S4 Table Sequence based classification of carbohydrate active enzymes (CAE) predicted through 16S gene sequences by PICRUSt2 in the archaeal communities of *Capra hircus* GITs.

EC number	**Enzyme**	**Classification**	
EC:2.4.1.1	Glycogen phosphorylase	GT	
EC:2.4.1.15	Alpha,alpha-trehalose-phosphate synthase (UDP-forming)	GT	
EC:2.4.1.227	acetylglucosaminyltransferase	GT	
EC:2.4.1.83	Dolichyl-phosphate beta-D-mannosyltransferase	GT	
EC:2.4.99.18	Dolichyl-diphosphooligosaccharide--protein glycotransferase	GT	
EC:3.1.3.12	Trehalose-phosphatase	GT	
EC:3.2.1.1	Alpha-amylase	GH	CBM
EC:3.2.1.4	Cellulase	GH	CBM

Glycoside Hydrolase (GH), Glycosyl transferase (GT), and Carbohydrate Binding Module (CBM).