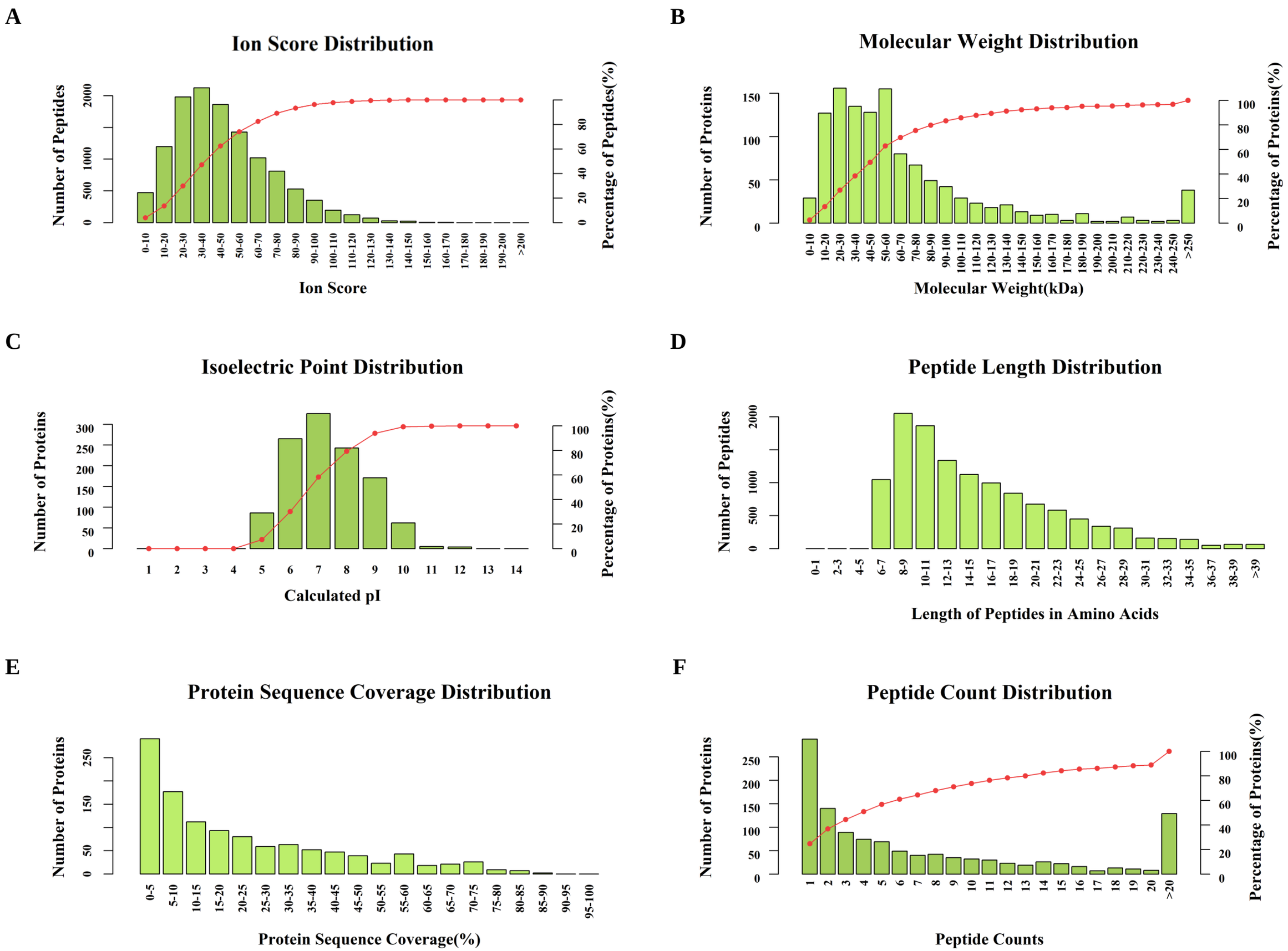

Fig. S1. The qualities of the proteome dataset. (A) Ion score distribution of the identified proteins with ≥ 1 unique peptide. **(B)** Molecular weight distribution of identified proteins proved that there is no bias in the protein extraction process. **(C)** Isoelectric point distribution of the identified proteins to show that protein extraction was unbiased. **(D-F)** Peptide length, protein sequence coverage, and peptide count distribution of the identified proteins.

