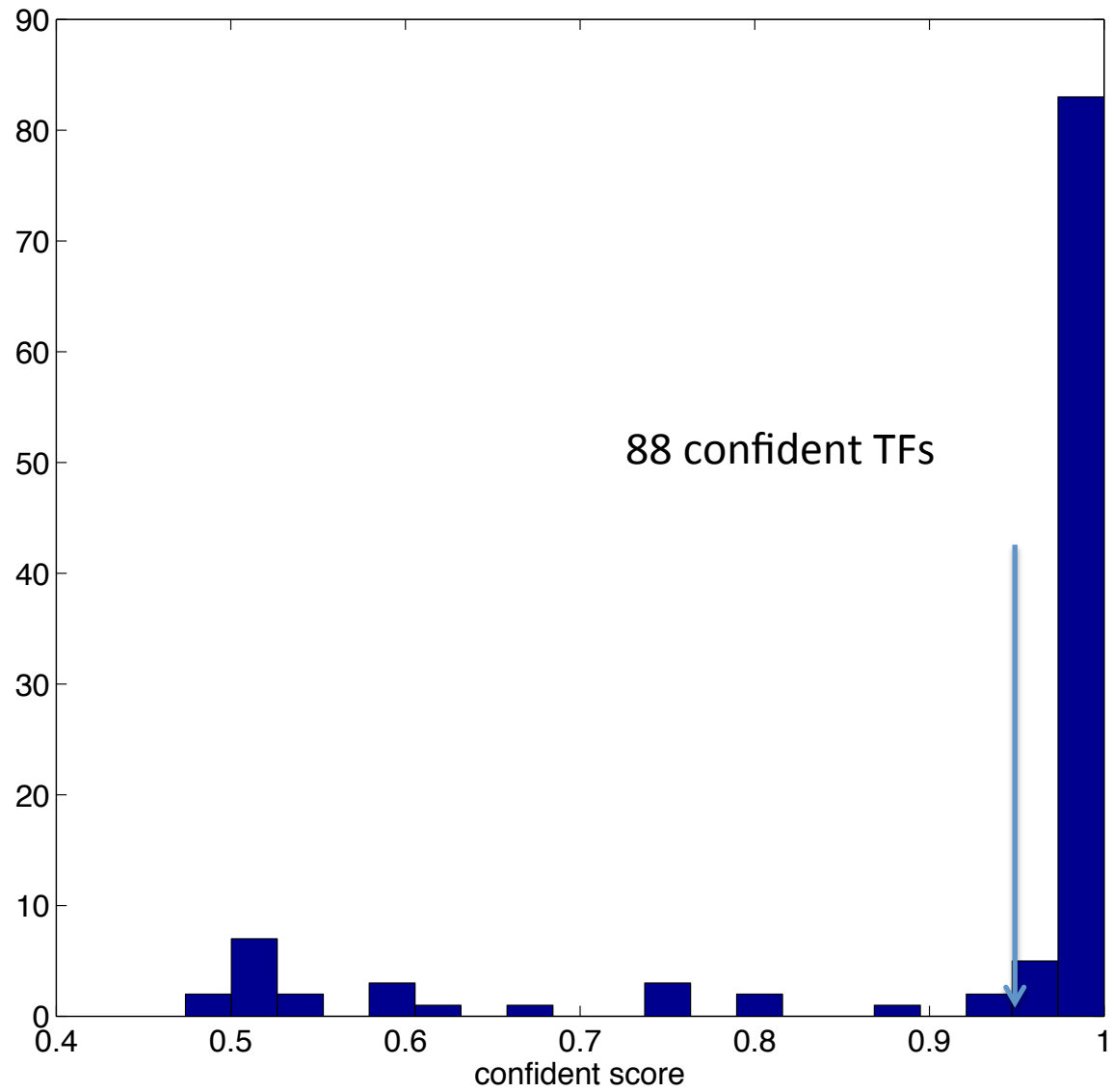


- Probabilistic nature of the hierarchy assignment, every output is slightly different
- Define a confident score of each TF assignment by running the algorithm 1000 times
- 88 confident TFs with score > 0.95 (33+21+34)



|    | A  | B          | C           | D         | E           | F                | G             |
|----|--|------------|-------------|-----------|-------------|------------------|---------------|
| 1  |  |            | all 112 TFs |           |             | 88 confident TFs |               |
| 2  |  | 1 vs 2     | 1 vs3       | 2 vs 3    | 1 vs 2      | 1 vs3            | 2 vs 3        |
| 3  | Average expression in34 human tissues                      | 0.29526    | 0.2715      | 0.49009   | 0.089196    | 0.16612          | 0.23691       |
| 4  | maximum Spearman Correlation of Tf binding with expression | 0.012593   | 0.018401    | 0.42777   | 0.0040738   | 0.0099273        | 0.27316 x     |
| 5  | tissue spec  | 0.31084    | 0.10627     | 0.18809   | 0.095605    | 0.10453          | 0.3789        |
| 6  | deg PPI (Ideker)   | 0.037536   | 0.0083216   | 0.22252   | 0.019956    | 0.0013394        | 0.24787 x     |
| 7  | deg PPI (BIOGRID)  | 0.43021    | 0.048729    | 0.087639  | 0.4809      | 0.035102         | 0.071495 x    |
| 8  | num. of kinases interaction                                | 0.22367    | 0.48164     | 0.13279   | 0.49241     | 0.37706          | 0.30722       |
| 9  | num. of mirna interaction                                  | 0.0046344  | 0.044758    | 0.14357   | 0.066976    | 0.011501         | 0.32133 ?     |
| 10 | num. targets in reg. net                                   | 0.00017006 | 0.00012202  | 0.49185   | 0.00012846  | 0.000046774      | 0.41427 x     |
| 11 | num. targets (TF) in reg. net                              | 0.00071373 | 2.7962E-06  | 0.032963  | 0.0010004   | 2.1834E-06       | 0.08145       |
| 12 | corr. between binding and gene expression                  | 0.17952    | 0.21795     | 0.46022   | 0.11007     | 0.090375         | 0.416         |
| 13 | binding matching score                                     | 0.016935   | 0.01371     | 0.29865   | 0.022732    | 0.023763         | 0.30838       |
| 14 | level of hierarchy (CC)                                    | 8.6554E-08 | 1.8789E-07  | 0.024019  | 0.000034609 | 1.5457E-06       | 0.0019698     |
