SANTA CRUZ BIOTECHNOLOGY, INC.

FOXC1 siRNA (m): sc-145221

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The Power to Question

BACKGROUND

The forkhead transcription factor genes FOXC1 (Mf1) and FOXC2 (Mfh1) interact with the Notch signaling pathway and are required for the prepatterning of anterior and posterior domains in the presumptive somites through a putative Notch/Delta/Mesp regulatory loop. The genes have similar, dose-dependent functions, and compensate for each other in the early development of the heart, blood vessels and somites. Both FOXC1 and FOXC2 are expressed in the mesenchyme from which the ocular drainage structures derive. FOXC1 and FOXC2 also interact in kidney and heart development. Mutations in the FOXC1 gene result in Axenfeld-Rieger malformations of the anterior segment of the eye and lead to an increased susceptibility of glaucoma, including juvenile glaucoma. Functional regions in FOXC1 are required for nuclear localization and transcriptional regulation. Specifically, two regions in the FOXC1 forkhead domain, one rich in basic amino acid residues, and a second, highly conserved among all FOX proteins, are necessary for nuclear localization of the FOXC1 protein.

REFERENCES

1. Smith, R.S., et al. 2000. Haploinsufficiency of the transcription factors FOXC1 and FOXC2 results in aberrant ocular development. Hum. Mol. Genet. 9: 1021-1032.
2. Kume, T., et al. 2000. Murine forkhead/winged helix genes FOXC1 (Mf1) and FOXC2 (Mfh1) are required for the early organogenesis of the kidney and urinary tract. Development 127: 1387-1395.
3. Kawase, C., et al. 2001. Screening for mutations of Axenfeld-Rieger syndrome caused by FOXC1 gene in Japanese patients. J. Glaucoma 10: 477-482.
4. Kume, T., et al. 2001. The murine winged helix transcription factors, FOXC1 and FOXC2, are both required for cardiovascular development and somitogenesis. Genes Dev. 15: 2470-2482.
5. Berry, F.B., et al. 2002. FOXC1 transcriptional regulation is mediated by N- and C-terminal activation domains and contains a phosphorylated transcriptional inhibitory domain. J. Biol. Chem. 277: 10292-10297.

CHROMOSOMAL LOCATION

Genetic locus: Foxc1 (mouse) mapping to 13 A3.2.

PRODUCT

FOXC1 siRNA (m) is a pool of 3 target-specific 19-25 nt siRNAs designed to knock down gene expression. Each vial contains 3.3 nmol of lyophilized siRNA, sufficient for a 10 µM solution once resuspended using protocol below. Suitable for 50-100 transfections. Also see FOXC1 shRNA Plasmid (m): sc-145221-SH and FOXC1 shRNA (m) Lentiviral Particles: sc-145221-V as alternate gene silencing products.

For independent verification of FOXC1 (m) gene silencing results, we also provide the individual siRNA duplex components. Each is available as 3.3 nmol of lyophilized siRNA. These include: sc-145221A, sc-145221B and sc-145221C.

STORAGE AND RESUSPENSION

Store lyophilized siRNA duplex at -20° C with desiccant. Stable for at least one year from the date of shipment. Once resuspended, store at -20° C, avoid contact with RNAses and repeated freeze thaw cycles.

Resuspend lyophilized siRNA duplex in 330 µl of the RNAse-free water provided. Resuspension of the siRNA duplex in 330 µl of RNAse-free water makes a 10 µM solution in a 10 µM Tris-HCl, pH 8.0, 20 mM NaCl, 1 mM EDTA buffered solution.

APPLICATIONS

FOXC1 siRNA (m) is recommended for the inhibition of FOXC1 expression in mouse cells.

SUPPORT REAGENTS

For optimal siRNA transfection efficiency, Santa Cruz Biotechnology's siRNA Transfection Reagent: sc-29528 (0.3 ml), siRNA Transfection Medium: sc-36868 (20 ml) and siRNA Dilution Buffer: sc-29527 (1.5 ml) are recommended. Control siRNAs or Fluorescein Conjugated Control siRNAs are available as 10 µM in 66 µl. Each contain a scrambled sequence that will not lead to the specific degradation of any known cellular mRNA. Fluorescein Conjugated Control siRNAs include: sc-36869, sc-44239, sc-44240 and sc-44241. Control siRNAs include: sc-37007, sc-44230, sc-44231, sc-44232, sc-44233, sc-44234, sc-44235, sc-44236, sc-44237 and sc-44238.

GENE EXPRESSION MONITORING

FOXC1 (4D11): sc-293455 is recommended as a control antibody for monitoring of FOXC1 gene expression knockdown by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000) or immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500).

To ensure optimal results, the following support reagents are recommended: 1) Western Blotting: use m-IgGκ BP-HRP: sc-516102 or m-IgGκ BP-HRP (Cruz Marker): sc-516102-CM (dilution range: 1:1000-1:10000), Cruz Marker™ Molecular Weight Standards: sc-2035, UltraCruz® Blocking Reagent: sc-516214 and Western Blotting Luminol Reagent: sc-2048. 2) Immunofluorescence: use m-IgGκ BP-FITC: sc-516140 or m-IgGκ BP-PE: sc-516141 (dilution range: 1:50-1:200) with UltraCruz® Mounting Medium: sc-24941 or UltraCruz® Hard-set Mounting Medium: sc-359850.

RT-PCR REAGENTS

Semi-quantitative RT-PCR may be performed to monitor FOXC1 gene expression knockdown using RT-PCR Primer: FOXC1 (m)-PR: sc-145221-PR (20 µl). Annealing temperature for the primers should be 55-60° C and the extension temperature should be 68-72° C.

SELECT PRODUCT CITATIONS

1. Mott, L., et al. 2018. Evaluation of FOXC1 as a therapeutic target for basal-like breast cancer. Cancer Gene Ther. 25: 84-91.

RESEARCH USE

For research use only, not for use in diagnostic procedures.