Germline Mutations and Phenotypic Associations in Korean Patients With Pheochromocytoma and Paraganglioma: A Multicenter Study and Literature Review

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Supplemental Data Table S1. Characteristics of cohort with PPGL (N=59) were obtained from six university hospitals

Characteristics	% (N)
Female sex	67.8% (40)
Age at diagnosis, yrs	52.5±14.3
Family history	6.8% (4)
Type	
PCC	88.1% (52)
PGL	10.2% (6)
PCC & PGL	1.7% (1)
Location	
Adrenal, unilateral	83.1% (49)
Adrenal, bilateral	5.1% (3)
Adrenal and Head & Neck	1.7% (1)
Head & Neck	0% (0)
Other sites	10.2% (6)
Multiple tumors	15.3% (9)
Tumor size, cm	4.3 (2.6–6.0)
Metastasis	6.8% (4)
Recurrence	12.3% (7/57)
Biochemical status	
Adrenergic	5.1% (3)
Noradrenergic	47.5% (28)
Adrenergic/Noradrenergic	40.7% (24)
Silent	6.8% (4)
Presence of other tumors	18.6% (11)

Values are expressed as mean±standard deviation, number (%), or median (interquartile range).

Abbreviations: PPGL, pheochromocytoma and paraganglioma; PCC, pheochromocytoma; PGL, paraganglioma.

Supplemental Data Table S2. Pathogenic mutations from Korean PPGL patients. (current study and literature review)

