



siPOOL™

Human Kinase Library

RNAi Screening Results You Can Trust



For the first time, medium to high-throughput RNAi screening with siPOOLS is enabled with the siPOOL human kinase library.

Key Benefits

Reliable RNAi screening results

The exceptional targeting specificity and efficient gene silencing by siPOOLS:

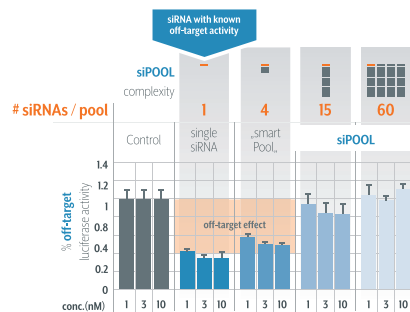
- reduces false positives and improves detection of true hits
- eases data analysis
- improves consistency between screens

Save time and resources

- Simplify screening with one siPOOL per gene
- Obtain results quickly (easily applied across cell lines with results in days)
- Avoid inefficient testing of multiple siRNAs to confirm hits

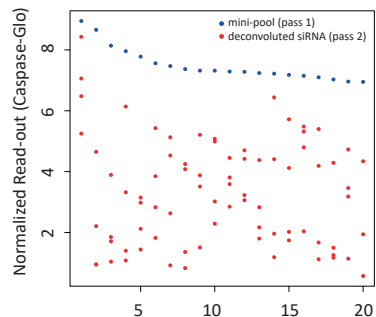
Problems faced with single siRNA/pools of 3-4 siRNAs

Off-target effects that give rise to variable, mixed phenotypes



Off-target spiking experiment demonstrates high complexity pools > 15 siRNAs required to dilute off-target effects.

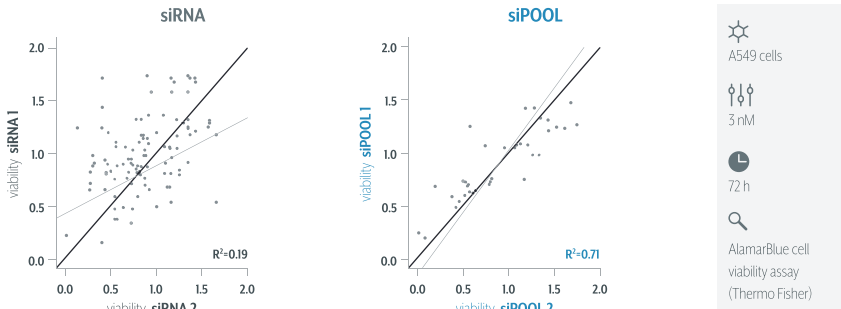
Variable results between siRNAs limit data interpretation



Falkenberg et al. show that siRNA results are widely divergent upon deconvolution of siGENOME smartpools.

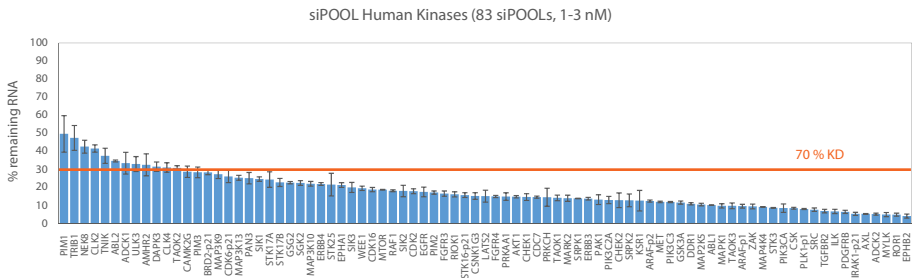
Data with the siPOOL Human Kinase Library

Reproducible phenotypes



siPOOLS efficiently counter siRNA variability. Two siPOOLS against the same gene (36 tested) produced more reproducible phenotypes than single siRNAs.

Efficient gene silencing at low nanomolar concentrations



Majority of human kinase siPOOLS tested (71 of 83) produced $\geq 70\%$ gene knockdown at 1-3 nM in standard cell lines (A549, MCF7, HeLa) as measured by rt-qPCR.

Efficient at very low concentrations, siPOOLS can be multiplexed with other treatments or siPOOLS without risk of side-effects (applicable for synthetic lethality screens).

Ordering information

- Provided in 96/384-well plates or 2D barcoded tubes
- Available lyophilized or in solution
- 0.1 – 1 nmol scales
- Plate arraying service available
- Custom extensions possible

Please contact us or our distributors for pricing
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References:

Falkenberg, K. J., Gould, C. M., Johnstone, R. W. & Simpson, K. J. Genome-wide functional genomic and transcriptomic analyses for genes regulating sensitivity to vorinostat. *Sci. Data* 2014 1 1, 140017 (2014).