**miRNA Analysis:**

miRNA was analyzed using sRNA Detection module of Oasis [1]. It examines sample qualities, as well as quantifies known and novel sRNAs for each submitted sample. A principal component analysis (PCA) plot was generated to understand sample similarities based on sRNA expression, followed by trimming reads filtered for being too short or too long. By pressing the different buttons at the top, the bars can be shown (solid button) or hidden (hollow button). sRNAs in Oasis are grouped into various species, including micro RNA (miRNA), piwi RNA (piRNA), small nucleolar RNA (snoRNA), small nuclear RNA (snRNA) and ribosomal RNA (rRNA). *T*rimming is followed by length filtering and mapping reads to the reference genome. Finally count files for all known sRNA species, as well as novel, predicted miRNAs, are generated for each sample. Differential miRNA analysis was performed using package DESeq(dds), followed by sizeFactors(dds) and dispersions(dds) [2]. By comparing WT\_4\_Ct\_Cx and SAMP8\_Ct\_Cx8, 147 miRNA’s and SAMP8\_Ct\_Cx8.csv and SAMP8\_UNC0642 comparison with 25 miRNA’s were found to have a significant P value (<0.05) and fold change (>2). The list of these miRNA’s is provided in files WT\_4\_Ct\_Cx\_vs\_SAMP8\_Ct\_Cx8.csv and SAMP8\_Ct\_Cx8.csv\_vs\_SAMP8\_UNC0642.csv.

**References:**

1. Capece, V., Garcia Vizcaino, J. C., Vidal, R., Rahman, R.-U., Pena Centeno, T., Shomroni, O., … Bonn, S. (2015). Oasis: online analysis of small RNA deep sequencing data. Bioinformatics, 31(13), 2205–2207. <http://doi.org/10.1093/bioinformatics/btv113>
2. Anders, S., Huber, W. Differential expression analysis for sequence count data. *Genome Biol* **11,**R106 (2010). https://doi.org/10.1186/gb-2010-11-10-r106