



Figure 2. Significant upregulated homolog groups in three core stemness studies: a.) We designed a scoring method that would capture groups that showed high levels of upregulation as a group (such as groups A and C) in stem cell populations and will not score highly very tissue-specific (group F), or unrelated (group B) groups. b.) Homolog groups showed a significant shift in score from randomized groups. We selected significant homolog groups, based on the deviation of their score from randomness and identified 210 significant groups, of which 91 had two or more member genes. c.) The 91 significant homolog groups did not show dependence of their significance score on group size.