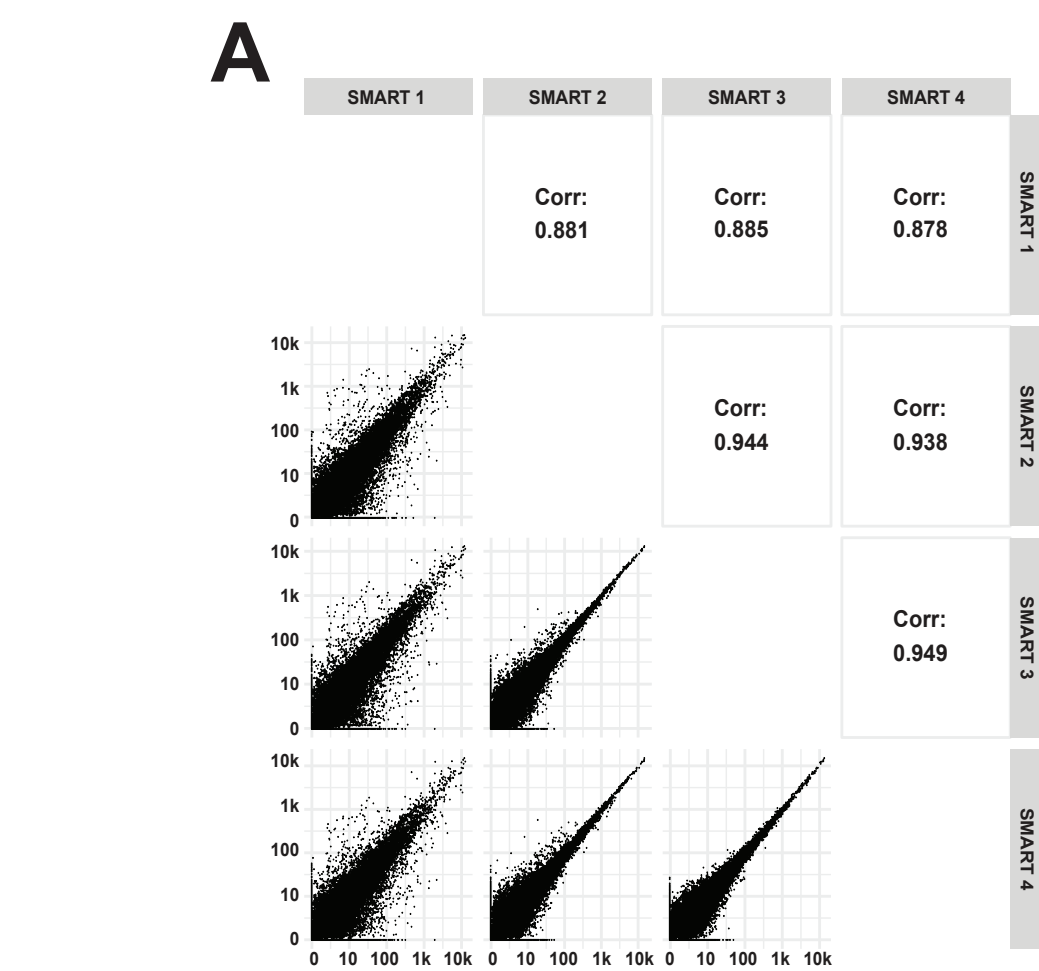

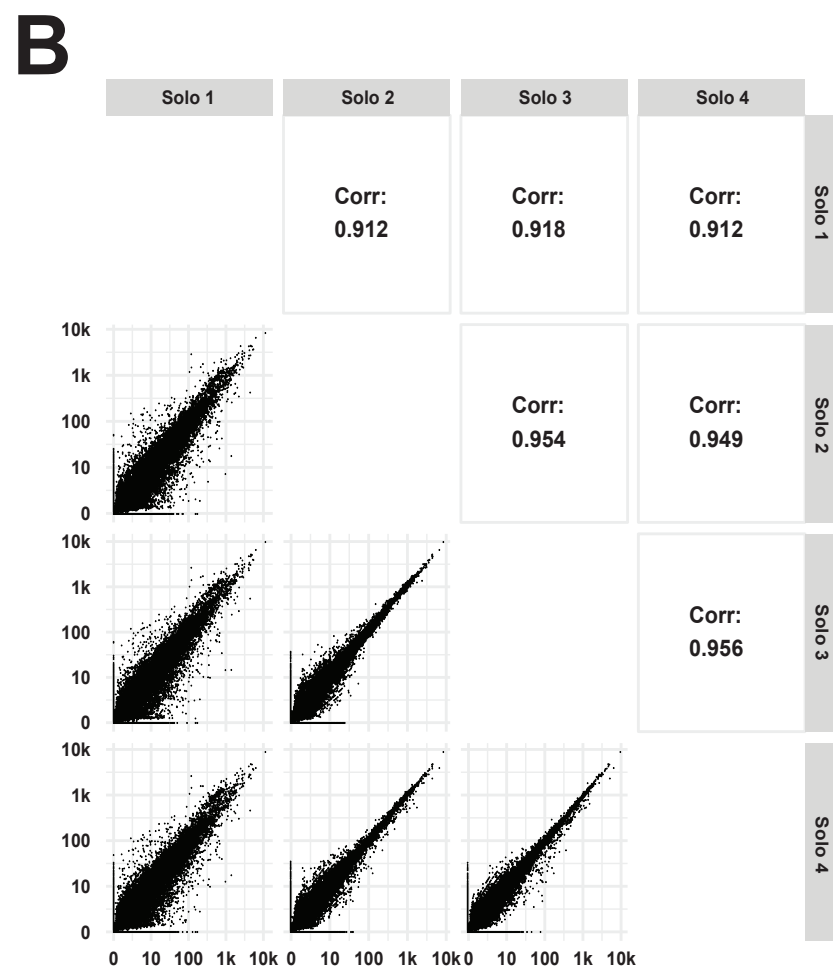

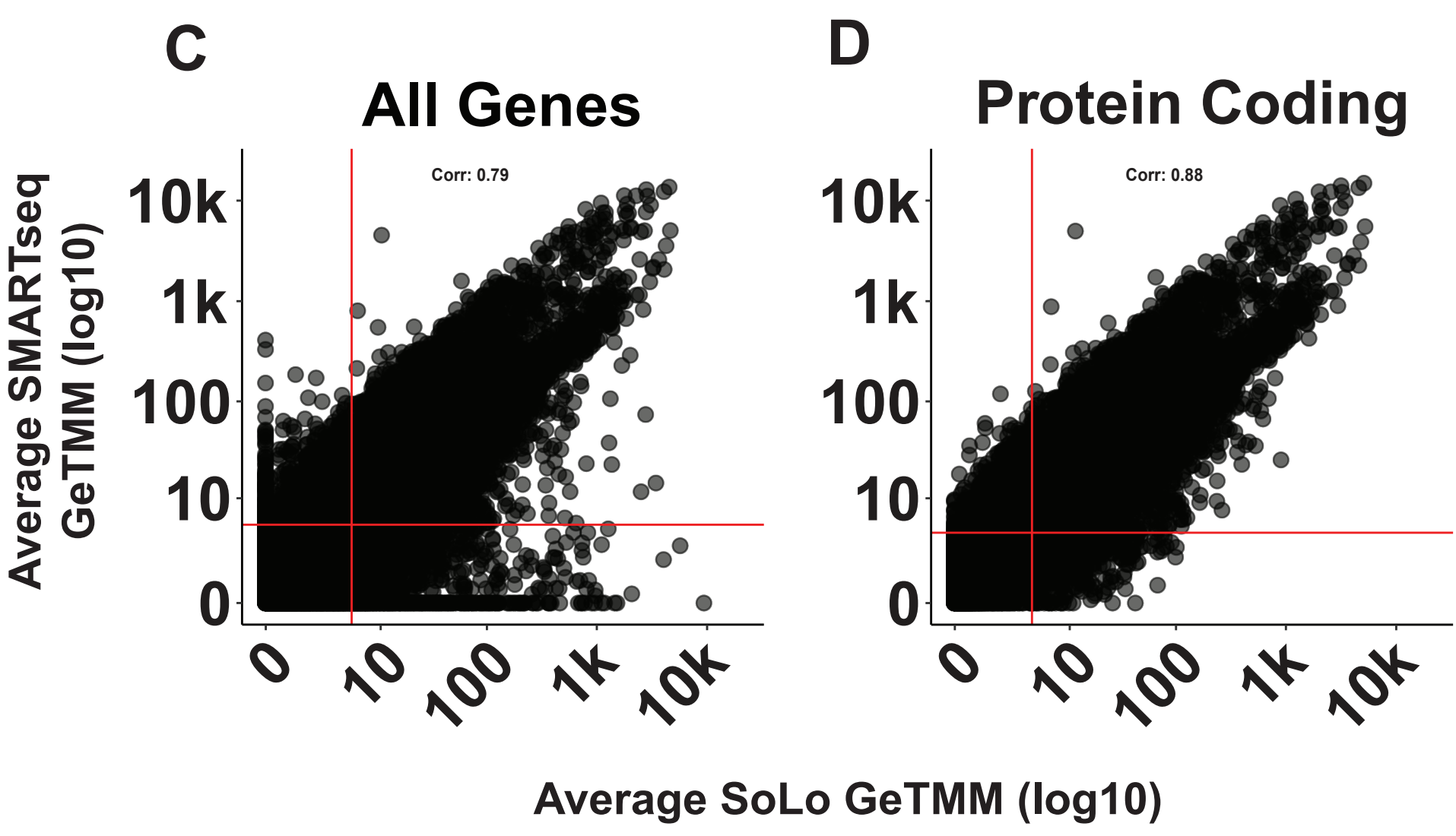

Figure S1: GeTMM values correlate within and between techniques A-B) Scatter plots with correlation values for all pairwise replicates within SMARTseq (A) and SoLo (B) samples. C-D) Scatter plots showing averaged log10 GeTMM values for SoLo and SMARTseq samples using all genes (C), and just protein coding genes (D), red lines indicate 5 GeTMM.