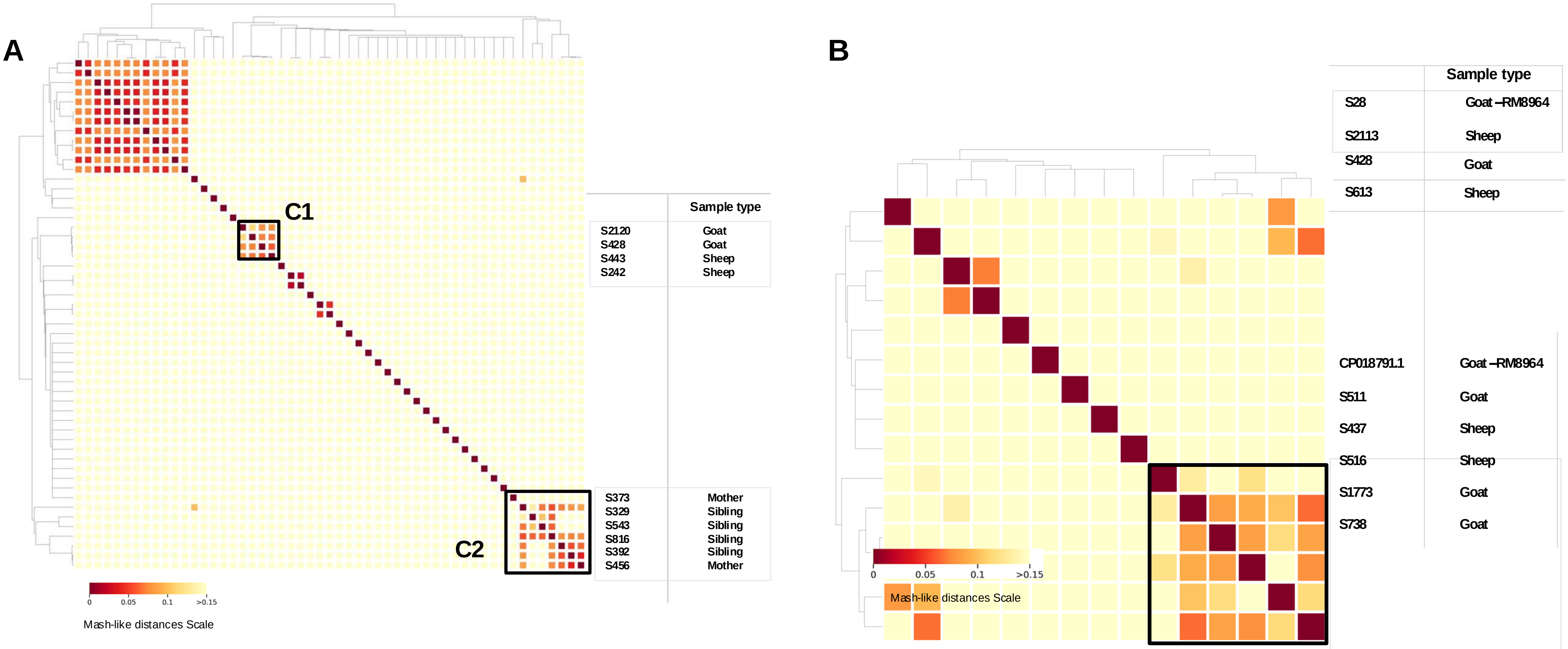

	Sample type
S2120	Goat
S428	Goat
S443	Sheep
S242	Sheep
S373	Mother
S329	Sibling
S543	Sibling
S816	Sibling
S392	Sibling
S456	Mother

	Sample type
S28	Goat –RM8964
S2113	Sheep
S428	Goat
S613	Sheep
CP018791.1	Goat –RM8964
S511	Goat
S437	Sheep
S516	Sheep
S1773	Goat
S738	Goat

Figure S1. *Pairwise Mash-like distances for A) Campylobacter concisus B) Campylobacter vicugnae. Each sample in the dataset was compared to itself and all other samples. The colors in the matrix represent the range of Mash-like distances (refer to the scale). The diagonal line compares each sample to itself, resulting in dark red squares, indicating zero differences between the sequences. Black boxes are used to show clustering of samples (C1 and C2 in A), and on the right side, sample metadata, including samples and host species are utilized to support the genetic similarities observed in the metagenomic dataset.*