Upregulated

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
214298_x_at	37870	septin 6	**0.0000**	**-0.0018**	-0.3994	-0.1260	**0.0148**	178 ± 8	186 ± 10	228 ± 20	279 ± 38
205056_s_at	A	protein "A"	**0.0410**	-0.3550	0.4930	**0.0523**	0.4430	430 ± 38	443 ± 116	493 ± 21	563 ± 41
205986_at	AATK	apoptosis-associated tyrosine kinase	**0.0229**	**-0.0469**	0.0979	-0.3946	**0.0212**	2012 ± 85	2454 ± 180	1958 ± 129	3320 ± 611
204177_s_at	AB026190	Kelch motif containing protein	**0.0017**	**-0.0012**	0.0959	**-0.0389**	**0.0023**	344 ± 23	396 ± 11	498 ± 32	504 ± 50
203505_at	ABCA1	ATP-binding cassette, sub-family A , member 1	**0.0009**	**-0.0024**	**0.0432**	-0.2938	**0.0084**	802 ± 124	1093 ± 209	1153 ± 127	2307 ± 574
212772_s_at	ABCA2	ATP-binding cassette, sub-family A , member 2	**0.0085**	-0.0607	0.4103	-0.1981	0.2286	2149 ± 243	2713 ± 235	3010 ± 268	3321 ± 773
203192_at	ABCB6	ATP-binding cassette, sub-family B , member 6	**0.0382**	-0.3080	-0.4790	0.4942	0.3859	381 ± 19	390 ± 40	364 ± 33	452 ± 51
203981_s_at	ABCD4	ATP-binding cassette, sub-family D , member 4	0.2780	**-0.0112**	0.4061	-0.0865	0.1593	316 ± 27	366 ± 25	341 ± 12	418 ± 54
202123_s_at	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	**0.0018**	**-0.0247**	0.4739	0.4913	0.0929	989 ± 118	1154 ± 138	1371 ± 137	1561 ± 257
210461_s_at	ABLIM1	actin binding LIM protein 1	**0.0159**	**-0.0266**	-0.4038	-0.2723	0.0624	96 ± 14	92 ± 20	132 ± 22	171 ± 31
202366_at	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	**0.0128**	**-0.0019**	0.0607	-0.1022	**0.0042**	161 ± 12	216 ± 16	253 ± 20	323 ± 53
203164_at	ACATN	acetyl-Coenzyme A transporter	0.2331	**-0.0035**	-0.3973	-0.0775	0.1115	343 ± 21	359 ± 14	382 ± 20	416 ± 28
204241_at	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	0.2933	**-0.0340**	0.3973	0.1675	0.1455	274 ± 18	279 ± 25	304 ± 39	375 ± 43
207973_x_at	ACRV1	acrosomal vesicle protein 1	0.8153	**-0.0215**	**0.0500**	-0.0634	**0.0397**	220 ± 14	280 ± 25	247 ± 23	321 ± 32
208223_s_at	ACVR1B	activin A receptor, type IB	**0.0068**	**-0.0026**	-0.4471	0.4256	**0.0045**	79 ± 13	93 ± 7	93 ± 13	167 ± 27
207953_at	AD7C-NTP	neuronal thread protein	**0.0006**	**-0.0147**	-0.3379	-0.0562	**0.0351**	200 ± 17	235 ± 14	389 ± 71	383 ± 74
205745_x_at	ADAM17	a disintegrin and metalloproteinase domain 17	**0.0227**	**-0.0249**	**-0.0299**	-0.4591	0.0691	406 ± 31	389 ± 7	481 ± 30	477 ± 29
207665_at	ADAM21	a disintegrin and metalloproteinase domain 21	0.1526	**-0.0427**	0.4568	0.4805	**0.0454**	213 ± 22	281 ± 38	244 ± 25	334 ± 35
206134_at	ADAMDEC1	ADAM-like, decysin 1	0.0693	**-0.0210**	0.2733	-0.4496	**0.0092**	55 ± 5	69 ± 8	105 ± 15	89 ± 10
220287_at	ADAMTS9	a disintegrin-like and metalloprotease	0.1781	**-0.0340**	0.2568	-0.0761	0.2487	303 ± 31	323 ± 32	329 ± 36	411 ± 55
220648_at	ADAR3	double-stranded RNA specific adenosine deaminase	0.0842	**-0.0006**	-0.1342	0.3729	**0.0069**	323 ± 56	316 ± 37	379 ± 45	545 ± 34
213217_at	ADCY2	adenylate cyclase 2	**0.0034**	**-0.0137**	0.4392	0.4272	0.0568	3323 ± 178	3330 ± 215	4453 ± 552	4496 ± 513
209320_at	ADCY3	adenylate cyclase 3	0.5995	**-0.0159**	0.1650	-0.2960	0.1846	543 ± 36	545 ± 39	622 ± 36	675 ± 74
203741_s_at	ADCY7	adenylate cyclase 7	**0.0464**	**-0.0129**	0.1193	**-0.0061**	0.1919	228 ± 33	311 ± 39	292 ± 20	340 ± 56
201753_s_at	ADD3	adducin 3	**0.0071**	**-0.0032**	**0.0287**	-0.0699	**0.0009**	4514 ± 321	5928 ± 566	8335 ± 749	7237 ± 742
209613_s_at	ADH1B	alcohol dehydrogenase IB , beta polypeptide	**0.0069**	**-0.0201**	0.2979	-0.0827	0.1403	48 ± 7	48 ± 10	79 ± 20	87 ± 16
201792_at	AEBP1	AE binding protein 1	**0.0001**	**-0.0004**	-0.1628	-0.2006	**0.0085**	293 ± 46	305 ± 48	530 ± 72	643 ± 123
218735_s_at	AF020591	zinc finger protein	**0.0143**	-0.2315	**0.0427**	-0.0670	0.3397	496 ± 25	506 ± 21	596 ± 66	564 ± 46
206840_at	AFM	afamin	**0.0374**	**-0.0301**	0.1782	0.4366	**0.0124**	98 ± 17	119 ± 18	105 ± 9	179 ± 22
221788_at	AGM1	N-acetylglucosamine-phosphate mutase	0.8955	**-0.0164**	-0.1862	**-0.0265**	0.3263	259 ± 27	313 ± 56	322 ± 39	400 ± 80
219792_at	AGMAT	agmatine ureohydrolase	0.0777	**-0.0254**	-0.3096	-0.4473	0.0649	214 ± 21	224 ± 24	229 ± 15	306 ± 36
32837_at	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2	0.2503	**-0.0078**	0.1110	-0.0851	0.0766	468 ± 24	490 ± 44	556 ± 32	637 ± 79
217419_x_at	AGRN	agrin	**0.0265**	-0.3160	0.0613	-0.3947	0.6315	554 ± 44	633 ± 80	652 ± 36	697 ± 143
205357_s_at	AGTR1	angiotensin II receptor, type 1	**0.0017**	**-0.0003**	0.1517	**-0.0147**	**0.0075**	79 ± 6	105 ± 14	122 ± 10	138 ± 14
213592_at	AGTRL1	angiotensin II receptor-like 1	**0.0444**	**-0.0459**	**0.0168**	**-0.0327**	**0.0253**	897 ± 172	1599 ± 422	3549 ± 921	2433 ± 622
212543_at	AIM1	absent in melanoma 1	0.1970	**-0.0054**	**0.0184**	-0.1655	**0.0408**	177 ± 19	215 ± 22	218 ± 13	289 ± 44
202587_s_at	AK1	adenylate kinase 1	**0.0442**	-0.0894	0.3108	-0.2714	0.4005	1489 ± 121	1525 ± 133	1768 ± 241	1863 ± 205
212172_at	AK2	adenylate kinase 2	**0.0417**	-0.1628	0.0649	-0.3466	0.1369	143 ± 15	134 ± 19	142 ± 20	243 ± 68
201674_s_at	AKAP1	A kinase anchor protein 1	**0.0301**	-0.8514	0.2896	-0.2216	0.8298	584 ± 36	634 ± 55	655 ± 65	622 ± 77
222024_s_at	AKAP13	A kinase anchor protein 13	**0.0059**	**-0.0026**	**0.0412**	**-0.0187**	**0.0097**	441 ± 42	513 ± 52	641 ± 79	869 ± 138
209534_x_at	AKAP13	A kinase anchor protein 13	**0.0005**	**-0.0310**	0.2242	-0.4919	0.0865	551 ± 31	553 ± 47	690 ± 70	746 ± 94

Probe set	**Name**	**Description**	**NFT_O**	**MMSE_O**	**NFT_I**	**MMSE_I**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
215483_at	AKAP9	A kinase anchor protein 9	0.1518	**-0.0230**	0.4615	**-0.0231**	0.0890	205 ± 45	275 ± 27	408 ± 75	354 ± 77
216594_x_at	AKR1C2	aldo-keto reductase family 1, member C2	0.3738	**-0.0407**	**-0.0361**	0.1419	0.0685	726 ± 75	639 ± 50	792 ± 22	876 ± 50
209160_at	AKR1C3	aldo-keto reductase family 1, member C3	0.3544	**-0.0094**	-0.3514	-0.4961	**0.0263**	352 ± 49	324 ± 33	575 ± 67	538 ± 98
219393_s_at	AKT3	protein kinase B, gamma	**0.0257**	-0.1261	0.0552	0.4652	0.1281	153 ± 15	199 ± 24	198 ± 24	243 ± 40
207016_s_at	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	**0.0515**	**-0.0053**	**-0.0403**	0.0805	**0.0055**	212 ± 27	157 ± 19	400 ± 70	569 ± 138
202054_s_at	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	0.5623	**-0.0027**	**-0.0002**	0.2161	**0.0473**	868 ± 46	750 ± 56	1014 ± 52	1217 ± 226
214220_s_at	ALMS1	Alstrom syndrome 1	0.0641	**-0.0127**	**0.0028**	**-0.0399**	0.1605	160 ± 17	203 ± 18	228 ± 23	252 ± 52
214221_at	ALMS1	Alstrom syndrome 1	**0.0201**	**-0.0029**	0.3626	0.3114	**0.0120**	257 ± 22	256 ± 15	313 ± 25	369 ± 35
214707_x_at	ALMS1	Alstrom syndrome 1	**0.0006**	**-0.0270**	0.4931	**-0.0255**	0.0720	701 ± 38	892 ± 69	1091 ± 117	1316 ± 304
210170_at	ALP	alpha-actinin-2-associated LIM protein	0.0597	**-0.0185**	0.0807	0.3478	0.1315	76 ± 8	102 ± 14	95 ± 6	141 ± 37
202125_s_at	ALS2CR3	ALS 2 chromosome region, candidate 3	**0.0046**	**-0.0159**	0.3688	-0.1876	**0.0515**	1607 ± 144	1664 ± 150	2244 ± 194	2186 ± 295
203002_at	AMOTL2	angiomotin like 2	**0.0196**	-0.0580	0.1666	-0.1487	0.2241	847 ± 58	1017 ± 115	1077 ± 60	1222 ± 231
207992_s_at	AMPD3	adenosine monophosphate deaminase	**0.0317**	**-0.0129**	0.1057	0.3435	**0.0281**	569 ± 37	683 ± 134	645 ± 52	933 ± 100
205609_at	ANGPT1	angiopoietin 1	0.0907	**-0.0043**	0.1258	**-0.0190**	0.1030	346 ± 42	388 ± 76	523 ± 89	556 ± 62
205608_s_at	ANGPT1	angiopoietin 1	**0.0010**	**-0.0019**	-0.4103	0.3450	**0.0057**	301 ± 35	294 ± 37	363 ± 26	469 ± 38
213004_at	ANGPTL2	angiopoietin-like 2	**0.0000**	**-0.0393**	**0.0122**	-0.1088	**0.0460**	98 ± 8	133 ± 15	161 ± 8	173 ± 35
201305_x_at	ANP32B	acidic nuclear p32 family, member B	**0.0029**	**-0.0014**	0.2229	**-0.0488**	**0.0179**	720 ± 86	850 ± 111	1215 ± 197	1253 ± 114
201306_s_at	ANP32B	acidic nuclear p32 family, member B	**0.0012**	**-0.0029**	-0.4955	-0.2924	**0.0171**	4717 ± 455	4986 ± 670	5555 ± 604	8019 ± 1168
201012_at	ANXA1	annexin A1	**0.0169**	**-0.0043**	0.3733	-0.2274	0.0704	309 ± 36	327 ± 48	654 ± 176	914 ± 296
201590_x_at	ANXA2	annexin A2	0.0805	**-0.0024**	0.2680	-0.4418	**0.0493**	1027 ± 111	1161 ± 103	1347 ± 154	1564 ± 152
213503_x_at	ANXA2	annexin A2	0.1193	**-0.0147**	**-0.0311**	0.4328	0.0689	1001 ± 119	878 ± 75	1011 ± 143	1423 ± 200
210427_x_at	ANXA2	annexin A2	**0.0039**	**-0.0007**	0.2420	-0.0920	**0.0347**	951 ± 63	1032 ± 98	1252 ± 160	1456 ± 144
207064_s_at	AOC2	amine oxidase, copper containing 2	0.1172	**-0.0414**	0.0591	-0.2237	**0.0121**	216 ± 16	286 ± 25	225 ± 16	335 ± 43
200845_s_at	AOP2	acidic calcium-independent phospholipase A2	0.0819	**-0.0387**	**0.0292**	-0.4848	**0.0547**	2495 ± 180	2674 ± 239	4147 ± 588	3524 ± 606
205423_at	AP1B1	adaptor-related protein complex 1, beta 1 subunit	**0.0366**	-0.1486	-0.3909	-0.2217	0.2246	340 ± 35	314 ± 32	424 ± 34	407 ± 64
202398_at	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	**0.0262**	**-0.0250**	-0.4886	-0.4378	0.1517	70 ± 13	81 ± 20	88 ± 23	134 ± 24
215148_s_at	APBA3	a beta precursor protein-binding, family A, member 3	**0.0481**	-0.1362	-0.2320	0.2067	0.1586	469 ± 41	464 ± 73	479 ± 49	663 ± 108
218555_at	APC2	anaphase-promoting complex subunit 2	**0.0418**	-0.0709	0.1166	0.1431	0.0825	620 ± 120	544 ± 79	592 ± 41	1054 ± 246
220237_at	APG3	autophagy Apg3p/Aut1p-like	0.0750	**-0.0209**	**0.0384**	-0.1811	**0.0440**	60 ± 7	50 ± 9	91 ± 10	127 ± 38
204902_s_at	Apg4B	KIAA0943 protein	0.6193	**-0.0411**	-0.1332	-0.1610	0.0855	353 ± 38	304 ± 54	328 ± 25	470 ± 63
207175_at	APM1	adipose most abundant gene transcript 1	0.0615	**-0.0426**	0.4119	0.3825	0.3306	83 ± 12	91 ± 19	111 ± 19	133 ± 32
207158_at	APOBEC1	apolipoprotein B mRNA editing enzyme, catalytic 1	0.2954	**-0.0074**	-0.2239	-0.2207	**0.0451**	157 ± 27	160 ± 29	155 ± 8	263 ± 43
213553_x_at	APOC1	apolipoprotein C-I	0.2519	**-0.0489**	**0.0396**	-0.3988	0.1150	1261 ± 161	1713 ± 237	1606 ± 135	1865 ± 143
206738_at	APOC4	apolipoprotein C-IV	**0.0014**	**-0.0267**	**0.0024**	-0.2108	**0.0482**	179 ± 11	235 ± 25	281 ± 13	305 ± 60
221013_s_at	APOL2	apolipoprotein L, 2	0.1087	**-0.0013**	0.0910	**-0.0378**	**0.0066**	162 ± 20	180 ± 13	256 ± 17	250 ± 30
211277_x_at	APP	a beta precursor protein	**0.0065**	**-0.0024**	**0.0521**	**-0.0046**	**0.0319**	345 ± 18	385 ± 28	458 ± 24	573 ± 108
218527_at	APTX	aprataxin	**0.0130**	-0.3520	-0.3766	0.4755	0.8193	700 ± 39	688 ± 57	730 ± 57	761 ± 79
209047_at	AQP1	aquaporin 1	0.1381	**-0.0152**	0.4508	-0.3638	0.1509	3845 ± 804	3974 ± 762	5294 ± 1026	6422 ± 799
216219_at	AQP6	aquaporin 6, kidney specific	0.1343	**-0.0479**	0.2267	-0.1735	0.1153	339 ± 30	340 ± 18	349 ± 40	482 ± 77
203025_at	ARD1	ARD1 homolog, N-acetyltransferase	**0.0212**	-0.0851	0.3202	-0.4038	0.2991	525 ± 41	498 ± 49	577 ± 55	692 ± 126
214182_at	ARF6	ADP-ribosylation factor 6	0.1885	**-0.0027**	0.3874	**-0.0262**	0.0753	143 ± 10	128 ± 26	181 ± 23	190 ± 11
217888_s_at	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	0.2345	**-0.0486**	0.1206	**-0.0101**	0.3263	602 ± 43	658 ± 36	744 ± 76	735 ± 84

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
203945_at	ARG2	arginase, type II	**0.0321**	**-0.0063**	0.2004	-0.4407	**0.0071**	320 ± 20	355 ± 24	371 ± 20	492 ± 57
221790_s_at	ARH	LDL receptor adaptor protein	**0.0246**	-0.0754	-0.3521	0.4210	0.1923	260 ± 42	204 ± 42	339 ± 53	460 ± 150
57082_at	ARH	LDL receptor adaptor protein	**0.0483**	**-0.0506**	-0.3702	0.3490	0.0559	422 ± 44	473 ± 114	441 ± 66	799 ± 173
202117_at	ARHGAP1	Rho GTPase activating protein 1	**0.0243**	-0.0643	0.1319	0.3211	0.1404	2789 ± 229	3196 ± 376	3283 ± 271	4023 ± 573
206167_s_at	ARHGAP6	Rho GTPase activating protein 6	0.1337	**-0.0476**	0.1965	0.2431	0.1326	348 ± 31	377 ± 58	457 ± 20	486 ± 66
216620_s_at	ARHGEF10	Rho guanine nucleotide exchange factor 10	**0.0020**	**-0.0082**	0.2725	-0.4057	**0.0305**	654 ± 67	765 ± 91	946 ± 70	921 ± 69
217348_x_at	ARHGEF15	Rho guanine nucleotide exchange factor 15	0.5720	**-0.0164**	**0.0480**	**-0.0151**	0.0821	199 ± 18	235 ± 31	226 ± 24	295 ± 30
208009_s_at	ARHGEF16	Rho guanine exchange factor 16	**0.0199**	**-0.0043**	0.2112	-0.2052	**0.0149**	173 ± 25	176 ± 17	276 ± 27	291 ± 46
201230_s_at	ARIH2	ariadne homolog 2	0.2864	**-0.0309**	-0.3318	0.2833	0.0939	932 ± 32	906 ± 52	958 ± 55	1129 ± 107
201954_at	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	**0.0177**	**-0.0194**	**0.0218**	-0.2238	0.1227	394 ± 26	492 ± 59	536 ± 56	553 ± 53
222047_s_at	ARS2	arsenate resistance protein ARS2	**0.0099**	**-0.0053**	0.4491	0.4489	0.0706	1624 ± 85	1755 ± 149	2029 ± 163	2187 ± 203
210385_s_at	ARTS-1	type 1 TNF receptor shedding aminopeptidase regulator	0.1149	**-0.0082**	0.3852	**-0.0417**	0.1942	187 ± 26	199 ± 29	215 ± 10	267 ± 36
213702_x_at	ASAH1	N-acylsphingosine amidohydrolase 1	0.6440	**-0.0304**	0.4006	-0.4250	0.2972	5013 ± 132	4860 ± 196	5092 ± 270	5595 ± 425
212818_s_at	ASB1	ankyrin repeat and SOCS box-containing 1	0.1412	**-0.0108**	0.3778	0.3963	0.0806	821 ± 40	783 ± 30	853 ± 51	999 ± 91
209988_s_at	ASCL1	achaete-scute complex-like 1	0.3369	**-0.0183**	0.3420	-0.1386	0.1160	772 ± 52	764 ± 56	984 ± 92	969 ± 108
209987_s_at	ASCL1	achaete-scute complex-like 1	**0.0416**	**-0.0042**	**0.0197**	-0.1938	**0.0184**	353 ± 37	537 ± 111	502 ± 78	832 ± 153
204244_s_at	ASK	activator of S phase kinase	0.8717	**-0.0304**	**0.0294**	-0.2094	0.3078	107 ± 7	97 ± 10	110 ± 7	126 ± 14
208033_s_at	ATBF1	AT-binding transcription factor 1	**0.0526**	**-0.0240**	0.0612	-0.0685	**0.0415**	140 ± 25	176 ± 20	243 ± 23	206 ± 33
204998_s_at	ATF5	activating transcription factor 5	**0.0079**	-0.0980	0.1389	0.4472	0.0816	216 ± 19	280 ± 46	269 ± 10	320 ± 29
212096_s_at	ATIP1	AT2 receptor-interacting protein 1	0.3979	**-0.0223**	**-0.0549**	-0.3781	0.2176	2652 ± 258	2649 ± 463	3344 ± 306	3342 ± 227
213238_at	ATP10D	ATPase, Class V, type 10D	0.1324	**-0.0307**	**0.0384**	-0.2089	0.2592	289 ± 19	297 ± 28	317 ± 35	370 ± 39
214149_s_at	ATP6V0E	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e	0.0989	**-0.0102**	-0.2467	-0.0745	0.0973	344 ± 27	345 ± 61	368 ± 6	493 ± 59
214150_x_at	ATP6V0E	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e	**0.0086**	**-0.0001**	-0.4607	-0.1644	**0.0069**	3051 ± 283	2997 ± 267	3623 ± 256	4448 ± 364
214923_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	**0.0084**	**-0.0074**	0.1493	**-0.0531**	**0.0149**	340 ± 17	392 ± 39	381 ± 22	536 ± 72
205197_s_at	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	0.1930	**-0.0192**	0.2878	0.4453	**0.0270**	122 ± 19	115 ± 22	111 ± 12	195 ± 28
205198_s_at	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	**0.0026**	**-0.0015**	0.1093	-0.0686	**0.0141**	232 ± 19	276 ± 21	297 ± 17	365 ± 47
214594_x_at	ATP8B1	ATPase, Class I, type 8B, member 1	**0.0051**	**-0.0400**	0.2453	**-0.0306**	0.0561	1259 ± 205	1462 ± 119	2399 ± 338	2176 ± 557
206251_s_at	AVPR1A	arginine vasopressin receptor 1A	**0.0103**	**-0.0048**	**-0.0548**	0.2142	**0.0134**	54 ± 4	52 ± 8	68 ± 11	101 ± 17
209309_at	AZGP1	alpha-2-glycoprotein 1, zinc	0.1755	**-0.0020**	-0.1857	-0.1359	0.0582	148 ± 32	153 ± 22	250 ± 71	307 ± 30
209413_at	B4GALT2	1,4- galactosyltransferase, polypeptide 2	**0.0150**	-0.2865	-0.3149	**0.0217**	0.2782	637 ± 30	571 ± 77	710 ± 42	764 ± 116
220974_x_at	BA108L7.2	similar to rat tricarboxylate carrier-like protein	**0.0450**	-0.8301	0.1331	0.4391	0.1871	1030 ± 60	1094 ± 91	1268 ± 92	1085 ± 83
221234_s_at	BACH2	basic leucine zipper transcription factor 2	0.1147	**-0.0124**	0.4399	-0.4112	0.1052	314 ± 25	350 ± 36	366 ± 24	424 ± 38
209364_at	BAD	BCL2-antagonist of cell death	**0.0183**	**-0.0380**	0.2296	0.2838	0.2043	544 ± 37	561 ± 60	680 ± 49	749 ± 140
202666_s_at	BAF53A	BAF53	0.6228	**-0.0222**	-0.4574	-0.1521	0.2152	235 ± 30	269 ± 26	314 ± 41	314 ± 22
202387_at	BAG1	BCL2-associated athanogene	0.1238	**-0.0437**	0.1509	**-0.0545**	0.2868	746 ± 29	745 ± 68	767 ± 58	876 ± 56
213105_s_at	BAIAP3	BAI1-associated protein 3	0.1084	**-0.0263**	**0.0289**	-0.4828	0.1003	312 ± 19	353 ± 48	382 ± 25	433 ± 42
219966_x_at	BANP	BTG3 associated nuclear protein	**0.0530**	**-0.0020**	-0.1251	-0.3183	**0.0276**	525 ± 24	452 ± 75	495 ± 59	801 ± 140
217986_s_at	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	0.4382	**-0.0466**	-0.1131	-0.3254	0.5147	191 ± 29	174 ± 24	201 ± 23	238 ± 37
201353_s_at	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	**0.0022**	-0.1658	-0.0797	-0.1746	0.3146	275 ± 31	246 ± 16	376 ± 41	362 ± 103
203080_s_at	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	**0.0015**	**-0.0049**	-0.2754	-0.2383	0.0749	1215 ± 117	1277 ± 148	1528 ± 109	1748 ± 230
214139_at	BCAA	RBP1-like protein	0.8617	**-0.0325**	-0.4738	-0.3532	0.2877	133 ± 12	139 ± 19	149 ± 13	178 ± 24
221623_at	BCAN	chondroitin sulfate proteoglycan BEHAB/brevican	**0.0537**	**-0.0052**	-0.4303	-0.4111	0.0674	378 ± 29	374 ± 31	496 ± 63	529 ± 58

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
203576_at	BCAT2	branched chain aminotransferase 2, mitochondrial	**0.0107**	**-0.0089**	0.4821	-0.0728	0.1003	428 ± 50	453 ± 50	538 ± 35	585 ± 56
204872_at	BCE-1	BCE-1 protein	0.0987	**-0.0433**	-0.1150	-0.2518	0.3342	2317 ± 176	2238 ± 310	2563 ± 176	2812 ± 276
203685_at	BCL2	B-cell CLL/lymphoma 2	**0.0206**	**-0.0003**	-0.1509	0.2748	**0.0021**	992 ± 105	821 ± 72	1193 ± 141	1514 ± 79
203140_at	BCL6	B-cell CLL/lymphoma 6	0.0984	**-0.0029**	-0.1477	-0.1755	0.0958	3035 ± 407	3028 ± 315	3862 ± 668	4927 ± 811
210679_x_at	BCL7A	B-cell CLL/lymphoma 7A	**0.0250**	**-0.0016**	**0.0430**	-0.0731	**0.0023**	744 ± 103	784 ± 87	1431 ± 127	1264 ± 199
218056_at	BFAR	bifunctional apoptosis regulator	**0.0001**	**-0.0056**	-0.3329	0.4813	**0.0177**	425 ± 21	395 ± 9	490 ± 39	590 ± 71
206956_at	BGLAP	bone gamma-carboxyglutamate protein	**0.0015**	-0.1275	0.2620	-0.1442	0.4224	135 ± 18	150 ± 10	174 ± 25	190 ± 40
213905_x_at	BGN	biglycan	0.1015	**-0.0428**	0.1989	-0.4413	0.1359	558 ± 72	738 ± 130	666 ± 74	892 ± 121
201261_x_at	BGN	biglycan	**0.0134**	**-0.0022**	**0.0318**	**-0.0015**	**0.0133**	424 ± 33	557 ± 32	544 ± 47	717 ± 94
203278_s_at	BHC80	BRAF35/HDAC2 complex	0.0622	**-0.0421**	**-0.0035**	0.2633	**0.0148**	568 ± 62	407 ± 24	683 ± 70	666 ± 43
219902_at	BHMT2	betaine-homocysteine methyltransferase 2	**0.0027**	-0.7079	0.4322	0.0813	0.4214	75 ± 11	94 ± 22	131 ± 28	104 ± 31
214716_at	BIKE	BMP-2 inducible kinase	**0.0251**	-0.5080	0.1746	-0.3795	0.4249	96 ± 10	98 ± 7	122 ± 7	115 ± 21
202931_x_at	BIN1	bridging integrator 1	**0.0006**	-0.1185	0.2379	-0.4332	0.2381	2447 ± 132	3112 ± 625	3191 ± 371	4028 ± 829
210201_x_at	BIN1	bridging integrator 1	**0.0009**	-0.1085	0.2134	0.3594	0.1475	4504 ± 315	5412 ± 892	5137 ± 456	7213 ± 1462
214439_x_at	BIN1	bridging integrator 1	**0.0121**	**-0.0210**	0.2010	-0.3430	0.0882	2478 ± 189	2989 ± 282	3309 ± 329	4413 ± 963
214643_x_at	BIN1	bridging integrator 1	**0.0007**	**-0.0351**	0.3823	-0.4420	0.0697	889 ± 59	1098 ± 196	1079 ± 142	1619 ± 310
222199_s_at	BIN3	bridging integrator 3	**0.0243**	-0.1004	-0.0655	-0.1899	**0.0066**	417 ± 14	384 ± 39	553 ± 44	463 ± 26
204861_s_at	BIRC1	baculoviral IAP repeat-containing 1	**0.0089**	**-0.0287**	0.0822	-0.2118	0.0917	235 ± 39	308 ± 38	323 ± 52	439 ± 85
202076_at	BIRC2	baculoviral IAP repeat-containing 2	0.1764	**-0.0004**	-0.2373	-0.2328	**0.0047**	1322 ± 44	1230 ± 81	1333 ± 92	1672 ± 103
219520_s_at	BM042	uncharacterized bone marrow protein BM042	0.1508	**-0.0118**	0.3688	-0.1907	0.0557	675 ± 74	871 ± 109	841 ± 46	1007 ± 98
208292_at	BMP10	bone morphogenetic protein 10	0.1511	**-0.0399**	**-0.0343**	0.2072	0.1133	182 ± 18	157 ± 14	198 ± 18	233 ± 30
213578_at	BMPR1A	bone morphogenetic protein receptor, type IA	0.1070	**-0.0081**	0.4084	-0.2047	0.1331	558 ± 47	601 ± 38	716 ± 85	769 ± 94
215016_x_at	BPAG1	bullous pemphigoid antigen 1, 230/240kDa	**0.0534**	**-0.0039**	-0.4014	-0.2492	**0.0282**	5282 ± 187	5147 ± 325	6388 ± 444	6107 ± 310
212254_s_at	BPAG1	bullous pemphigoid antigen 1, 230/240kDa	0.0744	**-0.0088**	0.3068	-0.0936	0.0654	5158 ± 301	5655 ± 403	6553 ± 553	6347 ± 288
220142_at	BRAL1	brain link protein-1	**0.0405**	**-0.0038**	-0.1426	0.3367	**0.0011**	510 ± 40	372 ± 71	446 ± 41	888 ± 149
213473_at	BRAP	BRCA1 associated protein	**0.0364**	**-0.0024**	**0.0192**	**-0.0153**	**0.0087**	177 ± 16	231 ± 19	241 ± 11	253 ± 17
41512_at	BRAP	BRCA1 associated protein	**0.0202**	**-0.0068**	0.0881	-0.1793	**0.0154**	198 ± 6	204 ± 14	250 ± 18	259 ± 22
204531_s_at	BRCA1	breast cancer 1, early onset	**0.0108**	-0.0747	0.2649	0.3185	0.1295	94 ± 11	128 ± 23	149 ± 22	154 ± 24
204520_x_at	BRD1	bromodomain containing 1	0.1618	**-0.0103**	0.2763	**-0.0170**	**0.0053**	556 ± 49	617 ± 46	776 ± 16	675 ± 36
214911_s_at	BRD2	bromodomain containing 2	**0.0253**	**-0.0489**	-0.4998	0.4433	0.2672	1066 ± 126	1052 ± 94	1268 ± 111	1341 ± 130
203825_at	BRD3	bromodomain containing 3	**0.0019**	**-0.0499**	0.1745	-0.3258	0.1166	1333 ± 129	1593 ± 221	2030 ± 210	2257 ± 525
202102_s_at	BRD4	bromodomain containing 4	**0.0008**	-0.2748	0.2483	0.2147	0.3608	1564 ± 94	1513 ± 146	1805 ± 190	1884 ± 237
202103_at	BRD4	bromodomain containing 4	**0.0042**	**-0.0008**	0.4088	-0.2915	**0.0054**	358 ± 36	338 ± 19	434 ± 27	520 ± 46
204481_at	BRPF1	bromodomain and PHD finger containing, 1	**0.0119**	**-0.0021**	0.3547	-0.1542	**0.0183**	256 ± 38	308 ± 40	316 ± 25	456 ± 63
207369_at	BRS3	bombesin-like receptor 3	0.0584	**-0.0210**	**0.0075**	-0.0861	0.0734	119 ± 14	145 ± 15	163 ± 26	210 ± 32
203542_s_at	BTEB1	basic transcription element binding protein 1	**0.0045**	**-0.0004**	-0.3359	-0.0642	**0.0033**	493 ± 48	485 ± 59	611 ± 49	857 ± 117
201236_s_at	BTG2	BTG family, member 2	0.0738	**-0.0134**	-0.3544	-0.4104	0.0727	772 ± 86	791 ± 44	809 ± 50	1051 ± 114
205548_s_at	BTG3	BTG family, member 3	0.3501	**-0.0034**	-0.2933	-0.4369	**0.0160**	603 ± 48	641 ± 84	620 ± 48	975 ± 137
213134_x_at	BTG3	BTG family, member 3	0.1027	**-0.0115**	0.4256	-0.1352	**0.0321**	625 ± 28	826 ± 69	790 ± 80	977 ± 118
215425_at	BTG3	BTG family, member 3	**0.0290**	**-0.0044**	0.0825	0.4505	**0.0091**	92 ± 6	120 ± 15	135 ± 16	175 ± 26
204821_at	BTN3A3	butyrophilin, subfamily 3, member A3	0.4096	**-0.0381**	0.4254	-0.1324	0.3087	96 ± 18	93 ± 20	127 ± 16	146 ± 33
217207_s_at	BTNL3	butyrophilin-like 3	**0.0425**	**-0.0474**	-0.3797	-0.1285	0.2296	302 ± 24	303 ± 34	323 ± 24	391 ± 48

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
216091_s_at	BTRC	beta-transducin repeat containing	0.1195	**-0.0202**	-0.2478	0.4764	0.0933	197 ± 18	189 ± 11	201 ± 13	247 ± 20
202096_s_at	BZRP	benzodiazapine receptor	0.3296	**-0.0440**	-0.3461	-0.2356	0.4039	627 ± 65	620 ± 74	674 ± 61	767 ± 59
217928_s_at	C11orf23	chromosome 11 open reading frame 23	0.5503	**-0.0417**	-0.2945	0.4476	0.1577	617 ± 42	520 ± 25	624 ± 30	685 ± 69
204073_s_at	C11orf9	chromosome 11 open reading frame 9	**0.0046**	**-0.0116**	-0.4375	0.3976	0.0567	1722 ± 260	1813 ± 253	2488 ± 293	3448 ± 814
218374_s_at	C12orf4	chromosome 12 open reading frame 4	0.3940	**-0.0368**	0.2320	-0.4711	0.1436	343 ± 13	323 ± 24	342 ± 17	403 ± 37
218183_at	C16orf5	chromosome 16 open reading frame 5	**0.0024**	**-0.0003**	0.4460	-0.2017	**0.0115**	307 ± 23	318 ± 27	368 ± 25	505 ± 75
209574_s_at	C18orf1	chromosome 18 open reading frame 1	0.8664	**-0.0129**	0.4174	-0.4672	**0.0309**	341 ± 12	330 ± 28	301 ± 13	479 ± 78
213390_at	C19orf7	chromosome 19 open reading frame 7	**0.0015**	-0.1056	0.1669	-0.4800	0.2720	995 ± 72	1134 ± 143	1286 ± 121	1340 ± 210
209883_at	C1orf17	chromosome 1 open reading frame 17	0.3038	**-0.0320**	0.4297	0.3759	0.2095	1089 ± 88	1156 ± 104	1180 ± 78	1396 ± 143
220992_s_at	C1orf25	chromosome 1 open reading frame 25	0.7491	**-0.0408**	0.3573	**-0.0354**	0.1346	177 ± 12	194 ± 27	175 ± 8	234 ± 24
212067_s_at	C1R	complement component 1, r subcomponent	0.7171	**-0.0331**	-0.1028	0.3522	0.2474	287 ± 49	260 ± 41	283 ± 27	390 ± 58
208747_s_at	C1S	complement component 1, s subcomponent	**0.0210**	**-0.0118**	-0.1632	-0.1282	**0.0419**	442 ± 55	424 ± 54	793 ± 167	739 ± 120
207482_at	C20orf10	chromosome 20 open reading frame 10	**0.0423**	**-0.0337**	0.1532	0.3122	**0.0355**	149 ± 16	146 ± 19	168 ± 12	274 ± 61
206567_s_at	C20orf104	chromosome 20 open reading frame 104	**0.0457**	-0.2828	0.4684	0.3248	0.3914	610 ± 43	643 ± 89	764 ± 60	682 ± 81
209422_at	C20orf104	chromosome 20 open reading frame 104	0.1491	**-0.0113**	**0.0243**	**-0.0391**	0.1277	882 ± 55	1015 ± 77	1019 ± 38	1102 ± 76
209020_at	C20orf111	chromosome 20 open reading frame 111	0.1097	**-0.0411**	-0.2008	0.3022	0.1830	392 ± 14	373 ± 24	419 ± 30	461 ± 42
208880_s_at	C20orf14	chromosome 20 open reading frame 14	**0.0087**	-0.7205	**0.0539**	0.4275	0.6000	304 ± 26	385 ± 67	342 ± 28	421 ± 112
218010_x_at	C20orf149	chromosome 20 open reading frame 149	**0.0490**	**-0.0527**	0.1466	-0.4514	0.1982	683 ± 80	738 ± 77	806 ± 27	979 ± 168
210357_s_at	C20orf16	chromosome 20 open reading frame 16	**0.0002**	**-0.0030**	0.2860	-0.0934	**0.0111**	904 ± 84	1144 ± 80	1239 ± 89	1440 ± 166
207713_s_at	C20orf18	chromosome 20 open reading frame 18	**0.0038**	**-0.0159**	0.2209	-0.4076	**0.0437**	517 ± 35	540 ± 47	705 ± 48	755 ± 115
221827_at	C20orf18	chromosome 20 open reading frame 18	**0.0144**	**-0.0221**	**0.0456**	0.2796	**0.0226**	430 ± 28	456 ± 22	456 ± 64	622 ± 19
218586_at	C20orf20	chromosome 20 open reading frame 20	**0.0107**	-0.4800	0.4614	0.4958	0.5419	379 ± 37	393 ± 45	458 ± 40	442 ± 61
219706_at	C20orf29	chromosome 20 open reading frame 29	0.4606	**-0.0206**	0.1750	-0.3770	0.0785	485 ± 19	480 ± 41	504 ± 31	628 ± 71
218089_at	C20orf4	chromosome 20 open reading frame 4	0.1009	**-0.0044**	-0.4318	-0.3579	**0.0095**	622 ± 24	666 ± 40	680 ± 36	833 ± 62
218145_at	C20orf97	chromosome 20 open reading frame 97	**0.0014**	**-0.0047**	0.1287	-0.3686	**0.0052**	327 ± 21	340 ± 31	314 ± 32	492 ± 56
203996_s_at	C21orf2	chromosome 21 open reading frame 2	**0.0190**	**-0.0308**	-0.3788	0.3050	**0.0283**	274 ± 27	257 ± 26	298 ± 18	412 ± 64
220543_at	C21orf62	chromosome 21 open reading frame 62	0.1357	**-0.0059**	0.4862	0.1216	**0.0030**	125 ± 17	124 ± 14	127 ± 12	217 ± 26
220941_s_at	C21orf91	chromosome 21 open reading frame 91	**0.0011**	**-0.0087**	-0.1983	-0.3222	**0.0057**	153 ± 26	151 ± 18	155 ± 11	302 ± 56
204402_at	C22orf3	chromosome 22 open reading frame 3	**0.0378**	-0.1521	0.3266	-0.3165	0.5188	148 ± 12	152 ± 21	172 ± 20	184 ± 21
217622_at	C22orf3	chromosome 22 open reading frame 3	**0.0401**	**-0.0221**	0.0616	**-0.0150**	0.0752	120 ± 10	142 ± 29	204 ± 35	241 ± 52
216305_s_at	C2orf3	chromosome 2 open reading frame 3	0.1514	**-0.0269**	0.0619	-0.2066	0.1066	193 ± 12	256 ± 30	256 ± 20	278 ± 36
201298_s_at	C2orf6	chromosome 2 open reading frame 6	**0.0060**	-0.1575	-0.2365	-0.2771	0.6045	307 ± 23	271 ± 37	304 ± 48	356 ± 60
214428_x_at	C4A	complement component 4A	**0.0169**	**-0.0024**	-0.4946	-0.1759	**0.0361**	2009 ± 348	2233 ± 417	2694 ± 281	3836 ± 692
208451_s_at	C4B	complement component 4B	**0.0417**	**-0.0115**	0.4895	0.3056	**0.0518**	2358 ± 463	1849 ± 298	2910 ± 305	3553 ± 440
205500_at	C5	complement component 5	**0.0406**	-0.1233	0.2302	**-0.0336**	0.2194	183 ± 14	212 ± 19	240 ± 21	243 ± 38
48031_r_at	C5orf4	chromosome 5 open reading frame 4	**0.0116**	**-0.0182**	**0.0422**	-0.3703	**0.0303**	543 ± 35	755 ± 125	768 ± 54	975 ± 157
221766_s_at	C6orf37	chromosome 6 open reading frame 37	0.0579	**-0.0121**	0.1136	**-0.0463**	0.1911	184 ± 31	240 ± 41	285 ± 32	304 ± 57
208469_s_at	C6orf8	chromosome 6 open reading frame 8	**0.0141**	-0.2490	0.0712	0.4707	0.4058	138 ± 19	192 ± 46	190 ± 24	245 ± 74
204265_s_at	C6orf9	chromosome 6 open reading frame 9	**0.0431**	**-0.0024**	0.0892	**-0.0045**	**0.0429**	408 ± 44	471 ± 31	547 ± 41	622 ± 83
202992_at	C7	complement component 7	**0.0004**	**-0.0114**	0.0940	-0.0771	0.1185	65 ± 12	76 ± 15	117 ± 28	128 ± 28
212247_at	C7orf14	chromosome 7 open reading frame 14	0.0838	**-0.0103**	-0.3710	-0.1692	**0.0079**	277 ± 18	330 ± 27	289 ± 13	388 ± 29
204024_at	C8orf1	chromosome 8 open reading frame 1	**0.0076**	**-0.0220**	0.1528	-0.1242	**0.0526**	251 ± 15	259 ± 33	259 ± 26	347 ± 30

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
221543_s_at	C8orf2	chromosome 8 open reading frame 2	0.1488	**-0.0194**	**0.0309**	-0.1725	0.2136	763 ± 76	839 ± 29	884 ± 30	938 ± 58
222166_at	C9orf16	chromosome 9 open reading frame 16	-0.8040	**-0.0361**	0.3006	0.4738	0.1189	131 ± 9	112 ± 12	122 ± 9	163 ± 24
212848_s_at	C9orf3	chromosome 9 open reading frame 3	**0.0365**	**-0.0171**	0.3396	0.4588	0.1084	545 ± 55	648 ± 106	724 ± 73	819 ± 71
61874_at	C9orf7	chromosome 9 open reading frame 7	0.1132	**-0.0001**	0.0699	-0.0607	**0.0067**	678 ± 33	815 ± 53	848 ± 36	1030 ± 106
205949_at	CA1	carbonic anhydrase I	0.1709	**-0.0334**	-0.4004	-0.3545	0.1119	170 ± 23	165 ± 11	170 ± 19	239 ± 34
218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex like	**0.0030**	-0.0629	-0.2588	-0.2545	0.1607	647 ± 36	722 ± 51	722 ± 51	836 ± 84
210770_s_at	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A	**0.0296**	-0.1755	-0.3549	**0.0190**	0.0739	842 ± 86	600 ± 108	824 ± 171	1334 ± 295
210380_s_at	CACNA1G	calcium channel, voltage-dependent, alpha 1G subunit	**0.0359**	-0.6883	0.3657	-0.1288	0.9121	110 ± 16	110 ± 31	129 ± 18	118 ± 26
205525_at	CALD1	caldesmon 1	0.0677	**-0.0174**	0.3032	-0.2790	0.1691	245 ± 29	310 ± 40	336 ± 33	363 ± 55
214880_x_at	CALD1	caldesmon 1	0.1284	**-0.0197**	**0.0449**	**-0.0125**	0.1927	103 ± 8	146 ± 15	162 ± 10	160 ± 42
201616_s_at	CALD1	caldesmon 1	**0.0071**	**-0.0215**	-0.1260	-0.1370	0.1422	152 ± 20	161 ± 8	224 ± 25	203 ± 36
213956_at	CAP350	centrosome-associated protein 350	0.0676	**-0.0213**	0.0893	**-0.0111**	**0.0257**	326 ± 44	357 ± 29	624 ± 83	501 ± 116
204373_s_at	CAP350	centrosome-associated protein 350	**0.0158**	**-0.0069**	0.1450	**-0.0194**	0.0557	548 ± 44	661 ± 46	722 ± 99	809 ± 56
210944_s_at	CAPN3	calpain 3,	**0.0344**	-0.0585	0.4311	-0.3479	0.2365	1953 ± 281	2232 ± 473	2295 ± 305	3153 ± 613
212707_s_at	CAPRI	Ca2+-promoted Ras inactivator	**0.0063**	-0.1193	0.0917	-0.0768	0.2382	213 ± 17	286 ± 28	357 ± 64	341 ± 84
212512_s_at	CARM1	coactivator-associated arginine methyltransferase-1	**0.0025**	-0.1770	0.2979	**0.0375**	0.2178	825 ± 28	888 ± 121	966 ± 109	1186 ± 210
211208_s_at	CASK	calcium/calmodulin-dependent serine protein kinase	**0.0015**	**-0.0229**	0.3791	-0.4989	0.1543	625 ± 45	619 ± 53	711 ± 59	780 ± 62
61297_at	CASKIN2	cask-interacting protein 2	**0.0358**	-0.1118	0.3470	-0.1709	**0.0343**	185 ± 25	211 ± 9	296 ± 25	241 ± 38
202763_at	CASP3	caspase 3, apoptosis-related cysteine protease	0.4648	**-0.0042**	**-0.0319**	0.2221	**0.0154**	244 ± 13	214 ± 14	256 ± 21	335 ± 43
213596_at	CASP4	caspase 4, apoptosis-related cysteine protease	**0.0155**	**-0.0002**	0.1019	-0.0769	**0.0099**	123 ± 9	146 ± 21	159 ± 14	206 ± 19
211464_x_at	CASP6	caspase 6, apoptosis-related cysteine protease	**0.0005**	**-0.0328**	0.2753	**-0.0058**	0.1579	104 ± 17	143 ± 17	189 ± 36	206 ± 58
210775_x_at	CASP9	caspase 9, apoptosis-related cysteine protease	**0.0351**	**-0.0070**	-0.1949	-0.1976	**0.0296**	524 ± 29	542 ± 27	530 ± 26	649 ± 41
209701_at	CAST	calpastatin	**0.0467**	-0.1267	0.3898	0.3006	0.1231	173 ± 17	177 ± 20	162 ± 16	256 ± 53
212586_at	CAST	calpastatin	0.2290	**-0.0017**	0.0618	**-0.0001**	**0.0236**	947 ± 34	1222 ± 104	1143 ± 61	1316 ± 113
202370_s_at	CBFB	core-binding factor, beta subunit	0.1357	**-0.0129**	-0.1676	0.4665	0.2039	2103 ± 223	2117 ± 130	2462 ± 234	2647 ± 193
209682_at	CBLB	Cas-Br-M ecotropic retroviral transforming sequence b	**0.0047**	**-0.0019**	-0.2344	0.4864	**0.0211**	271 ± 27	255 ± 13	308 ± 25	384 ± 43
206559_x_at	CCND1	cyclin D1	**0.0377**	-0.1808	-0.2346	-0.4917	0.4216	8340 ± 1675	18791 ± 961	418 ± 1318	0668 ± 1887
201700_at	CCND3	cyclin D3	**0.0115**	**-0.0099**	0.4261	0.4103	**0.0202**	1297 ± 62	1238 ± 81	1306 ± 110	1645 ± 106
208656_s_at	CCNI	cyclin I	0.1799	**-0.0493**	-0.0681	0.4341	0.1501	5148 ± 233	5220 ± 474	5192 ± 262	6191 ± 455
220671_at	CCRN4L	CCR4 carbon catabolite repression 4-like	0.1917	**-0.0279**	0.0808	**-0.0514**	0.2738	317 ± 34	337 ± 33	388 ± 35	448 ± 84
215049_x_at	CD163	CD163 antigen	0.6135	**-0.0102**	-0.0945	-0.3960	0.1006	422 ± 84	361 ± 61	481 ± 81	689 ± 125
208405_s_at	CD164	CD164 antigen, sialomucin	-0.9469	**-0.0441**	-0.2522	-0.0675	0.6400	2494 ± 162	2415 ± 235	2474 ± 206	2795 ± 276
205789_at	CD1D	CD1D antigen, d polypeptide	0.9905	**-0.0477**	0.2226	-0.3644	0.0753	52 ± 13	61 ± 8	41 ± 8	93 ± 21
207995_s_at	CD209L	CD209 antigen-like	0.2358	**-0.0036**	**0.0504**	-0.0713	**0.0090**	111 ± 9	130 ± 9	129 ± 14	193 ± 28
204581_at	CD22	CD22 antigen	0.1308	**-0.0156**	-0.2997	-0.4034	0.0705	206 ± 46	223 ± 44	435 ± 90	370 ± 89
202256_at	CD2BP2	CD2 antigen binding protein 2	**0.0003**	**-0.0044**	-0.4117	-0.4526	**0.0071**	365 ± 20	382 ± 34	411 ± 28	523 ± 43
204192_at	CD37	CD37 antigen	**0.0393**	**-0.0287**	0.2019	-0.2060	0.1453	141 ± 21	185 ± 33	180 ± 30	234 ± 26
212014_x_at	CD44	CD44 antigen	0.1574	**-0.0011**	-0.3565	**-0.0400**	**0.0245**	202 ± 43	251 ± 20	345 ± 58	450 ± 76
212063_at	CD44	CD44 antigen	0.1240	**-0.0039**	-0.0830	-0.2795	0.0774	1535 ± 362	1422 ± 297	2392 ± 556	2962 ± 529
209835_x_at	CD44	CD44 antigen	0.1756	**-0.0060**	-0.4856	-0.1959	0.0595	284 ± 54	360 ± 47	409 ± 58	525 ± 65
204489_s_at	CD44	CD44 antigen	0.1072	**-0.0252**	-0.1584	-0.0662	0.3795	550 ± 104	633 ± 139	877 ± 150	957 ± 313
204490_s_at	CD44	CD44 antigen	**0.0114**	**-0.0021**	0.4591	-0.2108	**0.0287**	190 ± 33	254 ± 19	327 ± 50	419 ± 81

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
205173_x_at	CD58	CD58 antigen	-0.6922	**-0.0360**	0.4973	**-0.0105**	0.6313	204 ± 23	219 ± 42	205 ± 38	270 ± 58
211189_x_at	CD84	CD84 antigen	0.4477	**-0.0468**	0.2165	-0.1569	0.1496	203 ± 21	245 ± 34	228 ± 16	289 ± 34
205685_at	CD86	CD86 antigen	0.1727	**-0.0199**	0.0656	-0.1265	0.2488	135 ± 25	183 ± 33	174 ± 19	226 ± 46
205288_at	CDC14A	CDC14 cell division cycle 14 homolog A	0.0944	**-0.0002**	**0.0000**	**-0.0166**	**0.0313**	51 ± 5	68 ± 8	72 ± 8	99 ± 17
209658_at	CDC16	CDC16 cell division cycle 16 homolog	**0.0049**	-0.0551	**-0.0478**	0.3723	0.1444	1445 ± 138	1318 ± 118	1536 ± 90	2047 ± 400
209659_s_at	CDC16	CDC16 cell division cycle 16 homolog	**0.0222**	-0.0572	0.3535	0.3460	0.2377	1144 ± 85	1171 ± 111	1349 ± 92	1463 ± 197
201853_s_at	CDC25B	cell division cycle 25B	**0.0444**	-0.0807	**-0.0429**	-0.3220	0.5325	681 ± 75	687 ± 43	761 ± 57	795 ± 69
212401_s_at	CDC2L1	cell division cycle 2-like 1	**0.0008**	**-0.0044**	-0.3227	-0.3547	**0.0464**	841 ± 72	826 ± 55	979 ± 76	1162 ± 134
210473_s_at	CDC2L2	cell division cycle 2-like 2	**0.0022**	**-0.0040**	0.0912	**-0.0263**	0.0661	718 ± 34	845 ± 83	1021 ± 146	1119 ± 136
207318_s_at	CDC2L5	cell division cycle 2-like 5	**0.0117**	-0.3694	0.3608	0.4445	0.5772	798 ± 58	877 ± 63	882 ± 67	940 ± 102
210965_x_at	CDC2L5	cell division cycle 2-like 5	**0.0222**	-0.0848	-0.3203	**0.0448**	0.0795	55 ± 12	42 ± 13	67 ± 11	90 ± 14
212540_at	CDC34	cell division cycle 34	**0.0010**	**-0.0076**	0.1914	-0.4306	**0.0154**	661 ± 28	673 ± 53	792 ± 34	822 ± 33
218062_x_at	CDC42EP4	CDC42 effector protein 4	0.0635	**-0.0030**	0.2132	-0.1759	**0.0433**	1525 ± 178	1932 ± 169	2119 ± 155	2491 ± 380
214721_x_at	CDC42EP4	CDC42 effector protein 4	**0.0425**	**-0.0042**	**0.0381**	**-0.0265**	0.1068	845 ± 77	1065 ± 139	1164 ± 62	1311 ± 225
209057_x_at	CDC5L	CDC5 cell division cycle 5-like	0.3540	**-0.0401**	**0.0015**	-0.0797	0.1905	325 ± 20	385 ± 31	375 ± 41	437 ± 43
203968_s_at	CDC6	CDC6 cell division cycle 6 homolog	**0.0137**	-0.2598	-0.2975	-0.2560	0.1934	95 ± 6	77 ± 14	112 ± 10	104 ± 15
206866_at	CDH4	cadherin 4, type 1, R-cadherin	**0.0222**	**-0.0089**	0.2027	0.2995	**0.0126**	409 ± 43	350 ± 20	553 ± 36	563 ± 76
201253_s_at	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	**0.0092**	-0.0557	0.1247	0.0875	0.0743	2104 ± 169	2319 ± 354	2368 ± 132	3127 ± 376
203468_at	CDK10	cyclin-dependent kinase 10	**0.0024**	-0.1007	-0.4625	0.1474	0.1340	219 ± 33	183 ± 32	282 ± 38	298 ± 43
204252_at	CDK2	cyclin-dependent kinase 2	0.7921	**-0.0196**	-0.1799	-0.3622	0.2063	325 ± 48	340 ± 31	349 ± 23	441 ± 49
201938_at	CDK2AP1	CDK2-associated protein 1	0.4430	**-0.0078**	0.3673	**-0.0038**	0.2039	6126 ± 401	6628 ± 886	3130 ± 1006	8106 ± 951
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C	0.8162	**-0.0347**	-0.3622	0.1172	0.1428	3177 ± 375	2602 ± 246	3068 ± 430	4329 ± 776
204159_at	CDKN2C	cyclin-dependent kinase inhibitor 2C	**0.0401**	**-0.0092**	0.2967	-0.1842	0.1311	382 ± 44	488 ± 60	500 ± 54	600 ± 96
204039_at	CEBPA	CCAAT/enhancer binding protein , alpha	**0.0472**	-0.1038	**0.0184**	0.4440	0.1807	597 ± 48	774 ± 100	786 ± 93	830 ± 61
213006_at	CEBPD	CCAAT/enhancer binding protein , delta	**0.0539**	**-0.0127**	-0.3282	0.3574	**0.0041**	77 ± 6	76 ± 7	78 ± 13	126 ± 12
212437_at	CENPB	centromere protein B, 80kDa	**0.0025**	-0.1993	0.0900	-0.2449	0.2886	360 ± 40	459 ± 67	540 ± 52	520 ± 126
90265_at	CENTA1	centaurin, alpha 1	**0.0446**	-0.3566	0.2010	0.0866	0.3929	3918 ± 394	4256 ± 851	4261 ± 531	5753 ± 1312
212477_at	CENTB2	centaurin, beta 2	0.3075	**-0.0126**	-0.4842	0.3100	**0.0529**	75 ± 9	69 ± 8	87 ± 5	106 ± 13
214102_at	CENTD1	centaurin, delta 1	**0.0056**	**-0.0098**	**0.0096**	-0.1393	**0.0116**	395 ± 32	628 ± 62	696 ± 60	790 ± 141
213618_at	CENTD1	centaurin, delta 1	**0.0369**	**-0.0145**	-0.3047	-0.2844	**0.0451**	1503 ± 160	1624 ± 204	2190 ± 189	1992 ± 200
34206_at	CENTD2	centaurin, delta 2	**0.0114**	-0.0714	-0.2073	0.4744	0.2501	506 ± 64	510 ± 62	642 ± 28	715 ± 148
219746_at	CERD4	cer-d4 homolog	**0.0156**	**-0.0006**	**0.0173**	0.4469	**0.0000**	294 ± 13	424 ± 62	382 ± 25	599 ± 35
209508_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	0.1552	**-0.0064**	0.1718	-0.1971	**0.0483**	258 ± 23	259 ± 14	321 ± 31	348 ± 29
211862_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	0.0629	**-0.0129**	**0.0302**	-0.0682	0.2689	270 ± 13	291 ± 33	329 ± 41	345 ± 18
214486_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	**0.0028**	**-0.0002**	0.2733	-0.1001	**0.0019**	226 ± 21	232 ± 21	318 ± 34	365 ± 22
211316_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	**0.0084**	**-0.0195**	-0.1291	-0.1853	0.1004	667 ± 53	651 ± 35	768 ± 85	888 ± 85
48580_at	CGBP	CpG binding protein	**0.0069**	-0.1018	-0.3274	0.4843	0.3010	1841 ± 118	1982 ± 213	2096 ± 136	2326 ± 263
206861_s_at	CGGBP1	CGG triplet repeat binding protein 1	**0.0112**	**-0.0006**	0.2764	0.4898	**0.0007**	747 ± 47	698 ± 64	792 ± 58	1250 ± 152
212405_s_at	CGI-01	CGI-01 protein	**0.0066**	-0.1276	0.1575	-0.1003	0.4228	294 ± 16	288 ± 35	337 ± 27	337 ± 28
212407_at	CGI-01	CGI-01 protein	**0.0356**	**-0.0269**	0.1279	-0.0781	**0.0212**	417 ± 19	453 ± 35	422 ± 12	537 ± 43
202938_x_at	CGI-96	CGI-96 protein	**0.0377**	-0.1320	-0.1858	-0.1763	0.2128	189 ± 10	150 ± 24	188 ± 30	251 ± 53
210672_s_at	CGTHBA	Conserved gene telomeric to alpha globin cluster	**0.0461**	-0.3931	0.0799	-0.4967	0.3067	640 ± 39	619 ± 53	587 ± 52	739 ± 84

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
214273_x_at	CGTHBA	Conserved gene telomeric to alpha globin cluster	0.0751	**-0.0216**	-0.3683	0.4655	0.1113	512 ± 53	499 ± 29	633 ± 42	749 ± 140
206932_at	CH25H	cholesterol 25-hydroxylase	0.3227	**-0.0402**	0.4733	0.2922	0.1271	214 ± 38	224 ± 20	211 ± 25	355 ± 82
204258_at	CHD1	chromodomain helicase DNA binding protein 1	**0.0430**	-0.0665	-0.3121	0.4113	0.1449	327 ± 17	334 ± 18	395 ± 32	374 ± 22
203461_at	CHD2	chromodomain helicase DNA binding protein 2	**0.0015**	**-0.0001**	0.1545	**-0.0180**	**0.0000**	143 ± 11	178 ± 33	184 ± 21	352 ± 35
205022_s_at	CHES1	checkpoint suppressor 1	**0.0476**	**-0.0093**	-0.1288	-0.2885	0.1187	298 ± 34	265 ± 37	363 ± 44	400 ± 48
218803_at	CHFR	checkpoint with forkhead and ring finger domains	**0.0342**	**-0.0315**	0.1311	**0.0361**	0.0612	717 ± 33	782 ± 80	890 ± 35	1000 ± 125
220210_at	CHRNA10	cholinergic receptor, nicotinic, alpha polypeptide 10	0.4964	**-0.0465**	0.1777	-0.0845	0.3789	93 ± 13	97 ± 15	115 ± 10	122 ± 14
207568_at	CHRNA6	cholinergic receptor, nicotinic, alpha polypeptide 6	0.1486	**-0.0233**	0.4311	0.4926	0.1019	229 ± 31	234 ± 30	234 ± 20	341 ± 55
210943_s_at	CHS1	Chediak-Higashi syndrome 1	0.5176	**-0.0465**	0.1558	-0.1652	0.1034	498 ± 37	480 ± 34	496 ± 41	645 ± 77
209834_at	CHST3	carbohydrate sulfotransferase 3	0.1458	**-0.0035**	-0.2076	-0.2966	0.1017	555 ± 103	579 ± 59	625 ± 62	853 ± 104
32094_at	CHST3	carbohydrate sulfotransferase 3	**0.0096**	**-0.0003**	-0.1875	-0.3537	**0.0133**	485 ± 69	513 ± 38	713 ± 91	815 ± 91
221059_s_at	CHST6	carbohydrate sulfotransferase 6	**0.0221**	**-0.0014**	**0.0043**	-0.4750	**0.0085**	650 ± 50	658 ± 70	926 ± 115	1061 ± 113
201953_at	CIB1	calcium and integrin binding 1	0.0627	**-0.0202**	0.3059	0.3883	**0.0068**	721 ± 40	757 ± 48	705 ± 38	942 ± 57
205516_x_at	CIZ1	Cip1-interacting zinc finger protein	**0.0077**	-0.3116	-0.0616	-0.4456	0.1239	969 ± 85	911 ± 42	1224 ± 87	1043 ± 142
200999_s_at	CKAP4	cytoskeleton-associated protein 4	**0.0394**	-0.2797	-0.3599	-0.4826	0.3189	539 ± 46	523 ± 42	643 ± 44	604 ± 69
217947_at	CKLFSF6	chemokine-like factor super family 6	0.0564	**-0.0011**	0.2061	-0.1641	**0.0481**	644 ± 45	750 ± 54	836 ± 85	944 ± 96
214135_at	CLDN18	claudin 18	**0.0325**	-0.1671	**0.0338**	0.4801	0.0680	123 ± 15	187 ± 22	172 ± 17	192 ± 27
204482_at	CLDN5	claudin 5	**0.0230**	-0.0576	**0.0011**	-0.3048	**0.0121**	684 ± 76	1053 ± 123	1262 ± 153	1111 ± 109
221698_s_at	CLECSF12	C-type lectin, superfamily member 12	0.0650	**-0.0036**	**0.0522**	-0.4612	**0.0332**	225 ± 22	314 ± 44	326 ± 39	415 ± 66
209732_at	CLECSF2	C-type lectin, superfamily member 2	**0.0140**	-0.2275	-0.4506	0.4686	0.5504	166 ± 39	204 ± 32	200 ± 35	250 ± 57
208659_at	CLIC1	chloride intracellular channel 1	0.8258	**-0.0403**	-0.2440	**-0.0457**	0.4004	486 ± 71	534 ± 50	627 ± 22	614 ± 94
222043_at	CLU	clusterin	**0.0230**	**-0.0176**	**0.0040**	**0.0373**	**0.0226**	1111 ± 60	982 ± 60	1716 ± 273	1584 ± 207
61732_r_at	CMG1	capillary morphogenesis protein 1	**0.0002**	**-0.0158**	**0.0069**	**-0.0166**	**0.0255**	21 ± 4	31 ± 4	35 ± 5	62 ± 18
201774_s_at	CNAP1	chromosome condensation-related SMC-associated protein 1	0.1620	**-0.0075**	0.3686	**-0.0276**	0.2398	147 ± 18	152 ± 31	179 ± 13	202 ± 10
222182_s_at	CNOT2	CCR4-NOT transcription complex, subunit 2	**0.0001**	**-0.0047**	-0.2017	0.3898	**0.0108**	738 ± 65	662 ± 50	1115 ± 104	1163 ± 201
208912_s_at	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	0.0801	**-0.0264**	0.1639	-0.4091	0.1319	4700 ± 260	5089 ± 574	6190 ± 593	7447 ± 1606
203073_at	COG2	component of oligomeric golgi complex 2	0.3151	**-0.0400**	-0.4490	-0.4517	0.1009	703 ± 33	780 ± 66	776 ± 54	883 ± 44
212189_s_at	COG4	component of oligomeric golgi complex 4	**0.0119**	-0.1525	**0.0294**	-0.4694	0.2053	335 ± 46	423 ± 42	448 ± 31	486 ± 82
209082_s_at	COL18A1	collagen, type XVIII, alpha 1	**0.0048**	**-0.0359**	0.1687	-0.1700	0.1127	219 ± 22	265 ± 32	286 ± 18	332 ± 52
202403_s_at	COL1A2	collagen, type I, alpha 2	**0.0342**	**-0.0031**	-0.1468	-0.4837	**0.0165**	191 ± 20	200 ± 30	197 ± 9	294 ± 32
208096_s_at	COL21A1	collagen, type XXI, alpha 1	0.1289	**-0.0035**	-0.1983	-0.1062	**0.0334**	330 ± 40	348 ± 59	414 ± 77	601 ± 87
222073_at	COL4A3	collagen, type IV, alpha 3	**0.0521**	**-0.0010**	-0.4617	-0.4398	**0.0059**	121 ± 16	126 ± 10	161 ± 20	232 ± 36
213110_s_at	COL4A5	collagen, type IV, alpha 5	0.3377	**-0.0133**	0.3257	-0.2960	0.1181	1168 ± 129	1592 ± 264	1661 ± 169	1862 ± 273
209156_s_at	COL6A2	collagen, type VI, alpha 2	0.0823	**-0.0015**	-0.2691	-0.4149	**0.0233**	136 ± 24	134 ± 10	157 ± 28	331 ± 92
201438_at	COL6A3	collagen, type VI, alpha 3	0.2859	**-0.0267**	0.2059	0.4789	0.1675	67 ± 12	96 ± 32	153 ± 47	172 ± 43
204136_at	COL7A1	collagen, type VII, alpha 1	**0.0279**	-0.1322	0.1597	0.2291	0.2043	197 ± 14	241 ± 73	313 ± 26	310 ± 60
52651_at	COL8A2	collagen, type VIII, alpha 2	**0.0147**	**-0.0006**	**0.0083**	**-0.0204**	**0.0028**	216 ± 20	311 ± 28	317 ± 24	355 ± 24
208817_at	COMT	catechol-O-methyltransferase	0.2906	**-0.0093**	-0.0950	0.4285	0.0734	644 ± 57	575 ± 42	658 ± 48	853 ± 119
201358_s_at	COPB	coatomer protein complex, subunit beta	0.2386	**-0.0283**	0.0666	-0.1164	0.1351	3174 ± 113	3629 ± 299	3601 ± 165	3994 ± 337
209746_s_at	COQ7	COQ7 coenzyme Q, 7 homolog ubiquinone	**0.0231**	-0.1475	0.1429	0.2421	0.0726	319 ± 19	358 ± 33	307 ± 27	424 ± 47
214282_at	CP	ceruloplasmin	0.2097	**-0.0147**	-0.4169	0.3578	0.1093	38 ± 5	39 ± 9	58 ± 9	69 ± 15
206100_at	CPM	carboxypeptidase M	0.1786	**-0.0370**	0.2926	**-0.0122**	0.1208	196 ± 25	301 ± 49	301 ± 53	346 ± 44

Probe set	Name	Description	NFT$_{O}$	MMSE$_{O}$	NFT$_{I}$	MMSE$_{I}$	ANOVA	Control	Incipient	Moderate	Severe
202118_s_at	CPNE3	copine III	**0.0249**	**-0.0163**	0.2366	**-0.0141**	**0.0019**	258 ± 28	317 ± 36	424 ± 17	345 ± 23
201639_s_at	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	**0.0052**	-0.1161	0.4582	-0.0721	0.3101	385 ± 38	502 ± 91	497 ± 71	601 ± 121
33132_at	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	**0.0495**	-0.1760	**0.0362**	**-0.0518**	0.0953	483 ± 39	707 ± 77	759 ± 73	713 ± 129
210069_at	CPT1B	carnitine palmitoyltransferase I, muscle	**0.0011**	**-0.0028**	-0.1709	-0.3727	**0.0181**	227 ± 24	200 ± 25	301 ± 40	383 ± 65
210070_s_at	CPT1B	carnitine palmitoyltransferase I, muscle	**0.0136**	**-0.0098**	0.4551	-0.2809	0.0811	263 ± 26	311 ± 33	344 ± 24	388 ± 49
204264_at	CPT2	carnitine palmitoyltransferase II	0.1620	**-0.0001**	**0.0063**	**-0.0319**	**0.0017**	104 ± 6	133 ± 12	132 ± 13	177 ± 14
217552_x_at	CR1	complement component receptor 1	0.1135	**-0.0040**	0.3839	**-0.0237**	0.0830	19 ± 7	35 ± 11	43 ± 13	63 ± 14
217484_at	CR1	complement component receptor 1	**0.0466**	**-0.0450**	**0.0420**	-0.3210	**0.0206**	131 ± 11	187 ± 23	165 ± 10	213 ± 27
205076_s_at	CRA	cisplatin resistance associated	0.0631	**-0.0038**	0.4665	-0.3701	0.0619	406 ± 40	398 ± 33	465 ± 36	573 ± 71
209833_at	CRADD	CASP2 and RIPK1 domain	0.0606	**-0.0268**	-0.3374	-0.4958	0.0583	392 ± 14	371 ± 19	384 ± 14	452 ± 33
209432_s_at	CREB3	cAMP responsive element binding protein 3	**0.0006**	**-0.0104**	-0.1206	0.3873	**0.0014**	708 ± 32	678 ± 31	922 ± 49	831 ± 53
202160_at	CREBBP	CREB binding protein	**0.0020**	**-0.0115**	0.1311	-0.1158	**0.0122**	1011 ± 56	1138 ± 97	1388 ± 96	1278 ± 76
205984_at	CRHBP	corticotropin releasing hormone binding protein	**0.0076**	**-0.0334**	-0.3448	0.4704	0.2320	122 ± 17	128 ± 17	155 ± 26	187 ± 34
219226_at	CRK7	CDC2-related protein kinase 7	-0.8701	**-0.0116**	0.4451	-0.4041	**0.0483**	126 ± 18	106 ± 9	107 ± 10	183 ± 32
206184_at	CRKL	v-crk sarcoma virus CT10 oncogene homolog -like	0.2573	**-0.0417**	-0.4839	-0.1358	0.0794	228 ± 19	260 ± 20	237 ± 21	312 ± 32
206315_at	CRLF1	cytokine receptor-like factor 1	0.1669	**-0.0156**	0.2908	-0.4871	0.1171	136 ± 41	92 ± 32	240 ± 72	270 ± 59
209716_at	CSF1	colony stimulating factor 1	0.2485	**-0.0008**	0.1086	**-0.0167**	**0.0039**	367 ± 39	506 ± 50	500 ± 44	722 ± 98
202329_at	CSK	c-src tyrosine kinase	**0.0014**	**-0.0100**	0.0856	-0.0762	**0.0362**	526 ± 46	614 ± 38	799 ± 62	850 ± 148
208865_at	CSNK1A1	casein kinase 1, alpha 1	0.3689	**0.0000**	-0.1906	-0.1298	**0.0125**	2970 ± 138	2918 ± 50	3518 ± 81	3846 ± 407
208866_at	CSNK1A1	casein kinase 1, alpha 1	0.1292	**-0.0081**	-0.3952	-0.1598	**0.0060**	324 ± 22	323 ± 10	426 ± 24	384 ± 24
202332_at	CSNK1E	casein kinase 1, epsilon	**0.0057**	**-0.0027**	0.3337	0.0660	**0.0054**	570 ± 58	503 ± 33	746 ± 83	1068 ± 183
203575_at	CSNK2A2	casein kinase 2, alpha prime polypeptide	**0.0004**	**-0.0530**	**0.0046**	-0.1334	0.0685	370 ± 8	389 ± 13	459 ± 37	437 ± 31
221731_x_at	CSPG2	chondroitin sulfate proteoglycan 2	**0.0516**	**-0.0024**	-0.4981	-0.1574	**0.0258**	2094 ± 293	2434 ± 296	3450 ± 377	3298 ± 448
204620_s_at	CSPG2	chondroitin sulfate proteoglycan 2	0.4794	**-0.0147**	-0.1054	-0.2114	0.2851	1776 ± 245	1626 ± 168	2017 ± 218	2228 ± 227
204619_s_at	CSPG2	chondroitin sulfate proteoglycan 2	0.1038	**-0.0247**	0.0746	**-0.0042**	0.1689	389 ± 31	519 ± 63	575 ± 85	558 ± 63
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	0.0726	**-0.0047**	-0.2915	-0.2565	**0.0218**	443 ± 41	444 ± 69	432 ± 32	657 ± 74
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	**0.0026**	**-0.0037**	-0.1732	-0.2394	**0.0369**	391 ± 42	381 ± 78	446 ± 45	660 ± 112
205670_at	CST	cerebroside sulfotransferase	**0.0216**	-0.0799	0.0935	-0.1898	0.1771	85 ± 27	145 ± 60	105 ± 23	240 ± 86
220957_at	CTAGE-1	CTAGE-1 protein	0.3922	**-0.0278**	0.3270	0.2087	0.0796	126 ± 14	136 ± 25	129 ± 13	207 ± 40
213980_s_at	CTBP1	C-terminal binding protein 1	**0.0411**	-0.3020	-0.3468	-0.4501	**0.0442**	2235 ± 150	1972 ± 57	2554 ± 137	2284 ± 115
201220_x_at	CTBP2	C-terminal binding protein 2	**0.0064**	**-0.0149**	0.1692	-0.3864	0.0726	1894 ± 191	1724 ± 93	2254 ± 271	2556 ± 243
210835_s_at	CTBP2	C-terminal binding protein 2	**0.0001**	**-0.0270**	0.2167	0.2175	**0.0381**	2070 ± 200	2304 ± 324	2897 ± 281	3192 ± 374
218923_at	CTBS	chitobiase, di-N-acetyl-	**0.0262**	**-0.0332**	0.1312	-0.0678	0.0832	207 ± 22	264 ± 22	333 ± 56	315 ± 38
210844_x_at	CTNNA1	catenin , alpha 1 (102kDa	0.4535	**-0.0044**	-0.1227	-0.1602	0.1983	1553 ± 152	1572 ± 212	1888 ± 193	2026 ± 167
221021_s_at	CTNNBL1	catenin, beta like 1	0.2123	**-0.0093**	0.1529	-0.1693	**0.0256**	283 ± 24	353 ± 25	359 ± 12	392 ± 34
36566_at	CTNS	cystinosis, nephropathic	**0.0432**	**-0.0324**	0.1469	-0.3789	0.0759	284 ± 35	323 ± 40	334 ± 13	422 ± 51
219080_s_at	CTPS2	CTP synthase II	0.1321	**-0.0001**	**0.0362**	-0.2678	**0.0003**	93 ± 11	112 ± 11	109 ± 13	196 ± 24
206297_at	CTRC	chymotrypsin C	0.3537	**-0.0247**	**0.0352**	-0.4192	**0.0299**	162 ± 22	195 ± 30	181 ± 29	293 ± 43
214377_s_at	CTRL	chymotrypsin-like	**0.0061**	-0.1180	-0.1313	0.4411	0.2503	208 ± 24	220 ± 28	226 ± 15	285 ± 42
213141_at	CTRL	chymotrypsin-like	0.0569	**-0.0238**	-0.1651	-0.3981	0.1252	328 ± 33	307 ± 17	348 ± 18	471 ± 92
213275_x_at	CTSB	cathepsin B	**0.0307**	**-0.0190**	0.2080	-0.3207	0.0729	3611 ± 346	3316 ± 265	3940 ± 318	5016 ± 695
202295_s_at	CTSH	cathepsin H	0.1658	**-0.0362**	-0.4007	-0.0755	0.3380	1821 ± 234	1787 ± 351	2375 ± 324	2354 ± 294

Probe set	Name	Description	NFT_O	MMSE_O	NFT_I	MMSE_I	ANOVA	Control	Incipient	Moderate	Severe
202087_s_at	CTSL	cathepsin L	0.5555	**-0.0272**	-0.4994	**-0.0402**	0.6177	647 ± 40	679 ± 62	733 ± 60	743 ± 80
202902_s_at	CTSS	cathepsin S	**0.0368**	-0.4058	0.2206	-0.3935	0.2152	166 ± 18	236 ± 23	173 ± 22	238 ± 51
202901_x_at	CTSS	cathepsin S	0.4358	**-0.0489**	**0.0065**	-0.0708	0.1185	95 ± 8	144 ± 18	134 ± 18	149 ± 22
201424_s_at	CUL4A	cullin 4A	**0.0516**	**-0.0168**	0.2723	**-0.0061**	**0.0353**	336 ± 21	386 ± 43	483 ± 46	441 ± 28
203533_s_at	CUL5	cullin 5	0.1935	**-0.0367**	-0.1648	-0.0905	**0.0401**	225 ± 19	188 ± 27	266 ± 13	254 ± 16
214743_at	CUTL1	cut-like 1, CCAAT displacement protein	**0.0013**	**-0.0014**	0.2620	0.0981	**0.0042**	801 ± 35	714 ± 86	943 ± 81	1255 ± 154
209774_x_at	CXCL2	chemokine ligand 2	0.1268	**-0.0015**	-0.3813	-0.3027	**0.0389**	120 ± 15	146 ± 21	199 ± 31	209 ± 24
213681_at	CYHR1	cysteine and histidine rich 1	**0.0110**	**-0.0373**	-0.1514	-0.0675	0.1174	204 ± 22	220 ± 18	207 ± 17	285 ± 39
216809_at	CYLC1	cylicin, basic protein of sperm head cytoskeleton 1	**0.0074**	**0.0000**	0.1655	-0.1105	**0.0001**	106 ± 11	128 ± 15	151 ± 10	239 ± 29
211031_s_at	CYLN2	cytoplasmic linker 2	**0.0373**	-0.1178	-0.3140	-0.1301	**0.0252**	1267 ± 154	1318 ± 90	1908 ± 142	1380 ± 229
204309_at	CYP11A	cytochrome P450, subfamily XIA	0.1618	**-0.0057**	0.2687	**-0.0285**	**0.0499**	119 ± 12	143 ± 6	150 ± 6	175 ± 23
217558_at	CYP2C9	cytochrome P450, subfamily IIC , polypeptide 9	0.0985	**-0.0008**	0.1531	-0.4189	**0.0084**	78 ± 11	76 ± 5	93 ± 13	144 ± 21
220432_s_at	CYP39A1	cytochrome P450, subfamily XXXIX , polypeptide 1	0.0859	**-0.0161**	**0.0101**	-0.1890	0.1692	31 ± 5	40 ± 9	45 ± 5	57 ± 12
205998_x_at	CYP3A4	cytochrome P450, subfamily IIIA , polypeptide 4	0.0692	**-0.0135**	0.2344	-0.3041	**0.0389**	606 ± 28	722 ± 91	711 ± 44	868 ± 68
206515_at	CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	0.0923	**-0.0010**	**0.0075**	-0.3227	**0.0230**	124 ± 17	143 ± 30	229 ± 52	367 ± 94
204190_at	D13S106E	highly charged protein	**0.0156**	-0.2346	-0.1781	0.2969	0.2799	551 ± 44	567 ± 45	522 ± 43	688 ± 105
202646_s_at	D1S155E	NRAS-related gene	**0.0484**	-0.1550	**0.0010**	-0.1643	0.3444	2687 ± 151	2897 ± 196	3029 ± 101	2993 ± 141
216060_s_at	DAAM1	dishevelled associated activator of morphogenesis 1	**0.0015**	-0.1112	0.2206	0.2471	0.0891	839 ± 26	824 ± 50	1042 ± 111	964 ± 15
212793_at	DAAM2	dishevelled associated activator of morphogenesis 2	**0.0038**	**-0.0114**	0.1578	-0.0982	0.0608	3452 ± 394	4531 ± 634	5302 ± 359	5565 ± 939
205417_s_at	DAG1	dystroglycan 1	0.1294	**-0.0107**	0.2535	-0.4654	0.0928	1326 ± 94	1328 ± 86	1592 ± 102	1639 ± 148
206878_at	DAO	D-amino-acid oxidase	0.2293	**-0.0445**	**0.0137**	-0.3370	0.0682	270 ± 15	335 ± 60	321 ± 32	432 ± 50
206324_s_at	DAPK2	death-associated protein kinase 2	**0.0267**	**-0.0082**	0.0843	**-0.0030**	**0.0044**	122 ± 15	174 ± 16	141 ± 7	267 ± 50
203891_s_at	DAPK3	death-associated protein kinase 3	**0.0397**	**-0.0080**	0.0604	-0.4720	**0.0043**	100 ± 10	139 ± 21	134 ± 9	214 ± 33
201623_s_at	DARS	aspartyl-tRNA synthetase	0.6838	**-0.0082**	**0.0183**	-0.0978	0.1298	1240 ± 48	1426 ± 57	1476 ± 115	1625 ± 181
208281_x_at	DAZ3	deleted in azoospermia 3	0.5587	**-0.0330**	0.3063	-0.2133	0.1894	111 ± 13	126 ± 13	129 ± 15	160 ± 16
218443_s_at	DAZAP1	DAZ associated protein 1	**0.0020**	**-0.0492**	0.1234	0.3117	0.1403	439 ± 32	505 ± 53	523 ± 35	598 ± 70
214334_x_at	DAZAP2	DAZ associated protein 2	0.4612	**-0.0221**	-0.4577	-0.4672	0.1398	4825 ± 241	5432 ± 532	5819 ± 442	6184 ± 491
201678_s_at	DC12	DC12 protein	0.0959	**-0.0222**	-0.1699	-0.4385	**0.0528**	541 ± 49	490 ± 40	533 ± 40	674 ± 45
209759_s_at	DCI	dodecenoyl-Coenzyme A delta isomerase	0.0751	**-0.0024**	0.2597	-0.4718	**0.0158**	303 ± 27	310 ± 50	338 ± 23	491 ± 66
219678_x_at	DCLRE1C	DNA cross-link repair 1C	**0.0015**	**-0.0240**	0.3760	-0.4335	0.1549	658 ± 71	694 ± 84	955 ± 161	993 ± 171
209335_at	DCN	decorin	0.6224	**-0.0495**	0.4554	**-0.0316**	0.3997	246 ± 17	292 ± 13	282 ± 28	317 ± 47
210749_x_at	DDR1	discoidin domain receptor family, member 1	**0.0327**	-0.0610	0.3706	-0.2586	0.1939	2892 ± 340	3354 ± 267	3910 ± 344	3776 ± 498
208779_x_at	DDR1	discoidin domain receptor family, member 1	**0.0030**	**-0.0014**	0.2272	-0.1356	**0.0103**	2859 ± 317	3596 ± 440	4527 ± 383	4669 ± 516
207169_x_at	DDR1	discoidin domain receptor family, member 1	**0.0026**	**-0.0048**	0.2248	-0.3244	**0.0137**	2385 ± 270	3067 ± 372	3934 ± 363	3896 ± 494
205168_at	DDR2	discoidin domain receptor family, member 2	**0.0177**	**-0.0001**	0.0891	-0.1388	**0.0017**	295 ± 53	323 ± 32	471 ± 51	773 ± 146
208895_s_at	DDX18	DEAD/H box polypeptide 18	**0.0017**	-0.1057	-0.3871	0.4609	0.1582	1132 ± 90	1086 ± 73	1076 ± 99	1460 ± 223
208152_s_at	DDX21	DEAD/H box polypeptide 21	0.4080	**-0.0177**	0.4509	0.4093	**0.0318**	885 ± 53	943 ± 101	828 ± 32	1192 ± 130
221780_s_at	DDX27	DEAD/H box polypeptide 27	**0.0125**	-0.0791	-0.4820	0.3839	0.2228	162 ± 31	152 ± 31	208 ± 23	237 ± 39
215693_x_at	DDX27	DEAD/H box polypeptide 27	**0.0022**	**-0.0129**	-0.2769	-0.4938	0.0625	857 ± 64	878 ± 80	937 ± 56	1121 ± 85
201584_s_at	DDX39	DEAD/H box polypeptide 39	**0.0009**	**-0.0061**	0.3404	-0.4461	**0.0148**	585 ± 43	730 ± 89	749 ± 47	971 ± 114
204909_at	DDX6	DEAD/H box polypeptide 6	**0.0213**	**-0.0113**	0.1479	-0.1763	0.0629	184 ± 27	163 ± 21	241 ± 21	298 ± 60
207269_at	DEFA4	defensin, alpha 4, corticostatin	0.1017	**-0.0383**	0.3230	0.3105	**0.0133**	121 ± 17	93 ± 10	114 ± 14	192 ± 32

