Supplementary Material

Comprehensive Analysis of the mRNA-lncRNA Co-expression Profile and ceRNA Networks Patterns in Chronic Hepatitis B

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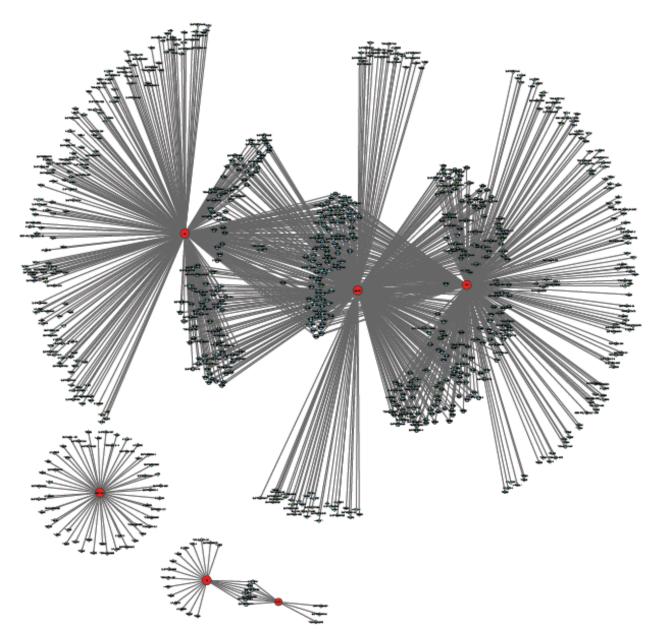


Fig. (1A). The co-expression network of complement and coagulation cascades.

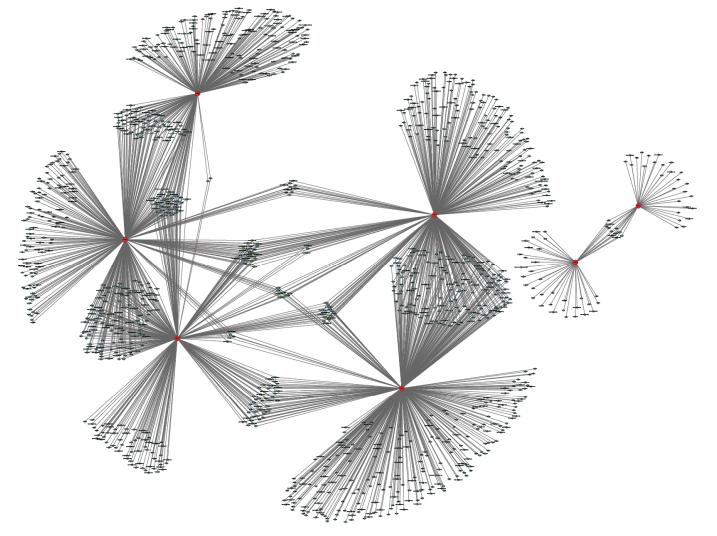


Fig. (1B). The co-expression network of TGF- β signaling pathway.

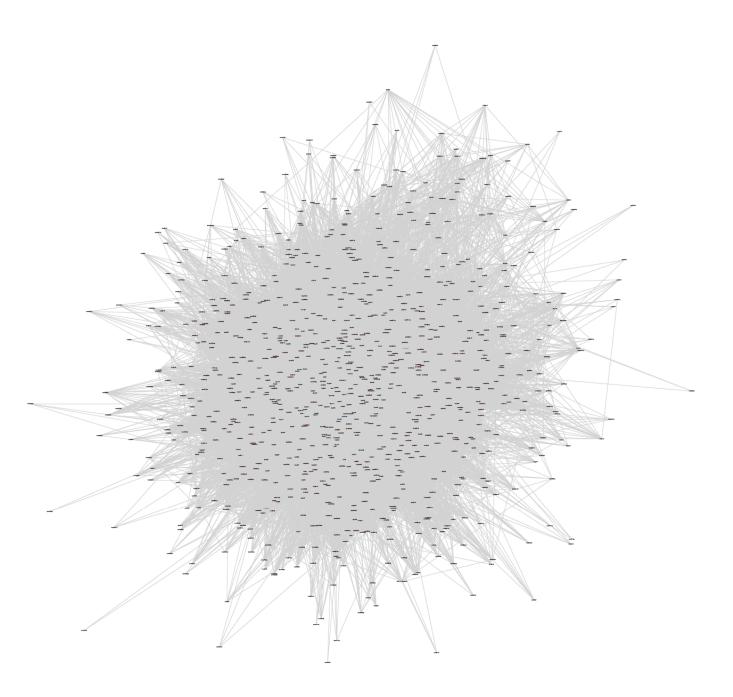


Fig. (2). ceRNAs for the top 10 up/downregulated lncRNAs.

