Supplementary Table S2. Association of Number of Mutations with Clinicopathological Parameters

	No. of mutations, median (range)	p
Age (years)		
≥45	48 (32–89)	0.797
<45	56 (13–95)	
Sex		
Female	48 (13–59)	0.518
Male	52 (32–95)	
Histology		
Classical variant	48 (34–88)	0.127
Follicular variant	47 (13–58)	
Tall cell variant	77 (59–95)	
Extrathyroidal extension		
Present	51.5 (13–89)	1.000
Absent	46 (32–95)	
Stage		
II	56 (13–95)	0.797
IV	48 (32–89)	

Supplementary Table S7. Pathway Analysis Using g:Profiler and Ingenuity Pathway Analysis

	Ingenuity Pathway Analysis of the genes restricted to metastasis		
No.	*Ingenuity canonical pathways*	*Genes*	p
1	Nonsmall cell lung cancer signaling	TP53, NRAS, HRAS, SIN3A	<0.0001
2	Bladder cancer signaling	TP53, NRAS, HRAS, SIN3A	<0.0001
3	Prostate cancer signaling	TP53, NRAS, HRAS, SIN3A	<0.0001
4	Chronic myeloid leukemia signaling	TP53, NRAS, HRAS, SIN3A	<0.0001
5	Glioma signaling	TP53, NRAS, HRAS, SIN3A	<0.0001
6	DNA methylation and transcriptional repression signaling	CHD4, RBBP7, SIN3A	<0.0001
7	Ovarian cancer signaling	TP53, NRAS, HRAS, SIN3A	<0.0001
8	Thyroid cancer signaling	TP53, NRAS, HRAS	<0.0001
9	UVC-induced MAPK signaling	TP53, NRAS, HRAS	<0.0001
10	Cancer drug resistance by drug efflux	TP53, NRAS, HRAS	<0.0001
	Ingenuity Pathway Analysis of the genes restricted to metastasis (excluding the genes present with >1% frequency in TCGA thyroid)		
No.	*Ingenuity canonical pathways*	*Genes*	p
1	DNA methylation and transcriptional repression signaling	CHD4, RBBP7, SIN3A	<0.0001
2	L-Dopachrome biosynthesis	TYR	0.0004074
3	Biotin-carboxyl carrier protein assembly	ACACB	0.0012303
4	Adipogenesis pathway	RBBP7, SIN3A	0.0012882
5	Eumelanin biosynthesis	TYR	0.0020417
6	Transcriptional regulatory network in embryonic stem cells	EOMES	0.0218776
7	Nur77 signaling in T lymphocytes	SIN3A	0.0239883
8	Cell cycle: G1/S checkpoint regulation	SIN3A	0.0269153
9	Nonsmall cell lung cancer signaling	SIN3A	0.0309030
10	Cyclins and cell cycle regulation	SIN3A	0.0331131
	g:Profiler pathway analysis of the genes restricted to metastasis (excluding the genes present with >1% frequency in TCGA thyroid)		
No.	*g:Profiler pathway*	*Genes*	p
1	Epigenetic regulation of gene expression	CHD4, RBBP7, SIN3A	0.0269
2	Regulation of TP53 activity through acetylation	CHD4, RBBP7	0.0411

MAPK, mitogen-activated protein kinase; TCGA, The Cancer Genome Atlas; UVC, ultraviolet light short wavelength.