Supplementary Table S1. PCR primers used for the validation of stable clones and microarray data.

Gene	Accession no.	Primer sequence (5'-3')	T_m (°C)	Amplicon size (bp)	Reference
RPL35A	NM_000996.2	F: GGGTACAGCATCACTCGGA R: ACGCCCGAGATGAAACAG	58	220	(15)
TSC2	X75621	F: CCGTCTTCCACATCGCCACCCTG R:ACGATCACGTGGACAAAGTTGAACTG	67	168	(25)
ANO2	NM_020373.2	F: AAGTGCGGCTCGATGCAAAGAAG R: CGGAGGTGATCGCAATGACAAAAG	62	152	-
MAPK4	NM_002747	F: TCTTCATCAGCACAGAGGACCTC R: GGAGCAGTCGTGGGGAACGG	62	138	-
EREG	NM_001432	F: ACAACTGTGATTCCATCATGTATCC R: CTACACTTTGTTATTGACACTTGAGC	62	109	-
UCA1	NR_015379.2	F: GAGCTTCGGGTAACTCTTACGG R: GATGGACGGCAGTTGGTGTGC	62	153	-
TSC2 (TAD1)	X75621	F: TGTGCAGGAGAAGACGAACC R: GGCACCGACAGTGACTTGTA	58	240	-
TSC2 (TAD2)	X75621	F: GGTGTCCCTGCAGTGCAGGAAA R: GAGCCGCTTGATGTGGCGGAG	56	205	-

Abbreviations: F, forward primer; R, reverse primer; T_m, annealing temperature; and, bp, base pairs

Supplementary Table S2. Details of PCR primers used in the generation of different deletion constructs.

Construct	Primer sequence (5' – 3')	T_m (°C)	Amplicon size (bp)	Reference
pFP1EREG	F:TAGCCTCGAGCTCCATCAGCATAGGCAGGAA (*Xho*I) R:TAGCAGATCTCGGCGATGGGAGCGGGCGCT (*Bgl*II)	53	1022	(17)
pFP2EREG	F:TAGCCTCGAGACAATGACTCGACTTTGAGG (*Xho*I) R:TAGCAGATCTCGGCGATGGGAGCGGGCGCT (*Bgl*II)	58	733	(17)
pFP3EREG	F:TAGCCTCGAGCACTACTCTCAGGTGCTCCAG (*Xho*I) R:TAGCAGATCTCGGCGATGGGAGCGGGCGCT (*Bgl*II)	58	328	(17)
pFP4EREG	F:TAGCAGATCTCTCCATCAGCATAGGCAGGAA (*Bgl*II) R:TAGCAAGCTTCCTCAAAGTCGAGTCATTGTGA (*Hind* III)	58	309	-
pFP1EREG-mut	F:ACCACCCACTACAGGGCAGG R:GTTCCCCATACATGCCTTTGGA	56	966	-
pcDNA3.1(+)/TSC2-NLSdel	F:GAGGAAGCCGCCTACTCCAAC R:GGCAATCCACTTGGAGGGGTAG	58	5385	-

Supplementary Table S3. PCR primers used for the chromatin immunoprecipitation (ChIP) analysis.

Primer	Pimer sequence (5' – 3')	T_m (°C)	Amplicon size (bp)	Reference
EREGF	CTCCATCAGCATAGGCAGGAA	57	554	-
EREGR	GGTTGCTCAGGGTGACGGACATA			
EREGF1	TATGTCCGTCACCCTGAGCAACC	57	491	-
EREGR1	CGGCGATGGGAGCGGGCGCT			
SP1F	GGTACCGCTCCAAGGTTGCCTTCTCTATGA	56	601	(19)
SP1R	CTCGAGGGCCAACCTCGGCCCTTCCTG			

Supplementary Table S4. Sequences of the probes used in EMSA.

Oligo	Sequence(5' - 3')	Size (bp)	Probe*
TS1F	CTCCATCAGCATAGGCAGGAAAGTGGGAGTGAGGAAAGGCTTAGAGTTTT	50	Probe 1 (-857 bp
TS1R	AAAACTCTAAGCCTTTCCTCACTCCCACTTTCCTGCCTATGCTGATGGAG	50	to -807 bp)
TS2F	CCAGCCTGGCTGGGGTCAGACAATTTGCCTGGGGAAATAGTGGGAGCTGA	50	Probe 2 (-807 bp
TS2R	TCAGCTCCCACTATTTCCCCAGGCAAATTGTCTGACCCCAGCCAGGCTGG	50	to -757 bp)
TS3F	GGTTGAAAAGACCGATTGGCTTCACGTTTGTGGCAGGCCTTGTCCAAAAAG	51	Probe 3 (-757bp
TS3R	CTTTTTGGACAAGGCCTGCCACAAACGTGAAGCCAATCGGTCTTTTCAACC	51	to -706 bp)
TS4F	CAATAGGAAGTCGTTGAAAGGTTTTGTGCAGGGGAGCGACAGGATTAAGG	50	Probe 4 (-706 bp
TS4R	CCTTAATCCTGTCGCTCCCCTGCACAAAACCTTTCAACGACTTCCTATTG	50	to -656 bp)
TS5F	CACTACTTAGTAGGAAGTCATATCAAAAGCAGCAACCTGACAAATGGCAAA	51	Probe 5 (-656 bp
TS5R	TTTGCCATTTGTCAGGTTGCTGCTTTTGATATGACTTCCTACTAAGTAGTG	51	to -605 bp)
TS6F	TACGACAGAAGGAAAAAAAATAACAGGAATTTTCTTCACAATGACTCGACTT	52	Probe 6 (-605 bp
TS6R	AAGTCGAGTCATTGTGAAGAAAATTCCTGTTATTTTTTTTCCTTCTGTCGTA	52	to -553 bp)
TS7F	TGAGGTAATAAATGCCTGAGCCACATTGGAAGCAGGGGTCTCAGAAGGAA	50	Probe 7 (-553 bp
TS7R	TTCCTTCTGAGACCCCTGCTTCCAATGTGGCTCAGGCATTTATTACCTCA	50	to -503 bp)
TS8F	GGCGCAGATGGGAAAGGCTTTTCTGGGCGGTGGCGTTTCAATGCAAGGAG	50	Probe 8 (-503 bp
TS8R	CTCCTTGCATTGAAACGCCACCGCCCAGAAAAGCCTTTCCCATCTGCGCC	50	to -453 bp)
TS9F	GGCGCTTGAATCACTGACAGACTTCAAGTTAAGGGAGTTTTCGTGGCTGAG	51	Probe 9 (-453 bp
TS9R	CTCAGCCACGAAAACTCCCTTAACTTGAAGTCTGTCAGTGATTCAAGCGCC	51	to -402 bp)
TS10F	GTTAGTAAGTCACACGCACAGCTCTCCAAAGGCATGTATGGGGAACGCCA	50	Probe 10 (-402 bp
TS10R	TGGCGTTCCCCATACATGCCTTTGGAGAGCTGTGCGTGTGACTTACTAAC	50	to -352 bp)
TS11F	GCCTTGGCTAAAAGACTGATTCAAGTTATGTCCGTCACCCTGAGCAACC	49	Probe 11 (-352 bp
TS11R	GGTTGCTCAGGGTGACGGACATAACTTAATCAGTCTTTTAGCCAAGGC	49	to -303 bp)

***** A double-stranded probe was made by mixing equal amount of each of the two oligos.
Abbreviation: bp, base pairs.