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
208024_s_at	DGCR6	DiGeorge syndrome critical region gene 6	**0.0406**	-0.7078	**0.0413**	-0.1414	0.0739	771 ± 56	849 ± 30	1027 ± 59	835 ± 113
206395_at	DGKG	diacylglycerol kinase, gamma 90kDa	**0.0084**	**-0.0392**	-0.4413	-0.2059	**0.0488**	415 ± 25	441 ± 37	550 ± 62	632 ± 95
32032_at	DGSI	DiGeorge syndrome critical region gene DGSI	**0.0363**	-0.1100	0.2119	0.2163	**0.0549**	492 ± 20	594 ± 74	496 ± 46	727 ± 98
204383_at	DGSI	DiGeorge syndrome critical region gene DGSI	**0.0490**	**-0.0081**	**0.0315**	-0.1106	0.0821	276 ± 16	273 ± 19	319 ± 22	364 ± 43
202532_s_at	DHFR	dihydrofolate reductase	**0.0360**	-0.0568	0.2614	0.4053	0.0922	284 ± 32	297 ± 42	385 ± 45	395 ± 29
202534_x_at	DHFR	dihydrofolate reductase	0.1505	**-0.0174**	**0.0503**	0.3447	**0.0405**	546 ± 25	644 ± 95	733 ± 71	810 ± 64
213632_at	DHODH	dihydroorotate dehydrogenase	0.1321	**-0.0017**	-0.3591	0.4442	**0.0095**	152 ± 16	139 ± 13	153 ± 9	252 ± 44
205603_s_at	DIAPH2	diaphanous homolog 2	**0.0285**	-0.0631	0.1489	0.2158	0.0581	163 ± 17	213 ± 49	267 ± 20	273 ± 41
206061_s_at	DICER1	Dicer1, Dcr-1 homolog	0.1312	**-0.0282**	0.4132	**-0.0319**	0.1687	469 ± 33	533 ± 77	596 ± 59	637 ± 55
215529_x_at	DIP2	disco-interacting protein 2 homolog	**0.0041**	-0.1117	0.1679	**-0.0180**	0.4337	600 ± 77	753 ± 83	844 ± 170	923 ± 226
221191_at	DKFZP434A0131	DKFZp434A0131 protein	**0.0032**	**-0.0032**	0.0734	**-0.0199**	**0.0211**	230 ± 25	271 ± 18	398 ± 64	399 ± 50
203486_s_at	DKFZP434A043	DKFZp434A043 protein	**0.0054**	**-0.0200**	0.3453	-0.2310	**0.0136**	675 ± 38	678 ± 35	808 ± 24	772 ± 15
210129_s_at	DKFZP434B103	DKFZP434B103 protein	**0.0011**	-0.0860	**0.0038**	**-0.0434**	0.2406	229 ± 14	326 ± 29	364 ± 36	433 ± 138
212886_at	DKFZP434C171	DKFZP434C171 protein	0.1514	**-0.0330**	**0.0518**	-0.1119	0.1027	79 ± 13	125 ± 24	114 ± 21	147 ± 19
212132_at	DKFZP434D1335	DKFZP434D1335 protein	**0.0327**	-0.1083	-0.1890	-0.1157	0.5608	505 ± 33	521 ± 49	578 ± 49	579 ± 60
222099_s_at	DKFZP434D1335	DKFZP434D1335 protein	**0.0181**	**-0.0028**	-0.2633	-0.1173	**0.0342**	687 ± 47	717 ± 26	869 ± 30	898 ± 102
204495_s_at	DKFZP434H132	DKFZP434H132 protein	**0.0489**	-0.1455	0.1412	0.4398	0.1976	169 ± 15	211 ± 39	191 ± 19	257 ± 42
214699_x_at	DKFZP434J154	DKFZP434J154 protein	**0.0064**	**-0.0010**	-0.4882	-0.2742	**0.0004**	287 ± 13	293 ± 15	326 ± 30	535 ± 71
212665_at	DKFZP434J214	DKFZP434J214 protein	**0.0059**	**-0.0015**	0.3889	-0.0698	**0.0265**	826 ± 66	956 ± 73	983 ± 59	1192 ± 112
47553_at	DKFZP434N014	DKFZP434N014 protein	**0.0023**	-0.0667	-0.1178	0.3747	0.2084	441 ± 58	381 ± 38	572 ± 93	602 ± 104
221887_s_at	DKFZP434N014	DKFZP434N014 protein	**0.0221**	-0.8832	-0.2535	0.4834	0.8025	369 ± 53	434 ± 72	474 ± 72	413 ± 119
214766_s_at	DKFZP434N093	DKFZP434N093 protein	**0.0077**	**-0.0173**	-0.0777	-0.4819	0.0620	164 ± 20	162 ± 10	211 ± 16	232 ± 32
206819_at	DKFZP434P211	DKFZp434P211 protein	0.1624	**-0.0045**	-0.3518	-0.4518	0.0917	95 ± 15	88 ± 22	107 ± 13	176 ± 44
212177_at	DKFZp564B0769	SR rich protein	**0.0193**	**-0.0481**	-0.0557	-0.4678	0.0916	504 ± 60	447 ± 30	660 ± 65	667 ± 110
205673_s_at	DKFZP564L0862	DKFZP564L0862 protein	**0.0391**	**-0.0037**	0.1477	-0.3968	**0.0037**	88 ± 11	80 ± 12	85 ± 9	171 ± 31
216263_s_at	DKFZP564O092	DKFZP564O092 protein	**0.0526**	**-0.0244**	0.3606	-0.2653	0.0714	48 ± 8	57 ± 7	56 ± 11	95 ± 21
212447_at	DKFZP566C134	DKFZP566C134 protein	**0.0490**	**-0.0008**	**-0.0274**	-0.3491	**0.0185**	1166 ± 76	1081 ± 86	1403 ± 98	1466 ± 104
209703_x_at	DKFZP586A0522	DKFZP586A0522 protein	**0.0276**	**-0.0183**	**0.0191**	-0.0581	**0.0358**	986 ± 135	1536 ± 227	1930 ± 271	1817 ± 338
213488_at	DKFZP586B2420	DKFZP586B2420 protein	**0.0035**	**-0.0001**	**0.0478**	-0.0804	**0.0026**	265 ± 31	369 ± 46	404 ± 33	514 ± 54
212256_at	DKFZp586H0623	putative UDP-GalNAc:polypeptide	**0.0098**	**-0.0120**	**0.0328**	**-0.0510**	**0.0363**	415 ± 30	521 ± 58	624 ± 66	591 ± 57
208015_at	DKFZP586M0622	DKFZP586M0622 protein	0.0589	**-0.0262**	0.3512	**0.0419**	0.0557	145 ± 9	128 ± 31	144 ± 14	207 ± 23
206257_at	DKFZP586M1019	DKFZP586M1019 protein	0.0666	**-0.0043**	0.0700	0.4183	**0.0193**	409 ± 15	418 ± 21	439 ± 22	554 ± 58
214274_s_at	DLEC1	deleted in lung and esophageal cancer 1	**0.0222**	-0.2592	0.2302	0.2129	0.3234	891 ± 39	971 ± 86	1061 ± 63	1033 ± 88
205677_s_at	DLEU1	deleted in lymphocytic leukemia, 1	0.3159	**-0.0123**	0.4122	0.4914	0.0961	271 ± 25	302 ± 36	306 ± 18	384 ± 42
201681_s_at	DLG5	discs, large homolog 5	**0.0001**	**-0.0012**	**-0.0242**	0.2884	**0.0057**	459 ± 43	493 ± 67	689 ± 62	718 ± 63
208216_at	DLX4	distal-less homeobox 4	0.1211	**-0.0191**	**0.0476**	**-0.0375**	0.0790	118 ± 14	138 ± 11	154 ± 21	194 ± 30
208382_s_at	DMC1	DMC1 dosage suppressor of mck1 homolog	0.2943	**-0.0442**	**0.0145**	**-0.0010**	**0.0125**	121 ± 6	187 ± 24	132 ± 16	219 ± 34
208386_x_at	DMC1	DMC1 dosage suppressor of mck1 homolog	**0.0066**	**-0.0070**	-0.4795	-0.1730	**0.0394**	60 ± 8	57 ± 8	78 ± 10	103 ± 18
207660_at	DMD	dystrophin	0.1838	**-0.0095**	0.2682	0.4240	**0.0290**	168 ± 19	140 ± 14	171 ± 13	252 ± 41
212730_at	DMN	desmuslin	**0.0011**	**-0.0008**	**-0.0045**	-0.4739	**0.0005**	2024 ± 230	1812 ± 243	3472 ± 380	3170 ± 269
37996_s_at	DMPK	dystrophia myotonica-protein kinase	**0.0096**	**-0.0077**	-0.4543	0.2331	**0.0150**	515 ± 33	459 ± 49	621 ± 38	758 ± 109
213231_at	DMWD	dystrophia myotonica-containing WD repeat motif	0.0833	**-0.0299**	0.2695	-0.0789	0.2256	249 ± 35	270 ± 21	328 ± 30	339 ± 49

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
33768_at	DMWD	dystrophia myotonica-containing WD repeat motif	**0.0464**	**-0.0080**	-0.4711	0.3340	**0.0430**	1105 ± 72	1202 ± 128	1491 ± 125	1560 ± 177
202500_at	DNAJB2	DnaJ homolog, subfamily B, member 2	**0.0000**	-0.0820	-0.1415	-0.3158	0.2546	1044 ± 126	1000 ± 134	1484 ± 188	1612 ± 479
206782_s_at	DNAJC4	DnaJ homolog, subfamily C, member 4	0.1528	**-0.0196**	0.3372	0.1169	0.0948	237 ± 15	223 ± 31	242 ± 10	314 ± 42
221677_s_at	DONSON	downstream neighbor of SON	0.2701	**-0.0462**	-0.0867	-0.4673	0.1337	270 ± 31	269 ± 29	270 ± 18	348 ± 24
220483_s_at	DORFIN	double ring-finger protein, Dorfin	**0.0000**	**-0.0042**	0.1766	0.4139	**0.0131**	85 ± 10	103 ± 22	151 ± 21	169 ± 25
222041_at	DPH2L1	diptheria toxin resistance protein	0.0901	**-0.0076**	0.2567	0.4324	**0.0406**	284 ± 20	289 ± 26	322 ± 24	382 ± 30
201431_s_at	DPYSL3	dihydropyrimidinase-like 3	0.1273	**-0.0169**	0.1126	-0.3099	**0.0408**	1944 ± 171	1972 ± 138	3087 ± 420	2680 ± 414
206590_x_at	DRD2	dopamine receptor D2	**0.0231**	**-0.0193**	-0.2246	-0.4492	**0.0327**	250 ± 26	251 ± 9	273 ± 20	359 ± 44
206032_at	DSC3	desmocollin 3	**0.0398**	**-0.0466**	0.2311	0.1407	0.0591	105 ± 18	102 ± 14	133 ± 11	191 ± 43
200606_at	DSP	desmoplakin	0.3852	**-0.0076**	0.2251	0.3171	**0.0227**	157 ± 16	189 ± 21	286 ± 38	347 ± 81
205741_s_at	DTNA	dystrobrevin, alpha	0.0794	**-0.0375**	-0.1328	-0.2852	0.2491	781 ± 138	714 ± 106	934 ± 162	1260 ± 331
38037_at	DTR	diphtheria toxin receptor	**0.0040**	**0.0000**	-0.2801	0.3925	**0.0002**	200 ± 16	195 ± 20	228 ± 19	329 ± 25
205777_at	DUSP9	dual specificity phosphatase 9	**0.0234**	**-0.0209**	-0.1090	0.2903	**0.0348**	273 ± 38	223 ± 21	322 ± 32	409 ± 60
208955_at	DUT	dUTP pyrophosphatase	0.2888	**-0.0354**	-0.2468	0.3855	**0.0106**	309 ± 24	309 ± 16	300 ± 9	404 ± 34
222247_at	DXS542	putative X-linked retinopathy protein	0.4498	**-0.0042**	0.1001	**-0.0160**	**0.0358**	117 ± 8	141 ± 15	147 ± 13	175 ± 17
203262_s_at	DXS9928E	DNA segment on chromosome X 9928 expressed sequence	**0.0101**	**-0.0060**	-0.1346	0.3718	**0.0316**	882 ± 87	929 ± 92	987 ± 52	1250 ± 113
208713_at	E1B-AP5	E1B-55kDa-associated protein 5	0.0926	**-0.0300**	**0.0236**	-0.2869	**0.0231**	611 ± 39	810 ± 73	758 ± 39	837 ± 67
222051_s_at	E2F5	E2F transcription factor 5, p130-binding	**0.0540**	**-0.0236**	0.3119	-0.4168	**0.0105**	81 ± 12	121 ± 28	91 ± 10	219 ± 55
201749_at	ECE1	endothelin converting enzyme 1	**0.0323**	**-0.0025**	0.4218	-0.1976	**0.0488**	367 ± 65	371 ± 39	524 ± 53	660 ± 131
217497_at	ECGF1	endothelial cell growth factor 1	0.0970	**-0.0138**	0.1474	-0.2875	**0.0452**	106 ± 18	76 ± 12	109 ± 19	158 ± 19
204858_s_at	ECGF1	endothelial cell growth factor 1	-0.9602	**-0.0401**	0.4880	0.3053	**0.0314**	258 ± 41	221 ± 14	206 ± 23	428 ± 92
206101_at	ECM2	extracellular matrix protein 2	**0.0530**	**-0.0115**	0.1719	-0.1344	**0.0308**	249 ± 29	301 ± 44	493 ± 112	471 ± 48
220048_at	EDAR	ectodysplasin 1, anhidrotic receptor	**0.0458**	-0.0953	0.1863	0.1967	**0.0539**	270 ± 26	305 ± 62	268 ± 14	417 ± 48
209058_at	EDF1	endothelial differentiation-related factor 1	**0.0272**	-0.4963	0.1657	0.1372	0.6451	1566 ± 70	1531 ± 71	1730 ± 205	1798 ± 251
204464_s_at	EDNRA	endothelin receptor type A	**0.0209**	-0.1151	0.0798	**-0.0423**	0.4552	178 ± 16	211 ± 21	217 ± 22	229 ± 33
200919_at	EDR2	early development regulator 2	0.4775	**-0.0291**	0.2193	0.4029	0.0627	1650 ± 93	1859 ± 107	1756 ± 85	2114 ± 182
213614_x_at	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	**0.0016**	-0.0986	0.4804	0.1604	**0.0275**	16900 ± 813	16222 ± 317	548 ± 1268	9010 ± 1956
213477_x_at	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	**0.0022**	-0.1639	0.3792	-0.1628	**0.0209**	0405 ± 1281	21758 ± 869	374 ± 1469	2836 ± 2475
213583_x_at	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	**0.0057**	-0.0949	-0.4400	-0.3968	**0.0019**	12703 ± 735	13073 ± 203	7045 ± 859	14179 ± 984
203113_s_at	EEF1D	eukaryotic translation elongation factor 1 delta	**0.0083**	-0.2413	-0.2392	0.3612	0.4500	2217 ± 280	2326 ± 314	2813 ± 234	2750 ± 448
200689_x_at	EEF1G	eukaryotic translation elongation factor 1 gamma	**0.0189**	-0.5812	0.1266	-0.2644	0.1342	6523 ± 381	7297 ± 471	8204 ± 669	6937 ± 528
201843_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	0.1235	**-0.0246**	0.2269	**-0.0413**	0.2709	518 ± 50	673 ± 145	812 ± 189	935 ± 191
206580_s_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	**0.0049**	**-0.0071**	**0.0496**	-0.0812	**0.0171**	682 ± 79	701 ± 61	1081 ± 90	1051 ± 173
209356_x_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	**0.0006**	**-0.0194**	0.2244	0.3746	**0.0087**	368 ± 24	335 ± 17	524 ± 34	480 ± 70
202023_at	EFNA1	ephrin-A1	**0.0080**	**-0.0304**	-0.0845	-0.3531	0.1948	334 ± 51	325 ± 57	468 ± 65	517 ± 115
204400_at	EFS2	signal transduction protein	**0.0025**	**-0.0284**	0.0723	-0.2872	0.1001	575 ± 52	765 ± 115	806 ± 79	1099 ± 275
206254_at	EGF	epidermal growth factor	0.0576	**-0.0481**	-0.3784	-0.4958	0.0743	84 ± 7	98 ± 15	86 ± 21	156 ± 35
211551_at	EGFR	epidermal growth factor receptor oncogene homolog, avian)	0.2659	**-0.0047**	0.2270	-0.1849	**0.0266**	235 ± 24	255 ± 16	284 ± 19	342 ± 33
201984_s_at	EGFR	epidermal growth factor receptor oncogene homolog, avian)	0.3982	**-0.0187**	0.4366	-0.1343	0.1500	271 ± 33	273 ± 22	308 ± 16	351 ± 25
220956_s_at	EGLN2	egl nine homolog 2	0.0983	**-0.0275**	0.2139	-0.1987	0.2456	622 ± 54	591 ± 55	649 ± 31	739 ± 55
208112_x_at	EHD1	EH-domain containing 1	**0.0002**	**0.0000**	0.2233	-0.0891	**0.0000**	264 ± 33	348 ± 29	453 ± 37	609 ± 61
209039_x_at	EHD1	EH-domain containing 1	**0.0047**	**-0.0014**	-0.3383	-0.3237	**0.0007**	717 ± 47	786 ± 69	841 ± 64	1257 ± 141

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
212351_at	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon	**0.0149**	-0.0731	**-0.0084**	-0.2207	0.2530	423 ± 18	398 ± 29	437 ± 31	485 ± 38
218287_s_at	EIF2C1	eukaryotic translation initiation factor 2C, 1	**0.0175**	-0.1229	**0.0238**	-0.4644	0.1303	476 ± 30	586 ± 56	592 ± 30	663 ± 89
203462_x_at	EIF3S9	eukaryotic translation initiation factor 3, subunit 9 eta	**0.0066**	**-0.0008**	-0.4073	0.4087	**0.0073**	1209 ± 43	1209 ± 83	1354 ± 57	1521 ± 74
211937_at	EIF4B	eukaryotic translation initiation factor 4B	**0.0003**	-0.0967	0.0971	0.3661	0.1363	1205 ± 67	1275 ± 176	1660 ± 136	1506 ± 208
208707_at	EIF5	eukaryotic translation initiation factor 5	**0.0526**	**-0.0043**	0.1410	-0.2343	**0.0385**	549 ± 24	568 ± 40	648 ± 50	695 ± 36
219325_s_at	ELAC1	elaC homolog 1	**0.0252**	**-0.0430**	**0.0539**	0.4195	**0.0400**	48 ± 8	66 ± 17	66 ± 5	98 ± 14
203822_s_at	ELF2	E74-like factor 2	0.2468	**-0.0281**	-0.3003	-0.4960	**0.0337**	774 ± 47	849 ± 77	748 ± 41	1010 ± 83
31845_at	ELF4	E74-like factor 4	0.1010	**-0.0203**	0.2169	0.3826	**0.0539**	97 ± 14	126 ± 27	112 ± 10	182 ± 34
203617_x_at	ELK1	ELK1, member of ETS oncogene family	**0.0366**	-0.1253	0.3243	0.4405	0.2507	1084 ± 116	1339 ± 214	1423 ± 72	1547 ± 242
220366_at	ELSPBP1	epididymal sperm binding protein 1	**0.0329**	-0.0602	0.1542	0.4590	0.1215	153 ± 17	186 ± 31	183 ± 16	259 ± 53
204398_s_at	EML2	echinoderm microtubule associated protein like 2	0.0821	**-0.0482**	0.3391	-0.3220	0.0842	591 ± 60	662 ± 57	591 ± 33	819 ± 108
201324_at	EMP1	epithelial membrane protein 1	**0.0170**	**-0.0010**	-0.3348	-0.0792	**0.0249**	232 ± 41	216 ± 45	347 ± 46	501 ± 117
213895_at	EMP1	epithelial membrane protein 1	**0.0086**	**-0.0379**	0.4527	0.3056	0.1096	103 ± 16	107 ± 16	121 ± 13	155 ± 17
217820_s_at	ENAH	enabled homolog	**0.0499**	**-0.0125**	0.2796	**-0.0357**	**0.0402**	1003 ± 42	1081 ± 99	1448 ± 189	1348 ± 61
37408_at	ENDO180	endocytic receptor	0.0634	**-0.0157**	0.0815	-0.0639	**0.0048**	436 ± 41	509 ± 23	384 ± 29	751 ± 127
213579_s_at	EP300	E1A binding protein p300	**0.0097**	**-0.0009**	0.1249	**-0.0004**	**0.0051**	203 ± 25	266 ± 19	246 ± 21	348 ± 36
212376_s_at	EP400	E1A binding protein p400	**0.0274**	-0.2770	**0.0508**	0.4744	0.2432	371 ± 17	379 ± 16	445 ± 18	421 ± 53
210825_s_at	EPB72	erythrocyte membrane protein band 7.2	**0.0250**	-0.1139	0.1575	0.4327	**0.0259**	9039 ± 421	9554 ± 256	1051 ± 622	10300 ± 434
201061_s_at	EPB72	erythrocyte membrane protein band 7.2	**0.0032**	**-0.0020**	0.3088	-0.3868	**0.0282**	2615 ± 197	2692 ± 271	3102 ± 203	3571 ± 263
209963_s_at	EPOR	erythropoietin receptor	**0.0052**	-0.0703	0.1661	-0.0774	0.1755	141 ± 11	164 ± 14	163 ± 9	188 ± 23
37986_at	EPOR	erythropoietin receptor	0.0984	**-0.0019**	-0.2489	-0.3140	**0.0129**	223 ± 21	210 ± 33	216 ± 10	344 ± 47
200842_s_at	EPRS	glutamyl-prolyl-tRNA synthetase	**0.0067**	-0.0694	-0.4863	-0.1668	0.1271	594 ± 52	576 ± 58	682 ± 75	844 ± 135
202609_at	EPS8	epidermal growth factor receptor pathway substrate 8	0.4848	**-0.0113**	0.3343	**-0.0202**	0.3262	813 ± 39	849 ± 102	1025 ± 88	1024 ± 174
212087_s_at	ERAL1	Era G-protein-like 1	0.2567	**-0.0210**	**0.0372**	**-0.0020**	0.0745	589 ± 26	656 ± 33	633 ± 55	783 ± 75
217941_s_at	ERBB2IP	erbb2 interacting protein	**0.0126**	**-0.0033**	-0.4232	**-0.0457**	**0.0032**	2624 ± 324	3068 ± 269	4899 ± 635	4093 ± 386
206794_at	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	**0.0094**	-0.5273	0.1832	-0.2239	0.7749	86 ± 11	97 ± 11	97 ± 9	108 ± 25
207347_at	ERCC6	excision repair cross-complementing rodent repair def. 6	0.0610	**-0.0303**	0.1977	-0.3328	0.0963	225 ± 23	227 ± 17	247 ± 23	326 ± 50
203643_at	ERF	Ets2 repressor factor	**0.0076**	**-0.0039**	**0.0463**	-0.1209	**0.0003**	181 ± 32	363 ± 33	447 ± 52	420 ± 48
208958_at	ERp44	endoplasmic reticulum resident protein 44 kDa	0.6145	**-0.0404**	0.1841	-0.0993	0.0730	154 ± 11	150 ± 9	213 ± 22	188 ± 24
208658_at	ERP70	protein disulfide isomerase related protein	**0.0124**	-0.0576	-0.3718	0.4224	0.3098	369 ± 40	361 ± 45	413 ± 37	485 ± 74
213873_at	ESDN	endothelial and smooth muscle cell-derived neuropilin-like	0.0565	**-0.0356**	**0.0192**	-0.1737	0.1039	152 ± 10	205 ± 20	195 ± 16	256 ± 53
202081_at	ETR101	immediate early protein	0.2720	**-0.0060**	-0.2287	0.2698	**0.0254**	1192 ± 82	1165 ± 157	1286 ± 107	1676 ± 141
204774_at	EVI2A	ecotropic viral integration site 2A	0.6624	**-0.0052**	0.2425	-0.3038	0.2040	1650 ± 156	1820 ± 291	2110 ± 241	2297 ± 237
211742_s_at	EVI2B	ecotropic viral integration site 2B	0.5752	**-0.0168**	0.3591	-0.0897	0.2783	438 ± 56	486 ± 57	508 ± 40	578 ± 42
209214_s_at	EWSR1	Ewing sarcoma breakpoint region 1	**0.0184**	**-0.0015**	0.3634	**-0.0204**	**0.0153**	1151 ± 47	1317 ± 96	1371 ± 42	1466 ± 69
50376_at	EZF-2	endothelial zinc finger protein 2	**0.0047**	-0.0929	**0.0357**	-0.4982	0.0750	943 ± 78	1307 ± 234	1181 ± 136	1619 ± 229
218707_at	EZF-2	endothelial zinc finger protein 2	**0.0040**	**-0.0007**	-0.3312	-0.2959	**0.0047**	218 ± 37	151 ± 27	323 ± 42	395 ± 62
203989_x_at	F2R	coagulation factor II receptor	0.2415	**-0.0155**	**0.0442**	-0.0761	**0.0227**	49 ± 8	67 ± 7	63 ± 10	100 ± 18
219429_at	FAAH	fatty acid hydroxylase	0.7656	**-0.0105**	0.4165	-0.4211	0.1621	1173 ± 105	1066 ± 129	1304 ± 156	1625 ± 264
201963_at	FACL2	fatty-acid-Coenzyme A ligase, long-chain 2	0.9855	**-0.0127**	-0.1234	-0.2482	0.1972	1446 ± 132	1425 ± 189	1375 ± 132	1975 ± 350
208962_s_at	FADS1	fatty acid desaturase 1	**0.0077**	**-0.0010**	0.0692	**-0.0475**	**0.0059**	1176 ± 114	1536 ± 158	2085 ± 232	2454 ± 398
204257_at	FADS3	fatty acid desaturase 3	**0.0517**	**-0.0355**	0.4612	0.1031	0.1085	490 ± 26	472 ± 25	499 ± 40	629 ± 78

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
209405_s_at	FAM3A	family with sequence similarity 3, member A	**0.0042**	-0.2095	**0.0299**	0.2812	0.1813	267 ± 9	341 ± 45	397 ± 54	369 ± 52
38043_at	FAM3A	family with sequence similarity 3, member A	**0.0027**	**-0.0302**	0.0835	-0.3574	0.0887	462 ± 37	483 ± 56	503 ± 25	709 ± 134
220255_at	FANCE	Fanconi anemia, complementation group E	**0.0172**	**-0.0410**	-0.4864	-0.1755	0.1587	106 ± 13	95 ± 24	123 ± 12	155 ± 23
202995_s_at	FBLN1	fibulin 1	**0.0296**	-0.1146	0.3952	0.2100	0.2188	190 ± 15	188 ± 17	200 ± 16	272 ± 59
202766_s_at	FBN1	fibrillin 1	**0.0393**	**-0.0008**	-0.3708	**-0.0354**	**0.0410**	303 ± 25	313 ± 18	385 ± 24	395 ± 39
203184_at	FBN2	fibrillin 2	**0.0038**	**-0.0005**	**0.0026**	-0.1568	**0.0004**	73 ± 8	100 ± 4	95 ± 10	156 ± 21
213940_s_at	FBP17	formin-binding protein 17	**0.0310**	-0.2360	**0.0351**	-0.1219	0.0597	266 ± 35	377 ± 65	485 ± 71	346 ± 52
212288_at	FBP17	formin-binding protein 17	0.0699	**-0.0131**	0.3263	-0.1196	0.0979	1483 ± 125	1845 ± 265	1954 ± 55	2071 ± 201
208988_at	FBXL11	F-box and leucine-rich repeat protein 11	**0.0420**	-0.3816	-0.3414	-0.2992	0.4891	917 ± 80	790 ± 31	958 ± 52	941 ± 111
209005_at	FBXL5	F-box and leucine-rich repeat protein 5	**0.0149**	-0.1215	0.4708	0.3412	0.3649	1150 ± 68	1165 ± 102	1220 ± 61	1339 ± 90
213249_at	FBXL7	F-box and leucine-rich repeat protein 7	0.0883	**-0.0007**	0.4879	-0.2287	**0.0496**	580 ± 50	623 ± 32	719 ± 42	774 ± 74
219305_x_at	FBXO2	F-box only protein 2	0.1118	**-0.0089**	-0.4853	-0.1051	0.1061	1464 ± 100	1512 ± 186	1764 ± 156	2076 ± 273
212991_at	FBXO9	F-box only protein 9	**0.0175**	-0.0685	-0.3605	-0.3832	0.1810	534 ± 53	464 ± 29	675 ± 76	814 ± 207
214623_at	FBXW3	F-box and WD-40 domain protein 3	**0.0084**	**-0.0163**	**0.0019**	-0.0990	**0.0179**	34 ± 9	69 ± 18	80 ± 18	134 ± 35
208647_at	FDFT1	farnesyl-diphosphate farnesyltransferase 1	0.1174	**-0.0001**	**-0.0372**	-0.3202	**0.0044**	3066 ± 241	2739 ± 279	3693 ± 128	4054 ± 317
201275_at	FDPS	farnesyl diphosphate synthase	0.1716	**-0.0040**	-0.2270	-0.2568	**0.0348**	495 ± 36	491 ± 41	623 ± 47	646 ± 52
37384_at	FEM-2	partner of PIX 2	**0.0099**	**-0.0029**	-0.0720	0.2527	**0.0063**	601 ± 49	481 ± 38	687 ± 45	819 ± 90
214417_s_at	FETUB	fetuin B	**0.0390**	**-0.0034**	**0.0538**	-0.2644	**0.0002**	74 ± 7	111 ± 9	95 ± 9	152 ± 18
203562_at	FEZ1	fasciculation and elongation protein zeta 1	0.1361	**-0.0112**	0.4477	0.4564	0.1458	8620 ± 513	9094 ± 1000	9994 ± 861	11074 ± 716
210704_at	FEZ2	fasciculation and elongation protein zeta 2	**0.0206**	-0.0694	0.2365	0.3726	0.0849	125 ± 10	157 ± 16	148 ± 15	194 ± 30
205117_at	FGF1	fibroblast growth factor 1	**0.0335**	**-0.0466**	0.3218	-0.2871	0.1717	2890 ± 414	3520 ± 567	4195 ± 455	4073 ± 418
214284_s_at	FGF18	fibroblast growth factor 18	**0.0350**	-0.2066	0.1269	-0.4345	0.1048	79 ± 10	78 ± 11	130 ± 18	106 ± 25
211535_s_at	FGFR1	fibroblast growth factor receptor 1	**0.0308**	**-0.0134**	-0.3851	-0.0706	0.1287	553 ± 44	624 ± 78	706 ± 85	776 ± 64
207822_at	FGFR1	fibroblast growth factor receptor 1	**0.0419**	**-0.0219**	-0.3246	0.2605	0.0933	162 ± 23	132 ± 13	186 ± 30	230 ± 28
204379_s_at	FGFR3	fibroblast growth factor receptor 3	**0.0009**	**-0.0075**	**0.0018**	-0.1005	**0.0349**	1925 ± 183	2388 ± 291	3023 ± 414	3684 ± 718
205305_at	FGL1	fibrinogen-like 1	**0.0010**	**-0.0038**	0.2055	**-0.0102**	**0.0214**	158 ± 14	189 ± 13	223 ± 23	286 ± 50
203734_at	FHX	FOXJ2 forkhead factor	**0.0165**	**-0.0008**	0.0703	-0.1768	**0.0004**	538 ± 24	628 ± 47	556 ± 30	832 ± 71
40850_at	FKBP8	FK506 binding protein 8, 38kDa	**0.0214**	-0.8156	-0.3324	-0.3505	0.1388	789 ± 109	959 ± 155	1328 ± 141	871 ± 279
222065_s_at	FLII	flightless I homolog	**0.0534**	**-0.0288**	-0.4035	**-0.0297**	0.2726	324 ± 17	359 ± 46	386 ± 10	395 ± 31
218993_at	FLJ10581	putative RNA methyltransferase	**0.0125**	-0.1307	0.1828	**-0.0363**	**0.0507**	348 ± 13	364 ± 13	329 ± 30	430 ± 36
218485_s_at	FLJ11320	GDP-fucose transporter 1	0.1421	**-0.0224**	0.1217	**-0.0303**	**0.0163**	182 ± 15	202 ± 12	180 ± 17	270 ± 33
218658_s_at	FLJ12934	likely ortholog of mouse actin-related protein 8 homolog	**0.0081**	**-0.0206**	**0.0037**	-0.1453	**0.0018**	205 ± 13	313 ± 38	300 ± 7	330 ± 21
208919_s_at	FLJ13052	NAD kinase	0.1013	**-0.0038**	-0.2803	0.1632	**0.0083**	637 ± 23	640 ± 45	798 ± 37	823 ± 69
219020_at	FLJ14249	hypothetical protein FLJ14249	**0.0129**	**-0.0078**	0.1252	0.4713	**0.0262**	572 ± 40	666 ± 72	645 ± 27	840 ± 93
220349_s_at	FLJ21865	endo-beta-N-acetylglucosaminidase	**0.0002**	**-0.0027**	0.4989	-0.2325	**0.0199**	290 ± 28	307 ± 34	353 ± 50	515 ± 84
65635_at	FLJ21865	endo-beta-N-acetylglucosaminidase	**0.0018**	**-0.0152**	0.2788	0.4974	**0.0397**	1096 ± 83	1206 ± 141	1257 ± 113	1711 ± 248
219677_at	FLJ22393	SPRY domain-containing SOCS box protein SSB-1	**0.0150**	-0.1910	0.2423	0.4844	0.2943	271 ± 33	347 ± 60	337 ± 25	406 ± 76
220078_at	FLJ23277	FLJ23277 protein	**0.0286**	**-0.0037**	0.2386	-0.0590	**0.0332**	153 ± 22	197 ± 23	218 ± 14	255 ± 34
213746_s_at	FLNA	filamin A, alpha	**0.0389**	-0.0994	0.2038	0.3077	0.2700	211 ± 17	204 ± 28	310 ± 52	296 ± 74
214752_x_at	FLNA	filamin A, alpha	**0.0016**	**-0.0016**	0.0618	0.3999	**0.0197**	375 ± 32	376 ± 33	504 ± 52	631 ± 103
200859_x_at	FLNA	filamin A, alpha	**0.0088**	**-0.0235**	0.1556	0.4354	0.1889	593 ± 51	583 ± 83	705 ± 57	810 ± 124
207876_s_at	FLNC	filamin C, gamma	**0.0000**	**-0.0031**	**0.0096**	-0.2264	**0.0220**	296 ± 28	363 ± 88	487 ± 52	576 ± 90

Probe set	Name	Description	NFT$_{O}$	MMSE$_{O}$	NFT$_{I}$	MMSE$_{I}$	ANOVA	Control	Incipient	Moderate	Severe
211726_s_at	FMO2	flavin containing monooxygenase 2	**0.0111**	**-0.0001**	0.1205	-0.2048	**0.0038**	213 ± 17	221 ± 11	313 ± 27	371 ± 52
213729_at	FNBP3	formin binding protein 3	**0.0244**	-0.1181	0.4285	-0.0703	0.1529	743 ± 71	909 ± 74	866 ± 53	982 ± 99
218053_at	FNBP3	formin binding protein 3	**0.0032**	**-0.0028**	**0.0247**	**-0.0094**	**0.0012**	820 ± 51	979 ± 63	1334 ± 126	1194 ± 80
211303_x_at	FOLH1	folate hydrolase 1	0.5866	**-0.0116**	0.4028	-0.0704	0.0734	209 ± 15	182 ± 33	319 ± 66	389 ± 88
202724_s_at	FOXO1A	forkhead box O1A	**0.0008**	**0.0000**	0.3261	-0.1806	**0.0002**	429 ± 27	514 ± 47	638 ± 44	745 ± 56
204131_s_at	FOXO3A	forkhead box O3A	**0.0016**	**-0.0039**	0.2351	-0.2294	**0.0246**	1779 ± 163	1890 ± 150	2030 ± 170	2696 ± 329
219889_at	FRAT1	frequently rearranged in advanced T-cell lymphomas	**0.0287**	**-0.0351**	0.1516	0.3567	**0.0079**	253 ± 17	290 ± 35	269 ± 15	387 ± 36
203592_s_at	FSTL3	follistatin-like 3	**0.0135**	-0.0880	-0.1028	0.3068	0.1070	342 ± 33	340 ± 38	331 ± 31	517 ± 107
214211_at	FTH1	ferritin, heavy polypeptide 1	**0.0031**	**-0.0120**	0.0583	-0.2873	**0.0508**	5115 ± 224	5411 ± 567	6197 ± 500	6658 ± 227
213187_x_at	FTL	ferritin, light polypeptide	**0.0008**	-0.1316	0.3645	0.1251	0.1597	12189 ± 926	1772 ± 1300	508 ± 1226	4232 ± 1771
220856_x_at	FTL	ferritin, light polypeptide	**0.0000**	**-0.0276**	0.2405	-0.4983	0.0794	2021 ± 198	2210 ± 258	2776 ± 225	2989 ± 451
210608_s_at	FUT2	fucosyltransferase 2	**0.0025**	**-0.0411**	**0.0107**	-0.3321	0.0771	150 ± 8	165 ± 12	164 ± 13	209 ± 27
202419_at	FVT1	follicular lymphoma variant translocation 1	**0.0037**	**-0.0255**	0.2682	**-0.0355**	0.1621	1159 ± 84	1279 ± 108	1477 ± 108	1416 ± 139
201635_s_at	FXR1	fragile X mental retardation, autosomal homolog 1	**0.0053**	-0.2314	-0.4560	-0.3281	0.4178	339 ± 36	349 ± 38	322 ± 39	468 ± 125
218204_s_at	FYCO1	FYVE and coiled-coil domain containing 1	**0.0017**	**-0.0002**	-0.3794	-0.2551	**0.0004**	189 ± 24	190 ± 11	214 ± 22	338 ± 30
212486_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.1121	**-0.0214**	0.2110	**-0.0053**	0.0766	729 ± 44	807 ± 99	1057 ± 118	954 ± 113
210105_s_at	FYN	FYN oncogene related to SRC, FGR, YES	**0.0168**	**-0.0301**	0.1020	-0.1987	0.0776	4639 ± 246	5050 ± 186	5724 ± 525	5746 ± 313
219764_at	FZD10	frizzled homolog 10	0.2412	**-0.0097**	0.0959	-0.2894	0.0755	154 ± 14	174 ± 25	161 ± 11	219 ± 21
209414_at	FZR1	Fzr1 protein	0.0802	**-0.0120**	**0.0051**	**-0.0004**	**0.0042**	114 ± 9	162 ± 8	177 ± 15	194 ± 22
209416_s_at	FZR1	Fzr1 protein	0.2781	**-0.0435**	0.4026	-0.3404	0.3116	360 ± 31	409 ± 61	409 ± 16	471 ± 38
202275_at	G6PD	glucose-6-phosphate dehydrogenase	**0.0001**	-0.1379	0.1634	-0.1570	0.0760	233 ± 17	289 ± 23	355 ± 31	309 ± 57
203853_s_at	GAB2	GRB2-associated binding protein 2	**0.0202**	-0.2032	0.0723	-0.4535	0.4749	1281 ± 77	1465 ± 172	1393 ± 72	1660 ± 308
220886_at	GABRQ	gamma-aminobutyric acid receptor, theta	0.1085	**-0.0081**	**0.0039**	**-0.0035**	**0.0053**	98 ± 11	188 ± 27	155 ± 13	205 ± 29
209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, beta	0.4308	**-0.0124**	-0.2865	-0.2601	0.1684	200 ± 83	252 ± 88	251 ± 57	529 ± 174
207574_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta	0.6976	**-0.0411**	-0.1461	0.4709	0.1877	826 ± 194	569 ± 82	1189 ± 215	1206 ± 309
204121_at	GADD45G	growth arrest and DNA-damage-inducible, gamma	**0.0529**	**-0.0019**	-0.2213	0.3086	**0.0079**	135 ± 17	140 ± 34	178 ± 18	256 ± 31
207086_x_at	GAGE4	G antigen 4	**0.0403**	-0.0749	0.2067	-0.3665	**0.0374**	118 ± 14	138 ± 16	119 ± 9	213 ± 48
208155_x_at	GAGE6	G antigen 6	**0.0492**	**-0.0148**	0.2833	0.2955	**0.0531**	126 ± 10	127 ± 19	169 ± 12	181 ± 25
40225_at	GAK	cyclin G associated kinase	**0.0110**	**-0.0547**	0.4185	0.2943	0.0997	1839 ± 167	1896 ± 349	1959 ± 92	2761 ± 433
202281_at	GAK	cyclin G associated kinase	**0.0158**	-0.1064	-0.3730	0.2430	0.3096	547 ± 52	491 ± 102	643 ± 53	709 ± 129
201723_s_at	GALNT1	UDP-N-acetyl-alpha-D-galactosamine 1	0.3002	**-0.0336**	0.4142	-0.1813	0.1038	512 ± 23	533 ± 16	585 ± 26	600 ± 43
219956_at	GALNT6	UDP-N-acetyl-alpha-D-galactosamine 6	0.5226	**-0.0081**	-0.2252	-0.3535	0.0998	316 ± 33	323 ± 28	361 ± 80	539 ± 87
220929_at	GALNT8	UDP-N-acetyl-alpha-D-galactosamine: 8	**0.0011**	-0.0598	-0.2898	0.3891	0.2407	132 ± 12	144 ± 9	163 ± 20	192 ± 37
205354_at	GAMT	guanidinoacetate N-methyltransferase	**0.0054**	-0.0940	**0.0021**	-0.1239	0.1569	317 ± 31	370 ± 30	364 ± 43	478 ± 80
204028_s_at	GAPCENA	rab6 GTPase activating protein	**0.0039**	**-0.0231**	0.1198	-0.3690	**0.0537**	1472 ± 78	1620 ± 85	1747 ± 129	1902 ± 121
208138_at	GAS	gastrin	0.6262	**-0.0311**	0.1528	-0.1679	0.0704	223 ± 24	270 ± 29	240 ± 22	327 ± 37
204457_s_at	GAS1	growth arrest-specific 1	**0.0047**	**-0.0060**	-0.1530	-0.2460	0.0807	331 ± 37	349 ± 63	390 ± 66	526 ± 51
31874_at	GAS2L1	growth arrest-specific 2 like 1	0.2561	**-0.0327**	0.4090	0.2762	0.1216	1999 ± 167	2135 ± 280	2363 ± 166	3051 ± 551
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.4795	**-0.0005**	0.4933	**-0.0312**	**0.0459**	84 ± 17	90 ± 16	154 ± 26	164 ± 33
202269_x_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.0872	**-0.0160**	-0.2118	-0.2896	0.1216	123 ± 26	108 ± 10	200 ± 42	186 ± 34
202748_at	GBP2	guanylate binding protein 2, interferon-inducible	0.0695	**-0.0181**	0.4744	-0.3312	0.0969	261 ± 48	207 ± 28	288 ± 38	375 ± 48
218912_at	GCC1	golgi coiled coil 1	0.2364	**-0.0155**	-0.4072	0.3610	0.1502	397 ± 33	383 ± 12	466 ± 33	479 ± 44

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
202923_s_at	GCLC	glutamate-cysteine ligase, catalytic subunit	0.3378	**-0.0329**	-0.3315	-0.3267	0.3079	721 ± 30	772 ± 84	786 ± 79	890 ± 51
206397_x_at	GDF1	growth differentiation factor 1	**0.0007**	**-0.0021**	**0.0047**	0.1810	**0.0013**	3388 ± 448	3988 ± 621	4835 ± 615	9008 ± 1706
221314_at	GDF9	growth differentiation factor 9	0.2946	**-0.0145**	0.0757	-0.2874	0.0774	188 ± 17	194 ± 17	208 ± 19	265 ± 29
204472_at	GEM	GTP binding protein overexpressed in skeletal muscle	0.3951	**-0.0200**	**-0.0220**	-0.3777	0.1794	528 ± 93	462 ± 42	558 ± 82	775 ± 150
203540_at	GFAP	glial fibrillary acidic protein	**0.0007**	**-0.0047**	0.2849	-0.3598	**0.0028**	9575 ± 2303	2303 ± 2309	4655 ± 3370	1436 ± 3898
205100_at	GFPT2	glutamine-fructose-6-phosphate transaminase 2	**0.0024**	**-0.0031**	-0.1919	-0.2648	**0.0390**	473 ± 53	509 ± 63	534 ± 37	735 ± 100
210260_s_at	GG2-1	TNF-induced protein	0.2697	**-0.0056**	0.1440	-0.1486	**0.0337**	89 ± 9	87 ± 14	82 ± 9	132 ± 16
208296_x_at	GG2-1	TNF-induced protein	**0.0052**	**-0.0010**	-0.1026	-0.3941	**0.0051**	137 ± 17	114 ± 10	176 ± 13	205 ± 24
50277_at	GGA1	golgi assoc., gamma adaptin ear cont., ARF binding 1	**0.0087**	**-0.0094**	0.1813	0.2164	**0.0065**	2115 ± 127	2236 ± 261	2197 ± 145	3273 ± 392
45572_s_at	GGA1	golgi assoc., gamma adaptin ear cont., ARF binding 1	**0.0079**	**-0.0332**	0.1441	0.1918	**0.0153**	2083 ± 124	2157 ± 175	2082 ± 142	2916 ± 319
214233_at	GGA2	golgi assoc., gamma adaptin ear cont., ARF binding 2	0.2847	**-0.0221**	0.3788	-0.4479	**0.0146**	201 ± 28	234 ± 14	188 ± 23	336 ± 50
202321_at	GGPS1	geranylgeranyl diphosphate synthase 1	0.0578	**-0.0398**	0.1741	0.4364	0.2752	283 ± 21	262 ± 8	295 ± 27	330 ± 25
207131_x_at	GGT1	gamma-glutamyltransferase 1	**0.0498**	-0.5682	0.3518	-0.3872	0.6655	228 ± 15	251 ± 32	242 ± 12	281 ± 57
219571_s_at	GIOT-3	GIOT-3 for gonadotropin inducible transcription repressor-3	**0.0101**	**-0.0263**	0.4362	0.4414	**0.0373**	385 ± 21	402 ± 20	479 ± 32	451 ± 22
201667_at	GJA1	gap junction protein, alpha 1, 43kDa	**0.0088**	**-0.0029**	0.2614	**-0.0394**	**0.0066**	8527 ± 616	9294 ± 933	145 ± 1106	1958 ± 1320
204973_at	GJB1	gap junction protein, beta 1, 32kDa	0.5627	**-0.0024**	-0.3942	-0.1613	0.0559	259 ± 33	245 ± 32	338 ± 31	414 ± 74
207034_s_at	GLI2	GLI-Kruppel family member GLI2	**0.0394**	**-0.0313**	**0.0002**	**-0.0537**	**0.0125**	53 ± 6	94 ± 16	93 ± 8	96 ± 9
208240_s_at	GLIO703	acid fibroblast growth factor-like protein	**0.0193**	-0.4557	0.1676	-0.2935	0.4785	436 ± 71	591 ± 110	626 ± 85	608 ± 137
216021_s_at	GLRA3	glycine receptor, alpha 3	0.2047	**-0.0032**	-0.1144	-0.2517	**0.0145**	69 ± 19	53 ± 12	67 ± 12	134 ± 22
217807_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	0.0973	**-0.0335**	0.0961	0.3195	0.0610	5524 ± 762	6032 ± 1154	5937 ± 422	9236 ± 1566
222251_s_at	GMEB2	glucocorticoid modulatory element binding protein 2	**0.0036**	**-0.0040**	**-0.0161**	0.0936	**0.0060**	456 ± 17	447 ± 57	510 ± 45	748 ± 102
44146_at	GMEB2	glucocorticoid modulatory element binding protein 2	**0.0193**	**-0.0230**	0.1818	-0.4741	0.1046	942 ± 47	984 ± 95	1064 ± 58	1255 ± 154
202543_s_at	GMFB	glia maturation factor, beta	**0.0300**	-0.2118	0.4027	-0.4285	**0.0298**	258 ± 26	283 ± 36	436 ± 57	312 ± 50
218350_s_at	GMNN	geminin, DNA replication inhibitor	0.1277	**-0.0353**	-0.4888	-0.3441	0.2385	557 ± 48	531 ± 44	677 ± 69	691 ± 92
204187_at	GMPR	guanosine monophosphate reductase	**0.0020**	**-0.0003**	-0.2771	**-0.0474**	**0.0068**	302 ± 34	346 ± 63	558 ± 102	663 ± 97
214431_at	GMPS	guanine monphosphate synthetase	**0.0463**	-0.3648	0.1747	0.3103	0.5494	224 ± 24	224 ± 8	265 ± 28	265 ± 40
221737_at	GNA12	guanine nucleotide binding protein alpha 12	**0.0009**	**-0.0057**	0.1159	0.3704	**0.0240**	683 ± 54	714 ± 119	949 ± 83	1050 ± 119
201180_s_at	GNAI3	guanine nucleotide binding protein, alpha inhibiting activity 3	0.1123	**-0.0083**	0.3466	**-0.0228**	0.0947	946 ± 113	1147 ± 112	1067 ± 82	1310 ± 81
204993_at	GNAZ	guanine nucleotide binding protein , alpha z polypeptide	**0.0099**	**-0.0145**	**0.0088**	-0.0983	**0.0075**	943 ± 54	1089 ± 18	1052 ± 71	1320 ± 104
203383_s_at	GOLGA1	golgi autoantigen, golgin subfamily a, 1	0.2846	**-0.0406**	**-0.0077**	0.1321	**0.0387**	562 ± 48	476 ± 28	527 ± 40	673 ± 55
202106_at	GOLGA3	golgi autoantigen, golgin subfamily a, 3	**0.0078**	-0.1783	0.1386	-0.3005	0.4777	578 ± 32	640 ± 43	632 ± 57	698 ± 81
201567_s_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	0.5147	**-0.0185**	0.4713	**-0.0085**	0.2212	740 ± 42	859 ± 75	879 ± 78	934 ± 62
201056_at	GOLGB1	golgi autoantigen, golgin subfamily b, macrogolgin , 1	**0.0162**	-0.1767	0.4898	-0.4079	0.3962	591 ± 38	653 ± 70	653 ± 42	730 ± 79
204324_s_at	GOLPH4	golgi phosphoprotein 4	**0.0002**	-0.0585	0.0616	0.3239	0.1384	194 ± 24	176 ± 18	283 ± 35	308 ± 77
204630_s_at	GOSR1	golgi SNAP receptor complex member 1	**0.0004**	-0.0829	0.1248	-0.0587	0.2339	1205 ± 69	1251 ± 38	1597 ± 206	1693 ± 345
213206_at	GOSR2	golgi SNAP receptor complex member 2	**0.0171**	-0.2925	0.3581	**-0.0243**	0.1655	82 ± 14	96 ± 16	139 ± 13	122 ± 31
213180_s_at	GOSR2	golgi SNAP receptor complex member 2	0.1599	**-0.0367**	-0.1493	-0.4145	**0.0150**	222 ± 12	182 ± 20	205 ± 18	265 ± 16
222058_at	GP	goliath protein	**0.0234**	**-0.0021**	-0.2028	-0.3028	**0.0280**	364 ± 41	402 ± 38	410 ± 46	554 ± 48
204984_at	GPC4	glypican 4	0.1666	**-0.0028**	0.3112	-0.2522	**0.0219**	252 ± 27	306 ± 38	333 ± 41	415 ± 33
209167_at	GPM6B	glycoprotein M6B	0.2911	**-0.0011**	0.4608	-0.1684	**0.0395**	5522 ± 1053	15349 ± 337	8872 ± 810	9279 ± 1859
209170_s_at	GPM6B	glycoprotein M6B	0.5022	**-0.0203**	-0.2370	-0.1752	0.2397	16565 ± 956	6441 ± 1640	9620 ± 1469	9438 ± 1756
214605_x_at	GPR1	G protein-coupled receptor 1	**0.0121**	-0.1013	-0.1805	0.1836	0.1079	99 ± 16	66 ± 18	111 ± 18	168 ± 50

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
211977_at	GPR107	G protein-coupled receptor 107	0.1652	**-0.0414**	**0.0094**	-0.4349	0.0648	280 ± 16	355 ± 44	305 ± 22	424 ± 61
220565_at	GPR2	G protein-coupled receptor 2	0.0626	**-0.0228**	-0.4947	0.1235	**0.0097**	137 ± 13	123 ± 21	135 ± 15	229 ± 36
206960_at	GPR23	G protein-coupled receptor 23	**0.0237**	-0.5581	**0.0386**	**-0.0143**	0.2369	61 ± 9	86 ± 17	97 ± 12	76 ± 12
206236_at	GPR4	G protein-coupled receptor 4	0.1179	**-0.0222**	0.1394	-0.3591	0.0902	131 ± 15	166 ± 34	164 ± 19	221 ± 29
206361_at	GPR44	G protein-coupled receptor 44	0.0688	**-0.0232**	0.2274	**-0.0518**	**0.0404**	158 ± 15	193 ± 28	161 ± 19	261 ± 44
213880_at	GPR49	G protein-coupled receptor 49	-0.9964	**-0.0292**	-0.4843	-0.3200	0.3585	310 ± 22	269 ± 26	391 ± 74	392 ± 71
212070_at	GPR56	G protein-coupled receptor 56	**0.0227**	**-0.0076**	0.0824	-0.2145	0.0914	2205 ± 241	2498 ± 267	2691 ± 85	2995 ± 154
206002_at	GPR64	G protein-coupled receptor 64	0.4096	**-0.0444**	-0.1669	-0.2039	0.1291	94 ± 12	112 ± 16	134 ± 17	138 ± 9
214467_at	GPR65	G protein-coupled receptor 65	0.0978	**-0.0058**	0.2720	**-0.0545**	0.0601	65 ± 8	92 ± 12	119 ± 23	126 ± 19
203632_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	0.5907	**-0.0031**	-0.1174	-0.2951	0.0812	9378 ± 775	10323 ± 997	10702 ± 893	2968 ± 1198
204396_s_at	GPRK5	G protein-coupled receptor kinase 5	**0.0191**	-0.0629	0.3653	-0.2351	0.1079	260 ± 18	296 ± 30	292 ± 23	357 ± 35
210981_s_at	GPRK6	G protein-coupled receptor kinase 6	**0.0252**	-0.3525	-0.4139	-0.3627	0.3867	253 ± 32	306 ± 45	340 ± 45	327 ± 36
214091_s_at	GPX3	glutathione peroxidase 3	0.0722	**-0.0468**	-0.4047	0.1236	0.1524	487 ± 69	402 ± 27	536 ± 54	999 ± 377
205068_s_at	GRAF	GTPase regulator assoc. with focal adhesion kinase pp125	**0.0153**	**-0.0480**	-0.2873	-0.4590	0.1240	363 ± 18	347 ± 20	358 ± 35	448 ± 44
210999_s_at	GRB10	growth factor receptor-bound protein 10	**0.0198**	**-0.0152**	**-0.0308**	0.3708	**0.0133**	195 ± 25	149 ± 18	204 ± 20	329 ± 62
212244_at	GRINL1A	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	0.1961	**-0.0272**	-0.2613	-0.1004	0.3773	735 ± 71	761 ± 78	834 ± 76	901 ± 26
208035_at	GRM6	glutamate receptor, metabotropic 6	0.1456	**-0.0001**	0.2317	**-0.0015**	**0.0001**	281 ± 17	306 ± 24	286 ± 29	492 ± 46
205801_s_at	GRP3	guanine nucleotide exchange factor for Rap1	0.1063	**-0.0016**	0.3245	0.4359	**0.0067**	263 ± 33	223 ± 36	493 ± 94	494 ± 64
209945_s_at	GSK3B	glycogen synthase kinase 3 beta	**0.0279**	-0.0703	0.1326	**-0.0481**	**0.0448**	419 ± 24	548 ± 55	559 ± 18	616 ± 77
210912_x_at	GSTM4	glutathione S-transferase M4	0.1168	**-0.0165**	0.4771	-0.0925	**0.0192**	474 ± 30	511 ± 45	462 ± 17	591 ± 12
205752_s_at	GSTM5	glutathione S-transferase M5	**0.0035**	**-0.0005**	0.4310	-0.4405	**0.0088**	1039 ± 164	997 ± 93	1324 ± 157	1926 ± 287
205439_at	GSTT2	glutathione S-transferase theta 2	0.0609	**-0.0499**	-0.2853	-0.3129	0.1187	107 ± 16	147 ± 30	133 ± 29	195 ± 23
202451_at	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	0.0620	**-0.0457**	**0.0252**	-0.1414	**0.0349**	653 ± 49	743 ± 56	894 ± 63	815 ± 59
222104_x_at	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	**0.0188**	**-0.0183**	**0.0120**	-0.1941	**0.0192**	267 ± 26	447 ± 70	546 ± 75	523 ± 79
210892_s_at	GTF2I	general transcription factor II, i	**0.0414**	-0.2977	0.0907	0.0999	0.5006	97 ± 14	95 ± 13	97 ± 12	123 ± 16
210891_s_at	GTF2I	general transcription factor II, i	0.2744	**-0.0106**	0.4968	**-0.0119**	0.0945	7358 ± 359	7783 ± 546	8911 ± 158	8478 ± 660
35671_at	GTF3C1	general transcription factor IIIC, polypeptide 1, alpha 220kDa	**0.0086**	-0.2387	-0.2871	0.1669	0.2613	1670 ± 76	1675 ± 150	2015 ± 130	2016 ± 274
204366_s_at	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	0.2079	**-0.0237**	0.2826	-0.2680	**0.0363**	902 ± 49	983 ± 106	856 ± 43	1247 ± 162
213835_x_at	GTPBG3	mitochondrial GTP binding protein	**0.0418**	-0.1445	0.0926	-0.2526	0.3571	493 ± 36	569 ± 63	572 ± 50	634 ± 76
218088_s_at	GTR2	Rag C protein	**0.0001**	**-0.0002**	-0.4090	0.2745	**0.0007**	1041 ± 36	1013 ± 82	1218 ± 67	1411 ± 69
211040_x_at	GTSE1	G-2 and S-phase expressed 1	0.3915	**-0.0119**	-0.1952	-0.1168	0.2177	848 ± 64	867 ± 25	926 ± 51	1045 ± 102
202605_at	GUSB	glucuronidase, beta	**0.0180**	-0.2020	-0.3251	0.4929	0.4342	628 ± 68	704 ± 87	685 ± 28	873 ± 195
215695_s_at	GYG2	glycogenin 2	**0.0496**	**-0.0128**	0.1616	-0.0860	0.1524	155 ± 25	150 ± 29	198 ± 25	227 ± 24
216833_x_at	GYPB	glycophorin B	0.3405	**-0.0236**	0.0623	-0.1498	0.1241	133 ± 20	124 ± 17	165 ± 14	190 ± 27
215093_at	H105E3	NAD dependent steroid dehydrogenase-like; H105e3	**0.0019**	**-0.0135**	0.2719	**-0.0205**	**0.0545**	187 ± 12	219 ± 14	229 ± 11	258 ± 28
221667_s_at	H11	protein kinase H11	**0.0325**	**-0.0110**	-0.2135	-0.1292	0.2250	3080 ± 407	3136 ± 396	3949 ± 579	4552 ± 813
209398_at	H1F2	H1 histone family, member 2	**0.0025**	**0.0000**	-0.4224	-0.1851	**0.0012**	200 ± 21	197 ± 19	292 ± 20	424 ± 74
204805_s_at	H1FX	H1 histone family, member X	0.3343	**-0.0103**	0.2358	0.1958	**0.0086**	802 ± 157	717 ± 47	750 ± 37	1503 ± 271
220936_s_at	H2AFJ	H2A histone family, member J	0.0934	**-0.0112**	0.4641	**-0.0283**	**0.0453**	95 ± 12	100 ± 17	91 ± 12	145 ± 16
214290_s_at	H2AFO	H2A histone family, member O	0.1840	**-0.0258**	-0.3274	0.2912	**0.0236**	626 ± 55	566 ± 63	448 ± 71	911 ± 173
218280_x_at	H2AFO	H2A histone family, member O	**0.0516**	**-0.0376**	**-0.0310**	0.1351	**0.0355**	336 ± 21	281 ± 25	254 ± 30	449 ± 86
205436_s_at	H2AFX	H2A histone family, member X	0.1529	**-0.0294**	0.2264	0.1686	**0.0226**	1393 ± 98	1471 ± 142	1372 ± 81	1995 ± 252

Probe set	Name	Description	NFT_O	MMSE_O	NFT_I	MMSE_I	ANOVA	Control	Incipient	Moderate	Severe
212205_at	H2AV	histone H2A.F/Z variant	**0.0383**	-0.1289	0.1438	**-0.0485**	**0.0417**	3246 ± 90	3551 ± 178	4050 ± 157	3704 ± 314
222067_x_at	H2BFB	H2B histone family, member B	0.1840	**-0.0138**	**-0.0056**	**0.0508**	**0.0319**	232 ± 18	192 ± 18	197 ± 35	359 ± 74
209911_x_at	H2BFB	H2B histone family, member B	0.1416	**-0.0143**	-0.1819	0.2089	0.0617	584 ± 53	509 ± 37	608 ± 63	783 ± 103
202708_s_at	H2BFQ	H2B histone family, member Q	0.2363	**-0.0142**	-0.1293	0.0613	0.0888	898 ± 127	681 ± 39	867 ± 86	1271 ± 256
213828_x_at	H3F3A	H3 histone, family 3A	-0.7117	**-0.0295**	-0.0908	0.2397	0.1105	7795 ± 500	6487 ± 387	7403 ± 384	9931 ± 1756
211940_x_at	H3F3A	H3 histone, family 3A	0.9045	**-0.0299**	-0.1043	0.3697	**0.0458**	5312 ± 467	4361 ± 327	4678 ± 194	6807 ± 1017
211998_at	H3F3B	H3 histone, family 3B	**0.0179**	**-0.0191**	**0.0119**	-0.3470	**0.0432**	1123 ± 66	1487 ± 171	1755 ± 138	1810 ± 328
208180_s_at	H4FH	H4 histone family, member H	**0.0408**	-0.3376	0.1906	0.2131	0.2174	82 ± 4	88 ± 14	83 ± 8	115 ± 18
208181_at	H4FH	H4 histone family, member H	**0.0170**	**-0.0073**	0.3022	0.1819	**0.0110**	35 ± 7	28 ± 6	39 ± 11	80 ± 16
208630_at	HADHA	hydroxyacyl-Coenzyme A dehydrogenase, alpha subunit	**0.0118**	**-0.0521**	0.4725	0.2224	0.0996	688 ± 47	605 ± 39	803 ± 76	853 ± 99
221744_at	HAN11	WD-repeat protein	**0.0483**	-0.3463	0.1168	-0.2447	0.4583	289 ± 29	328 ± 36	358 ± 22	350 ± 49
221745_at	HAN11	WD-repeat protein	0.3014	**-0.0207**	0.2287	-0.1814	0.2937	353 ± 43	329 ± 12	415 ± 27	452 ± 79
220801_s_at	HAO2	hydroxyacid oxidase 2	0.1094	**-0.0016**	**0.0467**	**-0.0357**	**0.0027**	145 ± 12	200 ± 20	176 ± 20	288 ± 42
209102_s_at	HBP1	HMG-box containing protein 1	**0.0491**	**-0.0149**	-0.0662	-0.2922	0.1785	862 ± 68	836 ± 71	1029 ± 104	1062 ± 94
218166_s_at	HBXAP	hepatitis B virus x associated protein	**0.0084**	**-0.0001**	-0.3952	-0.0954	**0.0067**	182 ± 15	170 ± 17	219 ± 12	251 ± 19
218662_s_at	HCAP-G	chromosome condensation protein G	0.2099	**-0.0134**	**0.0298**	-0.2702	0.0556	53 ± 6	80 ± 13	68 ± 17	107 ± 17
216229_x_at	HCGII-7	HCGII-7 protein	0.1128	**-0.0199**	0.2201	-0.1481	0.1208	468 ± 49	475 ± 56	589 ± 57	672 ± 92
217965_s_at	HCNGP	transcriptional regulator protein	**0.0073**	**-0.0217**	**0.0403**	-0.4671	**0.0494**	306 ± 15	374 ± 52	394 ± 48	526 ± 88
42361_g_at	HCR	HCR	**0.0006**	-0.1657	0.2218	-0.4724	0.3324	98 ± 9	113 ± 15	117 ± 16	143 ± 26
201209_at	HDAC1	histone deacetylase 1	**0.0383**	**-0.0168**	0.2007	-0.1396	**0.0366**	487 ± 57	591 ± 78	749 ± 66	680 ± 61
204225_at	HDAC4	histone deacetylase 4	0.1689	**-0.0037**	-0.2977	0.2746	**0.0177**	444 ± 34	410 ± 20	484 ± 34	579 ± 42
217937_s_at	HDAC7A	histone deacetylase 7A	**0.0145**	-0.1376	0.1337	-0.3190	0.0779	169 ± 29	200 ± 42	306 ± 21	258 ± 56
212785_s_at	HDCMA18P	HDCMA18P protein	0.6277	**-0.0403**	0.3208	**-0.0189**	0.2753	437 ± 37	520 ± 45	520 ± 41	530 ± 30
200896_x_at	HDGF	hepatoma-derived growth factor	0.1432	**-0.0302**	**-0.0260**	-0.4717	0.2466	1827 ± 135	1806 ± 54	1899 ± 78	2144 ± 185
203674_at	HELZ	helicase with zinc finger domain	**0.0327**	-0.9466	0.4966	0.4583	0.4163	984 ± 56	1153 ± 118	1166 ± 53	1079 ± 124
203903_s_at	HEPH	hephaestin	**0.0097**	**-0.0143**	0.4726	-0.3213	**0.0041**	809 ± 59	802 ± 57	1139 ± 33	1007 ± 107
206087_x_at	HFE	hemochromatosis	**0.0204**	-0.1680	0.0694	0.3967	0.1289	303 ± 22	380 ± 57	419 ± 14	415 ± 47
206910_x_at	HFL3	H factor -like 3	0.1493	**-0.0194**	0.0671	-0.2142	**0.0244**	164 ± 20	200 ± 7	179 ± 15	242 ± 19
217130_at	HFSE-1	HFSE-1 protein	**0.0252**	-0.2062	0.4533	0.4596	0.3994	251 ± 24	263 ± 40	281 ± 32	334 ± 48
209960_at	HGF	hepatocyte growth factor	**0.0058**	**-0.0061**	0.3819	-0.1260	**0.0037**	61 ± 8	56 ± 12	106 ± 12	95 ± 9
38340_at	HIP12	huntingtin interacting protein 12	**0.0084**	-0.1084	0.0666	-0.3375	0.2182	2668 ± 169	3342 ± 376	3288 ± 204	4164 ± 977
209558_s_at	HIP12	huntingtin interacting protein 12	**0.0017**	**-0.0211**	0.1561	0.4829	0.0613	1415 ± 66	1747 ± 160	2174 ± 83	2530 ± 580
219028_at	HIPK2	homeodomain interacting protein kinase 2	**0.0100**	-0.0715	0.1187	-0.2245	0.1298	801 ± 125	1247 ± 214	1548 ± 266	1356 ± 327
213537_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.1330	**-0.0039**	**0.0403**	**-0.0453**	**0.0316**	115 ± 19	177 ± 30	218 ± 39	245 ± 31
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	0.5562	**-0.0241**	-0.4147	-0.2074	0.1962	64 ± 31	255 ± 93	328 ± 126	365 ± 143
200904_at	HLA-E	major histocompatibility complex, class I, E	**0.0412**	**-0.0143**	0.2928	-0.4695	0.0838	802 ± 84	838 ± 102	1191 ± 194	1169 ± 129
207565_s_at	HLALS	major histocompatibility complex, class I-like sequence	**0.0540**	**-0.0034**	0.1439	**-0.0397**	**0.0099**	56 ± 8	64 ± 11	59 ± 12	112 ± 16
209399_at	HLCS	holocarboxylase synthetase] ligase)	0.3150	**-0.0340**	0.1826	-0.1758	0.1571	298 ± 20	296 ± 10	299 ± 22	369 ± 40
203040_s_at	HMBS	hydroxymethylbilane synthase	0.6340	**-0.0112**	-0.0965	-0.4070	0.0658	380 ± 30	387 ± 36	363 ± 17	495 ± 56
219959_at	HMCS	molybdenum cofactor sulfurase	0.9247	**-0.0283**	0.2754	0.3527	0.1241	88 ± 14	76 ± 10	75 ± 8	134 ± 31
210719_s_at	HMG20B	high-mobility group 20B	0.0729	**-0.0051**	0.1253	-0.2553	**0.0067**	267 ± 27	385 ± 36	344 ± 25	458 ± 50
203744_at	HMGB3	high-mobility group box 3	0.1438	**-0.0269**	**0.0253**	**-0.0227**	0.1632	568 ± 20	585 ± 30	642 ± 25	697 ± 79

Probe set	Name	Description	NFT_O	MMSE_O	NFT_I	MMSE_I	ANOVA	Control	Incipient	Moderate	Severe
202772_at	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	0.0799	**-0.0355**	0.1149	0.2023	0.1349	617 ± 24	641 ± 70	704 ± 38	793 ± 83
209377_s_at	HMGN3	high mobility group nucleosomal binding domain 3	0.5215	**-0.0142**	**-0.0158**	-0.1120	**0.0340**	3728 ± 155	3686 ± 480	4919 ± 422	4500 ± 209
203665_at	HMOX1	heme oxygenase 1	0.3369	**-0.0480**	-0.0964	0.4185	0.2454	542 ± 62	446 ± 13	518 ± 42	649 ± 100
212109_at	HN1L	HN1 like	**0.0011**	**-0.0131**	-0.2089	0.1081	**0.0259**	211 ± 19	181 ± 17	268 ± 25	343 ± 68
214280_x_at	HNRPA1	heterogeneous nuclear ribonucleoprotein A1	**0.0088**	**-0.0475**	**-0.0056**	-0.4787	0.1727	1718 ± 140	1554 ± 46	1834 ± 106	2140 ± 325
210110_x_at	HNRPH3	heterogeneous nuclear ribonucleoprotein H3	**0.0363**	**-0.0458**	-0.1545	-0.1360	0.3048	383 ± 26	419 ± 49	417 ± 45	509 ± 69
200072_s_at	HNRPM	heterogeneous nuclear ribonucleoprotein M	0.0839	**-0.0330**	0.2808	-0.0780	0.1649	874 ± 44	951 ± 123	975 ± 81	1197 ± 142
215489_x_at	HOMER-3	Homer, neuronal immediate early gene, 3	0.1252	**-0.0136**	0.2486	0.4751	**0.0009**	409 ± 31	452 ± 47	403 ± 18	710 ± 93
204647_at	HOMER-3	Homer, neuronal immediate early gene, 3	**0.0285**	**-0.0003**	0.2780	-0.3614	**0.0011**	438 ± 54	492 ± 81	614 ± 32	879 ± 109
206848_at	HOXA7	homeo box A7	0.1568	**-0.0235**	0.1134	**-0.0550**	0.1396	235 ± 25	287 ± 30	329 ± 34	383 ± 81
205600_x_at	HOXB5	homeo box B5	**0.0237**	-0.0572	**0.0509**	**-0.0233**	0.0765	277 ± 24	379 ± 36	342 ± 31	461 ± 85
206194_at	HOXC4	homeo box C4	**0.0040**	**-0.0004**	**0.0495**	**-0.0181**	**0.0030**	153 ± 14	189 ± 20	167 ± 18	295 ± 46
212259_s_at	HPIP	hematopoietic PBX-interacting protein	**0.0266**	-0.1653	0.2625	0.4229	0.1652	507 ± 95	658 ± 136	950 ± 111	760 ± 225
214177_s_at	HPIP	hematopoietic PBX-interacting protein	**0.0008**	**-0.0133**	0.0638	-0.3815	**0.0099**	1382 ± 115	1987 ± 266	2668 ± 314	2541 ± 422
221170_at	HRH4	histamine H4 receptor	0.4048	**-0.0029**	0.4627	0.2943	**0.0029**	65 ± 4	63 ± 11	62 ± 7	126 ± 23
209972_s_at	HRI	heme-regulated initiation factor 2-alpha kinase	**0.0104**	**-0.0153**	-0.0963	0.3186	**0.0121**	155 ± 16	150 ± 11	169 ± 11	234 ± 28
202795_x_at	HRIHFB2122	Tara-like protein	**0.0164**	-0.0772	0.1455	0.4316	0.2472	651 ± 52	717 ± 96	747 ± 70	924 ± 157
216210_x_at	HRIHFB2122	Tara-like protein	**0.0042**	**-0.0021**	0.0635	-0.0825	**0.0193**	711 ± 69	768 ± 84	951 ± 117	1468 ± 321
202098_s_at	HRMT1L1	HMT1 hnRNP methyltransferase-like 1	**0.0087**	-0.2161	-0.4997	-0.2943	0.6701	1239 ± 83	1279 ± 108	1313 ± 85	1404 ± 116
203394_s_at	HRY	hairy homolog	**0.0467**	-0.0976	-0.4651	0.4699	0.0900	403 ± 50	438 ± 56	584 ± 68	520 ± 18
203395_s_at	HRY	hairy homolog	0.8275	**-0.0298**	0.0850	-0.0597	0.1046	226 ± 18	275 ± 18	310 ± 16	336 ± 58
203283_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	0.1550	**-0.0449**	**0.0280**	**-0.0483**	0.1457	182 ± 14	200 ± 27	245 ± 19	236 ± 25
217760_at	HSA249128	DIPB protein	0.3976	**-0.0047**	0.3018	**-0.0278**	**0.0323**	1139 ± 32	1173 ± 42	1158 ± 25	1397 ± 119
217759_at	HSA249128	DIPB protein	0.1238	**-0.0439**	-0.2991	-0.4561	0.3261	2284 ± 91	2430 ± 139	2527 ± 175	2640 ± 125
218508_at	HSA275986	transcription factor	**0.0008**	-0.1117	0.2660	0.4488	0.1461	562 ± 27	599 ± 47	595 ± 47	708 ± 59
200941_at	HSBP1	heat shock factor binding protein 1	**0.0483**	-0.1191	-0.3705	-0.1979	0.5439	1858 ± 112	1786 ± 145	2012 ± 130	2056 ± 199
220081_x_at	HSD17B7	hydroxysteroid dehydrogenase 7	**0.0012**	**-0.0018**	0.0627	-0.1158	**0.0182**	664 ± 70	935 ± 112	1138 ± 128	1248 ± 190
221771_s_at	HSMPP8	M-phase phosphoprotein, mpp8	**0.0335**	**-0.0193**	-0.3458	-0.3883	0.1061	1038 ± 58	985 ± 28	1152 ± 62	1215 ± 104
218826_at	HSNOV1	novel protein	**0.0117**	**-0.0068**	**0.0375**	**-0.0022**	**0.0004**	349 ± 28	544 ± 56	451 ± 31	590 ± 35
205824_at	HSPB2	heat shock 27kDa protein 2	0.0792	**-0.0101**	-0.4014	-0.2725	**0.0544**	241 ± 36	244 ± 32	374 ± 37	373 ± 70
219284_at	HSPBAP1	HSPB associated protein 1	**0.0321**	-0.0871	-0.1388	-0.3041	0.3554	306 ± 40	322 ± 12	332 ± 24	385 ± 38
219357_at	HSPC018	HSPC018 protein	**0.0042**	**-0.0086**	0.1314	-0.4463	**0.0256**	567 ± 26	545 ± 35	813 ± 65	901 ± 168
218936_s_at	HSPC128	HSPC128 protein	0.0594	**-0.0119**	0.3851	**-0.0222**	0.1222	325 ± 11	348 ± 31	354 ± 28	434 ± 54
221046_s_at	HSPC135	HSPC135 protein	**0.0003**	-0.0720	0.3881	-0.4735	0.1749	535 ± 42	527 ± 53	601 ± 51	762 ± 148
214328_s_at	HSPCA	heat shock 90kDa protein 1, alpha	0.1638	**-0.0187**	**-0.0232**	0.3004	0.0833	1402 ± 1190	3042 ± 1353	2437 ± 1827	5463 ± 2900
213645_at	HSRTSBETA	rTS beta protein	**0.0150**	-0.2776	**0.0081**	0.3794	0.3304	368 ± 48	511 ± 95	669 ± 156	688 ± 233
208360_s_at	HSU88895	endogenous retrovirus H D1 leader region	0.4625	**-0.0383**	0.0816	**-0.0392**	0.2937	264 ± 28	302 ± 30	293 ± 30	372 ± 65
209448_at	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	**0.0003**	**-0.0052**	-0.4350	-0.1846	0.0702	437 ± 40	489 ± 67	630 ± 66	684 ± 104
206639_x_at	HTN1	histatin 1	0.2992	**-0.0285**	0.1227	-0.1586	**0.0100**	72 ± 13	103 ± 21	60 ± 11	158 ± 33
205956_x_at	HUMGT198A	GT198, complete ORF	**0.0035**	**-0.0230**	**0.0304**	-0.4651	**0.0162**	232 ± 15	335 ± 62	326 ± 26	402 ± 33
213230_at	HUMPPA	paraneoplastic antigen	**0.0069**	**-0.0184**	-0.2988	0.3277	0.1046	308 ± 35	343 ± 57	412 ± 31	534 ± 121
201904_s_at	HYA22	HYA22 protein	0.0821	**-0.0240**	0.4130	-0.3512	0.1796	387 ± 71	430 ± 71	485 ± 45	616 ± 101

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
201906_s_at	HYA22	HYA22 protein	**0.0099**	**-0.0080**	-0.4795	-0.3534	**0.0472**	565 ± 54	607 ± 47	738 ± 41	738 ± 65
212493_s_at	HYPB	Huntingtin interacting protein B	0.0589	**-0.0002**	-0.2118	-0.3614	**0.0062**	760 ± 40	677 ± 35	959 ± 66	1050 ± 123
219910_at	HYPE	Huntingtin interacting protein E	**0.0157**	**-0.0208**	0.3751	0.3312	**0.0199**	385 ± 33	421 ± 49	437 ± 35	622 ± 89
64064_at	IAN4L1	immune associated nucleotide 4 like 1	0.3988	**-0.0081**	0.2504	**-0.0512**	0.0912	798 ± 100	892 ± 58	862 ± 52	1135 ± 137
202638_s_at	ICAM1	intercellular adhesion molecule 1 , human rhinovirus receptor	0.7981	**-0.0215**	0.2416	-0.1320	0.1649	145 ± 22	178 ± 22	176 ± 4	212 ± 25
203337_x_at	ICAP-1A	integrin cytoplasmic domain-associated protein 1	0.1185	**-0.0153**	0.3539	-0.3135	**0.0193**	639 ± 91	486 ± 91	568 ± 42	856 ± 65
207826_s_at	ID3	inhibitor of DNA binding 3	0.5310	**-0.0253**	**-0.0239**	-0.4252	0.0887	330 ± 61	265 ± 75	505 ± 35	424 ± 83
209292_at	ID4	inhibitor of DNA binding 4	0.4504	**-0.0427**	0.1727	**-0.0110**	0.2324	918 ± 142	1154 ± 160	1429 ± 245	1321 ± 192
209291_at	ID4	inhibitor of DNA binding 4	**0.0455**	**-0.0005**	0.1097	-0.0608	**0.0090**	2633 ± 276	3180 ± 368	4522 ± 521	4569 ± 639
210045_at	IDH2	isocitrate dehydrogenase 2 , mitochondrial	**0.0491**	-0.1209	0.1369	-0.0940	0.3844	634 ± 59	811 ± 126	869 ± 78	960 ± 244
213918_s_at	IDN3	IDN3 protein	**0.0345**	-0.5216	-0.3798	-0.2337	0.6084	224 ± 21	265 ± 20	240 ± 20	260 ± 35
212483_at	IDN3	IDN3 protein	**0.0020**	**-0.0039**	0.2102	-0.3477	**0.0188**	425 ± 37	454 ± 44	570 ± 24	604 ± 68
205058_at	IDUA	iduronidase, alpha-L-	**0.0112**	-0.0736	0.1242	**-0.0002**	0.4207	136 ± 17	176 ± 24	178 ± 20	200 ± 48
201026_at	IF2	translation initiation factor IF2	**0.0304**	-0.1449	0.1937	0.4380	0.2928	208 ± 26	238 ± 27	242 ± 16	281 ± 35
214314_s_at	IF2	translation initiation factor IF2	0.0593	**-0.0046**	**0.0239**	-0.1421	0.0879	149 ± 21	176 ± 29	212 ± 36	264 ± 38
201025_at	IF2	translation initiation factor IF2	0.1548	**-0.0273**	0.3045	-0.3080	0.1312	413 ± 14	448 ± 23	455 ± 26	529 ± 59
201024_x_at	IF2	translation initiation factor IF2	**0.0006**	**-0.0043**	0.2736	-0.4404	**0.0111**	878 ± 96	839 ± 30	1133 ± 133	1577 ± 268
208965_s_at	IFI16	interferon, gamma-inducible protein 16	**0.0073**	**-0.0071**	0.4553	**-0.0544**	**0.0483**	124 ± 22	139 ± 19	162 ± 4	203 ± 24
201315_x_at	IFITM2	interferon induced transmembrane protein 2	0.3289	**-0.0388**	**-0.0310**	-0.4588	0.3639	2361 ± 394	2300 ± 275	2505 ± 283	3232 ± 572
208448_x_at	IFNA16	interferon, alpha 16	0.4667	**-0.0035**	0.1753	0.4397	**0.0072**	128 ± 11	106 ± 11	122 ± 8	180 ± 22
214569_at	IFNA5	interferon, alpha 5	0.2400	**-0.0137**	**0.0216**	**-0.0291**	0.0697	101 ± 10	117 ± 15	118 ± 13	175 ± 34
210354_at	IFNG	interferon, gamma	0.5036	**-0.0139**	**0.0368**	**-0.0010**	**0.0536**	110 ± 11	154 ± 22	119 ± 16	189 ± 32
202146_at	IFRD1	interferon-related developmental regulator 1	**0.0327**	**-0.0262**	-0.2574	-0.3113	0.3104	1169 ± 136	1038 ± 96	1252 ± 96	1469 ± 257
209100_at	IFRD2	interferon-related developmental regulator 2	0.0966	**-0.0379**	-0.3982	0.2574	0.2415	559 ± 51	610 ± 62	699 ± 60	722 ± 85
203628_at	IGF1R	insulin-like growth factor 1 receptor	0.2267	**-0.0415**	0.1521	-0.0660	0.0931	244 ± 40	320 ± 39	483 ± 104	414 ± 51
203425_s_at	IGFBP5	insulin-like growth factor binding protein 5	**0.0141**	-0.1448	0.3618	0.0852	0.2220	144 ± 12	130 ± 15	158 ± 14	182 ± 24
221453_at	IGRP	islet-specific glucose-6-phosphatase catalytic subunit-related	**0.0275**	**-0.0103**	0.2944	-0.3287	**0.0052**	285 ± 28	336 ± 42	311 ± 14	509 ± 76
206420_at	IGSF6	immunoglobulin superfamily, member 6	0.1250	**-0.0056**	0.1719	-0.2739	**0.0135**	77 ± 9	91 ± 8	87 ± 13	129 ± 13
204912_at	IL10RA	interleukin 10 receptor, alpha	**0.0029**	**0.0000**	0.0744	**-0.0319**	**0.0006**	247 ± 18	309 ± 23	333 ± 32	473 ± 57
209575_at	IL10RB	interleukin 10 receptor, beta	**0.0476**	**-0.0406**	0.0583	**-0.0115**	0.1471	180 ± 17	244 ± 21	233 ± 28	269 ± 43
201887_at	IL13RA1	interleukin 13 receptor, alpha 1	0.2656	**-0.0087**	**0.0103**	-0.0713	**0.0294**	618 ± 64	815 ± 64	768 ± 66	918 ± 79
212300_at	IL14	interleukin 14	**0.0148**	-0.0722	-0.2701	-0.2278	**0.0018**	404 ± 25	375 ± 39	576 ± 35	455 ± 40
217371_s_at	IL15	interleukin 15	0.4004	**-0.0023**	0.1822	-0.1245	**0.0124**	47 ± 7	50 ± 7	55 ± 8	86 ± 10
205992_s_at	IL15	interleukin 15	0.4956	**-0.0204**	-0.4547	0.3268	0.0609	130 ± 10	125 ± 19	137 ± 22	191 ± 13
205707_at	IL17R	interleukin 17 receptor	0.4245	**-0.0297**	**0.0266**	-0.2735	0.1405	427 ± 39	498 ± 53	540 ± 72	641 ± 77
206295_at	IL18	interleukin 18	0.2454	**-0.0423**	0.1406	**-0.0014**	0.3269	70 ± 13	88 ± 13	84 ± 10	109 ± 22
208200_at	IL1A	interleukin 1, alpha	**0.0236**	**-0.0002**	0.2490	-0.4684	**0.0029**	98 ± 9	102 ± 14	112 ± 10	159 ± 6
202948_at	IL1R1	interleukin 1 receptor, type I	0.0693	**-0.0185**	0.3273	-0.1392	**0.0525**	353 ± 63	461 ± 89	605 ± 61	547 ± 51
220663_at	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	0.1197	**-0.0447**	-0.3947	-0.4324	0.1236	824 ± 66	895 ± 89	1134 ± 124	1028 ± 110
220056_at	IL22R	interleukin 22 receptor	**0.0121**	-0.0863	0.4088	0.4312	0.1247	167 ± 12	182 ± 29	189 ± 18	247 ± 36
204116_at	IL2RG	interleukin 2 receptor, gamma	-0.8498	**-0.0379**	**0.0390**	**-0.0105**	0.4319	338 ± 34	394 ± 33	428 ± 30	421 ± 68
205207_at	IL6	interleukin 6	-0.8048	**-0.0436**	-0.3757	-0.3026	0.0573	148 ± 14	163 ± 23	130 ± 21	227 ± 37

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
205945_at	IL6R	interleukin 6 receptor	0.3942	**-0.0099**	**0.0431**	-0.1237	0.0575	138 ± 14	157 ± 17	178 ± 15	204 ± 20
204863_s_at	IL6ST	interleukin 6 signal transducer	**0.0045**	-0.0988	0.2054	-0.0903	0.1647	240 ± 21	259 ± 23	326 ± 17	313 ± 56
221548_s_at	ILKAP	integrin-linked kinase-associated serine/threonine pptase 2C	**0.0050**	**-0.0198**	0.3352	0.3466	**0.0346**	386 ± 23	402 ± 26	450 ± 33	552 ± 71
215838_at	ILT11	leukocyte immunoglobulin-like receptor, B7	0.0840	**-0.0273**	0.2746	-0.2116	0.1102	75 ± 15	95 ± 20	104 ± 7	131 ± 18
205981_s_at	ING1L	inhibitor of growth family, member 1-like	0.4275	**-0.0276**	-0.2699	0.1529	**0.0500**	276 ± 28	270 ± 30	269 ± 31	376 ± 27
205070_at	ING3	inhibitor of growth family, member 3	**0.0279**	**-0.0308**	-0.2624	-0.4706	**0.0134**	353 ± 37	317 ± 23	485 ± 49	420 ± 11
48825_at	ING4	candidate tumor suppressor p33 ING1 homolog	0.1851	**-0.0393**	**-0.0523**	-0.1946	0.2793	393 ± 16	383 ± 39	453 ± 34	447 ± 32
202794_at	INPP1	inositol polyphosphate-1-phosphatase	0.4936	**-0.0044**	-0.4137	-0.4802	**0.0315**	1793 ± 74	1683 ± 164	1780 ± 80	2192 ± 137
201598_s_at	INPPL1	inositol polyphosphate phosphatase-like 1	**0.0032**	-0.0573	0.1656	-0.4308	0.0901	438 ± 36	578 ± 61	547 ± 44	658 ± 97
201625_s_at	INSIG1	insulin induced gene 1	0.2919	**-0.0215**	-0.2624	0.2973	0.1513	207 ± 23	197 ± 30	229 ± 35	291 ± 30
213792_s_at	INSR	insulin receptor	**0.0001**	**-0.0122**	0.3332	0.2521	**0.0168**	630 ± 54	702 ± 88	846 ± 106	1319 ± 279
219843_at	IPP	intracisternal A particle-promoted polypeptide	**0.0356**	-0.0841	**0.0191**	-0.0551	0.1628	153 ± 22	226 ± 37	193 ± 14	241 ± 43
221974_at	IPW	imprinted in Prader-Willi syndrome	**0.0170**	**-0.0071**	-0.3939	-0.0576	0.0763	391 ± 46	393 ± 53	545 ± 80	550 ± 30
213446_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	**0.0390**	-0.1261	**-0.0497**	0.3772	0.0998	113 ± 19	110 ± 5	121 ± 11	174 ± 32
203474_at	IQGAP2	IQ motif containing GTPase activating protein 2	**0.0022**	**-0.0507**	-0.0679	0.3583	0.0697	80 ± 13	83 ± 13	91 ± 10	150 ± 36
201587_s_at	IRAK1	interleukin-1 receptor-associated kinase 1	0.2154	**-0.0004**	0.1876	-0.3026	**0.0109**	828 ± 81	819 ± 87	1121 ± 103	1294 ± 157
219618_at	IRAK4	interleukin-1 receptor associated kinase 4	0.1283	**-0.0010**	0.2831	-0.1557	**0.0120**	85 ± 14	120 ± 12	128 ± 15	164 ± 21
202621_at	IRF3	interferon regulatory factor 3	**0.0036**	**-0.0363**	**-0.0294**	-0.4987	0.1216	421 ± 52	372 ± 50	480 ± 50	570 ± 72
208436_s_at	IRF7	interferon regulatory factor 7	0.1181	**-0.0034**	0.4770	-0.1925	0.0739	223 ± 37	223 ± 29	267 ± 31	425 ± 108
209184_s_at	IRS2	insulin receptor substrate 2	**0.0469**	**-0.0162**	0.2325	0.2139	0.0642	2760 ± 155	2867 ± 224	3221 ± 424	3863 ± 283
222126_at	IRS3L	insulin receptor substrate 3-like	0.0826	**-0.0055**	**0.0235**	**-0.0016**	**0.0082**	404 ± 19	573 ± 55	596 ± 59	611 ± 31
207191_s_at	ISLR	immunoglobulin superfamily containing leucine-rich repeat	**0.0425**	-0.2678	**0.0411**	**-0.0151**	0.3381	136 ± 15	197 ± 20	193 ± 37	212 ± 50
214660_at	ITGA1	integrin, alpha 1	**0.0126**	**-0.0056**	0.1753	**-0.0072**	**0.0405**	17 ± 2	23 ± 5	22 ± 5	49 ± 15
206766_at	ITGA10	integrin, alpha 10	0.1222	**-0.0207**	0.2957	-0.1090	0.0823	363 ± 35	379 ± 30	365 ± 13	474 ± 45
201656_at	ITGA6	integrin, alpha 6	0.3613	**-0.0391**	0.0840	**-0.0130**	0.3150	369 ± 34	501 ± 75	508 ± 78	516 ± 77
216331_at	ITGA7	integrin, alpha 7	0.0848	**-0.0186**	**0.0047**	0.4410	**0.0169**	794 ± 44	1013 ± 116	1377 ± 137	1358 ± 228
204990_s_at	ITGB4	integrin, beta 4	**0.0000**	**-0.0027**	0.2021	0.4038	**0.0090**	581 ± 102	733 ± 162	1106 ± 146	1302 ± 210
214020_x_at	ITGB5	integrin, beta 5	0.1007	**-0.0029**	0.4578	**-0.0295**	0.0715	301 ± 24	350 ± 54	414 ± 36	477 ± 75
201125_s_at	ITGB5	integrin, beta 5	**0.0013**	**0.0000**	0.1029	-0.1493	**0.0009**	498 ± 49	611 ± 65	704 ± 53	954 ± 114
201124_at	ITGB5	integrin, beta 5	**0.0472**	**-0.0014**	0.2332	-0.2319	**0.0103**	480 ± 39	524 ± 46	538 ± 28	684 ± 51
214021_x_at	ITGB5	integrin, beta 5	**0.0015**	**-0.0178**	0.4349	0.1124	**0.0478**	48 ± 5	48 ± 11	57 ± 10	80 ± 6
205816_at	ITGB8	integrin, beta 8	**0.0013**	**-0.0003**	0.1977	-0.4076	**0.0049**	93 ± 14	104 ± 19	145 ± 16	171 ± 14
37201_at	ITIH4	inter-alpha inhibitor H4	**0.0124**	-0.2896	0.1498	0.2076	0.3251	300 ± 21	342 ± 43	322 ± 26	429 ± 94
210740_s_at	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	0.2014	**-0.0094**	0.4446	0.3792	**0.0311**	2826 ± 150	2665 ± 127	3357 ± 193	3334 ± 241
203723_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	**0.0093**	**-0.0017**	-0.1140	-0.3123	**0.0230**	2349 ± 446	2585 ± 171	4220 ± 708	4519 ± 781
213076_at	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	0.1334	**-0.0097**	-0.1257	-0.4305	0.0626	532 ± 35	531 ± 24	586 ± 42	761 ± 116
35776_at	ITSN1	intersectin 1	**0.0464**	**-0.0081**	0.4158	-0.3448	**0.0504**	894 ± 95	1048 ± 115	1069 ± 100	1367 ± 152
218517_at	Jade-1	PHD protein Jade-1	**0.0016**	**-0.0002**	-0.4109	0.3962	**0.0008**	529 ± 38	567 ± 53	658 ± 38	848 ± 75
207187_at	JAK3	Janus kinase 3	0.1097	**-0.0064**	0.1080	**-0.0339**	0.1091	400 ± 21	444 ± 30	438 ± 35	540 ± 66
214037_s_at	JM1	JM1 protein	**0.0116**	-0.0699	0.2736	-0.4667	0.3091	95 ± 14	107 ± 12	105 ± 7	137 ± 26
209217_s_at	JM5	JM5 protein	**0.0080**	**-0.0142**	0.2165	-0.2095	0.0621	669 ± 31	678 ± 32	715 ± 52	841 ± 63
37872_at	JRK	jerky homolog	0.0757	**-0.0002**	0.0915	**-0.0121**	**0.0076**	283 ± 17	303 ± 17	339 ± 16	383 ± 26

