Supplemental Table S1: Sequences of the oligonucleotides used for this study

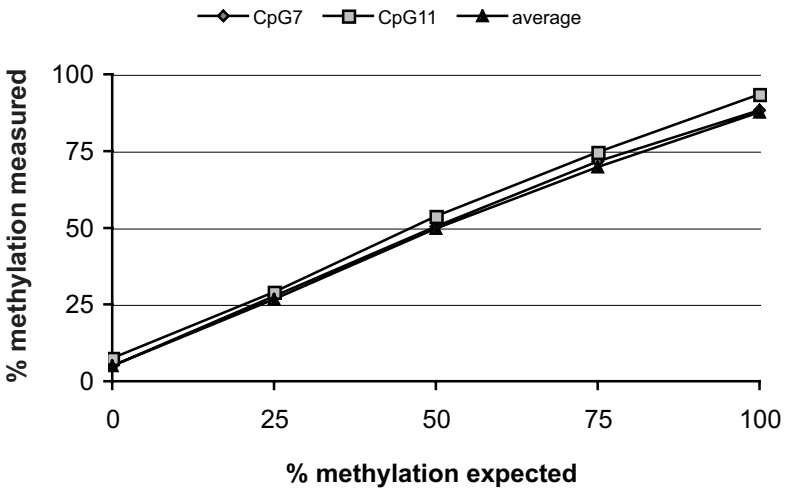
Methylation analyses		
mGlut4bi1Fornest mGlut4bi1For mGlut4bi1Rev	TTTGTTTTTTGGGTTTTTTTTAAGA AATATCCCAACCTATCCCAAAC TTTTTTTTGAATTGAGTTTTTTTT	PCR amplification
mGlut41_seq1 mGlut41_seq2	GGATGGGTTAGTAGGTA GTTTTTAGATATATTAGGA	Pyrosequencing
mGlut4RT_for mGlut4RT_rev	CCCTTTAAGGCTCCATCTCC TGTGTGTATGCCCCGAAGTA	Real time PCR after FauI
mSHIPprom_for mSHIPprom_rev	CATGGAAATGGGCATCAATA AAAGTGATAGCAAGGCCACG	Real time PCR after FauI
ChIP analyses		
mGlut4ChIP1For mGlut4ChIP1Rev	CCTGTCCCTTGGGTCCCCTCCAAGA GGTGTCCCAGCCTGTCCCAGGC	Conventional PCR
mGlut4ChIPRTFor mGlut4ChIPRTRev	CCCTTTAAGGCTCCATCTCC TGTGTGTATGCCCCGAAGTA	Real time PCR
mGlut4_4ChIPRTFor mGlut4_4ChIPRTRev	GTGGGTTGTGGCAGTGAGTCCCACCA GAAAAACTGGACCAGATTTCCCAAT	Real time PCR
mDag1ChIPFor mDag1ChIPRev	AGCTACCCGGACTGGCTAAG GCACCTCTCTGCCCATT	Real time PCR
mLactoferinChIPFor mLactoferinChIPRev	TCTAGGCTGACTCCGCTCTC TAGAGGTGGGACATGGGGTA	Conventional and real time PCR
Gene expression analyses		
18SFor 18SRev	CGGCTACCACATCCAAGGAA GCTGGAATTACCGCGGCT	
maP2For maP2Rev	TGGAAGACAGCTCCTCCTCG AATCCCCATTTACGCTGATGATC	
mLXRαFor mLXRαRev	GCAGGAGATTGTTGACTTTGC GTCCTCCCTGCTGAGCTGTA	
mGlut4For mGlut4Rev	TCATTGTCGGCATGGGTTTC CGGCAAATAGAAGGAAGACGTA	
hERβFor hERβRev	TGGAGTCTGGTCGTGTGAAG CTCTTGCGCCGGTTTTTAT	
Gelshift assays		
Sp1cont_for Sp1cont_rev	ACGTTGCAGCCGGGGCGGGGCTTCTGCA TGCAGAAGCCCCGCCCCGGCTGCAACGT	Sp1 control sequence (Karin et al., PNAS 1989)
Seq1_for Seq1_rev	CCTTTGCCCTCCCCCGCCTGGGACAGGC GCCTGTCCCAGGCGGGGGAGGGCAAAGG	
Seq1mut_for Seq1mut_rev	CCTTTGCCCTATTATGCCTGGGACAGGC GCCTGTCCCAGGCATAATAGGGCAAAGG	Mutated Sp1 and RXR binding site
Seq1mutSp1_for Seq1mutSp1_rev	CCTTTGCCCTCCTATGCCTGGGACAGGC GCCTGTCCCAGGCATAGGAGGGCAAAGG	Mutated Sp1 binding site
Seq7_for Seq7_rev	TCGCGGACCCTTTAAGGCTCCATCTCCT AGGAGATGGAGCCTTAAAGGGTCCGCGA	

