#12136 Store at -20°C

SignalSilence® Sall4 siRNA I

☑ 10 µM in 300 µl (3 nmol)

Cell Signaling TECHNOLOGY®

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New 08/12

For Research Use Only. Not For Use In Diagnostic Procedures.

Species Cross-Reactivity: H

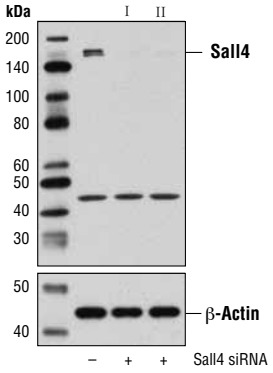
Description: SignalSilence® Sall4 siRNA I from Cell Signaling Technology (CST) allows the researcher to specifically inhibit Sall4 expression using RNA interference, a method whereby gene expression can be selectively silenced through the delivery of double stranded RNA molecules into the cell. All SignalSilence® siRNA products from CST are rigorously tested in-house and have been shown to reduce target protein expression by western analysis.

Background: Members of the SALL gene family encode putative zinc finger transcription factors highly expressed during development (1). Sall4 is expressed very early in development with other pluripotency regulators, such as Oct-4 and Nanog (2). Recent studies suggest Sall4 works as a master regulator that controls its own expression and the expression of Oct-4 in a transcriptional regulation feedback loop governing stem cell pluripotency and stem cell fate (2,3). Immunohistochemical studies indicate that Sall4 is a sensitive and specific diagnostic marker for primary germ cell tumors and yolk sac tumors (4,5). Research studies have shown that Sall4 is constitutively expressed in acute myeloid leukemia (AML) and is a probable effector of the Wnt/β-catenin signaling pathway in this disease (6). In addition, mutations in Sall4 have been implicated in human malformation syndromes including Duane-radial ray syndrome (Okihiro syndrome) and Acro-renal-ocular syndrome (7).

Directions for Use: CST recommends transfection with 100 nM SignalSilence® Sall4 siRNA I 48 to 72 hours prior to cell lysis. For transfection procedure, follow protocol provided by the transfection reagent manufacturer. Please feel free to contact CST with any questions on use.

Each vial contains the equivalent of 100 transfections, which corresponds to a final siRNA concentration of 100 nM per transfection in a 24-well plate with a total volume of 300 µl per well.

Quality Control: Oligonucleotide synthesis is monitored base by base through trityl analysis to ensure appropriate coupling efficiency. The oligo is subsequently purified by affinity-solid phase extraction. The annealed RNA duplex is further analyzed by mass spectrometry to verify the exact composition of the duplex. Each lot is compared to the previous lot by mass spectrometry to ensure maximum lot-to-lot consistency.



Western blot analysis of extracts from NTERA-2 cl.D1 cells, transfected with 100 nM SignalSilence® Control siRNA (Unconjugated) #6568 (-), SignalSilence® Sall4 siRNA I (+), or SignalSilence® Sall4 siRNA II #12111 (+), using Sall4 (D16H12) Rabbit mAb #8459 (upper) or β-Actin (D6A8) Rabbit mAb #8457 (lower). The Sall4 (D16H12) Rabbit mAb confirms silencing of Sall4 expression, while the β-Actin (D6A8) Rabbit mAb is used as a loading control.

Entrez-Gene ID #57167
Swiss-Prot Acc. #Q9UJQ4

Storage: Sall4 siRNA I is supplied in RNAse-free water. *Aliquot and store at -20ºC.*

Please visit www.cellsignal.com for a complete listing of recommended companion products.

Background References:

(1) Sweetman, D. and Münsterberg, A. (2006) *Dev Biol* 293, 285-93.

(2) Yang, J. et al. (2008) *Proc Natl Acad Sci USA* 105, 19756-61.

(3) Yang, J. et al. (2010) *PLoS One* 5, e10766.

(4) Mei, K. et al. (2009) *Mod Pathol* 22, 1628-36.

(5) Miertus, J. et al. (2006) *Hum Genet* 119, 154-61.

(6) Ma, Y. et al. (2006) *Blood* 108, 2726-35.

(7) Al-Baradie, R. et al. (2002) *Am J Hum Genet* 71, 1195-9.

Applications Key: **W**—Western **IP**—Immunoprecipitation **IHC**—Immunohistochemistry **ChIP**—Chromatin Immunoprecipitation **IF**—Immunofluorescence **F**—Flow cytometry **E-P**—ELISA-Peptide

Species Cross-Reactivity Key: **H**—human **M**—mouse **R**—rat **Hm**—hamster **Mk**—monkey **Mi**—mink **C**—chicken **Dm**—D. melanogaster **X**—Xenopus **Z**—zebrafish **B**—bovine **Dg**—dog **Pg**—pig **Sc**—S. cerevisiae **Ce**—C. elegans **Hr**—Horse **All**—all species expected Species enclosed in parentheses are predicted to react based on 100% homology.