A novel meta-analysis approach of cancer transcriptomes reveals prevailing transcriptional networks in cancer cells

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Although microarray technology has revealed transcriptomic diversities underlining various cancer phenotypes, transcriptional programs controlling them have not been well elucidated. To decode transcriptional programs governing cancer transcriptomes, we have recently developed a computational method termed EEM, which searches for significantly coherent expression modules from prescribed gene sets defined by prior biological knowledge like *cis*-regulatory elements. In this study, to systematically analyze transcriptional programs in broad types of cancer, we apply EEM to 122 microarray data sets retrieved from public databases. The data sets contain about 15000 experiments for tumor samples of various tissue origins including breast, colon, lung and so on. This EEM based meta-analysis successfully identified expression modules activated in broad types of cancer transcriptomes. Furthermore, we predicted transcriptional networks governing these expression modules as "meta-networks", which suggest that cell-cycle and immune related transcriptional programs is employed by various types of cancer cells. This study demonstrates broad applicability of our method, and opens a way to comprehensive understanding of transcriptional networks in cancer cells.