

Table S5. Predicted EVI1 binding sites and primers used for ChIP assays.

Gene	Genomic coordinates (hg19) Forward/reverse (consensus binding site)	Forward primer (5'-3')	Reverse primer (5'-3')
Predicted targets (Transfac, GSEA)			
<i>SCUBE3</i> (1)	chr6:35,178,411-35,178,420 Reverse (V\$EVI1_05): TTTTCTATATATTATCTCATTAA	CCAAACACTTGGGCTTTTGT	GGGATAAAAACCTCGTAGGG
<i>SCUBE3</i> (2)	chr6:35,179,860-35,179,868 Reverse (V\$EVI1_06): ACCATTCTCTTGTGGGGGCAAA	AGCTCCTCGGCTCTCTCTCT	TGTGTAGGGTTGGAGGACAAG
<i>TCF4</i>	chr18:53,256,680-53,256,686 Forward (V\$EVI1_06): ACAGATTACAAGATTATGCACCT	TGGTGAAAATGCAAAAACC	TCTCACATGTGTATCCCCAAA
mTOR pathway			
<i>AKT3</i>	chr1:244,008,880-244,008,896 Forward (V\$EVI1_02 and V\$EVI1_04): AAAAAAAAAAGAAAAGA AAAGAAAAAGAAT	TGAGGCTCCCAAGACAGATT	CCTGGGTGCTACAGTGAGAA
<i>RHEB</i>	chr7:151,218,309-151,218,316 Reverse (V\$EVI1_06): GTCGTTTTTATCCTG TGGATTCCGAT	AACACCGTGGTGAGGGTATC	CATGAAATGTTGAGGTTTACGC
<i>RPS6KA1</i> (1)	chr1:26,854,187-26,854,197 Forward (V\$EVI1_02): TCTCAAAAAGAAAAGAAAAAATTA	CAGCCTGTTGACAGAGCAAG	CTGCAGCCTTGAACCTTCTGG
<i>RPS6KA1</i> (2)	chr1:26,870,070-26,870,080 Forward (V\$EVI1_03 and V\$EVI1_05): CCCCTGAAGATAAGATTGTGTCTCC	CACCCACTCCTCCATCTGTC	TGCCTAAAACCCCTTCTCCT
<i>RPTOR</i>	chr17:78,519,829-78,519,843 Forward (V\$EVI1_04): CTAATTCAGATAATAAAAAGTTAAGCAAAT	TGGTTGAAAATGGAAAATGC	GCATGTAAATACTCGCAATGCT
Lung metastasis signature			
<i>FSCN1</i>	chr7:5,630,468-5,630,477 Reverse (V\$EVI1_02): CCCGAGATTCTCTTTTC CCCCGTCCGG	AAACAAACAAAACCCCGAGA	GTGAGTGAGTGAGCCCTGGT
<i>SPARC</i> (1)	chr5:151,068,565-151,068,551 Forward (V\$EVI1_04): GGTAAGAGCAAATGCAAAGATACTGGGCA	GGCCCTAAGGAGGTGACATT	ACAAGTCTGAGCCACCATGC
<i>SPARC</i> (2)	chr5:151,067,151-151,067,139 Forward (V\$EVI1_02, V\$EVI1_03 and V\$EVI1_05): ATTGAACAGATAAGGTAATTGATGA	CCAGGTGATCATAGGCAAGTTA	GACATCTAGCTGGTGGACCTG
<i>SPARC</i> (3)	chr5:151,066,999-151,066,992 Forward (V\$EVI1_02 and V\$EVI1_06): ACTGTACAGACAAGACAAGCTGCTA	CCAGTTCCAAATCATCAAGGA	TTCAAGGGGGTTGTATTTGC
SOX9 target based on ChIP data (probe A_17_P10450589)			
	chr17:70,117,112 -70,117,268	CTCTAAGGTGAGGCGGAGTA	CACCCCTTCTCTTCTCCTCC