

Supplementary Table 1. Putative 18 bp target sites in the VE-cadherin gene locus (50 Kb). The starting position of the found subsequence is relative to the start of transcription of the VE-cadherin mRNA (accession number NM_001795, Suzuki,S., Sano,K. and Tanihara,H., Diversity of the cadherin family: evidence for eight new cadherins, Cell Regul. 2 (4), 261-270 (1991)) in the corresponding gene sequence from Homo sapiens chromosome 16 reference genomic contig NT_010546 (gi|22068154:1200574-1251030). The number of matching residues and DNA strand are indicated. Matching and unmatching positions are in uppercase and lowercase letters, respectively.

Protein	Expected target site	Position	#Res.Matched	DNA strand	Subseq Found
CD144-3	GTAGGTTGGGAAAGAGGA	+13959	14/18	-	GcAGGgTGGGAgAGAGGt
		+18355	14/18	+	GgAGGTgGGGAcAGAGcA
CD144-4	TGAGCGGCTTGAGGGGTC	-6327	13/18	-	TGAGtGGgcTGAGaGGTg
		+5493	13/18	-	gGAGgGcCcTGAtGGGTC
CD144-5	GCTAGAGCAGTTGACTAA	-11971	13/18	+	cCTAGctCAGaTtACTAA
		+35544	13/18	+	aCcAGAcAAGTTGAaTAA
CD144-13	GCAGACGGTTAGGACGCC	+31059	13/18	-	GCAGaAAGGTgAactCGCC
CD144-23	GTCAGAGGAGTAGGCGTA	+11420	14/18	-	GTCAGaAGAGcAGGgGTg
CD144-29	TGATGAGGTGTAGGCAAA	-3736	13/18	-	TGcTcAGtTacAGGCAAA
		+1710	13/18	+	TGgTGAGGgGTAGGggAg
		+12391	13/18	+	gGgTGAGGaGTAGGtAcA
		+12407	13/18	+	caAgGAaGTGTAGGgAAA
		+20723	13/18	+	TGAaGgttTGTAGGCcAA
		+34254	13/18	-	gGATaAGGaGTAGaCAgA
		+36556	13/18	+	gGATGAGaTGTgGcCAgA