Pakistan J. Zool., vol. 54(5), pp 2315-2327, 2022 **DOI**: https://dx.doi.org/10.17582/journal.pjz/20210713140738

Supplementary Material

Mining the SNPs of Human Low Density Lipoprotein (LDL) related Gene *APOB* through *in silico* Approaches

Muneeza Zafar[1,2,3], Fazli Rabbi Awan[2,*], Munazza Raza Mirza[3,*], Sumaira Nishat[2,4], Sajid Ali Rajput[5] and Imran Riaz Malik[1,*]

[1]*Department of Biotechnology, University of Sargodha, Sargodha*
[2]*Health Biotechnology Division, National Institute for Biotechnology and Genetic Engineering, Jhang Road, P.O. Box. 577, Faisalabad*
[3]*Dr. Panjwani Center for Molecular Medicine and Drug Research, International Center for Chemical and Biological Sciences, University of Karachi, Karachi-75270*
[4]*Department of Computer Science, University of Agriculture, Faisalabad*
[5]*Institute of Biotechnology and Genetie Engineering, University of Sindh, Jamshoro*

Supplementary Table I.- Working inputs and prediction score criteria used for 18 computational tools used in prediction of deleterious *APOB* SNPs.

S. No.	Tools	Criteria	Input
Sequence Based Tools and their prediction criteria			
1.	SIFT	Score > 0.5 Tolerable Score < 0.5 Deleterious	rs dbSNP
2.	PROVEAN	Score < -2.5 Deleterious Score > -2.5 Neutral	ENSP00000224605 63 A
3.	Mutation Assessor	Neutral /Low Medium/High	UniProt ID position Wild and variant
4.	PON-P2	Pathogenic Neutral Unknown	FASTA-format amino acid wild and mutant in header
5.	PhD-SNP	RI > 0.5 DiseaseRI < 0.5 Neutral	FASTA seq. or Swiss Port ID, AA position and new variable
Supervised Learned Based Tools and their prediction criteria			
6.	SNAP	-100 Neutral +100 Deleterious	FASTA Sequence
7.	SuSPect	0 - 100	UniPort Accession and mutations
8.	MutPred	Score > 0.5 Deleterious Score < 0.5 Neutral	Protein FASTA sequence along amino acid substitution in sequence header
Structure Based Tools and their prediction criteria			
9.	PolyPhen	0 – Benign 1 - Probably Damaging Between 0 – 1 Possibly Damaging	Protein FASTA seq. AA substitution and position
10.	I-Mutant3	Score > - 0.5 Stable Score < -0.5 Unstable	FASTA seq. or Swiss Port ID, AA position and new variable

* Corresponding author: munazzaraza@iccs.com
0030-9923/2022/0005-2315 $ 9.00/0

S. No.	Tools	Criteria	Input
Consensus Based Tools and their prediction criteria			
11.	Condel	0 – Neutral 1.0 − Deleterious	Identifier Substitutions
12.	MetaSNP	Output > 0.5 = Deleterious	Protein sequence and a list of comma separated mutations
13.	PredictSNP	Green – Neutral Red − Deleterious	Protein FASTA sequence along substitution
Evolutionary conservation based method			
14.	PANTHER	PT > 450 my Damaging PT < 200 my Neutral	FASTA seq. and substitutions
Tools used for prediction of non- coding region SNPs			
15.	RegulomeDB	1 (Likely to affect binding and liked expression) **2** (Likely to affect binding) **3** (Less likely to affect) **4 ,5, 6** (Minimal binding)	rs dbSNP ID
16.	PolymiRTs	**D** (Disturb) **N** (Disturb non conserved site) **C** (Create new allele) **O (**Ancestor allele not determined)	rs dbSNP ID
17.	SNPinfo	Y sSNP Splicing Regulation Stop Codon Polyphen Prediction SNPs3D Prediction TFBS Prediction miRNA Binding Site Prediction	rs dbSNP ID
18	HOPE	Structural features Different properties of amino acid Generate 3D models	Protein sequence and the mutation position

Supplementary Table II.- Retrieved Data of missense SNPs present in *APOB* by using from NCBI dbSNP data base.

