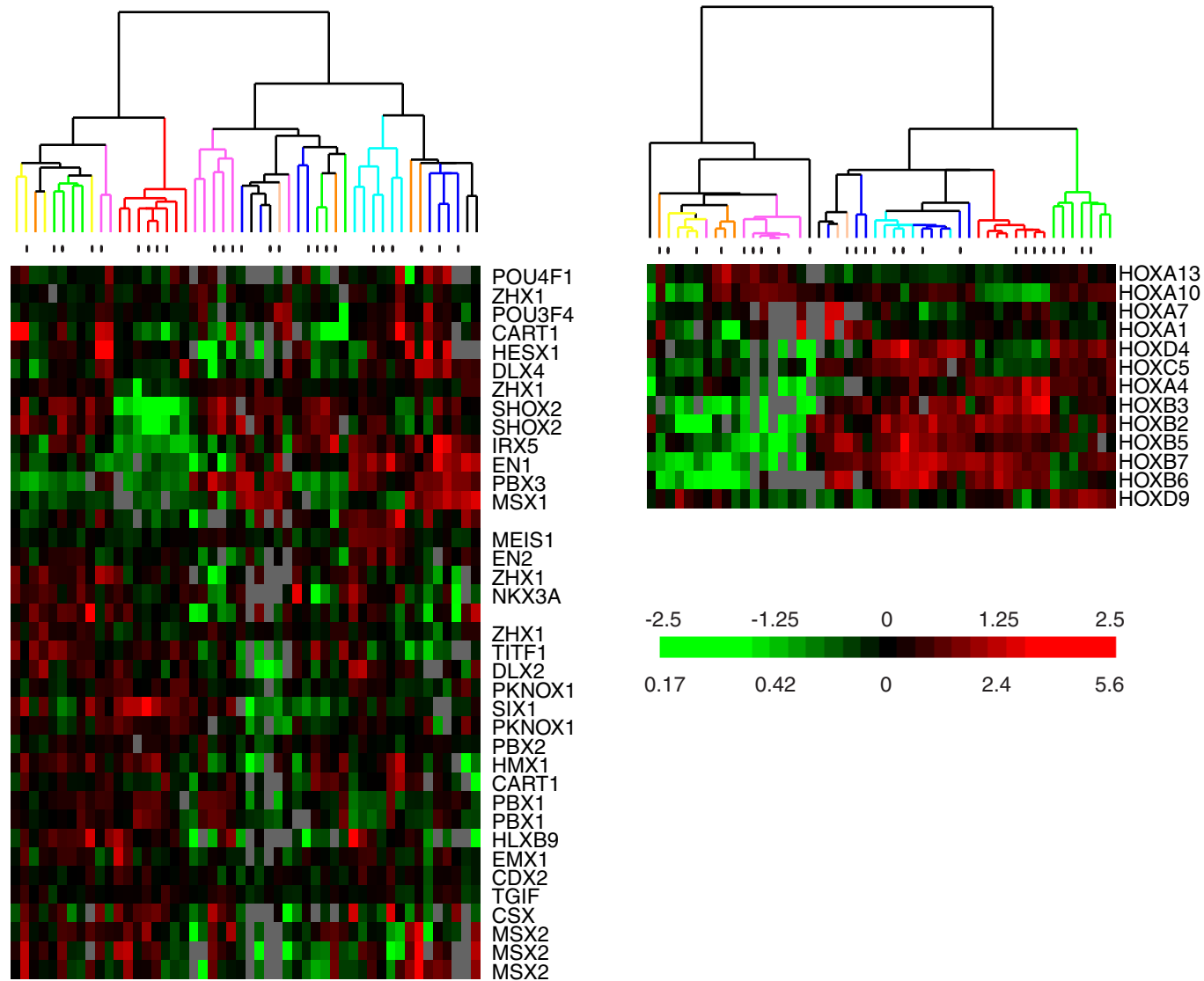


Supp Fig. 7



Supplemental Figure 7. Site classification by Hox genes versus other homeobox genes. The 51 homeobox genes identified in Fig 4A were separated into the two groups, and hierarchical clustering was performed. The data is shown in matrix format and the fibroblast sites color-coded as in Fig. 1C. Canonical Hox genes were superior in classifying fibroblasts sites of origin as indicated by the improved grouping of fibroblasts and the shorter branches of the dendrograms.