Probe set	Name	Description	NFT$_{O}$	MMSE$_{O}$	NFT$_{I}$	MMSE$_{I}$	ANOVA	Control	Incipient	Moderate	Severe
201466_s_at	JUN	v-jun sarcoma virus 17 oncogene homolog	0.1488	**-0.0383**	-0.1618	0.4803	0.1224	283 ± 36	249 ± 50	380 ± 78	438 ± 58
213281_at	JUN	v-jun sarcoma virus 17 oncogene homolog	**0.0123**	**-0.0462**	0.4313	0.4139	**0.0326**	231 ± 28	306 ± 39	288 ± 26	365 ± 21
203751_x_at	JUND	jun D proto-oncogene	0.9400	**-0.0486**	0.4937	0.3146	**0.0237**	593 ± 93	416 ± 57	426 ± 27	880 ± 190
203752_s_at	JUND	jun D proto-oncogene	**0.0006**	**-0.0284**	0.4697	**-0.0494**	0.1244	7987 ± 603	8307 ± 654	9983 ± 683	0792 ± 1603
222105_s_at	KBRAS2	I-kappa-B-interacting Ras-like protein 2	**0.0013**	-0.1363	**0.0507**	-0.2443	0.3500	221 ± 40	281 ± 34	343 ± 37	397 ± 142
205616_at	KCNA6	K+ VGC, shaker-related subfamily, member 6	0.6276	**-0.0233**	**-0.0192**	0.3894	**0.0328**	201 ± 22	125 ± 25	237 ± 15	280 ± 63
220776_at	KCNJ14	K+ inwardly-rectifying channel, J14	**0.0166**	**-0.0011**	**0.0401**	**-0.0048**	**0.0048**	110 ± 6	136 ± 12	132 ± 12	239 ± 47
211806_s_at	KCNJ15	K+ inwardly-rectifying channel, J15	**0.0213**	**-0.0012**	0.0722	-0.0810	**0.0117**	275 ± 21	303 ± 23	339 ± 33	443 ± 50
220727_at	KCNK10	potassium channel, subfamily K, member 10	**0.0043**	**-0.0101**	**0.0012**	-0.1831	**0.0120**	126 ± 9	154 ± 21	153 ± 8	222 ± 33
219615_s_at	KCNK5	potassium channel, subfamily K, member 5	**0.0035**	**-0.0001**	-0.2003	0.2202	**0.0001**	116 ± 12	100 ± 16	141 ± 13	239 ± 31
219287_at	KCNMB4	K+ large conductance Ca2+-activated channel, M beta 4	**0.0110**	-0.0714	0.4940	0.2051	0.1329	1214 ± 88	1213 ± 124	1246 ± 76	1612 ± 217
205902_at	KCNN3	K+ intermediate/small g Ca2+-activated channel, N3	**0.0037**	**-0.0049**	0.4348	-0.1493	**0.0194**	731 ± 117	798 ± 124	1374 ± 227	1393 ± 242
214185_at	KHDRBS1	KH domain containing, RNA binding, signal transd. assoc. 1	0.1717	**-0.0007**	-0.1785	0.1870	**0.0030**	200 ± 17	168 ± 23	209 ± 20	306 ± 34
212303_x_at	KHSRP	KH-type splicing regulatory protein	**0.0154**	-0.8695	0.1610	-0.4943	0.4099	667 ± 42	794 ± 47	825 ± 87	748 ± 102
213552_at	KIAA0836	likely homol. m. hep./hep. sulfate-glucuronic ac. C5-epimer.	**0.0013**	**-0.0236**	0.3785	-0.2352	0.0855	136 ± 13	140 ± 20	177 ± 11	182 ± 18
200897_s_at	KIAA0992	palladin	**0.0334**	**-0.0266**	0.4983	0.4183	0.1896	2067 ± 288	1852 ± 273	2794 ± 382	2981 ± 656
200906_s_at	KIAA0992	palladin	**0.0060**	**-0.0407**	**-0.0466**	0.4818	0.1323	140 ± 15	99 ± 17	164 ± 21	170 ± 33
222310_at	KIAA1172	pre-mRNA splicing SR protein rA4	**0.0043**	**-0.0362**	-0.3607	-0.2180	**0.0429**	220 ± 27	241 ± 33	360 ± 47	308 ± 40
202962_at	KIF13B	kinesin family member 13B	0.2037	**-0.0255**	0.3258	0.4888	0.0831	731 ± 60	895 ± 138	881 ± 81	1127 ± 140
206364_at	KIF14	kinesin family member 14	**0.0313**	**-0.0046**	0.1049	-0.1069	**0.0348**	45 ± 8	40 ± 8	61 ± 11	86 ± 15
203943_at	KIF3B	kinesin family member 3B	**0.0037**	-0.0697	0.0972	-0.2634	0.2003	1251 ± 98	1250 ± 61	1469 ± 117	1553 ± 178
201991_s_at	KIF5B	kinesin family member 5B	**0.0399**	-0.1585	-0.2502	-0.2047	0.5321	3698 ± 153	3734 ± 552	4224 ± 421	4506 ± 595
207029_at	KITLG	KIT ligand	**0.0439**	**-0.0404**	-0.3623	-0.1597	0.0622	65 ± 8	55 ± 6	80 ± 4	76 ± 6
210504_at	KLF1	Kruppel-like factor 1	**0.0353**	**-0.0131**	-0.2229	-0.0726	0.0907	101 ± 17	101 ± 12	101 ± 13	156 ± 25
219371_s_at	KLF2	Kruppel-like factor 2	0.2745	**-0.0500**	**0.0070**	-0.3375	0.0592	463 ± 36	681 ± 121	637 ± 46	800 ± 116
209212_s_at	KLF5	Kruppel-like factor 5	**0.0384**	**-0.0386**	-0.1339	-0.4130	**0.0518**	177 ± 14	156 ± 16	180 ± 6	237 ± 33
204334_at	KLF7	Kruppel-like factor 7	**0.0029**	-0.0743	**0.0547**	-0.0926	0.0601	664 ± 44	848 ± 69	759 ± 41	938 ± 122
205783_at	KLK13	kallikrein 13	**0.0193**	**-0.0176**	**-0.0057**	0.2616	**0.0263**	215 ± 14	215 ± 14	244 ± 29	314 ± 32
211519_s_at	KNSL6	kinesin-like 6	0.1543	**-0.0145**	0.0786	-0.1533	0.0704	172 ± 19	193 ± 14	194 ± 12	261 ± 41
213741_s_at	KPNA1	karyopherin alpha 1	0.5022	**-0.0144**	**-0.0111**	-0.4726	**0.0258**	256 ± 20	212 ± 36	236 ± 19	318 ± 9
212101_at	KPNA6	karyopherin alpha 6	0.4216	**-0.0240**	-0.2187	-0.3286	0.0978	763 ± 63	828 ± 78	789 ± 68	1028 ± 104
212102_s_at	KPNA6	karyopherin alpha 6	**0.0086**	**-0.0289**	-0.4737	0.2894	0.0758	126 ± 15	125 ± 16	139 ± 18	190 ± 25
213574_s_at	KPNB1	karyopherin beta 1	**0.0000**	**-0.0012**	0.3691	-0.1867	**0.0057**	1480 ± 67	1471 ± 104	1672 ± 66	2060 ± 201
213507_s_at	KPNB1	karyopherin beta 1	**0.0007**	**-0.0295**	0.4863	0.3391	0.0628	2130 ± 92	2140 ± 107	2308 ± 164	2857 ± 354
207657_x_at	KPNB2	karyopherin beta 2	**0.0201**	**-0.0015**	0.2631	-0.1281	**0.0160**	1078 ± 122	974 ± 83	1289 ± 93	1601 ± 192
221829_s_at	KPNB2	karyopherin beta 2	**0.0002**	**-0.0090**	0.1923	-0.0920	**0.0304**	2337 ± 359	2292 ± 235	4071 ± 573	5202 ± 1378
214715_x_at	KR18	KRAB zinc finger protein KR18	**0.0463**	**-0.0301**	0.0998	**-0.0290**	0.1092	1839 ± 257	1919 ± 186	3117 ± 542	2720 ± 558
200914_x_at	KTN1	kinectin 1	**0.0042**	**-0.0029**	**0.0276**	-0.0678	**0.0151**	1603 ± 117	1988 ± 199	2350 ± 166	2475 ± 279
204328_at	LAK-4P	expressed in activated T/LAK lymphocytes	**0.0060**	**-0.0056**	0.3675	-0.3177	**0.0220**	549 ± 58	562 ± 31	671 ± 84	966 ± 161
205116_at	LAMA2	laminin, alpha 2	**0.0478**	**-0.0026**	**0.0191**	-0.0749	**0.0315**	114 ± 10	149 ± 20	142 ± 7	214 ± 42
202202_s_at	LAMA4	laminin, alpha 4	**0.0258**	-0.1425	**0.0166**	-0.0851	0.2081	189 ± 23	243 ± 37	280 ± 26	251 ± 41
216081_at	LAMA4	laminin, alpha 4	**0.0214**	**-0.0311**	-0.3279	-0.1297	0.1438	276 ± 25	299 ± 21	323 ± 36	431 ± 85

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
200771_at	LAMC1	laminin, gamma 1	0.1222	**-0.0068**	-0.2206	**-0.0491**	0.2585	655 ± 58	659 ± 53	739 ± 48	831 ± 107
201553_s_at	LAMP1	lysosomal-associated membrane protein 1	**0.0005**	**-0.0216**	0.1481	-0.3812	0.0864	9662 ± 723	0480 ± 1002	2482 ± 987	5386 ± 3118
218816_at	LANO	LAP and no PDZ protein	0.2624	**-0.0241**	**-0.0383**	0.4164	0.2297	324 ± 55	277 ± 33	387 ± 63	425 ± 40
207790_at	LANO	LAP and no PDZ protein	**0.0009**	**-0.0118**	0.3932	-0.3220	**0.0418**	179 ± 26	262 ± 56	333 ± 60	412 ± 84
215538_at	LARGE	like-glycosyltransferase	0.4473	**-0.0173**	0.1346	-0.0892	0.0706	96 ± 14	107 ± 13	106 ± 8	151 ± 21
219813_at	LATS1	LATS, large tumor suppressor, homolog 1	**0.0107**	**-0.0175**	0.2652	0.4151	**0.0291**	76 ± 9	84 ± 7	87 ± 8	133 ± 25
204256_at	LCE	long-chain fatty-acyl elongase	**0.0081**	**-0.0282**	-0.3269	0.4712	0.0690	362 ± 12	311 ± 29	381 ± 29	420 ± 35
202068_s_at	LDLR	low density lipoprotein receptor	0.5777	**-0.0036**	-0.0779	-0.3718	**0.0505**	520 ± 65	480 ± 55	496 ± 32	735 ± 97
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	0.0871	**-0.0053**	0.3217	**-0.0455**	0.1730	249 ± 14	266 ± 32	308 ± 26	330 ± 40
200923_at	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.5752	**-0.0076**	-0.2317	0.4148	0.1643	944 ± 131	864 ± 76	1097 ± 81	1277 ± 184
203236_s_at	LGALS9	lectin, galactoside-binding, soluble, 9	**0.0020**	**-0.0105**	**0.0543**	-0.2117	**0.0060**	237 ± 15	260 ± 24	235 ± 21	366 ± 42
221670_s_at	LHX3	LIM homeobox protein 3	**0.0357**	-0.5179	-0.2224	0.1234	0.4417	360 ± 33	308 ± 37	348 ± 31	408 ± 61
205876_at	LIFR	leukemia inhibitory factor receptor	**0.0020**	-0.0629	-0.1000	0.1700	0.0824	87 ± 13	73 ± 11	92 ± 10	134 ± 27
207857_at	LILRA2	leukocyte immunoglobulin-like receptor, A2	**0.0418**	**-0.0039**	0.1243	-0.4168	**0.0360**	137 ± 19	150 ± 25	172 ± 11	224 ± 24
218850_s_at	LIMD1	LIM domains containing 1	0.1138	**-0.0460**	0.1431	0.4449	0.0733	266 ± 30	334 ± 47	314 ± 26	441 ± 72
202193_at	LIMK2	LIM domain kinase 2	**0.0058**	**-0.0005**	0.3244	**-0.0156**	**0.0096**	207 ± 22	238 ± 20	360 ± 64	402 ± 47
210582_s_at	LIMK2	LIM domain kinase 2	**0.0316**	**-0.0213**	-0.4022	0.4844	0.1292	500 ± 60	530 ± 52	669 ± 72	718 ± 100
220036_s_at	LIMR	lipocalin-interacting membrane receptor	**0.0188**	**-0.0294**	**-0.0343**	0.4145	**0.0315**	598 ± 33	501 ± 28	599 ± 56	759 ± 83
219181_at	LIPG	lipase, endothelial	**0.0430**	**-0.0122**	0.1300	0.3529	0.1010	165 ± 19	164 ± 10	205 ± 26	231 ± 21
203713_s_at	LLGL2	lethal giant larvae homolog 2	**0.0211**	**-0.0174**	-0.3217	-0.0773	0.1607	98 ± 14	93 ± 23	149 ± 20	161 ± 42
220132_s_at	LLT1	lectin-like NK cell receptor	0.4310	**-0.0278**	0.4441	0.1543	**0.0318**	46 ± 9	31 ± 5	53 ± 8	74 ± 12
203411_s_at	LMNA	lamin A/C	0.2624	**-0.0137**	-0.2059	0.4986	0.0897	377 ± 48	372 ± 22	443 ± 31	503 ± 44
203276_at	LMNB1	lamin B1	0.2466	**-0.0084**	-0.0865	-0.0733	0.0564	87 ± 21	79 ± 12	144 ± 18	124 ± 18
212714_at	LOC113251	c-Mpl binding protein	0.1719	**-0.0230**	-0.0951	-0.0881	0.2554	698 ± 37	718 ± 68	721 ± 36	881 ± 122
213779_at	LOC129080	putative emu1	**0.0037**	-0.1094	**0.0041**	-0.3719	0.2095	408 ± 27	537 ± 83	554 ± 41	642 ± 141
213089_at	LOC166994	integral membrane glycoprotein-like	0.1854	**-0.0153**	0.3178	0.2622	0.1533	897 ± 136	1043 ± 229	1225 ± 215	1683 ± 364
222056_s_at	LOC51011	CGI-105 protein	**0.0112**	-0.3071	0.1059	0.0967	0.2871	790 ± 32	810 ± 39	937 ± 74	891 ± 90
222158_s_at	LOC51029	CGI-146 protein	-0.7592	**-0.0061**	0.4618	0.4169	0.1225	109 ± 10	83 ± 11	131 ± 25	165 ± 36
201871_s_at	LOC51035	ORF	0.1092	**-0.0285**	0.2605	-0.4529	0.1719	733 ± 50	792 ± 76	895 ± 85	930 ± 29
218258_at	LOC51082	RNA polymerase I 16 kDa subunit	0.3085	**-0.0248**	0.2509	0.1511	0.0554	632 ± 31	590 ± 38	609 ± 39	760 ± 66
221131_at	LOC51146	alpha-1,4-N-acetylglucosaminyltransferase	**0.0548**	**-0.0012**	-0.4697	**-0.0502**	**0.0204**	193 ± 15	210 ± 17	256 ± 22	280 ± 24
219114_at	LOC51161	g20 protein	**0.0237**	-0.2277	0.1830	-0.3992	0.2764	276 ± 8	255 ± 18	334 ± 20	333 ± 63
210389_x_at	LOC51174	delta-tubulin	**0.0002**	**-0.0032**	**0.0480**	-0.2489	**0.0040**	137 ± 12	193 ± 19	211 ± 21	240 ± 21
219863_at	LOC51191	cyclin-E binding protein 1	0.1006	**0.0000**	0.0916	**-0.0333**	**0.0077**	252 ± 17	323 ± 30	336 ± 23	467 ± 73
221998_s_at	LOC51231	VRK3 for vaccinia related kinase 3	**0.0257**	-0.1420	0.1388	-0.1718	0.6446	122 ± 18	135 ± 28	149 ± 18	161 ± 30
221999_at	LOC51231	VRK3 for vaccinia related kinase 3	**0.0139**	**-0.0004**	**0.0261**	-0.2779	**0.0000**	330 ± 14	418 ± 42	369 ± 26	581 ± 24
219167_at	LOC51285	Ris	**0.0071**	**-0.0008**	0.1168	-0.1557	**0.0181**	701 ± 104	896 ± 140	1271 ± 204	1390 ± 197
207785_s_at	LOC51580	H-2K binding factor-2	0.4535	**-0.0452**	-0.2753	**-0.0126**	0.5700	1311 ± 84	1359 ± 130	1500 ± 64	1460 ± 157
219590_x_at	LOC51611	CGI-30 protein	**0.0095**	**-0.0163**	**0.0016**	-0.1407	**0.0243**	743 ± 14	872 ± 58	863 ± 35	917 ± 42
65521_at	LOC51619	ubiquitin-conjugating enzyme HBUCE1	0.0890	**-0.0262**	0.4014	0.1929	**0.0145**	575 ± 38	589 ± 24	580 ± 33	794 ± 84
201974_s_at	LOC51622	CGI-43 protein	0.3575	**-0.0097**	0.4065	0.4825	**0.0190**	231 ± 21	212 ± 22	252 ± 23	331 ± 33
217842_at	LOC51631	CGI-74 protein	**0.0059**	**-0.0279**	**0.0225**	-0.2132	**0.0411**	470 ± 39	553 ± 52	525 ± 21	671 ± 73

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
204097_s_at	LOC51634	CGI-79 protein	**0.0153**	-0.0716	-0.1577	0.4835	0.1456	446 ± 31	414 ± 50	468 ± 24	647 ± 139
208549_x_at	LOC51685	prothymosin a14	**0.0051**	-0.0679	0.2755	-0.2466	0.1181	1488 ± 127	1929 ± 316	1702 ± 152	2455 ± 459
212294_at	LOC55970	G-protein gamma-12 subunit	0.2331	**-0.0123**	-0.3488	-0.3390	0.1419	904 ± 80	944 ± 88	1131 ± 121	1225 ± 141
220371_s_at	LOC56996	cation-chloride cotransporter-interacting protein	**0.0319**	**-0.0158**	0.1159	-0.3570	**0.0280**	324 ± 23	399 ± 50	371 ± 29	529 ± 78
219366_at	LOC57099	cell death regulator aven	0.0851	**-0.0061**	-0.2302	-0.4037	0.0684	181 ± 26	163 ± 29	184 ± 19	261 ± 17
219307_at	LOC57107	candidate tumor suppressor protein	0.4561	**-0.0164**	0.4711	0.1795	0.2024	169 ± 11	167 ± 15	188 ± 17	219 ± 29
209944_at	LOC57862	clones 23667 and 23775 zinc finger protein	**0.0148**	-0.1498	-0.2433	0.3261	0.1760	1702 ± 163	1657 ± 157	2121 ± 185	1959 ± 143
219165_at	LOC59346	PDZ-LIM protein mystique	**0.0170**	**-0.0053**	0.1108	-0.4421	**0.0110**	231 ± 34	193 ± 25	318 ± 34	328 ± 23
215271_at	LOC63923	hypothetical protein similar to tenascin-R	**0.0431**	-0.0792	0.0656	-0.1605	0.1295	94 ± 12	92 ± 9	111 ± 22	170 ± 43
212274_at	LPIN1	lipin 1	**0.0003**	**-0.0016**	0.0580	-0.2010	**0.0060**	674 ± 76	813 ± 98	1051 ± 98	1104 ± 93
203549_s_at	LPL	lipoprotein lipase	0.9821	**-0.0368**	-0.2533	-0.1094	0.1573	686 ± 74	741 ± 75	733 ± 79	943 ± 98
202822_at	LPP	LIM domain containing preferred translocation partner in lipoma	0.1662	**-0.0049**	-0.3185	-0.3853	0.1172	895 ± 100	961 ± 79	1095 ± 64	1259 ± 167
221640_s_at	LRDD	leucine-rich and death domain containing	**0.0006**	-0.0957	0.4677	-0.2515	0.2483	153 ± 29	191 ± 30	256 ± 34	250 ± 71
201412_at	LRP10	low density lipoprotein receptor-related protein 10	**0.0119**	**-0.0002**	0.2710	-0.4640	**0.0106**	801 ± 70	911 ± 86	1052 ± 78	1233 ± 120
219188_s_at	LRP16	LRP16 protein	**0.0014**	**-0.0067**	-0.0644	0.2029	**0.0161**	285 ± 18	256 ± 36	303 ± 27	441 ± 68
212850_s_at	LRP4	low density lipoprotein receptor-related protein 4	0.4666	**-0.0341**	-0.2210	0.4485	0.3438	1505 ± 191	1604 ± 171	1890 ± 175	2036 ± 359
34697_at	LRP6	low density lipoprotein receptor-related protein 6	0.2235	**-0.0220**	0.2343	-0.3992	**0.0137**	224 ± 33	196 ± 30	351 ± 37	292 ± 21
201861_s_at	LRRFIP1	leucine rich repeat interacting protein 1	**0.0024**	**-0.0143**	0.4284	-0.3903	**0.0507**	341 ± 37	321 ± 20	384 ± 38	516 ± 81
220610_s_at	LRRFIP2	leucine rich repeat interacting protein 2	**0.0105**	-0.0587	-0.2315	0.3641	0.1545	232 ± 23	238 ± 35	314 ± 27	302 ± 42
37796_at	LRRN1	leucine-rich repeat protein, neuronal 1	**0.0222**	-0.1003	0.2211	0.4351	**0.0365**	452 ± 36	614 ± 131	437 ± 32	815 ± 149
90610_at	LRRN1	leucine-rich repeat protein, neuronal 1	**0.0021**	**-0.0214**	0.3330	0.1749	0.0649	458 ± 52	567 ± 128	653 ± 83	909 ± 191
202903_at	LSM5	U6 snRNA-associated Sm-like protein	**0.0173**	-0.0619	**0.0028**	**-0.0512**	**0.0217**	109 ± 11	168 ± 20	162 ± 8	187 ± 30
211018_at	LSS	lanosterol synthase	0.2231	**-0.0141**	**-0.0112**	-0.1288	0.1810	115 ± 22	87 ± 15	149 ± 23	165 ± 39
204682_at	LTBP2	latent transforming growth factor beta binding protein 2	**0.0068**	**-0.0219**	0.1621	-0.2944	**0.0367**	320 ± 32	415 ± 50	370 ± 22	529 ± 77
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	0.1899	**-0.0014**	0.4053	0.3169	**0.0141**	478 ± 41	399 ± 56	559 ± 49	844 ± 165
40093_at	LU	Lutheran blood group	**0.0257**	-0.0749	0.2284	0.1117	0.1643	296 ± 24	293 ± 79	380 ± 41	440 ± 60
220044_x_at	LUC7A	cisplatin resistance-associated overexpressed protein	0.0825	**-0.0013**	-0.3827	**-0.0459**	**0.0087**	1293 ± 69	1283 ± 114	1646 ± 48	1523 ± 98
203412_at	LZTR1	leucine-zipper-like transcriptional regulator, 1	**0.0046**	-0.1107	0.3603	-0.4392	0.1602	714 ± 48	808 ± 89	823 ± 70	986 ± 124
210302_s_at	MAB21L2	mab-21-like 2	**0.0025**	**0.0000**	0.0734	**-0.0369**	**0.0001**	145 ± 11	188 ± 9	197 ± 16	258 ± 21
208634_s_at	MACF1	microtubule-actin crosslinking factor 1	0.1273	**-0.0059**	0.2891	-0.3500	0.1213	6029 ± 397	6370 ± 490	7020 ± 245	7661 ± 793
212346_s_at	MAD4	MAX dimerization protein 4	**0.0010**	**-0.0265**	0.3865	-0.2169	0.0819	389 ± 46	423 ± 24	507 ± 19	658 ± 144
208037_s_at	MADCAM1	mucosal vascular addressin cell adhesion molecule 1	**0.0275**	-0.0619	0.1521	-0.4532	**0.0180**	315 ± 35	394 ± 66	311 ± 25	537 ± 78
203077_s_at	MADH2	MAD, mothers against decapentaplegic homolog 2	0.2862	**-0.0368**	-0.3903	-0.3001	0.3342	318 ± 14	306 ± 8	356 ± 23	355 ± 37
202526_at	MADH4	MAD, mothers against decapentaplegic homolog 4	-0.7954	**-0.0096**	0.0958	-0.1898	0.2556	92 ± 9	84 ± 7	108 ± 14	116 ± 13
205187_at	MADH5	MAD, mothers against decapentaplegic homolog 5	**0.0081**	**-0.0343**	0.1287	-0.1805	**0.0319**	53 ± 6	65 ± 12	97 ± 12	85 ± 12
218559_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B	0.2956	**-0.0035**	0.3005	0.1221	**0.0128**	407 ± 40	335 ± 25	412 ± 63	628 ± 80
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F	0.1017	**-0.0017**	-0.1085	-0.2944	**0.0421**	702 ± 150	781 ± 178	1614 ± 423	1741 ± 363
204970_s_at	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G	**0.0243**	**-0.0366**	-0.2613	0.1171	0.0816	813 ± 111	608 ± 41	890 ± 49	1083 ± 191
206218_at	MAGEB2	melanoma antigen, family B, 2	**0.0134**	**-0.0106**	-0.4312	0.3334	**0.0534**	106 ± 13	96 ± 12	119 ± 6	171 ± 35
210017_at	MALT1	mucosa assoc. lymphoid tissue lymphoma transloc. gene 1	**0.0422**	**-0.0071**	-0.3718	**-0.0078**	0.0655	101 ± 12	118 ± 17	142 ± 9	145 ± 12
65884_at	MAN1B1	mannosidase, alpha, class 1B, member 1	**0.0158**	-0.2430	0.1404	-0.0781	0.2107	374 ± 26	395 ± 24	465 ± 22	424 ± 53
202032_s_at	MAN2A2	mannosidase, alpha, class 2A, member 2	0.5956	**-0.0108**	0.4182	-0.0852	0.1884	1141 ± 70	1242 ± 51	1307 ± 114	1463 ± 152

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
209166_s_at	MAN2B1	mannosidase, alpha, class 2B, member 1	**0.0062**	**-0.0036**	-0.4465	-0.1480	**0.0134**	288 ± 31	298 ± 60	328 ± 33	509 ± 70
202424_at	MAP2K2	mitogen-activated protein kinase kinase 2	**0.0280**	-0.0812	-0.4688	0.3035	0.3280	2156 ± 174	1988 ± 117	2579 ± 289	3084 ± 800
215499_at	MAP2K3	mitogen-activated protein kinase kinase 3	**0.0097**	-0.1042	0.3736	-0.4656	0.0598	334 ± 25	382 ± 49	474 ± 43	422 ± 25
215498_s_at	MAP2K3	mitogen-activated protein kinase kinase 3	**0.0000**	**-0.0003**	0.1738	-0.1373	**0.0016**	207 ± 23	240 ± 27	319 ± 35	375 ± 28
216206_x_at	MAP2K7	mitogen-activated protein kinase kinase 7	**0.0135**	**-0.0257**	0.1166	-0.0778	0.0755	196 ± 25	197 ± 14	307 ± 43	292 ± 53
203652_at	MAP3K11	mitogen-activated protein kinase kinase kinase 11	**0.0016**	**-0.0166**	0.2092	0.3177	**0.0530**	704 ± 45	738 ± 87	863 ± 92	1180 ± 233
205192_at	MAP3K14	mitogen-activated protein kinase kinase kinase 14	**0.0340**	**-0.0191**	0.2121	-0.3673	0.1328	309 ± 42	367 ± 40	385 ± 33	480 ± 78
203514_at	MAP3K3	mitogen-activated protein kinase kinase kinase 3	**0.0016**	**-0.0190**	0.1606	-0.3785	0.0662	349 ± 29	414 ± 55	480 ± 26	540 ± 84
243_g_at	MAP4	microtubule-associated protein 4	**0.0076**	-0.1287	0.1900	-0.4409	0.2930	1991 ± 134	1954 ± 216	2538 ± 254	2367 ± 390
212567_s_at	MAP4	microtubule-associated protein 4	**0.0096**	-0.2729	0.3683	-0.3555	0.1948	1624 ± 178	1683 ± 227	2304 ± 164	1907 ± 390
212566_at	MAP4	microtubule-associated protein 4	**0.0186**	-0.1349	0.2724	0.1356	0.2787	5182 ± 271	4426 ± 263	5819 ± 566	6610 ± 1381
202890_at	MAP7	microtubule-associated protein 7	0.4108	**-0.0418**	-0.2125	-0.2200	0.3319	1664 ± 158	1720 ± 217	2051 ± 218	2005 ± 115
208351_s_at	MAPK1	mitogen-activated protein kinase 1	**0.0028**	**-0.0084**	-0.0824	0.0572	**0.0053**	212 ± 14	184 ± 12	226 ± 15	272 ± 20
206106_at	MAPK12	mitogen-activated protein kinase 12	**0.0116**	-0.1412	0.2112	-0.0892	0.2916	192 ± 21	238 ± 31	234 ± 16	298 ± 72
201460_at	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	**0.0088**	**-0.0414**	0.1902	0.2697	0.0992	644 ± 44	761 ± 104	763 ± 80	940 ± 98
202569_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	**0.0053**	**-0.0096**	-0.2661	-0.1510	**0.0082**	364 ± 27	358 ± 14	466 ± 23	435 ± 25
206449_s_at	MASP1	mannan-binding lectin serine protease 1	-0.5137	**-0.0187**	0.2096	0.3410	**0.0039**	117 ± 8	105 ± 8	87 ± 13	171 ± 24
215903_s_at	MAST205	microtubule assoc. testis spec. serine/threonine protein kinase	**0.0133**	**-0.0046**	0.2525	-0.2152	**0.0164**	562 ± 48	503 ± 48	703 ± 47	780 ± 90
213705_at	MAT2A	methionine adenosyltransferase II, alpha	0.1291	**-0.0001**	**0.0133**	**-0.0184**	**0.0038**	316 ± 29	434 ± 58	490 ± 25	733 ± 137
200768_s_at	MAT2A	methionine adenosyltransferase II, alpha	0.1428	**-0.0484**	-0.3430	-0.0566	0.3635	2439 ± 309	2542 ± 196	2992 ± 172	2956 ± 359
202350_s_at	MATN2	matrilin 2	0.1427	**-0.0007**	0.0691	**-0.0219**	**0.0266**	377 ± 45	508 ± 59	471 ± 46	634 ± 76
209331_s_at	MAX	MAX protein	**0.0335**	-0.1708	0.2483	-0.1402	0.3918	692 ± 41	737 ± 53	827 ± 51	770 ± 86
209332_s_at	MAX	MAX protein	0.0672	**-0.0078**	-0.1406	0.2432	**0.0402**	2796 ± 181	2330 ± 97	2998 ± 170	3381 ± 374
212064_x_at	MAZ	MYC-associated zinc finger protein	**0.0249**	-0.4632	**-0.0091**	0.3543	0.1634	1125 ± 75	1036 ± 57	1420 ± 97	1218 ± 206
204179_at	MB	myoglobin	0.3415	**-0.0084**	-0.1165	0.2485	0.0711	198 ± 24	185 ± 8	224 ± 19	276 ± 37
41160_at	MBD3	methyl-CpG binding domain protein 3	**0.0124**	**-0.0232**	0.2830	-0.3059	0.0881	1863 ± 130	1716 ± 106	2335 ± 218	2529 ± 404
210136_at	MBP	myelin basic protein	**0.0343**	**-0.0383**	**0.0285**	-0.4138	0.2970	1624 ± 245	1962 ± 326	2352 ± 674	3195 ± 956
205458_at	MC1R	melanocortin 1 receptor	0.2192	**-0.0198**	0.3825	0.4837	0.1997	212 ± 19	193 ± 23	261 ± 34	297 ± 57
205716_at	MCFP	mitochondrial carrier family protein	0.7286	**-0.0439**	0.1984	0.2795	0.0938	138 ± 13	120 ± 8	129 ± 13	173 ± 19
214057_at	MCL1	myeloid cell leukemia sequence 1	**0.0414**	**-0.0009**	**0.0519**	**-0.0378**	**0.0349**	209 ± 16	232 ± 21	253 ± 29	314 ± 29
200797_s_at	MCL1	myeloid cell leukemia sequence 1	**0.0203**	**-0.0030**	**-0.0489**	0.4306	0.0652	1766 ± 169	1533 ± 75	1987 ± 160	2475 ± 430
208795_s_at	MCM7	MCM7 minichromosome maintenance deficient 7	**0.0461**	-0.2606	-0.1340	0.2613	0.5904	439 ± 69	431 ± 52	535 ± 72	545 ± 101
213761_at	MDM1	nuclear protein double minute 1	0.2852	**-0.0015**	0.0725	**-0.0364**	**0.0135**	315 ± 13	386 ± 26	389 ± 21	418 ± 25
207078_at	MED6	RNA polymerase II transcriptional regulation mediator	0.1388	**-0.0413**	0.2022	-0.2359	0.1339	117 ± 10	153 ± 27	158 ± 22	183 ± 14
213816_s_at	MET	met proto-oncogene	**0.0087**	-0.0686	**0.0403**	-0.2312	0.0995	136 ± 13	182 ± 30	168 ± 17	220 ± 32
203406_at	MFAP1	microfibrillar-associated protein 1	**0.0001**	**-0.0001**	**0.0005**	**-0.0454**	**0.0004**	877 ± 21	956 ± 44	1096 ± 20	1111 ± 58
201126_s_at	MGAT1	mannosyl -glycoprot. β-1,2-N-acetylglucosaminyltransferase	**0.0216**	-0.1793	0.2577	-0.4527	0.3490	573 ± 43	603 ± 45	682 ± 46	677 ± 73
209497_s_at	MGC10871	hypothetical protein similar to RNA-binding protein lark	**0.0324**	-0.3426	-0.4598	0.3893	0.4320	601 ± 85	758 ± 106	710 ± 73	813 ± 119
64408_s_at	MGC4809	serologically defined breast cancer antigen NY-BR-20	**0.0268**	-0.0786	-0.4929	**-0.0433**	0.2675	65 ± 9	64 ± 9	89 ± 17	92 ± 14
205905_s_at	MICA	MHC class I polypeptide-related sequence A	0.0711	**-0.0399**	0.1274	-0.4064	0.1107	155 ± 13	180 ± 23	176 ± 19	261 ± 59
206247_at	MICB	MHC class I polypeptide-related sequence B	**0.0038**	**-0.0005**	0.1496	0.1426	**0.0044**	138 ± 10	122 ± 5	192 ± 27	283 ± 52
210694_s_at	MID1	midline 1	0.0751	**-0.0048**	-0.4117	-0.1303	0.0584	370 ± 40	422 ± 64	414 ± 29	577 ± 78

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
207233_s_at	MITF	microphthalmia-associated transcription factor	**0.0224**	-0.0609	0.1805	-0.2943	0.1083	407 ± 48	554 ± 66	537 ± 52	637 ± 96
218205_s_at	MKNK2	MAP kinase-interacting serine/threonine kinase 2	**0.0001**	**-0.0058**	0.3211	-0.3921	0.0601	1678 ± 152	1789 ± 282	2409 ± 305	2758 ± 418
218845_at	MKPX	mitogen-activated protein kinase phosphatase x	**0.0038**	**-0.0282**	0.3287	0.2653	**0.0136**	1014 ± 42	1014 ± 93	1046 ± 53	1457 ± 183
201285_at	MKRN1	makorin, ring finger protein, 1	0.2066	**-0.0168**	-0.1629	-0.4398	0.2428	1013 ± 33	1016 ± 51	1106 ± 36	1121 ± 65
208082_x_at	MKRN4	makorin, ring finger protein, 4	**0.0259**	-0.3632	0.2007	-0.1776	0.0991	900 ± 92	977 ± 114	1336 ± 126	1017 ± 188
206426_at	MLANA	melan-A	**0.0053**	-0.0574	**0.0085**	-0.3347	0.2505	57 ± 6	72 ± 14	83 ± 10	102 ± 27
213395_at	MLC1	megalencephalic leukoencephalopathy w/ subcortical cysts 1	**0.0201**	-0.1278	0.1608	-0.3273	0.0755	1076 ± 142	1294 ± 213	1793 ± 138	1416 ± 288
212079_s_at	MLLT2	myeloid/lymphoid or mixed-lineage leukemia	**0.0051**	**-0.0525**	0.2902	-0.2032	0.1785	145 ± 26	180 ± 23	206 ± 31	286 ± 83
201924_at	MLLT2	myeloid/lymphoid or mixed-lineage leukemia	**0.0059**	**-0.0009**	-0.3971	0.3371	**0.0224**	1667 ± 129	1606 ± 134	2181 ± 213	2576 ± 399
207842_s_at	MLN51	MLN51 protein	**0.0036**	**-0.0007**	0.2351	**-0.0527**	**0.0062**	1372 ± 115	1647 ± 183	2256 ± 256	2199 ± 212
204580_at	MMP12	matrix metalloproteinase 12	-0.9509	**-0.0303**	0.1792	0.2065	**0.0077**	116 ± 12	100 ± 9	99 ± 7	163 ± 19
207012_at	MMP16	matrix metalloproteinase 16	0.7754	**-0.0464**	0.1365	-0.1226	0.2746	100 ± 9	98 ± 8	114 ± 10	131 ± 21
201069_at	MMP2	matrix metalloproteinase 2	0.0807	**-0.0240**	0.1786	0.3588	**0.0292**	242 ± 30	327 ± 49	269 ± 24	419 ± 62
220201_at	MNAB	membrane-associated nucleic acid binding protein	0.5069	**-0.0365**	-0.2946	0.1330	**0.0309**	143 ± 15	95 ± 20	146 ± 20	195 ± 28
212452_x_at	MORF	monocytic leukemia zinc finger protein-related factor	**0.0139**	-0.0906	-0.1931	-0.2322	0.1619	479 ± 47	480 ± 21	605 ± 44	590 ± 77
212462_at	MORF	monocytic leukemia zinc finger protein-related factor	**0.0042**	**-0.0079**	0.4942	-0.3379	**0.0143**	803 ± 53	805 ± 25	962 ± 41	1075 ± 104
203524_s_at	MPST	mercaptopyruvate sulfurtransferase	**0.0052**	**-0.0287**	-0.1137	0.1436	**0.0278**	580 ± 61	565 ± 45	603 ± 78	875 ± 108
206538_at	MRAS	muscle RAS oncogene homolog	**0.0163**	-0.7755	0.4340	0.2705	0.2830	152 ± 29	208 ± 43	243 ± 29	203 ± 36
204387_x_at	MRP63	mitochondrial ribosomal protein 63	**0.0274**	**-0.0247**	0.3553	-0.2007	0.0973	806 ± 83	796 ± 43	1001 ± 72	1039 ± 117
221995_s_at	MRP63	mitochondrial ribosomal protein 63	**0.0236**	**-0.0306**	0.0945	0.4858	**0.0078**	234 ± 20	296 ± 32	249 ± 8	434 ± 74
41220_at	MSF	MLL septin-like fusion	**0.0201**	**-0.0019**	0.1894	0.4429	**0.0079**	3652 ± 302	3381 ± 172	4726 ± 414	5008 ± 399
210533_at	MSH4	mutS homolog 4	**0.0428**	-0.0565	-0.1952	-0.0760	0.1417	112 ± 11	116 ± 13	109 ± 12	173 ± 39
205932_s_at	MSX1	msh homeo box homolog 1	**0.0189**	**-0.0007**	0.2089	-0.1222	**0.0141**	596 ± 38	676 ± 106	778 ± 61	1163 ± 229
206461_x_at	MT1H	metallothionein 1H	0.4224	**-0.0184**	-0.4401	-0.1084	0.1491	7403 ± 686	8572 ± 632	8638 ± 906	0388 ± 1269
204326_x_at	MT1L	metallothionein 1L	0.1130	**-0.0139**	0.4215	-0.1706	**0.0272**	6290 ± 635	7881 ± 601	7372 ± 890	9500 ± 318
208581_x_at	MT1X	metallothionein 1X	0.7046	**-0.0358**	-0.2987	-0.1080	0.1314	0620 ± 1243	12186 ± 687	168 ± 1145	4632 ± 1617
212185_x_at	MT2A	metallothionein 2A	0.6080	**-0.0283**	-0.3102	-0.2349	0.1771	7870 ± 2129	8902 ± 1006	101 ± 1397	3863 ± 2800
211783_s_at	MTA1	metastasis associated 1	**0.0495**	**-0.0048**	-0.4272	0.2196	**0.0022**	917 ± 50	837 ± 17	944 ± 68	1368 ± 167
205323_s_at	MTF1	metal-regulatory transcription factor 1	**0.0336**	**-0.0001**	0.2922	-0.0566	**0.0111**	419 ± 32	476 ± 32	538 ± 22	570 ± 43
203433_at	MTHFS	5,10-methenyltetrahydrofolate synthetase	**0.0063**	-0.1228	0.2313	-0.0677	0.4588	260 ± 33	242 ± 53	274 ± 58	355 ± 63
203095_at	MTIF2	mitochondrial translational initiation factor 2	**0.0002**	**-0.0065**	0.0930	-0.2917	**0.0418**	411 ± 31	418 ± 35	522 ± 44	575 ± 63
207847_s_at	MUC1	mucin 1, transmembrane	0.0790	**-0.0180**	0.4843	0.3841	**0.0227**	254 ± 29	263 ± 35	267 ± 14	414 ± 64
217117_x_at	MUC3A	mucin 3A, intestinal	0.2290	**-0.0012**	0.0708	**-0.0535**	**0.0234**	411 ± 27	448 ± 40	480 ± 53	645 ± 77
207727_s_at	MUTYH	mutY homolog	**0.0200**	**-0.0354**	0.4997	0.4970	0.1024	634 ± 69	753 ± 92	729 ± 39	910 ± 99
36907_at	MVK	mevalonate kinase	0.0798	**-0.0020**	0.3448	0.4876	**0.0052**	1115 ± 24	1287 ± 95	1265 ± 96	1610 ± 105
204994_at	MX2	myxovirus resistance 2	0.5644	**-0.0276**	0.2472	-0.2149	0.1845	289 ± 25	311 ± 30	290 ± 26	432 ± 99
202364_at	MXI1	MAX interacting protein 1	**0.0543**	**-0.0153**	**-0.0209**	-0.3737	0.1029	4690 ± 458	4852 ± 492	5951 ± 413	5997 ± 504
213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog -like 1	0.0637	**-0.0039**	0.3402	-0.1240	**0.0518**	172 ± 15	197 ± 16	249 ± 36	245 ± 14
214087_s_at	MYBPC1	myosin binding protein C, slow type	0.1441	**-0.0324**	-0.2576	-0.3289	0.1974	1473 ± 271	1384 ± 106	2123 ± 249	2011 ± 441
209757_s_at	MYCN	v-myc myelocytomatosis viral related oncogene	0.1525	**-0.0008**	0.4780	-0.1110	**0.0260**	113 ± 12	130 ± 22	166 ± 17	180 ± 12
217274_x_at	MYL4	myosin, light polypeptide 4, alkali; atrial, embryonic	**0.0416**	**-0.0287**	0.3234	-0.2108	0.0551	220 ± 15	212 ± 10	227 ± 14	337 ± 68
202555_s_at	MYLK	myosin, light polypeptide kinase	**0.0195**	**-0.0367**	0.2422	-0.1911	0.1238	788 ± 87	970 ± 98	985 ± 124	1151 ± 104

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
201976_s_at	MYO10	myosin X	0.0988	**-0.0457**	**0.0290**	-0.2051	0.1025	3064 ± 290	3944 ± 556	4474 ± 301	4214 ± 576
59375_at	MYO15BP	myosin XVB pseudogene	**0.0454**	-0.2505	0.1104	0.4554	0.1478	560 ± 46	703 ± 99	528 ± 39	865 ± 200
211916_s_at	MYO1A	myosin IA	**0.0123**	**-0.0142**	-0.3886	**-0.0494**	**0.0495**	214 ± 13	229 ± 20	240 ± 13	314 ± 45
32811_at	MYO1C	myosin IC	0.2342	**-0.0186**	0.3034	-0.3232	0.0939	1185 ± 113	1162 ± 118	1272 ± 35	1621 ± 213
203072_at	MYO1E	myosin IE	0.1401	**-0.0248**	0.2110	-0.0881	**0.0100**	175 ± 22	239 ± 14	187 ± 17	265 ± 23
212667_at	MYO1F	myosin IF	0.0775	**0.0000**	-0.1813	-0.2269	**0.0012**	2144 ± 409	2016 ± 262	3497 ± 590	5316 ± 867
218966_at	MYO5C	myosin 5C	**0.0277**	**-0.0019**	0.2926	-0.3093	**0.0052**	512 ± 35	624 ± 61	579 ± 47	816 ± 83
203215_s_at	MYO6	myosin VI	**0.0181**	-0.2041	0.1624	-0.0700	0.3753	158 ± 40	217 ± 49	202 ± 30	323 ± 126
214780_s_at	MYO9B	myosin IXB	**0.0028**	**-0.0088**	0.1093	-0.3535	**0.0218**	490 ± 33	647 ± 68	738 ± 69	837 ± 119
205610_at	MYOM1	myomesin 1 185kDa	**0.0003**	**-0.0017**	0.3562	-0.0983	**0.0161**	85 ± 21	101 ± 16	179 ± 23	198 ± 46
32069_at	N4BP1	Nedd4 binding protein 1	**0.0019**	**-0.0011**	**-0.0359**	-0.4043	**0.0073**	327 ± 27	309 ± 42	374 ± 26	470 ± 20
207196_s_at	NAF1	Nef-associated factor 1	**0.0067**	**-0.0010**	0.0764	-0.0589	**0.0063**	465 ± 33	520 ± 39	633 ± 35	656 ± 59
202926_at	NAG	neuroblastoma-amplified protein	**0.0038**	-0.0877	**0.0297**	-0.1395	0.1210	589 ± 40	749 ± 55	715 ± 60	787 ± 89
202943_s_at	NAGA	N-acetylgalactosaminidase, alpha-	0.2581	**-0.0058**	0.2561	-0.3471	0.0625	403 ± 31	424 ± 25	433 ± 23	526 ± 46
218064_s_at	NAKAP95	neighbor of A-kinase anchoring protein 95	0.0589	**-0.0073**	-0.1590	**0.0080**	**0.0038**	772 ± 59	600 ± 55	859 ± 67	1579 ± 343
208754_s_at	NAP1L1	nucleosome assembly protein 1-like 1	**0.0526**	**-0.0111**	0.4410	**-0.0078**	**0.0357**	1696 ± 113	1839 ± 140	2296 ± 187	2036 ± 143
204528_s_at	NAP1L1	nucleosome assembly protein 1-like 1	**0.0216**	**-0.0102**	0.3438	**-0.0016**	0.1583	1207 ± 78	1335 ± 97	1497 ± 134	1493 ± 107
201414_s_at	NAP1L4	nucleosome assembly protein 1-like 4	**0.0326**	-0.2180	0.1773	0.4221	0.2869	919 ± 56	967 ± 94	1116 ± 44	1047 ± 116
218330_s_at	NAV2	neuron navigator 2	0.2265	**-0.0010**	-0.2585	**-0.0533**	**0.0269**	891 ± 93	972 ± 72	1264 ± 119	1392 ± 199
201913_s_at	NBP	nucleotide binding protein	0.2950	**-0.0249**	0.0855	-0.0581	0.3742	815 ± 57	869 ± 76	961 ± 143	1087 ± 140
212843_at	NCAM1	neural cell adhesion molecule 1	**0.0080**	-0.0607	-0.4805	0.2158	0.1489	4141 ± 191	4068 ± 411	4850 ± 375	5222 ± 565
211063_s_at	NCK1	NCK adaptor protein 1	**0.0501**	**-0.0283**	-0.4487	0.2968	0.0891	655 ± 25	566 ± 20	749 ± 71	735 ± 64
209061_at	NCOA3	nuclear receptor coactivator 3	0.2199	**-0.0442**	0.3014	**-0.0053**	0.1038	166 ± 24	218 ± 19	226 ± 12	279 ± 54
207760_s_at	NCOR2	nuclear receptor co-repressor 2	**0.0007**	**-0.0205**	0.3161	0.1962	**0.0084**	2231 ± 141	2095 ± 171	2767 ± 139	2938 ± 277
208759_at	NCSTN	nicastrin	**0.0022**	**-0.0148**	0.2609	0.3984	**0.0215**	604 ± 28	646 ± 50	620 ± 30	783 ± 54
202607_at	NDST1	N-deacetylase/N-sulfotransferase 1	0.0605	**-0.0342**	-0.4743	**-0.0392**	**0.0542**	499 ± 57	560 ± 55	761 ± 37	644 ± 102
207279_s_at	NEBL	nebulette	0.3703	**-0.0374**	0.4559	-0.0767	0.4722	241 ± 17	243 ± 27	265 ± 26	297 ± 38
203961_at	NEBL	nebulette	**0.0496**	**-0.0037**	-0.4161	**-0.0204**	0.0710	5126 ± 259	5476 ± 442	6672 ± 660	7214 ± 975
200015_s_at	NEDD5	neural precursor cell expressed, develop. down-reg. 5	0.1540	**-0.0053**	0.1331	-0.0581	**0.0533**	3651 ± 234	4068 ± 399	4858 ± 186	4633 ± 458
219396_s_at	NEIL1	nei endonuclease VIII-like 1	**0.0301**	-0.1547	-0.1070	0.3798	0.2915	331 ± 47	336 ± 78	402 ± 30	476 ± 77
213328_at	NEK1	NIMA -related kinase 1	**0.0326**	-0.1439	0.1019	-0.0865	0.0632	210 ± 28	296 ± 30	301 ± 21	281 ± 27
212530_at	NEK7	NIMA -related kinase 7	0.0951	**-0.0165**	0.3140	**-0.0241**	0.2232	1295 ± 132	1424 ± 170	1790 ± 261	1687 ± 165
212299_at	NEK9	NIMA - related kinase 9	**0.0231**	**-0.0037**	-0.0972	-0.0904	0.1022	671 ± 58	704 ± 101	796 ± 65	933 ± 87
206948_at	NEU3	sialidase 3	**0.0481**	-0.0903	-0.3657	0.3676	**0.0150**	204 ± 11	200 ± 28	165 ± 25	316 ± 55
214799_at	NFASC	neurofascin	**0.0403**	**-0.0143**	0.2598	-0.2121	0.0612	927 ± 155	1373 ± 236	1897 ± 324	1733 ± 352
211105_s_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, CaN-dep. 1	**0.0244**	**-0.0010**	-0.4702	-0.4771	**0.0178**	284 ± 29	294 ± 39	316 ± 25	502 ± 93
207416_s_at	NFATC3	nuclear factor of activated T-cells, cytoplasmic, CaN-dep 3	0.2278	**-0.0205**	0.4054	-0.4599	0.1522	159 ± 20	168 ± 24	209 ± 28	225 ± 10
200758_s_at	NFE2L1	nuclear factor -like 1	**0.0050**	-0.1564	0.4897	-0.1971	0.1493	2024 ± 97	2188 ± 57	2612 ± 102	2300 ± 337
200759_x_at	NFE2L1	nuclear factor -like 1	**0.0002**	**-0.0083**	-0.1371	0.1569	**0.0449**	3717 ± 135	3695 ± 357	4159 ± 99	4798 ± 473
214179_s_at	NFE2L1	nuclear factor -like 1	**0.0090**	**-0.0089**	-0.3975	0.1002	**0.0276**	2155 ± 138	2002 ± 130	2237 ± 152	2870 ± 323
204702_s_at	NFE2L3	nuclear factor -like 3	0.0981	**-0.0338**	0.1887	-0.2065	**0.0478**	81 ± 10	101 ± 8	95 ± 9	136 ± 22
209289_at	NFIB	nuclear factor I/B	0.0751	**-0.0266**	0.1744	0.3378	0.1231	2449 ± 153	2587 ± 188	2843 ± 141	3078 ± 286

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
209290_s_at	NFIB	nuclear factor I/B	0.2873	**-0.0407**	0.2379	-0.2492	0.1876	2753 ± 184	2756 ± 170	3347 ± 213	3249 ± 383
206929_s_at	NFIC	nuclear factor I/C	0.2432	**-0.0376**	0.2118	**-0.0474**	0.2191	318 ± 39	342 ± 32	352 ± 34	449 ± 68
213298_at	NFIC	nuclear factor I/C	**0.0026**	**-0.0056**	**0.0037**	**-0.0541**	**0.0127**	126 ± 10	158 ± 14	180 ± 8	234 ± 40
209239_at	NFKB1	NF of kappa light polypeptide gene enhancer in B-cells 1	**0.0219**	-0.3815	-0.3905	-0.3749	0.6568	458 ± 33	500 ± 42	493 ± 36	532 ± 59
201502_s_at	NFKBIA	NF of kappa light polypep. gene enhancer in B-cells inhib., α	**0.0057**	**-0.0011**	-0.2975	-0.2235	**0.0073**	1776 ± 294	1999 ± 377	2682 ± 493	4203 ± 735
210268_at	NFX1	nuclear transcription factor, X-box binding 1	**0.0025**	**-0.0222**	0.1403	-0.0758	0.0635	76 ± 14	112 ± 21	143 ± 23	148 ± 25
202008_s_at	NID	nidogen	0.2302	**-0.0339**	0.1322	-0.1095	**0.0045**	133 ± 8	204 ± 23	142 ± 12	230 ± 32
215338_s_at	NKTR	natural killer-tumor recognition sequence	**0.0129**	-0.1353	**0.0301**	-0.2544	**0.0117**	181 ± 13	225 ± 27	292 ± 21	234 ± 28
217844_at	NLI-IF	nuclear LIM interactor-interacting factor	**0.0141**	**-0.0102**	**0.0314**	**-0.0301**	**0.0436**	630 ± 82	791 ± 83	1116 ± 90	1117 ± 258
205204_at	NMB	neuromedin B	**0.0007**	**-0.0059**	**0.0169**	0.4550	**0.0383**	432 ± 33	482 ± 62	492 ± 42	737 ± 139
204862_s_at	NME3	non-metastatic cells 3, protein expressed in	**0.0016**	**-0.0005**	0.4648	-0.1352	**0.0022**	548 ± 38	582 ± 72	612 ± 22	914 ± 109
212739_s_at	NME4	non-metastatic cells 4, protein expressed in	**0.0080**	**-0.0083**	0.0959	-0.2639	**0.0036**	750 ± 43	692 ± 72	1036 ± 68	952 ± 85
202237_at	NNMT	nicotinamide N-methyltransferase	0.0773	**-0.0235**	-0.2385	0.1065	**0.0010**	201 ± 27	89 ± 20	147 ± 22	306 ± 48
214427_at	NOL1	nucleolar protein 1, 120kDa	**0.0218**	-0.2247	-0.1073	0.2250	0.3489	850 ± 66	796 ± 116	868 ± 80	1053 ± 143
200874_s_at	NOL5A	nucleolar protein 5A	**0.0194**	**-0.0054**	**-0.0087**	0.0914	**0.0318**	305 ± 13	272 ± 7	349 ± 38	399 ± 37
205895_s_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	**0.0422**	-0.1171	0.3146	-0.4466	0.5031	258 ± 22	263 ± 25	276 ± 25	306 ± 22
200057_s_at	NONO	non-POU domain containing, octamer-binding	**0.0360**	**-0.0029**	-0.4987	**-0.0379**	**0.0445**	3672 ± 99	3873 ± 104	4017 ± 165	4172 ± 110
217950_at	NOSIP	eNOS interacting protein	**0.0205**	-0.1487	-0.1308	0.0772	0.4777	502 ± 41	484 ± 26	553 ± 62	605 ± 88
205247_at	NOTCH4	Notch homolog 4	0.1144	**-0.0163**	**0.0329**	0.4330	**0.0348**	302 ± 17	360 ± 40	367 ± 28	474 ± 62
220316_at	NPAS3	basic-helix-loop-helix-PAS protein	0.0759	**-0.0001**	**0.0020**	-0.1486	**0.0011**	427 ± 16	554 ± 44	617 ± 17	796 ± 108
202679_at	NPC1	Niemann-Pick disease, type C1	-0.6334	**-0.0085**	-0.2478	-0.3528	0.2017	1188 ± 120	1093 ± 103	1197 ± 118	1503 ± 168
214107_x_at	NPEPPS	aminopeptidase puromycin sensitive	0.3775	**-0.0290**	-0.1239	-0.2002	0.2578	517 ± 41	478 ± 62	549 ± 31	615 ± 42
215090_x_at	NPEPPS	aminopeptidase puromycin sensitive	**0.0244**	**-0.0310**	-0.0994	-0.2947	0.2896	681 ± 46	704 ± 75	761 ± 48	822 ± 51
217041_at	NPTXR	neuronal pentraxin receptor	0.9277	**-0.0482**	-0.2217	-0.4873	0.3205	208 ± 20	207 ± 21	238 ± 18	273 ± 47
201468_s_at	NQO1	NADH dehydrogenase, quinone 1	0.4670	**-0.0390**	0.1347	0.0782	0.1421	496 ± 64	397 ± 40	503 ± 67	655 ± 86
31637_s_at	NR1D1	nuclear receptor subfamily 1, group D, member 1	**0.0110**	-0.4674	-0.3669	0.4310	0.4949	2771 ± 256	3307 ± 583	2925 ± 490	3686 ± 491
209506_s_at	NR2F1	nuclear receptor subfamily 2, group F, member 1	**0.0289**	-0.2429	0.1921	-0.0775	0.8210	542 ± 23	568 ± 23	596 ± 54	619 ± 106
209262_s_at	NR2F6	nuclear receptor subfamily 2, group F, member 6	**0.0482**	-0.0951	-0.4242	**0.0542**	0.0882	436 ± 32	408 ± 63	418 ± 32	613 ± 98
216979_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	0.2152	**-0.0037**	**0.0524**	-0.2079	**0.0265**	86 ± 7	88 ± 12	104 ± 12	150 ± 26
214632_at	NRP2	neuropilin 2	**0.0498**	-0.0981	-0.1788	-0.4201	0.1182	127 ± 14	86 ± 17	120 ± 12	145 ± 21
209982_s_at	NRXN2	neurexin 2	**0.0111**	-0.2299	-0.4993	-0.3509	0.2346	488 ± 41	542 ± 54	605 ± 48	677 ± 108
203718_at	NTE	neuropathy target esterase	**0.0077**	-0.7111	0.4995	-0.4016	0.9043	1308 ± 102	1387 ± 157	1466 ± 187	1459 ± 259
217033_x_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	**0.0020**	-0.0579	0.1423	0.4117	0.0866	806 ± 38	897 ± 106	1029 ± 81	1098 ± 102
222027_at	NUCKS	similar to rat nuclear ubiquitous casein kinase 2	**0.0064**	**-0.0546**	0.1786	-0.2575	0.1422	287 ± 34	298 ± 36	309 ± 24	473 ± 120
217802_s_at	NUCKS	similar to rat nuclear ubiquitous casein kinase 2	**0.0001**	**-0.0002**	**0.0099**	-0.1530	**0.0013**	4406 ± 107	4549 ± 104	5193 ± 244	5660 ± 313
210574_s_at	NUDC	nuclear distribution gene C homolog	**0.0143**	-0.6804	0.4860	0.3653	0.4315	1192 ± 56	1181 ± 70	1343 ± 67	1201 ± 118
218414_s_at	NUDE1	LIS1-interacting protein NUDE1, rat homolog	**0.0039**	**-0.0333**	0.2772	0.4052	0.1041	667 ± 108	780 ± 187	994 ± 161	1401 ± 366
205134_s_at	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	**0.0340**	**-0.0085**	0.0947	-0.2330	**0.0225**	252 ± 20	252 ± 11	353 ± 36	372 ± 50
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	**0.0008**	**-0.0052**	0.2004	**-0.0377**	**0.0547**	740 ± 72	879 ± 74	987 ± 66	1133 ± 170
207545_s_at	NUMB	numb homolog	0.3200	**-0.0075**	0.2505	**-0.0534**	**0.0465**	120 ± 8	119 ± 17	168 ± 17	167 ± 20
212709_at	NUP160	nucleoporin 160kDa	**0.0067**	**-0.0001**	0.4503	-0.0642	**0.0004**	151 ± 11	185 ± 12	213 ± 16	245 ± 11
202155_s_at	NUP214	nucleoporin 214kDa	**0.0128**	**-0.0011**	-0.4361	-0.0709	**0.0094**	390 ± 24	401 ± 44	445 ± 20	536 ± 33

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
219007_at	Nup43	nucleoporin Nup43	0.0636	**-0.0199**	0.1865	-0.3225	0.0635	539 ± 55	572 ± 39	710 ± 47	738 ± 92
203195_s_at	NUP98	nucleoporin 98kDa	**0.0044**	**-0.0001**	0.1507	**-0.0104**	**0.0000**	97 ± 10	154 ± 25	250 ± 12	233 ± 27
210793_s_at	NUP98	nucleoporin 98kDa	**0.0410**	**-0.0031**	0.1170	**-0.0122**	0.0780	229 ± 15	256 ± 24	278 ± 13	291 ± 19
221684_s_at	NYX	nyctalopin	**0.0154**	-0.0634	0.0984	-0.2008	0.1515	98 ± 14	117 ± 10	125 ± 9	180 ± 48
205660_at	OASL	2'-5'-oligoadenylate synthetase-like	0.6803	**-0.0071**	0.1457	-0.0822	0.0815	263 ± 27	299 ± 26	287 ± 21	382 ± 51
210797_s_at	OASL	2'-5'-oligoadenylate synthetase-like	0.3167	**-0.0139**	0.1112	**-0.0072**	0.1729	282 ± 34	335 ± 19	332 ± 25	399 ± 55
200790_at	ODC1	ornithine decarboxylase 1	0.1019	**-0.0166**	0.4136	-0.3532	**0.0544**	948 ± 48	879 ± 53	864 ± 35	1217 ± 176
203569_s_at	OFD1	oral-facial-digital syndrome 1	**0.0071**	**-0.0015**	-0.3908	-0.1424	**0.0326**	1060 ± 101	1179 ± 94	1411 ± 124	1546 ± 159
201282_at	OGDH	oxoglutarate dehydrogenase	**0.0460**	-0.9567	-0.2534	0.3984	**0.0340**	622 ± 72	623 ± 88	924 ± 73	586 ± 118
205301_s_at	OGG1	8-oxoguanine DNA glycosylase	0.1250	**-0.0181**	0.1970	**-0.0363**	0.0777	57 ± 7	71 ± 7	108 ± 20	103 ± 22
205760_s_at	OGG1	8-oxoguanine DNA glycosylase	**0.0016**	**-0.0030**	0.2250	-0.1113	**0.0319**	480 ± 47	532 ± 65	629 ± 70	843 ± 148
215136_s_at	OIP2	Opa-interacting protein 2	**0.0322**	**-0.0077**	0.0628	-0.1313	**0.0200**	267 ± 10	355 ± 36	334 ± 22	419 ± 50
206323_x_at	OPHN1	oligophrenin 1	**0.0084**	**-0.0069**	0.1390	-0.3364	**0.0301**	2393 ± 277	2949 ± 391	3096 ± 78	4482 ± 876
221460_at	OR2C1	olfactory receptor, family 2, subfamily C, member 1	**0.0335**	**-0.0144**	-0.4954	0.3644	0.0770	283 ± 40	259 ± 21	322 ± 47	468 ± 94
215770_at	OR7E2P	olfactory receptor, 7E2 pseudogene	0.5560	**-0.0046**	-0.0931	0.2537	**0.0094**	45 ± 6	30 ± 6	42 ± 13	86 ± 15
207408_at	ORCTL4	organic cationic transporter-like 4	**0.0328**	**-0.0158**	**-0.0380**	0.3543	**0.0312**	350 ± 25	337 ± 23	365 ± 30	506 ± 72
208735_s_at	OS4	conserved gene amplified in osteosarcoma	**0.0542**	**-0.0290**	**0.0126**	0.3074	0.0849	450 ± 25	483 ± 60	496 ± 27	609 ± 61
203445_s_at	OS4	conserved gene amplified in osteosarcoma	**0.0343**	**-0.0077**	0.4949	0.3445	0.0991	2495 ± 230	2660 ± 291	3025 ± 231	3476 ± 393
215399_s_at	OS-9	amplified in osteosarcoma	**0.0037**	-0.4339	**0.0377**	0.2597	0.4182	355 ± 24	395 ± 47	437 ± 20	415 ± 56
218304_s_at	OSBPL11	oxysterol binding protein-like 11	0.2868	**-0.0153**	-0.3162	**-0.0412**	0.2455	704 ± 69	837 ± 129	961 ± 110	993 ± 146
213039_at	P114-RHO-GEF	Rho-specific guanine nucleotide exchange factor p114	0.1011	**-0.0312**	-0.4892	**0.0337**	0.0606	1073 ± 35	1126 ± 163	1129 ± 81	1493 ± 150
202553_s_at	P29	GCIP-interacting protein p29	**0.0025**	-0.0574	0.1144	**-0.0131**	**0.0550**	998 ± 90	1164 ± 72	1308 ± 75	1189 ± 68
220408_x_at	P38IP	transcription factor	0.0884	**-0.0190**	-0.4874	-0.3214	**0.0123**	743 ± 68	763 ± 99	729 ± 49	1063 ± 44
220402_at	P53AIP1	p53-regulated apoptosis-inducing protein 1	0.0912	**-0.0004**	0.0885	**-0.0401**	**0.0000**	47 ± 9	57 ± 7	43 ± 8	125 ± 16
204064_at	P84	nuclear matrix protein p84	**0.0263**	-0.1264	-0.2149	0.4118	0.1330	917 ± 91	917 ± 73	1180 ± 78	1041 ± 109
212220_at	PA200	proteasome activator 200 kDa	**0.0035**	-0.0876	**0.0521**	-0.2996	0.3204	77 ± 6	87 ± 16	105 ± 13	124 ± 34
215157_x_at	PABPC1	poly binding protein, cytoplasmic 1	**0.0234**	**-0.0318**	0.1606	**-0.0525**	0.1582	3495 ± 151	3731 ± 242	4100 ± 273	4097 ± 223
208113_x_at	PABPC3	poly binding protein, cytoplasmic 3	**0.0287**	-0.1967	**0.0357**	-0.0759	0.3436	2272 ± 174	2625 ± 405	2907 ± 234	2622 ± 145
201544_x_at	PABPN1	poly binding protein, nuclear 1	**0.0050**	-0.1873	0.4933	0.1838	0.2529	4230 ± 288	4405 ± 488	4544 ± 448	5912 ± 1094
201651_s_at	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	0.1415	**-0.0026**	-0.1714	**0.0380**	**0.0176**	2223 ± 156	1874 ± 170	2533 ± 133	3396 ± 579
205719_s_at	PAH	phenylalanine hydroxylase	0.4106	**-0.0367**	0.1758	**-0.0028**	0.3914	99 ± 13	120 ± 18	121 ± 8	128 ± 6
208878_s_at	PAK2	p21 -activated kinase 2	0.4320	**-0.0374**	0.3637	-0.0987	0.1148	305 ± 24	363 ± 38	311 ± 18	408 ± 47
33814_at	PAK4	p21-activated kinase 4	**0.0089**	**-0.0114**	0.1352	**-0.0533**	0.0807	600 ± 39	625 ± 41	722 ± 44	847 ± 128
205815_at	PAP	pancreatitis-associated protein	0.0883	**-0.0061**	0.0663	-0.2791	**0.0332**	130 ± 10	171 ± 16	156 ± 13	221 ± 36
221527_s_at	PARD3	par-3 partitioning defective 3 homolog	**0.0117**	**-0.0031**	0.3044	-0.4089	**0.0163**	390 ± 40	350 ± 29	543 ± 60	563 ± 64
204004_at	PAWR	PRKC, apoptosis, WT1, regulator	0.2839	**-0.0029**	-0.2074	-0.0971	0.0977	274 ± 32	279 ± 33	330 ± 27	376 ± 32
205646_s_at	PAX6	paired box gene 6	**0.0003**	**0.0000**	0.2655	-0.1912	**0.0024**	1018 ± 115	1011 ± 98	1441 ± 189	2040 ± 299
220355_s_at	PB1	polybromo 1	**0.0209**	**-0.0348**	**0.0362**	**-0.0008**	**0.0027**	563 ± 20	639 ± 38	746 ± 32	650 ± 34
217739_s_at	PBEF	pre-B-cell colony-enhancing factor	0.5430	**-0.0205**	0.3250	**-0.0138**	0.2467	371 ± 34	411 ± 44	489 ± 58	499 ± 65
211097_s_at	PBX2	pre-B-cell leukemia transcription factor 2	**0.0481**	**-0.0013**	-0.4044	0.3876	**0.0127**	164 ± 11	143 ± 18	197 ± 14	225 ± 24
204476_s_at	PC	pyruvate carboxylase	**0.0001**	**-0.0409**	**0.0223**	-0.4650	0.1148	501 ± 40	596 ± 65	695 ± 67	713 ± 92
203845_at	PCAF	p300/CBP-associated factor	0.6531	**-0.0359**	0.3825	**-0.0295**	**0.0263**	1312 ± 103	1521 ± 167	2028 ± 200	1671 ± 164

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
217049_x_at	PCDH11Y	protocadherin 11 Y-linked	0.1777	**-0.0450**	**0.0483**	**-0.0071**	0.0645	112 ± 8	141 ± 21	125 ± 20	198 ± 36
205656_at	PCDH17	protocadherin 17	**0.0178**	-0.1013	0.0796	-0.4762	0.2160	2305 ± 195	2450 ± 219	2921 ± 243	2876 ± 341
219738_s_at	PCDH9	protocadherin 9	0.0769	**-0.0190**	0.4993	-0.1118	0.1086	2250 ± 176	2345 ± 232	2846 ± 206	2706 ± 160
214937_x_at	PCM1	pericentriolar material 1	**0.0260**	-0.2095	-0.2338	-0.1556	0.0725	1098 ± 66	1064 ± 91	1350 ± 70	1155 ± 99
214118_x_at	PCM1	pericentriolar material 1	0.0943	**-0.0377**	**-0.0541**	0.3889	0.1044	1313 ± 127	1299 ± 70	1282 ± 85	1636 ± 130
201933_at	PCOLN3	procollagen N-endopeptidase	**0.0036**	-0.6778	0.4751	0.4852	0.3157	580 ± 36	520 ± 68	708 ± 59	586 ± 115
205559_s_at	PCSK5	proprotein convertase subtilisin/kexin type 5	**0.0025**	**-0.0129**	-0.0647	0.3272	**0.0039**	180 ± 23	127 ± 17	238 ± 24	247 ± 25
212594_at	PDCD4	programmed cell death 4	**0.0001**	**-0.0014**	**0.0070**	**-0.0142**	**0.0029**	174 ± 14	234 ± 16	313 ± 33	296 ± 36
212593_s_at	PDCD4	programmed cell death 4	**0.0048**	**-0.0093**	0.4099	**-0.0001**	**0.0016**	674 ± 59	872 ± 116	1342 ± 16	1022 ± 179
204449_at	PDCL	phosducin-like	**0.0431**	-0.3051	**0.0069**	**-0.0113**	**0.0421**	175 ± 21	204 ± 11	271 ± 28	204 ± 28
206388_at	PDE3A	phosphodiesterase 3A, cGMP-inhibited	**0.0009**	**-0.0029**	0.0846	-0.1842	**0.0257**	133 ± 8	141 ± 16	165 ± 26	234 ± 36
206792_x_at	PDE4C	phosphodiesterase 4C, cAMP-specific	**0.0069**	**-0.0180**	**0.0220**	-0.1432	**0.0466**	4935 ± 632	6755 ± 1121	9049 ± 1345	8316 ± 1212
210837_s_at	PDE4D	phosphodiesterase 4D, cAMP-specific	**0.0031**	**-0.0055**	0.2113	-0.4434	**0.0044**	56 ± 6	57 ± 15	61 ± 10	127 ± 23
210836_x_at	PDE4D	phosphodiesterase 4D, cAMP-specific	**0.0374**	**-0.0457**	**-0.0044**	0.4461	0.0851	108 ± 13	79 ± 17	106 ± 11	153 ± 31
216061_x_at	PDGFB	platelet-derived growth factor beta polypeptide	0.1198	**-0.0065**	**0.0075**	**-0.0086**	0.1059	376 ± 20	423 ± 60	550 ± 46	531 ± 96
202273_at	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	**0.0221**	-0.0721	0.1187	-0.1005	0.0688	242 ± 26	334 ± 48	345 ± 24	346 ± 31
205137_x_at	PDZ-73/NY-CO-38	PDZ-73 protein	**0.0449**	**0.0000**	0.1158	**-0.0100**	**0.0004**	219 ± 34	300 ± 64	385 ± 32	565 ± 65
211184_s_at	PDZ-73/NY-CO-38	PDZ-73 protein	**0.0082**	**-0.0031**	0.0585	-0.2086	**0.0460**	275 ± 29	342 ± 61	368 ± 52	519 ± 91
208982_at	PECAM1	platelet/endothelial cell adhesion molecule	**0.0355**	**-0.0058**	0.4207	-0.0699	0.1173	519 ± 62	516 ± 49	660 ± 76	719 ± 83
215354_s_at	PELP1	proline and glutamic acid rich nuclear protein	**0.0040**	-0.0933	0.1963	-0.1487	0.2547	296 ± 43	314 ± 47	413 ± 43	400 ± 69
214989_x_at	PEPP2	phosphoinositol 3-phosphate-binding protein-2	**0.0188**	-0.0869	0.3103	-0.1503	0.3509	965 ± 95	945 ± 109	1226 ± 203	1265 ± 200
202861_at	PER1	period homolog 1	**0.0000**	**-0.0099**	0.2052	**-0.0479**	**0.0365**	271 ± 55	393 ± 44	479 ± 50	542 ± 107
36829_at	PER1	period homolog 1	**0.0020**	**-0.0105**	0.3087	-0.2764	**0.0267**	894 ± 96	1094 ± 107	1102 ± 53	1405 ± 175
205251_at	PER2	period homolog 2	**0.0146**	**-0.0004**	0.1440	-0.2737	**0.0063**	782 ± 65	883 ± 79	991 ± 63	1158 ± 71
213296_at	PEX10	peroxisome biogenesis factor 10	0.2588	**-0.0364**	-0.1705	0.1926	0.0961	554 ± 44	576 ± 58	568 ± 32	709 ± 32
202464_s_at	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0.2420	**-0.0098**	-0.2468	-0.2187	0.0817	1897 ± 261	1863 ± 98	2821 ± 385	2722 ± 459
205261_at	PGC	progastricsin	0.1265	**-0.0029**	-0.0870	0.3083	**0.0083**	164 ± 6	155 ± 16	170 ± 16	291 ± 53
203501_at	PGCP	plasma glutamate carboxypeptidase	0.4277	**-0.0302**	-0.1570	**-0.0239**	0.2750	430 ± 57	513 ± 66	603 ± 76	556 ± 64
218388_at	PGLS	6-phosphogluconolactonase	**0.0156**	-0.0720	0.2090	0.0703	0.1472	398 ± 41	418 ± 42	424 ± 51	573 ± 89
218387_s_at	PGLS	6-phosphogluconolactonase	**0.0128**	**-0.0074**	**0.0406**	0.2988	**0.0540**	719 ± 96	803 ± 82	880 ± 93	1140 ± 147
203314_at	PGPL	Pseudoautosomal GTP-binding protein-like	**0.0237**	**-0.0422**	-0.2159	-0.2081	0.1991	517 ± 48	492 ± 45	529 ± 36	652 ± 80
220558_x_at	PHEMX	pan-hematopoietic expression	0.6180	**-0.0087**	0.4042	-0.2646	0.0577	393 ± 35	369 ± 25	395 ± 46	572 ± 87
40446_at	PHF1	PHD finger protein 1	**0.0197**	**-0.0527**	-0.4096	-0.4306	**0.0503**	2651 ± 90	2777 ± 260	2681 ± 127	3481 ± 378
209439_s_at	PHKA2	phosphorylase kinase, alpha 2	**0.0023**	**-0.0017**	-0.0864	-0.3197	**0.0079**	306 ± 37	299 ± 17	408 ± 35	478 ± 55
218634_at	PHLDA3	pleckstrin homology-like domain, family A, member 3	**0.0057**	**-0.0113**	0.4370	0.2769	**0.0290**	709 ± 56	715 ± 78	804 ± 77	1052 ± 124
209345_s_at	PI4KII	phosphatidylinositol 4-kinase type II	**0.0394**	-0.1836	**0.0255**	-0.1561	0.4015	784 ± 53	835 ± 60	828 ± 52	913 ± 46
212881_at	PIASY	protein inhibitor of activated STAT protein PIASy	**0.0076**	**-0.0162**	0.1215	0.3572	0.0559	334 ± 30	417 ± 89	425 ± 42	598 ± 96
213239_at	PIBF1	progesterone-induced blocking factor 1	0.1800	**-0.0210**	0.3313	**-0.0049**	**0.0412**	126 ± 6	140 ± 13	132 ± 14	192 ± 29
200704_at	PIG7	LPS-induced TNF-alpha factor	0.4490	**-0.0187**	0.4384	-0.3985	0.1091	998 ± 126	909 ± 107	1141 ± 164	1394 ± 49
200706_s_at	PIG7	LPS-induced TNF-alpha factor	0.5757	**-0.0387**	0.1702	-0.1734	0.1294	664 ± 83	870 ± 122	926 ± 36	935 ± 112
205281_s_at	PIGA	phosphatidylinositol glycan, class A	0.4475	**-0.0485**	-0.3049	-0.4006	0.3726	276 ± 26	275 ± 19	332 ± 30	320 ± 35
204484_at	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	**0.0152**	**-0.0073**	-0.0821	0.1709	**0.0169**	778 ± 57	744 ± 122	978 ± 107	1382 ± 241

Probe set	Name	Description	NFT_O	MMSE_O	NFT_I	MMSE_I	ANOVA	Control	Incipient	Moderate	Severe
204297_at	PIK3C3	phosphoinositide-3-kinase, class 3	0.0844	**-0.0010**	0.1369	-0.4447	**0.0123**	321 ± 17	365 ± 31	362 ± 35	467 ± 35
206138_s_at	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	**0.0327**	**-0.0035**	-0.1265	**-0.0494**	0.1078	1331 ± 78	1291 ± 88	1500 ± 89	1585 ± 101
222218_s_at	PILR	paired immunoglobulin-like receptor alpha	0.1095	**-0.0303**	0.2959	-0.2963	0.1310	148 ± 21	181 ± 22	170 ± 17	214 ± 13
209193_at	PIM1	pim-1 oncogene	0.1210	**-0.0054**	-0.0846	-0.4711	0.0680	416 ± 66	362 ± 36	476 ± 62	594 ± 55
214224_s_at	PIN4	protein NIMA-interacting, 4	0.5067	**-0.0190**	0.4797	-0.3499	**0.0511**	474 ± 26	478 ± 19	481 ± 21	557 ± 18
214225_at	PIN4	protein NIMA-interacting, 4	**0.0466**	**-0.0141**	-0.3622	-0.1424	**0.0163**	180 ± 21	193 ± 16	192 ± 6	276 ± 34
207391_s_at	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	**0.0121**	**-0.0010**	0.1322	0.4337	**0.0020**	724 ± 49	817 ± 53	821 ± 95	1264 ± 143
205570_at	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	**0.0308**	**-0.0089**	-0.1953	-0.1431	0.1561	232 ± 26	234 ± 54	276 ± 24	346 ± 49
204146_at	PIR51	RAD51-interacting protein	0.0702	**-0.0492**	0.4145	0.3550	0.1439	65 ± 6	55 ± 6	86 ± 14	104 ± 26
214682_at	PKD1	polycystic kidney disease 1	**0.0106**	-0.3156	-0.0832	0.4934	0.6342	166 ± 28	162 ± 33	212 ± 68	243 ± 62
202328_s_at	PKD1	polycystic kidney disease 1	**0.0226**	-0.8845	-0.4643	0.1503	0.8066	875 ± 35	868 ± 106	932 ± 77	973 ± 114
38269_at	PKD2	protein kinase D2	**0.0088**	**-0.0229**	0.4274	0.2416	0.0702	603 ± 52	662 ± 96	667 ± 62	868 ± 72
206178_at	PLA2G5	phospholipase A2, group V	**0.0199**	-0.0741	-0.2008	0.1190	0.2547	539 ± 61	498 ± 81	590 ± 98	781 ± 157
215938_s_at	PLA2G6	phospholipase A2, group VI	**0.0013**	**-0.0435**	0.0710	-0.0647	0.1377	288 ± 23	341 ± 25	381 ± 31	476 ± 114
211918_x_at	PLAC3	placenta-specific 3	**0.0228**	**-0.0063**	0.0664	-0.1455	**0.0137**	361 ± 30	428 ± 23	469 ± 50	644 ± 102
205372_at	PLAG1	pleiomorphic adenoma gene 1	0.0731	**-0.0015**	**0.0333**	0.2767	**0.0049**	132 ± 13	121 ± 7	168 ± 20	209 ± 19
207943_x_at	PLAGL1	pleiomorphic adenoma gene-like 1	0.0851	**-0.0128**	-0.0981	0.4084	**0.0156**	275 ± 24	230 ± 25	310 ± 21	334 ± 9
202925_s_at	PLAGL2	pleiomorphic adenoma gene-like 2	**0.0075**	**-0.0098**	0.4766	-0.2048	0.0607	311 ± 25	327 ± 24	394 ± 15	405 ± 44
205111_s_at	PLCE1	phospholipase C, epsilon 1	**0.0043**	**-0.0439**	0.1239	-0.3028	**0.0336**	226 ± 20	286 ± 38	363 ± 46	343 ± 33
204613_at	PLCG2	phospholipase C, gamma 2	0.1598	**-0.0270**	0.3807	0.4970	**0.0522**	305 ± 30	344 ± 58	301 ± 43	497 ± 77
205934_at	PLCL1	phospholipase C-like 1	0.5862	**-0.0210**	-0.4694	-0.4231	0.2556	405 ± 48	419 ± 75	469 ± 91	594 ± 64
209643_s_at	PLD2	phospholipase D2	**0.0072**	**-0.0018**	**0.0324**	**-0.0437**	**0.0098**	332 ± 26	417 ± 33	506 ± 40	540 ± 73
201373_at	PLEC1	plectin 1, intermediate filament binding protein 500kDa	**0.0168**	**-0.0225**	-0.0787	-0.4002	0.1725	406 ± 48	421 ± 17	522 ± 46	606 ± 123
214415_at	PLGL	plasminogen-like	**0.0392**	-0.2956	0.1232	-0.3677	**0.0387**	161 ± 19	214 ± 46	292 ± 25	219 ± 35
205871_at	PLGL	plasminogen-like	0.0840	**-0.0107**	**-0.0372**	0.4935	**0.0519**	151 ± 26	114 ± 20	192 ± 26	217 ± 28
200827_at	PLOD	procollagen-lysine, 2-oxoglutarate 5-dioxygenase	0.0550	**-0.0284**	**-0.0271**	0.2514	0.1692	409 ± 45	344 ± 12	422 ± 28	517 ± 89
202619_s_at	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	0.2114	**-0.0253**	-0.3160	**-0.0328**	0.2518	251 ± 29	269 ± 40	267 ± 23	341 ± 39
202185_at	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	**0.0173**	**-0.0080**	-0.4297	0.4495	0.0720	1010 ± 117	1177 ± 152	1203 ± 94	1520 ± 152
56197_at	PLSCR3	phospholipid scramblase 3	0.1117	**-0.0403**	0.2329	0.2967	**0.0088**	1539 ± 107	1647 ± 196	1389 ± 51	2309 ± 302
208890_s_at	PLXNB2	plexin B2	**0.0023**	**-0.0039**	**0.0015**	-0.1719	**0.0193**	557 ± 42	905 ± 169	1134 ± 148	1277 ± 242
211014_s_at	PML	promyelocytic leukemia	0.1579	**-0.0006**	**0.0435**	**-0.0359**	**0.0090**	323 ± 19	352 ± 20	353 ± 15	446 ± 39
209640_at	PML	promyelocytic leukemia	0.0579	**-0.0070**	**0.0245**	**-0.0327**	0.0753	238 ± 12	267 ± 24	283 ± 23	359 ± 56
217226_s_at	PMX1	paired mesoderm homeo box 1	**0.0137**	-0.0925	0.3677	-0.1337	**0.0386**	655 ± 61	745 ± 48	882 ± 51	797 ± 54
205991_s_at	PMX1	paired mesoderm homeo box 1	**0.0076**	**-0.0227**	0.2348	-0.4575	**0.0173**	178 ± 19	227 ± 28	202 ± 15	285 ± 27
215281_x_at	POGZ	pogo transposable element with ZNF domain	**0.0119**	**-0.0094**	-0.4953	-0.2406	0.0773	217 ± 30	210 ± 41	314 ± 47	326 ± 35
219380_x_at	POLH	polymerase , eta	**0.0059**	**-0.0235**	**0.0199**	**-0.0327**	0.1005	40 ± 8	51 ± 11	70 ± 17	89 ± 20
209302_at	POLR2H	polymerase II polypeptide H	**0.0180**	-0.0630	0.3990	0.3664	0.2676	965 ± 56	957 ± 91	1036 ± 63	1147 ± 86
203782_s_at	POLRMT	polymerase mitochondrial	0.1055	**-0.0335**	0.3889	**0.0304**	**0.0295**	864 ± 15	797 ± 25	837 ± 50	1000 ± 69
210910_s_at	POMZP3	POM and ZP3 fusion	**0.0001**	**-0.0058**	0.2722	0.1599	**0.0309**	317 ± 38	321 ± 41	386 ± 53	512 ± 59
204148_s_at	POMZP3	POM and ZP3 fusion	**0.0079**	**-0.0156**	-0.4302	0.1304	0.0956	361 ± 47	335 ± 50	442 ± 80	538 ± 41
204839_at	POP5	RNase MRP/RNase P protein-like	0.0807	**-0.0192**	0.1514	0.4699	0.1272	767 ± 52	800 ± 69	884 ± 56	975 ± 75
207725_at	POU4F2	POU domain, class 4, transcription factor 2	0.2444	**-0.0179**	0.2280	-0.3741	**0.0090**	85 ± 11	117 ± 15	99 ± 4	156 ± 23

