Appendix E. Genes with multiple rare variants (MAF <1%) in three or more ACEi-A samples

						CATURAN.			Comment	. NICE	No of combinedvar		No. of		
					 MutationTas	FATHMM MKL Coding	GERP++		Sequence Ontology	in NIST callable	iants in ACEi- A samples	variants in ACEi-A	variants in control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	1	Pred (C)	RS	Gene Names	(Combined)	regions	A samples	samples	samples	NFE MAF	AFR MAF
1:1944676	C/T	rs148941537	9.1	-				UBR4	synonymous	True	3	1	. 0	0.0017508	0
1:1944788	G/A	rs34710232	0.24	-				UBR4	synonymous	True		1	. 1	0.0059756	0.00091954
1:1948907	T/A	rs150747540	24.2	0.502	Damaging	Damaging	5.68	UBR4	missense	True		1	. 0	0.0009072	0
1:1952820	T/C	rs61759879	17.56	-				UBR4	splice_region	True		1	. 0	0.0033709	0.00068823
1:2216000	C/T	rs112062179	23.3	-	Damaging	Damaging	2.11	HSPG2	missense	True	6	1	. 0	0.0049974	0.00080441
1:2216535	C/T	rs141963344	16.37	0.082				HSPG2	missense	True]	1	. 0	0.0047329	0.00022952
1:2217448	-/	rs142226974	21.3	0.176	Damaging	Damaging	4.94	HSPG2	missense	True		1	. 0	6.49E-05	0
1:2220248		rs62642528	16.99	0.31	Tolerated	Tolerated	3.46	HSPG2	missense	True		1	. 0	0.0089448	
1:2220697	·	rs143669458	22.3	0.09	Damaging	Damaging	4.53	HSPG2	missense	True		1	. 0	0.0042813	
1:2221519	'	rs149677207	6.714	-				HSPG2	missense	False		1	. 0	0.0067506	0.00022946
1:3979894	-	rs41270805	5.882	0.048	Tolerated	Tolerated	0.213	MACF1	missense	True	5	2	2 0	0.0085603	0.00195357
1:3979945	· ·	rs141334491	10.8	-				MACF1	synonymous	True		1	. 0	0.0080353	0.00091785
1:3982717		rs138428016	3.974	-				MACF1	synonymous	True		1	. 0	0.0003888	
1:3985364	<u> </u>	rs147777128	25.4	0.449	Damaging	Damaging	2.56	MACF1	missense	True		1	. 0	0.0051847	
1:4197637	/	rs200138511	6.259	0.034	Tolerated	Tolerated	0.154	HIVEP3	missense	True	4	1	1	0.0046759	0.00161327
1:4197916	-	rs140035336	0.073	-				HIVEP3	synonymous	True		1	. 0	0.0025328	
1:4197924	-	rs150644975	0.037	-				HIVEP3	synonymous	True		1	. 0	0.0043524	
1:4204887		rs369367320	17.21	-				HIVEP3	synonymous	True		1	. 0	0.0001299	0.00011505
1:5507500	-/	rs200747808	24.5	0.295	Damaging	Damaging	4.28	ACOT11,FAM151A	missense	True	4	1	. 0	0.0003891	0
1:5507545	- '	rs61744146	0.052	-				ACOT11,FAM151A	synonymous	True	1	1	. 0	0.0005835	0.00011473
1:5508184	-	rs142814457	0.029	-	Damaging	Tolerated	-0.209	ACOT11,FAM151A	missense	True	1	1	. 2	0.0072633	
1:5508564		rs17399297	24.7	0.292	Damaging	Damaging	4.48	ACOT11,FAM151A	missense	True		1	. 0	0.0064859	
1:8659057	/ -	rs10493784	7.209	0.034	Tolerated	Tolerated	-5	COL24A1	missense	True	4	1	. 0	0.0083442	0.00231481
1:1521864	<u> </u>	rs113556887	0.303	-				HRNR	synonymous	False	6	3	<u>'</u>	0.0042095	0.0108642
1:1521880		rs200444708	5.338	0.027	Tolerated	Tolerated	-6.74	HRNR	missense	False		3		0.0009855	
1:1521880	<u> </u>	rs79940627	5.787	0.017	Tolerated	Tolerated	-5.76	HRNR	missense	False	1	3	1	0.005424	
1:1521884	- 	rs377380707	0.562	-				HRNR	synonymous	False	1	2	2 0	0.0012502	0.00048544
1:1521889	· ·	rs149648668	2.042	-				HRNR	synonymous	False	4	2	2 2	0.0068561	0.00192505
1:1521890	-	rs145118416	9.772	-				HRNR	synonymous	False	1	1	. 2	0.0091572	
1:1521916	-	rs142633454	1.088	0.01	Tolerated	Tolerated	-2.18	HRNR	missense	False	4	1	. 0	0.0038247	
1:1521917		rs368316243	6.651	0.015	Tolerated	Tolerated	-6.13	HRNR	missense	False	4	1	. 0	0	<u> </u>
1:1521937	· '	rs148822876	6.66	0.061	Tolerated	Tolerated	-0.807	HRNR	missense	True	_	1	. 0	6.48E-05	
1:1522758	-	rs145079750	14.71	0.073	Tolerated	Tolerated	-3.19	FLG	missense	False	6	1	. 0	0.0013642	
1:1522758	- '	rs140464988	18.75	0.055	Tolerated	Tolerated	0.217	FLG	missense	False	4	1	. 0	0.0011035	
1:1522767	/	rs12732870	7.755	0.069	Tolerated	Tolerated	-6.21	FLG	missense	False	4	1	2	0.0015141	
1:1522768	- '	rs140287233	0.94	-			L	FLG	synonymous	False	4	1	. 0	0.0009786	
1:1522772	· ·	rs201591837	16.89	0.056	Tolerated	Tolerated	-0.788	FLG	missense	False	4	1	0	0.0015033	0.00011582
1:1522792		rs149520854	4.294	0.018	Tolerated	Tolerated	-6.51	FLG	missense	False	4	1	0	0.0007342	
1:1522806		rs116918835	1.856	0.037	Tolerated	Tolerated	-0.944	FLG	missense	False	4	1	0	0.0009012	
1:1522806	- 	rs117945779	4.653	0.03	Tolerated	Tolerated	-0.332	FLG	missense	False	4	1	0	0.0013309	
1:1522820	G/A	rs201021216	19.14	0.046	Tolerated	Tolerated	-1.39	FLG	missense	False		1	. 0	0.0001298] 0

											No of		Ī., ,		
						FATHMAM			6	NICT	combinedvar		No. of		
					MutationTag	FATHMM MKL Coding	GERP++		Sequence Ontology	in NIST callable	iants in ACEi- A samples	variants in ACEi-A	variants in control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)	Pred (C)	RS	Gene Names	(Combined)	regions	A samples	samples	samples	NFE MAF	AFR MAF
1:1523240	,	rs141384852	9.707	0.046	Tolerated	Tolerated	2.29	FLG2	missense	True	4	2	2 0	0.0056641	0.00069412
1:1523243	-	rs144875878	6.088	0.02	Tolerated	Tolerated	-5.38	FLG2	missense	True	†	1	0	0.0007899	0.00023507
1:1523243	-	rs149671990	0.031	0.03	Tolerated	Tolerated	-8.47	FLG2	missense	True		1	1 0	0.0006078	0.00024044
1:1523275	<u> </u>	rs12758283	0.106	-				FLG2	synonymous	False		1	1	0.005979	0.00135735
1:1523275	A/G	rs12754184	0.515	-				FLG2	synonymous	False		1	0	0.001632	0.00027078
1:1857037	C/A	rs143020055	4.469	-				HMCN1	5_prime_UTR	True	4	1	1 0	0.0020752	0.00034443
1:1859641	C/T	rs145595000	24.2	0.268	Damaging	Damaging	5.38	HMCN1	missense	True		1	. 0	0.0002593	0
1:1860831	C/T	rs141099682	22.9	0.402	Damaging	Damaging	3.08	HMCN1	missense	True	1	1	1 0	0.000454	0.00022962
1:1860991	G/A	rs201836712	29.9	0.791	Damaging	Damaging	5.62	HMCN1	missense	True	1	1	1 0	6.48E-05	0
1:2040857	G/A	rs371235736	18.92	-				SOX13	synonymous	True	3	1	1 0	0.0005185	0.00022962
1:2040914	T/C	rs61211343	5.278	-	Tolerated	Tolerated	4.42	SOX13	missense	True		1	1 0	0.0012343	0.119443
1:2040920	G/A	rs201772428	23.7	-	Damaging	Damaging	5.18	S0X13	missense	True	_	1	0	0.0018799	0.00045924
1:2040927	C/G	rs12088948	2.892	-				SOX13	splice_region	True		1	0	0.0012336	0.142923
1:2044030	G/A	rs144860399	17.3	-				PIK3C2B	synonymous	True	5	1	0	6.49E-05	0.00356322
1:2044183	G/A	rs17847754	2.117	-				PIK3C2B	synonymous	True		1	0	0.001556	0.0254023
1:2044261	C/A	rs61762602	19.16	0.092	Tolerated	Damaging	3.44	PIK3C2B	missense	True		1	0	0.0064868	0.00091996
1:2044289	G/C	rs17847745	6.265	-				PIK3C2B	splice_region	True		1	1 0	0.001428	0.0240009
1:2044297	T/C	rs61740681	8.326	-				PIK3C2B	synonymous	True		2	2 2	0.0049916	0.00057432
1:2044359	G/A	rs372874064	19.97	0.047	Damaging	Damaging	4.94	PIK3C2B	missense	True		1	1 0	0.0009725	0
1:2044362	·	rs140417606	-	-				PIK3C2B	5_prime_UTR	True		1	0	0.0003924	0.102558
1:2050270	/	rs147074435	9.186	-				CNTN2	synonymous	True	5	1	1	0.0032417	0.00022952
1:2050282	/	rs142502980	14.11	0.048	Damaging	Damaging	3.95	CNTN2	missense	True		1	0	0.0029816	0.00091764
1:2050305	/	rs139732336	15.21	0.105	Damaging	Damaging	2.15	CNTN2	missense	True		3	3 1	0.0073291	0.00149357
1:2050335	- '	rs79431021	0.002	0.059	Tolerated	Tolerated	-6.97	CNTN2	missense	True		1	1 0	0.0099248	0.0899471
1:2071343	-7	rs200461962	1.913	0.003	Tolerated	Tolerated	-1.55	FCAMR	missense	True	4	1	1 0	0.0020086	0.00011478
1:2071357		rs188207561	15.58	0.159	Tolerated	Tolerated	2.3	FCAMR	missense	True	_	1		0.0060304	0.00068886
1:2071358	- '	rs147389157	21.6	0.148	Damaging	Damaging	5.32	FCAMR	missense	True	_	1	· · · · ·	0.0067419	0.00160698
1:2071404	-	rs199884709	7.974	0.011	Tolerated	Tolerated	-5.32	FCAMR	missense	True	-	1		0.0032421	0.00126379
1:2082022	<u> </u>	rs113155197	19.53	-	1			PLXNA2	synonymous	True	5	1	· · ·	0.0069994	0.00057524
1:2082023		rs144314864	9.358	-	m 1 . 1		204	PLXNA2	synonymous	True	-	1	<u> </u>	0.0013617	0.00034507
1:2082526		rs143711247	22.3	0.081	Tolerated	Damaging	2.94	PLXNA2	missense	True	1	1	ij <u>0</u>	0.002982	0.00045924
1:2082526	-	rs41309627	26.6	0.487	Damaging	Damaging	5.6	PLXNA2	missense	True	4	1	1	0.0051881	0.00057405
1:2082700	-	rs150558490	10.82	0.092	Tolerated	Damaging	3.07	PLXNA2	missense	True	7		1	0.0050571	0.00195223
1:2251173	-	rs189391711	6.05	-	Tolerated	Tolerated	-1.43	DNAH14 DNAH14	missense	True	- 1′	1	· · ·	0.0066156	0.00160735 0.00142993
1:2251391	 	rs144132167 rs115240788	3.49 8.387	0.026	Tolongt- J	Tolomot- J	1.68	DNAH14 DNAH14	5_prime_UTR	False	1	- 1	2	0.0056436 0.0055088	
1:2252684	-	rs115240788 rs201300824	8.38/	0.026	Tolerated	Tolerated	1.68	DNAH14 DNAH14	missense	True True	4	1	2	0.0055088	0.00137709 0.00011531
1:2253284	-	rs201300824 rs202118490	0.124	-	Talamatad	Talamatad	0.51	DNAH14 DNAH14	splice_acceptor		-	1	0	0.0015668	0.00011531
1:2253284	-	rs202118490 rs187487970	0.609	 	Tolerated	Tolerated	0.51	DNAH14 DNAH14	missense	True True	1	1	0	0.0001951	0
1:2253805	-	rs191528375	10.89	0.008	Tolerated	Tolerated	-0.189	DNAH14	synonymous	True	1	1	-	0.0003894	0.00172176
1:2254636	+'	rs139192897	17.27	0.000	Tolerateu	Tolerated	-0.109	DNAH14	missense missense	True	1	1	`	0.0086308	0.00172176
1:2255281	-	rs184094753	51	- -	Damaging	Damaging	4.43	DNAH14	stop_gained	True	1	1	·	0.004804	0.00011481
1:2279162	-	rs112805433	5.592	1-	Damaging	Dailiagilig	T.43	SNAP47	non_coding_exon		4	1	0	0.0042783	0.00091764
1.44/9104	JC/ I	13114003433	J.J74	I	1	I		SINAF4/	Inon-counig_exon	i aise	η,	<u>_</u>	<u> </u>	0.0005122	0.0012339/

							1		T		No of				
											combinedvar	No. of	No. of		
						FATHMM	CERR		Sequence	in NIST	iants in ACEi-	variants in	variants in		
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	1	MKL Coding Pred (C)	RS RERP++	Gene Names	Ontology (Combined)	callable regions	A samples	ACEi-A samples	control samples	gnomAD NFE MAF	gnomAD AFR MAF
1:2279357	- , -	rs200031076	21.9	0.084	Damaging	Tolerated	3.08	SNAP47	missense	True		samples 1	Samples	6.48E-05	Ark MAI
1:2279468	,	rs140543368	14.33	-	Damaging	Tolcraccu	3.00	SNAP47	synonymous	True	1	1	0	0.0017496	0.00022952
1:2279683	•	rs41303119	0.035	0.025	Tolerated	Tolerated	0.928	SNAP47	missense	True	1	1	0	0.0017450	0.0022332
1:2284048		rs373521717	0.171	0.032	Tolerated	Tolerated	-0.69	OBSCN	missense	True	5	1	0	0.0001298	
	G/A	rs140550965	0.029	-				OBSCN	synonymous	True		1	. 0	0.0001296	
1:2284519		rs142188902	0.619	-				OBSCN	5_prime_UTR_pre	True	1	1	. 1	0.0053143	0.0021814
1:2284612	-	rs189809636	4.805	-	Damaging	Tolerated	1.53	OBSCN	missense	True	1	1	. 0	0.0087515	0.00275545
1:2284755	G/A	rs79290523	0.005	-				OBSCN	synonymous	True	1	1	. 0	0.0047329	0.00057392
1:2285057	A/C	rs200399314	23.2	0.399	Damaging	Damaging	4.51	OBSCN	missense	False	1	1	. 0	0.0004548	0
1:2285069	T/C	rs188302055	27.4	0.571	Damaging	Damaging	4.02	OBSCN	missense	True		1	. 0	0.0091016	0.00276434
1:2285209	G/A	rs56015866	17.74	0.061	Damaging	Damaging	2.24	OBSCN	missense	True	1	1	. 0	0.0090119	0.00286829
1:2308052	G/A	rs151309110	24.1	0.094	Damaging	Damaging	4.63	COG2	missense	True	4	1	. 0	0	0.00045924
1:2308108	T/C	rs113173809	6.954	-				COG2	synonymous	True	1	1	. 0	0.0054447	0.00126263
1:2308146	C/T	rs200705175	22.1	0.213	Damaging	Damaging	3.06	COG2	missense	True		1	. 0	6.48E-05	0
1:2308193	T/C	rs372067889	19.07	-				COG2	synonymous	True	1	1	. 0	0.0004539	0
1:2377118	G/A	rs149514924	23.5	0.696	Damaging	Damaging	5.73	RYR2	missense	True	3	1	. 0	0.0011015	0.00011478
1:2377780	C/T	rs193922628	0.004	-				RYR2	synonymous	True		1	. 0	0.0018792	0.00091785
1:2378118	C/T	rs143906555	2.143	-				RYR2	synonymous	True		1	. 0	0.0055102	0.00114837
1:2378212	T/C	rs201500134	24.5	0.594	Damaging	Damaging	6.17	RYR2	missense	True		1	. 0	0.0009107	0
2:3264003	A/C	rs150426823	22.9	0.327	Damaging	Damaging	3.83	BIRC6	missense	True	4	1	. 0	0.0036284	0.00114732
2:3264104	G/A	rs144184005	6.694	-				BIRC6	synonymous	True		1	. 0	0.0090756	0.0028729
2:3272471	C/G	rs150127918	22.9	0.316	Damaging	Damaging	4.99	BIRC6	missense	True		1	0	0.0023986	0.00022973
2:3274020	A/G	rs61754132	14.44	0.314				BIRC6	synonymous	True		1	1	0.0055116	0.0010333
2:4801823	G/T	rs3211299	24.3	0.539	Damaging	Damaging	2.34	FBXO11,MSH6	missense	True	3	1	. 0	0.001232	0.00045903
2:4802598	G/A	rs368318845	19.44	0.272	Damaging	Damaging	1.5	FBXO11,MSH6	missense	True		1	. 0	0.0002593	0
2:4802598	C/A	rs267608047	16.71	-				FBXO11,MSH6	synonymous	True		1	. 0	0.0002592	0.00011481
2:4802630	,	rs2020908	17.04	0.322	Damaging	Damaging	1.71	FBXO11,MSH6	missense	True		1	. 1	0.0077791	0.00091827
2:5020125	G/A	rs138066456	22.8	-				NRXN1	synonymous	True	4	1	. 0	0.0054439	0.00080294
2:5031852	,	rs201720955	32	0.712	Damaging	Damaging	5.54	NRXN1	missense	True		1	. 0	Ů	0.00011471
2:5125964	AGAAAGAC	rs138189924	-	-				NRXN1	5_prime_UTR	False		2	2 0	0.008838	0.00287443
2:5125964		rs138189924	-	-				NRXN1	5_prime_UTR	False		2	2 0	0.0043806	0.00635401
2:8474511		rs112166113	11.25	0.02	Tolerated	Tolerated	4.61	DNAH6	missense	True	5	1	. 0	0.008624	0.00206659
2:8477708		rs116693971	5.885	0.029	Tolerated	Tolerated	3.26	DNAH6	missense	True		1	. 0	0.0016885	0.00068997
2:8480062	,	rs138935163	0.318	0.023	Tolerated	Tolerated	0.414	DNAH6	missense	True		1	. 0	0.0005186	0.00011484
2:8492839		rs200844717	25	0.478	Damaging	Damaging	4.55	DNAH6	missense	True		1	. 0	0.0020739	0.00011484
2:8494027	,	rs72832548	20.7	0.083	Damaging	Damaging	3.87	DNAH6	missense	True	1	1	0	0.0046014	
2:8503286		rs75617902	18.23	-				DNAH6	synonymous	True		1	. 0	0.0049909	0.0012635
2:8504318		rs72836490	27	0.248	Damaging	Damaging	5.74	DNAH6	missense	True		1	. 0	0.0047959	0.00068966
2:1093359	,	rs138272224	8.172	-				RANBP2	5_prime_UTR	False	4	1	. 0	0.0047952	0.00172216
2:1093360	,	rs372373398	6.327	-				RANBP2	5_prime_UTR	False		1	. 0	0.0058961	0.00126205
2:1093478	,	rs140650569	9.394	-	ļ			RANBP2	synonymous	False		1	. 0	0.0002593	0.00022946
2:1093848		rs2949961	17.12	-				RANBP2	splice_region	False		1	. 0	0.006039	0.00137868
2:1524049	G/A	rs35707762	20.1	0.191	Tolerated	Tolerated	4.92	NEB	missense	True	6	1	. 0	0.0095954	0.00172137

