

## Supplementary Online Content

Ghani M, Reitz C, Cheng R, et al; Alzheimer's Disease Genetics Consortium. Association of long runs of homozygosity with Alzheimer disease among African American individuals. *JAMA Neurol*. Published online September 14, 2015. doi:10.1001/jamaneurol.2015.1700.

**eFigure 1.** Population STRUCTURE Analyses

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**eTable 1.** A 114-kb Consensus Region Flanked by SNPs rs6817611 and rs7669180 (chr4:152172448-152286356/hg18) Was Overlapped by ROHs>2Mb in 7 Cases and No Controls From the ADGC Data Set

**eTable 2.** A 202-kb Consensus Region Flanked by SNPs rs12442211 and rs11635599 (chr15: 72032728-72235049/hg18) Was Overlapped by >1Mb-ROHs in 5 Cases and No Controls (EMP1=0.0002; EMP2=0.023) From the CHAP-Indianapolis Data Set

**eTable 3.** Gene-Based Analyses of the Entire Data Set Revealed Several Genes on Chr3p21.31 That Were Intersected by ROHs>3Mb Significantly More Frequently in Cases Compared With Controls

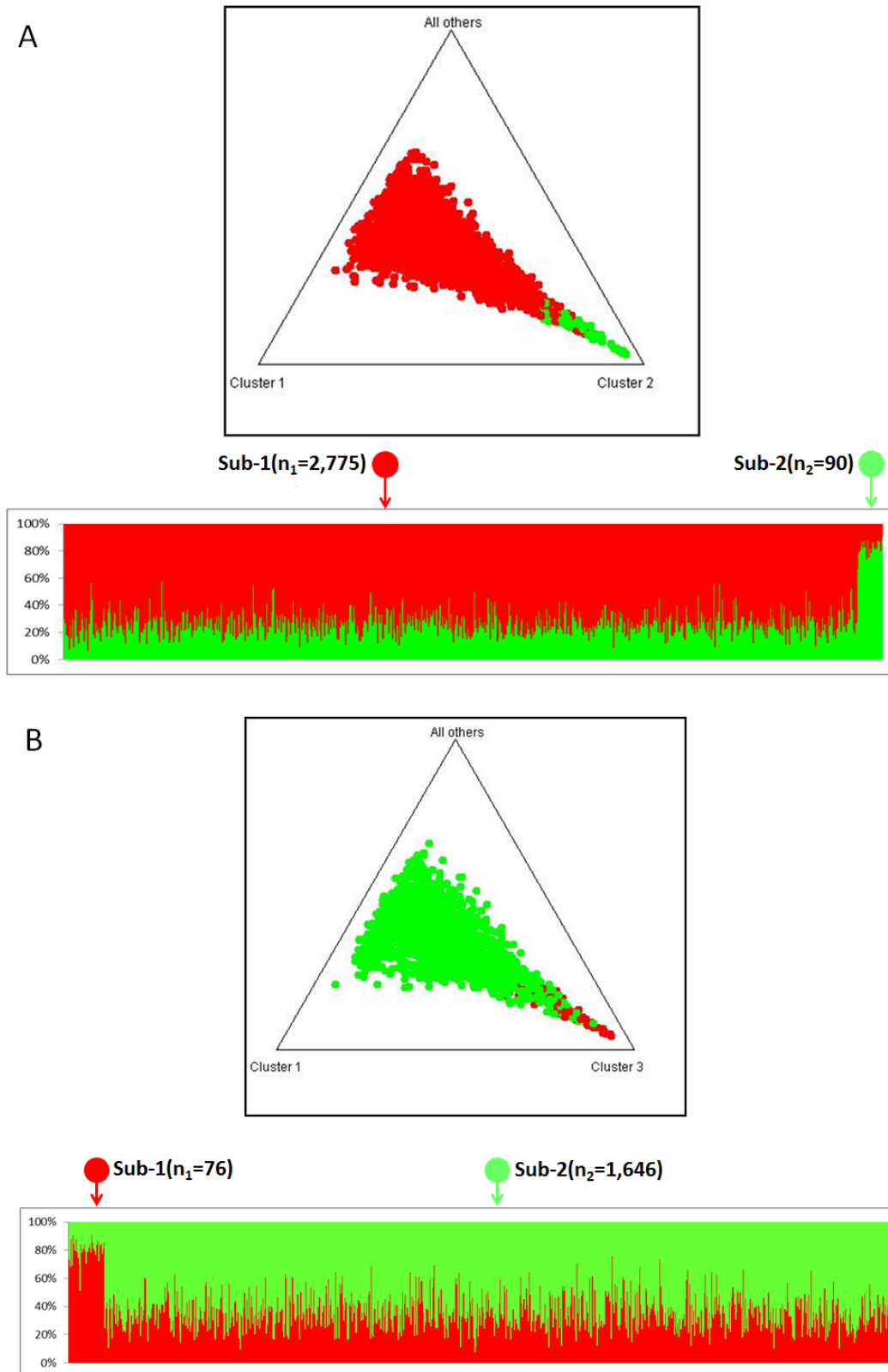
**eTable 4.** Nominally Significant Results Obtained in the Entire African American Data Set (AA) Compared With the Nominally Significant Results for the Caribbean Hispanic Data Set (HISP) (547 AD Cases and 542 Controls) Reported in Ghani et al, *JAMA Neurology* 2013

**eTable 5.** List of Nominally Significant Genes Intersected by ROHs in the ADGC and CHAP-Indianapolis (C-I) Data Sets

**eTable 6.** Potentially Damaging SNPs (With Their SIFT and Polyphen Scores For Missense Variants) Within the Canonical Transcripts of the Genes Inside the Consensus Regions Identified in the ADGC and CHAP-Indianapolis Data Sets

This supplementary material has been provided by the authors to give readers additional information about their work.

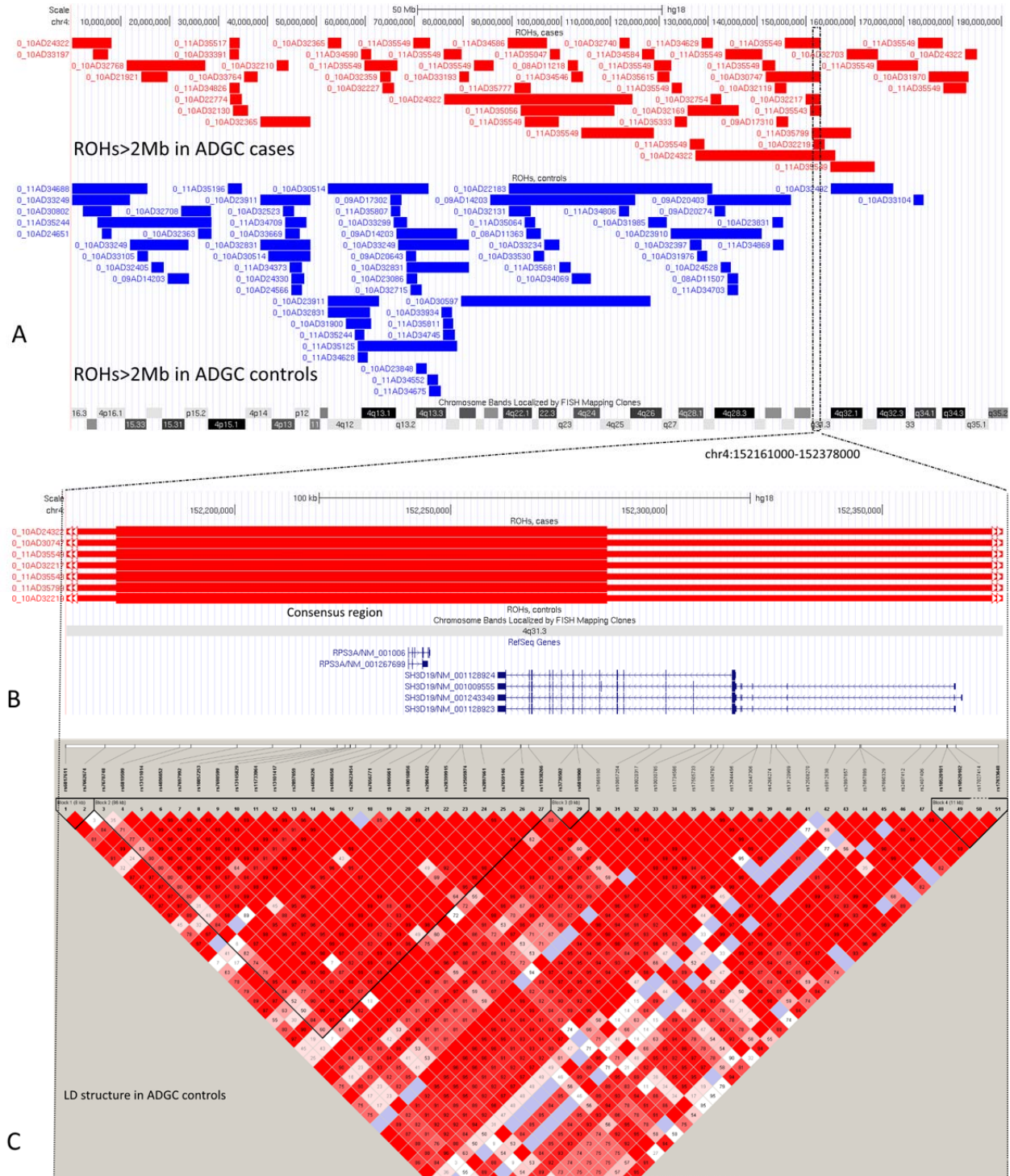
**eFigure 1. Population STRUCTURE Analyses**



**A.** Detection of 90 outliers in the ADGC dataset (using 452 selected independent SNPs). **B.** Detection of 76 outliers in the CHAP-Indianapolis dataset (using 518 selected independent SNPs).

