

## APPENDIX II

Table A 2.1 Obesity genes common in ADA

S.no.	Gene	S.no.	Gene	S.no.	Gene	S.no.	Gene	S.no.	Gene	S.no.	Gene
1	<i>ABCB1</i>	21	<i>CAVI</i>	41	<i>GAL</i>	61	<i>MAOA</i>	81	<i>PYY</i>	101	<i>IL6</i>
2	<i>ABCC8</i>	22	<i>CD14</i>	42	<i>GAPDH</i>	62	<i>MAOB</i>	82	<i>REN</i>	102	<i>IRS1</i>
3	<i>ABCG1</i>	23	<i>CD36</i>	43	<i>GCK</i>	63	<i>MME</i>	83	<i>RFC1</i>	103	<i>KCNJ11</i>
4	<i>ACE</i>	24	<i>CDX2</i>	44	<i>GLP1R</i>	64	<i>MMP3</i>	84	<i>RXRA</i>	104	<i>LIPE</i>
5	<i>ADAM17</i>	25	<i>CFB</i>	45	<i>GNB3</i>	65	<i>MTHFR</i>	85	<i>SCD</i>	105	<i>LIPF</i>
6	<i>ADRA2A</i>	26	<i>CFH</i>	46	<i>GRB14</i>	66	<i>MTR</i>	86	<i>SERPINE1</i>	106	<i>VEGFA</i>
7	<i>ADRB1</i>	27	<i>CHRNA2</i>	47	<i>GSK3B</i>	67	<i>NAT2</i>	87	<i>SIRT1</i>	107	<i>TLR4</i>
8	<i>ADRB3</i>	28	<i>CLU</i>	48	<i>GSTM1</i>	68	<i>NOS1</i>	88	<i>SLC2A2</i>	108	<i>TNFRSF1A</i>
9	<i>AGT</i>	29	<i>CNTF</i>	49	<i>GSTP1</i>	69	<i>NPY</i>	89	<i>SLC6A3</i>	109	<i>TNFRSF1B</i>
10	<i>AHSG</i>	30	<i>COMT</i>	50	<i>HFE</i>	70	<i>NTRK1</i>	90	<i>SMAD3</i>	110	<i>TNMD</i>
11	<i>AKT2</i>	31	<i>CRHBP</i>	51	<i>HMOX1</i>	71	<i>PARP1</i>	91	<i>SOAT1</i>	111	<i>TP53</i>
12	<i>ALDH2</i>	32	<i>CRP</i>	52	<i>HSD11B1</i>	72	<i>PDE3B</i>	92	<i>SREBF1</i>	112	<i>USF1</i>
13	<i>APOA1</i>	33	<i>CSN1S1</i>	53	<i>HSPA5</i>	73	<i>PLA2G1B</i>	93	<i>TARDBP</i>	113	<i>PPARA</i>
14	<i>APOA2</i>	34	<i>CST3</i>	54	<i>HTR2C</i>	74	<i>PLAT</i>	94	<i>TF</i>	114	<i>PPARD</i>
15	<i>APOA5</i>	35	<i>CYP19A1</i>	55	<i>IL10</i>	75	<i>PLG</i>	95	<i>TFAM</i>	115	<i>PPARG</i>
16	<i>APOB</i>	36	<i>CYP2C19</i>	56	<i>IL1A</i>	76	<i>PNLIPRP1</i>	96	<i>TGFB1</i>	116	<i>PPARGCIA</i>
17	<i>APOBEC1</i>	37	<i>DBH</i>	57	<i>IL1B</i>	77	<i>PON3</i>	97	<i>TIMP1</i>	117	<i>PTEN</i>
18	<i>APOE</i>	38	<i>DRD4</i>	58	<i>IL1RN</i>	78	<i>FGF1</i>	98	<i>BDNF</i>		
19	<i>APP</i>	39	<i>EIF2AK2</i>	59	<i>IL4</i>	79	<i>FOXO3</i>	99	<i>CASP3</i>		
20	<i>AVPR1A</i>	40	<i>BCHE</i>	60	<i>FABP4</i>	80	<i>F11R</i>	100	<i>PTGS2</i>		

Table A 2.2 Sequence based clustering of ADA genes

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
1	Cluster 0	XR_933974.1, NM_138568.3, NM_001294.3, NM_001282175.1, NM_001282176.1, NM_001013257.2, NM_005581.4, NM_012116.3, NM_001130852.1	23	Cluster 22	AAH38596.1
2	Cluster 1	NP_004516.2	24	Cluster 23	CAH71487.1
3	Cluster 2	NP_000375.2	25	Cluster 24	NP_002282.2
4	Cluster 3	NP_002323.2	26	Cluster 25	NP_001002029.3, NP_009224.2
5	Cluster 4	NP_005520.4	27	Cluster 26	NP_115907.2, NP_542197.3
6	Cluster 5	NP_005036.2	28	Cluster 27	NP_002327.2
7	Cluster 6	BAJ08045.1	29	Cluster 28	NP_005682.2, NP_000343.2
8	Cluster 7	AAI17181.1	30	Cluster 29	NP_056036.1
9	Cluster 8	NP_001597.2	31	Cluster 30	NP_000383.1
10	Cluster 9	NP_001126.3	32	Cluster 31	NP_003052.2
11	Cluster 10	NP_057425.3	33	Cluster 32	NP_000825.2
12	Cluster 11	NP_005119.2	34	Cluster 33	NP_000005.2
13	Cluster 12	NP_056472.2	35	Cluster 34	NP_006531.1
14	Cluster 13	NP_005493.2	36	Cluster 35	AAI50278.1
15	Cluster 14	NP_003096.1, NP_001009598.1	37	Cluster 36	NP_000611.1, NP_000594.2
16	Cluster 15	NP_085128.2	38	Cluster 37	NP_000544.2
17	Cluster 16	NP_036462.2	39	Cluster 38	NP_004929.2
18	Cluster 17	NP_005568.2, NP_000292.1	40	Cluster 39	NP_055680.3
19	Cluster 18	NP_004548.3	41	Cluster 40	NP_000866.1, NP_000199.2
20	Cluster 19	NP_079461.2	42	Cluster 41	NP_008870.2, NP_005624.2

