



Figure 2. Rumen microbiome metagenomics of twin lambs inoculated with rumen fluid from donor ewes divergent for feed efficiency. Analyses were performed using the core diversity analysis command in QIIME (Caporaso et al., 2010) using a sampling depth of 559 (minimum number of sequence reads per sample) to account for variation in total number of sequence reads per sample. **Recipients (L = lambs inoculated with low RFI donors; H = lambs inoculated with high RFI donors) and donors (DL = low RFI donor; DH = high RFI donor). (A) Phylum level rumen microbiome taxonomy summary; (B) Alpha diversity chao1 rarefaction curve; (C) Bray Curtis Emperor PCoA Plot.