sTable 1. Other nonsynonymous variants with P<1E-3

					Carrier rate		Fisher's Exact Test		FDR	Other variant information					Hopkins		Detroit		AFR, gnomAD		REVEL
Gene	cDNA	AminoAcid	Ref	Alt	Cases	Controls	OR	*P*	q-value	Chr	BP	ID	_Reference_Sequ	Exon	Carriers	Non-carriers	Carriers	Non-carriers	Carriers	Non-carriers	Score
PKP4	c.A1811G	p.D604G	A	G	0.53%	0.05%	10.76	5.12E-05	0.20	2	159,499,113	rs144866707	NM_003628	exon11	6	960	3	747	4	8127	0.68
BCL9	c.A1348G	p.M450V	A	G	0.47%	0.07%	6.29	9.75E-04	0.39	1	147,091,309	rs372306642	NM_004326	exon8	5	960	3	747	6	8018	0.17
AGT	c.T452G	p.L151W	A	C	0.47%	0.06%	7.65	4.56E-04	0.34	1	230,846,145	rs150161533	NM_000029	exon2	6	960	2	747	5	8126	0.33
AGBL5	c.G2399A	p.G800E	G	A	0.76%	0.17%	4.44	2.24E-04	0.23	2	27,292,484	rs150715804	NM_021831	exon14	7	960	6	747	14	8116	0.03
SPRED2	c.G906C	p.E302D	C	G	0.88%	0.27%	3.31	7.05E-04	0.38	2	65,540,986	rs142134790	NM_181784	exon6	11	960	4	747	21	7872	0.18
LMAN2L	c.A650G	p.N217S	T	C	0.47%	0.07%	6.35	9.25E-04	0.38	2	97,377,653	rs201001633	NM_001142292	exon6	3	960	5	747	6	8092	0.49
CNTN3	c.C2702T	p.T901M	G	A	0.76%	0.20%	3.80	6.41E-04	0.37	3	74,334,458	rs141921900	NM_020872	exon19	3	960	10	747	16	7944	0.09
WHSC1	c.C4025A	p.P1342H	C	A	0.47%	0.06%	7.39	5.59E-04	0.35	4	1,980,563	rs201619712	NM_133330	exon24	5	959	3	746	5	7839	0.19
AFM	c.T40G	p.F14V	T	G	0.59%	1.59%	0.37	8.21E-04	0.38	4	74,347,532	rs145217978	NM_001133	exon1	7	959	3	746	118	7422	0.03
PLA2G12A	c.G331A	p.D111N	C	T	0.70%	0.15%	4.79	2.47E-04	0.24	4	110,638,824	rs114816312	NM_030821	exon3	8	960	4	747	12	8128	0.44
IL7R	c.C1241T	p.T414M	C	T	0.59%	0.12%	4.78	8.25E-04	0.38	5	35,876,449	rs2229232	NM_002185	exon8	7	960	3	747	10	8125	0.11
RAD17	c.A1815C	p.E605D	A	C	0.76%	0.17%	4.45	2.21E-04	0.23	5	68,709,888	rs140350987	NM_133339	exon16	4	960	9	747	14	8128	0.06
ANKHD1-EIF4EBP3	c.A5986G	p.S1996G	A	G	0.47%	0.05%	9.56	2.07E-04	0.23	5	139,908,517	rs368415796	NM_020690	exon29	5	960	3	747	4	8128	0.08
C6orf222	c.G1126A	p.E376K	C	T	0.47%	0.07%	6.37	9.02E-04	0.38	6	36,293,102	rs375540037	NM_001010903	exon6	3	960	5	747	6	8128	0.01
CDCA7L	c.C100T	p.P34S	G	A	0.53%	0.06%	8.61	1.21E-04	0.23	7	21,956,437	rs144827468	NM_018719	exon2	4	960	5	747	5	8128	0.04
COBL	c.G2161C	p.E721Q	C	G	0.64%	0.11%	5.85	1.51E-04	0.23	7	51,096,803	rs369112275	NM_001287436	exon11	7	960	4	747	9	8127	0.04
PINX1	c.A150C	p.Q50H	T	G	0.59%	0.09%	6.24	2.75E-04	0.24	8	10,690,474	rs189959562	NM_017884	exon3	5	960	5	747	7	7417	0.25
OC90	c.G1366A	p.G456S	C	T	0.76%	0.18%	4.16	3.89E-04	0.30	8	133,036,796	rs190749924	NM_001080399	exon14	8	960	5	746	14	7599	0.02
TTC16	c.C854T	p.P285L	C	T	0.47%	0.06%	7.59	4.79E-04	0.34	9	130,485,594	rs371121543	NM_144965	exon7	2	960	6	746	5	8055	0.33
TSC1	c.T1163C	p.L388P	A	G	0.53%	0.07%	7.16	2.59E-04	0.24	9	135,786,058	rs377598226	NM_000368	exon12	6	960	3	747	6	8114	0.55
ADAMTS13	c.G58A	p.A20T	G	A	0.53%	0.10%	5.38	8.92E-04	0.38	9	136,287,621	rs142293909	NM_139025	exon1	6	960	3	747	8	8128	0.04
CARD9	c.A809T	p.E270V	T	A	0.47%	0.06%	7.27	6.15E-04	0.37	9	139,264,888	rs114895119	NM_052813	exon6	7	960	1	747	5	7720	0.04
