Supplementary Table 3: Legend of numeric attributes in the MetaCore TF analysis

Object name	network object name in MetaBase
Actual	number of targets in the activated dataset(s) regulated by the chosen transcription factor (TF)
n	number of network objects in the activated dataset(s)
R	number of targets in the complete database or background list regulated by the chosen TF
N	total number of gene-based objects in the complete database or background list
Expected	mean value for hypergeometric distribution (n*R/N)
Ratio	connectivity ratio (Actual/Expected)
z-score	z-score ((Actual-Expected)/sqrt(variance))
p-value	probability to have the given value of Actual or higher (or lower for negative z-score)