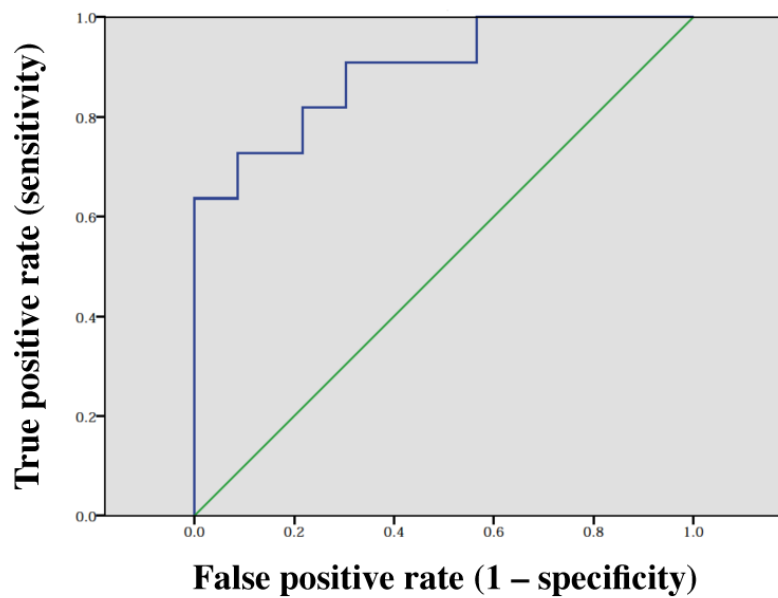
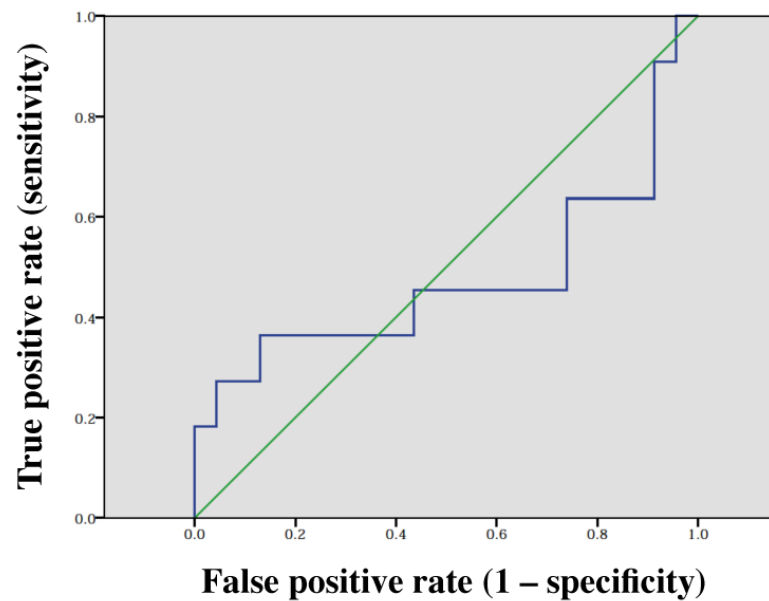


(a) Log2(NeuroD6) ROC curve



(b) Log2(NeuroD1) ROC curve



Supplementary Figure 1

25959	KANK2	KN motif and ankyrin repeat domains 2	chr19:11274791-11308243	2.812708414	0.00232257	3.056202208	0.000638422
58475	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	chr11:60145957-60185228	2.909860517	0.00654308	2.374609032	0.00163713
6876	TAGLN	transgelin	chr11:117070039-117075508	2.918748695	0.00232257	2.465585017	0.000638422
9457	FHL5	four and a half LIM domains 5	chr6:97010423-97071054	2.923729822	0.00654308	10.50620693	0.000638422
2828	GPR4	G protein-coupled receptor 4	chr19:46093022-46105466	3.075902983	0.00962874	2.233289068	0.00287725
150946	FAM59B	family with sequence similarity 59, member B	chr2:26395959-26413241	3.093628585	0.00232257	2.901783731	0.000638422
2872	MKMK2	MAP kinase interacting serine/threonine kinase 2	chr19:2037463-2051243	3.139881255	0.00762148	2.229793331	0.00287725
283755	HERC2P3	hect domain and RLD 2 pseudogene 3	chr15:20586683-20711433	3.172697556	0.00232257	6.604594557	0.000638422
134549	SHROOM1	shroom family member 1	chr5:132157663-132166703	3.256833576	0.00232257	2.504877412	0.000638422
353514	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	chr19:54818352-54824409	3.294272731	0.00232257	6.066986075	0.00396642
59	ACTA2	actin, alpha 2, smooth muscle, aorta	chr10:90694830-90777253	3.402251992	0.00865834	2.914806272	0.00825241
845	CASQ2	calsequestrin 2 (cardiac muscle)	chr1:116242519-116345204	3.491410523	0.00962874	5.322706439	0.000638422
23704	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	chr2:223916861-223920355	4.436801472	0.00232257	4.699574041	0.000638422
6279	SI00A8	SI00 calcium binding protein A8	chr1:153362507-153363664	5.018965399	0.00232257	2.142150734	0.0151369
871	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	chr11:75273100-75283870	5.437863735	0.00232257	2.129345418	0.0101566
6275	SI00A4	SI00 calcium binding protein A4	chr1:153516094-153518282	5.52659158	0.00232257	4.606560625	0.000638422
26266	SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4	chr7:135365246-135412933	6.580968881	0.00232257	2.996233377	0.000638422
3303	HSPA1A	heat shock 70kDa protein 1A	chr6:31777395-31785719	6.599057552	0.00232257	3.8880048	0.000638422
3304	HSPA1B	heat shock 70kDa protein 1B	chr6:31795511-31798031	6.599057552	0.00232257	2.366327899	0.000638422
375061	FAM89A	family with sequence similarity 89, member A	chr1:231154703-231175995	8.186858725	0.00232257	2.253222839	0.00248927
100500849	MIR3916	microRNA 3916	chr1:247342111-247374105	17.2291545	0.00762148	2.127294836	0.00287725

The core set of 522 DEGs in the frontal cortex of AD overlapping between EMU and UKY satisfying q-Value (FDR-corrected p-Value) < 0.05 and fold change greater than 2.0 or smaller than 0.5 were extracted by RNA-Seq data analysis of SRA060572. They are listed with Entrez Gene ID, Gene Symbol, Gene Name, Chromosomal Locus, Fold Change, and q-Value. NEUROD6 is underlined.

