Supplementary Data

A Blood Gene Expression Marker of Early Alzheimer's Disease

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Supplementary Table 1
Bilateral measures of regional cortical thickness and cortical volume used in the classifier analysis obtained by structural MRI analysis

Cortical volume	Left hemisphere regional cortical thickness	Right hemisphere regional cortical thickness
Left Lateral Ventricle	Average thickness bankssts	Average thickness bankssts
Left Inferior Lateral Ventricle	Average thickness caudal anterior cingulate	Average thickness caudal anterior cingulate
Left Cerebellum White Matter	Average thickness caudal middle frontal	Average thickness caudal middle frontal
Left Cerebellum Cortex	Average thickness cuneus	Average thickness cuneus
Left Thalamus Proper	Average thickness entorhinal	Average thickness entorhinal
Left Caudate	Average thickness fusiform	Average thickness fusiform
Left Putamen	Average thickness inferior parietal	Average thickness inferior parietal
Left Pallidum	Average thickness inferior temporal	Average thickness inferior temporal
3rd Ventricle	Average thickness isthmus cingulate	Average thickness isthmus cingulated
4th Ventricle	Average thickness lateral occipital	Average thickness lateral occipital
Brainstem	Average thickness lateral orbitofrontal	Average thickness lateral orbitofrontal
Left Hippocampus	Average thickness lingual	Average thickness lingual
Left Amygdala	Average thickness medial orbitofrontal	Average thickness medial orbitofrontal
CSF	Average thickness middle temporal	Average thickness middle temporal
Left Accumbens area	Average thickness parahippocampal	Average thickness parahippocampal
Left Ventral Diencephalon	Average thickness paracentral	Average thickness paracentral
Left vessel	Average thickness parsopercularis	Average thickness parsopercularis
Left choroid plexus	Average thickness parsorbitalis	Average thickness parsorbitalis
Right Lateral Ventricle	Average thickness parstriangularis	Average thickness parstriangularis
Right Inferior Lateral Ventricle	Average thickness pericalcarine	Average thickness pericalcarine
Right Cerebellum White Matter	Average thickness postcentral	Average thickness postcentral
Right Cerebellum Cortex	Average thickness posterior cingulate	Average thickness posterior cingulated
Right Thalamus Proper	Average thickness precentral	Average thickness precentral
Right Caudate	Average thickness precuneus	Average thickness precuneus
Right Putamen	Average thickness rostral anterior cingulate	Average thickness rostral anterior cingulate
Right Pallidum	Average thickness rostral middle frontal	Average thickness rostral middle frontal
Right Hippocampus	Average thickness superior frontal	Average thickness superior frontal
Right Amygdala	Average thickness superior parietal	Average thickness superior parietal
Right Accumbens area	Average thickness superior temporal	Average thickness superior temporal
Right Ventral DC	Average thickness supramarginal	Average thickness supramarginal
Right vessel	Average thickness frontal pole	Average thickness frontal pole
Right choroid-plexus	Average thickness temporal pole	Average thickness temporal pole
5th Ventricle	Average thickness transverse temporal	Average thickness transverse temporal
White matter hypointensities	Average thickness insula	Average thickness insula
non-white matter hypointensities		
Optic chiasm		
Corpus callosum Posterior		
Corpus callosum Mid Posterior		
Corpus callosum Central		
Corpus callosum Mid_Anterior		
Corpus callosum Anterior		

Supplementary Table 2

The 203 Illumina probes that were used for out of bag development of an AD diagnostic classifier. Bold indicates those probes included (50 Illumina probes; 48 genes) that best classify AD from control samples in the training cohort (Table 2)

