

**Supplementary data to:**

**Original article:**

**PLASMA LNCRNA PROFILING IDENTIFIED BC200 AND NEAT1  
LNCRNAs AS POTENTIAL BLOOD-BASED BIOMARKERS FOR  
LATE-ONSET ALZHEIMER'S DISEASE**

Majid Khodayi<sup>1</sup> , Mohammad Khalaj-Kondori<sup>1,\*</sup> , Mohammad Ali Hoseinpour Feizi<sup>1</sup> ,  
Mortaza Jabarpour Bonyadi<sup>1</sup> , Mahnaz Talebi<sup>2</sup> 

<sup>1</sup> Department of Animal Biology, Faculty of Natural Sciences, University of Tabriz,  
Tabriz, Iran

<sup>2</sup> Neurosciences Research Center, Tabriz University of Medical Sciences, Tabriz,  
Iran

\* **Corresponding author:** Mohammad Khalaj-Kondori, Department of Animal Biology,  
Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran. Tel. +984133392674;  
E-mail: [khalaj@tabrizu.ac.ir](mailto:khalaj@tabrizu.ac.ir)

<https://dx.doi.org/10.17179/excli2022-4764>

This is an Open Access article distributed under the terms of the Creative Commons Attribution License  
(<http://creativecommons.org/licenses/by/4.0/>).

**Raw data to Table 2:** Demographic data including age, gender, educational level, Mini-Mental State Examination score, and Apolipoprotein E genotype, were collected for all subjects. Fifty AD patients and fifty healthy controls were enrolled in the study.

Patient	Age	Gender	Education	MMSE	ApoE genotype	Control	Age	Gender	Education	MMSE
1	82	F	Literate	16	$\epsilon 2/\epsilon 3$	1	70	F	Illiterate	28
2	72	F	Literate	15	$\epsilon 2/\epsilon 4$	2	64	M	Literate	29
3	84	M	Literate	23	$\epsilon 3/\epsilon 3$	3	67	M	Literate	28
4	84	M	Literate	19	$\epsilon 3/\epsilon 3$	4	75	F	Literate	29
5	83	F	Illiterate	14	$\epsilon 3/\epsilon 3$	5	81	M	Literate	27
6	82	F	Literate	12	$\epsilon 3/\epsilon 3$	6	75	F	Illiterate	28
7	67	M	Literate	17	$\epsilon 3/\epsilon 3$	7	86	F	Literate	28
8	77	F	Literate	25	$\epsilon 3/\epsilon 3$	8	84	M	Illiterate	27
9	68	F	Literate	12	$\epsilon 3/\epsilon 3$	9	85	M	Literate	28
10	68	F	Illiterate	22	$\epsilon 3/\epsilon 3$	10	83	F	Illiterate	28
11	82	M	Literate	23	$\epsilon 3/\epsilon 3$	11	69	F	Literate	29
12	68	F	Literate	21	$\epsilon 3/\epsilon 3$	12	79	F	Literate	29
13	77	F	Literate	25	$\epsilon 3/\epsilon 3$	13	72	F	Literate	29
14	78	F	Illiterate	23	$\epsilon 3/\epsilon 3$	14	75	M	Literate	29
15	78	M	Literate	19	$\epsilon 3/\epsilon 3$	15	82	M	Literate	27
16	80	F	Illiterate	21	$\epsilon 3/\epsilon 3$	16	65	F	Literate	29
17	69	F	Literate	22	$\epsilon 3/\epsilon 3$	17	74	M	Literate	29
18	84	F	Illiterate	21	$\epsilon 3/\epsilon 3$	18	74	F	Literate	28
19	84	F	Illiterate	18	$\epsilon 3/\epsilon 4$	19	74	F	Literate	29
20	88	M	Literate	12	$\epsilon 3/\epsilon 4$	20	80	F	Illiterate	27
21	70	M	Illiterate	21	$\epsilon 3/\epsilon 4$	21	67	M	Literate	29
22	71	M	Literate	25	$\epsilon 3/\epsilon 4$	22	84	F	Literate	29
23	78	F	Illiterate	24	$\epsilon 3/\epsilon 4$	23	85	F	Illiterate	27
24	71	F	Literate	18	$\epsilon 3/\epsilon 4$	24	88	F	Literate	27
25	75	M	Literate	25	$\epsilon 3/\epsilon 4$	25	72	M	Literate	28
26	86	M	Illiterate	12	$\epsilon 3/\epsilon 4$	26	73	F	Literate	28
27	65	F	Literate	18	$\epsilon 4/\epsilon 4$	27	78	M	Literate	28
28	68	F	Illiterate	20	$\epsilon 4/\epsilon 4$	28	72	F	Literate	27
29	75	F	Literate	23	$\epsilon 4/\epsilon 4$	29	75	M	Literate	29
30	67	F	Literate	25	$\epsilon 3/\epsilon 4$	30	85	F	Illiterate	27
31	79	F	Literate	24	$\epsilon 3/\epsilon 4$	31	75	F	Literate	29
32	81	M	Literate	13	$\epsilon 3/\epsilon 3$	32	85	M	Literate	28
33	72	F	Literate	23	$\epsilon 3/\epsilon 3$	33	75	M	Literate	29
34	73	F	Literate	23	$\epsilon 3/\epsilon 3$	34	66	F	Illiterate	28
35	71	M	Literate	18	$\epsilon 3/\epsilon 3$	35	79	M	Literate	29
36	82	F	Illiterate	19	$\epsilon 3/\epsilon 3$	36	82	M	Literate	27
37	71	F	Literate	24	$\epsilon 3/\epsilon 3$	37	73	F	Literate	28
38	82	M	Illiterate	25	$\epsilon 3/\epsilon 3$	38	73	F	Literate	29
39	76	F	Literate	18	$\epsilon 3/\epsilon 3$	39	72	F	Literate	27
40	80	F	Illiterate	19	$\epsilon 3/\epsilon 3$	40	82	M	Illiterate	27
41	80	F	Literate	16	$\epsilon 3/\epsilon 3$	41	80	F	Literate	28
42	80	F	Literate	17	$\epsilon 3/\epsilon 3$	42	82	M	Illiterate	27
43	79	M	Illiterate	14	$\epsilon 3/\epsilon 4$	43	76	F	Literate	29
44	78	F	Literate	23	$\epsilon 3/\epsilon 4$	44	80	F	Illiterate	27
45	79	F	Literate	23	$\epsilon 3/\epsilon 4$	45	85	M	Literate	28
46	90	M	Illiterate	25	$\epsilon 3/\epsilon 4$	46	80	F	Literate	28
47	75	F	Illiterate	21	$\epsilon 3/\epsilon 4$	47	79	F	Literate	28
48	68	F	Literate	20	$\epsilon 3/\epsilon 4$	48	78	F	Literate	29
49	79	F	Literate	14	$\epsilon 3/\epsilon 4$	49	79	F	Literate	28
50		F	Literate	11	$\epsilon 4/\epsilon 4$	50	78	M	Literate	28

