

siPOOLS eliminate off-target effects

Short interfering RNAs (siRNA) are widely used for gene inactivation in basic research and increasingly in therapeutic applications. One major shortcoming of current RNAi reagents is frequent off-target effects: Functioning like endogenous microRNAs, siRNAs can inhibit the expression of partially complementary genes sharing as little as 6 bases of common

sequence. As a consequence, every single siRNA inhibits a broad range of largely unpredictable off-target genes that frequently dominate the phenotypic effect.

siPOOLS are complex pools of 30 precisely defined and carefully selected siRNAs that prevent off-target effects while showing reliable and efficient target gene knock down.

siPOOLS are defined Pools of selected siRNAs

siPOOLS silence target genes with highest reliability

siPOOLS do not show off-target effects

Customer Benefits are:

- **Reliable and interpretable results in one single experiment**
- **Cost saving:**
 - **no optimization for target gene knock down**
 - **radically reduced validation work**
- **Robust silencing of long non-coding RNAs**
- **Silencing of gene families and entire signaling cascades**
- **No unspecific toxicity**

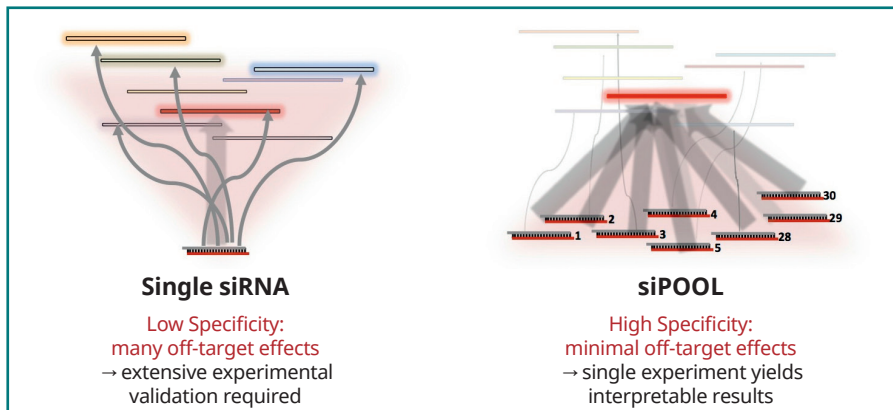


Fig.1: Diluting off-target effects with complex siRNA Pools: Every single siRNA has its own set of sequence-specific off-target effects (left). In complex siRNA pools, off-target effects of individual siRNAs are diluted below detection limit while cooperative on-target silencing remains reliably high.



Fig.2: Comparison of current siRNA reagents: Optimal siRNA sequences are dispersed along the entire gene transcript (top). Established siRNA reagents rely on the predicted activity of one to four siRNAs (bottom left and center). siPOOLS contain 30 selected siRNAs with highest silencing potential and optimized sequence diversity for off-target dilution (bottom right).

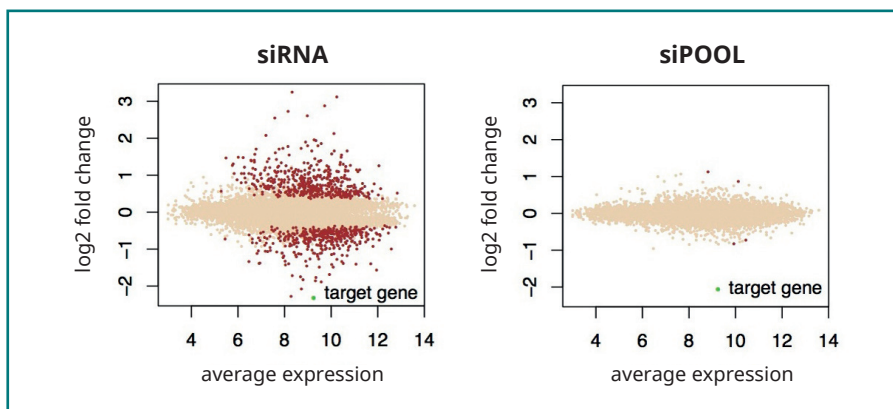


Fig.3: siPOOLS allow gene silencing with minimal side effects: A single siRNA (left) and a siPOOL (right) targeting human SCYL1 were transfected at 10nM concentration in HeLa cells and analyzed by expression profiling after 24h. Deregulation of gene expression is shown as shift on the y-axis. Applying a p-value cut-off of 1E-4, 890 genes were deregulated by the single siRNA (red dots). Only 4 off-targets were significantly affected by the siPOOL while the target gene (green dot) was efficiently silenced.

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Order Information:

siPOOLS are available for your selection of target genes:

- PAGE purified
- shipped with positive and negative control siPOOLS
- validated target gene silencing (on request)

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