Figure S1. PCA plot of long non-coding RNA expression profiles for samples from CI-AKI and control groups. Blue dots represent samples from CI-AKI group and red dots represent control samples. The X and Y-axis represent PC1 and PC2, respectively. The proportion of variance explained by PC1 is equal to 27.44 and 21.02% for PC2. PCA, Principal component analysis; CI-AKI, contrast-induced acute kidney injury; PC, principle component.
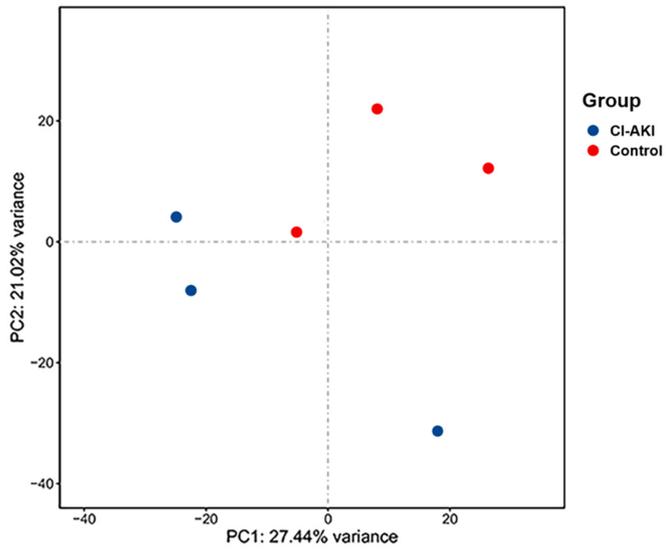
Figure S2. Functional enrichment analysis of the potential targets of differentially expressed long non-coding RNAs regulated in a *cis*-regulatory manner. (A) Significant GO terms enriched in the GO analysis. Red bars represent biological process, green bars represent cell component, and blue bars represent molecular function. (B) Significant pathways enriched in the Kyoto encyclopedia of genes and genomes enrichment analysis. GO, Gene Ontology.
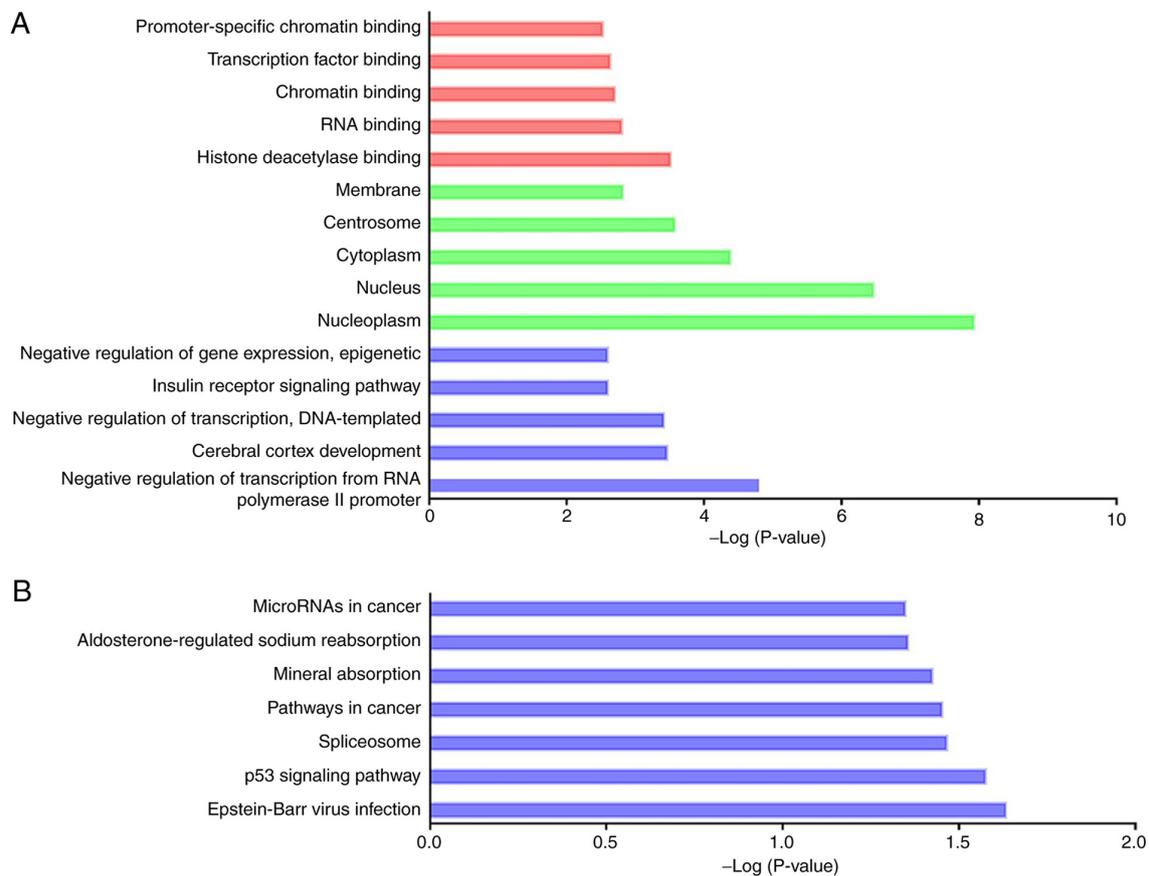
Figure S3. Functional enrichment analysis of the potential targets of differentially expressed long non-coding RNAs regulated in a *trans*-regulatory manner. (A) Significant GO terms enriched in the GO analysis. Red bars represent biological process, green bars represent cell component, and blue bars represent molecular function. (B) Significant pathways enriched in the Kyoto encyclopedia of genes and genomes enrichment analysis. GO, Gene Ontology.
