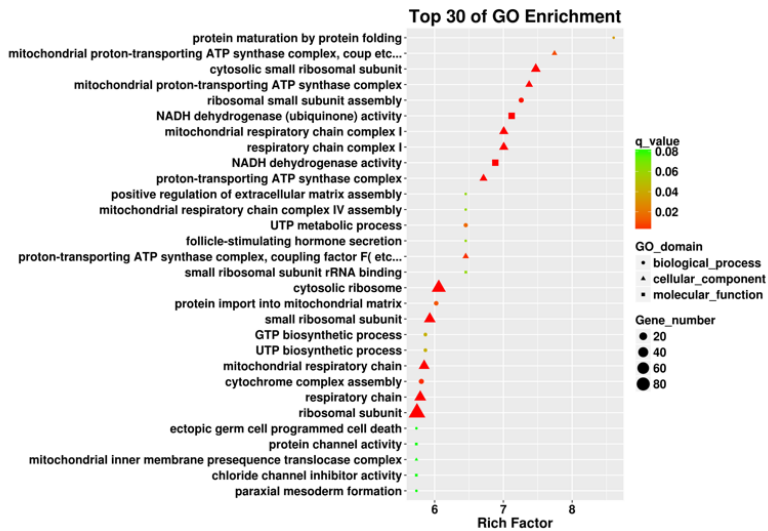


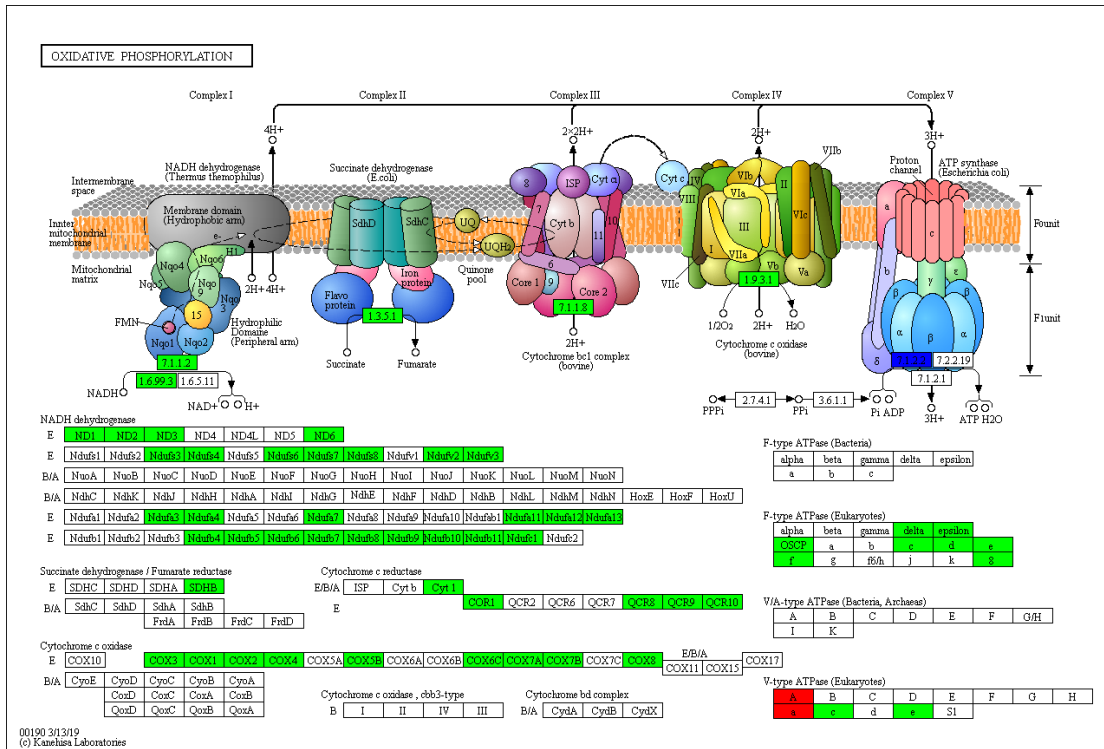
## Supplementary material

### Decreased neurotensin induces ovulatory dysfunction via the NTSR1/ERK/EGR1 axis in polycystic ovary syndrome

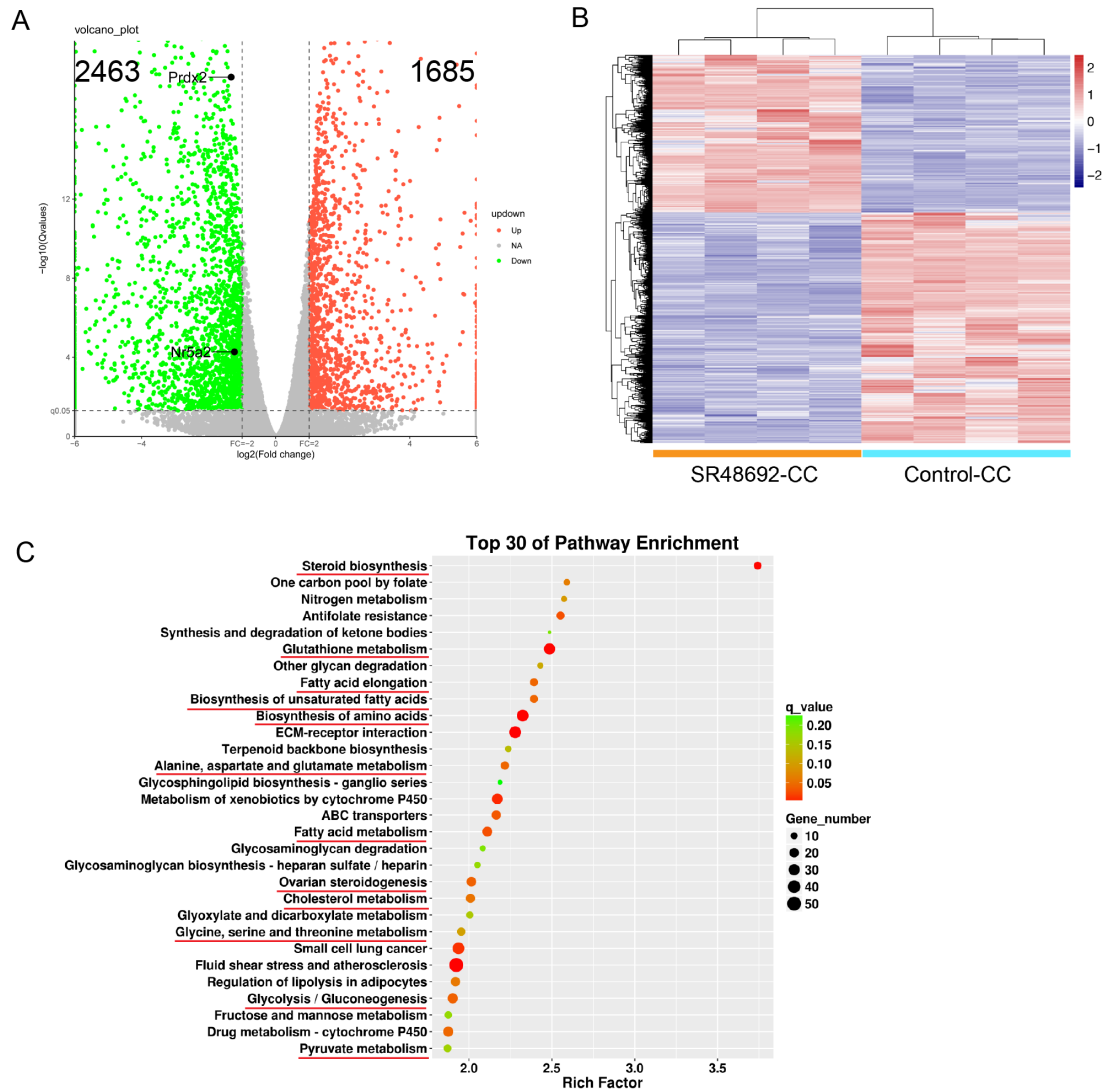
Dongshuang Wang<sup>1,2,\*</sup>, Meiling Zhang<sup>1,2,\*</sup>, Wang-Sheng Wang<sup>1,2</sup>, Weiwei Chu<sup>1,2</sup>, Junyu Zhai<sup>1,2</sup>, Yun Sun<sup>1,2</sup>, Zi-Jiang Chen (✉)<sup>1,2,3</sup>, Yanzhi Du (✉)<sup>1,2</sup>