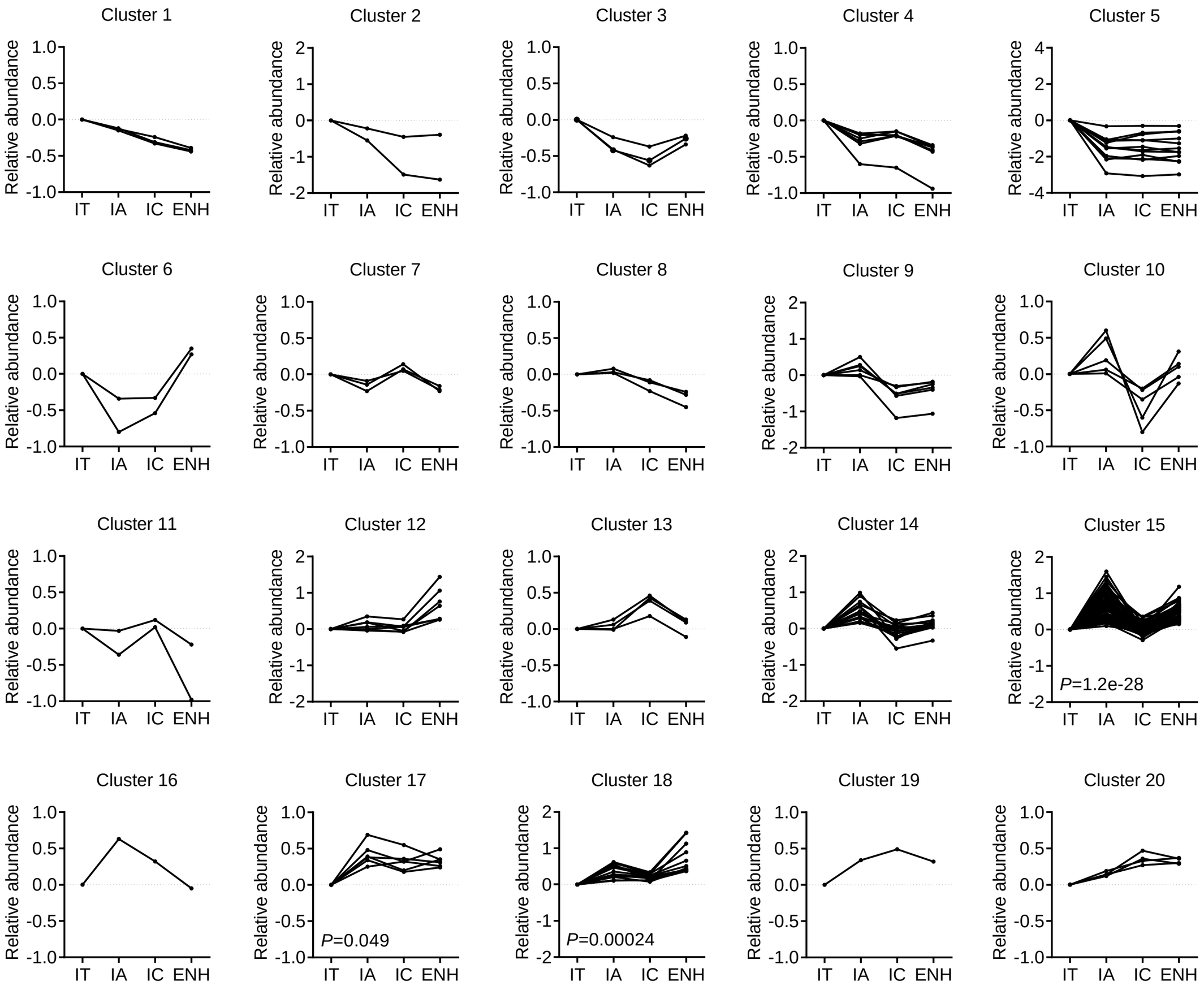

Fig. S2. Serum protein pattern analyses by the Short Time-series Expression Miner (STEM). IT, immune-tolerant phase; IA, immune reactive HBeAg-positive phase; IC, inactive HBV carrier state phase; ENH, HBeAg-negative chronic hepatitis B phase.

