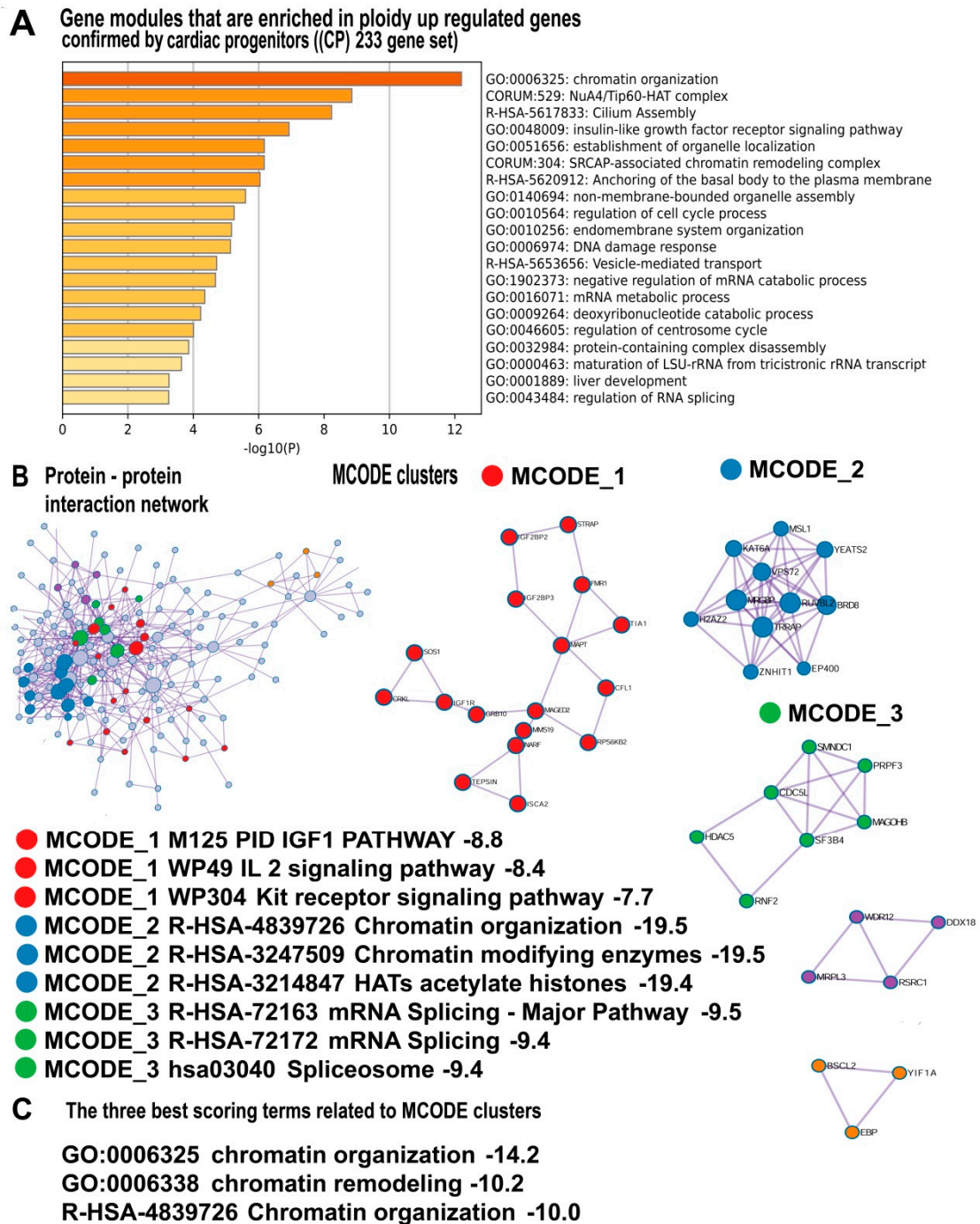


Supplementary Figures

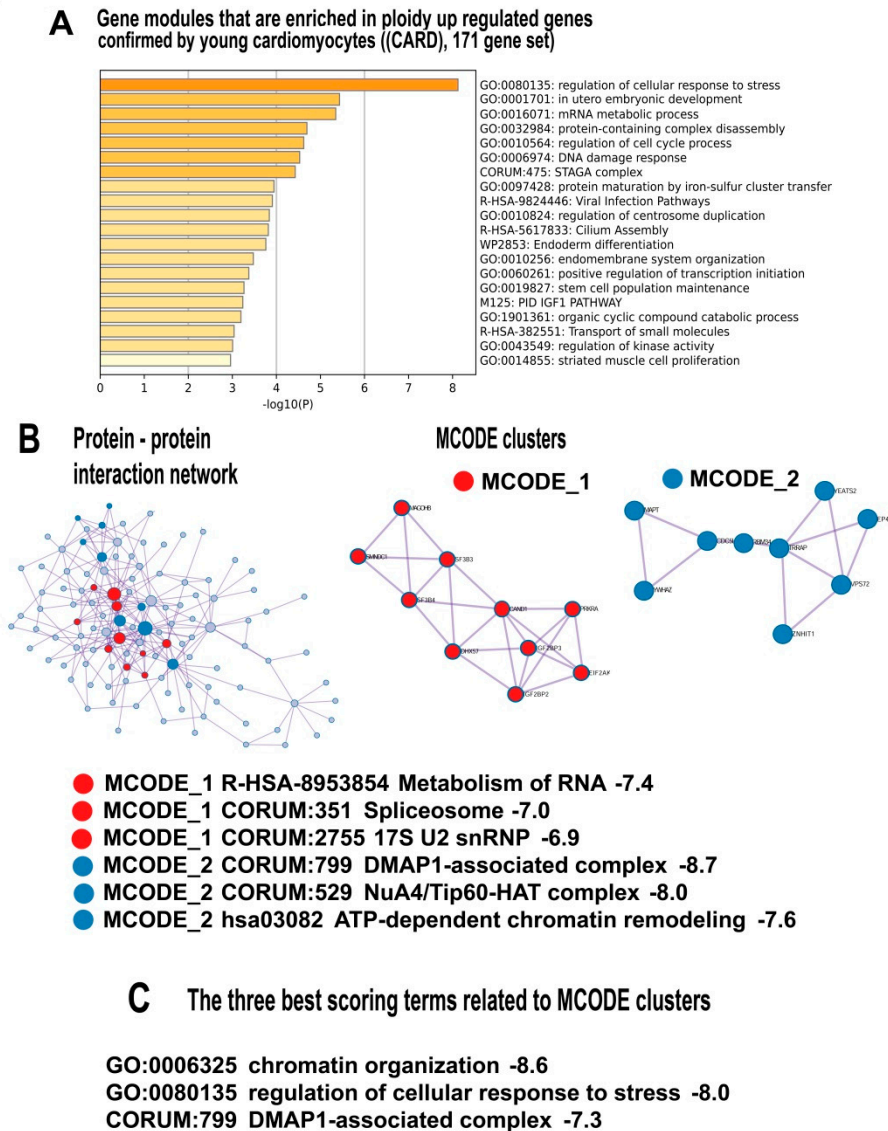
Supplementary Figure S1



Supplementary Figure S1. The enrichment of polyploidy-induced genes from the 233 gene set for CP. This gene set was obtained by comparison of ploidy-upregulated genes in cancer cells and MSC (358 gene set) and all ploidy-upregulated genes in cardiac progenitor cells (CP) obtained from iPS of fibroblastic origin [28]. (A)—Bar graph of enriched terms related to gene modules and processes. The statistical significance of enrichment is shown at the X-axis ($-\log_{10}(p)$). (B) — Protein interaction network and MCODE components (densely connected network components) identified in the gene list. The network and MCODE components were constructed on the base of physical interactions taken from String server (physical score > 0.4). The coding by color circles indicates the results of MCODE

component pathway and process enrichment analysis. (C) — The three best-scoring terms related to MCODE components. This Figure illustrates a good concordance between the data obtained for all 358 genes (for cancer cells and MSC) and for the 233 gene set (for CP derived from