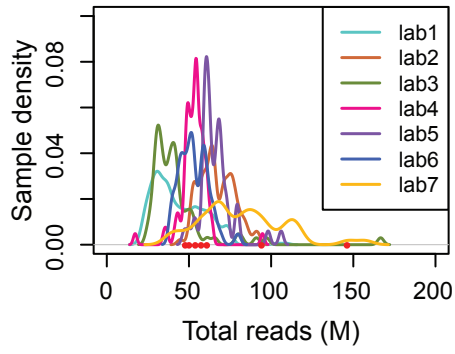
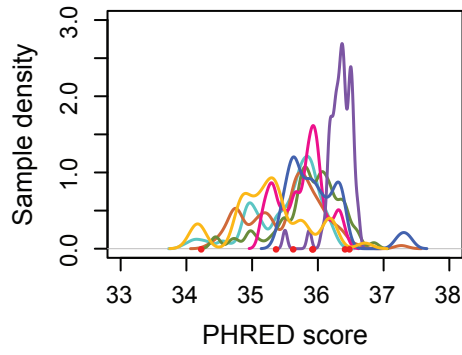


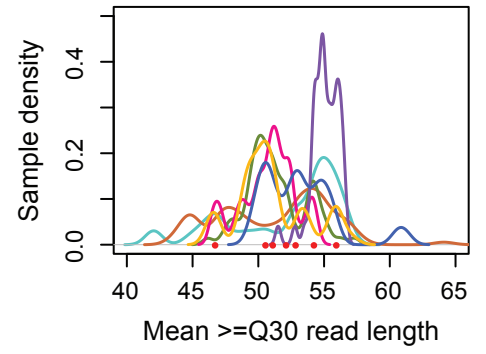
**A) Sequencing depth**



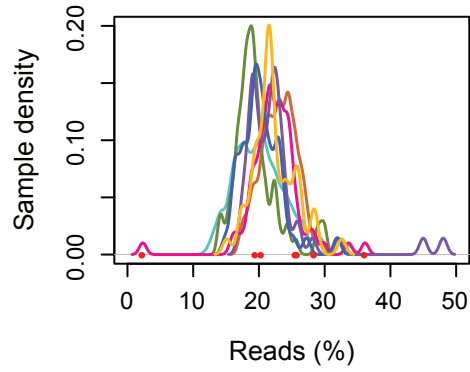
**B) Sequencing quality**



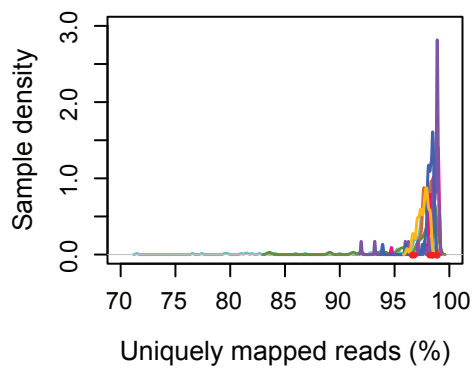