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
217730_at	PP1201	PP1201 protein	**0.0066**	**-0.0546**	0.0628	-0.4309	0.0612	481 ± 42	538 ± 103	747 ± 102	696 ± 51
203497_at	PPARBP	PPAR binding protein	0.0989	**-0.0008**	**0.0130**	**-0.0248**	**0.0219**	219 ± 16	274 ± 16	287 ± 24	323 ± 33
37152_at	PPARD	peroxisome proliferative activated receptor, delta	**0.0126**	**-0.0412**	0.1345	-0.3681	0.1062	1530 ± 160	1795 ± 206	1959 ± 137	2077 ± 143
210235_s_at	PPFIA1	protein tyrosine phosphatase, receptor type, f	**0.0046**	-0.0588	0.1933	-0.2761	0.0900	140 ± 8	167 ± 17	185 ± 18	220 ± 36
202066_at	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide	0.0733	**-0.0015**	-0.4499	-0.1055	**0.0264**	985 ± 130	1033 ± 109	1403 ± 101	1397 ± 133
202065_s_at	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide	**0.0011**	**-0.0365**	0.4079	-0.3017	0.1226	155 ± 14	151 ± 8	197 ± 9	246 ± 59
212841_s_at	PPFIBP2	PTPRF interacting protein, binding protein 2	**0.0484**	-0.1761	-0.2569	-0.4983	0.6289	392 ± 66	386 ± 64	454 ± 68	492 ± 57
208993_s_at	PPIG	peptidyl-prolyl isomerase G	**0.0083**	-0.5287	**0.0029**	-0.0878	0.3766	518 ± 51	638 ± 50	650 ± 52	628 ± 92
208994_s_at	PPIG	peptidyl-prolyl isomerase G	0.7292	**-0.0163**	0.2272	-0.3274	**0.0324**	530 ± 28	576 ± 67	508 ± 41	761 ± 94
220158_at	PPL13	placental protein 13-like protein	0.3020	**-0.0314**	0.4667	-0.3886	0.1124	206 ± 22	206 ± 15	208 ± 16	281 ± 38
209296_at	PPM1B	protein phosphatase 1B , magnesium-dependent, beta isoform	0.1784	**-0.0386**	-0.0717	-0.3369	0.4205	1708 ± 174	1626 ± 213	1967 ± 249	2108 ± 254
204566_at	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	0.3476	**-0.0252**	-0.2363	-0.4974	0.1160	263 ± 22	267 ± 31	251 ± 30	350 ± 36
200726_at	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	0.1435	**-0.0081**	-0.1204	-0.2027	0.1911	2398 ± 123	2317 ± 420	2673 ± 189	3037 ± 202
212680_x_at	PPP1R14B	protein phosphatase 1, regulatory subunit 14B	0.1825	**-0.0314**	0.4801	0.3522	0.0832	276 ± 33	226 ± 49	285 ± 40	438 ± 93
202014_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	**0.0098**	**-0.0082**	0.3147	**0.0340**	**0.0366**	186 ± 36	146 ± 20	211 ± 21	394 ± 109
37028_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	**0.0041**	**-0.0128**	-0.0903	0.1204	**0.0048**	601 ± 47	640 ± 96	576 ± 29	1078 ± 172
205478_at	PPP1R1A	protein phosphatase 1, regulatory subunit 1A	0.6284	**-0.0239**	-0.3431	-0.1275	0.1149	545 ± 34	533 ± 41	720 ± 33	848 ± 199
221088_s_at	PPP1R9A	protein phosphatase 1, regulatory subunit 9A	**0.0211**	-0.2320	0.3029	-0.3311	0.3112	447 ± 53	382 ± 27	519 ± 61	582 ± 120
202883_s_at	PPP2R1B	protein phosphatase 2 , regulatory subunit A , beta isoform	**0.0391**	**-0.0201**	-0.1117	-0.1160	0.2970	653 ± 51	691 ± 63	745 ± 27	808 ± 90
216105_x_at	PPP2R4	protein phosphatase 2A, regulatory subunit B'	**0.0346**	-0.9433	-0.2356	0.4966	0.3095	794 ± 38	739 ± 55	931 ± 85	769 ± 112
211159_s_at	PPP2R5D	protein phosphatase 2, regulatory subunit B , delta isoform	**0.0359**	-0.2226	**-0.0117**	0.2715	0.3967	196 ± 19	195 ± 17	208 ± 2	233 ± 21
209826_at	PPT2	palmitoyl-protein thioesterase 2	**0.0048**	-0.5098	0.1746	0.1236	0.7143	296 ± 20	304 ± 85	302 ± 46	380 ± 73
204086_at	PRAME	preferentially expressed antigen in melanoma	0.5153	**-0.0447**	0.1751	-0.2056	0.3703	173 ± 30	156 ± 16	175 ± 22	231 ± 41
201494_at	PRCP	prolylcarboxypeptidase	0.5735	**-0.0345**	-0.4344	**-0.0348**	0.4317	1333 ± 123	1500 ± 109	1544 ± 168	1687 ± 201
203057_s_at	PRDM2	PR domain containing 2, with ZNF domain	**0.0299**	-0.0576	0.4258	-0.1576	0.0737	376 ± 28	513 ± 62	444 ± 40	558 ± 73
209766_at	PRDX3	peroxiredoxin 3	0.1138	**-0.0099**	0.3414	0.3532	**0.0250**	177 ± 10	199 ± 16	196 ± 19	279 ± 40
37022_at	PRELP	proline arginine-rich end leucine-rich repeat protein	0.1874	**-0.0079**	0.0762	-0.3172	**0.0407**	698 ± 48	859 ± 86	837 ± 53	1062 ± 142
213052_at	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	**0.0117**	-0.1242	0.1244	-0.4929	0.1720	1170 ± 62	1354 ± 141	1398 ± 82	1483 ± 126
204842_x_at	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	**0.0028**	**-0.0302**	**0.0249**	-0.2060	**0.0425**	709 ± 64	984 ± 147	935 ± 68	1283 ± 234
204746_s_at	PRKCABP	protein kinase C, alpha binding protein	**0.0474**	-0.0758	0.1434	-0.2528	0.1499	391 ± 31	458 ± 71	446 ± 29	561 ± 72
202161_at	PRKCL1	protein kinase C-like 1	**0.0084**	**-0.0231**	0.0854	0.4515	0.1113	310 ± 14	361 ± 26	438 ± 38	515 ± 114
204211_x_at	PRKR	protein kinase, interferon-inducible double stranded RNA dep.	**0.0103**	**-0.0043**	**0.0395**	**-0.0064**	**0.0251**	246 ± 21	330 ± 33	325 ± 28	450 ± 78
39313_at	PRKWNK1	protein kinase, lysine deficient 1	**0.0064**	**-0.0496**	**0.0526**	-0.3309	0.1312	152 ± 17	206 ± 36	229 ± 35	266 ± 48
204061_at	PRKX	protein kinase, X-linked	0.1732	**-0.0020**	**-0.0415**	0.2905	**0.0240**	294 ± 40	215 ± 21	345 ± 35	435 ± 73
204060_s_at	PRKX	protein kinase, X-linked	**0.0024**	**-0.0001**	-0.1192	-0.4796	**0.0041**	374 ± 33	349 ± 12	465 ± 43	599 ± 74
205445_at	PRL	prolactin	0.4642	**-0.0011**	**0.0380**	**-0.0237**	**0.0194**	170 ± 7	198 ± 24	179 ± 5	252 ± 29
216638_s_at	PRLR	prolactin receptor	**0.0475**	-0.0855	-0.1510	0.4310	**0.0176**	57 ± 12	50 ± 9	38 ± 10	104 ± 22
220696_at	PRO0478	PRO0478 protein	0.1663	**-0.0464**	**0.0283**	**-0.0020**	**0.0355**	69 ± 12	90 ± 12	136 ± 21	92 ± 18
207401_at	PROX1	prospero-related homeobox 1	**0.0419**	**-0.0341**	-0.3715	0.2964	**0.0547**	68 ± 14	51 ± 11	80 ± 12	105 ± 13
202126_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B	**0.0258**	**-0.0201**	**0.0247**	-0.2297	0.0927	1002 ± 53	1076 ± 41	1159 ± 63	1199 ± 72
200000_s_at	PRPF8	PRP8 pre-mRNA processing factor 8 homolog	**0.0081**	**-0.0126**	-0.2210	0.4400	**0.0224**	1501 ± 72	1369 ± 71	1551 ± 80	1732 ± 41
209017_s_at	PRSS15	protease, serine, 15	**0.0418**	**-0.0462**	0.3570	0.1826	0.1744	759 ± 43	781 ± 98	783 ± 78	1053 ± 175

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
211152_s_at	PRSS25	protease, serine, 25	**0.0311**	**-0.0011**	0.3142	-0.3684	**0.0085**	232 ± 12	238 ± 9	313 ± 28	312 ± 21
202880_s_at	PSCD1	pleckstrin homology, Sec7 and coiled/coil domains 1	**0.0186**	**-0.0142**	**0.0530**	-0.0749	0.0937	531 ± 31	730 ± 103	799 ± 98	899 ± 170
203399_x_at	PSG3	pregnancy specific beta-1-glycoprotein 3	0.2826	**-0.0111**	0.1048	**-0.0100**	0.2034	71 ± 9	82 ± 13	76 ± 15	111 ± 18
201053_s_at	PSMF1	proteasome inhibitor subunit 1	0.5086	**-0.0246**	0.1422	-0.0754	0.1961	443 ± 38	514 ± 50	499 ± 31	586 ± 63
215233_at	PSR	phosphatidylserine receptor	**0.0030**	-0.1146	**-0.0022**	0.3050	0.0887	237 ± 31	113 ± 31	363 ± 75	327 ± 103
212722_s_at	PSR	phosphatidylserine receptor	**0.0066**	**-0.0227**	0.2791	0.2951	0.3001	121 ± 11	126 ± 14	146 ± 20	190 ± 50
212015_x_at	PTBP1	polypyrimidine tract binding protein 1	**0.0306**	-0.1288	-0.0822	0.2286	**0.0462**	362 ± 28	389 ± 68	536 ± 45	448 ± 40
211270_x_at	PTBP1	polypyrimidine tract binding protein 1	**0.0002**	**-0.0017**	-0.4944	-0.1343	**0.0160**	566 ± 51	683 ± 79	850 ± 87	870 ± 76
216306_x_at	PTBP1	polypyrimidine tract binding protein 1	**0.0000**	**-0.0080**	-0.3438	-0.1018	**0.0139**	655 ± 76	763 ± 67	1021 ± 101	962 ± 90
211271_x_at	PTBP1	polypyrimidine tract binding protein 1	**0.0004**	**-0.0203**	-0.1738	-0.1182	**0.0465**	492 ± 37	568 ± 84	714 ± 46	655 ± 57
209815_at	PTCH	patched homolog	0.3840	**-0.0278**	-0.3552	-0.1513	0.1068	580 ± 57	556 ± 45	760 ± 94	713 ± 35
211252_x_at	PTCRA	pre-T-cell receptor alpha precursor	0.0739	**-0.0054**	**0.0513**	-0.1717	**0.0429**	436 ± 31	557 ± 77	578 ± 60	713 ± 93
221005_s_at	PTDSS2	phosphatidylserine synthase 2	0.0767	**-0.0374**	0.2876	-0.2261	0.1245	300 ± 26	301 ± 15	404 ± 46	383 ± 50
210702_s_at	PTGIS	prostaglandin I2 synthase	**0.0487**	**-0.0404**	**0.0043**	-0.1266	0.0582	54 ± 9	94 ± 13	88 ± 20	126 ± 27
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1	**0.0239**	-0.0967	**0.0116**	-0.1446	0.1213	386 ± 39	521 ± 47	500 ± 62	571 ± 62
205911_at	PTHR1	parathyroid hormone receptor 1	**0.0004**	**-0.0490**	**0.0360**	-0.4442	0.0721	329 ± 20	454 ± 74	514 ± 48	551 ± 100
211921_x_at	PTMA	prothymosin, alpha	**0.0417**	**-0.0372**	0.2769	-0.2721	0.2916	3270 ± 222	3812 ± 583	4248 ± 432	4259 ± 440
208617_s_at	PTP4A2	protein tyrosine phosphatase type IVA, member 2	0.1686	**-0.0346**	0.4635	-0.2168	0.2035	4403 ± 445	4600 ± 465	5632 ± 441	5320 ± 491
208616_s_at	PTP4A2	protein tyrosine phosphatase type IVA, member 2	0.4269	**-0.0374**	-0.4687	-0.2230	0.4894	4527 ± 377	4492 ± 383	4925 ± 537	5371 ± 300
209695_at	PTP4A3	protein tyrosine phosphatase type IVA, member 3	**0.0443**	-0.2697	0.4945	0.4491	0.5277	419 ± 38	394 ± 20	508 ± 46	492 ± 111
200635_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	**0.0131**	-0.2112	0.4725	-0.0859	0.1438	329 ± 29	369 ± 28	469 ± 21	398 ± 76
208300_at	PTPRH	protein tyrosine phosphatase, receptor type, H	**0.0395**	-0.1097	0.4328	-0.3639	0.1764	141 ± 18	163 ± 14	164 ± 20	219 ± 39
203038_at	PTPRK	protein tyrosine phosphatase, receptor type, K	**0.0062**	**-0.0039**	-0.1297	-0.2852	**0.0461**	1992 ± 286	2153 ± 376	2732 ± 224	3066 ± 245
208789_at	PTRF	polymerase I and transcript release factor	**0.0011**	**-0.0027**	0.2795	-0.1749	**0.0513**	604 ± 87	709 ± 124	1004 ± 125	1088 ± 209
200677_at	PTTG1IP	pituitary tumor-transforming 1 interacting protein	**0.0351**	**-0.0001**	-0.2915	-0.2062	**0.0046**	2393 ± 185	2503 ± 330	3374 ± 265	3682 ± 326
201164_s_at	PUM1	pumilio homolog 1	**0.0068**	0.6643	-0.4315	**0.0272**	0.5530	968 ± 50	865 ± 38	1012 ± 88	895 ± 118
204021_s_at	PURA	purine-rich element binding protein A	0.0964	**-0.0050**	-0.0979	0.1572	**0.0017**	776 ± 70	603 ± 36	770 ± 54	1200 ± 161
204020_at	PURA	purine-rich element binding protein A	**0.0460**	**-0.0130**	-0.3091	-0.2161	0.1014	4505 ± 145	4334 ± 190	4796 ± 224	4982 ± 90
201087_at	PXN	paxillin	**0.0233**	**-0.0361**	0.1051	**-0.0319**	0.2670	602 ± 53	649 ± 37	735 ± 81	780 ± 89
207330_at	PZP	pregnancy-zone protein	0.1449	**-0.0106**	0.0668	-0.4680	**0.0022**	227 ± 28	328 ± 55	229 ± 18	448 ± 56
217846_at	QARS	glutaminyl-tRNA synthetase	**0.0059**	**-0.0209**	**0.0045**	-0.1218	0.0880	1227 ± 65	1356 ± 76	1427 ± 89	1581 ± 148
212263_at	QKI	homolog of mouse quaking QKI	**0.0521**	**-0.0290**	0.3669	-0.0868	0.1559	1853 ± 197	2286 ± 332	2395 ± 202	2604 ± 209
212636_at	QKI	homolog of mouse quaking QKI	**0.0005**	**-0.0010**	**0.0054**	**-0.0078**	**0.0031**	6635 ± 488	9010 ± 882	1099 ± 793	0982 ± 1262
212262_at	QKI	homolog of mouse quaking QKI	**0.0041**	**-0.0014**	**0.0180**	**-0.0428**	**0.0044**	503 ± 12	673 ± 57	759 ± 46	821 ± 100
210714_at	R3HDM	R3H domain containing	**0.0035**	**-0.0503**	-0.4702	0.4698	0.1971	219 ± 31	216 ± 45	268 ± 52	374 ± 90
217793_at	RAB11B	RAB11B, member RAS oncogene family	**0.0501**	**-0.0496**	0.1744	-0.1866	0.2098	336 ± 36	297 ± 35	348 ± 29	484 ± 112
202252_at	RAB13	RAB13, member RAS oncogene family	**0.0001**	**-0.0049**	0.2138	-0.3645	**0.0056**	897 ± 127	1125 ± 163	1695 ± 171	1586 ± 223
220964_s_at	RAB1B	RAB1B, member RAS oncogene family	**0.0197**	-0.5264	**0.0471**	**-0.0233**	0.3043	814 ± 93	1064 ± 130	1187 ± 103	1010 ± 241
208730_x_at	RAB2	RAB2, member RAS oncogene family	0.0716	**-0.0398**	0.0827	**-0.0213**	**0.0418**	511 ± 45	627 ± 41	576 ± 78	870 ± 153
218360_at	RAB22A	RAB22A, member RAS oncogene family	0.1373	**-0.0055**	0.2237	-0.1059	**0.0137**	289 ± 21	337 ± 19	306 ± 24	389 ± 17
217762_s_at	RAB31	RAB31, member RAS oncogene family	0.2297	**-0.0180**	0.2812	-0.1812	**0.0138**	1432 ± 102	1555 ± 112	1976 ± 122	1724 ± 118
217764_s_at	RAB31	RAB31, member RAS oncogene family	0.1283	**-0.0419**	0.4453	-0.4229	0.1264	3180 ± 207	3292 ± 251	3920 ± 186	3705 ± 343

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
217763_s_at	RAB31	RAB31, member RAS oncogene family	**0.0208**	**-0.0035**	0.1143	-0.3723	**0.0129**	1585 ± 103	1671 ± 198	2164 ± 133	2199 ± 186
213531_s_at	RAB3GAP	RAB3 GTPase-ACTIVATING PROTEIN	**0.0111**	-0.2783	-0.3024	0.4026	0.4796	3895 ± 362	3823 ± 552	4573 ± 696	5071 ± 894
203223_at	RAB5EP	rabaptin-5	**0.0111**	**-0.0026**	0.1192	**-0.0265**	**0.0280**	64 ± 10	100 ± 14	97 ± 16	137 ± 22
208641_s_at	RAC1	ras-related C3 botulinum toxin substrate 1	**0.0418**	-0.1343	0.4572	0.1130	0.1295	5886 ± 525	5738 ± 741	5720 ± 521	7954 ± 1103
204461_x_at	RAD1	RAD1 homolog	**0.0219**	-0.1051	**0.0180**	0.2628	0.1006	349 ± 32	361 ± 58	481 ± 44	502 ± 72
221523_s_at	RAGD	Rag D protein	**0.0095**	-0.0693	0.1697	0.0922	0.2760	619 ± 32	617 ± 51	654 ± 42	749 ± 79
218849_s_at	RAI	RelA-associated inhibitor	**0.0013**	**-0.0004**	**0.0538**	**-0.0466**	**0.0016**	328 ± 32	451 ± 31	451 ± 43	703 ± 108
212124_at	RAI17	retinoic acid induced 17	0.6879	**-0.0375**	**-0.0374**	-0.2345	0.1936	1912 ± 97	1941 ± 116	2173 ± 54	2087 ± 113
214435_x_at	RALA	v-ral simian leukemia viral oncogene homolog A	**0.0239**	**-0.0250**	0.0850	0.4558	**0.0393**	251 ± 13	274 ± 28	274 ± 14	369 ± 52
202844_s_at	RALBP1	ralA binding protein 1	0.2783	**-0.0415**	-0.3200	-0.4585	0.0736	485 ± 54	438 ± 38	459 ± 19	609 ± 55
209051_s_at	RALGDS	ral guanine nucleotide dissociation stimulator	**0.0342**	-0.1752	-0.1360	-0.4036	0.1803	732 ± 140	700 ± 79	1053 ± 106	866 ± 141
209050_s_at	RALGDS	ral guanine nucleotide dissociation stimulator	**0.0006**	**-0.0052**	-0.4854	0.4162	**0.0197**	2790 ± 314	2596 ± 203	3981 ± 659	6540 ± 1705
210552_s_at	RALGPS1A	Ral guanine nucleotide exchange factor RalGPS1A	0.3669	**-0.0258**	0.0968	-0.2394	0.3475	110 ± 8	121 ± 12	123 ± 13	148 ± 23
201271_s_at	RALY	RNA binding protein	0.2539	**-0.0393**	0.3665	0.2195	0.1213	490 ± 59	382 ± 36	477 ± 51	612 ± 80
204916_at	RAMP1	receptor activity modifying protein 1	0.1731	**-0.0038**	0.0603	0.4486	**0.0316**	866 ± 64	841 ± 51	962 ± 56	1099 ± 71
202640_s_at	RANBP3	RAN binding protein 3	**0.0251**	**-0.0191**	-0.3513	-0.3009	**0.0114**	381 ± 26	350 ± 34	543 ± 52	485 ± 56
212127_at	RANGAP1	Ran GTPase activating protein 1	**0.0015**	-0.2068	-0.2733	-0.4353	0.3901	551 ± 64	582 ± 35	607 ± 72	766 ± 163
209285_s_at	RAP140	KIAA1105 protein	0.0654	**-0.0039**	0.1381	**-0.0103**	**0.0547**	918 ± 67	1160 ± 142	1252 ± 71	1279 ± 119
205080_at	RARB	retinoic acid receptor, beta	0.1443	**-0.0395**	-0.1468	0.4361	0.0861	341 ± 42	322 ± 31	345 ± 18	451 ± 44
209496_at	RARRES2	retinoic acid receptor responder 2	**0.0109**	**-0.0005**	0.3095	0.2327	**0.0043**	281 ± 38	319 ± 47	414 ± 39	529 ± 64
204070_at	RARRES3	retinoic acid receptor responder 3	0.0720	**-0.0326**	0.3585	-0.1098	0.2308	498 ± 48	522 ± 77	633 ± 52	619 ± 36
214368_at	RASGRP2	RAS guanyl releasing protein 2	**0.0269**	-0.2404	-0.3323	-0.3678	0.0837	43 ± 11	71 ± 21	113 ± 18	85 ± 24
219214_s_at	RBAK	RB-associated KRAB repressor	**0.0374**	-0.3075	**0.0094**	-0.4507	0.1300	117 ± 10	188 ± 18	149 ± 27	181 ± 34
205062_x_at	RBBP1	retinoblastoma binding protein 1	**0.0209**	-0.2634	**0.0245**	0.3884	0.3650	223 ± 15	230 ± 18	260 ± 16	258 ± 24
202040_s_at	RBBP2	retinoblastoma binding protein 2	**0.0024**	**-0.0106**	0.1014	-0.3293	**0.0346**	535 ± 53	598 ± 73	644 ± 27	811 ± 96
205169_at	RBBP5	retinoblastoma binding protein 5	**0.0463**	-0.3678	-0.3349	**-0.0385**	0.7640	165 ± 13	176 ± 18	179 ± 25	196 ± 27
212781_at	RBBP6	retinoblastoma binding protein 6	**0.0095**	-0.2117	**0.0381**	-0.3574	0.2409	398 ± 32	464 ± 60	506 ± 27	476 ± 38
212783_at	RBBP6	retinoblastoma binding protein 6	**0.0354**	-0.0788	0.4745	0.3680	0.1531	765 ± 80	824 ± 124	1118 ± 149	1020 ± 132
205296_at	RBL1	retinoblastoma-like 1	**0.0004**	**-0.0027**	**0.0106**	**-0.0012**	**0.0095**	41 ± 6	77 ± 11	99 ± 10	109 ± 25
208984_x_at	RBM10	RNA binding motif protein 10	**0.0000**	-0.0610	0.0963	-0.4212	0.0690	396 ± 27	448 ± 43	627 ± 55	611 ± 130
219286_s_at	RBM15	RNA binding motif protein 15	**0.0074**	**-0.0401**	-0.0558	0.4091	**0.0318**	602 ± 62	457 ± 33	856 ± 127	787 ± 110
222026_at	RBM3	RNA binding motif protein 3	**0.0245**	-0.3758	0.1587	0.3906	0.6027	263 ± 23	274 ± 27	321 ± 23	310 ± 65
201967_at	RBM6	RNA binding motif protein 6	**0.0196**	-0.0963	-0.1343	-0.2604	0.2455	1276 ± 201	1245 ± 126	1734 ± 212	1591 ± 230
213852_at	RBM8A	RNA binding motif protein 8A	-0.9563	**-0.0198**	**0.0006**	-0.1022	**0.0384**	1490 ± 72	1804 ± 46	1806 ± 80	1888 ± 173
215127_s_at	RBMS1	RNA binding motif, single stranded interacting protein 1	0.1620	**-0.0343**	0.2688	-0.1520	0.2489	606 ± 45	595 ± 64	745 ± 70	740 ± 94
34187_at	RBMS2	RNA binding motif, single stranded interacting protein 2	**0.0003**	**-0.0097**	0.2625	-0.0838	**0.0413**	61 ± 10	61 ± 7	95 ± 10	101 ± 18
206767_at	RBMS3	RNA binding motif, single stranded interacting protein	0.1478	**-0.0101**	0.1234	-0.3970	**0.0487**	340 ± 33	353 ± 35	427 ± 23	459 ± 41
207836_s_at	RBPMS	RNA-binding protein gene with multiple splicing	**0.0493**	**-0.0006**	-0.3577	-0.1852	**0.0148**	72 ± 11	82 ± 9	93 ± 6	124 ± 16
209487_at	RBPMS	RNA-binding protein gene with multiple splicing	**0.0071**	**-0.0116**	0.1152	0.2701	**0.0534**	204 ± 25	245 ± 53	366 ± 67	386 ± 55
219382_at	RBT1	RPA-binding trans-activator	**0.0045**	**-0.0001**	0.2426	**-0.0062**	**0.0014**	287 ± 24	334 ± 12	346 ± 20	478 ± 55
212977_at	RDC1	G protein-coupled receptor	**0.0326**	**-0.0115**	-0.3993	-0.0569	**0.0410**	233 ± 21	274 ± 39	359 ± 40	348 ± 41
219155_at	RDGBB	retinal degeneration B beta	**0.0027**	**-0.0079**	0.2426	0.4367	**0.0486**	635 ± 58	702 ± 107	881 ± 78	929 ± 92

Probe set	**Name**	**Description**	**NFT$_{O}$**	**MMSE$_{O}$**	**NFT$_{I}$**	**MMSE$_{I}$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
219799_s_at	RDHL	NADP-dependent retinol dehydrogenase/reductase	0.4356	**-0.0359**	**0.0517**	-0.1756	**0.0119**	294 ± 32	447 ± 68	336 ± 44	534 ± 59
218599_at	REC8	Rec8p	0.2758	**-0.0057**	-0.2864	-0.1630	**0.0510**	367 ± 26	411 ± 53	409 ± 28	513 ± 33
211168_s_at	RENT1	regulator of nonsense transcripts 1	**0.0101**	**-0.0006**	0.3164	0.3478	**0.0013**	463 ± 22	468 ± 33	507 ± 30	676 ± 58
203600_s_at	RES4-22	gene with multiple splice variants near HD locus on 4p16.3	**0.0236**	-0.0741	0.3668	0.2766	0.1669	867 ± 26	965 ± 60	939 ± 72	1072 ± 80
214661_s_at	RES4-25	gene near HD on 4p16.3	0.0988	**-0.0121**	0.3328	0.3937	**0.0102**	265 ± 13	290 ± 29	271 ± 11	383 ± 40
212920_at	REST	RE1-silencing transcription factor	**0.0365**	**-0.0166**	-0.2577	0.4119	0.0974	145 ± 11	141 ± 13	162 ± 21	194 ± 14
212968_at	RFNG	radical fringe homolog	**0.0014**	-0.1213	-0.3207	0.3628	0.1974	424 ± 13	410 ± 22	484 ± 16	519 ± 78
207672_at	RFX4	regulatory factor X, 4	0.2115	**-0.0018**	-0.3907	-0.4004	**0.0403**	64 ± 18	87 ± 14	143 ± 34	184 ± 48
210751_s_at	RGN	regucalcin	0.0604	**-0.0079**	0.1159	-0.1632	**0.0119**	399 ± 36	473 ± 48	466 ± 19	610 ± 55
209639_s_at	RGS12	regulator of G-protein signalling 12	**0.0062**	**-0.0547**	0.4138	-0.4777	0.1434	175 ± 15	177 ± 20	230 ± 30	259 ± 44
205823_at	RGS12	regulator of G-protein signalling 12	0.2130	**-0.0047**	0.2099	-0.4334	**0.0454**	468 ± 20	480 ± 42	537 ± 37	614 ± 51
209324_s_at	RGS16	regulator of G-protein signalling 16	0.1043	**-0.0036**	-0.2729	-0.4144	**0.0083**	328 ± 30	341 ± 34	366 ± 43	517 ± 46
207525_s_at	RGS19IP1	regulator of G-protein signalling 19 interacting protein 1	**0.0238**	-0.1713	**0.0105**	-0.4184	0.2236	885 ± 24	1039 ± 77	1068 ± 64	1157 ± 163
206518_s_at	RGS9	regulator of G-protein signalling 9	**0.0317**	-0.2796	**0.0287**	-0.4574	0.5473	88 ± 6	110 ± 11	107 ± 23	120 ± 19
213409_s_at	RHEB2	Ras homolog enriched in brain 2	**0.0509**	**-0.0136**	0.1401	**-0.0536**	0.0964	148 ± 18	172 ± 23	179 ± 14	211 ± 8
216049_at	RHOBTB3	Rho-related BTB domain containing 3	0.0997	**-0.0038**	0.1935	-0.4185	**0.0024**	80 ± 10	72 ± 9	76 ± 13	161 ± 27
202975_s_at	RHOBTB3	Rho-related BTB domain containing 3	**0.0003**	**-0.0403**	0.1039	-0.2136	**0.0129**	1350 ± 103	1632 ± 149	2138 ± 216	1942 ± 184
203596_s_at	RI58	retinoic acid- and interferon-inducible protein	0.1430	**-0.0348**	-0.0773	0.3114	0.0765	353 ± 14	284 ± 54	362 ± 11	411 ± 33
218076_s_at	RICH1	homolog of rat nadrin	**0.0152**	**-0.0003**	0.2587	**-0.0162**	**0.0030**	536 ± 39	621 ± 47	614 ± 49	887 ± 99
221126_at	RIG	regulated in glioma	**0.0037**	**-0.0549**	0.4428	-0.2707	0.1835	79 ± 10	82 ± 11	104 ± 14	132 ± 32
221127_s_at	RIG	regulated in glioma	0.6704	**-0.0376**	0.4063	-0.2458	0.2803	977 ± 93	1080 ± 169	1178 ± 92	1326 ± 150
211564_s_at	RIL	LIM domain protein	0.1519	**-0.0077**	0.2047	0.4985	**0.0250**	118 ± 16	177 ± 24	172 ± 27	256 ± 45
215478_at	RIMS2	regulating synaptic membrane exocytosis 2	0.3706	**-0.0188**	0.3501	-0.1803	0.1450	57 ± 12	56 ± 7	66 ± 13	103 ± 24
60471_at	RIN3	Ras and Rab interactor 3	**0.0120**	**-0.0003**	0.1182	-0.2578	**0.0065**	302 ± 40	345 ± 41	402 ± 55	654 ± 121
219457_s_at	RIN3	Ras and Rab interactor 3	**0.0072**	**-0.0016**	0.1846	-0.3083	**0.0223**	99 ± 25	131 ± 29	163 ± 30	270 ± 63
219312_s_at	RINZF	zinc finger protein RINZF	**0.0077**	**-0.0001**	**0.0259**	**-0.0048**	**0.0024**	53 ± 4	64 ± 9	87 ± 9	92 ± 5
219041_s_at	RIP60	replication initiation region protein	**0.0112**	**-0.0004**	0.4222	0.3474	**0.0019**	986 ± 67	921 ± 60	1290 ± 99	1351 ± 78
211753_s_at	RLN1	relaxin 1	**0.0437**	**-0.0015**	0.2236	0.1966	**0.0035**	79 ± 9	85 ± 18	90 ± 8	154 ± 20
210524_x_at	RNAHP	RNA helicase-related protein	0.4991	**-0.0261**	0.3426	**-0.0369**	0.0738	3327 ± 296	4122 ± 268	3837 ± 200	5610 ± 1181
201788_at	RNAHP	RNA helicase-related protein	0.2647	**-0.0300**	0.2686	-0.4426	0.3034	1228 ± 77	1394 ± 168	1563 ± 147	1599 ± 206
213397_x_at	RNASE4	ribonuclease, RNase A family, 4	0.0777	**-0.0118**	-0.2765	-0.3788	0.1338	279 ± 31	307 ± 26	303 ± 23	397 ± 56
205158_at	RNASE4	ribonuclease, RNase A family, 4	0.1817	**-0.0206**	-0.4801	-0.4339	0.1381	107 ± 19	125 ± 19	118 ± 12	166 ± 19
217984_at	RNASE6PL	ribonuclease 6 precursor	0.7632	**-0.0432**	0.0616	**-0.0270**	**0.0356**	1671 ± 133	2260 ± 119	1887 ± 199	2454 ± 283
203022_at	RNASEH2A	ribonuclease H2, large subunit	0.0821	**-0.0344**	**0.0285**	-0.3617	**0.0019**	262 ± 18	311 ± 37	247 ± 7	380 ± 13
221154_at	RNF18	ring finger protein 18	**0.0296**	**-0.0216**	-0.1136	-0.4719	**0.0072**	37 ± 9	36 ± 4	31 ± 6	79 ± 16
210706_s_at	RNF24	ring finger protein 24	0.4464	**-0.0308**	0.1965	-0.2842	0.2294	535 ± 33	497 ± 51	554 ± 29	634 ± 65
203160_s_at	RNF8	ring finger protein 8	**0.0158**	-0.2849	-0.2667	0.4711	0.3334	487 ± 18	444 ± 24	453 ± 31	526 ± 54
204207_s_at	RNGTT	RNA guanylyltransferase and 5'-phosphatase	**0.0045**	-0.1523	0.2768	-0.2436	0.3457	196 ± 15	203 ± 16	196 ± 16	261 ± 56
211387_x_at	RNGTT	RNA guanylyltransferase and 5'-phosphatase	0.1952	**-0.0283**	0.0856	**-0.0485**	0.2043	235 ± 25	249 ± 32	336 ± 40	338 ± 69
212430_at	RNPC1	RNA-binding region containing 1	**0.0016**	**-0.0538**	0.2544	-0.2201	0.1628	324 ± 39	390 ± 42	446 ± 29	478 ± 86
218301_at	RNPEPL1	arginyl aminopeptidase -like 1	**0.0413**	**-0.0314**	-0.4549	-0.2899	0.1225	241 ± 34	239 ± 32	305 ± 18	348 ± 53
210230_at	RNU2	RNA, U2 small nuclear	**0.0326**	-0.1111	**0.0421**	-0.3610	0.4191	164 ± 45	273 ± 83	334 ± 95	419 ± 194

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
214349_at	RNU2	RNA, U2 small nuclear	0.3170	**-0.0059**	-0.3167	0.1602	**0.0021**	161 ± 16	108 ± 12	167 ± 15	227 ± 26
213044_at	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	0.0912	**-0.0066**	-0.2032	**-0.0507**	0.0977	1312 ± 131	1316 ± 87	1642 ± 116	1592 ± 111
214697_s_at	ROD1	ROD1 regulator of differentiation 1	**0.0344**	-0.1326	**0.0389**	-0.1794	0.4233	63 ± 8	76 ± 12	67 ± 14	92 ± 17
207569_at	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1	0.2563	**-0.0038**	0.1150	0.2559	**0.0252**	97 ± 8	87 ± 10	115 ± 8	145 ± 22
206169_x_at	RoXaN	ubiquitous tetratricopeptide containing protein RoXaN	**0.0425**	-0.0857	**0.0190**	-0.2736	0.1373	266 ± 33	380 ± 84	450 ± 54	399 ± 60
213323_s_at	RoXaN	ubiquitous tetratricopeptide containing protein RoXaN	0.0646	**-0.0040**	-0.4739	-0.2781	**0.0081**	392 ± 38	395 ± 23	417 ± 35	637 ± 90
205191_at	RP2	retinitis pigmentosa 2	0.1129	**-0.0490**	-0.4458	-0.3696	0.0698	85 ± 13	93 ± 9	131 ± 16	112 ± 10
209317_at	RPA40	RNA polymerase I subunit	**0.0131**	-0.6938	0.1284	0.3046	0.7692	331 ± 30	344 ± 43	365 ± 23	376 ± 38
207515_s_at	RPA40	RNA polymerase I subunit	**0.0081**	**-0.0308**	0.3626	0.1519	0.0682	322 ± 23	289 ± 12	360 ± 26	437 ± 65
210573_s_at	RPC62	polymerase III	0.1680	**-0.0280**	0.2938	-0.2901	**0.0138**	225 ± 19	273 ± 35	246 ± 25	377 ± 46
206608_s_at	RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	0.1067	**-0.0091**	0.4838	-0.1302	**0.0166**	197 ± 25	229 ± 13	193 ± 16	327 ± 55
200725_x_at	RPL10	ribosomal protein L10	**0.0003**	-0.1119	0.3732	-0.4860	0.2923	5597 ± 425	6042 ± 561	6726 ± 452	6950 ± 795
214351_x_at	RPL13	ribosomal protein L13	0.0760	**-0.0006**	0.3465	-0.3248	**0.0106**	2993 ± 328	2828 ± 223	3566 ± 113	4058 ± 219
212933_x_at	RPL13	ribosomal protein L13	**0.0008**	**-0.0258**	**0.0261**	0.3873	0.0595	7513 ± 381	8578 ± 982	9468 ± 458	10087 ± 800
208929_x_at	RPL13	ribosomal protein L13	**0.0381**	**-0.0359**	**0.0369**	0.4147	0.0945	6899 ± 609	8068 ± 1226	8219 ± 239	10016 ± 972
212790_x_at	RPL13A	ribosomal protein L13a	**0.0306**	-0.2866	0.4988	0.1618	0.1938	13630 ± 429	12677 ± 858	15136 ± 817	13971 ± 972
210646_x_at	RPL13A	ribosomal protein L13a	**0.0475**	-0.1785	-0.3915	0.3537	0.2442	15391 ± 767	14525 ± 824	16888 ± 817	16198 ± 913
200715_x_at	RPL13A	ribosomal protein L13a	**0.0009**	**-0.0003**	0.1337	0.2796	**0.0004**	2416 ± 99	2801 ± 288	3103 ± 293	4234 ± 331
200022_at	RPL18	ribosomal protein L18	**0.0171**	-0.2639	-0.2083	-0.3094	0.5468	4784 ± 300	4818 ± 203	5286 ± 88	5108 ± 407
213642_at	RPL27	ribosomal protein L27	0.0821	**-0.0035**	0.0880	-0.1178	**0.0125**	304 ± 30	377 ± 36	394 ± 14	539 ± 85
212044_s_at	RPL27A	ribosomal protein L27a	0.1105	**-0.0133**	0.1608	-0.2125	**0.0158**	336 ± 32	376 ± 44	353 ± 15	517 ± 63
200003_s_at	RPL28	ribosomal protein L28	**0.0400**	-0.5973	-0.4237	-0.3188	0.2660	6713 ± 424	6945 ± 420	8190 ± 391	6931 ± 996
201429_s_at	RPL37A	ribosomal protein L37a	**0.0472**	-0.1013	0.4372	0.4316	0.3401	9166 ± 1869	0157 ± 2225	3157 ± 1461	4277 ± 3380
214041_x_at	RPL37A	ribosomal protein L37a	**0.0023**	**-0.0101**	0.2570	-0.2179	**0.0355**	700 ± 67	962 ± 216	1143 ± 93	1689 ± 418
221943_x_at	RPL38	ribosomal protein L38	0.1029	**-0.0059**	-0.4825	-0.2224	0.0685	1826 ± 197	1930 ± 278	1966 ± 65	2624 ± 291
202028_s_at	RPL38	ribosomal protein L38	0.1085	**-0.0447**	0.3882	-0.2593	**0.0344**	1186 ± 105	1314 ± 160	1114 ± 44	1667 ± 183
208695_s_at	RPL39	ribosomal protein L39	**0.0024**	**-0.0154**	-0.2328	-0.0623	0.0702	12858 ± 725	12490 ± 725	15140 ± 764	14521 ± 936
200089_s_at	RPL4	ribosomal protein L4	**0.0164**	-0.2430	0.2975	0.3698	**0.0167**	5922 ± 227	5918 ± 255	7235 ± 393	6300 ± 356
210034_s_at	RPL5	ribosomal protein L5	-0.9684	**-0.0177**	0.0748	**-0.0500**	0.4285	81 ± 9	90 ± 7	92 ± 13	111 ± 20
213080_x_at	RPL5	ribosomal protein L5	**0.0000**	**-0.0011**	0.4544	-0.2809	**0.0074**	8949 ± 548	8805 ± 334	10816 ± 540	10998 ± 602
200909_s_at	RPLP2	ribosomal protein, large P2	**0.0314**	-0.1173	-0.1384	-0.4765	0.2375	5678 ± 292	5163 ± 197	6380 ± 415	6217 ± 671
220113_x_at	Rpo1-2	similar to DNA-directed RNA polymerase I	0.0667	**-0.0032**	0.0672	**-0.0129**	**0.0427**	902 ± 86	997 ± 95	1427 ± 189	1444 ± 235
214001_x_at	RPS10	ribosomal protein S10	**0.0045**	**-0.0073**	0.0694	**-0.0138**	**0.0169**	227 ± 34	364 ± 52	319 ± 29	477 ± 82
202649_x_at	RPS19	ribosomal protein S19	**0.0259**	-0.0560	0.2630	-0.2296	0.4124	6922 ± 444	7046 ± 500	7827 ± 439	7929 ± 727
213414_s_at	RPS19	ribosomal protein S19	**0.0216**	**-0.0189**	-0.1150	-0.3807	0.2190	8397 ± 545	7998 ± 597	8966 ± 388	9804 ± 858
208903_at	RPS28	ribosomal protein S28	**0.0054**	-0.2684	-0.0993	0.2320	0.3472	652 ± 27	717 ± 84	698 ± 47	793 ± 61
213347_x_at	RPS4X	ribosomal protein S4, X-linked	**0.0207**	-0.1661	0.1692	0.3259	**0.0430**	10105 ± 387	11438 ± 817	12669 ± 774	11631 ± 483
203379_at	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	**0.0073**	**-0.0290**	0.3845	-0.1808	0.0977	346 ± 68	350 ± 38	576 ± 70	583 ± 142
204635_at	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.9404	**-0.0281**	-0.4216	-0.0710	0.0763	635 ± 21	795 ± 79	705 ± 72	869 ± 71
204633_s_at	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	**0.0388**	**-0.0032**	-0.1274	-0.1023	0.0742	854 ± 48	946 ± 105	1126 ± 101	1139 ± 103
201204_s_at	RRBP1	ribosome binding protein 1 homolog 180kDa	**0.0020**	**-0.0366**	0.3385	-0.2930	**0.0485**	611 ± 119	841 ± 164	1277 ± 140	1190 ± 282
203704_s_at	RREB1	ras responsive element binding protein 1	0.1249	**-0.0122**	0.2622	-0.1804	**0.0544**	278 ± 32	315 ± 27	347 ± 10	407 ± 48

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
209527_at	RRP4	homolog of Yeast RRP4 , 3'-5'-exoribonuclease	**0.0298**	-0.1503	-0.1453	0.2872	0.1576	334 ± 14	291 ± 14	382 ± 45	390 ± 45
222368_at	RU2	RU2S	**0.0018**	**-0.0404**	0.1196	-0.4033	**0.0483**	729 ± 88	946 ± 135	874 ± 67	1678 ± 486
218243_at	RUFY1	RUN and FYVE domain-containing 1	**0.0314**	**-0.0162**	0.3917	0.3117	**0.0481**	1108 ± 76	1113 ± 130	1163 ± 45	1508 ± 159
216994_s_at	RUNX2	runt-related transcription factor 2	0.0766	**-0.0420**	0.2358	**-0.0082**	0.1172	103 ± 15	136 ± 21	122 ± 20	181 ± 34
209148_at	RXRB	retinoid X receptor, beta	**0.0056**	-0.3866	**0.0000**	-0.2507	0.1774	859 ± 39	981 ± 58	1037 ± 51	975 ± 90
205954_at	RXRG	retinoid X receptor, gamma	**0.0168**	**-0.0065**	0.2179	0.4743	**0.0058**	160 ± 16	194 ± 21	201 ± 10	251 ± 18
201846_s_at	RYBP	RING1 and YY1 binding protein	**0.0121**	**-0.0031**	-0.4537	-0.2667	**0.0212**	712 ± 65	799 ± 72	869 ± 66	1044 ± 78
201844_s_at	RYBP	RING1 and YY1 binding protein	**0.0457**	**-0.0454**	0.3750	0.3441	**0.0022**	1330 ± 164	1487 ± 190	1111 ± 54	2029 ± 142
214172_x_at	RYK	RYK receptor-like tyrosine kinase	0.5209	**-0.0458**	0.4641	-0.3741	0.3495	178 ± 19	175 ± 17	196 ± 15	222 ± 27
205863_at	S100A12	S100 calcium binding protein A12	0.4581	**-0.0009**	-0.4202	-0.2978	**0.0230**	150 ± 28	120 ± 17	166 ± 17	285 ± 64
208540_x_at	S100A14	S100 calcium binding protein A14	0.1051	**-0.0343**	-0.0895	0.3152	**0.0153**	560 ± 60	506 ± 14	514 ± 49	753 ± 67
203186_s_at	S100A4	S100 calcium binding protein A4	0.2738	**-0.0267**	0.4680	**-0.0031**	0.2427	176 ± 49	270 ± 80	312 ± 62	386 ± 93
217946_s_at	SAE1	SUMO-1 activating enzyme subunit 1	**0.0190**	-0.3629	0.0755	-0.4510	0.5748	890 ± 41	909 ± 40	985 ± 56	959 ± 74
213635_s_at	SAFB	scaffold attachment factor B	**0.0072**	**-0.0010**	0.2105	-0.2087	**0.0156**	122 ± 12	135 ± 18	166 ± 11	201 ± 28
213283_s_at	SALL2	sal-like 2	**0.0138**	**-0.0267**	0.3549	0.4857	**0.0426**	1603 ± 122	1758 ± 94	1682 ± 115	2089 ± 138
204900_x_at	SAP30	sin3-associated polypeptide, 30kDa	0.9324	**-0.0208**	-0.3346	-0.2982	0.1064	446 ± 21	468 ± 67	432 ± 50	625 ± 91
200051_at	SART1	squamous cell carcinoma antigen recognised by T cells	**0.0041**	**-0.0332**	0.3963	0.3809	0.1055	459 ± 33	485 ± 55	578 ± 49	620 ± 69
218854_at	SART2	squamous cell carcinoma antigen recognized by T cell	0.6623	**-0.0154**	-0.0957	-0.1797	0.1772	256 ± 26	244 ± 33	261 ± 26	334 ± 24
203227_s_at	SAS	sarcoma amplified sequence	0.1117	**-0.0446**	**0.0468**	**-0.0322**	0.1945	1098 ± 106	1315 ± 150	1433 ± 99	1431 ± 159
218143_s_at	SCAMP2	secretory carrier membrane protein 2	**0.0055**	**-0.0195**	0.3385	-0.2880	0.0722	743 ± 65	843 ± 66	856 ± 40	1083 ± 153
201771_at	SCAMP3	secretory carrier membrane protein 3	0.6291	**-0.0126**	-0.0764	0.4019	0.0953	899 ± 80	827 ± 42	971 ± 88	1126 ± 80
201819_at	SCARB1	scavenger receptor class B, member 1	0.3737	**-0.0220**	**0.0549**	-0.1425	**0.0429**	547 ± 34	559 ± 26	517 ± 37	685 ± 60
59705_at	SCLY	putative selenocysteine lyase	0.1838	**-0.0444**	**0.0003**	-0.2152	**0.0233**	108 ± 6	139 ± 12	118 ± 12	151 ± 10
212556_at	SCRIB	scribble	**0.0150**	**-0.0517**	0.3018	-0.4003	0.2333	708 ± 71	756 ± 119	828 ± 62	1023 ± 182
221513_s_at	SDCCAG16	serologically defined colon cancer antigen 16	0.0572	**-0.0409**	0.1271	-0.4150	0.3428	301 ± 9	281 ± 15	326 ± 19	346 ± 44
218427_at	SDCCAG3	serologically defined colon cancer antigen 3	**0.0432**	**-0.0235**	-0.1022	-0.2134	0.2393	250 ± 38	239 ± 13	298 ± 41	328 ± 26
212609_s_at	SDCCAG8	serologically defined colon cancer antigen 8	**0.0423**	-0.2550	0.1802	0.4689	0.3989	936 ± 79	979 ± 78	1105 ± 107	1100 ± 38
221621_at	SEC14L1	SEC14-like 1	0.2649	**-0.0188**	**0.0533**	**-0.0364**	0.0882	135 ± 14	141 ± 10	140 ± 11	196 ± 31
204541_at	SEC14L2	SEC14-like 2	**0.0028**	**-0.0011**	0.1077	0.2310	**0.0006**	191 ± 16	184 ± 21	289 ± 23	321 ± 34
218703_at	SEC22A	sec22 homolog	0.2462	**-0.0275**	0.1275	0.2372	0.1031	148 ± 16	148 ± 22	151 ± 16	212 ± 28
212900_at	SEC24A	SEC24 related gene family, member A	0.2023	**-0.0090**	0.1276	-0.0804	0.0915	548 ± 47	563 ± 78	647 ± 50	767 ± 83
202361_at	SEC24C	SEC24 related gene family, member C	**0.0439**	**-0.0408**	-0.0916	0.3909	0.1990	606 ± 33	593 ± 27	693 ± 64	728 ± 67
201915_at	SEC63L	SEC63 protein	**0.0064**	-0.3697	0.2389	-0.3916	0.2029	172 ± 14	206 ± 19	184 ± 15	217 ± 17
201914_s_at	SEC63L	SEC63 protein	0.0650	**-0.0238**	**0.0097**	-0.4574	**0.0479**	230 ± 6	244 ± 25	292 ± 12	322 ± 42
213716_s_at	SECTM1	secreted and transmembrane 1	0.6746	**-0.0168**	0.2184	-0.4093	0.2470	118 ± 23	102 ± 8	138 ± 38	270 ± 120
204563_at	SELL	selectin L	0.1906	**-0.0181**	0.2189	-0.2847	0.0964	250 ± 35	309 ± 45	290 ± 48	427 ± 68
203071_at	SEMA3B	sema domain 3B	**0.0018**	**-0.0242**	**0.0215**	0.2637	**0.0544**	472 ± 63	647 ± 128	701 ± 107	1161 ± 327
203788_s_at	SEMA3C	sema domain 3C	**0.0015**	**-0.0438**	0.1701	-0.3260	0.0616	173 ± 14	191 ± 22	201 ± 12	277 ± 50
35666_at	SEMA3F	sema domain 3F	0.4129	**-0.0220**	-0.2913	0.4963	0.0729	520 ± 48	490 ± 68	469 ± 40	702 ± 93
46665_at	SEMA4C	sema domain 4C	**0.0019**	**-0.0183**	0.2383	-0.1388	0.0865	1383 ± 103	1781 ± 331	1934 ± 186	2537 ± 544
208124_s_at	SEMA4F	sema domain 4F	**0.0145**	-0.1111	0.1946	0.3547	0.4600	300 ± 14	298 ± 18	312 ± 12	346 ± 40
219194_at	SEMA4G	sema domain 4G	**0.0297**	**-0.0307**	0.0967	-0.0836	0.0678	403 ± 35	465 ± 49	457 ± 56	654 ± 112

Probe set	Name	Description	NFT$_{O}$	MMSE$_{O}$	NFT$_{I}$	MMSE$_{I}$	ANOVA	Control	Incipient	Moderate	Severe
215114_at	SENP3	sentrin/SUMO-specific protease 3	**0.0403**	-0.1066	0.0943	-0.2966	0.3214	136 ± 14	167 ± 27	160 ± 27	194 ± 21
201427_s_at	SEPP1	selenoprotein P, plasma, 1	0.6326	**-0.0097**	-0.1597	-0.1533	0.1292	7932 ± 1018	7599 ± 949	772 ± 2027	1178 ± 1761
202376_at	SERPINA3	serine proteinase inhibitor, clade A , member 3	0.0641	**-0.0200**	-0.0574	0.4556	0.1254	4750 ± 1534	3185 ± 873	237 ± 2013	9225 ± 2380
213874_at	SERPINA4	serine proteinase inhibitor, clade A , member 4	0.0581	**-0.0033**	0.2556	0.4354	**0.0087**	170 ± 14	165 ± 26	206 ± 21	284 ± 35
210413_x_at	SERPINB4	serine proteinase inhibitor, clade B , member 4	0.3214	**-0.0186**	0.3165	-0.4704	**0.0524**	162 ± 12	152 ± 17	173 ± 20	244 ± 39
200986_at	SERPING1	serine proteinase inhibitor, clade G , member 1,	0.8450	**-0.0262**	-0.2840	-0.2578	**0.0455**	406 ± 57	377 ± 48	364 ± 43	565 ± 34
207636_at	SERPINI2	serine proteinase inhibitor, clade I , member 2	**0.0008**	**-0.0082**	0.1503	-0.1183	**0.0534**	158 ± 17	179 ± 34	202 ± 24	273 ± 42
210231_x_at	SET	SET translocation	0.1671	**-0.0221**	-0.2090	-0.0708	0.2605	3226 ± 134	3324 ± 187	3575 ± 116	3601 ± 189
213048_s_at	SET	SET translocation	**0.0357**	**-0.0450**	0.2813	**-0.0092**	0.2526	2167 ± 202	2368 ± 346	2853 ± 265	2679 ± 214
37462_i_at	SF3A2	splicing factor 3a, subunit 2, 66kDa	0.1671	**-0.0295**	0.0846	0.3454	0.1721	480 ± 33	570 ± 73	559 ± 39	669 ± 80
203818_s_at	SF3A3	splicing factor 3a, subunit 3, 60kDa	**0.0254**	**-0.0031**	0.2043	-0.2822	**0.0166**	500 ± 21	518 ± 19	521 ± 21	595 ± 18
200688_at	SF3B3	splicing factor 3b, subunit 3, 130kDa	**0.0050**	-0.0650	0.2027	0.1853	0.1305	479 ± 37	473 ± 46	539 ± 41	609 ± 50
33322_i_at	SFN	stratifin	**0.0105**	**-0.0004**	0.2461	**-0.0059**	**0.0000**	949 ± 44	1154 ± 24	1026 ± 46	1571 ± 140
33323_r_at	SFN	stratifin	**0.0137**	**-0.0217**	**0.0450**	-0.3218	**0.0213**	503 ± 41	697 ± 77	689 ± 96	972 ± 154
202037_s_at	SFRP1	secreted frizzled-related protein 1	**0.0284**	-0.2193	0.3824	-0.2465	0.3383	527 ± 57	699 ± 98	724 ± 97	696 ± 102
202035_s_at	SFRP1	secreted frizzled-related protein 1	**0.0007**	**-0.0031**	**0.0197**	**-0.0105**	**0.0265**	47 ± 5	70 ± 8	71 ± 6	95 ± 19
204051_s_at	SFRP4	secreted frizzled-related protein 4	0.3782	**-0.0463**	0.1317	-0.2424	0.4631	213 ± 26	215 ± 22	241 ± 14	259 ± 20
202775_s_at	SFRS8	splicing factor, arginine/serine-rich 8	0.0646	**-0.0284**	0.2639	0.1393	0.0695	995 ± 57	970 ± 98	1035 ± 124	1449 ± 215
38691_s_at	SFTPC	surfactant, pulmonary-associated protein C	**0.0087**	**-0.0129**	0.1265	-0.1077	**0.0249**	421 ± 45	612 ± 70	580 ± 76	771 ± 114
201739_at	SGK	serum/glucocorticoid regulated kinase	0.5440	**-0.0260**	-0.2537	**-0.0234**	0.2301	3269 ± 434	3649 ± 399	4770 ± 682	4333 ± 684
220357_s_at	SGK2	serum/glucocorticoid regulated kinase 2	0.1788	**-0.0397**	**0.0204**	0.4107	0.0981	263 ± 11	335 ± 55	304 ± 26	400 ± 55
212322_at	SGPL1	sphingosine-1-phosphate lyase 1	0.1367	**-0.0029**	-0.3805	-0.4287	0.0904	622 ± 55	665 ± 58	766 ± 57	874 ± 114
212321_at	SGPL1	sphingosine-1-phosphate lyase 1	**0.0111**	**0.0000**	0.2744	-0.1147	**0.0021**	489 ± 37	555 ± 42	668 ± 30	723 ± 61
201396_s_at	SGT	small glutamine-rich tetratricopeptide repeat -containing	**0.0021**	**-0.0531**	**0.0538**	0.3991	0.1722	324 ± 21	365 ± 83	391 ± 45	552 ± 120
209370_s_at	SH3BP2	SH3-domain binding protein 2	**0.0090**	**-0.0046**	0.2362	-0.3518	**0.0243**	318 ± 40	417 ± 56	571 ± 64	778 ± 192
205636_at	SH3GL3	SH3-domain GRB2-like 3	**0.0211**	**-0.0303**	0.4552	0.1000	**0.0247**	222 ± 19	193 ± 16	209 ± 23	362 ± 75
46323_at	SHAPY	apyrase	**0.0144**	-0.0552	0.2770	0.3441	0.1703	472 ± 25	479 ± 27	521 ± 27	550 ± 25
201996_s_at	SHARP	SMART/HDAC1 associated repressor protein	**0.0089**	**-0.0115**	-0.2994	-0.1248	**0.0238**	233 ± 26	238 ± 19	276 ± 23	357 ± 44
201997_s_at	SHARP	SMART/HDAC1 associated repressor protein	**0.0048**	**-0.0297**	-0.2410	0.2854	0.1376	1487 ± 108	1534 ± 197	1671 ± 131	1955 ± 155
214853_s_at	SHC1	SHC transforming protein 1	0.2562	**-0.0371**	-0.3108	0.2533	0.0865	1057 ± 105	786 ± 51	1094 ± 97	1239 ± 156
221519_at	SHFM3	split hand/foot malformation type 3	**0.0116**	**-0.0068**	**0.0149**	-0.1847	**0.0400**	1267 ± 89	1570 ± 221	1781 ± 166	1963 ± 217
214096_s_at	SHMT2	serine hydroxymethyltransferase 2	**0.0171**	-0.2061	0.4016	0.4485	0.4974	887 ± 59	857 ± 35	1000 ± 84	1020 ± 133
203759_at	SIAT4C	sialyltransferase 4C	**0.0119**	**-0.0034**	0.2510	-0.1040	**0.0158**	162 ± 17	172 ± 23	256 ± 21	270 ± 45
220937_s_at	SIAT7D	sialyltransferase 7D	0.4560	**-0.0035**	**0.0278**	**-0.0050**	0.0731	99 ± 8	109 ± 11	112 ± 7	130 ± 6
210073_at	SIAT8A	sialyltransferase 8A	**0.0492**	-0.3977	-0.3620	0.3443	0.5285	131 ± 13	116 ± 12	144 ± 19	146 ± 18
213485_s_at	SIMRP7	multidrug resistance-associated protein 7	**0.0175**	-0.2048	0.1870	-0.4495	0.4536	763 ± 75	878 ± 166	886 ± 59	1030 ± 157
220605_s_at	SIRT2	sirtuin silent mating type information regulation 2 homolog 2	**0.0142**	-0.0951	-0.2493	0.3597	0.3275	1964 ± 166	2090 ± 184	2263 ± 191	2694 ± 527
219613_s_at	SIRT6	sirtuin silent mating type information regulation 2 homolog 6	0.1807	**-0.0189**	**-0.0146**	-0.4220	**0.0150**	343 ± 44	300 ± 49	315 ± 12	490 ± 45
218797_s_at	SIRT7	sirtuin silent mating type information regulation 2 homolog 7	**0.0161**	**-0.0016**	-0.3114	-0.1519	**0.0416**	352 ± 39	362 ± 31	422 ± 33	489 ± 34
202782_s_at	SKIP	skeletal muscle and kidney enriched inositol phosphatase	0.6078	**-0.0005**	**0.0337**	-0.0870	**0.0078**	568 ± 24	568 ± 35	575 ± 36	720 ± 25
214734_at	SLAC2-B	SLAC2-B	**0.0024**	**-0.0017**	-0.4069	-0.2589	**0.0025**	374 ± 45	433 ± 30	428 ± 28	629 ± 66
206181_at	SLAM	signaling lymphocytic activation molecule	0.2031	**-0.0004**	**0.0027**	-0.1306	**0.0083**	86 ± 8	127 ± 17	125 ± 11	164 ± 20

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
217507_at	SLC11A1	solute carrier family 11 , member 1	0.1333	**-0.0248**	0.3909	0.0671	**0.0028**	64 ± 13	88 ± 26	37 ± 8	182 ± 43
215274_at	SLC12A3	solute carrier family 12 , member 3	0.1475	**-0.0065**	0.2175	**-0.0172**	**0.0233**	140 ± 14	174 ± 11	177 ± 25	250 ± 39
218066_at	SLC12A7	solute carrier family 12 , member 7	0.0825	**-0.0001**	0.0797	-0.0827	**0.0015**	807 ± 80	842 ± 93	929 ± 79	1489 ± 199
220502_s_at	SLC13A1	solute carrier family 13 , member 1	0.2660	**-0.0158**	-0.4419	0.3546	0.0951	17 ± 4	20 ± 5	31 ± 1	35 ± 9
205856_at	SLC14A1	solute carrier family 14 , member 1	**0.0048**	**-0.0001**	**0.0407**	-0.4844	**0.0056**	430 ± 69	517 ± 38	701 ± 91	1329 ± 326
211576_s_at	SLC19A1	solute carrier family 19 , member 1	**0.0195**	**0.0000**	**0.0320**	**-0.0004**	**0.0007**	209 ± 19	287 ± 25	344 ± 26	426 ± 52
210923_at	SLC1A7	solute carrier family 1 , member 7	0.2220	**-0.0490**	0.1444	0.4442	0.0581	295 ± 23	326 ± 41	301 ± 18	415 ± 46
210542_s_at	SLC21A11	solute carrier family 21 , member 11	0.8069	**-0.0138**	-0.4152	-0.2062	**0.0252**	1000 ± 60	1067 ± 85	961 ± 58	1327 ± 126
219229_at	SLC21A11	solute carrier family 21 , member 11	**0.0137**	**-0.0283**	-0.2105	-0.3714	0.1233	365 ± 43	389 ± 35	523 ± 75	493 ± 47
210010_s_at	SLC25A1	solute carrier family 25 , member 1	**0.0456**	**-0.0097**	-0.2451	0.4273	0.1721	494 ± 61	549 ± 79	623 ± 41	762 ± 147
220474_at	SLC25A21	solute carrier family 25 , member 21	**0.0499**	**-0.0323**	0.4538	-0.4170	**0.0470**	19 ± 5	23 ± 5	46 ± 11	42 ± 7
205097_at	SLC26A2	solute carrier family 26 , member 2	-0.9853	**-0.0327**	-0.1505	-0.1534	0.5196	197 ± 32	203 ± 17	232 ± 24	251 ± 36
204717_s_at	SLC29A2	solute carrier family 29 , member 2	**0.0052**	**-0.0049**	-0.0903	-0.4792	**0.0369**	95 ± 12	80 ± 15	133 ± 23	182 ± 42
201250_s_at	SLC2A1	solute carrier family 2 , member 1	0.3114	**-0.0358**	0.4063	0.4693	0.1211	1655 ± 125	1782 ± 270	1626 ± 73	2257 ± 279
218494_s_at	SLC2A4RG	SLC2A4 regulator	**0.0063**	-0.0954	0.1320	0.3725	0.1217	236 ± 21	279 ± 32	312 ± 30	337 ± 41
219991_at	SLC2A9	solute carrier family 2 , member 9	**0.0184**	**-0.0070**	0.1222	0.4332	**0.0006**	363 ± 28	432 ± 44	370 ± 21	601 ± 58
207440_at	SLC35A2	solute carrier family 35 , member 2	**0.0249**	**-0.0186**	0.1983	-0.4383	**0.0232**	110 ± 15	160 ± 23	188 ± 9	199 ± 34
209865_at	SLC35A3	solute carrier family 35 transporter), member 3	**0.0515**	**-0.0134**	**0.0066**	**-0.0023**	**0.0002**	78 ± 7	158 ± 10	140 ± 13	156 ± 15
218237_s_at	SLC38A1	solute carrier family 38, member 1	**0.0160**	-0.0633	0.2943	-0.1262	0.2556	1248 ± 44	1430 ± 134	1427 ± 134	1595 ± 143
210739_x_at	SLC4A4	solute carrier family 4	**0.0323**	**-0.0514**	0.1752	-0.1081	0.1841	692 ± 39	701 ± 42	739 ± 54	973 ± 193
209884_s_at	SLC4A7	solute carrier family 4	0.4631	**-0.0233**	0.2789	-0.0568	0.1319	206 ± 19	242 ± 23	268 ± 28	298 ± 41
210854_x_at	SLC6A8	solute carrier family 6 , member 8	**0.0049**	**-0.0103**	-0.3691	-0.4310	**0.0399**	703 ± 48	654 ± 36	774 ± 37	874 ± 72
202219_at	SLC6A8	solute carrier family 6 , member 8	**0.0012**	**-0.0366**	-0.3476	0.4949	0.1024	2750 ± 308	2602 ± 148	3752 ± 414	4381 ± 986
201195_s_at	SLC7A5	solute carrier family 7 , member 5	**0.0000**	**-0.0011**	0.3759	-0.0785	**0.0150**	1245 ± 84	1334 ± 81	1677 ± 108	1834 ± 225
203578_s_at	SLC7A6	solute carrier family 7 , member 6	0.2360	**-0.0183**	0.2629	0.0989	0.1376	77 ± 8	83 ± 10	99 ± 10	110 ± 15
203579_s_at	SLC7A6	solute carrier family 7 , member 6	**0.0120**	**-0.0325**	0.1937	-0.4160	**0.0275**	188 ± 11	164 ± 18	212 ± 20	285 ± 46
208039_at	SLC9A2	solute carrier family 9 , isoform 2	**0.0058**	**-0.0275**	0.3509	-0.3496	**0.0523**	164 ± 18	196 ± 26	205 ± 22	298 ± 57
206874_s_at	SLK	Ste20-related serine/threonine kinase	**0.0460**	-0.0917	0.0925	-0.0662	0.2044	1396 ± 72	1624 ± 80	1750 ± 114	1717 ± 211
214850_at	SMA3	SMA3	**0.0021**	-0.0652	0.1644	-0.1777	0.1696	225 ± 36	312 ± 49	414 ± 92	535 ± 184
206565_x_at	SMA3	SMA3	**0.0373**	-0.1716	0.1287	-0.2966	0.2043	286 ± 43	442 ± 67	507 ± 110	448 ± 80
215599_at	SMA4	SMA4	**0.0066**	-0.2286	0.0725	0.4557	0.2346	322 ± 52	563 ± 158	987 ± 351	791 ± 317
201073_s_at	SMARCC1	SWI/SNF rel., matrix assoc. actin dep. reg. of chromatin, c1	**0.0162**	-0.1204	-0.2783	**-0.0310**	0.4058	248 ± 36	293 ± 41	338 ± 19	319 ± 62
201320_at	SMARCC2	SWI/SNF rel., matrix assoc. actin dep. reg. of chromatin, c2	**0.0011**	-0.0747	0.3060	**-0.0167**	**0.0463**	932 ± 107	1146 ± 57	1502 ± 98	1293 ± 259
201321_s_at	SMARCC2	SWI/SNF rel., matrix assoc. actin dep. reg. of chromatin, c2	**0.0045**	**-0.0019**	-0.4013	-0.2896	**0.0108**	1161 ± 70	1090 ± 23	1549 ± 115	1656 ± 224
203183_s_at	SMARCD1	SWI/SNF rel., matrix assoc. actin dep. reg. of chromatin, d1	0.2408	**-0.0094**	0.3760	0.3416	**0.0334**	269 ± 21	253 ± 27	313 ± 23	390 ± 51
212152_x_at	SMARCF1	SWI/SNF rel., matrix assoc. actin dep. reg. of chromatin, f1	**0.0206**	**-0.0483**	0.2636	**-0.0423**	**0.0443**	1942 ± 116	2278 ± 95	2366 ± 123	2341 ± 130
201589_at	SMC1L1	SMC1 structural maintenance of chromosomes 1-like 1	0.3775	**-0.0049**	-0.2678	**-0.0381**	0.1786	620 ± 69	730 ± 100	824 ± 99	873 ± 78
215623_x_at	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1	0.9070	**-0.0084**	0.2061	-0.3477	**0.0209**	47 ± 5	54 ± 4	48 ± 9	84 ± 13
200739_s_at	SMT3H1	SMT3 suppressor of mif two 3 homolog 1	**0.0229**	-0.4166	0.3982	-0.1993	0.3171	227 ± 18	238 ± 28	222 ± 17	315 ± 72
213139_at	SNAI2	snail homolog 2	0.1765	**-0.0319**	-0.4459	-0.1751	0.3069	67 ± 8	67 ± 16	79 ± 10	97 ± 13
205443_at	SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	**0.0258**	-0.3086	**-0.0079**	**0.0182**	0.2461	99 ± 12	79 ± 10	106 ± 8	116 ± 17
204104_at	SNAPC2	small nuclear RNA activating complex, polypeptide 2, 45kDa	**0.0102**	**-0.0008**	0.3018	0.1674	**0.0007**	158 ± 10	170 ± 15	262 ± 21	263 ± 33

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
207474_at	SNRK	SNF-1 related kinase	0.6988	**-0.0487**	0.0826	**-0.0033**	0.3816	60 ± 12	79 ± 12	76 ± 10	98 ± 26
214004_s_at	SNRK	SNF-1 related kinase	**0.0161**	**-0.0380**	0.2111	0.3382	0.0750	447 ± 33	530 ± 101	721 ± 103	740 ± 104
201221_s_at	SNRP70	small nuclear ribonucleoprotein 70kDa polypeptide	**0.0151**	-0.0709	0.3048	0.3104	0.0651	2083 ± 140	2283 ± 358	2252 ± 288	3607 ± 741
203516_at	SNTA1	syntrophin, alpha 1	**0.0048**	-0.0674	0.1956	0.3795	**0.0179**	1068 ± 93	1166 ± 167	1772 ± 126	1439 ± 259
53912_at	SNX11	sorting nexin 11	**0.0078**	-0.0588	0.3747	0.1381	0.0916	659 ± 48	690 ± 68	775 ± 79	1139 ± 273
220140_s_at	SNX11	sorting nexin 11	**0.0211**	**-0.0482**	**0.0089**	-0.2493	**0.0174**	436 ± 36	594 ± 52	537 ± 52	646 ± 34
219793_at	SNX16	sorting nexin 16	**0.0177**	-0.0954	0.3075	**-0.0032**	0.3081	72 ± 8	89 ± 14	101 ± 8	97 ± 16
217789_at	SNX6	sorting nexin 6	**0.0032**	-0.0871	0.2358	-0.3492	0.2253	578 ± 53	770 ± 117	861 ± 96	963 ± 226
215078_at	SOD2	superoxide dismutase 2, mitochondrial	0.2895	**-0.0120**	-0.4533	0.1783	0.1261	32 ± 7	43 ± 6	52 ± 10	68 ± 16
204275_at	SOLH	small optic lobes homolog	**0.0498**	-0.2702	0.2357	-0.2695	0.2524	247 ± 20	232 ± 11	309 ± 18	276 ± 44
218087_s_at	SORBS1	sorbin and SH3 domain containing 1	**0.0146**	**-0.0500**	0.1965	-0.0631	**0.0032**	3538 ± 296	3953 ± 332	6032 ± 568	4431 ± 613
201563_at	SORD	sorbitol dehydrogenase	**0.0355**	**-0.0005**	0.4184	-0.1133	**0.0256**	384 ± 37	435 ± 44	519 ± 52	575 ± 48
204432_at	SOX12	SRY -box 12	**0.0323**	-0.1077	-0.4298	-0.2083	0.3770	179 ± 20	195 ± 23	249 ± 36	241 ± 51
38918_at	SOX13	SRY -box 13	0.0671	**-0.0135**	0.4324	-0.2430	**0.0320**	224 ± 23	245 ± 13	309 ± 10	283 ± 27
213721_at	SOX2	SRY -box 2	**0.0051**	-0.0886	0.2700	-0.3085	0.2874	911 ± 63	1027 ± 120	1106 ± 93	1159 ± 107
202935_s_at	SOX9	SRY -box 9	0.2072	**-0.0413**	0.4124	-0.1193	0.3201	1868 ± 242	1947 ± 226	2225 ± 200	2432 ± 256
202863_at	SP100	nuclear antigen Sp100	0.4149	**-0.0013**	-0.3967	-0.3193	**0.0095**	201 ± 17	207 ± 12	204 ± 22	306 ± 37
209761_s_at	SP110	SP110 nuclear body protein	**0.0074**	**-0.0083**	0.3462	-0.2521	0.0630	291 ± 33	323 ± 20	381 ± 33	442 ± 66
213168_at	SP3	Sp3 transcription factor	0.4829	**-0.0194**	-0.3456	**-0.0029**	0.1453	1062 ± 49	1073 ± 103	1305 ± 74	1185 ± 103
210117_at	SPAG1	sperm associated antigen 1	**0.0113**	**0.0000**	**0.0028**	-0.0951	**0.0005**	108 ± 9	143 ± 21	142 ± 13	215 ± 18
210033_s_at	SPAG6	sperm associated antigen 6	0.2245	**-0.0057**	-0.1899	0.4068	**0.0009**	140 ± 15	134 ± 5	124 ± 26	248 ± 21
212468_at	SPAG9	sperm associated antigen 9	0.3476	**-0.0233**	0.0609	-0.0580	0.1248	297 ± 30	387 ± 38	405 ± 32	422 ± 59
200665_s_at	SPARC	secreted protein, acidic, cysteine-rich	0.0672	**-0.0003**	-0.1639	-0.1010	**0.0226**	2913 ± 418	2930 ± 596	3905 ± 516	5716 ± 1081
201290_at	SPC18	signal peptidase complex	**0.0088**	**-0.0240**	0.2285	-0.1576	0.0671	1337 ± 91	1513 ± 121	1742 ± 101	1654 ± 144
219257_s_at	SPHK1	sphingosine kinase 1	0.1330	**-0.0402**	0.2499	-0.2398	0.1792	211 ± 31	277 ± 24	271 ± 29	302 ± 31
205861_at	SPIB	Spi-B transcription factor	**0.0352**	**-0.0016**	-0.4522	**-0.0102**	**0.0071**	145 ± 14	150 ± 23	153 ± 16	241 ± 29
204640_s_at	SPOP	speckle-type POZ protein	**0.0130**	**-0.0508**	0.3502	-0.2411	**0.0513**	1577 ± 128	1574 ± 47	1983 ± 71	1808 ± 165
208939_at	SPS	selenium donor protein	**0.0075**	**0.0000**	-0.3770	-0.1017	**0.0019**	613 ± 30	654 ± 55	762 ± 39	930 ± 91
203127_s_at	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	0.3684	**-0.0010**	-0.0919	-0.3287	**0.0036**	448 ± 40	418 ± 46	407 ± 30	670 ± 76
214072_x_at	SPUF	secreted protein of unknown function	0.5587	**-0.0258**	**0.0221**	**-0.0119**	0.0605	260 ± 12	331 ± 28	294 ± 19	340 ± 27
38766_at	SRCAP	Snf2-related CBP activator protein	**0.0051**	**-0.0128**	0.3534	-0.4363	**0.0079**	262 ± 30	364 ± 39	396 ± 17	446 ± 48
202308_at	SREBF1	sterol regulatory element binding transcription factor 1	**0.0157**	**-0.0249**	**0.0002**	-0.1787	**0.0319**	526 ± 42	967 ± 130	858 ± 105	1196 ± 268
201248_s_at	SREBF2	sterol regulatory element binding transcription factor 2	**0.0109**	**-0.0222**	0.3194	-0.3374	0.0764	514 ± 47	482 ± 23	647 ± 56	717 ± 112
203181_x_at	SRPK2	SFRS protein kinase 2	**0.0024**	**-0.0078**	0.2557	**-0.0211**	**0.0249**	653 ± 49	780 ± 42	898 ± 72	902 ± 75
204955_at	SRPX	sushi-repeat-containing protein, X chromosome	**0.0329**	**-0.0001**	0.3611	-0.1210	**0.0201**	555 ± 67	603 ± 91	759 ± 104	1030 ± 163
207435_s_at	SRRM2	serine/arginine repetitive matrix 2	**0.0455**	-0.0891	-0.1306	-0.3703	0.3390	1711 ± 263	1665 ± 142	2272 ± 275	2247 ± 471
208610_s_at	SRRM2	serine/arginine repetitive matrix 2	0.1392	**-0.0188**	0.1935	-0.1035	0.1846	922 ± 118	1020 ± 111	1178 ± 148	1420 ± 249
219405_at	SS-56	SSA protein SS-56	0.3120	**-0.0185**	-0.1404	-0.1418	0.2804	340 ± 33	345 ± 25	374 ± 17	411 ± 29
207520_at	SSA2	Sjogren syndrome antigen A2	0.3551	**-0.0294**	-0.4371	-0.0970	0.0787	59 ± 8	61 ± 8	61 ± 7	98 ± 20
212852_s_at	SSA2	Sjogren syndrome antigen A2	**0.0009**	**-0.0134**	0.1610	-0.4100	0.0711	1973 ± 193	2150 ± 259	2577 ± 179	2909 ± 392
46256_at	SSB-3	SPRY domain-containing SOCS box protein SSB-3	**0.0081**	**-0.0069**	0.4760	0.1705	**0.0072**	1667 ± 47	1832 ± 250	1808 ± 44	2744 ± 389
214060_at	SSBP1	single-stranded DNA binding protein	0.2778	**-0.0208**	-0.4106	0.2700	**0.0284**	255 ± 26	275 ± 21	242 ± 20	372 ± 50

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
202506_at	SSFA2	sperm specific antigen 2	**0.0486**	**-0.0010**	0.4770	**-0.0126**	**0.0542**	893 ± 105	1059 ± 103	1376 ± 188	1419 ± 174
221753_at	SSH1	slingshot 1	0.0640	**-0.0177**	0.1460	**-0.0289**	0.0711	355 ± 25	388 ± 18	427 ± 31	479 ± 50
51192_at	SSH-3	slingshot 3	**0.0014**	**-0.0009**	**0.0268**	-0.3388	**0.0044**	291 ± 21	370 ± 27	393 ± 23	619 ± 115
214105_at	SSI-3	suppressor of cytokine signaling 3	**0.0025**	**-0.0095**	0.4300	0.2982	**0.0089**	40 ± 5	42 ± 8	89 ± 7	107 ± 29
204964_s_at	SSPN	sarcospan	0.1982	**-0.0037**	0.3021	**-0.0074**	**0.0230**	285 ± 39	362 ± 66	426 ± 51	576 ± 98
204963_at	SSPN	sarcospan	0.2502	**-0.0128**	0.3774	-0.4936	**0.0367**	305 ± 31	318 ± 34	314 ± 33	481 ± 75
200652_at	SSR2	signal sequence receptor, beta	**0.0403**	-0.0640	**0.0499**	-0.2850	0.0660	1023 ± 47	1151 ± 63	1115 ± 26	1269 ± 101
202440_s_at	ST5	suppression of tumorigenicity 5	**0.0393**	**-0.0180**	0.2207	0.4519	0.0906	379 ± 36	336 ± 40	464 ± 35	472 ± 46
202294_at	STAG1	stromal antigen 1	0.0723	**-0.0294**	-0.1990	0.4287	**0.0288**	565 ± 30	568 ± 73	588 ± 27	791 ± 86
209022_at	STAG2	stromal antigen 2	0.3647	**-0.0303**	-0.2631	-0.1119	0.3818	2095 ± 162	2163 ± 221	2488 ± 182	2456 ± 237
209023_s_at	STAG2	stromal antigen 2	**0.0027**	**-0.0085**	0.3459	**-0.0066**	**0.0240**	506 ± 61	644 ± 21	837 ± 75	757 ± 122
202991_at	STARD3	START domain containing 3	**0.0225**	-0.1621	-0.3479	0.3569	0.4592	195 ± 15	194 ± 21	241 ± 33	241 ± 36
201331_s_at	STAT6	signal transducer and activator of transcription 6, IL4 induced	**0.0223**	**-0.0179**	0.4762	-0.3917	0.1537	618 ± 51	569 ± 29	640 ± 43	766 ± 88
213037_x_at	STAU	staufen, RNA binding protein	0.1214	**-0.0495**	**-0.0476**	-0.1455	0.0939	3023 ± 133	2850 ± 66	3353 ± 116	3251 ± 204
202764_at	STIM1	stromal interaction molecule 1	**0.0215**	**-0.0026**	0.0697	-0.1609	0.0654	253 ± 28	255 ± 23	324 ± 17	338 ± 33
40420_at	STK10	serine/threonine kinase 10	0.1280	**-0.0092**	0.1361	-0.1559	0.0553	223 ± 20	253 ± 28	240 ± 13	310 ± 26
41657_at	STK11	serine/threonine kinase 11	0.0944	**-0.0050**	0.1801	0.0657	**0.0056**	806 ± 99	738 ± 104	891 ± 35	1421 ± 215
212565_at	STK38L	serine/threonine kinase 38 like	0.2831	**-0.0388**	-0.2267	-0.3637	0.1654	494 ± 37	429 ± 52	515 ± 9	582 ± 66
203330_s_at	STX5A	syntaxin 5A	0.3823	**-0.0434**	0.1426	-0.0747	0.1213	190 ± 17	229 ± 15	210 ± 20	247 ± 7
215588_x_at	SUDD	sudD suppressor of bimD6 homolog	**0.0036**	**-0.0364**	0.1982	-0.1362	0.1386	1815 ± 216	1913 ± 136	2669 ± 330	3159 ± 836
206593_s_at	SURF5	surfeit 5	0.4824	**-0.0229**	0.0728	-0.1322	0.3090	393 ± 26	398 ± 37	439 ± 21	468 ± 36
219262_at	SUV39H2	suppressor of variegation 3-9 homolog 2	0.6039	**-0.0475**	0.2314	-0.4013	0.0841	39 ± 5	39 ± 10	41 ± 10	74 ± 17
204978_at	SWAP2	suppressor of white apricot homolog 2	**0.0017**	**-0.0242**	0.2863	-0.4042	**0.0522**	949 ± 115	1131 ± 161	1135 ± 118	1803 ± 405
206546_at	SYCP2	synaptonemal complex protein 2	**0.0032**	-0.0905	**0.0001**	-0.0670	0.2322	32 ± 3	45 ± 7	53 ± 7	55 ± 15
221276_s_at	SYNCOILIN	intermediate filament protein syncoilin	**0.0021**	**-0.0021**	0.3414	**-0.0113**	**0.0160**	119 ± 12	126 ± 22	165 ± 21	198 ± 18
221898_at	T1A-2	lung type-I cell membrane-associated glycoprotein	0.4797	**-0.0091**	-0.2149	-0.3009	0.1723	174 ± 32	143 ± 16	209 ± 17	232 ± 38
217437_s_at	TACC1	transforming, acidic coiled-coil containing protein 1	0.2180	**-0.0049**	**0.0210**	-0.2360	0.1797	458 ± 23	501 ± 27	555 ± 54	612 ± 79
215272_at	TADA3L	transcriptional adaptor 3-like	**0.0400**	-0.1427	0.4103	-0.4306	0.3476	79 ± 12	73 ± 18	82 ± 12	124 ± 38
209358_at	TAF11	TAF11 RNA polymerase II	0.0573	**-0.0315**	0.1939	-0.4966	0.0756	458 ± 39	485 ± 40	479 ± 38	613 ± 55
202840_at	TAF15	TAF15 RNA polymerase II	**0.0532**	**-0.0073**	0.0564	-0.0856	**0.0382**	351 ± 34	350 ± 32	504 ± 33	489 ± 77
210053_at	TAF5	TAF5 RNA polymerase II	0.0976	**-0.0345**	-0.2634	-0.2789	0.1180	321 ± 25	306 ± 36	398 ± 26	376 ± 34
205547_s_at	TAGLN	transgelin	**0.0000**	**-0.0120**	0.1651	-0.2519	**0.0289**	225 ± 31	239 ± 37	341 ± 22	362 ± 54
204877_s_at	TAO1	thousand and one amino acid protein kinase	0.6842	**-0.0399**	**0.0067**	0.3208	**0.0183**	114 ± 10	122 ± 9	97 ± 7	180 ± 33
202307_s_at	TAP1	transporter 1, ATP-binding cassette, sub-family B	0.7251	**-0.0383**	0.1327	-0.3236	0.1894	385 ± 48	418 ± 76	338 ± 42	653 ± 200
208829_at	TAPBP	TAP binding protein	**0.0159**	-0.1026	0.4846	-0.1862	0.0695	1245 ± 102	1233 ± 54	1582 ± 115	1433 ± 109
221444_at	TAS2R16	taste receptor, type 2, member 16	0.3909	**-0.0196**	0.1102	-0.2086	0.0559	146 ± 14	162 ± 15	152 ± 15	210 ± 23
206916_x_at	TAT	tyrosine aminotransferase	0.2259	**-0.0134**	-0.2050	-0.3071	**0.0128**	59 ± 11	52 ± 5	55 ± 9	105 ± 16
202132_at	TAZ	transcriptional co-activator with PDZ-binding motif	**0.0064**	-0.1504	0.1412	0.1375	**0.0358**	110 ± 13	90 ± 8	183 ± 31	148 ± 25
37278_at	TAZ	tafazzin ; endocardial fibroelastosis 2; Barth syndrome)	0.1651	**-0.0262**	0.1214	-0.1555	0.0706	539 ± 38	648 ± 69	592 ± 35	745 ± 61
202133_at	TAZ	transcriptional co-activator with PDZ-binding motif	0.0666	**-0.0279**	0.1714	**-0.0424**	**0.0029**	475 ± 84	634 ± 95	1340 ± 265	912 ± 106
222173_s_at	TBC1D2	TBC1 domain family, member 2	0.0991	**-0.0399**	-0.2686	-0.3220	**0.0371**	88 ± 18	66 ± 22	55 ± 11	160 ± 45
201813_s_at	TBC1D5	TBC1 domain family, member 5	**0.0284**	**-0.0129**	**0.0340**	**-0.0342**	**0.0431**	776 ± 19	890 ± 46	925 ± 74	1062 ± 103

