## 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.