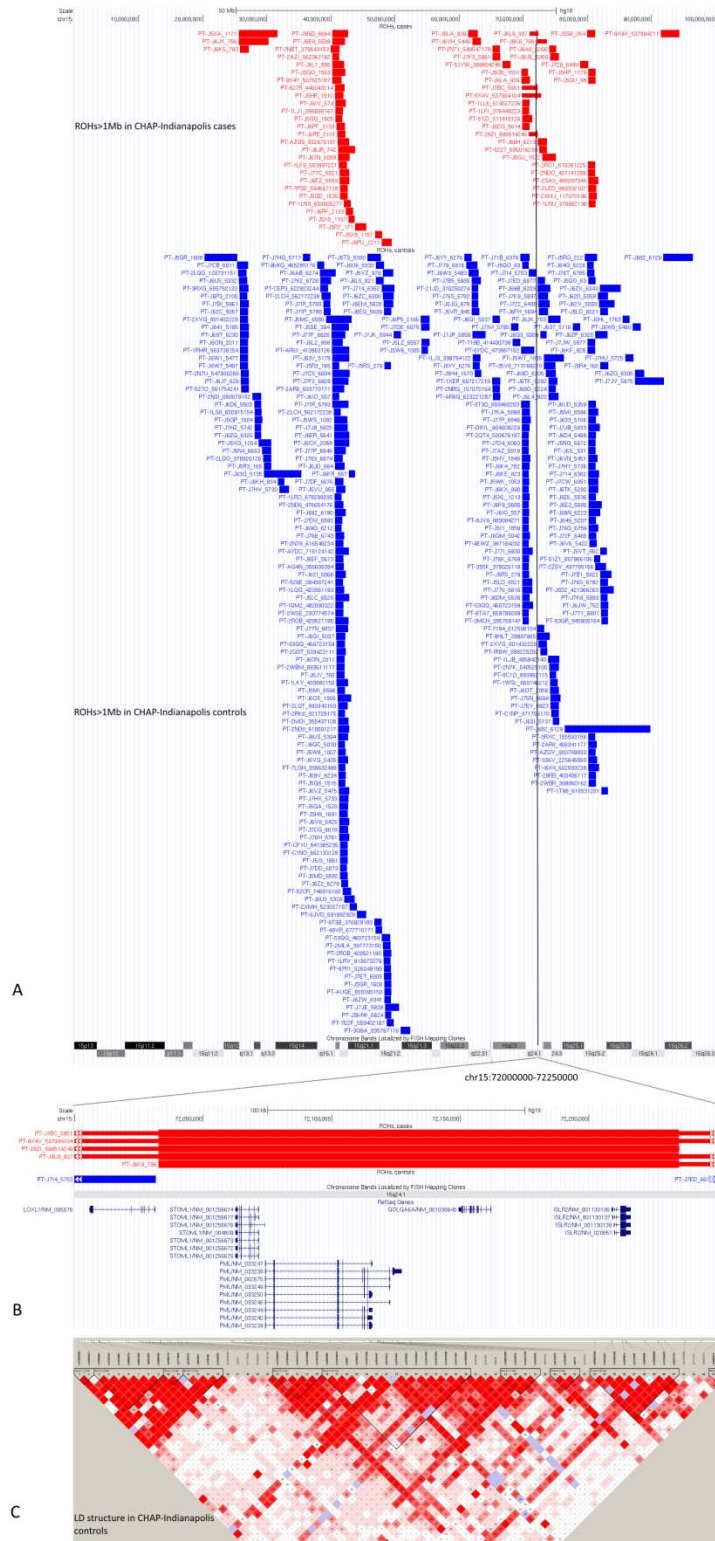
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**eFigure 2. Consensus Region on chr4q31.3 Associated With AD in the ADGC Data Set**



**A.** ROHs > 2Mb mapped to chromosome 4 among cases (n=871) and controls (n=1620) **B.** Significant consensus region at chr4q31.3 (dashed bar), which was overlapped by ROHs > 2Mb in 7 cases (thick red bars). **C.** LD structure of the Chr4:152161000-152378000/hg18 region among controls indicates that this consensus region belongs to a single LD block.

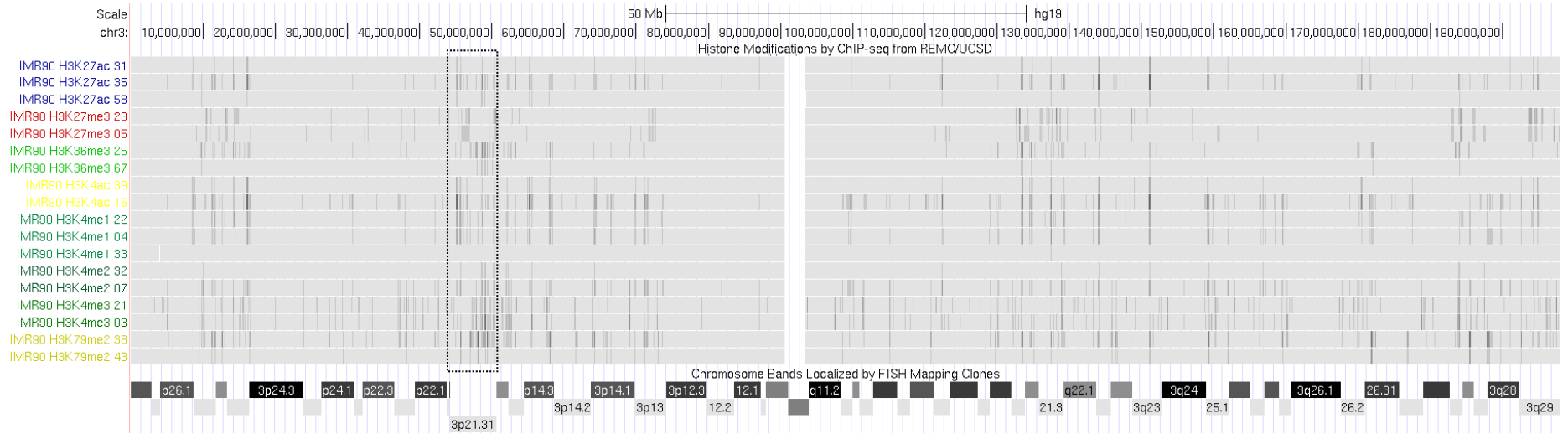
**eFigure 3. Consensus Region on chr15q24.1.3 Associated With AD in the CHAP-Indianapolis Data Set**



**A.** ROHs>1Mb on chromosome 15 among cases (n=279) and controls (n=1367). **B.** Significant consensus region on chr15q24.1 (vertical line), which was overlapped by ROHs>2Mb in 5 cases (thick red bars). **C.** LD structure of the Chr15:72000000-72250000/hg18 region among controls.

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**eFigure 4.** Histone Modifications Map of Chromosome 3 From the Roadmap Epigenomics Project (<http://www.roadmapepigenomics.org/>)



ChIP sequencing for the human cell line IMR90 revealed a dense accumulation of gene regulatory elements at Chr3p21.31 (dashed rectangle).

**eTable 1.** A 114-kb Consensus Region Flanked by SNPs rs6817611 and rs7669180 (chr4:152172448-152286356/hg18) Was Overlapped by ROHs>2Mb in 7 Cases and No Controls From the ADGC Data Set (EMP1=0.0008; EMP2=0.0438).

SNP	position	10AD24322	11AD35543	11AD35549	10AD32217	11AD35799	10AD30747	10AD32219
rs6817611	152172448	CC	CC	CC	CC	CC	CC	CC
rs7662674	152181140	CC	TT	TT	CC	TT	TT	TT
rs7678748	152187745	AA	AA	CC	CC	AA	AA	AA
rs6819599	152197581	TT	CC	CC	TT	TT	TT	TT
rs13131014	152200086	CC	CC	TT	CC	CC	CC	CC
rs4696652	152210222	AA	AA	AA	AA	CC	CC	CC
rs7697992	152218072	TT	GG	GG	GG	TT	TT	TT
rs10857253	152224234	TT	TT	TT	TT	CC	CC	CC
rs7698599	152232260	TT	TT	TT	TT	GG	GG	GG
rs13145829	152234103	GG	GG	GG	GG	AA	AA	AA
rs11733964	152235154	TT	TT	TT	TT	CC	CC	CC
rs13101417	152235226	CC	CC	CC	CC	TT	TT	TT
rs2897659	152236381	GG	GG	GG	GG	AA	AA	AA
rs4696226	152239679	CC	TT	TT	TT	CC	CC	CC
rs2280283	152240227	AA	GG	GG	GG	GG	GG	GG
rs4696658	152243776	TT	TT	TT	TT	GG	GG	GG
rs28523454	152244087	AA	AA	AA	AA	AA	AA	AA
rs7656771	152245419	CC	TT	TT	TT	TT	TT	TT
rs4696661	152250888	TT	CC	CC	CC	TT	TT	TT
rs10016856	152253885	AA	AA	AA	AA	AA	AA	AA
rs28644282	152254976	TT	TT	TT	TT	TT	TT	TT
rs28399915	152259414	GG	GG	GG	GG	GG	GG	GG
rs12505974	152259936	CC	CC	CC	CC	TT	TT	TT
rs2897661	152263998	TT	TT	TT	TT	TT	TT	TT
rs7659146	152272752	GG	AA	AA	AA	GG	GG	GG
rs7664483	152272858	GG	GG	GG	GG	AA	AA	AA
rs11938266	152274523	TT	CC	CC	CC	TT	TT	TT
rs3736502	152284647	TT	CC	CC	CC	CC	CC	CC
rs6818900	152285134	AA	AA	AA	AA	GG	AA	GA
rs7669180	152286356	AA	AA	AA	AA	CC	CC	CC

**eTable 2.** A 202-kb Consensus Region Flanked by SNPs rs12442211 and rs11635599 (chr15: 72032728-72235049/hg18) Was Overlapped by >1Mb-ROHs in 5 Cases and No Controls (EMP1=0.0002; EMP2=0.023) From the CHAP-Indianapolis Data Set. A shared haplotype was observed in 4 cases at the site of consensus region (red font).

