

Figure S1. Alpha and beta diversity in EOC patients during neoadjuvant or adjuvant chemotherapy.

A, Boxplots showing the distribution of the number of observed ASVs during neoadjuvant (left) or adjuvant (right) chemotherapy (Wilcoxon test, * for $p \leq 0.05$; # for $0.05 < p \leq 0.1$). **C**, chemotherapy cycle.

PCoA based on weighted UniFrac distances between the gut microbiota profiles of EOC patients receiving neoadjuvant (left) or adjuvant (right) chemotherapy, stratified by collection time (from T0 until follow-up, **B**) or patient (from M1 to M12, **C**). A significant separation by patient was found (permutation test with pseudo-F ratio, $p = 0.001$).

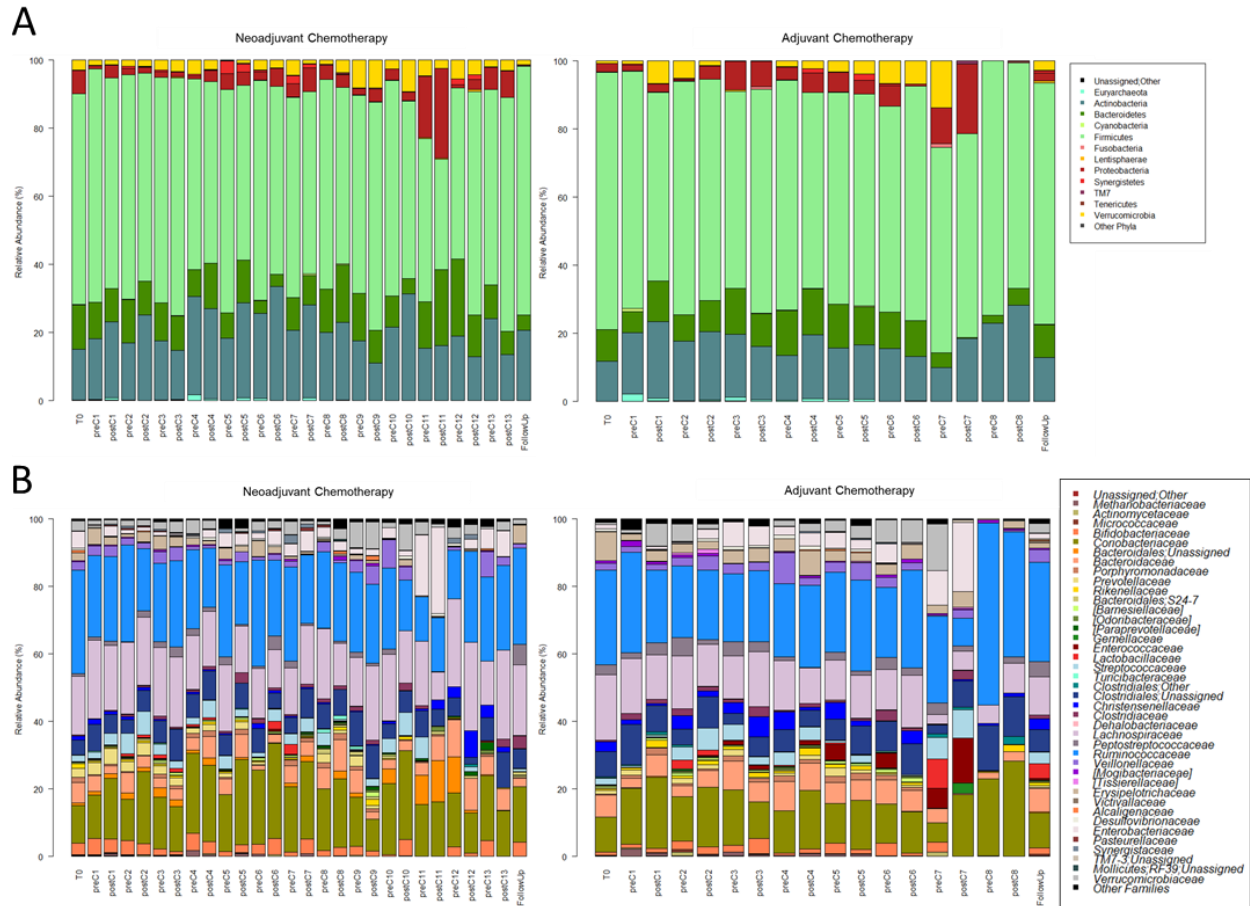


Figure S2. The compositional structure of the gut microbiota of EOC patients during neoadjuvant or adjuvant chemotherapy.

Bar plots showing the relative abundance of phyla (**A**) and families (**B**) of the gut microbiota of EOC patients during neoadjuvant (left) or adjuvant (right) chemotherapy. C, chemotherapy cycle. Only taxa with relative abundance > 0.1% in at least one sample are shown.

