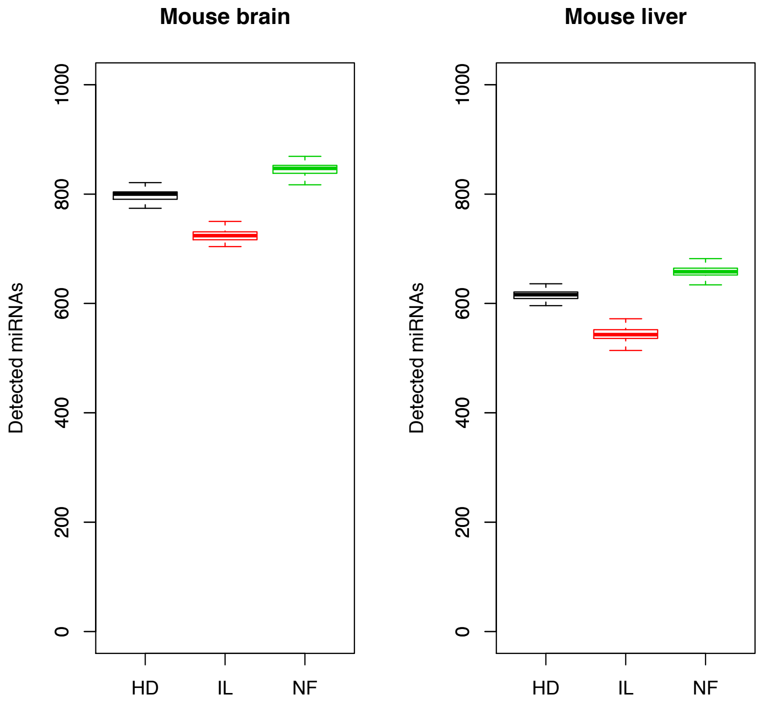

Supplemental Figure S1. Comparison between miRNA sequencing protocols. Libraries were prepared from one mouse brain and one mouse liver sample using three different protocols: HD (HD), Illumina (IL) and NEXTflex (Methods). Sequencing reads were processed and mapped as described in the main text. To compare miRNA coverage within each sequenced library, we counted the number of miRBase mature miRNAs that were represented by at least 1 read within sets of 1 million randomly subsampled mapped reads per library. Each boxplot corresponds to 100 subsampled sets.