Figure S1. GO enrichment analysis is composed of BP, CC and MF. (A) Number of GO enrichment items of source genes regulated by dysregulated lncRNAs. (B) Number of KEGG pathways associated with potential target genes of dysregulated lncRNAs. BP, biological process; CC, cellular component; MF, molecular function; lncRNA, long non-coding RNA; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

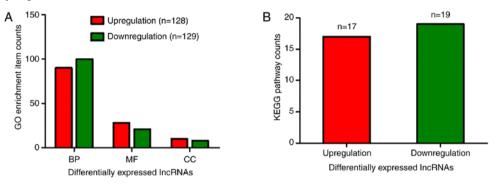


Figure S2. KEGG analysis of the potential biological functions of dysregulated lncRNAs, which are associated with Hashimoto's thyroiditis. KEGG analysis terms revealed that (A) 'thyroid hormone signaling pathway' and (B) 'calcium-regulated signaling pathway' were associated with the upregulated and downregulated lncRNAs in top 10 signaling pathways, respectively. KEGG, Kyoto Encyclopedia of Genes and Genomes.

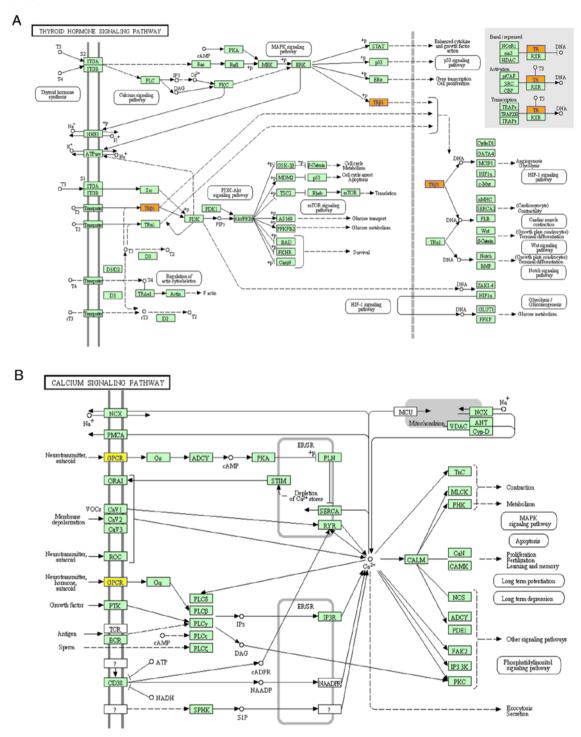


Figure S3. Longevity regulating pathway-mammal, non-alcoholic fatty liver disease and adipocytokine signaling pathway are potentially regulated by the dysregulated long non-coding RNAs. KEGG analysis terms revealed that (A) 'longevity regulating pathway-mammal', (B) 'non-alcoholic fatty liver disease' and (C) 'adipocytokine signaling pathway' contained NF-κB, JAK-STAT, PI3K-Akt and MAPK signaling pathways, which served a crucial role in the pathogenesis of Hashimoto's thyroiditis. KEGG, Kyoto Encyclopedia of Genes and Genomes.