Genes	Nucleic acid change	Amino Acid Change	Classification[a]	Source	ACMG classification
SDHD	c.119delT	p.Ile40ThrfsTer46	Pathogenic	current study	PVS1, PM2, PP4
VHL	c.640T>A	p.*214Argext*14	Likely-Pathogenic	current study	PM2, PM4, PP4, PP5
VHL	c.242C>T	p.Pro81Leu	Likely-Pathogenic	current study	PM1, PM2, PM5, PP4, PP5
VHL	c.499C>T	p.Arg167Trp	Likely-Pathogenic	current study	PM1, PM2, PM5, PP3, PP4, PP5
VHL	c.208G>A	p.Glu70Lys	Likely-Pathogenic	current study	PM1, PM2, PM5, PP3, PP4, PP5
NF1	c.1748A>G	p.Lys583Arg	Pathogenic	current study	PVS1, PM2, PP4, PP5
NF1	c.4800dup	p.Ala1601SerfsTer21	Pathogenic	current study	PVS1, PM2, PP4
NF1	c.7869+1G>A	p.?	Pathogenic	current study	PVS1, PM2, PP4, PP5
NF1	c.6596del	p.Leu2199*	Pathogenic	current study	PVS1, PM2, PP4
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	current study	PM1, PM2, PM5, PP3, PP4, PP5
RET	c.1902C>G	p.Cys634Trp	Likely-Pathogenic	current study	PM1, PM2, PM5, PP3, PP4, PP5
RET	c.1902C>G	p.Cys634Trp	Likely-Pathogenic	current study	PM1, PM2, PM5, PP3, PP4, PP5
RET	c.1902C>G	p.Cys634Trp	Likely-Pathogenic	current study	PM1, PM2, PM5, PP3, PP4, PP5
SDHA	c.511C>T	p.Arg171Cys	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM2, PP2, PP3, PP4, PP5
SDHB	c.757delT	p.Cys253Valfs*5	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
SDHB	c.137G>A	p.Arg48Gln	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
SDHB	c.392delC	p.Pro131Hisfs*5	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
VHL	c.482G>A	p.Arg161Gln	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
VHL	c.470C>T	p.Thr157Ile	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PP3, PP5
VHL	c.499C>T	p.Arg167Trp	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
VHL	c.262T>C	p.Trp88Arg	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PS1, PS3, PM1, PM2, PM5, PP3, PP5
VHL	c.208G>A	p.Glu70Lys	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
MAX	c.3G>A	p.Met1?	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2
NF1	c.6777del	p.Gly2260fs	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
NF1	c.6215delA	p.His2072Leufs*10	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2
RET	c.1900T>C	p.Cys634Arg	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
RET	c.1902C>G	p.Cys634Trp	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
RET	c.2753T>C	p.Met918Thr	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PS3, PM1, PM2, PM5, PP3, PP5
RET	c.1832G>A	p.Cys611Tyr	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
RET	c.1902C>G	p.Cys634Trp	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
RET	c.1832G>A	p.Cys611Tyr	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
SDHB	c.757delT	p.Cys253Valfs*5	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
SDHB	c.137G>A	p.Arg46Gln	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
SDHB	c.725G>A	p.Arg242His	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
SDHB	c.392delC	p.Pro131Hisfs*5	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
SDHB	c.392delC	p.Pro131Hisfs*5	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
SDHB	c.757delT	p.Cys253Valfs*5	Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
SDHD	c.49C>T	p.Arg17*	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PVS1, PM2, PP5
VHL	c.308C>T	p.Pro103Leu	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):858-872	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Clin Genet. 2014 Nov;86(5):482-6	PM1, PM2, PM5, PP3, PP5
VHL	c.242C>T	p.Pro81Leu	Likely-Pathogenic	Clin Genet. 2014 Nov;86(5):482-6	PM1, PM2, PM5, PP5
SDHB	c.392delC	p.Pro131Hisfs*5	Pathogenic	Clin Genet. 2014 Nov;86(5):482-6	PVS1, PM2, PP5
SDHB	c.666_678del	p.Arg223Glnfs*21	Pathogenic	Clin Genet. 2014 Nov;86(5):482-6	PVS1, PM2, PP5
SDHD	c.94_95delTC	p.Ala33Ilefs*35	Pathogenic	Clin Genet. 2014 Nov;86(5):482-6	PVS1, PM2, PP5
SDHB	c.757delT	p.Cys253Valfs*5	Pathogenic	Fam Cancer. 2010 Dec;9(4):643-6	PVS1, PM2, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Thyroid. 2006 Jun;16(6):609-14	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Thyroid. 2006 Jun;16(6):609-14	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Thyroid. 2006 Jun;16(6):609-14	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Thyroid. 2006 Jun;16(6):609-14	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Thyroid. 2006 Jun;16(6):609-14	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Thyroid. 2006 Jun;16(6):609-14	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	Korean J Med 2007;73(3):994-1002	PM1, PM2, PM5, PP3, PP5
VHL	c.250G>T	p.Val84Leu	Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PS1, PS3, PM1, PM2, PM5, PP3, PP5
VHL	c.262T>C	p.Trp88Arg	Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PS1, PS3, PM1, PM2, PM5, PP3, PP5
VHL	c.278G>A	p.Gly93Asp	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.361G>A	p.Asp121Asn	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.361G>A	p.Asp121Asn	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.445G>A	p.Ala149Thr	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.470C>T	p.Thr157Ile	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PP3, PP5
VHL	c.470C>T	p.Thr157Ile	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PP3, PP5
VHL	c.470C>T	p.Thr157Ile	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PP3, PP5
VHL	c.499C>T	p.Arg167Trp	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.499C>T	p.Arg167Trp	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.499C>T	p.Arg167Trp	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
VHL	c.500G>A	p.Arg167Gln	Likely-Pathogenic	J Hum Genet. 2014 Sep;59(9):488-93	PM1, PM2, PM5, PP3, PP5
SDHB	c.392delC	p.Pro131Hisfs*5	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2, PP5
SDHB	c.724C>T	p.Arg242Cys	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
SDHB	c.757delT	p.Cys253Valfs*5	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2, PP5
SDHD	c.112C>T	p.Arg38*	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2, PP5
SDHA	c.778G>A	p.Gly260Arg	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PS1, PM2, PP2, PP3, PP5
VHL	c.482G>C	p.Arg161Pro	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
VHL	c.592delC	p.L198Wfs*4	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2, PP5
VHL	c.208G>A	c.Glu70Lys	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
VHL	c.470C>T	p.Thr157Ile	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PP3, PP5
VHL	c.482G>A	p.Arg161Gln	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
VHL	c.640T>A	p.*214Argext*14	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM2, PM4, PP4, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5

