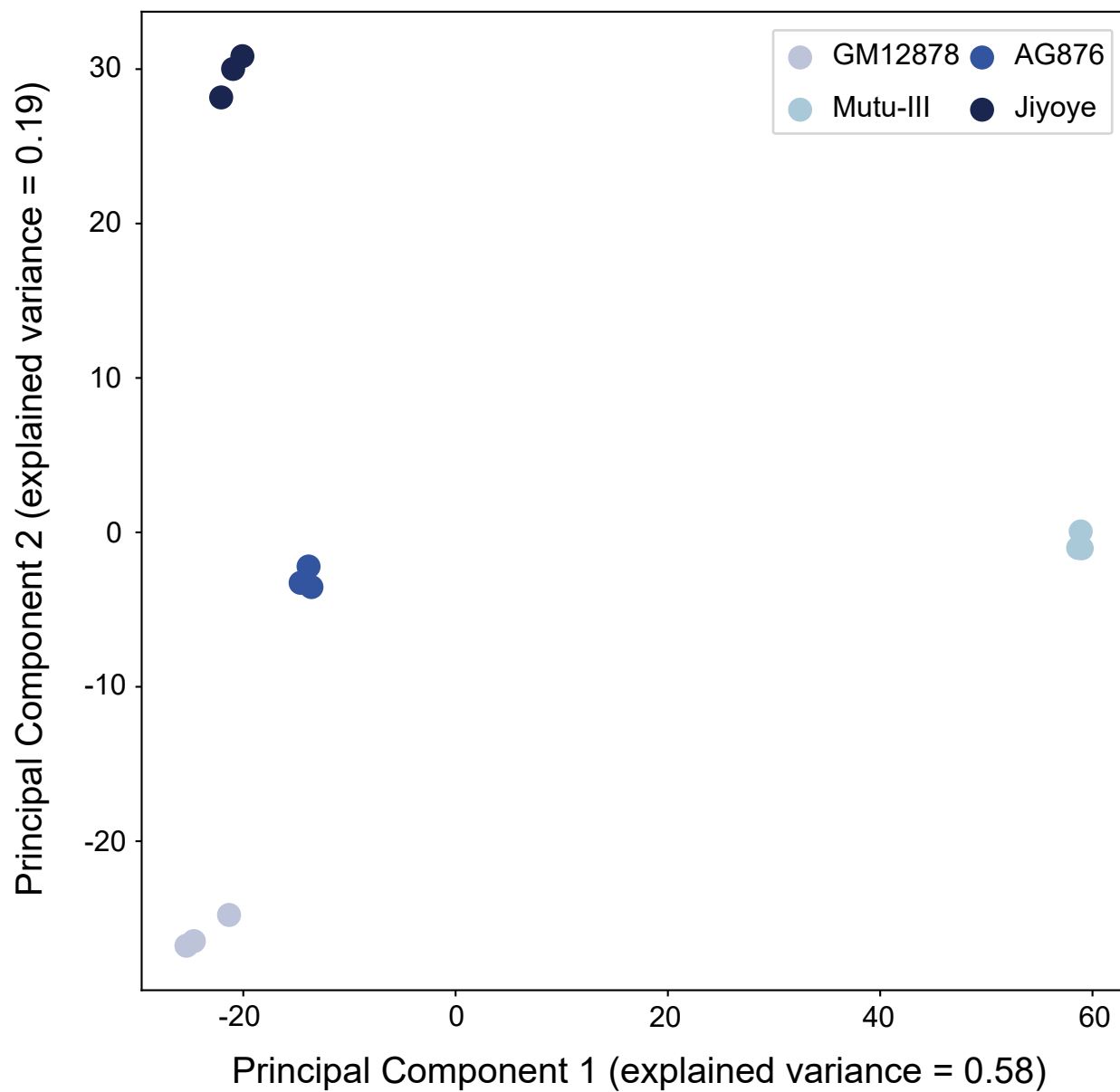




Additional File 7: Supplemental Figure 7. Comparison of RNA-seq datasets across type 1 and type 2 EBV B cell line replicates. Principal component analysis (PCA) on the 12 RNA-seq datasets used in this study. The publicly available Mutu-III RNA-seq dataset was sequenced single-end using a Poly(A) transcriptome library. AG876, Jiyoye, and GM12878 datasets (which were generated in this study) were sequenced paired-end using a whole transcriptome library. Experimental replicates cluster tightly together.