



Fig. E Variation among mouse strains. In order to quantify the level of relatedness of each of the strains relative to FVB/N we calculated the median absolute deviation (MAD) across the genome for all individuals from each of the different strains and averaged the MAD for each of the strains. We observed a range in MAD from 0.07 to 0.12. As expected, the closely related NIH strain has a MAD value comparable to FVB/N, since FVB/N was used as the reference in these hybridizations. We propose that the increased MAD in other strains is due to greater sequence divergence between different inbred strains.