

Figure S1. Uncropped western blot data. Uncropped images of western blot displayed in Fig. 1A (A), Fig. 3A (B), and Fig. 4A (C) are shown. The areas enclosed by red dashed lines indicate the portions used in the figures.

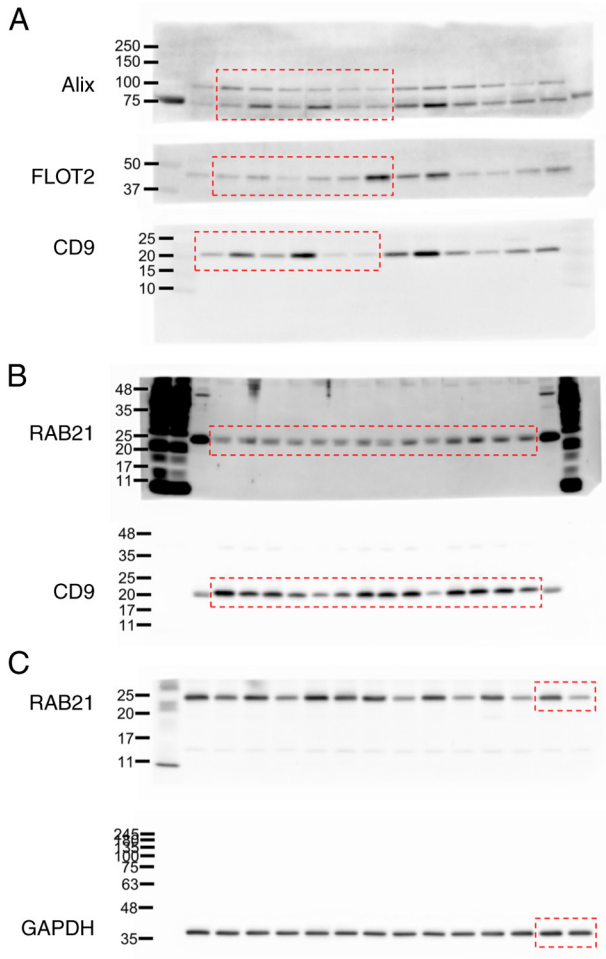


Figure S2. Plasma concentrations of proteins extracted from the Protein Atlas database. Proteins that were significantly abundant in serum EVs from FTC patients were subjected to analysis. The left table summarizes the plasma concentrations of the focused proteins and their ranks among 4,066 registered proteins. The right chart displays the distribution of all 4,066 proteins registered in the database. The positions of the proteins of interest are highlighted within the overall distribution. The URL for plasma concentration of proteins in the Protein Atlas database is as follows: <https://www.proteinatlas.org/humanproteome/blood/proteins+detected+in+ms>. EVs, extracellular vesicles; FTC, follicular thyroid carcinoma.

Gene symbol	Concentration	Rank from top among 4,066 proteins
KRT13	680 µg/l	319/4,066
LBP	1.3 mg/l	267/4,066
SAA1	11 mg/l	109/4,066
PGLYRP2	87 mg/l	30/4,066
RAB21	13 ng/l	3,858/4,066
FGA	140 mg/l	10/4,066

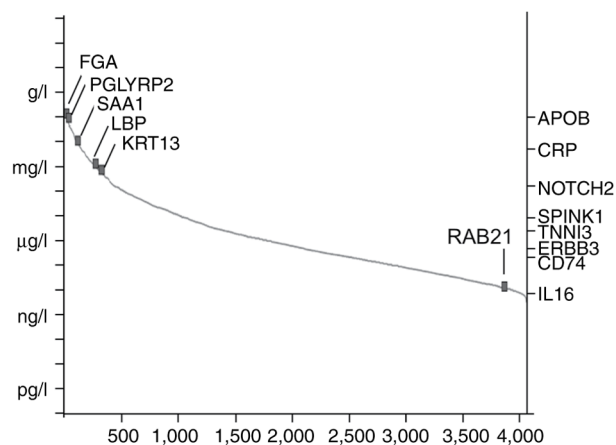


Figure S3. RAB21 mRNA expression extracted from the GEO public database. The mRNA expression values of RAB21 in FTA and FTC tissues were analyzed using the GSE15045 dataset from the GEO public database. Analysis was performed using the GEO2R website (<https://www.ncbi.nlm.nih.gov/geo/geo2r/>). The left bar graph shows the mRNA expression values of RAB21, and the right table summarizes the demographic characteristics and clinical backgrounds of each subject from the database. Gene expression data were analyzed using Welch's t-test. \*P<0.05. FTA, follicular thyroid adenoma; FTC, follicular thyroid carcinoma; GEO, Gene Expression Omnibus.