21	Cluster 20	NP_003897.2	43	Cluster 42	NP_000780.1
22	Cluster 21	NP_003793.2, NP_002463.2	44	Cluster 43	NP_002651.2

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
45	Cluster 44	NP_000918.2	67	Cluster 66	NP_004514.2	89	Cluster 88	NP_056219.3
46	Cluster 45	NP_004318.3	68	Cluster 67	AAI13370.1	90	Cluster 89	NP_037398.2
47	Cluster 46	NP_000245.2	69	Cluster 68	NP_055337.1	91	Cluster 90	NP_000850.1
48	Cluster 47	NP_001558.3	70	Cluster 69	NP_002763.1	92	Cluster 91	NP_003626.1
49	Cluster 48	NP_002883.3	71	Cluster 70	NP_004960.2	93	Cluster 92	NP_001005360.1
50	Cluster 49	NP_005535.1	72	Cluster 71	NP_036597.1	94	Cluster 93	EAW93480.1
51	Cluster 50	NP_055535.2	73	Cluster 72	NP_001609.2	95	Cluster 94	AAC50810.1
52	Cluster 51	NP_000177.2	74	Cluster 73	NP_001140.2	96	Cluster 95	NP_001612.1
53	Cluster 52	ACE87534.1	75	Cluster 74	NP_001073981.1	97	Cluster 96	NP_060117.3
54	Cluster 53	NP_055793.1, NP_065828.1, NP_001013049.1	76	Cluster 75	NR_028414.1, NM_001646.2, NR_028412.1, NR_028413.1,	98	Cluster 97	NP_000179.2, AAH64369.1, NP_000153.1
55	Cluster 54	NP_001035181.1, NP_006199.2	77	Cluster 76	NP_003374.3, NP_004622.2, NP_000518.1	99	Cluster 98	NP_004939.1
56	Cluster 55	NP_001005291.1	78	Cluster 77	NP_002705.2	100	Cluster 99	NP_004531.2
57	Cluster 56	NP_000616.3	79	Cluster 78	NP_004127.1	101	Cluster 100	NP_006394.1
58	Cluster 57	AAH51786.1	80	Cluster 79	NP_005947.3	102	Cluster 101	NP_002950.3
59	Cluster 58	NP_002702.2	81	Cluster 80	NP_001014797.1	103	Cluster 102	NP_001521.1
60	Cluster 59	AAI67432.1	82	Cluster 81	NP_003679.2	104	Cluster 103	AAI36784.1
61	Cluster 60	NP_056053.1	83	Cluster 82	NP_000035.2	105	Cluster 104	NP_000323.2
62	Cluster 61	NP_000913.2	84	Cluster 83	NP_005451.2	106	Cluster 105	NP_115896.1
63	Cluster 62	NP_055446.2	85	Cluster 84	ADE43428.1	107	Cluster 106	NP_000584.2
64	Cluster 63	NP_004913.2	86	Cluster 85	NP_005227.1	108	Cluster 107	NP_065164.2

65	Cluster 64	NP_005348.2	87	Cluster 86	NP_055864.2	109	Cluster 108	NP_009057.1
66	Cluster 65	NP_003364.1	88	Cluster 87	NP_003465.3	110	Cluster 109	NP_003257.1

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
111	Cluster 110	NP_037393.1	133	Cluster 132	NP_001101.1	155	Cluster 154	NP_003232.2
112	Cluster 111	NP_060676.2	134	Cluster 133	NP_036370.2	156	Cluster 155	NP_004412.2
113	Cluster 112	NP_005056.3	135	Cluster 134	NP_009102.3	157	Cluster 156	NP_000689.1
114	Cluster 113	NP_001017423.1	136	Cluster 135	NP_000241.1	158	Cluster 157	NP_001446.1
115	Cluster 114	NP_001741.4	137	Cluster 136	NP_001006933.2	159	Cluster 158	NP_008878.3
116	Cluster 115	NP_003162.2	138	Cluster 137	NP_001138508.1	160	Cluster 159	NP_004449.1
117	Cluster 116	NP_005418.1, NP_000537.3	139	Cluster 138	NP_068776.2, NP_002094.2	161	Cluster 160	NP_004906.3, NP_071452.2
118	Cluster 117	NP_005338.1, NP_005336.3, NP_005518.3	140	Cluster 139	NP_775098.2, NP_001155.1	162	Cluster 161	NP_001701.2, NP_000054.2
119	Cluster 118	NP_000280.1	141	Cluster 140	NP_001001438.1	163	Cluster 162	NP_003976.2
120	Cluster 119	NP_000167.1	142	Cluster 141	NP_000120.2	164	Cluster 163	AAI36410.1
121	Cluster 120	AAH40187.1	143	Cluster 142	NP_004997.4	165	Cluster 164	NP_005948.3
122	Cluster 121	NP_000475.1	144	Cluster 143	NP_001231.2	166	Cluster 165	NP_001005845.1
123	Cluster 122	NP_002324.2	145	Cluster 144	NP_036616.2	167	Cluster 166	NP_001036.1, NP_001035.1
124	Cluster 123	NP_002688.3	146	Cluster 145	NP_005447.1	168	Cluster 167	NP_001005743.1
125	Cluster 124	NP_061916.3	147	Cluster 146	NP_056146.1	169	Cluster 168	NP_071881.1
126	Cluster 125	NP_001387.2	148	Cluster 147	NP_001724.3	170	Cluster 169	NP_003446.2
127	Cluster 126	NP_079056.2	149	Cluster 148	NP_000535.3	171	Cluster 170	BAE06099.2
128	Cluster 127	NP_001007793.1	150	Cluster 149	NP_000224.2	172	Cluster 171	NP_036428.1
129	Cluster 128	NP_000391.1	151	Cluster 150	NP_001054.1	173	Cluster 172	NP_000234.1
130	Cluster 129	NP_001106818.1	152	Cluster 151	NP_777596.2	174	Cluster 173	NP_006288.2