Supplementary TABLE 2. The set of 60 differentially spliced genes in the frontal cortex of AD identified by RNA-Seq data analysis of SRA060752

Entrez Gene ID	Gene Symbol	Gene Name	Chromosome Locus	Sqrt JS	q-Value
5797	PTPRM	protein tyrosine phosphatase, receptor type, M	chr18:7567313-8406952	0.825781	0.0142952
5468	PPARG	peroxisome proliferator-activated receptor gamma	chr3:12329348-12476009	0.735183	0.0142952
2635	GBP3	guanylate binding protein 3	chr1:89472359-89488549	0.727772	0.035452
7516	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	chr7:152341056-152373250	0.721052	0.0142952
23348	DOCK9	dedicator of cytokinesis 9	chr13:99445739-99738687	0.712575	0.0142952
441869	LOC441869	hypothetical protein LOC441869	chr1:1352433-1357201	0.712559	0.0142952
94121	SYTL4	synaptotagmin-like 4	chrX:99929488-99987135	0.706969	0.0208722
5163	PDK1	pyruvate dehydrogenase kinase, isozyme 1	chr2:173420640-173464990	0.68768	0.0142952
23332	CLASP1	cytoplasmic linker associated protein 1	chr2:122095164-122407091	0.68699	0.035452
25788	RAD54B	RAD54 homolog B (S. cerevisiae)	chr8:95383956-95487343	0.676423	0.0302148
26091	HERC4	hect domain and RLD 4	chr10:69681655-69835103	0.638866	0.0142952
144406	WDR66	WD repeat domain 66	chr12:122356462-122441832	0.626485	0.0142952
26034	IPCEF1	interaction protein for cytohesin exchange factors 1	chr6:154331635-154677900	0.624585	0.0142952
27124	INPP5J	inositol polyphosphate-5-phosphatase J	chr22:31518727-31530683	0.61534	0.0142952
51454	GULP1	GULP, engulfment adaptor PTB domain containing 1	chr2:189156388-189460669	0.605783	0.0142952
57125	PLXDC1	plexin domain containing 1	chr17:37213271-37309211	0.586646	0.0142952
57476	GRAMD1B	GRAM domain containing 1B	chr11:123396297-123498480	0.58641	0.0142952
221	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	chr11:67776047-67796852	0.580375	0.035452
55036	CCDC40	coiled-coil domain containing 40	chr17:78010430-78074468	0.576498	0.0142952
8120	AP3B2	adaptor-related protein complex 3, beta 2 subunit	chr15:83211862-83378635	0.554378	0.0142952
11176	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	chr12:56915608-57030163	0.552978	0.0208722
158471	PRUNE2	prune homolog 2 (Drosophila)	chr9:79224615-79521133	0.549799	0.0142952
1503	CTPS	CTP synthase	chr1:41445006-41478403	0.546957	0.0142952
353189	SLCO4C1	solute carrier organic anion transporter family, member 4C1	chr5:101569536-101632253	0.544079	0.0142952
6599	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	chr3:47627377-47823405	0.524068	0.0208722
79000	AUNIP	aurora kinase A and ninein interacting protein	chr1:26159495-26185869	0.520829	0.0142952
606495	CYB5RL	cytochrome b5 reductase-like	chr1:54635094-54665746	0.504141	0.035452
6596	HLTF	helicase-like transcription factor	chr3:148747775-148804341	0.488028	0.0208722
23114	NFASC	neurofascin homolog (chicken)	chr1:204797781-204991955	0.476222	0.0302148
10919	EHMT2	euchromatic histone-lysine N-methyltransferase 2	chr6:31847534-31865464	0.468069	0.0142952
6829	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	chr19:39936185-39967308	0.467546	0.0142952
1454	CSNK1E	casein kinase 1, epsilon	chr22:38686650-38714174	0.464769	0.0216171
26038	CHD5	chromodomain helicase DNA binding protein 5	chr1:6161840-6240218	0.4647	0.0216171
165918	RNF168	ring finger protein 168	chr3:196195656-196230639	0.455392	0.0208722
64324	NSD1	nuclear receptor binding SET domain protein 1	chr5:176559969-176727214	0.448436	0.0142952
9256	BZRAP1	benzodiazapine receptor (peripheral) associated protein 1	chr17:56378585-56494931	0.422966	0.035452
57478	USP31	ubiquitin specific peptidase 31	chr16:23072727-23160591	0.416776	0.0142952
80255	SLC35F5	solute carrier family 35, member F5	chr2:114464233-114514862	0.416096	0.0142952
9760	TOX	thymocyte selection-associated high mobility group box	chr8:59717971-60031855	0.415069	0.0142952
57631	LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	chrX:114345175-114468635	0.411526	0.0302148
55183	RIF1	RAP1 interacting factor homolog (yeast)	chr2:152266396-152334001	0.407443	0.0208722
284161	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	chr17:57297827-57353330	0.40268	0.0208722
26052	DNM3	dynamamin 3	chr1:171810620-172381857	0.397641	0.0216171
440823	MIAT	myocardial infarction associated transcript (non-protein coding)	chr22:27042837-27072441	0.389809	0.0208722
6645	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16:69221049-69342955	0.389015	0.0216171
84864	MINA	MYC induced nuclear antigen	chr3:97540880-97691295	0.385104	0.035452
284677	C1orf204	chromosome 1 open reading frame 204	chr1:159796478-159832447	0.371537	0.0208722
391123	VSIG8	V-set and immunoglobulin domain containing 8	chr1:159796478-159832447	0.371537	0.0208722
6489	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	chr12:22346281-22487648	0.370318	0.0142952
29801	ZDHHC8	zinc finger, DHHC-type containing 8	chr22:20119363-20135632	0.364549	0.0216171
9321	TRIP11	thyroid hormone receptor interactor 11	chr14:92432265-92511291	0.364451	0.0142952
9631	NUP155	nucleoporin 155kDa	chr5:37286396-37371197	0.351752	0.0142952
57120	GOPC	golgi associated PDZ and coiled-coil motif containing	chr6:117803819-117923705	0.347199	0.0142952
55362	TMEM63B	transmembrane protein 63B	chr6:44095333-44123256	0.332719	0.0216171
23028	KDM1A	lysine (K)-specific demethylase 1	chr1:23345940-23410184	0.327325	0.0216171
23600	AMACR	alpha-methylacyl-CoA racemase	chr5:33987090-34124633	0.307388	0.0142952
5358	PLS3	plastin 3 (T isoform)	chrX:114795176-114885179	0.303812	0.0216171
55763	EXOC1	exocyst complex component 1	chr4:56719815-56771244	0.303033	0.0216171
80218	NAA50	N-acetyltransferase 13 (GCN5-related)	chr3:113432171-113465120	0.248626	0.0142952
23276	KLHL18	kelch-like 18 (Drosophila)	chr3:47205859-47392593	0.242977	0.0216171