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
1	ENSP00000233242.1	rs676210	21008652	0.3662	missense	C/A,	P [Pro] ⇒ Q [Gln]	NP_000375.2
2	ENSP00000233242.1	rs679899	21028042	0.485	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
3	ENSP00000233242.1	rs1042031	21002881	0.1278	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
4	ENSP00000233242.1	rs1042034	21002409	0.3704	missense	G/A	S [Ser] ⇒ N [Asn]	NP_000375.2
5	ENSP00000233242.1	rs1367117	21041028	0.1693	missense	C/T	T [Thr] ⇒ I [Ile]	NP_000375.2
6	ENSP00000233242.1	rs1801695	21001981	0.0142	missense	G/A	A [Ala] ⇒ T [Thr]	NP_000375.2
7	ENSP00000233242.1	rs1801696	21009172	0.0006	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
8	ENSP00000233242.1	rs1801701	21005955	0.0385	missense	G/A	R [Arg] ⇒ Q [Gln]	NP_000375.2
9	ENSP00000233242.1	rs1801702	2100261	0.0627	missense	G/C	R [Arg] ⇒ T [Thr]	NP_000375.2
10	ENSP00000233242.1	rs13306194	21029662	0.0274	missense	C/T	R [Arg] ⇒ W [Trp]	NP_000375.2
11	ENSP00000233242.1	rs61743502	21002628	0.002	missense	T/C	V [Val] ⇒ A [Ala]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
12	ENSP00000233242.1	rs72653092	21009583	0.0004	missense	T/A, T/G	S [Ser] ⇒ T [Thr], S [Ser] ⇒ A [Ala]	NP_000375.2
13	ENSP00000233242.1	rs72654423	21002482	0.0042	missense	A/G	I [Ile] ⇒ V [Val]	NP_000375.2
14	ENSP00000233242.1	rs533617	21011100	0.0162	missense	A/G	H [His] ⇒ R [Arg]	NP_000375.2
15	ENSP00000233242.1	rs568413	21012603	---	missense	G/A, G/C, G/T	C [Cys] ⇒ Y [Tyr], C [Cys]	NP_000375.2
16	ENSP00000233242.1	rs584542	21009931	0.0138	missense	G/T, G/A	V [Val] ⇒ I [Ile], V [Val] ⇒ F [Phe]	NP_000375.2
17	ENSP00000233242.1	rs1042023	21006574	0.0028	missense	C/G	Q [Gln] ⇒ E [Glu]	NP_000375.2
18	ENSP00000233242.1	rs1800480	21044060	0.0172	UTR-5	----/G	-------	------
19	ENSP00000233242.1	rs1801698	21004631	0.0004	missense	A/G	T [Thr] ⇒ A [Ala]	NP_000375.2
20	ENSP00000233242.1	rs1801699	21011127	0.0112	missense	A/G	N [Asn] ⇒ S [Ser]	NP_000375.2
21	ENSP00000233242.1	rs1801703	21003040	0.0034	missense	G/A, G/C, G/T	V [Val] ⇒ M [Met],V [Val]	NP_000375.2
22	ENSP00000233242.1	rs2163204	21008515	0.0118	missense	A/C	N [Asn] ⇒ H [His]	NP_000375.2
23	ENSP00000233242.1	rs6752026	21038062	0.0349	missense	C/T	P [Pro] ⇒ S [Ser]	NP_000375.2
24	ENSP00000233242.1	rs9282603	21041014	0.001	missense	T/C	Y [Tyr] ⇒ H [His]	NP_000375.2
25	ENSP00000233242.1	rs12691202	21026844	0.0142	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
26	ENSP00000233242.1	rs12713450	21001971	0.0383	missense	C/T	T [Thr] ⇒ M [Met]	NP_000375.2
27	ENSP00000233242.1	rs12713540	21005467	0.0004	missense	T/A	S [Ser] ⇒ T [Thr]	NP_000375.2
28	ENSP00000233242.1	rs12713559	21006196	0.0002	missense	C/T	R [Arg] ⇒ C [Cys]	NP_000375.2
29	ENSP00000233242.1	rs12713675	21009501	0.0222	missense	C/A	A [Ala] ⇒ D [Asp]	NP_000375.2
30	ENSP00000233242.1	rs12713681	21009973	0.0088	missense	G/C	D [Asp] ⇒ H [His]	NP_000375.2
31	ENSP00000233242.1	rs12713843	21015495	0.0028	missense	G/A	R [Arg] ⇒ H [His]	NP_000375.2
32	ENSP00000233242.1	rs12713844	21015541	0.003	missense	G/C	D [Asp] ⇒ H [His]	NP_000375.2
33	ENSP00000233242.1	rs12714192	21026810	0.0218	missense	C/A	T [Thr] ⇒ N [Asn]	NP_000375.2
34	ENSP00000233242.1	rs12714214	21028495	0.003	missense	C/G, C/T	P [Pro] ⇒ R [Arg] ,P [Pro] ⇒ L [Leu]	NP_000375.2
35	ENSP00000233242.1	rs12714225	21032483	0.0082	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
36	ENSP00000233242.1	rs12720763	21001550	0.0102	UTR-3	---/A	-------	--------
37	ENSP00000233242.1	rs12720854	21007033	0.0072	missense	A/G	S [Ser] ⇒ G [Gly]	NP_000375.2
38	ENSP00000233242.1	rs12720855	21006988	0.0224	missense	T/C	S [Ser] ⇒ P [Pro]	NP_000375.2
39	ENSP00000233242.1	rs13306187	21013213	0.004	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
40	ENSP00000233242.1	rs13306190	21032408	0.0002	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
41	ENSP00000233242.1	rs13306198	21037212	0.0142	missense	C/T	T [Thr] ⇒ M [Met]	NP_000375.2
42	ENSP00000233242.1	rs13306206	21019859	0.0018	missense	C/T	P [Pro] ⇒ S [Ser]	NP_000375.2
43	ENSP00000233242.1	rs41288783	21019741	0.001	missense	C/T	P [Pro] ⇒ L [Leu]	NP_000375.2
44	ENSP00000233242.1	rs61736761	21015135	0.0284	missense	C/A	L [Leu] ⇒ M [Met]	NP_000375.2
45	ENSP00000233242.1	rs61741164	21014550	0.0006	missense	A/G	Y [Tyr] ⇒ C [Cys]	NP_000375.2
46	ENSP00000233242.1	rs61741625	21035651	0.0026	missense	G/A	A [Ala] ⇒ T [Thr]	NP_000375.2
47	ENSP00000233242.1	rs61741974	21005611	0.0012	missense	T/C	F [Phe] ⇒ L [Leu]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
48	ENSP00000233242.1	rs61742331	21006807	0.0018	missense	C/G	A [Ala] ⇒ G [Gly]	NP_000375.2
49	ENSP00000233242.1	rs61743299	21002725	0.0224	missense	T/A	S [Ser] ⇒ T [Thr]	NP_000375.2
50	ENSP00000233242.1	rs61743313	21002656	0.0014	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
51	ENSP00000233242.1	rs61744153	21005391	0.0006	missense	C/A	T [Thr] ⇒ K [Lys]	NP_000375.2
52	ENSP00000233242.1	rs61744288	21006088	0.0018	missense	T/C	W[Trp] ⇒ R [Arg]	NP_000375.2
53	ENSP00000233242.1	rs61746672	21037187	0.0034	missense	A/T	E [Glu] ⇒ D [Asp]	NP_000375.2
54	ENSP00000233242.1	rs72653059	21037186	0.0042	missense	A/G	I [Ile] ⇒ V [Val]	NP_000375.2
55	ENSP00000233242.1	rs72653077	21015451	0.0015	missense	C/T	P [Pro] ⇒ S [Ser]	NP_000375.2
56	ENSP00000233242.1	rs72653078	21014578	0.001	missense	C/A	L [Leu] ⇒ I [Ile]	NP_000375.2
57	ENSP00000233242.1	rs72653091	21009626	0.003	missense	A/C	E [Glu] ⇒ D [Asp]	NP_000375.2
58	ENSP00000233242.1	rs72653095	21008406	0.0062	missense	C/T	P [Pro] ⇒ L [Leu]	NP_000375.2
59	ENSP00000233242.1	rs72653099	21007642	0.0014	missense	C/A	L[Leu] ⇒ M [Met]	NP_000375.2
60	ENSP00000233242.1	rs72654409	21005107	0.0034	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
62	ENSP00000233242.1	rs72654424	21002320	0.0008	missense	C/G	Q [Gln] ⇒ E [Glu]	NP_000375.2
63	ENSP00000233242.1	rs72654428	21001719	0.0084	UTR-3	----	------	-----
64	ENSP00000233242.1	rs72654430	21001501	0.003	UTR-3	-----	-----	-----
65	ENSP00000233242.1	rs140027955	21009645	0.0004	missense	C/T	S [Ser] ⇒ F [Phe]	NP_000375.2
66	ENSP00000233242.1	rs141225768	21012205	0.0002	missense	A/G	I [Ile] ⇒ V [Val]	NP_000375.2
67	ENSP00000233242.1	rs142114415	21032396	0.001	missense	G/A, G/T	R[Arg] ⇒ H [His] , R [Arg] ⇒ L [Leu]	NP_000375.2
68	ENSP00000233242.1	rs142151703	21001551	0.0022	UTR-3	----	-----	-----
69	ENSP00000233242.1	rs142422341	21007057	0.0002	missense	G/A	G [Gly] ⇒ S [Ser]	NP_000375.2
70	ENSP00000233242.1	rs143269114	21007377	0.0006	missense	C/T	T[Thr] ⇒ M [Met]	NP_000375.2
71	ENSP00000233242.1	rs143282164	21013198	0.001	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
72	ENSP00000233242.1	rs143425834	21026862	0.0002	missense	G/T	G [Gly] ⇒ C [Cys]	NP_000375.2
73	ENSP00000233242.1	rs143710616	21005514	0.0002	missense	C/T	T [Thr] ⇒ I [Ile]	NP_000375.2
74	ENSP00000233242.1	rs144467873	21006289	0.0004	missense	C/T	R[Arg] ⇒ W [Trp]	NP_000375.2
75	ENSP00000233242.1	rs145142090	21023544	0.0004	missense	T/C	V [Val] ⇒ A [Ala]	NP_000375.2
76	ENSP00000233242.1	rs145862664	21028508	0.0006	missense	G/C	D[Asp] ⇒ H [His]	NP_000375.2
77	ENSP00000233242.1	rs146152405	21037152	0.0004	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
78	ENSP00000233242.1	rs148170480	21009253	0.0016	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
79	ENSP00000233242.1	rs149227065	21033362	0.0002	missense	A/G, A/G	E [Glu] ⇒ G [Gly],E [Glu] ⇒ V [Val]	NP_000375.2
80	ENSP00000233242.1	rs151009667	21011802	0.0004	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
81	ENSP00000233242.1	rs151333262	21002239	0.0002	missense	G/A	G [Gly] ⇒ S [Ser]	NP_000375.2
82	ENSP00000233242.1	rs180874451	21011409	0.0006	missense	A/C	K [Lys] ⇒ T [Thr]	NP_000375.2
83	ENSP00000233242.1	rs183117027	21004340	0.0008	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
84	ENSP00000233242.1	rs183398286	21022990	0.0002	missense	A/G	N [Asn] ⇒ S [Ser]	NP_000375.2
85	ENSP00000233242.1	rs186299244	21006985	0.0004	missense	T/C	Y [Tyr] ⇒ H [His]	NP_000375.2
86	ENSP00000233242.1	rs186544754	21041033	0.0022	missense	G/T	Q[Gln] ⇒ H [His]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
87	ENSP00000233242.1	rs199510126	21011178	0.0002	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
88	ENSP00000233242.1	rs199668351	21003112	0.0006	missense	C/A	L[Leu] ⇒ M [Met]	NP_000375.2
89	ENSP00000233242.1	rs199859104	21015453	0.0002	missense	C/T	S [Ser] ⇒ L [Leu]	NP_000375.2
90	ENSP00000233242.1	rs200106845	21010212	0..0002	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
