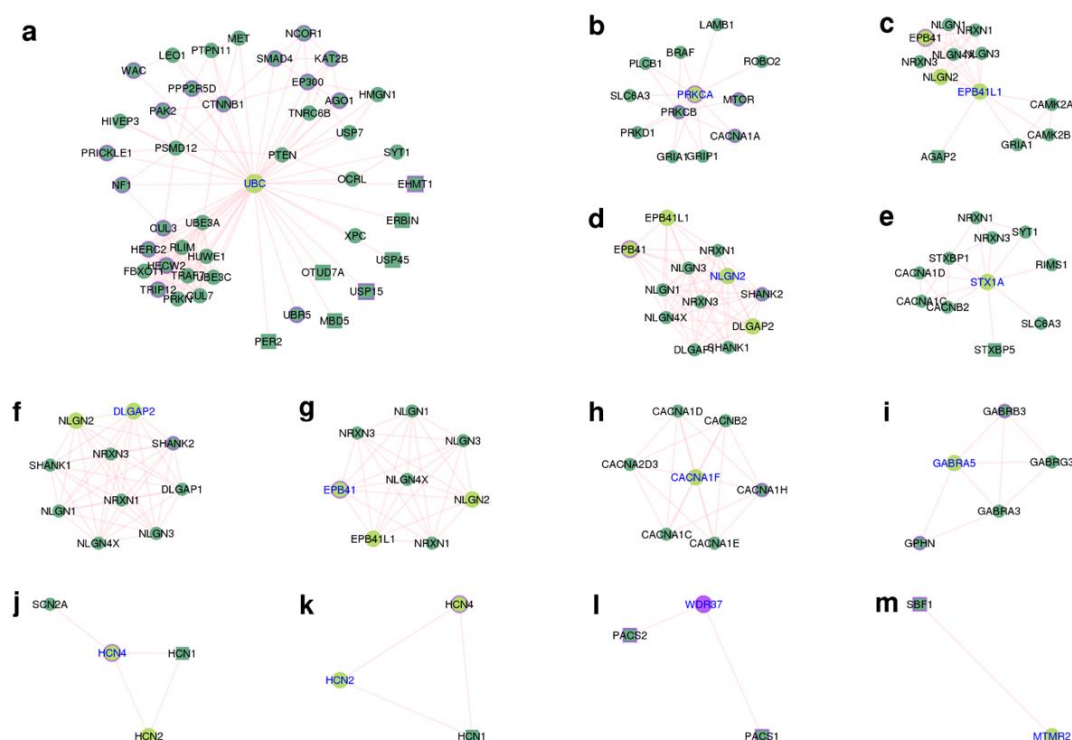
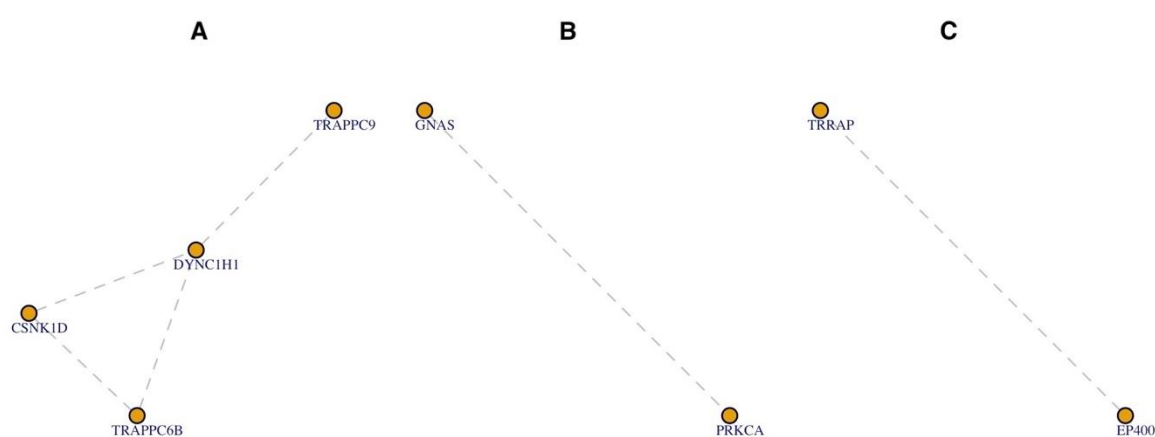