SNP	Position	PT-9X4V_537994104	PT-28ZI_899514246	PT-J6L9_937	PT-J6K8_796	PT-J7BC_5951
rs12442211	72032728	GG	GG	GG	GG	AA
rs12101466	72035441	AA	AA	AA	AA	GG
rs12102019	72035530	TT	TT	TT	TT	CC
rs11854876	72038358	TT	TT	TT	TT	TT
rs10152173	72039461	TT	TT	TT	TT	CC
rs10152898	72042174	GG	GG	GG	GG	TT
rs11072458	72043460	AA	AA	AA	AA	GG
rs4886809	72045502	CC	CC	CC	CC	CC
rs11636934	72062223	AA	AA	AA	AA	GG
rs2507	72062729	AA	AA	AA	AA	GG
rs2289413	72063281	AA	AA	AA	AA	AA
rs11072460	72067920	TT	TT	TT	TT	GG
rs3816197	72069933	CC	CC	CC	CC	CC
rs5742914	72073982	CC	CC	CC	CC	CC
rs3784563	72078046	CC	CC	CC	CC	CC
rs3784562	72078076	CC	CC	CC	CC	TT
rs10162627	72086923	AA	AA	AA	AA	AA
rs11072463	72090402	CC	CC	CC	CC	CC
rs11072464	72092235	AA	AA	AA	AA	AA
rs11072468	72099847	TT	TT	TT	TT	TT
rs2277599	72104096	AA	AA	AA	AA	AA
rs11855663	72112796	GG	GG	GG	GG	GG
rs743580	72115169	AA	AA	AA	AA	AA
rs743581	72115194	GG	GG	GG	GG	GG
rs9479	72115629	AA	AA	AA	AA	AA
rs10851869	72118136	TT	TT	TT	TT	TT
rs1550434	72118264	CC	CC	CC	CC	CC
rs12917449	72118712	AA	AA	AA	AA	AA
rs3784556	72119241	GG	GG	GG	GG	GG
rs876383	72120466	GG	GG	GG	GG	GG
rs5742915	72123686	TT	TT	TT	TT	TT
rs1036673	72125515	CC	CC	CC	CC	CC
rs6772	72125992	CC	CC	CC	CC	CC
rs723434	72130383	TT	TT	TT	TT	TT
rs28503548	72200687	GG	GG	GG	GG	AA
rs4454921	72206862	AA	AA	AA	AA	AA
rs12904268	72207279	TT	TT	TT	TT	TT
rs3910071	72211204	TT	TT	TT	TT	TT
rs3743207	72212463	TT	TT	TT	TT	TT
rs3889598	72212558	CC	CC	CC	CC	CC
rs16969056	72219707	GG	GG	GG	GG	AA
rs12164922	72224840	GG	GG	GG	GG	GG
rs8033129	72227472	AA	00	AA	AA	CC
rs11635599	72235049	TT	TT	TT	TT	TT



**eTable 3.** Gene-Based Analyses of the Entire Data Set Revealed Several Genes on Chr3p21.31 That Were Intersected by ROHs>3Mb Significantly More Frequently in Cases Compared With Controls

Gene	Reference Sequence	EMP1	EMP2	Cases	Controls	%cases	%controls	strand	txStart/hg18	txEnd/hg18	cdsStart/hg18	cdsEnd/hg18	exonCount
CSPG5	NM_001206942	0.0001	0.0392	31	23	1.62%	0.60%	-	47578731	47596734	47579093	47594105	5
PFKFB4	NM_004567	0.0001	0.0064	45	37	2.35%	0.96%	-	48530120	48569231	48532183	48569214	14
UCN2	NM_033199	0.0002	0.0131	46	40	2.40%	1.04%	-	48574154	48576205	48575222	48575561	2
COL7A1	NM_000094	0.0002	0.0131	46	40	2.40%	1.04%	-	48576509	48607597	48576842	48607596	118
UQCRC1	NM_003365	0.0002	0.0131	46	40	2.40%	1.04%	-	48611435	48622102	48611564	48622057	13
TMEM89	NM_001008269	0.0003	0.0296	46	41	2.40%	1.06%	-	48633278	48634193	48633278	48634193	2
SLC26A6	NM_001040454	0.0003	0.0320	46	42	2.40%	1.09%	-	48638159	48646283	48638422	48646032	20
CAMKV	NM_024046	0.0001	0.0391	48	45	2.50%	1.17%	-	49870425	49882373	49871754	49874825	11
MST1R	NM_002447	0.0001	0.0391	48	45	2.50%	1.17%	-	49899439	49916310	49899743	49916046	20
MON1A	NM_032355	0.0001	0.0391	48	45	2.50%	1.17%	-	49921305	49942449	49921450	49942323	6
RBM6	NM_001167582	0.0001	0.0391	48	45	2.50%	1.17%	+	49952480	50089689	50060690	50089570	17
RBM5	NM_005778	0.0001	0.0301	46	42	2.40%	1.09%	+	50101344	50131401	50102871	50130893	25
SEMA3F	NM_004186	0.0002	0.0420	47	44	2.45%	1.14%	+	50167851	50201512	50172059	50200552	19
SLC38A3	NM_006841	0.0001	0.0320	46	42	2.40%	1.09%	+	50217682	50233415	50226636	50232613	16
GNAI2	NM_001166425	0.0001	0.0320	46	42	2.40%	1.09%	+	50259329	50271790	50259504	50270126	9
SEMA3B	NM_001290060	0.0001	0.0320	46	42	2.40%	1.09%	+	50281430	50289606	50281676	50289141	17
LSMEM2	NM_153215	0.0001	0.0320	46	42	2.40%	1.09%	+	50291461	50300549	50291548	50299637	4
IFRD2	NM_006764	0.0001	0.0320	46	42	2.40%	1.09%	-	50300166	50305030	50300625	50304901	12
HYAL3	NM_001200029	0.0001	0.0320	46	42	2.40%	1.09%	-	50305262	50311297	50305680	50308037	4
NAT6	NM_001200018	0.0001	0.0320	46	42	2.40%	1.09%	-	50308836	50311324	50309037	50309898	2
HYAL1	NM_153281	0.0001	0.0320	46	42	2.40%	1.09%	-	50312323	50324816	50312917	50315391	6
TUSC2	NM_007275	0.0001	0.0320	46	42	2.40%	1.09%	-	50337343	50340673	50338555	50340534	3
RASSF1	NM_170712	0.0001	0.0320	46	42	2.40%	1.09%	-	50342220	50350668	50343015	50344493	6
ZMYND10	NM_015896	0.0001	0.0320	46	42	2.40%	1.09%	-	50353540	50358160	50353844	50358014	12
NPRL2	NM_006545	0.0001	0.0320	46	42	2.40%	1.09%	-	50359922	50363490	50360040	50363087	11
CYB561D2	NM_007022	0.0001	0.0320	46	42	2.40%	1.09%	+	50363129	50366500	50363868	50366179	4
TMEM115	NM_007024	0.0001	0.0320	46	42	2.40%	1.09%	-	50367183	50371943	50367777	50371498	2
CACNA2D2	NM_001291101	0.0001	0.0320	46	42	2.40%	1.09%	-	50375047	50516679	50377100	50488633	38
C3orf18	NM_001171741	0.0002	0.0392	45	41	2.35%	1.06%	-	50570459	50583462	50572091	50578134	5
HEMK1	NM_016173	0.0001	0.0301	45	40	2.35%	1.04%	+	50581912	50597425	50583539	50592852	11
CISH	NM_013324	0.0001	0.0279	45	39	2.35%	1.01%	-	50618888	50624266	50620041	50622878	4
MAPKAPK3	NM_001243926	0.0001	0.0279	45	39	2.35%	1.01%	+	50624296	50661732	50630000	50660481	13
DOCK3	NM_004947	0.0001	0.0279	45	39	2.35%	1.01%	+	50687675	51396669	50687698	51394030	53



**eTable 4.** Nominally Significant Results Obtained in the Entire African American Data Set (AA) Compared With the Nominally Significant Results for the Caribbean Hispanic Data Set (HISP) (547 AD Cases and 542 Controls) Reported in Ghani et al, *JAMA Neurology* 2013

Chr	Gene	RefSeq	Band	Dataset	EMP1	EMP2
3	NKTR	NM_005385	Chr3p22.1	AA	0.003	0.997
				HISP	0.038	1.000
3	SEC22C	NM_001201572	Chr3p22.1	AA	0.003	0.997
				HISP	0.038	1.000
3	SS18L2	NM_016305	Chr3p22.1	AA	0.003	0.997
				HISP	0.038	1.000
3	ZBTB47	NM_145166	Chr3p22.1	AA	0.001	0.789
				HISP	0.038	1.000
3	SCN5A	NM_001099405	Chr3p22.2	AA	0.018	1.000
				HISP	0.030	1.000
3	RBMS3	NM_001177711	Chr3p24.1	AA	0.045	1.000
				HISP	0.008	0.997
9	PAX5	NM_001280548	Chr9p13.2	AA	0.037	1.000
				HISP	0.007	0.997
9	ZCCHC7	NM_001289120	Chr9p13.2	AA	0.044	1.000
				HISP	0.007	0.997
9	NFX1	NM_002504	Chr9p13.3	AA	0.049	1.000
				HISP	0.035	1.000
9	AQP7	NM_001170	Chr9p13.3	AA	0.049	1.000
				HISP	0.035	1.000
19	INSR	NM_000208	Chr19p13.2	AA	0.037	1.000
				HISP	0.032	1.000
19	ZNF557	NM_024341	Chr19p13.2	AA	0.037	1.000
				HISP	0.016	1.000

