

## Physical activity changes gut microbiota

**SUPPLEMENTARY TABLE 1.** Alpha diversity measurements in gut microbiota within each group T1, T2, and T3 after 1-year of intervention and, as well as, across the three groups.

	Faith_pd p-value	Observed features p-value	Pielou-Evenness p-value
T1 (n = 99)	0.981	0.722	0.319
T2 (n = 99)	0.701	0.780	0.574
T3 (n = 99)	0.675	0.720	0.055
Across three groups	0.438	0.758	0.122

**SUPPLEMENTARY TABLE 2.** List of the predicted pathways between three groups.

BioCyc Pathway ID	Pathway
PWY-6562	norspermidine biosynthesis
BRANCHED-CHAIN-AA-SYN-PWY	superpathway of branched chain amino acid biosynthesis
ILEUSYN-PWY	L-isoleucine biosynthesis I (from threonine)
PWY-2942	L-lysine biosynthesis III
PWY-5101	L-isoleucine biosynthesis II
PWY-5103	L-isoleucine biosynthesis III
PWY-5104	L-isoleucine biosynthesis IV
PWY-6630	superpathway of L-tyrosine biosynthesis
VALSYN-PWY	L-valine biosynthesis
PWY-6628	superpathway of L-phenylalanine biosynthesis
PWY-5505	L-glutamate and L-glutamine biosynthesis
PWY0-1241	ADP-L-glycero-β;-D-manno-heptose biosynthesis
OANTIGEN-PWY	O-antigen building blocks biosynthesis ( <i>E. coli</i> )
KDO-NAGLIPASYN-PWY	superpathway of (Kdo) <sub>2</sub> -lipid A biosynthesis
PWY-5265	peptidoglycan biosynthesis II (staphylococci)
PWY-6891	thiazole component of thiamine diphosphate biosynthesis II
PWY-6895	superpathway of thiamine diphosphate biosynthesis II
PWY-7377	cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion)
PYRIDNUCSAL-PWY	NAD salvage pathway I (PNC VI cycle)
LPSSYN-PWY	superpathway of lipopolysaccharide biosynthesis
P125-PWY	superpathway of (R, R)-butanediol biosynthesis
PWY-5910	superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate)
PWY-5757	fosfomycin biosynthesis
PWY-922	mevalonate pathway I (eukaryotes and bacteria)
AEROBACTINSYN-PWY	aerobactin biosynthesis
ENTBACSYN-PWY	enterobactin biosynthesis
PWY-7431	aromatic biogenic amine degradation (bacteria)
CRNFORCAT-PWY	creatinine degradation I
ORNDEG-PWY	superpathway of ornithine degradation
PWY-5705	allantoin degradation to glyoxylate III
PWY-5499	vitamin B <sub>6</sub> degradation

**SUPPLEMENTARY TABLE 2.** Continue.

<b>PWY0-1533</b>	methylphosphonate degradation I
<b>GALACTARDEG-PWY</b>	D-galactarate degradation I
<b>GLUCARDEG-PWY</b>	D-glucarate degradation I
<b>GOLPDLCAT-PWY</b>	superpathway of glycerol degradation to 1,3-propanediol
<b>AST-PWY</b>	L-arginine degradation II (AST pathway)
<b>ARGDEG-PWY</b>	superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation
<b>ORNARGDEG-PWY</b>	superpathway of L-arginine and L-ornithine degradation
<b>BENZCOA-PWY</b>	anaerobic aromatic compound degradation ( <i>Thauera aromatica</i> )
<b>GLUCARGALACTSUPER-PWY</b>	superpathway of D-glucarate and D-galactarate degradation
<b>PWY-6588</b>	pyruvate fermentation to acetone
<b>PWY-7111</b>	pyruvate fermentation to isobutanol (engineered)
<b>PWY-5100</b>	pyruvate fermentation to acetate and lactate II
<b>NONOXIPENT-PWY</b>	pentose phosphate pathway (non-oxidative branch) I
<b>PWY-7254</b>	TCA cycle VII (acetate-producers)