Supplementary information, Figure S2

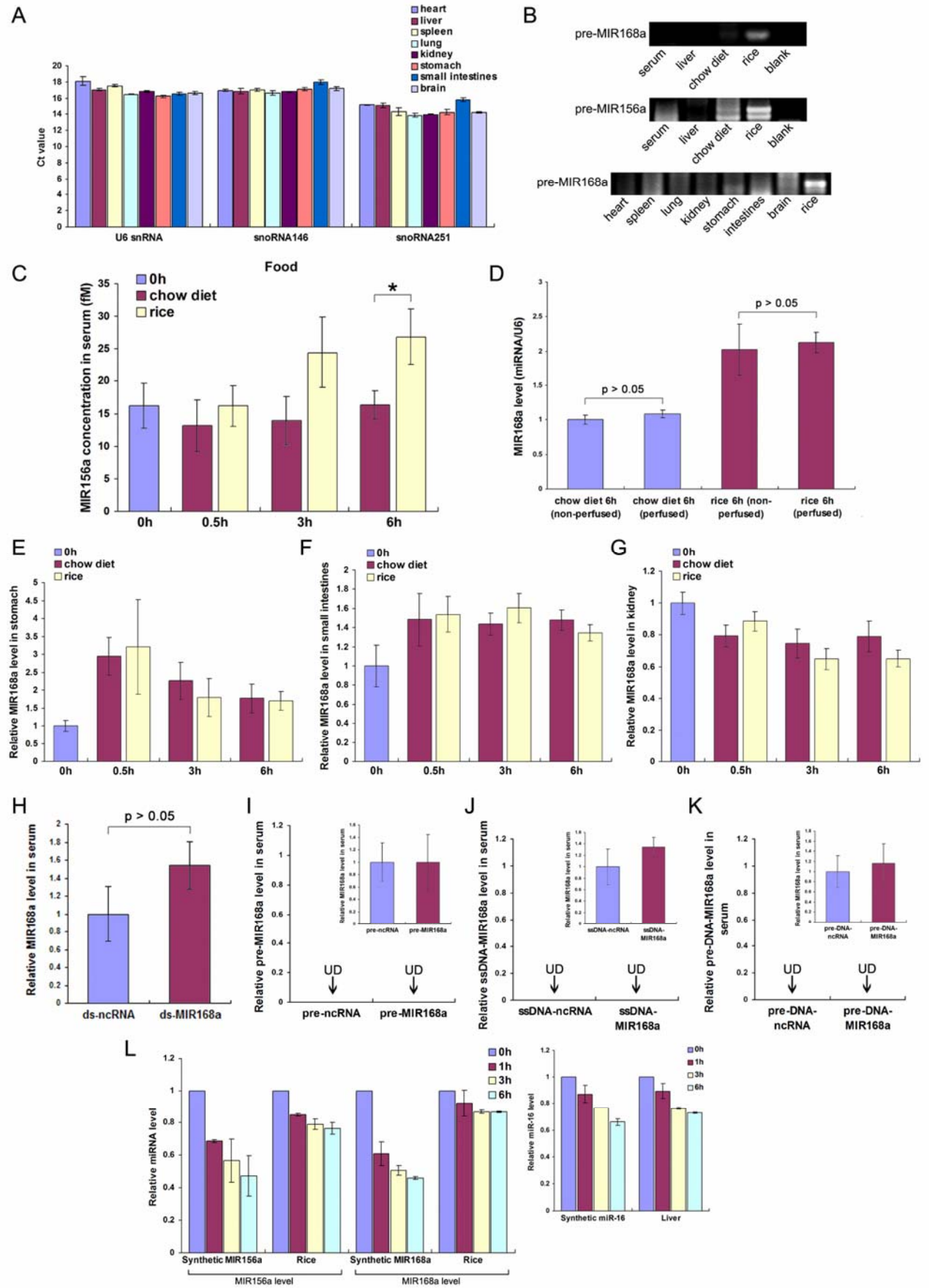

Figure S2 A quantitative analysis of plant miRNAs in mouse serum and various organs as well as the uptake of various forms of MIR168a by C57BL/6J mice. **(A)** The levels of U6, snoRNA146, and snoRNA251 in various mouse organs (*n* = 6). **(B)** The levels of pre-MIR168a and pre-MIR156a in various organs, chow diet, and rice. Accurate amplification of pre-MIR168a and pre-MIR156a was confirmed by Sanger-based method to sequence the PCR products. **(C)** The levels of MIR156a in mouse serum after feeding with chow diet or fresh rice (*n* = 8). **(D)** The levels of MIR168a in perfused or unperfused mouse livers after feeding with chow diet or rice (*n* = 6). **(E-G**) The levels of MIR168a in mouse stomach **(E)**, small intestine **(F)** and kidney **(G)** after feeding mice with chow diet or fresh rice for 0.5 h, 3 h, or 6 h (*n* = 8). **(H)** The level of MIR168a in mouse serum at 6 h after gavage feeding with dsRNA (ds-MIR168a; *n* = 5), with ds-ncRNA serving as the control. **(I)** The level of pre-MIR168a in mouse serum at 6 h after gavage feeding with pre-MIR168a (*n* = 5), with pre-ncRNA serving as the control. Insert, the level of mature MIR168a in mouse serum after gavage feeding with pre-MIR168a or pre-ncRNA. **(J)** The level of ss-DNA-MIR168a in mouse serum 6 h after gavage feeding with ssDNA (ss-DNA-MIR168a; *n* = 5), with ss-DNA-ncRNA serving as the control. Insert, the level of mature MIR168a in mouse serum after gavage feeding with ss-DNA-MIR168a or ss-DNA-ncRNA. **(K)** The level of pre-DNA-MIR168a in mouse serum 6 h after gavage feeding with preDNA (pre-DNA-MIR168a; *n* = 5), with pre-DNA-ncRNA serving as the control. Insert, the level of mature MIR168a in mouse serum after gavage feeding with pre-DNA-MIR168a or pre-DNA-ncRNA. UD, undetectable. **(L)** Synthetic miRNAs (without 2'-O-methylated 3' ends) and total RNA samples isolated from rice or mouse liver were left untreated (0 h) or acidified by HCl to pH 2.0 and incubated for 1 h, 3 h, or 6 h at 37 °C, and then subjected to RNA purification followed by qRT-PCR determination for the indicated miRNAs (*n* = 3). **P* < 0.05; ***P* < 0.01.