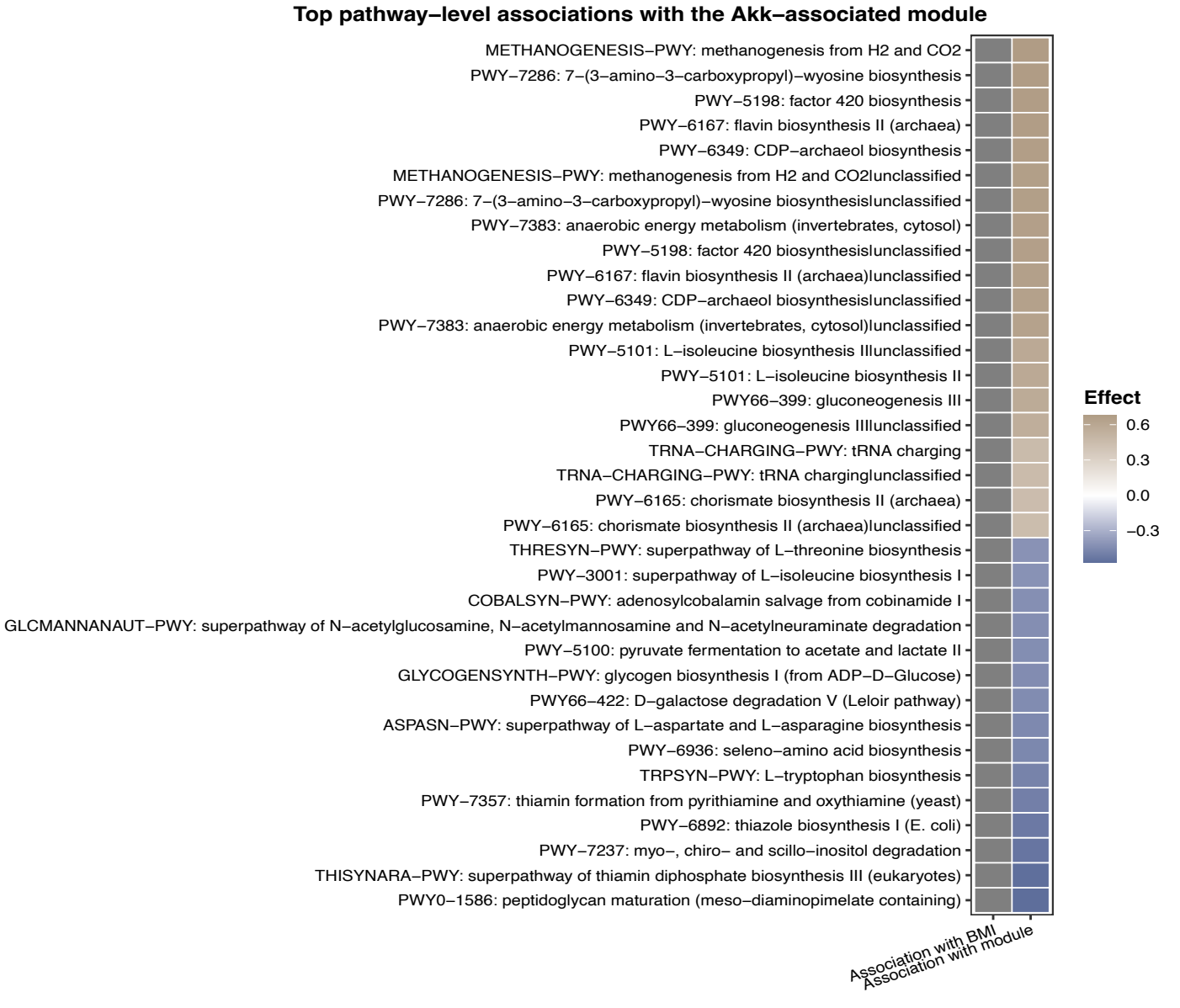
Top pathway−level associations with the Akk−associated module
METHANOGENESIS−PWY: methanogenesis from H2 and CO2
PWY−7286: 7−(3−amino−3−carboxypropyl)−wyosine biosynthesis
PWY−5198: factor 420 biosynthesis
PWY−6167: flavin biosynthesis II (archaea)
PWY−6349: CDP−archaeol biosynthesis
METHANOGENESIS−PWY: methanogenesis from H2 and CO2|unclassified
PWY−7286: 7−(3−amino−3−carboxypropyl)−wyosine biosynthesis|unclassified
PWY−7383: anaerobic energy metabolism (invertebrates, cytosol)
PWY−5198: factor 420 biosynthesis|unclassified
PWY−6167: flavin biosynthesis II (archaea)|unclassified
PWY−6349: CDP−archaeol biosynthesis|unclassified
PWY−7383: anaerobic energy metabolism (invertebrates, cytosol)|unclassified
PWY−5101: L−isoleucine biosynthesis III|unclassified
PWY−5101: L−isoleucine biosynthesis II
PWY66−399: gluconeogenesis III
PWY66−399: gluconeogenesis III|unclassified
TRNA−CHARGING−PWY: tRNA charging
TRNA−CHARGING−PWY: tRNA charging|unclassified
PWY−6165: chorismate biosynthesis II (archaea)
PWY−6165: chorismate biosynthesis II (archaea)|unclassified
THRESYN−PWY: superpathway of L−threonine biosynthesis
PWY−3001: superpathway of L−isoleucine biosynthesis I
COBALSYN−PWY: adenosylcobalamin salvage from cobinamide I
GLCMANNANAUT−PWY: superpathway of N−acetylglucosamine, N−acetylmannosamine and N−acetylneuraminate degradation
PWY−5100: pyruvate fermentation to acetate and lactate II
GLYCOGENSYNTH−PWY: glycogen biosynthesis I (from ADP−D−Glucose)
PWY66−422: D−galactose degradation V (Leloir pathway)
ASPASN−PWY: superpathway of L−aspartate and L−asparagine biosynthesis
PWY−6936: seleno−amino acid biosynthesis
TRPSYN−PWY: L−tryptophan biosynthesis
PWY−7357: thiamin formation from pyrithiamine and oxythiamine (yeast)
PWY−6892: thiazole biosynthesis I (E. coli)
PWY−7237: myo−, chiro− and scillo−inositol degradation
THISYNARA−PWY: superpathway of thiamin diphosphate biosynthesis III (eukaryotes)
PWY0−1586: peptidoglycan maturation (meso−diaminopimelate containing)
Association with BMI
Association with module
Effect
0.6
0.3
0.0
−0.3