



**Supplementary information, Figure S1. Strand-specific RNA-Seq of sham and 7 dpa adult hearts.** (A) PHRED quality scores across each position of reads. The central red line is the median value, the yellow box represents the inter-quartile range (25–75%), the upper and lower lines represent the 10% and 90% points, and the blue line represents the mean quality. (B) Evaluation of strand-specific strategy. For all of the four samples, >97% reads were generated with correct strand information. (C) Reads distribution on transcripts. The even distribution reveals well-controlled randomized fragmentation of the transcripts in the RNA-Seq experiments. Data are shown as mean  $\pm$  SD. (D) RPKM scores of exonic, intronic and intergenic regions. (E) For each position of the reads, mutation rates were calculated and summarized. The average mutation rate is less than 0.5 per read.