91	ENSP00000233242.1	rs375894411	21015174	0.0004	missense	G/A	D[Asp] ⇒ N [Asn]	NP_000375.2
92	ENSP00000233242.1	rs531273434	21009015	0.0004	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
93	ENSP00000233242.1	rs544542990	21014461	0.0002	missense	C/T, A/G	L [Leu] ⇒ F [Phe], R[Arg] ⇒ G [Gly]	NP_000375.2
94	ENSP00000233242.1	rs551178628	21005425	0.0004	missense	G/A, G/T	V[Val] ⇒ M [Met],V [Val] ⇒ L [Leu]	NP_000375.2
95	ENSP00000233242.1	rs558304720	21012282	0.0002	missense	G/A, G/T	G[Gly] ⇒ D [Asp] G[Gly] ⇒ V [Val]	NP_000375.2
96	ENSP00000233242.1	rs574725520	21007229	0.0002	missense	C/A	N [Asn] ⇒ K [Lys]	NP_000375.2
97	ENSP00000233242.1	rs575505383	21019079	0.0016	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
98	ENSP00000233242.1	rs12720801	21016515	0.0002	missense	G/A, G/C	G [Gly] ⇒ S [Ser], G [Gly] ⇒ R [Arg]	NP_000375.2
99	ENSP00000233242.1	rs61741467	21016646	0.0002	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
100	ENSP00000233242.1	rs61742323	21007728	0.0034	missense	C/G, C/T	T [Thr] ⇒ R [Arg], T [Thr] ⇒ M [Met]	NP_000375.2
101	ENSP00000233242.1	rs61744151	21005956	0.0002	missense,	C/A	R [Arg] ⇒ R [Arg]	NP_000375.2
102	ENSP00000233242.1	rs61746686	21005148	0.0006	missense	A/G	D [Asp] ⇒ G [Gly]	NP_000375.2
103	ENSP00000233242.1	rs72653060	21034825	0.001	missense	T/G	F [Phe] ⇒ V [Val]	NP_000375.2
104	ENSP00000233242.1	rs72653074	21016551	0.0002	missense	G/A	G [Gly] ⇒ R [Arg]	NP_000375.2
105	ENSP00000233242.1	rs72653076	21015496	0.0004	missense	C/T	R [Arg] ⇒ C [Cys]	NP_000375.2
106	ENSP00000233242.1	rs72653088	21010006	0.0002	missense	C/T	H [His] ⇒ Y [Tyr]	NP_000375.2
107	ENSP00000233242.1	rs72653100	21007626	0.0014	missense	G/A, G/C	S [Ser] ⇒ N [Asn],S [Ser] ⇒ T [Thr]	NP_000375.2
108	ENSP00000233242.1	rs72653101	21007547	0.0006	missense	C/G	N [Asn] ⇒ K [Lys]	NP_000375.2
109	ENSP00000233242.1	rs72653102	21007462	0.0004	missense	C/T	R [Arg] ⇒ C [Cys]	NP_000375.2
110	ENSP00000233242.1	rs72654404	21007001	0.0002	missense,	C/A, C/T	D [Asp] ⇒ E [Glu],T [Thr] ⇒ T [Thr]	NP_000375.2
111	ENSP00000233242.1	rs72654416	21004645	0.0026	missense	C/T	T [Thr] ⇒ M [Met]	NP_000375.2
112	ENSP00000233242.1	rs72654422	21002619	0.003	missense	T/C	M [Met] ⇒ T [Thr]	NP_000375.2
113	ENSP00000233242.1	rs72654425	21002183	0.0002	missense	C/G	N [Asn] ⇒ K [Lys]	NP_000375.2
114	ENSP00000233242.1	rs78875649	21015162	0.0006	missense	A/G	S [Ser] ⇒ G [Gly]	NP_000375.2
115	ENSP00000233242.1	rs80179164	21041083	0.0002	missense	G/C	V [Val] ⇒ L [Leu]	NP_000375.2
116	ENSP00000233242.1	rs138391809	21008559	0.0006	missense	C/T	T [Thr] ⇒ I [Ile]	NP_000375.2
117	ENSP00000233242.1	rs138529007	21007651	0.0002	missense	A/G	N [Asn] ⇒ D [Asp]	NP_000375.2
118	ENSP00000233242.1	rs139599466	21005607	0.0002	missense	C/T	T [Thr] ⇒ I [Ile]	NP_000375.2
119	ENSP00000233242.1	rs139857448	21010000	0.0002	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
120	ENSP00000233242.1	rs139929439	21006392	0.001	Missense,	T/A	I [Ile] ⇒ I [Ile]	NP_000375.2
121	ENSP00000233242.1	rs140246447	21012391	0.0002	missense	T/C	S [Ser] ⇒ P [Pro]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
122	ENSP00000233242.1	rs140647761	21006513	0.0002	missense	C/G, C/T	P [Pro] ⇒ R [Arg],P [Pro] ⇒ L [Leu]	NP_000375.2
123	ENSP00000233242.1	rs140773510	21013262	0.0002	missense	T/A	S [Ser] ⇒ T [Thr]	NP_000375.2
124	ENSP00000233242.1	rs140858817	21011824	0.0004	missense	A/G	M[Met] ⇒ V [Val]	NP_000375.2
125	ENSP00000233242.1	rs140877474	21012493	0.0014	missense	A/G	S [Ser] ⇒ G [Gly]	NP_000375.2
126	ENSP00000233242.1	rs141591543	21008019	0.0004	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
127	ENSP00000233242.1	rs142638069	21011758	0.0006	missense	G/A, G/T	A [Ala] ⇒ T [Thr] ,A [Ala] ⇒ S [Ser]	NP_000375.2
128	ENSP00000233242.1	rs142756262	21007986	0.0002	missense	A/G, A/T	N [Asn] ⇒ S [Ser],N [Asn] ⇒ I [Ile]	NP_000375.2
129	ENSP00000233242.1	rs143612660	21002671	0.0002	missense	A/G, G/C	I [Ile] ⇒ V [Val], S [Ser] ⇒ S [Ser]	NP_000375.2
130	ENSP00000233242.1	rs145324793	21012588	0.0002	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
131	ENSP00000233242.1	rs145424390	21010849	0.0008	missense	G/A	V[Val] ⇒ M [Met]	NP_000375.2
132	ENSP00000233242.1	rs146687572	21001752	0.0004	missense	G/C	G[Gly] ⇒ A [Ala]	NP_000375.2
133	ENSP00000233242.1	rs146687604	21006931	0.001	missense	C/A	L [Leu] ⇒ I [Ile]	NP_000375.2
134	ENSP00000233242.1	rs147173587	21027964	0.0002	missense	C/A	S [Ser] ⇒ Y [Tyr]	NP_000375.2
135	ENSP00000233242.1	rs147447233	21009964	0.0008	missense	G/A	G [Gly] ⇒ R [Arg]	NP_000375.2
136	ENSP00000233242.1	rs147564959	21005635	0.0002	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
137	ENSP00000233242.1	rs148126873	21033413	0.0002	missense	T/A	I [Ile] ⇒ N [Asn]	NP_000375.2
138	ENSP00000233242.1	rs148190577	21024958	0.0004	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
139	ENSP00000233242.1	rs148451559	21011717	0.0002	missense	G/A	M [Met] ⇒ I [Ile]	NP_000375.2
140	ENSP00000233242.1	rs148502464	21025111	0.0004	missense	G/A	G [Gly] ⇒ E [Glu]	NP_000375.2
141	ENSP00000233242.1	rs148503464	21041049	0.0002	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
142	ENSP00000233242.1	rs148987924	21008904	0.0002	missense	C/A, C/G	T [Thr] ⇒ N [Asn], T [Thr] ⇒ S [Ser]	NP_000375.2
143	ENSP00000233242.1	rs149349129	21009828	0.0002	missense	G/A	R[Arg] ⇒ K [Lys]	NP_000375.2
144	ENSP00000233242.1	rs149357946	21019061	0.0004	missense	G/A	A [Ala] ⇒ T [Thr]	NP_000375.2
145	ENSP00000233242.1	rs149887185	21006466	0.0002	missense	A/G	M[Met] ⇒ V [Val]	NP_000375.2
146	ENSP00000233242.1	rs150110189	21004370	0.0004	missense	G/A	G [Gly] ⇒ S [Ser]	NP_000375.2
147	ENSP00000233242.1	rs181143364	21029669	0.0002	Missense	G/A	Q[Gln] ⇒ Q [Gln]	NP_000375.2
148	ENSP00000233242.1	rs181570298	21016629	0.0004	missense	A/T	T [Thr] ⇒ S [Ser]	NP_000375.2
149	ENSP00000233242.1	rs181737266	21038061	0.0004	missense	C/T	P [Pro] ⇒ L [Leu]	NP_000375.2
150	ENSP00000233242.1	rs181877973	21011034	0.0002	missense	A/G	D[Asp] ⇒ G [Gly]	NP_000375.2
151	ENSP00000233242.1	rs183394803	21008487	0.0002	missense	C/T	T [Thr] ⇒ I [Ile]	NP_000375.2
152	ENSP00000233242.1	rs183475426	21008028	0.0006	missense	G/C	S [Ser] ⇒ T [Thr]	NP_000375.2
153	ENSP00000233242.1	rs183812948	21002053	0.0008	missense	G/A	D[Asp] ⇒ N [Asn]	NP_000375.2
154	ENSP00000233242.1	rs183950016	21024971	0.0002	missense	C/A	L[Leu] ⇒ M [Met]	NP_000375.2
155	ENSP00000233242.1	rs184512808	21010317	0.0002	missense	A/G	Y [Tyr] ⇒ C [Cys]	NP_000375.2
156	ENSP00000233242.1	rs184685800	21009814	0.0002	missense	C/G	Q [Gln] ⇒ E [Glu]	NP_000375.2
157	ENSP00000233242.1	rs185224477	21007420	0.0002	missense	T/C	F [Phe] ⇒ L [Leu]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
158	ENSP00000233242.1	rs185540148	21016457	0.0002	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
159	ENSP00000233242.1	rs186346145	21011685	0.0002	missense	A/G	N [Asn] ⇒ S [Ser]	NP_000375.2
160	ENSP00000233242.1	rs186480094	21011134	0.0004	missense	A/T	N[Asn] ⇒ Y [Tyr]	NP_000375.2
161	ENSP00000233242.1	rs187506285	21019873	0.0002	missense	C/T	T[Thr] ⇒ M [Met]	NP_000375.2
162	ENSP00000233242.1	rs188019153	21001699	0.0004	UTR' 3		-----	NP_000375.2
163	ENSP00000233242.1	rs188592517	21004369	0.0002	missense	G/A, G/T	G[Gly] ⇒ D [Asp], G[Gly] ⇒ V [Val]	NP_000375.2
164	ENSP00000233242.1	rs189341276	21011179	0.0006	missense	C/A, C/T	R [Arg] ⇒ S [Ser] ,R [Arg] ⇒ C [Cys]	NP_000375.2
165	ENSP00000233242.1	rs189880634	21023593	-----	missense	T/A	L[Leu] ⇒ M [Met]	NP_000375.2
166	ENSP00000233242.1	rs190114930	21006438	0.0002	missense	T/C	V [Val] ⇒ A [Ala]	NP_000375.2
167	ENSP00000233242.1	rs190134103	21037963	0.0002	missense	T/A, T/C	F [Phe] ⇒ I [Ile] ,F [Phe] ⇒ L [Leu]	NP_000375.2
168	ENSP00000233242.1	rs191145848	21012073	0.0004	missense	C/T	R [Arg] ⇒ C [Cys]	NP_000375.2
169	ENSP00000233242.1	rs192004342	21032448	-----	missense	G/A, G/C	E [Glu] ⇒ K [Lys], E [Glu] ⇒ Q [Gln]	NP_000375.2
170	ENSP00000233242.1	rs192491009	21008393	0.0002	missense	G/C	K[Lys] ⇒ N [Asn]	NP_000375.2
171	ENSP00000233242.1	rs192869978	21028037	0.0002	missense	A/G	K [Lys] ⇒ E [Glu]	NP_000375.2
172	ENSP00000233242.1	rs199585500	21011288	0.0002	missense	G/T	Q[Gln] ⇒ H [His]	NP_000375.2
173	ENSP00000233242.1	rs199590149	21007461	0.0002	missense	G/A, G/C	R[Arg] ⇒ H [His] R [Arg] ⇒ P [Pro]	NP_000375.2
174	ENSP00000233242.1	rs199689957	21006601	0.0002	missense	G/A	V[Val] ⇒ M [Met]	NP_000375.2
175	ENSP00000233242.1	rs199815987	21012003	0.0002	missense	A/G	H [His] ⇒ R [Arg]	NP_000375.2
176	ENSP00000233242.1	rs200034452	21009774	0.0004	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