	1	I	I	1			l		T		No of				
											combinedvar	No. of	No. of		1
						FATHMM			Sequence	in NIST	iants in ACEi-	variants in	variants in		
. n	D 6/41			DEV	1	MKL Coding	1		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
-	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)	Pred (C)	RS	Gene Names	(Combined)	regions		samples	samples	NFE MAF	AFR MAF
2:1524177	+	rs115631125	0.004	-				NEB	synonymous	True	-	1	. 0	0.0010000	
2:1524258	-	rs149881695	21.5	0.105	Damaging	Damaging	6.08	NEB	missense	True		1	. 1	0.0025272	
2:1524270	<u> </u>	rs140688592	0.408	-	<u> </u>			NEB	synonymous	True	-	1	· · · · · ·		
2:1525243	-	rs114089598	25.9	0.27	Damaging	Damaging	5.87	NEB	missense	True	4	1	. 0	0.0037311	0.00091806
2:1525342	-	rs146616621	2.529	0.044	Tolerated	Tolerated	-0.318	NEB	missense	True		1	. 0	0.0022032	0.00068855
2:1628657	 	rs115450134	15.06	-				DPP4	splice_region	True] ³	1	1	0.0079715	
2:1628901	-7	rs56179129	19.92	0.169	Damaging	Damaging	4.62	DPP4	missense	True	-	1	. 1	0.0044873	
2:1629299	+	rs148524083	17.3	-				DPP4	synonymous	True	 -	2		0.0027170	
2:1699853	C/T	rs34564141	22.4	-	Damaging	Damaging	5.75	LRP2	missense	True	5	3	0	0.0001071	0.00884041
2:1700632	+	rs149367019	8.276	-			4.60	LRP2	synonymous	True	-	1	. 1	0.0050577	0.00114863
2:1700829	- /	rs138070797	21.3	0.38	Damaging	Damaging	4.68	LRP2	missense	True		1	. 0	0.002722	
2:1700924	+-	rs141068435	5.954	-	1			LRP2	synonymous	True	-	1	. 0	0.0004538	
2:1700974	<u> </u>	rs202173572	10.62	-				LRP2	synonymous	True	10	1	. 0	0.0002030	
2:1793967	-	rs55866005	22.3	0.138	Damaging	Damaging	4.67	TTN	missense	True	10	2	1	0.007.0220	
2:1794193	+'	rs72648235	25.7	0.542	Damaging	Damaging	5.66	TTN	missense	True	-	1	. 0		
2:1794404	<u> </u>	rs370257707	26.3	0.41	Damaging	Damaging	4.8	TTN	missense	True	4	1	· ·		0.000
2:1794519	- 	rs72646857	17.52	-				TTN	synonymous	True	-	1	·		
2:1794723	-	rs72646808	25	0.368	Damaging	Damaging	5.99	TTN	missense	True	-	1	0	0.000	0.00068839
2:1794860	 	rs72677225	23.7	0.18	Damaging	Damaging	3.39	TTN	missense	True	-	2	1	0.007003	
2:1795296	-	rs199868380	8.022	-	Damaging	Tolerated	0.862	TTN	missense	True		1	. 0	0.0002370	
2:1795404	/	rs182428755	14.49	-	Damaging	Damaging	5.95	TTN	missense	True		1	. 0	0.0050750	0.00114811
2:1795474	 	rs115744476	7.054	-				TTN	synonymous	True	-	1	. 0	0.0071227	0.00080367
2:1795593	-7	rs72650019	22.4	-	Damaging	Damaging	6.07	TTN	missense	True		1	. 1	0.0026668	0.00011478
2:1795714	+'	rs72650003	19.35	-				TTN	synonymous	True		1	. 0	0.0031769	
2:1795829	-7	rs72648981	23.1	-	Damaging	Damaging	6.16	TTN	missense	True		1	. 0	0.000170	
2:1795867	+	rs72648969	16.97	-	Damaging	Tolerated	6.16	TTN	missense	True	-	1	. 0		
2:1795875	-	rs200128066	24.4	-	Damaging	Damaging	5.95	TTN	missense	True		1	. 0		0 00220516
2:1795932	+	rs76771282	20.8	-	D :	ъ .	5.60	TTN	synonymous	True	-	1	. 0		
2:1795935	+'	rs72648953	24.1	-	Damaging	Damaging	5.63	TTN	missense	True		1	. 0	0.0001110	
	G/A	rs72648950	17.42	-	D	D	5.99	TTN	synonymous	True	-	1	1	0.006293	0.00505166
2:1795953	T/C	rs146983095	23.3	-	Damaging	Damaging		TTN	missense	True	1	<u> </u>	. 0	0.0077222	0.0021814
2:1796123	-	rs145581345	12.19 22.5	-	Damaging	Damaging	4.64 5.55	TTN TTN	missense	True	-	1	. 0	0.0007136	
2:1796152	 	rs72647897	+	-	Damaging	Damaging	5.55		missense	True	-	2	1	+	
2:1796237 2:1796352	G/A C/T	rs45447891 rs143035953	22.8 14.17	0.14	Tolerated	Tolerated	3.31	TTN TTN	synonymous	True True	-		1 0	0.0071336	0.00126292 0.00424604
	-7	rs143035953 rs72647870	24.6	0.14			-	TTN	missense		-	<u> </u>	0	0.0048613	
2:1796459	-7			0./1	Damaging	Damaging	5.91		missense	True	4	1	. 0		
2:1925430	C/A	rs183007688	10.83	-	1			NABP1	5_prime_UTR	True	· •	- 2	0	0.0059602	
2:1925431	+	rs4386269	1.373	0.114	, ·	. ·	2 20	NABP1	5_prime_UTR	False	4	2	1	0 0040474	0.00084104
2:1984957	-	rs147133320	21.7	0.114	Damaging	Damaging	3.38	RFTN2	missense	True	 *	1	. 0		
2:1984985	+	rs143754556	10.23	0.103	Tolerated	Tolerated	-1.69	RFTN2	missense	True	-	1	. 0	0.0070127	
2:1985403		rs375642198	- 200	-				RFTN2	5_prime_UTR	False		3	<u> </u>	0.000	0.00388645
2:2182986	 ' 	rs187032950	2.209	-				DIRC3	non_coding_exon	True	3	1	. 0	0.0021070	
2:2184644	IC/T	rs73083149	0.345	-	I .	l	<u> </u>	DIRC3	non_coding_exon	True	J	1	. 0	0.0004537	0.108251

											No of combinedvar	No. of	No. of		
						FATHMM	arnn		Sequence	in NIST	iants in ACEi-	variants in	variants in	4.5	
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	1	MKL Coding Pred (C)	GERP++ RS	Gene Names	Ontology (Combined)	callable regions	A samples	ACEi-A samples	control samples	gnomAD NFE MAF	gnomAD AFR MAF
2:2184646		rs74677841	3.614	-	ter rrea (c)	rrea (c)	IKS	DIRC3	non_coding_exon			3ampies	o o	0.0004539	0.108055
2:2184650	<u> </u>	rs60796764	0.42	_				DIRC3	non_coding_exon		1	1	0	0.0004536	0.108316
2:2184650		rs58899448	0.103	_				DIRC3	non_coding_exon		1	1	0	0.000454	0.125201
2:2186043		rs11336139	-	-				DIRC3	splice_region	True	1	1	0	0.0064063	0.00137741
2:2186832	<u> </u>	rs2552525	0.42	-				TNS1	synonymous	True	4	1	1 0	0.0011022	0.224233
2:2186962	A/G	rs2552530	13.34	-				TNS1	synonymous	True	1	1	0	0.0009093	0.228782
2:2186998	G/A	rs138930905	6.647	-				TNS1	synonymous	True	1	1	0	0.0001946	0
2:2187136	C/T	rs61743889	7.277	-				TNS1	synonymous	True		1	0	6.50E-05	0.0764177
2:2187457	C/G	rs138239490	24.2	0.538	Damaging	Damaging	4.98	TNS1	missense	True		2	2 0	0.0051901	0.0009187
2:2202467	G/T	rs35723758	11.14	-				DNPEP	synonymous	True	3	1	0	0.00888	0.00126263
2:2202504	T/G	rs72963541	14.79	-	Damaging	Damaging	-0.959	DNPEP	missense	True		2	2 1	0.0079169	0.00149563
2:2202508	C/T	rs1132736	19.44	-				DNPEP	synonymous	True		1	0	0.0095405	0.0865562
2:2203376	G/T	rs55876679	10.84	-	Damaging	Damaging	3.27	SPEG	missense	True	4	1	0	0.0015562	0.00034451
2:2203424	C/T	rs79386296	7.945	-				SPEG	splice_region	True		1	0	0.0034367	0.00895934
2:2203491	T/A	rs201170917	27.4	0.371	Damaging	Damaging	3.42	SPEG	missense	True		1	0	0.0007795	0
2:2203555	G/A	rs200692984	14.61	0.065	Tolerated	Tolerated	4.05	SPEG	missense	True		1	0	0.0001297	0
2:2382805	G/A	rs35114079	0.035	-				COL6A3	synonymous	True	5	1	1	0.0090933	0.00172572
2:2382805	G/A	rs116505603	12.66	0.458	Tolerated	Tolerated	3.07	COL6A3	missense	True		1	1 0	0.0012325	0
2:2382899	G/C	rs113897824	7.22	0.115	Damaging	Tolerated	3.64	COL6A3	missense	True		1	1 0	0.0058991	0.00057379
2:2382899	C/G	rs112010940	22.8	0.521	Damaging	Damaging	4.4	COL6A3	missense	True		1	1 0	0.0058984	0.00057366
2:2382963		rs113716915	16.18	0.223	Damaging	Damaging	1.84	COL6A3	missense	True		2	2 1	0.0050564	0.00229568
2:2383227	C/T	rs113567254	9.219	-				COL6A3	5_prime_UTR	True		1	0	0.0020934	0.00057617
2:2419762		rs200313330	0.193	-				SNED1	synonymous	True	3	1	0	0.0001948	0.00011492
2:2419911	<u> </u>	rs138612536	14.71	-				SNED1	synonymous	True		1	•	0.0053233	0.00138058
2:2420023	/	rs372698242	0.019	-				SNED1	synonymous	True		1	· · · · ·	0.0001947	0
2:2420110	<u> </u>	rs182099291	22.9	0.334	Tolerated	Damaging	4.07	SNED1	missense	True		1	-	0.0007171	0.00011515
3:3922558		rs146284335	8.978	0.079	Tolerated	Tolerated	-8.03	XIRP1	missense	True	3	1	-	0.00849	0.00172137
3:3922717		rs151275736	25.4	0.124	Damaging	Damaging	4.29	XIRP1	missense	True		1	1	0.0049447	0.00034562
3:3922750		rs147374766	23.2	0.158	Damaging	Damaging	4.39	XIRP1	missense	True	_	1	1 0	0.0012982	0.00023015
3:3922877	<u> </u>	rs61736153	0.488	0.011	Tolerated	Tolerated	-6.01	XIRP1	missense	True	_	1	•	0.0055116	0.0308911
3:3922901	<u> </u>	rs74827471	1.963	-	-			XIRP1	synonymous	True	2	1		0.0084966	0.00172216
3:4672272	<u> </u>	rs57097145	0.447	-	-			ALS2CL	missense	True	3	1	<u> </u>	0.0063727	0.152701
3:4672461		rs147622923	16.88	-	-			ALS2CL	splice_region	True	_	1	•	0.0060952	0.00137773
3:4672477	/	rs138226157	0.115	-	m 1 . 1	m 1 . 1	0.0550	ALS2CL	synonymous	True	_	1	0	0.0025961	0
3:4672792	<u> </u>	rs34733632	4.311	0.019	Tolerated	Tolerated	-0.0779	ALS2CL	missense	True	4	1	0	0.0016257	0.00011508
3:4673502	<u> </u>	rs116751098	6.471	- 0.27	D .	ъ .	4.71	ALS2CL	5_prime_UTR	True	6]	0	0.0066122	0.171613
3:5238459		rs61734644	27.7	0.37	Damaging	Damaging	4.71	DNAH1	missense	True	- °	1 2	· · · ·	0.0076574	0.00091996 0.00160735
3:5238720		rs77639782	0.213	0.123	Damasin -	Damagi	4.52	DNAH1	synonymous	True	1	2		0.00616	
3:5240417		rs145673040	22.4	0.123	Damaging	Damaging	4.53 1.88	DNAH1 DNAH1	missense	True	-	1		0.0085748 0.0095318	0.00149357
3:5240625 3:5241000	<u> </u>	rs112505934 rs201299120	22.8	0.045	Damaging	Damaging		DNAH1 DNAH1	missense	True True	-		0	0.0095318	0.00091954 0.00068997
3:5241000	<u> </u>	rs182141515	18.93	0.054	Tolerated	Damaging	4.46 3.58	DNAH1 DNAH1	missense	True	1	- 1	0	0.0027252	0.00068997
	<u> </u>	_	1.548	0.30	Damaging	Damaging	3.30		missense		4	-	0	0.002593	
3:1867597	I _H /C	rs141772791	1.548	-				ST6GAL1	5_prime_UTR	True	J ⁻	L	41 0	0.0036941	0.0189394

