

SPOUT1 siRNA (h): sc-92746

BACKGROUND

Chromosome 9 consists of about 145 million bases and 4% of the human genome, encoding nearly 900 genes. Considered to play a role in gender determination, deletion of the distal portion of 9p can lead to development of male to female sex reversal, the phenotype of a female with a male X,Y genotype. Hereditary hemorrhagic telangiectasia, which is characterized by harmful vascular defects, is associated with the chromosome 9 gene-encoding Endoglin protein, ENG. Familial dysautonomia is also associated with chromosome 9 through the gene IKBKAP. Notably, chromosome 9 encompasses the largest interferon family gene cluster. Chromosome 9 is partnered with chromosome 22 in the translocation leading to the aberrant production of Bcr-Abl fusion protein often found in leukemias.

REFERENCES

1. Humphray, S.J., Oliver, K., Hunt, A.R., Plumb, R.W., Loveland, J.E., Howe, K.L., Andrews, T.D., Searle, S., Hunt, S.E., Scott, C.E., Jones, M.C., Ainscough, R., Almeida, J.P., Ambrose, K.D., Ashwell, R.I., et al. 2004. DNA sequence and analysis of human chromosome 9. *Nature* 429: 369-374.
2. Coppo, P., Flamant, S., De Mas, V., Jarrier, P., Guillier, M., Bonnet, M.L., Lacout, C., Guilhot, F., Vainchenker, W. and Turhan, A.G. 2006. Bcr-Abl activates Stat3 via JAK and MEK pathways in human cells. *Br. J. Haematol.* 134: 171-179.
3. Zheng, X., Güller, S., Beissert, T., Puccetti, E. and Ruthardt, M. 2006. Bcr and its mutants, the reciprocal t(9;22)-associated Abl/Bcr fusion proteins, differentially regulate the cytoskeleton and cell motility. *BMC Cancer* 7: 262.
4. Burmeister, T., Schwartz, S., Taubald, A., Jost, E., Lipp, T., Schneller, F., Diedrich, H., Thomssen, H., Mey, U.J., Eucker, J., Rieder, H., Gökbuget, N., Hoelzer, D. and Thiel, E. 2007. Atypical Bcr-Abl mRNA transcripts in adult acute lymphoblastic leukemia. *Haematologica* 92: 1699-1702.
5. Cottin, V., Dupuis-Girod, S., Lesca, G. and Cordier, J.F. 2007. Pulmonary vascular manifestations of hereditary hemorrhagic telangiectasia (Rendu-Osler disease). *Respiration* 74: 361-378.

CHROMOSOMAL LOCATION

Genetic locus: SPOUT1 (human) mapping to 9q34.11.

PRODUCT

SPOUT1 siRNA (h) 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 μ M solution once resuspended using protocol below. Suitable for 50-100 transfections. Also see SPOUT1 shRNA Plasmid (h): sc-92746-SH and SPOUT1 shRNA (h) Lentiviral Particles: sc-92746-V as alternate gene silencing products.

For independent verification of SPOUT1 (h) gene silencing results, we also provide the individual siRNA duplex components. Each is available as 3.3 nmol of lyophilized siRNA. These include: sc-92746A, sc-92746B and sc-92746C.

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 μ l of the RNase-free water provided. Resuspension of the siRNA duplex in 330 μ l of RNase-free water makes a 10 μ M solution in a 10 μ M Tris-HCl, pH 8.0, 20 mM NaCl, 1 mM EDTA buffered solution.

APPLICATIONS

SPOUT1 siRNA (h) is recommended for the inhibition of SPOUT1 expression in human 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 μ M in 66 μ l. 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

SPOUT1 (H-7): sc-393263 is recommended as a control antibody for monitoring of SPOUT1 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-IgG κ BP-HRP: sc-516102 or m-IgG κ 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-IgG κ BP-FITC: sc-516140 or m-IgG κ 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 SPOUT1 gene expression knockdown using RT-PCR Primer: SPOUT1 (h)-PR: sc-92746-PR (20 μ l). Annealing temperature for the primers should be 55-60° C and the extension temperature should be 68-72° C.

RESEARCH USE

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

PROTOCOLS

See our web site at www.scbt.com for detailed protocols and support products.