177	ENSP00000233242.1	rs200143030	21009537	0.0012	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
178	ENSP00000233242.1	rs200184366	21006280	0.0002	missense	G/A	V[Val] ⇒ M [Met]	NP_000375.2
179	ENSP00000233242.1	rs200222843	21003286	0.0002	missense	C/T	R[Arg] ⇒ W [Trp]	NP_000375.2
180	ENSP00000233242.1	rs200231583	21009139	0.0002	missense	A/C	M[Met] ⇒ L [Leu]	NP_000375.2
181	ENSP00000233242.1	s200318200	21041038	0.0002	missense	A/G	S [Ser] ⇒ G [Gly]	NP_000375.2
182	ENSP00000233242.1	rs200321839	1012618	0.0002	missense	C/T	T [Thr] ⇒ M [Met]	NP_000375.2
183	ENSP00000233242.1	rs200367807	21008233	0.0004	missense	A/T	N [Asn] ⇒ Y [Tyr]	NP_000375.2
184	ENSP00000233242.1	rs200370790	21010351	0.0002	missense	C/G	Q [Gln] ⇒ E [Glu]	NP_000375.2
185	ENSP00000233242.1	rs200464882	21043527	0.0002	missense	A/C	S [Ser] ⇒ T [Thr]	NP_000375.2
186	ENSP00000233242.1	rs200469887	21002080	0.0002	missense	A/T	I [Ile] ⇒ F [Phe]	NP_000375.2
187	ENSP00000233242.1	rs200524554	21025057	0.0002	missense	C/T	P [Pro] ⇒ L [Leu]	NP_000375.2
188	ENSP00000233242.1	rs200584734	21007345	0.0002	missense	G/C	A [Ala] ⇒ P [Pro]	NP_000375.2
189	ENSP00000233242.1	rs200759464	21009627	0.0002	missense	A/T	E [Glu] ⇒ V [Val]	NP_000375.2
190	ENSP00000233242.1	rs200783423	21009496	0.0002	missense	G/A, G/C	E [Glu] ⇒ K [Lys] ,E [Glu] ⇒ Q [Gln]	NP_000375.2
191	ENSP00000233242.1	rs200824333	21008143	0.0002	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
192	ENSP00000233242.1	rs200940198	21009879	0.0002	missense	T/A, T/C	V [Val] ⇒ E [Glu], V [Val] ⇒ A [Ala]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
193	ENSP00000233242.1	rs201152495	21009144	0.0002	missense	A/T, A/T	K [Lys] ⇒ I [Ile],A [Ala] ⇒ A [Ala]	NP_000375.2
194	ENSP00000233242.1	rs201270852	21013220	0.0008	missense	C/T	R[Arg] ⇒ W [Trp]	NP_000375.2
195	ENSP00000233242.1	rs201368319	21038109	0.0004	missense	A/G	Y [Tyr] ⇒ C [Cys]	NP_000375.2
196	ENSP00000233242.1	rs201448956	21003274	0.0002	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
197	ENSP00000233242.1	rs201461940	21008695	0.0002	missense	A/C	T [Thr] ⇒ P [Pro]	NP_000375.2
198	ENSP00000233242.1	rs201519465	21010096	0.0002	missense	A/G	I [Ile] ⇒ V [Val]	NP_000375.2
199	ENSP00000233242.1	rs201595604	21025036	0.0002	missense	C/A	R[Arg] ⇒ H [His]	NP_000375.2
200	ENSP00000233242.1	rs201606169	21037137	0.0004	missense	C/A	R[Arg] ⇒ H [His]	NP_000375.2
201	ENSP00000233242.1	rs201764222	21019889	0.0002	missense	G/T	V [Val] ⇒ F [Phe]	NP_000375.2
202	ENSP00000233242.1	rs201874707	21008757	0.0002	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
203	ENSP00000233242.1	rs201985284	21008617	0.0002	missense/	G/A, G/T	E [Glu] ⇒ K [Lys] ,E[Glu]	NP_000375.2
204	ENSP00000233242.1	rs201990496	21005124	0.0002	missense	C/G, C/T	S [Ser] ⇒ C [Cys] ,S [Ser] ⇒ F [Phe]	NP_000375.2
205	ENSP00000233242.1	rs202001155	21027991	0.0002	missense	G/A	R[Arg] ⇒ Q [Gln]	NP_000375.2
206	ENSP00000233242.1	rs202213088	21005706	0.0002	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
207	ENSP00000233242.1	rs202229735	21009840	----	missense	A/G, A/T	E [Glu] ⇒ G [Gly],E [Glu] ⇒ V [Val]	NP_000375.2
208	ENSP00000233242.1	rs267599180	21006843	0.0008	missense	C/T	S [Ser] ⇒ F [Phe]	NP_000375.2
209	ENSP00000233242.1	rs367788462	21028530	0.0004	missense/	G/A	E [Glu] ⇒ E [Glu]	NP_000375.2
210	ENSP00000233242.1	rs368779816	21013297	0.0002	missense	C/T	T[Thr] ⇒ M [Met]	NP_000375.2
211	ENSP00000233242.1	rs369430233	21007848	0.0002	missense	T/A, T/C	M[Met] ⇒ K [Lys], M[Met] ⇒ T [Thr]	NP_000375.2
212	ENSP00000233242.1	rs369472561	21008013	0.0002	missense	G/T	G[Gly] ⇒ V [Val]	NP_000375.2
213	ENSP00000233242.1	rs371987644	21016525	0.0002	missense	A/C	E [Glu] ⇒ D [Asp]	NP_000375.2
214	ENSP00000233242.1	rs372035579	21009927	0.006	missense	T/C	L [Leu] ⇒ P [Pro]	NP_000375.2
215	ENSP00000233242.1	rs372154910	21013525	0.0002	missense	G/A	R[Arg] ⇒ Q [Gln]	NP_000375.2
216	ENSP00000233242.1	rs373272476	21009291	0.0002	missense	T/C	M[Met] ⇒ T [Thr]	NP_000375.2
217	ENSP00000233242.1	rs373995960	21006007	0.0002	missense	G/A, G/T	A [Ala] ⇒ T [Thr] ,A [Ala] ⇒ S [Ser]	NP_000375.2
218	ENSP00000233242.1	rs374402922	21011669	0.0002	missense	A/T	Q[Gln] ⇒ H [His]	NP_000375.2
219	ENSP00000233242.1	rs374411400	21005850	0.0002	missense	A/G	K [Lys] ⇒ R [Arg]	NP_000375.2
220	ENSP00000233242.1	rs375294575	21016458	0.0002	missense	G/A	A [Ala] ⇒ T [Thr]	NP_000375.2
221	ENSP00000233242.1	rs375855688	21009109	0.0004	missense	G/C	V [Val] ⇒ L [Leu]	NP_000375.2
222	ENSP00000233242.1	rs376250460	21008385	0.0002	missense	T/C, G/T	V [Val] ⇒ A [Ala], T [Thr] ⇒ T [Thr]	NP_000375.2
223	ENSP00000233242.1	rs528503563	21011474	0.0002	missense	A/G	T [Thr] ⇒ A [Ala]	NP_000375.2
224	ENSP00000233242.1	rs530171166	21032507	0.0004	missense	G/A	R[Arg] ⇒ H [His]	NP_000375.2
225	ENSP00000233242.1	rs530601244	21012550	0.0002	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
226	ENSP00000233242.1	rs530659716	21006064	0.0002	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
227	ENSP00000233242.1	rs531341535	21015435	0.0002	missense	T/A	L [Leu] ⇒ H [His]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
228	ENSP00000233242.1	rs532531549	21009513	0.0006	missense	G/C	G[Gly] ⇒ A [Ala]	NP_000375.2
229	ENSP00000233242.1	rs532575330	21002364	0.0002	missense	G/A	C[Cys] ⇒ Y [Tyr]	NP_000375.2
230	ENSP00000233242.1	rs533551460	21002457	0.0002	missense	T/G	F [Phe] ⇒ C [Cys]	NP_000375.2
231	ENSP00000233242.1	rs534116066	21008505	0.0008	missense	G/A, G/T	G[Gly] ⇒ D [Asp], G[Gly] ⇒ V [Val]	NP_000375.2
232	ENSP00000233242.1	rs534924739	21012249	0.0002	missense	G/T	G[Gly] ⇒ V [Val]	NP_000375.2
233	ENSP00000233242.1	rs535011070	21006202	0.0002	missense	C/A, C/T	L [Leu] ⇒ I [Ile] ,L [Leu] v F [Phe]	NP_000375.2
234	ENSP00000233242.1	rs535977033	21006385	0.0002	missense	T/A, C/T	S [Ser] ⇒ T [Thr], V [Val] ⇒ V [Val]	NP_000375.2
235	ENSP00000233242.1	rs536328155	21025043	0.0002	missense	T/C	Y [Tyr] ⇒ H [His]	NP_000375.2
236	ENSP00000233242.1	rs536537735	21037107	0.0002	missense	A/G	K [Lys] ⇒ R [Arg]	NP_000375.2
237	ENSP00000233242.1	rs537054558	21014559	0.0004	missense	G/A	S [Ser] ⇒ N [Asn]	NP_000375.2
238	ENSP00000233242.1	rs539614975	21015499	0.0002	missense	C/T	P [Pro] ⇒ S [Ser]	NP_000375.2
239	ENSP00000233242.1	rs540075453	21001479	0.0002	UTR-3	A/G	----------	-----
240	ENSP00000233242.1	rs540192015	21002629	0.0002	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
241	ENSP00000233242.1	rs540387864	21007339	0.0002	missense	T/A, T/C	Y [Tyr] ⇒ N [Asn]	NP_000375.2
242	ENSP00000233242.1	rs540530658	21038007	0.0002	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
243	ENSP00000233242.1	rs540978306	21016481	0.0004	missense	A/G	Q [Gln] ⇒ R [Arg]	NP_000375.2
244	ENSP00000233242.1	rs542107305	21026829	0.0002	missense	G/A	V[Val] ⇒ M [Met]	NP_000375.2
245	ENSP00000233242.1	rs543698457	21035637	0.0004	missense/	T/A	H [His] ⇒ Q [Gln]	NP_000375.2
246	ENSP00000233242.1	rs544303971	21002250	0.0002	missense	C/T	P [Pro] ⇒ L [Leu]	NP_000375.2
247	ENSP00000233242.1	rs544521341	21007174	0.0004	missense	A/G, C/T	K [Lys] ⇒ E [Glu]T [Thr] ⇒ T [Thr]	NP_000375.2
248	ENSP00000233242.1	rs546392030	21009396	0.0002	missense	T/C	L [Leu]⇒ S [Ser]	NP_000375.2
249	ENSP00000233242.1	rs546684381	21032559	0.0002	missense	G/A, G/T	V [Val] ⇒ I [Ile] V [Val] ⇒ F [Phe]	NP_000375.2
250	ENSP00000233242.1	rs546747242	21007551	0.0002	missense	A/G	N [Asn] ⇒ S [Ser]	NP_000375.2
251	ENSP00000233242.1	rs547372326	21009611	0.0002	missense	C/G	F [Phe] ⇒ L [Leu]	NP_000375.2
252	ENSP00000233242.1	rs548108916	21027992	0.0002	Missense/	C/A	R [Arg] ⇒ R [Arg]	NP_000375.2
253	ENSP00000233242.1	rs548321407	21027842	0.0002	missense	G/C	A [Ala] ⇒ P [Pro]	NP_000375.2
254	ENSP00000233242.1	rs549741449	21012192	0.0004	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2
255	ENSP00000233242.1	rs549983245	21012114	0.0004	missense	A/T	N [Asn] ⇒ I [Ile]	NP_000375.2
256	ENSP00000233242.1	rs551773082	21012643	0.0002	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
257	ENSP00000233242.1	rs552302745	21002383	0.0002	missense	T/G	L [Leu] ⇒ V [Val]	NP_000375.2
258	ENSP00000233242.1	rs552447556	21008910	0.0002	missense	T/G	L [Leu] ⇒ R [Arg]	NP_000375.2
259	ENSP00000233242.1	rs552692138	21007029	0.0002	missense	T/A	M[Met] ⇒ K [Lys]	NP_000375.2
260	ENSP00000233242.1	rs553689397	21044034	0.0006	UTR-5	---/C	----------	-----
261	ENSP00000233242.1	rs554045156	21009330	0.0002	missense	G/A	R[Arg] ⇒ Q [Gln]	NP_000375.2
262	ENSP00000233242.1	rs554648284	21009718	0.0002	missense	G/T	V [Val] ⇒ F [Phe]	NP_000375.2
263	ENSP00000233242.1	rs556582055	21010805	0.0002	Missense/	C/G	D[Asp] ⇒ E [Glu]	NP_000375.2

