

Figure S1. Building of the FE model and the FEA process. (A-D) Construction of the 3D stereolithography model of the thyroid gland using the CT data. (E) The FE model of the thyroid with the trachea. (F) The side surface and (G) the bottom side of the thyroid in contact with the trachea. FEA, finite element analysis.

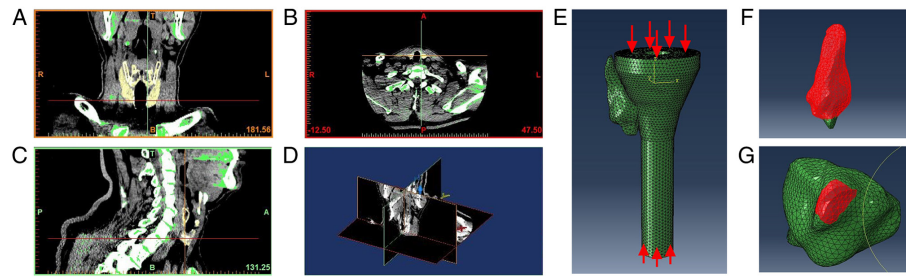


Figure S2. Identification of PTMC stiffness using nanoindentation technology. (A) The displacement increases with the increase of the experimental load. (B) The image of the nanoindentation instrument, which includes the stepping motor, mechanical sensor and adjustable pan tilt. The continuous change of load was controlled by a computer, and the pressing depth was monitored online. (C) The association between the displacement and the experimental load (nm). (D) The results of PTMC stiffness among the 33 samples. PTMC, papillary thyroid microcarcinoma. Y-axis represent PTMC stiffness (kPa). hr, residual indentation depth; S, slope of the unloading curve at the beginning; Pmax, maximum load; hmax, maximum indentation depth.

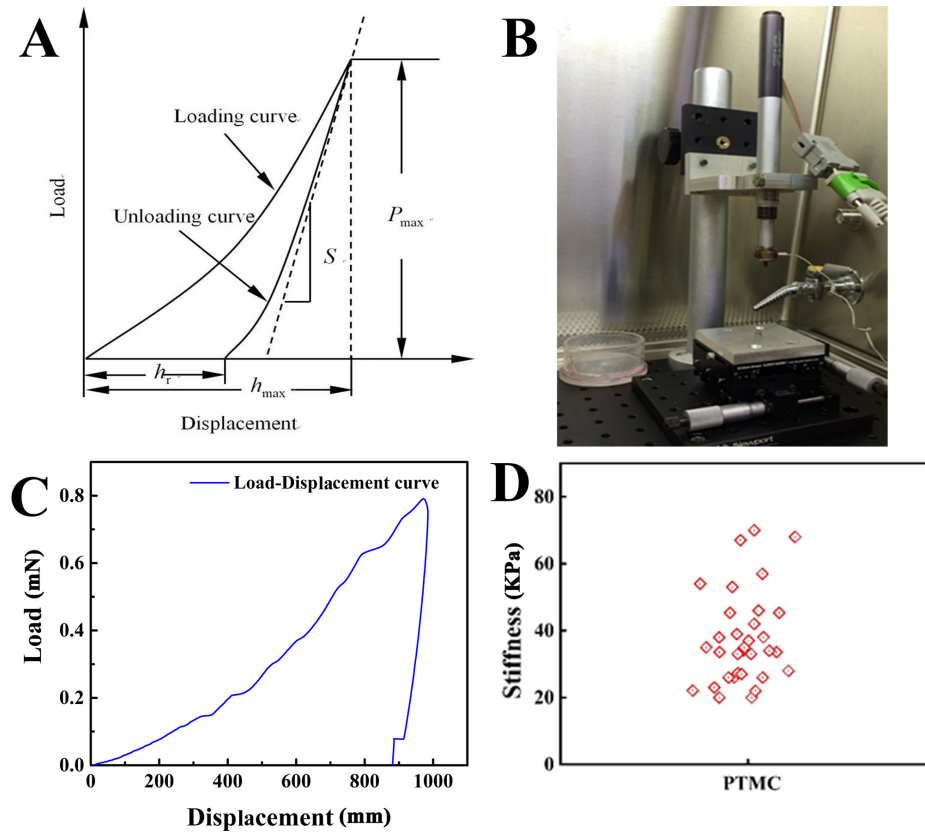


Figure S3. Gene expression in adjacent normal tissue, PTMC from the interior and lateral thyroid. (A) *Piezo2* and *CHD3*, (B) *Runx2* and *Twist1* and (C) *ADORA1* and *GABBR2* expression was increased in the PTMC from the interior compared with that in the lateral groups. *P<0.05 vs. PTMC in lateral groups. PTMC, papillary thyroid microcarcinoma.

