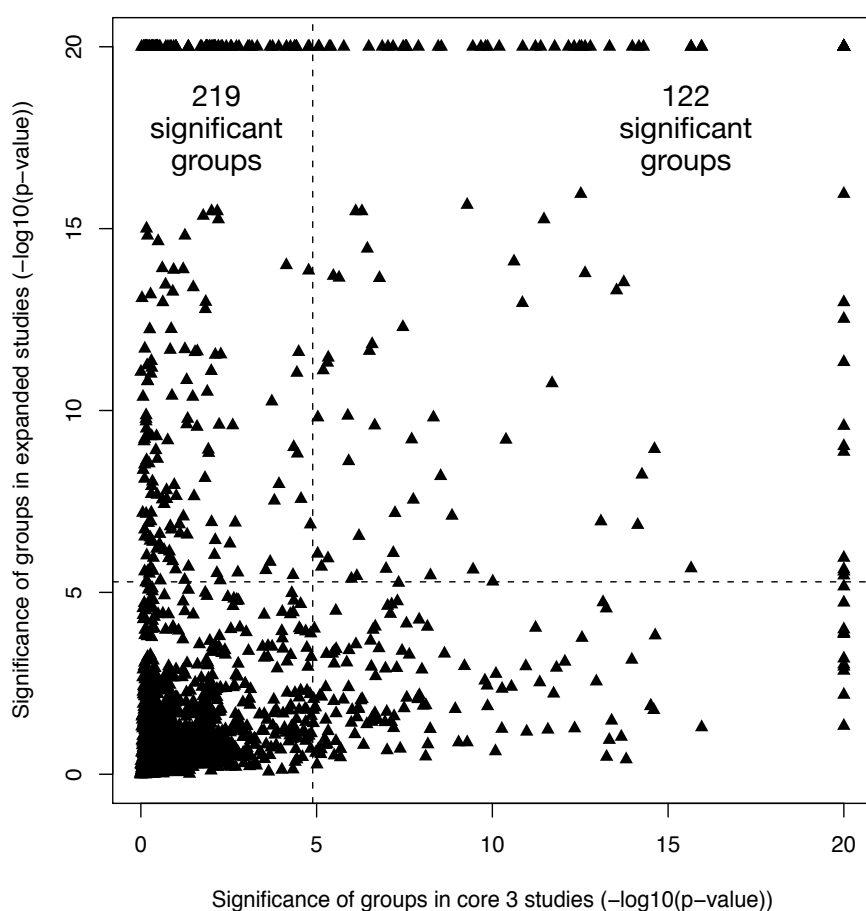
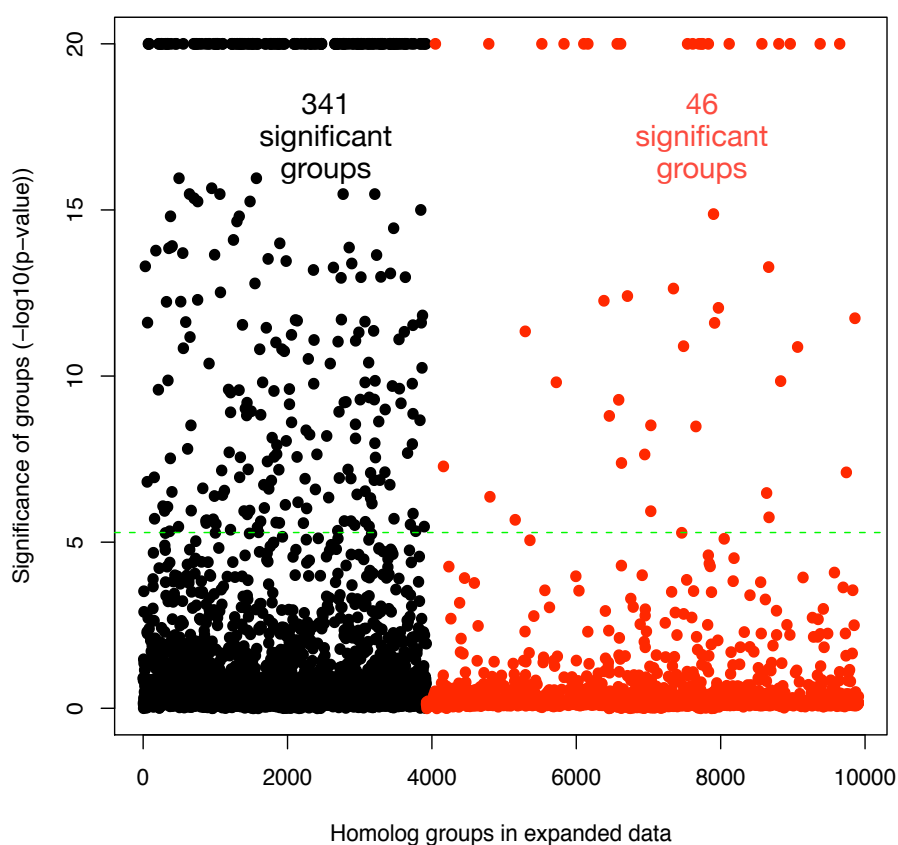