No.	ENSP ID	SNP ID	Chromo. Position	MAF Value	Type of SNP	Nuc. Chan	AA Change	Protein ID
264	ENSP00000233242.1	rs557580138	21011760	0.0002	missense	C/A	A [Ala] ⇒ D [Asp]	NP_000375.2
265	ENSP00000233242.1	rs558626935	21015538	0.0002	missense	A/G	T [Thr] ⇒ A [Ala]	NP_000375.2
266	ENSP00000233242.1	rs559224730	21005385	0.0002	missense	C/T	P [Pro] ⇒ L [Leu]	NP_000375.2
267	ENSP00000233242.1	rs561304247	21002277	0.0002	missense	T/C	M[Met] ⇒ T [Thr]	NP_000375.2
268	ENSP00000233242.1	rs561774487	21009939	0.0008	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
269	ENSP00000233242.1	rs562608061	21032376	0.0002	missense	G/A	A [Ala] ⇒ T [Thr]	NP_000375.2
270	ENSP00000233242.1	rs562624518	21008918	0.0002	missense	T/G	F [Phe] ⇒ L [Leu]	NP_000375.2
271	ENSP00000233242.1	rs564030306	21023012	0.0002	missense	G/A	V[Val] ⇒ M [Met]	NP_000375.2
272	ENSP00000233242.1	rs565114521	21012510	0.0002	missense	T/C	L [Leu] ⇒ P [Pro]	NP_000375.2
273	ENSP00000233242.1	rs565184018	21006055	0.0002	missense	A/G	S [Ser] ⇒ G [Gly]	NP_000375.2
274	ENSP00000233242.1	rs565963363	21013304	0.0002	missense	C/G, C/T	L [Leu] ⇒ V [Val]	NP_000375.2
275	ENSP00000233242.1	rs566501266	21013243	0.0002	missense	C/A	T [Thr] ⇒ N [Asn]	NP_000375.2
276	ENSP00000233242.1	rs566674173	21023538	0.0006	missense	T/A	L [Leu] ⇒ Q [Gln]	NP_000375.2
277	ENSP00000233242.1	rs568054660	21002743	0.0002	missense	G/A	V [Val] ⇒ I [Ile]	NP_000375.2
278	ENSP00000233242.1	rs568176871	21009751	0.0002	missense	A/T	T [Thr] ⇒ S [Ser]	NP_000375.2
279	ENSP00000233242.1	rs569794936	21009667	0.0002	missense	G/C	V [Val] ⇒ L [Leu]	NP_000375.2
280	ENSP00000233242.1	rs570097888	21012169	0.0002	missense	G/A	E [Glu] ⇒ K [Lys]	NP_000375.2
281	ENSP00000233242.1	rs570383610	21011700	0.0002	missense	G/T	S [Ser] ⇒ I [Ile]	NP_000375.2
282	ENSP00000233242.1	rs570782024	21002841	0.0002	missense	T/C	I [Ile] ⇒ T [Thr]	NP_000375.2
283	ENSP00000233242.1	rs571485213	21005512	0.0008	missense	C/T	L [Leu] ⇒ F [Phe]	NP_000375.2
284	ENSP00000233242.1	rs571626569	21009249	0.0018	missense	G/T	G[Gly] ⇒ V [Val]	NP_000375.2
285	ENSP00000233242.1	rs571728141	21012283	0.0002	missense	G/A	G [Gly] ⇒ S [Ser]	NP_000375.2
286	ENSP00000233242.1	rs572653083	21011094	0.0002	missense	G/A	G [Gly] ⇒ E [Glu]	NP_000375.2
287	ENSP00000233242.1	rs572869977	21042384	0.0002	missense	A/G	S [Ser] ⇒ G [Gly]	NP_000375.2
288	ENSP00000233242.1	rs573286918	21011926	0.0002	missense	G/A	G [Gly] ⇒ S [Ser]	NP_000375.2
289	ENSP00000233242.1	rs573308525	21037144	0.0002	missense	C/T	P [Pro] ⇒ S [Ser]	NP_000375.2
290	ENSP00000233242.1	rs573670976	21006319	0.0002	missense	G/A	A [Ala] ⇒ T [Thr]	NP_000375.2
291	ENSP00000233242.1	rs574659380	21002013	0.0002	missense	C/A	S [Ser] ⇒ Y [Tyr]	NP_000375.2
292	ENSP00000233242.1	rs574791609	21003113	0.0002	Missense/	G/A	K[Lys] ⇒ K [Lys]	NP_000375.2
293	ENSP00000233242.1	rs577157373	21008554	0.0002	missense	G/A, G/C	D[Asp] ⇒ N [Asn]	NP_000375.2
294	ENSP00000233242.1	rs577157440	21002175	0.0002	missense	T/C	V [Val] ⇒ A [Ala]	NP_000375.2
295	ENSP00000233242.1	rs577437570	21009351	0.0002	missense	C/T	A [Ala] ⇒ V [Val]	NP_000375.2

