Transcriptome-based identification of drug mechanisms (KMAP Express_Education)

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Genes are pleiotropic, having multiple functions according to cell type, developmental stage, and conditions. A single gene is frequently involved in multiple pathways, and thus, its function is most comprehensively understood in a global or genome-level context. Conventional in vitro and in vivo assays reveal a tiny fraction of a drug's activities. In contrast, genome-scale transcriptomic profiling broadens our view on drug action unbiased. The drug discovery process is similar to a long journey along a complex trail in a dark forest where it is easy to get lost. KMAP ExpressTM is like having a map, showing you shorter and cost-/time-saving paths along your journey to successful drug discovery. Developed by KaiPharm, KMAP® is a high-quality NGS-generated full transcriptomic profiling dataset for thousands of small molecule drugs approved in the United States, the European Union, and Japan at three concentrations in two cell lines with triple replicates across all conditions. The transcriptomic profiles of customer's drug candidates are generated under identical conditions as those of KMAP® and comparatively analyzed against ~2,700 approved drugs, covering a broad range of targets and indications. In contrast to other assays or experimental approaches, the dimension of comparison in KMAP ExpressTM is unparalleled interrogating 20,000 genes in 50,000 samples for each requested expression profile.