iPS). This is clearly seen for general chromatin remodeling (A-C) and chromatin remodeling associated with NuA4/Tip60 histone acetylating complex. It also uncovers the activation of housekeeping and developmental processes (A, B), and ciliogenesis (A).

Supplementary Figure S2

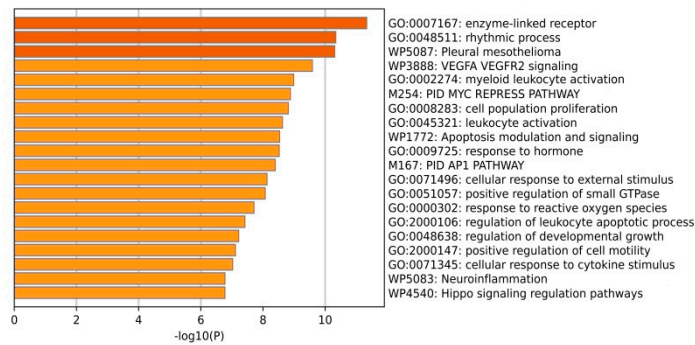


Supplementary Figure S2. The enrichment of polyploidy-induced genes from the 171 gene set for young CARD . This gene set was obtained by comparison of ploidy-upregulated genes in cancer cells and MSC (358 gene set) and all ploidy-upregulated genes in young cardiomyocytes (CARD) obtained from iPS of fibroblastic origin [28]. (A)—Bar graph of enriched terms related to gene modules and processes. The statistical significance of enrichment is shown at the X-axis ($-\log_{10}(p)$). (B) — Protein interaction network and MCODE components (densely connected network components) identified in the gene list. The network and MCODE components were constructed on the base of physical interactions taken from String server (physical score > 0.4). The coding by color circles indicates the results of MCODE component pathway and process enrichment analysis. (C) — The three best-scoring terms

