

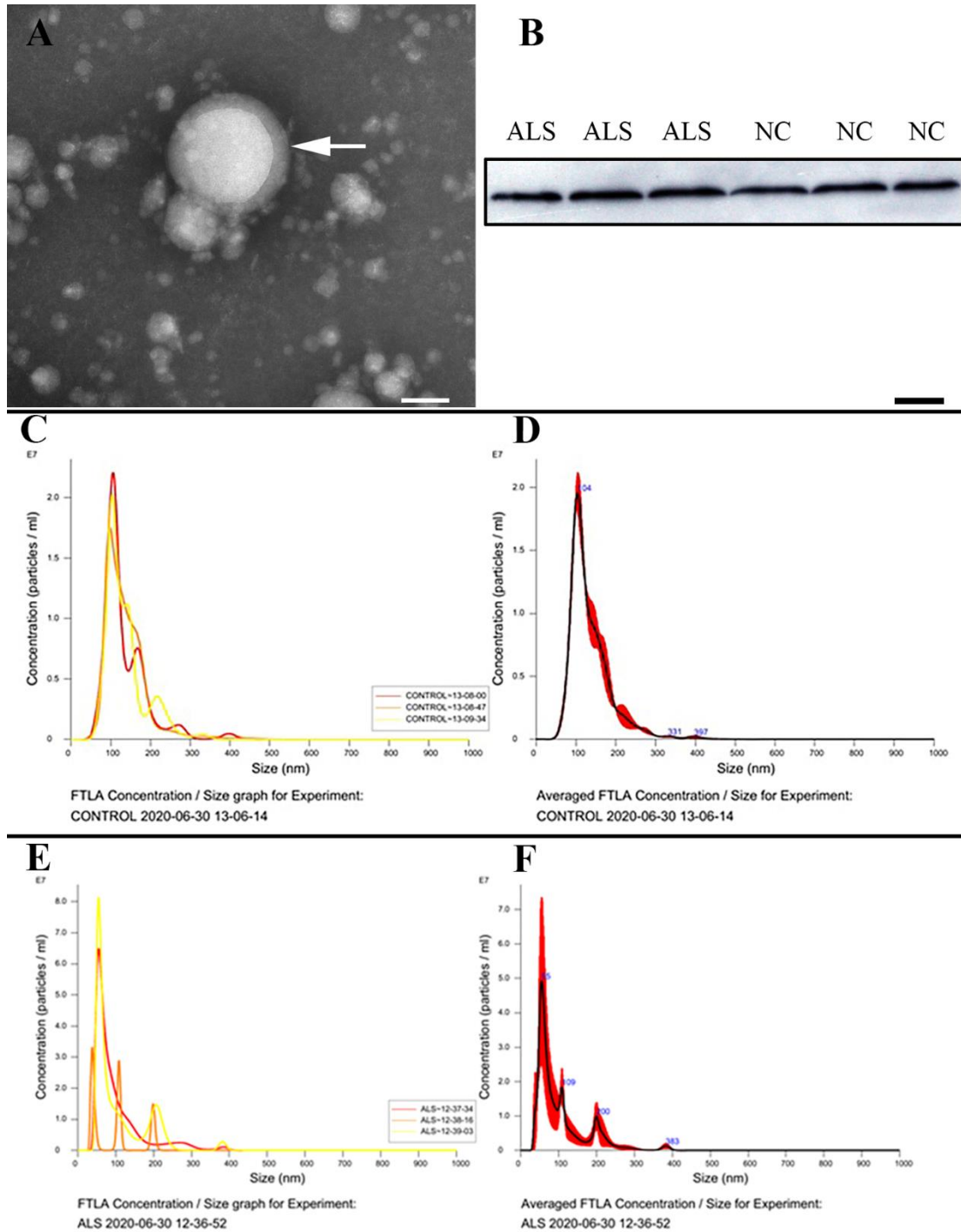


Figure 1. Exosomes were extracted in the plasma. (A) Exosomes from the plasma under scanning electron microscope (white arrow: exosome, scale bar = 100 μ m). (B) Expression of exosomal CD9 as a positive exosomal marker (ALS: ALS patients, NC: healthy controls). (C, D) The fitting curves of exosomal concentration with different diameters in the plasma of healthy controls. (E, F) The fitting curves of exosomal concentration with different diameters in the plasma of ALS patients.