M= Male, F= Female, MMSE= Mini-Mental State Examination, ApoE= Apolipoprotein E

**Raw data to Figure 1:** The fold changes of 90 different lncRNAs as well as five housekeeping genes including RNU43 snoRNA, 18S rRNA, U6B snRNA, GAPDH, Lamin A/C, in plasma samples of 10 AD and 10 healthy controls were obtained by the human lncRNA Profiler qPCR Array Kit.

Well	lncRNAs	Fold change
A1	21A	0.0757
A2	7SK	1.2634
A3	7SL	9.3655
A4	Air	1.2634
A5	AK023948	0.5203
A6	Alpha 280	0.6865
A7	Alpha 250	1.2634
A8	ANRIL	1.2634
A9	anti-NOS2A	3.6486
A10	antiPeg11	1.2634
A11	BACE1AS (family)	43.937
A12	BC200	84.294
B1	CAR Intergenic 10	1.2634
B2	DHFR upstream transcripts (family)	0.1716
B3	Dio3os (family)	20.783
B4	DISC2 (family)	1.2634
B5	DLG2AS (family)	0.4436
B6	E2F4 antisense	3.6234
B7	EgoA	0.5239
B8	EGO B	1.2634
B9	Emx2os	1.2634
B10	Evf1 and EVF2	0.2968
B11	GAS5-family	1.5447
B12	Gomafu	10.537
C1	H19	84.294
C2	H19 antisense	15.005
C3	H19 upstream conserved 1 & 2	38.515
C4	HAR1A	1.2634
C5	HAR1B	1.1626
C6	HOTAIR	2.1248
C7	HOTAIRM1	13.337
C8	HOTTIP	9.8311
C9	Hoxa11as	10.61
C10	HOXA3as	9.8995
C11	HOXA6as	1.2634
C12	HULC	21.22
D1	IGF2AS (family)	3.9105
D2	IPW	1.2634
D3	Jpx	0.1494
D4	Kcnq1ot1	1.2634
D5	KRAS P1	1.2634
D6	L1PA16	0.01
D7	lincRNA-p21	42.44
D8	lincRNA-RoR	0.0225
D9	lincRNA-SFMBT2	0.1878
D10	lincRNA-VLDLR	0.1239
D11	LOC285194	0.1086
D12	LUST	0.1612

**Raw data to Figure 1 (cont.):** The fold changes of 90 different lncRNAs as well as five housekeeping genes including RNU43 snoRNA, 18S rRNA, U6B snRNA, GAPDH, Lamin A/C, in plasma samples of 10 AD and 10 healthy controls were obtained by the human lncRNA Profiler qPCR Array Kit.

