Figure 4. Pattern analysis of the 91 candidate stemness homolog groups in the three core stemness studies : a.) Idealized patterns that represent the possible distributions of genes in each homolog group. b.) We estimated a stemness and gene-usage normalize entropy score that allowed us to distinguish several different pattern types. The most commonly occuring pattern was "few genes-few tissues," while close to a third of the groups represented a "one dominant gene - many tissues" type of pattern. c.) Examples of homolog groups of the two most common pattern types. The group heatmaps show the distribution of upregulation for each gene in each population type.