| 15 | dnds   | 0.27182    | 0.16433     | 0.05803   | 0.39654     | 0.13674          | 0.22403       |
| 16 | snpdensity   | 0.31172    | 0.017835    | 0.0045973 | 0.33824     | 0.0079265        | 0.0063617 x   |
| 17 | Level in hierarchy (BFS by NB)                             | 0.029415   | 0.3485      | 0.015662  | 0.049017    | 0.24823          | 0.01435       |
| 18 | Motif.All.SNP.DAF<0.05                                     | 0.28617    | 0.23959     | 0.37797   | 0.14661     | 0.22785          | 0.38926       |
| 19 | Motif.Favorable.SNP.DAF<0.05                               | 0.13554    | 0.35973     | 0.034642  | 0.077353    | 0.4376           | 0.062735 ?    |
| 20 | Motif.Favorable.SNP.DAF>0.95                               | 0.16311    | 0.39871     | 0.055234  | 0.25597     | 0.44664          | 0.10547       |
| 21 | Motif.Unfavorable.SNP.DAF<0.05                             | 0.42786    | 0.32915     | 0.4728    | 0.25096     | 0.35671          | 0.27681       |
| 22 | Motif.Unfavorable.SNP.DAF>0.95                             | 0.1339     | 0.30308     | 0.0089035 | 0.090003    | 0.41307          | 0.023293      |
| 23 | num. ncRNA targets   | 0.0034976  | 0.00060624  | 0.39533   | 0.0018068   | 0.00078737       | 0.44831       |
| 24 | num. miRNA targets   | 0.00136    | 0.00060226  | 0.44719   | 0.0010314   | 0.00079817       | 0.3451        |
| 25 | num. miscRNA targets                                       | 0.00434    | 0.035137    | 0.34139   | 0.0050079   | 0.045643         | 0.31058       |
| 26 | num. snRNA targets   | 0.0001845  | 0.0022095   | 0.13948   | 0.00097365  | 0.0014401        | 0.23067       |
| 27 | num. snoRNA targets  | 0.0005997  | 0.003628    | 0.22335   | 0.00049549  | 0.0062647        | 0.15739       |
| 28 | num. lincRNA targets                                       | 0.0061756  | 0.00060591  | 0.25182   | 0.0042034   | 0.00082169       | 0.38087       |
| 29 | num. processed transcript targets                          | 0.0041468  | 0.00064015  | 0.36425   | 0.0023227   | 0.00091441       | 0.48273       |
| 30 | Ave_targets_Short_PolyA-                                   | 0.0082414  | 0.038096    | 0.20908   | 0.019233    | 0.043518         | 0.28905       |
| 31 | Ave_targets_PolyA+   | 0.012223   | 0.069524    | 0.18613   | 0.018277    | 0.08631          | 0.19223       |
| 32 | Betweenness  | 0.48394    | 0.0011442   | 0.0060366 | 0.019782    | 0.0012294        | 0.000049096 x |