GENETICS

# BETTER THAN THE DELPHI ORACLE

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A new paper shows a nice workflow how to do an *in vitro* prediction which drug will suppress a certain tumor. The authors are simply linking the phenotype of the cell line “50% inhibitory concentration by drug X” with its expression signature. The good news are that doing both in one vial (phenotyping and expression analysis) is leading to excellent results.

Is there any trick to do this also system-wide e.g. for the metabolism of a substance and its signalling pathway? Pharmacogenetics would greatly benefit from such an approach, nay, nay.