Figure S3

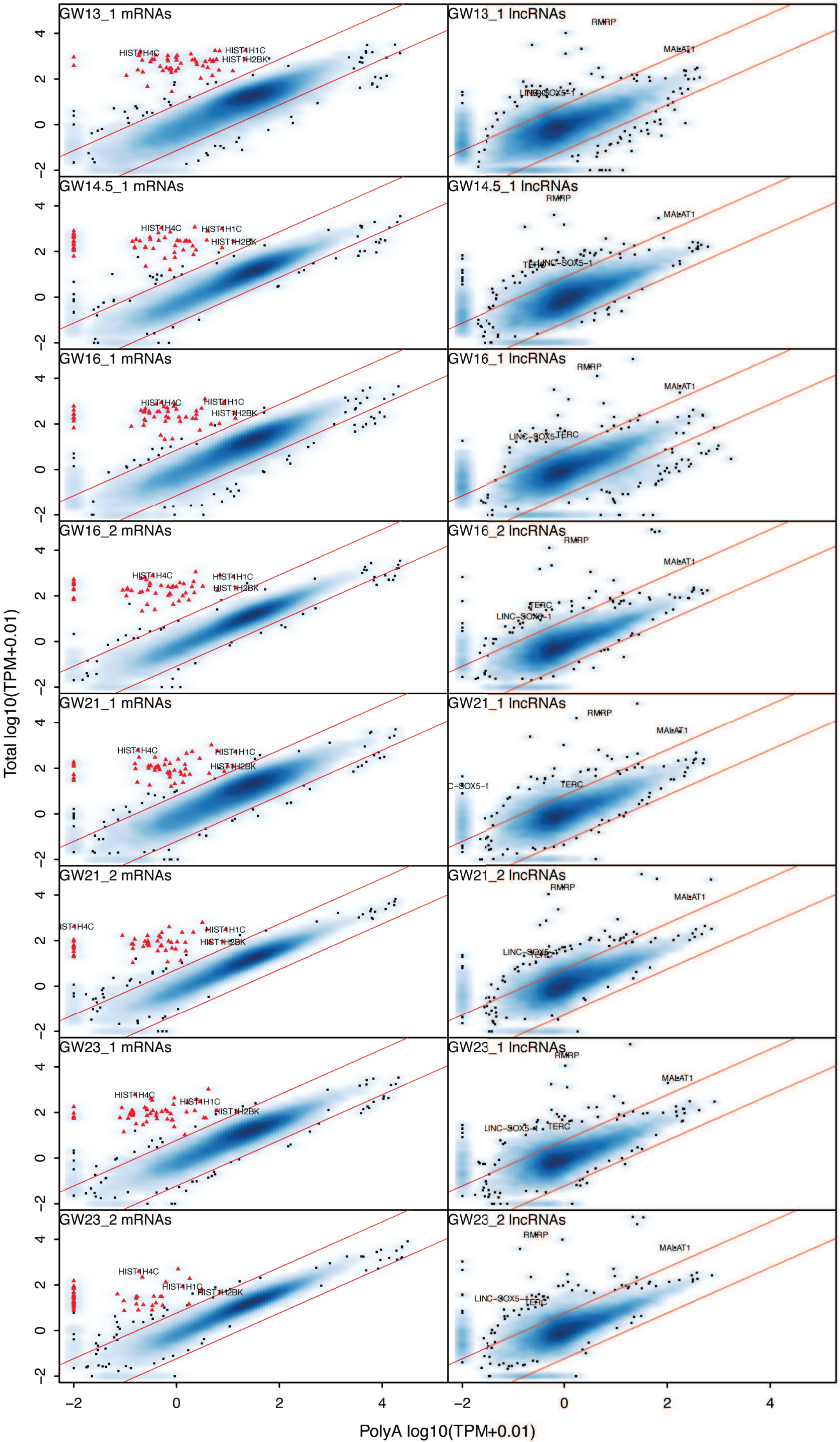

Figure S3. Identification of lncRNAs enriched in total RNA-seq

Smooth scatter plot comparisons of mRNA (left) and lncRNA (right) expression levels between polyA RNA-seq and total RNA-seq in all 8 samples. Genes not expressed either polyA or total RNA-seq were omitted. 58 mRNAs and 85 lncRNAs were consistently > 10 fold enriched in total RNA-seq across all samples. Only one gene, NDUFC2-KCTD14, was identified as consistently enriched in the polyA selected RNA-seq. Red diagonals represent 10 fold enrichment in either total (upper) or polyA (lower) fractions. Red triangles, histone subunits enriched > 10 fold in total RNA. TPM, Transcripts per Million.