131	Cluster 130	NP_037514.2	153	Cluster 152	NP_005849.1	175	Cluster 174	NP_001089.1
132	Cluster 131	NP_000893.2	154	Cluster 153	NP_000076.2	176	Cluster 175	NP_066264.3

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
177	Cluster 176	NP_000734.2, NP_000735.1, NP_000739.1, NP_004189.1, NP_000733.2, NP_000741.1	199	Cluster 198	NP_002121.4, NP_005509.1, NP_005509.1	221	Cluster 220	NP_001428.1, NP_000116.2, NP_000116.2
178	Cluster 177	NP_002582.3, NP_001018083.2	200	Cluster 199	NP_005563.1	222	Cluster 221	NP_036516.1
179	Cluster 178	NP_000778.3	201	Cluster 200	NP_068600.4	223	Cluster 222	NP_038466.2
180	Cluster 179	NP_000656.1, NP_000046.1	202	Cluster 201	AAI10388.1	224	Cluster 223	NP_001743.1
181	Cluster 180	NP_000468.1	203	Cluster 202	NP_000921.1	225	Cluster 224	NP_002769.1
182	Cluster 181	NP_001156.1	204	Cluster 203	NP_003892.2	226	Cluster 225	NP_066955.1
183	Cluster 182	NP_002948.1, NP_068811.	205	Cluster 204	NP_005543.2	227	Cluster 226	NP_000331.1
184	Cluster 183	NP_000954.1	206	Cluster 205	NP_006242.5	228	Cluster 227	NP_006573.2
185	Cluster 184	NP_110383.2	207	Cluster 206	NP_000449.1	229	Cluster 228	NP_000887.2
186	Cluster 185	NP_001025173.1, NP_004481.2	208	Cluster 207	NP_000748.3	230	Cluster 229	NP_001376.1
187	Cluster 186	NP_647536.1, NP_000737.1	209	Cluster 208	NP_000062.1	231	Cluster 230	NP_002078.1
188	Cluster 187	NP_036237.2, NP_036236.1	210	Cluster 209	NP_001005463.1	232	Cluster 231	NP_000681.2
189	Cluster 188	NP_000608.1, NP_000569.3	211	Cluster 210	NP_002750.1	233	Cluster 232	NP_055577.1
190	Cluster 189	NP_004111.2	212	Cluster 211	NP_003092.4	234	Cluster 233	AAI57844.1
191	Cluster 190	NP_000231.1, NP_000889.3	213	Cluster 212	NP_001001549.1	235	Cluster 234	NP_000490.1
192	Cluster 191	NP_055040.2	214	Cluster 213	NP_000192.2	236	Cluster 235	NP_005496.4
193	Cluster 192	NP_055391.2	215	Cluster 214	AAH13200.1	237	Cluster 236	NP_000099.2
194	Cluster 193	NP_821079.3	216	Cluster 215	NP_001036189.1	238	Cluster 237	ABY87534.1
195	Cluster 194	NP_055965.1	217	Cluster 216	NP_002028.1	239	Cluster 238	NP_005578.1
196	Cluster 195	NP_001008212.1	218	Cluster 217	NP_000148.2	240	Cluster 239	NP_000094.2

197	Cluster 196	NP_004272.2	219	Cluster 218	1NP_065087.1	241	Cluster 240	NP_001234.3
198	Cluster 197	NP_004201.3	220	Cluster 219	NP_003046.2	242	Cluster 241	NP_005644.2

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
243	Cluster 242	NP_066961.2	265	Cluster 264	NP_000377.1	287	Cluster 286	NP_852556.2
244	Cluster 243	NP_006659.1	266	Cluster 265	NP_000390.2	288	Cluster 287	NP_005169.2
245	Cluster 244	NP_002413.1, NP_002413.1, NP_002412.1	267	Cluster 266	NP_001864.1	289	Cluster 288	NP_001001890.1
246	Cluster 245	NP_001219.2	268	Cluster 267	NP_065172.1	290	Cluster 289	NP_001924.2
247	Cluster 246	NP_001213.2	269	Cluster 268	NP_000448.3	291	Cluster 290	NP_004374.1
248	Cluster 247	NP_000069.2	270	Cluster 269	NP_000063.2	292	Cluster 291	NP_001822.3
249	Cluster 248	NP_000097.3, NP_000761.3, NP_000760.1	271	Cluster 270	NP_000859.1, NP_000612.1	293	Cluster 292	NP_001001928.1, NP_005028.4, NP_006229.1
250	Cluster 249	NP_612380.1	272	Cluster 271	NP_057677.2	294	Cluster 293	NP_821133.1
251	Cluster 250	NP_060292.3	273	Cluster 272	AAH15017.1	295	Cluster 294	BAF31287.1
252	Cluster 251	NP_000925.2	274	Cluster 273	NP_001109.2	296	Cluster 295	NP_001120853.1
253	Cluster 252	NP_000675.1, NP_000015.1, NP_000016.1	275	Cluster 274	NP_000012.1, NP_000438.2	297	Cluster 296	NP_000227.1, NP_000228.1
254	Cluster 253	NP_004888.2	276	Cluster 275	NP_006220.1	298	Cluster 297	NP_478067.2
255	Cluster 254	NP_055774.2	277	Cluster 276	NP_006138.1	299	Cluster 298	NP_110418.1
256	Cluster 255	NP_000020.1	278	Cluster 277	NP_000671.2	300	Cluster 299	NP_000862.1
257	Cluster 256	NP_006812.3	279	Cluster 278	NP_000672.3	301	Cluster 300	NP_000265.1
258	Cluster 257	NP_006847.1	280	Cluster 279	NP_002053.3	302	Cluster 301	NP_006673.1
259	Cluster 258	NP_001617.1	281	Cluster 280	NP_001057.1	303	Cluster 302	AAH04101.1
260	Cluster 259	NP_004170.1	282	Cluster 281	NP_009052.3	304	Cluster 303	NP_079379.1
261	Cluster 260	AAI04857.1	283	Cluster 282	NP_000729.2	305	Cluster 304	NP_001053.2
262	Cluster 261	NP_005901.2	284	Cluster 283	AAF88068.1	306	Cluster 305	NP_002084.2

