

Supplementary Materials: *Asx12*^{-/-} Mice Exhibit De Novo Cardiomyocyte Production during Adulthood

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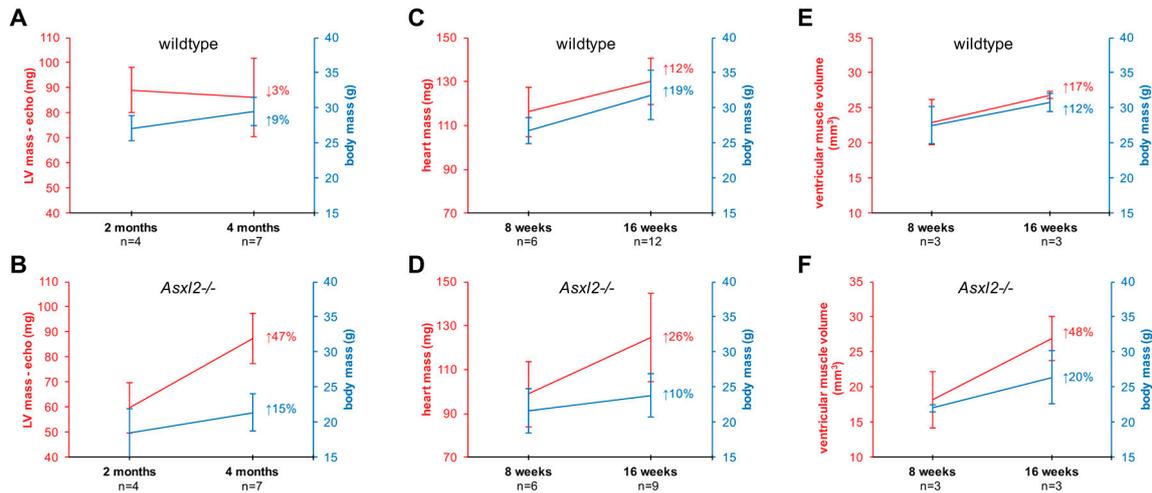


Figure S1. Assessment of cardiac versus body growth in wildtype and *Asx12*^{-/-} mice. (A,B) Left ventricular (LV) mass calculated via echocardiography (echo) at two and four months of age in wildtype (A) and *Asx12*^{-/-} (B) animals; (C,D) heart mass of freshly dissected hearts at 8 and 16 weeks of age in wildtype (C) and *Asx12*^{-/-} (D) animals; (E,F) quantitative morphometric analysis of ventricular muscle volume at 8 and 16 weeks of age in wildtype (E) and *Asx12*^{-/-} (F). Sample size is shown below the graphs. Bars represent standard deviation.

