

Improving Target Identification with Phenovault

- Database & Analysis Suite for RNAi/CRISPR Screens

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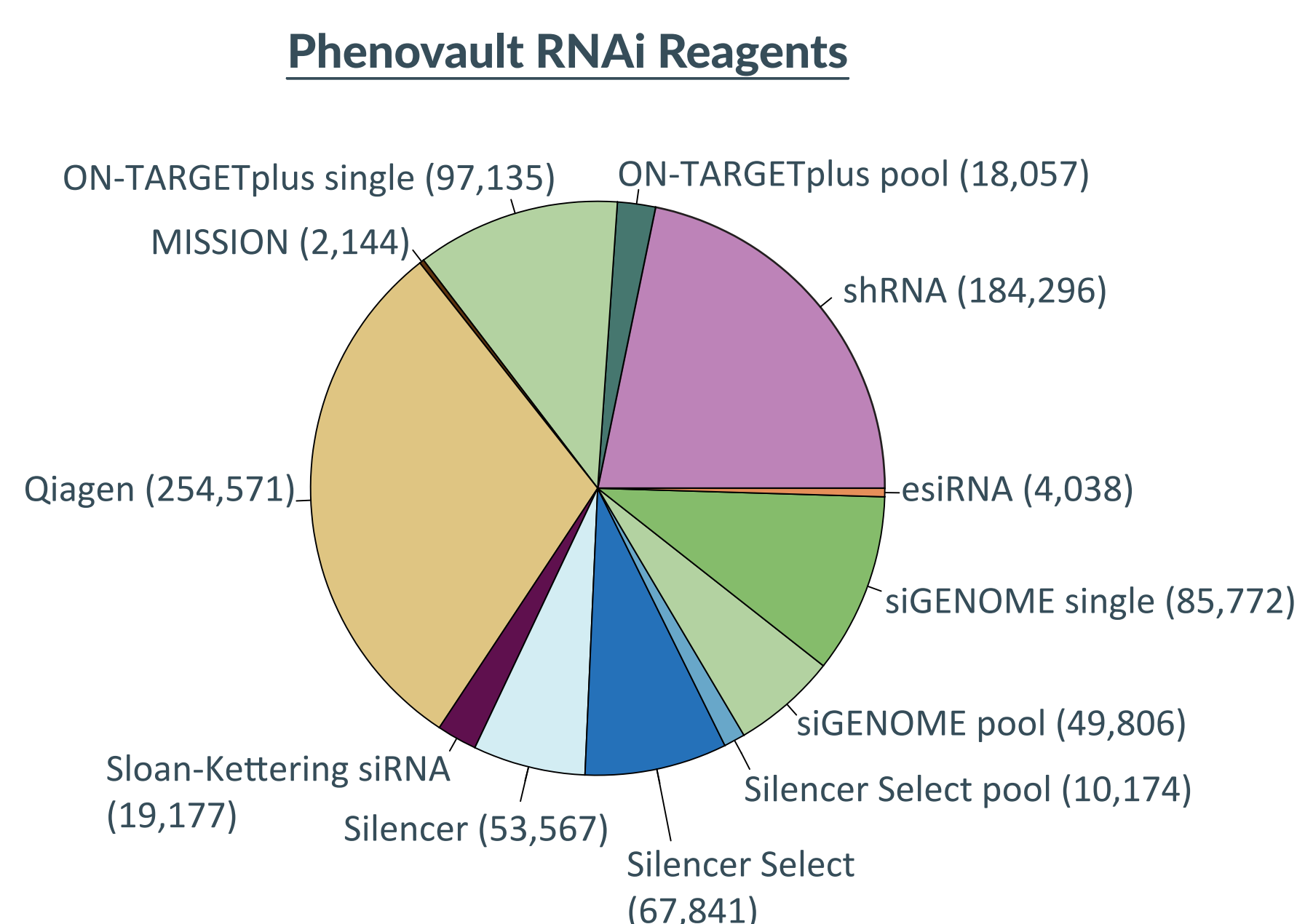
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RNA interference (RNAi) and CRISPR screens produce a wealth of information on gene function. However, published analyses only focus on a few top-scoring genes. Most of the information lies buried in supplementary materials, invisible and untapped. Phenovault is a growing database and analysis suite hosted by siTOOLS Biotech that contains complete datasets from published RNAi/CRISPR screens. With over 100 million data-points, Phenovault is the largest curated RNAi screening repository. siTOOLS uses public and proprietary algorithms to reveal seed-based hit genes from customer RNAi screens. For example, a kinome screen of 700 genes can be used to find seed-based hits in the entire human genome, thus transforming a narrowly focussed screen into a genome-wide RNAi screen. Phenovault algorithms uncover single genes with strong effect and gene networks that drive phenotypes.