Gene symbol	Illumina probe[a]	Meng score[b]	*q*-value[c]	Bootstrap count[d]
RPS27A	**ILMN_2048326**	**1.87E-02**	**2.11E-05**	**200**
CHMP4A	**ILMN_1715607**	**1.71E-02**	**4.10E-03**	**200**
SFRS17A	**ILMN_1807737**	**1.68E-02**	**1.97E-03**	**198**
POMP	**ILMN_1693287**	**1.67E-02**	**3.62E-05**	**147**
C5ORF41	**ILMN_2195821**	**1.66E-02**	**9.41E-05**	**142**
FTHL7	**ILMN_2234016**	**1.65E-02**	**2.28E-03**	**67**
LOC401206	**ILMN_1792528**	**1.59E-02**	**3.62E-05**	**115**
AK2	**ILMN_1716053**	**1.58E-02**	**2.34E-03**	**161**
UQCRB	**ILMN_1759453**	**1.55E-02**	**3.64E-03**	**200**
LOC653505	**ILMN_1776260**	**1.55E-02**	**4.95E-05**	**134**
PGS1	**ILMN_2075051**	**1.51E-02**	**2.34E-03**	**58**
NRBP2	**ILMN_1733248**	**1.50E-02**	**1.85E-03**	**197**
UTP14A	**ILMN_2095820**	**1.47E-02**	**2.34E-03**	**57**
DICER1	**ILMN_1772692**	**1.46E-02**	**4.32E-04**	**180**
RPL36AL	**ILMN_2189936**	**1.44E-02**	**3.62E-05**	**200**
ATP5EP2	**ILMN_2225887**	**1.42E-02**	**5.76E-03**	**145**
SIRPG	**ILMN_1771801**	**1.39E-02**	**2.34E-03**	**20**
LSM3	**ILMN_2229242**	**1.36E-02**	**8.15E-03**	**200**
APBB3	**ILMN_2320513**	**1.33E-02**	**2.89E-03**	**177**
MRPL51	**ILMN_2097421**	**1.32E-02**	**2.19E-07**	**200**
RELL2	**ILMN_1652540**	**1.30E-02**	**5.10E-03**	**187**
CETN2	**ILMN_1695645**	**1.29E-02**	**2.11E-05**	**195**
PWP1	**ILMN_1743049**	**1.18E-02**	**5.07E-03**	**81**
KIAA0146	**ILMN_1887174**	**1.15E-02**	**7.55E-04**	**100**
LOC388720	**ILMN_1754990**	**1.14E-02**	**2.12E-04**	**101**
CIP29	**ILMN_1680967**	**1.11E-02**	**5.41E-03**	**191**
LOC388621	**ILMN_1677262**	**1.11E-02**	**4.75E-03**	**139**
SFRS17A	**ILMN_2117716**	**1.10E-02**	**4.87E-04**	**182**
PCBP1	**ILMN_1673215**	**1.09E-02**	**4.23E-04**	**100**
ATP5J2	**ILMN_2310621**	**1.08E-02**	**3.09E-05**	**65**
H2AFY	**ILMN_2373495**	**1.07E-02**	**6.30E-03**	**163**
COX17	**ILMN_2187718**	**1.07E-02**	**1.21E-05**	**5**
IDS	**ILMN_1758626**	**1.07E-02**	**2.34E-03**	**162**
SHFM1	**ILMN_2128128**	**1.07E-02**	**2.80E-04**	**173**
LOC651064	**ILMN_1782417**	**1.03E-02**	**6.09E-03**	**53**
STX16	**ILMN_1741942**	**9.95E-03**	**1.91E-03**	**160**
GDPD1	**ILMN_2106265**	**9.93E-03**	**4.88E-03**	**179**
C6ORF166	**ILMN_2148847**	**9.85E-03**	**5.31E-03**	**27**
ING3	**ILMN_2237746**	**9.83E-03**	**5.42E-03**	**158**
CACNA2D4	**ILMN_1696317**	**9.61E-03**	**7.73E-03**	**47**
PLEK	**ILMN_1795762**	**9.22E-03**	**2.84E-03**	**3**
NDUFA1	**ILMN_1784286**	**9.04E-03**	**2.45E-06**	**198**
CDKN1B	**ILMN_1722811**	**7.90E-03**	**7.93E-03**	**199**
RGS19	**ILMN_1677085**	**7.62E-03**	**5.48E-03**	**165**
RPS27A	**ILMN_1755883**	**7.61E-03**	**2.77E-04**	**180**
LOC731640	**ILMN_1661174**	**7.41E-03**	**8.33E-03**	**66**
AHSA1	**ILMN_1703617**	**6.98E-03**	**1.74E-03**	**58**
BXDC1	**ILMN_1664167**	**6.43E-03**	**4.29E-04**	**0**
KARS	**ILMN_1777584**	**5.54E-03**	**2.56E-03**	**5**
UBE2G1	**ILMN_1814465**	**−4.62E-04**	**1.74E-03**	**105**
NDUFS5	ILMN_1776104	N/A	4.69E-06	64
CALML4	ILMN_1815707	N/A	2.11E-05	35
LOC646200	ILMN_1732328	N/A	2.11E-05	12
UQCRH	ILMN_2232936	N/A	2.18E-05	8
RPA3	ILMN_1716895	N/A	3.62E-05	22
RPS25	ILMN_1746516	N/A	4.95E-05	68
ATP5I	ILMN_1726603	N/A	7.74E-05	0
UFC1	ILMN_2110281	N/A	8.19E-05	0
C5ORF41	ILMN_1776788	N/A	1.10E-04	123
RPL36AL	ILMN_2189933	N/A	2.12E-04	161