											No of combinedvar	No. of	No. of		
						FATHMM			Sequence	in NIST	iants in ACEi-	variants in	variants in		
					I .	MKL Coding	GERP++		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
		Identifier	cadd score	REVEL score	ter Pred (C)	Pred (C)	RS	Gene Names	(Combined)	regions		samples	samples	NFE MAF	AFR MAF
3:1867597	/	rs141772791	1.548	-				ST6GAL1	5_prime_UTR	True	-	1	0	0.0021387	0.00057392
3:1867934	- '	rs147859392	5.92	-				ST6GAL1	synonymous	True	2	1	· · ·	0.0009072	0.0003442
3:1930027	-	rs145262666	0.547	-				ATP13A5	synonymous	True	3	1	<u> </u>	0.0011016	
3:1930328	- '	rs74478656	23.8	0.662	Damaging	Damaging	4.68	ATP13A5	missense	True	_	1	· ·	0.0088312	0.00126553
3:1930515	/	rs201926626	16.38	-	m 1 . 1	m 1 . 1	0.055	ATP13A5	splice_region	True	_	1	•	0.0002593	0.00011486
3:1930810	/	rs201387347	8.297	0.019	Tolerated	Tolerated	0.275	ATP13A5	missense	True	7	1	1	0.0031744	0.00057366
3:1954960	/ -	rs147627958	19.59	-	Tolerated	Damaging	4.21	MUC4	missense	True		1	0	0.0002595	0 00003461
3:1955051	- '	rs201282456	0.484	-	m 1 . 1	m 1 . 1		MUC4	stop_gained	False	_	1	0	0.0023741	0.0003461
3:1955065	-	rs368695884	6.913	-	Tolerated	Tolerated		MUC4	missense	False	_		0	0.0014303	0 0525044
3:1955070		rs76083001	0.076	-	Tolerated	Tolerated	1.10	MUC4	missense	False	-		1	0.0089924	0.0535844
3:1955083	-7	rs425562	9.739	-	Tolerated	Tolerated	-1.49	MUC4	missense	False	4	1	· · ·	0.0008364	
3:1955107		rs77303944	1.219	-	m 1 . 1	m 1 . 1		MUC4	synonymous	False	_	3	1 -	0.0063452	0.00247525
3:1955107	- '	rs77250903	10.63	-	Tolerated	Tolerated		MUC4	missense	False		2	1	0.0021507	0.00255673
3:1955114	- 	rs201835572	1.16	-	m 1 . 1	m 1 . 1	0.044	MUC4	synonymous	False	_	1	1	0.0044594	0.0040696
3:1955131		rs201824339	4.968	-	Tolerated	Tolerated	0.844	MUC4	missense	False	_	1	0	0.00195	0.00035596
3:1955137	-	rs57614388	0.001	-	Damaging	Tolerated		MUC4	missense	False	4	1	1	0.0083133	0.00691866
3:1955163	- '	rs201534662	8.663	-	Tolerated	Tolerated	0.55	MUC4	missense	True	4	1	•	0.0012362	0.00069316
3:1955944	-/	rs148323328	3.42	0.051	Tolerated	Tolerated	4.74	TNK2	missense	True	4	1	2	0.0080719	0.00207517
3:1955946	-	rs148423089	24	0.081	Damaging	Damaging	5.06	TNK2	missense	True	-	1	0	0.002341	0.00023073
3:1955949	- '	rs62283329	0.007	-				TNK2	synonymous	True	_	1	3	0.0074403	0.00150602
3:1955950		rs139268974	0.013	-				TNK2	synonymous	True		1	· · ·	0.0022153	0.00011547
		rs200573341	-	-				CRIPAK	5_prime_UTR	True	3	1	·	0.0096452	0.0499036
4:1388790	/ -	rs79415192	5.299	0.004	Tolerated	Tolerated	-2.49	CRIPAK	missense	False	4	1	•	0.001954	
4:1389192		rs146804633	4.959	0.036	Tolerated	Tolerated	-1.63	CRIPAK	missense	False	4	1	0	0.0009617	0.0017188
4:1389210	· ·	rs113156931	3.247	0.015	Tolerated	Tolerated	-1.63	CRIPAK	missense	False	<u> </u>	1	0	0.0001672	0.00014274
4:2306600		rs140095568	6.183	-				ZFYVE28	synonymous	True	5	1	•	0.0025937	0.00068918
4:2307125		rs143836367	0.021	-				ZFYVE28	synonymous	True	_	1	1 0	0.0046668	0.00068871
4:2366219	<u> </u>	rs148576290	2.075	-				ZFYVE28	5_prime_UTR	True	4	2	2 0	0.005903	0.00114758
4:2420036		rs115545770	22.5	-				ZFYVE28	synonymous	True		2	2 0	0.0019634	0.0640698
4:8605845	-	rs115804488	7.418	-				CPZ,GPR78	synonymous	True	3	1	1 0	0.0085514	0.00321543
4:8607856		rs141203560	24.1	0.363	Damaging	Damaging	3.41	CPZ,GPR78	missense	True	_	1	1 0	0.0033701	0.00057471
4:8620153	-/	rs12650877	7.025	-				CPZ,GPR78	splice_region	True		1	•	0.0084966	
4:8621089	- '	rs34486568	0.001	-				CPZ,GPR78	synonymous	True	_	1	· ·	0.0033048	0.00149219
4:1552444	-	rs145036588	-	-				DCHS2	splice_region	False	3	2		0.0056159	0.003327
4:1552545	-	rs79215995	19.89	0.294	Damaging	Tolerated	-6.01	DCHS2	missense	True	4	1	-	0.006028	0.00080386
4:1554121	-	rs148953504	34	0.876	Damaging	Damaging	4.92	DCHS2	missense	True		2	 	0.0035015	0.00034483
4:1875103	-	rs34174591	1.25	-				FAT1	synonymous	True	6	1	1 0	0.0099857	0.0867816
4:1875181	/	rs72716245	0.002	-				FAT1	synonymous	True	4	2	2 0	0.0037594	0.00080367
4:1875189	-	rs202166446	0.036	0.237	Tolerated	Tolerated	-11.7	FAT1	missense	True	1	1	· · · ·	0.0007777	0.00022967
4:1875273	-	rs74424517	6.103	-				FAT1	synonymous	True	4	1	1 0	0.0097656	0.00207996
4:1875428	-	rs183343406	26.1	0.337	Damaging	Damaging	5.09	FAT1	missense	True	1	1	0	0.0023998	0.00103353
4:1875493		rs111886222	25.7	0.227	Damaging	Damaging	5.49	FAT1	missense	True	4	1	1 0	0.0083647	0.00241158
4:1875579	C/T	rs113970444	23.4	0.306	Damaging	Damaging	5.04	FAT1	missense	True		1	L] 0	0.0082318	0.00183781

		ı	1	1	1	ı	I	ī	ı	1	No of		1	ı	1
											No of combinedvar	No. of	No. of		
						FATHMM			Sequence	in NIST	iants in ACEi-	variants in	variants in		
					MutationTas	MKL Coding	GERP++		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)	Pred (C)	RS	Gene Names	(Combined)	regions	ir sumpres	samples	samples	NFE MAF	AFR MAF
5:3141092	G/A	rs61748189	0.632	-				DROSHA	synonymous	True	6	2	. 1	0.0081659	0.00240936
5:3142197	A/-	rs70955711	-	-				DROSHA	splice_region	False	1	1	. 1	0.0097926	0.0774411
5:3143597	G/A	rs17485810	14.17	-				DROSHA	synonymous	True	1	1	. 0	0.001886	0.00070505
5:3151525	C/T	rs200485820	11.13	0.019	Tolerated	Damaging	4.76	DROSHA	missense	True	1	1	. 0	6.48E-05	0
5:3152679	G/A	rs149389256	26.6	0.325	Damaging	Damaging	5.41	DROSHA	missense	True		1	. 1	0.0052858	0.00138953
5:7902474	C/A	rs189499447	16.47	0.116	Tolerated	Damaging	0.828	CMYA5	missense	True	3	1	. 1	0.0058442	0.00149528
5:7902508	A/G	rs72635618	8.838	0.015	Tolerated	Tolerated	2.07	CMYA5	missense	True		1	. 0	0.0038232	0.00080312
5:7902637	T/G	rs72635619	0.861	0.181	Tolerated	Tolerated	-4.33	CMYA5	missense	True	1	1	. 0	0.0036951	0.00080349
5:7902832	G/A	rs199784482	18.94	0.07	Tolerated	Damaging	4.42	CMYA5	missense	True]	1	. 0	0.0025279	0.00068855
5:7903378	C/T	rs370580149	6.483	-				CMYA5	synonymous	True		1	. 0	0.0001945	0
5:8994965	A/G	rs61740119	6.601	-				GPR98	synonymous	True	5	1	. 0	0.0037584	0.0107947
5:9004157	T/C	rs13171868	15.17	0.057	Damaging	Tolerated	1.67	GPR98	missense	True		1	0	0.0086866	0.00172137
5:9005927	C/A	rs199839743	23.1	0.211	Damaging	Damaging	4.34	GPR98	missense	True		1	. 1	0.0046086	0.00149357
5:9007006	G/A	rs202067248	7.206	0.064	Tolerated	Tolerated	0.403	GPR98	missense	True		1	. 0	0.0001296	0.00022952
5:9008695	G/A	rs41304892	4.968	0.088	Tolerated	Tolerated	-7.1	GPR98	missense	True		2	2 1	0.0045378	0.00091827
5:1402076	G/A	rs78362045	2.186	-				PCDHA1,PCDHA2,PCD	5_prime_UTR	True	4	1	. 0	0.0031108	0.00160661
5:1402091	G/A	rs61730777	15.64	-				PCDHA1,PCDHA2,PCD	synonymous	False		1	. 0	0.0042796	0.00068966
5:1402149	G/A	rs17844309	0.342	0.039	Tolerated	Tolerated	0.0401	PCDHA1,PCDHA2,PCD	missense	False		1	. 0	0.0083085	0.00861079
5:1402163	G/A	rs143805132	15.2	0.06	Tolerated	Tolerated	3.44	PCDHA1,PCDHA2,PCD	missense	True		1	. 0	0.0003244	0
5:1791932	C/T	rs376959601	1.54	-				MAML1	synonymous	True	6	1	. 0	0	0
5:1791933	C/T	rs61748799	9.505	-				MAML1	synonymous	True		1	. 0	0.004731	0.00114784
5:1792012	C/T	rs61753466	14.85	0.042	Tolerated	Damaging	0.661	MAML1	missense	True		2	2 2	0.0094768	0.00229621
5:1792189	/ -	rs79329237	0.024	-				MAML1	non_coding_exon	True		2	2 0	0.0046068	0.00068886
5:1792204	C/A	rs183808429	0.303	-				MAML1	non_coding_exon	True		2	2 0	0.0095393	0.00309846
6:2932324	G/C	rs41271546	22.8	0.317	Tolerated	Damaging	5.01	OR5V1	missense	True	3	1	1	0.0071966	0.00103258
6:2932366	T/C	rs28359952	4.86	-				OR5V1	synonymous	True		1	. 0	0.0099299	0.00252932
6:2936468	G/A	rs36210740	11.98	-	Tolerated	Tolerated	2.22	OR5V1,OR12D2	missense	False		1	0	0.0025924	0.00780891
6:2936487	,	rs11752608	9.253	-	Damaging	Tolerated	3.94	OR5V1,OR12D2	missense	False		1	. 0	0.002594	0.0109095
6:2940795	C/T	rs17184009	38	-	Damaging	Damaging	3.73	OR10C1,OR11A1	stop_gained	True	3	2	2 0	0.0043433	0.0716747
6:2940797	C/T	rs11755177	5.501	-				OR10C1,OR11A1	synonymous	True		3	0	0.0073892	0.10944
6:2940805	C/A	rs11755182	7.171	-	Damaging	Tolerated	2.44	OR10C1,OR11A1	missense	True		3	0	0.007393	0.109335
6:2940815	,	rs17177639	20.2	-	Damaging	Damaging	3.11	OR10C1,OR11A1	missense	True	1	2		0.0043444	0.0722656
6:2940820	,	rs17177646	15.93	-	Tolerated	Tolerated	-1.24	OR10C1,OR11A1	missense	True		2	1 0	0.0042785	0.0663757
6:2940872		rs11968123	0.357	-	Tolerated	Tolerated	0.0822	OR10C1,OR11A1	missense	False		2	2 0	0.0042813	0.0551081
6:3067145		rs77465266	2.599	-				MDC1	synonymous	True	3	1	. 0	0.005575	0.00240881
6:3067176	/	rs75355880	0.879	0.018	Tolerated	Tolerated	-4.12	MDC1	missense	True	1	1	. 0	0.0056428	
6:3067196	,	rs80087328	0.201	0.006	Tolerated	Tolerated	-4.79	MDC1	missense	True		1	. 0	0.0055109	0.00241268
6:3067271		rs74590481	1.48	-				MDC1	synonymous	True	1	1	. 0	0.0056609	0.00233318
6:3067318	,	rs143042499	6.578	-				MDC1	synonymous	True		1	. 0	0.0045494	
6:3067328		rs114458930	1	-				MDC1	synonymous	False	1	1	. 0	0.0075793	
6:3067334	,	rs144700924	1.142	0.033	Tolerated	Tolerated	2.07	MDC1	missense	False		1	. 0	0.0082229	
6:3067335		rs149535951	0.041	-				MDC1	synonymous	False		1	. 0	0.0030057	0.00715198
6:3067335	T/G	rs143258964	0.311	0.017	Tolerated	Tolerated	-2.3	MDC1	missense	False]	1	. 0	0.003779	0.010117

					1						No of				
												No. of	No. of		
					MantationToo	FATHMM MKL Coding	CEDD		Sequence	in NIST	iants in ACEi-	variants in ACEi-A	variants in	AD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)		RS	Gene Names	Ontology (Combined)	callable regions	A samples	samples	control samples	gnomAD NFE MAF	AFR MAF
6:3068025		rs61733210	0.046	-	ter rreu (e)	Trea (c)	l l	MDC1	synonymous	True		3diffpies 1	1	0.0083679	0.00195357
6:3088316	<u> </u>	rs199858134	14.47	-				VARS2	synonymous	False	3	1	0	0.0003075	
6:3088356	<u> </u>	rs141408930	16.67	_	Damaging	Damaging	4.5	VARS2	initiator codon	False	1	1	1 0	0.0064885	
6:3088547		rs147636694	14.44	-	1 10 0	1 10 0		VARS2	synonymous	False	1	1	0	0.0022032	0.00505166
6:3089098	-	rs55865499	10.72	0.022	Tolerated	Tolerated	-3.03	VARS2	missense	False	1	1	0	0.0055088	0.00080331
6:3150311	G/A	rs7753431	16.5	-				ATP6V1G2-DDX39B,D	missense	False	3	1	0	0.0091475	0.0531034
6:3150968	C/T	rs62395765	5.409	-				ATP6V1G2-DDX39B,D	5_prime_UTR	False		2	2 0	0.0090096	0.00964852
6:3151003	A/C	rs62395766	6.839	-				ATP6V1G2-DDX39B,D	I5_prime_UTR	False		2	2 0	0.0097631	0.0154271
6:3879595	G/T	rs61748602	2.705	-				DNAH8	splice_region	True	5	2	2 1	0.0074675	0.00045935
6:3880575	G/A	rs45622336	0.147	-				DNAH8	synonymous	True		1	0	0.0058351	0.00080349
6:3881341	G/T	rs61757219	7.862	0.062	Tolerated	Tolerated	-2.42	DNAH8	missense	True		1	1 0	0.0066105	0.00114758
6:3897667	-/	rs189023122	23.6	0.295	Damaging	Damaging	4.79	DNAH8	missense	True		1	1	0.0001955	0
6:3982413	<u> </u>	rs199767843	16.48	0.354	Damaging	Damaging	6.11	DAAM2	missense	True	4	2	2 0	0.0055772	
6:3983930		rs200668867	33	0.655	Damaging	Damaging	5.05	DAAM2	missense	True		1	1 0	0.0003241	0.00022967
6:3986500	<u> </u>	rs61748650	22.9	0.177	Damaging	Damaging	4.93	DAAM2	missense	True	_	1	`	0.0062856	
6:4300601	<u> </u>	rs147493246	27.1	0.592	Damaging	Damaging	5.5	CUL7	missense	True	3	1	· ·	0.0097899	
6:4300640		rs41274912	22.4	0.467	Damaging	Damaging	2.26	CUL7	missense	True		1	0	0.0097226	0.00137804
6:4301876		rs372224208	-	-			- 00	CUL7,KLC4	inframe_deletion	True		1	0	0.0053247	0.0006895
6:4302039		rs141692693	19.58	-	Tolerated	Tolerated	-7.88	CUL7,KLC4	missense	True	3	1	0	0.0001944	0.00367309
6:1353072		rs149162146	7.531	-	m 1 . 1	m 1 . 1	6.00	HBS1L	synonymous	True	3	1	0	0.0005836	0.00034467
6:1353239	-/	rs111758776	6.182	-	Tolerated	Tolerated	-6.99	HBS1L HBS1L	missense	True	-	2	- v	0.0084878	0.00126292
6:1353577 6:1524562		rs186634007 rs41291047	15.23 26.3	0.479	Damaging	Damaging	4.39	SYNE1	missense	False True	5		2 0	0.009085 0.0007776	0.00137804
6:1524562	,	rs35686213	1.618	0.479	Damaging	Damaging	6.16	SYNE1	missense synonymous	True	1	1	1 1	0.0007776	0.00011473
6:1526296		rs76160752	18.3	0.018	Damaging	Damaging	3.16	SYNE1	missense	True	1	1	0	0.0009123	0.00092143
6:1526296		rs148493518	0.021	0.016	Damaging	Damaging	3.10	SYNE1	synonymous	True	-	1	1 1	0.0077454	0.0377497
6:1526882		rs200275358	0.072	-				SYNE1	synonymous	True	1	1	1 0	0.0000303	
6:1527494		rs138617999	0.154	0.021	Tolerated	Tolerated	-1.26	SYNE1	missense	True	1	1	0	0.0013012	
6:1604539		rs142637746	1.166	0.06	Tolerated	Tolerated	-0.354	IGF2R	missense	True	5	1	0	0.0010200	0.000031113
6:1604555		rs147711556	28.3	0.357	Damaging	Damaging	5.5	IGF2R	missense	True	1	1	0	0.0009071	0.00011476
6:1604695	<u> </u>	rs8191808	18.1	0.125	Damaging	Damaging	4.31	IGF2R	missense	True	1	1	1	0.0066736	0.00068839
6:1604828		rs146152775	5.31	0.086	Tolerated	Tolerated	2.74	IGF2R	missense	True	1	1	1 0	0	0.00011476
6:1605011		rs76130099	1.225	0.106	Tolerated	Damaging	1.62	IGF2R	missense	True	1	1	1 0	0.0060928	
6:1605921		rs145650284	1.611	-		0 0		SLC22A2	non_coding_exon	True	4	1	0	0.0080363	0.00183697
6:1606634	T/G	rs8177517	24.5	-	Tolerated	Damaging	5.13	SLC22A2	missense	True	1	1	0	0.0003888	0.0252525
6:1606646	G/A	rs8177515	0.01	-				SLC22A2	synonymous	True	1	2	2 0	0.0056398	0.00091891
6:1675600	G/A	rs186514078	1.11	-				TCP10L2	non_coding_exon	True	5	1	0	0.0062848	0.00091806
6:1675857	C/T	rs186539787	0.032	-				TCP10L2	synonymous	False	1	1	1 0	0.0001299	0.00644122
6:1675953	C/T	rs146018563	28	-	Damaging	Tolerated	1.64	TCP10L2	stop_gained	False]	1	0	0.0035653	0.00019372
6:1675953	T/C	rs202096111	0.986	-				TCP10L2	synonymous	False		3	3 2	0.0086885	0.00819113
7:2740393	C/T	rs112599565	0.606	-				AMZ1	splice_region	True	4	1	0	0.0019453	0.00045914
7:2742363	C/T	rs149317306	0.196	-				AMZ1	synonymous	True]	1	0	0.0041526	0.00103472
7:2748787	T/C	rs150799683	0.035	0.002	Tolerated	Tolerated	-5.63	AMZ1	missense	True]	1	0	0.0039022	0.00034515