**C) Sequencing quality**



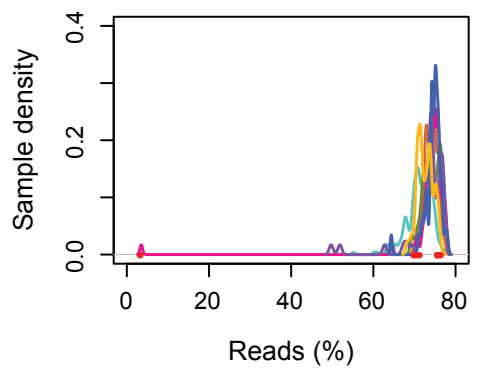
**D) Duplicates**

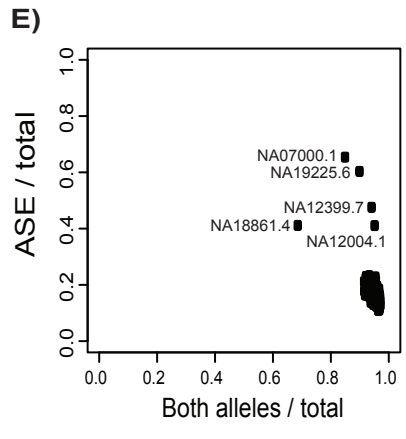
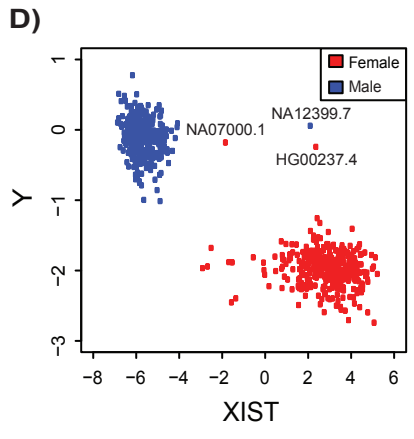
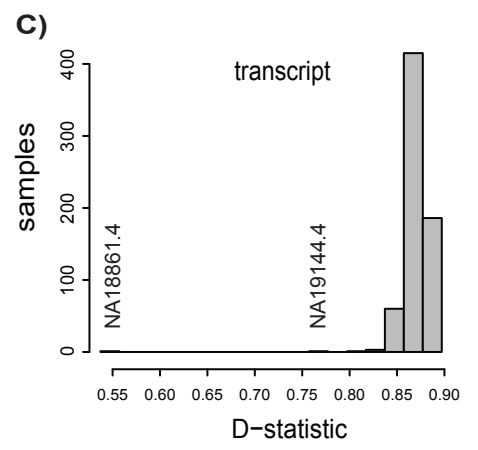
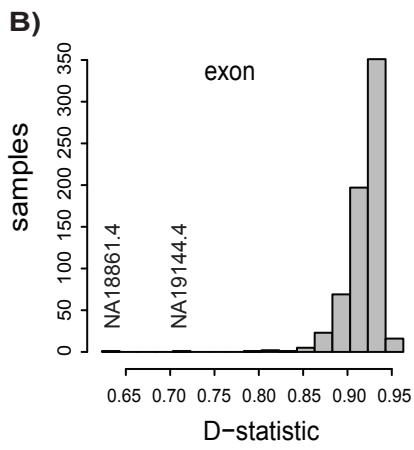
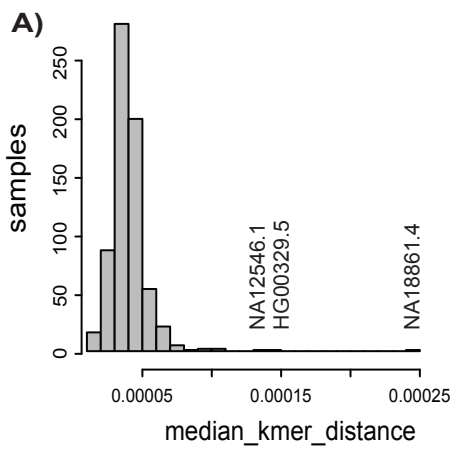


