## Sheng\_Supplementary Figure S2

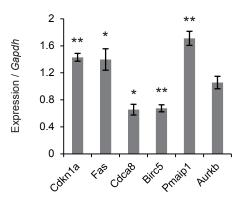


Figure S2 Analysis of Gene Expression Changes in SMN-depleted Mouse Primary Cardiomyocytes. Cardiomyocytes were isolated from P2 heterozygous mice; mouse SMN was efficiently knocked down with siRNA-2 (Fig. 6). Cells were collected 48 hrs post siRNA treatment, and cell cycle- and apoptosis- related genes were analyzed with quantitative PCR. Data were first normalized to *Gapdh* and then normalized to the control siRNA. \* P < 0.05, \*\* P < 0.01, N = 3.