

Supplementary Table 1. SNPs shared by both III-29 and IV-18 resulting in a missense or nonsense amino acid change or occurring at a splice site with minor allele frequency (MAF) less than 5% or unknown. Chromosome positions are based on the hg19 human reference genome build.

Gene	dbSNP ID#	MAF	Amino Acid Change	Nucleotide change	PolyPhen2 prediction	Chromosome	Position
AASDH	rs61978622	0.018062	D → N	G → A	benign	chr4	57215969
ABCA8	rs35621847	0.039862	A → V	C → T	benign	chr17	66924083
ABCC8		Unknown	I → V	A → G	benign	chr11	17428614
ABCG8	rs144200355	0.001325	T → S	A → T	possibly damaging	chr2	44099435
ABI3	rs616338	0.003599	F → S	T → C	benign	chr17	47297297
ABO	rs8176696	0.022458	G → R	G → A	possibly damaging	chr9	136136773
ABO	rs34229678	Unknown	R → H	A → G	benign	chr9	136135238
ACAN	rs117116488	0.002166	S → L	C → T	probably damaging	chr15	89390513
ACAN	rs11638262	Unknown	A → T	G → A	benign	chr15	89399453
ACAN		Unknown	A → T	G → A	benign	chr15	89399510
ACAN		Unknown	A → T	G → A	benign	chr15	89399909
ACOT4	rs3742819	0.001825	R → C	C → T	possibly damaging	chr14	74058832
ACP6	rs143920833	0.003297	D → G	A → G	possibly damaging	chr1	147131553
ACSBG2	rs79266675	0.010834	D → E	T → A	benign	chr19	6141593
ACSF3	rs11547019	0.044738	A → P	G → C	benign	chr16	89167138
ACSM5	rs12931877	0.02458	H → R	A → G	benign	chr16	20441077
ACTN3	rs71457732	0.006843	R → C	C → T	probably damaging	chr11	66330533
ADAMTS10	rs62621197	0.025665	R → Q	G → A	benign	chr19	8670147
ADAT3	rs139117131	Unknown	T → M	C → T	possibly damaging	chr19	1912594
AGAP4		Unknown	R → H	G → A	probably damaging	chr10	46321904
AGAP7	rs4043618	Unknown	R → Q	G → A	probably damaging	chr10	51465650
AGAP7	rs61850063	Unknown	D → E	C → G	benign	chr10	51464656
AGAP7	rs61850064	Unknown	Y → N	T → A	benign	chr10	51465552
AGXT		Unknown	P → L	C → T	probably damaging	chr2	241808314
AHNAK	rs114515655	0.008014	V → M	G → A	probably damaging	chr11	62286666

AHNAK2	rs28737397	Unknown	S → G	A → G	benign	chr14	105411971
AHNAK2	rs2013462	0.002735	V → A	T → C	benign	chr14	105416959
AKAP12	rs61748676	0.019596	S → C	A → T	probably damaging	chr6	151672185
AKAP13	rs79101360	Unknown	T → P	A → C	possibly damaging	chr15	86287035
AKAP9		Unknown	A → T	G → A	benign	chr7	91632004
AKR1E2	rs17133693	0.04326	K → R	A → G	benign	chr10	4875591
ALDH3B1		Unknown	K → R	A → G	benign	chr11	67786273
ALX1	rs115440539	0.007053	H → R	A → G	benign	chr12	85674221
ANGPTL4	rs140744493	0.001845	R → C	C → T	probably damaging	chr19	8436373
ANKLE2		Unknown	V → I	G → A	benign	chr12	133313556
ANKRD11	rs76793093	0.042505	P → S	C → T	benign	chr16	89346163
ANKRD11	rs60520302	0.045494	A → P	G → C	benign	chr16	89346883
ANKRD18B	rs41305300	0.044333	Q → R	A → G	probably damaging	chr9	38577239
ANKRD20A3		Unknown	A → S	G → T	probably damaging	chr9	67968287
ANKRD20A3		Unknown	A → V	C → T	possibly damaging	chr9	67934748
ANKRD20A3		Unknown	E → G	A → G	benign	chr9	67927015
ANKRD20A4		Unknown	A → S	G → T	probably damaging	chr9	69423550
ANKRD20A4		Unknown	V → E	T → A	probably damaging	chr9	69423863
ANKRD20A4	rs79777643	Unknown	I → T	T → C	possibly damaging	chr9	69423521
ANKRD20A4		Unknown	Q → E	C → G	possibly damaging	chr9	69423844
ANKRD20A4	rs112196072	Unknown	A → V	C → T	benign	chr9	69423368
ANKRD20A4	rs77680263	Unknown	D → E	C → A	benign	chr9	69423519
ANKRD20A4	rs79174276	Unknown	E → K	G → A	benign	chr9	69423700
ANKRD20A4	rs2982939	Unknown	A → T	G → A	benign	chr9	69423721
ANKRD20A4	rs77404847	Unknown	S → T	G → C	benign	chr9	69423755
ANKRD20A4		Unknown	S → L	C → T	benign	chr9	69423770
ANKRD20A4		Unknown	T → I	C → T	benign	chr9	69423821
ANKRD20A4		Unknown	Q → K	C → A	benign	chr9	69423823
ANKRD20A4		Unknown	N → S	A → G	benign	chr9	69423887

ANKRD30A	rs41304589	0.026965	Q → E	C → G	benign	chr10	37454048
ANKRD36	rs62156909	Unknown	V → L	G → T	benign	chr2	97909629
ANKRD36B	rs148539055	Unknown	Y → C	A → G	probably damaging	chr2	98128196
ANKRD36B	rs13001324	Unknown	D → N	G → A	possibly damaging	chr2	98164020
ANKRD43	rs40274	0.016856	R → P	G → C	benign	chr5	132149684
ANO2	rs3741901	0.048286	P → S	C → T	benign	chr12	6030301
ANXA8L2	rs2271519	Unknown	A → V	C → T	possibly damaging	chr10	47754794
APOB48R	rs34395441	0.014612	E → K	G → A	benign	chr16	28508892
AQP7	rs4008658	0.021028	K → T	A → C	benign	chr9	33387047
ARFGAP3	rs9607957	0.02585	S → G	A → G	benign	chr22	43218397
ARHGEF5	rs3823677	Unknown	T → I	C → T	benign	chr7	144060802
ARRB1		Unknown	T → P	A → C	benign	chr11	74989724
ASPM	rs12138336	0.044173	Q → H	G → C	benign	chr1	197070521
ATF1	rs2230674	0.016437	P → A	C → G	probably damaging	chr12	51208122
ATM	rs3218707	0.008777	V → I	G → A	benign	chr11	108114727
ATP12A	rs56291145	0.023348	N → H	A → C	benign	chr13	25267017
ATP5I	rs76028807	0.010738	L → F	C → T	benign	chr4	668009
B3GALT6		Unknown	A → V	C → T	benign	chr1	1168173
BAG1	rs1071545	0.031378	G → R	G → C	benign	chr9	33264540
BCAP31		Unknown	N → S	A → G	benign	chrX	152969493
BCLAF1	rs1967446	0.011848	Y → D	T → G	possibly damaging	chr6	136597288
BCMO1	rs143238312	0.007692	G → A	G → C	probably damaging	chr16	81323953
BMP2K	rs116710382	0.005633	N → Y	A → T	benign	chr4	79832870
BMPR1A	rs3182217	Unknown	P → T	C → A	benign	chr10	88635779
BRIP1	rs147755155	0.00044	P → L	C → T	probably damaging	chr17	59853772
BSG	rs144824657	Unknown	V → F	G → T	possibly damaging	chr19	577782
C12orf10	rs71453838	Unknown	Q → H	A → C	benign	chr12	53693533
C14orf73	rs34558946	Unknown	Q → E	C → G	benign	chr14	103576444
C16orf11	rs113068385	0.012785	R → Q	G → A	benign	chr16	615048