	· ·	Identifier	cadd score	REVEL score	MutationTas ter Pred (C)	FATHMM MKL Coding Pred (C)	GERP++ RS	Gene Names	Sequence Ontology (Combined)	in NIST callable regions	No of combinedvar iants in ACEi- A samples	No. of variants in ACEi-A samples	No. of variants in control samples	gnomAD NFE MAF	gnomAD AFR MAF
7:2752155		rs147110889	0.777	-				AMZ1	synonymous	True		1	. 0	0.0041537	0
7:2162901		rs191266255	8.608	-				DNAH11	synonymous	True]3	1	. 0		0.00034435
7:2167548	-	rs62447794	5.573	-				DNAH11	splice_region	True		1	. 0		0.00103282
7:2178165	· ·	rs72657364	2.859	0.033	Tolerated	Tolerated	-1.27	DNAH11	missense	True		1	. 0	0.0000100	0.00964409
-	C/T	rs62445328	0.05	-				DNAH11	synonymous	True	_	1	1	0.0063496	0.00137804
	C/G	rs202148932	0.013	-	Tolerated	Tolerated	1.61	DNAH11	missense	True	_	1	. 0	0.0007136	0.00011497
7:4787659	/	rs112879160	0.024	-				HUS1,PKD1L1	synonymous	True	15	1	. 0	0.0023337	0.00068871
7:4788014	-	rs116988549	18.22	0.09		Damaging	5.51	HUS1,PKD1L1	missense	True	-	1	1	0.0060928	0.00126292
7:4789274		rs150396842	13.27	0.033	Tolerated	Tolerated	2.69	HUS1,PKD1L1	missense	True		1	. 1	0.0015554	0.00034443
7:4792552	-/	rs141646493	0.06	0.028	Tolerated	Tolerated	-8.7	HUS1,PKD1L1	missense	True	4	3	0	0.0075266	0.00252525
7:4821109	-	rs144916268	1.03	0.106	Tolerated	Tolerated	-2.61	ABCA13	missense	True	4	1	. 0	0.0003889	0
7:4828416		rs186683711	3.628	-	m 1 . 1		0.60	ABCA13	splice_region	True	-	1	. 0	0.0068724	0.00264064
7:4831415	-	rs142391487	18.54			0 0	3.62	ABCA13	missense	True		1	. 1	0.0091369	
7:4841178	,	rs78147863	19.97	0.593	Damaging	Damaging	5.7	ABCA13	missense	True	4	1	. 0	0.0010210	
7:7392975	<u> </u>	rs138159923	0.202	0.116	D .	ъ .	2.16	GTF2IRD1	synonymous	True	4	2	· · · · ·		
7:7396979 7:7397199	,	rs145912521	22.7	0.116	1 0 0		2.16	GTF2IRD1	missense	False	-	1	. 0		0.00068839
	-	rs149209759	21.9	0.143	 	Damaging	4.2	GTF2IRD1	missense	False	4	1	. 0		0.00034427
7:8258029		rs199626449	15.21	0.045	Damaging	Damaging	1.29	PCLO PCLO	missense	True	4	1	0	0.0012703	0.00022962
7:8258487 7:8276355		rs372909168 rs183301643	5.618 2.84	-				PCLO	synonymous	True True	-	1	0	0.0011018	0.00049542
7:8276355	-	rs183301643	2.84	-	1			PCLO	splice_region	True	1	1	1	0.0026106	0.00049542
7:8276439	/	rs617301643	15.61	0.066	Tolerated	Damaging	3.65	PCLO	splice_region missense	True	1	1	0		0.00210332
7:9160305	C/T	rs142401936	24.5	0.000	Tolerated	Tolerated	1.66	AKAP9	missense	True	5	1	0		0.00091800
7:9166082		rs192046591	11.76	-	Tolerateu	Tolerateu	1.00	AKAP9	splice_region	True	-	2	0	0.002014	0.00080332
	A/G	rs73226383	27.5	0.291	Damaging	Damaging	5.62	AKAP9	missense	True	-	1	0	0.0002370	0.00022732
7:9170872		rs61757672	0.957	0.271	Damaging	Damaging	3.02	AKAP9	synonymous	True		1	0	0.001102	0.00034433
	<u> </u>	rs199830571	3.466	0.099	Tolerated	Tolerated	-0.962	MUC12	missense	False	4	1	0		
7:1006370	/	rs199836803	9.859	0.034	Tolerated	Tolerated	-1.02	MUC12	missense	False	1	1	1		
7:1006445	-	rs141500497	5.259	0.015	Tolerated	Tolerated	-0.234	MUC12	missense	False	1	1	0		0.00024462
7:1006458	-	rs371001202	18.45	0.012	Tolerated	Tolerated	-0.964	MUC12	missense	False	1	1	0	-	0.00082256
7:1006461	-	rs139823939	0.199	0.037	Tolerated	Tolerated	-0.585	MUC12	missense	False		1	0	0.0001118	0.00017501
7:1006464	<u> </u>	rs202045957	14.4	0.013	Tolerated	Tolerated	-2.13	MUC12	missense	False		1	0	0.0004097	0.00028361
7:1006772	· ·	rs79084107	0.356	0.01	Tolerated	Tolerated	-1.61	MUC17	missense	False	4	4	1	0.0044331	0.0315657
7:1006816		rs144494200	0.003	0.006	Tolerated	Tolerated	-1.95	MUC17	missense	True	1	1	. 0	0	0.00011748
7:1006817		rs138331718	0.058	0.015	Tolerated	Tolerated	-2.1	MUC17	missense	True	1	1	. 0	0.0006482	0.00022999
7:1006995	-/	rs147613804	10.75	-				MUC17	synonymous	True	1	1	. 1	0.0058351	0.00103282
7:1171888		rs147422190	25.1	0.83	Damaging	Damaging	2.5	CFTR	missense	False	3	1	. 0	0.0003888	0.00011471
7:1172304		rs1800098	22	0.665		Damaging	4.83	CFTR	missense	True	1	1	. 0	0.0066874	0.00137836
7:1172322	-	rs1800100	23.4	0.706		Damaging	4.51	CFTR	missense	True	1	1	. 0	0.0083636	0.00172216
7:1172326	/	rs1800103	22.8	0.738	1 0	Damaging	-4.45	CFTR	missense	True	1	1	. 1	0.0004537	0.00011471
7:1172506	-	rs1800112	23.1	0.569	 	Damaging	6.16	CFTR	missense	True	1	1	. 0		0.00011486
7:1318654	-	rs144287352	0.025	-				PLXNA4	synonymous	True	4	1	. 0	0.001557	0.00022967
7:1318874	-	rs117847895	7.438	-				PLXNA4	synonymous	True	1	1	. 0	0.0014256	0.00022946

											No of	No. of	No. of		
						FATHMM			Sequence	in NIST	combinedvar iants in ACEi-	variants in	variants in		
					MutationTas	MKL Coding	GERP++		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)	Pred (C)	RS	Gene Names	(Combined)	regions	P-55	samples	samples	NFE MAF	AFR MAF
7:1319131	C/T	rs190791576	14.48	0.073	Damaging	Damaging	4	PLXNA4	missense	True		1	. 0	6.48E-05	0
7:1319259	C/T	rs112682233	16.57	0.127	Damaging	Damaging	5.23	PLXNA4	missense	True	1	1	. 0	0.0029804	0.00045903
8:2033501	G/A	rs147335228	0.004	-				MYOM2	synonymous	False	5	1	. 0	0.0002611	0.00011647
8:2040178	C/A	rs34004023	0.01	-				MYOM2	synonymous	True	1	1	. 0	0.0068742	0.00241102
8:2046731	C/T	rs142781583	0.131	-				MYOM2	synonymous	True		2	2 1	0.0062208	0.00195133
8:2048729	C/T	rs191644656	19.3	0.261	Damaging	Damaging	5.67	MYOM2	missense	True		1	. 0	0.0004535	0.00011478
8:2063891	G/C	rs143305181	26.6	0.45	Damaging	Damaging	5.32	MYOM2	missense	True		1	. 0	0.0093925	0.00081339
8:5950821	C/T	rs117413256	13.32	-				NSMAF	synonymous	True	5	1	. 0	0.0049007	0.00080478
8:5953580	C/T	rs150658908	24.1	0.403	Damaging	Damaging	5.72	NSMAF	missense	True		1	. 0	0.0001298	0
8:5957198	C/T	rs144534227	9.719	-				NSMAF	5_prime_UTR	True		1	. 0	0.0043557	0.00069093
8:5957235	C/T	rs146530407	13.35	-				NSMAF	5_prime_UTR	True		2	2 0	0.0029466	0.00162715
8:1007791	G/A	rs61753725	2.883	-				VPS13B	synonymous	True	4	1	. 0	0.0049929	0.00114732
8:1008322	A/G	rs28940272	25.6	0.666	Damaging	Damaging	6.06	VPS13B	missense	True		1	. 0	0.0038232	0.00103282
8:1008611	C/T	rs138127778	1.125	0.099	Tolerated	Tolerated	3.89	VPS13B	missense	True		1	. 1	0.0092005	0.00172176
8:1008715	,	rs61754107	1.106	-				VPS13B	synonymous	True		1	. 0	0.0009736	0.00045945
8:1048976	,	rs17854256	17.52	0.05	Damaging	Damaging	5.31	RIMS2	missense	True	3	1	. 0	0.0061608	
8:1048979	G/A	rs202004651	7.416	-				RIMS2	synonymous	True		1	. 0	0.0029839	0.00034467
8:1049489		rs17854257	6.196	-				RIMS2	synonymous	True		1	. 0	0.0062922	0.00114863
8:1051609		rs188924401	21.2	-				RIMS2	synonymous	True		1	. 0	0.0034393	0.00091849
8:1132777		rs61759499	22.3	0.097	Damaging	Damaging	5.44	CSMD3	missense	True	5	1	. 0	0.0042153	0.00022962
8:1135048		rs61754527	24.2	0.384	Damaging	Damaging	4.9	CSMD3	missense	True		1	. 0	0.0028523	0.00103306
8:1136490		rs61753739	28.9	0.433	Damaging	Damaging	5.74	CSMD3	missense	True		1	+ +	0.0059206	0.00069654
8:1137021	- /	rs146167541	7.069	-				CSMD3	synonymous	True		2	2 0	0.0060398	0.0010333
8:1449403		rs200585601	12.28	0.347	Tolerated	Tolerated	0.661,0.66	EPPK1	missense	False	4	3	3	0.0080235	0.0680195
8:1449408	-7	rs188369736	0.005	-				EPPK1	synonymous	False		1	. 0	0.0045443	0.00057366
8:1449423		rs199598193	33	0.805	Damaging	Damaging	4,4,4	EPPK1	missense	True		1	1	0.0033078	
8:1449470		rs377574983	0.006	-		m 1 . 1	4.40	EPPK1	synonymous	True	-	1	1	0.0016868	
8:1449471		rs150047119	16.76	0.626	Damaging	Tolerated	4.42	EPPK1	missense	True	(1	. 0	0.0036312	
8:1449915		rs200575172	0.093	-				PLEC	synonymous	True	6	1	. 0	0.0001298	
8:1449919		rs113137721	0.156	-				PLEC	synonymous	True		1	. 0	0.0032463	0.00057524
8:1449920		rs148865812	2.87	0.100	m 1 . 1	m 1 . 1	0.46	PLEC	synonymous	True	-	1	1	0.0081797	
8:1449940	,	rs34132016 rs141002386	5.92	0.102 0.622	Tolerated	Tolerated	-8.46 3.9	PLEC PLEC	missense	True	-	1	. 0	0.0071929 6.49E-05	0.00160587
8:1449945 8:1449973		rs62641756	3.622	0.622	Damaging	Damaging	0.864	PLEC	missense	True True	-	1	. 0	0.0005189	0.0116065
8:1449973 8:1449975		rs117962829	22	0.077	Tolerated	Tolerated	4.98	PLEC	missense missense	True	1	1	0	0.0003189	0.0116065
8:1449973		rs201430180	16.87	0.042	Damaging	Damaging		PLEC		True	1	1	0	0.0005241	0.00011497
8:1449994 8:1450012	/	rs148465219	0.157	0.042	Tolerated	Damaging	4.49	PLEC	missense		1	1	1 0	0.0055281	
8:1450012 8:1450038	-,	rs148465219 rs200482255	0.006	[PLEC	synonymous synonymous	True True	1	1	- 0	0.0014916	
8:1450038		rs201818691	0.249	-				PLEC	splice region	True	1	1	. 0	0.001556	
8:1450044		rs36078464	5.478	-		Tolerated	3.47	RECOL4	missense	True	4	1	0	0.0031826	
8:1457419	,	rs34159914	0.489	-	1	1 OICI ALEU	J.T/	RECQL4	synonymous	True	 ^	2	0	0.0054447	
9:7922829		rs76157996	2.541	_	 			PRUNE2	splice_acceptor	True	3	1	. U	0.0031206	
9:7932255		rs73650283	23.1	0.108	Tolerated	Damaging	4.08	PRUNE2	missense	True	 	1	0	0.0004330	
7.7334433	u/A	113/3030403	43.1	0.100	i oiei ateu	Daniaging	17.00	I KONEZ	IIII35EII5E	Titue]	1	1 0	0.000369	0.00073317

