**Supplementary Text S3:** Pseudo-code of attractor metagene finding algorithm

1. Start from a seed gene $g\_{seed}$.
2. Calculate the associations $I(g\_{seed}; g\_{i})$ between each gene $g\_{i}$ and $g\_{seed}$
3. Create a metagene $m\_{0}$ using the weighted average of all the genes, with the weights $w\_{i}$ being a function of $I(g\_{seed};g\_{i})$, i.e., $w\_{i}=f(I(g\_{seed};g\_{i}))$
4. Given metagene $m\_{0}$, calculate the associations $I(m\_{0};g\_{i})$ between metagene $m\_{0}$ and each gene $g\_{i}$
5. Create metagene $m\_{1}$ using $w\_{i}=f(I(m\_{0};g\_{i}))$
6. Repeat iteration until $m\_{j+1}=m\_{j}$, or until a preset maximum iteration number is reached.
7. The converged $m\_{j}$ is the attractor metagene given by $g\_{seed}$