Figure S1: The distribution of genes by number of expressing tissues remains bi-modal when gene expression thresholds are relaxed. Most genes are either globally expressed or tissue-specific, yet the tendency for global expression is enhanced. GNF refers to the study of Su AI et al., PNAS 2004. HPA refers to data of the human protein atlas (Berglund L. et al., Mol Cell Proteomics 2008). RNA-seq refers to RNA-sequencing data (Bradley RK et al, PLoS Biol 2012). GNF genes were considered as expressed in a tissue if their intensity value was above 30, and RNA-seq genes were considered as expressed in a tissue if their RPKM was at least 0.3. Total is the combined expression dataset.