Supplementary Table III.- *APOB* SNPs present in non-coding region with their Regulome DB scores.

S No.	Chromosome location	dbSNP IDs	Rank	Score	SNP type
1	chr2:21224372..21224373	rs72654430	4	0.60906	3 UTR
2	chr2:21224421..21224422	rs12720763	4	0.60906	3 UTR
3	chr2:21224422..21224423	rs142151703	4	0.60906	3 UTR
4	chr2:21224590..21224591	rs72654428	4	0.60906	3 UTR

S No.	Chromosome location	dbSNP IDs	Rank	Score	SNP type
5	chr2:21044060	rs1800480	4	0.60906	5 UTR
6	chr2:21226400..21226401	rs141644795	4	0.60906	intronic
7	chr2:21226486..21226487	rs187296678	5	0.58955	intronic
8	chr2:21226873..21226874	rs542404934	4	0.60906	intronic
9	chr2:21227850..21227851	rs72654410	5	0.58955	intronic
10	chr2:21227935..21227936	rs139704306	4	0.60906	intronic
11	chr2:21235564..21235565	rs12713771	3a	0.24403	intronic
12	chr2:21235604..21235605	rs566982035	3a	1	intronic
13	chr2:21235618..21235619	rs72653080	3a	0.65649	intronic
14	chr2:21235809..21235810	rs183128193	3a	0.75931	intronic
15	chr2:21235827..21235828	rs118002564	4	0.60906	intronic
16	chr2:21235847..21235848	rs12720844	5	0.58955	intronic
17	chr2:21235943..21235944	rs190865121	5	0.58955	intronic
18	chr2:21235981..21235982	rs12713776	4	0.60906	intronic
19	chr2:21236481..21236482	rs488329	2b	0.66759	intronic
20	chr2:21236732..21236733	rs143870044	3a	0.75713	intronic
21	chr2:21236739..21236740	rs536749646	3a	0.50689	intronic
22	chr2:21236831..21236832	rs147270037	5	0.955	intronic
23	chr2:21237145..21237146	rs139828082	5	0.58955	intronic
24	chr2:21237236..21237237	rs187401851	5	0.9375	intronic
25	chr2:21237296..21237297	rs569993957	4	0.60906	intronic
26	chr2:21237674..21237675	rs534008508	4	0.60906	intronic
27	chr2:21237851..21237852	rs78580569	4	0.60906	intronic
28	chr2:21238515..21238516	rs182561283	5	0.58955	intronic
29	chr2:21238763..21238764	rs146764589	4	0.60906	intronic
30	chr2:21238797..21238798	rs140225127	4	0.60906	intronic
31	chr2:21238825..21238826	rs541923839	4	0.60906	intronic
32	chr2:21238983..21238984	rs150956240	5	0.58955	intronic
33	chr2:21238992..21238993	rs12720800	5	0.58955	intronic
34	chr2:21239082..21239083	rs12720802	5	0.58955	intronic
35	chr2:21239583..21239584	rs12713868	3a	0.35836	intronic
36	chr2:21239584..21239585	rs12713869	3a	0.29248	intronic
37	chr2:21239594..21239595	rs12713870	5	0.225	intronic
38	chr2:21239610..21239611	rs12713871	5	0.58955	intronic
39	chr2:21239622..21239623	rs13306202	5	0.58955	intronic
40	chr2:21239652..21239653	rs191090985	5	0.88556	intronic
41	chr2:21239682..21239683	rs545349871	5	0.58955	intronic
42	chr2:21239711..21239712	rs187182863	5	0.58955	intronic
43	chr2:21239718..21239719	rs12720819	5	0.58955	intronic
44	chr2:21239727..21239728	rs571625076	5	0.58955	intronic

