#### SUPPLEMENTAL METHODS

#### Ultrasound-guided core-needle biopsy

Following local anesthesia with 2% lidocaine, patients underwent ultrasound-guided core-needle biopsy (CNB) utilizing 18-gauge disposable needles with a double-action spring-activated mechanism (1.1- or 1.6-cm excursion; TSK Ace-cut, Create Medic, Yokohama, Japan) [1]. The core-needle was advanced towards the target nodule using a freehand technique, starting from the isthmus of the thyroid. Once the needle tip reached the periphery of the nodule, the stylet and cutting cannula of the needle were sequentially activated. After the CNB, the biopsy site received firm, localized compression for a duration of 10 to 20 minutes [2].

## Immunohistochemical staining of the HBME-1 and galectin-3

The CNB samples underwent standard paraffin embedding and subsequent hematoxylin and eosin (H&E) staining. For immunohistochemistry, representative paraffin blocks containing both tumor and normal thyroid tissue were selected. Galectin-3 (Gal-3, dilution 1:200, BenchMark XT auto-immunostainer, Novo, Ventana, AZ, USA) and Hector Battifora mesothelial-1 (HBME-1, dilution 1:200; BenchMark XT auto-immunostainer, Dako, Carpinteria, CA, USA) were used for immunohistochemical staining. Galectin-3 exhibited expression in the cytoplasm and/or nucleus, while HBME-1 showed cytoplasmic and cell membrane expression. The expression of these markers was assessed based on the following criteria: negative (0), focal positive (1, less than 25% of cells), and positive (2, more than 25% of cells), considering the positive expression of tumor cells. In the statistical analysis, cases showing any level of positive staining were categorized as positive [3].

# DNA isolation and detection of the $BRAF^{V600E}$ and RAS mutation

Genomic DNA was isolated from formalin-fixed, paraffin-embedded tissue sections representing each archival tissue block. The QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) was utilized for DNA purification. The purified DNA was directly subjected to polymerase chain reaction (PCR) with primers designed to detect each mutation site. The amplification targeted exon 15 of the BRAF gene, which contains V600E mutation and exons 2 and 3 of the NRAS, HRAS, and KRAS genes. The amplification protocol consisted of initial denaturation at 95°C for 15 minutes, followed by 45 cycles of denaturation at 95°C for 30 seconds, primer annealing at 55°C to 65°C for 30 seconds, primer extension at 72°C for 30 seconds, and a final extension at 72°C for 5 minutes. The PCR reaction was then cooled to 4°C [4]. The final PCR products was verified through electrophoresis. To determine any genetic mutation, DNA sequencing was carried out employing the antisense primers. The DNA sequences were subsequently analyzed using a DNA analyzer (Bioedit v7.2.0, Ibis Biosciences, Carlsbad, CA, USA). To confirm the presence of BRAF and RAS mutations, each DNA sample was analyzed at least twice.

### SUPPLEMENTAL REFERENCES

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