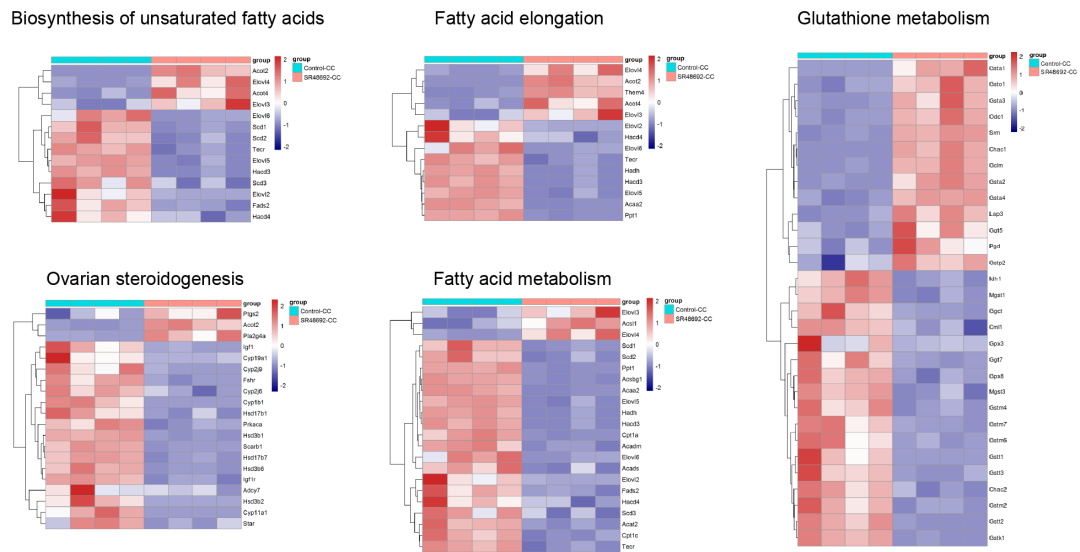
**Fig. S1** Gene ontology (GO) terms of different expressed genes (DEGs) enrichment between control and SR48692-treated oocytes.



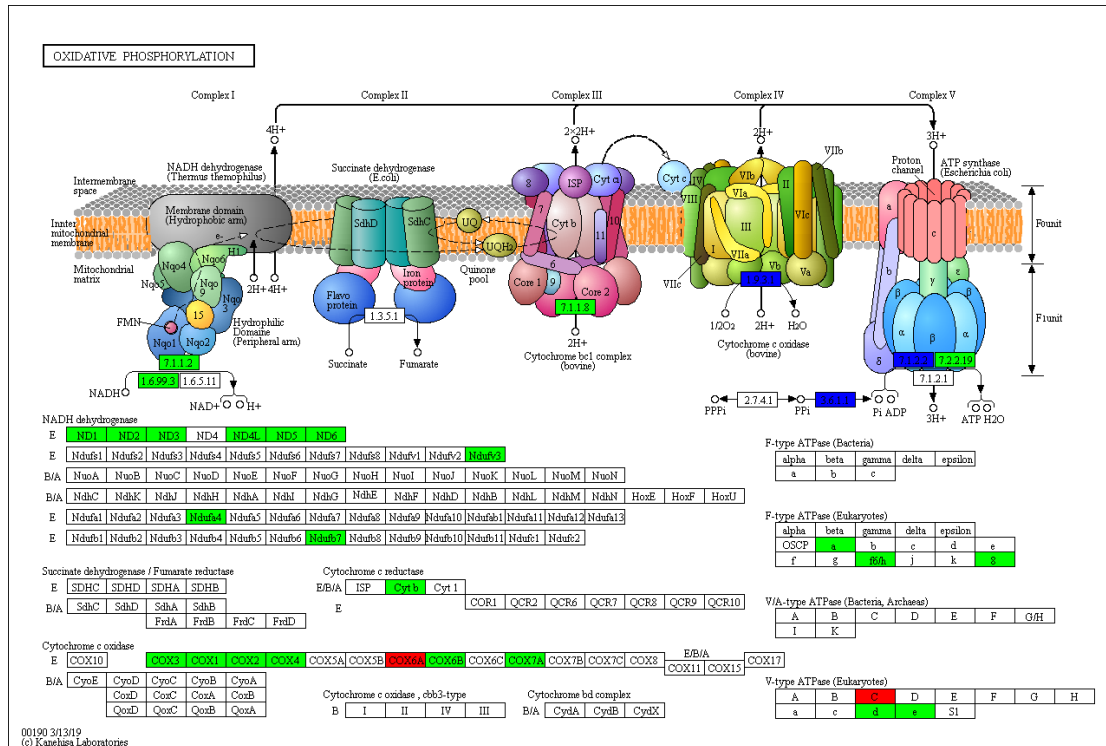
**Fig. S2** The KEGG pathway of the oxidative phosphorylation responds to SR48692-treated oocytes. Gene expression levels were indicated as significantly higher (red) or lower (green) in the SR48692-treated group compared to the control group.



