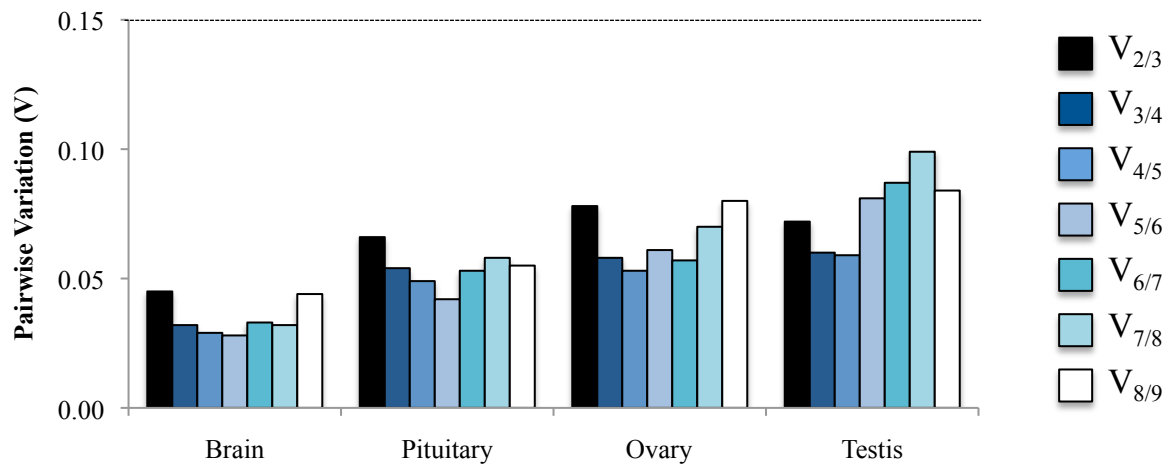


### A. Zebra finch



### B. White-throated sparrow

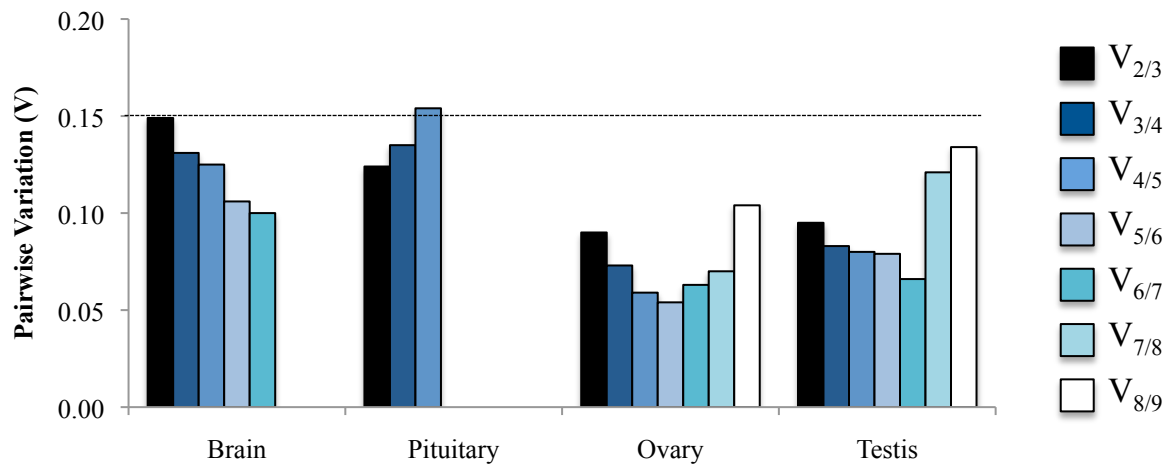


Figure S1: Determination of the optimal number of reference genes using geNorm. Pairwise variation ( $V_n/V_{n+1}$ ) analysis between sequential normalization factors ( $NF_n$  and  $NF_{n+1}$ ) for each set of tissues (x-axis) was used to determine the optimal number of control genes. Each bar represents the pairwise variation between the normalization factors calculated for  $n$  and  $n+1$  genes. A value of 0.15 is used as the suggested cut-off, below which addition of the next most stable gene does not have a significant effect (Vandesompele et al., 2002). On the basis of these data, the two most stable reference genes were sufficient for normalization in all tissues, as addition of the third most stable gene did not have a significant effect on the normalization factor ( $V_{2/3} < 0.15$ ).