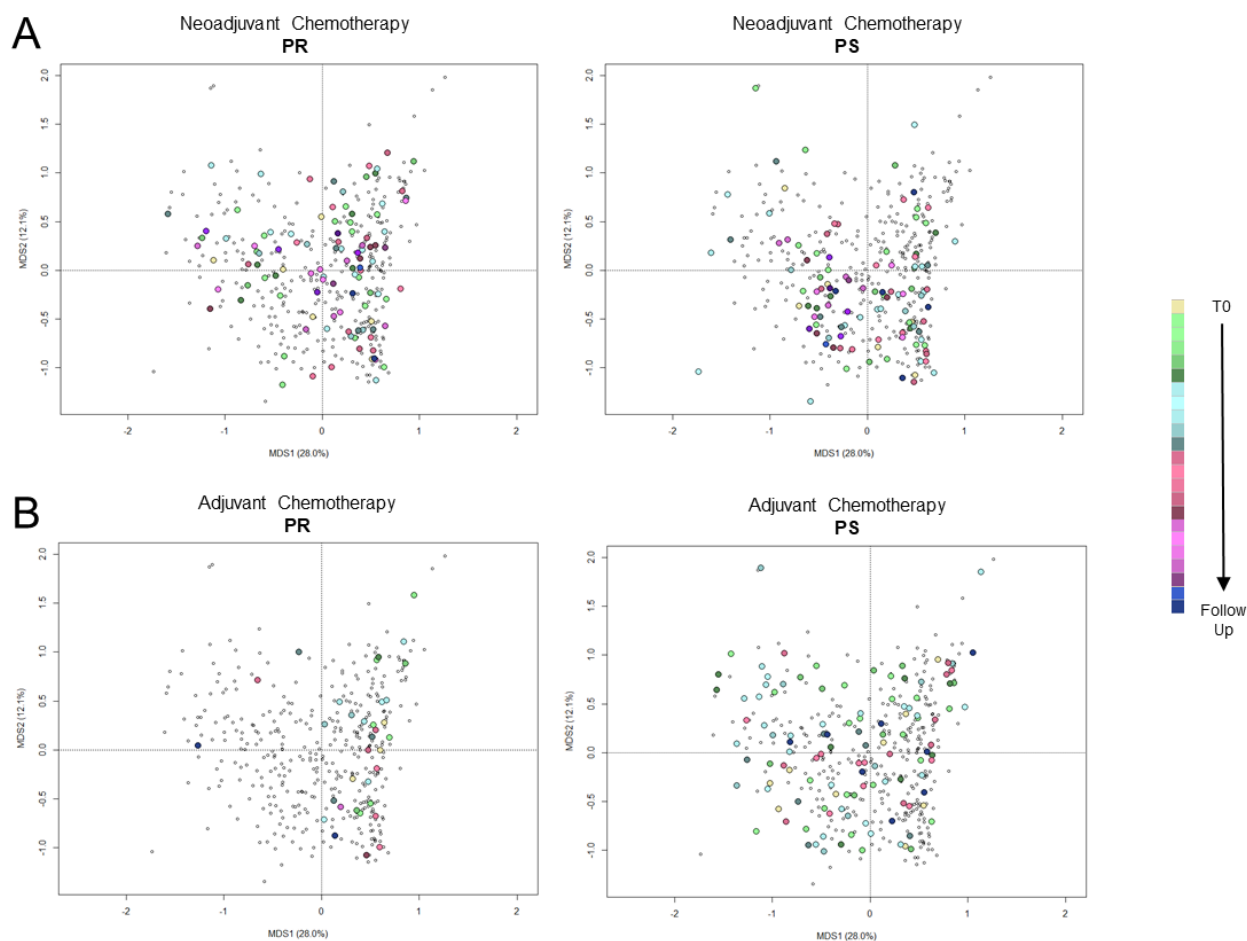


Figure S3. Beta diversity in EOC patients stratified by therapeutic response, during neoadjuvant and adjuvant chemotherapy.

PCoA based on weighted UniFrac distances between the gut microbiota profiles of platinum-resistant (*i.e.*, PR, left) and platinum-sensitive (*i.e.*, PS, right) EOC patients during neoadjuvant (A) or adjuvant (B) chemotherapy, stratified by collection time (from T0 until follow-up). No significant separation was found (permutation test with pseudo-F ratio, $p > 0.05$).