RET	c.1891G>T	p.Asp631Tyr	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
RET	c.1900T>C	p.Cys634Arg	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
RET	c.1901G>A	p.Cys634Tyr	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
RET	c.1902C>G	p.Cys634Trp	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PM1, PM2, PM5, PP3, PP5
RET	c.2753T>C	p.Met918Thr	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PS3, PM1, PM2, PM5, PP3, PP5
NF1	c.928delC	p.His310Metfs*7	Likely-Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2
NF1	c.4029dupT	p.Glu1344*	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2, PP5
MAX	c.289C>T	p.Gln97*	Pathogenic	J Med Genet 2022 Vol. 59(1):56-64	PVS1, PM2, PP5
RET	c.1900T>C	p.Cys634Arg	Likely-Pathogenic	Endocr J. 1998 Aug;45(4):555-61	PM1, PM2, PM5, PP3, PP5
RET	c.1900T>C	p.Cys634Arg	Likely-Pathogenic	Endocr J. 1998 Aug;45(4):555-61	PM1, PM2, PM5, PP3, PP5
RET	c.1852T>C	p.Cys618Arg	Likely-Pathogenic	Endocr J. 1998 Aug;45(4):555-61	PM1, PM2, PM5, PP3, PP5
RET	c.1901G>A	p.Cys634Tyr	Likely-Pathogenic	Endocr J. 1998 Aug;45(4):555-61	PM1, PM2, PM5, PP3, PP5
RET	c.1901G>A	p.Cys634Tyr	Likely-Pathogenic	Endocr J. 1998 Aug;45(4):555-61	PM1, PM2, PM5, PP3, PP5
SDHB	c.757delT	p.Cys253Valfs*5	Pathogenic	Fam Cancer. 2016 Oct;15(4):601-6	PVS1, PM2, PP5
SDHA	c.778G>A	p.Gly260Arg	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):909-917	PS1, PM2, PP2, PP3, PP5
KIF1B	c.2787-2A>C	p.?	Likely-Pathogenic	Endocrinol Metab (Seoul). 2020 Dec;35(4):909-917	PVS1, PM2
RET	c.2692G>T	p.Asp898Tyr	Likely-Pathogenic	Endocrinol. 2018 Apr 15;2018:8657914	PM1, PM2, PP3, PP5

Several variants (RET p.Gln214His, RET 634 codon mutation without further information, SDHD p.Val111Ile, VHL p.Val114Arg, VHL p.Leu85Phe) from literature review has been reclassified as VUSs and subsequently excluded from the mutation(+) group.

[a]Pathogenicity of variants from literature review were reclassified according to ACMG/AMP guideline [15].

