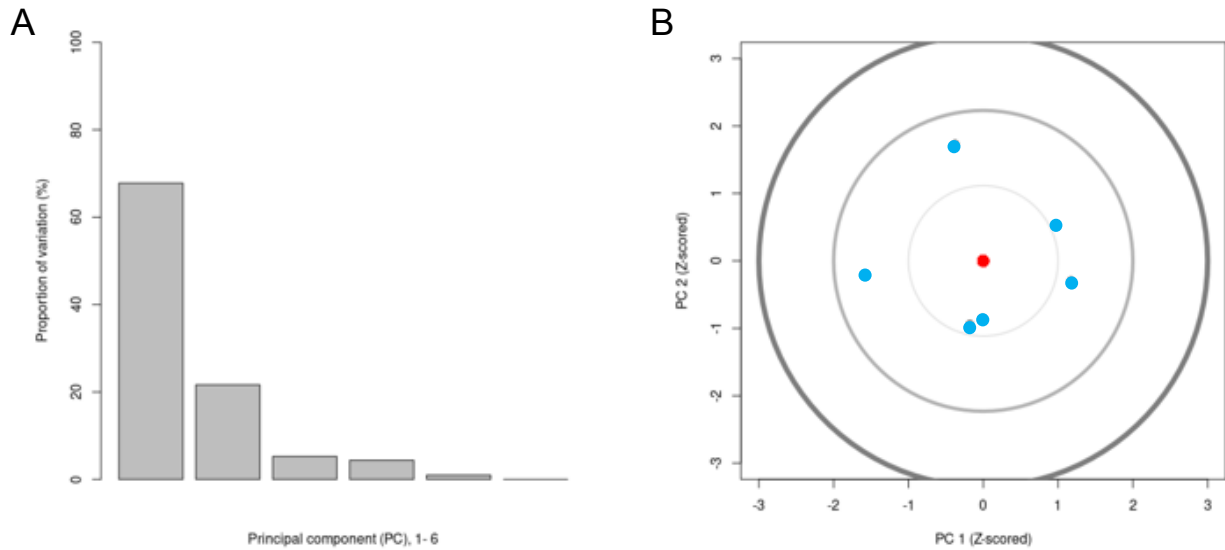




Supplementary Figure 2. Transcriptomics principal component analysis. (A) Scree plot showing the proportion of transcriptomic variation explained by each principal component. **(B)** Scatter plot tracking each sample (blue dots) on normalized (Z) principal component coordinates. The red dot indicates $Z_1=0$, $Z_2=0$, while grey circles indicate increasing $Z = \sqrt{(Z_1^2 + Z_2^2)}$, $Z=1$ (thin line), $Z=2$ (medium line), $Z=3$ (thick line). All samples lie within $Z=2$, thus all transcriptomics data was deemed uniform (P-value > 0.05 from $Z < 2$) and used for the analyses.