Supplemental Figure S1.
A: Bisulfite-Pyrosequencing of unmethylated and methylated DNA, and different ratios thereof. 5-AZA-dC treated genomic DNA from MEFs (0% methylation) and Universal Methylated Mouse DNA (100% methylation) were bisulfite treated, PCR amplified, and mixed in ratios 4:1 (25% methylation), 1:1 (50% methylation), and 1:4 (75% methylation). The DNA was analysed by Pyrosequencing and results blotted versus the expected percentage of methylation.
B: DNA methylation at CpG11 in wt, erko, and berko MEFs derived from three different mice, assessed by bisulfite-Pyrosequencing.
C: Methylation analysis by methylation sensitive restriction enzyme digest using FauI, followed by real time PCR for *Glut4*. Genomic DNA of wt, erko, and berko MEFs was subjected to FauI digest. Subsequently, the amount of uncut *Glut4* promoter was determined using real time PCR. The results were normalized to *18S* rRNA or *SHIP* promoter, which both do not exhibit a FauI recognition site. Percent methylation was calculated by generating a standard curve using FauI digested unmethylated and methylated DNA, and different ratios thereof.

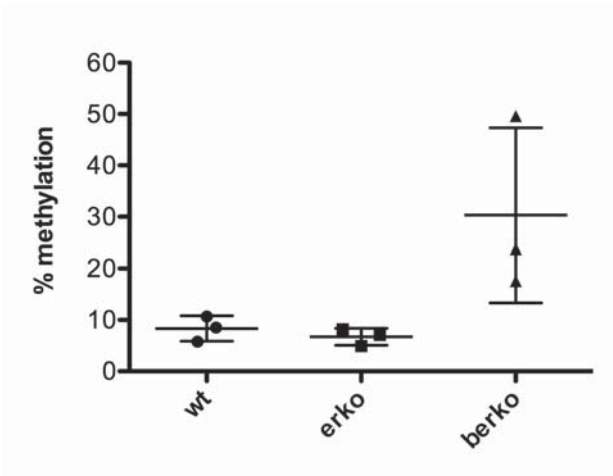
Supplemental Figure S2.
ERα recruitment to the ERE on the *lactoferrin* promoter in wt MEFs. Cells were treated with 10 nM E2 for 45 min. ChIPs were analysed by real time PCR and results were normalized to inputs and recruitment in erko MEFs. Data are represented as mean + SD.

Suppl. Figure 1

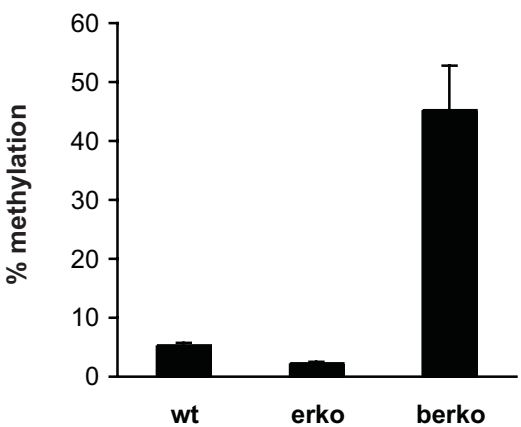
A



B



C



Suppl. Figure 2