C16orf38	rs61751878	0.005263	R → H	G → A	possibly damaging	chr16	1536466
C16orf68	rs1731000	0.008601	A → T	G → A	benign	chr16	8738499
C19orf38	rs73009507	0.041096	P → A	C → G	probably damaging	chr19	10961024
C1orf63	rs34619962	0.004256	Y → H	T → C	probably damaging	chr1	25573016
C1orf88	rs15396	0.042455	K → N	A → C	benign	chr1	111891170
C1QTNF9	rs3751356	Unknown	R → Q	G → A	benign	chr13	24895437
C20orf114	rs61739245	0.012184	I → F	A → T	probably damaging	chr20	31877713
C2orf50		Unknown	P → A	C → G	benign	chr2	11284061
C6orf10	rs7775397	0.03022	K → Q	A → C	probably damaging	chr6	32261252
C6orf103	rs78851618	0.02643	I → T	T → C	possibly damaging	chr6	147047296
C6orf15	rs2233982	0.040062	M → I	G → A	possibly damaging	chr6	31079440
C6orf201	rs13200786	0.042705	D → V	A → T	probably damaging	chr6	4087949
C6orf211	rs140681772	0.001067	H → Y	C → T	possibly damaging	chr6	151790096
C6orf27	rs3101017	0.043845	T → A	A → G	benign	chr6	31733466
C7orf28B	rs62441800	Unknown	M → I	G → C	benign	chr7	6844574
C8orf45	rs17332410	0.044768	L → V	C → G	possibly damaging	chr8	67796120
C8orf85	rs111477672	0.035192	Q → H	G → T	probably damaging	chr8	117950758
CA9	rs77984049	0.044944	R → W	A → T	probably damaging	chr9	35674347
CACNA1F	rs34162630	0.016741	R → Q	G → A	probably damaging	chrX	49082499
CACNA1G	rs116920450	0.004333	R → Q	G → A	benign	chr17	48653130
CALD1	rs61755271	0.002123	R → K	G → A	benign	chr7	134617996
CALHM1	rs41287500	0.014416	M → I	G → A	benign	chr10	105215091
CALHM1	rs41287502	0.014653	G → C	G → T	benign	chr10	105215216
CARS2		Unknown	N → S	A → G	benign	chr13	111340361
CASP9	rs2308941	0.007995	T → I	C → T	benign	chr1	15844718
CATSPERB	rs72629402	0.043168	V → A	T → C	benign	chr14	92159558
CBX2	rs141957173	0.004819	P → A	C → G	benign	chr17	77758653
CCDC144A	rs3869489	Unknown	E → K	G → A	benign	chr17	16664991
CCDC76	rs35216047	Unknown	A → V	C → T	benign	chr1	100598867

CCL25	rs74959615	0.037695	R → H	G → A	benign	chr19	8121096
CD200R1	rs71625219	0.5	P → T	A → C	probably damaging	chr3	112648127
CD248	rs74818906	0.007567	A → T	G → A	benign	chr11	66083043
CDC27	rs75661039	Unknown	H → Q	T → A	probably damaging	chr17	45214604
CDC27	rs74390782	Unknown	R → W	C → T	probably damaging	chr17	45214690
CDC27	rs62075657	Unknown	L → F	A → C	probably damaging	chr17	45216132
CDC27	rs62077268	Unknown	A → T	G → A	probably damaging	chr17	45249365
CDC27	rs62077279	Unknown	E → G	A → G	probably damaging	chr17	45266522
CDC27	rs62077280	Unknown	T → A	A → G	probably damaging	chr17	45266535
CDC27	rs74496366	Unknown	M → R	T → G	possibly damaging	chr17	45219364
CDC27	rs77095606	Unknown	L → W	T → G	possibly damaging	chr17	45234477
CDC27	rs78043820	Unknown	R → G	A → G	benign	chr17	45234481
CDC27	rs74398156	Unknown	A → T	G → A	benign	chr17	45235653
CDK5RAP2	rs34523498	0.032542	G → E	G → A	benign	chr9	123205981
CDRT1	rs3826385	Unknown	N → D	A → G	possibly damaging	chr17	15510988
CEP110	rs77083332	0.022983	L → V	C → G	benign	chr9	123875921
CEP350		Unknown	S → C	C → G	probably damaging	chr1	179983108
CES1	rs3826193	Unknown	I → V	A → G	benign	chr16	55862791
CES1	rs3826192	0.002451	V → I	G → A	benign	chr16	55862824
CHPF	rs62191582	0.016065	A → G	C → G	possibly damaging	chr2	220404484
CHTF18	rs61745756	0.049377	R → H	G → A	benign	chr16	839600
CILP	rs60240130	Unknown	G → S	G → A	benign	chr15	65489128
CIT	rs55707601	0.01485	S → C	C → G	benign	chr12	120263003
CLN5	rs138611001	0.009162	N → K	C → A	probably damaging	chr13	77574606
CNNM2	rs76057237	0.037262	R → Q	G → A	possibly damaging	chr10	104678350
CNR2	rs35761398	Unknown	Q → R	A → G	benign	chr1	24201920
CNTNAP3	rs10974151	Unknown	S → Y	C → A	benign	chr9	39118205
COL14A1	rs11774228	0.007086	V → I	G → A	benign	chr8	121267490
COL22A1	rs10111520	0.047515	P → T	C → A	benign	chr8	139749799

COL9A3	rs45628843	0.040847	P → L	C → T	benign	chr20	61459315
CORO1B	rs11601245	0.008226	A → T	G → A	benign	chr11	67206234
CPA5	rs17388190	0.020798	P → S	C → T	probably damaging	chr7	129989852
CPN1	rs61751507	0.03176	G → D	G → A	possibly damaging	chr10	101829514
CPS1	rs113635180	Unknown	T → A	A → G	benign	chr2	211456637
CRB2	rs2488601	0.003643	T → A	A → G	benign	chr9	126135715
CSPG4		Unknown	P → L	C → T	benign	chr15	75982186
CSRP2BP	rs139667492	0.001538	Y → N	T → A	benign	chr20	18162405
CTAGE4		Unknown	P → L	C → T	probably damaging	chr7	143964428
CTSS	rs41271951	0.047612	V → A	T → C	benign	chr1	150737220
CUBN	rs45569534	0.014999	E → Q	G → C	benign	chr10	16930419
CUL7	rs61748654	Unknown	Q → R	A → G	benign	chr6	43014299
CYFIP1	rs149042952	0.008352	A → V	C → T	possibly damaging	chr15	22993121
CYP4X1		Unknown	S → G	A → G	benign	chr1	47514254
DAPL1	rs61740880	0.019806	A → V	C → T	possibly damaging	chr2	159672251
DCHS2	rs146032523	0.002275	T → I	C → T	possibly damaging	chr4	155191162
DCLK2	rs67917234	Unknown	P → R	C → G	benign	chr4	151177341
DCLK3	rs35704209	0.004562	E → D	G → T	benign	chr3	36756867
DCTN4	rs35772018	0.009531	Y → C	A → G	probably damaging	chr5	150110239
DDX49	rs139869066	0.006044	G → S	G → A	possibly damaging	chr19	19030611
DDX51	rs17418886	Unknown	Q → R	A → G	possibly damaging	chr12	132626668
DGKH	rs17646069	0.044617	V → A	T → C	benign	chr13	42803263
DGUOK	rs74874677	0.013947	Q → R	A → G	probably damaging	chr2	74177777
DHX16	rs9262138	0.032054	D → G	A → G	benign	chr6	30627867
DIP2A	rs7283507	0.038516	P → A	C → G	benign	chr21	47918662
DKFZp434M131	rs62579097	Unknown	T → A	A → G	benign	chr9	90745671
DKFZp686I15204	rs62538181	Unknown	M → I	G → C	benign	chr9	43915893
DNAH10	rs145483216	Unknown	M → V	A → G	probably damaging	chr12	124323006
DNAJC13	rs79953286	0.038622	Y → C	A → G	probably damaging	chr3	132226100