DCHS1	c.C1245A	p.S415R	G	T	0.94%	0.24%	3.99	1.03E-04	0.23	11	6,661,600	rs117368891	NM_003737	exon2	7	960	9	747	19	8039	0.13
FAM90A1	c.G614A	p.G205E	C	T	0.64%	0.15%	4.42	7.98E-04	0.38	12	8,375,199	rs201524812	NM_018088	exon7	7	959	4	747	11	7511	0.06
KMT2D	c.A10192G	p.M3398V	T	C	0.88%	0.27%	3.24	8.58E-04	0.38	12	49,430,947	rs75937132	NM_003482	exon34	10	960	5	747	21	7700	0.27
LIG4	c.C691T	p.P231S	G	A	0.94%	0.25%	3.83	1.43E-04	0.23	13	108,862,926	rs3093765	NM_002312	exon2	7	959	9	747	20	8104	0.55
CHAC1	c.A452G	p.K151R	A	G	0.94%	0.25%	3.83	1.40E-04	0.23	15	41,247,629	rs147487857	NM_024111	exon3	7	960	9	747	20	8125	0.12
NEDD4	c.C809T	p.P270L	G	A	1.00%	0.31%	3.26	3.46E-04	0.28	15	56,208,221	rs147060928	NM_001284338	exon1	12	960	5	747	25	8125	0.23
CYP1A1	c.C1390A	p.R464S	G	T	0.82%	0.20%	4.20	1.92E-04	0.23	15	75,012,979	rs41279188	NM_000499	exon7	8	959	6	747	16	8128	0.52
DNAH3	c.C5283A	p.D1761E	G	T	0.47%	0.05%	9.56	2.07E-04	0.23	16	21,042,523	rs371102224	NM_017539	exon37	4	960	4	747	4	8128	0.80
SLC5A2	c.A1961G	p.N654S	A	G	0.64%	0.15%	4.36	7.67E-04	0.38	16	31,501,798	rs61742739	NM_003041	exon14	7	960	4	747	12	8072	0.67
PEX12	c.A102T	p.R34S	T	A	0.47%	0.07%	6.37	9.02E-04	0.38	17	33,904,939	rs147530802	NM_000286	exon1	7	960	1	747	6	8128	0.54
KAT7	c.C137T	p.S46L	C	T	0.47%	0.07%	6.37	9.02E-04	0.38	17	47,869,369	rs147141932	NM_007067	exon2	3	960	5	747	6	8128	0.14
PRX	c.G1483C	p.E495Q	C	G	0.82%	0.23%	3.66	5.14E-04	0.35	19	40,902,776	rs146789340	NM_181882	exon7	9	958	5	746	18	7976	0.02
ZNF460	c.G1657A	p.G553R	G	A	0.53%	0.09%	6.01	5.73E-04	0.35	19	57,803,566	rs137997052	NM_006635	exon3	4	960	5	747	7	7944	0.09
CDH26	c.T1343C	p.V448A	T	C	0.88%	0.22%	3.99	1.65E-04	0.23	20	58,567,492	rs34866303	NM_177980	exon10	8	960	7	747	18	8128	0.37

CDH26 Of the 54 different cell types and organs in Gtexportal.org, prostate shows the highest expression level. In addition to conventional Ca++, dependent homophilic interactions, as well as interactions with

NEDD4 this gene codes for a HECT ubiquitin ligase that functions in the ubiquitin proteasome system of protein degradation. The encoded protein contains an N-terminal calcium and phospholipid binding C2

RAD17 is a cell cycle checkpoint gene required for cell cycle arrest and DNA damage repair. The protein is phosphorylated by the checkpoint kinase ATR, and recruits the RAD1-RAD9-HUS1 checkpoint protein

PINX1 is a nucleolar protein that has been shown to act as a telomerase inhibitor (7). It mediates TRF1 and TERT accumulation in nucleolus and enhances TRF1 binding to telomeres. Both over- and under-

LIG4 The protein encoded by this gene is a DNA ligase that joins single-strand breaks in double-stranded DNA in an ATP-dependent reaction. This protein is essential for DNA double-strand break repair through

PKP4 is a component of desmosomal and other adhesion plaques and is thought to be involved in regulating junctional plaque organization and cadherin function. It is involved in positive regulation of GTPase

Supplementary references

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