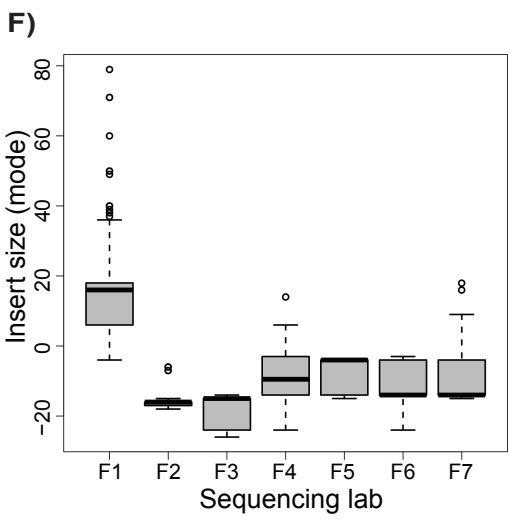
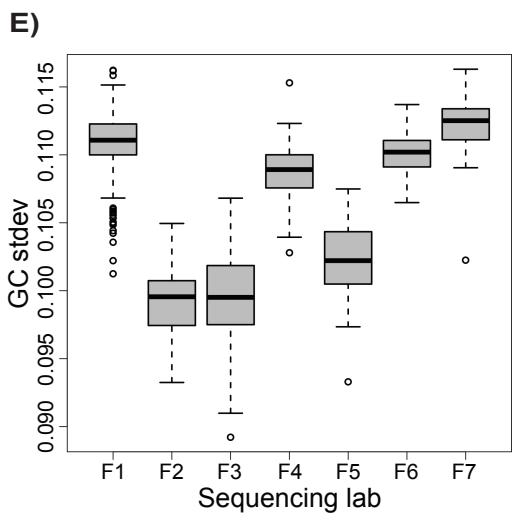
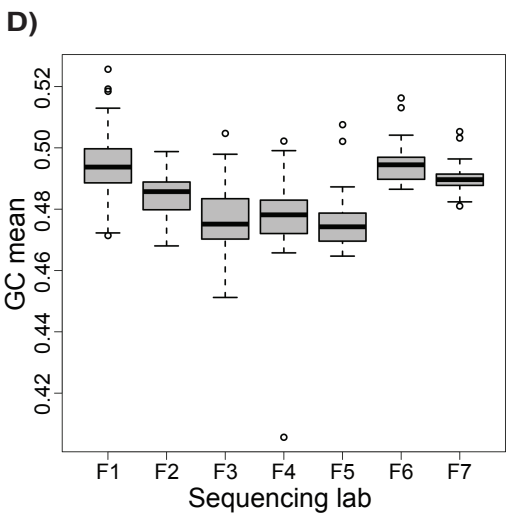