DOCK5		Unknown	H → Y	C → T	benign	chr8	25159907
DSC1	rs35338395	0.039435	S → F	C → T	benign	chr18	28737407
DSG2	rs2230234	0.0375	I → V	A → G	probably damaging	chr18	29104714
DSPP		Unknown	D → N	G → A	probably damaging	chr4	88537268
DSPP	rs140656082	Unknown	N → D	A → G	benign	chr4	88537232
DSTYK		Unknown	E → A	A → C	benign	chr1	205156631
DTHD1	rs56412718	0.015901	P → T	C → A	probably damaging	chr4	36340755
DTX2	rs12534498	0.011409	V → I	G → A	benign	chr7	76111938
DUSP5	rs35834951	Unknown	A → V	C → T	benign	chr10	112266823
DYDC2	rs1047951	0.019731	G → S	G → A	benign	chr10	82126600
E2F7	rs61754233	0.010537	P → R	C → G	possibly damaging	chr12	77439823
ECT2L	rs138935097	Unknown	V → A	T → C	benign	chr6	139202137
EFEMP2		Unknown	I → V	A → G	benign	chr11	65636053
EFHB	rs76398910	0.028053	T → I	C → T	possibly damaging	chr3	19924058
EGFLAM	rs113400125	0.019881	R → C	C → T	benign	chr5	38406251
EIF4G1	rs111924994	0.001797	A → P	G → C	benign	chr3	184040371
EIF5AL1	rs1250783	Unknown	V → L	G → C	possibly damaging	chr10	81272814
ELL3	rs34636853	0.00339	P → L	C → T	possibly damaging	chr15	44066904
EPS8L1	rs144463157	0.006817	G → R	G → C	probably damaging	chr19	55593837
ERI2	rs149105300	0.001103	G → R	G → A	possibly damaging	chr16	20814940
ERO1LB	rs35648587	0.00353	K → N	A → C	benign	chr1	236433208
FAAH	rs114795065	0.000958	R → H	G → A	probably damaging	chr1	46871409
FAM113A	rs147321844	0.00044	P → L	C → T	benign	chr20	2816292
FAM120B	rs113032155	0.041588	D → G	A → G	benign	chr6	170627695
FAM122C	rs45447592	0.030882	P → S	C → T	benign	chrX	133963268
FAM133A	rs34123774	0.030604	E → K	G → A	benign	chrX	92964617
FAM157B		Unknown	T → R	C → G	possibly damaging	chr9	141111600
FAM164A	rs77219198	0.013064	S → F	C → T	probably damaging	chr8	79629586
FAM171A1		Unknown	M → R	T → G	probably damaging	chr10	15262960

FAM186A		Unknown	T → P	A → C	benign	chr12	50745703
FAM189A1	rs34232112	Unknown	H → R	A → G	benign	chr15	29418574
FAM22D	rs139769515	Unknown	C → S	G → C	benign	chr10	89120661
FAM22F	rs2479282	Unknown	R → G	A → G	benign	chr9	97087707
FAM26F	rs11544160	0.044724	E → K	G → A	benign	chr6	116784797
FAM75A2	rs6476797	Unknown	A → T	G → A	benign	chr9	39360949
FAM75A6	rs10907643	Unknown	P → L	C → T	benign	chr9	43625382
FANCB	rs41309679	0.048599	G → E	G → A	probably damaging	chrX	14877404
FANCM	rs45547534	0.009053	I → M	A → G	probably damaging	chr14	45606387
FARP1	rs61749894	0.002861	R → C	C → T	probably damaging	chr13	99092998
FASN	rs12946178	0.003426	E → K	G → A	probably damaging	chr17	80046994
FAT1	rs1280098	0.002245	Q → P	A → C	benign	chr4	187538942
FAT4	rs72675395	0.014396	R → K	G → A	probably damaging	chr4	126412154
FCGBP	rs6508919	Unknown	G → S	G → A	probably damaging	chr19	40367567
FCRL2	rs138710224	0.001318	L → M	C → A	possibly damaging	chr1	157738309
FER1L6	rs56132579	0.038562	R → Q	G → A	probably damaging	chr8	125115420
FEZ2	rs1544655	0.00228	P → L	C → T	benign	chr2	36825137
FGFR1OP	rs61751042	0.021158	T → I	C → T	possibly damaging	chr6	167435928
FGFR1OP	rs17856382	0.030109	K → N	G → T	benign	chr6	167438276
FGFR1OP	rs34585172	0.021577	S → P	T → C	benign	chr6	167438364
FHOD3	rs61735994	0.021945	Q → R	A → G	benign	chr18	34289142
FLG	rs77166567	Unknown	D → N	G → A	probably damaging	chr1	152280347
FNBP4	rs112054219	Unknown	T → S	C → G	benign	chr11	47788731
FNDC1	rs62432291	0.024201	P → S	C → T	probably damaging	chr6	159621087
FNDC3A	rs45604939	0.042696	T → A	A → G	possibly damaging	chr13	49775997
FOLH1B	rs145858863	0.020774	V → A	T → C	benign	chr11	89413795
FOXD4L1		Unknown	A → P	G → C	possibly damaging	chr2	114257590
FOXO3	rs111556510	0.029224	A → V	C → T	benign	chr6	108882830
FOXQ1	rs148598230	Unknown	L → P	T → C	probably damaging	chr6	1312998

FRG1	rs1803592	Unknown	K → E	A → G	benign	chr4	190873379
FRG1	rs1061653	Unknown	G → E	G → A	benign	chr4	190876242
FRG1	rs150472183	Unknown	Q → K	C → A	benign	chr4	190876301
FRG1	rs184307882	Unknown	K → E	A → G	benign	chr4	190881933
FRG1	rs75206851	Unknown	R → Q	G → A	benign	chr4	190883051
FRG2B		Unknown	D → H	G → C	possibly damaging	chr10	135440144
FRG2B		Unknown	I → T	T → C	benign	chr10	135440080
FRG2B	rs78279965	Unknown	T → S	A → T	benign	chr10	135440159
FRG2B	rs75987380	Unknown	H → Q	C → G	benign	chr10	135440214
FRG2B	rs79777505	Unknown	H → Y	C → T	benign	chr10	135440216
FRMD1	rs73028318	0.00371	R → Q	G → A	benign	chr6	168464402
FRYL	rs145522900	Unknown	V → I	G → A	benign	chr4	48583490
GAL3ST2		Unknown	D → E	C → A	probably damaging	chr2	242743392
GBP1	rs75161612	0.016957	S → N	G → A	benign	chr1	89523911
GGT1	rs186765281	Unknown	I → V	A → G	possibly damaging	chr22	25010855
GIMAP6	rs62000976	0.002349	S → L	C → T	benign	chr7	150325372
GLB1L	rs147143842	0.008884	R → W	C → T	probably damaging	chr2	220107997
GLYCTK	rs121909448	0.00022	F → C	T → G	probably damaging	chr3	52327048
GNAS	rs61749697	0.02253	P → L	C → T	benign	chr20	57429447
GOLGA6A		Unknown	E → K	G → A	probably damaging	chr15	74367283
GOLGA6A		Unknown	Q → R	A → G	benign	chr15	74367066
GOLGA6A		Unknown	Q → L	A → T	benign	chr15	74367120
GOLGA6A		Unknown	P → L	C → T	benign	chr15	74367333
GOLGA6B		Unknown	R → Q	G → A	benign	chr15	72954890
GOLGA6B		Unknown	R → W	C → T	benign	chr15	72958170
GOLGA6D	rs3895102	Unknown	D → G	A → G	benign	chr15	75552784
GOT2	rs11076256	0.049418	G → S	G → A	possibly damaging	chr16	58752466
GPA33	rs72689400	0.008754	V → F	G → T	probably damaging	chr1	167038219
GPR115	rs115890838	0.010834	V → I	G → A	benign	chr6	47682212