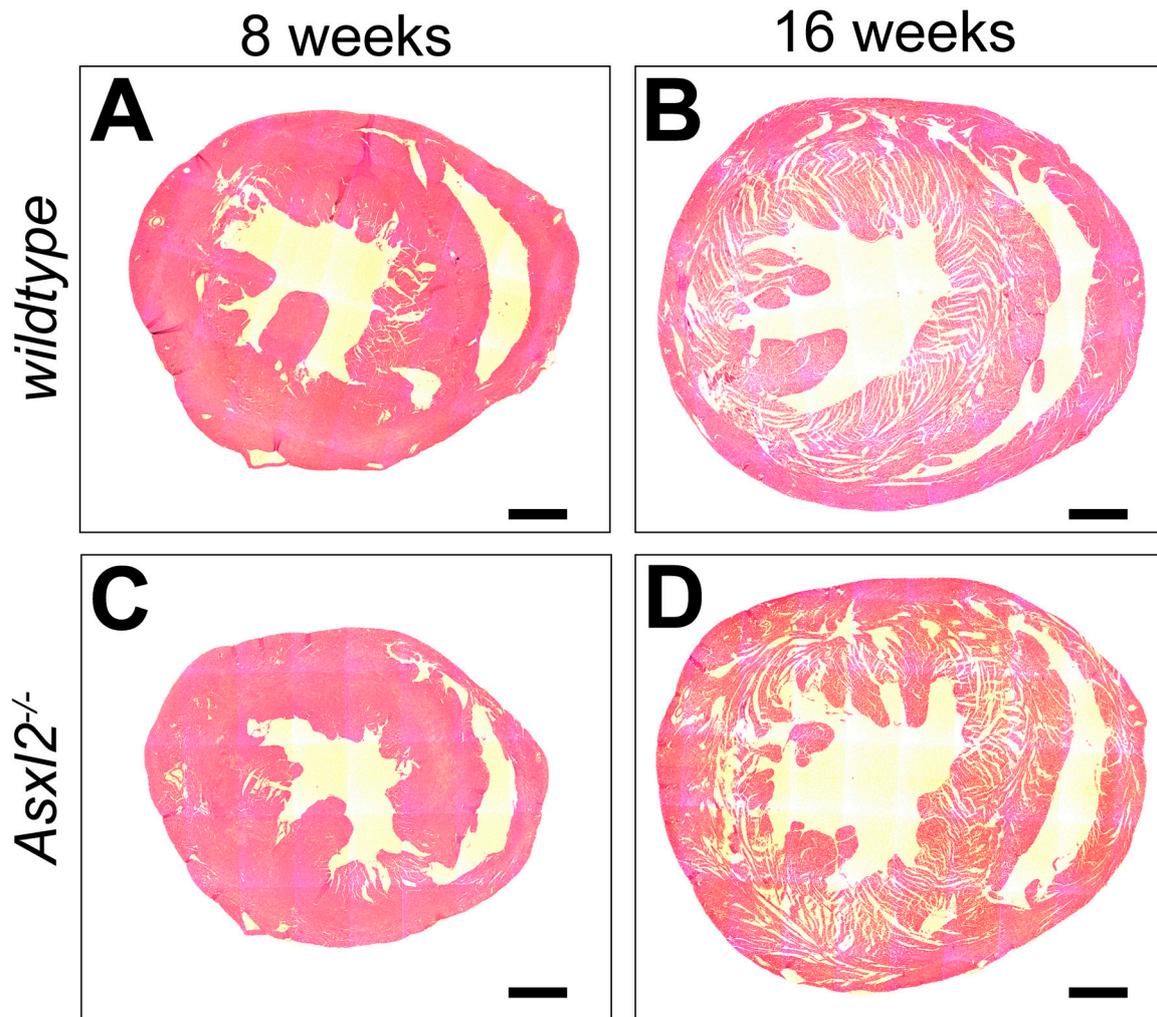


Figure S2. Histological examination of *Asxl2*^{-/-} hearts. Shown are representative hematoxylin and eosin stained cross-sections from (A) wildtype heart at 8 weeks of age; (B) wildtype heart at 16 weeks of age; (C) *Asxl2*^{-/-} heart at 8 weeks of age; and (D) *Asxl2*^{-/-} heart at 16 weeks of age. Body masses of mice with heart cross-sections represented here are (A) 24.5 grams; (B) 30.0 grams; (C) 22.5 grams; (D) 28.6 grams. Scale bar = 500 μ m.