**eTable 5.** List of Nominally Significant Genes Intersected by ROHs in the ADGC and CHAP-Indianapolis (C-I) Data Sets

Gene	EMP1	EMP2	dataset	ROHs>	Cytoband	Transcript	txStart/hg18	txEnd/hg18	cdsStart/hg18	cdsEnd/hg18	exonCount
POMGNT2	0.0433	1.0000	ADGC	1Mb	3p22.1	NM_032806	43095724	43122579	43096184	43097927	2
POMGNT2	0.0291	1.0000	C-I	1Mb	3p22.1	NM_032806	43095724	43122579	43096184	43097927	2
CDC25A	0.0359	0.9962	ADGC	3Mb	3p21.31	NM_001789	48173671	48204805	48175438	48204441	15
CDC25A	0.0052	0.2407	C-I	3Mb	3p21.31	NM_001789	48173671	48204805	48175438	48204441	15
CDC25A	0.0220	0.9990	C-I	2Mb	3p21.31	NM_001789	48173671	48204805	48175438	48204441	15
MIR4443	0.0359	0.9962	ADGC	3Mb	3p21.31	NR_039645	48213057	48213110	48213110	48213110	1
MIR4443	0.0052	0.2407	C-I	3Mb	3p21.31	NR_039645	48213057	48213110	48213110	48213110	1
MIR4443	0.0220	0.9990	C-I	2Mb	3p21.31	NR_039645	48213057	48213110	48213110	48213110	1
CAMP	0.0359	0.9962	ADGC	3Mb	3p21.31	NM_004345	48239840	48241985	48239996	48241918	4
CAMP	0.0052	0.2407	C-I	3Mb	3p21.31	NM_004345	48239840	48241985	48239996	48241918	4
CAMP	0.0220	0.9990	C-I	2Mb	3p21.31	NM_004345	48239840	48241985	48239996	48241918	4
ZNF589	0.0234	0.9896	ADGC	3Mb	3p21.31	NM_016089	48257599	48287483	48257665	48285280	4
ZNF589	0.0052	0.2407	C-I	3Mb	3p21.31	NM_016089	48257599	48287483	48257665	48285280	4
ZNF589	0.0220	0.9990	C-I	2Mb	3p21.31	NM_016089	48257599	48287483	48257665	48285280	4
NME6	0.0234	0.9896	ADGC	3Mb	3p21.31	NM_005793	48310592	48317852	48311130	48317806	6
NME6	0.0052	0.2407	C-I	3Mb	3p21.31	NM_005793	48310592	48317852	48311130	48317806	6
NME6	0.0220	0.9990	C-I	2Mb	3p21.31	NM_005793	48310592	48317852	48311130	48317806	6
SPINK8	0.0234	0.9896	ADGC	3Mb	3p21.31	NM_001080525	48323339	48344835	48323485	48344835	5
SPINK8	0.0052	0.2407	C-I	3Mb	3p21.31	NM_001080525	48323339	48344835	48323485	48344835	5
SPINK8	0.0220	0.9990	C-I	2Mb	3p21.31	NM_001080525	48323339	48344835	48323485	48344835	5
FBXW12	0.0234	0.9896	ADGC	3Mb	3p21.31	NM_001159929	48388712	48411194	48388781	48411128	10
FBXW12	0.0015	0.1976	C-I	3Mb	3p21.31	NM_001159929	48388712	48411194	48388781	48411128	10
FBXW12	0.0076	0.9971	C-I	2Mb	3p21.31	NM_001159929	48388712	48411194	48388781	48411128	10
FBXW12	0.0266	1.0000	C-I	1Mb	3p21.31	NM_001159929	48388712	48411194	48388781	48411128	10
PLXNB1	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0015	0.1976	C-I	3Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0015	0.1976	C-I	3Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0015	0.1976	C-I	3Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0015	0.1976	C-I	3Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0076	0.9971	C-I	2Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0076	0.9971	C-I	2Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0076	0.9971	C-I	2Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0076	0.9971	C-I	2Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0076	0.9971	C-I	2Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0266	1.0000	C-I	1Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0266	1.0000	C-I	1Mb	3p21.31	NM_001130082	48420264	48446464	48420896	48441024	38
PLXNB1	0.0266	1.0000	C-I	1Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
PLXNB1	0.0266	1.0000	C-I	1Mb	3p21.31	NM_002673	48420264	48445876	48420896	48441024	38
CCDC51	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_001256966	48448583	48456533	48448821	48450270	4
CCDC51	0.0015	0.1976	C-I	3Mb	3p21.31	NM_001256966	48448583	48456533	48448821	48450270	4
CCDC51	0.0076	0.9971	C-I	2Mb	3p21.31	NM_001256966	48448583	48456533	48448821	48450270	4
CCDC51	0.0266	1.0000	C-I	1Mb	3p21.31	NM_001256966	48448583	48456533	48448821	48450270	4
TMA7	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_015933	48456689	48460541	48456710	48460294	4
TMA7	0.0015	0.1976	C-I	3Mb	3p21.31	NM_015933	48456689	48460541	48456710	48460294	4
TMA7	0.0076	0.9971	C-I	2Mb	3p21.31	NM_015933	48456689	48460541	48456710	48460294	4
TMA7	0.0266	1.0000	C-I	1Mb	3p21.31	NM_015933	48456689	48460541	48456710	48460294	4
ATRIP	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0309	0.9947	ADGC	3Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0468	1.0000	ADGC	2Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0468	1.0000	ADGC	2Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0015	0.1976	C-I	3Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0015	0.1976	C-I	3Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0119	0.9977	C-I	2Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0119	0.9977	C-I	2Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0253	1.0000	C-I	1Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12
ATRIP	0.0253	1.0000	C-I	1Mb	3p21.31	NM_032166	48463117	48482058	48463253	48481957	12



SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0119	0.9977	C-I	2Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272066	48484200	48517263	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272067	48484200	48517251	48485509	48513713	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_001272068	48484200	48516487	48485509	48513713	7
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0350	1.0000	C-I	1Mb	3p21.31	NM_016479	48484200	48516686	48485509	48516531	6
SHISA5	0.0359	1.0000	C-I	1Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0359	1.0000	C-I	1Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0359	1.0000	C-I	1Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
SHISA5	0.0359	1.0000	C-I	1Mb	3p21.31	NM_001272083	48484200	48489746	48485740	48489427	3
MIR6823	0.0441	1.0000	ADGC	3Mb	3p21.31	NR_106881	48562397	48562458	48562458	48562458	1
MIR6823	0.0010	0.0329	C-I	3Mb	3p21.31	NR_106881	48562397	48562458	48562458	48562458	1
MIR6823	0.0064	0.9971	C-I	2Mb	3p21.31	NR_106881	48562397	48562458	48562458	48562458	1
MIR6823	0.0410	1.0000	C-I	1Mb	3p21.31	NR_106881	48562397	48562458	48562458	48562458	1
MIR711	0.0490	1.0000	ADGC	1Mb	3p21.31	NR_031756	48591338	48591414	48591414	48591414	1
MIR711	0.0010	0.0329	C-I	3Mb	3p21.31	NR_031756	48591338	48591414	48591414	48591414	1
MIR711	0.0064	0.9971	C-I	2Mb	3p21.31	NR_031756	48591338	48591414	48591414	48591414	1
CELSR3-AS1	0.0341	1.0000	ADGC	1Mb	3p21.31	NR_111921	48676204	48681607	48681607	48681607	3
CELSR3-AS1	0.0014	0.1982	C-I	3Mb	3p21.31	NR_111921	48676204	48681607	48681607	48681607	3
CELSR3-AS1	0.0103	0.9973	C-I	2Mb	3p21.31	NR_111921	48676204	48681607	48681607	48681607	3
NCKIPSD	0.0217	1.0000	ADGC	1Mb	3p21.31	NM_016453	48686275	48698370	48686980	48698244	13
NCKIPSD	0.0014	0.1982	C-I	3Mb	3p21.31	NM_016453	48686275	48698370	48686980	48698244	13
NCKIPSD	0.0103	0.9973	C-I	2Mb	3p21.31	NM_016453	48686275	48698370	48686980	48698244	13
IP6K2	0.0103	1.0000	ADGC	1Mb	3p21.31	NM_001005909	48700439	48729715	48700709	48707728	6