Differentially spliced genes in the frontal cortex compared between AD versus NC derived from EMU and UKY extracted by RNA-Seq data analysis of SRA060752 were combined. The spliced genes satisfying q-Value (FDR-corrected p-Value) < 0.05 are listed with Entrez Gene ID, Gene Symbol, Gene Name, Chromosomal Locus, the square root of the Jensen-Shannon divergence (Sqrt JS), and q-Value.

Supplementary TABLE 3. The set of 215 DEGs in cortical neurons of the superior frontal gyrus of AD identified by microarray data analysis of GSE5281

Entrez Gene ID	Gene Symbol	Gene Title	Fold Change (AD vs NC)	p-Value
116	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)	0.069636923	1.26039E-07
6750	SST	somatostatin	0.078547047	2.49899E-05
25859	PART1	prostate androgen-regulated transcript 1 (non-protein coding)	0.09979003	7.81005E-07
10556	RPP30	ribonuclease P/MRP 30kDa subunit	0.121421574	1.15361E-05
7306	TYRP1	tyrosinase-related protein 1	0.12391224	2.91523E-06
729870	LOC729870	uncharacterized LOC729870	0.125916106	1.14639E-07
10001	MED6	mediator complex subunit 6	0.127676215	1.04388E-05
5771	PTPN2	protein tyrosine phosphatase, non-receptor type 2	0.129512873	1.61631E-05
126068	ZNF441	zinc finger protein 441	0.135568912	3.65191E-06
9040	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	0.140010654	9.52306E-06
2563	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta	0.142042327	2.57797E-05
57452	GALNT16	polypeptide N-acetylgalactosaminyltransferase 16	0.143744955	8.22479E-06
1412	CRYBA2	crystallin, beta A2	0.145842233	9.60478E-05
53918	PELO	pelota homolog (Drosophila)	0.147274585	3.97322E-05
10777	ARPP21	cAMP-regulated phosphoprotein, 21kDa	0.1474134	4.52823E-06
64105	CENPK	centromere protein K	0.148647796	2.45922E-05
158228	FAM201A	family with sequence similarity 201, member A	0.149625358	3.40468E-08
196294	IMMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.15002806	1.03281E-05
158326	FREM1	FRAS1 related extracellular matrix 1	0.15200796	2.39567E-07
283401	FLJ33996	Hypothetical protein FLJ33996	0.154423179	2.77206E-05
8754	ADAM9	ADAM metalloproteinase domain 9	0.154955285	3.00411E-07
6511	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	0.156759363	4.74541E-05
5605	MAP2K2	mitogen-activated protein kinase kinase 2	0.157368364	6.95049E-06
51230	PHF20	PHD finger protein 20	0.157471386	2.87845E-05
5600	MAPK11	mitogen-activated protein kinase 11	0.16197929	3.94138E-08
81573	ANKRD13C	ankyrin repeat domain 13C	0.165393484	9.22967E-05
221264	AKD1	adenylate kinase domain containing 1	0.167076883	2.44999E-05
8539	API5	apoptosis inhibitor 5	0.169466	6.32302E-05
57379	AICDA	activation-induced cytidine deaminase	0.171641877	6.25246E-07
728192	LINC00460	long intergenic non-protein coding RNA 460	0.171656016	8.49002E-07
201626	PDE12	Phosphodiesterase 12	0.172443023	1.6E-05
23304	UBR2	ubiquitin protein ligase E3 component n-recogin 2	0.17290985	4.0324E-05
90632	C6orf176	chromosome 6 open reading frame 176	0.174179808	1.05824E-05
256471	MFSD8	major facilitator superfamily domain containing 8	0.178004149	3.08466E-06
1846	DUSP4	dual specificity phosphatase 4	0.180708065	3.17436E-05
56915	EXOSC5	exosome component 5	0.18089212	4.4006E-05
81602	CDADC1	cytidine and dCMP deaminase domain containing 1	0.181221497	5.63843E-06
22843	PPM1E	protein phosphatase, Mg2+/Mn2+ dependent, 1E	0.181354038	9.88435E-05
891	CCNB1	cyclin B1	0.182817517	1.34014E-05
2762	GMDS	GDP-mannose 4,6-dehydratase	0.183086528	3.97601E-06
7062	TCHH	trichohyalin	0.183269147	9.68165E-06
6835	SURF2	surfeit 2	0.184390125	3.26572E-05
81491	GPR63	G protein-coupled receptor 63	0.186613153	3.74939E-05
55172	C14orf104	chromosome 14 open reading frame 104	0.186734612	8.42116E-07
3914	LAMB3	laminin, beta 3	0.189677043	4.52811E-06
523	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	0.190442377	8.45909E-05
51086	TNNI3K	TNNI3 interacting kinase	0.192973193	1.79598E-05
169200	TMEM164	transmembrane protein 64	0.193218848	4.05358E-06
9734	HDAC9	histone deacetylase 9	0.19323932	1.28179E-05
79693	YRDC	yrdC domain containing (E. coli)	0.193557047	8.18589E-07
4801	NFYB	nuclear transcription factor Y, beta	0.194719115	3.02116E-05
93426	SYCE1	synaptonemal complex central element protein 1	0.195656453	1.51885E-05
84520	C14orf142	chromosome 14 open reading frame 142	0.19704676	2.13813E-05
9481	SLC25A27	solute carrier family 25, member 27	0.198188373	8.25666E-05
6708	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	0.198230692	1.01877E-05
2936	GSR	glutathione reductase	0.199527565	1.63443E-06
10562	OLFM4	olfactomedin 4	0.199647096	1.15847E-05
7991	TUSC3	tumor suppressor candidate 3	0.200399391	3.74354E-05
10681	GNB5	guanine nucleotide binding protein (G protein), beta 5	0.201370766	5.0234E-05
23040	MYT1L	myelin transcription factor 1-like	0.204647283	8.31875E-05
22901	ARSG	arylsulfatase G	0.208725376	5.32396E-05
10279	PRSS16	protease, serine, 16 (thymus)	0.210284553	7.90389E-05
54939	COMM4	COMM domain containing 4	0.210664422	4.94578E-05
1770	DNAH9	dynein, axonemal, heavy chain 9	0.212595043	9.92987E-06
894	CCND2	cyclin D2	0.213765457	6.53823E-05
7356	SCGB1A1	secretoglobin, family 1A, member 1 (uteroglobulin)	0.214429919	7.1649E-05
283484	LOC283484	uncharacterized LOC283484	0.216069327	3.39563E-05
57650	KIAA1524	KIAA1524	0.216374441	1.19481E-05
4139	MARK1	MAP/microtubule affinity-regulating kinase 1	0.217306843	9.01463E-05
27098	CLUL1	clusterin-like 1 (retinal)	0.217430566	1.7684E-05
8301	PICALM	phosphatidylinositol binding clathrin assembly protein	0.218691398	9.96687E-06
55110	MAGOHB	mago-nashi homolog B (Drosophila)	0.21950427	5.82891E-05
163081	ZNF567	zinc finger protein 567	0.219687149	4.08174E-05
80700	UBXN6	UBX domain protein 6	0.22029261	5.64717E-05
1731	SEPT1	septin 1	0.220367831	4.45004E-05
54414	SIAE	sialic acid acetyltransferase	0.222876791	6.67167E-05

