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## **Pheno-RNA, a method to associate genes with a specific phenotype, identifies genes linked to cellular transformation**

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Cellular transformation is associated with dramatic changes in gene expression, but it is difficult to determine which regulated genes are oncogenically relevant. Here we describe Pheno-RNA, a general approach to identifying candidate genes associated with a specific phenotype. Specifically, we generate a “phenotypic series” by treating a nontransformed breast cell line with a wide variety of molecules that induce cellular transformation to various extents. By performing transcriptional profiling across this phenotypic series, the expression profile of every gene can be correlated with the strength of the transformed phenotype. We identify ~200 genes whose expression profiles are very highly correlated with the transformation phenotype, strongly suggesting their importance in transformation. Within biological categories linked to cancer, some genes show high correlations with the transformed phenotype, but others do not. Many genes whose expression profiles are highly correlated with transformation have never been associated with cancer, suggesting the involvement of heretofore unknown genes in cancer.

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