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IP6K2	0.0103	1.0000	ADGC	1Mb	3p21.31	NM_001005909	48700439	48729715	48700709	48707728	6
IP6K2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001005909	48700439	48729715	48700709	48707728	6
IP6K2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001005909	48700439	48729715	48700709	48707728	6
IP6K2	0.0103	0.9973	C-I	2Mb	3p21.31	NM_001005909	48700439	48729715	48700709	48707728	6
IP6K2	0.0103	0.9973	C-I	2Mb	3p21.31	NM_001005909	48700439	48729715	48700709	48707728	6
IP6K2	0.0103	1.0000	ADGC	1Mb	3p21.31	NM_001146179	48705886	48729715	48706900	48707728	4
IP6K2	0.0103	1.0000	ADGC	1Mb	3p21.31	NM_001146179	48705886	48729715	48706900	48707728	4
IP6K2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001146179	48705886	48729715	48706900	48707728	4
IP6K2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001146179	48705886	48729715	48706900	48707728	4
IP6K2	0.0103	0.9973	C-I	2Mb	3p21.31	NM_001146179	48705886	48729715	48706900	48707728	4
IP6K2	0.0103	0.9973	C-I	2Mb	3p21.31	NM_001146179	48705886	48729715	48706900	48707728	4
PRKAR2A	0.0144	1.0000	ADGC	1Mb	3p21.31	NM_004157	48763096	48860274	48764021	48860033	11
PRKAR2A	0.0014	0.1982	C-I	3Mb	3p21.31	NM_004157	48763096	48860274	48764021	48860033	11
PRKAR2A	0.0120	0.9977	C-I	2Mb	3p21.31	NM_004157	48763096	48860274	48764021	48860033	11
PRKAR2A-AS1	0.0124	1.0000	ADGC	1Mb	3p21.31	NR_109996	48860373	48864419	48864419	48864419	2
PRKAR2A-AS1	0.0124	1.0000	ADGC	1Mb	3p21.31	NR_109996	48860373	48864419	48864419	48864419	2
PRKAR2A-AS1	0.0014	0.1982	C-I	3Mb	3p21.31	NR_109996	48860373	48864419	48864419	48864419	2
PRKAR2A-AS1	0.0014	0.1982	C-I	3Mb	3p21.31	NR_109996	48860373	48864419	48864419	48864419	2
PRKAR2A-AS1	0.0120	0.9977	C-I	2Mb	3p21.31	NR_109996	48860373	48864419	48864419	48864419	2
PRKAR2A-AS1	0.0120	0.9977	C-I	2Mb	3p21.31	NR_109996	48860373	48864419	48864419	48864419	2
SLC25A20	0.0124	1.0000	ADGC	1Mb	3p21.31	NM_000387	48869359	48911430	48870146	48911231	9
SLC25A20	0.0014	0.1982	C-I	3Mb	3p21.31	NM_000387	48869359	48911430	48870146	48911231	9
SLC25A20	0.0120	0.9977	C-I	2Mb	3p21.31	NM_000387	48869359	48911430	48870146	48911231	9
ARIH2OS	0.0124	1.0000	ADGC	1Mb	3p21.31	NM_001123040	48930224	48931822	48930713	48931586	1
ARIH2OS	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001123040	48930224	48931822	48930713	48931586	1
ARIH2OS	0.0120	0.9977	C-I	2Mb	3p21.31	NM_001123040	48930224	48931822	48930713	48931586	1
ARIH2	0.0075	1.0000	ADGC	1Mb	3p21.31	NM_006321	48931284	48997975	48939995	48995707	16
ARIH2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_006321	48931284	48997975	48939995	48995707	16
ARIH2	0.0295	1.0000	C-I	2Mb	3p21.31	NM_006321	48931284	48997975	48939995	48995707	16
P4HTM	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_177938	49002344	49019585	49002693	49019344	9
P4HTM	0.0014	0.1982	C-I	3Mb	3p21.31	NM_177938	49002344	49019585	49002693	49019344	9
P4HTM	0.0226	0.9991	C-I	2Mb	3p21.31	NM_177938	49002344	49019585	49002693	49019344	9
WDR6	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_018031	49019640	49028390	49019778	49027725	6
WDR6	0.0014	0.1982	C-I	3Mb	3p21.31	NM_018031	49019640	49028390	49019778	49027725	6
WDR6	0.0226	0.9991	C-I	2Mb	3p21.31	NM_018031	49019640	49028390	49019778	49027725	6
DALRD3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_001009996	49027925	49031045	49028024	49031001	12
DALRD3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_001009996	49027925	49031045	49028024	49031001	12
DALRD3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_018114	49027925	49033508	49028024	49030266	12
DALRD3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_018114	49027925	49033508	49028024	49030266	12
DALRD3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001009996	49027925	49031045	49028024	49031001	12
DALRD3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001009996	49027925	49031045	49028024	49031001	12
DALRD3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_018114	49027925	49033508	49028024	49030266	12
DALRD3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_018114	49027925	49033508	49028024	49030266	12
DALRD3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001009996	49027925	49031045	49028024	49031001	12
DALRD3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001009996	49027925	49031045	49028024	49031001	12
DALRD3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_018114	49027925	49033508	49028024	49030266	12
DALRD3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_018114	49027925	49033508	49028024	49030266	12
MIR425	0.0105	1.0000	ADGC	1Mb	3p21.31	NR_029948	49032584	49032671	49032671	49032671	1
MIR425	0.0014	0.1982	C-I	3Mb	3p21.31	NR_029948	49032584	49032671	49032671	49032671	1
MIR425	0.0226	0.9991	C-I	2Mb	3p21.31	NR_029948	49032584	49032671	49032671	49032671	1
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199074	49032911	49035930	49034876	49035609	5
MIR191	0.0105	1.0000	ADGC	1Mb	3p21.31	NR_029690	49033054	49033146	49033146	49033146	1
MIR191	0.0014	0.1982	C-I	3Mb	3p21.31	NR_029690	49033054	49033146	49033146	49033146	1
MIR191	0.0226	0.9991	C-I	2Mb	3p21.31	NR_029690	49033054	49033146	49033146	49033146	1
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5

NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199073	49033621	49035930	49034876	49035609	5
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
NDUFAF3	0.0226	0.9991	C-I	2Mb	3p21.31	NM_199070	49034077	49035930	49034876	49035609	5
IMPDH2	0.0105	1.0000	ADGC	1Mb	3p21.31	NM_000884	49036765	49041879	49036819	49041787	14
IMPDH2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_000884	49036765	49041879	49036819	49041787	14
IMPDH2	0.0226	0.9991	C-I	2Mb	3p21.31	NM_000884	49036765	49041879	49036819	49041787	14
QRICH1	0.0118	1.0000	ADGC	1Mb	3p21.31	NM_198880	49042145	49106508	49042888	49089454	10
QRICH1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_198880	49042145	49106508	49042888	49089454	10
QRICH1	0.0226	0.9991	C-I	2Mb	3p21.31	NM_198880	49042145	49106508	49042888	49089454	10
QARS	0.0092	1.0000	ADGC	1Mb	3p21.31	NM_005051	49108368	49117566	49108465	49117170	24
QARS	0.0014	0.1982	C-I	3Mb	3p21.31	NM_005051	49108368	49117566	49108465	49117170	24
QARS	0.0226	0.9991	C-I	2Mb	3p21.31	NM_005051	49108368	49117566	49108465	49117170	24
MIR6890	0.0092	1.0000	ADGC	1Mb	3p21.31	NR_106950	49112290	49112351	49112351	49112351	1
MIR6890	0.0014	0.1982	C-I	3Mb	3p21.31	NR_106950	49112290	49112351	49112351	49112351	1
MIR6890	0.0226	0.9991	C-I	2Mb	3p21.31	NR_106950	49112290	49112351	49112351	49112351	1
USP19	0.0092	1.0000	ADGC	1Mb	3p21.31	NM_001199162	49120482	49133375	49120848	49131582	27
USP19	0.0092	1.0000	ADGC	1Mb	3p21.31	NM_001199162	49120482	49133375	49120848	49131582	27
USP19	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001199162	49120482	49133375	49120848	49131582	27
USP19	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001199162	49120482	49133375	49120848	49131582	27
USP19	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001199162	49120482	49133375	49120848	49131582	27
USP19	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001199162	49120482	49133375	49120848	49131582	27
USP19	0.0092	1.0000	ADGC	1Mb	3p21.31	NM_001199160	49121109	49133375	49121394	49131582	27
USP19	0.0092	1.0000	ADGC	1Mb	3p21.31	NM_001199160	49121109	49133375	49121394	49131582	27
USP19	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001199160	49121109	49133375	49121394	49131582	27
USP19	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001199160	49121109	49133375	49121394	49131582	27
USP19	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001199160	49121109	49133375	49121394	49131582	27
USP19	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001199160	49121109	49133375	49121394	49131582	27
LAMB2	0.0111	1.0000	ADGC	1Mb	3p21.31	NM_002292	49133550	49145603	49133662	49145304	32
LAMB2	0.0014	0.1982	C-I	3Mb	3p21.31	NM_002292	49133550	49145603	49133662	49145304	32
LAMB2	0.0226	0.9991	C-I	2Mb	3p21.31	NM_002292	49133550	49145603	49133662	49145304	32
LAMB2P1	0.0111	1.0000	ADGC	1Mb	3p21.31	NR_004405	49165295	49166838	49166838	49166838	1
LAMB2P1	0.0014	0.1982	C-I	3Mb	3p21.31	NR_004405	49165295	49166838	49166838	49166838	1
LAMB2P1	0.0226	0.9991	C-I	2Mb	3p21.31	NR_004405	49165295	49166838	49166838	49166838	1
CCDC71	0.0111	1.0000	ADGC	1Mb	3p21.31	NM_022903	49174971	49178789	49175241	49176645	2
CCDC71	0.0014	0.1982	C-I	3Mb	3p21.31	NM_022903	49174971	49178789	49175241	49176645	2
CCDC71	0.0226	0.9991	C-I	2Mb	3p21.31	NM_022903	49174971	49178789	49175241	49176645	2
KLHDC8B	0.0132	1.0000	ADGC	1Mb	3p21.31	NM_173546	49184021	49188923	49185206	49188238	6
KLHDC8B	0.0014	0.1982	C-I	3Mb	3p21.31	NM_173546	49184021	49188923	49185206	49188238	6
KLHDC8B	0.0226	0.9991	C-I	2Mb	3p21.31	NM_173546	49184021	49188923	49185206	49188238	6
C3orf84	0.0132	1.0000	ADGC	1Mb	3p21.31	NM_001080528	49190072	49204295	49190072	49204208	4
C3orf84	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001080528	49190072	49204295	49190072	49204208	4
C3orf84	0.0226	0.9991	C-I	2Mb	3p21.31	NM_001080528	49190072	49204295	49190072	49204208	4
CCDC36	0.0138	1.0000	ADGC	1Mb	3p21.31	NM_178173	49210864	49270541	49224217	49269719	10
CCDC36	0.0138	1.0000	ADGC	1Mb	3p21.31	NM_178173	49210864	49270541	49224217	49269719	10
CCDC36	0.0014	0.1982	C-I	3Mb	3p21.31	NM_178173	49210864	49270541	49224217	49269719	10
CCDC36	0.0014	0.1982	C-I	3Mb	3p21.31	NM_178173	49210864	49270541	49224217	49269719	10
CCDC36	0.0166	0.9990	C-I	2Mb	3p21.31	NM_178173	49210864	49270541	49224217	49269719	10
CCDC36	0.0166	0.9990	C-I	2Mb	3p21.31	NM_178173	49210864	49270541	49224217	49269719	10
CCDC36	0.0138	1.0000	ADGC	1Mb	3p21.31	NM_001135197	49211936	49270541	49224217	49269719	8

