Inventory of Supplementary Materials:
Supplementary Figures:
Figure S1, related to Figure 1
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Table S1, related to Figure 1. Tab1. Names of cell types. Tab2. Reads mapped in each library. Tab3. Correlation between array and RNAseq, and between cufflinks and stringtie.

Table S2, related to Figure 2. Tab1. List of local alternative acceptor events. Tab2. List of local alternative donor events. Tab3. List of local exon skipping events. Tab4. List of type I and type II intron retention events.

Table S3, related to Figure 4 and Figure 7. Tab1. List of primers used in the RT-PCR validation. Tab2. Expression levels of significantly differentially expressed lincRNAs.

Table S4, related to Figure 5. Tab1. Peptide quantification. Tab2. Quantification of protein abundance. Tab3. Peptides uniquely mapped to alternative spliced isoforms.

Table S5, related to Figure 4. Average expression level of all isoforms.

File S6, related to Figure 1. Newly assembled protein coding gene models.

File S7, related to Figure 7. Genomic locations for the newly identified and modified lincRNAs.

External Databases: Raw read data were deposited in NCBI SRA database under BioProject PRJNA323955.

Supplemental Experimental Procedures