**Table S5, extended. Extended AGO-CLIP RNAi network map**

Matrix including genomic locations of all peaks called across the 97 samples included in this study. Peak identifiers (peakID) were assigned in the format “chromosome:start\_end:strand”; these are also described in individual columns and the width of the peak is included. Peaks were annotated and gene information is given including genic region (annotation), genes starts, ends, lengths, IDs, corresponding transcript IDs (LVP\_AGWG strain AaegL5.2 gene set), and peak distance to transcriptional start site (distanceToTSS). Information pertaining to filtering is also given by sample type at each specific peak location; number of replicates where the peak was called (peakBC), raw counts (counts), normalized counts in reads per million mapped (counts\_norm), number of peaks containing at least 10 raw reads (nhipeaks), and number of replicates containing at least one read (BCsample) are shown. Peaks were searched for high-confidence small RNAs and where applicable, small RNA information was appended by peak, including 6mer sequence(s) of all small RNA families potentially targeting the peak (six\_mer), predicted 6mer target sequence(s) (Psix\_target), the small RNA family name(s) (PsmallRNA\_family), the genomic coordinates of the 70nt extended peak in the format “chromosome:start\_end:strand” (extendedPeak), the extended peak sequence, which was searched for small RNA 6mers (seqUnderExtendedPeak), the 18mer(s) surrounding any 6mer match(es) (PSeqExtended), the start and end of the 6mer pattern(s) found in the format “chromosome:start\_end” (PsiteOfPattern) or its center in the format “chromosome:position” (PcenterOfPattern), the absolute distance of the 6mer(s) from the peak center (Pdistance\_to\_peak\_center), if the small RNA(s) was one of the most abundant or targeting small RNAs, and in which sample type (Ptop\_smallRNA), the number of sites at that peak separated by family (Psites\_within\_family), and the number of unique families targeting that peak (Psites\_unique\_families). Predicted targets were classified by seed pairing rules (Bartel, 2009) and Pseven\_A1\_target (family name), Pseven\_M8\_target (individual family members), and Peight\_target (individual family members) are shown. We additionally included an alternative 8mer in which the 3′ end of the target was not an A but was fully complementary to the small RNA (Peight\_target\_alt; individual family members). Predicted targets that were complementary to nt 1-18 of the small RNA with 0 mismatches (Pperfect\_18mer\_target) or with 1 mismatch (Pone\_mis\_18mer\_target) are shown and were only searched for the most abundant known and novel AGO2-loaded small RNAs (family name is shown). Chimera information is given by peak for each sample type, in the format “small RNA name x number of reads” (chimera) and whether the chimera(s) was one of the most abundant or targeting small RNAs, and in which sample type (top\_smallRNA\_chimera) is indicated. Multiple small RNA entries per peak are described and are separated by “:” if the small RNAs are within the same family, and by “;” if they are from different families. High-confidence peaks meeting stringent filtering conditions (filtered\_peak) and the high-confidence peaks supported by a chimera or predicted 6mer target (hi\_confidence\_target) are indicated.