CCDC36	0.0138	1.0000	ADGC	1Mb	3p21.31	NM_001135197	49211936	49270541	49224217	49269719	8
CCDC36	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001135197	49211936	49270541	49224217	49269719	8
CCDC36	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001135197	49211936	49270541	49224217	49269719	8
CCDC36	0.0166	0.9990	C-I	2Mb	3p21.31	NM_001135197	49211936	49270541	49224217	49269719	8
CCDC36	0.0166	0.9990	C-I	2Mb	3p21.31	NM_001135197	49211936	49270541	49224217	49269719	8
C3orf62	0.0138	1.0000	ADGC	1Mb	3p21.31	NM_198562	49281033	49289512	49283616	49289309	3
C3orf62	0.0014	0.1982	C-I	3Mb	3p21.31	NM_198562	49281033	49289512	49283616	49289309	3
C3orf62	0.0166	0.9990	C-I	2Mb	3p21.31	NM_198562	49281033	49289512	49283616	49289309	3
MIR4271	0.0138	1.0000	ADGC	1Mb	3p21.31	NR_036233	49286556	49286623	49286623	49286623	1
MIR4271	0.0014	0.1982	C-I	3Mb	3p21.31	NR_036233	49286556	49286623	49286623	49286623	1
MIR4271	0.0166	0.9990	C-I	2Mb	3p21.31	NR_036233	49286556	49286623	49286623	49286623	1
USP4	0.0141	1.0000	ADGC	1Mb	3p21.31	NM_199443	49289580	49352540	49290729	49352461	21
USP4	0.0141	1.0000	ADGC	1Mb	3p21.31	NM_199443	49289580	49352540	49290729	49352461	21
USP4	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199443	49289580	49352540	49290729	49352461	21
USP4	0.0014	0.1982	C-I	3Mb	3p21.31	NM_199443	49289580	49352540	49290729	49352461	21
USP4	0.0166	0.9990	C-I	2Mb	3p21.31	NM_199443	49289580	49352540	49290729	49352461	21
USP4	0.0166	0.9990	C-I	2Mb	3p21.31	NM_199443	49289580	49352540	49290729	49352461	21
USP4	0.0093	1.0000	ADGC	1Mb	3p21.31	NM_001251877	49324221	49352540	49324803	49352461	7
USP4	0.0093	1.0000	ADGC	1Mb	3p21.31	NM_001251877	49324221	49352540	49324803	49352461	7
USP4	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001251877	49324221	49352540	49324803	49352461	7
USP4	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001251877	49324221	49352540	49324803	49352461	7
USP4	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001251877	49324221	49352540	49324803	49352461	7
USP4	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001251877	49324221	49352540	49324803	49352461	7
GPX1	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_000581	49369612	49370795	49369824	49370715	2
GPX1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_000581	49369612	49370795	49369824	49370715	2
GPX1	0.0126	0.9977	C-I	2Mb	3p21.31	NM_000581	49369612	49370795	49369824	49370715	2
RHOA	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_001664	49371582	49424530	49372645	49388026	5
RHOA	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001664	49371582	49424530	49372645	49388026	5
RHOA	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001664	49371582	49424530	49372645	49388026	5
TCTA	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_022171	49424642	49428913	49424863	49427299	3
TCTA	0.0014	0.1982	C-I	3Mb	3p21.31	NM_022171	49424642	49428913	49424863	49427299	3
TCTA	0.0126	0.9977	C-I	2Mb	3p21.31	NM_022171	49424642	49428913	49424863	49427299	3
AMT	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_001164712	49429214	49435115	49429780	49434887	10
AMT	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001164712	49429214	49435115	49429780	49434887	10
AMT	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001164712	49429214	49435115	49429780	49434887	10
NICN1	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_032316	49434769	49441761	49437269	49441676	6
NICN1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_032316	49434769	49441761	49437269	49441676	6
NICN1	0.0126	0.9977	C-I	2Mb	3p21.31	NM_032316	49434769	49441761	49437269	49441676	6
DAG1	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_001177643	49481139	49548055	49522971	49545636	3
DAG1	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_001177643	49481139	49548055	49522971	49545636	3
DAG1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001177643	49481139	49548055	49522971	49545636	3
DAG1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001177643	49481139	49548055	49522971	49545636	3
DAG1	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001177643	49481139	49548055	49522971	49545636	3
DAG1	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001177643	49481139	49548055	49522971	49545636	3
DAG1	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_001177644	49482568	49548055	49522971	49545636	3
DAG1	0.0094	1.0000	ADGC	1Mb	3p21.31	NM_001177644	49482568	49548055	49522971	49545636	3
DAG1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001177644	49482568	49548055	49522971	49545636	3
DAG1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001177644	49482568	49548055	49522971	49545636	3
DAG1	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001177644	49482568	49548055	49522971	49545636	3
DAG1	0.0126	0.9977	C-I	2Mb	3p21.31	NM_001177644	49482568	49548055	49522971	49545636	3
BSN-AS2	0.0160	1.0000	ADGC	1Mb	3p21.31	NR_038866	49561742	49566803	49566803	49566803	3
BSN-AS2	0.0160	1.0000	ADGC	1Mb	3p21.31	NR_038866	49561742	49566803	49566803	49566803	3
BSN-AS2	0.0014	0.1982	C-I	3Mb	3p21.31	NR_038866	49561742	49566803	49566803	49566803	3
BSN-AS2	0.0014	0.1982	C-I	3Mb	3p21.31	NR_038866	49561742	49566803	49566803	49566803	3
BSN-AS2	0.0126	0.9977	C-I	2Mb	3p21.31	NR_038866	49561742	49566803	49566803	49566803	3
BSN-AS2	0.0126	0.9977	C-I	2Mb	3p21.31	NR_038866	49561742	49566803	49566803	49566803	3
BSN	0.0184	1.0000	ADGC	1Mb	3p21.31	NM_003458	49566925	49683986	49567039	49677276	12
BSN	0.0014	0.1982	C-I	3Mb	3p21.31	NM_003458	49566925	49683986	49567039	49677276	12
BSN	0.0221	0.9991	C-I	2Mb	3p21.31	NM_003458	49566925	49683986	49567039	49677276	12
APEH	0.0138	1.0000	ADGC	1Mb	3p21.31	NM_001640	49686438	49695938	49686838	49695779	22
APEH	0.0014	0.1982	C-I	3Mb	3p21.31	NM_001640	49686438	49695938	49686838	49695779	22
APEH	0.0389	1.0000	C-I	2Mb	3p21.31	NM_001640	49686438	49695938	49686838	49695779	22
MST1	0.0339	1.0000	ADGC	1Mb	3p21.31	NM_020998	49696383	49701200	49696464	49701128	18

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MST1	0.0014	0.1982	C-I	3Mb	3p21.31	NM_020998	49696383	49701200	49696464	49701128	18
MST1	0.0389	1.0000	C-I	2Mb	3p21.31	NM_020998	49696383	49701200	49696464	49701128	18
RBM6	0.0440	1.0000	ADGC	2Mb	3p21.31	NM_005777	49952480	50089689	49975078	50089570	21
RBM6	0.0014	0.1982	C-I	3Mb	3p21.31	NM_005777	49952480	50089689	49975078	50089570	21
RBM5	0.0440	1.0000	ADGC	2Mb	3p21.31	NR_036627	50101344	50131401	50131401	50131401	24
RBM5	0.0014	0.1982	C-I	3Mb	3p21.31	NR_036627	50101344	50131401	50131401	50131401	24
RBM5-AS1	0.0440	1.0000	ADGC	2Mb	3p21.31	NR_045388	50112039	50113425	50113425	50113425	1
RBM5-AS1	0.0440	1.0000	ADGC	2Mb	3p21.31	NR_045388	50112039	50113425	50113425	50113425	1
RBM5-AS1	0.0014	0.1982	C-I	3Mb	3p21.31	NR_045388	50112039	50113425	50113425	50113425	1
RBM5-AS1	0.0014	0.1982	C-I	3Mb	3p21.31	NR_045388	50112039	50113425	50113425	50113425	1
HCN4	0.0294	1.0000	ADGC	1Mb	15q24-q25	NM_005477	71399252	71448658	71401874	71447664	8
HCN4	0.0271	1.0000	C-I	1Mb	15q24-q25	NM_005477	71399252	71448658	71401874	71447664	8
REC114	0.0214	1.0000	ADGC	1Mb	15q24.1	NM_001042367	71522551	71639406	71522579	71639310	6
REC114	0.0205	1.0000	C-I	1Mb	15q24.1	NM_001042367	71522551	71639406	71522579	71639310	6
CD276	0.0452	1.0000	ADGC	1Mb	15q23-q24	NM_025240	71763674	71793912	71779033	71792350	8
CD276	0.0030	0.9805	C-I	1Mb	15q23-q24	NM_025240	71763674	71793912	71779033	71792350	8
CD276	0.0294	0.9952	C-I	2Mb	15q23-q24	NM_025240	71763674	71793912	71779033	71792350	8
ZFP14	0.0339	1.0000	ADGC	1Mb	19q13.12	NM_020917	41517194	41561945	41522965	41550634	5
ZFP14	0.0382	1.0000	C-I	1Mb	19q13.12	NM_020917	41517194	41561945	41522965	41550634	5

**eTable 6.** Potentially Damaging SNPs (With Their SIFT and Polyphen Scores For Missense Variants) Within the Canonical Transcripts of the Genes Inside the Consensus Regions Identified in the ADGC and CHAP-Indianapolis Data Sets; with their minor allele frequency in 1000Genomes combined population (GMAF), African American (AA\_MAF), African (AFR\_MAF), American (AMR\_MAF), Asian (ASN\_MAF), European (EUR\_MAF) and European American (EA\_MAF).

