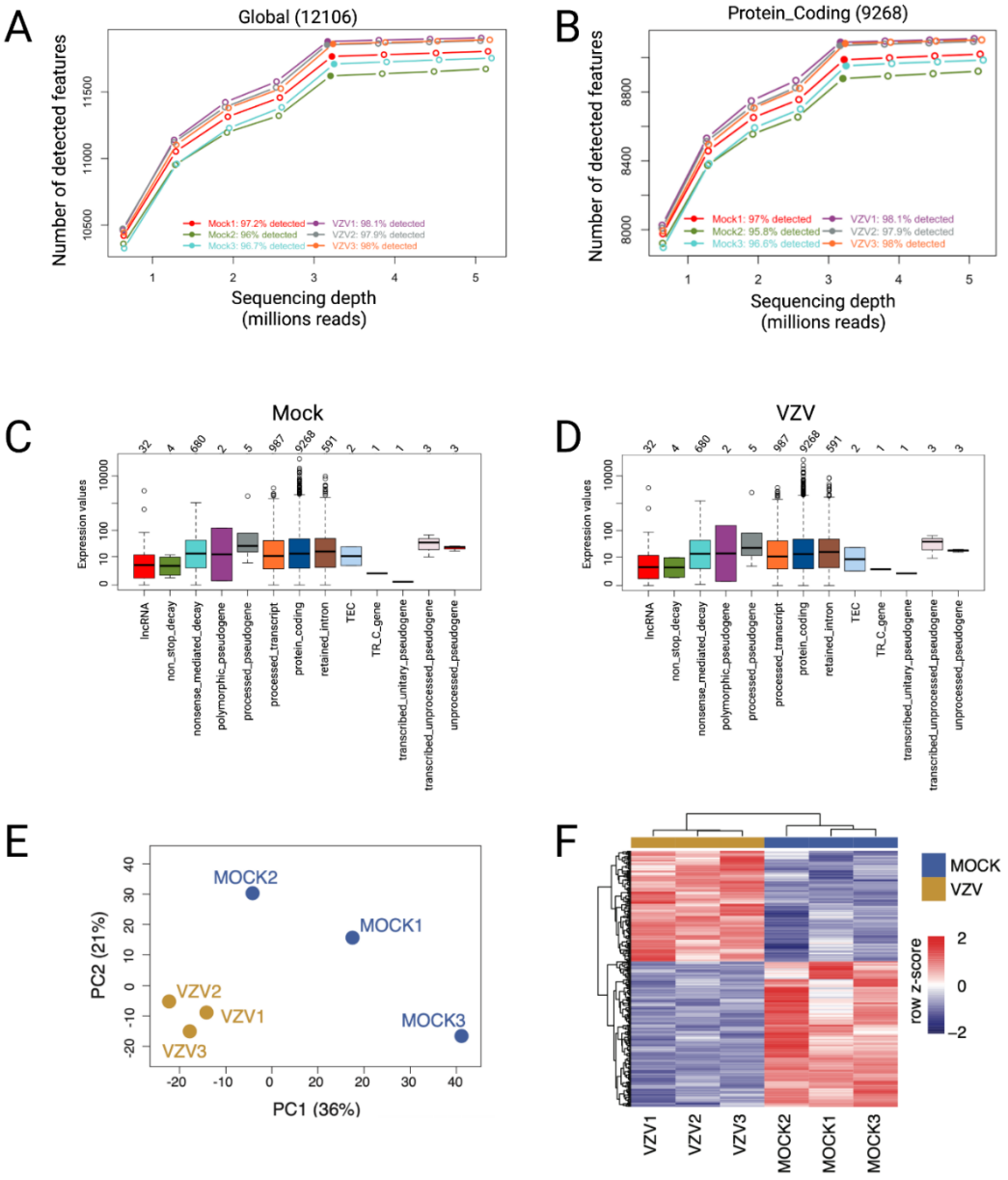
eFigure 1 Whole-transcriptome profiling of mock and VZV-infected HBVAFs

(A) Saturation plot of sequencing depth and number of detected features (all RNA biotypes) for each sample. Solid circle denotes observed number of detected features, open circles are predicted number of detected features simulated at higher depths (increasing number of reads; right x-axis) or lower depths (decreasing number of reads; left x-axis). (B) Saturation plot of sequencing depth and number of detected features of all samples for protein coding RNA only. (C) Distribution of expression values by RNA biotype for mock-infected HBVAFs and (D) VZV-infected HBVAFs. (E) Principal component analysis (PCA) reduces the dimensions of large data sets, allowing a description of data sets and their variance with a reduced number of variables. PCA shows tight clustering of HBVAFs samples based on infection status (VZV- or mock-infected, gold and blue circles, respectively). (F) Heat map of all 320 DEGs show a clear clustering of genes based on infection status (blue denotes mock-infected samples, gold denotes VZV-infected samples).



eFigure 2 Biodetection Plots for Individual Samples

Gray bar corresponds to the percentage of each biotype in the genome, stripped color bar is the proportion detected in the samples, and the solid color bar is the percentage of each biotype within the sample. Vertical green line separates the most abundant biotypes (left side x-axis) from the rest (right side x-axis).