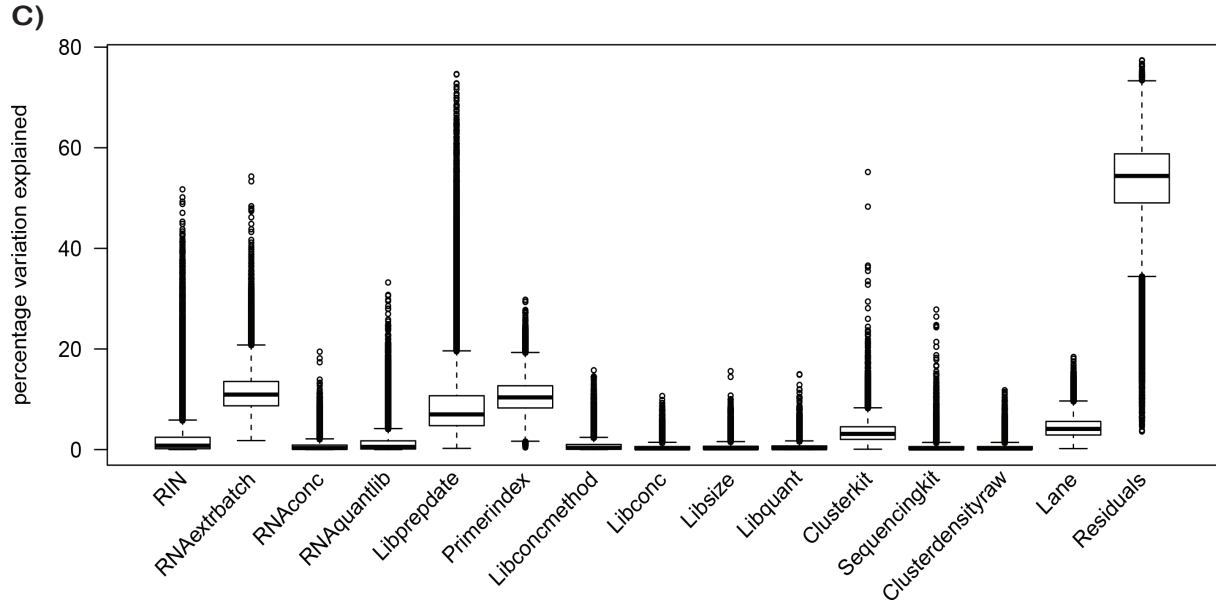
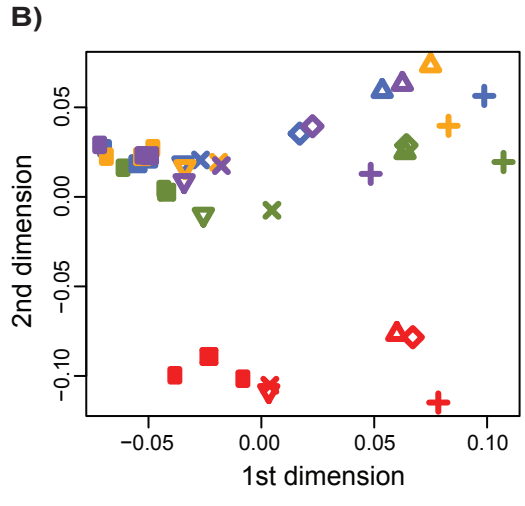
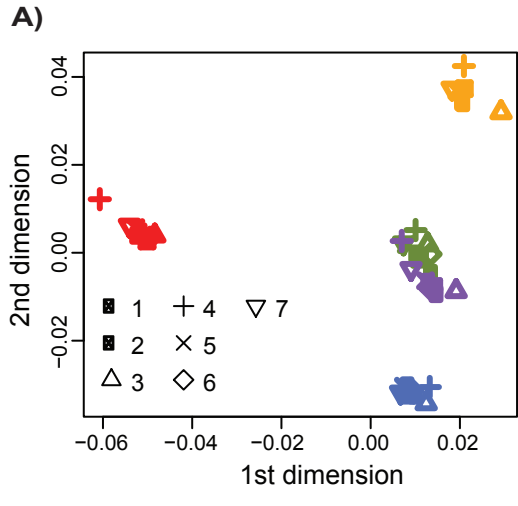
**E) Mapping**