Supplementary Table 2
(*continued*)

Gene symbol	Illumina probe[a]	Meng score[b]	q-value[c]	Bootstrap count[d]
RPL32	ILMN_1663799	N/A	2.25E-04	61
LOC653658	ILMN_1652073	N/A	2.25E-04	54
THYN1	ILMN_2357361	N/A	2.77E-04	8
GTF2H5	ILMN_1739497	N/A	2.77E-04	0
ATP5O	ILMN_1791332	N/A	2.93E-04	3
CD3D	ILMN_2325837	N/A	4.32E-04	0
HSPE1	ILMN_1803775	N/A	4.71E-04	64
ATP6V1E1	ILMN_2339779	N/A	4.86E-04	72
NGDN	ILMN_2324998	N/A	4.86E-04	8
PRMT1	ILMN_1692473	N/A	4.93E-04	91
MRPS21	ILMN_1655765	N/A	5.67E-04	6
AIF1	ILMN_1792473	N/A	6.99E-04	3
NME1	ILMN_1741133	N/A	6.99E-04	0
PRDX1	ILMN_2366388	N/A	7.87E-04	41
CEBPB	ILMN_1693014	N/A	7.87E-04	13
C14ORF156	ILMN_1661945	N/A	8.43E-04	94
LOC731365	ILMN_1656662	N/A	1.03E-03	0
LOC285900	ILMN_1657612	N/A	1.22E-03	1
PRDX1	ILMN_2366391	N/A	1.25E-03	1
CBX3	ILMN_1790625	N/A	1.51E-03	1
GIMAP7	ILMN_1776678	N/A	1.51E-03	0
PTPRE	ILMN_1734543	N/A	1.58E-03	40
HS.569831	ILMN_1873075	N/A	1.84E-03	101
CD3D	ILMN_2261416	N/A	1.85E-03	0
HS.5724	ILMN_1839019	N/A	1.92E-03	67
SSBP1	ILMN_1809478	N/A	1.94E-03	20
ALOX5	ILMN_1680996	N/A	1.99E-03	0
KCTD21	ILMN_1809708	N/A	2.16E-03	73
MRPS33	ILMN_1741264	N/A	2.16E-03	0
PTPRE	ILMN_2383611	N/A	2.18E-03	40
THYN1	ILMN_2334042	N/A	2.28E-03	4
ARHGAP9	ILMN_1663916	N/A	2.34E-03	0
PSMC3	ILMN_1809010	N/A	2.34E-03	31
RPS12	ILMN_1782621	N/A	2.34E-03	16
MKNK1	ILMN_1750429	N/A	2.34E-03	11
MYBPC3	ILMN_1781184	N/A	2.34E-03	2
TOMM7	ILMN_1674069	N/A	2.34E-03	0
MAN2A2	ILMN_1815148	N/A	2.34E-03	0
TOMM7	ILMN_2087060	N/A	2.34E-03	0
C16ORF7	ILMN_1693630	N/A	2.43E-03	2
TYK2	ILMN_1676955	N/A	2.44E-03	6
LOC646483	ILMN_1673738	N/A	2.44E-03	0
CWC15	ILMN_1713482	N/A	2.44E-03	0
NPEPL1	ILMN_1724194	N/A	2.44E-03	0
SPN	ILMN_1801040	Meng	2.48E-03	128
MRPL22	ILMN_1748819	N/A	2.54E-03	49
ENY2	ILMN_2166865	N/A	2.54E-03	0
ATP5J2	ILMN_2307883	N/A	2.56E-03	30
C20ORF24	ILMN_2387599	N/A	2.56E-03	14
SNRPD2	ILMN_2369785	N/A	2.56E-03	3
ZMAT2	ILMN_1745343	N/A	2.61E-03	26
LOC440567	ILMN_1718136	N/A	2.63E-03	4
CCDC53	ILMN_1715569	N/A	2.78E-03	0
EEF1D	ILMN_1782543	N/A	2.82E-03	0
CETN3	ILMN_2224031	N/A	2.88E-03	12
BUD31	ILMN_1710697	N/A	2.89E-03	89
PDLIM7	ILMN_2396639	N/A	2.89E-03	81
SNRPB2	ILMN_1771620	N/A	2.89E-03	43
TBCA	ILMN_1726239	N/A	2.89E-03	12
ATP6V1E1	ILMN_1798485	N/A	2.89E-03	2
NGDN	ILMN_1690049	N/A	2.89E-03	0