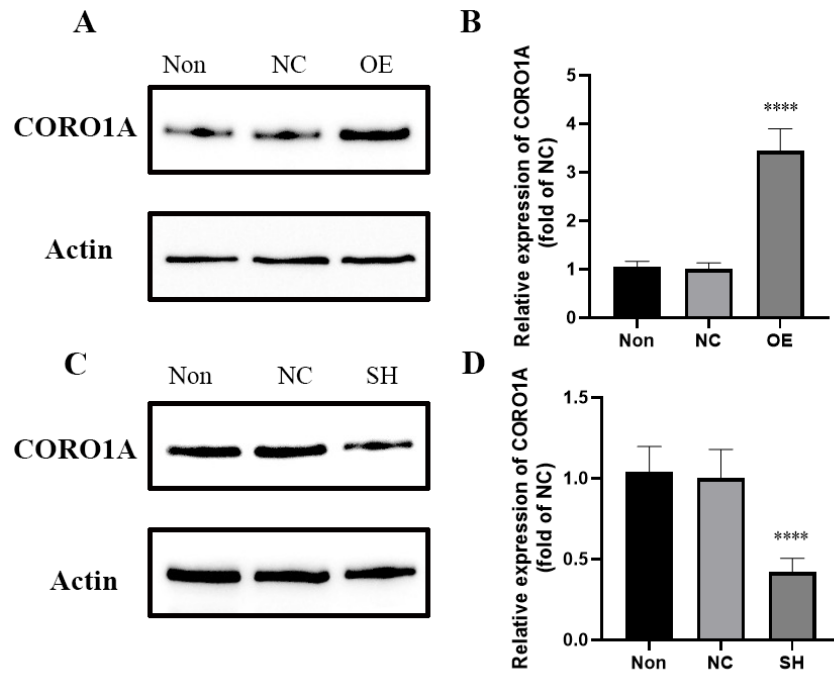


Figure 2. The functional efficiency of the overexpressing or shRNA vector was identified by western blot. (A, B) Western blot and quantitative analysis of the expression of CORO1A in the NSC-34 cells with overexpressing vector. (C, D) Western blot and quantitative analysis of the expression of CORO1A in the NSC-34 cells with shRNA vector. **** $p < 0.0001$ vs the NC group. (Non: the non-transfected cells, NC: cells transfected with the blank vector, OE: cells transfected with the overexpressing vector, SH: cells transfected with the shRNA vector)

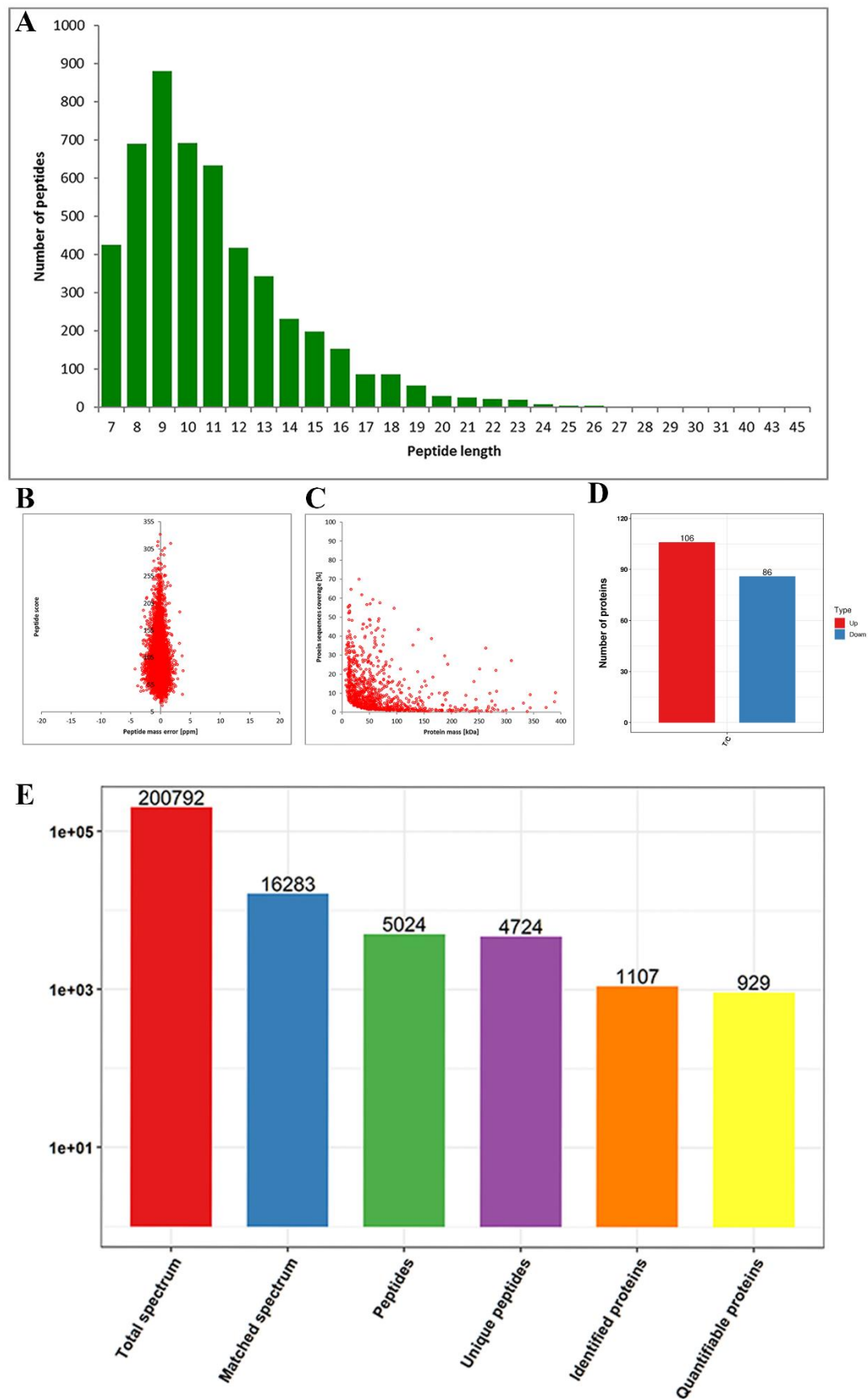


Figure 3. Proteomic analysis of exosomal proteins. (A) Number of identified peptides of different

length. (B) The peptide score (ordinate) is a simple approach to evaluate whether a result is significant or not; peptide mass error (abscissa) is the parts per million ratio of peptide mass error between theory and practice. (C) Protein sequence coverage (percent of the identified peptide sequence covering the protein sequence) in different protein masses. (D) Differentially expressed proteins between ALS patients and controls. (E) Number of detected spectra, peptides and proteins.