GPR137C	rs147785041	Unknown	S → G	A → G	benign	chr14	53019944
GPR88	rs2809819	0.000913	V → I	G → A	benign	chr1	101005090
GPRIN2	rs71185249	Unknown	S → G	A → G	benign	chr10	46999190
GPX1	rs1050450	0.036435	P → L	C → T	benign	chr3	49394834
GSPT1	rs424518	0.003643	V → A	T → C	benign	chr16	12009279
GTPBP5		Unknown	M → V	A → G	benign	chr20	60773906
GTSF1L	rs17826038	0.016799	L → V	C → G	probably damaging	chr20	42355169
HACL1		Unknown	E → Q	G → C	benign	chr3	15628058
HAPLN1		Unknown	F → L	C → G	benign	chr5	82940384
HAUS6	rs4977493	Unknown	S → I	G → T	probably damaging	chr9	19058483
HCN4	rs143090627	Unknown	G → E	G → A	benign	chr15	73660505
HDGFL1		Unknown	E → K	G → A	possibly damaging	chr6	22570483
HEATR5A	rs61754287	0.007799	M → T	T → C	benign	chr14	31819145
HEPH	rs17216603	0.003094	A → T	G → A	benign	chrX	65418789
HERC2	rs2525965	Unknown	F → L	C → G	possibly damaging	chr15	28566562
HGF	rs5745687	0.040296	E → K	G → A	benign	chr7	81359051
HLA-A	rs3180267	Unknown	I → R	T → G	benign	chr6	29911063
HLA-A	rs1059526	0	A → T	G → A	benign	chr6	29911218
HLA-DQA1	rs1129957	Unknown	Q → K	C → A	benign	chr6	32610009
HOMER3	rs1059240	0.007706	S → R	C → G	benign	chr19	19040312
HOOK1	rs41312662	0.016831	I → V	A → G	benign	chr1	60299125
HOXA4		Unknown	L → M	T → A	probably damaging	chr7	27169047
HPS1	rs11592273	0.044384	G → W	G → T	probably damaging	chr10	100189568
HR	rs117197822	0.014067	R → Q	G → A	probably damaging	chr8	21981218
HRNR	rs76549374	Unknown	E → K	G → A	possibly damaging	chr1	152190945
HS3ST4	rs2943336	0.000913	R → Q	A → G	possibly damaging	chr16	25704145
HS6ST1		Unknown	S → T	G → C	benign	chr2	129076016
HYAL4	rs149028871	0.000222	L → F	C → T	benign	chr7	123508397
HYDIN	rs1798314	0.027638	E → Q	G → C	probably damaging	chr16	70884524

HYDIN	rs3817211	0.009017	N → D	A → G	probably damaging	chr16	71098649
HYDIN	rs1774449	0.004072	I → S	T → G	benign	chr16	70942688
HYDIN	rs1774513	0.020548	V → L	G → C	benign	chr16	71026076
IFIH1	rs35667974	0.00796	I → V	A → G	probably damaging	chr2	163124637
IFNA7	rs149946231	0.005275	V → L	G → T	benign	chr9	21201780
IGSF11		Unknown	Q → H	G → T	benign	chr3	118623641
IGSF22	rs11024769	0.044015	L → F	C → T	possibly damaging	chr11	18735465
IGSF3	rs76151115	0.004955	R → Q	G → A	probably damaging	chr1	117142613
IGSF3	rs76417519	0.002655	R → W	C → T	probably damaging	chr1	117142641
IGSF5	rs142105354	0.002419	R → Q	G → A	benign	chr21	41173190
IL17RD	rs143416217	0.000452	T → I	C → T	benign	chr3	57137154
IL28B	rs62120527	0.00939	E → K	G → A	probably damaging	chr19	39734352
IL28B	rs138893424	0.011664	L → F	C → T	benign	chr19	39735517
INA	rs34440112	0.022594	I → L	A → C	benign	chr10	105048217
INSM2	rs144835486	Unknown	P → S	C → T	benign	chr14	36003618
IRAK1BP1	rs41269339	0.022941	P → R	C → G	benign	chr6	79577412
IRS1	rs13306469	0.011407	G → S	G → A	benign	chr2	227661291
IRX3	rs1450355	0.003643	L → P	T → C	benign	chr16	54318528
ISCU	rs67681514	0.5	F → C	T → G	benign	chr12	108956418
JPH3	rs149647215	0.003175	G → S	G → A	benign	chr16	87677887
KANK4	rs34591898	0.024802	A → V	C → T	benign	chr1	62703977
KCNJ14	rs73050908	0.007895	A → V	C → T	benign	chr19	48968015
KIAA0284	rs62641737	0.0124	S → F	C → T	possibly damaging	chr14	105352651
KIAA0564	rs2274810	0.041474	E → K	G → A	benign	chr13	42264380
KIAA1409	rs79866114	0.010089	L → V	C → G	probably damaging	chr14	93963563
KIF15	rs138043992	0.002141	R → L	G → T	probably damaging	chr3	44843459
KIF21B	rs140589352	0.014499	S → L	C → T	possibly damaging	chr1	200978027
KIF26A	rs61743202	0.026009	K → R	A → G	benign	chr14	104644212
KIF4A		Unknown	L → R	T → G	probably damaging	chrX	69595143

KLHDC9	rs1128750	0.038997	A → T	G → A	benign	chr1	161069544
KLHL38	rs71505429	Unknown	H → R	A → G	benign	chr8	124664874
KLRC2	rs1141715	Unknown	S → F	T → C	benign	chr12	10587111
KRT17		Unknown	R → L	G → T	benign	chr17	39778707
KRT39	rs143643076	0.006661	G → E	G → A	benign	chr17	39115049
KRT6B	rs144860693	0.037265	G → R	G → A	benign	chr12	52845574
KRT6C	rs28538343	Unknown	S → N	G → A	benign	chr12	52867094
KRT86	rs58717266	Unknown	Q → P	A → C	possibly damaging	chr12	52696930
KRTAP10-1	rs233316	0.004096	P → L	C → T	probably damaging	chr21	45959195
KRTAP10-1	rs233319	0.003643	V → M	G → A	probably damaging	chr21	45959733
KRTAP10-1	rs34549147	Unknown	D → Y	G → T	possibly damaging	chr21	45959559
KRTAP10-6	rs75991593	Unknown	R → H	G → A	benign	chr21	46012181
KRTAP10-7	rs7410162	Unknown	R → C	C → T	benign	chr21	46020720
KRTAP10-7	rs4818725	Unknown	R → H	G → A	benign	chr21	46020721
KRTAP10-9	rs142813376	Unknown	V → M	G → A	possibly damaging	chr21	46047779
KRTAP22-1	rs724849	0.029769	Y → C	A → G	benign	chr21	31973525
KRTAP4-7	rs11650261	Unknown	R → H	G → A	probably damaging	chr17	39240790
KRTAP4-7	rs9894966	Unknown	S → C	A → T	benign	chr17	39240795
KRTAP5-5	rs147101544	Unknown	P → H	C → A	probably damaging	chr11	1651555
KRTAP5-7	rs147685834	Unknown	C → S	G → C	possibly damaging	chr11	71238453
LAMA4	rs71543223	Unknown	A → E	C → A	benign	chr6	112508770
LAMB1	rs35915664	0.014378	I → T	T → C	probably damaging	chr7	107569962
LAX1	rs41264261	0.020323	P → S	C → T	possibly damaging	chr1	203743798
LBP	rs5744212	0.004267	L → F	C → T	possibly damaging	chr20	36997672
LCMT2	rs142368943	0.004344	T → I	C → T	benign	chr15	43621741
LDLRAD3		Unknown	H → P	A → C	probably damaging	chr11	36248854
LGALS8	rs35499589	Unknown	M → V	A → G	benign	chr1	236702210
LGR6		Unknown	V → A	T → C	benign	chr1	202287443
LIG4	rs1805389	0.045323	A → V	C → T	benign	chr13	108863609