1741	DLG3	discs, large homolog 3 (Drosophila)	0.222930685	8.59311E-06
152756	C4orf39	chromosome 4 open reading frame 39	0.222995615	8.84069E-06
169270	ZNF596	zinc finger protein 596	0.223311428	7.30718E-06
5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	0.224140879	2.69271E-05
9869	SETDB1	SET domain, bifurcated 1	0.2253656	1.81497E-05
7270	TTF1	transcription termination factor, RNA polymerase I	0.226659218	2.28839E-05
2794	GNL1	guanine nucleotide binding protein-like 1	0.226797093	3.09869E-06
23332	CLASP1	Cytoplasmic linker associated protein 1	0.226910712	7.3493E-05
283310	C12orf64	chromosome 12 open reading frame 64	0.22780007	4.15357E-05
51275	C12orf47	chromosome 12 open reading frame 47	0.230619235	7.53242E-05
90317	ZNF616	zinc finger protein 616	0.230715995	9.38919E-05
284656	EPHA10	EPH receptor A10	0.230742139	1.67301E-05
160518	DENND5B	DENN/MADD domain containing 5B	0.231022895	6.26944E-05
64398	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	0.232247403	4.09094E-05
8543	LMO4	LIM domain only 4	0.232544867	4.43493E-05
1982	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	0.233795543	7.04498E-05
57528	KCTD16	potassium channel tetramerisation domain containing 16	0.234745918	5.32779E-05
63974	NEUROD6	neurogenic differentiation 6	0.237572737	6.60728E-05
51496	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	0.240790778	2.02993E-05
79783	SUGCT	succinyl-CoA:glutarate-CoA transferase	0.241107758	3.62348E-05
51608	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae)	0.241383495	5.94325E-06
515	ATP5F1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	0.241431174	1.40459E-05
1984	EIF5A	eukaryotic translation initiation factor 5A	0.241553721	2.19357E-06
27319	BHLHE22	basic helix-loop-helix family, member e22	0.242258502	8.42321E-05
147645	VSIG10L	V-set and immunoglobulin domain containing 10 like	0.242683646	8.85379E-05
56993	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	0.243163969	5.41726E-06
56052	ALG1	asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae)	0.247020898	1.48808E-05
151195	CCNYL1	cyclin Y-like 1	0.247698446	4.9648E-05
22948	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	0.247856464	6.15965E-05
80224	NUBPL	nucleotide binding protein-like	0.248161621	7.20475E-05
10658	CELF1	CUGBP, Elav-like family member 1	0.248454389	9.33091E-05
9677	PIPK5K1	diphosphoinositol pentakisphosphate kinase 1	0.249381978	1.35708E-07
3382	ICA1	islet cell autoantigen 1, 69kDa	0.249762845	2.41638E-05
54148	MRPL39	mitochondrial ribosomal protein L39	0.25067943	8.7033E-05
55862	ECHDC1	enoyl CoA hydratase domain containing 1	0.251455215	4.37292E-05
642924	LINC00535	long intergenic non-protein coding RNA 535	0.252893819	6.83023E-06
7881	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	0.253379497	1.54E-05
645191	LINGO3	leucine rich repeat and Ig domain containing 3	0.25400303	3.56459E-05
147007	TMEM199	transmembrane protein 199	0.254036375	2.23978E-06
100132884	LOC100132884	uncharacterized LOC100132884	0.2546586	8.09859E-05
101928498	LOC101928498	uncharacterized LOC101928498	0.257003889	1.71389E-06
9470	EIF4E2	eukaryotic translation initiation factor 4E family member 2	0.259272145	9.46231E-05
6945	MLX	MAX-like protein X	0.260489569	6.51217E-05
10775	POP4	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	0.260614809	7.92389E-06
286359	LOC286359	uncharacterized LOC286359	0.261719351	1.21654E-05
51105	PHF20L1	PHD finger protein 20-like 1	0.261767529	3.50347E-05
100507557	LOC100507557	uncharacterized LOC100507557	0.262771642	8.02713E-05
51111	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	0.263004871	4.22888E-05
1807	DPYS	dihydropyrimidinase	0.263121132	4.91402E-06
7336	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	0.268049344	4.64289E-05
55027	HEATR3	HEAT repeat containing 3	0.269701101	4.01842E-05
78991	PCYOX1L	prenylcysteine oxidase 1 like	0.269715877	4.43934E-05
3419	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	0.271499204	9.95633E-05
9063	PIAS2	Protein inhibitor of activated STAT, 2	0.271684484	4.41772E-05
1084	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	0.271821968	5.7677E-05
844	CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	0.271852315	3.03481E-05
10237	SLC35B1	solute carrier family 35, member B1	0.272823999	7.92528E-05
65244	SPATS2	spermatogenesis associated, serine-rich 2	0.273482519	6.42035E-05
91147	TMEM67	transmembrane protein 67	0.273483738	8.15071E-05
285440	CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2	0.27381825	1.39834E-06
1785	DNM2	dynamain 2	0.274895786	2.11917E-05
29761	USP25	ubiquitin specific peptidase 25	0.274909483	3.05449E-05
11218	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	0.275382525	1.28363E-05
255352	C10orf93	chromosome 10 open reading frame 93	0.275661283	8.60497E-05
79183	TTPAL	tocopherol (alpha) transfer protein-like	0.27810543	1.92919E-05
22869	ZNF510	zinc finger protein 510	0.278916363	3.72453E-05
5599	MAPK8	mitogen-activated protein kinase 8	0.280823911	1.47051E-05
7024	TFCP2	transcription factor CP2	0.281014494	4.15538E-05
11130	ZWINT	ZW10 interactor	0.281253181	2.7161E-07
9788	MTSS1	metastasis suppressor 1	0.282059367	5.65722E-05
129285	KLRAQ1	KLRAQ motif containing 1	0.286866593	3.05391E-06
1662	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	0.287532559	3.55595E-05
11034	DSTN	Destrin (actin depolymerizing factor)	0.287674004	2.96698E-05
6880	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	0.289512359	7.06464E-05
286144	C8orf83	chromosome 8 open reading frame 83	0.291989129	6.82599E-05
54039	PCBP3	poly(rC) binding protein 3	0.292139459	9.23825E-05
5645	PRSS2	protease, serine, 2 (trypsin 2)	0.29347403	3.63464E-05
84451	KIAA1804	mixed lineage kinase 4	0.293869593	2.47971E-05
339965	CCDC158	coiled-coil domain containing 158	0.294669218	9.13572E-06
22949	PTGR1	prostaglandin reductase 1	0.295070422	2.10552E-05