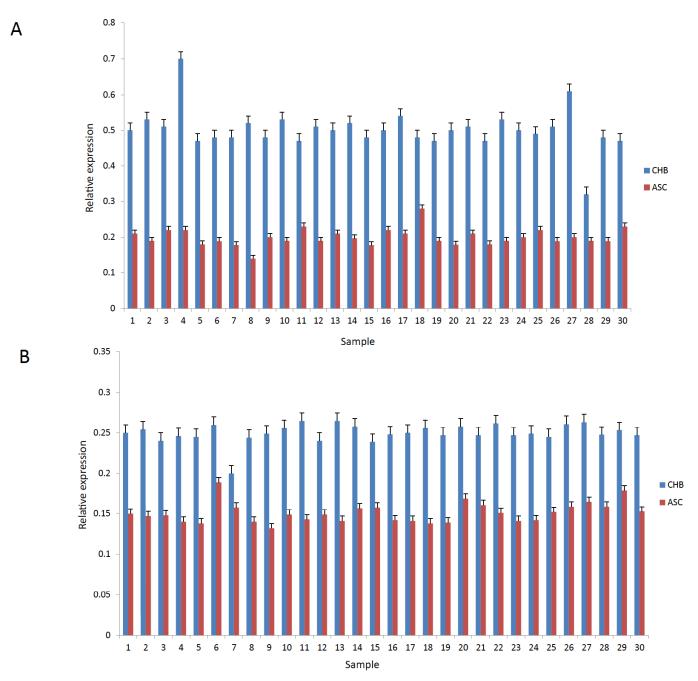


Fig. (3). Validation of the expression of ZFP57 (A) and T039096 (B) by qRT-PCR in 30 CHB and ASC samples, respectively. Sample 1, 2 and 3 stand for the three CHB and ASC sample, which were used to sequencing analysis.

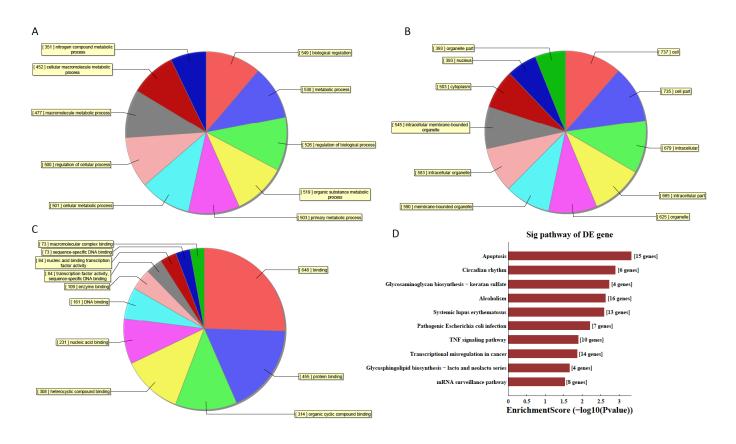


Fig. (4). GO and KEGG pathway analyses. Enrichment of biological process (A), cellular component (B) and molecular function (C) in downregulated mRNA. (D) KEGG pathway enrichment analysis of downregulated mRNAs.

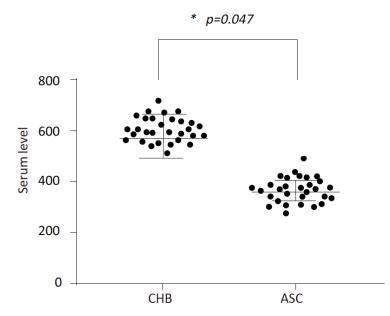


Fig. (5). Validation of protein level of ZFP57 by ELISA.

Table 1. Primers used for the examined mRNAs and lncRNAs.

	Forward Primer	Reverse Primer
T039096	ACACTGGTTTGGCTTGCTGA	ATGTTCAAAGCCCACTTCCCA
ZFP57	TAGCCCCAGGAAGGAATCCA	CTGGCTTCTTCTTCACCCGT

Table 2. Correlations between ZFP57 expression and clinical signature.

Characteristics	Number of Patients	M (P ₂₅ , P ₇₅)	Р
HBV-DNA			
>average value	8	0.00566 (0.00217, 0.01457)	0.765
<average td="" value<=""><td>22</td><td>0.00385 (0.00126, 0.00640)</td></average>	22	0.00385 (0.00126, 0.00640)	
ALT			
>average value	18	0.00393 (0.00105, 0.00531)	0.038
<average td="" value<=""><td>12</td><td>0.00573 (0.00364, 0.01574)</td><td></td></average>	12	0.00573 (0.00364, 0.01574)	
AST			
>average value	11	0.00535 (0.00431, 0.00674)	0.676
<average td="" value<=""><td>19</td><td>0.00395 (0.00145, 0.01367)</td><td></td></average>	19	0.00395 (0.00145, 0.01367)	
TB			
>nromal value	12	0.00523 (0.00378, 0.03125)	0.553
<normal td="" value<=""><td>18</td><td>0.00463 (0.0030, 0.009656)</td><td></td></normal>	18	0.00463 (0.0030, 0.009656)	