

## **Appendices**

**Appendix A: Maximum Illumina/Solexa high-throughput sequencing read depths for each of the miRNAs both pre and post normalisation in addition to log fold change and adjusted P-values for a comparison between normalised read depths in the heterozygotes and homozygous mutants.** Listed are all miRNAs with a prenormalised maximum read depth of at least 1 in a single sample. The miRNAs are ordered according to their normalised expression in the *Dgcr8*<sup>+/+</sup> cell line.

**Appendix B: Additional GO term and KEGG pathway analyses of the genes up regulated upon the depletion of DGCR8 (Including an HTML representation of Table 5.1).** Genes up regulated upon the depletion of DGCR8 (*P*-value < 0.05, LFC > log<sub>2</sub>(1.1)) were subjected to GO term and KEGG pathway enrichment and depletion analyses. Presented are the results of 8 analyses including both the over and under-representation of “Biological Process” (BP), “Molecular Function” (MF) and “Cellular Compartment” (CC) GO terms and KEGG pathways associated with genes within this list. Hyperlinks connect to relevant databases.

**Appendix C: HTML representations of the tables included in Table 5.3. These summarise the annotation associated with the candidate targets of mmu-miR-25 and mmu-miR-291a-3p.** The tables contain the probe IDs that fulfilled the criteria required to be associated with a miRNA target. The “Gene Symbols”, “Gene Name” and “Entrez ID” for each probe were annotated according to the *lumiMouseAll* Bioconductor library. Where these annotations were not available, “Gene Symbols” and “Entrez ID” were annotated according to the annotations of Dr. Cei Abreu-Goodger (derived from Ensembl, Nov 2008) and marked with an asterisk. Also included are the LFCs and *P*-values associated with each array experiment used to define the set, associated GO terms and KEGG pathway information, relevant miRNA seed counts within the 3'UTRs of associated transcripts and TargetScan (v4.2) and miRBase Target predictions for each gene for the respective miRNA. Hyperlinks connect to relevant databases.