9802	DAZAP2	DAZ associated protein 2	0.295709943	6.90278E-05
2170	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	0.298322552	9.02347E-05
84557	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	0.299830163	1.36819E-06
113174	SAAL1	serum amyloid A-like 1	0.30157444	7.69427E-06
56256	SERTAD4	SERTA domain containing 4	0.302069796	5.66397E-05
84798	C19orf48	chromosome 19 open reading frame 48	0.304409689	2.50785E-05
9577	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.306075086	9.92354E-05
84900	RNFT2	ring finger protein, transmembrane 2	0.306171729	4.52424E-05
261726	TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	0.307187952	4.81912E-05
166379	BBS12	Bardet-Biedl syndrome 12	0.307793398	1.64386E-05
11144	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	0.309237619	5.48091E-06
55216	C11orf57	chromosome 11 open reading frame 57	0.311048275	1.04698E-05
23329	TBC1D30	TBC1 domain family, member 30	0.31573145	5.64438E-05
8745	ADAM23	ADAM metalloproteinase domain 23	0.317318146	4.87044E-05
84142	FAM175A	family with sequence similarity 175, member A	0.318203448	2.67463E-05
55786	ZNF415	zinc finger protein 415	0.320643226	2.88337E-05
401442	LOC401442	uncharacterized LOC401442	0.323075963	3.91753E-05
80820	EEDP1	endonuclease/exonuclease/phosphatase family domain containing 1	0.323089105	5.1179E-05
23185	LARP4B	La ribonucleoprotein domain family, member 4B	0.323170088	4.43628E-05
92	ACVR2A	activin A receptor, type IIA	0.327396714	6.95311E-06
154215	NKAIN2	Na ⁺ /K ⁺ transporting ATPase interacting 2	0.327625458	7.47158E-05
162394	SLFN5	schlafen family member 5	0.327952908	9.92377E-05
79644	SRD5A3	steroid 5 alpha-reductase 3	0.328233834	5.36134E-05
135295	SRSF12	serine/arginine-rich splicing factor 12	0.330721489	3.56501E-05
8417	STX7	syntaxin 7	0.331856143	4.05275E-05
8882	ZNF259	zinc finger protein 259	0.332476459	4.81463E-06
11143	MYST2	MYST histone acetyltransferase 2	0.332553475	7.67737E-05
441061	MARCH11	membrane-associated ring finger (C3HC4) 11	0.333104755	3.48392E-05
168667	BMPER	BMP binding endothelial regulator	0.333885173	6.68363E-05
151194	FAM119A	family with sequence similarity 119, member A	0.334401486	8.06696E-05
9329	GTF3C4	general transcription factor IIC, polypeptide 4, 90kDa	0.3354717	3.24135E-05
60526	C2orf43	chromosome 2 open reading frame 43	0.336549456	1.18393E-05
8498	RANBP3	RAN binding protein 3	0.336838662	4.15908E-05
8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	0.342786093	4.27269E-05
8396	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	0.346321233	7.98368E-05
26002	MOXD1	monooxygenase, DBH-like 1	0.350988747	8.95184E-05
6419	SETMAR	SET domain and mariner transposase fusion gene	0.35787671	2.36463E-05
23096	IQSEC2	IQ motif and Sec7 domain 2	0.358468105	8.59696E-05
3754	KCNF1	potassium voltage-gated channel, subfamily F, member 1	0.359533309	4.95636E-05
9515	STXBPSL	syntaxin binding protein 5-like	0.360338998	8.58457E-05
47	ACLY	ATP citrate lyase	0.361128893	9.52106E-05
55973	BCAP29	B-cell receptor-associated protein 29	0.3634238	5.20388E-05
9131	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1	0.368230385	6.62156E-05
388272	C16orf87	chromosome 16 open reading frame 87	0.371197394	1.52935E-05
11285	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	0.372874153	7.20649E-06
91543	RSAD2	radical S-adenosyl methionine domain containing 2	0.383620394	8.54968E-05
23184	MESDC2	mesoderm development candidate 2	0.39605989	3.45543E-05
23041	MON2	MON2 homolog (S. cerevisiae)	0.404470706	8.63572E-05
22929	SEPHS1	selenophosphate synthetase 1	0.404606953	3.40831E-05
81545	FBXO38	F-box protein 38	0.416551062	4.34948E-05
10360	NPM3	nucleophosmin/nucleoplasm 3	0.417979562	2.84678E-05
100303728	SLC25A5-AS1	SLC25A5 antisense RNA 1	0.436709024	8.65633E-05
8111	GPR68	G protein-coupled receptor 68	0.442242867	7.38844E-05
54884	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.460077878	1.06392E-05
720	C4A	complement component 4A (Rodgers blood group)	2.992510275	8.64066E-05
9117	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	3.326491174	2.84927E-05
56288	PARD3	par-3 family cell polarity regulator	3.762403671	1.03744E-05
94	ACVRL1	activin A receptor type II-like 1	5.081871823	7.65974E-05
202181	LOC202181	SUMO-interacting motifs containing 1 pseudogene	6.913531993	5.09011E-06