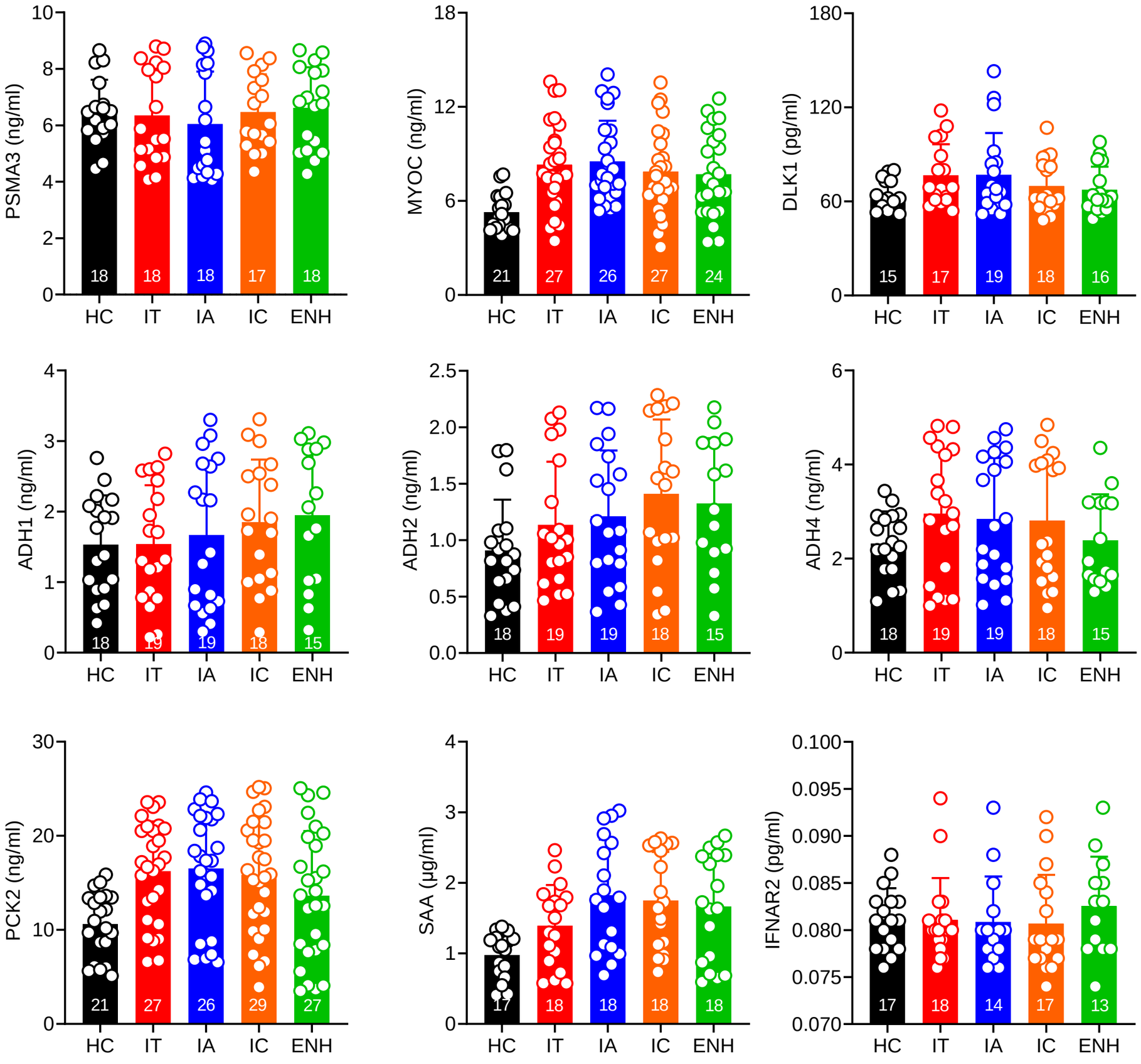

Fig. S3. Serum expression of various proteins in healthy controls and patients at different phases of chronic HBV infection as assessed by ELISA. PSMA3, proteasome subunit alpha type 3; MYOC, myocilin; DLK1, delta-like 1 homolog; ADH, alcohol Dehydrogenase; PCK2, Phosphoenolpyruvate carboxykinase [GTP], mitochondrial; SAA, serum amyloid A protein; IFNAR2, interferon alpha/beta receptor 2; HC, healthy controls (black); IT, immune-tolerant phase (red); IA, immune reactive HBeAg-positive phase (blue); IC, inactive HBV carrier state phase (orange); ENH, HBeAg-negative chronic hepatitis B phase (green). Each circle represents an individual sample. Data were presented as the mean±SD.