		ı	1	1		ı	1	I	Ι	I	lwc		1	ı	1
											No of combinedvar	No. of	No. of		
						FATHMM			Sequence	in NIST	iants in ACEi-	variants in	variants in		
					MutationTas	MKL Coding	GERP++		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score		Pred (C)	RS	Gene Names	(Combined)	regions	A samples	samples	samples	NFE MAF	AFR MAF
9:7932385	C/T	rs200875180	23.3	0.205	Tolerated	Damaging	5.94	PRUNE2	missense	True		1	. 0	0.00324	0.00068871
9:7932397	G/T	rs73650284	0.034	-		0 0		PRUNE2	synonymous	True	1	1	. 1	0.0022686	0.00919329
9:7932605	G/C	rs185829648	25.4	0.277	Damaging	Damaging	4.94	PRUNE2	missense	True	1	1	. 0	0.0060928	0.00149185
9:1128985	C/T	rs151065500	19.47	0.046	Damaging	Damaging	4.36	AKAP2,PALM2-AKAP2	missense	True	3	1	. 0	0.0085581	0.00608077
9:1128990	C/T	rs115538409	22.1	0.122				AKAP2,PALM2-AKAP2	synonymous	True		1	. 0	0.0085659	0.00608636
9:1128997	C/A	rs112958283	6.489	0.026	Tolerated	Tolerated	3.57	AKAP2,PALM2-AKAP2	missense	True		2	2 1	0.0048651	0.00091849
9:1131632		rs185633813	24	0.208	Damaging	Damaging	3.72	SVEP1	missense	True	3	1	. 0	0.0018795	0.00114758
9:1131690	G/A	rs191479924	23	0.088	Tolerated	Damaging	4.66	SVEP1	missense	True		1	. 0	0.0018142	0.00091827
9:1131702	-,	rs143931457	10.48	0.093	Tolerated	Tolerated	-0.482	SVEP1	missense	True		2	2 0	0.0062865	0.00149322
9:1132653		rs117475463	17.84	0.056	Damaging	Damaging	4.62	SVEP1	missense	True		1	. 0	0.0073339	0.0126321
9:1144542	,	rs150006859	13.31	0.031	Tolerated	Tolerated	-2.96	C9orf84	missense	True	4	1	. 0	0.000909	0.00126466
9:1144754		rs77603777	18.18	0.051	Tolerated	Damaging	1.57	C9orf84	missense	True		1	. 0	0.0010375	0.00022941
9:1145103		rs144324654	13.67	0.026	Tolerated	Damaging	1.15	C9orf84	missense	True		1	. 0	0.0001948	
9:1145381		rs148914231	21.2	0.222	Tolerated	Damaging	4.65	C9orf84	missense	True		1	. 0	0.0013608	
9:1178087	,	rs61734387	28.3	0.288	Damaging	Damaging	4.92	TNC	missense	True	4	1	. 0	0.0023992	
9:1178402		rs61737739	18.48	0.032	Tolerated	Damaging	1.64	TNC	missense	False		1	· · · ·	0.0007134	0.00022957
9:1178486		rs145086096	24.2	0.244	Damaging	Damaging	5.06	TNC	missense	False		1	. 0	0.0078439	0.00103425
$\overline{}$	C/T	rs144032672	26.4	0.376	Damaging	Damaging	5.19	TNC	missense	False		1	0	0.0027213	0.00068855
9:1178773		rs138862103	-	-			. = 0	TNC	splice_region	True	3	1	. 0	0.0050544	0.00068855
9:1244410		rs201300206	23.5	0.108	Tolerated	Damaging	4.72	DAB2IP	missense	True	3	2	2 0	0.0020093	0.00091849
9:1245224 9:1245261		rs34839326 rs368910721	10.64	0.622	ъ .	ъ .	5.27	DAB2IP DAB2IP	synonymous	True	-	1	. 0	0.0033722 0.0001296	0.00091912
9:1245261		rs181428257	7.951	0.622	Damaging	Damaging	-3.5	HMCN2	missense	True	3	1	0	0.0001296	0.00011484
9:1332693	,	rs80073481	10.34	-		Tolerated	-3.5	HMCN2	non_coding_exon non coding exon		ľ	2	1 2	0.0028349	0.00043943
9:1332830		rs146082211	14.65	-		Damaging	3.73	HMCN2	non coding exon		1	2	2 2	0.0034284	0.00172374
9:1338847	-,	rs201962705	13.75	0.114	Tolerated	Tolerated	2.55	LAMC3	missense	True	3	1	1 1	0.0016627	0.00037417
9:1339450		rs199535979	1.843	0.114	Tolcraccu	Tolcraccu	2.55	LAMC3	splice_region	True	Ĭ	1	0	0.0003433	
9:1339469	,	rs149131135	22	0.063	Tolerated	Tolerated	4.2	LAMC3	missense	True	1	1	0	0.0003243	
9:1339480	,	rs146221263	11.72	0.027	Tolerated	Tolerated	1.1	LAMC3	missense	True		1	0	0.0048682	0.00138058
9:1339481		rs140955110	20.8	0.025	Tolerated	Damaging	4	LAMC3	missense	True	1	1	. 0	0.0048657	0.00126408
9:1339609		rs141724499	0.992	-		- 0 0		LAMC3	synonymous	False	1	1	. 0	0.0053784	0.00137678
9:1397307		rs143341441	0.047	-				RABL6	5_prime_UTR	True	3	2	2 0	0.0048651	0.00172453
9:1397337	,	rs188586555	1.177	0.018	Tolerated	Tolerated	0.166	RABL6	missense	False	1	1	. 1	0.0046056	0.00022999
9:1397350	T/C	rs45457892	2.002	-	Tolerated	Tolerated	0.976	RABL6	missense	False]	1	. 0	0.0019541	0.00080608
10:149650	A/T	rs41299658	24.3	0.177	Damaging	Damaging	4.34	DCLRE1C	5_prime_UTR_pre	True	3	1	. 0	0.0007127	0.0003442
10:149841	C/T	rs12250184	0.68	-				DCLRE1C	5_prime_UTR	False]	1	. 0	0.0018154	0.0808824
10:149962	A/G	rs12411686	6.436	-				DCLRE1C	5_prime_UTR	True]	1	. 2	0.0055757	0.0003442
10:149963	G/C	rs140710760	6.098	-				DCLRE1C	5_prime_UTR	True		1	. 0	0.0016202	0.0144628
10:169558	C/T	rs201001705	0.007	-				CUBN	synonymous	False	4	1	. 0	0.0014264	0.00034483
10:169673	C/T	rs11254278	2.061	-				CUBN	synonymous	False	4	1	. 1	0.0070651	0.00390356
10:169674	T/C	rs144360241	23.9	0.322	Damaging	Damaging	5.32	CUBN	missense	False]	1	0	0.0066736	0.00091785
10:170871	G/A	rs1873469	4.074	-				CUBN	synonymous	True]	1	. 1	0.005848	0.284246
10:171101	G/A	rs201802902	7.436	-				CUBN	synonymous	True]	1	. 0	6.48E-05	0.00011478

									I		No of				
												No. of	No. of		
					MutationTag	FATHMM MKL Coding	CEDD		Sequence	in NIST callable	iants in ACEi	variants in ACEi-A	variants in	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	1	Pred (C)	RS	Gene Names	Ontology (Combined)	regions	A samples	samples	control samples	NFE MAF	AFR MAF
10:171263	<u> </u>	rs7905349	10.22	0.05	Tolerated	Damaging	-2.62	CUBN	missense	True		1	1	0.0059609	
10:171529		rs150309054	2.966	-	Toteratea	Dumaging	2.02	CUBN	synonymous	True	1	1	0	0.00033003	
10:374474		rs16937417	14.84	0.081	Tolerated	Tolerated	-3.17	ANKRD30A	missense	False	3	1	. 0	0.006741	
10:374517	C/T	rs41276126	0.049	-				ANKRD30A	synonymous	False]	1	. 0	0.0063877	0.00229727
10:374517	A/G	rs41276128	0.189	-				ANKRD30A	synonymous	False		1	. 0	0.0061214	0.0033318
10:374666		rs202042210	0.162	-				ANKRD30A	splice_region	False		1	. 0	0.0064772	0.00440581
10:375079	A/G	rs193176695	2.127	0.044	Tolerated	Tolerated	0.215	ANKRD30A	missense	False]	1	. 0	0.0032629	0.00034483
10:375082	G/C	rs141194244	0.005	0.023	Tolerated	Tolerated	-5.61	ANKRD30A	missense	False		1	. 0	0.0097157	
10:618197	T/G	rs201055213	20.2	-				ANK3	missense	True	3	1	. 0	0.000908	0.00022962
10:618306	T/C	rs140902380	25	0.498	Damaging	Damaging	5.48	ANK3	missense	True		1	. 0	0	0.00011481
10:618334	,	rs148904927	27.2	0.256	Damaging	Damaging	5.8	ANK3	missense	True		1	. 0	0.0055844	
10:618346	<u> </u>	rs147209108	18.88	0.116	Tolerated	Tolerated	1.14	ANK3	missense	True		1	. 0	6.48E-05	
10:618403		rs75052415	18.39	-				ANK3	synonymous	True		1	. 0	0.0004568	
10:820095		rs373346984	5.065	-				AL359195.1	5_prime_UTR	False	3	3		0.0050436	0.00327243
10:820095		rs148292259	1.938	-				AL359195.1	5_prime_UTR	False	1	3	3 2	0.0007846	0.00117005
10:820125		rs146823840	5.879	-				AL359195.1	missense	False		1	. 0	0.0025285	0.00011481
10:129904		rs146273614	6.266	0.043	Tolerated	Tolerated	-8.82	MKI67	missense	True	5	2	2 0	0.0079715	
10:129905		rs2782871	10.76	0.044	Tolerated	Tolerated	-3.42	MKI67	missense	True	1	1	. 0	0.0027919	
10:129905		rs141046519	0.913	-				MKI67	synonymous	True	1	1		0.0050571	
10:129905		rs141964620	0.001	0.015	Tolerated	Tolerated	-7.48	MKI67	missense	True		1	0	0.000584	
11:126148		rs141821939	0.03	-				MUC5B	synonymous	True	6	1	. 0	0.0005189	
11:126429		rs61997210	5.268	-	Tolerated	Tolerated	-1.97	MUC5B	missense	False	-	1	. 0	0.0071475	
11:126473		rs201750183	15.64	-	Tolerated	Tolerated	0.725	MUC5B	missense	False	-	1	. 0	7.38E-05	0.00012435
11:126763		rs375374640	0.001	-			0.44	MUC5B	synonymous	False	-	1	. 0	0.0001965	0.00023294
11:126881		rs71469871	16.1	0.08	Tolerated	Tolerated	2.61	MUC5B	missense	False	-	1	. 0	0.000561	0.00071685
11:127184	- / -	rs76174982	0.766	-	m 1 . 1	m 1 . 1	0.007	MUC5B	synonymous	True	-	1	. 0	0.0040914	0.00080869
11:127278		rs190158159	17.75	0.02	Tolerated	Tolerated	-0.336	MUC5B	missense	True	-	1	. 0	0.0003891	0 00104505
11:127643		rs55893724	5.822	-	Tolerated	Tolerated	-8.11	MUC5B	missense	False	-	1	. 2	0.0096406	0.00104505
11:127673		rs199967813	16.16	-	Tolerated	Tolerated	0.186	MUC5B TH	missense	False	4	2	0	0.0001301	0 00114063
11:218867		rs11564716	6.226	-	D .	ъ .	2.44	TH	synonymous	True	4		1	0.0081116 6.49E-05	
11:218934		rs139807727 rs76240471	9.262	-	Damaging	Damaging	3.44	TH	missense	True True	-	1	. 0	0.0033164	
11:219092 11:769401		rs11041525	15.27	0.286	T-1	T-14	4.06	CYB5R2	missense	True	3	3	1	0.0033164	
11:769401	L'	rs3903566	6.668	0.286	Tolerated	Tolerated	4.06	CYB5R2	missense 5_prime_UTR	True	3	3	1	0.0087549	0.0937069
11:403138		rs186079357	1.517	-				LRRC4C		True	4	2	1 1	0.0089622	0.0937336
11:403136		rs76244463	8.453	-	-			LRRC4C	5_prime_UTR	False	1	1	0	0.0036321	0.00390446
11:403142		rs146880928	9.598	-	 			LRRC4C	5_prime_UTR 5 prime UTR	True	1	1	2	0.0008323	0.00404214
11:403136		rs186195231	2.45	0.026	Tolerated	Tolerated	1.89	GLYATL2	missense	False	4	1	2	0.0003474	0.00126292
11:586047	<u> </u>	rs191895872	7.326	0.020	Tolerateu	roierateu	1.07	GLYATL2 GLYATL2	5_prime_UTR	False	1	1	1 0	0.0003888	
11:586121		rs187069348	0.02	-				GLYATL2 GLYATL1	5_prime_UTR	True	4	1	. 0	0.0045372	
11:587071		rs368951690	0.002	<u>-</u>	 		 	GLYATL1	splice_region	True	1	1	. 0	0.0093325	
11:567223	C/G	rs17157907	0.889	0.116	Tolerated	Tolerated	-0.175	SLC22A10.SLC22A25	missense	True	3	1	. 0	0.0001299	0.0008046
11:629320	-/	rs148517822	18.86	0.116	Tolerated	Tolerated	3.61		missense	True	 	1	1 0	6.48E-05	
11.049340	L-/ G	1314031/022	10.00	0.17/	1 olei aleu	1 oiei ateu	3.01	SECZZATU,SECZZAZS	Impsense	rrue	1	1	1 0	0.40E-03	0.00034433

											No of		Ī., .		
						FATHMM			Cognongo	in MICT		No. of	No. of variants in		
					MutationTag	MKL Coding	CERP++		Sequence Ontology	in NIST callable	iants in ACEi- A samples	variants in ACEi-A	control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)		RS	Gene Names	(Combined)	regions	A samples	samples	samples	NFE MAF	AFR MAF
11:629851	•	rs61746630	4.409	-		(5)		SLC22A10,SLC22A25	synonymous	True		1	0	0.0058328	0.00126176
11:629960	,	rs1783657	24.5	-	Damaging	Damaging	3.47	SLC22A10,SLC22A25	splice_acceptor	True	1	1	0	0.0069399	
11:629968	,	rs35722529	23.9	0.154	Tolerated	Tolerated	3.64	SLC22A10,SLC22A25	missense	True	1	1	. 0	0.0058984	
11:630648		rs77350650	15.51	0.209	Tolerated	Tolerated	1.14	SLC22A10	missense	True	3	1	. 0	0.0058351	0.0181317
11:630784	A/-	rs10718324	#N/A	#N/A				SLC22A10	frameshift	True	1	1	. 0	0.006579	0.0480125
11:774123	C/T	rs140281656	22.5	0.338	Damaging	Damaging	4.32	RSF1	missense	True	3	1	. 1	0.0060311	0.00172255
11:774127	C/T	rs141555749	0.554	0.121	Tolerated	Tolerated	-0.845	RSF1	missense	True	1	1	. 0	0.0060288	0.00137741
11:774139	G/T	rs144279798	0.265	-				RSF1	5_prime_UTR	True	1	1	. 1	0.0061214	0.00172453
11:775318	G/A	rs145506885	9.474	-				RSF1	5_prime_UTR	True		1	. 0	0.0005192	0
12:190884	A/G	rs55971855	24	-	Damaging	Damaging	4.08	CACNA2D4	missense	True	5	1	0	0.0068146	0.00091933
12:192964	C/T	rs115020705	6.211	-				CACNA2D4,LRTM2	5_prime_UTR	True		1	. 0	0.0003242	0.0137773
12:193725	C/T	rs181436784	6.221	-				CACNA2D4,LRTM2	5_prime_UTR	True		1	. 0	0.0011691	0.0002301
12:198760	C/T	rs79680317	0.378	-				CACNA2D4	missense	True		1	. 0	0.009467	0.134023
12:202769	C/T	rs184264198	0.063	-				CACNA2D4	5_prime_UTR	True		1	. 0	0.0029855	0.00057458
12:606168	C/G	rs149834874	20.4	0.135	Tolerated	Tolerated	2.2	VWF	missense	True	4	1	. 0	0.0018787	0.00034443
12:606270	,	rs61751302	4.234	0.106	Tolerated	Tolerated	-3.81	VWF	missense	True		1		0.0049255	
12:610365	·	rs61750615	26.9	0.437	Damaging	Damaging	4.91	VWF	missense	True		2	2 1	0.0066788	
\vdash	C/T	rs180837208	16.04	-				C12orf57	5_prime_UTR	True	5	1	. 0	0.0005836	0.00057366
12:705308		rs79145172	0.002	-				C12orf57	5_prime_UTR	True		2	2 1	0.009659	0.00252409
12:705312	,	rs373012829	#N/A	#N/A				C12orf57	5_prime_UTR	True		1	. 0	0.0027871	0.00068855
12:705381		rs376817694	-	-				C12orf57	frameshift	True		1	. 0	0.0024029	
12:837450	,	rs148315042	2.051	-	_	L		FAM90A1	synonymous	False	4	1	. 0	0.0016866	0.00022957
12:837508	,	rs146432845	35	-	Damaging	Tolerated	0.849	FAM90A1	stop_gained	False	-	1	1	0.0008432	0.00068855
12:837519	,	rs201524812	9.043	0.055	Tolerated	Tolerated	-1.11	FAM90A1	missense	False	-	1	. 0	0.000005	0.00091849
12:837741	,	rs147681712	1.37	0.009	Tolerated	Tolerated	-0.719	FAM90A1	missense	False	3	1	. 0	0.002085	0.00069849
12:408349	,	rs151020006	10.89 0.007	-				MUC19 MUC19	synonymous	True	3	1	. 0	0.0044736 0.0030488	
12:408541 12:408743	,	rs191493043 rs149170137	0.375	-				MUC19	missense	True True	1	1	1 1	0.0030488	0.00045924
12:406743	,	rs117275013	3.588	-				MUC19	synonymous stop_gained	True	1	1	1	0.0090827	
12:409297	,	rs200578414	23.2	0.414	Damaging	Damaging	3.18	KMT2D	<u> </u>	True	4	1	0	0.0099896	0.00232641
12:494347	,	rs201623566	16.31	0.414	Tolerated	Damaging	3.33	KMT2D	missense missense	True	1	1	0	0.0004344	0.00011303
12:494453		rs202076833	21.2	0.178	Tolerated	Damaging	3.52	KMT2D	missense	True	1	1	0	0.0014731	0.00103734
12:494456	,	rs113282510	0.179	-	Tolcraccu	Damaging	3.32	KMT2D	synonymous	True	1	1	0	0.0017074	
12:652122		rs79129123	#N/A	#N/A				TBC1D30	splice_region	True	4	2	0	0.0020447	0.0830092
12:652122	,	rs79129123	#N/A	#N/A				TBC1D30	splice_region	True	1	1	0	0.0054038	
12:652184		rs9804897	11.85	-				TBC1D30	5 prime UTR	True	1	1	1	0.0081095	0.0416283
12:652690	-, -	rs78100345	15.44	0.083	Tolerated	Tolerated	-2.06	TBC1D30	missense	True	1	1	0	0.0092785	0.00735801
12:652692	-,	rs193199722	16.36	0.099	Tolerated	Tolerated	5.32	TBC1D30	missense	True	1	1	. 0	0.0007136	
12:854502	,	rs140862066	7.895	0.036	Tolerated	Tolerated	2.77	LRRIQ1	missense	True	4	2	2 1	0.0034519	
12:854591	,	rs143253287	10.29	0.051	Tolerated	Tolerated	-2.99	LRRIQ1	missense	True	1	1	0	0.0012317	
12:854977	,	rs141856803	5.954	0.224	Tolerated	Tolerated	-3.95	LRRIQ1	missense	True	1	1	. 0	0.0064262	0.00011542
12:125608	,	rs118099322	0.503	-				AACS	5_prime_UTR	True	3	1	. 0	0.0081106	0.00160883
12:125611	A/G	rs148547406	2.802	-				AACS	5_prime_UTR	True	1	1	. 0	0.004027	0.00091806

