnitine"
[5] "s__Bacteroides_cellulosilyticus"	[5] "g__HISDEG-PWY: L-histidine degradation I g__Synergistes.s__Synergistes_sp_3_1_syn1"	[5] "m__C14:0 SM"
[6] "s__Bacteroides_eggerthii"	[6] "g__NONMEVIPP-PWY: methylerythritol phosphate pathway I g__Bacteroides.s__Bacteroides_sp_2_1_22"	[6] "m__C14:1 carnitine"
[7] "s__Bacteroides_fluxus"	[7] "g__NONMEVIPP-PWY: methylerythritol phosphate pathway I g__Dysgonomonas.s__Dysgonomonas_mossii"	[7] "m__C14:2 carnitine"
[8] "s__Bacteroides_fragilis"	[8] "g__PANTO-PWY: phosphopantothenate biosynthesis I g__Alistipes.s__Alistipes_sp_HGB5"	[8] "m__C16-OH carnitine"
[9] "s__Bacteroides_massiliensis"	[9] "g__PANTO-PWY: phosphopantothenate biosynthesis I g__Dysgonomonas.s__Dysgonomonas_gadei"	[9] "m__C18:1 LPC plasmalogen"
[10] "s__Bacteroides_ovatus"	[10] "g__PANTO-PWY: phosphopantothenate biosynthesis I g__Dysgonomonas.s__Dysgonomonas_mossii"	[10] "m__C18:1-OH carnitine"
[11] "s__Bacteroides_sp_1_1_30"	[11] "g__PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing) g__Collinsella.s__Collinsella_aerofaciens"	[11] "m__C20:1 LPC"
[12] "s__Bacteroides_sp_2_1_22"	[12] "g__PWY-1042: glycolysis IV (plant cytosol) g__Megamonas.s__Megamonas_funiformis"	[12] "m__C22:6 LPC"
[13] "s__Bacteroides_sp_4_3_47FAA"	[13] "g__PWY-2942: L-lysine biosynthesis III g__Dysgonomonas.s__Dysgonomonas_gadei"	[13] "m__C38:3 PC"
[14] "s__Bacteroides_sp_9_1_42FAA"	[14] "g__PWY-2942: L-lysine biosynthesis III g__Dysgonomonas.s__Dysgonomonas_mossii"	[14] "m__C38:4 PC plasmalogen"
[15] "s__Barnesiella_intestinihominis"	[15] "g__PWY-3001: superpathway of L-isoleucine biosynthesis I g__Megamonas.s__Megamonas_hypermegale"	[15] "m__C38:4 PC"

[16] "s__Bifidobacterium_adolescentis"	[16] "g__PWY-5097: L-lysine biosynthesis VI g__Dysgonomonas.s__Dysgonomonas_gadei"	[16] "m__C38:6 PC"
[17] "s__Butyricicoccus_pullicaecorum"	[17] "g__PWY-5097: L-lysine biosynthesis VI g__Dysgonomonas.s__Dysgonomonas_mossii"	[17] "m__C4 carnitine"
[18] "s__Butyrivibrio_crossotus"	[18] "g__PWY-5188: tetrapyrrole biosynthesis I (from glutamate) g__Ruminococcus.s__Ruminococcus_callidus"	[18] "m__C46:1 TAG"
[19] "s__Clostridium_bolteae"	[19] "g__PWY-5659: GDP-mannose biosynthesis g__Alistipes.s__Alistipes_sp_HGB5"	[19] "m__C46:2 TAG"
[20] "s__Collinsella_aerofaciens"	[20] "g__PWY-5667: CDP-diacylglycerol biosynthesis g__Alistipes.s__Alistipes_sp_HGB5"	[20] "m__C48:3 TAG"
[21] "s__Collinsella_intestinalis"	[21] "g__PWY-5667: CDP-diacylglycerol biosynthesis g__Bacteroides.s__Bacteroides_finegoldii"	[21] "m__C50:5 TAG"
[22] "s__Coprococcus_eutactus"	[22] "g__PWY-5667: CDP-diacylglycerol biosynthesis g__Dysgonomonas.s__Dysgonomonas_gadei"	[22] "m__C52:6 TAG"
[23] "s__Coprococcus_sp_ART55_1"	[23] "g__PWY-5667: CDP-diacylglycerol biosynthesis g__Dysgonomonas.s__Dysgonomonas_mossii"	[23] "m__C52:7 TAG"
[24] "s__Desulfovibrio_desulfuricans"	[24] "g__PWY-5686: UMP biosynthesis g__Bacteroides.s__Bacteroides_finegoldii"	[24] "m__C58:10 TAG"
[25] "s__Dorea_longicatena"	[25] "g__PWY-5690: TCA cycle II (plants and fungi) g__Megamonas.s__Megamonas_funiformis"	[25] "m__Citruiline - Cholate"
[26] "s__Dysgonomonas_gadei"	[26] "g__PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation g__Dysgonomonas.s__Dysgonomonas_gadei"	[26] "m__Citruiline - chenodeoxycholate"
[27] "s__Dysgonomonas_mossii"	[27] "g__PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation g__Dysgonomonas.s__Dysgonomonas_mossii"	[27] "m__Isoallolithocholate [2M-H] -"
[28] "s__Erysipelotrichaceae_bacterium_5_2_54FAA"	[28] "g__PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis g__Alistipes.s__Alistipes_sp_HGB5"	[28] "m__N1-acetylserpine"
