



Figure 3. Upregulation patterns of significant homolog groups: a.) The upregulation patterns of the 210 significant homolog groups were examined by cell population and study. The spot for each group in a population was estimated as the average of the member gene upregulation score in that population. b.) The upregulation patterns of the 91 groups with two or more member genes. The bar on the right shows the significance of individual groups, where the most significant groups are shown in black and the least significant groups are shown in white. All profiles were hierarchically clustered in both the group and population dimensions.