SUPPORTING INFORMATION TABLES

Supporting Information Table 1. 48 cancer hotspot genes.

ABL1	AKT1	ALK	APC	ATM	BRAF
CSF1R	CTNNB1	EGFR	ERBB2	FBXW7	FGFR1
FLT3	GNA11	GNAS	GNAQ	HNF1A	HRAS
JAK3	KDR	KIT	KRAS	MET	MLH1
NPM1	NRAS	PDGFRA	PIK3CA	PTEN	PTPN11
SMAD4	SMARCB1	SMO	STK11	SRC	TP53
CDKN2A	FGFR3	JAK2	NOTCH1	RET	ERBB4
CDH1	FGFR2	IDH1	MPL	RB1	VHL

Supporting Information Table 2. Clinical characteristics of the 88 PTC patients.

Characteristics	Data (n = 88)
Age, Mean (SD)	45.7 (13.1)
Sex ratio (F/M)	63/25
Lesion (L/R/I)	39/40/9
Size (median)	8 (mm)
ETE (Absence/Presence)	63/25
LN (0/1A/1B)	43/23/22
Stage (I/III/IV)	63/7/18

Abbreviations: L, left lobe; R, right lobe; I, isthmus; ETE, extrathyroidal extension; LN, lymph node.

Supporting Information Table 3. Association of the number of total exonic mutations and missense SNV mutations with tumor invasive characteristics of the PTC patients.

Invasive characteristics		Total mutation number (mean±SD)	Missense SNV number (mean±SD)
LNM	Absence	1.28±1.45	0.93±1.06
	Presence	1.60±1.76	1.13±1.34
	P-value	0.353	0.431
ETE	Absence	1.35±1.33	0.98±1.01
	Presence	1.68±2.19	1.16±1.62
	P-value	0.487	0.618

Abbreviations: ETE, extrathyroidal extension; LNM, lymph node metastasis. P-values were from Student's t tests.

SUPPORTING INFORMATION FIGURE LEGENDS

Figure S1

The distribution of 2,158 pairs of amplicons depth. (A) Box plots show amplicon sequencing depth of the 48 genes in all samples. (B) Density plots show the distribution of the amplicon depth in each of the 88 PTC samples. Sample ID, such as TGC10A, is shown at the top of each plot. The x-axis represents $\log_2$-scaled amplicon depth, and y-axis represents the density of the given depth.

Figure S2

Genome browser screen shot of sequencing coverages in *NOTCH1*, *EGFR*, *RET* and *TP53* genes. Gene structure is shown by exons (blue blocks) and introns (dotted lines). The logarithmic transformed sequencing depth of two representative samples are shown for each gene.