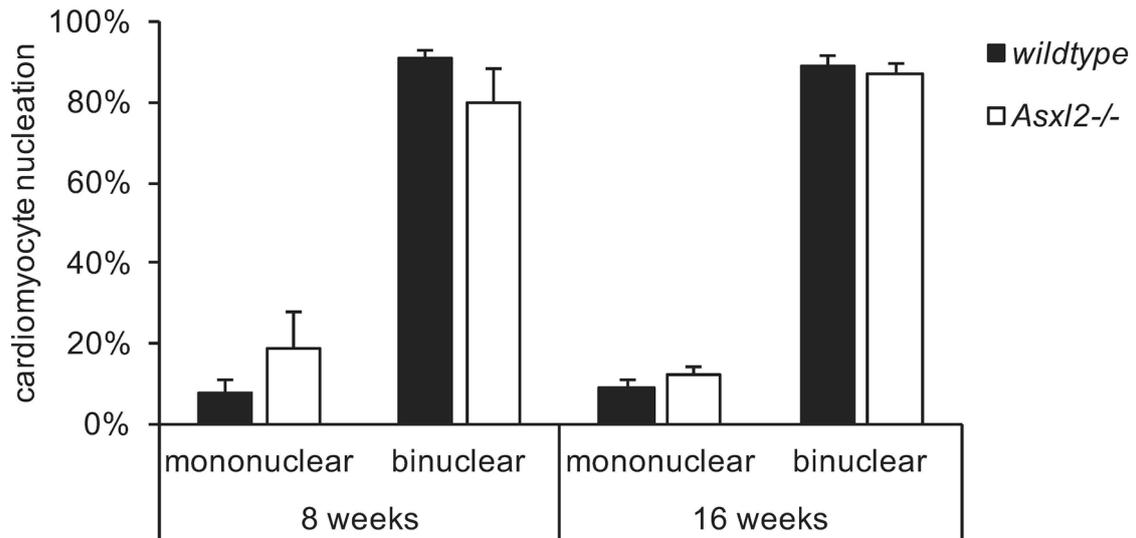


Figure S3. Analysis of cardiomyocyte nucleation status in *Asx12^{-/-}* and wildtype hearts. Cardiomyocytes were isolated from 8- and 16-week wildtype (8-week time-point: $n = 4$; 16-week time-point: $n = 5$) and *Asx12^{-/-}* ($n = 3$ per time-point) hearts and assessed for number of nuclei per cardiomyocyte. Bars represent standard deviation. No significant differences were observed (Student's t -test).

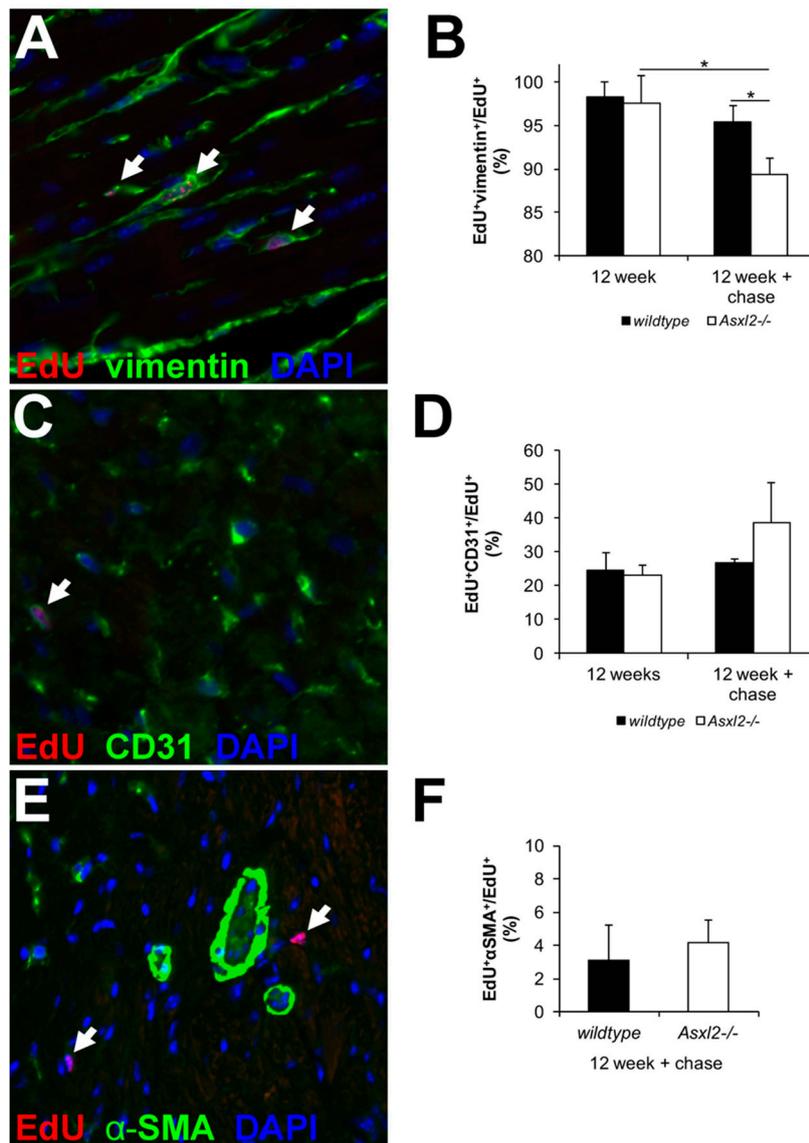


Figure S4. Analysis of vimentin, CD31, and α -SMA expression among EdU⁺ cells in chased *Asxl2*^{-/-} hearts. (A) Representative image of EdU, DAPI, and vimentin labeling; (B) quantification of percentage of EdU⁺ cells positive for vimentin; (C) Representative image of EdU, DAPI, and CD31 labeling; (D) quantification of percentage of EdU⁺ cells positive for CD31; (E) Representative image of EdU, DAPI, and α -SMA; (F) quantification of percentage of EdU⁺ cells positive for α -SMA. At least three non-consecutive sections, 25 images/section, from three animals per genotype/timepoint were assessed. Arrows indicate EdU⁺ nuclei. Bars represent standard deviation. * *p*-Value (Student's *t*-test) < 0.05.

