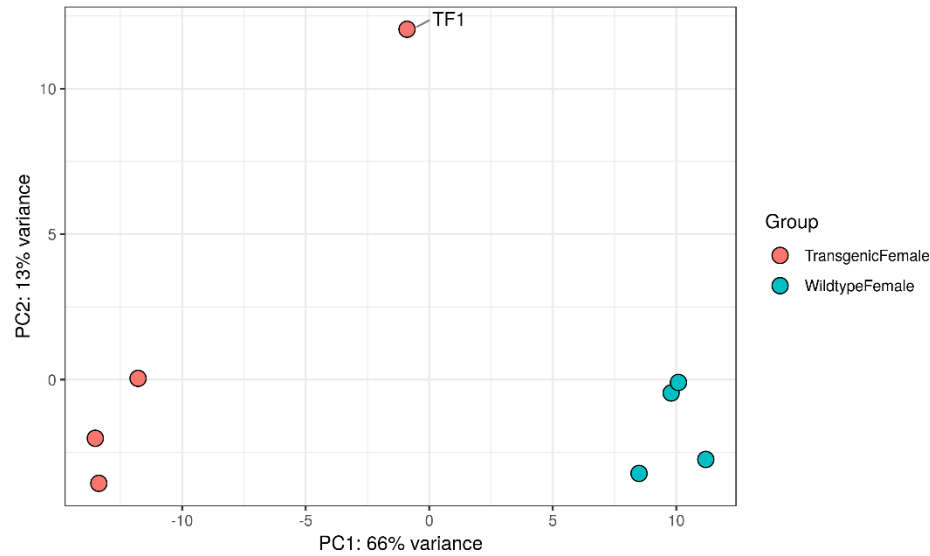


A



B

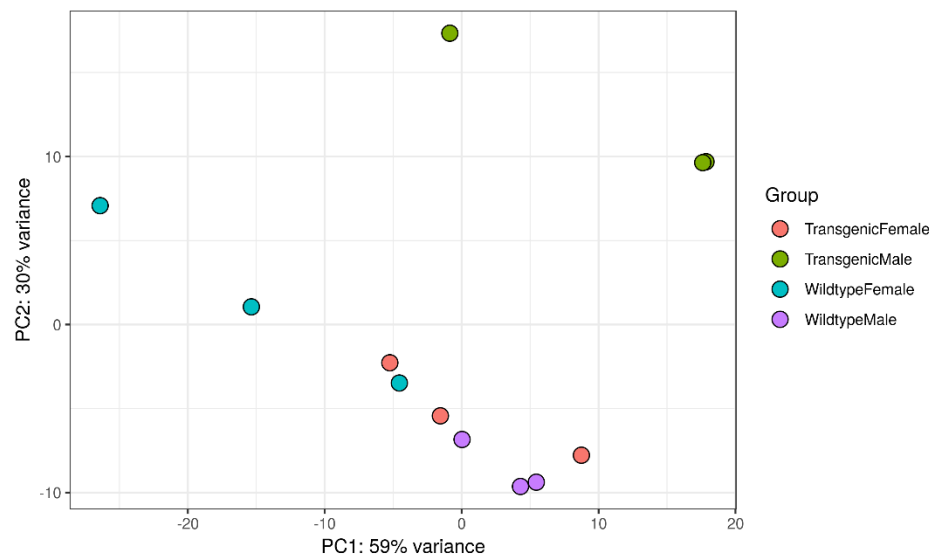


Figure 1-figure supplement 1. Principal component analysis of replicates from Experiment A (Panel A, two genotypes from *nGuy1_2*) and Experiment B (Panel B, 4 genotypes from *nGuy1_1*). The Euclidean distance between samples was calculated based on the *regularized-logarithm* transformed count data, implemented in the package DESeq2. In Panel A, one of the four transgenic female replicates (TF1) was excluded when transgenic female replicates were analyzed as a group.