263	Cluster 262	NP_003241.2	285	Cluster 284	NP_002766.1	307	Cluster 306	NP_004096.2
264	Cluster 263	NP_001007098.1	286	Cluster 285	NP_001056.1	308	Cluster 307	NP_002649.1

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
309	Cluster 308	AAA60958.1	331	Cluster 330	NP_000187.3	353	Cluster 352	NP_443200.2
310	Cluster 309	NP_002498.1	332	Cluster 331	NP_001127.1	354	Cluster 353	NP_006105.1
311	Cluster 310	NP_000346.2	333	Cluster 332	NP_005054.3	355	Cluster 354	NP_000305.3, AAC52017.1
312	Cluster 311	NP_000367.1	334	Cluster 333	NP_000593.1	356	Cluster 355	NP_002058.2
313	Cluster 312	NP_005794.1	335	Cluster 334	NP_057632.2	357	Cluster 356	NP_002328.1
314	Cluster 313	NP_005893.1	336	Cluster 335	NP_002491.2	358	Cluster 357	NP_004181.1, NP_000226.2
315	Cluster 314	NP_004171.2	337	Cluster 336	NP_001048.2	359	Cluster 358	NP_000437.3, NP_000296.2 , NP_000931.1
316	Cluster 315	NP_000401.1	338	Cluster 337	NP_005882.2	360	Cluster 359	NP_000667.1, NP_000666.2
317	Cluster 316	NP_003384.2	339	Cluster 338	NP_000473.2	361	Cluster 360	NP_000286.3, NP_001076.2
318	Cluster 317	NP_061979.3	340	Cluster 339	NP_000651.3	362	Cluster 361	NP_000788.2, AAI28123.1
319	Cluster 318	NP_001995.1	341	Cluster 340	NP_001035282.1	363	Cluster 362	NP_005267.2
320	Cluster 319	NP_000697.1	342	Cluster 341	NP_004367.2	364	Cluster 363	NP_002231.1, NP_000516.3
321	Cluster 320	NP_036227.1	343	Cluster 342	NP_002066.1	365	Cluster 364	NP_009053.1, NP_003358.1
322	Cluster 321	NP_055199.1	344	Cluster 343	NP_005243.1	366	Cluster 365	NP_002533.1
323	Cluster 322	AAH95435.1	345	Cluster 344	NP_001170.2	367	Cluster 366	NP_001123214.1
324	Cluster 323	NP_002070.1	346	Cluster 345	NP_001216.1	368	Cluster 367	NP_006184.2
325	Cluster 324	AAH29051.1	347	Cluster 346	NP_001604.1	369	Cluster 368	BAH83534.1, AAH44218.1
326	Cluster 325	NP_000522.3	348	Cluster 347	NP_000582.1	370	Cluster 369	NP_000498.2
327	Cluster 326	NP_001900.1, NP_000528.1	349	Cluster 348	NP_000638.1, NP_000570.1	371	Cluster 370	AAI09054.1
328	Cluster 327	NP_001020537.2	350	Cluster 349	NP_071419.3	372	Cluster 371	NP_000034.1

329	Cluster 328	NP_002037.2, NP_055179.1	351	Cluster 350	NP_065133.1	373	Cluster 372	NP_004070.3
330	Cluster 329	NP_000285.1	352	Cluster 351	NP_001613.2	374	Cluster 373	NP_001621.2

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
375	Cluster 374	NP_001035307.1	397	Cluster 396	AAG10713.1	419	Cluster 418	NP_000030.1
376	Cluster 375	NP_998766.1	398	Cluster 397	NP_004083.3	420	Cluster 419	NP_036374.1
377	Cluster 376	NP_001777.1 , NP_004926.1	399	Cluster 398	NP_000653.3, NP_000006.2	421	Cluster 420	NP_001120676.1 , NP_002124.1
378	Cluster 377	NP_002701.1, NP_002701.1	400	Cluster 399	NP_000261.2	422	Cluster 421	NP_112591.2, NP_057106.2
379	Cluster 378	AAH00039.1	401	Cluster 400	NP_658985.2	423	Cluster 422	NP_115749.2
380	Cluster 379	NP_001873.2	402	Cluster 401	NP_003811.2	424	Cluster 423	NP_001902.1
381	Cluster 380	NP_114412.2	403	Cluster 402	NP_002677.1	425	Cluster 424	NP_002620.1
382	Cluster 381	NP_071427.2	404	Cluster 403	NP_060294.1	426	Cluster 425	NP_000302.1
383	Cluster 382	NP_065390.1	405	Cluster 404	NP_001241.1	427	Cluster 426	NP_001030337.1
384	Cluster 383	NP_005389.1	406	Cluster 405	NP_002790.1	428	Cluster 427	NP_001700.2
385	Cluster 384	NP_003006.2	407	Cluster 406	NP_004337.2	429	Cluster 428	NP_003192.1
386	Cluster 385	NP_000032.1, NP_000032.1	408	Cluster 407	NP_003318.1	430	Cluster 429	NP_004823.1, NP_899062.1
387	Cluster 386	NP_002248.1	409	Cluster 408	NP_000894.1	431	Cluster 430	NP_002497.2
388	Cluster 387	NP_001256.3	410	Cluster 409	NP_002534.1	432	Cluster 431	NP_000844.2
389	Cluster 388	NP_003346.2	411	Cluster 410	CAK22320.1	433	Cluster 432	NP_000624.2
390	Cluster 389	NP_003876.1	412	Cluster 411	NP_003947.1	434	Cluster 433	NP_001076087.1
391	Cluster 390	NP_058642.1	413	Cluster 412	NP_005390.1	435	Cluster 434	NP_001635.2
392	Cluster 391	NP_005797.1	414	Cluster 413	NP_000745.1	436	Cluster 435	AAI18551.1
393	Cluster 392	NP_000520.1	415	Cluster 414	NP_000566.3	437	Cluster 436	NP_000585.2

394	Cluster 393	NP_036471.1	416	Cluster 415	NP_002720.1	438	Cluster 437	NP_006570.1
395	Cluster 394	NP_001217.2	417	Cluster 416	NP_254274.1	439	Cluster 438	NP_001005413.1
396	Cluster 395	NP_005516.1	418	Cluster 417	NP_000567.1	440	Cluster 439	NP_061838.1