Phenovault - Largest Curated RNAi Database & Analysis Suite

Inside the Phenovault

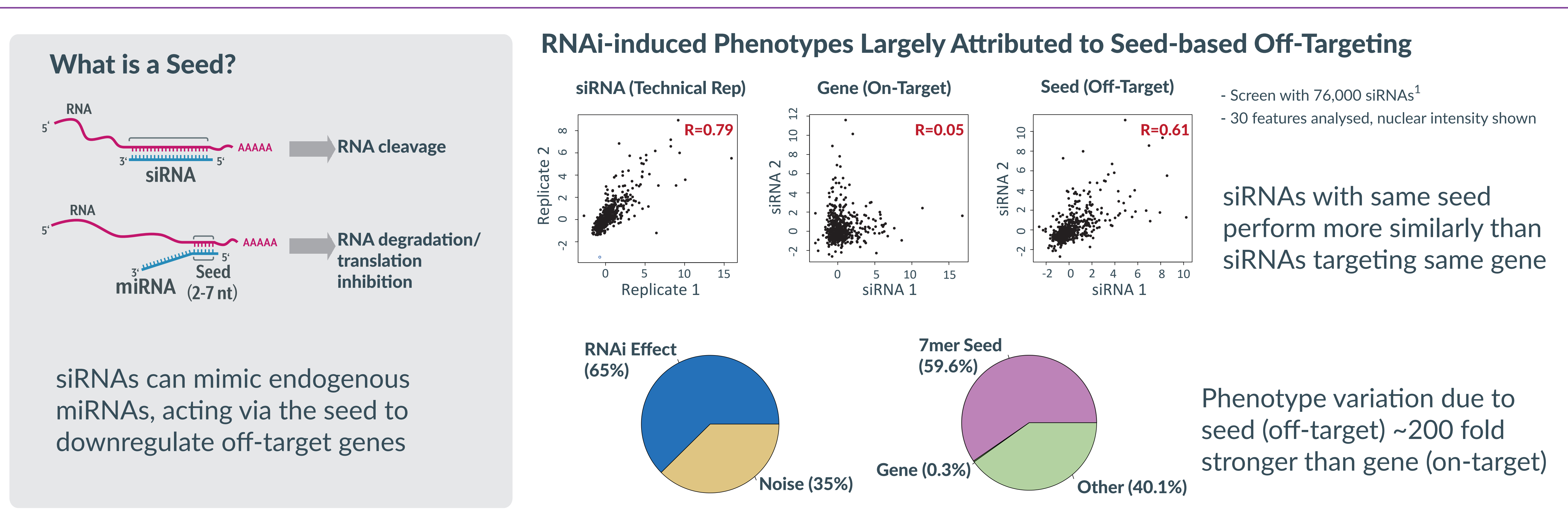
- > 100 million data-points
- > 2000 screening features
- Over a dozen published and proprietary analysis algorithms



