**Legends for Supplementary Files**

Supplementary File 1. Flax genome derived miRNA hairpin structures. All flax genome predicted miRNAs and their pre-cursors are shown with the hairpin structures of the miRNAs and the position of the mature miRNA marked and the sequence given.

Supplementary File 2. Flax UNIGENE derived miRNA hairpin structures. All flax UNIGENE predicted miRNAs and their pre-cursors are shown with the hairpin structures of the miRNAs and the position of the mature miRNA marked and the sequence given.

Supplementary File 3. Discarded flax genome derived hairpin structures. All flax genome predicted hairpin sequences which were discarded as potential pre-miRNAs on the basis of current standards for miRNA prediction are provided.

Supplementary File 4. Discarded flax UNGENE derived hairpin structures. All flax UNIGENE predicted hairpin sequences which were discarded as potential pre-miRNAs on the basis of current standards for miRNA prediction are provided.

Supplementary File 5. Predicted targets for Unigene derived miRNAs. All flax UNIGENE predicted miRNAs which were found to have targets using the program psRNATarget as well as the parameters used, the sequences of the miRNA and target site as well as mode of inhibition as determined by the sequenced complimentarity at positions 9-11 nt of the mature miRNA are provided.

Supplementary File 6. miRNA:target duplex structures for Contig6926. psRNATarget predicted targeting of Contig6926 by multiple novoMIR predicted miRNAs. The miRNA:target duplex structure for the targets is shown for each match as well as the parameters used.

Supplementary File 7. miRNA:target duplex structures for Contig3977. psRNATarget predicted targeting of Contig3977 by multiple novoMIR predicted miRNAs. The miRNA:target duplex structure for the targets is shown for each match as well as the parameters used.

Supplementary File 8. miRNA:target duplex structures for miRNA:5208. Multiple psRNATarget predicted targets for novoMIR predicted miRNA:5208. The miRNA:target duplex structure for the targets is shown for each match as well as the parameters used.

Supplementary File 9. miRNA:target duplex structures for pre-miRNA:932. Multiple psRNATarget predicted targets for novoMIR predicted pre-miRNA:932. The miRNA:target duplex structure for the targets is shown for each match as well as the parameters used.

Supplementary File 10. miRNA:target duplex structures for Scaffold1966 miRNAs. Multiple psRNATarget predicted targets for novoMIR predicted miRNAs mapping to the same region of Scaffold1966 and overlapping by 204 nt. The miRNA:target duplex structure for the targets is shown for each match as well as the parameters used.

Supplementary File 11. miRNA:target duplex structures for pre-miRNA:1209. Multiple psRNATarget predicted targets for novoMIR predicted pre-miRNA:1209. The miRNA:target duplex structure for the targets is shown for each match as well as the parameters used.

Supplementary File 12. Targets of flax miRNAs. Putative Flax miRNAs were found to target 1063 Unigenes. These targets were analyzed using the KEGG Automated Annotation Server which was able to categorize the targets according to their predicted function and network hierarchy. These 175 targets from the 1063 unigenes had KEGG orthology to proteins with a known function.

Supplementary File 13. KEGG Pathway Analysis of Linum putative miRNA targets - breakdown by heirarchy subcategory. The KO values distinguishing targets by their orthology allowed them to be classified into all related pathways using KEGG BRITE. Each KO may be classified into more than one subcategory as well as more than one heirarchy. For the four heirarchies of Metabolism, Genetic Information Processing, Environmental Processing and Cellular Processes 59, 18, 4, and 19 (respectively) pathways were found to be associated with the flax putative miRNA targets.

Supplementary File 14. The complete dataset for all miRNAs derived from the flax genome with predicted targets. The 4,247 target/miRNA combinations were identified from 220 distinct miRNA gene units. Mature and precursor sequences are listed as well as the predicted targets, the psRNATarget parameters of the match, the sequence of the target found complimentary to the miRNA, as well as the Kyoto Encyclopedia of Genes and Genomic information (KEGG) data used to categorize targets to biological networks.