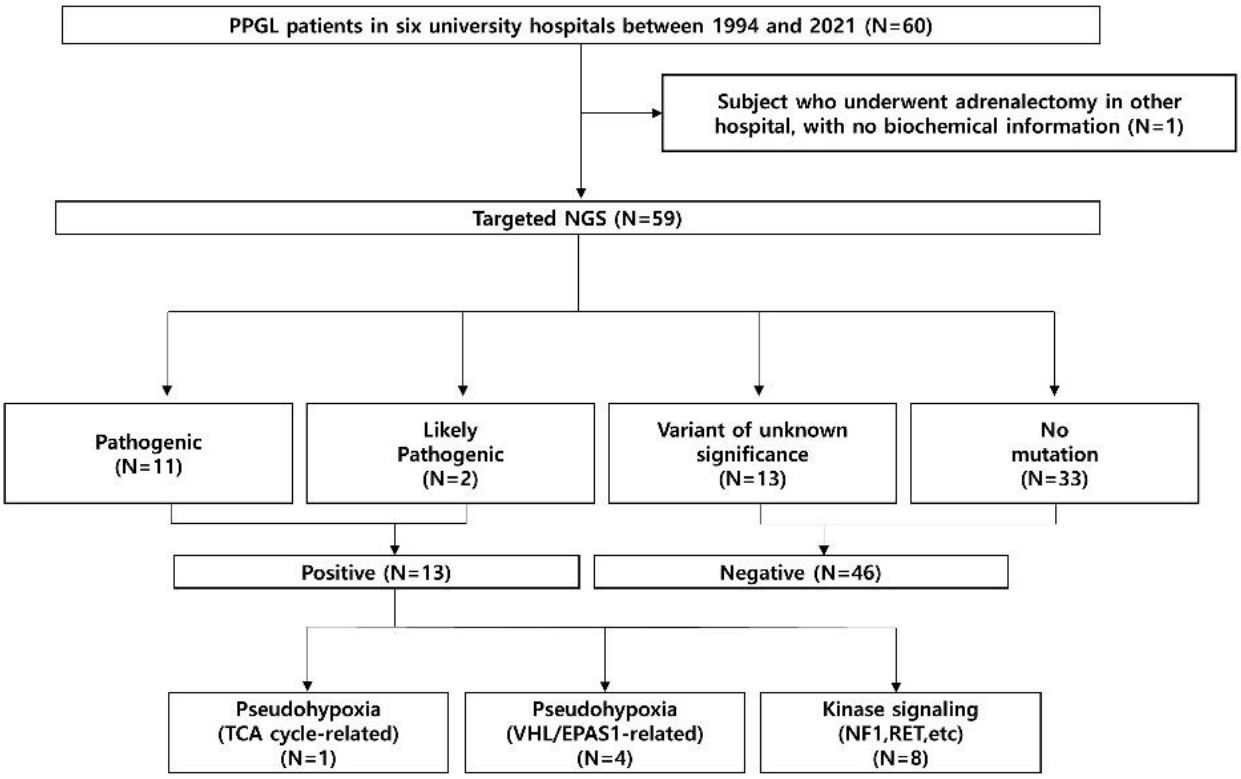
Supplemental Data Table S3. Common genotypic and phenotypic characteristics of all Korean PPGL cases

Characteristic	*SDHB* (N=16)[a]	*VHL* (N=30)[a]	*NF1* (N=8)[a]	*RET* (N= 31)[a]	*P*-value
Female sex	30.8% (4/13)	58.3% (14/24)	33.3% (2/6)	81.0% (17/21)	0.050
Age at diagnosis, yrs	40.2 ± 18.4 (13/13)	37.8 ± 16.3 (21/21)	45.5 ± 16.5 (6/6)	48.7 ± 12.6 (21/21)	0.246
Family history	50% (1/2)	52.9% (9/17)	0% (0/4)	73.7% (14/19)	0.055
Type					**<0.001**
PCC	46.2% (6/13)	91.6% (22/24)	100% (6/6)	100% (26/26)	
PGL	53.8% (7/13)	8.3% (2/24)	0% (0/6)	0% (0/26)	
PCC & PGL	0% (0/13)	0% (0/24)	0% (0/6)	0% (0/26)	
Location					**<0.001**
Adrenal, unilateral	40% (4/10)	34.8% (8/23)	100% (6/6)	53.3% (8/15)	
Adrenal, bilateral	0% (0/10)	56.5% (13/23)	0% (0/6)	46.7% (7/15)	
Adrenal & Head & Neck	0% (0/10)	0% (0/23)	0% (0/6)	0% (0/15)	
Head & Neck	10% (1/10)	0% (0/23)	0% (0/6)	0% (0/15)	
Other sites	50% (5/10)	8.7% (2/23)	0% (0/6)	0% (0/15)	
Multiple tumors	0% (0/3)	40% (2/5)	0% (0/4)	44.4% (4/9)	0.238
Tumor diameter, cm	4.5 (3.5–9.0; 10/10)	3.5 (2.4–4.3; 10/10)	5.3 (4.3–7.2; 6/6)	4.7 (3.2–6.0; 16/16)	**0.014**
Metastasis	58.3% (7/12)	36.4% (4/11)	0% (0/6)	0% (0/16)	**0.002**
Recurrence	25.0% (3/12)	27.3% (3/11)	16.7% (1/6)	6.25% (1/16)	0.290
Biochemical status					**0.001**
Adrenergic	0% (0/12)	0% (0/11)	0% (0/6)	17.6% (3/17)	
Noradrenergic	83.3% (10/12)	72.7% (8/11)	33.3% (2/6)	17.6% (3/17)	
Adrenergic/Noradrenergic	0% (0/12)	0% (0/11)	50% (3/6)	58.8% (10/17)	
Silent	16.7% (2/12)	27.3% (3/11)	16.7% (1/6)	5.9% (1/17)	
Presence of other tumors	0% (0/10)	40% (4/10)	66.7% (4/6)	92.8% (13/14)	**<0.001**
Consequences					**<0.001**
Frameshift	75.0% (12/16)	3.3% (1/30)	50% (4/8)	0% (0/33)	
Missense	25.0% (4/16)	86.7% (26/30)	12.5% (1/8)	100% (33/33)	
Nonsense	0% (0/16)	3.3% (1/30)	25.0% (2/8)	0% (0/33)	
Splicing	0% (0/16)	0% (0/30)	12.5% (1/8)	0% (0/33)	
Stop loss	0% (0/16)	6.6% (2/30)	0% (0/8)	0% (0/33)	

