Table S1 Sequences of the 3 siRNAs targeting OXR1 and miR-668-3p mimic or inhibitor

siRNA symbol	Forward oligonucleotide 5'-3'	Reverse oligonucleotide 5'-3'
si-OXR1-1	GAAUAAACUAGCAAUUGUAUU	UACAAUUGCUAGUUUAUUCUA
si-OXR1-2	GAAUGUUCAAGAAGCAAUACA	UAUUGCUUCUUGAACAUUCCA
si-OXR1-3	GUAGUAGACAAUACUGUAAUU	UUACAGUAUUGUCUACUACAG
si-NC	GCUGCUUGGACAAGGCUAUC	UAGCCUAGUCCAAAGCAGCAT
Sequences of miR-668-3p mimic or inhibitor 5'-3'		
Mimic NC	CUCUCUGCGCCGUCCAAGUCACCG	
Mimic	UGUCACUCGGCUCGGCCCACUACC	
Inhibitor NC	CAGUACUUUUGUGUAGUACAA	
Inhibitor	GGTAGTGGGCCGAGCCGAGTGACA	

Table S2 Primer sequences used for RT-qPCR analysis

Gene symbol	Forward primer 5'-3'	Reverse primer 5'-3'
miR-668-3p	ACACTCCAGCTGGGUGUCACUCGGCUCGGCCC	CTCAACTGGTGTCGTGGA
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
OXR1	TGCTAGGGCTGGTGTCCTAA	TTTGGCCAGTGTGTAGGTCC
GAPDH	GGTGAAGGTCGGTGTGAACG	CTCGCTCCTGGAAGATGGTG

U6 was used to normalize miR-668-3p expression, and GAPDH was used to normalize OXR1 expression.

Table S3 Differentially expressed miRNAs in healthy individuals and patients with Alzheimer's disease

Transcript ID	Fold change	P value
hsa-miR-93-3p	10.08	0.0002
hsa-miR-1299	9.31	0.0116
hsa-miR-323a-5p	8.61	0.002
hsa-miR-668-3p	6.5	0.0362
hsa-miR-1202	6.42	0.0027
hsa-miR-935	5.01	0.0317
hsa-miR-128-2-5p	4.83	0.002
hsa-miR-30c-1-3p	4.07	0.0257
hsa-miR-4443	3.75	0.0016
hsa-miR-486-5p	3.13	0.0219
hsa-miR-431-5p	3.11	0.0027
hsa-miR-629-5p	2.96	0.0036
hsa-miR-5187-5p	2.89	0.0263
hsa-miR-4433-3p	2.83	0.0055
hsa-miR-543	2.66	0.0128
hsa-miR-433-3p	2.59	0.0125
hsa-miR-3162-5p	2.56	0.0367
hsa-miR-346	2.34	0.0083
hsa-miR-671-3p	2.3	0.0109
hsa-miR-485-5p	2.27	0.0013
hsa-miR-1973	2.27	0.0091
hsa-miR-744-5p	2.26	0.0026
hsa-miR-486-3p	2.24	0.0006
hsa-miR-1224-5p	2.2	0.034
hsa-let-7d-3p	2.19	0.0495
hsa-miR-760	2.13	0.0037
hsa-miR-125a-3p	2.11	0.0037
hsa-miR-146b-5p	2.09	0.0012
hsa-miR-4492	2.05	0.0007
hsa-miR-320e	2.03	0.0001
hsa-miR-187-3p	2	0.0122
hsa-miR-4440	−2.03	0.0159
hsa-miR-1207-5p	−2.04	0.0009

Table S3 (*continued*)

Table S3 (*continued*)

Transcript ID	Fold change	P value
hsa-miR-6765-3p	−2.07	0.0012
hsa-miR-3188	−2.07	0.0219
hsa-miR-4667-5p	−2.13	0.0029
hsa-mir-663a	−2.16	0.0001
hsa-miR-4640-5p	−2.18	0.0041
hsa-miR-1273d	−2.22	0.0023
hsa-miR-5006-5p	−2.26	0.0007
hsa-miR-6800-5p	−2.32	0.0003
hsa-miR-4732-5p	−2.35	0.0016
hsa-miR-642a-3p	−2.36	0.0411
hsa-miR-6774-5p	−2.43	0.0022
hsa-miR-4454	−2.48	0.0042
hsa-miR-7975	−2.59	0.0029
hsa-miR-1273f	−2.6	0.0018
hsa-miR-4298	−2.63	0.0168
hsa-miR-6778-5p	−2.65	0.0019
hsa-miR-3195	−2.77	0.0025
hsa-miR-4646-5p	−2.8	0.0101
hsa-miR-6806-5p	−2.97	0.0213
hsa-miR-3175	−2.99	0.0235
hsa-miR-6797-5p	−3.05	0.0268
hsa-miR-1285-3p	−3.32	0.0008
hsa-miR-4286	−3.74	0.0003
hsa-miR-1273e	−3.78	0.0136
hsa-miR-6865-5p	−3.93	0.0003
hsa-miR-1273g-3p	−4.59	0.0017
hsa-miR-6754-5p	−4.82	0.0013
hsa-miR-4417	−5.34	0.0002
hsa-mir-4449	−5.72	0.0042
hsa-miR-4449	−6.15	0.0003
hsa-miR-3648	−6.21	0.0188
hsa-miR-1246	−6.84	0.0001
hsa-miR-1972	−7.14	0.0089
hsa-miR-3651	−11.13	0.0001

Table S4 MRNAs with potential binding sites for miR-668-3p

Potential gene
PGM2L1
PIK3R1
SLC24A2
CACNA2D1
SYT4
PTPN4
NCALD
IPCEF1
NEDD4L
ENO2
SCAMP5
SCN1A
MYO5A
ETS2
CD200
NECAB1
SCN3A
EPHA4
UBE2QL1
PCDH19
CCND2
NRSN1
MAL2
TMEM33
GABRB3
GSK3B
OXR1
GDAP1
SORL1
KCNS2
BAG4
HOMER1
RAB2A
DYNLL2

Table S4 (*continued*)

Table S4 (*continued*)

Potential gene
CELF2
DUSP4
MAP4K4
IWS1
PAIP2B
DOCK5