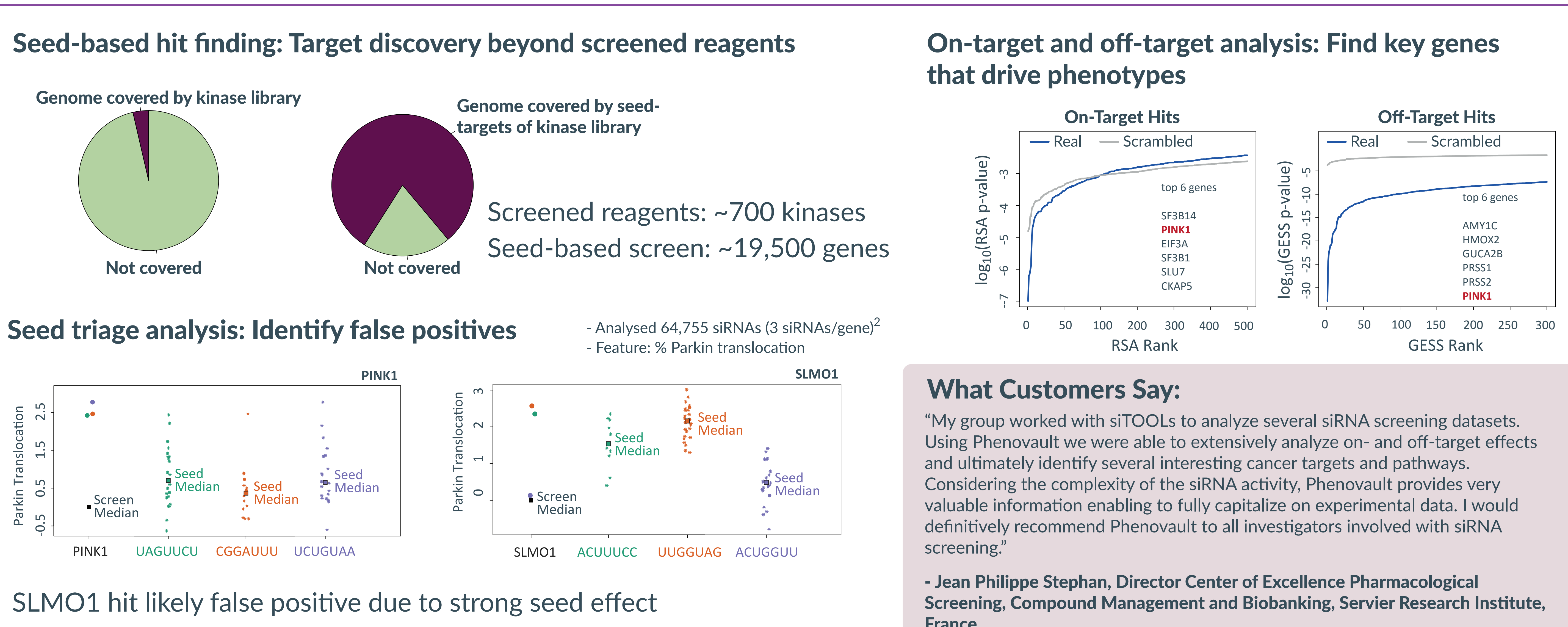
Applications

- Novel genome-wide hit detection based on siRNA seed effects
- Quality assessment of RNAi screen hits (detect false positives, counteract screening artefacts)
- Prioritize screening features or gene targets for follow-up validation work

Seed Effects Dominate RNAi Screens



Using Seed Effects to Find Novel Targets & Data Insights



References 1. Balestra, F. R., Strnad, P., Flückiger, I., and Gönczy, P. (2013) Discovering Regulators of Centriole Biogenesis through siRNA-Based Functional Genomics in Human Cells. Dev. Cell. 25, 555-571 2. Hasson, S. A., Kane, L. A., Yamano, K., Huang, C.-H., Sliter, D. A., Buehler, E., Wang, C., Heman-Ackah, S. M., Hessa, T., Guha, R., Martin, S. E., and Youle, R. J. (2013) High-content genome-wide RNAi screens identify regulators of parkin upstream of mitophagy. Nature. 504, 291-5