								I			No of		Ī., .		
						E A TEXANDA				. NICT		No. of	No. of		
					MutationTag	FATHMM MKL Coding	CEDD		Sequence Ontology	in NIST	iants in ACEi-	variants in ACEi-A	variants in	mom AD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)		RS	Gene Names	(Combined)	callable regions	A samples	samples	control samples	gnomAD NFE MAF	AFR MAF
12:125612		rs151126662	0.014	-	ter rrea (e)	i i cu (c)	IKS .	AACS	5 prime UTR	True		1	o n	0.0018807	0.00011478
12:125619		rs146803379	10.09	0.072				AACS	missense	True	1	1	0	0.0010007	
12:133308	,	rs35568769	0.501	-				ANKLE2	5_prime_UTR	False	4	1	0	0.0001230	
12:133333	,	rs191525323	3.591	_				ANKLE2	5_prime_UTR	True	1	1	0	0.0004543	
12:133333		rs190915987	2.138	_	<u> </u>			ANKLE2	5_prime_UTR	True	1	1	0	0.0023343	
12:133333		rs138648071	2.56	-				ANKLE2	5_prime_UTR	False	1	1	0	6.49E-05	0.073942
13:327829		rs182574298	10.64	0.099	Damaging	Damaging	5.41	FRY	synonymous	True	3	1	0	0.0032413	
13:328283	,	rs148908035	9.011	-				FRY	splice_region	True		1	. 0	0.003046	
13:328284		rs192351218	18.51	0.047	Damaging	Damaging	3.21	FRY	missense	True	1	1	. 0	0.0030468	0.00034443
13:328358	,	rs144509680	9.036	-	Damaging	Damaging	3.93	FRY	missense	True	1	1	. 0	0.0001296	0
13:411346		rs139436481	3.366	-		0 0		FOXO1	synonymous	True	4	1	. 0	0.0061592	0.0011489
13:411347	A/G	rs45624735	9.679	-				FOXO1	synonymous	True	1	1	. 0	0.0014256	0
13:412401	C/T	rs34733279	22.9	0.27	Damaging	Damaging	3.44	FOXO1	missense	True	1	1	. 0	0.0079681	0.00426338
13:412403	G/A	rs202030645	14.46	-				FOXO1	5_prime_UTR	True		1	. 1	0.0097309	0.00254394
13:994494	G/A	rs41279128	0.213	-				DOCK9	synonymous	True	4	1	. 1	0.0058336	0.00160661
13:995546	C/T	rs142267943	0.012	-				DOCK9	synonymous	True		1	. 0	0.0062914	0.00080367
13:995824	C/T	rs199901746	24.5	0.268	Damaging	Damaging	5.68	DOCK9	missense	True]	1	. 0	0.0013615	0.00034427
13:996301	C/T	rs147408595	17.11	-				DOCK9	synonymous	True]	1	. 2	0.0082977	0.00160661
14:644456	G/A	rs117567094	7.125	-				SYNE2	synonymous	True	5	1	. 0	0.0098522	0.00172176
14:644493	C/T	rs192061494	9.636	0.227	Tolerated	Tolerated	4.13	SYNE2	missense	True		1	. 0	0.0007784	0
14:644577	C/G	rs34449017	21.4	0.119	Damaging	Damaging	6.06	SYNE2	missense	True		3	0	0.0036307	0.00022957
14:644738	A/G	rs187183308	0.341	-				SYNE2	synonymous	True		1	. 0	0.0016846	0
14:709898	-,	rs139422733	33	-	Damaging	Tolerated	-9.32	ADAM20	stop_gained	True	4	1	. 0	0.0020104	0.00057392
14:709899	T/C	rs45554935	23.8	0.18	Tolerated	Damaging	3.46	ADAM20	missense	True		1	. 1	0.0021387	0.00057419
14:709904	,	rs375968717	8.483	-				ADAM20	synonymous	True		1	. 0	6.48E-05	0
14:709911		rs144800201	12.53	-				ADAM20	synonymous	True		1	. 0	0.0005834	
14:105408		rs372622112	0.036	-				AHNAK2	synonymous	False	9	1	. 0	0.0008681	0.00035486
14:105409		rs199609161	-	-				AHNAK2	frameshift	False		1	. 0	0.0020201	0.00081075
14:105410		rs148191664	0.065	-				AHNAK2	synonymous	False		1	. 0	0.0058464	
14:105410		rs201588593	3.83	0.017	Tolerated	Tolerated	-6.54	AHNAK2	missense	False		1	. 0	0.0004554	0.00011571
14:105413	,	rs145247381	0.181	-	-			AHNAK2	synonymous	False		2	·	0.0089695	0.00165563
14:105414	,	rs191205927	0.128	-				AHNAK2	synonymous	False		2	2 0	0.0088588	
14:105415	·	rs201874096	0.03	0.08	Tolerated	Tolerated	-0.475	AHNAK2	missense	False	-	1	2	0.0004127	
14:105417	,	rs201127992	2.194	0.074	Tolerated	Tolerated	1.34	AHNAK2	missense	False		1	. 0	0.0068586	0.00298507
14:105417	·	rs2819430	0.805	-	-		-	AHNAK2	synonymous	False	-	1	0	0.0035073	
14:105417		rs143593141	2.672	0.022	T-1	T-1	F 20	AHNAK2	synonymous	False	1	1	1 1	0 0000466	
14:105417 14:105418	<i>,</i> -	rs2013232 rs181067637	0.005 1.335	0.023	Tolerated	Tolerated	-5.38	AHNAK2 AHNAK2	missense	False	-	1	1	0.0008466 0.0062346	
14:105418		rs45448397	5.74	0.048	Tolorated	Tolorated	-3.51	AHNAK2 AHNAK2	synonymous	False	1	1	. 0	0.0062346	
14:105420	,	rs45448397 rs117585192	2.08	0.048	Tolerated	Tolerated	-3.51	BRF1	missense 5 prime UTR	True True	5	1	0	0.0073911	
14:105688		rs117585192 rs117732489	7.579	-	+		-	BRF1	 -i 		-	1	. 0	0.0055109	
14:105692	,	rs139282295	10.76	-	+			BRF1,PACS2	synonymous 5 prime UTR	True True	1	7	0	0.0056479	0.00218441
14:105767		rs149060227	0.465	[1			BRF1,PACS2	5_prime_UTR	True	1	1	- 0	0.0099571	
14.103//0	1/6	1314700044/	10.403	1-	1	l	1	IDIVLT'L WOOF	19_brune_01K	Titue	1	1	1 0	0.0076033	0.00113161

!											No of combinedvar	No. of	No. of		
						FATHMM	CERR		Sequence	in NIST	iants in ACEi-	variants in	variants in		
Chr:Pos Re	lef/Alt	Identifier	cadd score	REVEL score	MutationTas ter Pred (C)	MKL Coding Pred (C)	GERP++ RS	Gene Names	Ontology (Combined)	callable regions	A samples	ACEi-A samples	control samples	gnomAD NFE MAF	gnomAD AFR MAF
14:105779 C/	., .	rs148025879	1.021	-	ter rreu (e)	Trea (e)	I C	BRF1.PACS2	5 prime UTR	True		3diffpies 1	o o	0.0096603	0.00160735
15:229257 G/		rs139395765	15.16	_				CYFIP1	5_prime_UTR	True	4	1	1	0.0090003	0.00149391
15:229391 G/	,	rs142622793	17.13	-				CYFIP1	synonymous	True	1	1	0	0.0076112	0.00068934
15:229931 C/		rs149042952	24.3	-				CYFIP1	missense	True	1	1	1	0.0098778	0.00310917
15:229977 C/		rs189070691	1.462	-				CYFIP1	splice_region	True	1	1	0	0.0013613	0
15:236865 C/	,	rs192811250	0.597	-				GOLGA6L2	synonymous	False	5	1	1 0	0.0097339	0.00172176
15:236892 A/	/G	rs117712234	18.57	0.025	Tolerated	Tolerated		GOLGA6L2	missense	False	1	1	1 0	0.0062856	0.00137709
15:236904 C/	/T	rs2344895	7.454	-				GOLGA6L2	splice_region	False	1	3	3	0.002623	0.292462
15:309187 C/	/G	rs114851315	12.01	-				ARHGAP11B	5_prime_UTR	False	3	1	0	0.0069716	0.0640166
15:310610 G/	/T	rs182387718	3.597	-				ARHGAP11B	non_coding_exon	False		1	1 0	0.002271	0.00057485
15:310610 C/	/T	rs186792445	2.189	-				ARHGAP11B	non_coding_exon	False		1	0	0.0084689	0.00176762
15:310617 T/	'/C	rs2339018	3.448	-				ARHGAP11B	non_coding_exon	False		1	0	0.0020104	0.00103353
15:419620 C/	/G	rs182187974	16.02	0.411	Tolerated	Damaging	4.69	MGA	missense	True	4	3	0	0.005771	0.00206754
15:419890 G/	C/C	rs191457035	4.502	0.049	Tolerated	Tolerated	-3.05	MGA	missense	True		1	0	6.48E-05	0.00011471
15:759689 C/	/T	rs117177957	15.05	0.03	Tolerated	Tolerated	0.605	CSPG4	missense	True	4	1	1 0	0.0035719	0.00068997
15:759820 G/	i/A	rs77681934	22.7	0.146	Damaging	Damaging	5.26	CSPG4	missense	False		1	1 0	0.0050868	0.0105968
15:759820 C/	/T	rs79463888	24.3	0.258	Damaging	Damaging	5.26	CSPG4	missense	False		3	3 1	0.006748	0.00199063
15:759854 A/	,	rs112660485	28.1	0.837	Damaging	Damaging	4.78	CSPG4	missense	False		1	1	0.0090873	0.109759
15:860871 C/	/G	rs146115074	24.5	0.16	Tolerated	Damaging	4.71	AKAP13	missense	True	5	1	0	0.0007134	0.00034451
15:861237 A/	/T	rs114705815	3.035	0.019	Tolerated	Tolerated	1.28	AKAP13	missense	True		1	0	0.0077811	0.00080349
15:861248 G/	,	rs115468498	5.473	-				AKAP13	synonymous	True		1	0	0.0085581	0.00114916
15:862623 G/	<i>'</i>	rs79991499	0.405	-				AKAP13	synonymous	True		2	2 0	0.0032438	0.00045945
15:862867 G/		rs147284419	23.5	0.199	Damaging	Damaging	3.84	AKAP13	missense	True		1	1 0	6.48E-05	0
16:334763 C/		rs200501001	14.06	0.04	Tolerated	Tolerated	1.26	PDIA2	missense	True	4	1	1 0	0.0008438	
16:335185 G/	,	rs45503892	0.617	-				PDIA2	synonymous	False	1	1	1 1	0.0066148	
16:336730 C/		rs118177911	3.915	-				PDIA2	synonymous	False		1	1 0	0.0042142	0.00229568
16:336731 G/	,	rs116969376	22.5	0.061	Tolerated	Tolerated	3.41	PDIA2	missense	False		1	2	0.0058351	0.00126205
16:124550 G/		rs60593994	23	0.589	Tolerated	Damaging	2.7	CACNA1H	missense	True	6	1	0	0.0064252	0.00046062
16:125026 A/		rs200520956	20.3	0.222	Tolerated	Damaging	0.875	CACNA1H	missense	True	-	1	0	0.0005838	0
16:125702 C/	,	rs372701359	6.574	-				CACNA1H	synonymous	True	-	1	0	0.0001302	0
16:125733 C/		rs59090452	15.27	-	m 1 . 1	<u> </u>	0.00	CACNA1H	synonymous	True	-	1	0	0.0044782	0.00022989
16:125803 G/		rs41292285	20.3	0.309	Tolerated	Damaging	3.02	CACNA1H	missense	True	-	1	2	0.0075935	0.00126466
16:125929 C/		rs61319429	8.687	0.172	Tolerated	Tolerated	1.31	CACNA1H	missense	True	-	1	0	0.0011032	0.00023031
16:126825 C/ 16:214742 C/	,	rs60218977 rs140189010	17.64 14.19	0.067	Tolorated	Tolerated	2.21	CACNA1H PKD1	synonymous	True False	6	1	0	0.0067427 0.0054482	0.00068839
16:214742 C/ 16:215334 C/		rs140189010 rs147788838	14.19	0.067	Tolerated		3.95	PKD1	missense	False	l°	1	0	0.0034482	
16:215334 C/		rs149151043	23.5	0.165	Damaging	Damaging Damaging	3.59	PKD1	missense	False	1	1	1 0	0.0020099	0.00114863
16:215361 C/	,	rs149151043	15.08	0.099	Tolerated Tolerated	Damaging Damaging	3.24	PKD1	missense missense	False	1	1	1 0	0.0075895	
16:215385 G/		rs150568356	7.389	0.099	Tolerated	Tolerated	1.17	PKD1	missense	False	1	1	1 0	0.0013216	
16:215365 G/	,	rs148496347	20.6	0.101	Tolerated	Damaging	2.27	PKD1	missense	False		1	1 0	0.0014499	0.00033104
16:216060 A/		rs143843155	9.652	-	1 olei ateu	Damaging	4.47	PKD1	synonymous	False	1	1	0	0.0014931	0.00034307
16:216104 G/	,	rs373088132	9.772	_				PKD1	synonymous	False	1	1	0	0.000303	0.00011492
16:216245 C/		rs148727945	7.421	-				PKD1	synonymous	False	1	1	0	0.0018804	