a.



b.



c.

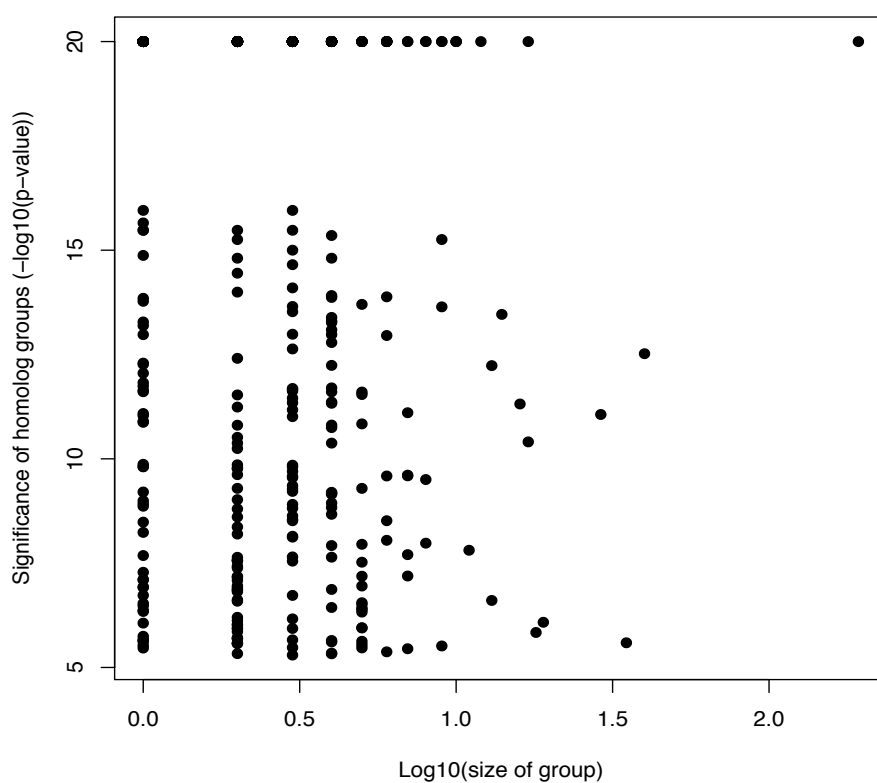


Figure 4. Putative stemness homolog confirmation after data source expansion: a.) We applied our method to an expanded set of transcriptional profiling studies. We compared the significance of the homolog groups that had been tested in the core 3 stemness studies with their significance after the addition of new data sources. We found that 122 groups were commonly identified as significant, as well as 219 groups that were previously not significant, but new data had provided support for their significance. Significance cutoffs are shown by dashed lines. b.) Most significant groups within the expanded data sources had already been discovered within the set of genes, tested in the three core studies. However, we also picked up 46 new significant homolog groups that could not have been previously identified, because their member genes had not been tested. The significance cutoff is indicated by a dashed green line. c.) We did not find any dependence between the size of the 387 significant homolog groups, identified by the expanded analysis and their significance level.