S No.	Chromosome location	dbSNP IDs	Rank	Score	SNP type
45	chr2:21239771..21239772	rs12720817	5	0.58955	intronic
46	chr2:21239817..21239818	rs549394363	5	0.99722	intronic
47	chr2:21239913..21239914	rs138999114, rs573286852	5	0.83105	intronic
48	chr2:21239920..21239921	rs112745407	3a	0.63742	intronic
49	chr2:21240044..21240045	rs115755929	3a	0.47482	intronic
50	chr2:21240110..21240111	rs144876159	4	0.60906	intronic
51	chr2:21240125..21240126	rs189046815	3a	1	intronic
52	chr2:21240147..21240148	rs180931378	3a	0.8738	intronic
53	chr2:21240184..21240185	rs535824398	4	0.60906	intronic
54	chr2:21240407..21240408	rs572186909	2c	0.58033	intronic
55	chr2:21240502..21240503	rs76693756	4	0.60906	intronic
56	chr2:21240537..21240538	rs12713911	4	0.60906	intronic
57	chr2:21240937..21240938	rs147100637	4	0.60906	intronic
58	chr2:21240958..21240959	rs374897675	4	0.60906	intronic
59	chr2:21241210..21241211	rs147720589	5	0.58955	intronic
60	chr2:21241289..21241290	rs12720825	4	0.60906	intronic
62	chr2:21241301..21241302	rs12720821	3a	0.75713	intronic
63	chr2:21241641..21241642	rs181346861	4	0.60906	intronic
64	chr2:21242235..21242236	rs560821395	4	0.60906	intronic
65	chr2:21242328..21242329	rs185721706	4	0.60906	intronic
66	chr2:21242795..21242796	rs72653069	5	0.72379	intronic
67	chr2:21242852..21242853	rs561979139	5	0.58955	intronic
68	chr2:21243043..21243044	rs12720785	4	0.60906	intronic
69	chr2:21243400..21243401	rs139313355	2c	1	intronic
70	chr2:21243967..21243968	rs114471564	5	1	intronic
71	chr2:21244126..21244127	rs563121607	4	0.60906	intronic
72	chr2:21244127..21244128	rs531867731	4	0.60906	intronic
73	chr2:21244259..21244260	rs191606984	4	0.60906	intronic
74	chr2:21244655..21244656	rs542314665	5	0.85033	intronic
75	chr2:21244983..21244984	rs111825526	4	0.60906	intronic
76	chr2:21245081..21245082	rs564571506	4	0.60906	intronic
77	chr2:21245203..21245204	rs149677861	4	0.60906	intronic
78	chr2:21245365..21245366	rs145511260	5	0.99471	intronic
79	chr2:21245560..21245561	rs372178138	5	0.58955	intronic
80	chr2:21245630..21245631	rs558233757	4	0.60906	intronic
81	chr2:21246381..21246382	rs72653066	3a	0.4701	intronic
82	chr2:21246960..21246961	rs142557833	5	0.58955	intronic
83	chr2:21247013..21247014	rs529641466	5	0.87837	intronic
84	chr2:21247022..21247023	rs547734093	5	0.99722	intronic