Supplementary Table 2
(*continued*)

Gene symbol	Illumina probe[a]	Meng score[b]	q-value[c]	Bootstrap count[d]
LOC645688	ILMN_1772888	N/A	2.89E-03	0
LSM5	ILMN_1737947	N/A	2.92E-03	0
LDHB	ILMN_1728132	N/A	3.03E-03	0
SOD1	ILMN_1662438	N/A	3.10E-03	1
RPL6	ILMN_1712155	N/A	3.10E-03	0
LOC653103	ILMN_1746706	N/A	3.50E-03	0
EEF1B2	ILMN_2318725	N/A	3.50E-03	0
LOC440055	ILMN_1700316	N/A	3.51E-03	21
LOC654121	ILMN_1753892	N/A	3.52E-03	82
TCIRG1	ILMN_1711994	N/A	3.52E-03	1
LOC388532	ILMN_1656292	N/A	3.56E-03	72
MRPS17	ILMN_1804851	N/A	3.64E-03	22
C1ORF63	ILMN_1760556	N/A	3.83E-03	165
MRPL33	ILMN_1706326	N/A	3.83E-03	6
COMMD1	ILMN_1761242	N/A	3.87E-03	4
MRPL27	ILMN_1811327	N/A	3.94E-03	0
SP140	ILMN_2246882	N/A	4.29E-03	17
KIAA2010	ILMN_1678097	N/A	4.33E-03	24
ATP5J	ILMN_1772929	N/A	4.75E-03	81
LOC341457	ILMN_1688127	N/A	4.75E-03	16
SSB	ILMN_1672006	N/A	4.75E-03	1
LPP	ILMN_1651254	N/A	4.79E-03	66
APBB3	ILMN_1740772	N/A	4.79E-03	19
C14ORF43	ILMN_1763091	N/A	4.92E-03	39
IFFO	ILMN_2348268	N/A	5.05E-03	73
TMSB10	ILMN_1812392	N/A	5.07E-03	22
WBP5	ILMN_1679838	N/A	5.10E-03	117
MRPS18C	ILMN_1658416	N/A	5.10E-03	38
RAC2	ILMN_1709795	N/A	5.10E-03	27
MRPL35	ILMN_2341952	N/A	5.10E-03	0
NSMCE1	ILMN_1697962	N/A	5.31E-03	165
FAM126B	ILMN_1779486	N/A	5.31E-03	34
USP34	ILMN_1739454	N/A	5.31E-03	24
METTL5	ILMN_1691570	N/A	5.31E-03	14
NUDT1	ILMN_2330243	N/A	5.31E-03	14
GTF2B	ILMN_1737857	N/A	5.31E-03	6
LOC649548	ILMN_1672755	N/A	5.31E-03	3
KLF6	ILMN_1735014	N/A	5.31E-03	2
AIF1	ILMN_1703538	N/A	5.31E-03	1
RPS24	ILMN_1656625	N/A	5.31E-03	0
DNAJA1	ILMN_1672496	N/A	5.31E-03	0
BOLA3	ILMN_1786658	N/A	5.31E-03	0
BEX2	ILMN_2181892	N/A	5.43E-03	18
ATP5EP2	ILMN_1756674	N/A	5.70E-03	39
RPL21	ILMN_2290808	N/A	5.70E-03	0
PAX7	ILMN_1761061	N/A	5.82E-03	1
ITGA3	ILMN_1685397	N/A	5.95E-03	4
NDUFA9	ILMN_1760741	N/A	6.27E-03	9
ATP5I	ILMN_1772506	N/A	6.28E-03	0
ZFP36	ILMN_1720829	N/A	6.29E-03	0
NFAT5	ILMN_1780291	N/A	6.30E-03	2
SNX27	ILMN_1714401	N/A	6.40E-03	33
LOC642210	ILMN_1715926	N/A	6.40E-03	3
PFDN5	ILMN_1755536	N/A	6.40E-03	1
CR1	ILMN_1742601	N/A	6.40E-03	1
RBMS1	ILMN_1666444	N/A	6.48E-03	32
TRAPPC4	ILMN_1814650	N/A	6.53E-03	7
UCHL3	ILMN_1660111	N/A	6.53E-03	0
RBM23	ILMN_2363106	N/A	6.53E-03	0
IL10RB	ILMN_2230892	N/A	6.57E-03	102
PSMA3	ILMN_2387553	N/A	6.72E-03	0

