Supplemental Data Table S11. *In silico* analyses of mutations identified in association positive cases

Gene	NT alteration	AA alteration	Conventional criteria	ACMG criteria	1000G	ExAC	ESP6500	SIFT	Polyphen2	LRT	Mutation taster	Mutation assessor	FATHMM	GERP++
DUOX2	c.1232G>A	p.R411K	EP	VUS	ND	0	ND	T	B	D	D	M	NA	5.36
DUOX2	c.1588A>T	p.K530X	KP	P	0.0006	0.0007	ND	T	NA	N	A	NA	NA	4.63
DUOX2	c.2654G>A	p.R885Q	KP	LP	ND	0.0001	ND	NA	D	D	D	L	NA	4.29
DUOX2	c.4010G>T	p.G1337V	EP	VUS	ND	ND	ND	D	D	D	D	H	NA	5.57
DUOX2	c.1462G>A	p.G488R	KP	LP	ND	ND	ND	NA	NA	NA	NA	NA	NA	NA
DUOX2	c.2635G>A	p.E879K	KP	LP	ND	0	ND	D	D	D	D	H	NA	5.23
DUOX2	c.3616G>A	p.A1206T	EP	VUS	ND	0	ND	D	D	D	D	M	NA	5.69
DUOX2	c.3329G>A	p.R1110Q	KP	LP	0.0004	0.0002	ND	D	D	D	D	H	NA	5.6
DUOX2	c.1319G>A	p.S440N	EP	VUS	ND	ND	ND	T	B	D	D	M	NA	4.18
DUOX2	c.227C>T	p.P76L*	EP	VUS	ND	0	ND	T	D	D	D	M	NA	5.84
DUOXA2	c.413dupA	p.Y138X	KP	LP	ND	0.0002	ND	NA	NA	NA	NA	NA	NA	NA
DUOXA2	c.535T>C	p.Y179H**	EP	VUS	ND	0.0001	ND	D	D	D	D	M	T	5.3
DUOXA2	c.738C>G	p.Y246X	KP	P	ND	0.0002	ND	T	NA	N	D	NA	NA	-2.3
DUOXA2	c.280C>T	p.R94C	EP	VUS	ND	ND	ND	D	D	N	N	M	T	5.38
GALE	c.1002G>A	p.W334X	EP	P	ND	ND	ND	T	NA	D	D	NA	NA	4.89
GALE	c.47G>A	p.S16N	EP	VUS	ND	ND	ND	D	D	D	D	H	D	4.89
GALE	c.905G>A	p.G302D	KP	LP	ND	0	ND	D	D	D	A	H	D	4.47
GALE	c.264delT	p.F88fs	EP	LP	ND	ND	ND	NA	NA	NA	NA	NA	NA	NA
GALE	c.38A>G	p.Y13C	EP	VUS	ND	ND	ND	D	D	D	D	H	D	4.89
GALE	c.10A>G	p.K4E	EP	VUS	ND	ND	ND	T	B	N	D	M	D	3.74
GALK1	c.1159G>A	p.A387T	EP	VUS	0.0002	0	ND	T	D	N	D	M	D	4.84
GALT	c.50+1G>A	c.50+1G>A	KP	P	ND	0	ND	NA	NA	NA	D	NA	NA	5.53
GALT	c.998G>A	p.R333Q	KP	LP	ND	0	ND	D	D	U	A	M	D	5.2
GALT	c.1034C>A	p.A345D	KP	LP	ND	ND	ND	T	PD	U	A	M	D	5.21
MCCC1	c.475T>C	p.C159R	KP	LP	ND	0	ND	D	D	D	D	H	D	5.46
MCCC1	c.288+2T>A	NA	KP	P	0.0002	0	ND	NA	NA	NA	D	NA	NA	5.9
MUT	c.2179C>T	p.R727X	KP	P	ND	0	ND	T	NA	D	D	NA	NA	4.67
MUT	c.322C>T	p.R108C	KP	LP	0.0002	0.0001	ND	D	D	D	A	H	D	5.61
MUT	c.1228A>G	p.I410V	EP	VUS	ND	ND	ND	D	PD	D	D	M	D	5.49
PAH	c.1065+1G>A	NA	KP	P	ND	ND	ND	NA	NA	NA	D	NA	NA	5.81
PAX8	c.300dupTACC	p.M102fs	EP	LP	ND	ND	ND	NA	NA	NA	NA	NA	NA	NA
PAX8	c.192G>C	p.R64S	EP	VUS	ND	ND	ND	D	D	D	D	H	D	5.18
PAX8	c.739G>A	p.E247K	EP	VUS	ND	ND	ND	D	PD	D	D	L	D	4.54
SLC25A13	c.851delGTAT	p.M285Pfs*2	KP	P	0.0008	0.0003	ND	NA	NA	NA	NA	NA	NA	NA
SLC25A13	c.1180+1G>A	NA	KP	P	0.0008	0.0001	ND	NA	NA	NA	A	NA	NA	4.72
SLC5A5	c.1060A>C	p.T354P	KP	LP	ND	0	ND	D	D	D	A	H	D	4.36
SLC5A5	c.1605del	p.G535fs	EP	LP	ND	ND	ND	NA	NA	NA	NA	NA	NA	NA
TPO	c.1061G>T	p.W354L	EP	VUS	ND	ND	ND	D	D	D	D	M	T	5.3
TSHR	c.1454C>A	p.A485D***	EP	VUS	ND	ND	ND	D	D	D	D	M	D	5.64
TSHR	c.403A>T	p.N135Y	EP	VUS	ND	ND	ND	D	D	D	D	M	D	5.8

