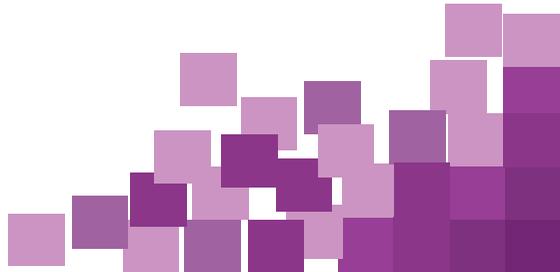


# The Phenovault

Database and Analysis Suite for  
RNAi/CRISPR Screens

*Uncover new insights into gene function,  
siRNA reagents and screening data*

Free Access!



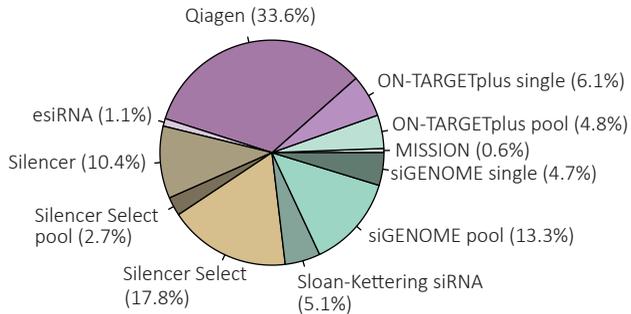
The **Phenovault** is a carefully curated database and analysis suite for RNAi and CRISPR screening data developed by siTOOLS Biotech.

Harnessing the power of large datasets and leveraging “seed”-based behaviour of siRNAs, the Phenovault unlocks new insights into existing RNAi screening data, siRNA reagents and gene targets.

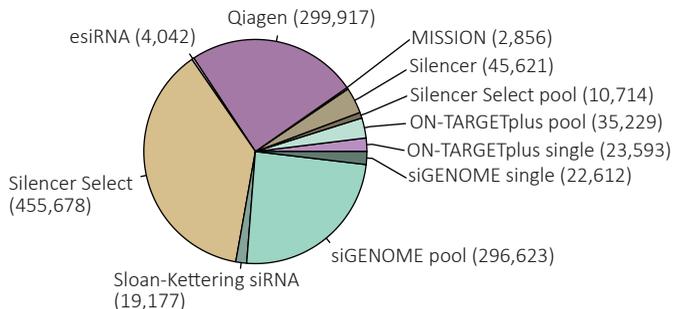
## Inside the Phenovault

- 48 screening publications and growing
- 374,364 unique reagents
- 20 million data points
- 845 screening features

### Phenovault RNAi reagents

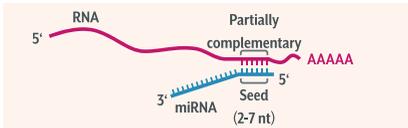
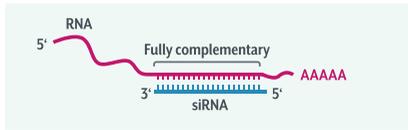


### Screen count per Phenovault RNAi reagent



# Leveraging seed-based siRNA off-target effects

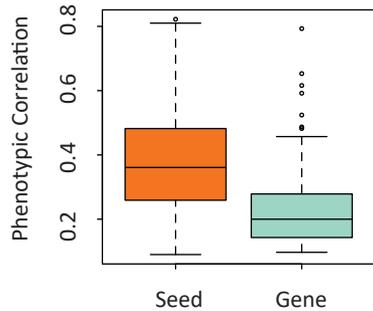
## What is a seed?



*microRNAs use the seed to recognise and downregulate transcripts*

The seed is a 6 base sequence at position 2 to 7 of the siRNA guide strand that dictates siRNA off-target activity based on microRNA mimicry.

## Seed effects dominate phenotypes



Correlation analysis of 300 phenotypic features show siRNAs sharing the same seed produce more closely related phenotypes than siRNAs targeting the same gene.

## What Phenovault can do

Combining large screening datasets with seed-based behaviour, Phenovault can:

### Evaluate siRNA specificity

Determine potential for off-targeting by a given siRNA sequence and obtain a list of candidate off-target genes.

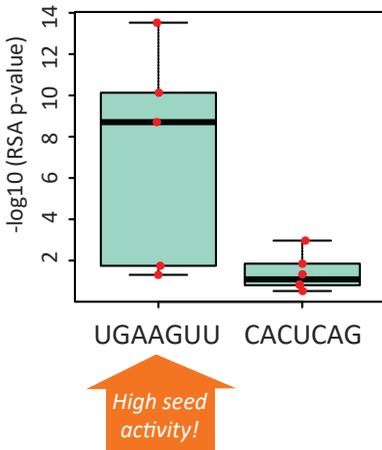
### Evaluate gene targets

Understand gene targets through their past performance in RNAi/CRISPR screens and obtain information on indicated phenotypes.