Supplementary Table 2
(*continued*)

Gene symbol	Illumina probe[a]	Meng score[b]	*q*-value[c]	Bootstrap count[d]
LATS2	ILMN_1703412	N/A	6.87E-03	1
LOC730994	ILMN_1680774	N/A	6.87E-03	0
ZNF746	ILMN_1706342	N/A	7.05E-03	17
C11ORF56	ILMN_1713402	N/A	7.05E-03	2
PIK3CB	ILMN_1763347	N/A	7.05E-03	1
SNRPB2	ILMN_1690706	N/A	7.36E-03	0
BTF3	ILMN_2319414	N/A	7.71E-03	55
RPL11	ILMN_2114876	N/A	7.80E-03	0
IGBP1	ILMN_1717165	N/A	7.82E-03	2
COX6A1	ILMN_1783636	N/A	7.92E-03	0
RPL6	ILMN_1690494	N/A	7.93E-03	0
TXN	ILMN_1680314	N/A	8.00E-03	3
MRPL21	ILMN_1744835	N/A	8.44E-03	0
ISY1	ILMN_1781099	N/A	8.50E-03	20
MRPL55	ILMN_1799289	N/A	8.54E-03	0
C10ORF54	ILMN_2205963	N/A	8.54E-03	0
DBI	ILMN_2305544	N/A	8.68E-03	73
MRPL39	ILMN_1726391	N/A	8.95E-03	0
PSMC2	ILMN_1768784	N/A	9.32E-03	0
MYL6	ILMN_2326071	N/A	9.44E-03	34
C11ORF10	ILMN_1786759	N/A	9.59E-03	0

[a]The 50 illumina probes (48 genes) that best classify AD from normal elderly control subjects in the training cohort are shown in bold. [b]An estimate of variable (probe) importance in the Random Forest classifier model comparing AD and control samples. [c]*q*-value from a *t*-test comparing AD and control samples. [d]The number of times each probe appeared in the 200 bootstrap iteration.