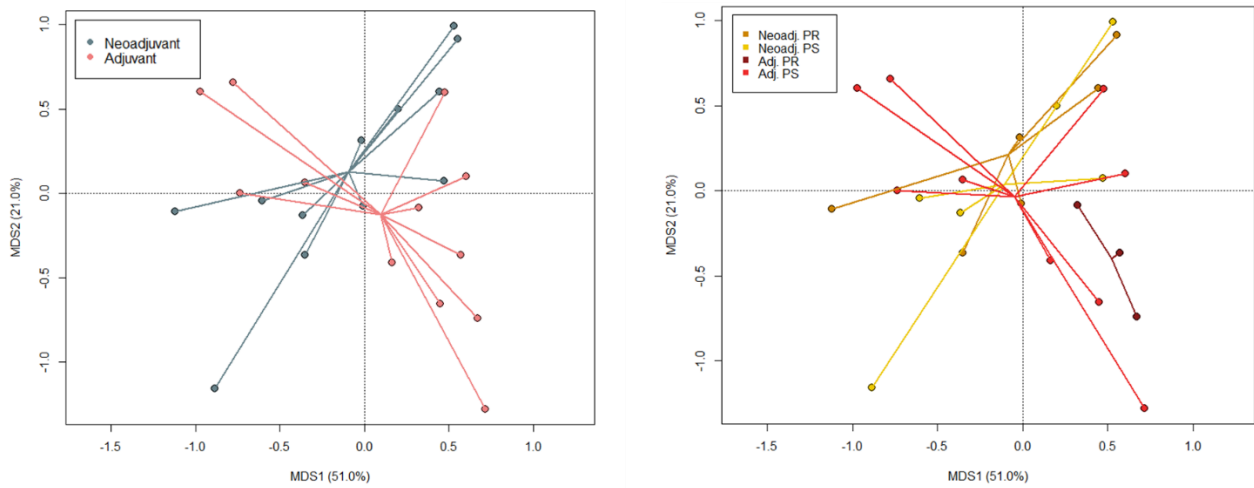
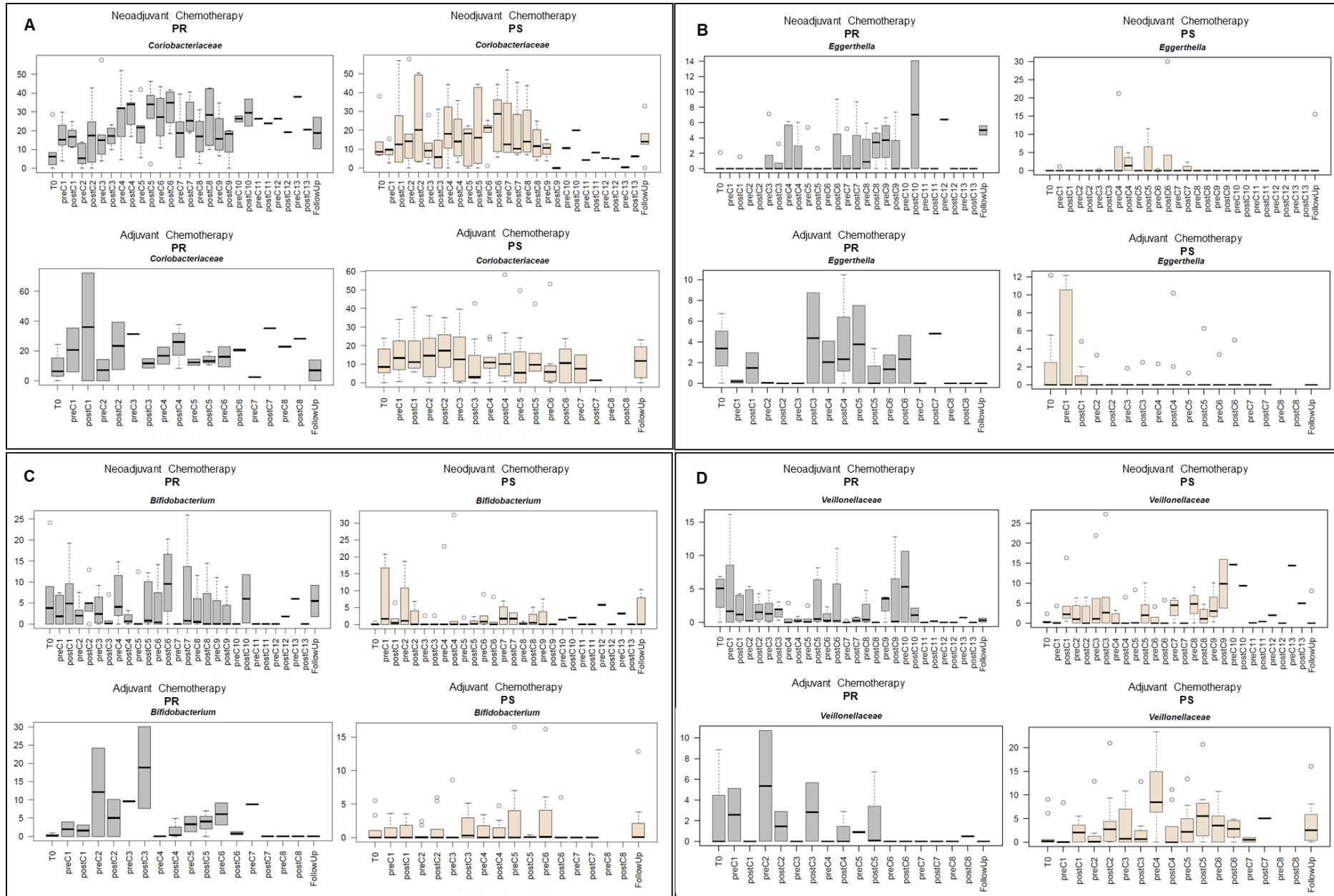
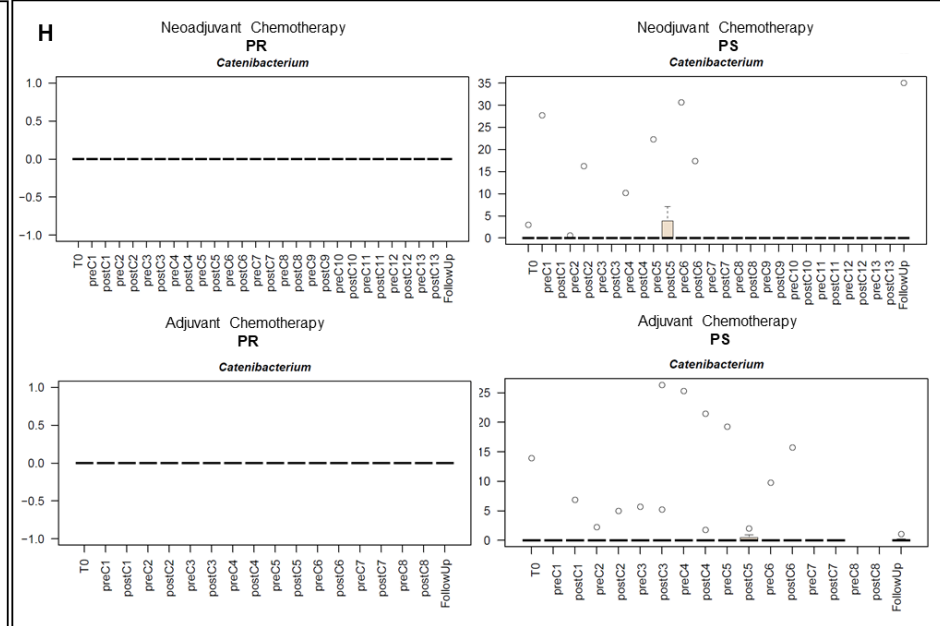
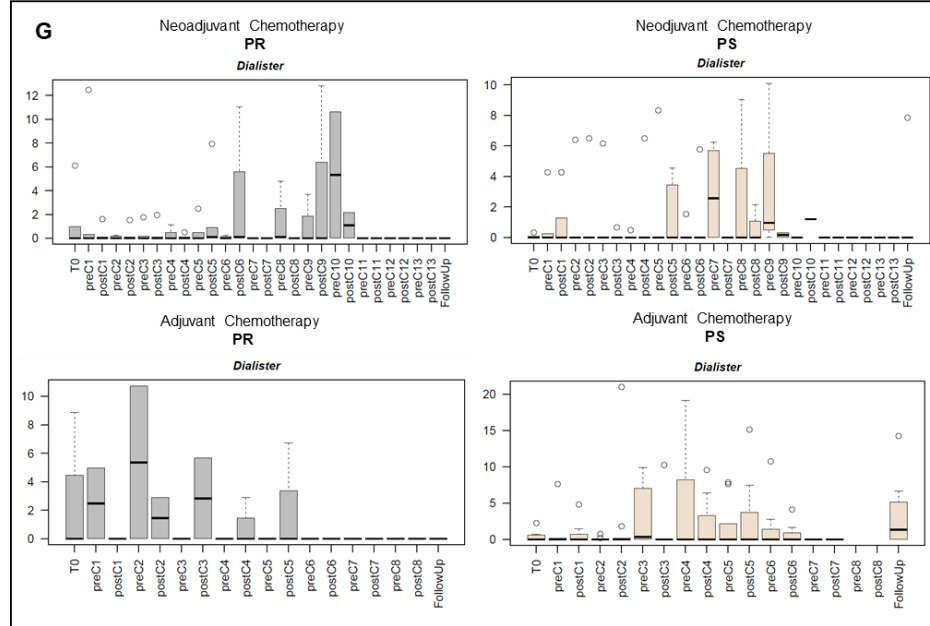
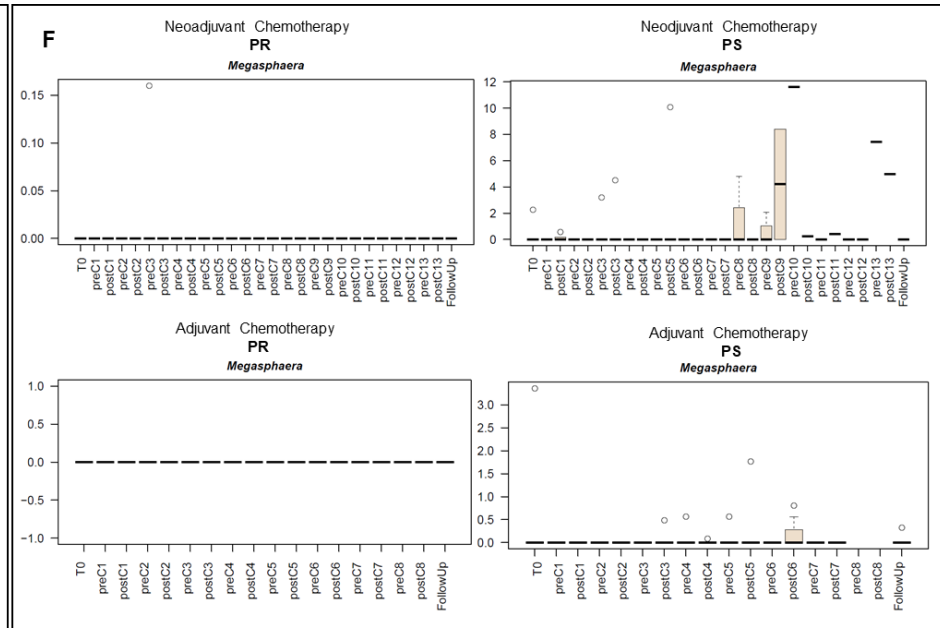
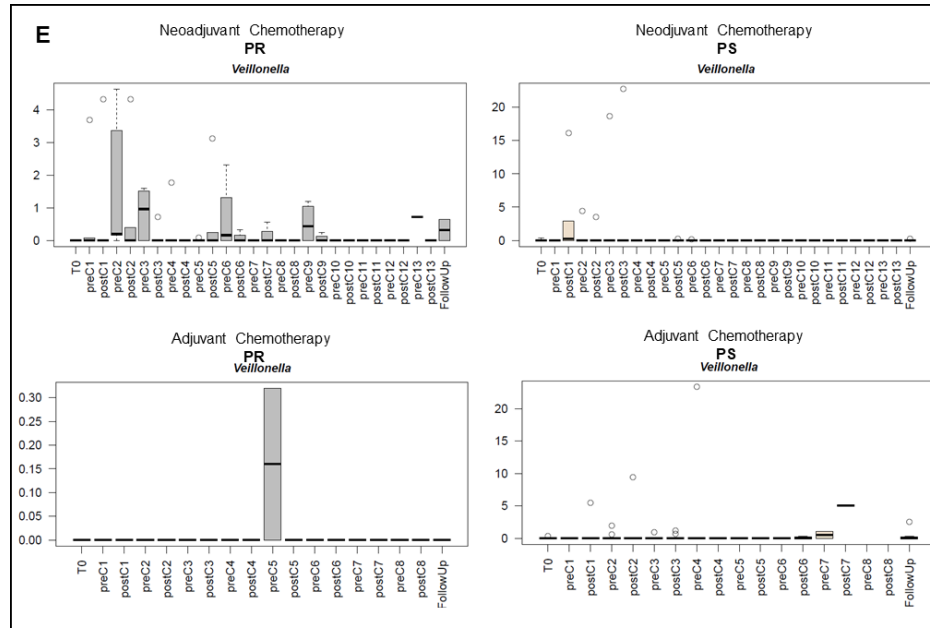


Figure S4. The gut microbiota of EOC patients at diagnosis does not stratify by disease severity or therapeutic response.