SNP	Gene	Consequence	SIFT	PolyPhen	GMAF	AA_MAF	AFR_MAF	AMR_MAF	ASN_MAF	EUR_MAF	EA_MAF
rs145488707	STOML1	missense_variant	deleterious(0)	probably_damaging(1)	-	T:0	-	-	-	-	T:0.000116
rs371570677	STOML1	missense_variant	deleterious(0)	probably_damaging(0.993)	-	A:0	-	-	-	-	A:0.000116
rs1061082	STOML1	missense_variant	deleterious(0.01)	probably_damaging(0.996)	-	-	-	-	-	-	-
rs146505992	STOML1	missense_variant	deleterious(0.01)	benign(0.052)	-	A:0	-	-	-	-	A:0.000116
rs141134528	STOML1	missense_variant	tolerated(0.2)	possibly_damaging(0.641)	-	C:0.000227	-	-	-	-	C:0
rs368495173	STOML1	missense_variant	deleterious(0.05)	possibly_damaging(0.67)	-	A:0.000227	-	-	-	-	A:0
rs148196033	STOML1	missense_variant	deleterious(0.02)	benign(0.394)	-	G:0.000682	-	-	-	-	G:0
rs141171144	STOML1	missense_variant	tolerated(0.1)	probably_damaging(0.958)	-	T:0.000455	-	-	-	-	T:0.000349
rs2277600	STOML1	missense_variant	deleterious(0.02)	possibly_damaging(0.803)	-	-	-	-	-	-	-
rs34524642	STOML1	frameshift_variant	-	-	-	-	-	-	-	-	-
rs151058454	STOML1	missense_variant	deleterious(0.01)	benign(0.283)	-	T:0.002983	-	-	-	-	T:0
rs373693671	STOML1	missense_variant	deleterious(0)	possibly_damaging(0.871)	-	A:0.000461	-	-	-	-	A:0.000234
rs368108098	STOML1	missense_variant	deleterious(0.02)	possibly_damaging(0.785)	-	A:0	-	-	-	-	A:0.000118
rs114483410	STOML1	missense_variant	deleterious(0)	benign(0)	A:0.0005	A:0	A:0.0020	-	-	-	A:0.000116
rs116083516	STOML1	missense_variant	deleterious(0)	probably_damaging(0.979)	A:0.0000	-	-	-	-	-	-
rs199575995	STOML1	missense_variant	deleterious(0.01)	benign(0.221)	-	-	-	-	-	-	-
rs150164503	STOML1	missense_variant	deleterious(0.03)	possibly_damaging(0.671)	-	A:0	-	-	-	-	A:0.000116
rs200693933	STOML1	missense_variant	tolerated(0.08)	possibly_damaging(0.686)	-	-	-	-	-	-	-
rs112182005	STOML1	missense_variant	deleterious(0)	benign(0.211)	-	-	-	-	-	-	-
rs143464424	STOML1	missense_variant	tolerated(0.07)	possibly_damaging(0.472)	-	A:0.000227	-	-	-	-	A:0
rs369331084	STOML1	missense_variant	deleterious(0.01)	possibly_damaging(0.879)	-	T:0	-	-	-	-	T:0.000116
rs137978751	STOML1	missense_variant	tolerated(0.11)	possibly_damaging(0.748)	-	T:0	-	-	-	-	T:0.000233
rs200662895	STOML1	missense_variant	tolerated(0.17)	possibly_damaging(0.677)	-	-	-	-	-	-	-
rs199911341	STOML1	missense_variant	deleterious(0.01)	possibly_damaging(0.822)	-	A:0	-	-	-	-	A:0.000350
rs34228316	PML	frameshift_variant	-	-	-	-	-	-	-	-	-
rs372639541	PML	missense_variant	tolerated(0.08)	probably_damaging(0.999)	-	G:0	-	-	-	-	G:0.000116
rs141544943	PML	missense_variant	deleterious(0)	probably_damaging(0.931)	-	T:0	-	-	-	-	T:0.000116
rs370861713	PML	missense_variant	tolerated(0.11)	probably_damaging(0.926)	-	G:0	-	-	-	-	G:0.000116
rs200708179	PML	missense_variant	deleterious(0)	probably_damaging(0.981)	A:0.0000	-	-	-	-	-	-
rs368684793	PML	missense_variant	tolerated(0.06)	possibly_damaging(0.573)	-	G:0	-	-	-	-	G:0.000116
rs200143816	PML	missense_variant	tolerated(0.16)	probably_damaging(0.984)	-	-	-	-	-	-	-
rs373742710	PML	missense_variant	tolerated(0.06)	probably_damaging(0.918)	-	A:0	-	-	-	-	A:0.000116
rs138345086	PML	missense_variant	deleterious(0.01)	probably_damaging(0.928)	-	T:0	-	-	-	-	T:0.000116
rs34681920	PML	frameshift_variant	-	-	-	-	-	-	-	-	-
rs140050477	PML	missense_variant	deleterious(0.01)	benign(0.219)	-	T:0.000456	-	-	-	-	T:0.001289
rs377549937	PML	missense_variant	deleterious(0.02)	possibly_damaging(0.632)	-	T:0.000228	-	-	-	-	T:0
rs371084483	PML	missense_variant	deleterious(0.02)	benign(0.386)	-	G:0	-	-	-	-	G:0.000117
rs199516006	PML	missense_variant	tolerated(0.07)	possibly_damaging(0.777)	A:0.0005	-	-	-	A:0.0017	-	-
rs375594567	PML	missense_variant	deleterious(0.03)	benign(0.168)	-	A:0	-	-	-	-	A:0.000117
rs74471420	PML	missense_variant	deleterious(0.04)	probably_damaging(0.977)	-	-	-	-	-	-	-
rs371413149	PML	missense_variant	deleterious(0.02)	possibly_damaging(0.458)	-	A:0	-	-	-	-	A:0.000116
rs149871195	PML	missense_variant	deleterious(0.03)	benign(0.219)	A:0.0005	A:0.000228	A:0.0020	-	-	-	A:0
rs145863996	PML	missense_variant	deleterious(0.01)	possibly_damaging(0.828)	-	C:0	-	-	-	-	C:0.000233
rs11555843	PML	missense_variant	tolerated(0.09)	possibly_damaging(0.776)	-	A:0	-	-	-	-	A:0.000465
rs143771296	PML	missense_variant	deleterious(0)	probably_damaging(0.998)	-	T:0.000227	-	-	-	-	T:0
rs200123201	PML	missense_variant	deleterious(0.05)	benign(0.298)	T:0.0005	-	-	-	-	T:0.0013	-
rs202019975	PML	missense_variant	deleterious(0)	benign(0.033)	T:0.0005	-	-	-	-	T:0.0013	-
rs374199653	PML	missense_variant	deleterious(0.01)	benign(0.12)	-	A:0	-	-	-	-	A:0.000116
rs200546578	PML	missense_variant	deleterious(0.04)	benign(0.219)	A:0.0005	-	A:0.0020	-	-	-	-
rs375611361	PML	missense_variant	deleterious(0)	probably_damaging(0.992)	-	A:0	-	-	-	-	A:0.000116
rs193112596	PML	splice_region_variant,intron_variant	-	-	A:0.0005	-	-	-	-	A:0.0013	-
rs147197708	PML	missense_variant	deleterious(0)	probably_damaging(0.991)	-	C:0	-	-	-	-	C:0.000116
rs140558473	PML	missense_variant	deleterious(0.01)	probably_damaging(0.997)	-	G:0.000227	-	-	-	-	G:0
rs373236341	PML	missense_variant	deleterious(0.01)	benign(0.266)	-	-	-	-	-	-	-
rs142900813	PML	missense_variant	deleterious(0.01)	possibly_damaging(0.591)	T:0.0009	T:0	T:0.0020	T:0.0028	-	-	T:0.000233
rs373296015	PML	missense_variant	deleterious(0)	probably_damaging(0.935)	-	G:0	-	-	-	-	G:0.000116
rs112105465	PML	missense_variant	deleterious(0.02)	possibly_damaging(0.838)	-	-	-	-	-	-	-
rs138817062	PML	missense_variant	deleterious(0.04)	benign(0.001)	-	T:0	-	-	-	-	T:0.000116
rs368187335	GOLGA6A	missense_variant	deleterious(0)	probably_damaging(0.994)	-	G:0.011396	-	-	-	-	G:0.000163
rs375959536	GOLGA6A	missense_variant	deleterious(0.04)	benign(0.209)	-	G:0	-	-	-	-	G:0.000119
rs369741080	GOLGA6A	missense_variant	deleterious(0.03)	possibly_damaging(0.477)	-	T:0	-	-	-	-	T:0.000190
rs370452591	GOLGA6A	missense_variant	deleterious(0.01)	possibly_damaging(0.747)	-	C:0	-	-	-	-	C:0.000125
rs199527610	GOLGA6A	missense_variant	tolerated(0.17)	possibly_damaging(0.492)	-	-	-	-	-	-	-
rs374121270	GOLGA6A	missense_variant	tolerated(0.09)	possibly_damaging(0.885)	-	A:0	-	-	-	-	A:0.000117
rs376685732	GOLGA6A	missense_variant	deleterious(0.02)	benign(0.051)	-	C:0.000455	-	-	-	-	C:0
rs370916628	GOLGA6A	missense_variant	deleterious(0.03)	benign(0.055)	-	C:0	-	-	-	-	C:0.000117