Well	lncRNAs	fold change
E1	Malat1	1.2634
E2	mascrRNA	1.2634
E3	MEG3 (family)	0.0049
E4	MEG9	16.534
E5	MER11C	42.147
E6	ncR-uPAR	0.1646
E7	NDM29	20.64
E8	NEAT1 (family)	0.9122
E9	Nespas	1.2811
E10	NRON	10.038
E11	NTT	41.567
E12	p53 mRNA	1.2634
F1	PCGEM1	9.8995
F2	PR antisense transcripts	0.2927
F3	PRINS	1.2634
F4	PSF inhibiting RNA	10.392
F5	PTENP1	0.5853
F6	RNCR3	1.2634
F7	SAF	0.623
F8	SCA8	30.64
F9	snaR	1.29
F10	SNHG1	0.3181
F11	SNHG3	1.1387
F12	SNHG4	4.6183
G1	SNHG5	1.2634
G2	SNHG6	0.4405
G3	Sox2ot	1.2634
G4	SRA	20.075
G5	ST7OT	83.133
G6	TEA ncRNAs (family)	13.337
G7	Tmevpg1	42.44
G8	TncRNA	3.2207
G9	Tsix	1.373
G10	TUG1 (family)	0.303
G11	UCA1	1.2634
G12	UM9-5	6.5312
H1	WT1-AS	1.2634
H2	Xist	21.368
H3	Y RNA-1	8.2669
H4	Zeb2NAT	1.2634
H5	Zfas1	0.9443
H6	Zfhx2as	2.1846
H7	18S rRNA	1.8592
H8	RNU43 (snoRNA)	2.1347
H9	GAPDH	0.6512
H10	LAMIN A/C	0.7173
H11	U6 snRNA	1.0127

**Raw data to Figure 7:** The following table lists log2 fold changes and *p* values of the 46 differentially expressed lncRNAs (33 up-regulated and 13 down-regulated). If the log2 fold change value is higher than 1, that gene has increased in the Alzheimer's sample compared to the normal sample, and if the log2 fold change value is less than 0, that gene has decreased in the Alzheimer's sample compared to the normal sample. *p*-value < 0.05 was considered statistically significant.

LncRNA	log2foldchange	p-value
AC015977.6	5.021876	0.040735
AC002116.7	4.302559	0.040735
LINC01533	4.079406	0.01525
RP1-297M16.2	3.924566	0.040735
RP11-77M5.1	3.415254	0.00291
CTD-2207A17.1	2.818729	0.040735
MCM8-AS1	2.812686	0.02881
RP11-181C3.1	2.261071	0.01851
SRGAP3-AS4	2.070602	0.049145
RP11-130C19.3	1.942549	0.001645
RP11-268P4.4	1.902838	0.015735
RP11-426C22.8	1.818981	0.036895
RP11-354A14.1	1.7962	0.039575
RP11-77G23.5	1.669089	0.036895
RP11-388K2.1	1.363121	0.039925
RP11-420K8.1	1.318804	0.029875
RP3-522J7.6	1.30376	0.029875
RP11-650J17.2	1.194805	0.03949
RP11-1H15.2	1.18612	0.01234
RP5-943J3.2	1.179981	0.040505
RP11-730K11.1	1.17893	0.00288
RP11-264K23.1	1.142734	0.00288
UBOX5-AS1	1.125041	0.03949
RP11-283G6.5	1.08542	0.03949
CCDC13-AS1	1.065485	0.02756
RP11-120D5.1	1.056605	0.004935
APOA1-AS	1.042099	0.01851
FAM225A	1.026811	0.03949
CTC-506B8.1	1.019807	0.001645
RP3-414A15.2	1.016449	0.02756
LINC01266	1.013907	0.01234
GNG12-AS1	1.011789	0.01851
ZBTB20-AS3	1.009658	0.03949
LINC00907	-1.00639	0.001645
RP1-122O8.7	-1.05226	0.03949
AC064875.2	-1.07047	0.01234
RP3-512E2.2	-1.08153	0.03949
RP11-461L13.5	-1.21311	0.03949
MIR3180-3	-1.25054	0.007815
MIR3180-2	-1.26425	0.007815
AC009005.2	-1.30897	0.01851
RP11-554A11.9	-1.30987	0.03949
RP11-453A12.1	-1.78919	0.005905
LINC01580	-1.94511	0.005495
CTA-929C8.8	-2.57173	0.03034
RP11-473M20.5	-4.10312	0.004195