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
213400_s_at	TBL1X	transducin -like 1X-linked	**0.0024**	**-0.0002**	0.2245	0.3880	**0.0007**	853 ± 75	949 ± 126	1106 ± 68	1624 ± 196
215122_at	TBX6	T-box 6	0.0593	**-0.0294**	-0.2407	**-0.0532**	0.0981	33 ± 9	42 ± 9	74 ± 18	78 ± 22
207554_x_at	TBXA2R	thromboxane A2 receptor	0.3649	**-0.0094**	**0.0037**	-0.1471	**0.0080**	171 ± 19	203 ± 20	171 ± 21	284 ± 35
214449_s_at	TC10	ras-like protein TC10	0.4970	**-0.0215**	-0.1950	0.3304	0.2737	228 ± 29	223 ± 27	269 ± 37	301 ± 26
212122_at	TC10	ras-like protein TC10	**0.0055**	**-0.0006**	0.0599	**-0.0001**	**0.0012**	154 ± 17	247 ± 26	292 ± 20	280 ± 36
212119_at	TC10	ras-like protein TC10	**0.0311**	**-0.0112**	-0.3316	**-0.0225**	**0.0356**	1844 ± 156	2098 ± 183	2545 ± 208	2401 ± 161
212931_at	TCF20	transcription factor 20	**0.0210**	-0.4521	-0.4258	0.1709	0.2903	870 ± 25	848 ± 79	1067 ± 63	979 ± 158
209153_s_at	TCF3	transcription factor 3	**0.0003**	**-0.0005**	0.1557	**-0.0216**	**0.0069**	224 ± 32	293 ± 34	438 ± 66	468 ± 72
221016_s_at	TCF-3	HMG-box transcription factor TCF-3	**0.0004**	**-0.0048**	0.1881	-0.1469	**0.0108**	355 ± 24	444 ± 45	455 ± 37	563 ± 51
205255_x_at	TCF7	transcription factor 7	**0.0052**	**-0.0263**	0.1623	-0.4557	**0.0352**	804 ± 96	1143 ± 180	970 ± 104	1628 ± 325
212761_at	TCF7L2	transcription factor 7-like 2	**0.0147**	**-0.0006**	0.1012	-0.3033	**0.0261**	1861 ± 116	2134 ± 213	2302 ± 127	2883 ± 396
212762_s_at	TCF7L2	transcription factor 7-like 2	**0.0078**	**-0.0274**	0.2111	-0.0889	0.1190	422 ± 47	448 ± 27	590 ± 69	572 ± 75
204043_at	TCN2	transcobalamin II; macrocytic anemia	0.4467	**-0.0281**	**0.0083**	**-0.0053**	0.0877	239 ± 16	320 ± 30	293 ± 32	345 ± 41
202384_s_at	TCOF1	Treacher Collins-Franceschetti syndrome 1	**0.0040**	-0.1318	0.4932	**-0.0009**	0.0595	150 ± 14	177 ± 18	268 ± 38	209 ± 44
201999_s_at	TCTEL1	t-complex-associated-testis-expressed 1-like 1	**0.0401**	**-0.0003**	-0.1117	-0.1475	**0.0192**	1062 ± 71	1086 ± 66	1309 ± 108	1498 ± 154
203742_s_at	TDG	thymine-DNA glycosylase	**0.0043**	**-0.0134**	**-0.0461**	-0.3433	**0.0227**	181 ± 19	158 ± 6	194 ± 14	287 ± 55
201737_s_at	TEB4	similar to S. cerevisiae SSM4	**0.0373**	**-0.0279**	0.2946	**-0.0212**	0.0551	1927 ± 111	2131 ± 127	2717 ± 277	2452 ± 245
200804_at	TEGT	testis enhanced gene transcript	0.0924	**-0.0081**	0.2297	-0.0781	**0.0132**	5273 ± 269	5521 ± 350	6661 ± 244	6016 ± 364
221680_s_at	TEL2	transcription factor ets	**0.0211**	**-0.0004**	0.1299	-0.1338	**0.0126**	145 ± 12	176 ± 10	211 ± 21	240 ± 29
219025_at	TEM1	tumor endothelial marker 1 precursor	**0.0036**	**-0.0122**	-0.4062	-0.1802	0.0713	280 ± 24	301 ± 7	352 ± 47	451 ± 77
217853_at	TEM6	tumor endothelial marker 6	0.1228	**-0.0027**	**0.0146**	-0.2218	**0.0210**	2462 ± 159	2999 ± 448	4169 ± 468	4407 ± 725
220147_s_at	TERA	TERA protein	0.1892	**-0.0370**	-0.1013	-0.2693	0.2641	428 ± 43	460 ± 21	458 ± 30	530 ± 40
202720_at	TES	testis derived transcript	0.4626	**-0.0111**	0.4356	-0.1491	0.0955	215 ± 34	199 ± 43	225 ± 27	321 ± 33
218020_s_at	TEX27	testis expressed sequence 27	0.3407	**-0.0397**	-0.4504	0.3833	0.1559	1007 ± 52	1111 ± 69	1120 ± 57	1210 ± 71
214063_s_at	TF	transferrin	0.1738	**-0.0017**	0.4695	-0.0883	**0.0396**	6535 ± 841	6388 ± 707	3136 ± 1103	1139 ± 1856
204653_at	TFAP2A	transcription factor AP-2 alpha	0.3762	**-0.0453**	-0.1267	0.3997	**0.0021**	125 ± 20	109 ± 17	85 ± 17	218 ± 34
212457_at	TFE3	transcription factor binding to IGHM enhancer 3	**0.0362**	-0.1708	-0.0995	-0.2453	**0.0150**	1132 ± 81	937 ± 92	1393 ± 111	1134 ± 58
50221_at	TFEB	transcription factor EB	0.0654	**-0.0085**	0.1780	-0.4414	0.1582	677 ± 82	790 ± 133	891 ± 123	1170 ± 249
221866_at	TFEB	transcription factor EB	0.0694	**-0.0315**	0.3967	-0.2969	0.2704	197 ± 34	230 ± 29	296 ± 48	297 ± 57
206715_at	TFEC	transcription factor EC	0.0706	**-0.0235**	-0.4850	-0.0634	**0.0440**	72 ± 13	87 ± 13	78 ± 10	123 ± 13
203085_s_at	TGFB1	transforming growth factor, beta 1	0.3127	**-0.0033**	0.2759	0.4450	**0.0134**	402 ± 33	364 ± 16	406 ± 47	644 ± 107
209651_at	TGFB1I1	transforming growth factor beta 1 induced transcript 1	0.0569	**-0.0001**	0.1423	-0.3400	**0.0016**	258 ± 29	257 ± 32	351 ± 30	515 ± 76
209908_s_at	TGFB2	transforming growth factor, beta 2	**0.0337**	-0.0575	0.2625	-0.4716	0.1398	123 ± 25	171 ± 38	174 ± 7	234 ± 50
209909_s_at	TGFB2	transforming growth factor, beta 2	**0.0458**	**-0.0137**	-0.2768	-0.0691	**0.0277**	57 ± 6	52 ± 10	66 ± 9	95 ± 15
204731_at	TGFBR3	transforming growth factor, beta receptor III	**0.0048**	**-0.0001**	0.3427	**-0.0168**	**0.0091**	339 ± 33	413 ± 40	512 ± 66	630 ± 87
203313_s_at	TGIF	TGFB-induced factor	0.1384	**-0.0075**	**-0.0130**	0.1977	0.0637	204 ± 31	160 ± 11	275 ± 22	298 ± 62
216262_s_at	TGIF2	TGFB-induced factor 2	0.3764	**-0.0102**	0.2323	-0.0885	**0.0367**	200 ± 24	229 ± 22	197 ± 14	295 ± 36
212596_s_at	THC211630	partial transcript encompassing THC211630 gene	**0.0016**	-0.1049	0.2030	0.3692	0.2414	575 ± 47	640 ± 100	767 ± 109	951 ± 247
208104_s_at	THG-1	TSC-22-like	**0.0367**	**-0.0213**	**0.0196**	**-0.0480**	**0.0386**	730 ± 59	968 ± 139	1231 ± 136	1097 ± 142
222122_s_at	THO2	Tho2	**0.0404**	-0.0989	-0.4113	**-0.0364**	0.2425	398 ± 39	377 ± 36	369 ± 29	470 ± 38
1316_at	THRA	thyroid hormone receptor, alpha oncogene homolog, avian)	0.0787	**-0.0041**	0.1177	-0.1348	**0.0089**	161 ± 10	200 ± 19	204 ± 18	278 ± 36
202039_at	TIAF1	TGFB1-induced anti-apoptotic factor 1	**0.0012**	-0.0569	0.1168	-0.3206	0.1704	1417 ± 134	1796 ± 259	2099 ± 192	2348 ± 562

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
203317_at	TIC	SEC7 homolog	**0.0203**	**-0.0014**	**0.0514**	0.3490	**0.0044**	78 ± 17	94 ± 10	173 ± 19	172 ± 33
213301_x_at	TIF1	transcriptional intermediary factor 1	**0.0015**	**-0.0051**	0.0706	-0.0954	**0.0450**	357 ± 21	407 ± 15	464 ± 39	501 ± 59
204391_x_at	TIF1	transcriptional intermediary factor 1	**0.0019**	**-0.0483**	**-0.0013**	0.0578	0.1005	485 ± 13	469 ± 49	558 ± 39	611 ± 62
203046_s_at	TIMELESS	timeless homolog	**0.0374**	-0.0640	-0.3186	-0.0681	0.1319	172 ± 20	240 ± 38	208 ± 16	284 ± 55
215168_at	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A	**0.0198**	-0.0772	-0.4583	-0.2471	0.1773	31 ± 10	26 ± 6	32 ± 4	61 ± 20
203092_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog	**0.0045**	-0.3013	-0.2335	0.1153	0.4589	367 ± 28	305 ± 36	369 ± 38	471 ± 139
203093_s_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog	**0.0215**	**-0.0010**	0.2759	**0.0405**	**0.0199**	221 ± 8	232 ± 26	276 ± 18	356 ± 56
209154_at	TIP-1	Tax interaction protein 1	**0.0516**	**-0.0025**	**0.0013**	-0.0847	**0.0353**	1652 ± 192	2510 ± 446	2896 ± 347	3486 ± 649
202122_s_at	TIP47	cargo selection protein	0.0586	**-0.0315**	0.3834	-0.4372	0.2473	685 ± 82	743 ± 105	825 ± 87	953 ± 110
217367_s_at	TIX1	triple homeobox 1	**0.0000**	**0.0000**	**0.0370**	**-0.0144**	**0.0001**	511 ± 47	593 ± 47	761 ± 57	913 ± 74
202085_at	TJP2	tight junction protein 2	**0.0172**	**-0.0007**	-0.4256	-0.0691	0.0605	1428 ± 145	1570 ± 296	1904 ± 182	2266 ± 271
47608_at	TJP4	tight junction protein 4	**0.0064**	-0.0907	0.1283	-0.1933	0.2218	1175 ± 140	1563 ± 222	1462 ± 164	1948 ± 458
206472_s_at	TLE3	transducin-like enhancer of split 3 homolog, Drosophila)	**0.0026**	-0.1135	-0.4060	0.2597	0.0932	87 ± 11	98 ± 20	84 ± 16	151 ± 30
212769_at	TLE3	transducin-like enhancer of split 3 homolog, Drosophila)	**0.0083**	**-0.0002**	0.0571	-0.1175	**0.0016**	90 ± 8	86 ± 7	135 ± 13	141 ± 10
214688_at	TLE4	transducin-like enhancer of split 4 homolog, Drosophila)	0.1134	**-0.0428**	-0.4730	-0.3002	**0.0285**	121 ± 10	123 ± 10	107 ± 16	179 ± 26
206415_at	TLL1	tolloid-like 1	**0.0503**	**-0.0293**	0.0840	-0.3975	**0.0103**	32 ± 3	28 ± 5	33 ± 5	67 ± 15
208942_s_at	TLOC1	translocation protein 1	**0.0074**	-0.1167	0.4150	-0.2947	**0.0269**	2138 ± 96	2214 ± 163	2738 ± 172	2411 ± 124
210176_at	TLR1	toll-like receptor 1	0.0766	**-0.0018**	-0.3761	**-0.0390**	**0.0162**	71 ± 9	93 ± 16	100 ± 4	120 ± 7
209108_at	TM4SF6	transmembrane 4 superfamily member 6	0.2463	**-0.0003**	-0.3779	-0.1027	**0.0075**	526 ± 47	518 ± 40	616 ± 78	881 ± 111
217974_at	TM7SF3	seven transmembrane protein TM7SF3	-0.8483	**-0.0293**	-0.4844	**-0.0116**	0.4008	159 ± 16	146 ± 22	164 ± 19	193 ± 19
221882_s_at	TMEM8	transmembrane protein 8	**0.0232**	-0.5294	**0.0337**	-0.4415	0.5615	147 ± 13	174 ± 33	198 ± 35	227 ± 69
220177_s_at	TMPRSS3	transmembrane protease, serine 3	0.2412	**-0.0226**	0.1712	-0.4257	0.0644	175 ± 16	147 ± 15	210 ± 20	229 ± 29
201645_at	TNC	tenascin C	0.2291	**-0.0475**	**0.0459**	-0.4827	0.0633	231 ± 46	284 ± 46	479 ± 100	391 ± 35
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	**0.0177**	**-0.0070**	0.0628	-0.3436	**0.0137**	289 ± 24	366 ± 30	335 ± 26	446 ± 45
209295_at	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	0.9726	**-0.0366**	-0.2500	0.2795	0.3513	385 ± 36	352 ± 21	396 ± 44	478 ± 78
204932_at	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	**0.0240**	**-0.0018**	**0.0407**	-0.1543	**0.0031**	48 ± 4	59 ± 6	74 ± 12	109 ± 16
207643_s_at	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	**0.0207**	**-0.0163**	0.0995	-0.4246	**0.0240**	563 ± 44	743 ± 72	700 ± 72	895 ± 90
207536_s_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	**0.0028**	**-0.0428**	**0.0490**	0.4553	**0.0101**	116 ± 8	173 ± 26	146 ± 7	239 ± 42
202687_s_at	TNFSF10	tumor necrosis factor superfamily, member 10	**0.0134**	-0.2852	0.2810	-0.2411	0.3852	50 ± 8	69 ± 9	70 ± 15	91 ± 27
217931_at	TNRC5	trinucleotide repeat containing 5	**0.0064**	**-0.0369**	**0.0095**	-0.1251	0.0788	237 ± 16	312 ± 37	308 ± 23	403 ± 75
206093_x_at	TNXB	tenascin XB	**0.0008**	**-0.0023**	-0.2677	-0.2116	**0.0057**	262 ± 39	225 ± 28	460 ± 39	412 ± 83
213451_x_at	TNXB	tenascin XB	**0.0001**	**-0.0026**	0.3414	**-0.0126**	**0.0062**	198 ± 45	236 ± 53	447 ± 45	388 ± 68
216333_x_at	TNXB	tenascin XB	**0.0002**	**-0.0121**	**0.0109**	**-0.0060**	**0.0003**	163 ± 24	236 ± 47	451 ± 47	332 ± 55
222243_s_at	TOB2	transducer of ERBB2, 2	**0.0020**	**-0.0011**	-0.3341	**-0.0540**	**0.0476**	794 ± 106	881 ± 108	1132 ± 74	1189 ± 153
221496_s_at	TOB2	transducer of ERBB2, 2	**0.0071**	**-0.0014**	0.1255	-0.3897	**0.0355**	406 ± 86	506 ± 154	805 ± 136	1017 ± 228
202807_s_at	TOM1	target of myb1	**0.0059**	-0.0865	0.1112	-0.2997	**0.0236**	255 ± 22	230 ± 20	376 ± 22	316 ± 59
204946_s_at	TOP3A	topoisomerase III alpha	**0.0429**	-0.3092	0.1462	-0.3943	0.3966	371 ± 38	471 ± 76	398 ± 46	523 ± 111
201746_at	TP53	tumor protein p53	**0.0053**	**-0.0211**	0.1652	-0.3715	0.0912	166 ± 20	203 ± 27	238 ± 26	265 ± 41
204071_s_at	TP53BPL	tumor protein p53-binding protein	**0.0054**	**-0.0199**	**0.0400**	-0.1030	0.0925	233 ± 9	264 ± 22	270 ± 29	324 ± 31
201691_s_at	TPD52	tumor protein D52	**0.0017**	**-0.0030**	**0.0206**	0.4724	**0.0047**	222 ± 19	263 ± 17	294 ± 28	362 ± 35
203786_s_at	TPD52L1	tumor protein D52-like 1	0.1937	**-0.0273**	-0.1000	**-0.0374**	0.1145	2979 ± 178	3119 ± 229	3012 ± 332	4117 ± 598
201379_s_at	TPD52L2	tumor protein D52-like 2	**0.0048**	-0.5364	0.2441	-0.4572	0.1182	652 ± 68	761 ± 109	990 ± 66	740 ± 161

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
210050_at	TPI1	triosephosphate isomerase 1	**0.0410**	-0.1561	-0.1123	0.4421	0.2218	166 ± 10	128 ± 17	176 ± 8	196 ± 41
203671_at	TPMT	thiopurine S-methyltransferase	0.1615	**-0.0012**	0.0561	-0.1834	**0.0077**	284 ± 36	322 ± 23	383 ± 20	469 ± 57
218855_at	TPRA40	seven transmembrane domain orphan receptor	**0.0168**	-0.2582	-0.2730	0.3201	0.4693	222 ± 16	237 ± 20	267 ± 21	268 ± 39
220865_s_at	TPT	trans-prenyltransferase	0.2911	**-0.0165**	**0.0521**	**-0.0410**	0.0691	264 ± 21	292 ± 19	278 ± 34	362 ± 27
211943_x_at	TPT1	tumor protein, translationally-controlled 1	0.1925	**-0.0405**	**-0.0026**	0.3018	0.1084	16377 ± 877	5133 ± 1005	637 ± 1213	8266 ± 1229
220205_at	TPTE	transmembrane phosphatase with tensin homology	0.6237	**-0.0317**	0.0599	-0.2294	0.0731	38 ± 7	57 ± 11	49 ± 11	83 ± 18
201398_s_at	TRAM	translocating chain-associating membrane protein	0.3401	**-0.0005**	0.2403	**-0.0534**	**0.0280**	1596 ± 80	1807 ± 103	2141 ± 124	2218 ± 267
213043_s_at	TRAP100	thyroid hormone receptor-associated protein	0.0597	**-0.0485**	-0.2229	-0.4669	0.1912	591 ± 38	540 ± 17	624 ± 61	708 ± 65
201986_at	TRAP240	thyroid hormone receptor-associated protein	**0.0027**	**-0.0063**	0.3155	-0.1257	**0.0475**	1278 ± 74	1446 ± 109	1468 ± 90	1664 ± 99
213193_x_at	TRB	T cell receptor beta locus	**0.0254**	**-0.0319**	0.0866	-0.1659	0.1197	328 ± 38	383 ± 51	377 ± 33	512 ± 88
34689_at	TREX1	three prime repair exonuclease 1	0.0831	**-0.0176**	0.1211	-0.0637	**0.0251**	759 ± 42	885 ± 59	870 ± 62	1059 ± 95
207891_s_at	TREX2	three prime repair exonuclease 2	**0.0488**	-0.0640	0.2984	**-0.0508**	0.3501	282 ± 29	344 ± 23	338 ± 32	397 ± 80
213334_x_at	TREX2	three prime repair exonuclease 2	0.1386	**-0.0008**	-0.3420	-0.3220	**0.0256**	643 ± 68	558 ± 37	755 ± 58	949 ± 132
218425_at	TRIAD3	TRIAD3 protein	**0.0203**	-0.3308	**0.0550**	-0.0816	0.2094	340 ± 32	455 ± 41	486 ± 25	463 ± 97
210579_s_at	TRIM10	tripartite motif-containing 10	0.4299	**-0.0071**	**0.0511**	-0.0920	**0.0176**	91 ± 21	120 ± 16	83 ± 16	208 ± 49
203147_s_at	TRIM14	tripartite motif-containing 14	0.5999	**-0.0382**	0.0999	-0.1836	0.2182	336 ± 37	348 ± 47	435 ± 26	474 ± 89
203148_s_at	TRIM14	tripartite motif-containing 14	**0.0159**	**-0.0057**	0.0854	0.3826	**0.0182**	161 ± 17	220 ± 38	268 ± 22	342 ± 70
202702_at	TRIM26	tripartite motif-containing 26	0.0738	**-0.0002**	0.3671	-0.2454	**0.0008**	447 ± 30	513 ± 16	468 ± 28	655 ± 51
203568_s_at	TRIM38	tripartite motif-containing 38	0.3111	**-0.0378**	**0.0073**	**-0.0026**	0.3079	202 ± 19	264 ± 14	262 ± 41	292 ± 53
202734_at	TRIP10	thyroid hormone receptor interactor 10	**0.0172**	**-0.0498**	0.3782	-0.3294	0.2308	428 ± 52	559 ± 97	590 ± 67	670 ± 122
203732_at	TRIP4	thyroid hormone receptor interactor 4	0.1021	**-0.0063**	-0.2594	-0.0905	**0.0025**	398 ± 17	429 ± 33	366 ± 13	509 ± 30
202656_s_at	TRIP-Br2	transcript. reg. interacting with the PHS-bromodomain 2	**0.0002**	**0.0000**	0.2766	-0.1218	**0.0002**	425 ± 26	477 ± 33	596 ± 38	670 ± 50
212318_at	TRN-SR	transportin-SR	**0.0078**	**-0.0136**	0.2962	-0.2555	**0.0357**	757 ± 63	738 ± 39	964 ± 70	1083 ± 151
218502_s_at	TRPS1	trichorhinophalangeal syndrome I	**0.0169**	**-0.0163**	0.1541	-0.3020	0.0692	666 ± 89	793 ± 117	1044 ± 137	998 ± 100
219632_s_at	TRPV1	transient receptor potential cation channel, V1	**0.0073**	-0.0696	0.1670	0.4987	0.0741	327 ± 34	420 ± 62	398 ± 32	592 ± 126
212689_s_at	TSGA	zinc finger protein	0.0668	**-0.0156**	-0.3911	-0.2230	0.2925	766 ± 67	810 ± 71	896 ± 45	978 ± 131
214606_at	TSPAN-2	tetraspan 2	**0.0427**	-0.1270	0.0584	0.2183	0.0692	20 ± 5	30 ± 9	26 ± 4	46 ± 9
209890_at	TSPAN-5	tetraspan 5	**0.0336**	**-0.0055**	0.3119	**-0.0086**	**0.0455**	225 ± 9	259 ± 31	264 ± 40	354 ± 35
213968_at	TSPAN-5	tetraspan 5	**0.0358**	**-0.0168**	**0.0430**	**-0.0235**	**0.0331**	82 ± 12	115 ± 12	110 ± 25	187 ± 40
209803_s_at	TSSC3	tumor suppressing subtransferable candidate 3	**0.0384**	-0.0625	**-0.0085**	0.3506	0.0790	60 ± 11	34 ± 14	61 ± 15	92 ± 18
204771_s_at	TTF1	transcription termination factor, RNA polymerase I	**0.0304**	-0.0653	-0.3904	0.3638	0.1252	372 ± 19	361 ± 11	476 ± 52	456 ± 52
204772_s_at	TTF1	transcription termination factor, RNA polymerase I	**0.0008**	**-0.0039**	0.2616	-0.0552	**0.0162**	177 ± 13	170 ± 27	212 ± 15	283 ± 41
219728_at	TTID	titin immunoglobulin domain protein	0.3587	**-0.0302**	0.4675	-0.0786	0.1657	252 ± 42	378 ± 52	530 ± 159	515 ± 77
208195_at	TTN	titin	**0.0050**	**0.0000**	**0.0059**	**-0.0187**	**0.0001**	124 ± 12	165 ± 19	168 ± 18	286 ± 32
211460_at	TTTY9	testis-specific transcript, Y-linked 9	**0.0363**	-0.1631	**0.0267**	-0.4758	0.1257	133 ± 11	195 ± 45	155 ± 12	232 ± 44
209074_s_at	TU3A	TU3A protein	**0.0001**	**-0.0002**	0.1100	-0.0901	**0.0016**	11683 ± 777	2319 ± 1038	6105 ± 756	6779 ± 1386
207547_s_at	TU3A	TU3A protein	**0.0188**	**-0.0045**	0.3494	-0.1434	**0.0013**	8632 ± 884	8454 ± 416	3215 ± 898	11306 ± 980
210527_x_at	TUBA2	tubulin, alpha 2	0.1207	**-0.0184**	0.2401	-0.3468	0.0671	455 ± 34	496 ± 25	506 ± 50	603 ± 34
209118_s_at	TUBA3	tubulin, alpha 3	**0.0225**	**-0.0270**	0.4465	-0.1753	0.0798	17518 ± 697	5982 ± 1634	214 ± 1907	0551 ± 1861
220069_at	TUBA8	tubulin, alpha 8	0.1944	**-0.0196**	0.3686	0.1901	0.0958	66 ± 6	78 ± 13	92 ± 10	115 ± 22
205854_at	TULP3	tubby like protein 3	**0.0010**	**-0.0300**	0.4674	-0.4840	0.1208	470 ± 66	481 ± 75	591 ± 55	746 ± 141
201009_s_at	TXNIP	thioredoxin interacting protein	**0.0020**	-0.0559	0.0682	-0.1020	0.0793	1333 ± 152	1840 ± 221	2148 ± 152	2017 ± 364

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
201010_s_at	TXNIP	thioredoxin interacting protein	**0.0366**	-0.0629	0.2336	-0.3598	0.1092	3342 ± 546	4285 ± 516	5646 ± 693	4997 ± 980
205546_s_at	TYK2	tyrosine kinase 2	**0.0372**	-0.0565	-0.3490	**-0.0534**	0.0864	365 ± 50	505 ± 57	564 ± 68	538 ± 49
205300_s_at	U1SNRNPBP	U1-snRNP binding protein homolog	**0.0067**	-0.1553	-0.2911	0.2136	0.2862	213 ± 18	198 ± 25	243 ± 20	292 ± 62
213876_x_at	U2AF1RS2	U2 small nuc. ribonucleoprotein auxiliary factor, small sub. 2	**0.0029**	**-0.0028**	0.4005	0.1366	**0.0117**	1007 ± 68	962 ± 126	1230 ± 122	1782 ± 300
208174_x_at	U2AF1RS2	U2 small nuc. ribonucleoprotein auxiliary factor, small sub. 2	**0.0038**	**-0.0404**	0.1980	-0.4998	0.1201	1129 ± 102	1359 ± 294	1312 ± 139	1791 ± 224
218381_s_at	U2AF65	U2 small nuclear ribonucleoprotein auxiliary factor	0.1736	**-0.0317**	**-0.0046**	-0.3796	**0.0079**	756 ± 37	635 ± 29	875 ± 51	831 ± 54
219192_at	UBAP2	ubiquitin associated protein 2	**0.0005**	**-0.0506**	0.0809	-0.2586	0.1268	778 ± 51	931 ± 110	1125 ± 95	1197 ± 231
202954_at	UBE2C	ubiquitin-conjugating enzyme E2C	0.0761	**-0.0146**	0.1097	-0.1087	**0.0333**	385 ± 21	417 ± 28	408 ± 21	551 ± 70
200676_s_at	UBE2L3	ubiquitin-conjugating enzyme E2L 3	**0.0230**	-0.3251	-0.2593	-0.3165	0.1420	1172 ± 97	1166 ± 64	1557 ± 153	1275 ± 190
201003_x_at	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	**0.0432**	**-0.0014**	0.2601	0.3578	**0.0018**	689 ± 37	627 ± 17	724 ± 52	899 ± 50
213822_s_at	UBE3B	ubiquitin protein ligase	**0.0439**	**-0.0003**	-0.4631	-0.1843	**0.0020**	184 ± 12	213 ± 40	223 ± 25	345 ± 18
209088_s_at	UBN1	ubinuclein 1	**0.0234**	**-0.0052**	0.1980	**-0.0516**	**0.0131**	392 ± 42	406 ± 39	461 ± 29	704 ± 128
205687_at	UBPH	similar to ubiquitin binding protein	**0.0255**	-0.0580	-0.4609	0.1409	**0.0353**	223 ± 10	235 ± 20	222 ± 21	319 ± 44
206072_at	UCN	urocortin	**0.0379**	**-0.0042**	-0.4247	-0.4671	0.0782	124 ± 17	112 ± 19	161 ± 22	215 ± 45
204881_s_at	UGCG	UDP-glucose ceramide glucosyltransferase	0.1100	**-0.0123**	-0.0983	-0.2782	**0.0477**	544 ± 27	558 ± 37	625 ± 39	667 ± 27
221304_at	UGT1A	UDP glycosyltransferase 1 family, polypeptide A cluster	0.2831	**-0.0213**	**0.0476**	-0.1752	**0.0113**	74 ± 9	88 ± 8	68 ± 7	123 ± 18
206094_x_at	UGT1A6	UDP glycosyltransferase 1 family, polypeptide A6	0.0845	**-0.0153**	**0.0327**	-0.4902	**0.0146**	200 ± 12	237 ± 37	228 ± 29	336 ± 33
204063_s_at	ULK2	unc-51-like kinase 2	0.3861	**-0.0324**	0.3022	0.4991	0.0712	446 ± 36	408 ± 22	434 ± 20	543 ± 47
212144_at	UNC84B	unc-84 homolog B	**0.0249**	**-0.0083**	-0.1889	-0.0949	0.1144	1657 ± 188	1813 ± 174	2261 ± 306	2366 ± 242
202330_s_at	UNG	uracil-DNA glycosylase	**0.0164**	**-0.0148**	-0.2500	-0.0828	**0.0352**	417 ± 36	427 ± 11	531 ± 35	522 ± 37
214323_s_at	UPF3A	similar to yeast Upf3, variant A	0.6766	**-0.0295**	0.4306	-0.0881	0.3369	1877 ± 56	2054 ± 221	2182 ± 204	2313 ± 169
222236_s_at	UPLC1	up-regulated in liver cancer 1	**0.0029**	**-0.0212**	-0.2315	-0.2488	0.1559	449 ± 63	494 ± 33	528 ± 29	634 ± 81
208971_at	UROD	uroporphyrinogen decarboxylase	**0.0146**	-0.2858	0.0884	**-0.0153**	0.3630	373 ± 26	416 ± 32	464 ± 23	441 ± 68
214879_x_at	USF2	upstream transcription factor 2, c-fos interacting	**0.0307**	-0.0687	0.0761	-0.1302	0.1382	523 ± 100	711 ± 111	645 ± 83	861 ± 107
202152_x_at	USF2	upstream transcription factor 2, c-fos interacting	0.1494	**-0.0250**	0.1606	0.3764	0.1205	1178 ± 107	1321 ± 162	1321 ± 79	1682 ± 226
202413_s_at	USP1	ubiquitin specific protease 1	**0.0362**	**-0.0028**	0.2163	**-0.0304**	**0.0357**	615 ± 25	700 ± 60	818 ± 56	802 ± 66
209136_s_at	USP10	ubiquitin specific protease 10	**0.0400**	-0.3576	0.4631	0.3590	0.4683	216 ± 17	211 ± 20	202 ± 22	258 ± 42
205356_at	USP13	ubiquitin specific protease 13	**0.0082**	-0.0799	0.1951	-0.4696	0.1907	506 ± 27	537 ± 40	544 ± 62	679 ± 92
214674_at	USP19	ubiquitin specific protease 19	0.0744	**-0.0118**	**0.0007**	**-0.0251**	**0.0021**	107 ± 7	208 ± 23	184 ± 27	229 ± 23
200083_at	USP22	ubiquitin specific protease 22	**0.0168**	-0.2529	0.2062	0.3971	0.2349	2573 ± 114	2652 ± 161	2909 ± 107	2933 ± 219
221654_s_at	USP3	ubiquitin specific protease 3	0.2221	**-0.0010**	-0.1238	0.4590	**0.0088**	314 ± 23	313 ± 15	328 ± 21	446 ± 48
211800_s_at	USP4	ubiquitin specific protease 4	0.3448	**-0.0044**	0.1192	-0.1600	**0.0456**	733 ± 37	777 ± 33	852 ± 25	871 ± 45
202682_s_at	USP4	ubiquitin specific protease 4	0.0971	**-0.0050**	0.1366	-0.1162	0.1598	1196 ± 76	1189 ± 87	1389 ± 117	1594 ± 223
201498_at	USP7	ubiquitin specific protease 7	**0.0121**	-0.1105	0.4675	-0.4097	0.1883	1397 ± 77	1464 ± 82	1646 ± 121	1804 ± 234
205139_s_at	UST	uronyl-2-sulfotransferase	**0.0095**	**-0.0170**	0.2404	0.4676	**0.0150**	351 ± 15	337 ± 31	462 ± 39	459 ± 34
203991_s_at	UTX	ubiquitously transcribed tetratricopeptide repeat gene X chrom	**0.0000**	**-0.0071**	-0.3630	-0.4187	**0.0066**	226 ± 15	260 ± 35	376 ± 26	360 ± 48
203241_at	UVRAG	UV radiation resistance associated gene	0.5963	**-0.0300**	**-0.0057**	0.0995	**0.0418**	370 ± 12	329 ± 43	353 ± 15	439 ± 27
201336_at	VAMP3	vesicle-associated membrane protein 3	**0.0120**	**-0.0041**	0.4627	-0.3955	**0.0338**	2793 ± 240	3110 ± 425	3813 ± 281	4085 ± 404
208626_s_at	VAT1	vesicle amine transport protein 1 homolog	**0.0329**	-0.0792	-0.3879	-0.1109	0.3873	905 ± 107	1035 ± 94	1110 ± 135	1152 ± 80
203868_s_at	VCAM1	vascular cell adhesion molecule 1	**0.0476**	**-0.0100**	0.3036	-0.0610	0.0610	185 ± 32	221 ± 27	350 ± 86	358 ± 31
214843_s_at	VDU1	pVHL-interacting deubiquitinating enzyme 1	0.2428	**-0.0113**	**0.0512**	-0.1063	0.1790	472 ± 25	500 ± 35	551 ± 13	590 ± 71
203683_s_at	VEGFB	vascular endothelial growth factor B	0.1062	**-0.0186**	0.0747	0.4652	0.1145	332 ± 12	397 ± 43	411 ± 41	494 ± 77

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
209946_at	VEGFC	vascular endothelial growth factor C	0.1971	**-0.0003**	0.2166	-0.1999	**0.0113**	152 ± 19	141 ± 19	159 ± 6	238 ± 31
203255_at	VIT1	vitiligo-associated protein VIT-1	**0.0054**	**-0.0066**	-0.3252	-0.4356	**0.0270**	813 ± 110	629 ± 63	1033 ± 81	1192 ± 195
207671_s_at	VMD2	vitelliform macular dystrophy	**0.0154**	-0.2132	-0.3657	-0.3952	0.3530	258 ± 36	338 ± 64	303 ± 37	383 ± 67
203292_s_at	VPS11	vacuolar protein sorting 11	0.4016	**-0.0474**	0.0573	-0.3676	0.0595	886 ± 60	908 ± 68	870 ± 62	1127 ± 89
205126_at	VRK2	vaccinia related kinase 2	0.1704	**-0.0024**	-0.4979	-0.1383	0.0759	439 ± 39	502 ± 44	521 ± 41	672 ± 109
221593_s_at	VRP	vascular Rab-GAP/TBC-containing	0.0752	**-0.0372**	0.1684	-0.0774	0.3441	472 ± 47	507 ± 34	523 ± 23	590 ± 66
38964_r_at	WAS	Wiskott-Aldrich syndrome	0.1578	**-0.0080**	**0.0339**	-0.2478	**0.0251**	1682 ± 175	2132 ± 324	1683 ± 153	2946 ± 505
221725_at	WASF2	WAS protein family, member 2	**0.0063**	**-0.0020**	0.4336	-0.1712	**0.0232**	592 ± 67	693 ± 100	801 ± 54	949 ± 100
221247_s_at	WBSCR16	Williams-Beuren syndrome chromosome region 16	0.1451	**-0.0280**	0.2930	0.4353	0.1813	370 ± 18	416 ± 40	439 ± 20	468 ± 49
213670_x_at	WBSCR20B	Williams-Beuren Syndrome critical region protein 20 copy B	**0.0115**	-0.5489	**-0.0301**	-0.2821	0.7051	378 ± 36	353 ± 67	445 ± 31	427 ± 104
213460_x_at	WBSCR20B	Williams-Beuren Syndrome critical region protein 20 copy B	**0.0232**	-0.1149	-0.1290	0.3295	0.2308	577 ± 42	537 ± 76	563 ± 30	732 ± 115
211768_at	WBSCR5	Williams-Beuren syndrome chromosome region 5	**0.0095**	**-0.0109**	-0.3131	0.0705	**0.0266**	199 ± 23	167 ± 13	233 ± 27	329 ± 59
217734_s_at	WDR6	WD repeat domain 6	**0.0018**	**-0.0121**	-0.2191	-0.2255	0.1072	1095 ± 136	1158 ± 98	1469 ± 146	1650 ± 286
203892_at	WFDC2	WAP four-disulfide core domain 2	0.1074	**-0.0181**	0.3771	0.2102	**0.0384**	229 ± 22	217 ± 27	309 ± 23	339 ± 51
202908_at	WFS1	Wolfram syndrome 1	**0.0297**	-0.5950	-0.2990	0.4335	0.0925	1434 ± 121	1411 ± 112	1836 ± 155	1454 ± 128
203112_s_at	WHSC2	Wolf-Hirschhorn syndrome candidate 2	**0.0389**	-0.1075	0.1413	-0.0696	**0.0169**	279 ± 20	327 ± 21	413 ± 22	332 ± 49
34225_at	WHSC2	Wolf-Hirschhorn syndrome candidate 2	0.0571	**-0.0013**	-0.3942	-0.1258	**0.0158**	435 ± 26	474 ± 11	500 ± 40	594 ± 42
212050_at	WIRE	WIRE protein	**0.0183**	**-0.0502**	0.0931	-0.3836	0.1597	1550 ± 84	1773 ± 172	1856 ± 129	1968 ± 157
217681_at	WNT7B	wingless-type MMTV integration site family, member 7B	0.4679	**-0.0473**	0.2906	-0.4688	0.0730	93 ± 15	89 ± 25	96 ± 23	172 ± 32
205667_at	WRN	Werner syndrome	0.4775	**-0.0413**	0.2670	-0.0975	0.1858	175 ± 14	167 ± 19	213 ± 16	199 ± 17
218276_s_at	WW45	WW45 protein	**0.0011**	**-0.0002**	0.4794	-0.3976	**0.0028**	309 ± 11	323 ± 28	351 ± 21	435 ± 28
219077_s_at	WWOX	WW domain containing oxidoreductase	0.4111	**-0.0026**	-0.0585	-0.2335	**0.0539**	1243 ± 109	1412 ± 189	1500 ± 106	1972 ± 296
204022_at	WWP2	Nedd-4-like ubiquitin-protein ligase	**0.0472**	-0.1550	0.0681	0.3055	0.2263	541 ± 14	607 ± 63	592 ± 62	706 ± 68
210200_at	WWP2	Nedd-4-like ubiquitin-protein ligase	0.0806	**-0.0011**	**0.0066**	**-0.0105**	**0.0036**	216 ± 15	268 ± 19	241 ± 18	354 ± 43
213900_at	X123	Friedreich ataxia region gene X123	**0.0034**	**-0.0007**	0.2036	-0.3521	**0.0089**	835 ± 93	1026 ± 104	1221 ± 137	1533 ± 207
219126_at	XAP135	PHD zinc finger protein XAP135	**0.0473**	**-0.0135**	-0.0979	-0.4817	**0.0474**	437 ± 40	393 ± 21	416 ± 43	573 ± 61
200670_at	XBP1	X-box binding protein 1	**0.0110**	-0.1117	-0.3637	-0.4808	0.1401	465 ± 45	450 ± 46	448 ± 36	596 ± 66
202933_s_at	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	**0.0385**	**-0.0042**	**0.0391**	**-0.0003**	**0.0156**	609 ± 56	847 ± 86	991 ± 125	942 ± 67
200047_s_at	YY1	YY1 transcription factor	0.1469	**-0.0372**	-0.4687	-0.2020	0.3365	1668 ± 53	1596 ± 103	1823 ± 108	1861 ± 181
213051_at	ZAP	likely ortholog of rat zinc-finger antiviral protein	**0.0498**	**-0.0005**	-0.3714	-0.4265	**0.0400**	714 ± 80	722 ± 88	877 ± 39	1137 ± 187
219266_at	ZBRK1	zinc-finger protein ZBRK1	**0.0089**	-0.1478	**0.0012**	-0.1152	**0.0170**	100 ± 8	155 ± 18	131 ± 10	158 ± 16
221646_s_at	ZDHHC11	zinc finger, DHHC domain containing 11	**0.0096**	**-0.0202**	-0.2738	-0.1884	**0.0245**	835 ± 178	873 ± 97	1677 ± 285	1364 ± 242
219779_at	ZFH4	zinc finger homeodomain 4	**0.0272**	-0.1113	0.1320	-0.1867	0.4714	684 ± 81	695 ± 71	796 ± 52	880 ± 160
213130_at	ZFP100	zinc finger protein ZFP100	**0.0123**	**-0.0033**	-0.2703	-0.4641	**0.0442**	153 ± 18	172 ± 19	210 ± 19	256 ± 42
201531_at	ZFP36	zinc finger protein 36, C3H type, homolog	0.6731	**-0.0278**	**-0.0342**	-0.3656	0.3619	803 ± 167	737 ± 212	999 ± 204	1300 ± 334
211962_s_at	ZFP36L1	zinc finger protein 36, C3H type-like 1	0.2179	**-0.0104**	**-0.0346**	-0.1701	0.1437	1600 ± 135	1459 ± 191	2069 ± 235	2092 ± 339
211965_at	ZFP36L1	zinc finger protein 36, C3H type-like 1	**0.0088**	**-0.0101**	-0.1681	-0.1960	0.0972	321 ± 49	322 ± 37	453 ± 56	490 ± 79
201368_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	0.7238	**-0.0045**	-0.3152	-0.0679	0.1357	1486 ± 163	1660 ± 105	2105 ± 305	2219 ± 360
201369_s_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	**0.0119**	**0.0000**	0.1361	**-0.0031**	**0.0011**	177 ± 26	227 ± 23	238 ± 22	409 ± 66
214310_s_at	ZFPL1	zinc finger protein-like 1	**0.0041**	-0.0657	-0.3436	-0.2014	0.1842	105 ± 14	108 ± 15	118 ± 8	164 ± 36
206373_at	ZIC1	Zic family member 1	0.0963	**-0.0008**	0.2570	-0.1077	**0.0193**	687 ± 91	1023 ± 124	1439 ± 202	1568 ± 335
221842_s_at	ZNF131	zinc finger protein 131	**0.0011**	**-0.0492**	0.4043	-0.4449	**0.0060**	505 ± 42	574 ± 95	837 ± 65	677 ± 58

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
37254_at	ZNF133	zinc finger protein 133	**0.0157**	**-0.0360**	-0.2098	0.1119	0.0962	404 ± 13	387 ± 26	445 ± 31	500 ± 51
206240_s_at	ZNF136	zinc finger protein 136	**0.0039**	**0.0000**	**0.0098**	**-0.0071**	**0.0001**	248 ± 13	321 ± 14	323 ± 30	480 ± 48
207394_at	ZNF137	zinc finger protein 137	0.2121	**-0.0119**	0.3015	-0.1603	0.2581	191 ± 18	197 ± 14	210 ± 20	243 ± 21
205883_at	ZNF145	zinc finger protein 145	**0.0001**	**-0.0142**	-0.1180	0.1035	**0.0247**	1629 ± 100	1486 ± 174	2137 ± 318	2501 ± 292
203318_s_at	ZNF148	zinc finger protein 148	**0.0199**	-0.1740	**0.0544**	-0.2266	0.2069	910 ± 96	1146 ± 153	1250 ± 113	1332 ± 229
203602_s_at	ZNF151	zinc finger protein 151	0.0937	**-0.0387**	-0.2431	0.1093	0.0618	381 ± 23	372 ± 28	354 ± 24	504 ± 74
202173_s_at	ZNF161	zinc finger protein 161	0.0762	**-0.0023**	0.3347	**-0.0528**	**0.0296**	479 ± 56	618 ± 84	770 ± 84	799 ± 103
202171_at	ZNF161	zinc finger protein 161	0.3381	**-0.0428**	-0.3664	**-0.0544**	0.5698	528 ± 57	567 ± 78	591 ± 71	655 ± 48
202172_at	ZNF161	zinc finger protein 161	**0.0477**	**-0.0028**	-0.4341	-0.2214	**0.0338**	942 ± 91	1065 ± 133	1089 ± 42	1345 ± 79
205497_at	ZNF175	zinc finger protein 175	**0.0370**	-0.4099	0.4828	0.4024	0.4257	310 ± 28	335 ± 39	386 ± 15	341 ± 44
219495_s_at	ZNF180	zinc finger protein 180	0.9872	**-0.0375**	0.0582	-0.1923	0.3723	177 ± 14	184 ± 23	182 ± 12	228 ± 36
204234_s_at	ZNF195	zinc finger protein 195	**0.0390**	-0.4104	-0.1744	0.4659	0.5731	298 ± 20	318 ± 24	361 ± 19	356 ± 73
210282_at	ZNF198	zinc finger protein 198	-0.6918	**-0.0065**	-0.4328	**-0.0098**	0.3303	61 ± 8	59 ± 12	67 ± 6	86 ± 16
202778_s_at	ZNF198	zinc finger protein 198	**0.0119**	**-0.0137**	0.2370	**-0.0015**	**0.0046**	929 ± 42	961 ± 43	1140 ± 37	1030 ± 41
204327_s_at	ZNF202	zinc finger protein 202	**0.0068**	**-0.0290**	-0.4696	0.4615	0.1103	285 ± 15	322 ± 33	329 ± 27	403 ± 51
205437_at	ZNF211	zinc finger protein 211	0.0657	**-0.0412**	0.4292	-0.4840	0.2890	324 ± 17	349 ± 17	365 ± 29	417 ± 60
202423_at	ZNF220	zinc finger protein 220	**0.0064**	**-0.0099**	-0.2274	-0.3115	0.1206	1533 ± 121	1603 ± 87	1884 ± 160	1925 ± 160
219123_at	ZNF232	zinc finger protein 232	**0.0264**	-0.0696	0.2808	-0.3583	0.0920	322 ± 25	395 ± 54	357 ± 23	479 ± 69
47571_at	ZNF236	zinc finger protein 236	0.1353	**-0.0078**	0.4862	0.4037	**0.0314**	373 ± 26	362 ± 8	374 ± 13	504 ± 64
206744_s_at	ZNF237	zinc finger protein 237	**0.0516**	**-0.0092**	0.2369	-0.2584	**0.0063**	51 ± 12	47 ± 7	51 ± 7	116 ± 23
215948_x_at	ZNF237	zinc finger protein 237	**0.0393**	**-0.0042**	0.3199	**-0.0229**	**0.0185**	90 ± 8	101 ± 14	144 ± 9	133 ± 18
203247_s_at	ZNF24	zinc finger protein 24	**0.0036**	**-0.0204**	0.4647	**-0.0326**	0.1285	808 ± 84	951 ± 65	988 ± 90	1108 ± 105
206900_x_at	ZNF253	zinc finger protein 253	0.0950	**-0.0357**	**0.0014**	**-0.0328**	**0.0342**	203 ± 10	310 ± 33	283 ± 33	308 ± 30
206862_at	ZNF254	zinc finger protein 254	**0.0076**	-0.2379	0.1219	**-0.0074**	0.3517	60 ± 7	78 ± 10	76 ± 4	103 ± 35
202049_s_at	ZNF262	zinc finger protein 262	0.0945	**-0.0077**	-0.0884	0.4896	**0.0122**	324 ± 22	282 ± 19	295 ± 13	418 ± 48
205917_at	ZNF264	zinc finger protein 264	**0.0017**	**-0.0477**	0.0676	-0.2724	**0.0475**	490 ± 25	610 ± 59	647 ± 44	711 ± 80
209989_at	ZNF268	zinc finger protein 268	**0.0017**	**-0.0202**	**0.0242**	0.2564	0.0568	131 ± 11	165 ± 44	211 ± 20	238 ± 32
204937_s_at	ZNF274	zinc finger protein 274	0.3553	**-0.0252**	-0.2940	-0.3504	0.1133	646 ± 41	660 ± 51	622 ± 44	782 ± 52
215887_at	ZNF277	zinc finger protein 277	0.2193	**-0.0037**	**-0.0292**	0.3394	0.0562	300 ± 24	275 ± 24	330 ± 19	424 ± 63
209494_s_at	ZNF278	zinc finger protein 278	**0.0149**	**-0.0202**	-0.0578	0.4757	0.1088	341 ± 21	358 ± 28	408 ± 26	465 ± 64
205383_s_at	ZNF288	zinc finger protein 288	**0.0042**	**-0.0001**	0.2082	0.4022	**0.0012**	2784 ± 275	2856 ± 331	3603 ± 335	4851 ± 478
211975_at	ZNF289	zinc finger protein 289, ID1 regulated	**0.0399**	-0.7879	**0.0395**	-0.4225	0.8304	1223 ± 88	1336 ± 130	1362 ± 117	1331 ± 150
209538_at	ZNF32	zinc finger protein 32	0.6879	**-0.0458**	-0.2701	**-0.0232**	0.4415	418 ± 23	462 ± 85	507 ± 34	548 ± 89
37860_at	ZNF337	zinc finger protein 337	**0.0273**	-0.1559	-0.2914	0.2961	0.3364	563 ± 60	527 ± 65	632 ± 63	688 ± 69
214760_at	ZNF337	zinc finger protein 337	**0.0389**	-0.1521	0.1032	-0.4603	0.1407	534 ± 46	642 ± 99	730 ± 56	700 ± 54
219379_x_at	ZNF358	zinc finger protein 358	**0.0004**	**-0.0158**	0.3941	0.4081	**0.0189**	599 ± 27	678 ± 106	792 ± 62	1086 ± 185
206135_at	ZNF387	zinc finger protein 387	**0.0436**	-0.0790	-0.2317	-0.3400	0.3980	1062 ± 174	1094 ± 214	1379 ± 171	1416 ± 176
204139_x_at	ZNF42	zinc finger protein 42	**0.0297**	-0.0567	-0.3626	0.1590	**0.0134**	615 ± 61	475 ± 19	545 ± 69	842 ± 109
40569_at	ZNF42	zinc finger protein 42	0.0578	**-0.0342**	-0.1281	**0.0257**	**0.0091**	1031 ± 75	785 ± 51	982 ± 61	1469 ± 230
210336_x_at	ZNF42	zinc finger protein 42	**0.0104**	**-0.0313**	-0.3599	-0.1998	0.0591	506 ± 44	458 ± 40	540 ± 59	736 ± 112
206695_x_at	ZNF43	zinc finger protein 43	0.2268	**-0.0016**	0.1529	**-0.0241**	**0.0354**	228 ± 15	264 ± 17	272 ± 17	310 ± 24
205089_at	ZNF7	zinc finger protein 7	0.1458	**-0.0103**	-0.4816	**-0.0204**	0.0576	174 ± 11	185 ± 12	191 ± 11	226 ± 18

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
221645_s_at	ZNF83	zinc finger protein 83	0.6657	**-0.0478**	0.1521	**-0.0133**	0.1220	283 ± 27	394 ± 44	432 ± 51	388 ± 54
204453_at	ZNF84	zinc finger protein 84	**0.0001**	**-0.0192**	0.2051	**-0.0099**	0.0592	87 ± 10	96 ± 13	133 ± 19	138 ± 21
208472_at	ZNFN1A4	zinc finger protein, subfamily 1A, 4	**0.0335**	-0.1455	**0.0288**	**-0.0211**	0.3678	102 ± 11	138 ± 26	121 ± 12	149 ± 31
218548_x_at	ZSIG11	putative secreted protein ZSIG11	0.1565	**-0.0164**	0.0785	**-0.0459**	0.1738	177 ± 23	203 ± 17	207 ± 14	239 ± 20
	Downregulated										
213666_at	37870	septin 6	**-0.0230**	**0.0374**	-0.4156	-0.3670	**0.0001**	886 ± 50	881 ± 73	635 ± 68	467 ± 42
200902_at	37879	15 kDa selenoprotein	**-0.0197**	0.1069	-0.3704	-0.2702	0.2214	983 ± 59	990 ± 133	908 ± 119	712 ± 43
202169_s_at	AASDHPPT	aminoadipate-semiald. dehydrog.-phosphopantetheinyl transf.	**-0.0065**	**0.0039**	0.2772	0.3595	0.1701	3196 ± 304	2882 ± 381	2542 ± 245	2128 ± 449
209994_s_at	ABCB1	ATP-binding cassette, sub-family B , member 1	-0.0567	**0.0281**	-0.4331	-0.1299	**0.0161**	185 ± 13	141 ± 35	139 ± 24	63 ± 23
209993_at	ABCB1	ATP-binding cassette, sub-family B , member 1	**-0.0352**	**0.0005**	**0.0166**	0.4480	**0.0346**	323 ± 17	306 ± 16	259 ± 18	217 ± 44
203196_at	ABCC4	ATP-binding cassette, sub-family C , member 4	**-0.0395**	-0.9594	0.1817	**-0.0025**	0.7244	189 ± 19	208 ± 25	176 ± 23	168 ± 33
201873_s_at	ABCE1	ATP-binding cassette, sub-family E , member 1	**-0.0048**	**0.0115**	**-0.0127**	0.1005	**0.0000**	516 ± 33	619 ± 27	557 ± 20	367 ± 19
221669_s_at	ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	**-0.0041**	**0.0074**	0.2274	-0.3825	**0.0036**	518 ± 21	404 ± 30	387 ± 28	376 ± 30
205412_at	ACAT1	acetyl-Coenzyme A acetyltransferase 1	**-0.0004**	**0.0034**	-0.1477	0.2538	**0.0143**	1199 ± 62	1204 ± 102	917 ± 106	853 ± 51
206690_at	ACCN1	amiloride-sensitive cation channel 1, neuronal	-0.4668	**0.0239**	-0.2025	-0.4684	0.1186	608 ± 62	484 ± 114	558 ± 135	269 ± 81
205378_s_at	ACHE	acetylcholinesterase	-0.3873	**0.0453**	0.4731	0.3744	0.2221	179 ± 20	163 ± 33	160 ± 25	104 ± 25
200793_s_at	ACO2	aconitase 2, mitochondrial	**-0.0023**	**0.0009**	0.3895	0.4085	**0.0008**	3157 ± 201	2668 ± 344	1879 ± 142	2027 ± 185
201630_s_at	ACP1	acid phosphatase 1, soluble	**-0.0018**	**0.0018**	-0.3912	-0.1132	**0.0035**	1359 ± 109	1259 ± 116	982 ± 43	886 ± 63
217827_s_at	ACP33	acid cluster protein 33	**-0.0455**	0.2177	-0.1581	0.0626	0.3864	1323 ± 71	1294 ± 50	1128 ± 74	1186 ± 144
206013_s_at	ACTL6	actin-like 6	-0.0778	**0.0372**	-0.3814	0.4915	0.2907	205 ± 43	194 ± 62	119 ± 29	103 ± 44
208637_x_at	ACTN1	actinin, alpha 1	-0.2078	**0.0309**	-0.1291	**0.0461**	**0.0405**	903 ± 46	722 ± 42	770 ± 44	720 ± 63
200720_s_at	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha	-0.0866	**0.0210**	0.4297	0.2111	0.0647	573 ± 62	592 ± 47	581 ± 24	413 ± 24
202135_s_at	ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta	**-0.0104**	0.4508	**-0.0249**	0.2736	0.6529	967 ± 60	860 ± 83	886 ± 62	868 ± 73
200729_s_at	ACTR2	ARP2 actin-related protein 2 homolog	**-0.0195**	**0.0277**	-0.4331	-0.1967	**0.0019**	881 ± 64	852 ± 132	641 ± 78	376 ± 56
200728_at	ACTR2	ARP2 actin-related protein 2 homolog	**-0.0005**	**0.0137**	0.3870	-0.1555	0.0807	1130 ± 100	1120 ± 245	892 ± 52	651 ± 46
200996_at	ACTR3	ARP3 actin-related protein 3 homolog	**-0.0455**	0.2131	-0.3638	-0.2805	0.3749	1348 ± 130	1232 ± 245	941 ± 88	1004 ± 259
206833_s_at	ACYP2	acylphosphatase 2, muscle type	**-0.0180**	0.1385	-0.1283	0.4894	0.0966	971 ± 52	869 ± 47	769 ± 76	806 ± 48
218147_s_at	AD-017	glycosyltransferase AD-017	**-0.0327**	**0.0463**	-0.3830	0.3037	**0.0131**	282 ± 21	295 ± 27	224 ± 17	194 ± 21
202266_at	AD022	TRAF and TNF receptor-associated protein	**-0.0451**	**0.0326**	0.4807	-0.4890	0.2624	1243 ± 122	1185 ± 75	1053 ± 93	957 ± 129
205746_s_at	ADAM17	a disintegrin and metalloproteinase domain 17	**-0.0138**	**0.0227**	-0.4412	-0.3215	**0.0264**	139 ± 14	184 ± 20	127 ± 18	96 ± 21
206046_at	ADAM23	a disintegrin and metalloproteinase domain 23	-0.2007	**0.0081**	0.2818	0.2990	**0.0266**	501 ± 35	473 ± 51	350 ± 21	369 ± 53
213219_at	ADCY2	adenylate cyclase 2	-0.0656	**0.0064**	0.0836	0.1310	0.0996	763 ± 85	785 ± 147	608 ± 90	441 ± 86
204497_at	ADCY9	adenylate cyclase 9	**-0.0439**	0.0849	0.4070	0.2887	0.3834	884 ± 86	795 ± 76	697 ± 46	699 ± 137
208848_at	ADH5	alcohol dehydrogenase 5 , chi polypeptide	**-0.0002**	**0.0182**	-0.4369	0.1306	0.0743	1093 ± 93	1035 ± 124	820 ± 88	759 ± 94
204120_s_at	ADK	adenosine kinase	**-0.0269**	0.2225	-0.2766	-0.3496	0.3324	160 ± 15	151 ± 8	168 ± 18	124 ± 23
205891_at	ADORA2B	adenosine A2b receptor	**-0.0083**	**0.0066**	-0.2831	0.4497	**0.0179**	423 ± 11	396 ± 42	288 ± 20	305 ± 49
208644_at	ADPRT	ADP-ribosyltransferase polymerase)	**-0.0020**	0.1298	**-0.0196**	-0.4561	0.1858	1196 ± 67	1111 ± 70	1092 ± 77	970 ± 60
217729_s_at	AES	amino-terminal enhancer of split	-0.0963	**0.0162**	-0.3097	0.2767	**0.0310**	1037 ± 85	944 ± 63	1011 ± 82	722 ± 58
211071_s_at	AF1Q	ALL1-fused gene from chromosome 1q	**-0.0076**	**0.0058**	-0.2779	0.3669	0.0888	8001 ± 717	7003 ± 903	5924 ± 594	5054 ± 1146
219308_s_at	AK5	adenylate kinase 5	**-0.0069**	**0.0166**	-0.3194	0.3453	**0.0220**	6484 ± 741	4905 ± 604	4274 ± 512	3541 ± 708

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
203156_at	AKAP11	A kinase anchor protein 11	**-0.0012**	**0.0001**	0.2438	0.0977	0.0794	3946 ± 346	3433 ± 587	2904 ± 249	2523 ± 392
210517_s_at	AKAP12	A kinase anchor protein 12	**-0.0186**	**0.0063**	**0.0503**	-0.3574	**0.0003**	1105 ± 80	1081 ± 61	989 ± 100	596 ± 48
202759_s_at	AKAP2	A kinase anchor protein 2	**-0.0251**	0.0691	**-0.0136**	-0.3125	0.2230	1219 ± 79	1193 ± 83	1141 ± 118	928 ± 129
201425_at	ALDH2	aldehyde dehydrogenase 2 family	-0.0615	**0.0161**	**-0.0228**	0.0997	**0.0039**	6579 ± 227	5151 ± 261	5117 ± 384	4890 ± 401
203608_at	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	-0.0816	**0.0336**	-0.3654	0.1285	0.1291	1539 ± 160	1230 ± 124	1319 ± 141	1025 ± 162
202022_at	ALDOC	aldolase C, fructose-bisphosphate	**-0.0254**	**0.0221**	-0.3021	-0.2986	**0.0162**	9235 ± 722	1254 ± 1578	118 ± 1163	5884 ± 497
218694_at	ALEX1	ALEX1 protein	**-0.0168**	**0.0163**	-0.3278	0.4239	0.0691	1010 ± 96	941 ± 101	740 ± 60	701 ± 113
204174_at	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	**-0.0089**	0.5289	**-0.0055**	0.3400	0.2616	771 ± 118	622 ± 75	475 ± 73	661 ± 144
202203_s_at	AMFR	autocrine motility factor receptor	**-0.0407**	**0.0203**	-0.0615	0.1140	0.0561	727 ± 104	657 ± 169	466 ± 91	300 ± 78
202811_at	AMSH	associated molecule with the SH3 domain of STAM	**-0.0444**	0.9850	0.3239	0.1350	0.6043	892 ± 36	871 ± 37	789 ± 57	876 ± 96
208498_s_at	AMY1A	amylase, alpha 1A; salivary	**-0.0232**	0.0582	-0.4186	-0.3594	0.2628	319 ± 32	348 ± 27	284 ± 23	262 ± 39
204727_at	AND-1	AND-1 protein	-0.1046	**0.0354**	-0.1270	0.0735	0.2635	56 ± 8	42 ± 6	46 ± 11	32 ± 5
209442_x_at	ANK3	ankyrin 3, node of Ranvier	-0.0607	**0.0314**	**0.0408**	0.2900	0.0931	1076 ± 39	1167 ± 82	1011 ± 55	939 ± 60
209860_s_at	ANXA7	annexin A7	**-0.0265**	0.1204	-0.3583	-0.1762	0.2317	1257 ± 99	1232 ± 145	1024 ± 58	1010 ± 109
200615_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit	**-0.0012**	**0.0001**	-0.4392	**0.0096**	**0.0413**	916 ± 42	763 ± 87	716 ± 49	677 ± 71
200613_at	AP2M1	adaptor-related protein complex 2, mu 1 subunit	-0.1009	**0.0229**	-0.4039	-0.1683	**0.0251**	2336 ± 116	2446 ± 364	2352 ± 185	1423 ± 209
208074_s_at	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	-0.0822	**0.0310**	-0.2196	0.4482	0.2109	1045 ± 91	992 ± 164	929 ± 37	724 ± 118
205678_at	AP3B2	adaptor-related protein complex 3, beta 2 subunit	-0.0587	**0.0056**	0.3870	0.1584	0.0674	1011 ± 132	778 ± 40	727 ± 87	634 ± 87
202442_at	AP3S1	adaptor-related protein complex 3, sigma 1 subunit	**-0.0078**	**0.0026**	0.4166	0.3811	**0.0011**	4853 ± 235	4193 ± 84	3928 ± 179	3611 ± 226
210277_at	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	**-0.0204**	0.1534	-0.1719	-0.3086	0.2052	126 ± 12	100 ± 17	110 ± 13	82 ± 17
203008_x_at	APACD	ATP binding protein associated with cell differentiation	**-0.0080**	0.1172	-0.3643	-0.3679	0.2875	674 ± 78	607 ± 98	470 ± 38	482 ± 111
211758_x_at	APACD	ATP binding protein associated with cell differentiation	**-0.0271**	**0.0094**	-0.3485	0.1203	**0.0110**	945 ± 98	781 ± 108	660 ± 60	513 ± 38
209871_s_at	APBA2	amyloid beta precursor protein-binding, family A, member 2	**-0.0111**	**0.0003**	-0.1928	**0.0461**	**0.0308**	4088 ± 350	3329 ± 423	2735 ± 284	2915 ± 277
203527_s_at	APC	adenomatosis polyposis coli	**-0.0070**	**0.0077**	-0.4214	-0.3631	**0.0021**	637 ± 20	511 ± 73	472 ± 57	241 ± 95
210027_s_at	APEX	APEX nuclease	**-0.0207**	**0.0185**	-0.2345	0.4053	**0.0246**	1413 ± 86	1505 ± 114	1246 ± 79	1100 ± 53
205543_at	APG-1	heat shock protein	**-0.0062**	**0.0126**	-0.0603	0.3192	**0.0155**	285 ± 25	223 ± 27	207 ± 21	164 ± 19
214875_x_at	APLP2	amyloid beta precursor-like protein 2	**-0.0508**	**0.0339**	0.4931	0.2839	0.0861	436 ± 51	390 ± 53	275 ± 43	320 ± 38
208703_s_at	APLP2	amyloid beta precursor-like protein 2	**-0.0511**	**0.0390**	-0.2066	-0.2359	0.0661	2060 ± 288	1965 ± 317	1960 ± 155	1076 ± 311
208704_x_at	APLP2	amyloid beta precursor-like protein 2	**-0.0322**	**0.0414**	-0.2457	-0.3323	**0.0334**	4958 ± 387	4375 ± 267	4473 ± 260	3468 ± 387
208248_x_at	APLP2	amyloid beta precursor-like protein 2	**-0.0075**	**0.0020**	**-0.0526**	0.0889	**0.0111**	5472 ± 321	5486 ± 288	5755 ± 212	4263 ± 377
214953_s_at	APP	amyloid beta precursor protein	**-0.0484**	0.5727	-0.1783	0.4867	0.2791	4578 ± 289	4597 ± 499	5130 ± 577	3717 ± 578
202268_s_at	APPBP1	amyloid beta precursor protein binding protein 1, 59kDa	**-0.0159**	0.5330	-0.1010	-0.4897	0.6402	937 ± 46	840 ± 69	875 ± 58	816 ± 113
201176_s_at	ARCN1	archain 1	**-0.0338**	0.0587	**-0.0229**	-0.4217	0.1365	1095 ± 51	1044 ± 110	948 ± 44	814 ± 130
200065_s_at	ARF1	ADP-ribosylation factor 1	**-0.0030**	**0.0003**	-0.3908	**0.0486**	**0.0080**	5134 ± 329	4211 ± 323	4202 ± 316	3330 ± 377
200734_s_at	ARF3	ADP-ribosylation factor 3	**-0.0363**	**0.0379**	-0.2526	0.2591	**0.0072**	6169 ± 535	5151 ± 427	4503 ± 419	3636 ± 524
200011_s_at	ARF3	ADP-ribosylation factor 3	**-0.0040**	**0.0032**	-0.3809	0.4246	0.2742	4470 ± 387	4035 ± 478	3904 ± 387	3305 ± 405
201097_s_at	ARF4	ADP-ribosylation factor 4	**-0.0249**	0.0967	0.4321	-0.3210	0.1529	2597 ± 175	2907 ± 90	2232 ± 76	2277 ± 361
201526_at	ARF5	ADP-ribosylation factor 5	-0.1202	**0.0013**	0.3219	0.2452	**0.0238**	1067 ± 97	1088 ± 100	965 ± 92	675 ± 90
218098_at	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2	**-0.0464**	**0.0005**	-0.3888	0.3052	**0.0224**	1113 ± 71	1204 ± 65	991 ± 77	808 ± 109

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
204288_s_at	ARGBP2	Arg/Abl-interacting protein ArgBP2	**-0.0372**	**0.0460**	0.4211	0.2355	**0.0037**	666 ± 64	588 ± 45	607 ± 72	330 ± 41
218501_at	ARHGEF3	Rho guanine nucleotide exchange factor 3	**-0.0087**	**0.0047**	-0.2544	0.0844	0.1657	1997 ± 266	1700 ± 177	1353 ± 184	1370 ± 275
211891_s_at	ARHGEF4	Rho guanine nucleotide exchange factor 4	-0.2452	**0.0486**	0.3604	**0.0476**	0.5472	461 ± 58	421 ± 40	406 ± 45	364 ± 33
203264_s_at	ARHGEF9	Cdc42 guanine nucleotide exchange factor 9	**-0.0080**	**0.0398**	-0.0682	0.1120	0.0903	2514 ± 265	2053 ± 361	1782 ± 211	1483 ± 325
215506_s_at	ARHI	ras homolog gene family, member I	-0.0710	**0.0287**	-0.0997	0.4589	0.1225	154 ± 18	132 ± 8	115 ± 21	102 ± 10
201228_s_at	ARIH2	ariadne homolog 2	**-0.0154**	0.1633	0.1764	-0.3651	0.0896	166 ± 13	196 ± 23	135 ± 8	144 ± 20
201659_s_at	ARL1	ADP-ribosylation factor-like 1	**-0.0294**	**0.0387**	-0.2117	0.2681	**0.0280**	361 ± 21	309 ± 31	251 ± 19	278 ± 31
202206_at	ARL7	ADP-ribosylation factor-like 7	**-0.0232**	**0.0060**	0.4689	0.2053	0.0985	451 ± 60	365 ± 53	291 ± 41	305 ± 33
202986_at	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	**-0.0216**	**0.0180**	0.1596	-0.4914	**0.0023**	2960 ± 138	2340 ± 220	2708 ± 198	1963 ± 93
218868_at	ARP3BETA	actin-related protein 3-beta	-0.1288	**0.0209**	0.3049	0.1522	0.0718	782 ± 141	520 ± 69	466 ± 47	452 ± 80
200950_at	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	**-0.0223**	0.0982	0.4727	0.2339	0.3586	1375 ± 147	1270 ± 182	992 ± 69	1047 ± 279
208679_s_at	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	**-0.0318**	0.0553	-0.4284	0.3142	0.2933	1696 ± 185	1625 ± 267	1311 ± 101	1220 ± 236
213513_x_at	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	**-0.0425**	**0.0321**	0.3714	-0.2868	0.0922	3327 ± 350	3014 ± 187	2846 ± 138	2398 ± 213
208736_at	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	**-0.0400**	**0.0210**	-0.4489	0.4450	0.1092	1115 ± 100	1082 ± 137	920 ± 73	760 ± 124
211963_s_at	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	**-0.0202**	0.6260	0.1618	0.2179	0.7378	1601 ± 65	1695 ± 82	1526 ± 141	1562 ± 129
221482_s_at	ARPP-19	cyclic AMP phosphoprotein, 19 kD	-0.0612	**0.0090**	-0.4479	0.4854	**0.0512**	2398 ± 315	2248 ± 244	2087 ± 163	1459 ± 110
217776_at	ARSDR1	androgen-regulated short-chain dehydrogenase/reductase 1	**-0.0167**	0.0941	0.4113	-0.4799	0.3016	1893 ± 177	1817 ± 207	1558 ± 136	1426 ± 256
204742_s_at	AS3	androgen-induced prostate proliferative shutoff associated	**-0.0354**	**0.0134**	0.3775	-0.3333	0.1775	694 ± 91	643 ± 112	531 ± 48	444 ± 74
213902_at	ASAH1	N-acylsphingosine amidohydrolase 1	-0.0909	**0.0061**	0.2001	0.1464	**0.0434**	1133 ± 135	919 ± 40	818 ± 73	703 ± 120
209517_s_at	ASH2L	ash2 -like	**-0.0055**	0.0721	0.3679	0.4077	0.0913	1287 ± 88	1330 ± 58	1041 ± 96	1141 ± 91
36554_at	ASMTL	acetylserotonin O-methyltransferase-like	**-0.0021**	**0.0017**	**-0.0265**	0.2221	**0.0458**	275 ± 22	276 ± 36	249 ± 25	172 ± 17
202024_at	ASNA1	arsA arsenite transporter, ATP-binding, homolog 1	**-0.0422**	0.0578	-0.2595	-0.1976	0.1275	638 ± 64	674 ± 83	628 ± 45	445 ± 82
209135_at	ASPH	aspartate beta-hydroxylase	**-0.0213**	0.2701	-0.3514	-0.1039	0.3476	929 ± 80	938 ± 80	966 ± 103	747 ± 92
210896_s_at	ASPH	aspartate beta-hydroxylase	**-0.0027**	**0.0014**	-0.3201	0.3528	**0.0005**	561 ± 45	350 ± 40	374 ± 51	246 ± 20
213197_at	ASTN	astrotactin	**-0.0197**	**0.0488**	**-0.0069**	0.1614	**0.0133**	1692 ± 157	1448 ± 203	1238 ± 168	888 ± 118
208758_at	ATIC	IMP cyclohydrolase	**-0.0177**	0.2268	**-0.0028**	0.1027	**0.0220**	1080 ± 27	987 ± 65	748 ± 99	981 ± 87
203295_s_at	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	-0.4108	**0.0472**	**0.0293**	-0.0678	0.0707	3247 ± 179	3350 ± 295	3451 ± 224	2494 ± 274
201243_s_at	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	**-0.0223**	0.2349	-0.2176	-0.2624	0.4412	10569 ± 551	9972 ± 1011	10155 ± 496	8878 ± 930
209186_at	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	**-0.0086**	**0.0040**	0.3046	0.4770	**0.0508**	3230 ± 62	2685 ± 287	2553 ± 162	2404 ± 294
215716_s_at	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	**-0.0241**	**0.0005**	0.2534	0.2047	**0.0342**	1788 ± 270	1625 ± 233	1154 ± 91	893 ± 232
216120_s_at	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	-0.1357	**0.0147**	-0.3664	-0.3966	**0.0083**	268 ± 25	231 ± 25	267 ± 20	159 ± 21
204685_s_at	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	**-0.0066**	**0.0022**	-0.3724	0.4763	**0.0151**	2397 ± 264	2403 ± 254	2013 ± 304	1201 ± 48
211137_s_at	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	**-0.0489**	0.2059	**0.0257**	-0.1215	0.2042	655 ± 48	733 ± 41	629 ± 32	576 ± 69
213738_s_at	ATP5A1	ATP synthase, mitochondrial F1 alpha 1	**-0.0098**	**0.0276**	-0.2752	0.3967	**0.0135**	4827 ± 452	4315 ± 520	3405 ± 479	2586 ± 329
201322_at	ATP5B	ATP synthase, mitochondrial F1 beta	**-0.0012**	**0.0016**	0.4908	0.3063	0.0944	3478 ± 372	3040 ± 478	2251 ± 281	2151 ± 572
213366_x_at	ATP5C1	ATP synthase, mitochondrial F1 gamma 1	**-0.0009**	**0.0018**	-0.3409	0.2362	**0.0109**	3990 ± 407	3464 ± 431	2580 ± 224	2253 ± 431
205711_x_at	ATP5C1	ATP synthase, mitochondrial F1 gamma 1	**-0.0018**	**0.0071**	0.3667	0.3274	**0.0066**	3292 ± 302	2777 ± 293	2034 ± 171	1969 ± 369
208870_x_at	ATP5C1	ATP synthase, mitochondrial F1 gamma 1	**-0.0235**	**0.0145**	0.2506	-0.2572	**0.0284**	4060 ± 484	3868 ± 438	2572 ± 192	2741 ± 450
217801_at	ATP5E	ATP synthase, mitochondrial F1 epsilon	**-0.0084**	**0.0391**	-0.4077	0.1998	**0.0327**	5191 ± 250	4834 ± 452	4800 ± 274	3806 ± 307

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
211755_s_at	ATP5F1	ATP synthase, mitochondrial F0 b 1	**-0.0175**	**0.0355**	0.1719	-0.4570	0.0996	3548 ± 347	2974 ± 389	2407 ± 251	2435 ± 482
207507_s_at	ATP5G3	ATP synthase, mitochondrial F0 c 3	**-0.0236**	0.0938	-0.2152	-0.4837	0.2957	1998 ± 237	1706 ± 304	1337 ± 216	1335 ± 376
207508_at	ATP5G3	ATP synthase, mitochondrial F0 c 3	**-0.0133**	**0.0201**	-0.4996	0.2836	0.0730	2559 ± 328	2249 ± 262	1626 ± 211	1695 ± 306
210149_s_at	ATP5H	ATP synthase, mitochondrial F0 d	**-0.0097**	**0.0254**	-0.1686	0.2712	0.0551	4108 ± 577	3508 ± 548	2431 ± 258	2522 ± 487
202325_s_at	ATP5J	ATP synthase, mitochondrial F0 F6	**-0.0131**	**0.0098**	-0.2612	0.3466	0.0874	2953 ± 210	2575 ± 296	2501 ± 93	1970 ± 389
202961_s_at	ATP5J2	ATP synthase, mitochondrial F0 f 2	**-0.0035**	**0.0049**	-0.3091	-0.4530	0.0980	2930 ± 213	2729 ± 380	2246 ± 277	1895 ± 382
210453_x_at	ATP5L	ATP synthase, mitochondrial F0 g	**-0.0291**	**0.0504**	-0.4626	0.2114	0.1852	2666 ± 259	2430 ± 290	1864 ± 239	1946 ± 417
208746_x_at	ATP5L	ATP synthase, mitochondrial F0 g	**-0.0443**	0.0778	-0.3199	0.1824	0.1672	2449 ± 251	2149 ± 323	1618 ± 157	1817 ± 386
208745_at	ATP5L	ATP synthase, mitochondrial F0 g	**-0.0183**	**0.0054**	-0.2001	0.3686	**0.0379**	1204 ± 87	1193 ± 157	903 ± 128	743 ± 132
207573_x_at	ATP5L	ATP synthase, mitochondrial F0 g	**-0.0049**	**0.0097**	-0.3982	0.3684	**0.0470**	1768 ± 123	1686 ± 274	1364 ± 140	1045 ± 152
200818_at	ATP5O	ATP synthase, mitochondrial F1 O	**-0.0224**	**0.0239**	0.4487	0.1979	0.0717	3259 ± 265	2919 ± 281	2509 ± 230	2123 ± 448
207809_s_at	ATP6IP1	ATPase, H+ transporting, lysosomal interacting protein 1	**-0.0538**	**0.0238**	-0.2033	0.0852	0.0640	2289 ± 324	1795 ± 272	1395 ± 177	1469 ± 126
201443_s_at	ATP6IP2	ATPase, H+ transporting, lysosomal interacting protein 2	**-0.0097**	0.0843	-0.4499	0.3486	0.2785	3605 ± 404	3098 ± 467	2734 ± 269	2553 ± 497
201444_s_at	ATP6IP2	ATPase, H+ transporting, lysosomal interacting protein 2	**-0.0044**	**0.0025**	-0.1328	0.1932	0.0732	1106 ± 231	873 ± 154	545 ± 80	556 ± 161
36994_at	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	**-0.0333**	0.1039	-0.2408	0.4923	0.2577	6835 ± 564	6391 ± 715	5204 ± 323	5395 ± 965
201971_s_at	ATP6V1A1	ATPase, lysosomal V1 A 1	**-0.0446**	0.0933	-0.2416	-0.4302	0.1629	168 ± 38	162 ± 43	73 ± 14	113 ± 33
202872_at	ATP6V1C1	ATPase, lysosomal V1 C 1	-0.1005	**0.0013**	-0.3820	-0.3411	**0.0143**	850 ± 66	858 ± 20	712 ± 43	595 ± 80
208898_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	**-0.0167**	**0.0052**	-0.1532	0.0754	**0.0036**	3577 ± 314	2604 ± 363	2232 ± 250	1974 ± 279
208899_x_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	**-0.0056**	**0.0016**	-0.4344	0.1406	**0.0094**	1449 ± 142	1160 ± 177	813 ± 81	920 ± 133
208678_at	ATP6V1E1	ATPase, lysosomal V1 E 1	**-0.0392**	**0.0232**	-0.1981	-0.2157	**0.0220**	3167 ± 409	2667 ± 438	2000 ± 163	1677 ± 307
201527_at	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	**-0.0079**	**0.0009**	0.4995	0.2629	0.0629	2988 ± 209	3036 ± 347	2711 ± 260	2007 ± 314
214762_at	ATP6V1G2	ATPase, lysosomal V1 G 2	**-0.0067**	**0.0020**	-0.4839	0.2505	**0.0068**	3258 ± 540	2582 ± 468	1551 ± 245	1192 ± 219
221504_s_at	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	**-0.0002**	**0.0003**	-0.0948	0.1710	**0.0289**	2552 ± 336	2233 ± 475	1589 ± 185	1170 ± 305
219659_at	ATP8A2	ATPase, aminophospholipid transporter-like, I 8A 2	-0.0779	**0.0336**	0.4087	-0.3513	0.1941	842 ± 106	768 ± 108	641 ± 74	571 ± 73
209903_s_at	ATR	ataxia telangiectasia and Rad3 related	**-0.0244**	0.0957	-0.2102	0.3627	0.1287	917 ± 77	786 ± 99	700 ± 28	701 ± 68
212517_at	ATRN	attractin	**-0.0373**	**0.0235**	-0.1717	0.1017	**0.0024**	1123 ± 41	1052 ± 69	901 ± 46	764 ± 93
208861_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	**-0.0206**	0.1848	-0.3421	-0.1373	0.4447	3094 ± 118	2988 ± 217	2946 ± 139	2681 ± 240
205052_at	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	**-0.0069**	0.0843	-0.4071	0.3211	0.3314	858 ± 95	795 ± 72	733 ± 66	657 ± 70
202686_s_at	AXL	AXL receptor tyrosine kinase	**-0.0344**	0.6565	-0.1005	-0.2097	0.7703	697 ± 68	735 ± 40	685 ± 76	630 ± 75
216231_s_at	B2M	beta-2-microglobulin	**-0.0485**	0.2655	-0.1112	-0.3310	0.4688	7997 ± 1038	6813 ± 1385	5780 ± 1676	5051 ± 961
217452_s_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 2	-0.1651	**0.0332**	-0.4916	-0.1578	**0.0209**	378 ± 48	395 ± 69	415 ± 39	189 ± 26
206233_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase 6	-0.0624	**0.0076**	-0.2410	0.4600	**0.0452**	428 ± 60	342 ± 80	347 ± 45	181 ± 42
215728_s_at	BACH	brain acyl-CoA hydrolase	**-0.0326**	0.3261	-0.4015	-0.3714	0.1547	223 ± 32	212 ± 38	129 ± 18	173 ± 36
202985_s_at	BAG5	BCL2-associated athanogene 5	**-0.0406**	**0.0034**	0.4526	**0.0301**	0.1562	1489 ± 81	1355 ± 86	1379 ± 26	1250 ± 75
204966_at	BAI2	brain-specific angiogenesis inhibitor 2	**-0.0156**	**0.0024**	0.3747	0.2132	**0.0029**	2809 ± 219	2051 ± 120	2491 ± 244	1672 ± 149
205638_at	BAI3	brain-specific angiogenesis inhibitor 3	**-0.0339**	**0.0293**	-0.1654	0.4614	**0.0291**	2137 ± 289	1773 ± 187	1474 ± 173	1199 ± 145
205084_at	BAP29	B-cell receptor-associated protein BAP29	-0.5328	**0.0442**	-0.4716	-0.3510	0.0891	148 ± 19	137 ± 20	146 ± 10	87 ± 19
213318_s_at	BAT3	HLA-B associated transcript 3	-0.0874	**0.0288**	-0.4008	-0.2591	**0.0357**	1678 ± 137	1814 ± 88	1683 ± 102	1302 ± 116
211703_s_at	BBP	beta-amyloid binding protein precursor	**-0.0158**	0.1296	-0.3977	-0.2633	0.1250	388 ± 35	440 ± 24	283 ± 47	320 ± 66

Probe set	**Name**	**Description**	**NFT$_{O}$**	**MMSE$_{O}$**	**NFT$_{I}$**	**MMSE$_{I}$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
202121_s_at	BC-2	putative breast adenocarcinoma marker	-0.1174	**0.0225**	0.2527	-0.1914	0.0719	955 ± 74	945 ± 119	871 ± 93	620 ± 55
219107_at	BCAN	chondroitin sulfate proteoglycan BEHAB/brevican	**-0.0120**	**0.0013**	0.2249	0.1422	0.0932	615 ± 106	640 ± 32	457 ± 78	337 ± 96
203053_at	BCAS2	breast carcinoma amplified sequence 2	-0.1778	**0.0458**	-0.4704	0.3028	0.0751	778 ± 106	703 ± 80	461 ± 32	570 ± 100
219497_s_at	BCL11A	B-cell CLL/lymphoma 11A	**-0.0336**	**0.0150**	-0.3391	0.1646	**0.0178**	718 ± 94	570 ± 58	512 ± 95	328 ± 46
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B	**-0.0127**	**0.0281**	0.1457	0.4365	0.0807	1046 ± 138	786 ± 122	767 ± 119	581 ± 97
202518_at	BCL7B	B-cell CLL/lymphoma 7B	-0.2025	**0.0406**	0.2065	0.3203	0.2600	823 ± 86	795 ± 82	676 ± 83	613 ± 77
208946_s_at	BECN1	beclin 1	**-0.0084**	**0.0030**	-0.2274	0.1509	0.0975	546 ± 40	581 ± 43	531 ± 42	415 ± 46
202710_at	BET1	BET1 homolog	-0.0824	**0.0328**	0.2249	0.0656	0.2736	661 ± 40	608 ± 32	584 ± 67	520 ± 55
218332_at	BEX1	brain expressed, X-linked 1	**-0.0023**	**0.0202**	-0.2446	0.2807	0.0574	7804 ± 510	7299 ± 721	5861 ± 599	5633 ± 699
201170_s_at	BHLHB2	basic helix-loop-helix domain containing, class B, 2	**-0.0048**	**0.0136**	-0.2592	0.4721	0.0723	2077 ± 211	2024 ± 245	1613 ± 131	1365 ± 239
221702_s_at	BLP2	BBP-like protein 2	**-0.0031**	**0.0008**	-0.2221	0.1544	0.0623	3015 ± 303	2599 ± 328	2211 ± 129	1969 ± 330
203840_at	BLZF1	basic leucine zipper nuclear factor 1	**-0.0341**	0.1739	-0.4715	**-0.0096**	0.1845	165 ± 14	147 ± 30	131 ± 18	99 ± 21
32088_at	BLZF1	basic leucine zipper nuclear factor 1	**-0.0120**	**0.0099**	0.4173	0.4551	**0.0038**	85 ± 9	67 ± 6	63 ± 8	40 ± 8
201849_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	**-0.0221**	**0.0241**	0.4302	0.0848	**0.0326**	4048 ± 394	3440 ± 384	3065 ± 119	2666 ± 268
221478_at	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	**-0.0455**	0.0866	0.3862	-0.1853	**0.0537**	2755 ± 131	3236 ± 153	2674 ± 284	2335 ± 126
205550_s_at	BRE	brain and reproductive organ-expressed	**-0.0138**	**0.0120**	-0.3178	-0.4768	0.2589	845 ± 54	808 ± 80	697 ± 47	725 ± 60
208906_at	BSCL2	Bernardinelli-Seip congenital lipodystrophy 2	**-0.0312**	**0.0461**	-0.2136	0.3797	0.0772	2986 ± 347	2493 ± 611	2097 ± 389	1370 ± 366
208677_s_at	BSG	basigin	-0.0571	**0.0295**	-0.1860	0.3601	0.1526	789 ± 108	782 ± 105	716 ± 69	484 ± 112
204586_at	BSN	bassoon	**-0.0234**	**0.0005**	0.3272	0.2580	0.1293	990 ± 141	729 ± 114	708 ± 98	593 ± 113
203944_x_at	BTN2A1	butyrophilin, subfamily 2, member A1	**-0.0240**	0.6333	-0.1731	0.2806	0.5435	500 ± 26	489 ± 30	437 ± 19	479 ± 54
218048_at	BUP	BUP protein	**-0.0261**	0.1184	-0.4689	-0.2383	0.2276	861 ± 54	930 ± 72	775 ± 27	769 ± 76
215241_at	C11orf25	chromosome 11 open reading frame 25	**-0.0145**	**0.0149**	0.0598	**-0.0039**	**0.0095**	1945 ± 278	1857 ± 312	1471 ± 258	599 ± 120
219099_at	C12orf5	chromosome 12 open reading frame 5	**-0.0068**	**0.0031**	-0.3120	0.1009	**0.0381**	234 ± 11	250 ± 15	229 ± 19	175 ± 23
202279_at	C14orf2	chromosome 14 open reading frame 2	**-0.0058**	**0.0044**	-0.4460	0.1046	**0.0128**	3699 ± 375	2787 ± 349	2540 ± 211	2207 ± 282
210532_s_at	C14orf2	chromosome 14 open reading frame 2	**-0.0109**	**0.0036**	0.4404	0.1401	**0.0353**	6081 ± 629	5182 ± 647	4197 ± 390	3708 ± 671
201491_at	C14orf3	chromosome 14 open reading frame 3	**-0.0027**	0.0614	**-0.0040**	0.2347	**0.0385**	1439 ± 66	1180 ± 124	1136 ± 74	1008 ± 124
209755_at	C1orf15	chromosome 1 open reading frame 15	**-0.0208**	**0.0251**	-0.4381	-0.4971	**0.0140**	1460 ± 221	1155 ± 161	741 ± 76	772 ± 136
221272_s_at	C1orf21	chromosome 1 open reading frame 21	**-0.0126**	**0.0054**	0.2226	-0.3614	0.1142	769 ± 28	781 ± 66	731 ± 45	607 ± 57
219443_at	C20orf13	chromosome 20 open reading frame 13	-0.1798	**0.0281**	0.3201	-0.4428	0.0706	258 ± 30	217 ± 32	172 ± 7	172 ± 25
217935_s_at	C20orf44	chromosome 20 open reading frame 44	-0.1049	**0.0092**	0.3013	0.2834	0.0892	951 ± 90	919 ± 56	793 ± 42	717 ± 46
218359_at	C20orf98	chromosome 20 open reading frame 98	-0.5784	**0.0478**	0.3913	0.4624	0.0705	992 ± 131	1088 ± 169	1142 ± 135	590 ± 166
206436_at	C22orf1	chromosome 22 open reading frame 1	-0.2720	**0.0362**	0.0949	0.4410	0.1990	637 ± 43	710 ± 98	621 ± 62	489 ± 73
209418_s_at	C22orf19	chromosome 22 open reading frame 19	**-0.0034**	0.3665	0.3584	0.0707	0.5568	252 ± 17	228 ± 8	213 ± 25	211 ± 36
202614_at	C4orf1	chromosome 4 open reading frame 1	**-0.0050**	**0.0017**	0.2290	-0.3963	**0.0230**	1240 ± 143	1158 ± 144	1021 ± 92	663 ± 65
209829_at	C6orf32	chromosome 6 open reading frame 32	**-0.0356**	**0.0495**	0.4126	-0.4550	**0.0125**	646 ± 49	639 ± 88	530 ± 57	357 ± 53
202241_at	C8FW	phosphoprotein regulated by mitogenic pathways	**-0.0085**	**0.0369**	0.1424	**0.0373**	0.1839	552 ± 48	489 ± 38	462 ± 39	426 ± 18
204480_s_at	C9orf16	chromosome 9 open reading frame 16	**-0.0422**	0.0659	0.2070	**0.0500**	0.4089	3883 ± 324	4271 ± 733	3433 ± 509	3056 ± 441
222165_x_at	C9orf16	chromosome 9 open reading frame 16	**-0.0444**	**0.0110**	0.1698	0.3104	0.3484	1259 ± 123	1250 ± 136	1089 ± 162	914 ± 176
209726_at	CA11	carbonic anhydrase XI	**-0.0369**	**0.0053**	-0.3455	0.4228	**0.0003**	2445 ± 151	2410 ± 219	2809 ± 227	1500 ± 106

