Figure S1

[Diagram showing three 180d sows with labels for heart, liver, lung, fat, muscle, brain, and ovary. The diagram indicates the use of WGS and RNA-seq with 150bp PE.]
Figure S2
S2-1

DNA

RNA

Chr1: 3656278
A->G

Chr1: 3656302
+ A->G

Chr1: 3656326
+ A->G

Chr1: 3656327
+ A->G

Chr1: 3656343
+ A->G

Chr1: 3656357
+ A->G
Figure S6

[Image of a network diagram showing various biological processes and their significance across different tissues (Brain, Fat, Heart, Liver, Lung, Muscle, Ovary). The diagram includes terms such as dendrite development, mRNA processing, cytoskeleton-dependent intracellular transport, and various metabolic processes. The visualization uses color coding to indicate the q-value and GeneRatio, with darker colors representing higher significance.]
Figure S7
Figure S9

(a) ADAR1 (FPKM) vs. Number of A-to-G sites

\[ r = 0.96 \]

\[ P < 0.01 \]

(b) ADAR2 (FPKM) vs. Number of A-to-G sites

\[ r = 0.65 \]

\[ P = 0.11 \]

(c) ADAR1 (FPKM) vs. Overall RNA editing level

\[ r = 0.95 \]

\[ P < 0.01 \]

(d) ADAR2 (FPKM) vs. Overall RNA editing level

\[ r = 0.63 \]

\[ P = 0.13 \]