Item S1: SARS-CoV-2 RNA extraction procedures and quantification.

Urine samples were collected in Corning 50-ml conical tubes and centrifuged at 2,000 *g* for 20 minutes within 4 hours of collection. Cell pellets were washed one time with PBS and stored until mRNA extraction. The biopsy fragment was de-embedded from Optimal cutting temperature compound and lyzed in a tissue lysis buffer.
Urine supernatant, urine cell pellets, plasma (140 µL) and biopsy fragment SARS-CoV-2 RNA were extracted using QIAamp® Viral RNA Mini Kit (QIAGEN®, Hilden, Germany), according to manufacturer's instructions. SARS-CoV-2 RNA was quantified at each time point by droplet-based Crystal Digital PCR™ (Stilla Technologies, Villejuif, France) on the Naica™ System (Stilla Technologies, Villejuif, France), which includes primers and FAM- and HEX- labeled probes specific to two distinct regions [ORF1ab and Nucleocapside (N) genes] of the SARS-CoV-2 positive strand RNA genome. The 3rd channel of the Naica™ system was used as an endogenous PCR control detecting a human housekeeping gene with a Cy5-labeled probe. This single assay design permits the simultaneous detection of two independent SARS-CoV-2 sequences reported as conserved, while concurrently monitoring PCR effectiveness using the third channel of detection. Samples with one of the two ORF1 or N genes or both genes detected were considered as positive samples and results were automatically analyzed using "Crystal reader" (Stilla) and "Crystal Miner" software (Stilla) based on the most amplified gene positive droplets. SARS-CoV-2 RNA concentrations (cp/mL) were finally calculated considering the extracted volume of plasma.

Item S2: Research ethics approval and informed consent.

The policy of in terms of data and patient protection are that each patient admitted in this hospital is advised that medical data is gathered in a database in order to conduct health research. The informed patient is provided with an objection form, and may opt out of research participation by filing this form, which does not require any explanation or justification.

Figure S1: Evolution of inflammatory markers during follow-up.

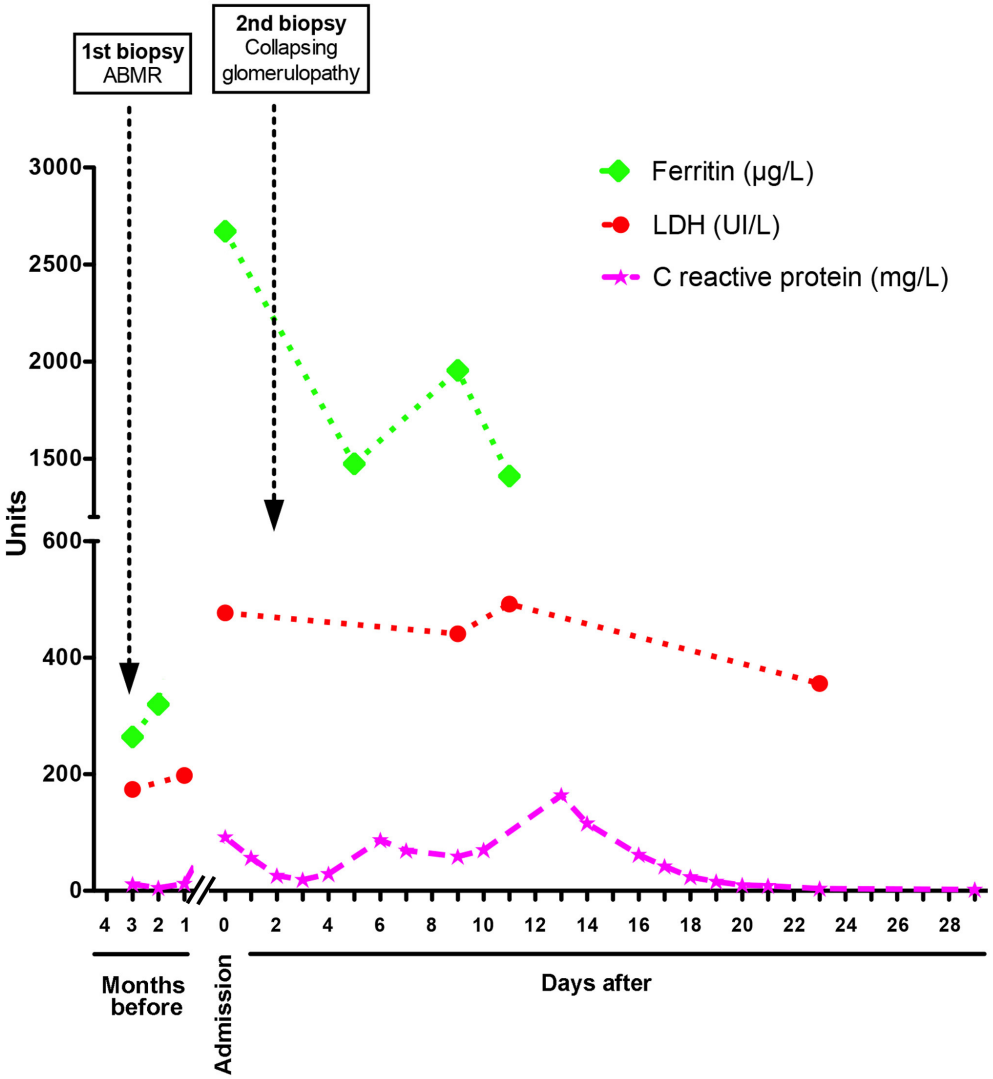

Figure S2: Evolution of serum albumin and protein-creatinine ratio during follow-up.