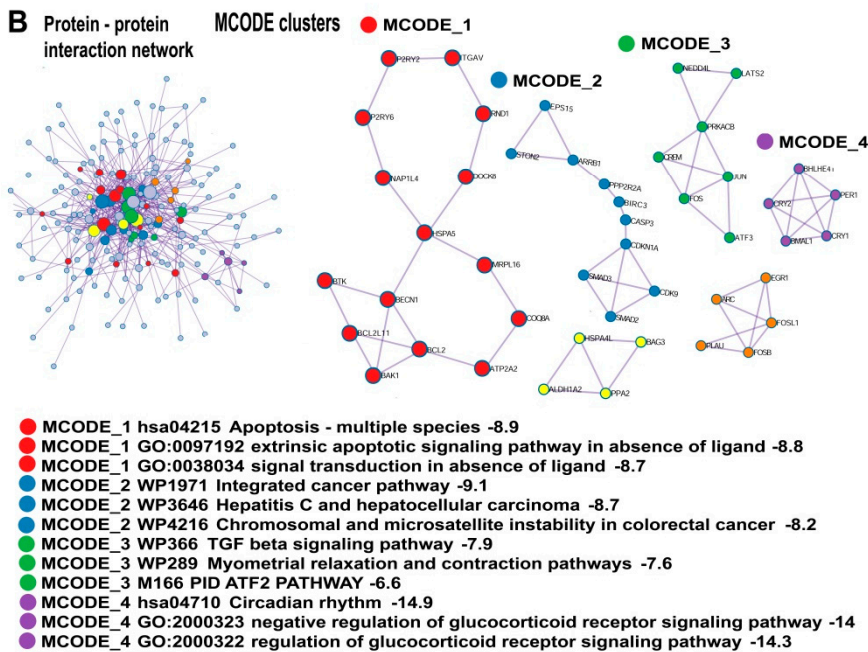
related to MCODE components. This Figure illustrates a good concordance between the data obtained for all 358 genes (for cancer cells and MSC) and for the 171 gene set (for CP derived from iPS). This is clearly seen for general chromatin remodeling (A-C) and chromatin remodeling associated with NuA4/Tip60 histone acetylating complex. It also uncovers the activation of housekeeping and developmental processes, DNA damage response (A, B), and ciliogenesis (A).

Supplementary Figure S3

A Gene modules that are enriched in ploidy down regulated genes confirmed by cardiac progenitors (CP) 244 gene set



B Protein - protein interaction network



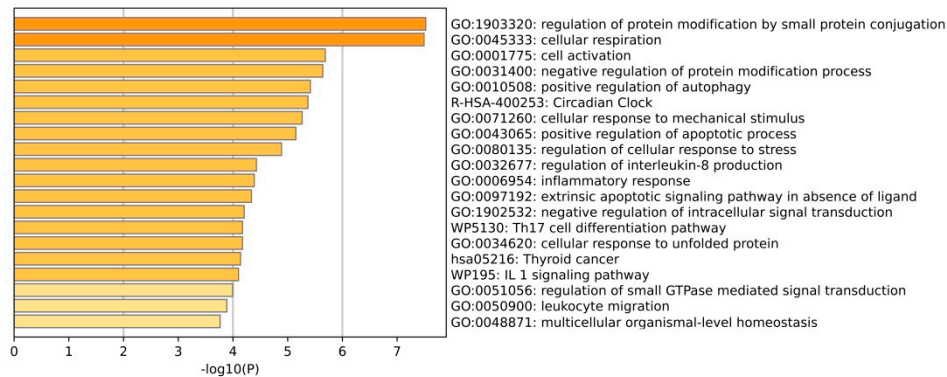
C The three best scoring terms related to MCODE clusters

WP5087 Pleural mesothelioma -11.0
GO:0007167 enzyme-linked receptor protein signaling pathway -10.8
GO:0048511 rhythmic process -10.7