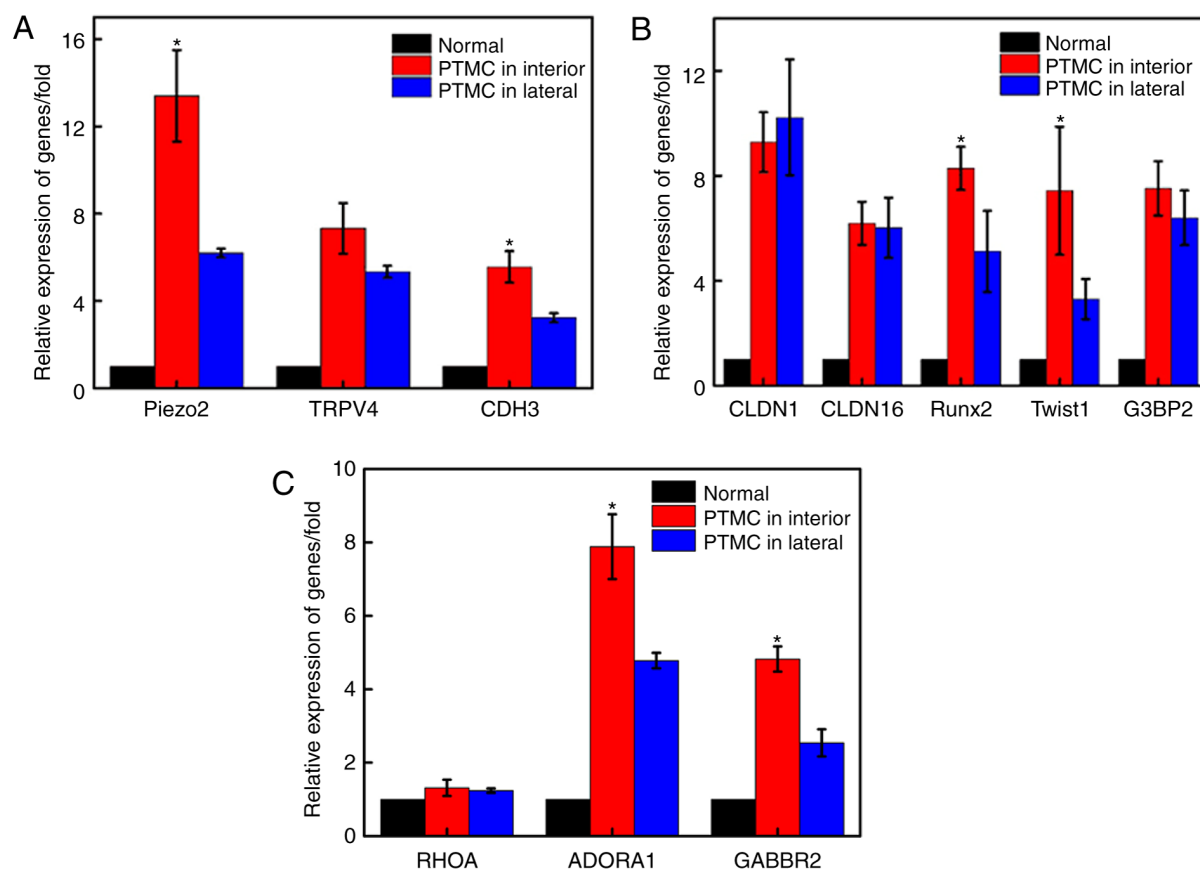


Figure S4. Gene expression levels in PTMC and adjacent normal tissues. (A) Venn diagram of the differentially expressed genes in three samples. I, II and III represent three different patients. Flow diagram of the enriched GO terms for biological process, for the (B) up- and (C) downregulated DEGs between the papillary thyroid microcarcinoma and adjacent normal tissue. The number of DEGs and the P-value are shown for each GO term. (D) KEGG pathway analysis of the DEGs. The x-axis represents the number of DEGs and the y-axis represents the KEGG pathway terms. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially expressed genes.