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
208321_s_at	CABP1	calcium binding protein 1	**-0.0527**	**0.0163**	-0.2668	0.4356	0.1159	1148 ± 167	891 ± 104	838 ± 183	575 ± 132
210181_s_at	CABP1	calcium binding protein 1	**-0.0232**	**0.0251**	-0.2262	0.3577	**0.0435**	539 ± 130	478 ± 110	274 ± 59	149 ± 28
207776_s_at	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	**-0.0469**	**0.0500**	-0.4754	0.3215	0.0952	342 ± 40	283 ± 50	235 ± 25	227 ± 18
213714_at	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	**-0.0011**	**0.0002**	-0.3438	0.4533	0.0965	699 ± 135	447 ± 98	373 ± 75	375 ± 87
206384_at	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	**-0.0065**	**0.0008**	0.0601	-0.4690	**0.0009**	1378 ± 179	1050 ± 144	889 ± 134	396 ± 91
204814_at	CADPS	Ca2+-dependent activator protein for secretion	**-0.0307**	**0.0525**	**0.0209**	**-0.0307**	**0.0009**	465 ± 16	625 ± 43	405 ± 49	419 ± 16
209563_x_at	CALM1	calmodulin 1	-0.0799	**0.0328**	-0.3477	0.4814	**0.0483**	9478 ± 582	8506 ± 417	6800 ± 613	7797 ± 1024
200622_x_at	CALM3	calmodulin 3	**-0.0071**	**0.0003**	-0.4056	0.1882	**0.0068**	1472 ± 147	1607 ± 210	1149 ± 54	905 ± 93
212952_at	CALR	calreticulin	**-0.0412**	0.2092	-0.3119	-0.2369	0.4102	780 ± 96	748 ± 65	676 ± 44	612 ± 68
217128_s_at	CAMK1G	calcium/calmodulin-dependent protein kinase IG	**-0.0193**	0.0825	0.3546	-0.2861	0.0804	343 ± 50	486 ± 98	314 ± 46	251 ± 31
215161_at	CAMK1G	calcium/calmodulin-dependent protein kinase IG	**-0.0081**	**0.0127**	-0.2239	0.1883	**0.0030**	527 ± 98	367 ± 88	255 ± 65	49 ± 11
213108_at	CAMK2A	calcium/calmodulin-dependent protein kinase II alpha	**-0.0149**	**0.0028**	0.4553	**0.0438**	0.0930	5507 ± 582	4530 ± 733	4188 ± 944	2766 ± 316
212252_at	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	**-0.0041**	**0.0200**	-0.2774	0.3730	0.0569	889 ± 47	825 ± 31	778 ± 96	626 ± 56
200625_s_at	CAP	adenylyl cyclase-associated protein	**-0.0379**	**0.0089**	0.3239	0.2932	**0.0193**	3145 ± 172	2707 ± 149	2605 ± 77	2415 ± 221
212551_at	CAP2	adenylyl cyclase-associated protein 2	-0.1058	**0.0282**	0.2603	0.2038	0.1583	1894 ± 362	1588 ± 321	1106 ± 121	1173 ± 202
212554_at	CAP2	adenylyl cyclase-associated protein 2	**-0.0037**	**0.0146**	0.2367	0.4717	0.0881	3701 ± 716	2980 ± 526	2384 ± 170	1740 ± 470
200001_at	CAPNS1	calpain, small subunit 1	**-0.0042**	**0.0058**	-0.3994	0.2378	0.0954	3062 ± 173	3120 ± 252	2919 ± 222	2278 ± 340
215153_at	CAPON	C-terminal PDZ domain ligand of neuronal NO synthase	-0.2234	**0.0056**	0.4427	**0.0549**	0.0951	793 ± 97	710 ± 115	704 ± 160	370 ± 72
208534_s_at	CAPRI	Ca2+-promoted Ras inactivator	-0.6048	**0.0484**	-0.4573	-0.3170	0.0602	281 ± 27	332 ± 24	285 ± 26	214 ± 27
219342_at	CAS1	O-acetyltransferase	**-0.0318**	**0.0019**	-0.1775	-0.4263	0.0552	1152 ± 130	1043 ± 129	880 ± 57	721 ± 110
222201_s_at	CASP8AP2	CASP8 associated protein 2	**-0.0193**	**0.0233**	0.2591	-0.3218	**0.0001**	510 ± 37	483 ± 41	518 ± 21	272 ± 20
216903_s_at	CBARA1	calcium binding atopy-related autoantigen 1	**-0.0085**	**0.0210**	-0.1862	0.2157	0.0914	1141 ± 26	1193 ± 44	1081 ± 43	1048 ± 50
205528_s_at	CBFA2T1	core-binding factor, runt domain, alpha subunit 2	-0.3651	**0.0316**	0.1555	-0.2604	0.0870	189 ± 24	180 ± 8	122 ± 14	138 ± 25
205827_at	CCK	cholecystokinin	**-0.0036**	**0.0149**	0.4920	-0.2213	**0.0385**	2013 ± 305	1517 ± 459	815 ± 147	1078 ± 252
205899_at	CCNA1	cyclin A1	**-0.0452**	0.1029	-0.2604	0.0793	0.0834	383 ± 41	296 ± 38	251 ± 20	288 ± 46
200953_s_at	CCND2	cyclin D2	**-0.0066**	**0.0166**	-0.3090	0.1804	**0.0351**	1669 ± 104	1683 ± 156	1318 ± 139	1178 ± 161
211559_s_at	CCNG2	cyclin G2	**-0.0017**	**0.0205**	-0.2864	0.3676	**0.0191**	303 ± 33	247 ± 15	233 ± 24	175 ± 28
204093_at	CCNH	cyclin H	**-0.0087**	**0.0396**	**-0.0258**	0.2629	0.0891	977 ± 90	907 ± 144	692 ± 68	645 ± 120
201947_s_at	CCT2	chaperonin containing TCP1, subunit 2	-0.1040	**0.0442**	-0.1558	**0.0115**	0.1182	1961 ± 144	1737 ± 60	1436 ± 110	1562 ± 265
200910_at	CCT3	chaperonin containing TCP1, subunit 3	**-0.0068**	0.1135	**-0.0039**	0.2583	0.1063	1682 ± 105	1396 ± 100	1491 ± 67	1288 ± 162
200877_at	CCT4	chaperonin containing TCP1, subunit 4	**-0.0136**	0.0565	-0.2119	**0.0384**	0.1370	2441 ± 400	1690 ± 221	1675 ± 194	1460 ± 323
208696_at	CCT5	chaperonin containing TCP1, subunit 5	**-0.0357**	0.4168	**-0.0205**	0.1860	0.1592	1481 ± 115	1170 ± 176	967 ± 43	1225 ± 251
200985_s_at	CD59	CD59 antigen p18-20	**-0.0140**	0.1447	-0.1724	0.2436	0.2818	2247 ± 184	1909 ± 202	1786 ± 167	1696 ± 299
200983_x_at	CD59	CD59 antigen p18-20	**-0.0232**	**0.0060**	**-0.0030**	0.1676	0.1173	1412 ± 273	1082 ± 143	1137 ± 172	663 ± 88
217881_s_at	CDC27	cell division cycle 27	**-0.0092**	**0.0005**	0.4716	0.2351	**0.0080**	148 ± 15	110 ± 17	120 ± 18	58 ± 11
214230_at	CDC42	cell division cycle 42	-0.0724	**0.0236**	-0.4514	0.4286	0.0905	822 ± 128	654 ± 102	466 ± 80	499 ± 113
210232_at	CDC42	cell division cycle 42	**-0.0403**	**0.0029**	0.4667	0.1006	**0.0034**	542 ± 63	523 ± 52	317 ± 36	321 ± 33
209056_s_at	CDC5L	CDC5 cell division cycle 5-like	**-0.0165**	**0.0004**	-0.3898	0.1676	**0.0145**	676 ± 37	624 ± 48	578 ± 26	492 ± 41
220115_s_at	CDH10	cadherin 10, type 2	**-0.0143**	**0.0106**	-0.4841	0.4099	**0.0006**	1441 ± 129	1128 ± 93	903 ± 74	830 ± 60

Probe set	**Name**	**Description**	**NFT_O**	**MMSE_O**	**NFT_I**	**MMSE_I**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
207172_s_at	CDH11	cadherin 11, type 2, OB-cadherin	**-0.0038**	**0.0303**	**0.0208**	-0.4522	0.0659	248 ± 23	218 ± 44	164 ± 11	153 ± 26
207173_x_at	CDH11	cadherin 11, type 2, OB-cadherin	**-0.0493**	**0.0075**	-0.1495	0.1995	0.0991	892 ± 65	835 ± 64	721 ± 72	668 ± 69
204726_at	CDH13	cadherin 13, H-cadherin	**-0.0062**	**0.0005**	0.3355	0.3721	0.0665	136 ± 20	107 ± 25	75 ± 19	61 ± 10
206280_at	CDH18	cadherin 18, type 2	-0.2637	**0.0094**	0.2671	0.2251	0.1480	650 ± 70	638 ± 112	575 ± 97	385 ± 56
217574_at	CDH8	cadherin 8, type 2	**-0.0110**	0.7485	0.3316	-0.4476	0.2528	123 ± 11	123 ± 19	80 ± 12	121 ± 28
204247_s_at	CDK5	cyclin-dependent kinase 5	**-0.0323**	**0.0150**	-0.4969	-0.2199	**0.0131**	1026 ± 97	935 ± 76	781 ± 66	573 ± 118
204995_at	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1	**-0.0163**	**0.0021**	**-0.0137**	**0.0265**	0.1154	2690 ± 232	2480 ± 274	2387 ± 227	1808 ± 286
211297_s_at	CDK7	cyclin-dependent kinase 7	**-0.0063**	**0.0161**	-0.2259	0.3587	**0.0118**	219 ± 12	186 ± 9	169 ± 32	105 ± 24
210240_s_at	CDKN2D	cyclin-dependent kinase inhibitor 2D	**-0.0150**	0.4288	-0.0701	0.3124	0.2412	298 ± 27	216 ± 31	204 ± 28	232 ± 53
204154_at	CDO1	cysteine dioxygenase, type I	**-0.0050**	**0.0016**	**0.0131**	0.2700	**0.0331**	1251 ± 133	1046 ± 147	742 ± 76	829 ± 133
212864_at	CDS2	CDP-diacylglycerol synthase 2	**-0.0128**	0.5775	0.2281	0.0688	0.0878	830 ± 22	852 ± 27	731 ± 27	831 ± 59
215080_s_at	CENTG1	centaurin, gamma 1	**-0.0185**	**0.0128**	**-0.0028**	-0.4291	**0.0065**	161 ± 25	133 ± 16	86 ± 18	58 ± 13
219375_at	CEPT1	choline/ethanolaminephosphotransferase	**-0.0270**	**0.0252**	-0.2786	0.4410	**0.0060**	636 ± 68	500 ± 83	568 ± 34	294 ± 31
205651_x_at	CGEF2	cAMP-regulated guanine nucleotide exchange factor II	**-0.0226**	0.0665	-0.1317	-0.1712	0.0794	1436 ± 127	1375 ± 125	1386 ± 189	918 ± 47
217783_s_at	CGI-127	yippee protein	**-0.0040**	**0.0331**	-0.2083	0.1157	0.1751	2867 ± 234	2640 ± 289	2266 ± 224	2124 ± 301
209526_s_at	CGI-142	hepatoma-derived growth factor 2	**-0.0189**	0.0558	-0.1429	-0.4209	0.1904	1273 ± 161	1152 ± 152	977 ± 118	868 ± 91
216693_x_at	CGI-142	hepatoma-derived growth factor 2	**-0.0239**	**0.0352**	0.4068	-0.1320	0.0738	1144 ± 111	998 ± 86	818 ± 73	872 ± 91
209524_at	CGI-142	hepatoma-derived growth factor 2	**-0.0183**	**0.0099**	0.1093	0.1474	0.0948	1729 ± 173	1629 ± 161	1518 ± 117	1206 ± 102
201570_at	CGI-51	CGI-51 protein	-0.0857	**0.0497**	-0.4275	-0.3504	0.1967	511 ± 44	546 ± 65	468 ± 35	395 ± 50
201569_s_at	CGI-51	CGI-51 protein	**-0.0099**	**0.0054**	-0.4190	0.4325	0.0657	249 ± 25	249 ± 14	205 ± 23	173 ± 14
204697_s_at	CHGA	chromogranin A	-0.0921	**0.0243**	-0.3461	0.2845	0.1283	1633 ± 242	1343 ± 329	960 ± 186	972 ± 118
204591_at	CHL1	cell adhesion molecule with homology to L1CAM	**-0.0507**	**0.0103**	0.4956	-0.2069	**0.0491**	1953 ± 265	1870 ± 314	1710 ± 211	970 ± 202
212624_s_at	CHN1	chimerin 1	**-0.0129**	**0.0385**	-0.0672	0.4678	**0.0413**	3955 ± 1705	1533 ± 1498	088 ± 1397	7492 ± 1820
214665_s_at	CHP	calcium binding protein P22	**-0.0504**	**0.0411**	0.3693	0.3649	0.1622	1473 ± 178	1461 ± 209	1035 ± 124	1062 ± 201
200884_at	CKB	creatine kinase, brain	-0.1076	**0.0380**	**0.0523**	0.4316	0.3358	4370 ± 295	4522 ± 248	4302 ± 434	3598 ± 438
202712_s_at	CKMT1	creatine kinase, mitochondrial 1	-0.1097	**0.0103**	-0.4046	0.4797	0.1204	1283 ± 145	1158 ± 166	1060 ± 187	749 ± 93
204170_s_at	CKS2	CDC28 protein kinase 2	**-0.0239**	0.2937	**-0.0140**	0.1114	0.1372	225 ± 36	139 ± 12	191 ± 10	154 ± 31
212308_at	CLASP2	cytoplasmic linker associated protein 2	-0.1006	**0.0364**	**0.0528**	-0.1170	**0.0391**	1088 ± 119	1226 ± 103	1096 ± 80	796 ± 57
212306_at	CLASP2	cytoplasmic linker associated protein 2	**-0.0008**	**0.0006**	**-0.0275**	0.0899	**0.0371**	2139 ± 97	1732 ± 218	1741 ± 177	1385 ± 178
205328_at	CLDN10	claudin 10	**-0.0275**	**0.0082**	-0.3097	0.0867	**0.0059**	1243 ± 103	975 ± 50	847 ± 137	666 ± 105
213415_at	CLIC2	chloride intracellular channel 2	**-0.0493**	0.0763	**-0.0229**	0.1437	**0.0401**	105 ± 30	30 ± 8	55 ± 15	24 ± 5
212358_at	CLIPR-59	CLIP-170-related protein	-0.2073	**0.0011**	**-0.0029**	0.2576	**0.0076**	4117 ± 165	3717 ± 244	3897 ± 334	2845 ± 187
200614_at	CLTC	clathrin, heavy polypeptide	**-0.0037**	**0.0005**	-0.4060	-0.2603	**0.0410**	7243 ± 670	6486 ± 304	5105 ± 392	5126 ± 842
206731_at	CNK2	connector enhancer of KSR2	-0.1118	**0.0353**	0.2282	0.2341	0.1553	862 ± 201	683 ± 164	411 ± 88	483 ± 108
220166_at	CNNM1	cyclin M1	**-0.0196**	**0.0047**	-0.4636	0.4948	**0.0024**	616 ± 35	621 ± 78	523 ± 66	302 ± 20
218250_s_at	CNOT7	CCR4-NOT transcription complex, subunit 7	**-0.0004**	**0.0007**	-0.1001	0.1061	**0.0237**	1628 ± 56	1649 ± 58	1422 ± 65	1344 ± 117
213436_at	CNR1	cannabinoid receptor 1	**-0.0111**	**0.0357**	-0.0599	**0.0418**	**0.0005**	1329 ± 131	910 ± 166	520 ± 65	578 ± 149
219301_s_at	CNTNAP2	contactin associated protein-like 2	**-0.0096**	0.0561	-0.2951	0.2199	0.0670	629 ± 91	485 ± 73	339 ± 32	408 ± 89
211980_at	COL4A1	collagen, type IV, alpha 1	**0.0000**	**0.0006**	**-0.0327**	**0.0227**	**0.0339**	689 ± 86	447 ± 65	423 ± 66	381 ± 79

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
221729_at	COL5A2	collagen, type V, alpha 2	**0.0000**	**0.0007**	**-0.0116**	**0.0176**	**0.0000**	4206 ± 290	1922 ± 298	766 ± 124	1310 ± 522
221730_at	COL5A2	collagen, type V, alpha 2	**-0.0096**	**0.0051**	-0.0944	0.1228	**0.0000**	1659 ± 134	724 ± 123	195 ± 45	456 ± 222
202143_s_at	COP9	COP9 homolog	**-0.0456**	**0.0086**	0.3430	0.1456	**0.0303**	415 ± 52	304 ± 50	251 ± 29	211 ± 61
202141_s_at	COP9	COP9 homolog	**-0.0315**	**0.0162**	-0.2004	0.1845	**0.0427**	3053 ± 330	2455 ± 262	2320 ± 136	1995 ± 226
202142_at	COP9	COP9 homolog	**-0.0366**	**0.0154**	-0.1159	-0.2309	**0.0287**	1267 ± 78	1187 ± 102	930 ± 80	1000 ± 75
208684_at	COPA	coatomer protein complex, subunit alpha	**-0.0473**	0.3604	-0.4467	-0.1221	0.6131	1527 ± 68	1631 ± 56	1440 ± 142	1457 ± 109
218042_at	COPS4	COP9 constitutive photomorphogenic homolog subunit 4	**-0.0414**	**0.0530**	0.4664	0.1270	0.1017	1411 ± 162	1218 ± 149	929 ± 87	1040 ± 166
201652_at	COPS5	COP9 constitutive photomorphogenic homolog subunit 5	**-0.0029**	0.1119	**-0.0347**	0.4678	0.2415	1170 ± 60	1079 ± 167	885 ± 84	916 ± 127
209029_at	COPS7A	COP9 constitutive photomorphogenic homolog subunit 7A	**-0.0187**	**0.0086**	0.4964	-0.4636	0.0642	1094 ± 75	1102 ± 102	1009 ± 74	797 ± 87
211727_s_at	COX11	COX11 homolog, cytochrome c oxidase assembly protein	**-0.0002**	**0.0008**	-0.0663	0.4055	**0.0520**	627 ± 86	578 ± 87	492 ± 48	330 ± 42
202698_x_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	**-0.0062**	**0.0061**	-0.4319	0.2970	**0.0040**	9240 ± 396	8813 ± 577	7597 ± 578	6651 ± 418
200086_s_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	**-0.0001**	**0.0005**	-0.1103	0.3323	**0.0099**	4745 ± 303	4355 ± 244	4522 ± 295	3153 ± 438
203663_s_at	COX5A	cytochrome c oxidase subunit Va	**-0.0477**	0.3337	-0.4746	-0.2231	0.3107	2564 ± 323	2615 ± 373	1815 ± 166	2233 ± 435
211025_x_at	COX5B	cytochrome c oxidase subunit Vb	**-0.0171**	0.0881	-0.2443	-0.3922	0.2782	3810 ± 296	3875 ± 584	3088 ± 274	2881 ± 526
200925_at	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	**-0.0087**	**0.0019**	-0.1796	0.1680	**0.0020**	12723 ± 648	1497 ± 1254	10636 ± 698	7477 ± 934
201441_at	COX6B	cytochrome c oxidase subunit VIb	**-0.0011**	**0.0045**	-0.4819	0.4836	**0.0084**	3088 ± 164	2698 ± 207	2729 ± 175	2067 ± 236
201754_at	COX6C	cytochrome c oxidase subunit VIc	**-0.0365**	**0.0106**	0.2968	**0.0477**	**0.0241**	7154 ± 660	6528 ± 778	4910 ± 480	4418 ± 813
201597_at	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2	**-0.0016**	**0.0510**	-0.4257	-0.1955	**0.0486**	5682 ± 223	5448 ± 435	5574 ± 386	4261 ± 465
201256_at	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	**-0.0042**	**0.0011**	-0.4572	-0.4843	**0.0134**	2624 ± 221	2158 ± 70	1833 ± 81	1970 ± 221
202110_at	COX7B	cytochrome c oxidase subunit VIIb	**-0.0033**	**0.0009**	-0.2401	**0.0316**	**0.0081**	3112 ± 202	2907 ± 267	2298 ± 200	1876 ± 366
213846_at	COX7C	cytochrome c oxidase subunit VIIc	**-0.0075**	**0.0219**	-0.4041	0.3766	**0.0021**	1180 ± 99	916 ± 81	841 ± 31	748 ± 66
201134_x_at	COX7C	cytochrome c oxidase subunit VIIc	**-0.0285**	**0.0352**	0.0873	-0.0800	0.1328	4528 ± 388	4138 ± 386	3705 ± 372	3135 ± 494
201119_s_at	COX8	cytochrome c oxidase subunit VIII	**-0.0387**	0.0862	-0.4139	0.2828	0.2939	2745 ± 212	2695 ± 174	2211 ± 241	2146 ± 419
210408_s_at	CPNE6	copine VI	-0.0711	**0.0434**	0.2474	0.2488	0.2977	805 ± 117	738 ± 161	631 ± 87	490 ± 74
202469_s_at	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	**-0.0235**	**0.0378**	0.2689	**0.0300**	**0.0032**	445 ± 21	475 ± 20	482 ± 10	348 ± 36
205630_at	CRH	corticotropin releasing hormone	**-0.0206**	**0.0113**	-0.3332	-0.3983	0.0581	247 ± 48	186 ± 39	108 ± 10	154 ± 21
211698_at	CRI1	CREBBP/EP300 inhibitory protein 1	-0.1183	**0.0156**	0.1867	-0.1807	**0.0117**	1411 ± 183	1546 ± 64	1405 ± 132	790 ± 105
208669_s_at	CRI1	CREBBP/EP300 inhibitory protein 1	**-0.0489**	**0.0212**	0.4501	0.1914	**0.0455**	1687 ± 244	1599 ± 311	1072 ± 114	835 ± 143
202551_s_at	CRIM1	cysteine-rich motor neuron 1	**-0.0068**	0.0796	-0.1490	**-0.0470**	0.0951	701 ± 55	659 ± 55	650 ± 64	494 ± 56
202517_at	CRMP1	collapsin response mediator protein 1	**-0.0033**	**0.0014**	-0.1276	0.1445	0.2375	1857 ± 55	1938 ± 205	1651 ± 187	1501 ± 153
219913_s_at	CRNKL1	Crn, crooked neck-like 1	**-0.0108**	**0.0004**	-0.1169	0.3803	**0.0197**	631 ± 27	605 ± 56	546 ± 25	456 ± 34
221517_s_at	CRSP6	cofactor required for Sp1 transcriptional activation 6	-0.1315	**0.0491**	**-0.0479**	-0.4372	0.0973	315 ± 24	267 ± 28	228 ± 17	201 ± 54
205489_at	CRYM	crystallin, mu	-0.1000	**0.0105**	0.2397	0.2176	0.0930	2634 ± 628	2301 ± 413	2238 ± 440	944 ± 114
202950_at	CRYZ	crystallin, zeta	**-0.0306**	**0.0259**	0.3843	-0.0611	**0.0128**	538 ± 53	502 ± 70	399 ± 49	268 ± 34
208660_at	CS	citrate synthase	-0.1882	**0.0473**	-0.1043	0.3386	0.3413	2407 ± 105	2485 ± 164	2251 ± 147	2168 ± 97
201112_s_at	CSE1L	CSE1 chromosome segregation 1-like	**-0.0247**	**0.0095**	**-0.0112**	**0.0262**	**0.0255**	1033 ± 76	1145 ± 116	881 ± 60	779 ± 46
220768_s_at	CSNK1G3	casein kinase 1, gamma 3	**-0.0100**	**0.0104**	**-0.0453**	0.2267	**0.0277**	368 ± 22	297 ± 25	303 ± 13	271 ± 30
212072_s_at	CSNK2A1	casein kinase 2, alpha 1 polypeptide	-0.0859	**0.0012**	0.2070	-0.2860	**0.0128**	780 ± 53	794 ± 56	682 ± 37	550 ± 64
206075_s_at	CSNK2A1	casein kinase 2, alpha 1 polypeptide	**-0.0231**	**0.0028**	-0.3590	-0.2245	**0.0423**	431 ± 17	386 ± 20	359 ± 40	289 ± 47

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
205143_at	CSPG3	chondroitin sulfate proteoglycan 3	-0.1035	**0.0019**	0.0768	-0.3863	**0.0046**	3646 ± 284	4419 ± 467	3632 ± 352	2396 ± 230
39966_at	CSPG5	chondroitin sulfate proteoglycan 5	**-0.0179**	**0.0012**	-0.2967	**0.0206**	**0.0009**	4013 ± 159	4238 ± 394	4309 ± 330	2498 ± 302
205373_at	CTNNA2	catenin , alpha 2	-0.0821	**0.0434**	0.2489	-0.3519	0.1447	1375 ± 150	1337 ± 202	1309 ± 249	772 ± 182
207614_s_at	CUL1	cullin 1	-0.0760	**0.0394**	-0.0723	0.1441	**0.0406**	749 ± 47	605 ± 54	547 ± 30	557 ± 84
203078_at	CUL2	cullin 2	-0.1008	**0.0283**	**0.0280**	0.1258	0.2557	134 ± 20	158 ± 25	101 ± 20	101 ± 26
203079_s_at	CUL2	cullin 2	**-0.0181**	**0.0129**	-0.3447	0.0778	**0.0190**	431 ± 28	382 ± 40	331 ± 17	304 ± 29
218002_s_at	CXCL14	chemokine ligand 14	**-0.0304**	**0.0177**	-0.2114	**0.0005**	0.0835	1243 ± 171	1009 ± 147	827 ± 167	634 ± 145
201828_x_at	CXX1	CAAX box 1	**-0.0429**	0.0994	0.3519	0.0817	0.3273	6288 ± 695	6106 ± 505	4886 ± 517	5410 ± 580
201066_at	CYC1	cytochrome c-1	**-0.0331**	0.2562	-0.4541	-0.4342	0.2587	1110 ± 98	1027 ± 71	858 ± 65	975 ± 116
204716_at	D10S170	DNA segment on chromosome 10 170	**-0.0329**	0.0615	0.2104	0.2419	0.2427	434 ± 16	415 ± 32	417 ± 31	347 ± 45
208872_s_at	D5S346	DNA segment, single copy probe LNS-CAI/LNS-CAII	**-0.0067**	**0.0407**	-0.1455	0.4736	0.1083	681 ± 58	591 ± 54	524 ± 46	495 ± 68
208873_s_at	D5S346	DNA segment, single copy probe LNS-CAI/LNS-CAII	**-0.0002**	**0.0003**	-0.1752	0.2336	0.1670	4398 ± 307	3919 ± 387	3731 ± 291	3318 ± 379
209763_at	dA141H5.1	similar to neuralin 1	**-0.0130**	**0.0018**	-0.2837	0.2859	**0.0029**	576 ± 33	505 ± 54	436 ± 44	335 ± 38
201624_at	DARS	aspartyl-tRNA synthetase	**-0.0207**	0.1639	-0.4876	-0.1835	0.3841	760 ± 63	748 ± 104	660 ± 71	573 ± 98
205818_at	DBCCR1	deleted in bladder cancer chromosome region candidate 1	**-0.0512**	**0.0406**	0.4569	0.2781	0.2044	1115 ± 137	957 ± 154	780 ± 112	791 ± 96
218482_at	DC6	DC6 protein	**-0.0211**	**0.0050**	-0.3244	0.4498	**0.0158**	579 ± 55	545 ± 64	470 ± 33	335 ± 55
201894_s_at	DCN	decorin	**-0.0235**	0.4632	0.3054	**-0.0087**	0.2726	552 ± 36	649 ± 58	554 ± 72	484 ± 51
200932_s_at	DCTN2	dynactin 2	**-0.0167**	**0.0102**	-0.4887	-0.2150	**0.0238**	1164 ± 85	1134 ± 92	994 ± 61	814 ± 62
208675_s_at	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	**-0.0015**	**0.0043**	-0.0671	0.4050	**0.0313**	835 ± 61	858 ± 98	730 ± 48	567 ± 44
202929_s_at	DDT	D-dopachrome tautomerase	**-0.0197**	0.1039	0.3307	-0.2800	0.1649	351 ± 26	390 ± 42	301 ± 22	241 ± 79
201241_at	DDX1	DEAD/H box polypeptide 1	**-0.0266**	**0.0002**	0.4827	-0.2906	**0.0171**	1351 ± 68	1201 ± 145	980 ± 73	936 ± 112
200033_at	DDX5	DEAD/H box polypeptide 5	**-0.0471**	0.5049	**-0.0209**	0.3871	0.6756	4816 ± 211	4787 ± 203	4361 ± 380	4314 ± 594
209407_s_at	DEAF1	deformed epidermal autoregulatory factor 1	**-0.0458**	0.0854	**-0.0015**	**0.0319**	0.1909	1447 ± 115	1121 ± 108	1175 ± 121	1145 ± 139
207431_s_at	DEGS	degenerative spermatocyte homolog, lipid desaturase	**-0.0142**	0.1882	-0.4856	-0.1448	0.2535	343 ± 28	413 ± 54	333 ± 42	278 ± 53
220482_s_at	DELGEF	deafness locus associated putative guanine nucleotide exch.	**-0.0037**	0.1192	0.1919	-0.4365	**0.0541**	161 ± 12	154 ± 20	168 ± 18	101 ± 20
216307_at	DGKB	diacylglycerol kinase, beta 90kDa	-0.3368	**0.0304**	-0.3492	0.1441	0.2894	191 ± 11	202 ± 31	188 ± 23	142 ± 10
203816_at	DGUOK	deoxyguanosine kinase	**-0.0023**	**0.0053**	0.3178	0.2036	**0.0005**	196 ± 21	228 ± 14	162 ± 22	72 ± 28
201790_s_at	DHCR7	7-dehydrocholesterol reductase	**-0.0050**	0.1341	-0.1588	0.4425	0.2613	676 ± 80	723 ± 98	565 ± 26	513 ± 92
203700_s_at	DIO2	deiodinase, iodothyronine, type II	**-0.0174**	**0.0025**	0.3598	-0.4399	**0.0202**	533 ± 50	497 ± 39	404 ± 46	332 ± 40
219619_at	Di-Ras2	Di-Ras2	**-0.0150**	**0.0403**	0.2672	-0.3548	**0.0373**	4346 ± 475	4114 ± 441	3577 ± 370	2499 ± 486
214193_s_at	DJ434O14.5	novel putative prot. similar to YIL091C	**-0.0193**	**0.0030**	-0.2614	0.1317	0.1003	211 ± 13	202 ± 14	184 ± 14	163 ± 14
203427_at	DKFZP547E2110	DKFZP547E2110 protein	**-0.0279**	0.2871	-0.0684	-0.3776	0.3995	650 ± 23	661 ± 59	667 ± 42	559 ± 67
203428_s_at	DKFZP547E2110	DKFZP547E2110 protein	-0.2265	**0.0100**	0.4096	**0.0338**	0.1291	273 ± 22	269 ± 28	220 ± 19	214 ± 9
217948_at	DKFZP564B147	DKFZP564B147 protein	**-0.0104**	0.1534	-0.0639	0.1180	**0.0206**	351 ± 31	253 ± 16	249 ± 14	278 ± 25
209708_at	DKFZP564G202	DKFZP564G202 protein	**-0.0376**	0.1774	-0.4433	0.4103	0.1341	493 ± 50	432 ± 57	342 ± 33	385 ± 36
221896_s_at	DKFZP564K247	DKFZP564K247 protein	**-0.0207**	**0.0055**	-0.2442	0.2262	**0.0216**	2539 ± 308	2101 ± 247	1687 ± 128	1533 ± 124
210006_at	DKFZP564O243	DKFZP564O243 protein	**-0.0371**	0.0731	-0.4892	0.3331	0.2586	1022 ± 110	863 ± 47	804 ± 85	791 ± 102
209300_s_at	DKFZP566B183	DKFZP566B183 protein	**-0.0013**	**0.0408**	0.4924	-0.2372	**0.0223**	1208 ± 178	1003 ± 205	645 ± 66	601 ± 82
216338_s_at	DKFZP566C243	DKFZP566C243 protein	-0.1978	**0.0176**	-0.1042	**0.0320**	**0.0400**	426 ± 21	314 ± 40	332 ± 31	285 ± 44

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
209001_s_at	DKFZP566D193	DKFZP566D193 protein	**-0.0071**	**0.0001**	0.4896	0.0832	**0.0249**	3677 ± 100	3677 ± 218	3001 ± 205	3240 ± 192
207170_s_at	DKFZP586A011	cervical cancer 1 protooncogene	**-0.0064**	**0.0354**	-0.3168	0.1824	**0.0042**	1107 ± 57	1080 ± 82	919 ± 76	747 ± 36
212453_at	DKFZP586B0923	DKFZP586B0923 protein	**-0.0487**	**0.0263**	-0.2710	0.2155	0.0693	1145 ± 108	1006 ± 120	769 ± 76	822 ± 133
213617_s_at	DKFZP586M1523	DKFZP586M1523 protein	**-0.0217**	**0.0181**	0.4689	0.2180	0.2533	434 ± 33	405 ± 43	353 ± 58	323 ± 26
201863_at	DKFZP586O0120	DKFZP586O0120 protein	-0.0914	**0.0064**	0.2499	0.4905	**0.0453**	910 ± 21	955 ± 53	829 ± 48	805 ± 14
213149_at	DLAT	dihydrolipoamide S-acetyltransferase	-0.3097	**0.0266**	0.4711	-0.4529	0.2396	465 ± 44	418 ± 69	438 ± 16	316 ± 68
209095_at	DLD	dihydrolipoamide dehydrogenase	**-0.0206**	**0.0009**	**-0.0275**	0.2242	0.1371	1235 ± 225	1096 ± 130	916 ± 101	690 ± 143
206253_at	DLG2	discs, large homolog 2, chapsyn-110	-0.0954	**0.0038**	-0.1550	0.4551	**0.0449**	195 ± 21	191 ± 11	139 ± 17	134 ± 20
206489_s_at	DLGAP1	discs, large homolog-associated protein 1	-0.0651	**0.0174**	-0.4121	0.2295	**0.0324**	125 ± 21	99 ± 14	61 ± 14	71 ± 6
210227_at	DLGAP2	discs, large homolog-associated protein 2	**-0.0190**	**0.0036**	-0.3302	0.3555	**0.0238**	1305 ± 73	1150 ± 147	1015 ± 128	789 ± 76
203881_s_at	DMD	dystrophin	**-0.0066**	**0.0055**	-0.3755	0.1129	**0.0112**	1080 ± 110	932 ± 42	765 ± 63	701 ± 69
200881_s_at	DNAJA1	DnaJ homolog, subfamily A, member 1	**-0.0115**	0.0951	**-0.0059**	0.4265	0.0987	1620 ± 249	1215 ± 132	1296 ± 172	903 ± 68
200880_at	DNAJA1	DnaJ homolog, subfamily A, member 1	**-0.0185**	0.3614	-0.1832	-0.3597	0.4671	2897 ± 185	2620 ± 261	2488 ± 195	2487 ± 219
202842_s_at	DNAJB9	DnaJ homolog, subfamily B, member 9	**-0.0185**	**0.0009**	0.3331	0.1874	**0.0114**	1925 ± 161	1839 ± 66	1375 ± 95	1469 ± 139
204720_s_at	DNAJC6	DnaJ homolog, subfamily C, member 6	**-0.0200**	0.0663	-0.1231	-0.2312	0.1939	5519 ± 319	5305 ± 691	5030 ± 218	4098 ± 632
212490_at	DNAJC8	DnaJ homolog, subfamily C, member 8	-0.2041	**0.0406**	0.2941	**0.0026**	**0.0437**	276 ± 20	215 ± 16	261 ± 22	200 ± 22
211928_at	DNCH1	dynein, cytoplasmic, heavy polypeptide 1	-0.2795	**0.0277**	-0.1075	0.3555	0.0799	3656 ± 126	3325 ± 273	3588 ± 248	2797 ± 306
205348_s_at	DNCI1	dynein, cytoplasmic, intermediate polypeptide 1	**-0.0206**	**0.0459**	-0.3530	0.3640	**0.0100**	2489 ± 291	2366 ± 267	1631 ± 112	1493 ± 153
211684_s_at	DNCI2	dynein, cytoplasmic, intermediate polypeptide 2	**-0.0399**	0.3712	-0.1479	-0.1333	0.2865	2985 ± 92	2999 ± 331	3062 ± 257	2484 ± 172
217976_s_at	DNCLI1	dynein, cytoplasmic, light intermediate polypeptide 1	**-0.0059**	**0.0020**	-0.0611	0.2493	0.1058	545 ± 67	465 ± 58	352 ± 48	347 ± 86
217918_at	DNLC2A	dynein light chain 2A	-0.2113	**0.0387**	-0.1272	-0.4797	0.1685	5575 ± 232	5027 ± 711	4537 ± 355	4209 ± 500
203105_s_at	DNM1L	dynamin 1-like	**-0.0152**	**0.0028**	-0.1914	0.3169	**0.0031**	403 ± 27	351 ± 24	292 ± 10	272 ± 35
213482_at	DOCK3	dedicator of cyto-kinesis 3	**-0.0156**	**0.0137**	**-0.0392**	-0.4163	**0.0241**	521 ± 80	421 ± 74	350 ± 43	202 ± 74
203258_at	DRAP1	DR1-associated protein 1	**-0.0342**	**0.0142**	0.1622	0.1439	**0.0287**	762 ± 50	617 ± 106	573 ± 57	419 ± 82
204751_x_at	DSC2	desmocollin 2	**-0.0377**	-0.8438	-0.2203	0.0944	0.7515	100 ± 11	94 ± 10	84 ± 7	101 ± 20
203498_at	DSCR1L1	Down syndrome critical region gene 1-like 1	-0.1169	**0.0130**	-0.4289	0.2339	0.0768	1848 ± 291	1701 ± 249	1650 ± 226	971 ± 95
203405_at	DSCR2	Down syndrome critical region gene 2	**-0.0060**	0.1123	0.3201	0.2474	0.2319	427 ± 28	423 ± 26	349 ± 26	381 ± 42
221689_s_at	DSCR5	Down syndrome critical region gene 5	**-0.0023**	0.1583	-0.4931	-0.3598	0.0686	828 ± 44	892 ± 57	701 ± 42	772 ± 56
202276_at	DSS1	Deleted in split-hand/split-foot 1 region	**-0.0445**	0.3622	0.1571	-0.3598	0.6194	524 ± 33	524 ± 14	456 ± 21	486 ± 72
209457_at	DUSP5	dual specificity phosphatase 5	**-0.0034**	0.2196	-0.0655	0.1422	**0.0493**	291 ± 32	245 ± 27	153 ± 30	229 ± 47
208892_s_at	DUSP6	dual specificity phosphatase 6	**-0.0421**	0.0795	-0.4189	0.3208	0.1768	640 ± 74	541 ± 36	539 ± 75	425 ± 56
208891_at	DUSP6	dual specificity phosphatase 6	**-0.0327**	**0.0259**	-0.1200	-0.3969	**0.0438**	1130 ± 189	832 ± 37	752 ± 113	564 ± 118
202348_s_at	DYT1	dystonia 1, torsion	-0.1608	**0.0200**	0.4272	0.2288	0.1102	366 ± 32	362 ± 31	277 ± 23	298 ± 34
204557_s_at	DZIP1	zinc-finger protein DZIP1	**-0.0003**	**0.0027**	-0.2519	0.3703	**0.0327**	625 ± 28	538 ± 83	593 ± 62	389 ± 39
220942_x_at	E2IG5	hypothetical protein, estradiol-induced	**-0.0028**	**0.0199**	-0.1262	0.1473	**0.0098**	1915 ± 143	1728 ± 181	1292 ± 104	1290 ± 172
208833_s_at	E46L	like mouse brain protein E46	**-0.0203**	**0.0074**	-0.3761	-0.4133	**0.0077**	3421 ± 300	2758 ± 228	2011 ± 182	2483 ± 358
202735_at	EBP	emopamil binding protein	-0.4425	**0.0342**	**0.0171**	-0.1000	0.1573	185 ± 17	188 ± 15	179 ± 13	136 ± 22
200789_at	ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	**-0.0045**	0.0751	**-0.0010**	0.1452	0.2163	795 ± 40	728 ± 41	688 ± 26	651 ± 85
219787_s_at	ECT2	epithelial cell transforming sequence 2 oncogene	**-0.0435**	0.6363	0.2693	-0.2427	0.4048	155 ± 20	155 ± 12	118 ± 20	147 ± 15

Probe set	Name	Description	NFT_O	MMSE_O	NFT_I	MMSE_I	ANOVA	Control	Incipient	Moderate	Severe
204642_at	EDG1	endothelial differentiation, sphingolipid GPCR 1	-0.1163	**0.0444**	0.3601	-0.3498	**0.0494**	975 ± 67	1023 ± 124	979 ± 87	687 ± 60
208399_s_at	EDN3	endothelin 3	-0.0572	**0.0134**	0.0593	-0.4652	0.0590	144 ± 36	162 ± 23	74 ± 19	71 ± 24
204905_s_at	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	**-0.0243**	0.1460	-0.4260	0.4063	0.3245	515 ± 45	440 ± 62	392 ± 45	393 ± 71
203354_s_at	EFA6R	ADP-ribosylation factor guanine nucleotide factor 6	**-0.0024**	**0.0004**	-0.1873	0.1572	0.0574	595 ± 43	624 ± 138	507 ± 62	303 ± 39
202668_at	EFNB2	ephrin-B2	**-0.0017**	**0.0221**	**-0.0174**	0.2218	**0.0004**	1863 ± 123	1516 ± 91	1329 ± 68	1216 ± 99
201632_at	EIF2B1	eukaryotic translation initiation factor 2B1 alpha	**-0.0165**	0.1292	**-0.0242**	0.1385	0.1055	1099 ± 39	994 ± 24	897 ± 73	920 ± 85
218488_at	EIF2B3	eukaryotic translation initiation factor 2B, 3 gamma	**-0.0392**	**0.0341**	0.3706	0.3375	**0.0271**	443 ± 41	406 ± 23	303 ± 13	328 ± 50
201142_at	EIF2S1	eukaryotic translation initiation factor 2 1 alpha	**-0.0213**	**0.0428**	-0.1048	0.1164	0.2022	661 ± 68	623 ± 74	527 ± 59	476 ± 49
200005_at	EIF3S7	eukaryotic translation initiation factor 3, 7 zeta	**-0.0430**	0.1540	-0.4749	-0.3078	0.1272	1140 ± 47	1175 ± 66	1128 ± 51	978 ± 55
208290_s_at	EIF5	eukaryotic translation initiation factor 5	**-0.0247**	**0.0418**	0.1212	**-0.0157**	0.1245	492 ± 82	355 ± 52	329 ± 40	294 ± 44
206051_at	ELAVL4	ELAV -like 4	-0.0733	**0.0090**	-0.3688	0.2806	0.0864	2362 ± 351	1887 ± 327	1753 ± 292	1205 ± 197
204513_s_at	ELMO1	engulfment and cell motility 1	**-0.0472**	0.3646	-0.4274	-0.3889	0.5308	2231 ± 168	2110 ± 298	1841 ± 177	1803 ± 341
221528_s_at	ELMO2	engulfment and cell motility 2	-0.2807	**0.0498**	-0.3200	**0.0314**	0.3301	828 ± 36	772 ± 70	732 ± 67	662 ± 86
213712_at	ELOVL2	elongation of very long chain fatty acids -like 2	**-0.0071**	**0.0102**	-0.2900	0.2102	0.0564	415 ± 14	449 ± 74	395 ± 60	244 ± 46
219532_at	ELOVL4	elongation of very long chain fatty acids -like 4	-0.0607	**0.0470**	0.4544	-0.1750	0.3105	566 ± 64	563 ± 75	512 ± 81	369 ± 99
201341_at	ENC1	ectodermal-neural cortex	**-0.0277**	**0.0251**	-0.3999	-0.2935	0.1253	9931 ± 1082	8003 ± 1360	446 ± 1365	5447 ± 1794
201313_at	ENO2	enolase 2,	**-0.0079**	**0.0003**	0.1580	0.2694	0.0973	3317 ± 330	3654 ± 583	2571 ± 323	2190 ± 436
202596_at	ENSA	endosulfine alpha	**-0.0045**	**0.0020**	-0.1906	0.0977	**0.0021**	1892 ± 235	1930 ± 187	1667 ± 152	821 ± 87
206191_at	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	**-0.0028**	**0.0209**	0.4758	-0.3541	**0.0071**	782 ± 78	642 ± 89	465 ± 31	476 ± 54
204505_s_at	EPB49	erythrocyte membrane protein band 4.9	-0.0769	**0.0035**	-0.2731	0.3281	**0.0213**	1621 ± 180	1485 ± 155	1519 ± 132	965 ± 71
206114_at	EPHA4	EphA4	-0.0806	**0.0436**	-0.3691	-0.2538	0.2281	579 ± 63	498 ± 82	382 ± 39	399 ± 117
206852_at	EPHA7	EphA7	-0.0910	**0.0373**	0.2443	-0.3807	**0.0280**	66 ± 7	76 ± 21	31 ± 3	37 ± 9
209589_s_at	EPHB2	EphB2	-0.0852	**0.0341**	0.3128	0.0661	0.2759	176 ± 17	185 ± 29	172 ± 25	123 ± 10
217886_at	EPS15	epidermal growth factor receptor pathway substrate 15	**-0.0406**	0.0624	0.4171	0.4492	**0.0368**	2459 ± 163	2233 ± 129	1809 ± 102	2056 ± 221
209009_at	ESD	esterase D/formylglutathione hydrolase	**-0.0060**	0.0958	-0.3487	-0.1029	0.1337	2421 ± 100	2433 ± 275	2068 ± 72	1935 ± 210
201931_at	ETFA	electron-transfer-flavoprotein, alpha polypeptide	**-0.0019**	**0.0017**	-0.3895	0.2345	**0.0249**	581 ± 34	579 ± 19	481 ± 30	459 ± 42
201329_s_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2	-0.0614	**0.0132**	0.4498	-0.2522	**0.0077**	276 ± 10	312 ± 27	290 ± 20	208 ± 11
205756_s_at	F8	coagulation factor VIII, procoagulant component	**-0.0057**	**0.0081**	-0.3027	0.1887	**0.0388**	750 ± 29	728 ± 47	687 ± 44	576 ± 47
203274_at	F8A	coagulation factor VIII-associated	**-0.0104**	**0.0071**	-0.1157	0.1640	**0.0371**	1569 ± 149	1331 ± 153	1151 ± 71	1014 ± 136
205738_s_at	FABP3	fatty acid binding protein 3, muscle and heart	-0.3339	**0.0366**	**0.0435**	-0.4552	0.3537	322 ± 37	323 ± 39	272 ± 19	250 ± 36
205030_at	FABP7	fatty acid binding protein 7, brain	**-0.0052**	**0.0103**	-0.4668	-0.4013	**0.0237**	3122 ± 423	2424 ± 336	2602 ± 474	1232 ± 104
205029_s_at	FABP7	fatty acid binding protein 7, brain	**-0.0053**	**0.0094**	-0.3508	0.4110	**0.0517**	689 ± 100	643 ± 110	534 ± 99	286 ± 101
201660_at	FACL3	fatty-acid-Coenzyme A ligase, long-chain 3	**-0.0220**	0.0749	0.1956	0.4906	0.2314	2717 ± 258	2589 ± 54	2240 ± 163	2228 ± 212
201662_s_at	FACL3	fatty-acid-Coenzyme A ligase, long-chain 3	**-0.0057**	**0.0164**	-0.4662	-0.2358	**0.0429**	973 ± 113	876 ± 95	747 ± 86	569 ± 90
204283_at	FARS1	phenylalanine-tRNA synthetase	**-0.0108**	0.1441	0.4891	0.3153	0.3641	202 ± 18	187 ± 14	159 ± 21	162 ± 25
214436_at	FBXL2	F-box and leucine-rich repeat protein 2	-0.0577	**0.0035**	-0.3235	-0.4576	**0.0286**	883 ± 55	796 ± 63	737 ± 66	625 ± 44
212231_at	FBXO21	F-box only protein 21	**-0.0429**	0.0590	-0.4226	0.4384	0.3762	1295 ± 70	1346 ± 151	1174 ± 130	1057 ± 127
212229_s_at	FBXO21	F-box only protein 21	**-0.0478**	0.2087	0.4360	-0.3589	0.5363	1872 ± 110	1832 ± 216	1614 ± 78	1612 ± 220
218432_at	FBXO3	F-box only protein 3	**-0.0224**	**0.0394**	-0.4570	0.4527	**0.0373**	864 ± 74	786 ± 110	652 ± 59	544 ± 70

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
218751_s_at	FBXW7	F-box and WD-40 domain protein 7	-0.1629	**0.0077**	0.4004	-0.4998	**0.0474**	1404 ± 220	1282 ± 188	1257 ± 193	613 ± 50
204232_at	FCER1G	Fc fragment of IgE, high affinity I	**-0.0190**	0.1445	**-0.0266**	0.3763	0.1576	1292 ± 193	1037 ± 91	944 ± 58	921 ± 83
216950_s_at	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor for	**-0.0493**	0.1039	-0.1366	-0.2976	0.3182	391 ± 75	380 ± 42	274 ± 43	264 ± 53
203116_s_at	FECH	ferrochelatase	**-0.0071**	**0.0121**	-0.4317	0.3058	0.1240	626 ± 34	652 ± 30	557 ± 29	550 ± 43
205110_s_at	FGF13	fibroblast growth factor 13	**-0.0085**	**0.0057**	0.3789	0.2858	0.0930	3707 ± 518	3219 ± 728	2269 ± 252	1974 ± 584
204380_s_at	FGFR3	fibroblast growth factor receptor 3	**-0.0448**	**0.0032**	0.3180	0.1246	0.0747	149 ± 23	142 ± 21	114 ± 25	68 ± 17
214170_x_at	FH	fumarate hydratase	**-0.0431**	0.2927	0.2571	0.2846	0.5091	936 ± 135	839 ± 83	729 ± 50	789 ± 106
203033_x_at	FH	fumarate hydratase	-0.1500	**0.0499**	0.2010	0.2412	0.0923	651 ± 49	647 ± 46	497 ± 55	547 ± 47
206492_at	FHIT	fragile histidine triad gene	**-0.0156**	0.3462	-0.4097	-0.3905	0.4292	318 ± 18	323 ± 21	268 ± 24	277 ± 49
214505_s_at	FHL1	four and a half LIM domains 1	-0.2094	**0.0486**	0.3758	**0.0415**	0.2475	526 ± 76	515 ± 94	329 ± 38	387 ± 96
202041_s_at	FIBP	fibroblast growth factor intracellular binding protein	**-0.0074**	**0.0218**	0.2725	**0.0184**	**0.0441**	1083 ± 84	1009 ± 58	952 ± 54	791 ± 51
209931_s_at	FKBP1B	FK506 binding protein 1B, 12.6 kDa	-0.1172	**0.0244**	0.1758	-0.2405	0.1069	253 ± 38	263 ± 46	169 ± 21	161 ± 33
206857_s_at	FKBP1B	FK506 binding protein 1B, 12.6 kDa	**-0.0499**	**0.0081**	-0.3837	-0.4594	0.0794	2493 ± 299	2116 ± 186	1592 ± 196	1751 ± 286
218003_s_at	FKBP3	FK506 binding protein 3, 25kDa	**-0.0397**	**0.0035**	0.2565	0.1299	**0.0349**	1565 ± 83	1395 ± 113	1388 ± 74	1160 ± 99
219499_at	FLJ10578	Sec61 alpha form 2	-0.0565	**0.0499**	0.4279	0.3337	0.0856	463 ± 44	475 ± 48	354 ± 17	374 ± 30
220925_at	FLJ21613	hypothetical protein FLJ21613	-0.0668	**0.0464**	**0.0316**	0.3920	0.1755	339 ± 23	341 ± 18	294 ± 7	300 ± 20
218175_at	FLJ22471	limkain beta 2	-0.1001	**0.0187**	0.1973	0.1228	0.2449	7621 ± 380	8391 ± 909	7113 ± 632	6512 ± 599
204359_at	FLRT2	fibronectin leucine rich transmembrane protein 2	-0.2159	**0.0206**	0.4729	0.3440	0.0658	1599 ± 190	1325 ± 109	1140 ± 111	1063 ± 147
216442_x_at	FN1	fibronectin 1	-0.0914	**0.0087**	0.3020	0.0574	**0.0140**	1830 ± 216	1506 ± 178	1684 ± 126	1005 ± 119
211719_x_at	FN1	fibronectin 1	-0.4478	**0.0312**	0.1474	0.2829	**0.0085**	1456 ± 135	1400 ± 131	1617 ± 139	910 ± 64
212464_s_at	FN1	fibronectin 1	-0.0664	**0.0478**	0.2867	0.2583	**0.0145**	1253 ± 164	1113 ± 99	1362 ± 150	672 ± 121
210495_x_at	FN1	fibronectin 1	**-0.0149**	**0.0274**	0.3979	0.2650	**0.0073**	1804 ± 201	1582 ± 146	1640 ± 107	983 ± 132
206018_at	FOXG1B	forkhead box G1B	**-0.0423**	0.0667	-0.2474	0.4724	0.2127	3556 ± 390	3137 ± 432	2699 ± 248	2537 ± 398
215160_x_at	FRG1	FSHD region gene 1	**-0.0003**	**0.0012**	0.4544	0.3929	**0.0525**	314 ± 13	326 ± 21	254 ± 31	260 ± 6
219170_at	FSD1	fibronectin type 3 and SPRY domain-containing protein	-0.3995	**0.0208**	**-0.0207**	0.1889	0.1650	1016 ± 65	848 ± 121	823 ± 106	703 ± 101
208310_s_at	FSTL1	follistatin-like 1	**-0.0432**	**0.0221**	0.3415	0.2117	**0.0057**	356 ± 28	350 ± 22	269 ± 25	234 ± 28
218373_at	FTS	fused toes homolog	**-0.0200**	**0.0172**	-0.2737	0.3411	0.1226	1474 ± 182	1319 ± 135	1136 ± 123	937 ± 182
202838_at	FUCA1	fucosidase, alpha-L- 1, tissue	**-0.0248**	0.1201	0.0782	-0.3119	0.2657	472 ± 33	505 ± 49	450 ± 44	368 ± 65
217897_at	FXYD6	FXYD domain containing ion transport regulator 6	**-0.0485**	**0.0032**	0.4744	0.3027	**0.0432**	3867 ± 465	2976 ± 473	2667 ± 450	2124 ± 184
220131_at	FXYD7	FXYD domain containing ion transport regulator 7	**-0.0141**	**0.0406**	-0.4220	0.3561	0.0621	867 ± 103	991 ± 135	762 ± 108	544 ± 83
208841_s_at	G3BP2	Ras-GTPase activating protein SH3 domain-binding protein 2	**-0.0172**	**0.0150**	0.1570	0.4393	0.1857	2239 ± 241	2019 ± 275	1669 ± 144	1563 ± 300
202812_at	GAA	glucosidase, alpha; acid	**-0.0382**	**0.0016**	0.1947	0.3817	0.1572	655 ± 18	655 ± 48	578 ± 37	551 ± 48
203146_s_at	GABBR1	gamma-aminobutyric acid B receptor, 1	**-0.0057**	**0.0160**	-0.0682	0.0892	**0.0075**	4399 ± 399	5093 ± 551	4248 ± 492	2697 ± 208
207014_at	GABRA2	gamma-aminobutyric acid A receptor, alpha 2	-0.0578	**0.0232**	0.2467	-0.3925	0.1946	528 ± 60	505 ± 113	402 ± 69	301 ± 78
205850_s_at	GABRB3	gamma-aminobutyric acid A receptor, beta 3	**-0.0089**	**0.0515**	-0.3541	**0.0264**	0.3529	157 ± 17	138 ± 24	111 ± 15	118 ± 26
205278_at	GAD1	glutamate decarboxylase 1	**-0.0365**	**0.0336**	-0.1256	0.1361	**0.0413**	2633 ± 303	1633 ± 340	1469 ± 285	1401 ± 437
206780_at	GAD2	glutamate decarboxylase 2	**-0.0456**	**0.0014**	0.3795	**0.0130**	**0.0114**	1015 ± 92	657 ± 96	458 ± 101	641 ± 156
204417_at	GALC	galactosylceramidase	**-0.0243**	0.2171	-0.4908	-0.2056	0.3357	1253 ± 48	1293 ± 140	1110 ± 59	1123 ± 67
206435_at	GALGT	UDP-N-acetyl-alpha-D-galactosamine	**-0.0098**	**0.0037**	-0.2652	0.1629	**0.0116**	647 ± 76	501 ± 61	407 ± 47	388 ± 21

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
204471_at	GAP43	growth associated protein 43	**-0.0463**	**0.0129**	-0.1279	0.3797	**0.0320**	2527 ± 419	1819 ± 315	1326 ± 238	1093 ± 388
217398_x_at	GAPD	glyceraldehyde-3-phosphate dehydrogenase	-0.1171	**0.0443**	-0.0564	0.4857	**0.0218**	7816 ± 1199	7119 ± 1731	773 ± 1102	2382 ± 1718
213453_x_at	GAPD	glyceraldehyde-3-phosphate dehydrogenase	**-0.0047**	**0.0148**	0.2472	-0.3722	**0.0306**	14914 ± 757	494 ± 1121	4695 ± 766	0854 ± 1435
201816_s_at	GBAS	glioblastoma amplified sequence	**-0.0188**	**0.0193**	0.3339	-0.4120	0.0577	1429 ± 184	1376 ± 175	1034 ± 62	879 ± 154
201738_at	GC20	translation factor sui1 homolog	-0.0831	**0.0334**	-0.2666	0.1112	0.2023	2748 ± 223	2633 ± 124	2225 ± 100	2088 ± 421
204224_s_at	GCH1	GTP cyclohydrolase 1	**-0.0093**	0.1634	-0.1284	0.4031	0.1779	230 ± 11	187 ± 13	202 ± 11	176 ± 30
214005_at	GGCX	gamma-glutamyl carboxylase	-0.0827	**0.0157**	**0.0169**	0.3015	0.0605	216 ± 16	242 ± 35	215 ± 21	145 ± 7
209248_at	GHITM	growth hormone inducible transmembrane protein	**-0.0187**	**0.0324**	-0.1177	0.3383	0.0615	3766 ± 500	3188 ± 361	2607 ± 259	2286 ± 391
209249_s_at	GHITM	growth hormone inducible transmembrane protein	**-0.0316**	**0.0299**	-0.4064	0.2521	0.0758	2140 ± 265	1815 ± 264	1352 ± 127	1365 ± 297
219137_s_at	GL004	GL004 protein	-0.0894	**0.0360**	-0.1503	0.0771	0.1230	1403 ± 91	1335 ± 46	1106 ± 99	1114 ± 156
200681_at	GLO1	glyoxalase I	**-0.0240**	0.0961	-0.3395	0.3674	0.2520	2702 ± 217	2459 ± 274	2065 ± 198	2124 ± 346
205279_s_at	GLRB	glycine receptor, beta	-0.0745	**0.0183**	-0.4049	0.1353	**0.0516**	515 ± 104	386 ± 61	245 ± 38	288 ± 48
205280_at	GLRB	glycine receptor, beta	**-0.0252**	**0.0020**	-0.1477	0.1717	0.0916	778 ± 142	545 ± 112	421 ± 88	393 ± 112
206662_at	GLRX	glutaredoxin	-0.0728	**0.0340**	-0.4513	**0.0457**	**0.0196**	1484 ± 231	829 ± 69	846 ± 76	829 ± 166
203158_s_at	GLS	glutaminase	**-0.0238**	**0.0149**	-0.2128	0.3964	**0.0057**	369 ± 40	282 ± 19	238 ± 15	223 ± 31
203159_at	GLS	glutaminase	**-0.0018**	**0.0029**	0.4161	0.0655	0.0992	4277 ± 509	3496 ± 587	2869 ± 391	2548 ± 575
200947_s_at	GLUD1	glutamate dehydrogenase 1	**-0.0132**	**0.0043**	-0.2764	0.1425	**0.0154**	3533 ± 227	3447 ± 269	3268 ± 157	2427 ± 314
200946_x_at	GLUD1	glutamate dehydrogenase 1	**-0.0138**	**0.0113**	-0.4296	0.3589	**0.0293**	2361 ± 224	2204 ± 226	2169 ± 231	1452 ± 124
215794_x_at	GLUD2	Glutamate dehydrogenase-2	**-0.0324**	**0.0321**	**-0.0247**	0.4324	**0.0429**	773 ± 90	686 ± 96	530 ± 31	495 ± 10
200648_s_at	GLUL	glutamate-ammonia ligase	**-0.0268**	**0.0005**	-0.1397	-0.1009	0.0844	2336 ± 499	1694 ± 273	1658 ± 161	978 ± 281
220108_at	GNA14	guanine nucleotide binding protein , alpha 14	**-0.0085**	**0.0126**	0.1015	0.3239	**0.0000**	324 ± 22	346 ± 18	330 ± 26	139 ± 32
206355_at	GNAL	guanine nucleotide binding protein , alpha activating	**-0.0046**	**0.0088**	-0.2666	-0.4524	0.0962	373 ± 43	369 ± 41	325 ± 25	242 ± 40
204762_s_at	GNAO1	guanine nucleotide binding protein , alpha activating O	**-0.0011**	**0.0023**	**-0.0079**	0.1545	**0.0233**	1172 ± 122	1272 ± 160	738 ± 49	819 ± 163
200780_x_at	GNAS	GNAS complex locus	**-0.0186**	0.0570	**-0.0278**	0.1798	0.1125	15851 ± 558	14022 ± 958	5087 ± 805	2419 ± 1638
200981_x_at	GNAS	GNAS complex locus	**-0.0305**	**0.0024**	**-0.0022**	**0.0457**	**0.0103**	15590 ± 672	3173 ± 1079	3330 ± 573	0715 ± 1378
212273_x_at	GNAS	GNAS complex locus	**-0.0219**	**0.0040**	-0.4654	0.1431	**0.0151**	15346 ± 513	12684 ± 969	3037 ± 942	0407 ± 1560
214157_at	GNAS	GNAS complex locus	**-0.0060**	**0.0054**	**-0.0275**	0.2411	**0.0355**	1042 ± 146	815 ± 44	752 ± 77	610 ± 57
211858_x_at	GNAS	GNAS complex locus	**-0.0035**	**0.0316**	**-0.0004**	0.1307	**0.0152**	11748 ± 890	9345 ± 1392	7661 ± 752	6971 ± 1309
214548_x_at	GNAS	GNAS complex locus	**-0.0375**	**0.0242**	-0.2501	0.1925	0.0904	16408 ± 419	3885 ± 1321	3321 ± 650	2347 ± 1837
200744_s_at	GNB1	guanine nucleotide binding protein , beta polypeptide 1	**-0.0362**	0.2471	**-0.0395**	0.1740	0.1601	662 ± 73	474 ± 52	538 ± 58	482 ± 70
200745_s_at	GNB1	guanine nucleotide binding protein , beta polypeptide 1	**-0.0438**	**0.0026**	0.3629	0.4306	0.1644	3025 ± 216	2635 ± 201	2490 ± 136	2385 ± 290
222005_s_at	GNG3	guanine nucleotide binding protein , gamma 3	**0.0000**	**0.0012**	-0.2590	0.4586	**0.0265**	1904 ± 212	1866 ± 278	1615 ± 235	908 ± 115
210425_x_at	GOLGIN-67	golgin-67	**-0.0029**	**0.0176**	-0.1951	-0.2947	**0.0045**	1183 ± 100	960 ± 107	735 ± 120	581 ± 132
208798_x_at	GOLGIN-67	golgin-67	**-0.0213**	**0.0129**	-0.3284	0.2218	0.0616	1634 ± 134	1319 ± 108	1349 ± 188	978 ± 206
208843_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa	**-0.0307**	0.2282	**0.0177**	**-0.0397**	0.2384	1527 ± 62	1706 ± 66	1525 ± 55	1460 ± 136
207812_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa	**-0.0325**	0.0642	0.2441	-0.1270	0.0905	1314 ± 49	1373 ± 90	1258 ± 63	1096 ± 99
208813_at	GOT1	glutamic-oxaloacetic transaminase 1, soluble	**-0.0001**	**0.0276**	-0.4403	-0.1149	0.0628	1289 ± 242	987 ± 207	671 ± 139	546 ± 206
200708_at	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial	**-0.0218**	**0.0169**	0.0578	0.3800	**0.0222**	2442 ± 80	2450 ± 260	1863 ± 149	1913 ± 147
211060_x_at	GPAA1	GPAA1P anchor attachment protein 1 homolog	**-0.0332**	0.0627	0.2325	0.4906	0.2260	823 ± 51	843 ± 100	751 ± 70	639 ± 41

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
207174_at	GPC5	glypican 5	**-0.0112**	**0.0051**	0.4731	-0.3603	**0.0406**	282 ± 19	325 ± 57	299 ± 23	186 ± 23
208308_s_at	GPI	glucose phosphate isomerase	-0.0830	**0.0070**	-0.0721	0.3316	0.0886	3211 ± 320	2880 ± 412	2543 ± 252	1965 ± 388
209469_at	GPM6A	glycoprotein M6A	-0.0599	**0.0113**	-0.3806	-0.3004	0.0619	8482 ± 449	8256 ± 723	8168 ± 941	5772 ± 770
209470_s_at	GPM6A	glycoprotein M6A	**-0.0178**	**0.0038**	-0.2145	0.3256	**0.0334**	8036 ± 601	7569 ± 1000	6653 ± 847	4586 ± 876
221288_at	GPR22	G protein-coupled receptor 22	-0.0612	**0.0004**	-0.2999	**0.0149**	**0.0054**	335 ± 43	240 ± 40	141 ± 30	152 ± 48
209991_x_at	GPR51	G protein-coupled receptor 51	-0.1557	**0.0310**	-0.4349	-0.3161	0.1829	931 ± 85	1053 ± 219	883 ± 141	571 ± 141
209990_s_at	GPR51	G protein-coupled receptor 51	**-0.0048**	**0.0018**	-0.4705	0.1291	**0.0470**	5017 ± 552	4018 ± 595	3662 ± 651	2590 ± 496
211520_s_at	GRIA1	glutamate receptor, ionotropic, AMPA 1	-0.1427	**0.0179**	0.2507	0.1108	0.1953	259 ± 44	215 ± 38	173 ± 18	162 ± 29
209793_at	GRIA1	glutamate receptor, ionotropic, AMPA 1	**-0.0082**	**0.0078**	-0.4700	-0.0656	**0.0099**	2199 ± 276	1690 ± 389	993 ± 98	1055 ± 232
205358_at	GRIA2	glutamate receptor, ionotropic, AMPA 2	-0.3308	**0.0212**	-0.4981	0.1884	0.1726	7425 ± 317	7290 ± 456	7576 ± 717	5752 ± 860
206730_at	GRIA3	glutamate receptor, ionotrophic, AMPA 3	**-0.0076**	**0.0200**	-0.4489	-0.1211	**0.0056**	418 ± 23	513 ± 60	330 ± 34	297 ± 43
206534_at	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	**-0.0037**	**0.0104**	-0.2958	0.3293	**0.0454**	224 ± 30	262 ± 50	154 ± 34	112 ± 26
205541_s_at	GSPT2	G1 to S phase transition 2	-0.0554	**0.0482**	-0.2396	0.1623	0.0653	688 ± 62	493 ± 77	483 ± 36	471 ± 85
202967_at	GSTA4	glutathione S-transferase A4	**-0.0039**	**0.0238**	-0.2333	0.3244	**0.0393**	1906 ± 167	1579 ± 177	1373 ± 177	1230 ± 146
202554_s_at	GSTM3	glutathione S-transferase M3	**-0.0494**	0.5239	0.3724	-0.1898	0.5830	1344 ± 137	1484 ± 233	1133 ± 190	1206 ± 170
201470_at	GSTTLp28	glutathione-S-transferase like	**-0.0192**	**0.0057**	-0.4297	0.2103	0.1335	2576 ± 113	2481 ± 163	2180 ± 147	2180 ± 172
202678_at	GTF2A2	general transcription factor IIA, 2, 12kDa	**-0.0174**	0.1775	-0.0760	**0.0448**	0.1555	825 ± 39	670 ± 49	635 ± 64	683 ± 89
203817_at	GUCY1B3	guanylate cyclase 1, soluble, beta 3	**-0.0070**	**0.0084**	0.2298	0.0799	**0.0305**	2116 ± 325	1694 ± 248	1201 ± 176	1128 ± 205
200075_s_at	GUK1	guanylate kinase 1	**-0.0218**	**0.0216**	-0.2739	0.2388	0.0972	2769 ± 282	2417 ± 185	2167 ± 104	1947 ± 285
217717_s_at	GW128	GW128 protein	**-0.0375**	0.0797	-0.3434	-0.4699	0.2079	1948 ± 186	1734 ± 385	1256 ± 116	1349 ± 343
217718_s_at	GW128	GW128 protein	**-0.0360**	**0.0099**	-0.4800	0.2452	0.2347	11085 ± 706	10473 ± 927	9320 ± 633	8682 ± 1220
207168_s_at	H2AFY	H2A histone family, member Y	-0.1291	**0.0403**	0.4183	-0.3448	0.1239	2313 ± 103	2354 ± 77	2015 ± 99	1983 ± 224
212206_s_at	H2AV	histone H2A.F/Z variant	**-0.0090**	0.0697	-0.1319	-0.4535	0.1102	1000 ± 59	924 ± 60	831 ± 57	834 ± 33
201036_s_at	HADHSC	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	**-0.0441**	0.3749	0.4509	**-0.0162**	0.2154	760 ± 40	785 ± 78	792 ± 51	617 ± 82
211569_s_at	HADHSC	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-0.2232	**0.0493**	**-0.0326**	0.4335	0.2136	323 ± 24	333 ± 17	286 ± 24	272 ± 17
205635_at	HAPIP	huntingtin-associated protein interacting protein	**-0.0209**	**0.0174**	-0.4418	0.1694	0.0648	1278 ± 131	1066 ± 130	923 ± 98	855 ± 96
222230_s_at	HARP11	uncharacterized hypothalamus protein HARP11	**-0.0452**	**0.0330**	-0.3547	0.3908	0.0877	2093 ± 351	1677 ± 307	1216 ± 142	1178 ± 275
204018_x_at	HBA1	hemoglobin, alpha 1	-0.1249	**0.0122**	0.0574	-0.2787	**0.0051**	4439 ± 1068	7014 ± 1153	4733 ± 561	1422 ± 269
209458_x_at	HBA1	hemoglobin, alpha 1	-0.1122	**0.0231**	0.1172	-0.3316	**0.0324**	4638 ± 1110	6385 ± 1043	4326 ± 633	2051 ± 621
211699_x_at	HBA1	hemoglobin, alpha 1	-0.2131	**0.0305**	0.1510	-0.4571	**0.0498**	3245 ± 717	4454 ± 686	3322 ± 416	1756 ± 481
211745_x_at	HBA2	hemoglobin, alpha 2	-0.1882	**0.0257**	0.0684	-0.2924	**0.0165**	4677 ± 1127	7230 ± 1226	5047 ± 702	2120 ± 625
211696_x_at	HBB	hemoglobin, beta	-0.0567	**0.0299**	0.1455	-0.1629	**0.0259**	3914 ± 1009	5946 ± 1422	3800 ± 727	1259 ± 161
209116_x_at	HBB	hemoglobin, beta	-0.0697	**0.0419**	0.0576	-0.1058	**0.0134**	2072 ± 526	3804 ± 962	2316 ± 538	572 ± 78
202300_at	HBXIP	hepatitis B virus x interacting protein	**-0.0064**	**0.0042**	-0.2895	0.2019	0.0836	1516 ± 111	1377 ± 152	1137 ± 62	1147 ± 137
218467_at	HCCA3	hepatocellular carcinoma susceptibility protein	**-0.0231**	**0.0106**	-0.2880	-0.4819	**0.0164**	1907 ± 89	1799 ± 104	1547 ± 99	1462 ± 128
203745_at	HCCS	holocytochrome c synthase	**-0.0009**	**0.0072**	-0.3093	-0.4453	0.0609	587 ± 37	552 ± 66	474 ± 20	419 ± 56
208905_at	HCS	cytochrome c	**-0.0075**	**0.0032**	**-0.0511**	-0.2885	**0.0341**	5741 ± 469	5213 ± 723	4540 ± 314	3586 ± 502
218306_s_at	HERC1	hect carboxyl terminus) domain and RCC1 -like domain 1	**-0.0202**	**0.0071**	0.3356	0.2379	**0.0046**	1929 ± 123	1768 ± 140	1779 ± 167	1217 ± 52
217902_s_at	HERC2	hect domain and RLD 2	**-0.0264**	0.1259	-0.0589	-0.4307	0.4833	914 ± 68	869 ± 74	845 ± 64	762 ± 69

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
201944_at	HEXB	hexosaminidase B	**-0.0050**	**0.0543**	-0.0906	0.1638	0.2112	602 ± 45	581 ± 24	504 ± 43	487 ± 56
218839_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1	**-0.0400**	0.0615	0.3790	-0.4520	0.1372	726 ± 55	661 ± 94	684 ± 55	486 ± 92
200093_s_at	HINT1	histidine triad nucleotide binding protein 1	**-0.0001**	**0.0021**	**-0.0204**	0.2548	**0.0470**	2390 ± 334	2006 ± 222	1694 ± 160	1348 ± 172
218946_at	HIRIP5	HIRA interacting protein 5	**-0.0280**	0.0832	-0.4160	0.4486	0.3137	454 ± 48	424 ± 43	385 ± 32	348 ± 39
208729_x_at	HLA-B	major histocompatibility complex, class I, B	**-0.0055**	0.0931	-0.0585	-0.2397	0.1480	1209 ± 202	1093 ± 192	949 ± 112	649 ± 142
209140_x_at	HLA-B	major histocompatibility complex, class I, B	**-0.0074**	0.4501	-0.1541	-0.1751	0.4639	3521 ± 406	3219 ± 488	2945 ± 350	2575 ± 478
211529_x_at	HLA-G	HLA-G histocompatibility antigen, class I, G	**-0.0485**	0.1848	**-0.0247**	0.2852	0.1475	1182 ± 209	823 ± 174	1040 ± 189	580 ± 158
218152_at	HMG20A	high-mobility group 20A	**-0.0392**	0.1617	0.4775	-0.1772	0.4909	623 ± 55	614 ± 37	595 ± 43	520 ± 59
212434_at	HMGE	GrpE-like protein cochaperone	**-0.0009**	**0.0001**	-0.4224	-0.2795	**0.0095**	548 ± 25	486 ± 57	400 ± 41	333 ± 56
202579_x_at	HMGN4	high mobility group nucleosomal binding domain 4	**-0.0404**	**0.0126**	0.1915	-0.4326	**0.0002**	1078 ± 39	1052 ± 68	935 ± 35	741 ± 29
212626_x_at	HNRPC	heterogeneous nuclear ribonucleoprotein C	**-0.0328**	0.1576	**-0.0548**	-0.2072	**0.0372**	2259 ± 234	1908 ± 231	2192 ± 149	1408 ± 137
209330_s_at	HNRPD	heterogeneous nuclear ribonucleoprotein D	**-0.0248**	**0.0076**	0.3495	-0.3117	0.0614	540 ± 80	528 ± 42	411 ± 32	332 ± 26
209067_s_at	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	**-0.0418**	**0.0476**	0.1833	-0.1610	**0.0231**	1361 ± 155	1401 ± 193	1067 ± 121	755 ± 54
200097_s_at	HNRPK	heterogeneous nuclear ribonucleoprotein K	**-0.0275**	**0.0232**	0.2932	0.0725	0.0874	1828 ± 167	1974 ± 257	1650 ± 128	1260 ± 160
208766_s_at	HNRPR	heterogeneous nuclear ribonucleoprotein R	**-0.0354**	0.1974	-0.1714	0.3809	0.3686	2330 ± 131	2401 ± 73	2127 ± 92	2105 ± 202
205454_at	HPCA	hippocalcin	**-0.0190**	**0.0017**	-0.4129	0.2393	0.1540	5236 ± 932	4404 ± 1192	2761 ± 479	2990 ± 610
219671_at	HPCAL4	hippocalcin like 4	**-0.0541**	**0.0247**	-0.3544	0.1130	**0.0315**	1789 ± 211	1136 ± 179	1463 ± 196	994 ± 153
202854_at	HPRT1	hypoxanthine phosphoribosyltransferase 1	**-0.0033**	**0.0422**	-0.4344	-0.0586	**0.0108**	1908 ± 362	1344 ± 202	1012 ± 156	620 ± 101
217736_s_at	HRI	heme-regulated initiation factor 2-alpha kinase	**-0.0371**	**0.0462**	-0.1269	-0.3178	**0.0001**	2116 ± 111	2547 ± 55	1731 ± 75	1969 ± 113
206445_s_at	HRMT1L2	HMT1 hnRNP methyltransferase-like 2	**-0.0053**	**0.0027**	0.2747	0.1676	0.1883	1529 ± 115	1516 ± 170	1273 ± 33	1194 ± 159
219697_at	HS3ST2	heparan sulfate 3-O-sulfotransferase 2	**-0.0155**	**0.0099**	0.4324	0.1425	**0.0345**	1043 ± 105	945 ± 86	792 ± 95	649 ± 83
204722_at	HSA243396	voltage-gated sodium channel beta-3 subunit	**-0.0315**	**0.0123**	0.3146	0.0675	**0.0275**	4699 ± 791	3133 ± 355	2303 ± 321	2462 ± 668
204723_at	HSA243396	voltage-gated sodium channel beta-3 subunit	**-0.0202**	**0.0077**	0.2978	0.3616	**0.0337**	3718 ± 631	2296 ± 225	2073 ± 276	1984 ± 442
204405_x_at	HSA9761	putative dimethyladenosine transferase	**-0.0189**	0.3875	-0.4826	-0.0860	0.2417	874 ± 39	858 ± 50	883 ± 29	753 ± 70
218608_at	HSA9947	putative ATPase	-0.6319	**0.0398**	0.3550	0.3491	0.2830	929 ± 85	943 ± 109	877 ± 113	678 ± 99
217869_at	HSD17B12	hydroxysteroid dehydrogenase 12	**-0.0439**	0.7493	-0.3927	0.3385	0.6994	1847 ± 107	1619 ± 199	1624 ± 116	1700 ± 213
209657_s_at	HSF2	heat shock transcription factor 2	**-0.0239**	0.2089	0.4017	-0.0727	0.2622	275 ± 11	307 ± 42	258 ± 14	230 ± 33
212922_s_at	HSKM-B	HSKM-B protein	**-0.0012**	**0.0082**	**-0.0337**	0.0777	**0.0489**	829 ± 118	860 ± 93	665 ± 51	501 ± 41
208744_x_at	HSP105B	heat shock 105kD	**-0.0010**	**0.0119**	-0.3269	0.2570	**0.0150**	462 ± 55	309 ± 77	228 ± 37	220 ± 38
206976_s_at	HSP105B	heat shock 105kD	**-0.0018**	**0.0149**	**-0.0090**	0.1392	**0.0184**	5310 ± 630	3838 ± 557	2990 ± 331	2767 ± 715
211936_at	HSPA5	heat shock 70kDa protein 5	**-0.0218**	**0.0340**	-0.0645	0.1923	**0.0186**	2203 ± 259	1540 ± 177	1408 ± 167	1183 ± 238
221891_x_at	HSPA8	heat shock 70kDa protein 8	**-0.0347**	0.0939	-0.3889	0.2171	0.2543	5448 ± 810	4206 ± 773	4465 ± 691	3213 ± 602
210338_s_at	HSPA8	heat shock 70kDa protein 8	**-0.0108**	**0.0485**	-0.1140	0.1012	0.1169	3681 ± 862	2343 ± 602	2288 ± 441	1248 ± 553
208687_x_at	HSPA8	heat shock 70kDa protein 8	**-0.0044**	**0.0283**	-0.2667	0.1426	0.1074	3821 ± 653	2452 ± 466	2597 ± 396	2005 ± 444
200691_s_at	HSPA9B	heat shock 70kDa protein 9B	**-0.0072**	**0.0030**	**-0.0466**	0.2915	0.1030	1920 ± 102	1834 ± 86	1657 ± 78	1578 ± 141
218291_at	HSPC003	HSPC003 protein	**-0.0101**	**0.0046**	-0.4183	0.2948	**0.0218**	422 ± 16	406 ± 48	378 ± 35	284 ± 21
218026_at	HSPC009	HSPC009 protein	**-0.0461**	**0.0521**	0.2627	-0.3230	0.1358	2261 ± 60	2363 ± 282	2200 ± 117	1811 ± 151
218190_s_at	HSPC051	ubiquinol-cytochrome c reductase complex	**-0.0261**	**0.0071**	-0.4421	-0.4124	**0.0263**	6097 ± 570	6171 ± 548	4410 ± 394	4266 ± 643
221570_s_at	HSPC133	HSPC133 protein	**-0.0390**	0.0792	-0.2256	0.4812	0.1497	874 ± 70	782 ± 80	636 ± 80	671 ± 97