LILRB3		Unknown	G → R	G → A	possibly damaging	chr19	54725913
LILRB3		Unknown	H → Y	C → T	benign	chr19	54724443
LILRB3	rs1052995	0.000913	Y → C	A → G	benign	chr19	54724457
LILRB3	rs1052968	Unknown	T → N	C → A	benign	chr19	54725798
LILRB3	rs4023899	Unknown	R → G	C → G	benign	chr19	54725835
LIPI	rs141732671	0.009894	H → D	C → G	probably damaging	chr21	15579196
LMAN1	rs1043302	0.032366	R → Q	G → A	benign	chr18	57026436
LOC390594	rs146917406	Unknown	G → D	G → A	probably damaging	chr15	65369947
LOC440563	rs1737105	Unknown	D → G	A → G	benign	chr1	13183511
LOC643854	rs4897534	Unknown	L → V	C → G	probably damaging	chr6	132030966
LOC643854		Unknown	I → V	A → G	benign	chr6	132032010
LOC653545		Unknown	G → S	G → A	probably damaging	chr10	135491077
LOC653545		Unknown	G → S	G → A	benign	chr10	135491056
LOC653545		Unknown	G → S	G → A	benign	chr10	135491083
LPHN2	rs112681863	0.008639	P → S	C → T	probably damaging	chr1	82416040
LPL	rs1801177	0.025829	D → N	G → A	benign	chr8	19805708
LRRRC16B	rs117092113	0.025292	R → H	G → A	probably damaging	chr14	24533474
LRRRC37A3	rs62071406	Unknown	S → T	T → A	possibly damaging	chr17	62892271
LRRFIP2	rs36068826	0.017485	Y → C	A → G	benign	chr3	37151157
LRRK2	rs35303786	0.008914	M → T	T → C	benign	chr12	40713899
LRWD1	rs35310665	0.042009	K → R	A → G	benign	chr7	102108263
LYZL1	rs2532753	Unknown	K → R	A → G	possibly damaging	chr10	29578084
MAD1L1	rs1801368	0.00928	R → H	G → A	benign	chr7	1976457
MAGEA4	rs41302158	0.002402	S → F	C → T	benign	chrX	151092258
MAPK15	rs56038219	0.021231	S → P	T → C	probably damaging	chr8	144804299
MARVELD2	rs139854607	0.003956	Q → R	A → G	benign	chr5	68715712
MASP2	rs141145402	0.000662	T → M	C → T	probably damaging	chr1	11106642
MAST2	rs33931638	0.035714	V → M	G → A	possibly damaging	chr1	46500251
MAST2	rs1052607	0.035072	K → R	A → G	benign	chr1	46499526

MAST3		Unknown	R → H	G → A	possibly damaging	chr19	18241327
MBD4	rs78782061	0.001986	N → S	A → G	possibly damaging	chr3	129152704
MCC	rs348942	0.000913	S → G	A → G	benign	chr5	112824039
MED25	rs145770066	0.004491	A → V	C → T	benign	chr19	50334047
MEGF6		Unknown	A → T	G → A	possibly damaging	chr1	3416227
METTL2A	rs2319055	0.000913	L → P	T → C	benign	chr17	60503921
MGLL		Unknown	N → I	A → T	benign	chr3	127411093
MIA3	rs2936053	0.000453	K → E	A → G	benign	chr1	222802006
MICALCL	rs3812754	Unknown	T → P	A → C	possibly damaging	chr11	12316389
MLL3	rs4024419	Unknown	G → E	G → A	probably damaging	chr7	151935910
MLL3	rs56850341	Unknown	L → F	C → T	probably damaging	chr7	151970931
MLL3	rs4024453	0.049522	S → L	C → T	possibly damaging	chr7	151945204
MLL3	rs13231116	0.017429	P → T	C → A	benign	chr7	151877127
MLL4	rs80216638	0.040295	T → N	C → A	benign	chr19	36211742
MMEL1	rs147088948	0.00022	S → G	A → G	probably damaging	chr1	2523012
MMP27	rs61754772	0.012621	K → R	A → G	benign	chr11	102575379
MPDZ	rs150038177	Unknown	K → E	A → G	possibly damaging	chr9	13186355
MPDZ	rs189005767	Unknown	T → S	A → T	benign	chr9	13190235
MPP2	rs70964679	Unknown	H → Q	C → G	benign	chr17	41960634
MRC2	rs143651722	0.000417	R → Q	G → A	probably damaging	chr17	60767078
MRPL4	rs113197610	0.011048	K → T	A → C	benign	chr19	10363251
MRPL53	rs141704877	0.010545	K → E	A → G	benign	chr2	74699715
MRVI1	rs35857561	0.048063	P → S	C → T	benign	chr11	10650367
MSH4	rs5745459	0.006049	Y → C	A → G	probably damaging	chr1	76345823
MSN		Unknown	E → G	A → G	benign	chrX	64956743
MT1E	rs72818417	0.04822	G → D	G → A	possibly damaging	chr16	56660816
MTFR1	rs151130367	0.00022	D → G	A → G	possibly damaging	chr8	66620110
MUC16	rs12459532	0.023737	P → L	C → T	benign	chr19	9059181
MUC16	rs59168469	0.025571	R → H	G → A	benign	chr19	9060915

MUC2		Unknown	A → T	G → A	benign	chr11	1092715
MUC4	rs147904363	Unknown	Q → H	G → C	unknown	chr3	195507372
MUC4	rs142066159	Unknown	P → L	C → T	probably damaging	chr3	195506974
MUC4	rs142559357	Unknown	T → P	A → C	probably damaging	chr3	195510707
MUC4		Unknown	T → M	C → T	probably damaging	chr3	195514279
MUC4		Unknown	D → G	A → G	possibly damaging	chr3	195514768
MUC4	rs77359000	Unknown	P → S	C → T	benign	chr3	195506933
MUC4	rs79358488	Unknown	L → P	T → C	benign	chr3	195507166
MUC4		Unknown	V → A	T → C	benign	chr3	195507226
MUC4		Unknown	S → A	T → G	benign	chr3	195507338
MUC4		Unknown	R → P	G → C	benign	chr3	195507412
MUC4	rs71187742	0.5	A → T	G → A	benign	chr3	195507683
MUC4		Unknown	D → N	G → A	benign	chr3	195507686
MUC4		Unknown	L → F	C → T	benign	chr3	195507827
MUC4	rs145853807	Unknown	V → A	T → C	benign	chr3	195510217
MUC4		Unknown	E → D	G → C	benign	chr3	195510228
MUC4	rs142766505	Unknown	A → T	G → A	benign	chr3	195511523
MUC4	rs6805660	Unknown	T → A	A → G	benign	chr3	195512042
MUC4		Unknown	D → V	A → T	benign	chr3	195512107
MUC4		Unknown	I → V	A → G	benign	chr3	195512186
MUC4		Unknown	M → T	T → C	benign	chr3	195514471
MUC4		Unknown	A → V	C → T	benign	chr3	195514489
MUC4		Unknown	A → S	G → T	benign	chr3	195514733
MUC5AC	rs2860722	Unknown	T → M	C → T	possibly damaging	chr11	1265786
MUC5AC	rs4963055	Unknown	T → I	C → T	possibly damaging	chr11	1269398
MUC5AC	rs3021164	Unknown	G → R	G → C	benign	chr11	1270663
MUC6	rs34232586	Unknown	Q → H	G → T	benign	chr11	1017338
MXRA5	rs66465405	Unknown	A → V	C → T	benign	chrX	3240343
MYADML2	rs62077244	0.014986	R → W	C → T	probably damaging	chr17	79898933

MYBPC2	rs61731791	0.02866	T → M	C → T	benign	chr19	50940778
MYH13		Unknown	M → T	T → C	benign	chr17	10265747
MYOM1	rs3765623	0.046955	D → N	G → A	possibly damaging	chr18	3086065
NAT8	rs181152984	Unknown	T → I	C → T	probably damaging	chr2	73868226
NAV2	rs146720224	0.003516	E → K	G → A	probably damaging	chr11	20119222
NBAS	rs75566418	0.002228	Y → H	T → C	probably damaging	chr2	15542296
NBEA	rs11538677	0.038918	I → V	A → G	possibly damaging	chr13	36202269
NBEA	rs41292197	0.021918	S → G	A → G	benign	chr13	35747681
NBPF10		Unknown	T → I	C → T	probably damaging	chr1	145313405
NBPF10		Unknown	D → N	A → G	possibly damaging	chr1	145327548
NBPF10		Unknown	Q → L	A → T	possibly damaging	chr1	145333841
NBPF10		Unknown	L → V	C → G	possibly damaging	chr1	145352701
NBPF10		Unknown	E → K	A → G	possibly damaging	chr1	145359049
NBPF10		Unknown	E → D	G → T	possibly damaging	chr1	145366857
NBPF10		Unknown	A → S	G → T	benign	chr1	145302676
NBPF10	rs3926769	Unknown	R → K	A → G	benign	chr1	145302704
NBPF10	rs3930826	Unknown	R → H	A → G	benign	chr1	145330829
NBPF10		Unknown	V → A	T → C	benign	chr1	145333820
NBPF11		Unknown	V → I	G → A	benign	chr1	146039032
NBPF11		Unknown	E → G	A → G	benign	chr1	146039133
NBPF11		Unknown	E → G	A → G	benign	chr1	147580910
NBPF14	rs147480284	0.047327	S → I	G → T	possibly damaging	chr1	148004783
NBPF14	rs141981140	0.044921	M → T	T → C	possibly damaging	chr1	148009349
NBPF16		Unknown	Q → L	A → T	probably damaging	chr1	148754942
NBPF16		Unknown	G → S	G → A	possibly damaging	chr1	148756448
NBPF16		Unknown	V → A	T → C	benign	chr1	148754858
NBPF16		Unknown	V → L	G → T	benign	chr1	148756607
NCOR1	rs76780359	Unknown	E → K	G → A	probably damaging	chr17	16068340
NDUFAF1	rs35227875	0.0232	E → K	G → A	possibly damaging	chr15	41688732