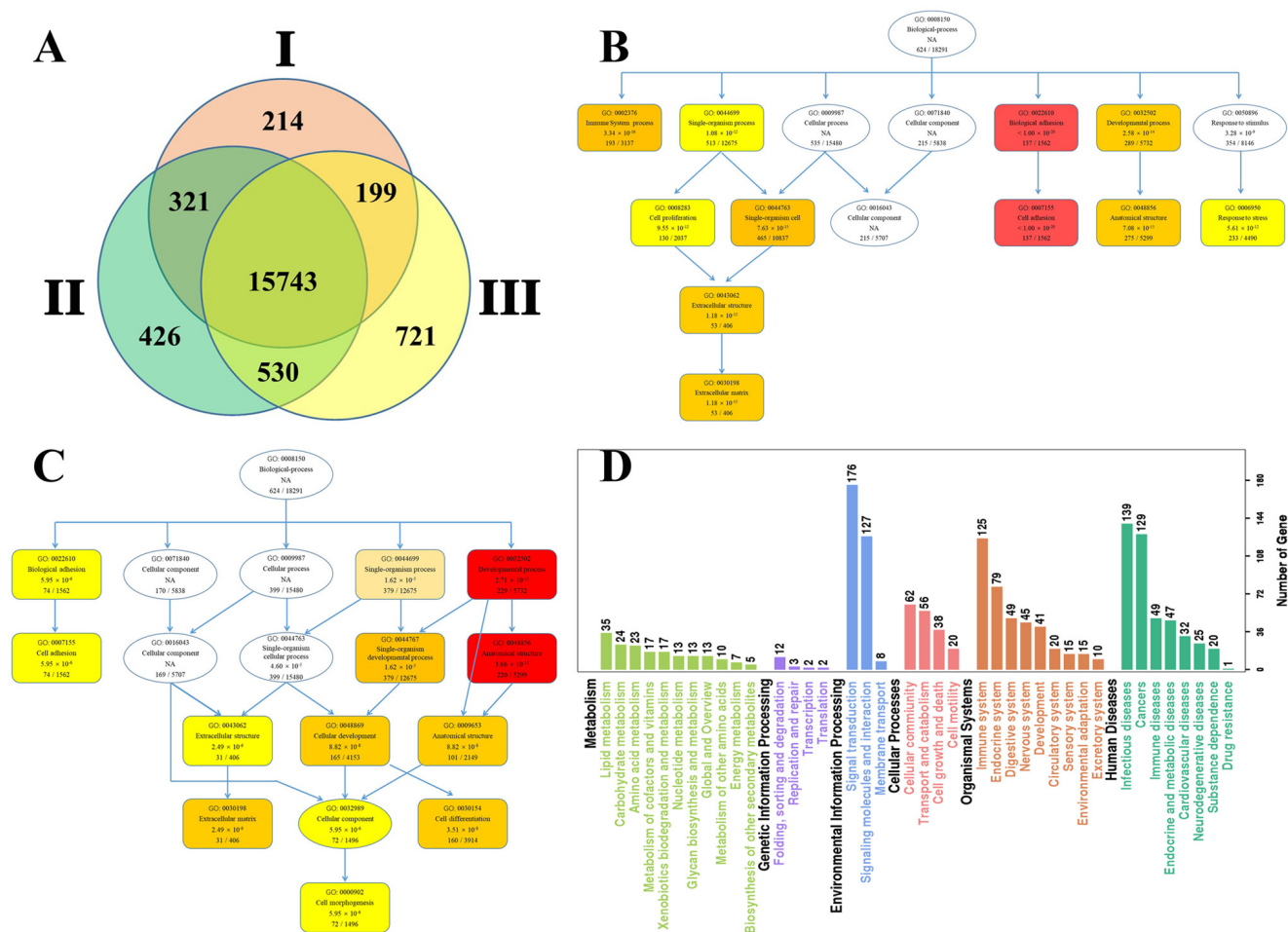


Table SI. Gene specific primers used for reverse transcription-quantitative PCR.

Gene name	Sense primer (5'-3')	Anti-sense primer (5'-3')
Piezo2	GCCCAACAAAGCCAGTTGAA	GGGCTGTGGTCCACAAAGA
TWIST1	CAGCGGGTCATGGCTAAC	CAGCTTGCCATCTTGGAGTC
G3BP2	CCCGAGTATTTGCACAGGTT	TCACTCAAGGTTGCATGAGC
CLDN1	TACGAGGGGCTGTGGATGTC	ATCACTCCCAGGAGGATGCC
CLDN16	TTTGGTTGGTCCTGTTGGC	TGTGCGAGGGGCTGAGTAT
CDH3	TGACCACAAGCCCAAGTTTAC	TAAGCAACCACCCCATTGTAG
TRPV4	TCTTCACCCTCACCGCCTACT	TCCACTGTGGTCCGGTAAG
Runx2	TCTTAGAACAATTCTGCCCTTT	TGCTTTGGTCTTGAAATCACA
RHOA	CAAGCATTCTGTCCCAACG	CAATCCTGTTTGCCATATCTCTG
ADORA1	TGCTGTGGA CCG CTA CCT C	CTCCACCGCACTCAGATTGTT
GABBR2	GCGAAGGACAGTGGAGAAGT	CCCAAGCTAAGAAACAACCG
18srRNA	GTAACCCGTTGAACCCCAT	CCATCCAATCGGTAGTAGCG