Probe set	Name	Description	$\mathrm{NFT_O}$	$\mathrm{MMSE_O}$	$\mathrm{NFT_I}$	$\mathrm{MMSE_I}$	ANOVA	Control	Incipient	Moderate	Severe
218491_s_at	HSPC144	HSPC144 protein	**-0.0004**	**0.0000**	-0.3992	0.1759	**0.0413**	989 ± 63	1049 ± 44	855 ± 54	741 ± 117
221597_s_at	HSPC171	HSPC171 protein	**-0.0009**	**0.0018**	**-0.0232**	0.0583	**0.0008**	718 ± 36	690 ± 54	576 ± 19	500 ± 21
211968_s_at	HSPCA	heat shock 90kDa protein 1, alpha	**-0.0382**	0.1059	**-0.0100**	0.1738	0.1110	4154 ± 682	2608 ± 460	3120 ± 537	2216 ± 401
200064_at	HSPCB	heat shock 90kDa protein 1, beta	**-0.0059**	**0.0203**	-0.0723	0.2991	**0.0042**	8350 ± 770	5982 ± 745	5472 ± 549	4407 ± 725
214359_s_at	HSPCB	heat shock 90kDa protein 1, beta	**-0.0001**	**0.0105**	**-0.0529**	-0.4753	0.0889	2432 ± 468	1818 ± 373	1593 ± 223	942 ± 393
200806_s_at	HSPD1	heat shock 60kDa protein 1	**-0.0402**	0.0995	-0.0793	-0.3346	0.1587	852 ± 128	675 ± 131	701 ± 67	475 ± 68
205133_s_at	HSPE1	heat shock 10kDa protein 1	**-0.0012**	**0.0065**	-0.1683	0.2496	**0.0188**	887 ± 40	834 ± 73	708 ± 44	631 ± 67
204521_at	HSU79274	protein predicted by clone 23733	**-0.0397**	**0.0532**	-0.3176	-0.2337	0.1279	783 ± 67	699 ± 80	594 ± 32	587 ± 67
221622_s_at	HT007	uncharacterized hypothalamus protein HT007	**-0.0187**	0.2901	-0.1958	-0.3127	0.2623	1619 ± 117	1583 ± 184	1251 ± 118	1417 ± 159
201595_s_at	HT010	uncharacterized hypothalamus protein HT010	**-0.0020**	**0.0087**	-0.3344	-0.2897	**0.0099**	1367 ± 109	1118 ± 133	973 ± 56	842 ± 123
204565_at	HT012	uncharacterized hypothalamus protein HT012	**-0.0020**	**0.0010**	-0.2409	0.1205	**0.0114**	685 ± 40	744 ± 51	524 ± 53	543 ± 59
219288_at	HT021	HT021	**-0.0346**	**0.0483**	-0.3616	-0.1653	**0.0053**	1391 ± 111	1120 ± 96	1007 ± 62	903 ± 93
207404_s_at	HTR1E	5-hydroxytryptamine receptor 1E	**-0.0485**	**0.0083**	0.4628	0.0563	**0.0346**	159 ± 31	165 ± 29	80 ± 10	85 ± 18
207135_at	HTR2A	5-hydroxytryptamine receptor 2A	-0.0763	**0.0076**	0.2894	0.4294	0.0662	955 ± 188	869 ± 142	633 ± 44	464 ± 66
200825_s_at	HYOU1	hypoxia up-regulated 1	**-0.0057**	**0.0135**	0.4911	0.3321	0.1428	3543 ± 82	3708 ± 359	3273 ± 264	2947 ± 126
204744_s_at	IARS	isoleucine-tRNA synthetase	**-0.0267**	**0.0046**	0.0880	0.0946	**0.0499**	2385 ± 217	2026 ± 159	1940 ± 159	1570 ± 229
203336_s_at	ICAP-1A	integrin cytoplasmic domain-associated protein 1	-0.1459	**0.0425**	0.3127	0.2854	0.1714	619 ± 92	658 ± 52	593 ± 60	422 ± 75
210418_s_at	IDH3B	isocitrate dehydrogenase 3 beta	**-0.0194**	**0.0505**	-0.3092	-0.1913	0.1327	678 ± 69	744 ± 128	574 ± 53	461 ± 55
210014_x_at	IDH3B	isocitrate dehydrogenase 3 beta	-0.0667	**0.0284**	0.3542	-0.1530	**0.0413**	1156 ± 85	1236 ± 91	1027 ± 47	915 ± 58
206342_x_at	IDS	iduronate 2-sulfatase	**-0.0071**	**0.0243**	-0.1804	0.1371	0.0975	771 ± 86	757 ± 103	670 ± 47	510 ± 55
202439_s_at	IDS	iduronate 2-sulfatase	**-0.0021**	**0.0006**	-0.2939	0.0865	0.3498	999 ± 53	989 ± 162	878 ± 91	765 ± 75
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	-0.1041	**0.0315**	-0.1982	-0.4728	**0.0451**	630 ± 73	636 ± 36	476 ± 68	352 ± 95
201642_at	IFNGR2	interferon gamma receptor 2	**-0.0005**	**0.0040**	-0.0768	0.2327	**0.0124**	1607 ± 83	1491 ± 26	1404 ± 66	1291 ± 42
202147_s_at	IFRD1	interferon-related developmental regulator 1	**-0.0121**	**0.0056**	0.2550	0.1383	**0.0093**	271 ± 31	235 ± 25	216 ± 28	116 ± 27
209541_at	IGF1	insulin-like growth factor 1	**-0.0322**	**0.0104**	-0.3300	-0.2736	0.1265	191 ± 16	186 ± 16	152 ± 14	140 ± 23
217805_at	ILF3	interleukin enhancer binding factor 3, 90kDa	**-0.0173**	**0.0027**	-0.3045	0.4752	**0.0016**	500 ± 38	502 ± 28	510 ± 18	340 ± 20
200084_at	IMAGE145052	small acidic protein	**-0.0305**	0.0878	0.4675	-0.3261	0.2146	2933 ± 219	2958 ± 284	2738 ± 245	2230 ± 302
204465_s_at	INA	internexin neuronal intermediate filament protein, alpha	**-0.0144**	**0.0006**	0.1510	0.4609	**0.0086**	2274 ± 293	2067 ± 333	1214 ± 134	1265 ± 119
214787_at	IRLB	c-myc promoter-binding protein	-0.0709	**0.0048**	**-0.0217**	0.1709	**0.0004**	214 ± 13	177 ± 9	207 ± 7	134 ± 15
210213_s_at	ITGB4BP	integrin beta 4 binding protein	**-0.0357**	0.1221	-0.1010	-0.3136	0.1684	498 ± 19	480 ± 61	469 ± 36	372 ± 30
217732_s_at	ITM2B	integral membrane protein 2B	**-0.0143**	0.1480	-0.3062	-0.3015	0.3425	7753 ± 278	8144 ± 340	6804 ± 759	6473 ± 1132
205874_at	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	-0.2895	**0.0031**	0.2679	0.2537	0.0842	363 ± 43	339 ± 46	290 ± 41	208 ± 41
203710_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	**-0.0267**	**0.0144**	0.3065	-0.4208	**0.0054**	1591 ± 180	1503 ± 153	1287 ± 124	810 ± 107
216944_s_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	**-0.0231**	**0.0260**	-0.4587	0.4591	0.0691	405 ± 70	325 ± 56	264 ± 44	188 ± 47
211323_s_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	**-0.0098**	**0.0472**	-0.1619	-0.2128	0.1661	187 ± 37	203 ± 50	114 ± 18	100 ± 39
209898_x_at	ITSN2	intersectin 2	-0.0950	**0.0147**	-0.4033	-0.2382	**0.0492**	1119 ± 96	1021 ± 84	1008 ± 59	797 ± 46
205842_s_at	JAK2	Janus kinase 2	-0.4365	**0.0469**	0.4782	-0.4874	0.1167	108 ± 10	123 ± 11	121 ± 12	83 ± 15
218976_at	JDP1	J domain containing protein 1	**-0.0270**	**0.0459**	-0.2447	0.3642	0.2171	1613 ± 64	1600 ± 285	1316 ± 126	1154 ± 190
203456_at	JM4	JM4 protein	**-0.0127**	0.1020	-0.1452	0.1227	0.2817	840 ± 50	776 ± 80	668 ± 40	712 ± 91

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
220188_at	JPH3	junctophilin 3	**-0.0210**	**0.0080**	-0.3868	0.1673	0.0710	243 ± 32	184 ± 43	138 ± 25	116 ± 35
205206_at	KAL1	Kallmann syndrome 1 sequence	**-0.0107**	**0.0035**	-0.3143	0.1739	0.0768	1764 ± 205	1563 ± 117	1447 ± 179	1100 ± 150
203162_s_at	KATNB1	katanin p80 subunit B 1	-0.0638	**0.0477**	0.2589	**0.0540**	0.4090	1834 ± 283	1631 ± 225	1405 ± 107	1363 ± 220
203163_at	KATNB1	katanin p80 subunit B 1	**-0.0045**	**0.0072**	0.2291	0.3477	**0.0546**	245 ± 28	229 ± 39	189 ± 27	125 ± 31
210078_s_at	KCNAB1	K+ VGC, shaker-related beta 1	**-0.0350**	**0.0088**	0.2890	0.1088	**0.0519**	1426 ± 219	1429 ± 270	894 ± 104	752 ± 188
210471_s_at	KCNAB1	K+ VGC, shaker-related beta 1	**-0.0120**	**0.0015**	0.4633	0.2535	**0.0206**	1031 ± 256	612 ± 125	315 ± 19	332 ± 63
203402_at	KCNAB2	K+ VGC, shaker-related beta 2	-0.1121	**0.0059**	-0.4954	0.0568	**0.0206**	1702 ± 110	1719 ± 263	1793 ± 187	1061 ± 65
207103_at	KCND2	K+ VGC, Shal-related 2	**-0.0303**	**0.0362**	-0.2481	**0.0262**	**0.0063**	599 ± 77	477 ± 67	334 ± 41	301 ± 50
210263_at	KCNF1	potassium voltage-gated channel, subfamily F, member 1	-0.2113	**0.0157**	0.1906	0.2435	0.1031	302 ± 39	284 ± 37	273 ± 47	165 ± 33
221307_at	KCNIP1	Kv channel interacting protein 1	**-0.0206**	**0.0139**	0.1317	0.1823	0.1303	255 ± 18	209 ± 25	201 ± 15	174 ± 38
207142_at	KCNJ3	K+ VGC inwardly-rectifying J 3	**-0.0253**	**0.0061**	0.2089	0.3596	0.0989	137 ± 26	136 ± 20	91 ± 13	72 ± 18
204679_at	KCNK1	potassium channel, subfamily K, member 1	-0.0952	**0.0487**	-0.4763	0.3852	0.4129	1263 ± 134	1316 ± 50	1146 ± 108	1007 ± 178
220116_at	KCNN2	K+ intermediate/small g Ca2+ activated channel N2	**-0.0196**	**0.0176**	0.1590	0.3121	**0.0323**	1195 ± 198	1025 ± 117	702 ± 60	658 ± 102
205737_at	KCNQ2	K+ VGC, KQT-like 2	-0.0579	**0.0165**	-0.3753	0.0906	0.1774	3002 ± 309	2645 ± 404	2203 ± 305	2083 ± 214
200698_at	KDELR2	KDEL endoplasmic reticulum protein retention receptor 2	**-0.0349**	0.1439	-0.1632	0.3752	0.2144	573 ± 46	557 ± 34	553 ± 93	395 ± 37
200040_at	KHDRBS1	KH domain containing, RNA binding, signal transd. assoc. 1	**-0.0081**	**0.0028**	0.4395	**0.0182**	0.0563	1524 ± 161	1641 ± 190	1178 ± 120	1093 ± 50
202753_at	KIAA0107	26S proteosome non-ATPase regulatory subunit	**-0.0121**	0.0856	-0.2772	0.2780	0.0835	1356 ± 110	1281 ± 137	961 ± 82	1106 ± 136
212215_at	KIAA0436	putative L-type neutral amino acid transporter	-0.0731	**0.0432**	-0.2785	-0.3937	**0.0468**	4121 ± 362	3701 ± 464	4198 ± 214	2676 ± 481
214788_x_at	KIAA0749	KIAA0749 protein/ Dendrin	**-0.0008**	**0.0080**	**-0.0137**	-0.2660	0.0565	3347 ± 309	3178 ± 591	2570 ± 333	1852 ± 351
210616_s_at	KIAA0905	yeast Sec31p homolog	-0.4756	**0.0264**	-0.1846	-0.2220	0.1029	1265 ± 62	1270 ± 46	1267 ± 51	1101 ± 43
200945_s_at	KIAA0905	yeast Sec31p homolog	**-0.0132**	**0.0047**	-0.3342	-0.2212	**0.0108**	2166 ± 81	1972 ± 97	1952 ± 102	1608 ± 156
215518_at	KIAA1006	tomosyn-like	**-0.0015**	**0.0020**	**-0.0208**	0.0694	**0.0480**	605 ± 42	628 ± 57	525 ± 44	446 ± 44
212163_at	KIDINS220	likely homolog of rat kinase D-interacting substance	**-0.0261**	**0.0233**	0.4004	0.3889	**0.0088**	2276 ± 58	2107 ± 68	1908 ± 62	1641 ± 238
209234_at	KIF1B	kinesin family member 1B	**-0.0038**	0.1867	**-0.0227**	0.2863	0.4746	5189 ± 229	4970 ± 315	4743 ± 209	4688 ± 277
203087_s_at	KIF2	kinesin heavy chain member 2	-0.0631	**0.0365**	0.4930	-0.2882	0.0784	710 ± 34	698 ± 73	600 ± 22	538 ± 62
203389_at	KIF3C	kinesin family member 3C	**-0.0286**	**0.0237**	-0.4724	0.1346	**0.0436**	2242 ± 292	1719 ± 177	1508 ± 161	1426 ± 151
203129_s_at	KIF5C	kinesin family member 5C	**-0.0269**	0.0934	-0.3165	-0.2285	0.3600	1174 ± 84	1206 ± 109	989 ± 104	1013 ± 115
203130_s_at	KIF5C	kinesin family member 5C	**-0.0446**	0.1471	**-0.0291**	0.4904	0.4423	9415 ± 336	8693 ± 827	8447 ± 608	8112 ± 467
203333_at	KIFAP3	kinesin-associated protein 3	**-0.0155**	**0.0191**	-0.4195	0.1154	0.1020	1100 ± 182	856 ± 128	669 ± 68	637 ± 162
205051_s_at	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncog. homolog	**-0.0041**	**0.0027**	0.2804	0.3225	**0.0200**	1882 ± 310	1350 ± 286	778 ± 44	1034 ± 200
205978_at	KL	klotho	**-0.0003**	**0.0033**	0.3164	-0.4851	**0.0238**	435 ± 84	390 ± 87	267 ± 41	143 ± 32
212877_at	KNS2	kinesin 2 60/70kDa	-0.0828	**0.0204**	-0.3794	0.1587	0.1179	2289 ± 394	1697 ± 330	1382 ± 231	1219 ± 328
212878_s_at	KNS2	kinesin 2 60/70kDa	-0.1316	**0.0477**	-0.3089	0.1352	0.2105	1692 ± 311	1254 ± 208	1092 ± 142	1020 ± 263
201088_at	KPNA2	karyopherin alpha 2	**-0.0066**	**0.0081**	-0.1845	-0.4971	**0.0015**	2522 ± 177	2083 ± 197	1668 ± 155	1585 ± 143
211762_s_at	KPNA2	karyopherin alpha 2	**-0.0060**	**0.0057**	-0.2107	0.3263	**0.0223**	828 ± 61	695 ± 98	529 ± 35	522 ± 93
221502_at	KPNA3	karyopherin alpha 3	**-0.0138**	**0.0084**	0.0589	-0.1254	**0.0502**	2414 ± 124	2197 ± 205	2077 ± 141	1716 ± 219
208975_s_at	KPNB1	karyopherin beta 1	**-0.0132**	**0.0031**	-0.4496	0.3078	**0.0362**	506 ± 21	527 ± 69	404 ± 16	365 ± 40
211952_at	KPNB3	karyopherin beta 3	**-0.0139**	0.1522	-0.1459	0.2778	0.1613	520 ± 25	428 ± 29	467 ± 50	395 ± 52
204584_at	L1CAM	L1 cell adhesion molecule syndrome, spastic paraplegia 1)	**-0.0373**	**0.0373**	-0.3482	0.2040	**0.0145**	1150 ± 186	1054 ± 148	613 ± 53	597 ± 40

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
211597_s_at	LAGY	lung cancer-associated Y protein	**-0.0129**	**0.0060**	0.2778	0.1769	0.1144	2302 ± 194	1797 ± 154	1639 ± 221	1573 ± 332
202020_s_at	LANCL1	LanC lantibiotic synthetase component C-like 1	**-0.0101**	0.1851	-0.3821	0.4683	0.5044	4720 ± 276	4653 ± 622	4430 ± 364	3857 ± 465
215543_s_at	LARGE	like-glycosyltransferase	**-0.0087**	**0.0010**	-0.3993	0.1717	0.0571	1140 ± 101	1081 ± 158	834 ± 66	770 ± 87
214039_s_at	LC27	putative integral membrane transporter	**-0.0154**	0.4047	0.2847	-0.1397	0.5371	2458 ± 147	2600 ± 299	2326 ± 93	2187 ± 221
206481_s_at	LDB2	LIM domain binding 2	**-0.0002**	**0.0015**	-0.0827	-0.3715	**0.0074**	1740 ± 347	1243 ± 204	796 ± 104	560 ± 95
200650_s_at	LDHA	lactate dehydrogenase A	**-0.0092**	**0.0320**	-0.4322	0.3628	**0.0054**	5673 ± 285	4997 ± 758	4079 ± 292	3184 ± 540
204454_at	LDOC1	leucine zipper, down-regulated in cancer 1	**-0.0214**	0.0792	-0.3766	0.3726	0.1781	2494 ± 326	2308 ± 440	1660 ± 111	1850 ± 203
209867_s_at	LEC3	KIAA0768 protein	**-0.0021**	**0.0067**	**-0.0271**	-0.4897	0.0902	719 ± 65	633 ± 76	647 ± 98	425 ± 80
203619_s_at	LFG	lifeguard	**0.0000**	**0.0033**	**-0.0256**	-0.3466	**0.0416**	2634 ± 203	2468 ± 295	2140 ± 163	1807 ± 135
208936_x_at	LGALS8	lectin, galactoside-binding, soluble, 8	**-0.0056**	**0.0037**	-0.4613	0.1241	**0.0073**	532 ± 12	528 ± 40	388 ± 35	379 ± 57
208934_s_at	LGALS8	lectin, galactoside-binding, soluble, 8	**-0.0102**	**0.0088**	0.4526	0.1155	**0.0242**	354 ± 37	301 ± 36	222 ± 27	201 ± 49
211219_s_at	LHX2	LIM homeobox protein 2	**-0.0293**	0.0822	0.4641	0.2976	0.3964	464 ± 31	451 ± 23	369 ± 59	373 ± 66
209205_s_at	LMO4	LIM domain only 4	**-0.0432**	**0.0057**	0.3782	-0.1588	**0.0324**	3592 ± 560	2627 ± 498	1970 ± 239	1845 ± 387
213510_x_at	LOC220594	TL132 protein	**-0.0384**	0.5947	0.2075	**-0.0214**	0.6152	2490 ± 121	2565 ± 153	2429 ± 226	2220 ± 211
219363_s_at	LOC51001	CGI-12 protein	**-0.0019**	**0.0013**	0.4726	-0.4585	**0.0060**	416 ± 17	431 ± 12	384 ± 25	318 ± 26
218628_at	LOC51019	CGI-116 protein	**-0.0326**	0.5029	-0.2642	-0.0944	0.5482	408 ± 25	434 ± 72	436 ± 27	338 ± 73
218193_s_at	LOC51026	CGI-141 protein	-0.0662	**0.0287**	-0.3640	0.4606	0.0793	254 ± 17	239 ± 21	214 ± 22	169 ± 31
209092_s_at	LOC51031	CGI-150 protein	**-0.0073**	**0.0070**	0.1319	0.2019	**0.0026**	738 ± 55	652 ± 72	571 ± 64	369 ± 42
219065_s_at	LOC51072	C21orf19-like protein	**-0.0034**	0.7906	-0.1375	-0.3174	0.7946	708 ± 20	670 ± 53	657 ± 27	652 ± 67
217748_at	LOC51094	CGI-45 protein	**-0.0424**	**0.0340**	0.4373	-0.0725	**0.0130**	1141 ± 45	1214 ± 78	994 ± 28	985 ± 51
203721_s_at	LOC51096	CGI-48 protein	**-0.0007**	0.1188	-0.1623	**0.0444**	0.1178	783 ± 50	697 ± 16	621 ± 19	667 ± 83
201825_s_at	LOC51097	CGI-49 protein	**-0.0471**	0.2683	-0.3802	-0.2278	**0.0524**	488 ± 40	484 ± 53	320 ± 31	417 ± 64
218664_at	LOC51102	CGI-63 protein	**-0.0135**	**0.0156**	0.4146	0.4646	**0.0255**	237 ± 18	283 ± 17	244 ± 20	146 ± 49
218059_at	LOC51123	HSPC038 protein	**-0.0401**	0.4048	**0.0097**	**-0.0067**	**0.0004**	1544 ± 49	1855 ± 57	1203 ± 79	1552 ± 126
217720_at	LOC51142	16.7Kd protein	**-0.0265**	0.0969	-0.4313	0.1931	0.1023	5411 ± 491	4552 ± 626	3525 ± 209	4180 ± 696
219212_at	LOC51182	likely ortholog of mouse heat shock protein, 70 kDa 4	**-0.0317**	**0.0224**	-0.0907	0.2725	0.1240	294 ± 42	260 ± 45	185 ± 31	168 ± 50
218671_s_at	LOC51189	ATPase inhibitor precursor	**-0.0214**	0.0607	0.4905	-0.2050	0.3419	903 ± 86	923 ± 113	798 ± 79	682 ± 121
218657_at	LOC51195	Link guanine nucleotide exchange factor II	-0.1778	**0.0184**	**-0.0451**	**0.0488**	**0.0305**	760 ± 53	459 ± 72	633 ± 128	377 ± 110
220890_s_at	LOC51202	hqp0256 protein	**-0.0156**	**0.0362**	-0.2420	-0.2503	0.0973	917 ± 34	821 ± 77	812 ± 45	720 ± 60
221069_s_at	LOC51204	clone HQ0477 PRO0477p	-0.5506	**0.0201**	-0.4025	0.1120	0.2245	362 ± 30	334 ± 11	311 ± 25	290 ± 26
218915_at	LOC51219	clone FLB5214	**-0.0481**	0.0815	-0.1092	0.1043	0.3074	1333 ± 145	1144 ± 122	1190 ± 31	1036 ± 86
218135_at	LOC51290	CDA14	**-0.0061**	**0.0187**	0.3293	-0.1997	0.0999	548 ± 29	510 ± 46	484 ± 20	420 ± 47
217990_at	LOC51292	GMPR2 for guanosine monophosphate reductase isolog	-0.0575	**0.0338**	0.0754	-0.0959	0.0894	640 ± 20	636 ± 60	584 ± 21	487 ± 67
205331_s_at	LOC51308	SGC32445 protein	-0.1475	**0.0292**	0.4047	0.2224	0.1718	721 ± 52	796 ± 91	743 ± 76	573 ± 49
219872_at	LOC51313	AD021 protein	-0.4511	**0.0442**	0.1116	0.1389	0.2708	93 ± 14	85 ± 15	80 ± 19	49 ± 16
221488_s_at	LOC51596	divalent cation tolerant protein CUTA	**-0.0174**	0.1974	0.3259	0.3374	0.2527	3518 ± 253	3562 ± 235	2957 ± 75	3196 ± 292
201973_s_at	LOC51622	CGI-43 protein	**-0.0414**	**0.0150**	-0.2863	0.0971	**0.0446**	2750 ± 146	2793 ± 181	2536 ± 108	2178 ± 188
203763_at	LOC51626	CGI-60 protein	-0.1172	**0.0009**	0.0572	-0.3188	**0.0179**	437 ± 36	462 ± 43	377 ± 41	280 ± 35
203762_s_at	LOC51626	CGI-60 protein	-0.0721	**0.0086**	0.3567	0.3152	0.0763	300 ± 49	235 ± 28	204 ± 44	144 ± 33

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
218732_at	LOC51651	CGI-147 protein	**-0.0060**	0.1236	0.0673	-0.3140	0.0950	419 ± 27	458 ± 6	340 ± 32	343 ± 60
215691_x_at	LOC51668	HSPCO34 protein	-0.1426	**0.0099**	0.4755	0.1328	**0.0148**	1060 ± 77	878 ± 36	916 ± 40	782 ± 30
203960_s_at	LOC51668	HSPCO34 protein	-0.0671	**0.0149**	-0.4219	0.2746	0.1197	166 ± 21	155 ± 18	125 ± 26	89 ± 28
217811_at	LOC51714	selenoprotein T	**-0.0356**	**0.0094**	-0.2472	-0.4963	0.0779	1080 ± 125	956 ± 95	736 ± 96	694 ± 142
220046_s_at	LOC57018	cyclin L ania-6a	**-0.0176**	0.5403	**-0.0028**	0.4446	0.1491	851 ± 54	707 ± 32	702 ± 33	755 ± 78
221679_s_at	LOC57406	lipase protein	-0.1809	**0.0211**	-0.1301	0.2143	0.1288	154 ± 32	157 ± 31	139 ± 16	71 ± 25
45288_at	LOC57406	lipase protein	**-0.0287**	**0.0117**	0.1829	0.1629	**0.0178**	1012 ± 41	915 ± 40	867 ± 37	805 ± 55
221020_s_at	LOC81034	folate transporter/carrier	**-0.0162**	**0.0047**	-0.4168	0.2421	0.0596	450 ± 62	369 ± 17	342 ± 9	276 ± 44
206953_s_at	LPHH1	latrophilin 1	**-0.0127**	**0.0020**	0.0665	-0.3828	**0.0322**	387 ± 42	327 ± 44	306 ± 21	213 ± 42
219643_at	LRP1B	low density lipoprotein-related protein 1B	**-0.0047**	**0.0216**	0.2200	-0.3432	**0.0119**	685 ± 73	705 ± 54	628 ± 62	404 ± 53
205282_at	LRP8	low density lipoprotein receptor-related protein 8	**-0.0340**	**0.0214**	-0.4762	0.2861	0.0920	476 ± 41	481 ± 48	421 ± 28	342 ± 48
211971_s_at	LRPPRC	leucine-rich PPR-motif containing	-0.0824	**0.0091**	0.4138	0.3324	0.0602	982 ± 112	1016 ± 109	845 ± 21	669 ± 54
209840_s_at	LRRN3	leucine-rich repeat protein, neuronal 3	-0.0560	**0.0405**	0.3458	-0.0574	0.0842	461 ± 37	507 ± 57	461 ± 33	343 ± 46
202209_at	LSM3	Lsm3 protein	**-0.0355**	**0.0075**	0.3358	0.2455	0.1840	710 ± 49	696 ± 76	584 ± 46	545 ± 81
202736_s_at	LSM4	U6 snRNA-associated Sm-like protein	**-0.0249**	0.1251	-0.4933	-0.4034	0.2614	415 ± 35	469 ± 21	382 ± 27	344 ± 75
211747_s_at	LSM5	U6 snRNA-associated Sm-like protein	**-0.0108**	0.0794	0.4092	-0.2786	0.2686	460 ± 26	480 ± 33	391 ± 14	388 ± 69
202904_s_at	LSM5	U6 snRNA-associated Sm-like protein	**-0.0187**	**0.0002**	-0.2231	0.1074	**0.0151**	92 ± 9	95 ± 9	93 ± 7	55 ± 6
218729_at	LXN	latexin protein	**-0.0155**	0.1529	-0.4764	0.3223	0.1136	139 ± 20	111 ± 15	65 ± 16	94 ± 33
219042_at	LZTS1	leucine zipper, putative tumor suppressor 1	**-0.0492**	**0.0008**	-0.4643	0.0945	**0.0024**	350 ± 44	266 ± 29	253 ± 46	118 ± 22
47550_at	LZTS1	leucine zipper, putative tumor suppressor 1	**-0.0046**	**0.0021**	0.2507	-0.4562	**0.0242**	558 ± 38	504 ± 56	462 ± 47	359 ± 30
212716_s_at	M9	muscle specific gene	**-0.0036**	**0.0046**	-0.4584	0.3427	**0.0120**	1812 ± 153	1708 ± 148	1434 ± 93	1186 ± 79
210501_x_at	M9	muscle specific gene	**-0.0051**	**0.0091**	-0.3337	0.1736	**0.0154**	1979 ± 170	1775 ± 185	1597 ± 92	1251 ± 79
221494_x_at	M9	muscle specific gene	**-0.0160**	**0.0095**	0.2801	0.3368	**0.0501**	2060 ± 141	1816 ± 197	1684 ± 138	1446 ± 56
209704_at	M96	likely ortholog of m. metal resp. element binding t.f. 2	-0.0781	**0.0340**	**0.0307**	-0.2700	0.0634	100 ± 9	122 ± 12	103 ± 11	74 ± 14
209014_at	MAGED1	melanoma antigen, family D, 1	**-0.0033**	**0.0015**	0.2771	0.4525	**0.0369**	3178 ± 433	2993 ± 317	2108 ± 176	2053 ± 181
219894_at	MAGEL2	MAGE-like 2	-0.1227	**0.0232**	0.4401	0.0626	0.3472	260 ± 29	219 ± 17	203 ± 36	186 ± 32
221760_at	MAN1A1	mannosidase, alpha, class 1A, member 1	**-0.0251**	**0.0034**	**-0.0281**	**0.0459**	**0.0099**	1111 ± 134	1039 ± 197	703 ± 68	531 ± 73
212741_at	MAOA	monoamine oxidase A	**-0.0452**	**0.0185**	-0.4700	0.1163	**0.0208**	1373 ± 102	1190 ± 59	1159 ± 76	993 ± 58
212508_at	MAP-1	modulator of apoptosis 1	**-0.0403**	**0.0202**	**-0.0292**	0.1064	**0.0272**	3675 ± 630	2771 ± 366	1647 ± 146	2163 ± 459
203151_at	MAP1A	microtubule-associated protein 1A	-0.2343	**0.0081**	-0.3772	0.1957	0.0963	11713 ± 600	1413 ± 1101	1388 ± 1115	8799 ± 488
202670_at	MAP2K1	mitogen-activated protein kinase kinase 1	-0.0653	**0.0425**	0.4379	0.0944	0.1021	2563 ± 551	1749 ± 385	1204 ± 88	1449 ± 403
217971_at	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting 1	-0.1034	**0.0370**	-0.2423	0.3544	0.1706	586 ± 30	599 ± 25	518 ± 32	484 ± 63
203266_s_at	MAP2K4	mitogen-activated protein kinase kinase 4	**-0.0172**	**0.0071**	-0.4511	-0.4046	**0.0378**	1519 ± 123	1249 ± 198	936 ± 93	1072 ± 171
218311_at	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	**-0.0286**	0.1537	0.2173	-0.4260	0.3954	587 ± 58	562 ± 64	479 ± 38	479 ± 62
212271_at	MAPK1	mitogen-activated protein kinase 1	**-0.0209**	0.0785	-0.2387	0.1111	0.3031	2107 ± 208	1703 ± 270	1471 ± 231	1562 ± 348
204813_at	MAPK10	mitogen-activated protein kinase 10	**-0.0432**	0.1331	0.2602	0.4829	0.3283	2161 ± 145	2139 ± 175	1800 ± 144	1930 ± 184
202530_at	MAPK14	mitogen-activated protein kinase 14	-0.1179	**0.0099**	0.4739	0.1149	0.1209	508 ± 23	480 ± 42	468 ± 29	401 ± 17
213014_at	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	**-0.0340**	0.2862	0.2459	0.0680	0.4696	217 ± 31	189 ± 16	158 ± 12	187 ± 34
203218_at	MAPK9	mitogen-activated protein kinase 9	**-0.0439**	**0.0247**	-0.3259	0.2509	0.0858	805 ± 82	747 ± 87	645 ± 44	536 ± 82

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
214270_s_at	MAPRE3	microtubule-associated protein, RP/EB family, member 3	**-0.0472**	0.0614	-0.4599	0.3210	0.2952	357 ± 56	316 ± 50	295 ± 36	216 ± 60
203841_x_at	MAPRE3	microtubule-associated protein, RP/EB family, member 3	**0.0000**	**0.0001**	**-0.0004**	0.1363	0.0948	269 ± 50	205 ± 61	132 ± 29	117 ± 44
213672_at	MARS	methionine-tRNA synthetase	**-0.0226**	0.3944	-0.1594	0.4726	0.6085	318 ± 38	341 ± 50	272 ± 43	268 ± 46
201475_x_at	MARS	methionine-tRNA synthetase	**-0.0446**	**0.0036**	0.3505	0.2150	**0.0000**	1803 ± 60	1457 ± 118	1293 ± 46	1100 ± 71
217956_s_at	MASA	E-1 enzyme	**-0.0234**	**0.0007**	0.0920	0.3833	**0.0204**	1996 ± 152	2047 ± 77	1881 ± 36	1455 ± 177
206267_s_at	MATK	megakaryocyte-associated tyrosine kinase	**-0.0206**	0.1345	-0.3783	-0.2390	0.2885	272 ± 30	307 ± 49	284 ± 41	195 ± 42
200626_s_at	MATR3	matrin 3	-0.0676	**0.0097**	-0.2578	0.2684	0.0855	4287 ± 485	4195 ± 251	3500 ± 364	2701 ± 604
218440_at	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1	**-0.0475**	0.2399	0.2557	-0.3499	0.2535	569 ± 36	614 ± 34	565 ± 47	499 ± 26
209623_at	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2	**-0.0180**	0.1887	0.3108	0.3034	0.3790	912 ± 55	895 ± 27	754 ± 53	812 ± 129
222036_s_at	MCM4	MCM4 minichromosome maintenance deficient 4	**-0.0130**	**0.0129**	0.4999	0.2440	**0.0106**	222 ± 24	248 ± 14	186 ± 15	151 ± 20
218163_at	MCT-1	MCT-1 protein	**-0.0418**	0.0853	-0.4930	0.3843	0.1596	567 ± 87	495 ± 97	338 ± 38	378 ± 84
200978_at	MDH1	malate dehydrogenase 1, NAD	**-0.0225**	**0.0067**	-0.4993	0.2123	0.0694	6822 ± 1292	5583 ± 1159	3397 ± 658	3337 ± 1012
213333_at	MDH2	malate dehydrogenase 2, NAD	**-0.0290**	0.0646	-0.2571	0.1177	**0.0172**	841 ± 51	728 ± 28	654 ± 34	718 ± 22
209036_s_at	MDH2	malate dehydrogenase 2, NAD	**-0.0333**	**0.0106**	0.3196	0.3564	**0.0251**	1706 ± 193	1448 ± 138	1135 ± 72	1085 ± 178
218877_s_at	MDS024	MDS024 protein	**-0.0061**	0.0959	0.3106	0.4829	0.3173	410 ± 43	399 ± 48	339 ± 33	304 ± 56
218597_s_at	MDS029	uncharacterized hematopoietic stem/progenitor cells MDS029	-0.0895	**0.0429**	-0.4335	0.1578	0.1530	1009 ± 189	709 ± 144	639 ± 66	585 ± 118
221706_s_at	MDS032	uncharacterized hematopoietic stem/progenitor cells MDS032	-0.1350	**0.0151**	0.0706	0.2262	0.0562	263 ± 15	290 ± 41	256 ± 8	190 ± 23
204059_s_at	ME1	malic enzyme 1, NADP-dependent, cytosolic	-0.2868	**0.0186**	0.3213	0.2996	0.2666	699 ± 32	692 ± 20	671 ± 50	585 ± 61
204663_at	ME3	malic enzyme 3, NADP-dependent, mitochondrial	-0.1852	**0.0115**	0.1769	0.2631	0.1509	510 ± 77	522 ± 56	417 ± 42	342 ± 12
207079_s_at	MED6	RNA polymerase II transcriptional regulation mediator	**-0.0332**	0.5551	-0.3561	-0.2726	0.7401	269 ± 15	266 ± 32	253 ± 26	227 ± 43
212535_at	MEF2A	MADS box transcription enhancer factor 2, polypeptide A	**-0.0192**	0.6612	**-0.0416**	-0.2256	0.4413	1536 ± 46	1513 ± 128	1675 ± 133	1375 ± 181
209199_s_at	MEF2C	MADS box transcription enhancer factor 2, polypeptide C	**-0.0450**	0.2145	-0.2858	**-0.0316**	0.2992	668 ± 59	749 ± 83	625 ± 62	562 ± 58
212732_at	MEG3	maternally expressed 3	-0.1756	**0.0205**	-0.3999	0.3011	0.2164	1063 ± 73	1062 ± 123	1031 ± 128	781 ± 83
203510_at	MET	met proto-oncogene	**-0.0023**	**0.0158**	**-0.0349**	-0.2853	**0.0457**	731 ± 191	652 ± 190	275 ± 45	240 ± 72
212673_at	METAP1	methionyl aminopeptidase 1	**-0.0418**	0.1857	0.2926	0.2774	0.3786	946 ± 66	877 ± 51	822 ± 41	828 ± 66
217043_s_at	MFN1	mitofusin 1	**-0.0095**	0.2386	**-0.0507**	-0.1041	0.2106	327 ± 27	324 ± 25	303 ± 22	244 ± 43
207098_s_at	MFN1	mitofusin 1	**-0.0095**	**0.0143**	**-0.0216**	0.4838	**0.0226**	247 ± 13	248 ± 20	238 ± 17	175 ± 20
212945_s_at	MGA	MAX dimerization protein 5	**-0.0120**	**0.0423**	0.4682	-0.3527	**0.0362**	254 ± 36	219 ± 15	225 ± 36	111 ± 27
217800_s_at	MGC10924	hypothetical protein MGC10924	**-0.0276**	**0.0013**	0.4876	**0.0005**	0.1601	3223 ± 379	3042 ± 423	2440 ± 218	2133 ± 455
212411_at	MGC19606	similar to HYPOTHETICAL 34.0 KDA PROTEIN ZK795.3	**-0.0051**	**0.0004**	**-0.0014**	**0.0302**	**0.0063**	911 ± 42	761 ± 36	763 ± 53	673 ± 42
203545_at	MGC2840	hypothetical protein MGC2840	**-0.0177**	**0.0033**	-0.1921	**0.0069**	**0.0000**	701 ± 15	636 ± 19	517 ± 19	569 ± 18
220966_x_at	MGC3038	hypothetical protein similar to actin related protein 2/3 5	**-0.0506**	**0.0283**	-0.4716	0.4071	0.1756	1548 ± 158	1445 ± 107	1260 ± 81	1202 ± 102
200899_s_at	MGEA5	meningioma expressed antigen 5	**-0.0275**	0.7519	-0.2568	0.1994	0.8733	2114 ± 128	1937 ± 176	1989 ± 173	1954 ± 187
211026_s_at	MGLL	monoglyceride lipase	**-0.0015**	**0.0080**	-0.3895	0.4265	0.0667	2671 ± 109	2619 ± 222	2221 ± 173	2142 ± 133
201403_s_at	MGST3	microsomal glutathione S-transferase 3	**-0.0137**	**0.0019**	**-0.0088**	**0.0224**	**0.0493**	4095 ± 297	3818 ± 369	3422 ± 281	2804 ± 353
209209_s_at	MIG2	mitogen inducible 2	**-0.0057**	0.0745	-0.3279	-0.3744	0.1408	304 ± 38	266 ± 59	190 ± 25	190 ± 29
218138_at	MKKS	McKusick-Kaufman syndrome	**-0.0008**	**0.0034**	0.2264	0.3450	**0.0006**	850 ± 26	662 ± 68	568 ± 29	589 ± 52
201318_s_at	MLCB	myosin, light polypeptide, regulatory, non-sarcomeric	**-0.0026**	**0.0101**	0.4656	0.3700	**0.0274**	1451 ± 65	1399 ± 151	1156 ± 131	916 ± 172
221474_at	MLC-B	myosin regulatory light chain	**-0.0223**	**0.0152**	0.1860	0.2933	0.1091	4248 ± 449	4205 ± 714	3291 ± 379	2589 ± 574

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
200948_at	MLF2	myeloid leukemia factor 2	**-0.0239**	0.0678	-0.2245	-0.1881	0.2238	2621 ± 195	2764 ± 300	2411 ± 169	2102 ± 229
203414_at	MMD	monocyte to macrophage differentiation-associated	**-0.0466**	**0.0279**	-0.4554	0.2713	0.0775	4073 ± 602	3966 ± 1019	2254 ± 250	2240 ± 430
204959_at	MNDA	myeloid cell nuclear differentiation antigen	**-0.0468**	0.3856	**0.0000**	**-0.0024**	0.0823	90 ± 7	140 ± 19	104 ± 27	69 ± 15
217873_at	MO25	MO25 protein	**-0.0105**	**0.0013**	-0.2833	0.2293	0.0849	1409 ± 149	1172 ± 151	985 ± 73	978 ± 150
218212_s_at	MOCS2	molybdenum cofactor synthesis 2	**-0.0526**	**0.0175**	-0.2544	0.3474	0.1032	691 ± 51	620 ± 84	582 ± 42	443 ± 99
209582_s_at	MOX2	antigen identified by monoclonal antibody MRC OX-2	**-0.0077**	**0.0053**	-0.2712	0.2555	**0.0115**	309 ± 42	260 ± 25	204 ± 13	174 ± 18
209583_s_at	MOX2	antigen identified by monoclonal antibody MRC OX-2	**-0.0089**	**0.0063**	-0.0604	0.2531	**0.0284**	1448 ± 162	1191 ± 134	1053 ± 109	874 ± 85
205273_s_at	MP1	metalloprotease 1	**-0.0035**	**0.0023**	-0.1599	-0.4753	0.0917	891 ± 69	873 ± 72	724 ± 68	660 ± 84
202974_at	MPP1	membrane protein, palmitoylated 1, 55kDa	**-0.0365**	**0.0486**	0.2817	-0.2191	**0.0250**	916 ± 68	890 ± 63	764 ± 38	623 ± 96
214071_at	MPPE1	metallo phosphoesterase	**-0.0229**	**0.0117**	**-0.0429**	0.3221	0.1863	314 ± 21	346 ± 44	296 ± 24	226 ± 56
203466_at	MPV17	MpV17 transgene, murine homolog, glomerulosclerosis	**-0.0019**	**0.0002**	**-0.0220**	**0.0269**	0.0767	315 ± 46	286 ± 69	181 ± 51	136 ± 47
204386_s_at	MRP63	mitochondrial ribosomal protein 63	**-0.0483**	0.3436	-0.4124	0.4109	0.3709	2267 ± 164	2117 ± 110	1886 ± 111	2071 ± 206
218049_s_at	MRPL13	mitochondrial ribosomal protein L13	**-0.0183**	0.0815	0.3909	0.1454	0.4149	237 ± 15	216 ± 20	198 ± 15	181 ± 43
218027_at	MRPL15	mitochondrial ribosomal protein L15	**-0.0022**	**0.0004**	0.3348	0.1211	**0.0001**	692 ± 42	522 ± 42	394 ± 49	399 ± 32
217980_s_at	MRPL16	mitochondrial ribosomal protein L16	**-0.0428**	**0.0046**	0.2555	0.4913	**0.0046**	627 ± 42	555 ± 12	485 ± 55	402 ± 9
217907_at	MRPL18	mitochondrial ribosomal protein L18	**-0.0397**	0.1117	0.4519	-0.4517	**0.0485**	1080 ± 49	1025 ± 68	850 ± 29	927 ± 89
203465_at	MRPL19	mitochondrial ribosomal protein L19	-0.2313	**0.0268**	-0.3700	0.2463	0.0643	172 ± 16	178 ± 24	188 ± 32	100 ± 18
220526_s_at	MRPL20	mitochondrial ribosomal protein L20	**-0.0023**	**0.0030**	-0.2427	0.2419	**0.0349**	1511 ± 153	1513 ± 43	1209 ± 109	1043 ± 127
218339_at	MRPL22	mitochondrial ribosomal protein L22	**-0.0332**	0.8265	-0.0710	-0.2524	0.8795	375 ± 23	361 ± 38	361 ± 14	340 ± 44
208787_at	MRPL3	mitochondrial ribosomal protein L3	**-0.0023**	**0.0002**	0.0934	0.0856	**0.0275**	1304 ± 99	1199 ± 125	1024 ± 55	880 ± 114
218106_s_at	MRPS10	mitochondrial ribosomal protein S10	-0.0944	**0.0169**	**0.0258**	-0.4331	0.0617	709 ± 47	825 ± 50	681 ± 24	625 ± 67
221437_s_at	MRPS15	mitochondrial ribosomal protein S15	-0.3056	**0.0267**	-0.2717	0.2956	0.0923	206 ± 25	163 ± 30	120 ± 18	119 ± 38
219819_s_at	MRPS28	mitochondrial ribosomal protein S28	**-0.0275**	0.1570	0.3632	-0.1572	0.3578	389 ± 32	374 ± 62	302 ± 28	285 ± 64
209421_at	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1	-0.2981	**0.0487**	-0.4509	-0.4918	0.1766	255 ± 25	208 ± 29	197 ± 21	176 ± 29
217772_s_at	MTCH2	mitochondrial carrier homolog 2	**-0.0203**	0.6855	0.2472	0.4905	0.8003	592 ± 27	599 ± 53	536 ± 56	586 ± 63
202309_at	MTHFD1	methylenetetrahydrofolate dehydrogenase	**-0.0054**	**0.0126**	-0.1471	0.2275	**0.0026**	911 ± 76	868 ± 86	722 ± 34	554 ± 44
216095_x_at	MTMR1	myotubularin related protein 1	**-0.0096**	0.1270	-0.2918	0.3099	0.3767	1334 ± 78	1252 ± 56	1249 ± 39	1151 ± 95
212277_at	MTMR4	myotubularin related protein 4	**-0.0251**	0.4555	-0.1919	0.3735	0.3577	893 ± 39	854 ± 43	759 ± 55	796 ± 91
213278_at	MTMR9	myotubularin related protein 9	-0.0762	**0.0041**	-0.4788	0.2304	**0.0424**	1222 ± 67	1093 ± 54	979 ± 74	969 ± 78
203517_at	MTX2	metaxin 2	**-0.0250**	**0.0019**	-0.3111	0.3382	**0.0269**	651 ± 65	488 ± 78	438 ± 54	375 ± 58
211276_at	my048	my048 protein	**-0.0012**	**0.0006**	-0.1518	0.1210	**0.0200**	4285 ± 328	3738 ± 337	3392 ± 309	2771 ± 318
210016_at	MYT1L	myelin transcription factor 1-like	**-0.0200**	**0.0138**	-0.2545	0.4071	**0.0097**	4307 ± 343	3359 ± 488	2698 ± 385	2224 ± 531
219368_at	NAP1L2	nucleosome assembly protein 1-like 2	**-0.0071**	**0.0274**	-0.2094	-0.4379	**0.0370**	2608 ± 419	1948 ± 373	1304 ± 172	1302 ± 348
200027_at	NARS	asparaginyl-tRNA synthetase	**-0.0088**	**0.0024**	-0.4416	0.2773	**0.0324**	5969 ± 298	5177 ± 478	5037 ± 112	4550 ± 340
201521_s_at	NCBP2	nuclear cap binding protein subunit 2, 20kDa	-0.4544	**0.0299**	-0.2954	0.3438	0.3870	186 ± 15	177 ± 22	165 ± 27	131 ± 26
209159_s_at	NDRG4	NDRG family member 4	**-0.0050**	**0.0006**	-0.0851	0.0636	**0.0369**	4100 ± 455	3612 ± 619	2957 ± 380	2038 ± 470
217860_at	NDUFA10	NADH dehydrogenase 1 alpha subcomplex, 10, 42kDa	**-0.0434**	**0.0368**	0.3786	-0.1656	**0.0057**	2018 ± 143	1727 ± 104	1598 ± 74	1384 ± 129
209224_s_at	NDUFA2	NADH dehydrogenase 1 alpha subcomplex, 2, 8kDa	**-0.0036**	**0.0006**	0.3884	0.2012	0.0767	1716 ± 111	1767 ± 170	1625 ± 99	1297 ± 134
218563_at	NDUFA3	NADH dehydrogenase 1 alpha subcomplex, 3, 9kDa	**-0.0545**	**0.0039**	-0.4208	0.0993	**0.0447**	3350 ± 308	2820 ± 142	2831 ± 265	2282 ± 170

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
217773_s_at	NDUFA4	NADH dehydrogenase 1 alpha subcomplex, 4, 9kDa	**-0.0144**	**0.0013**	0.4001	0.4492	**0.0071**	6163 ± 670	5522 ± 595	4688 ± 346	3212 ± 376
201304_at	NDUFA5	NADH dehydrogenase 1 alpha subcomplex, 5, 13kDa	**-0.0071**	**0.0002**	0.3567	0.1482	**0.0095**	2449 ± 361	2224 ± 321	1732 ± 161	988 ± 155
202785_at	NDUFA7	NADH dehydrogenase 1 alpha subcomplex, 7, 14.5kDa	-0.2010	**0.0456**	-0.3884	0.2929	0.1759	249 ± 37	207 ± 66	219 ± 38	105 ± 40
218160_at	NDUFA8	NADH dehydrogenase 1 alpha subcomplex, 8, 19kDa	**-0.0060**	**0.0107**	0.4807	-0.3705	**0.0043**	1703 ± 159	1552 ± 98	1284 ± 79	1073 ± 99
202077_at	NDUFAB1	NADH dehydrogenase 1, alpha/beta subcomplex, 1, 8kDa	**-0.0410**	0.1346	-0.2825	-0.4230	0.2644	2399 ± 265	2293 ± 364	1626 ± 260	1837 ± 366
206790_s_at	NDUFB1	NADH dehydrogenase 1 beta subcomplex, 1, 7kDa	**-0.0081**	**0.0173**	-0.2001	0.1919	0.0554	3317 ± 277	3188 ± 328	2827 ± 65	2319 ± 282
218201_at	NDUFB2	NADH dehydrogenase 1 beta subcomplex, 2, 8kDa	**-0.0063**	0.1520	0.4852	-0.4253	0.2779	1311 ± 73	1229 ± 86	1132 ± 93	1058 ± 135
218200_s_at	NDUFB2	NADH dehydrogenase 1 beta subcomplex, 2, 8kDa	**-0.0237**	**0.0393**	-0.1550	0.4898	0.0642	3210 ± 265	2755 ± 243	2524 ± 198	2284 ± 261
203371_s_at	NDUFB3	NADH dehydrogenase 1 beta subcomplex, 3, 12kDa	-0.1416	**0.0104**	**-0.0468**	**0.0024**	**0.0302**	1218 ± 95	961 ± 31	1007 ± 66	877 ± 92
218226_s_at	NDUFB4	NADH dehydrogenase 1 beta subcomplex, 4, 15kDa	**-0.0197**	**0.0142**	-0.4017	0.4832	0.0593	3537 ± 236	3153 ± 440	2255 ± 156	2471 ± 541
203621_at	NDUFB5	NADH dehydrogenase 1 beta subcomplex, 5, 16kDa	**-0.0026**	**0.0001**	**-0.0405**	0.1912	0.1054	1380 ± 145	1304 ± 128	1092 ± 137	909 ± 137
201227_s_at	NDUFB8	NADH dehydrogenase 1 beta subcomplex, 8, 19kDa	-0.1365	**0.0281**	-0.3266	-0.4453	**0.0533**	4664 ± 273	4595 ± 281	4721 ± 222	3774 ± 221
201226_at	NDUFB8	NADH dehydrogenase 1 beta subcomplex, 8, 19kDa	**-0.0379**	**0.0221**	-0.1945	0.0709	**0.0007**	2559 ± 119	2383 ± 192	2165 ± 199	1444 ± 95
218101_s_at	NDUFC2	NADH dehydrogenase 1, subcomplex unknown, 2, 14.5kDa	**-0.0241**	0.0889	0.4872	0.4107	0.2271	3256 ± 364	2834 ± 422	2387 ± 244	2325 ± 404
201966_at	NDUFS2	NADH dehydrogenase Fe-S protein 2, 49kDa	**-0.0469**	**0.0066**	0.2873	0.3658	0.1620	1533 ± 101	1437 ± 125	1245 ± 63	1249 ± 138
201740_at	NDUFS3	NADH dehydrogenase Fe-S protein 3, 30kDa	**-0.0299**	**0.0107**	0.4564	0.1919	0.0721	1888 ± 202	1832 ± 172	1513 ± 128	1282 ± 174
209303_at	NDUFS4	NADH dehydrogenase Fe-S protein 4, 18kDa	**-0.0010**	**0.0002**	0.4638	0.3367	**0.0113**	870 ± 127	679 ± 76	454 ± 25	502 ± 58
202941_at	NDUFV2	NADH dehydrogenase flavoprotein 2, 24kDa	**-0.0189**	**0.0007**	0.3506	0.1201	**0.0012**	1319 ± 117	1252 ± 97	970 ± 63	753 ± 66
201840_at	NEDD8	neural precursor cell expressed, develop. down-reg. 8	**-0.0509**	**0.0349**	**-0.0109**	0.2999	0.0880	1296 ± 78	1003 ± 166	1033 ± 79	817 ± 193
205113_at	NEF3	neurofilament 3	**-0.0257**	**0.0041**	0.4448	0.1919	**0.0111**	4061 ± 648	3177 ± 430	2827 ± 587	1320 ± 203
33767_at	NEFH	neurofilament, heavy polypeptide 200kDa	-0.1762	**0.0214**	-0.4405	0.0567	0.0786	2478 ± 444	1742 ± 392	2283 ± 617	817 ± 213
204412_s_at	NEFH	neurofilament, heavy polypeptide 200kDa	-0.1085	**0.0260**	-0.3640	-0.4297	0.1779	780 ± 113	873 ± 164	582 ± 181	422 ± 125
221805_at	NEFL	neurofilament, light polypeptide 68kDa	**-0.0234**	**0.0352**	0.4124	0.2082	**0.0383**	4381 ± 1058	3055 ± 656	2244 ± 574	1184 ± 340
206089_at	NELL1	NEL-like 1	-0.0574	**0.0067**	-0.2908	**0.0448**	**0.0042**	285 ± 72	88 ± 20	72 ± 13	50 ± 10
203413_at	NELL2	NEL-like 2	**-0.0190**	**0.0033**	-0.2954	0.2036	0.1661	4911 ± 740	4055 ± 797	2973 ± 346	3149 ± 780
206949_s_at	NESCA	nesca protein	-0.1969	**0.0457**	-0.2894	0.3162	**0.0259**	1761 ± 77	1782 ± 215	1217 ± 80	1556 ± 148
217979_at	NET-6	transmembrane 4 superfamily member tetraspan NET-6	**-0.0016**	**0.0002**	-0.3553	0.0663	**0.0359**	3470 ± 405	2691 ± 451	2277 ± 298	1814 ± 427
218888_s_at	NETO2	neuropilin and tolloid -like 2	**-0.0017**	**0.0020**	-0.1374	0.1561	**0.0046**	617 ± 68	501 ± 87	367 ± 35	273 ± 64
206282_at	NEUROD1	neurogenic differentiation 1	**-0.0024**	**0.0087**	-0.3558	0.0902	**0.0017**	681 ± 46	546 ± 94	334 ± 47	351 ± 71
220045_at	NEUROD6	neurogenic differentiation 6	**-0.0058**	**0.0007**	-0.1649	0.4237	**0.0141**	1251 ± 143	1088 ± 203	552 ± 40	781 ± 176
202216_x_at	NFYC	nuclear transcription factor Y, gamma	**-0.0018**	**0.0080**	-0.2709	0.3458	**0.0039**	327 ± 28	343 ± 13	304 ± 17	215 ± 19
217963_s_at	NGFRAP1	nerve growth factor receptor associated protein 1	**-0.0051**	**0.0000**	-0.0980	**0.0174**	**0.0515**	4275 ± 1218	2004 ± 1573	560 ± 1114	8777 ± 1681
201077_s_at	NHP2L1	NHP2 non-histone chromosome protein 2-like 1	**-0.0095**	**0.0417**	-0.1985	-0.3776	**0.0001**	1996 ± 74	1860 ± 49	1599 ± 43	1487 ± 108
218133_s_at	NIF3L1	NIF3 NGG1 interacting factor 3-like 1	**-0.0289**	0.1257	-0.4701	-0.2797	0.3518	413 ± 40	418 ± 61	301 ± 47	305 ± 95
202475_at	NIFIE14	seven transmembrane domain protein	**-0.0038**	0.1706	**-0.0091**	0.1416	0.1809	1663 ± 77	1554 ± 159	1268 ± 99	1392 ± 193
209075_s_at	NIFU	nitrogen fixation cluster-like	**-0.0278**	0.0597	-0.4466	0.1517	**0.0328**	4324 ± 578	3463 ± 363	2433 ± 141	3145 ± 409
201709_s_at	NIPSNAP1	nipsnap homolog 1	-0.2214	**0.0386**	0.2985	-0.4741	0.2267	1968 ± 141	1988 ± 146	1730 ± 237	1517 ± 148
218557_at	NIT2	Nit protein 2	-0.1438	**0.0447**	0.1931	0.3439	0.2335	346 ± 38	410 ± 36	326 ± 32	293 ± 46
203830_at	NJMU-R1	protein kinase Njmu-R1	**-0.0108**	**0.0074**	-0.3828	-0.1864	0.0931	58 ± 6	59 ± 10	34 ± 10	37 ± 9

Probe set	**Name**	**Description**	**$\mathrm{NFT_O}$**	**$\mathrm{MMSE_O}$**	**$\mathrm{NFT_I}$**	**$\mathrm{MMSE_I}$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
201577_at	NME1	non-metastatic cells 1, protein expressed in	**-0.0002**	**0.0132**	-0.0693	0.0805	**0.0177**	1677 ± 98	2013 ± 333	1526 ± 93	996 ± 222
201268_at	NME2	non-metastatic cells 2, protein expressed in	**-0.0145**	**0.0032**	-0.2512	0.3514	**0.0064**	1952 ± 82	1698 ± 146	1798 ± 89	1366 ± 127
203103_s_at	NMP200	nuclear matrix protein NMP200	**-0.0341**	**0.0024**	**0.0429**	0.3751	**0.0176**	1385 ± 113	1182 ± 120	1138 ± 89	879 ± 87
204239_s_at	NNAT	neuronatin	**-0.0396**	0.1151	0.0817	-0.3799	0.1211	1299 ± 171	1763 ± 335	1005 ± 133	1085 ± 222
202783_at	NNT	nicotinamide nucleotide transhydrogenase	**-0.0029**	**0.0114**	-0.1005	0.1905	**0.0063**	341 ± 38	362 ± 27	314 ± 38	174 ± 21
202784_s_at	NNT	nicotinamide nucleotide transhydrogenase	**-0.0013**	**0.0122**	-0.1247	0.4157	**0.0449**	198 ± 31	156 ± 19	134 ± 16	103 ± 11
211951_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	**-0.0409**	**0.0022**	-0.3290	0.3990	**0.0121**	1501 ± 60	1406 ± 72	1202 ± 68	1241 ± 78
214321_at	NOV	nephroblastoma overexpressed gene	-0.1281	**0.0404**	0.2049	0.1919	0.2718	1006 ± 317	910 ± 184	678 ± 104	443 ± 104
204743_at	NP25	neuronal protein	**-0.0241**	**0.0106**	0.4970	0.4269	**0.0145**	2850 ± 382	2492 ± 307	2221 ± 204	1447 ± 56
39548_at	NPAS2	neuronal PAS domain protein 2	-0.5133	**0.0117**	**0.0311**	0.4752	0.0715	177 ± 11	187 ± 20	172 ± 9	137 ± 4
39549_at	NPAS2	neuronal PAS domain protein 2	**-0.0119**	**0.0014**	-0.2237	0.2086	**0.0114**	522 ± 41	458 ± 64	499 ± 29	309 ± 42
209460_at	NPD009	NPD009 protein	-0.1446	**0.0279**	-0.1857	0.1349	**0.0510**	2303 ± 212	1766 ± 64	2044 ± 227	1564 ± 55
201455_s_at	NPEPPS	aminopeptidase puromycin sensitive	-0.0614	**0.0161**	-0.1344	0.1045	0.1133	926 ± 91	891 ± 58	690 ± 86	625 ± 142
206001_at	NPY	neuropeptide Y	**-0.0072**	**0.0138**	-0.3774	0.2133	**0.0025**	1142 ± 89	1099 ± 195	535 ± 42	672 ± 126
210519_s_at	NQO1	NADH dehydrogenase, quinone 1	**-0.0358**	0.2118	-0.1587	0.2682	0.3495	642 ± 66	552 ± 39	532 ± 43	522 ± 42
204791_at	NR2C1	nuclear receptor subfamily 2, group C, member 1	**-0.0041**	0.1308	-0.4607	-0.3655	0.2050	472 ± 19	454 ± 23	431 ± 13	402 ± 36
204081_at	NRGN	neurogranin	-0.1228	**0.0144**	0.4557	0.4226	0.1521	7959 ± 1379	7205 ± 1175	415 ± 1423	3975 ± 469
202599_s_at	NRIP1	nuclear receptor interacting protein 1	**-0.0056**	**0.0128**	-0.4870	0.1262	**0.0152**	1262 ± 102	1025 ± 115	1138 ± 41	818 ± 96
218625_at	NRN1	neuritin 1	**-0.0024**	**0.0003**	-0.2290	0.2579	**0.0422**	3559 ± 427	2601 ± 201	2165 ± 159	2177 ± 540
209915_s_at	NRXN1	neurexin 1	**-0.0079**	**0.0137**	-0.1905	-0.3132	**0.0018**	579 ± 84	426 ± 80	276 ± 46	185 ± 48
209914_s_at	NRXN1	neurexin 1	**-0.0029**	**0.0383**	**-0.0535**	0.1016	0.0756	560 ± 66	470 ± 78	368 ± 45	327 ± 72
216096_s_at	NRXN1	neurexin 1	**-0.0097**	**0.0029**	0.1970	-0.2620	**0.0116**	283 ± 34	184 ± 19	191 ± 8	176 ± 21
209025_s_at	NSAP1	NS1-associated protein 1	**-0.0216**	**0.0264**	**0.0432**	-0.0668	**0.0043**	421 ± 21	441 ± 42	415 ± 40	255 ± 20
203939_at	NT5E	5'-nucleotidase, ecto	**-0.0245**	**0.0286**	-0.2781	0.1989	**0.0176**	201 ± 9	220 ± 22	193 ± 30	116 ± 22
208093_s_at	NUDEL	LIS1-interacting protein NUDEL; endooligopeptidase A	-0.1093	**0.0245**	-0.0876	0.4134	0.1349	1368 ± 79	1202 ± 169	1170 ± 142	954 ± 76
219855_at	NUDT11	nudix -type motif 11	**-0.0020**	**0.0004**	-0.1390	0.4005	0.1961	822 ± 117	698 ± 107	530 ± 129	530 ± 81
205136_s_at	NUFIP1	nuclear fragile X mental retardation protein interacting 1	**-0.0020**	**0.0369**	-0.2454	-0.1031	**0.0055**	524 ± 17	536 ± 22	481 ± 19	437 ± 10
209073_s_at	NUMB	numb homolog	-0.0627	**0.0119**	-0.0953	-0.4586	**0.0273**	404 ± 19	394 ± 17	388 ± 19	314 ± 30
202097_at	NUP153	nucleoporin 153kDa	**-0.0134**	**0.0004**	-0.2728	0.2734	0.0851	831 ± 37	871 ± 83	777 ± 38	662 ± 53
201599_at	OAT	ornithine aminotransferase	**-0.0105**	**0.0067**	0.4922	**0.0457**	**0.0057**	3989 ± 367	3826 ± 163	3166 ± 292	2391 ± 306
201364_s_at	OAZ2	ornithine decarboxylase antizyme 2	-0.1004	**0.0379**	-0.0793	0.3236	0.2038	1194 ± 102	1069 ± 117	1035 ± 83	847 ± 150
212461_at	OAZIN	ornithine decarboxylase antizyme inhibitor	**-0.0493**	0.0727	0.3947	0.3702	0.1639	1273 ± 105	1195 ± 142	978 ± 74	997 ± 87
205728_at	ODZ1	odz, odd Oz/ten-m homolog 1	**-0.0164**	**0.0062**	-0.0712	0.3985	**0.0306**	386 ± 51	257 ± 15	252 ± 40	215 ± 33
207564_x_at	OGT	O-linked N-acetylglucosamine transferase	**-0.0084**	**0.0004**	-0.4563	0.3596	**0.0238**	555 ± 75	450 ± 73	458 ± 50	243 ± 39
205591_at	OLFM1	olfactomedin 1	**-0.0251**	0.0739	-0.4644	0.0994	0.3852	6279 ± 762	5627 ± 798	5286 ± 494	4436 ± 725
207093_s_at	OMG	oligodendrocyte myelin glycoprotein	**-0.0155**	0.2818	-0.3327	-0.2008	0.5925	2977 ± 180	3050 ± 321	2794 ± 229	2606 ± 241
214306_at	OPA1	optic atrophy 1	-0.2031	**0.0313**	-0.3732	**0.0246**	0.1938	883 ± 65	859 ± 76	909 ± 91	677 ± 49
212214_at	OPA1	optic atrophy 1	**-0.0093**	**0.0040**	0.3319	0.1592	**0.0053**	1264 ± 89	1152 ± 77	988 ± 66	857 ± 74
212213_x_at	OPA1	optic atrophy 1	**-0.0418**	**0.0255**	-0.3638	0.0986	**0.0276**	1940 ± 198	1709 ± 69	1346 ± 122	1362 ± 141

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
210028_s_at	ORC3L	origin recognition complex, subunit 3-like	**-0.0078**	**0.0054**	-0.4835	0.0662	**0.0397**	441 ± 40	384 ± 36	428 ± 38	268 ± 58
204957_at	ORC5L	origin recognition complex, subunit 5-like	**-0.0425**	0.0823	**-0.0323**	0.3690	0.4154	562 ± 18	506 ± 62	497 ± 34	462 ± 48
219073_s_at	OSBPL10	oxysterol binding protein-like 10	-0.0608	**0.0010**	-0.3575	0.4733	**0.0007**	324 ± 34	288 ± 50	325 ± 28	122 ± 14
202780_at	OXCT	3-oxoacid CoA transferase	**-0.0106**	**0.0157**	0.3498	0.4755	**0.0185**	1429 ± 195	1041 ± 43	883 ± 85	849 ± 127
218197_s_at	OXR1	oxidation resistance 1	**-0.0311**	**0.0019**	**0.0539**	-0.4047	0.0559	406 ± 72	326 ± 53	244 ± 37	202 ± 38
201832_s_at	P115	vesicle docking protein p115	**-0.0128**	0.0672	-0.3007	0.4243	0.1143	978 ± 96	858 ± 150	654 ± 41	653 ± 131
209175_at	P125	Sec23-interacting protein p125	**-0.0101**	**0.0456**	-0.3456	0.2038	**0.0041**	343 ± 16	369 ± 23	308 ± 13	275 ± 10
218320_s_at	P17.3	neuronal protein 17.3	**-0.0130**	**0.0255**	0.4359	0.1730	0.2742	1269 ± 108	1360 ± 88	1223 ± 60	1086 ± 87
200627_at	P23	unactive progesterone receptor, 23 kD	**-0.0356**	0.3229	-0.0748	-0.3196	0.5814	3914 ± 362	3739 ± 501	3559 ± 288	3082 ± 473
201310_s_at	P311	P311 protein	**-0.0241**	**0.0082**	-0.2780	-0.2836	**0.0451**	2591 ± 247	2064 ± 73	2288 ± 222	1723 ± 190
219825_at	P450RAI-2	cytochrome P450 retinoid metabolizing protein	**-0.0156**	**0.0352**	**-0.0474**	0.1346	**0.0113**	381 ± 68	348 ± 78	356 ± 59	89 ± 32
217831_s_at	p47	p47	-0.2827	**0.0279**	**-0.0362**	0.2512	0.2037	381 ± 39	345 ± 46	331 ± 24	270 ± 32
207543_s_at	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase , alpha I	**-0.0110**	0.0648	-0.0619	-0.3645	0.1284	784 ± 116	721 ± 66	660 ± 45	478 ± 72
208639_x_at	P5	protein disulfide isomerase-related protein	**-0.0129**	0.2781	**-0.0052**	0.3345	0.0898	961 ± 72	781 ± 73	932 ± 97	691 ± 47
207668_x_at	P5	protein disulfide isomerase-related protein	**-0.0257**	0.1825	**-0.0037**	0.2605	0.1631	884 ± 84	743 ± 92	855 ± 87	622 ± 45
200813_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase, Ib alpha	**-0.0129**	**0.0117**	-0.4800	0.4024	0.0989	1369 ± 154	1104 ± 121	1125 ± 90	890 ± 137
208051_s_at	PAIP1	polyadenylate binding protein-interacting protein 1	**-0.0267**	**0.0141**	-0.4156	0.4076	0.2375	1268 ± 93	1295 ± 128	1127 ± 119	919 ± 198
209064_x_at	PAIP1	polyadenylate binding protein-interacting protein 1	**-0.0474**	**0.0005**	-0.4297	**0.0191**	0.1220	2361 ± 246	1952 ± 195	2073 ± 83	1464 ± 407
210076_x_at	PAI-RBP1	PAI-1 mRNA-binding protein	-0.0715	**0.0091**	-0.0828	**0.0437**	**0.0003**	760 ± 53	507 ± 44	562 ± 22	509 ± 26
214607_at	PAK3	p21 -activated kinase 3	**-0.0213**	**0.0125**	-0.4008	0.3293	**0.0403**	3105 ± 117	2810 ± 340	2598 ± 311	2016 ± 192
219461_at	PAK6	p21-activated kinase 6	-0.1484	**0.0085**	0.1117	0.1009	0.1197	538 ± 46	472 ± 46	483 ± 60	363 ± 41
202336_s_at	PAM	peptidylglycine alpha-amidating monooxygenase	-0.0618	**0.0160**	0.4777	0.2203	0.0995	3470 ± 502	2627 ± 424	2615 ± 303	1932 ± 393
212958_x_at	PAM	peptidylglycine alpha-amidating monooxygenase	**-0.0002**	**0.0016**	-0.2800	0.2760	0.0704	2255 ± 227	1815 ± 329	1599 ± 204	1329 ± 226
218771_at	PANK4	pantothenate kinase 4	-0.4683	**0.0294**	-0.3618	-0.3598	0.1265	363 ± 31	373 ± 34	327 ± 25	274 ± 19
204715_at	PANX1	pannexin 1	**-0.0343**	0.0906	**-0.0089**	0.2841	0.0762	164 ± 17	120 ± 22	111 ± 6	102 ± 22
209043_at	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	**-0.0039**	**0.0071**	0.4994	0.3565	**0.0100**	2555 ± 140	2424 ± 222	2112 ± 97	1703 ± 237
217908_s_at	PC326	PC326 protein	**-0.0158**	**0.0027**	0.4009	0.2370	**0.0513**	603 ± 82	530 ± 53	451 ± 43	362 ± 40
221727_at	PC4	activated RNA polymerase II transcription cofactor 4	**-0.0078**	**0.0122**	-0.3851	0.1149	**0.0283**	2553 ± 473	2166 ± 448	1397 ± 195	967 ± 197
214512_s_at	PC4	activated RNA polymerase II transcription cofactor 4	**-0.0068**	**0.0163**	-0.1728	0.4287	**0.0185**	789 ± 101	588 ± 96	434 ± 43	447 ± 90
212857_x_at	PC4	activated RNA polymerase II transcription cofactor 4	**-0.0015**	**0.0283**	0.3702	-0.3935	**0.0489**	4244 ± 257	3621 ± 495	3166 ± 296	2818 ± 434
203860_at	PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide	**-0.0499**	0.1059	-0.1605	0.1538	0.1963	297 ± 18	247 ± 22	226 ± 21	243 ± 39
212694_s_at	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	**-0.0049**	**0.0251**	-0.0580	-0.3601	0.0763	356 ± 28	358 ± 47	271 ± 23	256 ± 37
210292_s_at	PCDH11X	protocadherin 11 X-linked	**-0.0497**	**0.0120**	-0.3257	-0.2192	**0.0146**	311 ± 36	217 ± 51	164 ± 25	143 ± 26
210273_at	PCDH7	BH-protocadherin	-0.1650	**0.0388**	0.1026	0.3394	0.2562	873 ± 62	941 ± 114	771 ± 105	699 ± 54
210674_s_at	PCDHA12	protocadherin alpha 12	**-0.0492**	0.0954	-0.4893	-0.4816	0.2197	828 ± 93	707 ± 97	692 ± 62	589 ± 47
213558_at	PCLO	piccolo	-0.1420	**0.0107**	-0.3489	0.1684	0.1069	2361 ± 276	2045 ± 296	2102 ± 266	1348 ± 186
205202_at	PCMT1	protein-L-isoaspartate O-methyltransferase	**-0.0375**	0.1014	0.4182	0.3935	0.3436	3286 ± 405	2972 ± 433	2490 ± 231	2460 ± 425
201202_at	PCNA	proliferating cell nuclear antigen	**-0.0342**	0.3086	-0.2987	-0.0732	0.4688	565 ± 54	534 ± 75	517 ± 65	409 ± 95
203660_s_at	PCNT2	pericentrin 2	**-0.0063**	0.1465	**-0.0208**	-0.4415	0.2669	1071 ± 43	995 ± 130	880 ± 55	890 ± 75

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
205549_at	PCP4	Purkinje cell protein 4	-0.0731	**0.0132**	-0.3427	**0.0067**	**0.0098**	2632 ± 442	1385 ± 316	2131 ± 138	1094 ± 196
205825_at	PCSK1	proprotein convertase subtilisin/kexin type 1	-0.0760	**0.0201**	0.3026	0.3018	0.1015	359 ± 117	225 ± 62	185 ± 45	70 ± 20
204870_s_at	PCSK2	proprotein convertase subtilisin/kexin type 2	**-0.0450**	**0.0133**	0.2045	-0.4055	0.0735	625 ± 85	600 ± 172	438 ± 72	265 ± 38
204869_at	PCSK2	proprotein convertase subtilisin/kexin type 2	**-0.0332**	**0.0098**	0.4376	0.0683	0.0737	1857 ± 373	1579 ± 349	1418 ± 240	714 ± 96
207239_s_at	PCTK1	PCTAIRE protein kinase 1	-0.1262	**0.0343**	-0.1361	0.1521	0.2667	547 ± 58	510 ± 70	507 ± 38	394 ± 17
221918_at	PCTK2	PCTAIRE protein kinase 2	**-0.0434**	0.2272	-0.3523	0.3467	0.5912	2675 ± 247	2497 ± 329	2336 ± 155	2201 ± 264
213581_at	PDCD2	programmed cell death 2	**-0.0162**	**0.0467**	-0.2544	-0.2499	0.2017	407 ± 33	385 ± 25	339 ± 16	321 ± 43
219275_at	PDCD5	programmed cell death 5	**-0.0043**	**0.0001**	**-0.0098**	0.2160	0.1481	221 ± 13	199 ± 20	208 ± 18	156 ± 27
204134_at	PDE2A	phosphodiesterase 2A, cGMP-stimulated	-0.1847	**0.0032**	0.2138	0.2123	**0.0489**	2889 ± 141	3178 ± 355	2889 ± 331	2049 ± 212
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific	**-0.0326**	0.3534	-0.1073	-0.4451	0.4626	1664 ± 158	1521 ± 211	1541 ± 204	1219 ± 233
204491_at	PDE4D	phosphodiesterase 4D, cAMP-specific	-0.2492	**0.0324**	-0.4339	-0.4607	0.1627	461 ± 36	439 ± 37	400 ± 17	358 ± 37
214130_s_at	PDE4DIP	phosphodiesterase 4D interacting protein	**-0.0469**	0.6333	-0.1268	**-0.0530**	0.6667	73 ± 19	68 ± 19	65 ± 14	42 ± 17
200980_s_at	PDHA1	pyruvate dehydrogenase alpha 1	**0.0000**	**0.0012**	0.4392	-0.3941	**0.0016**	1331 ± 26	1249 ± 64	1146 ± 59	1028 ± 43
208911_s_at	PDHB	pyruvate dehydrogenase beta	**-0.0269**	0.5494	-0.3129	-0.3853	0.7384	343 ± 41	340 ± 52	281 ± 46	303 ± 46
211023_at	PDHB	pyruvate dehydrogenase beta	**-0.0050**	**0.0044**	0.4320	-0.2444	**0.0021**	3184 ± 249	3117 ± 327	2159 ± 209	1913 ± 242
203067_at	PDX1	Pyruvate dehydrog. complex, lipoyl-cont. comp. X	-0.1471	**0.0135**	-0.4208	**0.0339**	0.1166	893 ± 86	775 ± 67	773 ± 53	630 ± 78
212094_at	PEG10	paternally expressed 10	**-0.0231**	**0.0035**	-0.2648	0.2707	**0.0103**	2795 ± 318	3278 ± 614	1807 ± 154	1498 ± 305
209242_at	PEG3	paternally expressed 3	-0.0608	**0.0314**	-0.2267	-0.3472	0.1349	6585 ± 539	5817 ± 759	5968 ± 512	4532 ± 618
213791_at	PENK	proenkephalin	**-0.0085**	0.3223	-0.0637	0.1760	0.1527	288 ± 19	252 ± 28	183 ± 30	264 ± 55
215023_s_at	PEX1	peroxisome biogenesis factor 1	**-0.0210**	**0.0114**	0.4575	-0.2887	**0.0214**	132 ± 17	142 ± 26	96 ± 24	43 ± 14
202658_at	PEX11B	peroxisomal biogenesis factor 11B	**-0.0459**	**0.0450**	0.0908	0.4108	**0.0122**	1041 ± 88	1127 ± 110	740 ± 73	799 ± 78
203972_s_at	PEX3	peroxisomal biogenesis factor 3	**-0.0160**	**0.0037**	-0.4727	-0.2367	**0.0399**	288 ± 24	314 ± 16	215 ± 20	245 ± 35
205420_at	PEX7	peroxisomal biogenesis factor 7	**-0.0283**	0.3050	0.2090	-0.4465	0.1660	123 ± 14	174 ± 21	105 ± 17	112 ± 35
201507_at	PFDN1	prefoldin 1	-0.1288	**0.0469**	0.4326	0.4238	0.1706	795 ± 47	832 ± 63	792 ± 58	669 ± 24
218336_at	PFDN2	prefoldin 2	-0.0804	**0.0083**	**-0.0340**	0.3985	**0.0337**	1546 ± 105	1423 ± 134	1446 ± 118	1053 ± 107
205361_s_at	PFDN4	prefoldin 4	**-0.0030**	**0.0021**	-0.2792	0.2061	**0.0154**	466 ± 53	452 ± 70	383 ± 42	221 ± 20
210976_s_at	PFKM	phosphofructokinase, muscle	**-0.0063**	**0.0173**	-0.4324	0.3557	**0.0159**	3250 ± 260	2841 ± 286	2238 ± 289	2084 ± 244
204992_s_at	PFN2	profilin 2	**-0.0062**	**0.0008**	0.4195	0.2011	0.0682	10014 ± 859	8675 ± 1185	7037 ± 748	6590 ± 1195
204604_at	PFTK1	PFTAIRE protein kinase 1	**-0.0082**	**0.0079**	0.4874	0.0678	**0.0263**	2379 ± 154	2415 ± 218	2107 ± 182	1635 ± 192
200886_s_at	PGAM1	phosphoglycerate mutase 1	**-0.0209**	**0.0344**	-0.3238	0.1918	**0.0493**	6674 ± 616	5443 ± 351	5129 ± 395	4757 ± 510
200738_s_at	PGK1	phosphoglycerate kinase 1	**-0.0116**	**0.0043**	-0.3625	0.1837	0.0812	3233 ± 352	2505 ± 356	2002 ± 222	2079 ± 536
201968_s_at	PGM1	phosphoglucomutase 1	**-0.0012**	0.0599	-0.1703	0.4710	0.2213	1613 ± 64	1554 ± 102	1436 ± 151	1305 ± 103
201121_s_at	PGRMC1	progesterone receptor membrane component 1	**-0.0344**	0.2342	-0.3081	0.2832	0.6955	3884 ± 251	3788 ± 569	3419 ± 222	3362 ± 464
219394_at	PGS1	phosphatidylglycerophosphate synthase	**-0.0119**	0.0730	**-0.0015**	**0.0068**	0.1517	380 ± 20	315 ± 21	302 ± 39	259 ± 55
222125_s_at	PH-4	putative proline 4-hydroxylase	**-0.0156**	**0.0312**	-0.1491	-0.4629	**0.0173**	2289 ± 154	2043 ± 127	1689 ± 70	1770 ± 168
210191_s_at	PHTF1	putative homeodomain transcription factor 1	**-0.0012**	0.0927	-0.0597	0.3532	0.4203	321 ± 13	300 ± 25	274 ± 23	272 ± 34
217862_at	PIAS1	protein inhibitor of activated STAT, 1	**-0.0438**	0.9802	0.3200	-0.2490	0.2407	645 ± 37	644 ± 39	535 ± 40	662 ± 75
214152_at	PIGB	phosphatidylinositol glycan, class B	**-0.0091**	**0.0388**	-0.4914	0.1408	**0.0261**	818 ± 64	713 ± 54	795 ± 85	527 ± 22
209707_at	PIGK	phosphatidylinositol glycan, class K	**-0.0265**	0.4780	-0.2272	-0.4830	0.6416	483 ± 30	502 ± 70	422 ± 64	428 ± 40

Probe set	Name	Description	NFT_O	MMSE_O	NFT_I	MMSE_I	ANOVA	Control	Incipient	Moderate	Severe
212740_at	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	**-0.0226**	**0.0073**	-0.4351	0.2147	0.2305	579 ± 38	577 ± 28	526 ± 41	475 ± 46
207081_s_at	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	**-0.0149**	**0.0411**	-0.1314	-0.2358	**0.0169**	1741 ± 224	1294 ± 76	1108 ± 121	1053 ± 119
200703_at	PIN	dynein, cytoplasmic, light polypeptide 1	**-0.0047**	**0.0048**	-0.3047	0.2102	0.1285	10172 ± 672	9066 ± 1571	8219 ± 1035	6224 ± 1413
209018_s_at	PINK1	PTEN induced putative kinase 1	-0.0835	**0.0070**	-0.4977	0.1649	0.1454	1321 ± 101	1254 ± 65	1192 ± 52	1067 ± 66
205632_s_at	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	**-0.0484**	**0.0185**	-0.4943	**0.0280**	**0.0040**	795 ± 62	784 ± 94	499 ± 25	566 ± 38
212518_at	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	**-0.0351**	**0.0209**	-0.3586	0.2206	0.1774	2340 ± 126	2152 ± 147	2124 ± 169	1847 ± 173
201192_s_at	PITPN	phosphotidylinositol transfer protein	**-0.0448**	0.1686	0.2374	0.0707	0.2133	457 ± 48	414 ± 19	343 ± 12	390 ± 57
201191_at	PITPN	phosphotidylinositol transfer protein	**-0.0255**	**0.0044**	0.4938	0.4076	0.1057	499 ± 53	419 ± 68	419 ± 38	289 ± 74
202522_at	PITPNB	phosphotidylinositol transfer protein, beta	**-0.0081**	**0.0383**	-0.3010	0.2193	**0.0115**	2399 ± 134	2343 ± 122	1950 ± 105	1958 ± 33
218667_at	PJA1	praja 1	**-0.0004**	**0.0001**	-0.1957	0.2023	0.0772	1719 ± 111	1664 ± 117	1259 ± 98	1443 ± 210
222171_s_at	PKNOX2	PBX/knotted 1 homeobox 2	-0.0738	**0.0180**	-0.2567	0.4167	**0.0097**	246 ± 17	219 ± 32	253 ± 26	129 ± 19
219046_s_at	PKNOX2	PBX/knotted 1 homeobox 2	-0.0740	**0.0203**	-0.3309	-0.4078	**0.0159**	398 ± 18	436 ± 41	299 ± 23	346 ± 29
213222_at	PLCB1	phospholipase C, beta 1	**-0.0091**	**0.0147**	-0.4156	0.2477	**0.0011**	5460 ± 376	4232 ± 431	3604 ± 419	2688 ± 564
213309_at	PLCL2	phospholipase C-like 2	**-0.0238**	**0.0199**	-0.0635	0.1993	**0.0540**	412 ± 55	327 ± 76	232 ± 39	213 ± 49
212891_s_at	PLINP-1	papillomavirus L2 interacting nuclear protein 1	**-0.0472**	**0.0036**	-0.2520	0.1091	0.0831	249 ± 28	192 ± 39	179 ± 26	138 ± 24
214781_at	PLXNA1	plexin A1	**-0.0217**	**0.0420**	-0.1991	0.3972	**0.0064**	396 ± 34	281 ± 28	306 ± 27	228 ± 34
201682_at	PMPCB	peptidase beta	**-0.0375**	0.5359	-0.0911	-0.3878	0.5202	1241 ± 63	1205 ± 125	1055 ± 84	1130 ± 110
209598_at	PNMA2	paraneoplastic antigen MA2	**-0.0029**	**0.0101**	0.3527	-0.2843	0.2358	5459 ± 569	4556 ± 780	4025 ± 669	3556 ± 747
212036_s_at	PNN	pinin, desmosome associated protein	-0.3193	**0.0376**	-0.3043	0.2412	0.1625	600 ± 32	564 ± 25	580 ± 39	488 ± 44
212296_at	POH1	26S proteasome-associated pad1 homolog	**-0.0428**	**0.0314**	-0.2466	-0.4642	0.0667	2288 ± 146	2228 ± 157	1924 ± 125	1752 ± 190
201803_at	POLR2B	polymerase II polypeptide B, 140kDa	**-0.0146**	**0.0129**	-0.4616	-0.0801	0.1129	1187 ± 85	1058 ± 131	945 ± 48	887 ± 97
202306_at	POLR2G	polymerase II polypeptide G	**-0.0254**	0.0847	-0.2151	0.0849	**0.0410**	1643 ± 137	1460 ± 111	1187 ± 44	1378 ± 84
216242_x_at	POLR2J2	DNA directed RNA polymerase II polypeptide J-related gene	**-0.0261**	**0.0024**	0.0954	-0.3703	**0.0083**	685 ± 82	869 ± 123	579 ± 24	439 ± 47
202634_at	POLR2K	polymerase II polypeptide K, 7.0kDa	**-0.0026**	**0.0004**	-0.1484	-0.4865	**0.0185**	850 ± 66	837 ± 57	789 ± 35	590 ± 69
210830_s_at	PON2	paraoxonase 2	**-0.0143**	0.0971	-0.2201	-0.4042	0.2561	1418 ± 179	1234 ± 278	1158 ± 153	843 ± 179
217848_s_at	PP	pyrophosphatase	**-0.0039**	0.0898	**-0.0177**	0.2296	0.1549	4022 ± 416	3457 ± 163	2915 ± 234	3072 ± 483
211765_x_at	PPIA	peptidylprolyl isomerase A	**-0.0099**	**0.0111**	-0.1443	0.4468	**0.0019**	12957 ± 664	1961 ± 1290	10820 ± 656	7802 ± 521
201293_x_at	PPIA	peptidylprolyl isomerase A	**-0.0031**	**0.0032**	-0.0556	0.1031	0.0596	13811 ± 850	2487 ± 1497	11851 ± 732	9640 ± 1095
204186_s_at	PPID	peptidylprolyl isomerase D	**-0.0162**	**0.0393**	0.2221	0.0565	**0.0046**	331 ± 26	269 ± 33	218 ± 7	206 ± 23
201500_s_at	PPP1R11	protein phosphatase 1, regulatory subunit 11	**-0.0014**	**0.0037**	-0.4545	0.4563	0.2642	2295 ± 90	2259 ± 46	2200 ± 76	2059 ± 109
201604_s_at	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	**-0.0386**	**0.0340**	0.3262	0.4527	**0.0050**	327 ± 24	276 ± 47	267 ± 28	137 ± 28
201603_at	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	**-0.0152**	**0.0003**	0.2750	0.1201	0.1917	626 ± 80	592 ± 71	511 ± 33	437 ± 38
202166_s_at	PPP1R2	protein phosphatase 1, regulatory subunit 2	**-0.0145**	0.0976	-0.3351	-0.2773	0.1276	472 ± 47	455 ± 63	332 ± 30	362 ± 41
202165_at	PPP1R2	protein phosphatase 1, regulatory subunit 2	**-0.0052**	**0.0001**	-0.2934	**0.0502**	**0.0155**	444 ± 69	438 ± 54	333 ± 19	205 ± 24
213465_s_at	PPP1R7	protein phosphatase 1, regulatory subunit 7	-0.1161	**0.0246**	0.2748	-0.4794	0.1228	782 ± 63	795 ± 100	677 ± 60	572 ± 50
208652_at	PPP2CA	protein phosphatase 2 , catalytic subunit, alpha isoform	**-0.0338**	**0.0017**	0.3552	0.3446	**0.0028**	3155 ± 299	2770 ± 112	2256 ± 130	1841 ± 279
213849_s_at	PPP2R2B	protein phosphatase 2 , regulatory subunit B , beta isoform	**-0.0271**	**0.0457**	-0.4563	0.3413	**0.0079**	2047 ± 202	1733 ± 163	1729 ± 118	1173 ± 40
201877_s_at	PPP2R5C	protein phosphatase 2, regulatory subunit B , gamma isoform	**-0.0039**	**0.0069**	-0.2833	0.4574	0.2200	1900 ± 182	1677 ± 196	1504 ± 103	1420 ± 204
203338_at	PPP2R5E	protein phosphatase 2, regulatory B epsilon	**-0.0006**	**0.0001**	-0.0580	**0.0480**	0.1080	707 ± 26	717 ± 22	655 ± 27	576 ± 73