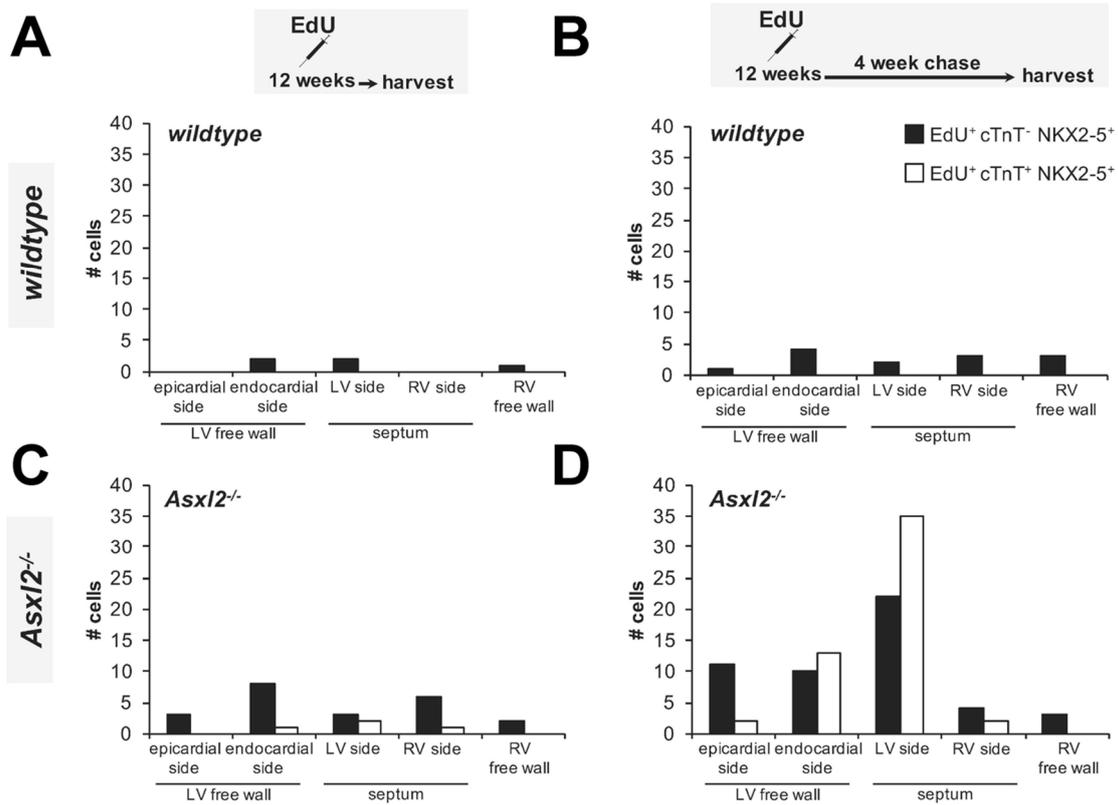


Figure S5. Number and distribution of EdU+cTnT-NKX2-5⁺ and EdU+cTnT+NKX2-5⁺ cells in unchased (A) and chased (B) wildtype, and unchased (C) and chased (D) *Asx12*^{-/-} hearts. EdU⁺ cells were classified according to whether they were cTnT-NKX2-5⁺ (black bars), cTnT+NKX2-5⁺ (white bars), or cTnT- NKX2-5⁻ (not shown). Sample size: *n* = 3 animals per genotype per scheme (unchased vs. chased); three non-consecutive sections/heart. Five 20× images/specific location per section were analyzed in unchased hearts. Whole sections (stitched from 20× images in ZenPro software) were analyzed in chased hearts.