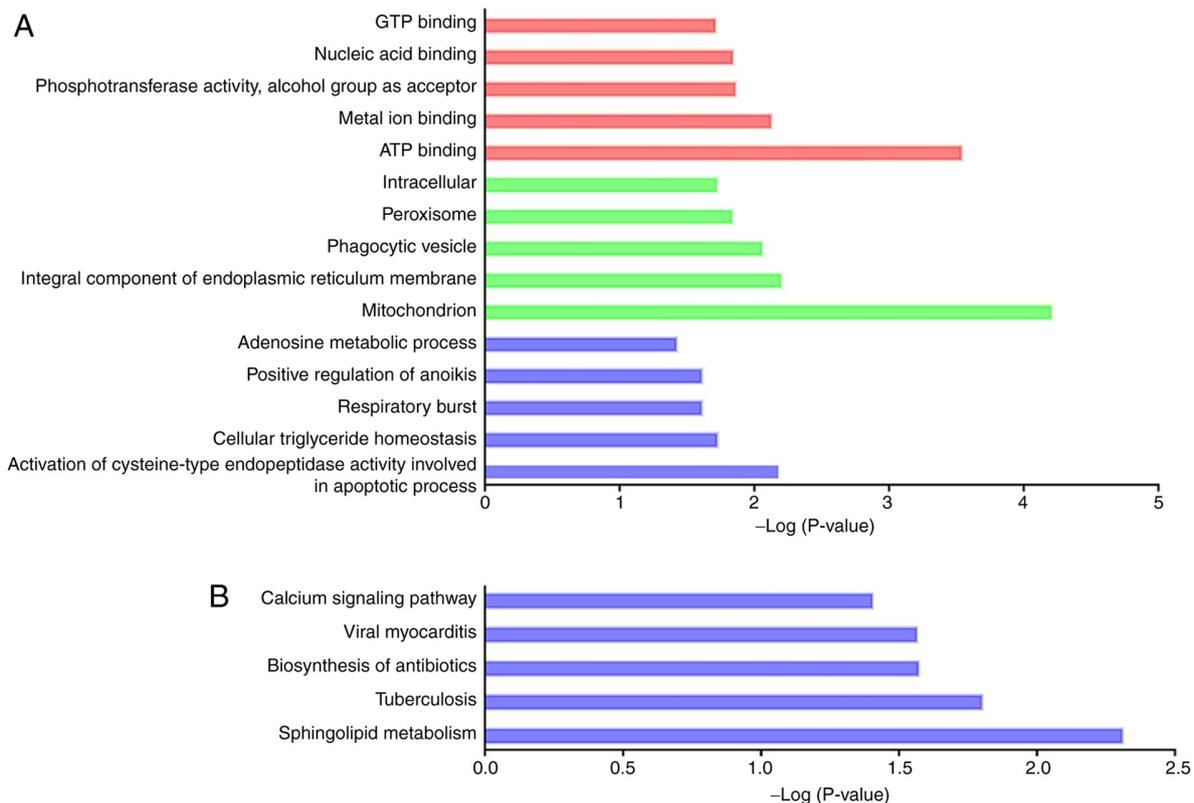
Table SIII. Relative expression of selected differentially expressed long non-coding RNAs through reverse transcription PCR.

LncRNA	Relative lncRNA levels (Mean ± SD)		Regulation	P-value
	Control	CI-AKI		
MSTRG.22041.2	1.03±0.28	6.44±4.35	Up	0.028
NONRATT000173.2	1.02±0.21	0.23±0.06	Down	<0.001
NONRATT005775.2	1.02±0.22	0.34±0.10	Down	<0.001
NONRATT016226.2	1.07±0.37	5.97±1.88	Up	0.001
NONRATT018005.2	1.02±0.22	3.52±1.19	Up	0.003
NONRATT023682.2	1.01±0.13	6.51±1.55	Up	<0.001
NONRATT027338.2	1.01±0.17	0.45±0.11	Down	<0.001
NONRATT027428.2	1.03±0.29	0.28±0.05	Down	0.001