**Abbreviations:** SRGAP3-AS4= SRGAP3 antisense RNA 4; MIR3180-2= MicroRNA 3180-2; FAM225A= Family with Sequence Similarity 225 Member A; CCDC13-AS1= CCDC13 Antisense RNA 1; LINC00907= Long Intergenic Non-Protein Coding RNA 907; MCM8-AS1= MCM8 Antisense RNA 1; UBOX5-AS1= UBOX5 Antisense RNA 1; APOA1-AS= APOA1 Antisense RNA; ZBTB20-AS3= ZBTB20 Antisense RNA 3

**Raw data to Gene ontology terms and pathways:** Pathway analysis of the differentially expressed lncRNAs obtained from GSE53697 RNA-seq dataset revealed potential involved pathways. LncRNAs and the most enriched pathways were listed here in the Table.

lncRNA	pathway
SRGAP3-AS4	The Visual Cycle
SRGAP3-AS4	Retinoate Biosynthesis I
CTD-2207A17.1	Chondroitin Sulfate Degradation
CTD-2207A17.1	Dermatan Sulfate Degradation
MIR3180-2	p38 MAPK Signaling
MIR3180-3	p38 MAPK Signaling
FAM225A	The Visual Cycle
CCDC13-AS1	The Visual Cycle
RP11-130C19.3	Chondroitin Sulfate Degradation
RP11-130C19.3	Dermatan Sulfate Degradation
RP11-130C19.3	The Visual Cycle
LINC00907	Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency
RP11-77G23.5	Chondroitin Sulfate Degradation
RP11-77G23.5	Dermatan Sulfate Degradation
RP11-77G23.5	The Visual Cycle
MCM8-AS1	iNOS Signaling
MCM8-AS1	Toll-like Receptor Signaling
RP1-122O8.7	iNOS Signaling
RP1-122O8.7	Toll-like Receptor Signaling
RP11-120D5.1	Cell Cycle Control of Chromosomal Replication
CTD-2207A17.1	Glioma Invasiveness Signaling
RP11-130C19.3	Retinoate Biosynthesis I
RP5-943J3.2	MIF-mediated Glucocorticoid Regulation
RP5-943J3.2	MIF Regulation of Innate Immunity
RP5-943J3.2	Phospholipases
RP5-943J3.2	Eicosanoid Signaling
RP5-943J3.2	Role of MAPK Signaling in the Pathogenesis of Influenza
RP5-943J3.2	VEGF Family Ligand-Receptor Interactions
MCM8-AS1	IL-1 Signaling
RP1-122O8.7	IL-1 Signaling
RP5-943J3.2	Antioxidant Action of Vitamin C
RP3-512E2.2	Leukocyte Extravasation Signaling
RP3-512E2.2	Chondroitin Sulfate Degradation
RP3-512E2.2	Dermatan Sulfate Degradation
RP11-77M5.1	MIF-mediated Glucocorticoid Regulation
RP11-77M5.1	MIF Regulation of Innate Immunity
RP11-77M5.1	Phospholipases
RP11-77M5.1	Eicosanoid Signaling
RP11-77M5.1	Role of MAPK Signaling in the Pathogenesis of Influenza

**Abbreviations:** SRGAP3-AS4= SRGAP3 antisense RNA 4; MIR3180-2= MicroRNA 3180-2; FAM225A= Family with Sequence Similarity 225 Member A; CCDC13-AS1= CCDC13 Antisense RNA 1; LINC00907= Long Intergenic Non-Protein Coding RNA 907; MCM8-AS1= MCM8 Antisense RNA 1; p38 MAPK= p38 mitogen-activated protein kinases; Oct4= Octamer-binding transcription factor 4; iNOS Signaling= inducible nitric oxide synthase Signaling; MIF= Macrophage migration inhibitory factor; VEGF= Vascular endothelial growth factor; IL-1= Interleukin-1; UBOX5-AS1= UBOX5 Antisense RNA 1; APOA1-AS= APOA1 Antisense RNA; ZBTB20-AS3= ZBTB20 Antisense RNA 3