**Table A 2.2 Sequence based clustering of ADA genes (continued)**

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
441	Cluster 440	NP_004735.2	463	Cluster 462	NP_068572.1
442	Cluster 441	AAH75054.1	464	Cluster 463	NP_064535.1
443	Cluster 442	NP_006780.1	465	Cluster 464	NP_003954.2
444	Cluster 443	NP_000558.2	466	Cluster 465	NP_000747.1
445	Cluster 444	NP_004896.1	467	Cluster 466	AAI48267.1
446	Cluster 445	NP_005857.1	468	Cluster 467	NP_001553.1
447	Cluster 446	NP_004172.2	469	Cluster 468	NP_006547.1
448	Cluster 447	NP_000627.2	470	Cluster 469	NP_001638.1
449	Cluster 448	NP_002791.1	471	Cluster 470	NP_061974.2
450	Cluster 449	NP_000841.1, NP_000552.2	472	Cluster 471	NP_004995.1
451	Cluster 450	NP_002077.1	473	Cluster 472	NP_006699.2
452	Cluster 451	NP_066279.2	474	Cluster 473	NP_001744.2, NP_001225.1
453	Cluster 452	NP_077718.3	475	Cluster 474	NP_000563.1
454	Cluster 453	NP_000591.1	476	Cluster 475	NP_036541.2
455	Cluster 454	NP_004486.2	477	Cluster 476	NP_001020275.1
456	Cluster 455	NP_000843.1	478	Cluster 477	NP_002486.1
457	Cluster 456	NP_003815.1	479	Cluster 478	NP_055037.1
458	Cluster 457	NP_003245.1	480	Cluster 479	NP_000610.2
459	Cluster 458	NP_000586.2	481	Cluster 480	NP_006389.2
460	Cluster 459	NP_005604.1	482	Cluster 481	NP_006212.1
461	Cluster 460	PODMR3.1	483	Cluster 482	NP_001504.2
462	Cluster 461	NP_000605.1	484	Cluster 483	AAH18538.1

Table A 2.2 Sequence based clustering of ADA genes (continued)

S.no.	Cluster	Accession no. of clustered sequence	S.no.	Cluster	Accession no. of clustered sequence
485	Cluster 484	NP_000568.1	506	Cluster 505	CCQ43987.1
486	Cluster 485	NP_002718.2	507	Cluster 506	NP_057057.2
487	Cluster 486	AFN61600.1	508	Cluster 507	NP_001039.1
488	Cluster 487	NP_002443.3	509	Cluster 508	NP_149097.1
489	Cluster 488	NP_000791.1	510	Cluster 509	NP_002406.1
490	Cluster 489	NP_002481.2	511	Cluster 510	NP_000198.1
491	Cluster 490	NP_000580.1	512	Cluster 511	NP_001502.1
492	Cluster 491	NP_006423.1	513	Cluster 512	NP_758844.1
493	Cluster 492	NP_067080.1	514	Cluster 513	NP_000474.2
494	Cluster 493	NP_000919.1	515	Cluster 514	NP_001634.1
495	Cluster 494	NP_000175.1	516	Cluster 515	NP_002973.1, NP_005614.2
496	Cluster 495	NP_003329.1	517	Cluster 516	NP_000031.1
497	Cluster 496	NP_000362.1	518	Cluster 517	NP_000575.1
498	Cluster 497	NP_000090.1	519	Cluster 518	NP_001556.2
499	Cluster 498	NP_001009.1	520	Cluster 519	NP_004151.3, NP_000896.1
500	Cluster 499	NP_000885.1	521	Cluster 520	NP_000600.1
501	Cluster 500	NP_003078.2, NP_001225.1	522	Cluster 521	NP_002976.2, NP_002974.1
502	Cluster 501	NP_004137.2	523	Cluster 522	NP_006263.1
503	Cluster 502	NP_001003704.1	524	Cluster 523	NP_004097.1
504	Cluster 503	NP_001433.1	525	Cluster 524	NP_004533.1

505	Cluster 504	NP_000125.2	526	Cluster 525	NP_001636.1
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S.no.	Gene	S.no.	Gene
1	GWA_20q13.33	16	MT-TT
2	PKP2P1	17	MT-TH
3	VR22	18	MT-TS2
4	LOC439999	19	MT-TL2
5	hCG2039140	20	MT-COI
6	GWA_7q31	21	MT-NC7
7	miRNA-29a/b	22	APOE_e2
8	LOC651924	23	APOC1P1
9	SG5	24	LOC388458
10	MT-DLOOP	25	GWA_15q21
11	MT-RNR1	26	GWA_14q31
12	MT-TI	27	GWA_9p24
13	MT-TQ	28	CDKN2BAS
14	MT-TG	29	PTENP1
15	MT-TR	30	GWA_7p15
		31	HLA

**Table A 2.3 Unmapped ADA genes in functional clustering**

**Table A 2.4 Biological processes in which all ADA genes clustered**

S.no.	Biological Process	No. of genes
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*Chapter 9*  
*Appendices*

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1	cellular component organization or biogenesis	47
2	cellular process	320
3	localization	85
4	reproduction	15
5	biological regulation	116
6	response to stimulus	137
7	developmental process	105
8	rhythmic process	1
9	multicellular organismal process	97
10	locomotion	18
11	biological adhesion	16
12	metabolic process	280
13	immune system process	79
14	cell killing	2
15	growth	1