		ı	1	1	1	ı	1	I	1	ī	No of		1	1	1
												No. of	No. of		
						FATHMM			Sequence	in NIST	iants in ACEi-	variants in	variants in		
					MutationTas	MKL Coding	GERP++		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)	Pred (C)	RS	Gene Names	(Combined)	regions	P-55	samples	samples	NFE MAF	AFR MAF
16:251013	A/G	rs373669956	14.64	-				C16orf59	5_prime_UTR	True	4	1	. 0	0.0058808	0.00185443
16:251104	C/T	rs200526529	7.413	-	Tolerated	Tolerated	0.207	C16orf59	missense	True	1	1	. 0	0.0026592	0.00057379
16:251111	G/A	rs199831316	4.127	-	Tolerated	Tolerated	-2.78	C16orf59	5_prime_UTR_pre	True	1	1	. 1	0.0054496	0.00057392
16:251417	G/A	rs200856167	3.949	-				C16orf59	synonymous	True	1	1	. 0	0.0012327	0.00045935
16:494092	G/A	rs375408619	0.243	-				PPL	splice_region	True	3	1	. 0	0.0021431	0.00022989
16:494188	G/A	rs79367056	0.019	-				PPL	synonymous	True		1	. 1	0.0041532	0.0012635
16:494323	C/T	rs139608681	21.2	0.314	Damaging	Damaging	4.1	PPL	missense	True		1	. 0	0.0017517	0.00011489
16:496085	C/G	rs142778222	11.51	0.04	Tolerated	Tolerated	1.74	PPL	missense	True		1	0	0.0015558	0.0003442
16:158026	G/T	rs111588143	15.28	-	Damaging	Damaging	2.08,2.08	MYH11,NDE1	missense	True	5	1	. 0	0.0018224	0.00988733
16:158088	C/G	rs113964173	24.3	0.562	Damaging	Damaging	1.09	MYH11,NDE1	missense	True		1	. 0	0.0051226	0.00321396
16:158089	C/T	rs150860193	18.99	-				MYH11,NDE1	synonymous	True		1	. 2	6.48E-05	0
16:158110	C/G	rs145252402	23.3	0.586	Damaging	Damaging	3.32	MYH11,NDE1	missense	True		1	. 0	0.0005833	0.00022957
16:158152	T/C	rs143288748	19.25	-				MYH11,NDE1	splice_region	True		1	. 0	0.0031116	0.00045893
16:576732	G/A	rs149097498	17.6	-				GPR56	5_prime_UTR	True	3	1	. 0	0.0029835	0.00103353
16:576739	C/T	rs141939880	1.498	-				GPR56	5_prime_UTR	True		1	. 2	0.0097302	0.00183613
16:576740	C/T	rs185069695	0.444	-				GPR56	5_prime_UTR	True		1	. 0	0.0010375	0.00022973
16:576808	C/T	rs118109420	0.678	-				GPR56	5_prime_UTR	True		1	. 2	0.0092701	0.0018395
	C/T	rs201745158	11	-				RLTPR	synonymous	True	3	1	. 0	0.0020096	0.00022952
16:676857		rs62059341	25.8	0.22	Damaging	Tolerated	5.37	RLTPR	missense	True		1	. 1	0.0072642	0.00068871
16:676862		rs144268948	-	-				RLTPR	inframe_deletion	True		1	. 1	0.0052529	
16:676880		rs114594028	9.984	-				RLTPR	synonymous	True		1	. 1	0.0053213	0.0364169
16:708891		rs375384248	19.03	-				HYDIN	synonymous	False	5	1	. 1	0.0062011	
16:708940	, -	rs149857179	26.2	-	Damaging	Damaging	5.51	HYDIN	missense	False		4	0	0.0014681	0.00306577
16:710090		rs201855097	7.981	-	Tolerated	Tolerated	-0.89	HYDIN	missense	False		1	. 0	0.0015368	0.0105263
16:710541	, -	rs183427172	9.144	0.088	Tolerated	Tolerated	-9.21	HYDIN	missense	False		1	. 0	0.0040867	0.00080331
16:710616		rs201092966	2.195	-				HYDIN	synonymous	False		1	. 0	0.0006802	
16:844420		rs78371901	0.93	0.333	Damaging	Tolerated	-0.135	ATP2C2	missense	True	6	1	. 1	0.0027919	
16:844822		rs62640930	0.443	-	<u> </u>			ATP2C2	synonymous	True		1	. 0	0.0029164	
16:844868		rs375405912	9.61	0.198	Tolerated	Tolerated	-0.845	ATP2C2	missense	True		1		0.0002596	
16:844943		rs62050917	1.431	0.287	Tolerated	Tolerated	-10.8	ATP2C2	missense	True		2	2 1	0.0090119	
16:844953		rs4782970	33	-	Damaging	Damaging	5.28	ATP2C2	splice_acceptor	True	-	1	. 0	0.0095967	0.00137931
16:844956		rs189686158	0.015	-				ATP2C2	synonymous	True	4	1	. 0	0.0001297	0.0265517
16:856450		rs375671352	4.188	-				GSE1	5_prime_UTR	True	4	1	. 0	0.0091773	0.00092251
16:856884		rs147629403	2.518	-				GSE1	synonymous	True		1	. 2	0.0076023	0.00195943
16:856901		rs371328519	0.305				5.40	GSE1	synonymous	True	-	1	. 0	0.000454	0.00034443
16:856966		rs61751198	33	0.45	Damaging	Damaging	5.48	GSE1	missense	True	2	1	0	0.006876	0.00137931
17:104040	,	rs61730794	25.1	0.796	Damaging	Damaging	5.45	MYH1	missense	True	3	1	0	0.0012963	0.00034459
17:104091		rs149164396	24.3	0.753	Damaging	Damaging	5.47	MYH1	missense	True	-	1	0	0.0032396	0 00161252
17:104112	•	rs150346984	23.4	0.342	Damaging	Tolerated	5.45	MYH1	missense	True	-	1	0	0.0053427	
17:104174		rs144345763	24.3	0.619	Damaging	Damaging	4.21	MYH1	missense	True	4	1	0	0.0012958	
17:104246 17:104290	,	rs34161789 rs61739663	29.4 1.318	-	Damaging	Damaging	5.55	MYH2 MYH2	missense	True	· ·	1	0	0.0062865 0.0045372	0.00137741
			24	0.693	Damaging	Damaging	5.15	MYH2 MYH2	synonymous	True	1	1	1 0	0.0045372	0.00436481
17:104331	L/ I	rs143872329	144	0.093	Damaging	Damaging	19.19	IVI 1 П 2	missense	True	j		1 0	0.006/436	0.00195178

		1		I	I		1			1	No of				
												No. of	No. of		
						FATHMM			Sequence	in NIST	iants in ACEi-	variants in	variants in		
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	mutationTas ter Pred (C)	MKL Coding	RS RERP++	Gene Names	Ontology (Combined)	callable regions	A samples	ACEi-A samples	control samples	gnomAD NFE MAF	gnomAD AFR MAF
17:104509		rs373848425	8.412	REVEL SCOTE	ter Freu (C)	Fieu (c)	IN3	MYH2	5 prime UTR	True		samples	Samples	0.0001297	0.00011478
17:104309	,	rs140218185	23.2	0.298	Tolerated	Tolerated	4.37	MYH3	missense	True	3	1	0	0.0001297	
17:105367	,	rs140074626	24	0.278	Damaging	Damaging	5.36	MYH3	missense	True		1	0	0.0010044	
17:105414		rs61735358	20.2	0.386	Damaging	Damaging	5.45	МҮНЗ	missense	True	1	1	0	0.0093519	
17:105416		rs145785711	27.4	0.631	Damaging	Damaging	5.45	мүнз	missense	True	1	1	0	0.0005189	
17:177181		rs45567732	14.42	-				SREBF1	splice_region	True	3	1	. 0	0.0028553	0.0280073
17:177199		rs7214136	16.2	0.01	Tolerated	Tolerated	2.36	SREBF1	missense	False	1	1	. 0	0.0012985	0.0607143
17:177203		rs2229591	16.1	-				SREBF1	synonymous	False	1	1	. 0	0.0011678	0.199171
17:177231	G/C	rs56174147	6.763	-				SREBF1	5_prime_UTR	True	1	1	. 0	0.0053143	0.00034459
17:180252	C/G	rs77565048	4.768	-	Tolerated	Tolerated	2.52	MYO15A	missense	True	3	1	. 0	0.0041553	0.0164255
17:180255	A/G	rs76468019	1.042	-	Tolerated	Tolerated	-3.48	MYO15A	missense	True	1	1	. 0	0.0016206	0.049299
17:180390	C/T	rs114328138	0.4	-				MYO15A	synonymous	True		1	. 0	0.0049261	0.0531451
17:180478	G/A	rs55688805	19.4	-				MYO15A	synonymous	True	1	1	. 0	0.0088892	0.00034475
17:180514	C/T	rs121908970	19.2	-	Damaging	Damaging	3.11	MYO15A	missense	True		1	. 0	0.0068129	0.00080423
17:180521	G/A	rs114274755	25.3	-	Damaging	Damaging	4.26	MYO15A	missense	True	1	1	. 0	0.0031777	0.0212644
17:181417	A/G	rs140298639	23.9	0.202	Damaging	Damaging	4.45	LLGL1	missense	True	3	1	. 0	0.0025282	0.00080423
17:181418	G/A	rs111836247	21	0.049	Tolerated	Damaging	4.54	LLGL1	missense	True		1	. 0	0.0017503	0.0516211
17:181418	C/T	rs72831933	5.269	-				LLGL1	synonymous	True		1	. 0	0.0088163	0.00034459
17:181440	C/T	rs112697370	6.025	-				LLGL1	synonymous	True		1	. 0	0.001817	0.0563105
17:181447	C/T	rs376243078	10.69	-				LLGL1	synonymous	True		1	. 0	6.49E-05	0
17:615545	G/C	rs1110991	13.19	-				ACE	synonymous	True	4	1	. 0	0.0013985	0.00023585
17:615549	G/C	rs7211207	7.062	-	Tolerated	Tolerated	1.96	ACE	missense	True		1	. 0	0.0014358	0.268678
17:615589	G/T	rs118145880	18.26	-				ACE	synonymous	True		1	. 0	0.0092088	0.00229674
17:615626	C/G	rs147429960	23.6	0.142	Tolerated	Damaging	2.87	ACE	5_prime_UTR_pre	True		1	. 0	0.0014293	0.00023026
17:615660	A/G	rs117647476	15.49	0.046	Damaging	Damaging	1.37	ACE	missense	False		1	. 1	0.005324	0.00080478
17:780554	C/G	rs191736683	9.465	0.021	Tolerated	Tolerated	-2.75	CCDC40	missense	False	4	1	. 0	0.0028509	
17:780640		rs374493149	10.56	-				CCDC40	synonymous	False		1	. 0	0.0031524	
17:780641		rs190696966	3.482	0.05	Tolerated	Tolerated		CCDC40	missense	False		2		0.0055934	0.00186567
17:780641		rs62075573	6.939	-				CCDC40	synonymous	False		2	1	0.0010442	0.00026076
17:780641		rs62075574	6.876	0.015	Tolerated	Tolerated		CCDC40	missense	False		2	2 1	0.0009775	0.00031095
17:780641		rs62075575	4.543	0.068	Tolerated	Tolerated		CCDC40	missense	False		2	1	0.0010213	0.000344
17:780641	,	rs60807430	-	-				CCDC40	frameshift	False		2	1 1	0.001396	0.00043215
17:780641	,	rs56241848	9.161	-	Tolerated	Tolerated		CCDC40	stop_lost	False		2	2 1	0.0013799	0.00037509
17:783060		rs139471994	0.156	-				RNF213	synonymous	True	3	1	. 0	0.003565	0.00022967
17:783132		rs147868237	23.7	0.171	Damaging	Damaging	4.76	RNF213	missense	True		1	. 0	0.0060311	0.00183739
17:783191		rs138044665	3.608	0.017	Tolerated	Tolerated	-1.85	RNF213	missense	True		1	. 1	0.0011664	0.00045924
17:783468		rs141329059	23.8	-	Damaging	Damaging	5.5	RNF213	missense	True		1	. 0	0.0042202	0.00080478
17:802872		rs185560154	3.057	-				SECTM1	5_prime_UTR	True	4	3	0	0.0099935	0.0021829
17:802873	,	rs373514410	0.423	-				SECTM1	5_prime_UTR	True		1	. 1	0.0033722	0.00080404
18:597131		rs201397391	14.11	0.021	Tolerated	Damaging	4.31	PIGN	missense	False	3	1	0	0.0023973	0.00022957
18:597683	, -	rs3764491	3.947	-				PIGN	synonymous	True		1	. 0	0.0008433	0
18:597742		rs147306123	6.691	-				PIGN	synonymous	True		1	. 0	0.0047959	
18:598296	T/C	rs17069514	4.88	-				PIGN	5_prime_UTR	True		1	. 0	0.0034393	0.00252699

						FATHMM			Sequence	in NIST	No of combinedvar iants in ACEi-	No. of variants in	No. of variants in		
			l		1	MKL Coding	1		Ontology	callable	A samples	ACEi-A	control	gnomAD	gnomAD
	Ref/Alt	Identifier	cadd score	REVEL score	· · · ·	Pred (C)	RS	Gene Names	(Combined)	regions	2	samples	samples	NFE MAF	AFR MAF
18:778935	/	rs78503084	18.56	0.347	Tolerated	Damaging	0.754	ADNP2	missense	True	- ³	1	2	0.0083593	0.00149185
18:778948		rs138162057	9.399	0.013	Tolerated	Tolerated	1.86	ADNP2	missense	True	_	2	2 0	0.0007000	
18:778962	-	rs75868400	21	0.124	Tolerated	Damaging	3.82	ADNP2	missense	True	2]	4	0.0079118	
19:489372	-	rs115452748	3.865	-				MADCAM1	5_prime_UTR	True	3	2	2 2	0.0052586	0.104447
19:489381	<u> </u>	rs116120082	6.468	-				MADCAM1	5_prime_UTR	True	-		2 2	0.001107	0.0878354
19:504830	- '	rs7246543	5.32	-		-		MADCAM1	synonymous	True	4		. 0	0.000150	0.0009223
19:373900	C/T	rs56138006	0.275	0.542	Di	D	4.60	TJP3	synonymous	True	- *		2 0	0.0023995	
19:374394	 	rs150181963	26 22.4	0.542	Damaging	Damaging	4.68	TJP3	missense	True	-		3	0.0038232 0.0070743	0.00080386
19:374649 19:815113	-	rs148817261 rs144887983	21.1	0.516	Damaging	Damaging Tolerated	-0.493 2.17	TJP3 FBN3	missense	True True	E	1	. 3	1	0.0014946
19:817106	-7	rs151274163	0.004	0.316	Damaging Tolerated	Tolerated	-0.849	FBN3	missense	True	- 3		0		
19:817106	/	rs1512/4163 rs143694434	4.616	0.301	i oiei ateu	roierated	-0.049	FBN3	missense synonymous	True	1	- 1	0		
19:817424	-/	rs139062839	0.007	-				FBN3	synonymous	True	-		. 0	0.0028542	0.00022978
19:820684		rs138635091	22	0.277	Damaging	Damaging	3.95	FBN3	missense	True	-		0		
19:820684	-	rs35525553	20.8	0.277	Tolerated	Damaging	0.677	FBN3	missense	True	-		0	+	
19:820985	-	rs117724347	17.68	0.233	Damaging	Damaging	-1.12	FBN3	missense	True	-	<u> </u>	0	<u> </u>	
19:897398	-	rs61745929	16.79	0.233	Tolerated	Tolerated	2.36	MUC16	missense	True	6	1	0		0.00172293
19:901816	-	rs202157654	3.306	0.043	Tolerated	Tolerated	-3.72	MUC16	missense	False	ď	<u> </u>	0	0.0044741	0.00011474
19:905779	-	rs143428939	0.026	-	Tolerateu	Tolerateu	-3.72	MUC16	synonymous	True	1	<u> </u>	0	0.0040187	0.00037311
19:906043	T/A	rs202027296	4.167	0.017	Tolerated	Tolerated	-1.04	MUC16	missense	True	1	<u> </u>	0	0.0031047	
19:906600	+'	rs151074528	6.062	0.032	Tolerated	Tolerated	0.412	MUC16	missense	True	1		0	0.0011310	
19:906793	-	rs200919021	16.62	0.035	Tolerated	Tolerated	0.77	MUC16	missense	True	1	1	0	0.0046086	
19:906849	-	rs113113198	0.007	-	Toleracea	Toteratea	0.77	MUC16	synonymous	True	1	1	0	†	!
19:128658	-	rs17706412	7.642	-				BEST2	synonymous	True	4	1	0	+	
19:128662	-/	rs112425354	6.246	-				BEST2	synonymous	True		1	1	0.0064851	0.00114863
19:128667	-/	rs137957583	9.041	-				BEST2	synonymous	True		1	0	0.0041505	
19:128688	-/	rs149797899	23.3	0.28	Damaging	Damaging	3.84	BEST2	missense	True	1	1	1	0.0087731	
19:150878	-	rs151268318	-	-				SLC1A6	splice_region	True	4	2	2 0	0.0054408	
19:150879	C/G	rs138883153	4.302	-				SLC1A6	5 prime UTR	True	1	2	2 0	0.0062979	0.00103472
19:154831	G/A	rs45479794	25.1	0.302	Damaging	Damaging	5.44	AKAP8	missense	True	4	1	. 0	0.0086263	0.00206517
19:154838	-	rs200383217	25.1	0.238	Damaging	Damaging	5.24	AKAP8	missense	True	1	1	. 0	0.0046711	0.00160957
19:154839	C/T	rs111389458	24.5	0.26	Damaging	Damaging	5.06	AKAP8	missense	True		1	. 0	0.0094095	0.00195492
19:154848	G/A	rs139511255	0.262	-				AKAP8	synonymous	True	1	1	. 0	t	0
19:403662		rs4029191	8.652	-				FCGBP	synonymous	True	6	1	. 1	0.0084955	0.00322432
19:403664	G/C	rs4029187	8.693	0.13	Tolerated	Tolerated	3.27	FCGBP	missense	True	1	2	2 0	0.0080509	0.0436691
19:403847	G/A	rs200692665	1.032	-				FCGBP	synonymous	False	1	2	. 1	0.004065	0
19:403959	G/A	rs150431034	3.342	-				FCGBP	synonymous	False		1	. 0	0.0023714	0.00061185
19:404060	<u> </u>	rs141349208	-	-				FCGBP	missense	False	1	1	. 1	0.0079626	0.00208092
19:428538	A/G	rs151116615	22.3	0.069	Damaging	Damaging	3.47	MEGF8	missense	True	3	1	. 0	0.0001949	0.00023031
19:428610	C/T	rs149279834	1.109	-				MEGF8	synonymous	True		1	. 1	0.0076534	0.00184077
19:428798	G/A	rs45623135	30	0.277	Damaging	Damaging	4.92	MEGF8	missense	True		1	. 0	0.0040286	0.00207517
19:428800	G/A	rs147133204	23.2	0.091	Damaging	Damaging	5.11	MEGF8	missense	True		1	. 0	0.0036293	0.00137931
19:495272	C/G	rs201342765	6.718	-				CGB,CTB-60B18.6	5_prime_UTR	False	4	2	2 0	0.00578	0.146181