Values are expressed as percentage (%), mean±standard deviation, number (%), or median (interquartile range). Clinical data for all characteristics were collected from available cases only (shown as the number of cases indicated / the number of descriptions of each characteristic).

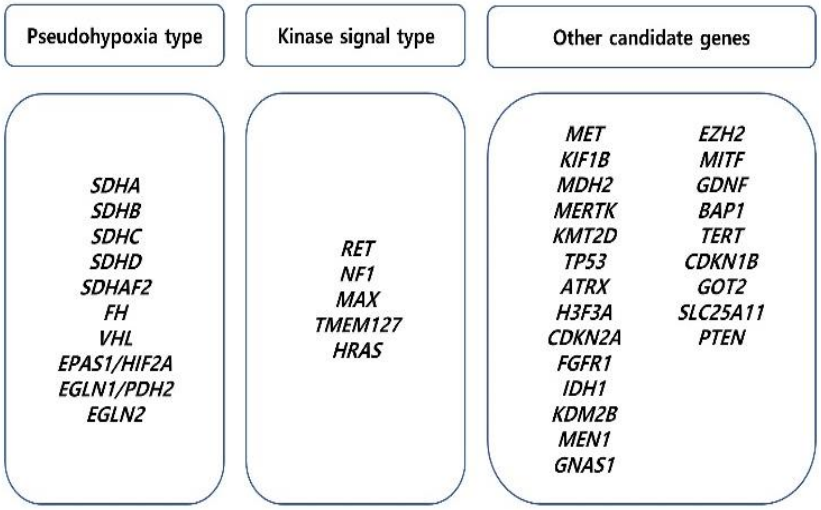
[a]Number of mutation-positive cases, including the literature review.

Abbreviations: PPGL, pheochromocytoma and paraganglioma; *SDH*, succinate dehydrogenase; *VHL*, von Hippel-Lindau; *NF1*, neurofibromatosis type 1; *RET*, rearranged during transformation; PCC, pheochromocytoma; PGL, paraganglioma.



Supplemental Data Fig. S1. Flow chart of this multicenter study.

Abbreviations: PPGL, pheochromocytoma and paraganglioma; TCA, tricarboxylic acid.