PCoA based on weighted UniFrac distances between the gut microbiota profiles of EOC patients at diagnosis, stratified by disease severity and consequently treatment administered (*i.e.*, neoadjuvant vs. adjuvant chemotherapy, left), or therapeutic response (PR, platinum-resistant vs. PS, platinum-sensitive for each treatment group, right). No significant separation was found (permutation test with pseudo-F ratio, $p > 0.05$).





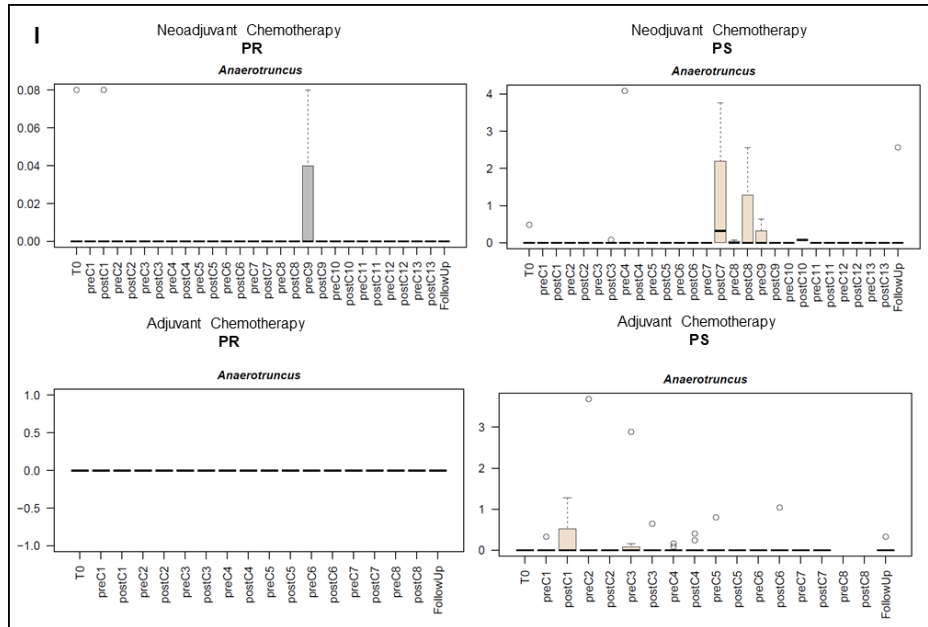


Figure S5. Temporal dynamics of the main discriminating taxa for platinum-resistant or platinum-sensitive EOC patients during neoadjuvant or adjuvant chemotherapy.

Boxplots showing the relative abundance distribution of the main taxa identified as discriminating for platinum-resistant (PR) or platinum-sensitive (PS) EOC patients, based on LEfSe analysis, during neoadjuvant or adjuvant chemotherapy. The following families and genera are shown: **A**, *Coriobacteriaceae*; **B**, *Eggerthella*; **C**, *Bifidobacterium*; **D**, *Veillonellaceae*; **E**, *Veillonella*; **F**, *Megasphaera*; **G**, *Dialister*; **H**, *Catenibacterium*; **I**, *Anaerotruncus*. For each panel, boxplots are shown in the following order: top, neoadjuvant group vs. bottom, adjuvant group; left, PR patients vs right, PS patients. C, chemotherapy cycle. See also **Figure 5**.

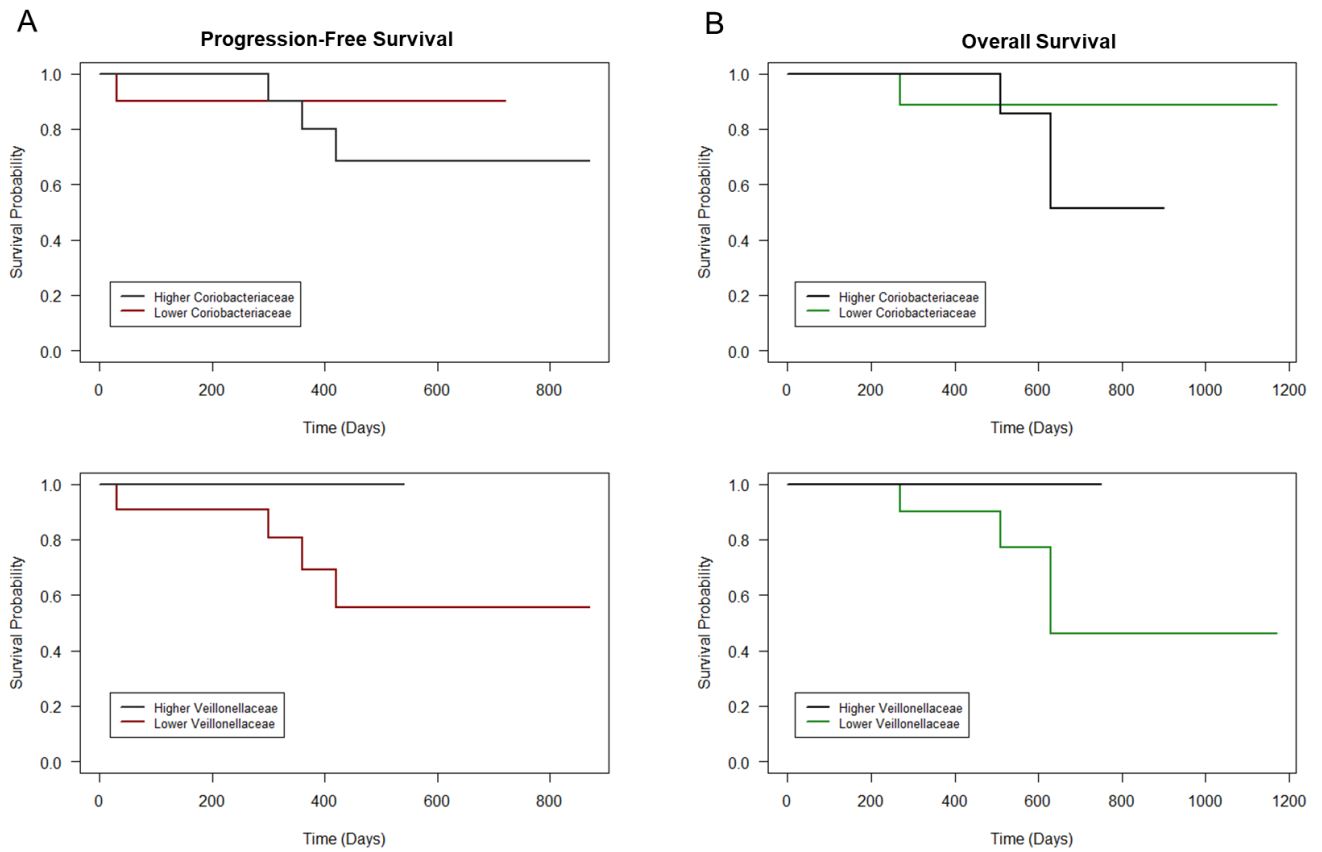


Figure S6. Association of gut microbial taxa and survival in EOC patients receiving chemotherapy treatments.

