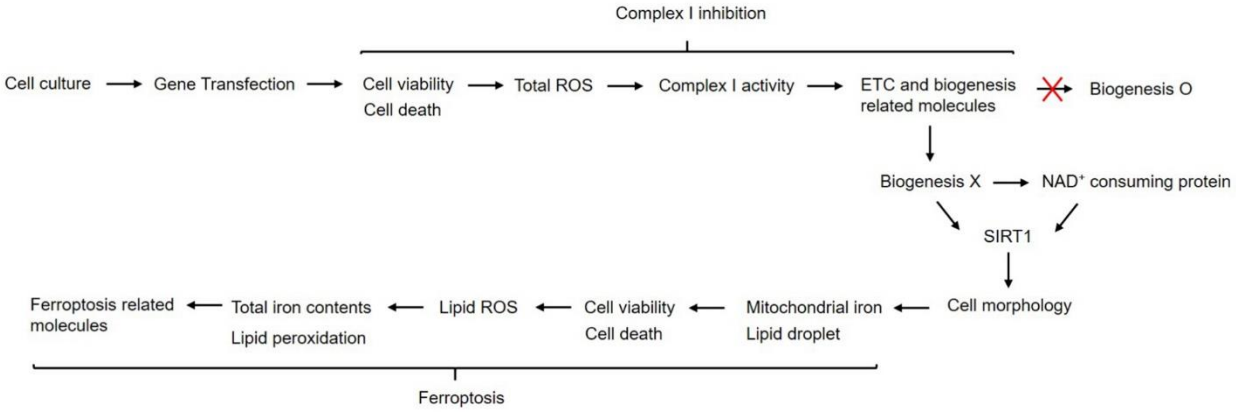

Figure S1. The flowchart of methodology. A series of experiments were performed in order.

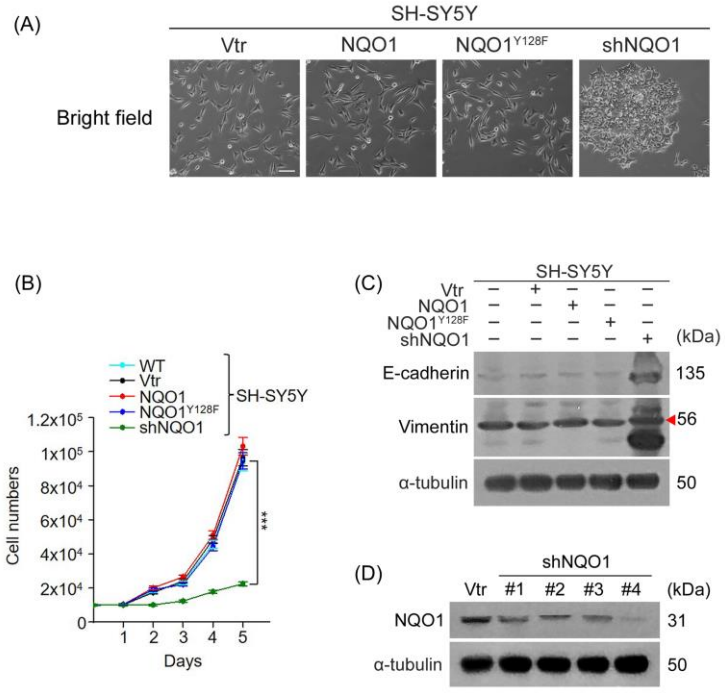

Figure S2. Cell morphology, cell growth rate, and immunoblot for NQO1knockdown and EMT-related molecules. (A) Bright-field microscope image. Original magnification, x 200. Scale bar size, 50 μm. **(B)** Proliferation was measured and quantified by counting cells for 5 days. Data are average ± SEM from three independent experiments. ns; not significant. ****P* < 0.001 relative to WT. WT; Wild type. **(C)** EMT-related molecules (E-cadherin and vimentin) were examined by immunoblot analysis. **(D)** Levels of NQO1 expression in cells using NQO1 knockdown constructs were confirmed by immunoblot analysis.

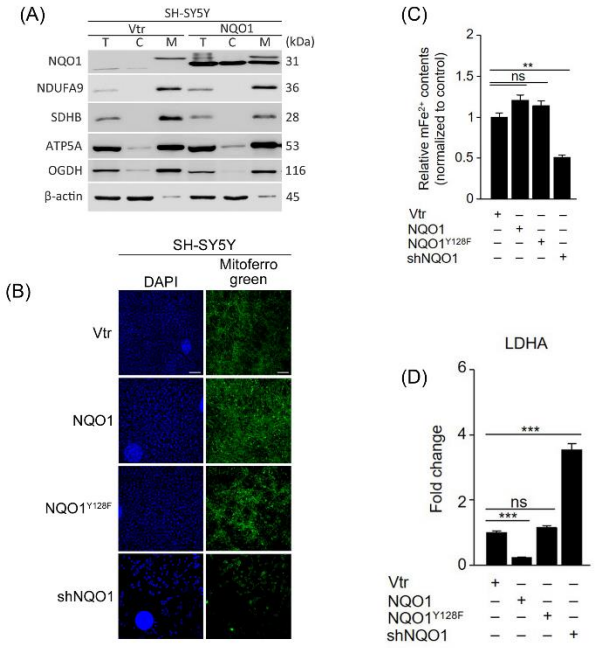

Figure S3. Examination of the primary energy metabolic proteins and iron contents in the mitochondria. (A) Mitochondrial proteins involved in energy metabolism were examined by immunoblot analysis. **(B, C)** Cells were stained with mitoferrogreen for 40 min to examine mitochondria ferrous iron contents. Fluorescent images were quantified using the Image J software. Original magnification, x 100. Scale bar size, 100 μm. Data are average ± SEM from three independent experiments. ns; not significant. ***P* < 0.01 relative to vector control. **(D)** Expression levels of *LDHA* were determined using RT-qPCR. Data are average ± SEM from three independent experiments. ns; not significant. ****P* < 0.001 relative to vector control.

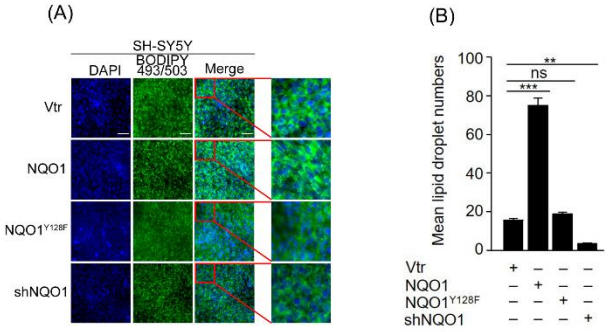

Figure S4. Comparing lipid droplet numbers among cells with Vtr, NOQ1, NQO1^{Y128F}, or shNQO1. (A, B) The number of cellular lipid droplets was determined by staining cells with BODYPY 493/503. Stained Images were quantified using the Image J software. Original magnification, × 200. Scale bar size, 50 μm. Data are average ± SEM from three independent experiments. ns; not significant. ***P* < 0.01, ****P* < 0.001 relative to vector control.