Table A 2.5 Pathways in which all ADA genes clustered

S. No.	Pathway	No. of genes	S.No.	Pathway	No. of genes
1	Axon guidance mediated by netrin	2	21	Parkinson disease	12
2	Axon guidance mediated by Slit/Robo	2	22	PI3 kinase pathway	14
3	Axon guidance mediated by semaphorins	5	23	PDGF signaling pathway	11
4	Apoptosis signaling pathway	22	24	Oxidative stress response	2
5	Gonadotropin-releasing hormone receptor pathway	47	25	Inflammation mediated by chemokine and cytokine signaling pathway	31
6	Angiogenesis	20	26	Nicotinic acetylcholine receptor signaling pathway	21
7	Alzheimer disease-presenilin pathway	27	27	Muscarinic acetylcholine receptor 2 and 4 signaling pathway	7
8	Alzheimer disease-amyloid secretase pathway	21	28	Muscarinic acetylcholine receptor 1 and 3 signaling pathway	11
9	Alpha adrenergic receptor signaling pathway	8	29	Metabotropic glutamate receptor group I pathway	4
10	Adrenaline and noradrenaline biosynthesis	7	30	Asparagine and aspartate biosynthesis	1
11	CCKR signaling map	26	31	Metabotropic glutamate receptor group III pathway	4
12	Ubiquitin proteasome pathway	1	32	Androgen/estrogene/progesterone biosynthesis	5
13	p53 pathway	15	33	Ionotropic glutamate receptor pathway	5
14	Wnt signaling pathway	17	34	Interleukin signaling pathway	15
15	VEGF signaling pathway	6	35	Interferon-gamma signaling pathway	1
16	Fructose galactose metabolism	2	36	Integrin signalling pathway	13
17	Toll receptor signaling pathway	3	37	Insulin/IGF pathway-protein kinase B signaling cascade	11
18	T cell activation	7	38	Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade	10
19	TCA cycle	1	39	p53 pathway feedback loops 2	5
20	Plasminogen activating cascade	8	40	Notch signalling pathway	12

Table A 2.5 Pathways in which all ADA genes clustered (continued)

S.No.	Pathway	No. of genes	S.No.	Pathway	No. of genes
41	p53 pathway by glucose deprivation	5	61	Pyruvate metabolism	2
42	B cell activation	6	62	Hypoxia response via HIF activation	4
43	Vitamin D metabolism and pathway	3	63	Endothelin signaling pathway	6
44	Triacylglycerol metabolism	2	64	EGF receptor signaling pathway	8
45	Vasopressin synthesis	1	65	Cytoskeletal regulation by Rho GTPase	4
46	Thyrotropin-releasing hormone receptor signaling pathway	5	66	5HT4 type receptor mediated signaling pathway	1
47	Ras Pathway	5	67	Blood coagulation	10
48	P53 pathway feedback loops 1	2	68	Beta2 adrenergic receptor signaling pathway	3
49	Oxytocin receptor mediated signaling pathway	5	69	Corticotropin releasing factor receptor signaling pathway	3
50	2-arachidonoylglycerol biosynthesis	1	70	Beta1 adrenergic receptor signaling pathway	3
51	Huntington disease	17	71	Cadherin signalling pathway	6
52	Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway	9	72	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway	10
53	p38 MAPK pathway	1	73	5HT3 type receptor mediated signaling pathway	1
54	Pentose phosphate pathway	2	74	5HT2 type receptor mediated signaling pathway	8
55	Glycolysis	6	75	5HT1 type receptor mediated signaling pathway	2
56	Nicotine pharmacodynamics pathway	12	76	5HT4 type receptor mediated signaling pathway	1
57	FGF signaling pathway	8	77	5-Hydroxytryptamine biosynthesis	1
58	Dopamine receptor mediated signaling pathway	13	78	Angiotensin II-stimulated signaling through G proteins and beta-arrestin	3
59	FAS signaling pathway	1	79	ALP23B signalling pathway	1
60	5-Hydroxytryptamine degradation	3	80	ATP synthesis	1

Table A 2.5 Pathways in which all ADA genes clustered (continued)

S.No.	Pathway	No. of genes	S.No.	Pathway	No. of genes
81	Arginine Biosynthesis	1	99	Metabotropic glutamate receptor group II pathway	2
82	Adenine and hypoxanthine salvage pathway	1	100	MYO signaling pathway	1
83	Activin beta signaling pathway	1	101	Methionine biosynthesis	1
84	Beta3 adrenergic receptor signaling pathway	2	102	Methylcitrate cycle	1
85	BMP/activin signaling pathway-drosophila	1	103	Opioid prodynorphin pathway	1
86	Cholesterol biosynthesis	5	104	Opioid proenkephalin pathway	1
87	Cysteine biosynthesis	1	105	Opioid proopiomelanocortin pathway	1
88	DNA replication	1	106	Plasminogen activating cascade	5
89	Endogenous cannabinoid signaling	1	107	Proline biosynthesis	1
90	FAS signaling pathway	7	108	Purine metabolism	1
91	Formyltetrahydroformate biosynthesis	1	109	Pyrimidine Metabolism	1
92	GABA-B receptor II signaling	1	110	S-adenosylmethionine biosynthesis	1
93	General transcription by RNA polymerase I	1	111	Xanthine and guanine salvage pathway	1
94	Hedgehog signaling pathway	1	112	T cell activation	4
95	Heme biosynthesis	1	113	TGF-beta signaling pathway	3
96	Heterotrimeric G-protein signaling pathway- Gi alpha and Gs alpha mediated pathway	13	114	Toll receptor signaling pathway	4
97	Histamine H1 receptor mediated signaling pathway	4	115	Transcription regulation by bZIP transcription factor	1
98	Histamine H2 receptor mediated signaling pathway (P04386)	1			

Table

A 2.6

S.no.	Protein classes	No. of genes
1	extracellular matrix protein	16
2	cytoskeletal protein	20
3	Transporter	56
4	transmembrane receptor regulatory protein	6
5	Transferase	58
6	Oxidoreductase	52
7	Lyase	12
8	cell adhesion molecule	12
9	Ligase	12
10	nucleic acid binding	59
11	signaling molecule	75
12	enzyme modulator	60
13	calcium-binding protein	15
14	defense/immunity protein	20
15	Hydrolase	75
16	transfer/carrier protein	16
17	membrane traffic protein	15
18	transcription factor	44
19	Chaperone	3
20	cell junction protein	4
21	structural protein	4
22	storage protein	5
23	Isomerise	7
24	receptor	68