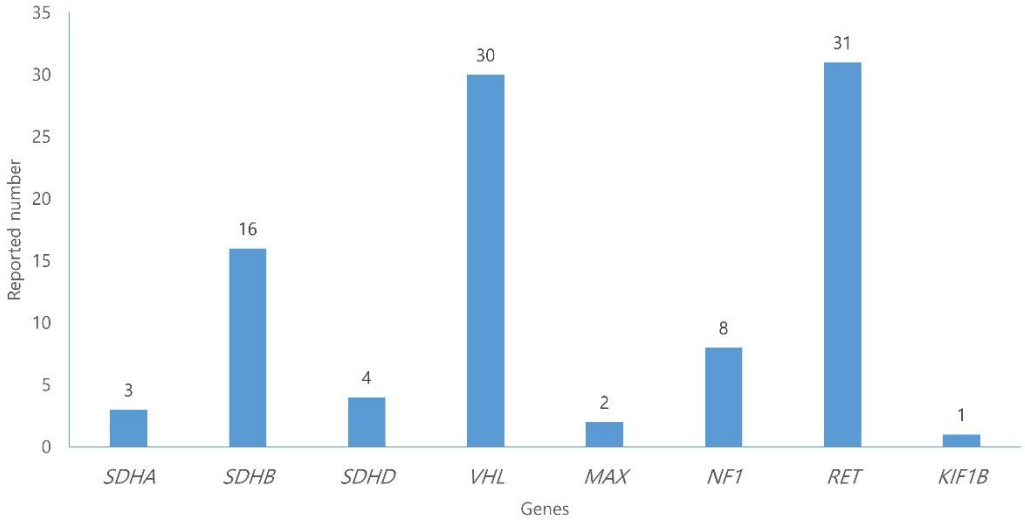


Abbreviations

Cluster1 Pseudohypoxia (N=10)	*SDHA*	Succinate dehydrogenase complex flavoprotein subunit A
	SDHB	Succinate dehydrogenase complex iron sulfur subunit B
	SDHC	Succinate dehydrogenase complex subunit C
	SDHD	Succinate dehydrogenase complex subunit D
	SDFAF2	Succinate dehydrogenase complex assembly factor 2
	FH	Fumarate hydratase
	VHL	Von Hippel-Lindau tumor suppressor
	EPAS1/HIF2A	Endothelial PAS domain protein 1
	EGLN1/PDH2	Egl-9 family hypoxia inducible factor 1
	EGLN2/PDH1	Egl-9 family hypoxia inducible factor 2
Cluster2 Kinase signaling (N=5)	*RET*	Ret proto-oncogene
	NF1	Neurofibromin 1
	MAX	MYC associated factor X
	TMEM127	Transmembrane protein 127
	HRAS	HRas proto-oncogene, GTPase
Other candidate genes (N=23)	*MET*	MET proto-oncogene, receptor tyrosine kinase
	KIF1B	Kinesin family member 1B
	MDH2	Malate dehydrogenase 2
	MERTK	MER proto-oncogene, tyrosine kinase
	KMT2D	Lysine methyltransferase 2D
	TP53	Tumor protein p53
	ATRX	ATRX chromatin remodeler
	H3F3A	H3 histone, family 3A
	CDKN2A	Cyclin dependent kinase inhibitor 2A
	FGFR1	Fibroblast growth factor receptor 1
	IDH1	Isocitrate dehydrogenase (NADP(+)) 1, cytosolic
	KDM2B	Lysine demethylase 2B
	MEN1	Menin 1
	GNAS1[GNAS]	GNAS complex locus 1
	EZH2	Enhancer of zeste 2 polycomb repressive complex 2 subunit
	MITF	Melanocyte inducing transcription factor
	GDNF	Glial cell derived neurotrophic factor
	BAP1	BRCA1 associated protein 1
	TERT	Telomerase reverse transcriptase
	CDKN1B	Cyclin dependent kinase inhibitor 1B
	GOT2	Glutamic-oxaloacetic transaminase 2
	SLC25A11	Solute carrier family 25 member 11
	PTEN	Phosphatase and tensin homolog

Supplemental Data Fig. S2. PPGL molecular clusters and related genes analyzed using NGS in this study.

Abbreviations: PPGL, pheochromocytoma and paraganglioma; NGS, next-generation sequencing.



Supplemental Data Fig. S3. Genotypes of Korean patients with PCC/PGL (N=95) in this multicenter study (N=13) and the literature (N=82).

Abbreviations: PPC, pheochromocytoma; PGL, paraganglioma.