NDUFS8	rs150278938	0.000879	R → C	C → T	possibly damaging	chr11	67799622
NEDD4	rs1912403	0.047977	M → V	A → G	benign	chr15	56208933
NEFH		Unknown	V → E	T → A	possibly damaging	chr22	29885722
NID2	rs61747585	0.04769	E → D	G → T	possibly damaging	chr14	52508842
NLRP6	rs6421985	0.005002	M → L	A → C	benign	chr11	280221
NLRP6	rs7482965	Unknown	Y → F	A → T	benign	chr11	280816
NMBR	rs138994608	0.022447	P → H	C → A	probably damaging	chr6	142400020
NOMO1	rs3895684	Unknown	A → V	C → T	benign	chr16	14989420
NOTCH2	rs61788900	Unknown	N → S	A → G	possibly damaging	chr1	120572547
NOTCH2	rs61788901	Unknown	E → K	G → A	benign	chr1	120572572
NSD1		Unknown	A → T	G → A	benign	chr5	176636958
NUP205	rs148613242	0.001099	A → G	C → G	probably damaging	chr7	135258511
OBSCN	rs1188732	0.005906	C → R	T → C	benign	chr1	228504472
OLA1		Unknown	P → S	C → T	probably damaging	chr2	175094043
OPLAH	rs55916375	0.047227	V → I	G → A	benign	chr8	145112983
OR10G3	rs45612332	0.036092	Y → C	A → G	probably damaging	chr14	22038562
OR10K2		Unknown	K → E	A → G	possibly damaging	chr1	158390389
OR13G1	rs56096718	0.042169	V → L	G → C	benign	chr1	247835779
OR11I	rs144766527	0.010765	S → T	T → A	benign	chr19	15198666
OR2A14	rs183164379	Unknown	A → V	C → T	benign	chr7	143826300
OR2H1	rs17184086	0.041667	V → M	G → A	probably damaging	chr6	29430213
OR2T10	rs41269353	0.014539	S → A	T → G	benign	chr1	248756502
OR4D9	rs17501584	0.032298	Q → R	A → G	probably damaging	chr11	59282861
OR4D9	rs141443392	0.001319	R → C	C → T	benign	chr11	59282575
OR4N2	rs146446158	0.002858	K → T	A → C	benign	chr14	20295873
OR4Q3	rs75664801	Unknown	L → I	C → A	benign	chr14	20215899
OR51A2	rs1817206	Unknown	G → E	G → A	benign	chr11	4976768
OR51L1	rs61729748	0.021445	N → Y	A → T	probably damaging	chr11	5020933
OR5H6	rs2173236	0.000908	S → L	C → T	benign	chr3	97983391

OR6P1	rs41273499	0.035095	R → W	C → T	probably damaging	chr1	158532614
OR7A17	rs139004201	0.008568	G → D	G → A	benign	chr19	14991881
OR8B3	rs507360	Unknown	Q → R	A → G	benign	chr11	124267177
OR9G9	rs71458233	Unknown	T → I	C → T	benign	chr11	56468048
OR9G9	rs11228735	0.03271	E → K	G → A	benign	chr11	56468416
OVGP1	rs3835606	Unknown	S → P	T → C	benign	chr1	111957592
P704P	rs71228614	0.5	S → L	C → T	probably damaging	chr14	20020201
PATL1		Unknown	I → T	T → C	probably damaging	chr11	59426391
PAX1	rs142565607	0.000665	K → R	A → G	possibly damaging	chr20	21687460
PCMTD1	rs62506083	Unknown	N → T	A → C	benign	chr8	52733128
PCNXL2	rs74503807	0.016031	A → V	C → T	possibly damaging	chr1	233353901
PCNXL2	rs41307684	0.016464	A → E	C → A	benign	chr1	233313594
PCOLCE	rs117595600	0.004168	R → W	C → T	possibly damaging	chr7	100205703
PDZK1	rs148919265	0.00713	G → S	G → A	benign	chr1	145748503
PER2	rs35333999	0.027829	V → I	G → A	probably damaging	chr2	239161957
PEX1		Unknown	I → M	A → G	benign	chr7	92132493
PGLYRP2	rs2304200	0.045739	R → W	C → T	possibly damaging	chr19	15580658
PHC2	rs41265897	0.02247	A → V	C → T	benign	chr1	33836164
PI4K2B	rs313549	0.000887	S → P	T → C	benign	chr4	25236017
PIGQ	rs71391136	0.5	C → Y	G → A	benign	chr16	633354
PIK3CG	rs61749915	0.0132	N → S	A → G	benign	chr7	106509571
PIK3R2	rs149081991	Unknown	A → T	G → A	benign	chr19	18280096
PITRM1	rs17849904	0.045187	V → I	G → A	benign	chr10	3181126
PKD1	rs40433	0.046207	R → Q	G → A	benign	chr16	2164808
PKD1L2	rs1453325	0.00771	N → D	A → G	benign	chr16	81190601
PKHD1L1	rs62508075	0.019635	I → V	A → G	probably damaging	chr8	110397780
PLEC1	rs35858667	0.04244	A → V	C → T	benign	chr8	144994888
PLEKHA4	rs62127976	0.019352	S → Y	C → A	probably damaging	chr19	49370819
PLXNA3	rs139336954	0.004341	P → L	C → T	benign	chrX	153693126

PLXNB2	rs11547731	0.002735	I → V	A → G	probably damaging	chr22	50722134
PMS2	rs1802683	Unknown	G → A	G → C	benign	chr7	6013049
PNMAL1	rs111356009	0.011337	V → M	G → A	possibly damaging	chr19	46973707
PNPLA7	rs61747535	0.043183	W → S	G → C	probably damaging	chr9	140373575
POLR1A	rs146078741	Unknown	R → P	G → C	benign	chr2	86317012
POP1	rs61743394	0.001082	G → D	G → A	probably damaging	chr8	99135639
POTEC	rs28709987	Unknown	H → D	C → G	benign	chr18	14542890
POTED	rs56121372	Unknown	H → Y	C → T	probably damaging	chr21	14987811
POTED	rs55653693	Unknown	D → Y	G → T	probably damaging	chr21	14987871
POTED		Unknown	M → T	T → C	benign	chr21	14982716
POTEE		Unknown	P → R	C → G	probably damaging	chr2	132021463
PPIAL4A	rs2691730	Unknown	L → P	T → C	benign	chr1	147955256
PPIAL4E	rs594576	Unknown	N → S	A → G	possibly damaging	chr1	148644408
PPIAL4G	rs4306185	Unknown	H → R	A → G	benign	chr1	143767643
PPP1R13L		Unknown	F → C	T → G	possibly damaging	chr19	45900279
PPP4R4	rs116524572	0.007576	R → W	C → T	probably damaging	chr14	94697644
PRAGMIN	rs28533138	0.028285	V → M	G → A	probably damaging	chr8	8176770
PRAGMIN	rs56351643	0.013877	P → T	C → A	benign	chr8	8233941
PRAMEF1	rs2982215	Unknown	P → L	C → T	benign	chr1	12856111
PRAMEF2	rs146271489	0.018976	A → T	G → A	benign	chr1	12921386
PRAMEF20	rs77164784	Unknown	D → N	G → A	possibly damaging	chr1	13743058
PRAMEF20		Unknown	R → G	A → G	benign	chr1	13743085
PRAMEF6	rs1967669	Unknown	C → S	G → C	possibly damaging	chr1	13001312
PRAMEF6	rs4285708	Unknown	K → T	A → C	possibly damaging	chr1	13365954
PRAMEF6	rs7419099	Unknown	C → Y	G → A	benign	chr1	13001186
PRB3		Unknown	R → H	G → A	benign	chr12	11420773
PRB4	rs12308381	Unknown	P → T	C → A	probably damaging	chr12	11461706
PRELID2	rs9324996	0.036818	N → S	A → G	benign	chr5	145197565
PRKAG3	rs33985460	0.035463	R → W	C → T	probably damaging	chr2	219691801