**Protein classes in which all ADA genes clustered**

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
1	<i>EFEMP1</i>	calcium ion binding	cellular movement	-	-	-
2	<i>ADAM9</i>	-	apoptotic process	-	-	Alzheimer disease-amyloid secretase pathway
3	<i>TTR</i>	transmembrane transporter	vitamin transport	-	transporter	-
4	<i>VLDLR</i>	-	-	-	receptor	-
5	<i>CHRNA2</i>	acetylcholine receptor activity	neurological system process	integral to membrane	GABA receptor	-
6	<i>NTRK2</i>	-	nervous system development	-	-	-
7	<i>GPD1</i>	oxidoreductase activity	phospholipid metabolic process	-	dehydrogenase	-
8	<i>EGR2</i>	-	-	-	-	Angiotensin II-stimulated signaling through G proteins and beta-arrestin
9	<i>ADRA1A</i>	G-protein coupled receptor activity	biosynthetic process	integral to membrane	G-protein coupled receptor	Alpha adrenergic receptor signaling pathway
10	<i>CRH</i>	hormone activity	blood circulation	-	peptide hormone	Corticotropin releasing factor receptor signaling pathway
11	<i>NOS2A</i>	oxidoreductase activity	biosynthetic process	-	-	PI3 kinase pathway
12	<i>SORL1</i>	lipid binding	lipid transport	-	receptor	-
13	<i>ARSB</i>	hydrolase activity	phospholipid metabolic	-	hydrolase	-
14	<i>SST</i>	hormone activity	cell surface receptor	extracellular	peptide hormone	-
15	<i>AGT</i>	transaminase activity	biosynthetic process	cytoplasm	transaminase	-

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
16	<i>MMP3</i>	-	-	extracellular	-	-
17	<i>NDUFS1</i>	binding	cellular process	cytoplasm	dehydrogenase	-
18	<i>SEL1L</i>	enzyme regulator	-	-	enzyme modulator	-
19	<i>TTR</i>	transmembrane transporter	vitamin transport	-	transfer/carrier protein	-
20	<i>UCHL1</i>	cysteine-type peptidase	cellular process	cytoplasm	cysteine protease	Parkinson disease
21	<i>SYN3</i>	-	-	-	membrane trafficking regulatory protein	
22	<i>SORCS2</i>	lipid binding	intracellular protein transport	-	receptor	-
23	<i>HMGCR</i>	oxidoreductase	biosynthetic process	-	-	Cholesterol biosynthesis
24	<i>HTR6</i>	receptor activity	cellular process	-	G-protein coupled receptor	Heterotrimeric G-protein signaling pathway
25	<i>IL1B</i>	cytokine receptor binding	multicellular organism process	extracellular	interleukin superfamily	Inflammation mediated by chemokine and cytokine signaling
26	<i>FOS</i>	-	-	-	-	Gonadotropin-releasing hormone receptor pathway
27	<i>UBQLN1</i>	-	proteolysis	-	-	-
28	<i>BDNF</i>	growth factor activity	cell differentiation	cytoplasm	neurotrophic factor	Huntington disease
29	<i>NRG1</i>	receptor binding	cell differentiation	extracellular	growth factor	EGF receptor signaling pathway
30	<i>VPS35</i>	transporter	cellular process	cytoplasm	membrane traffic protein	

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
31	<i>GOT1</i>	transaminase activity	biosynthetic process	cytosol	-	Asparagine and aspartate biosynthesis
32	<i>NCAM2</i>	-	-	-	immunoglobulin receptor	-
33	<i>IFT74</i>	cytoskeletal protein binding	cellular component biogenesis	cilium	-	-
34	<i>VEGF</i>	growth factor	angiogenesis		growth factor	Angiogenesis
35	<i>DHCR24</i>	-	steroid metabolic process	-	reductase	-
36	<i>SERPINA3</i>	serine-type endopeptidase inhibitor	regulation of biological process	extracellular	serine protease inhibitor	-
37	<i>GPD1</i>	oxidoreductase activity	phospholipid metabolic process	-	dehydrogenase	-
38	<i>EFEMP1</i>	calcium ion binding	cellular component movement	-	-	-
39	<i>HSPA5</i>	-	-	-	-	Apoptosis signaling
40	<i>DAPK1</i>	-	-	-	G-protein coupled receptor	-
41	<i>PICALM</i>	-	intracellular protein transport	cytoplasm	vesicle coat protein	-
42	<i>CXCL12</i>	chemokine activity	multicellular organism process	plasma membrane		Axon guidance mediated by Slit/Robo
43	<i>PPM1H</i>	kinase inhibitor	MAPK cascade	-	kinase inhibitor	-
44	<i>CPE</i>	metallopeptidase	cellular process	extracellular	metalloprotease	Vasopressin synthesis
45	<i>PRNP</i>	-	fatty acid metabolic process	-	-	-

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
46	<i>SORCS1</i>	lipid binding	intracellular protein transport	-	receptor	-
47	<i>CRHBP</i>	receptor binding	cellular process	-	signaling molecule	-
48	<i>UCHL1</i>	cysteine-type peptidase activity	cellular process	cytoplasm	cysteine protease	Parkinson disease
49	<i>SORCS2</i>	lipid binding	intracellular protein transport	-	receptor	-
50	<i>CHRNA2</i>	acetylcholine receptor activity	neurological system process	integral to membrane	GABA receptor	-
51	<i>VLDLR</i>	-	-	-	receptor	-
52	<i>ENPP2</i>	nucleotide phosphatase	metabolic process	-	nucleotide phosphatase	-
53	<i>NEUROD1</i>	nuclease activity	ectoderm development	-	nuclease	-
54	<i>NCOA2</i>	receptor binding	biosynthetic process	-	intracellular	acetyltransferase
55	<i>CLCNKB</i>	anion channel activity	anion transport	anion channel	-	-
56	<i>AGT</i>	serine-type endopeptidase inhibitor activity	regulation of biological process	-	extracellular space	serine protease inhibitor
57	<i>LHCGR</i>	G-protein coupled receptor activity	biosynthetic process	integral to membrane	receptor	Angiotensin II-stimulated signaling through G proteins and beta-arrestin
58	<i>NTRK2</i>		nervous system development	-	-	-
59	<i>EFEMP1</i>	calcium ion binding	cellular component movement	-	-	-