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Supplemental Data Table S11. Continued

Gene	NT alteration	AA alteration	Conventional criteria	ACMG criteria	1000G	ExAC	ESP6500	SIFT	Polyphen2	LRT	Mutation taster	Mutation assessor	FATHMM	GERP++
TSHR	c.1349G>A	p.R450H	KP	LP	0.0002	0.0003	ND	D	D	D	D	H	D	5.74
TSHR	c.611C>T	p.A204V	KP	LP	ND	0	ND	T	D	D	D	L	D	6.02
TSHR	c.1556G>A	p.R519H	EP	VUS	ND	0	ND	D	D	D	D	H	D	5.46
TSHR	c.1449C>A	p.N483K	EP	VUS	ND	ND	ND	D	D	D	D	M	D	5.64

Reference sequences of *MUT, MCCC1, SLC25A13, DUOX2, TSHR, DUOXA2, PAX8, GALE, GALT, GALT, PAH, SLC5A5, GALK1, TPO*, and *CYP21A2* were NM_000255, NM_001293273, NM_001160210, NM_014080, NM_000369, NM_207581, NM_003466, NM_001127621, NM_001258332, NM_000155, NM_000277, NM_000453, NM_000154, NM_175722, and NM_000500.7, respectively.

*KNIH1545408908 (allele frequency 0.00160772); **KNIH1545404850 (allele frequency 0.000803859); ***KNIH1481609856 (allele frequency 0.000803859) based on Korean Reference Genome DB

Abbreviations: KP, known pathogenic based on the Human Genome Mutation Database (DM) or ClinVar (pathogenic) databases; EP, expected pathogenic based on population frequency, *in silico* prediction, and mutation type (loss of function mutations); P, Pathogenic; LP, Likely pathogenic; VUS, variant of unknown significance; ND, not detected; NA, not applicable; D, damaging (in PolyPhen)/deleterious (in SIFT, LRT, FATHMM, RadialSVM, and LR); PD, possibly damaging (in PolyPhen); H, high (functional); M, medium (functional); N, neutral (nonfunctional); L, low(nonfunctional); T, tolerated (in SIFT); B, benign (in PolyPhen).