



Figure S3 Population structure assessed through principal component analysis (PCA) using 900K autosomal SNPs after LD pruning. (A) 154 DGRP inbred lines projected onto the plane spanned by the first two principal components (PC1, PC2). The points are colored according to the phenotype severity in the $hINS^{C96Y}$ crosses (red: severe, or first 25%; blue: intermediate, 25%-75%; green: mild, 75%-100%, percentiles in eye area distribution from small to large). (B) projection onto PC1 grouped by their phenotype severity showed no correlation between the two.