



Legend supplementary Figure 2:

Venn Mapping was performed on the merged breast/prostate data set with a varying cut-off fold ratio input. The results were analysed analogous to Figure 2. The number of significant ($p < 0.01$) overlaps were counted and depicted as the fraction of the maximum number of overlaps (blue line). Furthermore, the ratios of the genes of the same dataset were randomly redistributed among the different microarray experiments before Venn Mapping. The number of significant overlaps were again counted at different cut-off levels (red line).