Table 1. Examples of published candidate genes with mode of inheritance and corresponding ISPP scores

Autosomal Dominant			
Gene	ISPP_AD	ISPP_AR	ISPP_XL	Ref
APP	0.17(5%)	0.01(69%)	-	(Conidi, et al., 2015)
IRS1	0.12(6%)	0.04(29%)	-	(Rong, et al., 2015)
RET	0.17(5%)	0.01(69%)	-	(Figlioli, et al., 2012)
NCOR1	0.23(5%)	0.01(80%)	-	(Fozzatti, et al., 2011)
EGR2	0.20(5%)	0.01(76%)	-	(Lupski, et al., 2010)
Autosomal Recessive			
Gene	ISPP_AD	ISPP_AR	ISPP_XL	Ref
KMT2B	0.01(48%)	0.03(43%)	-	(Agha, et al., 2014)
APOB	0.11(6%)	0.25(8%)	-	(Hammer, et al., 2013)
GJB2	0.02(37%)	0.07(17%)	-	(Nikolay, et al., 2011)
FECH	0.01(46%)	0.18(8%)	-	(Balwani, et al., 2013)
ATF6	0.02(28%)	0.1(12%)	-	(Ansar, et al., 2015)
X-Linked			
Gene	ISPP_AD	ISPP_AR	ISPP_XL	Ref
POLA1	0.05(13%)	0.01(74%)	0.34(19%)	NIH
OGT	0.02(34%)	0.00(80%)	0.28(21%)	(Niranjan, et al., 2015)
GLUD2	0.01(57%)	0.00(80%)	0.18(24%)	(Cukier, et al., 2014)
BRCC3	0.00(63%)	0.02(61%)	0.16(26%)	(Huang, et al., 2015)
ZMYM3	0.00(63%)	0.00(80%)	0.25(22%)	(Philips, et al., 2014)
CLCN4	0.02(32%)	0.00(80%)	0.21(22%)	(Hu, et al., 2015)
CNKSR2	0.00(63%)	0.00(80%)	0.12(32%)	(Hu, et al., 2015)
FRMPD4	0.00(63%)	0.04(34%)	0.19(24%)	(Hu, et al., 2015)
KLHL15	0.03(27%)	0.00(80%)	0.19(24%)	(Hu, et al., 2015)
LAS1L	0.02(34%)	0.01(66%)	0.13(30%)	(Hu, et al., 2015)
RLIM	0.00(63%)	0.00(80%)	0.05(47%)	(Hu, et al., 2015)
USP27X	0.00(63%)	0.00(80%)	0.03(57%)	(Hu, et al., 2015)
CDK16	0.00(63%)	0.00(80%)	0.15(28%)	(Hu, et al., 2015)

By comparing ISPP scores of each gene, the possible inheritance mode of the gene could be estimated (S6 Text). The value in parentheses indicates the percentage among all in the inheritance-specific model. NIH indicates this x-linked disease candidate gene has not been published yet, but has been funded for conducting the research by NIH. Project#:1R56AI113274-01