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
60	<i>LPL</i>	lipase activity	phospholipid metabolic process	-	Esterase	
61	<i>SORL1</i>	lipid binding	intracellular protein transport	-	Receptor	2-arachidonoylglycerol biosynthesis
62	<i>ADAM9</i>	-	apoptotic process	-	-	
63	<i>SCD</i>	-	-	-	-	Alzheimer disease-amyloid secretase pathway
64	<i>GRB7</i>	-	-	-	transmembrane receptor regulatory protein	cell surface receptor signaling pathway
65	<i>PPM1H</i>	kinase inhibitor activity	MAPK cascade	-	kinase inhibitor	Angiogenesis
66	<i>LRRTM3</i>	kinase inhibitor activity	JAK-STAT cascade	cytoplasm	Cytokine	-
67	<i>PDE3B</i>	phosphoric diester hydrolase	cyclic nucleotide metabolic process		Phosphodiesterase	-
68	<i>SYN3</i>	-	-	-	membrane trafficking regulatory protein	-
69	<i>HMGCR</i>	oxidoreductase activity	biosynthetic process			-
70	<i>TP73</i>	chromatin binding	JNK cascade	chromosome	transcription factor	Cholesterol biosynthesis
71	<i>SNCAIP</i>	-	-	-	-	Huntington disease
72	<i>SEL1L</i>	enzyme regulator activity	-	-	enzyme modulator	Parkinson disease
73	<i>NCAM2</i>	-	-	-	immunoglobulin receptor superfamily	-
74	<i>CDKN2A</i>	kinase inhibitor	cell cycle	-	kinase inhibitor	p53 pathway

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
75	<i>C1R</i>	-	-	-	annexin	-
76	<i>HIF1A</i>	transcription factor	biosynthetic process	-	transcription factor	-
77	<i>GSTO2</i>	transferase activity	catabolic process	cytoplasm	cytoskeletal protein	Hypoxia response via HIF activation
78	<i>CPE</i>	metallopeptidase	cellular process	extracellular	metalloprotease	
79	<i>NDUFS1</i>	binding	cellular process	cytoplasm	dehydrogenase	Vasopressin synthesis
80	<i>LRP6</i>	protein binding	anatomical structure morphogenesis	plasma membrane	receptor	-
81	<i>GYS2</i>	-	-	-	-	Heterotrimeric G-protein signaling pathway
82	<i>COL25A1</i>	-	anatomical structure morphogenesis	-	-	-
83	<i>CECR2</i>	acetyltransferase	cellular process	-	acetyltransferase	-
84	<i>ESR1</i>	transcription factor	cellular process	-	nuclear hormone receptor	-
85	<i>ANK3</i>	cytoskeletal binding	cellular biogenesis	cytoplasm	cytoskeletal protein	-
86	<i>NGFR</i>	protein binding	apoptotic process	integral to membrane	tumor necrosis factor receptor	-
87	<i>ESR2</i>	transcription factor activity	cellular process	-	nuclear hormone receptor	-
88	<i>TFAM</i>	-	-	-	HMG box transcription factor	-

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
89	<i>NOS2A</i>	guanylate cyclase	biosynthetic process	-	-	PI3 kinase pathway
90	<i>PRKAB2</i>	kinase regulator	cholesterol metabolic process	-	kinase modulator	Gonadotropin-releasing hormone receptor pathway
91	<i>AKT2</i>	protein kinase activity	intracellular signal transduction	intracellular	annexin	Inflammation mediated by chemokine and cytokine signaling pathway
92	<i>DYRK1A</i>	tyrosine kinase	-	-	non-receptor serine/threonine protein kinase	-
93	<i>SOS1</i>	guanyl-nucleotide exchange factor	G-protein coupled receptor signaling pathway	-	guanyl-nucleotide exchange factor	Interleukin signaling pathway
94	<i>DLD</i>	oxidoreductase activity	ferredoxin metabolic process	-	dehydrogenase	-
95	<i>LAMB1</i>	receptor activity	cell-cell adhesion	extracellular matrix	receptor	Integrin signalling pathway
96	<i>CAND1</i>	-	cellular component organization	intracellular	transcription factor	-
97	<i>UBQLN1</i>	-	proteolysis	-	-	-
98	<i>ABCA1</i>	ATPase activity	catabolic process	intracellular	ATP-binding cassette (ABC) transporter	-
99	<i>PLCG1</i>	calcium ion binding	phospholipid metabolic process	-	calcium-binding protein	Axon guidance mediated by netrin
100	<i>ADRA1A</i>	G-protein coupled receptor	biosynthetic process	integral to membrane	G-protein coupled receptor	Alpha adrenergic receptor signaling pathway

Table A 2.7 Correlation of functional enrichment and expression of DGE ADA genes (continued)

S.no.	Gene	Molecular function	Biological process	Cellular component	Protein class	Pathway
101	<i>SERPINA3</i>	serine-type endopeptidase inhibitor activity	regulation of biological process	extracellular space	serine protease inhibitor	-
102	<i>GBP2</i>	GTPase activity	macrophage activation	heterotrimeric G-protein complex	heterotrimeric G-protein	-
103	<i>GNB3</i>	GTPase activity	G-protein coupled receptor signaling pathway	heterotrimeric G-protein complex	heterotrimeric G-protein	Angiotensin II-stimulated signaling through G proteins and beta-arrestin
104	<i>CYP39A1</i>	oxidoreductase activity	cholesterol metabolic process	-	oxygenase	
105	<i>CARD8</i>	sequence-specific DNA binding transcription factor activity	cellular defense response	-	nucleic acid binding	-
106	<i>AHSG</i>	peptidase inhibitor activity	regulation of biological process	extracellular space	cysteine protease inhibitor	-
107	<i>ABCA12</i>	ATPase activity	catabolic process	intracellular	ATP-binding cassette (ABC) transporter	-
108	<i>APOA2</i>	enzyme inhibitor	cellular component biogenesis	extracellular	apolipoprotein	-
109	<i>MT-ATP8</i>	cation transmembrane transporter	respiratory electron transport chain	-	ATP synthase	-