[29] "s__Eubacterium_biforme"	[29] "g__PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis g__Bacteroides.s__Bacteroides_sp_2_1_22"	[29] "m__NH4_C22:1 MAG"
[30] "s__Eubacterium_dolichum"	[30] "g__PWY-6386: UDP-N-acetyl/muramoyl-pentapeptide biosynthesis II (lysine-containing) g__Dysgonomonas.s__Dysgonomonas_mossii"	[30] "m__NH4_C46:3 TAG"
[31] "s__Haemophilus_pittmaniae"	[31] "g__PWY-6387: UDP-N-acetyl/muramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) g__Dysgonomonas.s__Dysgonomonas_mossii"	[31] "m__NH4_C48:3 TAG"
[32] "s__Lautropia_mirabilis"	[32] "g__PWY-6700: queuosine biosynthesis g__Dysgonomonas.s__Dysgonomonas_mossii"	[32] "m__NH4_C56:1 TAG"
[33] "s__Megamonas_funiformis"	[33] "g__PWY-6703: preQ0 biosynthesis g__Dysgonomonas.s__Dysgonomonas_mossii"	[33] "m__Val - chenodeoxycholate"

[34] "s__Megamonas_rupellensis"	[34] "g__PWY-7111: pyruvate fermentation to isobutanol (engineered) g__Haemophilus.s__Haemophilus_pittmaniae"	[34] "m__alpha-hydroxymetoprolol"
[35] "s__Odoribacter_laneus"	[35] "g__PWY-7199: pyrimidine deoxyribonucleosides salvage g__Alistipes.s__Alistipes_sp_HGB5"	[35] "m__biotin"
[36] "s__Odoribacter_splanchnicus"	[36] "g__PWY-7208: superpathway of pyrimidine nucleobases salvage g__Desulfovibrio.s__Desulfovibrio_desulfuricans"	[36] "m__cinnamoylglycine"
[37] "s__Parabacteroides_goldsteinii"	[37] "g__PWY-7219: adenosine ribonucleotides de novo biosynthesis g__Alistipes.s__Alistipes_sp_HGB5"	[37] "m__dTMP"
[38] "s__Parabacteroides_sp_D13"	[38] "g__PWY-7219: adenosine ribonucleotides de novo biosynthesis g__Dysgonomonas.s__Dysgonomonas_gadei"	[38] "m__dihydroorotate"
[39] "s__Paraprevotella_xylaniphila"	[39] "g__PWY-7219: adenosine ribonucleotides de novo biosynthesis g__Dysgonomonas.s__Dysgonomonas_mossii"	[39] "m__epiandrosterone"
[40] "s__Peptoniphilus_duerdenii"	[40] "g__PWY-7219: adenosine ribonucleotides de novo biosynthesis g__Synergistes.s__Synergistes_sp_3_1_syn1"	[40] "m__furosemide"
[41] "s__Phascolarctobacterium_succinatutens"	[41] "g__PWY-7221: guanosine ribonucleotides de novo biosynthesis g__Dysgonomonas.s__Dysgonomonas_mossii"	[41] "m__furoylglycine"
[42] "s__Prevotella_stercorea"	[42] "g__PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis I g__Dysgonomonas.s__Dysgonomonas_mossii"	[42] "m__gabapentin"
[43] "s__Prevotella_timonensis"	[43] "g__PWY0-1319: CDP-diacylglycerol biosynthesis II g__Alistipes.s__Alistipes_sp_HGB5"	[43] "m__guanidoacetic acid"
[44] "s__Pseudomonas_aeruginosa"	[44] "g__PWY0-1319: CDP-diacylglycerol biosynthesis II g__Bacteroides.s__Bacteroides_finegoldii"	[44] "m__heptanoate"
[45] "s__Ruminococcus_bromii"	[45] "g__PWY0-1319: CDP-diacylglycerol biosynthesis II g__Dysgonomonas.s__Dysgonomonas_gadei"	[45] "m__hydrochlorothiazide"
[46] "s__Ruminococcus_callidus"	[46] "g__PWY0-1319: CDP-diacylglycerol biosynthesis II g__Dysgonomonas.s__Dysgonomonas_mossii"	[46] "m__nicotinuric acid"
[47] "s__Ruminococcus_champanellensis"	[47] "g__PYRIDOXYN-PWY: pyridoxal 5'-phosphate biosynthesis I g__Dysgonomonas.s__Dysgonomonas_mossii"	[47] "m__porphobilinogen"
[48] "s__Ruminococcus_obeum"	[48] "g__UNINTEGRATED g__Clostridium.s__Clostridium_symbiosum"	[48] "m__quinine"
[49] "s__Streptococcus_intermedius"	[49] "g__UNINTEGRATED g__Lachnospiraceae_noname.s__Lachnospiraceae_bacterium_2_1_58FAA"	[49] "m__sulfapyridine"
[50] "s__Synergistes_sp_3_1_syn1"	[50] "g__VALSYN-PWY: L-valine biosynthesis g__Haemophilus.s__Haemophilus_pittmaniae"	[50] "m__xanthurenate"