					1				I		No of				
											combinedvar		No. of		
					MutationTag	FATHMM MKL Coding	CEDD		Sequence Ontology	in NIST callable	iants in ACEi-	variants in ACEi-A	variants in control	gnomAD	gnomAD
Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	ter Pred (C)		RS	Gene Names	(Combined)	regions	A samples	samples	samples	NFE MAF	AFR MAF
19:495274	,	rs369610551	6.899	-	(6)	1100 (0)	1.0	CGB,CTB-60B18.6	5 prime UTR	False		2	2 0	0.0041054	0.0733908
19:495354		rs143465240	1.646	-				CGB2,CTB-60B18.6	5 prime UTR	False	1	1	0	0.0080405	
19:495357		rs144929524	24.2	-	Damaging	Damaging	2.45	CGB2,CTB-60B18.6	missense	False	1	1	0	0.0064407	0.00228916
19:495358	C/G	rs369311910	23.1	-	Tolerated	Damaging	0.624	CGB2,CTB-60B18.6	missense	False	1	1	. 0	0.0082146	0.00271223
19:501541	G/A	rs151252460	22.6	0.071	Tolerated	Damaging	3.36	SCAF1	missense	True	3	1	. 0	0.0044526	0.00069784
19:501544	G/C	rs142052897	0.914	-	Tolerated	Tolerated	1.53	SCAF1	missense	True	1	1	. 0	0.0048739	0.00218692
19:501560	C/T	rs375947171	10.62	0.037	Tolerated	Tolerated	-1.66	SCAF1	missense	True]	1	. 0	0	0
19:501569	C/G	rs201476531	8.124	-				SCAF1	synonymous	True		1	. 0	0.0018151	0.00057405
19:518578	-/CCACAG	rs61361626	-	-				CTD-2616J11.11,ETFB	inframe_insertion	False	3	1	. 1	0.0053157	0.245442
19:518585	T/C	rs10419235	8.462	-				CTD-2616J11.11,ETFB	5_prime_UTR_pre	True		1	. 0	0.0011015	0.13259
19:518593	T/A	rs34601865	3.039	-				CTD-2616J11.11,ETFB	5_prime_UTR	True		1	1	0.0072492	0.313792
19:518598	C/T	rs11881186	3.741	-				CTD-2616J11.11,ETFB	5_prime_UTR	True		1	1	0.0068076	0.316521
19:518696	C/G	rs202118581	9.111	-				CTD-2616J11.11,ETFB	5_prime_UTR	False		2	2 0	0.0062938	0.00103425
19:547233	C/T	rs183638655	1.369	-	Tolerated	Tolerated	1.63	LILRA6,LILRB3,RPS9	missense	True	4	1	. 0	0.0088232	0.00080478
19:547263	C/T	rs200199363	0.001	-				LILRA6,LILRB3,RPS9	missense	False]	1	. 0	0	0.0162242
19:547447	G/C	rs201564548	17.73	0.034	Tolerated	Tolerated	-0.37	LILRA6,LILRB3,RPS9	missense	False		1	. 0	0.0024017	0.00034427
19:547466	C/T	rs181003692	8.126	-				LILRA6,RPS9	5_prime_UTR	False]	1	. 0	0.0025005	0.029196
19:547466	C/G	rs201578311	7.149	-				LILRA6,RPS9	5_prime_UTR	False		2	2 0	0.0034568	0.00043821
19:548481	C/T	rs141881690	0.102	0.028	Tolerated	Tolerated	-4.8	LILRA4	missense	True	5	1	. 0	0.0005207	0.00023202
19:548481		rs138326444	17.91	0.049				LILRA4	synonymous	True		1	. 0	0	0.00023256
19:548481	_	rs76665615	17.5	0.016	Tolerated	Tolerated	1.37	LILRA4	missense	True		1	. 0	0.0073789	
19:548487	<u> </u>	rs117434371	1.299	-				LILRA4	synonymous	True		1	. 1	0.0071429	
19:548487	,	rs150520656	5.187	-				LILRA4	synonymous	True		1	. 0	0.0033095	
19:548488		rs145556773	2.706	0.023	Tolerated	Tolerated	-5.02	LILRA4	missense	True		1	. 0	0.0051914	
19:548488		rs147736844	0.407	-				LILRA4	synonymous	True		1	. 0	0.0087013	
19:567330		rs202145068	0.016	-				ZSCAN5A	synonymous	True	5	1	. 0	0	0.00011471
19:567333	,	rs61736533	6.313	0.072	Tolerated	Tolerated	-3.68	ZSCAN5A	missense	True		1	. 2	0.0075178	
19:567555		rs61741090	0.226	-				ZSCAN5A,ZSCAN5D	synonymous	True		1	. 0	0.0066156	
19:567555		rs202218184	1.135	-	Tolerated	Tolerated	-0.858	ZSCAN5A,ZSCAN5D	missense	True		1	. 0	0.0066208	
19:567555		rs139065000	1.264	-	Tolerated	Tolerated	-1.12	ZSCAN5A,ZSCAN5D	missense	True		1	. 0	0.0035033	0.0008046
19:567585		rs375603262	0.358	-	Tolerated	Tolerated	0.702	ZSCAN5A,ZSCAN5D	missense	True		1	. 0	0.0002595	0
19:568262		rs145176985	6.886	-				ZSCAN5A	5_prime_UTR	True		1	. 0	0.0092749	
19:579316		rs201024371	0.058	0.008	Tolerated	Tolerated	-2.08	AC004076.7,ZNF17	missense	True	6	1	1 0	0.0003246	
19:579322		rs80002670	8.581	-				AC004076.7,ZNF17	synonymous	True		1	. 0	0.0046662	
19:579533		rs371417061	4.491	-				AC004076.9,ZNF749	splice_region	True		1	. 0	0.0009725	
19:579567	_	rs59258956	-	-		, .	0.50	AC004076.9,ZNF749	frameshift	True		1	0	0.0092208	
19:579871		rs73067111	36	-	Damaging	Damaging	3.52	AC004076.9,ZNF772	stop_gained	True		2	1	0.0068111	0.00057511
19:579887		rs192378379	8.75	-				AC004076.9,ZNF772	5_prime_UTR	True		1	0	0.0064186	
19:579888	/ -	rs115722058	10.45	0.054	T-1 1	T-1/ 1	0.215	AC004076.9,ZNF772	5_prime_UTR	True	4	1	0	0.006544	0.0564238
19:584202		rs147695123	22.9	0.054	Tolerated	Tolerated	-0.315	 	missense	False	4	1	0	0.0001296	
19:584212	<u> </u>	rs202002558	4.125	0.014	Tolerated	Tolerated	-2.84		missense	False		1	1	0.000821	0.00014397
19:584277		rs146519620	9.489	0.012	Tolerated	Tolerated	-0.389	CTD-2583A14.9,ZNF4		False		1	0	0.0080332	0.0021794
19:584279	L/A	rs181964445	4.962	l-			l	CTD-2583A14.9,ZNF4	5_prime_UTR	False		1	. [0	0.0073262	0.00126205

Chr:Pos I	Ref/Alt	Identifier	cadd score	REVEL score	MutationTas ter Pred (C)	FATHMM MKL Coding Pred (C)	GERP++ RS	Gene Names	Sequence Ontology (Combined)	in NIST callable regions	No of combinedvar iants in ACEi- A samples	No. of variants in ACEi-A samples	No. of variants in control samples	gnomAD NFE MAF	gnomAD AFR MAF
20:256617 (C/T	rs146492837	8.941	-	, ,			C20orf96	synonymous	True	4	1	. 0	0.0010369	0.00045924
20:271226 -	-/TTTTTA	rs3835237	-	-				C20orf96	splice_region	False	1	2	: 0	0.0068663	0.0340694
20:271336	A/G	rs77667040	8.506	-				C20orf96	5_prime_UTR	True	1	1	. 0	0.0004627	0.16261
20:271341	A/G	rs79138518	8.73	-				C20orf96	5_prime_UTR	True	1	1	. 0	0.0002638	0.118322
20:307296	G/A	rs117822199	22.7	0.061	Damaging	Damaging	3.56	TM9SF4	missense	True	4	3	0	0.0083603	0.00195223
20:307296	G/A	rs145247877	25.8	0.206	Damaging	Damaging	4.99	TM9SF4	missense	True		1	. 0	0.0001947	0
20:335703	C/T	rs145840864	10.9	-				МҮН7В	synonymous	True	3	1	. 0	0.002802	0.0009206
20:335754	C/T	rs200232362	21.4	0.297	Damaging	Damaging	3.53	МҮН7В	missense	True		1	. 0	0.0005191	0.00045945
20:335811	G/A	rs187028260	32	0.654	Damaging	Damaging	4.61	МҮН7В	missense	True		1	. 0	0.0062257	0.00057419
20:335849	C/T	rs374030911	1.447	-				МҮН7В	splice_region	True		1	. 0	0.0003903	0.00011508
20:335853	T/A	rs372086755	28.5	-	Damaging	Damaging	4.73	МҮН7В	missense	True		1	. 0	6.51E-05	0
20:608935	C/T	rs370777806	9.571	-				LAMA5	synonymous	True	4	1	. 0	0.0001334	0
20:608936	C/T	rs111653839	17.78	0.079	Tolerated	Tolerated	2.93	LAMA5	missense	True		1	. 0	0.0076511	0.00128355
20:608936	C/T	rs147290767	19.57	0.118	Damaging	Tolerated	1.46	LAMA5	missense	True		1	. 0	0.0037304	0.00058059
20:608939 (C/T	rs141245936	12.46	0.021	Tolerated	Tolerated	2.3	LAMA5	missense	True		1	. 0	0.0092292	0.00357885
20:608971	C/A	rs143066016	20.3	0.089	Tolerated	Damaging	2.78	LAMA5	missense	True		1	. 0	0.0024743	0.00011569
20:609084 (G/A	rs140927746	22.5	0.138	Damaging	Damaging	4.74	LAMA5	missense	True		1	. 0	0.0029213	0.00023026
21:4694587	T/A	rs202114789	26.6	0.838	Damaging	Damaging	4.51	SLC19A1	missense	True	4	1	. 0	6.48E-05	0
21:469506 (G/T	rs61338739	5.359	-				SLC19A1	splice_region	False		1	. 0	0.0030516	0.0003457
21:469514 (G/A	rs9282853	5.926	-				SLC19A1	synonymous	False		1	. 0	0.0037032	0.00023068
21:469564 (•	rs114130583	1.08	-				SLC19A1	splice_region	False		1	. 0	0.0000707	
21:478171 (rs199661615	8.967	0.026	Tolerated	Tolerated	-4.01	PCNT	missense	True	5	1	. 0	0.102 00	+
21:478172 (,	rs62224222	23.5	0.143	Tolerated	Damaging	3.31	PCNT	missense	True		2	1	0.0068085	
21:478173 (rs143796569	22.5	0.227	Tolerated	Damaging	5.46	PCNT	missense	True	4	1	. 0	0.000	
21:478458 (/ -	rs148384323	7.826	0.01	Tolerated	Tolerated	-0.351	PCNT	missense	True	4	1	. 0	0.0007733	
	C/T	rs150615481	2.706	0.022	Tolerated	Tolerated	-3.38	PCNT	missense	True	1.	1	. 0	0.000710	
-	A/C	rs376835455	5.379	-				AC008132.13	missense	False	4	2			
22:188471		rs374135010	-	-				AC008132.13	non_coding_exon	False	4	1	. 0		0.00170455
22:188480 7	,	rs370657728	1.365	-				AC008132.13	non_coding_exon	False	14	2	1	0.0041909	
	C/T	rs71312751	1.135	-				FAM230A,USP41	synonymous	False	- 4	1	. 1	0.0028728	0.00016234
22:207100 (rs111322070	7.757	-				FAM230A,USP41	synonymous	False	-	1	. 0	0.000121	0
22:207108 (,	rs74959292	8.278	-				FAM230A,USP41	missense	False	-	1	. 1	0.0093043	0.00184599
22:207108 (rs79754221	4.504	 -	-			FAM230A,USP41	missense	False	-	1	. 1	0.0084154	
22:207109 (rs182183609 rs369187745	7.355	-				FAM230A,USP41 OSBP2	synonymous	False	4	1	. 0		
22:311373 (,		9.497	-	-				synonymous	True	- 4	7			
22:311665 (,	rs189284083	7.237	-	-			OSBP2	splice_region	True	-		1 0	0.0090838	
22:312842 7	,	rs76606996 rs79945262	8.389 3.221	-	-			OSBP2 NOL12.TRIOBP	synonymous	True False	4.	1	1 1	0.0038885 0.0084444	
22:381203 (-/	rs202079450	11.01	1-	Tolorated	Tolerated	0.0434	NOL12,TRIOBP	1-7 - 7	False	- *	- I	1	0.0084444	
22:381206 /	,	rs199594270	0.334	-	Tolerated	Tolerated	0.0434	NOL12,TRIOBP	missense synonymous	True	┨	1	. 0	 	
22:381218 (,	rs34066624	28.6	 -	Damaging	Damaging	5.84	NOL12,TRIOBP	missense	True	┨	1	1 0	0.0011114	
22:467805 (•	rs147996421	0.003	1-	Damaging	Dailiagilig	3.04	CELSR1	synonymous	False	5	1 1	1	0.0029839	0.00080349
22:467805 (rs140242369	0.718	 -	 			CELSR1	splice_region	False	٦	1	0		

Chr:Pos	Ref/Alt	Identifier	cadd score	REVEL score	MutationTas ter Pred (C)	8	GERP++ RS	Gene Names	Sequence Ontology (Combined)	in NIST callable regions	A samples	No. of variants in ACEi-A samples	No. of variants in control samples		gnomAD AFR MAF
22:468588	G/A	rs11914038	0.555	-				CELSR1	missense	True		1	. 0	0.0077203	0.165977
22:469298	G/A	rs142438731	29.1	0.486	Damaging	Damaging	4.63	CELSR1	missense	True		2	2 0	0.0017521	0.00022994
22:469303	G/A	rs142177887	24.2	0.117	Tolerated	Damaging	3.41	CELSR1	missense	True		1	. 0	0.000324	0.00011473
22:506566	G/A	rs149152116	1.72	-	Damaging	Tolerated	-7.2	TUBGCP6	missense	True	3	1	. 0	0.0027919	0.0008046
22:506578	G/A	rs79022493	0.003	-	Damaging	Tolerated	-8.05	TUBGCP6	missense	True		1	. 0	0.0017523	0
22:506592	C/T	rs3747943	22.8	0.205	Damaging	Damaging	2.45	TUBGCP6	missense	True		1	. 0	0.0015618	0
22:506823	A/G	rs138586345	26.3	-	Damaging	Damaging	3.01	TUBGCP6	missense	True		1	. 0	0.0014945	0.00011497
X:1034950	G/C	rs76090537	1.846	0.048	Tolerated	Tolerated	-6.96	ESX1	missense	False	4	3	0	0	0
X:1034950	G/C	rs200088361	12.85	0.112	Tolerated	Tolerated	2.27	ESX1	missense	False		2	2 3	0	0
X:1409938	T/G	rs79905587	0.676	-	Tolerated	Tolerated		MAGEC1	missense	False	5	1	1	0.0051843	0.00128961
X:1409939	T/-	rs148942485	7.741	0.032				MAGEC1	frameshift	False		1	. 2	0	0
X:1409940	C/T	rs146798989	0.001	0.021	Tolerated	Tolerated		MAGEC1	missense	False		1	. 0	0.0006335	0.00049481
X:1409940	C/G	rs176043	6.763	0.088	Tolerated	Tolerated		MAGEC1	missense	False		1	. 0	0.0033545	0.00295619
X:1409940	G/T	rs176044	0.001	0.045	Damaging	Tolerated		MAGEC1	missense	False		2	2 0	0.005698	0.0106242
X:1409941	T/-	rs138660605	9.37	0.114				MAGEC1	frameshift	False		1	. 2	9.81E-05	0
X:1409958	T/C	rs150953847	0.727	0.009	Tolerated	Tolerated	-1.6	MAGEC1	missense	True		1	. 0	9.23E-05	0
X:1536897	G/A	rs34328761	0.009	-				PLXNA3	synonymous	True	5	1	. 0	0.0077737	0.00050684
X:1536925	G/A	rs151275064	4.626	-				PLXNA3	synonymous	True		1	0	0.0013147	0.00016943
X:1536959	C/T	rs140141994	1.471	-				PLXNA3	synonymous	True		1	0	0.0003781	0
X:1536984	G/A	rs375138921	24.2	0.38	Damaging	Damaging	5.02	PLXNA3	missense	True		1	. 0	0.0003715	0
X:1536998	T/C	rs143928608	6.966	-				PLXNA3	synonymous	True		1	0	9.37E-05	0