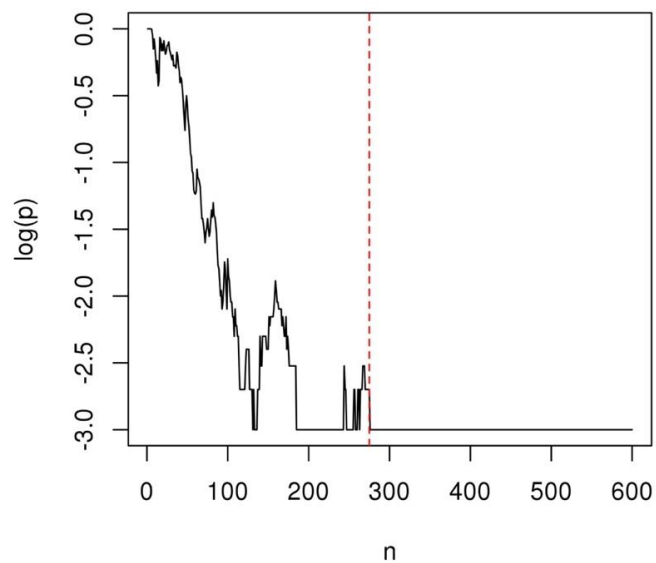
## 1 Supplementary Figures



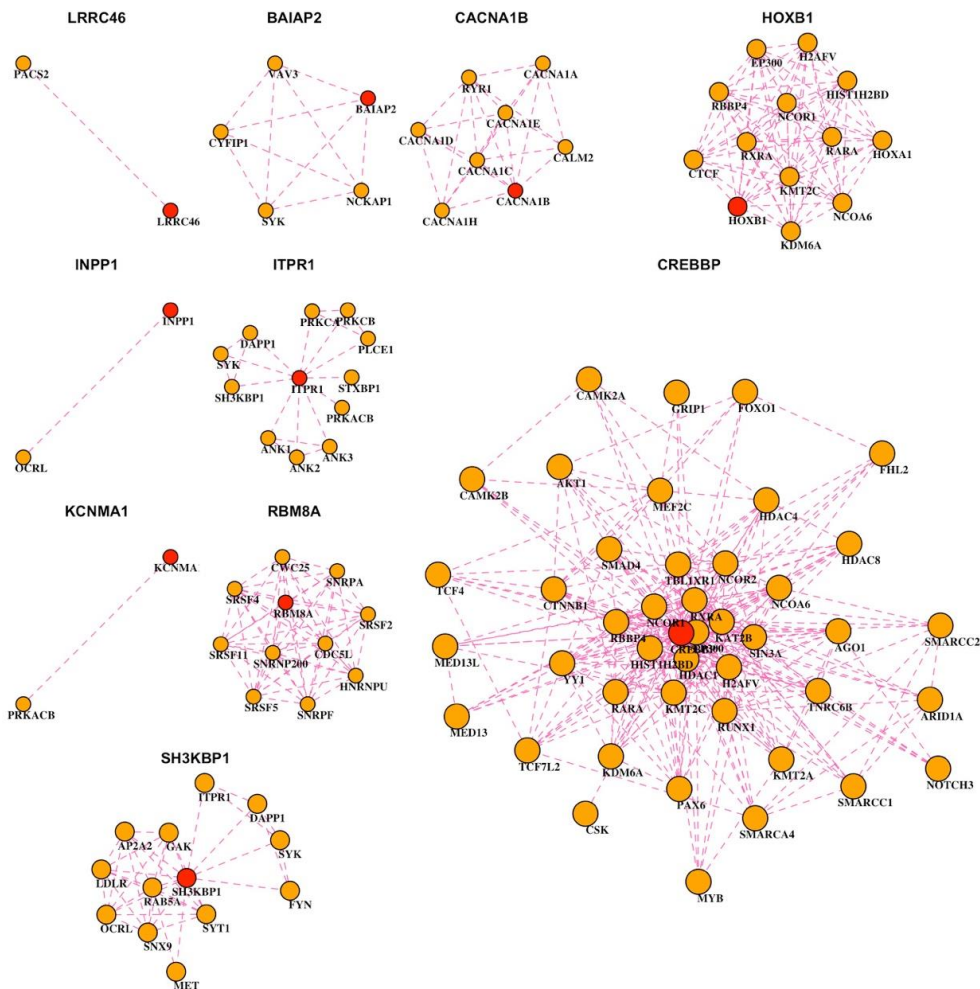
**Supplementary Figure S1. Interactors of the 13 genes that lie in network proximity to the CORE genes.** The 13 genes are indicated by blue labels. Shape: largest connected component (circle) and other components (square). Fill color: “GENOMICS-MINOR” (light green), SFARI genes (dark green) and no genomics evidence (purple). Border color: epigenetic and/or transcriptomic evidence (purple). Only members of the CORE+13 set are shown, while other direct interactors of the 13 genes are not reported.



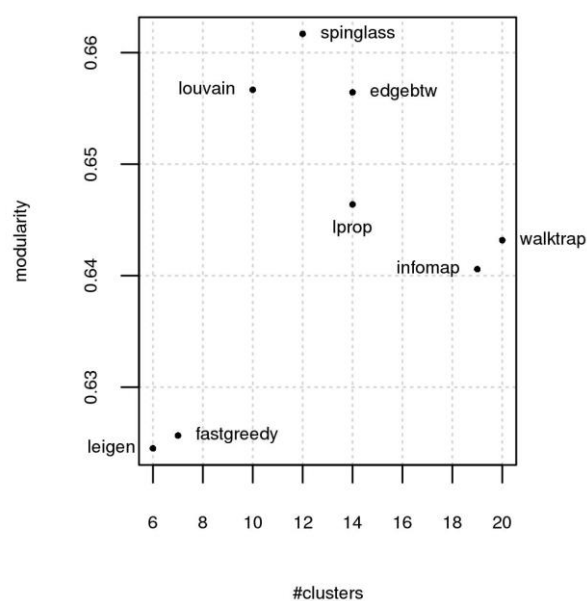
**Supplementary Figure S2. Interactions among the SHARED genes.** Only 8 of the 34 SHARED genes interact directly with at least another SHARED gene.



**Supplementary Figure S3. Network resampling on the genes top ranked by the multi-omics analysis.** Logarithm of  $p$ -value (y-axis) calculated for each rank of the gene list (x-axis) ordered by decreasing values of the global diffusion score.



**Supplementary Figure S4. Interactors of some genes belonging to the INT-MODULE.** Only the interactors that are member of the INT-MODULE are shown, while other interactors are not reported. See main text.



**Supplementary Figure S5. Modularity of different partitions of the INT-MODULE.** Modularity and number of clusters obtained partitioning the INT-MODULE by means of 8 community detection algorithms.