Kaplan-Meier curves for progression-free survival (**A**) and overall survival (**B**) in the whole cohort. EOC patients were stratified by higher or lower relative abundance of *Coriobacteriaceae* (top) and *Veillonellaceae* (bottom) (relative to median) at the preC7 (for neoadjuvant therapy) or preC4 (for adjuvant therapy) time-point. Log-rank test, $p \leq 0.1$ for *Veillonellaceae*.

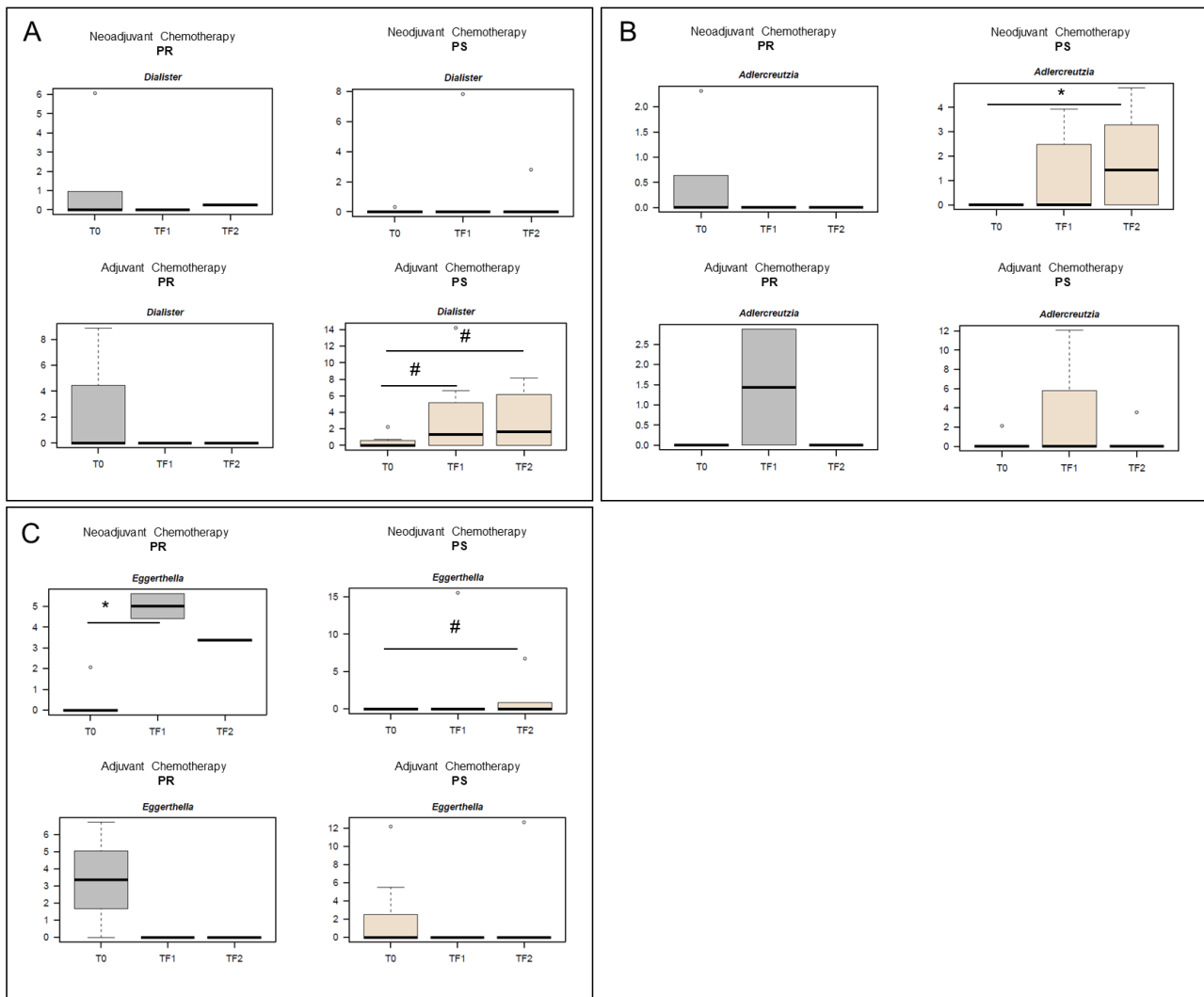
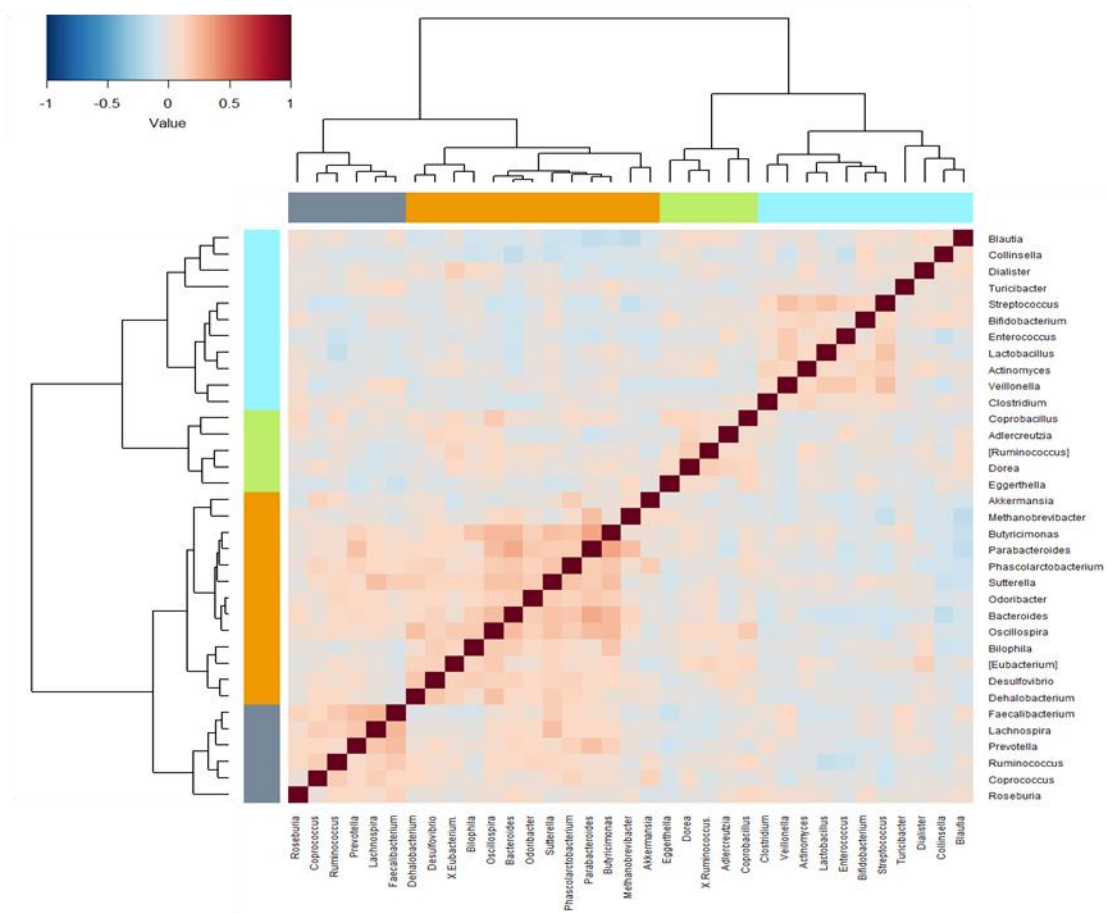


Figure S7. Variations in the potential gut microbial signatures of therapeutic response in the follow-up, up to 6 months after the end of therapy.