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rs372622676	GOLGA6A	missense_variant	deleterious(0.04)	benign(0.009)	-	A:0	-	-	-	-	A:0.000117
rs149223222	GOLGA6A	missense_variant	deleterious(0.01)	benign(0.295)	-	-	-	-	-	-	-
rs142259530	ISLR2	missense_variant	deleterious(0.03)	benign(0.289)	-	C:0	-	-	-	-	C:0.000116
rs370327397	ISLR2	missense_variant	deleterious(0.04)	probably_damaging(0.996)	-	T:0	-	-	-	-	T:0.000116
rs201306990	ISLR2	missense_variant	tolerated(0.07)	probably_damaging(0.998)	-	-	-	-	-	-	-
rs371096859	ISLR2	missense_variant	tolerated(0.2)	probably_damaging(0.997)	-	A:0	-	-	-	-	A:0.000116
rs201469990	ISLR2	missense_variant	deleterious(0.01)	probably_damaging(0.999)	-	-	-	-	-	-	-
rs150353936	ISLR2	missense_variant	tolerated(0.14)	possibly_damaging(0.515)	-	A:0.000227	-	-	-	-	A:0
rs3889598	ISLR2	missense_variant	tolerated(0.57)	probably_damaging(0.977)	T:0.0349	T:0.041401	T:0.07	T:0.02	T:0.03	T:0.02	T:0.014312
rs374707959	ISLR2	missense_variant	deleterious(0.01)	probably_damaging(0.998)	-	G:0	-	-	-	-	G:0.000116
rs149537427	ISLR2	missense_variant	tolerated(0.35)	possibly_damaging(0.673)	-	A:0	-	-	-	-	A:0.000465
rs368814186	ISLR2	missense_variant	tolerated(0.08)	possibly_damaging(0.537)	-	G:0	-	-	-	-	G:0.000116
rs202205145	ISLR2	missense_variant	tolerated(0.22)	probably_damaging(0.999)	-	T:0.000227	-	-	-	-	T:0.000116
rs368024378	ISLR2	missense_variant	tolerated(0.07)	probably_damaging(1)	-	C:0	-	-	-	-	C:0.000116
rs5813743	ISLR2	frameshift_variant	-	-	-	-	-	-	-	-	-
rs201210704	ISLR2	missense_variant	tolerated(0.97)	probably_damaging(0.93)	G:0.0014	-	G:0.01	-	-	-	-
rs369322354	ISLR2	missense_variant	tolerated(1)	probably_damaging(0.97)	-	C:0	-	-	-	-	C:0.000116
rs113946470	ISLR2	missense_variant	tolerated(0.14)	probably_damaging(0.985)	-	-	-	-	-	-	-
rs373225895	ISLR2	missense_variant	deleterious(0)	benign(0.079)	-	A:0	-	-	-	-	A:0.000118
rs374669132	ISLR2	missense_variant	deleterious(0.03)	probably_damaging(0.968)	-	G:0.000227	-	-	-	-	G:0
rs145379981	ISLR2	missense_variant	deleterious(0.02)	probably_damaging(0.996)	-	A:0	-	-	-	-	A:0.000116
rs372926193	ISLR2	missense_variant	deleterious(0)	probably_damaging(0.999)	-	C:0	-	-	-	-	C:0.000116
rs185463025	ISLR2	missense_variant	tolerated(0.08)	probably_damaging(0.991)	A:0.0009	A:0.000455	A:0.0041	-	-	-	A:0
rs200999608	ISLR2	missense_variant	tolerated(0.27)	probably_damaging(0.986)	G:0.0005	-	-	-	-	G:0.0013	-
rs144880828	ISLR2	missense_variant	deleterious(0.03)	probably_damaging(0.968)	-	G:0	-	-	-	-	G:0.000116
rs138774937	ISLR2	missense_variant	deleterious(0)	probably_damaging(0.98)	-	G:0.000456	-	-	-	-	G:0
rs376663143	RPS3A	missense_variant	tolerated(0.07)	possibly_damaging(0.816)	-	C:0.000227	-	-	-	-	C:0
rs199694166	SH3D19	missense_variant	deleterious(0.01)	benign(0.008)	-	-	-	-	-	-	-
rs146787893	SH3D19	missense_variant	deleterious(0.01)	probably_damaging(0.992)	-	G:0.000227	-	-	-	-	G:0
rs191202111	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.979)	C:0.0005	-	C:0.0020	-	-	-	-
rs376090399	SH3D19	missense_variant	deleterious(0.02)	benign(0.341)	-	T:0	-	-	-	-	T:0.000116
rs142870105	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.999)	-	T:0.002270	-	-	-	-	T:0
rs376194040	SH3D19	missense_variant	deleterious(0)	benign(0.103)	-	A:0	-	-	-	-	A:0.000116
rs370276794	SH3D19	missense_variant	tolerated(0.43)	possibly_damaging(0.812)	-	C:0	-	-	-	-	C:0.000116
rs192063486	SH3D19	missense_variant	tolerated(0.07)	probably_damaging(0.961)	A:0.0014	-	-	A:0.01	-	-	-
rs200083226	SH3D19	missense_variant	deleterious(0.04)	benign(0.013)	G:0.0005	-	-	-	-	G:0.0013	-
rs371735565	SH3D19	missense_variant	deleterious(0.01)	probably_damaging(0.988)	-	T:0	-	-	-	-	T:0.000116
rs372532779	SH3D19	missense_variant	deleterious(0.05)	possibly_damaging(0.764)	-	T:0	-	-	-	-	T:0.000116
rs372072781	SH3D19	missense_variant	deleterious(0)	possibly_damaging(0.721)	-	C:0.000227	-	-	-	-	C:0
rs150249923	SH3D19	missense_variant	deleterious(0)	possibly_damaging(0.703)	-	A:0	-	-	-	-	A:0.000116
rs183339685	SH3D19	missense_variant	tolerated(0.81)	possibly_damaging(0.597)	C:0.0018	-	-	-	C:0.01	-	-
rs186592293	SH3D19	missense_variant	tolerated(0.09)	possibly_damaging(0.657)	G:0.0005	-	G:0.0020	-	-	-	-
rs377758866	SH3D19	missense_variant	tolerated(0.08)	possibly_damaging(0.751)	-	A:0.000227	-	-	-	-	A:0
rs145726735	SH3D19	missense_variant	deleterious(0.01)	probably_damaging(0.998)	-	A:0	-	-	-	-	A:0.000116
rs146575678	SH3D19	missense_variant,splice_region_variant	deleterious(0.03)	benign(0.077)	A:0.0009	A:0.003177	A:0.0041	-	-	-	A:0
rs201329549	SH3D19	missense_variant	tolerated(0.39)	possibly_damaging(0.461)	-	A:0	-	-	-	-	A:0.000233
rs367960670	SH3D19	missense_variant	deleterious(0)	probably_damaging(1)	-	T:0.000227	-	-	-	-	T:0
rs78397848	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.98)	G:0.0354	G:0.001135	G:0.01	G:0.10	G:0.07	-	G:0.000349
rs111861991	SH3D19	missense_variant	tolerated(0.26)	probably_damaging(0.933)	-	-	-	-	-	-	-
rs146287053	SH3D19	missense_variant	deleterious(0.01)	probably_damaging(0.946)	-	A:0	-	-	-	-	A:0.000233
rs377710335	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.928)	-	A:0.000227	-	-	-	-	A:0
rs186990819	SH3D19	missense_variant	deleterious(0.02)	probably_damaging(0.999)	T:0.0005	-	-	-	T:0.0017	-	-
rs368920520	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.994)	-	A:0.000227	-	-	-	-	A:0
rs202081191	SH3D19	missense_variant	deleterious(0.01)	benign(0.341)	C:0.0005	-	C:0.0020	-	-	-	-
rs143505993	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.996)	C:0.0009	C:0.000227	C:0.0041	-	-	-	C:0
rs373289881	SH3D19	stop_gained	-	-	-	A:0	-	-	-	-	A:0.000116
rs34948591	SH3D19	frameshift_variant	-	-	-	-	-	-	-	-	-
rs150966759	SH3D19	missense_variant	tolerated(0.13)	probably_damaging(0.98)	T:0.0005	-	T:0.0020	-	-	-	-
rs142380318	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.964)	-	A:0.000227	-	-	-	-	A:0
rs147933255	SH3D19	missense_variant	tolerated(0.12)	possibly_damaging(0.836)	-	A:0	-	-	-	-	A:0.000116
rs147501781	SH3D19	missense_variant	deleterious(0)	benign(0.325)	A:0.0018	A:0.000908	-	A:0.01	-	A:0.0026	A:0.003953
rs201225279	SH3D19	missense_variant	deleterious(0.03)	probably_damaging(0.946)	T:0.0005	-	T:0.0020	-	-	-	-
rs201831997	SH3D19	missense_variant	deleterious(0.01)	probably_damaging(0.987)	T:0.0009	T:0.000227	-	-	T:0.0035	-	T:0
rs147112884	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.999)	-	A:0	-	-	-	-	A:0.000116
rs371516037	SH3D19	missense_variant	deleterious(0)	probably_damaging(1)	-	C:0	-	-	-	-	C:0.000116
rs201060063	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.994)	A:0.0000	-	-	-	-	-	-
rs27273740	SH3D19	missense_variant	deleterious(0.04)	benign(0.027)	C:0.0018	C:0.000227	-	C:0.01	-	C:0.0026	C:0.003721
rs375856466	SH3D19	missense_variant	tolerated(0.1)	possibly_damaging(0.623)	-	G:0.000227	-	-	-	-	G:0
rs149484381	SH3D19	missense_variant	deleterious(0)	probably_damaging(0.993)	-	A:0	-	-	-	-	A:0.000116
rs139285387	SH3D19	splice_acceptor_variant,5_prime_UTR_variant	-	-	-	-	-	-	-	-	-
rs183645038	SH3D19	splice_region_variant,intron_variant	-	-	T:0.0005	-	-	-	T:0.0017	-	-