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
202457_s_at	PPP3CA	protein phosphatase 3 , catalytic subunit, alpha isoform	**-0.0080**	**0.0031**	-0.4595	0.1890	**0.0048**	8074 ± 589	6655 ± 800	5487 ± 477	4384 ± 825
202429_s_at	PPP3CA	protein phosphatase 3 , catalytic subunit, alpha isoform	**-0.0086**	**0.0017**	0.4935	**0.0485**	**0.0199**	7798 ± 1142	6194 ± 1355	3797 ± 412	3682 ± 1035
202432_at	PPP3CB	protein phosphatase 3 , catalytic subunit, beta isoform	-0.0576	**0.0170**	-0.4889	0.4507	0.1383	4986 ± 606	4343 ± 765	3769 ± 498	2951 ± 582
204507_s_at	PPP3R1	protein phosphatase 3 , regulatory B alpha	**-0.0057**	**0.0049**	-0.2169	0.1539	**0.0136**	405 ± 62	300 ± 50	227 ± 13	191 ± 39
204506_at	PPP3R1	protein phosphatase 3 , regulatory B alpha	**-0.0070**	**0.0049**	-0.4510	-0.3620	**0.0015**	1234 ± 109	837 ± 95	799 ± 55	765 ± 55
200975_at	PPT1	palmitoyl-protein thioesterase 1	**-0.0440**	**0.0009**	0.2981	**0.0304**	**0.0099**	3582 ± 178	3607 ± 118	3458 ± 197	2708 ± 232
205839_s_at	PRAX-1	peripheral benzodiazepine receptor-associated protein 1	**-0.0031**	**0.0108**	-0.2184	0.4381	**0.0006**	844 ± 41	664 ± 54	584 ± 28	595 ± 51
39729_at	PRDX2	peroxiredoxin 2	-0.0596	**0.0292**	0.4614	0.2679	0.2009	3131 ± 291	2805 ± 242	2711 ± 227	2333 ± 241
201619_at	PRDX3	peroxiredoxin 3	**-0.0177**	**0.0517**	-0.2494	-0.4916	0.2653	1362 ± 178	1294 ± 186	1051 ± 125	927 ± 196
201923_at	PRDX4	peroxiredoxin 4	**-0.0476**	0.5869	-0.2450	-0.2642	0.5751	540 ± 48	557 ± 58	458 ± 49	503 ± 61
202918_s_at	PREI3	preimplantation protein 3	**-0.0317**	**0.0096**	-0.4853	0.3906	**0.0266**	544 ± 45	456 ± 51	424 ± 15	356 ± 37
37950_at	PREP	prolyl endopeptidase	**-0.0217**	0.2065	0.3111	-0.2782	0.2606	137 ± 11	143 ± 11	130 ± 9	111 ± 14
200603_at	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	**-0.0159**	0.1531	-0.1772	-0.4546	0.3804	4001 ± 272	3682 ± 469	3765 ± 326	3105 ± 417
200605_s_at	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	**-0.0412**	**0.0066**	-0.3807	0.3783	0.0619	2457 ± 401	2172 ± 408	1710 ± 255	1113 ± 134
212559_at	PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	**-0.0013**	**0.0006**	-0.3936	0.2274	**0.0372**	1397 ± 165	1280 ± 222	910 ± 122	778 ± 113
203680_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	**-0.0086**	**0.0013**	0.3263	0.2240	**0.0030**	1838 ± 216	1414 ± 188	1137 ± 59	873 ± 145
207957_s_at	PRKCB1	protein kinase C, beta 1	**-0.0164**	**0.0020**	0.3583	0.0780	**0.0057**	2455 ± 495	1584 ± 186	1158 ± 160	773 ± 138
209685_s_at	PRKCB1	protein kinase C, beta 1	**-0.0329**	**0.0238**	0.1049	-0.0685	**0.0382**	5398 ± 393	4710 ± 227	4601 ± 476	3284 ± 683
209678_s_at	PRKCI	protein kinase C, iota	**-0.0092**	**0.0119**	-0.4112	0.0685	**0.0150**	1222 ± 122	1455 ± 156	1036 ± 72	900 ± 26
203376_at	PRP17	pre-mRNA splicing factor 17	**-0.0032**	**0.0198**	0.3166	-0.2424	**0.0114**	1291 ± 84	1174 ± 92	914 ± 73	1034 ± 68
209440_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	**-0.0164**	**0.0146**	-0.4113	**0.0533**	**0.0369**	1058 ± 64	1066 ± 113	833 ± 62	826 ± 50
203089_s_at	PRSS25	protease, serine, 25	**-0.0097**	**0.0028**	0.3243	0.3347	0.0702	470 ± 47	403 ± 29	344 ± 22	318 ± 59
220892_s_at	PSA	phosphoserine aminotransferase	**-0.0491**	0.0753	-0.1058	-0.3851	0.2611	841 ± 138	796 ± 164	673 ± 145	444 ± 84
211746_x_at	PSMA1	proteasome subunit, alpha type, 1	**-0.0220**	0.0867	0.4527	0.1546	0.2335	2250 ± 231	2026 ± 189	1667 ± 156	1734 ± 311
201676_x_at	PSMA1	proteasome subunit, alpha type, 1	**-0.0012**	**0.0311**	0.4155	0.4945	**0.0166**	1522 ± 193	1403 ± 166	1027 ± 83	856 ± 95
210759_s_at	PSMA1	proteasome subunit, alpha type, 1	**-0.0135**	**0.0318**	-0.1441	0.1051	**0.0453**	1422 ± 104	1402 ± 135	983 ± 83	1037 ± 209
201274_at	PSMA5	proteasome subunit, alpha type, 5	**-0.0010**	**0.0070**	-0.0947	0.4506	0.0734	654 ± 50	536 ± 69	470 ± 29	482 ± 69
216088_s_at	PSMA7	proteasome subunit, alpha type, 7	**-0.0364**	0.3534	-0.4082	-0.4917	0.3533	328 ± 26	269 ± 31	268 ± 26	263 ± 39
200039_s_at	PSMB2	proteasome subunit, beta type, 2	**-0.0061**	**0.0082**	-0.3801	-0.3101	**0.0264**	1705 ± 102	1643 ± 163	1393 ± 92	1210 ± 127
201400_at	PSMB3	proteasome subunit, beta type, 3	**-0.0338**	**0.0077**	-0.4886	0.3569	**0.0157**	1653 ± 67	1735 ± 213	1418 ± 50	1133 ± 107
202243_s_at	PSMB4	proteasome subunit, beta type, 4	**-0.0233**	0.0990	-0.2697	0.1900	0.2296	1272 ± 123	1040 ± 129	959 ± 97	937 ± 168
202244_at	PSMB4	proteasome subunit, beta type, 4	**-0.0235**	0.0762	-0.1313	0.1674	0.2781	2345 ± 170	2055 ± 204	1982 ± 150	1896 ± 171
208799_at	PSMB5	proteasome subunit, beta type, 5	**-0.0208**	0.0767	-0.2765	0.1780	0.2478	1790 ± 120	1741 ± 233	1375 ± 72	1451 ± 255
208827_at	PSMB6	proteasome subunit, beta type, 6	**-0.0144**	0.1035	-0.3002	-0.4680	0.2908	884 ± 55	876 ± 54	847 ± 50	742 ± 61
201068_s_at	PSMC2	proteasome 26S subunit, ATPase, 2	**-0.0129**	0.1136	**-0.0444**	0.1440	0.2789	1438 ± 71	1274 ± 133	1140 ± 94	1142 ± 183
201699_at	PSMC6	proteasome 26S subunit, ATPase, 6	**-0.0152**	**0.0113**	-0.3002	-0.4475	**0.0520**	568 ± 51	521 ± 76	432 ± 43	347 ± 45
201198_s_at	PSMD1	proteasome 26S subunit, non-ATPase, 1	**-0.0011**	**0.0029**	-0.3606	0.3787	0.1306	1027 ± 50	1004 ± 89	929 ± 45	790 ± 102
219485_s_at	PSMD10	proteasome 26S subunit, non-ATPase, 10	**-0.0011**	**0.0283**	-0.3907	0.4622	**0.0140**	1407 ± 136	1358 ± 121	1079 ± 55	894 ± 88
208776_at	PSMD11	proteasome 26S subunit, non-ATPase, 11	**-0.0151**	0.2360	0.4594	-0.4007	0.1905	609 ± 92	492 ± 92	359 ± 55	447 ± 89

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
202353_s_at	PSMD12	proteasome 26S subunit, non-ATPase, 12	**-0.0073**	**0.0113**	-0.3918	-0.1008	0.1301	1128 ± 91	1048 ± 100	890 ± 58	850 ± 119
209853_s_at	PSME3	proteasome activator subunit 3	-0.0553	**0.0017**	0.2877	0.1113	**0.0124**	297 ± 30	275 ± 37	234 ± 24	129 ± 49
209852_x_at	PSME3	proteasome activator subunit 3	**-0.0081**	**0.0354**	-0.0945	0.1344	**0.0214**	1029 ± 35	1063 ± 71	982 ± 28	851 ± 45
218371_s_at	PSP1	paraspeckle protein 1	**-0.0227**	0.2295	-0.1960	-0.3731	0.3266	549 ± 28	514 ± 43	473 ± 34	483 ± 24
218477_at	PTD011	PTD011 protein	**-0.0284**	0.0700	-0.2274	-0.4150	0.1845	1798 ± 249	1474 ± 278	1369 ± 195	1097 ± 124
201433_s_at	PTDSS1	phosphatidylserine synthase 1	**-0.0302**	0.1749	-0.3827	-0.4934	0.4870	1860 ± 40	1859 ± 149	1665 ± 77	1721 ± 151
211711_s_at	PTEN	phosphatase and tensin homolog	**-0.0122**	**0.0023**	-0.4138	0.0631	**0.0260**	190 ± 8	162 ± 9	150 ± 11	143 ± 14
204897_at	PTGER4	prostaglandin E receptor 4	**-0.0468**	0.4669	-0.2958	-0.4613	0.3667	127 ± 10	104 ± 19	83 ± 16	97 ± 26
218083_at	PTGES2	prostaglandin E synthase 2	**-0.0253**	**0.0204**	0.4371	0.4251	**0.0389**	340 ± 39	335 ± 25	258 ± 33	195 ± 50
206772_at	PTHR2	parathyroid hormone receptor 2	**-0.0455**	-0.7974	-0.2897	0.2555	0.5778	223 ± 24	173 ± 30	195 ± 17	215 ± 37
203110_at	PTK2B	protein tyrosine kinase 2 beta	**-0.0123**	**0.0018**	0.4156	0.1991	0.2382	1756 ± 172	1795 ± 196	1617 ± 131	1321 ± 180
211737_x_at	PTN	pleiotrophin	-0.1183	**0.0101**	0.1067	-0.4360	**0.0046**	2175 ± 112	2594 ± 239	2397 ± 161	1574 ± 212
209466_x_at	PTN	pleiotrophin	**-0.0116**	**0.0092**	0.2051	0.4984	**0.0347**	1811 ± 127	1879 ± 143	1467 ± 182	1329 ± 98
221840_at	PTPRE	protein tyrosine phosphatase, receptor type, E	**-0.0421**	0.0803	-0.4168	0.4167	0.1692	1402 ± 155	1219 ± 85	1045 ± 48	1086 ± 144
203029_s_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	**-0.0017**	**0.0159**	0.3653	-0.4912	0.1272	2407 ± 350	2392 ± 270	1937 ± 215	1481 ± 318
210675_s_at	PTPRR	protein tyrosine phosphatase, receptor type, R	-0.5414	**0.0276**	**-0.0436**	0.0865	0.0904	325 ± 22	242 ± 31	262 ± 36	205 ± 38
206084_at	PTPRR	protein tyrosine phosphatase, receptor type, R	-0.6541	**0.0328**	0.2960	0.2296	0.3611	232 ± 25	236 ± 46	220 ± 27	161 ± 10
205948_at	PTPRT	protein tyrosine phosphatase, receptor type, T	-0.1792	**0.0374**	-0.2485	-0.1760	0.0830	472 ± 37	575 ± 149	370 ± 48	250 ± 76
209694_at	PTS	6-pyruvoyltetrahydropterin synthase	**-0.0377**	0.3707	-0.2676	0.3147	0.3071	1000 ± 84	912 ± 105	767 ± 64	912 ± 106
206157_at	PTX3	pentaxin-related gene, rapidly induced by IL-1 beta	-0.4309	**0.0154**	0.0565	0.3271	0.1006	90 ± 12	90 ± 12	52 ± 10	61 ± 17
216221_s_at	PUM2	pumilio homolog 2	**-0.0019**	0.1107	-0.1846	0.3783	0.3095	2907 ± 93	2774 ± 186	2738 ± 125	2508 ± 196
201706_s_at	PXF	peroxisomal farnesylated protein	**-0.0344**	0.0633	-0.4288	-0.4344	0.2202	524 ± 44	530 ± 76	454 ± 42	355 ± 92
201568_at	QP-C	low molecular mass ubiquinone-binding protein	**-0.0363**	**0.0020**	0.3897	0.0943	0.0604	3863 ± 229	3684 ± 223	3173 ± 248	2838 ± 390
205174_s_at	QPCT	glutaminyl-peptide cyclotransferase	**-0.0249**	**0.0036**	0.3491	0.4578	**0.0085**	217 ± 29	163 ± 22	117 ± 15	115 ± 19
202754_at	R3HDM	R3H domain containing	-0.0918	**0.0047**	-0.2158	-0.3046	**0.0186**	2101 ± 182	1776 ± 205	1855 ± 182	1246 ± 135
215548_s_at	RA410	vesicle transport-related protein	**-0.0111**	**0.0033**	0.2647	-0.4215	**0.0027**	617 ± 46	622 ± 30	614 ± 28	427 ± 37
200863_s_at	RAB11A	RAB11A, member RAS oncogene family	**-0.0118**	**0.0546**	-0.3706	-0.1627	0.1194	2222 ± 119	2025 ± 236	1824 ± 135	1635 ± 221
208734_x_at	RAB2	RAB2, member RAS oncogene family	-0.3161	**0.0293**	0.0814	0.2726	0.1268	598 ± 64	645 ± 48	468 ± 17	521 ± 62
208732_at	RAB2	RAB2, member RAS oncogene family	**-0.0192**	**0.0185**	0.4736	0.2287	**0.0239**	1327 ± 117	1367 ± 115	1157 ± 100	873 ± 80
208731_at	RAB2	RAB2, member RAS oncogene family	**-0.0145**	**0.0010**	-0.4806	0.3808	0.1065	3283 ± 379	2706 ± 326	2660 ± 252	2029 ± 397
204974_at	RAB3A	RAB3A, member RAS oncogene family	-0.1214	**0.0215**	0.1592	0.2433	0.2369	2346 ± 403	2236 ± 215	1790 ± 263	1548 ± 217
210406_s_at	RAB6A	RAB6A, member RAS oncogene family	**-0.0090**	**0.0055**	0.4432	0.2787	**0.0051**	2944 ± 286	2568 ± 395	2005 ± 160	1470 ± 141
201047_x_at	RAB6A	RAB6A, member RAS oncogene family	**-0.0090**	**0.0281**	-0.4386	0.2434	0.0552	3497 ± 310	3334 ± 381	2684 ± 230	2350 ± 353
211960_s_at	RAB7	RAB7, member RAS oncogene family	**-0.0011**	**0.0018**	-0.1173	**0.0339**	**0.0294**	628 ± 52	566 ± 47	433 ± 60	435 ± 44
203150_at	RAB9P40	Rab9 effector p40	-0.1689	**0.0439**	**0.0169**	0.4948	**0.0472**	512 ± 48	657 ± 95	483 ± 21	425 ± 21
201223_s_at	RAD23B	RAD23 homolog B	**-0.0139**	0.0691	-0.1518	-0.4530	0.1062	972 ± 52	853 ± 117	736 ± 55	747 ± 73
209849_s_at	RAD51C	RAD51 homolog C	**-0.0121**	**0.0382**	0.0662	-0.4592	**0.0009**	481 ± 35	400 ± 15	289 ± 22	318 ± 48
206066_s_at	RAD51C	RAD51 homolog C	**-0.0113**	**0.0382**	-0.4333	0.3324	0.1583	186 ± 30	211 ± 8	144 ± 25	128 ± 28
201628_s_at	RAGA	Ras-related GTP-binding protein	**-0.0065**	**0.0124**	-0.0669	-0.3912	0.0814	2592 ± 327	2187 ± 360	1542 ± 196	1702 ± 352

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
202100_at	RALB	v-ral simian leukemia viral oncogene homolog B	-0.2560	**0.0070**	0.1221	-0.4137	**0.0408**	1048 ± 73	1144 ± 91	875 ± 60	857 ± 78
212166_at	RANBP16	RAN binding protein 16	**-0.0195**	**0.0016**	**-0.0119**	0.1367	**0.0472**	761 ± 75	752 ± 89	590 ± 57	457 ± 107
201713_s_at	RANBP2	RAN binding protein 2	**-0.0019**	**0.0007**	**-0.0068**	0.1707	**0.0027**	939 ± 70	807 ± 36	833 ± 61	550 ± 65
200992_at	RANBP7	RAN binding protein 7	**-0.0221**	**0.0277**	-0.0931	0.4008	**0.0034**	1226 ± 50	1083 ± 44	1061 ± 54	922 ± 37
202583_s_at	RANBP9	RAN binding protein 9	**-0.0213**	**0.0406**	-0.1058	-0.4213	0.0888	590 ± 41	531 ± 42	504 ± 46	420 ± 48
202582_s_at	RANBP9	RAN binding protein 9	**-0.0016**	**0.0021**	**-0.0057**	0.4574	0.0615	2742 ± 173	2489 ± 268	2730 ± 80	1967 ± 291
201174_s_at	RAP1	TRF2-interacting telomeric RAP1 protein	-0.1245	**0.0243**	-0.3511	0.1460	0.0926	4273 ± 411	3538 ± 262	3286 ± 315	3120 ± 311
209444_at	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	**-0.0218**	0.2779	-0.1054	-0.3284	0.4242	1873 ± 104	1726 ± 188	1576 ± 78	1608 ± 177
219752_at	RASAL1	RAS protein activator like 1	**-0.0425**	0.0580	0.1507	0.1512	0.4003	754 ± 72	780 ± 94	662 ± 91	591 ± 45
202033_s_at	RB1CC1	RB1-inducible coiled-coil 1	**-0.0075**	**0.0143**	-0.3792	0.4869	**0.0026**	1687 ± 137	1333 ± 149	1271 ± 136	903 ± 84
202034_x_at	RB1CC1	RB1-inducible coiled-coil 1	**-0.0166**	**0.0044**	0.0712	-0.2828	**0.0203**	732 ± 69	605 ± 23	530 ± 32	523 ± 54
201092_at	RBBP7	retinoblastoma binding protein 7	**-0.0011**	0.5733	0.0803	**-0.0502**	0.5745	1637 ± 59	1700 ± 153	1564 ± 72	1503 ± 118
213762_x_at	RBMX	RNA binding motif protein, X chromosome	**-0.0310**	**0.0156**	-0.1546	-0.1673	**0.0007**	994 ± 74	1198 ± 83	816 ± 47	772 ± 13
218117_at	RBX1	ring-box 1	**-0.0101**	**0.0143**	0.4879	-0.4419	**0.0169**	1113 ± 48	1088 ± 139	1073 ± 58	744 ± 50
212820_at	RC3	rabconnectin-3	**-0.0025**	**0.0239**	0.3852	-0.4732	0.0887	1364 ± 169	1180 ± 148	1004 ± 130	809 ± 160
201485_s_at	RCN2	reticulocalbin 2, EF-hand calcium binding domain	**-0.0494**	0.1507	-0.4626	0.2110	0.3914	847 ± 150	659 ± 144	550 ± 98	591 ± 139
212612_at	RCOR	REST corepressor	**-0.0082**	**0.0050**	0.3048	-0.2285	0.0800	342 ± 20	326 ± 37	271 ± 24	254 ± 28
221532_s_at	REC14	recombination protein REC14	**-0.0030**	**0.0048**	-0.4217	0.2010	**0.0052**	806 ± 72	987 ± 50	741 ± 84	519 ± 72
205091_x_at	RECQL	RecQ protein-like	**-0.0363**	0.2159	-0.3520	0.2599	0.2323	108 ± 9	96 ± 14	105 ± 14	71 ± 16
219370_at	REPRIMO	candidate mediator of the p53-dependent G2 arrest	-0.5890	**0.0171**	-0.4041	0.3631	0.0584	610 ± 74	586 ± 100	612 ± 86	307 ± 85
203209_at	RFC5	replication factor C 5, 36.5kDa	-0.1559	**0.0312**	0.0806	0.1896	**0.0191**	310 ± 22	283 ± 18	219 ± 11	243 ± 27
214120_at	RFPL1S	ret finger protein-like 1 antisense	**-0.0056**	**0.0484**	-0.2988	**0.0201**	**0.0099**	1810 ± 258	1262 ± 206	874 ± 71	925 ± 233
214408_s_at	RFPL3S	ret finger protein-like 3 antisense	**-0.0118**	0.4082	-0.0807	-0.1593	0.6198	157 ± 12	153 ± 18	131 ± 18	135 ± 21
202963_at	RFX5	regulatory factor X, 5	**-0.0280**	0.0640	0.4011	**0.0520**	0.3412	320 ± 25	315 ± 31	291 ± 13	243 ± 53
38290_at	RGS14	regulator of G-protein signalling 14	**-0.0259**	**0.0456**	-0.4349	**0.0178**	0.0819	496 ± 50	410 ± 73	295 ± 29	362 ± 69
202388_at	RGS2	regulator of G-protein signalling 2, 24kDa	**-0.0462**	0.3204	-0.2343	0.0834	**0.0360**	1581 ± 225	886 ± 39	944 ± 75	1141 ± 242
210138_at	RGS20	regulator of G-protein signalling 20	**-0.0360**	**0.0074**	-0.2926	0.4766	0.1560	700 ± 58	579 ± 48	604 ± 54	525 ± 54
204339_s_at	RGS4	regulator of G-protein signalling 4	-0.2501	**0.0047**	0.4753	**0.0108**	0.0627	710 ± 97	548 ± 40	577 ± 65	419 ± 40
204337_at	RGS4	regulator of G-protein signalling 4	**-0.0070**	**0.0002**	-0.4824	0.0579	**0.0481**	3414 ± 635	2857 ± 869	2061 ± 340	1082 ± 207
206290_s_at	RGS7	regulator of G-protein signalling 7	**-0.0039**	**0.0005**	**-0.0362**	0.0617	**0.0063**	3660 ± 319	2949 ± 350	2458 ± 409	1779 ± 331
201453_x_at	RHEB2	Ras homolog enriched in brain 2	**-0.0132**	0.3169	-0.0716	0.3759	**0.0493**	3709 ± 199	3189 ± 261	2561 ± 170	3197 ± 447
206137_at	RIMS2	regulating synaptic membrane exocytosis 2	**-0.0032**	**0.0022**	0.3984	-0.3914	**0.0014**	733 ± 45	580 ± 26	547 ± 79	341 ± 67
206984_s_at	RIT2	Ras-like without CAAX 2	-0.1110	**0.0333**	-0.4794	0.3233	0.1997	346 ± 59	261 ± 45	279 ± 56	176 ± 43
217983_s_at	RNASE6PL	ribonuclease 6 precursor	**-0.0441**	0.3043	0.3740	0.4924	**0.0074**	1946 ± 172	2391 ± 165	1381 ± 90	1997 ± 250
208924_at	RNF11	ring finger protein 11	**-0.0106**	**0.0378**	-0.2098	0.2334	**0.0087**	3692 ± 286	3342 ± 291	3132 ± 201	2377 ± 201
201824_at	RNF14	ring finger protein 14	**-0.0227**	**0.0067**	0.3640	0.3373	0.2201	650 ± 41	605 ± 66	595 ± 35	508 ± 29
218528_s_at	RNF38	ring finger protein 38	-0.1884	**0.0467**	-0.2510	-0.1167	**0.0269**	1236 ± 53	1323 ± 46	1007 ± 41	1061 ± 126
209111_at	RNF5	ring finger protein 5	-0.0580	**0.0416**	-0.4001	0.3892	0.0834	753 ± 51	790 ± 41	726 ± 32	533 ± 125
203403_s_at	RNF6	ring finger protein 6	**-0.0250**	**0.0035**	0.3032	0.2629	**0.0500**	1619 ± 155	1603 ± 67	1251 ± 110	1112 ± 196

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
202683_s_at	RNMT	RNA methyltransferase	**-0.0229**	**0.0273**	**-0.0276**	0.2454	**0.0350**	1008 ± 65	1073 ± 77	978 ± 45	804 ± 45
204426_at	RNP24	coated vesicle membrane protein	-0.0658	**0.0373**	-0.2685	0.0970	0.1209	170 ± 24	144 ± 26	165 ± 23	93 ± 21
213194_at	ROBO1	roundabout, axon guidance receptor, homolog 1	**-0.0190**	**0.0339**	-0.4821	**0.0486**	0.0965	984 ± 82	859 ± 86	870 ± 61	676 ± 103
202762_at	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	**-0.0228**	**0.0031**	-0.1453	**0.0405**	0.2037	1227 ± 85	1081 ± 67	1081 ± 74	966 ± 109
221770_at	RPE	ribulose-5-phosphate-3-epimerase	**-0.0387**	**0.0374**	-0.4633	0.0552	**0.0123**	179 ± 24	155 ± 18	87 ± 15	99 ± 27
206196_s_at	RPIP8	RaP2 interacting protein 8	**-0.0217**	**0.0004**	-0.2493	**0.0482**	0.2763	5670 ± 362	5352 ± 569	4939 ± 628	4245 ± 543
200074_s_at	RPL14	ribosomal protein L14	**-0.0052**	**0.0196**	0.3355	0.4248	**0.0005**	2098 ± 88	2117 ± 133	2057 ± 86	1450 ± 105
221476_s_at	RPL15	ribosomal protein L15	**-0.0292**	0.1512	0.4066	0.3810	0.4572	9984 ± 466	9872 ± 444	9211 ± 408	9104 ± 585
200963_x_at	RPL31	ribosomal protein L31	**-0.0067**	**0.0345**	-0.4742	-0.2562	**0.0520**	13482 ± 533	13363 ± 650	1059 ± 1174	10731 ± 833
213687_s_at	RPL35A	ribosomal protein L35a	-0.0619	**0.0386**	-0.2630	0.3339	0.2020	3892 ± 155	3654 ± 208	3485 ± 320	3167 ± 251
202029_x_at	RPL38	ribosomal protein L38	-0.1238	**0.0136**	**-0.0222**	-0.4213	**0.0234**	12727 ± 476	12211 ± 521	12152 ± 629	10199 ± 636
213689_x_at	RPL5	ribosomal protein L5	**-0.0137**	0.1197	**-0.0144**	0.2009	0.1555	2350 ± 106	2050 ± 227	1983 ± 71	1911 ± 169
216044_x_at	RPL5	ribosomal protein L5	**-0.0033**	**0.0230**	**-0.0440**	-0.3552	0.0602	1544 ± 83	1545 ± 151	1264 ± 139	1145 ± 106
200034_s_at	RPL6	ribosomal protein L6	**-0.0061**	**0.0021**	-0.3376	0.2732	**0.0290**	5621 ± 278	4976 ± 478	5064 ± 363	3918 ± 311
208689_s_at	RPN2	ribophorin II	**-0.0299**	0.3807	**-0.0149**	0.4547	0.5514	1178 ± 115	1022 ± 100	992 ± 91	995 ± 127
209482_at	RPP20	POP7 homolog	**-0.0405**	0.1971	-0.4286	0.3070	**0.0432**	621 ± 52	564 ± 48	436 ± 6	537 ± 47
203436_at	RPP30	ribonuclease P	**-0.0199**	0.1517	-0.0989	0.0653	0.4253	511 ± 33	503 ± 35	450 ± 38	448 ± 30
200834_s_at	RPS21	ribosomal protein S21	**-0.0218**	0.0785	-0.0662	0.4424	0.1528	7013 ± 172	6143 ± 780	5753 ± 580	5211 ± 561
217753_s_at	RPS26	ribosomal protein S26	**-0.0237**	0.5177	0.3376	-0.2461	0.2265	3324 ± 215	3747 ± 252	3794 ± 440	2763 ± 521
201975_at	RSN	restin	-0.1203	**0.0322**	0.1531	-0.0649	**0.0286**	1621 ± 129	1694 ± 183	1670 ± 122	1092 ± 159
201980_s_at	RSU1	Ras suppressor protein 1	-0.0709	**0.0021**	**-0.0167**	0.2310	**0.0132**	451 ± 29	417 ± 11	343 ± 29	345 ± 23
203485_at	RTN1	reticulon 1	-0.2571	**0.0474**	0.3866	-0.2933	0.1433	8674 ± 664	8959 ± 762	9070 ± 804	6869 ± 531
210222_s_at	RTN1	reticulon 1	**-0.0274**	**0.0350**	-0.3646	-0.3413	**0.0198**	4900 ± 755	4110 ± 829	2660 ± 465	2077 ± 507
204217_s_at	RTN2	reticulon 2	**-0.0471**	0.1056	-0.2461	0.3288	0.1788	380 ± 28	354 ± 46	382 ± 39	277 ± 33
219549_s_at	RTN3	reticulon 3	**-0.0005**	**0.0017**	-0.2428	0.4707	0.1198	9500 ± 771	8770 ± 1125	7539 ± 384	6425 ± 1285
211509_s_at	RTN4	reticulon 4	**-0.0035**	0.0758	-0.1239	-0.3497	0.1659	12171 ± 355	12167 ± 350	11415 ± 534	10560 ± 855
212438_at	RY1	putative nucleic acid binding protein RY-1	**-0.0145**	0.1005	-0.1391	**0.0015**	**0.0074**	600 ± 51	452 ± 21	410 ± 32	478 ± 25
212440_at	RY1	putative nucleic acid binding protein RY-1	**-0.0161**	**0.0029**	-0.3721	-0.3424	**0.0075**	1292 ± 90	1307 ± 103	1090 ± 100	817 ± 83
213262_at	SACS	spastic ataxia of Charlevoix-Saguenay	**-0.0127**	**0.0479**	-0.1433	0.0913	**0.0066**	1103 ± 93	1018 ± 94	1022 ± 53	700 ± 54
208742_s_at	SAP18	sin3-associated polypeptide, 18kDa	-0.0582	**0.0179**	-0.4237	0.2564	0.0747	1663 ± 153	1465 ± 205	1176 ± 93	1051 ± 229
210592_s_at	SAT	spermidine/spermine N1-acetyltransferase	**-0.0037**	0.3238	**-0.0208**	0.4136	0.3122	5993 ± 501	5236 ± 280	4845 ± 324	4789 ± 827
211423_s_at	SC5DL	sterol-C5-desaturase -like	**-0.0282**	0.2729	-0.4559	0.3318	0.5457	1344 ± 119	1279 ± 120	1121 ± 118	1147 ± 156
203231_s_at	SCA1	spinocerebellar ataxia 1	-0.0856	**0.0133**	0.2071	0.3996	**0.0007**	558 ± 96	727 ± 98	183 ± 16	366 ± 95
212416_at	SCAMP1	secretory carrier membrane protein 1	**-0.0195**	0.1123	-0.1057	-0.3004	0.1636	3165 ± 134	2921 ± 221	3105 ± 132	2567 ± 296
206668_s_at	SCAMP1	secretory carrier membrane protein 1	**-0.0488**	**0.0290**	0.2270	-0.2586	0.2039	126 ± 19	102 ± 16	78 ± 8	82 ± 23
204362_at	SCAP2	src family associated phosphoprotein 2	**-0.0078**	**0.0063**	-0.2109	0.1617	0.1435	369 ± 31	365 ± 34	305 ± 23	281 ± 34
219196_at	SCG3	secretogranin III	**-0.0476**	**0.0119**	-0.2714	-0.3141	**0.0411**	477 ± 64	352 ± 62	301 ± 59	220 ± 61
204030_s_at	SCHIP1	schwannomin interacting protein 1	**-0.0223**	0.3671	0.4623	0.2794	0.2567	3214 ± 223	3205 ± 161	2592 ± 226	2927 ± 341
210383_at	SCN1A	sodium channel, voltage-gated, type I, alpha polypeptide	**-0.0438**	**0.0207**	0.2869	-0.0713	0.0931	684 ± 46	640 ± 141	531 ± 42	392 ± 75

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
206381_at	SCN2A2	sodium channel, voltage-gated, type II, alpha 2 polypeptide	**-0.0154**	**0.0222**	**-0.0122**	0.1496	0.0865	372 ± 43	390 ± 64	279 ± 27	235 ± 51
210432_s_at	SCN3A	sodium channel, voltage-gated, type III, alpha polypeptide	**-0.0104**	**0.0127**	-0.4237	-0.3692	0.0948	1177 ± 57	951 ± 143	1090 ± 179	673 ± 160
201339_s_at	SCP2	sterol carrier protein 2	**-0.0225**	0.0592	-0.3626	-0.4427	0.1686	810 ± 64	780 ± 119	612 ± 64	570 ± 105
205475_at	SCRG1	scrapie responsive protein 1	**-0.0080**	0.0694	-0.3106	0.3400	0.2099	3178 ± 354	2698 ± 308	2399 ± 387	2241 ± 220
202228_s_at	SDFR1	stromal cell derived factor receptor 1	**-0.0024**	**0.0112**	0.4220	0.2245	0.1066	8341 ± 809	7819 ± 1144	6616 ± 680	5052 ± 1179
201093_x_at	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein	**-0.0350**	0.0601	**-0.0064**	0.2115	**0.0214**	797 ± 39	635 ± 87	501 ± 13	574 ± 92
202675_at	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur	**-0.0209**	**0.0456**	-0.0635	0.2201	0.0899	342 ± 25	352 ± 28	295 ± 26	229 ± 59
202026_at	SDHD	succinate dehydrogenase complex D	**-0.0016**	**0.0009**	-0.2028	0.2856	**0.0464**	638 ± 65	520 ± 67	408 ± 34	443 ± 72
207707_s_at	SEC13L1	SEC13-like 1	**-0.0209**	0.3417	-0.1791	0.4572	0.4523	800 ± 38	771 ± 77	678 ± 23	754 ± 81
201583_s_at	SEC23B	Sec23 homolog B	-0.1008	**0.0249**	-0.0902	**0.0112**	**0.0198**	477 ± 37	371 ± 28	355 ± 20	372 ± 24
222127_s_at	SEC3	Sec3-like	**-0.0085**	0.1891	0.3149	-0.2923	0.3365	1597 ± 61	1554 ± 128	1483 ± 112	1315 ± 140
205352_at	SERPINI1	serine proteinase inhibitor, clade I , member 1	**-0.0017**	**0.0287**	0.1193	0.4948	**0.0022**	3672 ± 534	2816 ± 496	1752 ± 119	1388 ± 284
213609_s_at	SEZ6L	seizure related 6 homolog -like	-0.0849	**0.0390**	0.1896	0.1873	0.3119	1291 ± 245	1220 ± 164	896 ± 58	898 ± 208
211894_x_at	SEZ6L	seizure related 6 homolog -like	**-0.0360**	**0.0347**	0.0935	**-0.0057**	**0.0127**	522 ± 37	589 ± 60	375 ± 32	419 ± 57
201586_s_at	SFPQ	splicing factor proline/glutamine rich	-0.1449	**0.0385**	0.4017	-0.4022	0.1683	665 ± 38	664 ± 108	550 ± 68	417 ± 108
200754_x_at	SFRS2	splicing factor, arginine/serine-rich 2	**-0.0090**	0.3495	-0.1754	-0.2958	0.4427	1753 ± 72	1710 ± 151	1426 ± 117	1540 ± 267
214882_s_at	SFRS2	splicing factor, arginine/serine-rich 2	**-0.0175**	0.1984	-0.3325	0.4400	0.1506	807 ± 66	784 ± 44	601 ± 28	710 ± 100
208673_s_at	SFRS3	splicing factor, arginine/serine-rich 3	**-0.0366**	**0.0188**	-0.1667	0.3371	**0.0067**	572 ± 40	699 ± 94	582 ± 32	360 ± 44
212266_s_at	SFRS5	splicing factor, arginine/serine-rich 5	**-0.0087**	0.1147	-0.0891	0.0979	0.2947	3618 ± 287	3463 ± 268	3024 ± 153	3199 ± 204
210077_s_at	SFRS5	splicing factor, arginine/serine-rich 5	**-0.0321**	**0.0105**	-0.4921	0.1795	**0.0230**	173 ± 33	140 ± 17	154 ± 19	60 ± 13
203889_at	SGNE1	secretory granule, neuroendocrine protein 1	**-0.0266**	**0.0374**	-0.2030	-0.4626	**0.0527**	4541 ± 661	3594 ± 522	2643 ± 367	2566 ± 613
201312_s_at	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	**-0.0051**	0.1004	-0.4690	-0.1642	0.1710	3263 ± 211	3215 ± 450	2635 ± 204	2465 ± 307
201311_s_at	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	**-0.0441**	0.0571	-0.3366	0.2349	0.1859	673 ± 71	569 ± 104	499 ± 50	451 ± 65
218813_s_at	SH3GLB2	SH3-domain GRB2-like endophilin B2	**-0.0508**	**0.0307**	-0.4020	0.4245	0.0711	547 ± 41	600 ± 36	562 ± 30	426 ± 62
204019_s_at	SH3YL1	likely ortholog of mouse Sh3 domain YSC-like 1	**-0.0010**	**0.0004**	-0.2355	0.3404	0.0761	1622 ± 47	1566 ± 129	1560 ± 104	1283 ± 92
213308_at	SHANK2	SH3 and multiple ankyrin repeat domains 2	**-0.0229**	**0.0109**	0.2876	0.1151	**0.0111**	995 ± 60	943 ± 114	840 ± 71	600 ± 83
206330_s_at	SHC3	neuronal Shc	-0.3411	**0.0492**	-0.2830	-0.4775	0.1666	377 ± 82	386 ± 75	394 ± 107	138 ± 37
220979_s_at	SIAT7E	likely orth. m. sialyltransferase 7 E	**-0.0042**	**0.0044**	-0.1175	**0.0358**	**0.0339**	1914 ± 439	1296 ± 304	750 ± 68	697 ± 135
201381_x_at	SIP	Siah-interacting protein	**-0.0120**	**0.0257**	-0.1617	0.1517	0.0727	2353 ± 238	2264 ± 116	1901 ± 161	1598 ± 237
210691_s_at	SIP	Siah-interacting protein	**-0.0066**	**0.0462**	-0.2290	0.1790	0.0961	339 ± 47	268 ± 39	223 ± 16	207 ± 45
211761_s_at	SIP	Siah-interacting protein	**-0.0413**	**0.0253**	-0.4400	-0.2261	0.1357	3044 ± 308	2671 ± 295	2194 ± 185	2334 ± 283
217761_at	SIPL	SIPL protein	**-0.0337**	0.3120	0.1095	**-0.0294**	0.2446	1109 ± 72	1187 ± 113	994 ± 56	981 ± 53
221562_s_at	SIRT3	sirtuin silent mating type information regulation 2 homolog 3	**-0.0237**	**0.0048**	-0.4712	0.4585	**0.0463**	312 ± 22	281 ± 42	296 ± 29	192 ± 29
210040_at	SLC12A5	solute carrier family 12, member 5	**-0.0060**	**0.0024**	-0.4417	0.1041	**0.0310**	4065 ± 592	3201 ± 518	2646 ± 410	1941 ± 338
213664_at	SLC1A1	solute carrier family 1 , member 1	**-0.0351**	**0.0154**	0.2701	-0.1302	**0.0197**	1294 ± 135	1000 ± 111	894 ± 86	749 ± 136
209610_s_at	SLC1A4	solute carrier family 1 , member 4	-0.0626	**0.0145**	0.1458	0.2202	0.0557	1176 ± 82	1415 ± 179	1147 ± 143	862 ± 101
220460_at	SLC21A14	solute carrier family 21 , member 14	**-0.0291**	**0.0275**	-0.3200	0.3830	**0.0478**	1341 ± 118	1405 ± 217	1155 ± 173	796 ± 68
207088_s_at	SLC25A11	solute carrier family 25 , member 11	**-0.0002**	**0.0001**	-0.2924	0.1494	0.1177	599 ± 27	580 ± 48	464 ± 35	462 ± 82
203340_s_at	SLC25A12	solute carrier family 25 , member 12	**-0.0207**	**0.0246**	-0.3285	0.2534	**0.0006**	663 ± 59	551 ± 57	434 ± 36	335 ± 40

Probe set	**Name**	**Description**	**NFT$_O$**	**MMSE$_O$**	**NFT$_I$**	**MMSE$_I$**	**ANOVA**	**Control**	**Incipient**	**Moderate**	**Severe**
203339_at	SLC25A12	solute carrier family 25 , member 12	**-0.0199**	**0.0192**	-0.3401	0.0667	**0.0243**	664 ± 104	492 ± 72	333 ± 27	410 ± 48
211855_s_at	SLC25A14	solute carrier family 25 , member 14	**-0.0500**	**0.0498**	-0.3848	0.4708	0.2494	144 ± 19	137 ± 36	114 ± 15	80 ± 25
204587_at	SLC25A14	solute carrier family 25 , member 14	**-0.0349**	**0.0459**	-0.4448	0.0818	**0.0372**	692 ± 84	559 ± 62	421 ± 61	487 ± 39
200030_s_at	SLC25A3	solute carrier family 25 , member 3	**-0.0159**	**0.0195**	-0.1365	**0.0032**	0.1455	4444 ± 593	3704 ± 313	3094 ± 195	3191 ± 555
200657_at	SLC25A5	solute carrier family 25 , member 5	-0.0624	**0.0302**	-0.3340	0.1666	0.1062	2119 ± 332	1733 ± 233	1314 ± 146	1357 ± 256
212826_s_at	SLC25A6	solute carrier family 25 , member 6	**-0.0007**	**0.0011**	0.2718	-0.1912	**0.0121**	2006 ± 86	1710 ± 103	1907 ± 107	1518 ± 121
203306_s_at	SLC35A1	solute carrier family 35 , member 1	**-0.0492**	0.0717	0.2752	-0.3195	**0.0287**	1087 ± 70	1001 ± 94	1121 ± 82	792 ± 60
205918_at	SLC4A3	solute carrier family 4, anion exchanger, member 3	-0.0918	**0.0090**	-0.3207	0.2133	**0.0432**	603 ± 62	481 ± 67	552 ± 101	300 ± 53
205152_at	SLC6A1	solute carrier family 6 , member 1	**-0.0074**	**0.0049**	-0.1558	0.2176	**0.0012**	2529 ± 135	2837 ± 101	2305 ± 188	1605 ± 272
203909_at	SLC9A6	solute carrier family 9 , isoform 6	**-0.0040**	**0.0023**	-0.3805	0.3573	**0.0472**	3789 ± 290	3130 ± 379	2868 ± 278	2415 ± 420
209897_s_at	SLIT2	slit homolog 2	**-0.0028**	**0.0013**	-0.2865	0.2191	**0.0245**	681 ± 44	667 ± 72	572 ± 52	436 ± 60
218137_s_at	SMAP1	stromal membrane-associated protein	**-0.0024**	**0.0019**	0.4125	0.3581	**0.0050**	1008 ± 122	829 ± 134	551 ± 54	513 ± 52
206542_s_at	SMARCA2	SWI/SNF rel., matrix assoc., actin dep. reg. of chromatin, a2	**-0.0007**	**0.0031**	0.0674	0.4664	**0.0075**	1238 ± 120	1069 ± 111	912 ± 75	685 ± 68
202983_at	SMARCA3	SWI/SNF rel., matrix assoc., actin dep. reg. of chromatin, a3	**-0.0345**	**0.0420**	-0.4942	-0.4088	**0.0168**	1260 ± 105	1220 ± 75	1044 ± 85	860 ± 78
217766_s_at	SMP1	small membrane protein 1	**-0.0423**	0.3222	-0.0968	0.3462	0.5485	1146 ± 34	1158 ± 58	1178 ± 55	1005 ± 167
208739_x_at	SMT3H2	SMT3 suppressor of mif two 3 homolog 2	**-0.0161**	**0.0028**	-0.2627	0.2009	0.1111	1364 ± 153	1335 ± 208	927 ± 79	940 ± 178
202507_s_at	SNAP25	synaptosomal-associated protein, 25kDa	**-0.0365**	**0.0166**	-0.4790	-0.1824	**0.0246**	4545 ± 1074	3372 ± 874	1789 ± 394	1157 ± 298
202508_s_at	SNAP25	synaptosomal-associated protein, 25kDa	**-0.0109**	**0.0105**	-0.1152	0.2436	0.0643	11531 ± 866	1351 ± 1590	11315 ± 748	7036 ± 1824
213203_at	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19kDa	**-0.0223**	**0.0067**	-0.2161	0.4951	**0.0072**	1090 ± 95	923 ± 95	698 ± 46	767 ± 37
211546_x_at	SNCA	synuclein, alpha	-0.1254	**0.0248**	-0.4029	**0.0518**	**0.0294**	421 ± 53	362 ± 35	252 ± 16	322 ± 39
209877_at	SNCG	synuclein, gamma	**-0.0099**	**0.0014**	0.3211	0.2990	**0.0170**	500 ± 93	499 ± 100	472 ± 103	91 ± 12
201939_at	SNK	serum-inducible kinase	**-0.0402**	**0.0188**	0.2252	0.0980	**0.0166**	1700 ± 296	1462 ± 327	996 ± 190	523 ± 161
218033_s_at	SNN	stannin	**-0.0060**	**0.0059**	-0.4204	0.3482	0.1365	410 ± 40	344 ± 35	341 ± 23	299 ± 26
209481_at	SNRK	SNF-1 related kinase	**-0.0458**	**0.0478**	0.2770	-0.2004	**0.0199**	1464 ± 134	1252 ± 164	1046 ± 63	931 ± 106
206055_s_at	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	**-0.0468**	**0.0217**	0.3973	0.4243	0.0722	843 ± 113	942 ± 129	724 ± 53	542 ± 66
200826_at	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	**-0.0074**	**0.0012**	-0.4747	0.2642	**0.0252**	2611 ± 94	2699 ± 194	2648 ± 107	2013 ± 251
201522_x_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	-0.1142	**0.0481**	-0.4424	0.2609	0.2432	9644 ± 694	8567 ± 690	8324 ± 448	7725 ± 848
220405_at	SNTG1	syntrophin, gamma 1	-0.1008	**0.0247**	-0.4125	0.4880	0.0867	485 ± 39	404 ± 45	354 ± 45	358 ± 31
218404_at	SNX10	sorting nexin 10	**-0.0106**	**0.0007**	-0.3802	0.1610	**0.0152**	1338 ± 207	1134 ± 222	751 ± 106	571 ± 109
210648_x_at	SNX3	sorting nexin 3	-0.3846	**0.0327**	-0.0870	**0.0529**	0.2758	7787 ± 562	7691 ± 425	6730 ± 392	6211 ± 1031
212652_s_at	SNX4	sorting nexin 4	**-0.0242**	0.3432	0.4619	-0.2176	0.4826	1024 ± 54	1076 ± 36	939 ± 51	948 ± 103
214988_s_at	SON	SON DNA binding protein	**-0.0221**	0.6481	0.2869	-0.2735	0.6258	3173 ± 143	3018 ± 195	2882 ± 202	2875 ± 224
215522_at	SORCS3	VPS10 domain receptor protein SORCS 3	**-0.0007**	**0.0001**	0.2821	0.1608	**0.0060**	318 ± 33	260 ± 38	257 ± 39	126 ± 11
217927_at	SPC12	signal peptidase 12kDa	**-0.0437**	**0.0277**	-0.3702	0.3880	**0.0013**	2739 ± 273	2480 ± 219	1800 ± 131	1458 ± 138
210715_s_at	SPINT2	serine protease inhibitor, Kunitz type, 2	**-0.0203**	**0.0416**	-0.2731	-0.4742	0.2150	830 ± 102	717 ± 95	707 ± 80	529 ± 113
204675_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1	**-0.0534**	**0.0239**	0.2887	0.1791	0.0834	736 ± 146	514 ± 75	459 ± 58	379 ± 63
205335_s_at	SRP19	signal recognition particle 19kDa	**-0.0395**	0.1380	-0.1919	0.2972	0.5435	857 ± 38	852 ± 50	781 ± 49	766 ± 78
203605_at	SRP54	signal recognition particle 54kDa	**-0.0493**	-0.8298	0.4281	**-0.0091**	0.7820	562 ± 19	594 ± 30	541 ± 36	564 ± 55
208801_at	SRP72	signal recognition particle 72kDa	**-0.0268**	0.1835	0.4588	0.1944	0.5970	1397 ± 105	1357 ± 96	1239 ± 97	1223 ± 136

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
208802_at	SRP72	signal recognition particle 72kDa	**-0.0282**	**0.0004**	-0.3699	0.1928	0.1923	417 ± 24	400 ± 35	401 ± 36	317 ± 41
203182_s_at	SRPK2	SFRS protein kinase 2	-0.4388	**0.0328**	-0.1588	0.2489	0.2437	2148 ± 168	2067 ± 81	1953 ± 82	1711 ± 224
200918_s_at	SRPR	signal recognition particle receptor	-0.4038	**0.0146**	-0.1895	0.3093	0.1589	1232 ± 71	1283 ± 77	1129 ± 93	1033 ± 56
201138_s_at	SSB	Sjogren syndrome antigen B	**-0.0046**	0.1185	-0.1328	0.2347	0.1943	491 ± 24	443 ± 24	387 ± 26	412 ± 59
202591_s_at	SSBP1	single-stranded DNA binding protein	**-0.0182**	**0.0005**	-0.1698	**0.0036**	**0.0031**	785 ± 56	819 ± 60	631 ± 63	452 ± 72
213921_at	SST	somatostatin	**-0.0082**	**0.0213**	0.3244	0.4693	**0.0006**	1010 ± 123	551 ± 89	478 ± 88	401 ± 52
219631_at	ST7	suppression of tumorigenicity	**-0.0266**	**0.0008**	**-0.0283**	**0.0213**	0.0858	336 ± 37	317 ± 44	233 ± 21	241 ± 30
201837_s_at	STAF65	SPTF-associated factor 65 gamma	**-0.0062**	**0.0220**	-0.1010	0.1500	**0.0027**	773 ± 35	684 ± 51	689 ± 17	545 ± 44
203544_s_at	STAM	signal transducing adaptor molecule 1	**-0.0108**	**0.0064**	-0.4431	0.2823	0.1048	987 ± 40	935 ± 46	806 ± 50	780 ± 110
200887_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	**-0.0238**	0.1728	-0.4670	-0.3556	0.3253	1692 ± 167	1569 ± 215	1454 ± 106	1250 ± 151
203372_s_at	STATI2	STAT induced STAT inhibitor-2	-0.4851	**0.0220**	0.3330	-0.3020	0.2228	91 ± 11	96 ± 4	71 ± 11	65 ± 17
202557_at	STCH	stress 70 protein chaperone, microsome-associated, 60kDa	**-0.0340**	0.0895	-0.4335	0.2295	0.2793	2473 ± 393	1964 ± 360	1800 ± 80	1648 ± 325
208855_s_at	STK24	serine/threonine kinase 24	**-0.0370**	0.2495	-0.2624	0.0798	0.6884	3878 ± 100	3850 ± 249	3545 ± 216	3690 ± 330
208854_s_at	STK24	serine/threonine kinase 24	**-0.0227**	**0.0065**	-0.1862	0.2980	0.0627	587 ± 35	585 ± 54	514 ± 27	440 ± 51
203001_s_at	STMN2	stathmin-like 2	**-0.0542**	**0.0090**	-0.4918	0.2976	0.0902	3875 ± 683	3084 ± 568	2525 ± 541	1727 ± 482
218207_s_at	STMN3	stathmin-like 3	-0.0950	**0.0154**	0.0698	0.0613	0.2851	107 ± 14	110 ± 25	104 ± 8	66 ± 20
204701_s_at	STOML1	stomatin -like 1	-0.1453	**0.0049**	0.3473	0.2730	0.0936	636 ± 65	550 ± 45	523 ± 50	407 ± 80
203767_s_at	STS	steroid sulfatase , arylsulfatase C, isozyme S	**-0.0473**	0.2639	0.1749	0.2293	0.3079	316 ± 48	305 ± 41	211 ± 24	276 ± 53
204729_s_at	STX1A	syntaxin 1A	-0.0713	**0.0138**	-0.2916	0.0646	**0.0123**	1284 ± 103	982 ± 111	828 ± 88	938 ± 84
202260_s_at	STXBP1	syntaxin binding protein 1	**-0.0118**	**0.0389**	-0.2668	-0.4423	0.0843	7424 ± 848	6370 ± 1152	5270 ± 910	4162 ± 640
202930_s_at	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	**-0.0486**	**0.0101**	-0.1502	-0.3065	0.1587	857 ± 99	842 ± 115	608 ± 72	578 ± 140
219425_at	SULT4A1	sulfotransferase family 4A, member 1	**-0.0511**	**0.0355**	0.4968	0.2988	0.3413	1675 ± 215	1653 ± 288	1370 ± 186	1177 ± 169
201484_at	SUPT4H1	suppressor of Ty 4 homolog 1	**-0.0258**	**0.0037**	-0.3931	0.4284	**0.0407**	660 ± 23	603 ± 58	549 ± 24	519 ± 36
203069_at	SV2	synaptic vesicle glycoprotein 2	**-0.0128**	**0.0008**	-0.4907	0.3543	**0.0212**	3382 ± 509	2742 ± 431	1937 ± 302	1670 ± 207
205551_at	SV2B	synaptic vesicle protein 2B homolog	**-0.0430**	**0.0131**	-0.3641	0.2338	**0.0132**	4014 ± 470	3405 ± 373	2712 ± 439	1959 ± 380
202829_s_at	SYBL1	synaptobrevin-like 1	**-0.0280**	0.1421	0.0626	**-0.0182**	0.0859	1176 ± 44	1317 ± 76	1141 ± 82	1056 ± 61
221914_at	SYN1	synapsin I	**-0.0121**	**0.0009**	-0.2686	0.2340	0.2311	3781 ± 463	3337 ± 475	2951 ± 484	2442 ± 412
210315_at	SYN2	synapsin II	-0.0642	**0.0119**	-0.1093	0.1424	0.0898	145 ± 20	115 ± 22	94 ± 19	67 ± 23
204287_at	SYNGR1	synaptogyrin 1	-0.2070	**0.0343**	0.3140	0.4147	0.2651	2304 ± 257	2213 ± 292	1878 ± 233	1703 ± 106
205691_at	SYNGR3	synaptogyrin 3	**-0.0357**	**0.0081**	0.3796	0.2987	**0.0101**	2816 ± 360	2173 ± 386	1765 ± 304	1160 ± 214
212990_at	SYNJ1	synaptojanin 1	**-0.0145**	**0.0179**	-0.4354	0.1763	0.0558	2350 ± 384	1836 ± 246	1507 ± 188	1240 ± 241
207594_s_at	SYNJ1	synaptojanin 1	**-0.0051**	**0.0031**	-0.3540	0.3912	**0.0230**	192 ± 20	152 ± 17	125 ± 15	130 ± 6
203999_at	SYT1	synaptotagmin I	**-0.0196**	**0.0046**	-0.4110	0.3414	**0.0329**	3782 ± 1887	1079 ± 1556	3367 ± 1588	6527 ± 1869
203998_s_at	SYT1	synaptotagmin I	**-0.0073**	**0.0015**	-0.2139	**0.0132**	**0.0260**	471 ± 111	412 ± 131	127 ± 30	113 ± 42
206162_x_at	SYT5	synaptotagmin V	-0.0687	**0.0497**	0.2373	0.3148	0.2357	507 ± 140	385 ± 61	278 ± 67	249 ± 69
206552_s_at	TAC1	tachykinin, precursor 1	**-0.0117**	**0.0442**	-0.4349	0.4177	**0.0006**	1079 ± 171	432 ± 97	373 ± 80	305 ± 84
211382_s_at	TACC2	transforming, acidic coiled-coil containing protein 2	**-0.0027**	**0.0248**	0.1141	-0.0949	0.2703	352 ± 21	371 ± 28	323 ± 31	273 ± 52
201839_s_at	TACSTD1	tumor-associated calcium signal transducer 1	-0.3997	**0.0362**	0.1962	0.2095	0.2111	245 ± 60	199 ± 32	140 ± 18	143 ± 28
202168_at	TAF9	TAF9 RNA polymerase II, TATA box BP associated factor	**-0.0464**	**0.0125**	0.3732	0.1445	0.0726	1035 ± 72	1131 ± 93	1013 ± 85	765 ± 124

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
212978_at	TA-LRRP	T-cell activation leucine repeat-rich protein	**-0.0121**	**0.0502**	0.4617	0.3335	0.2215	986 ± 92	887 ± 114	774 ± 43	741 ± 109
212976_at	TA-LRRP	T-cell activation leucine repeat-rich protein	**-0.0024**	**0.0026**	0.2675	0.0968	**0.0260**	610 ± 94	427 ± 59	493 ± 50	293 ± 36
202813_at	TARBP1	TAR RNA binding protein 1	**-0.0361**	**0.0021**	**0.0402**	-0.2729	**0.0230**	777 ± 102	638 ± 49	567 ± 62	415 ± 72
203667_at	TBCA	tubulin-specific chaperone a	**-0.0001**	**0.0011**	**-0.0542**	0.1725	**0.0055**	1991 ± 145	2086 ± 150	1714 ± 59	1423 ± 65
218520_at	TBK1	TANK-binding kinase 1	**-0.0194**	0.0646	-0.1486	-0.4559	0.1405	933 ± 60	871 ± 85	838 ± 44	717 ± 68
208398_s_at	TBPL1	TBP-like 1	**-0.0193**	**0.0248**	-0.3780	-0.4171	**0.0018**	1556 ± 77	1228 ± 78	1154 ± 118	977 ± 96
204045_at	TCEAL1	transcription elongation factor A -like 1	**-0.0035**	**0.0061**	-0.4342	0.2097	0.0658	1302 ± 114	1181 ± 111	1004 ± 87	887 ± 140
202396_at	TCERG1	transcription elongation regulator 1	**-0.0046**	**0.0537**	-0.1867	0.3522	0.1322	1072 ± 67	951 ± 100	951 ± 51	809 ± 87
203303_at	TCTE1L	t-complex-associated-testis-expressed 1-like	**-0.0021**	**0.0025**	-0.2920	0.2183	**0.0488**	3263 ± 293	2829 ± 248	2601 ± 152	2249 ± 268
221471_at	TDE1	tumor differentially expressed 1	**-0.0034**	**0.0204**	0.1882	-0.2165	**0.0171**	1894 ± 138	1665 ± 190	1438 ± 98	1198 ± 175
200803_s_at	TEGT	testis enhanced gene transcript	**-0.0362**	0.1443	-0.0987	-0.4645	0.3182	1384 ± 176	1239 ± 142	1117 ± 132	1006 ± 64
212330_at	TFDP1	transcription factor Dp-1	**-0.0150**	0.1940	**-0.0179**	0.4048	0.3835	464 ± 13	404 ± 34	395 ± 37	392 ± 44
207332_s_at	TFRC	transferrin receptor	**-0.0219**	**0.0179**	-0.4813	0.3791	**0.0469**	832 ± 50	949 ± 58	770 ± 70	653 ± 90
213869_x_at	THY1	Thy-1 cell surface antigen	-0.2079	**0.0058**	0.3711	0.1148	0.1085	2286 ± 119	2493 ± 284	2287 ± 229	1749 ± 161
215171_s_at	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A	**-0.0084**	**0.0039**	-0.3795	-0.3761	0.1154	1688 ± 153	1444 ± 146	1360 ± 113	1189 ± 158
218118_s_at	TIMM23	translocase of inner mitochondrial membrane 23 homolog	**-0.0026**	**0.0310**	0.4872	0.4634	**0.0144**	411 ± 41	399 ± 84	326 ± 34	159 ± 35
208838_at	TIP120A	TBP-interacting protein	**-0.0431**	0.1078	-0.1124	0.3585	0.1451	808 ± 63	680 ± 80	663 ± 40	643 ± 13
202606_s_at	TLK1	tousled-like kinase 1	**-0.0070**	**0.0041**	-0.3843	-0.4396	**0.0530**	1258 ± 109	1102 ± 121	920 ± 83	853 ± 126
202242_at	TM4SF2	transmembrane 4 superfamily member 2	**-0.0122**	**0.0089**	0.3596	0.3278	**0.0470**	4879 ± 455	4802 ± 706	3690 ± 528	2830 ± 552
219892_at	TM6SF1	transmembrane 6 superfamily member 1	**-0.0109**	0.3514	0.3206	**-0.0518**	0.3221	385 ± 21	350 ± 53	297 ± 29	315 ± 40
205123_s_at	TMEFF1	TM protein with EGF-like and two follistatin-like domains 1	**-0.0237**	0.2855	0.4337	-0.3300	0.0646	296 ± 28	289 ± 37	191 ± 29	261 ± 18
202857_at	TMEM4	transmembrane protein 4	**-0.0225**	**0.0138**	-0.0604	**0.0329**	**0.0252**	1088 ± 71	1006 ± 37	961 ± 45	792 ± 88
204807_at	TMEM5	transmembrane protein 5	**-0.0456**	0.9518	**0.0098**	-0.2105	0.0987	162 ± 12	187 ± 10	136 ± 6	172 ± 22
203661_s_at	TMOD	tropomodulin	**-0.0043**	**0.0005**	-0.2794	-0.3898	0.0833	569 ± 30	480 ± 35	488 ± 35	436 ± 45
217733_s_at	TMSB10	thymosin, beta 10	**-0.0025**	**0.0188**	-0.2874	-0.2106	**0.0009**	11347 ± 750	0152 ± 1103	9556 ± 345	6674 ± 407
214581_x_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	**-0.0376**	**0.0426**	0.4443	0.1595	**0.0246**	191 ± 17	186 ± 36	127 ± 20	93 ± 26
218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	**-0.0060**	**0.0004**	-0.2306	**0.0133**	0.0902	1112 ± 81	1234 ± 128	916 ± 55	938 ± 99
215108_x_at	TNRC9	trinucleotide repeat containing 9	**-0.0057**	**0.0018**	-0.0905	0.1515	**0.0004**	298 ± 27	201 ± 22	216 ± 27	117 ± 14
214774_x_at	TNRC9	trinucleotide repeat containing 9	**-0.0045**	**0.0040**	**-0.0542**	0.0688	**0.0017**	523 ± 41	385 ± 56	383 ± 36	262 ± 33
216623_x_at	TNRC9	trinucleotide repeat containing 9	**-0.0082**	**0.0073**	**-0.0003**	0.0978	**0.0080**	320 ± 20	265 ± 23	222 ± 16	203 ± 34
200662_s_at	TOMM20-PENDING	translocase of outer mitochondrial membrane 20 homolog	-0.0556	**0.0054**	0.4855	0.4525	**0.0455**	4203 ± 626	3592 ± 668	3005 ± 357	1943 ± 207
201519_at	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A	**-0.0349**	0.2320	-0.4574	0.2939	0.4065	2502 ± 166	2452 ± 153	2104 ± 114	2350 ± 264
208901_s_at	TOP1	topoisomerase I	**-0.0078**	**0.0061**	-0.3674	0.1257	**0.0020**	997 ± 66	809 ± 63	932 ± 50	641 ± 45
204529_s_at	TOX	thymus high mobility group box protein TOX	-0.2258	**0.0222**	-0.4966	-0.4931	0.1277	350 ± 61	338 ± 78	287 ± 32	175 ± 21
203476_at	TPBG	trophoblast glycoprotein	**-0.0277**	0.1219	-0.2377	0.4886	0.1317	306 ± 34	277 ± 44	201 ± 22	236 ± 18
210372_s_at	TPD52L1	tumor protein D52-like 1	**-0.0341**	0.0569	**-0.0407**	-0.4850	0.1524	572 ± 63	493 ± 38	454 ± 27	428 ± 25
213011_s_at	TPI1	triosephosphate isomerase 1	**-0.0040**	**0.0071**	0.4451	0.4236	**0.0201**	5085 ± 324	4056 ± 207	4120 ± 421	3434 ± 384
200822_x_at	TPI1	triosephosphate isomerase 1	**-0.0152**	**0.0012**	0.3494	0.2671	**0.0367**	7114 ± 407	6712 ± 410	5459 ± 371	5381 ± 716
203846_at	TRIM32	tripartite motif-containing 32	**-0.0148**	0.1458	-0.4238	0.1861	**0.0109**	544 ± 32	511 ± 35	361 ± 14	490 ± 58

Probe set	Name	Description	NFT_O	$MMSE_O$	NFT_I	$MMSE_I$	ANOVA	Control	Incipient	Moderate	Severe
219736_at	TRIM36	tripartite motif-containing 36	**-0.0065**	**0.0128**	-0.2024	0.4147	**0.0053**	993 ± 201	688 ± 153	403 ± 78	271 ± 34
213009_s_at	TRIM37	tripartite motif-containing 37	**-0.0033**	**0.0105**	-0.1883	0.4345	0.0752	4165 ± 413	3528 ± 455	3064 ± 339	2753 ± 340
212544_at	TRIP3	thyroid hormone receptor interactor 3	**-0.0180**	**0.0043**	0.0631	-0.1050	**0.0310**	900 ± 45	847 ± 54	821 ± 24	687 ± 60
211700_s_at	TRO	trophinin	**-0.0280**	0.0977	**-0.0230**	-0.2825	0.1240	279 ± 17	262 ± 32	263 ± 28	189 ± 31
205803_s_at	TRPC1	transient receptor potential cation channel, C1	**-0.0098**	**0.0034**	-0.2895	-0.1139	**0.0043**	555 ± 56	593 ± 68	504 ± 41	292 ± 26
214908_s_at	TRRAP	transformation/transcription domain-associated protein	**-0.0019**	**0.0220**	0.3494	0.3063	**0.0002**	167 ± 15	164 ± 15	162 ± 9	63 ± 20
201758_at	TSG101	tumor susceptibility gene 101	**-0.0079**	0.1476	-0.2639	-0.3854	0.3445	1296 ± 70	1317 ± 112	1137 ± 52	1127 ± 137
203983_at	TSNAX	translin-associated factor X	**-0.0211**	0.0629	0.2829	-0.2806	0.0904	967 ± 94	1154 ± 181	927 ± 88	684 ± 58
200972_at	TSPAN-3	tetraspan 3	**-0.0472**	0.1121	-0.3408	-0.2407	0.2754	4622 ± 145	4394 ± 485	4124 ± 391	3599 ± 417
200973_s_at	TSPAN-3	tetraspan 3	**-0.0491**	0.0711	-0.2721	0.3264	0.2555	1013 ± 146	832 ± 203	627 ± 88	621 ± 188
221493_at	TSPYL	TSPY-like	-0.0808	**0.0179**	-0.4736	0.3621	0.0903	4396 ± 596	3623 ± 478	3813 ± 339	2544 ± 493
201434_at	TTC1	tetratricopeptide repeat domain 1	**-0.0032**	**0.0146**	-0.4034	0.1091	**0.0317**	882 ± 55	870 ± 30	722 ± 38	737 ± 53
208073_x_at	TTC3	tetratricopeptide repeat domain 3	**-0.0073**	**0.0298**	-0.3931	**0.0351**	0.0628	7305 ± 540	6413 ± 444	5710 ± 290	5751 ± 537
210645_s_at	TTC3	tetratricopeptide repeat domain 3	**-0.0062**	**0.0398**	-0.2237	0.4764	0.1376	5465 ± 512	4310 ± 409	3978 ± 454	3936 ± 710
208661_s_at	TTC3	tetratricopeptide repeat domain 3	**-0.0196**	**0.0034**	-0.3744	0.4543	0.3236	1102 ± 54	1056 ± 113	927 ± 51	917 ± 112
209372_x_at	TUBB	tubulin, beta polypeptide	-0.0937	**0.0151**	-0.2977	0.1141	0.0894	643 ± 171	416 ± 117	384 ± 112	122 ± 74
204141_at	TUBB	tubulin, beta polypeptide	**-0.0254**	**0.0031**	-0.1721	0.1147	**0.0237**	4264 ± 1764	1475 ± 1496	9752 ± 1404	7064 ± 1549
208977_x_at	TUBB2	tubulin, beta, 2	-0.0717	**0.0117**	-0.1275	0.1300	**0.0316**	5174 ± 691	3430 ± 671	3325 ± 440	2447 ± 702
213726_x_at	TUBB2	tubulin, beta, 2	**-0.0454**	**0.0071**	-0.2595	0.1838	**0.0223**	5931 ± 754	4528 ± 795	3982 ± 555	2703 ± 649
202154_x_at	TUBB4	tubulin, beta, 4	**-0.0493**	**0.0097**	-0.2211	0.0852	**0.0502**	4145 ± 593	3127 ± 660	2791 ± 400	1861 ± 539
213476_x_at	TUBB4	tubulin, beta, 4	**-0.0054**	**0.0000**	-0.3823	**0.0107**	0.0579	4953 ± 790	3568 ± 750	3288 ± 467	2154 ± 709
203894_at	TUBG2	tubulin, gamma 2	**-0.0004**	**0.0000**	0.4031	0.3653	**0.0000**	1044 ± 50	819 ± 38	788 ± 45	630 ± 20
201113_at	TUFM	Tu translation elongation factor, mitochondrial	-0.0712	**0.0437**	-0.2649	0.3000	0.2667	1379 ± 72	1367 ± 206	1172 ± 70	1068 ± 151
208864_s_at	TXN	thioredoxin	**-0.0261**	0.1063	-0.4860	0.2871	0.2129	1421 ± 136	1141 ± 134	1107 ± 101	1039 ± 179
209340_at	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	-0.0700	**0.0208**	0.1624	-0.4355	**0.0015**	631 ± 38	644 ± 40	694 ± 31	450 ± 50
208980_s_at	UBC	ubiquitin C	**-0.0071**	0.1540	**-0.0522**	0.4865	0.1939	0129 ± 1419	7932 ± 1243	7778 ± 489	6253 ± 1350
209115_at	UBE1C	ubiquitin-activating enzyme E1C	**-0.0279**	0.0992	-0.4097	**-0.0057**	**0.0180**	1170 ± 52	1242 ± 152	1239 ± 127	767 ± 47
201899_s_at	UBE2A	ubiquitin-conjugating enzyme E2A	**-0.0369**	0.1275	-0.4841	0.4540	0.2182	1501 ± 76	1459 ± 59	1336 ± 71	1300 ± 97
202333_s_at	UBE2B	ubiquitin-conjugating enzyme E2B	**-0.0244**	**0.0004**	0.4360	0.3814	**0.0047**	1251 ± 96	1220 ± 28	1114 ± 67	833 ± 58
200668_s_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3	**-0.0123**	0.1383	-0.0624	0.4014	0.3154	1701 ± 174	1461 ± 166	1428 ± 173	1237 ± 143
210024_s_at	UBE2E3	ubiquitin-conjugating enzyme E2E 3	**-0.0428**	0.2272	0.3539	-0.4538	0.6664	1951 ± 200	1924 ± 259	1628 ± 187	1670 ± 277
209142_s_at	UBE2G1	ubiquitin-conjugating enzyme E2G 1	**-0.0429**	**0.0213**	-0.0623	0.3811	0.0743	796 ± 41	835 ± 45	719 ± 51	640 ± 62
203109_at	UBE2M	ubiquitin-conjugating enzyme E2M	**-0.0220**	0.0756	-0.3919	0.2547	0.2814	1107 ± 136	924 ± 88	920 ± 74	799 ± 127
212751_at	UBE2N	ubiquitin-conjugating enzyme E2N	**-0.0062**	**0.0048**	0.4911	0.2554	**0.0496**	1362 ± 182	1173 ± 169	865 ± 115	755 ± 177
201524_x_at	UBE2N	ubiquitin-conjugating enzyme E2N	**-0.0183**	**0.0062**	-0.4656	-0.0682	**0.0070**	1417 ± 62	1508 ± 88	1309 ± 70	1096 ± 89
201002_s_at	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	**-0.0091**	**0.0088**	-0.2003	0.2026	**0.0155**	1546 ± 90	1389 ± 117	1095 ± 105	1170 ± 111
211069_s_at	UBL1	ubiquitin-like 1	-0.0602	**0.0082**	-0.3069	0.3080	**0.0521**	1848 ± 93	1904 ± 79	1798 ± 74	1468 ± 170
201534_s_at	UBL3	ubiquitin-like 3	**-0.0024**	0.1095	-0.2144	0.3032	0.3667	866 ± 115	808 ± 133	641 ± 102	601 ± 132
201535_at	UBL3	ubiquitin-like 3	**-0.0382**	0.3014	-0.4527	0.3896	0.5000	4421 ± 287	4207 ± 353	3838 ± 222	3950 ± 348

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
218011_at	UBL5	ubiquitin-like 5	**-0.0312**	**0.0229**	0.2939	0.3142	0.1035	830 ± 81	854 ± 35	630 ± 52	633 ± 109
218082_s_at	UBP1	upstream binding protein 1	-0.2317	**0.0211**	-0.2324	**0.0337**	**0.0186**	1056 ± 65	843 ± 74	970 ± 44	785 ± 62
212006_at	UBXD2	UBX domain containing 2	**-0.0091**	0.0800	0.4767	-0.0648	0.1506	584 ± 33	579 ± 47	485 ± 19	481 ± 58
201387_s_at	UCHL1	ubiquitin carboxyl-terminal esterase L1	-0.0663	**0.0467**	-0.2296	0.2168	0.1405	6962 ± 994	5602 ± 1002	3932 ± 611	4352 ± 1364
204616_at	UCHL3	ubiquitin carboxyl-terminal esterase L3	**-0.0093**	0.1875	-0.0760	-0.3619	0.2967	411 ± 32	338 ± 74	326 ± 25	271 ± 60
218801_at	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	**-0.0004**	**0.0002**	-0.4237	-0.3729	**0.0007**	614 ± 29	540 ± 59	472 ± 51	333 ± 26
205480_s_at	UGP2	UDP-glucose pyrophosphorylase 2	**-0.0388**	**0.0076**	-0.3493	0.2741	**0.0337**	3115 ± 243	2863 ± 250	2288 ± 58	2135 ± 354
202433_at	UGTREL1	UDP-galactose transporter related	**-0.0001**	**0.0006**	-0.0738	0.1137	**0.0016**	537 ± 28	470 ± 56	387 ± 24	324 ± 29
203790_s_at	UK114	translational inhibitor protein p14.5	**-0.0031**	**0.0082**	-0.1759	0.2522	**0.0374**	973 ± 101	803 ± 72	713 ± 83	613 ± 76
204062_s_at	ULK2	unc-51-like kinase 2	**-0.0209**	0.0989	-0.2918	0.3282	0.2445	830 ± 58	773 ± 69	771 ± 50	661 ± 54
202090_s_at	UQCR	ubiquinol-cytochrome c reductase subunit	**-0.0033**	**0.0268**	**-0.0514**	0.1684	**0.0307**	4040 ± 90	3663 ± 166	3747 ± 264	3133 ± 236
201903_at	UQCRC1	ubiquinol-cytochrome c reductase core protein I	**-0.0064**	**0.0060**	-0.3529	0.3425	**0.0308**	1596 ± 193	1347 ± 223	1265 ± 146	756 ± 189
212600_s_at	UQCRC2	ubiquinol-cytochrome c reductase core protein II	**-0.0057**	**0.0159**	-0.3826	0.2901	0.0695	2346 ± 219	2055 ± 195	1747 ± 157	1608 ± 247
200883_at	UQCRC2	ubiquinol-cytochrome c reductase core protein II	**-0.0457**	**0.0280**	-0.4999	0.3653	0.1309	635 ± 103	564 ± 87	412 ± 43	370 ± 104
202233_s_at	UQCRH	ubiquinol-cytochrome c reductase hinge protein	**-0.0044**	**0.0074**	-0.3256	0.4173	**0.0263**	2950 ± 274	2536 ± 328	2079 ± 190	1747 ± 331
203031_s_at	UROS	uroporphyrinogen III synthase	-0.1470	**0.0183**	0.2132	**0.0104**	**0.0280**	1484 ± 131	1086 ± 68	1181 ± 86	1068 ± 75
209137_s_at	USP10	ubiquitin specific protease 10	-0.0971	**0.0031**	-0.1373	-0.4759	**0.0250**	389 ± 28	335 ± 49	281 ± 32	215 ± 50
201672_s_at	USP14	ubiquitin specific protease 14	**-0.0401**	**0.0345**	-0.2163	0.1085	0.1164	1839 ± 106	1657 ± 98	1554 ± 42	1558 ± 106
209475_at	USP15	ubiquitin specific protease 15	**-0.0013**	**0.0097**	**-0.0193**	-0.4392	**0.0509**	850 ± 38	799 ± 80	734 ± 61	623 ± 20
220419_s_at	USP25	ubiquitin specific protease 25	**-0.0060**	**0.0005**	-0.3662	0.2669	**0.0018**	1310 ± 68	1243 ± 77	1073 ± 27	979 ± 53
206405_x_at	USP6	ubiquitin specific protease 6	**-0.0096**	0.5816	**-0.0089**	-0.3005	0.8362	2521 ± 189	2491 ± 258	2398 ± 266	2244 ± 196
201099_at	USP9X	ubiquitin specific protease 9, X chromosome	**-0.0355**	0.3307	0.4552	0.2730	0.7737	1032 ± 69	1004 ± 62	947 ± 48	950 ± 98
206624_at	USP9Y	ubiquitin specific protease 9, Y chromosome	**-0.0539**	**0.0298**	0.4829	-0.3926	**0.0380**	141 ± 31	83 ± 42	51 ± 21	25 ± 5
219675_s_at	UXS1	UDP-glucuronate decarboxylase 1	**-0.0131**	0.2276	-0.4129	-0.4291	0.4580	634 ± 26	557 ± 51	587 ± 38	523 ± 78
207100_s_at	VAMP1	vesicle-associated membrane protein 1	**-0.0274**	**0.0178**	**-0.0465**	0.3950	0.0562	335 ± 51	285 ± 70	272 ± 21	138 ± 15
214792_x_at	VAMP2	vesicle-associated membrane protein 2	-0.1776	**0.0237**	-0.2574	-0.4668	**0.0487**	1936 ± 135	1999 ± 219	2052 ± 226	1309 ± 185
201557_at	VAMP2	vesicle-associated membrane protein 2	-0.1559	**0.0449**	0.3258	0.2743	0.2215	2689 ± 238	2436 ± 101	2539 ± 264	2013 ± 230
201797_s_at	VARS2	valyl-tRNA synthetase 2	-0.4150	**0.0022**	0.3993	0.0710	**0.0377**	220 ± 14	231 ± 20	204 ± 18	158 ± 17
201472_at	VBP1	von Hippel-Lindau binding protein 1	**-0.0195**	0.0892	-0.4450	0.4495	0.2022	2796 ± 165	2523 ± 285	2324 ± 164	2174 ± 256
208649_s_at	VCP	valosin-containing protein	**-0.0483**	**0.0323**	-0.3824	0.4511	0.1692	757 ± 79	713 ± 65	635 ± 43	553 ± 69
212038_s_at	VDAC1	voltage-dependent anion channel 1	**-0.0163**	**0.0041**	-0.3186	0.3990	**0.0238**	1726 ± 263	1504 ± 287	1056 ± 109	726 ± 176
208846_s_at	VDAC3	voltage-dependent anion channel 3	**-0.0044**	0.1040	-0.1491	-0.4768	0.2434	719 ± 77	682 ± 66	533 ± 50	542 ± 118
212513_s_at	VDU1	pVHL-interacting deubiquitinating enzyme 1	**-0.0216**	0.0729	0.4101	-0.4185	0.1997	2189 ± 235	2038 ± 196	1773 ± 53	1646 ± 201
212171_x_at	VEGF	vascular endothelial growth factor	**-0.0468**	0.1701	-0.3508	-0.4864	**0.0506**	510 ± 47	483 ± 51	324 ± 31	425 ± 57
210512_s_at	VEGF	vascular endothelial growth factor	-0.0901	**0.0356**	0.4581	-0.3666	0.0853	1107 ± 238	1151 ± 221	602 ± 107	600 ± 122
206577_at	VIP	vasoactive intestinal peptide	**-0.0265**	0.0594	0.0878	0.4526	0.1772	175 ± 15	187 ± 23	172 ± 38	103 ± 27
209822_s_at	VLDLR	very low density lipoprotein receptor	**-0.0016**	**0.0124**	0.0791	0.3557	**0.0063**	377 ± 24	439 ± 33	306 ± 14	323 ± 26
220990_s_at	VMP1	likely ortholog of rat vacuole membrane protein 1	**-0.0025**	**0.0175**	0.4602	-0.2128	**0.0332**	922 ± 66	919 ± 80	759 ± 71	652 ± 43
44111_at	VPS33B	vacuolar protein sorting 33B	-0.3396	**0.0054**	0.0640	0.2743	0.1035	843 ± 60	855 ± 100	769 ± 85	589 ± 33

Probe set	Name	Description	NFT$_O$	MMSE$_O$	NFT$_I$	MMSE$_I$	ANOVA	Control	Incipient	Moderate	Severe
210849_s_at	VPS41	vacuolar protein sorting 41	**-0.0065**	**0.0297**	-0.1044	0.2867	**0.0305**	1264 ± 31	1059 ± 80	997 ± 72	1023 ± 77
203797_at	VSNL1	visinin-like 1	**-0.0075**	**0.0013**	-0.3812	-0.4878	**0.0099**	9648 ± 1630	8391 ± 1803	5029 ± 797	3272 ± 584
203798_s_at	VSNL1	visinin-like 1	**-0.0390**	**0.0026**	0.4303	0.1385	**0.0460**	816 ± 229	661 ± 144	347 ± 64	213 ± 81
202112_at	VWF	von Willebrand factor	**-0.0140**	**0.0076**	0.4462	-0.4464	**0.0183**	1310 ± 130	1518 ± 180	1201 ± 119	789 ± 167
204165_at	WASF1	WAS protein family, member 1	**-0.0045**	**0.0033**	-0.3634	0.3330	**0.0220**	5692 ± 502	4718 ± 836	3492 ± 491	3152 ± 651
217822_at	WBP11	WW domain binding protein 11	-0.1465	**0.0495**	0.1003	0.2961	0.2847	775 ± 85	765 ± 68	679 ± 27	611 ± 20
203599_s_at	WBP4	WW domain binding protein 4	**-0.0153**	0.0877	-0.3956	0.0905	0.1322	734 ± 55	704 ± 38	562 ± 56	620 ± 68
218512_at	WDR12	WD repeat domain 12	-0.0710	**0.0075**	-0.2317	0.1773	0.1246	627 ± 32	606 ± 46	576 ± 18	521 ± 24
212880_at	WDR7	WD repeat domain 7	**-0.0039**	**0.0039**	-0.2904	0.3777	**0.0297**	3046 ± 313	2624 ± 395	2044 ± 258	1752 ± 290
219478_at	WFDC1	WAP four-disulfide core domain 1	**-0.0005**	**0.0002**	-0.1372	**0.0313**	**0.0023**	780 ± 59	623 ± 63	535 ± 29	469 ± 65
204712_at	WIF1	WNT inhibitory factor 1	**-0.0048**	**0.0041**	-0.3439	0.1647	**0.0116**	1138 ± 243	813 ± 235	280 ± 33	379 ± 128
219628_at	WIG1	p53 target zinc finger protein	**-0.0247**	**0.0197**	**-0.0161**	0.4984	0.1305	794 ± 76	740 ± 108	725 ± 62	533 ± 61
202749_at	WRB	tryptophan rich basic protein	**-0.0034**	**0.0007**	-0.2827	**0.0453**	**0.0028**	3422 ± 298	3044 ± 155	2309 ± 141	2181 ± 295
203261_at	WS-3	novel RGD-containing protein	**-0.0125**	**0.0313**	-0.3433	0.1594	0.1371	1138 ± 119	1075 ± 160	799 ± 40	844 ± 120
221787_at	XAP135	PHD zinc finger protein XAP135	**-0.0096**	0.2054	0.1140	-0.4259	0.4842	353 ± 24	383 ± 26	302 ± 27	303 ± 77
206698_at	XK	Kell blood group precursor	-0.0947	**0.0364**	-0.4577	0.4347	**0.0197**	472 ± 51	422 ± 64	270 ± 9	354 ± 24
201352_at	YME1L1	YME1-like 1	**-0.0113**	0.0839	0.2457	-0.2831	0.1478	2050 ± 167	2119 ± 173	1659 ± 119	1756 ± 175
213655_at	YWHAE	tyrosine 3-/tryptophan 5-monooxygenase activ. epsilon	**-0.0093**	0.0606	-0.4302	-0.4287	0.2109	4052 ± 259	3746 ± 534	3401 ± 456	2899 ± 283
201020_at	YWHAH	tyrosine 3-/tryptophan 5-monooxygenase activ. eta	**-0.0183**	**0.0059**	-0.3574	0.2383	**0.0436**	3114 ± 602	2412 ± 540	1630 ± 246	1236 ± 284
200640_at	YWHAZ	tyrosine 3-/tryptophan 5-monooxygenase activ. zeta	**-0.0353**	**0.0518**	-0.4406	-0.3858	0.1973	4558 ± 489	4866 ± 985	3934 ± 520	2849 ± 632
200638_s_at	YWHAZ	tyrosine 3-/tryptophan 5-monooxygenase activ. zeta	**-0.0053**	**0.0009**	-0.4344	0.3967	**0.0074**	4107 ± 486	3585 ± 809	2781 ± 347	1280 ± 316
200639_s_at	YWHAZ	tyrosine 3-/tryptophan 5-monooxygenase activ. zeta	**-0.0291**	**0.0034**	0.3839	0.4706	**0.0087**	5410 ± 650	6158 ± 1020	5353 ± 534	2461 ± 193
200641_s_at	YWHAZ	tyrosine 3-/tryptophan 5-monooxygenase activ. zeta	**-0.0381**	**0.0047**	-0.2785	0.2296	**0.0440**	1473 ± 231	1282 ± 286	831 ± 52	715 ± 90
202982_s_at	ZAP128	peroxisomal long-chain acyl-coA thioesterase	-0.3188	**0.0470**	0.3975	0.0968	0.3398	414 ± 48	366 ± 17	328 ± 37	310 ± 56
201856_s_at	ZFR	zinc finger RNA binding protein	**-0.0286**	0.0984	**-0.0272**	0.4674	0.1207	626 ± 51	574 ± 74	469 ± 29	513 ± 19
209243_s_at	ZIM2	zinc finger, imprinted 2	-0.0802	**0.0421**	-0.4885	-0.1995	0.2032	282 ± 44	262 ± 45	224 ± 25	174 ± 26
204474_at	ZNF142	zinc finger protein 142	**-0.0161**	**0.0092**	-0.1410	0.0818	0.0847	537 ± 20	499 ± 48	415 ± 52	378 ± 60
213452_at	ZNF184	zinc finger protein 184	**-0.0280**	**0.0523**	0.3838	0.3711	0.1273	384 ± 57	325 ± 69	251 ± 21	226 ± 46
214823_at	ZNF204	zinc finger protein 204	**-0.0489**	**0.0430**	-0.3563	0.4082	0.2061	460 ± 64	394 ± 49	355 ± 47	299 ± 43
200828_s_at	ZNF207	zinc finger protein 207	**-0.0402**	0.5566	**-0.0106**	**0.0439**	0.2521	1262 ± 82	1123 ± 44	1074 ± 42	1195 ± 96
202051_s_at	ZNF262	zinc finger protein 262	**-0.0242**	**0.0081**	-0.3984	0.1513	0.1808	1099 ± 59	1042 ± 60	993 ± 64	897 ± 76
209741_x_at	ZNF291	zinc finger protein 291	-0.0696	**0.0231**	0.1863	0.2275	0.2204	815 ± 76	752 ± 78	685 ± 59	618 ± 50
215596_s_at	ZNF294	zinc finger protein 294	**-0.0327**	**0.0262**	-0.3439	-0.2542	0.0799	1070 ± 82	1032 ± 124	983 ± 76	732 ± 96
212749_s_at	ZNF363	zinc finger protein 363	**-0.0138**	0.0743	-0.1381	0.2829	**0.0410**	485 ± 31	384 ± 32	426 ± 41	334 ± 35
214813_at	ZNF75	zinc finger protein 75	**-0.0471**	0.3263	0.4446	0.1048	0.7372	158 ± 15	166 ± 21	140 ± 15	143 ± 23
204812_at	ZW10	ZW10 homolog, centromere/kinetochore protein	**-0.0153**	0.0935	**-0.0017**	0.1761	0.1609	548 ± 22	514 ± 26	447 ± 36	490 ± 40