Boxplots showing the relative abundance distribution of discriminating taxa for platinum-resistant (PR) or platinum-sensitive (PS) EOC patients, whose proportions remained high or increased in the follow-ups, at 3 (TF1) and 6 (TF2) months from the end of therapy, compared to baseline (T0). Discriminating taxa were identified by LEfSe (see **Figure 5**). The following genera are shown: **A**, *Dialister*; **B**, *Adlercreutzia*; **C**, *Eggerthella*. For each panel, boxplots are shown in the following order: top, neoadjuvant group vs. bottom, adjuvant group; left, PR patients vs right, PS patients. Wilcoxon test, * for $p \leq 0.05$; # for $0.05 < p \leq 0.1$.

A



B

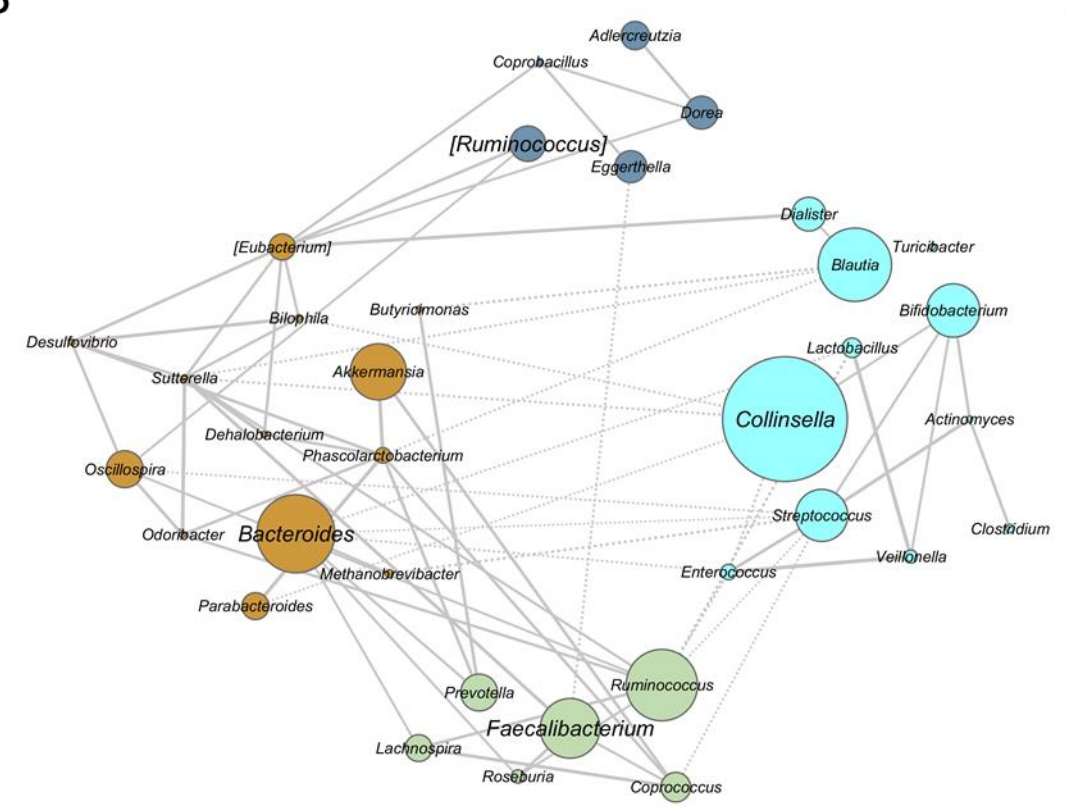


Figure S8. Assignment of bacterial co-abundance groups (CAGs).

A, Heat plot showing Kendall correlations between genera clustered by Spearman correlation coefficient and Ward linkage. The colors are indicative of the four CAGs identified.

B, Wiggum plot showing correlations between CAGs. The circle size is proportional to the genus abundance and connections between nodes represent positive and significant Kendall correlations between genera ($p < 0.05$).

MetaCyc ID	Pathway	Superclasses I	Superclasses II	Superclasses III
FASYN-ELONG-PWY	fatty acid elongation -- saturated	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis		
POLYISOPRENSYN-PWY	polyisoprenoid biosynthesis (E. coli)	Biosynthesis → Polyprenyl Biosynthesis → All-trans Polyprenyl Biosynthesis	Superpathways	
PWY-6700	queuosine biosynthesis I (de novo)	Macromolecule Modification → Nucleic Acid Processing → Queuosine Biosynthesis and Salvage		
PWY0-862	(5Z)-dodecenoate biosynthesis I	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis		
THISYN-PWY	superpathway of thiamine diphosphate biosynthesis I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Thiamine Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Thiamine Biosynthesis Superpathways	
PWY-7664	oleate biosynthesis IV (anaerobic)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis		
PWY-6969	TCA cycle V (2-oxoglutarate synthase)	Generation of Precursor Metabolites and Energy → TCA cycle		
PWY-6507	4-deoxy-L-threo-hex-4-enopyranuronate degradation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation		
PWY-6282	palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis		
PWY-5154	L-arginine biosynthesis III (via N-acetyl-L-citrulline)	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis		
PWYG-321	mycolate biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis		
PWY-6612	superpathway of tetrahydrofolate biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Single Carbon Carrier Biosynthesis → Folate Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Folate Biosynthesis Superpathways	
PWY-5989	stearate biosynthesis II (bacteria and plants)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Stearate Biosynthesis		
PWY-6519	8-amino-7-oxononanoate biosynthesis I	Biosynthesis → Other Biosynthesis → 8-Amino-7-oxononanoate Biosynthesis		

BIOTIN- BIOSYNTHESIS-PWY	biotin biosynthesis I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Biotin Biosynthesis	Superpathways	
P108-PWY	pyruvate fermentation to propanoate I	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Propanoate	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short- Chain Fatty Acids → Fermentation to Propanoate → Pyruvate Fermentation to Propanoate	
PRPP-PWY	superpathway of histidine, purine, and pyrimidine biosynthesis	Superpathways		
PWY-7242	D-fructuronate degradation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Sugar Acid Degradation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Acid Degradation	
FASYN-INITIAL-PWY	superpathway of fatty acid biosynthesis initiation (E. coli)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis	Superpathways	
FOLSYN-PWY	superpathway of tetrahydrofolate biosynthesis and salvage	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Single Carbon Carrier Biosynthesis → Folate Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Folate Biosynthesis	Superpathways
PWY0-845	superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Vitamin B6 BiosynthesisBiosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Vitamin B6 BiosynthesisSuperpathways	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Vitamin B6 Biosynthesis	Superpathways
GLUCONEO-PWY	gluconeogenesis I	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Gluconeogenesis		
PWY-1269	CMP-3-deoxy-D-manno- octulosonate biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → CMP-sugar Biosynthesis → CMP-3- deoxy-D-manno-octulosonate Biosynthesis		