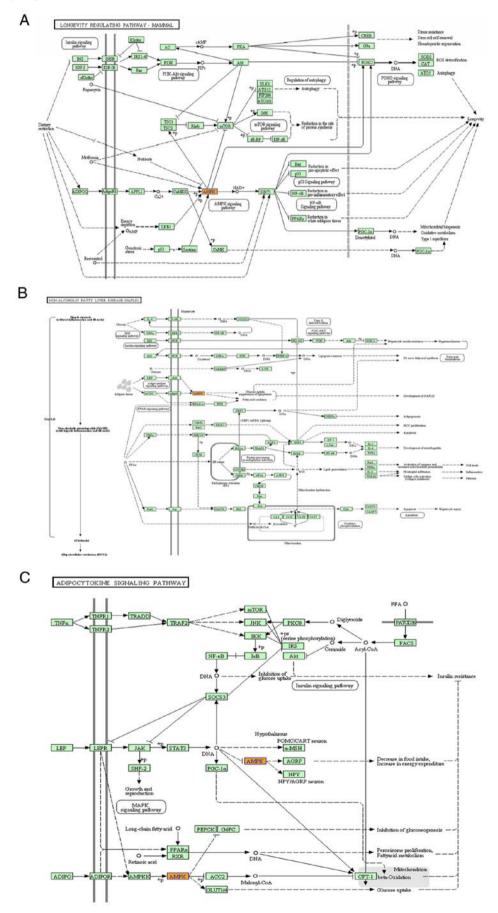


Figure S4. Prediction program used to predict the potential regulatory genes of lncRNA-LOC729737 and lncRNA-BC041964. The potential target genes were screened associated with the pathogenesis of HT, and the data indicated that STAT3 and IL-21R were the potential target genes of lncRNA-LOC729737 and lncRNA-BC041964, respectively. (A) Relative expression of STAT3 mRNA in PBMCs from patients with HT and healthy controls was detected via RT-qPCR. (B) Correlation between the transcript levels of STAT3 and lncRNA-LOC729737 in patients with HT. (C) Relative expression of IL-21R in PBMCs from patients with HT and healthy controls between the transcript levels of IL-21R and lncRNA-BC041964 in patients with HT. Each data point represents an individual subject, horizontal lines indicate the mean. \*P<0.05, \*\*\*P<0.001. HT, Hashimoto's thyroiditis; lncRNA, long non-coding RNA; RT-qPCR, reverse transcription-quantitative PCR.

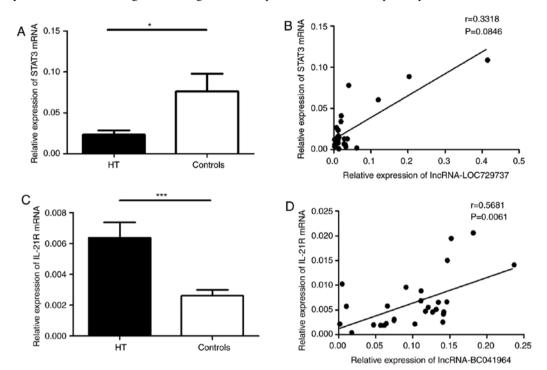


Table SI. Primer information of verified differentially expressed lncRNAs.

Gene	Туре	Primer sequence	Product size, bp
IncRNA-LOC100288778	Forward	5-CCCGCGTGTCAGACTCCA-3	235
	Reverse	5-CCAGCCTTCCGCTCCTTG-3	
IncRNA-EPT1	Forward	5-TCAGCACCAGGTCACAAGC-3	284
	Reverse	5-CAGTGGGACAGGATGAAAGAA-3	
IncRNA-BC041964	Forward	5-CGGTGGCTCACGCCTGTA-3	168
	Reverse	5-CCTGAGTAGCTGGGACGACA-3	
lncRNA-XLOC_I2_006631	Forward	5-GAATGCCAGAAACTGCTACCC-3	139
	Reverse	5-CTGCCCTCTTTGCCCACT-3	
lncRNA-AL137655_2	Forward	5-CAACAGGAGGAGATAAGGAAGC-3	199
	Reverse	5-CAGGAAGATGGGATGTAGAATGA-3	
IncRNA-LOC729737	Forward	5-TGGGCATAGGTTTGGTTTCC-3	267
	Reverse	5-TGTGGCTCCTTGCGGCTC-3	
β-actin	Forward	5-CACGAAACTACCTTCAACTCC-3	165
	Reverse	5-CATACTCCTGCTTGCTGATC-3	
STAT3	Forward	5-TCCATCAGCTCTACAGTGACAGC-3	134
	Reverse	5-TCCCAGGAGATTATGAAACACC-3	
IL-21R	Forward	5-CCCGACCTCGTCTGCTACA-3	101
	Reverse	5-TGGTCTTGCCAGGTAAGGGT-3	
MECP2	Forward	5-TCGCTCTAAAGTGGAGTTGATT-3	134
	Reverse	5-TGGGCTTCTTAGGTGGTTTC-3	

IncRNA, long non-coding RNA; MECP2, Methyl-CpG-binding protein 2.