S No.	Chromosome location	dbSNP IDs	Rank	Score	SNP type
85	chr2:21247174..21247175	rs151334814	3a	0.93733	intronic
86	chr2:21247286..21247287	rs12720839	3a	0.41664	intronic
87	chr2:21247728..21247729	rs78341608	3a	0.54807	intronic
88	chr2:21247764..21247765	rs72653065	4	0.60906	intronic
89	chr2:21248100..21248101	rs12720759	4	0.60906	intronic
90	chr2:21248236..21248237	rs566255530	4	0.60906	intronic
91	chr2:21248349..21248350	rs116255207	4	0.60906	intronic
92	chr2:21248484..21248485	rs186200586	3a	0.66969	intronic
93	chr2:21249179..21249180	rs531424311	4	0.60906	intronic
94	chr2:21249267..21249268	rs552569557	4	0.60906	intronic
95	chr2:21249403..21249404	rs190552864	4	0.60906	intronic
96	chr2:21249415..21249416	rs548617467	3a	0.30476	intronic
97	chr2:21249445..21249446	rs186828301	3a	0.144	intronic
98	chr2:21249870..21249871	rs78941963	3a	0.63742	intronic
99	chr2:21250254..21250255	rs78504102	4	0.60906	intronic
100	chr2:21250596..21250597	rs145100968	2b	0.79558	intronic
101	chr2:21251527..21251528	rs12714215	5	1	intronic
102	chr2:21252095..21252096	rs182312395	3a	0.59935	intronic
103	chr2:21252096..21252097	rs570904180	2b	0.59816	intronic
104	chr2:21252102..21252103	rs548067874	2b	0.33595	intronic
105	chr2:21252103..21252104	rs12720840	2b	0.549	intronic
106	chr2:21252183..21252184	rs184358787	3a	0.61437	intronic
107	chr2:21252303..21252304	rs146536216	4	0.60906	intronic
108	chr2:21252338..21252339	rs113010686	3a	0.6352	intronic
109	chr2:21252364..21252365	rs572597107, rs67556837	3a	0.8507	intronic
110	chr2:21252715..21252716	rs12720765	3a	0.33881	intronic
111	chr2:21253196..21253197	rs554117371	5	0.58955	intronic
112	chr2:21253200..21253201	rs6727706	5	0.58955	intronic
113	chr2:21253955..21253956	rs115200831	5	0.85033	intronic
114	chr2:21254108..21254109	rs140830032	5	0.58955	intronic
115	chr2:21254116..21254117	rs572158013	5	1	intronic
116	chr2:21254168..21254169	rs12720766	5	0.58955	intronic
117	chr2:21254384..21254385	rs12720769	4	0.60906	intronic
118	chr2:21254563..21254564	rs12720768	4	0.60906	intronic
119	chr2:21254735..21254736	rs201106138, rs377355276	2c	0.9925	intronic
120	chr2:21254738..21254739	rs143452815	2c	0.9925	intronic
121	chr2:21254837..21254838	rs114883958	5	0.58955	intronic
122	chr2:21255165..21255166	rs12714224	5	0.58955	intronic
123	chr2:21255763..21255764	rs184507838	4	0.60906	intronic

S No.	Chromosome location	dbSNP IDs	Rank	Score	SNP type
124	chr2:21255947..21255948	rs12714226	5	0.58955	intronic
125	chr2:21256002..21256003	rs576038819	5	0.58955	intronic
126	chr2:21256065..21256066	rs540340913	3a	0.75409	intronic
127	chr2:21256404..21256405	rs72653061	4	0.60906	intronic
128	chr2:21256412..21256413	rs12720811	4	0.60906	intronic
129	chr2:21256488..21256489	rs78610189	5	0.98	intronic
130	chr2:21257257..21257258	rs569321939	3a	0.68065	intronic
131	chr2:21257376..21257377	rs12720793	4	0.60906	intronic
132	chr2:21257413..21257414	rs78652877	4	0.60906	intronic
133	chr2:21257627..21257628	rs182257545	4	0.60906	intronic
134	chr2:21257676..21257677	rs148944625	4	0.60906	intronic
135	chr2:21257926..21257927	rs12720842	4	0.60906	intronic
136	chr2:21257975..21257976	rs114659957	4	0.60906	intronic
137	chr2:21257982..21257983	rs541372741	4	0.60906	intronic
138	chr2:21259328..21259329	rs12720853	4	0.60906	intronic
139	chr2:21259739..21259740	rs566540157	4	0.60906	intronic
140	chr2:21260189..21260190	rs191618417	2b	0.78832	intronic
141	chr2:21260298..21260299	rs13306197	4	0.60906	intronic
142	chr2:21260360..21260361	rs12720846	4	0.60906	intronic
143	chr2:21260371..21260372	rs139266444	4	0.60906	intronic
144	chr2:21261197..21261198	rs530005654	3a	0.57256	intronic
145	chr2:21261211..21261212	rs559799871	3a	0.57256	intronic
146	chr2:21261242..21261243	rs12714239	4	0.60906	intronic
147	chr2:21261269..21261270	rs569472006	3a	0.8227	intronic
148	chr2:21261845..21261846	rs142229577	2b	0.67017	intronic
149	chr2:21261997..21261998	rs12720796	3a	0.6851	intronic
150	chr2:21262034..21262035	rs146194270	3a	0.58328	intronic
151	chr2:21262190..21262191	rs12720797	2b	0.7516	intronic
152	chr2:21262314..21262315	rs12720798	3a	0.75713	intronic
153	chr2:21262374..21262375	rs12720794	4	0.60906	intronic
154	chr2:21262379..21262380	rs12720795	4	0.60906	intronic
155	chr2:21262667..21262668	rs12714248	5	0.58955	intronic
156	chr2:21262746..21262747	rs142459501	4	0.60906	intronic
157	chr2:21262755..21262756	rs12720789	3a	0.8507	intronic
158	chr2:21262771..21262772	rs555323073	4	0.60906	intronic
159	chr2:21262870..21262871	rs12720788	3a	0.57268	intronic
160	chr2:21262916..21262917	rs12720786	3a	0.39922	intronic
161	chr2:21263233..21263234	rs140139277	3a	0.57429	intronic
162	chr2:21263356..21263357	rs562375034	4	0.60906	intronic
163	chr2:21263636..21263637	rs1367116	5	0.97858	intronic

S No.	Chromosome location	dbSNP IDs	Rank	Score	SNP type
164	chr2:21263766..21263767	rs9282605	5	0.58955	intronic
165	chr2:21264077..21264078	rs548513084	4	0.60906	intronic
166	chr2:21264106..21264107	rs563016779	4	0.60906	intronic
167	chr2:21264181..21264182	rs191372114	4	0.60906	intronic
168	chr2:21264423..21264424	rs144729882	4	0.60906	intronic
169	chr2:21264998..21264999	rs531023775	2b	0.81166	intronic
170	chr2:21265897..21265898	rs12714268	2a	0.79886	intronic
171	chr2:21265934..21265935	rs72653055	4	0.60906	intronic
172	chr2:21266362..21266363	rs570818403	4	0.60906	intronic
173	chr2:21266658..21266659	rs12720762	2b	0.66261	Intronic

Supplementary Table IV.- Extracted non-coding SNPs of *APOB* through Regulome DB and SNP info.

dbSNP IDs	Regulome DB rank	Description	SNP info
rs12714268	2a	TF binding + matched TF motif + matched DNase Footprint + DNase peak	
rs488329	2b	TF binding + any motif + DNase Footprint + DNase peak	
rs145100968	2b	-----	
rs570904180	2b	-----	
rs548067874	2b	-----	
rs12720840	2b	-----	
rs191618417	2b	-----	
rs142229577	2b	-----	
rs12720797	2b	-----	
rs531023775	2b	-----	
rs12720762	2b	-----	Y (TFBS)
rs572186909	2c	TF binding + matched TF motif + DNase peak	
rs139313355	2c	------	
rs201106138, rs377355276	2c	-----	
rs143452815	2c	-----	

TFBS, Transcription factor binding cite; TF, Transcription factor.