PWY-6703	preQ0 biosynthesis	Biosynthesis → Secondary Metabolite Biosynthesis		
PWY-5695	inosine 5'-phosphate degradation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation		
NAGLIPASYN-PWY	lipid IVA biosynthesis (E. coli)	Biosynthesis → Cell Structure Biosynthesis → Lipopolysaccharide Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis	
PWY-6467	Kdo transfer to lipid IVA III (Chlamydia)	Biosynthesis → Cell Structure Biosynthesis → Lipopolysaccharide Biosynthesis → Kdo Transfer to Lipid IVA	Superpathways	
COLANSYN-PWY	colanic acid building blocks biosynthesis	Biosynthesis → Carbohydrate Biosynthesis	Superpathways	
PYRIDOXSYN-PWY	pyridoxal 5'-phosphate biosynthesis I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Vitamin B6 Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Vitamin B6 Biosynthesis	
RHAMCAT-PWY	L-rhamnose degradation I	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → L-rhamnose Degradation		
GALACTUROCAT-PWY	D-galacturonate degradation I	Degradation/Utilization/Assimilation → Carboxylate Degradation → Sugar Acid Degradation → D-Galacturonate Degradation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Acid Degradation → D-Galacturonate Degradation	
PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosynthesis I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Single Carbon Carrier Biosynthesis → Folate Biosynthesis → 6-Hydroxymethyl-Dihydropterin Diphosphate	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Folate Biosynthesis → 6-Hydroxymethyl-Dihydropterin Diphosphate Biosynthesis	

PWY-7539	6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Single Carbon Carrier Biosynthesis → Folate Biosynthesis → 6-Hydroxymethyl-Dihydropterin Diphosphate	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Folate Biosynthesis → 6-Hydroxymethyl-Dihydropterin Diphosphate Biosynthesis	
PWY-7254	TCA cycle VII (acetate-producers)	Generation of Precursor Metabolites and Energy → TCA cycle		
PWY-5918	superpathway of heme b biosynthesis from glutamate	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis	Biosynthesis → Tetrapyrrole Biosynthesis → Porphyrin Compound Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis	Superpathways
PWY0-1241	ADP-L-glycero-β-D-manno-heptose biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → ADP-sugar Biosynthesis		
PWY-7200	superpathway of pyrimidine deoxyribonucleoside salvage	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide Salvage	Superpathways	
PWY-5005	biotin biosynthesis II	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Biotin Biosynthesis		
HISDEG-PWY	L-histidine degradation I	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-histidine Degradation		
PWY-6478	GDP-D-glycero-α-D-manno-heptose biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → GDP-sugar Biosynthesis		
PWY0-1415	superpathway of heme b biosynthesis from uroporphyrinogen-III	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis	Biosynthesis → Tetrapyrrole Biosynthesis → Porphyrin Compound Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis	Superpathways
PWY-7255	ergothioneine biosynthesis I (bacteria)	Biosynthesis → Secondary Metabolite Biosynthesis → Ergothioneine Biosynthesis		

PWY-6163	chorismate biosynthesis from 3-dehydroquinate	Biosynthesis → Aromatic Compound Biosynthesis → Chorismate Biosynthesis		
DAPLYSINESYN-PWY	L-lysine biosynthesis I	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-lysine Biosynthesis		
P164-PWY	purine nucleobases degradation I (anaerobic)	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation	Generation of Precursor Metabolites and Energy → Fermentation	
PWY-7221	guanosine ribonucleotides de novo biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide De Novo Biosynthesis → Purine Ribonucleotide De Novo Biosynthesis		
PWY-5686	UMP biosynthesis I	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide De Novo Biosynthesis → Pyrimidine Ribonucleotide De Novo Biosynthesis → UMP Biosynthesis		
COA-PWY	coenzyme A biosynthesis I (prokaryotic)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Coenzyme A Biosynthesis		
ARO-PWY	chorismate biosynthesis I	Biosynthesis → Aromatic Compound Biosynthesis → Chorismate Biosynthesis	Superpathways	
PWY-6749	CMP-legionamate biosynthesis I	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → CMP-sugar Biosynthesis → CMP-legionamate biosynthesis		
ANAGLYCOLYSIS-PWY	glycolysis III (from glucose)	Generation of Precursor Metabolites and Energy → Glycolysis		
PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → 5-Aminoimidazole Ribonucleotide Biosynthesis		
COMPLETE-ARO-PWY	superpathway of aromatic amino acid biosynthesis	Biosynthesis → Amino Acid Biosynthesis	Superpathways	
THRESYN-PWY	superpathway of L-threonine biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-threonine Biosynthesis	Superpathways	
PWY0-1319	CDP-diacylglycerol biosynthesis II	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Phospholipid Biosynthesis → CDP-diacylglycerol Biosynthesis		
PWY-5667	CDP-diacylglycerol biosynthesis I	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Phospholipid Biosynthesis → CDP-diacylglycerol Biosynthesis		

CALVIN-PWY	Calvin-Benson-Bassham cycle	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis	Degradation/Utilization/Assimilation → C1 Compound Utilization and Assimilation → CO2 Fixation → Autotrophic CO2 Fixation	
PWY-6385	peptidoglycan biosynthesis III (mycobacteria)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan BiosynthesisSuperpathways	Superpathways	
PWY-6277	superpathway of 5-aminoimidazole ribonucleotide biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → 5-Aminoimidazole Ribonucleotide Biosynthesis	Superpathways	
PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → 5-Aminoimidazole Ribonucleotide Biosynthesis		
PWY-7219	adenosine ribonucleotides de novo biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide		
PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → UDP-N-Acetylmuramoyl-Pentapeptide Biosynthesis		
COBALSYN-PWY	superpathway of adenosylcobalamin salvage from cobinamide I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Cobamide Biosynthesis → Cobinamide Salvage → Adenosylcobalamin Salvage from Cobinamide	Superpathways	
PWY-6126	superpathway of adenosine nucleotides de novo biosynthesis II	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide De Novo Biosynthesis	Superpathways	
PWY-5384	sucrose degradation IV (sucrose phosphorylase)	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → Sucrose Degradation		
PWY-7229	superpathway of adenosine nucleotides de novo biosynthesis I	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide De Novo Biosynthesis	Superpathways	
PWY0-1298	superpathway of pyrimidine deoxyribonucleosides degradation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Pyrimidine Nucleotide Degradation	Superpathways	

PWY-7208	superpathway of pyrimidine nucleobases salvage	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide Salvage Superpathways	Superpathways	
PWY-5100	pyruvate fermentation to acetate and lactate II	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → pyruvate fermentation to lactate	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Acetate	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate → Pyruvate Fermentation to Acetate
REDCITCYC	TCA cycle VI (Helicobacter)	Generation of Precursor Metabolites and Energy → TCA cycle		
TRNA-CHARGING-PWY	tRNA charging	Biosynthesis → Aminoacyl-tRNA Charging	Metabolic Clusters	
PWY-3001	superpathway of L-isoleucine biosynthesis I	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis	Superpathways	
OANTIGEN-PWY	O-antigen building blocks biosynthesis (E. coli)	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis	Metabolic Clusters	Superpathways
PWY-5103	L-isoleucine biosynthesis III	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis		
PWY-5676	acetyl-CoA fermentation to butanoate II	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Butanoate	Superpathways	
PHOSLIPSYN-PWY	superpathway of phospholipid biosynthesis I (bacteria)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Phospholipid Biosynthesis	Superpathways	
PEPTIDOGLYCANSYN-PWY	peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan Biosynthesis	Superpathways	
PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → UDP-N-Acetylmuramoyl-Pentapeptide Biosynthesis		
PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Phospholipid Biosynthesis → Phosphatidylglycerol Biosynthesis	Superpathways	

