Figure S1. Module analysis of the non-functioning pituitary adenoma-related lncRNA-mRNA network using Molecular Complex Detection. (A and B) lncRNA-mRNA interactions in two modules and pathway enrichment of protein-coding genes in each corresponding module. (A) Module 4 and (B) Module 5. Square nodes represent lncRNAs and elliptical nodes represent mRNAs. Red indicates upregulation and green indicates downregulation. Inc, long non-coding.
Figure S2. Module analysis of the non-functioning pituitary adenoma-related IncRNA-mRNA network by Molecular Complex Detection. (A-C) IncRNA-mRNA interactions in three modules and pathway enrichment of protein-coding genes in each corresponding module. (A) Module 6, (B) Module 7 and (C) Module 8. Square nodes represent IncRNAs and elliptical nodes represent mRNAs. Red indicates upregulation and green indicates downregulation. Inc, long non-coding.

- Log10 P-value

Positive regulation of smooth muscle cell proliferation
Potassium channel complex
Malaria
Voltage-gated potassium channel activity
Voltage-gated potassium channel complex
Bladder cancer

- Log10 P-value

G-protein activated inward rectifier potassium channel activity
Ensheathment of neurons
Axon ensheathment
Estrogen signaling pathway
Colorectal cancer
Inward rectifier potassium channel activity

- Log10 P-value

MicroRNAs in cancer
Phosphoprotein binding
SnoRNA localization
Progesterone receptor signaling pathway
Regulation of ERBB signaling pathway
Negative regulation of blood coagulation
Figure S3. Analysis of hub genes and module gene expression levels in recurrence at ≥5 years (red boxes) or ≤1 year (blue boxes), including (A) REEP6, (B) SQRDL, (C) KCNJ6, (D) ANXA2, (E) SPRY2, (F) KCNS3, (G) ITM2C, (H) THBS2, (I) RP11-402C9.1, (J) LINC01203, (K) RP11-479G22.8, (L) RP11-615I2.1, (M) RP1-249I4.2, (N) RP11-116N8.2 and (O) RP11-288L9.4. FC, fold-change.