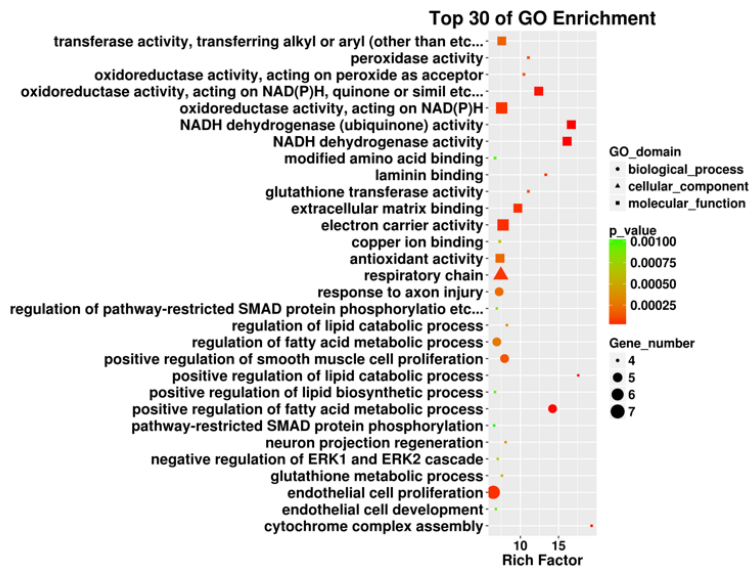
**Fig. S3** Transcriptome changes in SR48692-treated cumulus cells (CCs). (A) The corresponding volcano plot of SR48692-treated CCs versus controls showed 1685 upregulated (fold change > 2, q-value < 0.05, red) and 2463 downregulated (fold change < -2, q-value < 0.05, green) genes. (B) Expression heatmap of DEGs in SR48692-treated CCs compared to controls by RNA-seq. (C) Top 30 signaling pathways of the DEGs in KEGG enrichment analysis between control and SR48692-treated CCs.



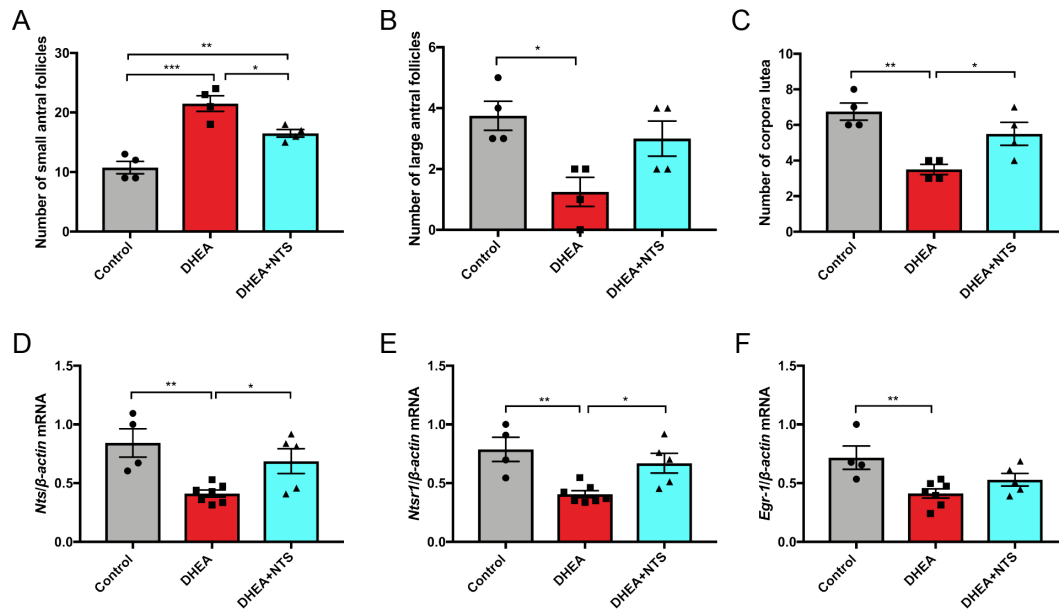
**Fig. S4** Heat maps of relative expressions of the indicated genes in distinct metabolic and steroidogenic pathways in control and SR48692-treated CCs. Each box corresponds to a different sample.