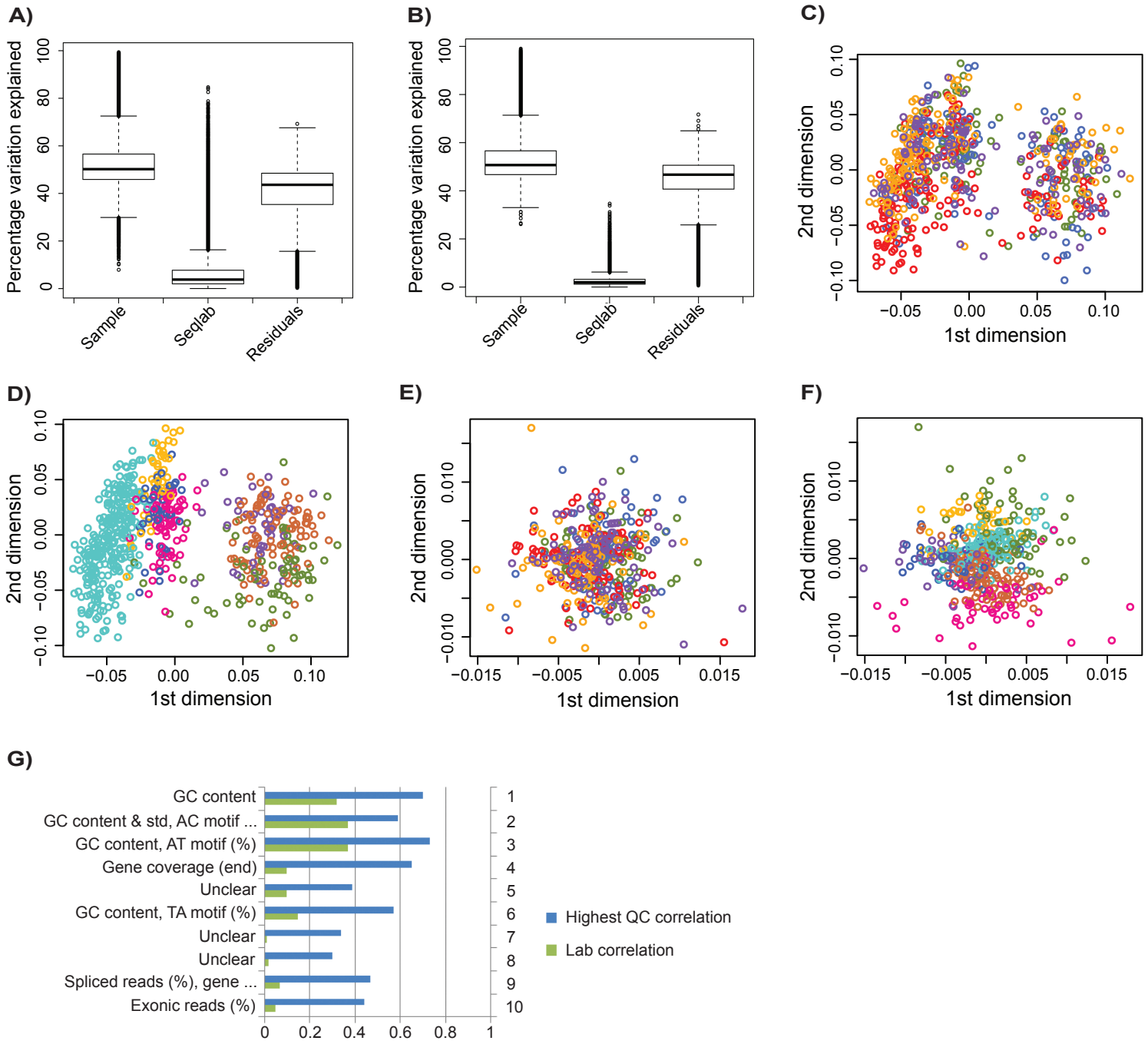


**F) Reads in exonic regions**



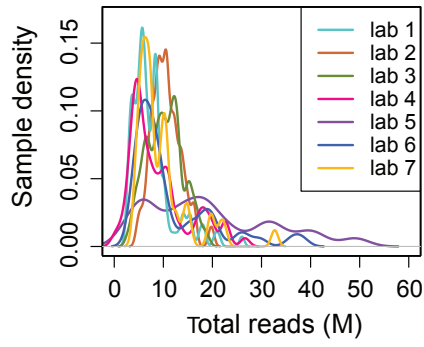




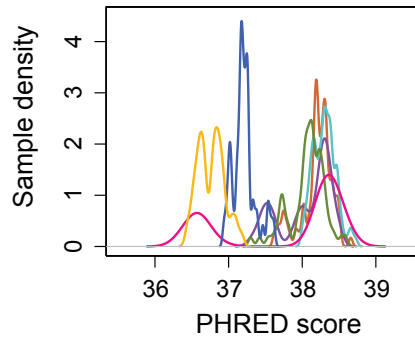


*t Hoen et al. Figure 4*

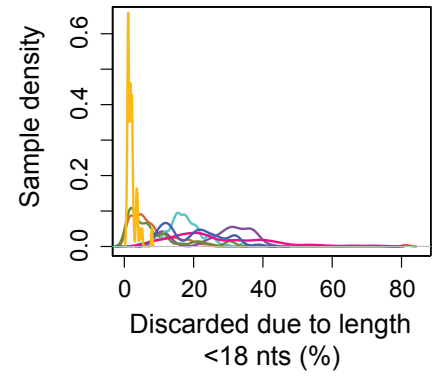
**A) Sequencing depth**



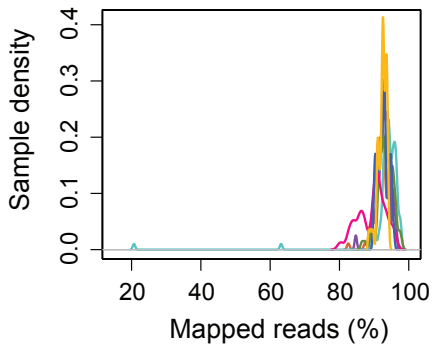
**B) Sequencing quality**



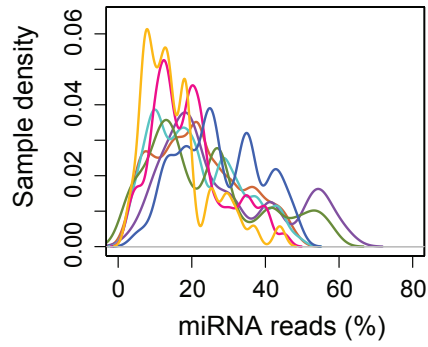
**C) Short reads**



**D) Mapping**



**E) miRNA content**



**F) miRNA genes**