PRMT10		Unknown	S → T	G → C	benign	chr4	148591832
PRR21	rs115609219	0.036269	H → Y	C → T	possibly damaging	chr2	240982312
PRR21		Unknown	C → R	T → C	benign	chr2	240981823
PRR21	rs148163158	0.00307	M → T	T → C	benign	chr2	240982047
PRSS3		Unknown	V → A	T → C	benign	chr7	142479915
PRSS3		Unknown	T → I	C → T	benign	chr7	142479954
PRSS3		Unknown	S → Y	C → A	benign	chr7	142480002
PRSS3		Unknown	P → S	C → T	benign	chr7	142480067
PRSS3		Unknown	M → L	A → C	benign	chr7	142481251
PRTN3	rs150802678	0.006266	R → H	G → A	probably damaging	chr19	847944
PSEN1	rs63750907	Unknown	T → I	C → T	probably damaging	chr14	73640375
PTF1A		Unknown	S → R	C → A	probably damaging	chr10	23482649
PTGFRN	rs71483896	Unknown	S → T	T → A	benign	chr1	117487711
PTPN12	rs2230602	0.04609	E → K	G → A	benign	chr7	77265140
PTPN3		Unknown	R → Q	G → A	probably damaging	chr9	112144053
PTPN3		Unknown	V → M	G → A	benign	chr9	112185089
PTPRE		Unknown	R → W	C → T	probably damaging	chr10	129847916
PTPRO	rs71459181	0.00712	V → I	G → A	possibly damaging	chr12	15661564
PTPRU	rs141378439	0.005326	R → Q	G → A	probably damaging	chr1	29609217
PVRL1	rs78809001	0.007571	R → Q	G → A	probably damaging	chr11	119548402
PWP1	rs11547907	0.034415	L → F	G → C	benign	chr12	108096769
RAB33A	rs11542874	0.014459	L → V	C → G	benign	chrX	129306052
RADIL	rs414035	0.00318	S → G	A → G	benign	chr7	4841470
RAPGEF5	rs28716840	0.026572	P → H	C → A	benign	chr7	22202046
RBM12B	rs150172581	Unknown	P → L	C → T	probably damaging	chr8	94746933
REST	rs61754065	0.004394	P → S	C → T	benign	chr4	57797230
REXO1L1	rs112143831	Unknown	P → T	C → A	possibly damaging	chr8	86575141
RFTN1	rs34276015	0.033441	E → K	G → A	possibly damaging	chr3	16419309
RGMB	rs2662263	0.004096	S → R	A → C	benign	chr5	98109838

RGNEF		Unknown	V → I	G → A	benign	chr5	73190313
RGPD3		Unknown	P → S	C → T	probably damaging	chr2	107039817
RGPD3	rs62152468	Unknown	E → Q	G → C	possibly damaging	chr2	107049714
RGPD3	rs2912695	Unknown	N → D	A → G	benign	chr2	107049681
RGPD3	rs2556281	Unknown	K → N	G → T	benign	chr2	107049703
RNF39	rs2301752	0.049311	A → T	G → A	possibly damaging	chr6	30039418
RNGTT	rs140205258	0.004673	G → D	G → A	benign	chr6	89601534
RP2	rs1805147	0.003018	R → W	C → T	possibly damaging	chrX	46719498
RRN3	rs2541719	Unknown	S → L	C → T	possibly damaging	chr16	15178499
RTEL1	rs3848668	0.04887	N → S	A → G	benign	chr20	62293272
RTN4RL1	rs181444163	Unknown	G → S	G → A	probably damaging	chr17	1840677
SACS	rs147099630	0.006608	N → S	A → G	benign	chr13	23913549
SBK2	rs620251	0.045061	A → P	G → C	benign	chr19	56041255
SCARF2	rs759612	0.028741	V → L	G → C	benign	chr22	20779946
SCARF2	rs70944210	Unknown	D → E	C → G	benign	chr22	20779947
SCNM1	rs1115	0.005394	E → K	G → A	benign	chr1	151140732
SCRN3	rs41270195	0.026449	S → I	G → T	benign	chr2	175289259
SDK2	rs117687984	0.006066	Y → H	T → C	possibly damaging	chr17	71468356
SDK2	rs2270716	0.04159	L → V	C → G	benign	chr17	71380087
SERPINI1	rs55872908	0.0113	A → T	G → A	benign	chr3	167512569
SETD4	rs2835239	0.033528	I → V	A → G	possibly damaging	chr21	37410477
SEZ6		Unknown	R → H	G → A	benign	chr17	27291138
SFT2D3	rs148183380	Unknown	E → D	G → T	benign	chr2	128459192
SH2D3A	rs143503063	0.001405	P → S	C → T	probably damaging	chr19	6754093
SHARPIN	rs11541805	0.017834	P → S	C → T	benign	chr8	145154910
SIGLEC12	rs61743142	0.012471	V → M	G → A	possibly damaging	chr19	52000187
SIGLEC6	rs60467951	0.025997	R → Q	G → A	possibly damaging	chr19	52034506
SKA3	rs17279819	0.042705	D → E	C → A	benign	chr13	21732175
SLC25A2	rs10075302	0.047014	G → C	G → T	possibly damaging	chr5	140682958

SLC26A3	rs34407351	0.029783	C → W	T → G	possibly damaging	chr7	107427322
SLC26A8		Unknown	C → R	T → C	probably damaging	chr6	35980088
SLC29A3	rs34040486	0.5	V → I	G → A	benign	chr10	73115942
SLC36A2	rs77010315	0.00727	G → V	G → T	probably damaging	chr5	150723155
SLC6A17	rs35600013	0.5	A → T	G → A	benign	chr1	110709720
SLC9A2		Unknown	S → P	T → C	benign	chr2	103317683
SLC9A9	rs2289491	0.021602	I → V	A → G	benign	chr3	142985717
SLCO1C1	rs36010656	0.037422	P → T	C → A	benign	chr12	20864342
SMC2		Unknown	D → H	G → C	possibly damaging	chr9	106887330
SON	rs34373121	Unknown	R → S	A → C	unknown	chr21	34948697
SORCS2	rs35935435	0.005296	D → E	C → A	benign	chr4	7666180
SOX17	rs189384157	Unknown	A → D	C → A	possibly damaging	chr8	55370796
SP100	rs57377576	Unknown	M → V	A → G	benign	chr2	231333763
SPDYE5	rs794362	0.000913	R → H	G → A	benign	chr7	75131251
SPIB	rs113934432	Unknown	A → P	G → C	benign	chr19	50926265
SPRN	rs2492666	0.00228	T → M	C → T	possibly damaging	chr10	135237166
SPZ1	rs2047589	0.041933	M → I	G → A	benign	chr5	79616544
SRRM4	rs140426282	Unknown	R → P	G → C	possibly damaging	chr12	119594512
STAB2	rs149382223	0.000659	Y → H	T → C	probably damaging	chr12	104089554
STARD8	rs55927581	0.017631	G → R	G → A	benign	chrX	67938269
STK36	rs16859180	0.046659	R → W	C → T	probably damaging	chr2	219553468
SVEP1	rs142508835	Unknown	S → T	T → A	possibly damaging	chr9	113192279
SYNE2	rs75568433	0.009944	P → T	C → A	probably damaging	chr14	64596823
SYNM	rs5030697	0.009593	P → L	C → T	benign	chr15	99671741
SYT8		Unknown	S → F	C → T	possibly damaging	chr11	1856580
TAF6L	rs144825291	0.011884	T → M	C → T	possibly damaging	chr11	62543398
TAF7L	rs147493489	0.005492	E → K	G → A	benign	chrX	100547853
TARS2		Unknown	R → C	C → T	probably damaging	chr1	150479448
TAS1R3	rs76755863	0.033124	A → T	G → A	benign	chr1	1266738