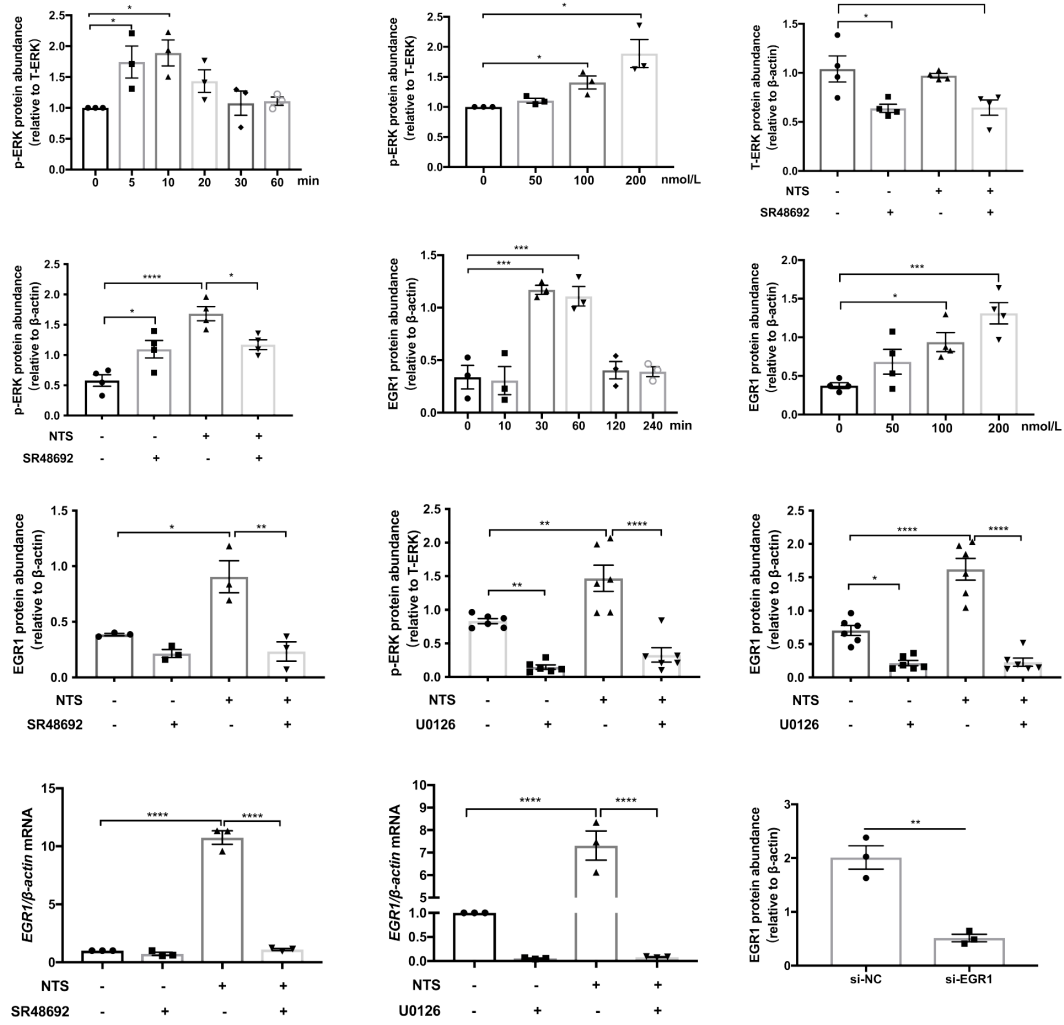
**Fig. S5** The KEGG pathway of the oxidative phosphorylation responds to SR48692-treated CCs. Gene expression levels were indicated as significantly higher (red) or lower (green) in the SR48692-treated group compared to the control group.



**Fig. S6** GO analyses of the overlap in transcripts that were downregulated in SR48692-treated oocytes and CCs.



**Fig. S7** Ovarian histological and molecular examinations in polycystic ovary syndrome (PCOS) mice. (A-C) The number of small antral follicles, large antral follicles, and corpora lutea in the half ovaries of mice from each group. (D-F) Quantitative real-time PCR (qRT-PCR) detection of *Nts*, *Ntsr1*, and *Egr1* expression in the ovaries of mice from each group. Data are shown as means  $\pm$  SEM. \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .