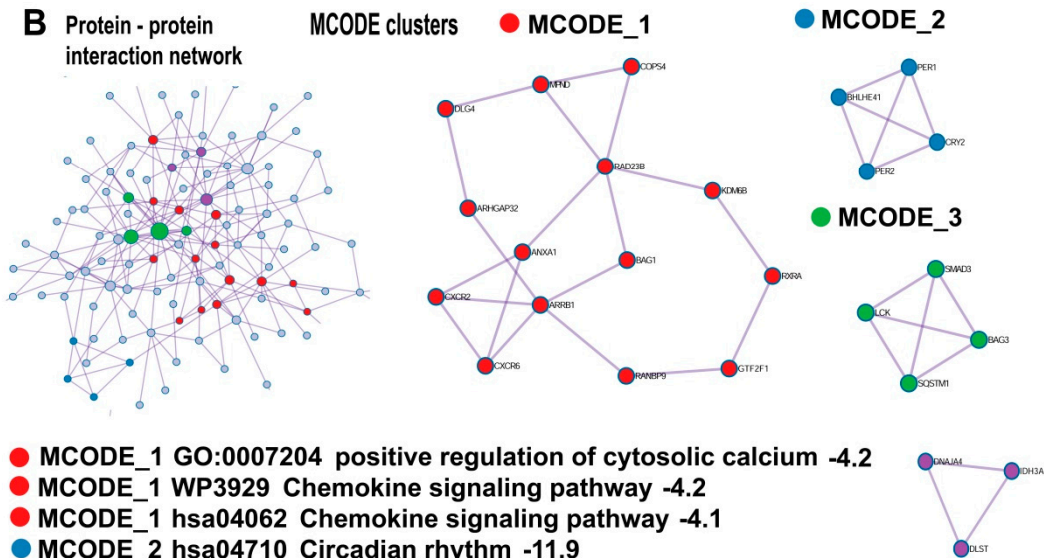
Supplementary Figure S3. The enrichment of polyploidy- downregulated genes from the 244 gene set. This gene set was obtained by comparison of ploidy-downregulated genes in cancer cells and MSC (425 gene set) and all ploidy-downregulated genes in cardiac progenitor cells (CP) obtained from iPS of fibroblastic origin [28]. The enrichment of polyploidy-inhibited genes from the 244 gene set . (A)—Bar graph of enriched terms related to gene modules and processes. The statistical significance of enrichment is shown at the X-axis ($-\log_{10}(p)$). (B) — Protein interaction network and MCODE components (densely connected network components) that were identified in the gene list. The network and MCODE components were constructed on the base of physical interactions taken from String server (physical score > 0.4). The coding by color circles indicates the results of MCODE component pathway and process enrichment analysis. (C) — Three best-scoring terms related to MCODE components. This Figure illustrates a good concordance between the data obtained for all 425 genes and 244 gene set. Especially, it is seen for the gene modules implicated in apoptosis, immunity (A-C), and circadian clock (A, B).

Supplementary Figure S4

A Gene modules that are enriched in ploidy down regulated genes confirmed by young cardiomyocytes derived from iPS ((CARD) 183 gene set



B Protein - protein interaction network



- MCODE_1 GO:0007204 positive regulation of cytosolic calcium -4.2
- MCODE_1 WP3929 Chemokine signaling pathway -4.2
- MCODE_1 hsa04062 Chemokine signaling pathway -4.1
- MCODE_2 hsa04710 Circadian rhythm -11.9
- MCODE_2 GO:0032922 circadian regulation of gene expression -10.6
- MCODE_2 R-HSA-400253 Circadian Clock -10.6
- MCODE_3 R-HSA-5663202 Diseases of signal transduction -4.8
- MCODE_3 R-HSA-449147 Signaling by Interleukins -4.8
- MCODE_3 GO:1903829 positive regulation of protein localization -4.8

C The three best scoring terms related to MCODE clusters

- GO:1903320 regulation of protein modification -7.5
- GO:1901873 regulation of post-translational protein modification -7.5
- GO:0045333 cellular respiration -6.8

Supplementary Figure S4. The enrichment of polyplody- downregulated genes from the 183 gene set. This gene set was obtained by comparison of ploidy-downregulated genes in cancer cells and MSC (425 gene set) and all ploidy-downregulated genes in young cardiomyocyte (CARD) obtained from iPS of fibroblastic origin [28]. The enrichment of polyplody-inhibited genes from the 183 gene set . (A)—Bar graph of enriched terms related to gene modules and processes. The statistical significance of enrichment is shown at the X-axis ($-\log_{10}(p)$). (B) — Protein interaction network and MCODE components (densely connected network components) that were identified in the gene list. The network and MCODE components were constructed on the base of physical interactions taken from String server (physical score > 0.4). The coding by color circles indicates the results of MCODE component pathway and process enrichment analysis. (C) — Three best-scoring terms related to MCODE components. This Figure illustrates a good concordance between the data obtained for all 425 genes and 183 gene set. Specifically, it is seen for the gene modules implicated in apoptosis, immunity (A-C), and circadian clock (A, B).