The set of 215 DEGs in LCM-captured cortical neurons of the superior frontal gyrus of AD satisfying p-Value < 0.0001 by two-tailed t-test and fold change greater than 2 or smaller than 0.5 were extracted by microarray data analysis of GSE5281. They are listed with Entrez Gene ID, Gene Symbol, Gene Name, Fold Change, and p-Value. NEUROD6 is underlined.

Supplementary TABLE 4. The set of 131 DEGs downregulated in the hippocampal CA1 region during progression of AD identified by microarray data analysis of GSE1297

Entrez Gene ID	Gene Symbol	Gene Name	Fold Change (Severe AD vs NC)	p-Value
57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG	0.119791216	0.00015044
1290	COL5A2	collagen, type V, alpha 2	0.137353439	0.003310089
7447	VSNL1	visinin-like 1	0.176659556	0.003811085
4253	CTAGE5	CTAGE family, member 5	0.187301453	0.000234565
11161	C14orf1	chromosome 14 open reading frame 1	0.200480779	0.005009542
56603	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	0.209620966	0.001291311
10675	CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)	0.212310725	0.003058062
10368	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	0.212906942	0.000645324
2115	ETV1	ets variant 1	0.22931704	0.000240241
55711	FAR2	fatty acyl CoA reductase 2	0.230090829	0.00066547
324	APC	adenomatous polyposis coli	0.240819317	0.000639442
1716	DGUOK	deoxyguanosine kinase	0.245686681	0.001149261
10197	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.251903297	0.001593785
9378	NRXN1	neurexin 1	0.260881827	0.009477858
1795	DOCK3	dedicator of cytokinesis 3	0.261184326	0.005551229
545	ATR	ataxia telangiectasia and Rad3 related	0.262908596	0.003036901
10769	PLK2	polo-like kinase 2	0.264329482	0.001588852
23026	MYO16	myosin XVI	0.264525437	0.003540514
6623	SNCG	synuclein, gamma (breast cancer-specific protein 1)	0.266115782	0.002115945
3084	NRG1	neuregulin 1	0.266870545	0.001406226
27292	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	0.275042863	0.002562807
6715	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	0.282086506	0.001299877
9331	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	0.284246871	0.005450676
11197	WIF1	WNT inhibitory factor 1	0.290913711	0.001653579
286	ANK1	ankyrin 1, erythrocytic	0.295816536	0.009830239
3040	HBA2	hemoglobin, alpha 2	0.299863012	0.004878631
5132	PDC	phosducin	0.301022115	0.003171501
55521	TRIM36	tripartite motif-containing 36	0.303428631	0.002870895
11178	LZTS1	leucine zipper, putative tumor suppressor 1	0.318678801	0.000656311
3043	HBB	hemoglobin, beta	0.320523818	0.005373169
55312	RFK	riboflavin kinase	0.326351561	0.000250327
4741	NEFM	neurofilament, medium polypeptide	0.334625635	0.001051236
5274	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	0.337526915	0.006332563
9409	PEX16	peroxisomal biogenesis factor 16	0.338900118	0.000820529
9079	LDB2	LIM domain binding 2	0.340999225	0.003326867
1268	CNR1	cannabinoid receptor 1 (brain)	0.344653589	0.008057005
5579	PRKCB	protein kinase C, beta	0.345004889	0.002186833
80742	PRR3	proline rich 3	0.357389253	0.009060604
100996492	LINC01314	long intergenic non-protein coding RNA 1314	0.366700351	0.009201076
63982	ANO3	anoctamin 3	0.372084936	0.008600399
114884	OSBPL10	oxysterol binding protein-like 10	0.377322152	1.56064E-05
6566	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.377389214	0.008899999
6045	RNF2	ring finger protein 2	0.379240231	0.00262118
51099	ABHD5	abhydrolase domain containing 5	0.38334089	0.005300446
9699	RIMS2	regulating synaptic membrane exocytosis 2	0.38701032	0.000579041
81831	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	0.393977566	0.000965658
9143	SYNGR3	synaptogyrin 3	0.397630789	0.005052114
1875	E2F5	E2F transcription factor 5, p130-binding	0.408606441	0.009410234
8548	BLZF1	basic leucine zipper nuclear factor 1	0.413990554	0.003290634
440270	GOLGA8B	golgin A8 family, member B	0.422538873	0.00471934
23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	0.43589904	0.001873881
2890	GRIA1	glutamate receptor, ionotropic, AMPA 1	0.436494345	0.009682402
93408	MYL10	myosin, light chain 10, regulatory	0.439384927	0.008276491
5937	RBMS1	RNA binding motif, single stranded interacting protein 1	0.441701035	0.009373718
8470	SORBS2	sorbin and SH3 domain containing 2	0.444625873	0.000784413
64771	C6orf106	chromosome 6 open reading frame 106	0.446598876	0.009694381
27324	TOX3	TOX high mobility group box family member 3	0.450425735	0.002724595
5994	RFXAP	regulatory factor X-associated protein	0.451935762	0.006501679
6000	RGS7	regulator of G-protein signaling 7	0.451971533	0.006045425
138046	RALYL	RALY RNA binding protein-like	0.453463038	0.001029166
53335	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.457377016	0.004390769
8604	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	0.457499507	0.00019237