### Seed-focussed analysis of RNAi screening data

Identify false positives and uncover novel targets via seed-based hit detection algorithms for a given RNAi screening dataset.

# Evaluate siRNA specificity

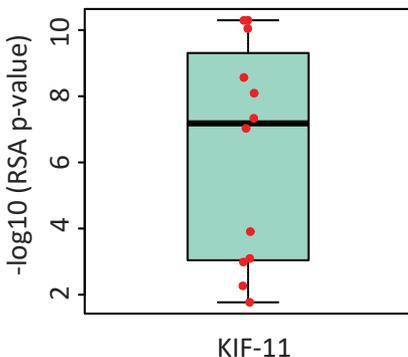


Our algorithms distinguish highly active seed sequences based on their enrichment in the top hits of Phenovault screens.

Using TargetScan (Lewis et al., 2015), a list of candidate off-target genes can be further provided.

*Boxplots represent publications where a given seed or gene was a significant hit. Each red dot represents one publication (note that one publication may include multiple screening features).*

# Evaluate gene targets



**Gene:** Kinesin Family Member 11, KIF-11

**Published role:** Motor protein that regulates spindle dynamics

**Phenovault info:**

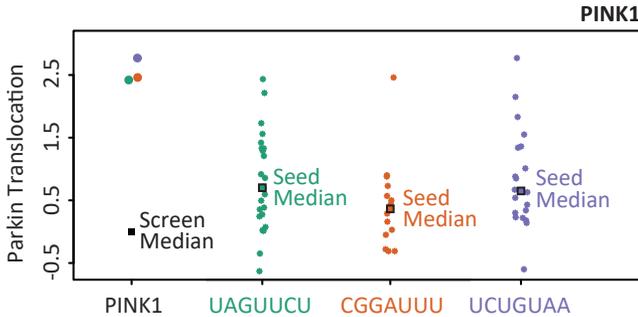
- Gene hit for 11 published screens (strong hit for 6 screens)
- Significantly regulated 12 screening features
- Phenotypes implicated include cell count, mitotic delay, EWS-FLI1 splicing and endocytosis

# Seed-focussed analysis of RNAi screening data

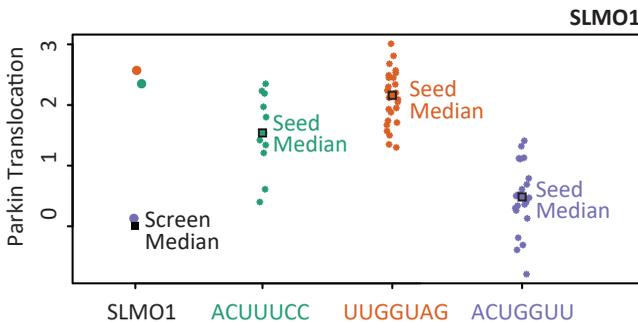
An RNAi screen for factors regulating Parkin mitochondrial translocation was analysed (Hasson et al., 2013).

## Identify false positives

With 3 siRNAs tested per gene, **seed triage analysis** could be performed for two top-ranked hits:

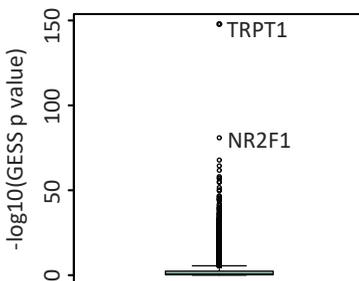


Minimal seed enrichment amongst 3 hit siRNAs indicates PINK1 is likely a true hit.



Significant seed enrichment for 2 of 3 hit siRNAs indicates SLMO1 is likely a false positive.

## Uncover novel hits



The Phenovault is equipped with various **seed-based hit-finding algorithms**.

The GESS algorithm (Sigoillot et al., 2012) applied here identified TRPT1 and NR2F1 as novel hits.

## How to access

Please submit your siRNA sequence, gene target, or screening data directly to us and receive your full Phenovault report by email.

Visit [www.phenovault.de](http://www.phenovault.de) for more information and updates.

### References:

Lewis BP, Burge CB, Bartel DP. (2005) Conserved Seed Pairing, Often Flanked by Adenosines, Indicates that Thousands of Human Genes are MicroRNA Targets. *Cell*, 120, 15-20 .

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, 291–295

Sigoillot, F. D., Lyman, S., Huckins, J. F., Adamson, B., Chung, E., Quattrochi, B., and King, R. W. (2012) A bioinformatics method identifies prominent off-targeted transcripts in RNAi screens. *Nat Meth*. 9, 363–366

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