**Fig. S8** Quantifications of western blot analysis and results of qRT-PCR in Fig. 8. Data are shown as means  $\pm$  SEM. \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ , \*\*\*\* $P < 0.0001$ .

**Supplementary tables****Table S1.** Clinical and biochemical indicators of women with and without PCOS in qRT-PCR.

	<b>Control (n=38)</b>	<b>PCOS (n=39)</b>	<b>P value</b>
Age (years)	27.63±3.43	27.64±2.68	0.989
BMI (kg/m <sup>2</sup> )	21.82±2.89	22.46±3.36	0.375
Basal FSH (mIU/ml)	6.21±1.32	5.75±1.54	0.176
Basal LH (mIU/ml)	5.47±3.01	9.70±7.29	0.002
LH/FSH	0.91±0.59	1.81±1.88	0.006
Basal E2 (pg/ml)	35.44±21.22	41.44±15.66	0.168
Basal T (mIU/ml)	0.95±0.37	1.32±0.54	0.007
AMH (ng/ml)	4.47±1.63	10.63±3.69	<0.0001

Data are presented as mean ± SD, BMI: body mass index, LH: luteinizing hormone, FSH: follicle stimulating hormone, T: testosterone, and AMH: anti-Müllerian hormone.

**Table S2.** Clinical and biochemical indicators of women with and without PCOS in ELISA.

	<b>Control (n=26)</b>	<b>PCOS (n=27)</b>	<b>P value</b>
Age (years)	30.39±3.40	30.85±3.67	0.633
BMI (kg/m <sup>2</sup> )	21.17±2.66	22.55±3.79	0.133
Basal FSH (mIU/ml)	6.27±1.24	5.99±1.58	0.476
Basal LH (mIU/ml)	5.47±1.69	8.45±4.46	0.003
LH/FSH	0.89±0.28	1.43±0.74	0.001
Basal E2 (pg/ml)	37.53±18.73	39.70±12.41	0.622
Basal T (mIU/ml)	1.01±0.33	1.38±0.60	0.029
AMH (ng/ml)	4.67±2.21	9.00±4.26	<0.0001

Data are presented as mean ± SD, BMI: body mass index, LH: luteinizing hormone, FSH: follicle stimulating hormone, T: testosterone, and AMH: anti-Müllerian hormone.

**Table S3.** Primer sequences used in the qRT-PCR analysis.

Target Genes	Species		Primer sequences (5'-3')
<i>ACTB</i>	Human	Forward	GGGAAATCGTGCGTGACATTAAG
		Reverse	TGTGTTGGCGTACAGGTCTTTG
<i>NTS</i>	Human	Forward	TGCTTTAGATGGCTTTAGCTTGG
		Reverse	TTCCTGGATTAACCTCCAGTGT
<i>EGR1</i>	Human	Forward	GGTCAGTGGCCTAGTGAGC
		Reverse	GTGCCGCTGAGTAAATGGGA
<i>Actb</i>	Mouse	Forward	GTGACGTTGACATCCGTAAAGA
		Reverse	GCCGGACTCATCGTACTCC
<i>Nts</i>	Mouse	Forward	GCAAGTCCTCCGTCTTGAAA
		Reverse	TGCCAACAAGGTCGTCATCAT
<i>Egr1</i>	Mouse	Forward	CAGTCCCATCTACTCGGCTG
		Reverse	TGTGGAAACAGATAGTCAGGGAT

**Table S4.** Primary antibodies used in the Western blot analysis.

Protein Name	Host	Dilution	Manufacturer
$\beta$ -Actin	Mouse monoclonal	WB: 1:3000	Proteintech
p44/42 MAPK (Erk1/2)	Rabbit monoclonal	WB: 1:1000	CST
Phospho-p44/42 MAPK (Erk1/2)	Rabbit monoclonal	WB: 1:1000 IF: 1:200	CST
EGR1	Rabbit monoclonal	WB: 1:1000 IF: 1:200	CST
NTS	Rabbit polyclonal	WB: 1:500	Abcam

**Table S5.** siRNA sequences used in the cell knockdown assay.

Oligo Name	Species	Sequence	
		sense (5'-3')	antisense (5'-3')
<i>si-Egr1</i>	Mouse	GGACAAGAAAGCAGACAA ATT	UUUGUCUGCUUUCUUGUCC TT
<i>si-EGR1</i>	Human	GGCAUACCAAGAUCACU UTT	AAGUGGAUCUUGGUAUGC CTT