22986	SORCS3	sortilin-related VPS10 domain containing receptor 3	0.459432107	0.003125207
5530	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	0.461727097	0.001385837
23392	KIAA0368	KIAA0368	0.462082599	0.003454136
1020	CDK5	cyclin-dependent kinase 5	0.464742579	0.00340998
5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	0.465879457	0.002607569

9856	KIAA0319	KIAA0319	0.466821918	0.003104747
9750	FAM65B	family with sequence similarity 65, member B	0.469502963	0.003648222
57863	CADM3	cell adhesion molecule 3	0.470400343	0.001417647
4121	MAN1A1	mannosidase, alpha, class 1A, member 1	0.470575788	0.007786277
23281	MTUS2	microtubule associated tumor suppressor candidate 2	0.475295934	0.007578628
23167	EFR3A	EFR3 homolog A (S. cerevisiae)	0.480846757	0.004322177
3039	HBA1	hemoglobin, alpha 1	0.481011431	0.006622563
4907	NT5E	5'-nucleotidase, ecto (CD73)	0.481199125	0.008511804
4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	0.482930377	0.004989266
3048	HBG2	hemoglobin, gamma G	0.483511346	0.001076114
3751	KCND2	potassium voltage-gated channel, Shal-related subfamily, member 2	0.489787298	0.004105453
27324	TOX3	TOX high mobility group box family member 3	0.490769258	0.005222024
10129	FRY	furry homolog (Drosophila)	0.49309084	0.00556954
3191	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.499634764	0.003832929
8502	PKP4	plakophilin 4	0.50203014	0.001264843
3708	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	0.50283747	0.002087049
6722	SRF	serum response factor (c-fos serum response element-binding transcription factor)	0.507259691	0.009083026
9071	CLDN10	claudin 10	0.512449482	0.005138908
2335	FN1	fibronectin 1	0.51287327	0.003377587
9922	IQSEC1	IQ motif and Sec7 domain 1	0.517453432	0.000135105
79567	FAM65A	family with sequence similarity 65, member A	0.517677872	0.005148038
23157	SEPT6	septin 6	0.521243095	1.94717E-05
6310	ATXN1	ataxin 1	0.529973111	0.000693097
1107	CHD3	chromodomain helicase DNA binding protein 3	0.531318284	0.002487892
79101	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	0.534934964	0.006396605
9821	RB1CC1	RB1-inducible coiled-coil 1	0.535541656	0.003745766
55757	UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	0.535558689	0.001405379
29114	TAGLN3	transgelin 3	0.536481218	0.00215522
9590	AKAP12	A kinase (PRKA) anchor protein 12	0.538894732	8.64065E-05
57496	MKL2	MKL/myocardin-like 2	0.541306767	0.009963246
53353	LRP1B	low density lipoprotein receptor-related protein 1B	0.541847962	0.004672477
23231	SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	0.542192244	0.007063601
56943	ENY2	enhancer of yellow 2 homolog (Drosophila)	0.544071595	0.009527721
79762	C1orf115	chromosome 1 open reading frame 115	0.546532572	0.005130192
10846	PDE10A	phosphodiesterase 10A	0.549157947	0.002263882
1349	COX7B	cytochrome c oxidase subunit VIIb	0.553088625	0.004051697
65981	CAPRN2	caprin family member 2	0.555441174	0.00066017
7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	0.556167619	0.006101886
1337	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	0.557465998	0.001751281
9353	SLIT2	slit homolog 2 (Drosophila)	0.558570719	0.009460307
26507	CNNM1	cyclin M1	0.5599908	0.005691077
93664	CADPS2	Ca ⁺⁺ -dependent secretion activator 2	0.560315994	0.002336932
509	ATP5C1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	0.563516199	0.005837604
491	ATP2B2	ATPase, Ca ⁺⁺ transporting, plasma membrane 2	0.564364625	0.008806963
91851	CHRDL1	chordin-like 1	0.565566821	0.003016121
56252	YLPM1	YLP motif containing 1	0.566024088	0.00755332
377	ARF3	ADP-ribosylation factor 3	0.567332148	0.005452724
4862	NPAS2	neuronal PAS domain protein 2	0.567397135	0.007890075
63974	<u>NEUROD6</u>	<u>neurogenic differentiation 6</u>	0.568549476	0.007199422
9452	ITM2A	integral membrane protein 2A	0.56961321	0.001581406
5162	PDHB	pyruvate dehydrogenase (lipoamide) beta	0.573206217	0.006116724
4714	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	0.578140448	0.001083971
22941	SHANK2	SH3 and multiple ankyrin repeat domains 2	0.580635291	0.006476589
6529	SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	0.582511461	0.004142352
58189	WFDC1	WAP four-disulfide core domain 1	0.582843283	0.002318206
1008	CDH10	cadherin 10, type 2 (T2-cadherin)	0.584467028	0.002335459
23518	R3HDM1	R3H domain containing 1	0.590781827	0.009081363
9994	CASP8AP2	caspase 8 associated protein 2	0.591049072	0.002678888
9168	TMSB10	thymosin beta 10	0.591288491	0.000133143
2744	GLS	glutaminase	0.591660135	0.007897416
2915	GRM5	glutamate receptor, metabotropic 5	0.592186084	0.00764757
576	BAI2	brain-specific angiogenesis inhibitor 2	0.593582138	0.008425238
64788	LMF1	lipase maturation factor 1	0.596678442	0.004542002
9847	KIAA0528	KIAA0528	0.599243843	0.006295878

