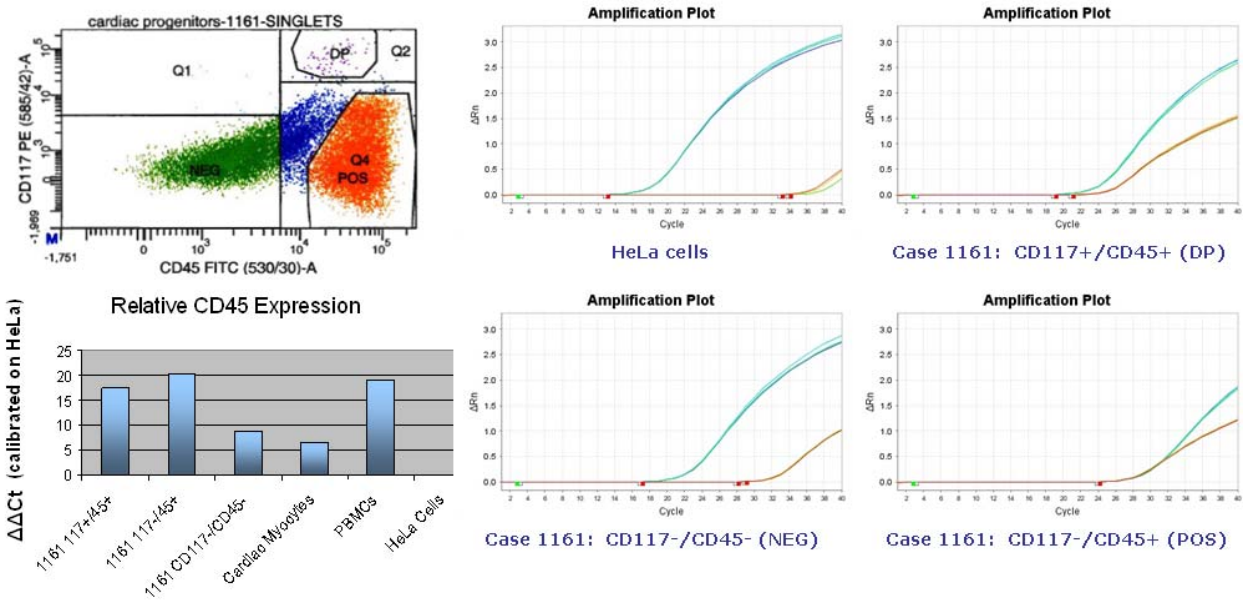
Data Supplement

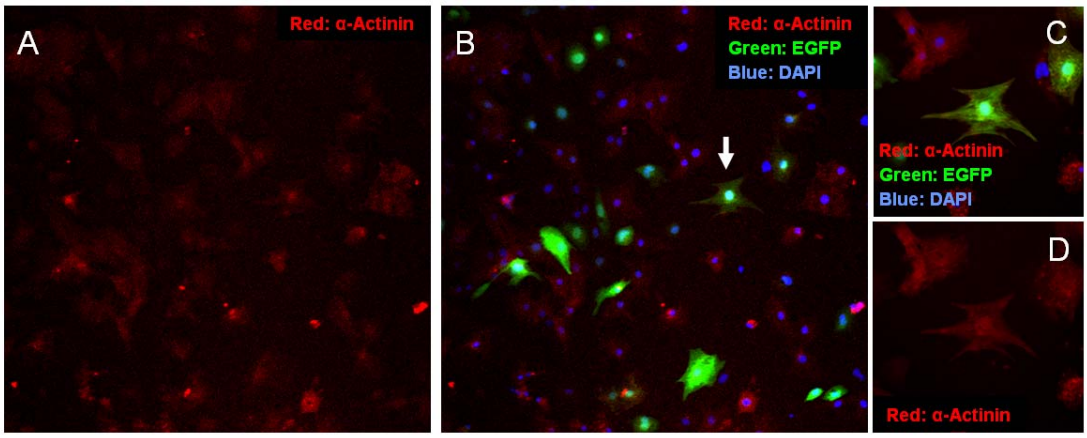
Supplemental Figure 1



Quantitative Real Time-PCR (QRT-PCR, TaqMan) for CD45 in FACS-sorted cells from a failing human heart. After initial gating to eliminate debris, aggregated cells and dead cells, the upper left panel depicts the cell sorting strategy and gates based on CD117 and CD45 staining. DP denotes double positive. POS denotes CD117-/CD45+ and excludes cells with nonspecific staining (blue). NEG denotes double negative. At center and right are four QRT-PCR amplification plots for these three sorted populations and HeLa cells as a negative control. In each amplification plot, the blue curve is GAPDH and the orange curve is CD45 which together are used to derive the ΔCt value for that sample. The lower left panel shows relative CD45 expression between cell populations expressed as the difference in their ΔCt values (ΔΔCt). Each ΔΔCt unit difference represents a two-fold difference in CD45 mRNA abundance between samples. These data indicate that CD45 expression in DP cells is much greater than in NEG

cells (~400-fold greater) and about 14% of that in POS cells, and parallel the flow cytometry fluorescence intensities. Peripheral blood mononuclear cells (PBMCs) and human cardiac myocytes are included as additional positive and negative controls, respectively. Differences in GAPDH amplification curves between samples reflect differences in total mRNA in the PCR reaction with HeLa cells having the greatest mRNA loaded and POS the least.

Supplemental Figure 2



Human c-kit enriched cardiac-derived progenitor cells (CPCs) co-cultured with neonatal rat ventricular myocytes (NRVMs). In a low magnification (20X) micrograph, after 18 hours in culture, A) shows α-actinin staining alone, and B) GFP, α-Actinin and DAPI overlay of the same field. C and D. Higher magnification (60X) view of a single cell (arrow in B).