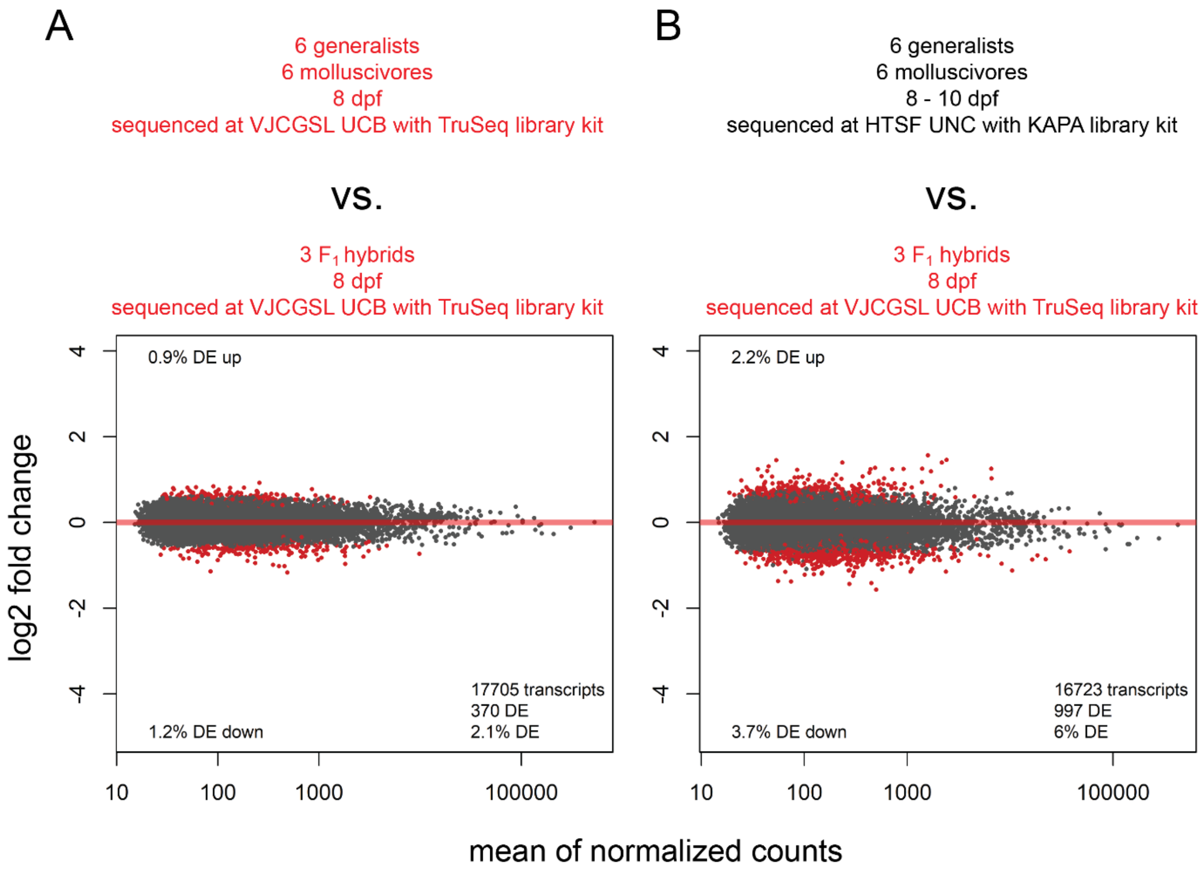

Fig S5. Estimating the effect of sequencing design on the proportion of genes misregulated in hybrids. The 8 dpf hybrids were sequenced at the same facility with the same library kit as the 17-20 dpf hybrids, while the 8-10 dpf parental species were sequenced at the same facility with the same library kit as the 17-20 dpf parental species. A) The comparison between 8 dpf parental species and 8 dpf hybrids revealed 370 genes (2.1%) misregulated. B) The comparison between 8 dpf hybrids and 8-10 dpf parental species revealed 997 (6%) genes misregulated – a 37% increase. We used this inflated estimate to adjust our estimate of misregulation in 17-20 dpf hybrid craniofacial tissues. Red points indicate genes detected as differentially expressed at 5% false discovery rate with Benjamini-Hochberg multiple testing adjustment. Grey points indicate genes showing no significant difference in expression between groups.