The set of 131 DEGs downregulated in the hippocampal CA1 region among incipient, moderate, and severe AD and NC groups by one-way ANOVA satisfying p-Value < 0.01 and fold change of severe AD versus NC smaller than 0.6 were extracted by microarray data analysis of GSE1297. They are listed with Entrez Gene ID, Gene Symbol, Gene Name, Fold Change, and p-Value. NEUROD6 is underlined.

Supplementary TABLE 5. The set of 31 DEGs downregulated in the hippocampus of Japanese AD patients identified by microarray data analysis of GSE36980

Entrez Gene ID	Gene Symbol	Gene Name	Fold Change (AD vs non-AD)	p-Value
4233	MET	met proto-oncogene (hepatocyte growth factor receptor)	0.347976759	0.001202064
63974	<u>NEUROD6</u>	<u>neurogenic differentiation 6</u>	0.433171474	0.001616741
5816	PVALB	parvalbumin	0.457320297	0.001537504
4885	NPTX2	neuronal pentraxin II	0.486879325	0.000695301
10368	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	0.496685808	0.004499281
3208	HPCA	hippocalcin	0.504149269	0.000333079
5176	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	0.522226034	0.00019849
348980	HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	0.523810594	0.004508668
376267	RAB15	RAB15, member RAS oncogene family	0.537387889	0.001299325
3595	IL12RB2	interleukin 12 receptor, beta 2	0.538167968	0.00328347
2675	GFRA2	GDNF family receptor alpha 2	0.539054643	0.001333403
407052	MIR95	microRNA 95	0.542735216	0.001639895
161145	TMEM229B	chromosome 14 open reading frame 83	0.545710178	0.000720208
5774	PTPN3	protein tyrosine phosphatase, non-receptor type 3	0.54910964	0.001537752
23349	KIAA1045	KIAA1045	0.55244187	0.003426591
8507	ENC1	ectodermal-neural cortex (with BTB-like domain)	0.559652363	0.003288053
266722	HS6ST3	heparan sulfate 6-O-sulfotransferase 3	0.560440342	0.001753288
53335	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.56767029	0.002900497
6304	SATB1	SATB homeobox 1	0.570165581	0.001900759
64409	WBSR17	Williams-Beuren syndrome chromosome region 17	0.572117803	0.003646413
84894	LINGO1	leucine rich repeat and Ig domain containing 1	0.574936403	0.000424171
84525	HOPX	HOP homeobox	0.577157339	0.000987151
2903	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	0.581203611	0.002390123
5138	PDE2A	phosphodiesterase 2A, cGMP-stimulated	0.583469267	0.002990823
51299	NRN1	neuritin 1	0.590013553	0.001828335
125113	KRT222	keratin 222 pseudogene	0.592296133	0.004941811
1428	CRYM	crystallin, mu	0.594516424	0.002824762
646113	LINC00643	long intergenic non-protein coding RNA 643	0.59477003	0.004445109
5923	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	0.59493107	0.004924286
221692	PHACTR1	phosphatase and actin regulator 1	0.597310446	0.002464967
23467	NPTXR	neuronal pentraxin receptor	0.597403904	4.42886E-05

The set of 31 DEGs downregulated in the hippocampus of Japanese AD patients satisfying p-Value < 0.005 by two-tailed t-test and fold change smaller than 0.6 were extracted by microarray data analysis of GSE36980. They are listed with Entrez Gene ID, Gene Symbol, Gene Name, Fold Change, and p-Value. NEUROD6 is underlined.