TAS2R43	rs113197337	Unknown	L → V	C → G	benign	chr12	11244687
TBC1D1	rs61731607	0.033657	A → P	G → C	benign	chr4	38023279
TBC1D1	rs61731610	0.041301	G → S	G → A	benign	chr4	38023294
TBC1D5	rs79960281	0.012166	Y → C	A → G	probably damaging	chr3	17349498
TBX15	rs61730011	0.030214	M → R	T → G	probably damaging	chr1	119427467
TCEB3C	rs74217850	0.5	S → C	C → G	possibly damaging	chr18	44555312
TCF19	rs7750641	0.036202	P → S	C → T	benign	chr6	31129310
TCF3	rs35354874	0.008314	L → P	T → C	probably damaging	chr19	1627365
TCN2	rs1131603	0.031902	L → S	T → C	probably damaging	chr22	31018975
TCP10L2	rs142318145	Unknown	A → T	G → A	possibly damaging	chr6	167585654
TEKT5	rs138126929	0.005492	V → I	G → A	benign	chr16	10788550
TESSP1	rs61747737	0.029386	F → C	T → G	probably damaging	chr16	2854507
TESSP5		Unknown	N → S	A → G	benign	chr3	46783919
TG	rs2069548	0.007662	G → D	G → A	probably damaging	chr8	133899575
THEM4	rs3748805	0.005455	L → R	T → G	benign	chr1	151881885
TIAM1	rs146645440	0.000439	A → T	G → A	benign	chr21	32492757
TJP2	rs41277907	0.049168	S → F	C → T	benign	chr9	71865988
TLR10	rs11466649	0.048838	A → S	G → T	benign	chr4	38776725
TMED9	rs57960711	0.034666	T → S	C → G	benign	chr5	177019262
TMEM146	rs139627891	Unknown	I → V	A → G	benign	chr19	5748257
TMEM217	rs150173395	0.002197	M → T	T → C	benign	chr6	37186394
TMEM223	rs118167825	0.010399	H → R	A → G	probably damaging	chr11	62559351
TMOD4	rs143662204	0.005492	M → V	A → G	benign	chr1	151143016
TMTC1		Unknown	A → V	C → T	probably damaging	chr12	29911688
TMX4	rs1135711	0.028128	Y → C	A → G	benign	chr20	7964476
TNIK	rs17857452	0.015436	A → T	G → A	benign	chr3	170802910
TNK1	rs1142390	Unknown	V → M	G → A	benign	chr17	7292107
TNP2	rs71383203	0.007306	Q → H	G → C	benign	chr16	11363003
TNXB	rs1150752	0.030842	T → A	A → G	benign	chr6	32064726

TOR1AIP1	rs17279712	0.043211	Q → H	A → C	benign	chr1	179877780
TP53RK	rs34983477	0.02987	R → Q	G → A	possibly damaging	chr20	45315786
TPSB2	rs1141965	Unknown	G → V	G → T	probably damaging	chr16	1279732
TPSB2	rs2272968	Unknown	R → P	G → C	benign	chr16	1279909
TPSB2		Unknown	N → S	A → G	benign	chr16	1279945
TREML1	rs138237630	0.002636	D → E	T → A	benign	chr6	41117594
TRIM73		Unknown	W → R	T → A	benign	chr7	75028434
TRPC4	rs73184536	0.040665	I → V	A → G	benign	chr13	38211105
TSC1		Unknown	M → T	T → C	benign	chr9	135786904
TSHR	rs2234919	0.038462	P → T	C → A	benign	chr14	81422178
TSHZ1	rs33930274	0.03125	A → T	G → A	benign	chr18	72998899
TSPAN10	rs34896443	0.03581	R → H	G → A	benign	chr17	79612541
TTC28	rs56085644	0.000457	R → H	G → A	benign	chr22	28378351
TTC28		Unknown	T → A	A → G	benign	chr22	29075678
TTC3	rs61999340	0.034687	L → V	C → G	probably damaging	chr21	38494273
TTC5	rs61741728	0.00616	Y → C	A → G	probably damaging	chr14	20763603
TLL10	rs114390380	0.01198	G → R	G → A	benign	chr1	1115548
TULP2	rs139577147	0.006157	R → H	G → A	benign	chr19	49392882
TULP4		Unknown	S → G	A → G	benign	chr6	158923156
TUT1	rs117162358	0.007927	R → H	G → A	probably damaging	chr11	62344743
TYMP	rs112723255	0.030165	A → T	G → A	benign	chr22	50964255
UGT2B4	rs67904882	Unknown	D → E	T → A	benign	chr4	70346565
UNC45B	rs11654824	0.048883	I → N	T → A	possibly damaging	chr17	33513337
UNC84A		Unknown	G → S	G → A	benign	chr7	897562
USP32		Unknown	N → S	A → G	benign	chr17	58288396
USP54	rs61761603	0.00905	G → A	G → C	possibly damaging	chr10	75258901
VCX2	rs5934423	Unknown	T → R	C → G	benign	chrX	8138641
VN1R4	rs12977715	Unknown	D → N	A → G	benign	chr19	53770261
VPS13B	rs142476821	0.002334	A → T	G → A	probably damaging	chr8	100874030

VPS37A	rs17502618	0.006298	I → F	A → T	benign	chr8	17132441
VRK3	rs35331034	0.000659	R → C	C → T	probably damaging	chr19	50491738
WASF3	rs17084492	0.047899	S → L	C → T	benign	chr13	27257004
WDR1	rs41268387	0.004113	H → R	A → G	benign	chr4	10089539
WDR86	rs4141455	0.003643	M → T	T → C	benign	chr7	151078735
WISP1	rs143089011	0.000463	A → T	G → A	benign	chr8	134233060
WSCD1	rs61735454	0.013158	P → L	C → T	benign	chr17	5984358
XRRA1	rs61736355	0.033539	A → V	C → T	probably damaging	chr11	74618265
YEATS2	rs74496163	0.040295	A → T	G → A	benign	chr3	183508714
ZBP1	rs41304401	0.004454	G → S	G → A	possibly damaging	chr20	56188219
ZC3H12A	rs17849897	0.016995	G → D	G → A	benign	chr1	37949052
ZFHx4	rs56261025	0.026014	V → L	G → C	benign	chr8	77616519
ZMYM4	rs77324819	0.001484	I → V	A → G	benign	chr1	35847342
ZNF22	rs3740093	0.042823	S → G	A → G	benign	chr10	45499009
ZNF257	rs140340371	Unknown	C → R	T → C	benign	chr19	22256303
ZNF286B	rs2654297	Unknown	V → A	T → C	benign	chr17	18584142
ZNF34		Unknown	S → P	T → C	benign	chr8	145999712
ZNF345	rs149031424	0.00331	T → I	C → T	benign	chr19	37368133
ZNF443	rs74181783	0.5	K → T	A → C	probably damaging	chr19	12541547
ZNF468	rs75548544	Unknown	E → G	A → G	possibly damaging	chr19	53344051
ZNF469	rs141255631	Unknown	A → E	C → A	benign	chr16	88497651
ZNF517	rs2976653	0.005906	V → A	T → C	benign	chr8	146033347
ZNF676	rs115951008	0.01778	Y → C	A → G	possibly damaging	chr19	22364031
ZNF717	rs71630106	0.5	V → I	G → A	benign	chr3	75786832
ZNF77	rs144419578	0.001762	Q → E	C → G	probably damaging	chr19	2936664
ZNF790		Unknown	R → T	G → C	benign	chr19	37311004
ZNF880	rs148392772	Unknown	R → Q	G → A	benign	chr19	52887603
ZP1	rs145067883	0.003298	V → I	G → A	benign	chr11	60636698