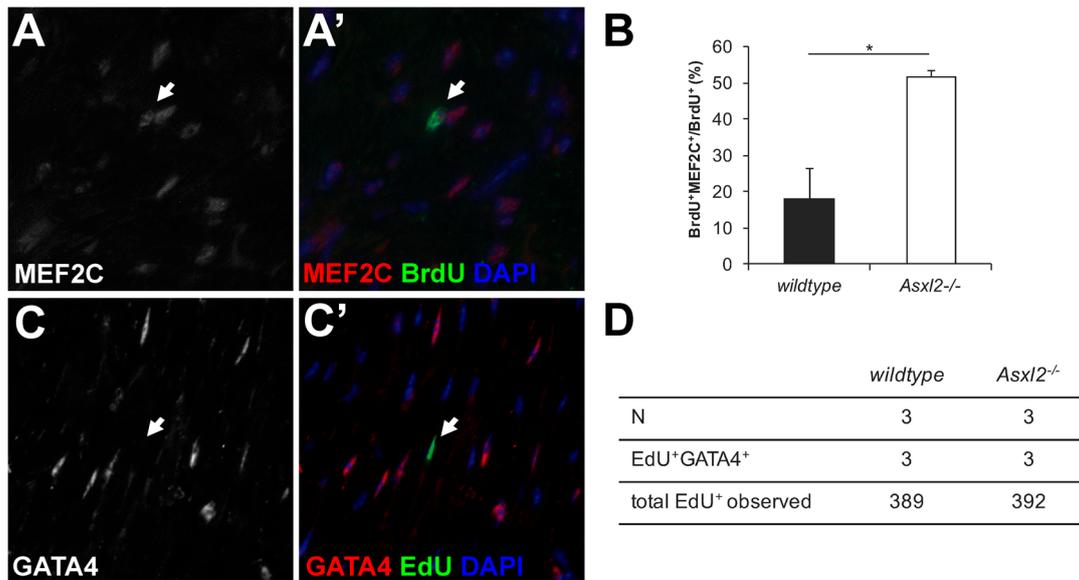


Figure S6. Expression of the cardiogenic markers MEF2C and GATA4 among BrdU⁺ or EdU⁺ cells in 12-week hearts. (A,A') Representative image of BrdU and Mef2C labeling; (B) Quantification of the percentage of BrdU⁺Mef2C⁺ cells in the left ventricle (*n* = 3 per genotype, three non-consecutive sections/heart, twenty-five 20× images/section); (C,C') Representative image of EdU and GATA-4 labeling; (D) EdU⁺GATA4⁺ cells in the left ventricles are rare in both the wildtype and *Asxl2*^{-/-}. Bars represent standard deviation. * *p*-Value (Student's *t*-test) < 0.05.

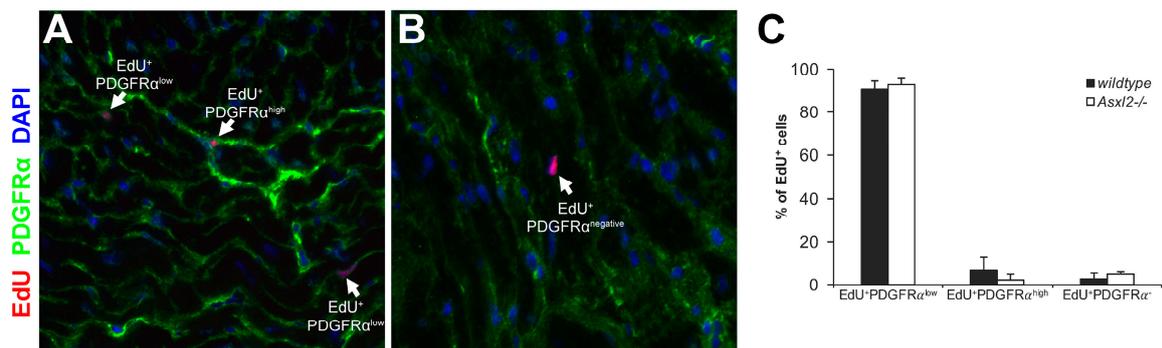


Figure S7. Examination of PDGFR α expression among EdU⁺ cells in 12-week hearts. (A,B) Representative images from frozen sections of EdU, anti-PDGFR α , and DAPI labeling; Overall, most small cells were positive for low levels of PDGFR α and many cells near blood vessels had high levels of PDGFR α , consistent with a previous report (Chong et al. 2011); (C) Quantification of the percentage of EdU⁺ cells that had low or high levels, as well as those that were negative for, PDGFR α . At least three non-consecutive sections from three animals per genotype were assessed. Bars represent standard deviation.