PWY4FS-7	phosphatidylglycerol biosynthesis I (plastidic)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Phospholipid Biosynthesis → Phosphatidylglycerol Biosynthesis	Superpathways	
PWY-6471	peptidoglycan biosynthesis IV (Enterococcus faecium)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan Biosynthesis Detoxification → Antibiotic Resistance	Superpathways	
VALSYN-PWY	L-valine biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-valine Biosynthesis		
ILEUSYN-PWY	L-isoleucine biosynthesis I (from threonine)	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis		
HISTSYN-PWY	L-histidine biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-histidine Biosynthesis		
NONMEVIP-PWY	methylerythritol phosphate pathway I	Biosynthesis → Secondary Metabolite Biosynthesis → Terpenoid	Biosynthesis → Hemiterpene Biosynthesis → Isopentenyl Diphosphate	Biosynthesis → Methylerythritol Phosphate Pathways
PWY-7560	methylerythritol phosphate pathway II	Biosynthesis → Secondary Metabolite Biosynthesis → Terpenoid	Biosynthesis → Hemiterpene Biosynthesis → Isopentenyl Diphosphate	Biosynthesis → Methylerythritol Phosphate Pathways
PWY-5121	superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)	Biosynthesis → Polyprenyl Biosynthesis → Geranylgeranyl Diphosphate Biosynthesis	Biosynthesis → Secondary Metabolite Biosynthesis → Terpenoid	Biosynthesis → Diterpenoid Biosynthesis
BRANCHED-CHAIN-AA-SYN-PWY	superpathway of branched chain amino acid biosynthesis	Biosynthesis → Amino Acid Biosynthesis	Superpathways	
PWY-5104	L-isoleucine biosynthesis IV	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis		
PWY-5101	L-isoleucine biosynthesis II	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis		
PWY-7111	pyruvate fermentation to isobutanol (engineered)	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Alcohols	
UDPNAGSYN-PWY	UDP-N-acetyl-D-glucosamine biosynthesis I	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → UDP-sugar Biosynthesis → UDP-N-acetyl-D-glucosamine Biosynthesis		

P161-PWY	acetylene degradation (anaerobic)	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Ethanol	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Alcohols → Pyruvate Fermentation to Ethanol
PWY0-1586	peptidoglycan maturation (meso-diaminopimelate containing)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan Biosynthesis		
GLYCOLYSIS-E-D	superpathway of glycolysis and the Entner-Doudoroff pathway	Generation of Precursor Metabolites and Energy	Superpathways	
SALVADEHYPOX-PWY	adenosine nucleotides degradation II	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation → Adenosine Nucleotide Degradation		
PWY-3781	aerobic respiration I (cytochrome c)	Generation of Precursor Metabolites and Energy → Electron Transfer Chains	Generation of Precursor Metabolites and Energy → Respiration → Aerobic Respiration	
P441-PWY	superpathway of N-acetylneuraminate degradation	Degradation/Utilization/Assimilation → Carboxylate Degradation	Superpathways	
P23-PWY	reductive TCA cycle I	Degradation/Utilization/Assimilation → C1 Compound Utilization and Assimilation → CO2 Fixation → Autotrophic CO2 Fixation → Reductive TCA Cycles		
PWY-6608	guanosine nucleotides degradation III	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation	Superpathways	
PWY-6353	purine nucleotides degradation II (aerobic)	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation	Superpathways	
METHYLGALLATE-DEGRADATION-PWY	methylgallate degradation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation		
GALLATE-DEGRADATION-I-PWY	gallate degradation II	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Gallate Degradation		
PWY-7663	gondoate biosynthesis (anaerobic)	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis		

PWY-6629	superpathway of L-tryptophan biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-tryptophan Biosynthesis	Superpathways	
GALLARATE-DEGRADATION-II-PWY	gallate degradation I	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Gallate Degradation		
PWY-6590	superpathway of Clostridium acetobutylicum acidogenic fermentation	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate	Superpathways	
P562-PWY	myo-inositol degradation I	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Alcohol Degradation		
PWY-5913	partial TCA cycle (obligate autotrophs)	Generation of Precursor Metabolites and Energy → TCA cycle		
PWY0-781	aspartate superpathway	Superpathways		
P122-PWY	heterolactic fermentation	Fermentation to Lactic Acid	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Alcohols → Pyruvate Fermentation to Ethanol	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Ethanol
PWY-7234	inosine-5'-phosphate biosynthesis III	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide De Novo Biosynthesis → Purine Ribonucleotide De Novo Biosynthesis → Inosine-5'-phosphate Biosynthesis		
PWY-6470	peptidoglycan biosynthesis V (β-lactam resistance)	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan Biosynthesis		
PWY-6317	D-galactose degradation I (Leloir pathway)	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → Galactose Degradation		
PWY-7237	myo-, chiro- and scyllo-inositol degradation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Alcohol Degradation	Superpathways	
GLCMANNANAUT-PWY	superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation	Degradation/Utilization/Assimilation → Amine and Polyamine Degradation	Superpathways	

PWY-6151	S-adenosyl-L-methionine salvage I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → S-adenosyl-L-methionine Biosynthesis		
PWY-6892	thiazole component of thiamine diphosphate biosynthesis I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Thiamine Biosynthesis → Thiazole Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Thiamine Biosynthesis → Thiazole Biosynthesis	
PYRIDNUCSAL-PWY	NAD salvage pathway I (PNC VI cycle)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → NAD Metabolism → NAD Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → NAD Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → NAD Metabolism → NAD Biosynthesis
FERMENTATION-PWY	mixed acid fermentation	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Ethanol	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Alcohols → Pyruvate Fermentation to Ethanol	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids
PWY-6737	starch degradation V	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Polysaccharide Degradation → Starch Degradation		
GLYCOLYSIS	glycolysis I (from glucose 6-phosphate)	Generation of Precursor Metabolites and Energy → Glycolysis		
PWY-5484	glycolysis II (from fructose 6-phosphate)	Generation of Precursor Metabolites and Energy → Glycolysis		
GLYCOCAT-PWY	glycogen degradation I	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Polysaccharide Degradation → Glycan Degradation		
ANAEROFRUCAT-PWY	homolactic fermentation	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Lactate	Superpathways	

P124-PWY	Bifidobacterium shunt	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Lactate	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Acetate	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate
P461-PWY	hexitol fermentation to lactate, formate, ethanol and acetate	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Lactate	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate	
PWY-621	sucrose degradation III (sucrose invertase)	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → Sucrose Degradation		
PWY0-1061	superpathway of L-alanine biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-alanine Biosynthesis	Superpathways	

Table S1. MetaCyc pathway and superclass information for the discriminating pathways between platinum-resistant and platinum-sensitive EOC patients receiving neoadjuvant or adjuvant chemotherapy. Differentially represented inferred functions were identified by linear discriminant analysis (LDA) effect size (LEfSe) analysis. See also **Figure 7**.