

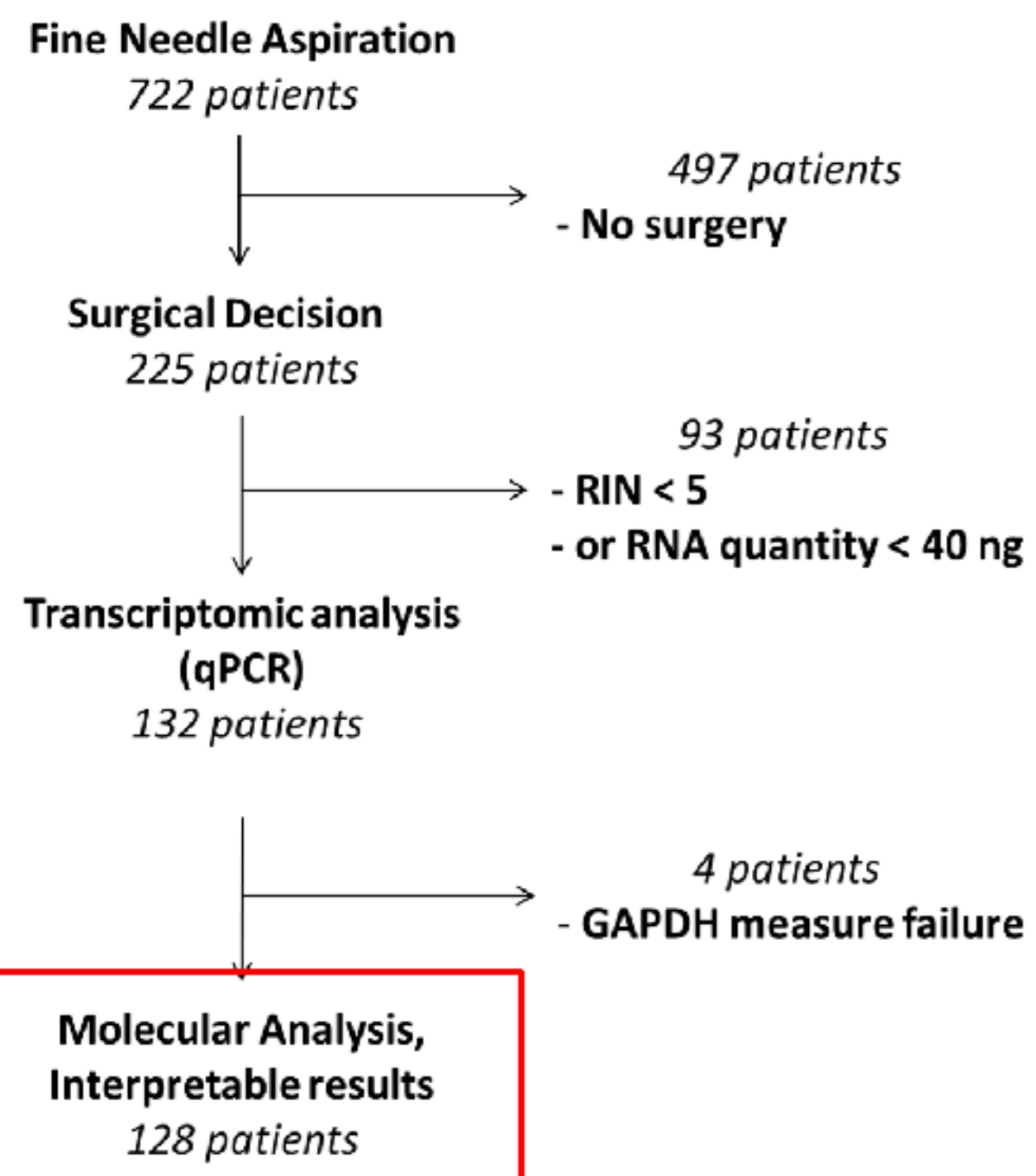
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Context : Thyroid nodules prediction of malignancy is based on ultrasonographic examination and cytological analysis. Up to 30% of thyroid nodules remain "indeterminate" after cytological examination using Bethesda Classification.

Objective : This monocentric prospective study aimed to identify a molecular signature to improve the accuracy of preoperative diagnosis of nodules, taking into account the prevalence of the disease and the differential clinical consequences of false-negative and false-positive results.

Material



722 patients, prospectively included, underwent Fine-needle-Aspiration (FNA) for 1 cm or more thyroid nodule. One sample was kept frozen. In case of surgical decision, based on clinician judgment, molecular analysis was performed.

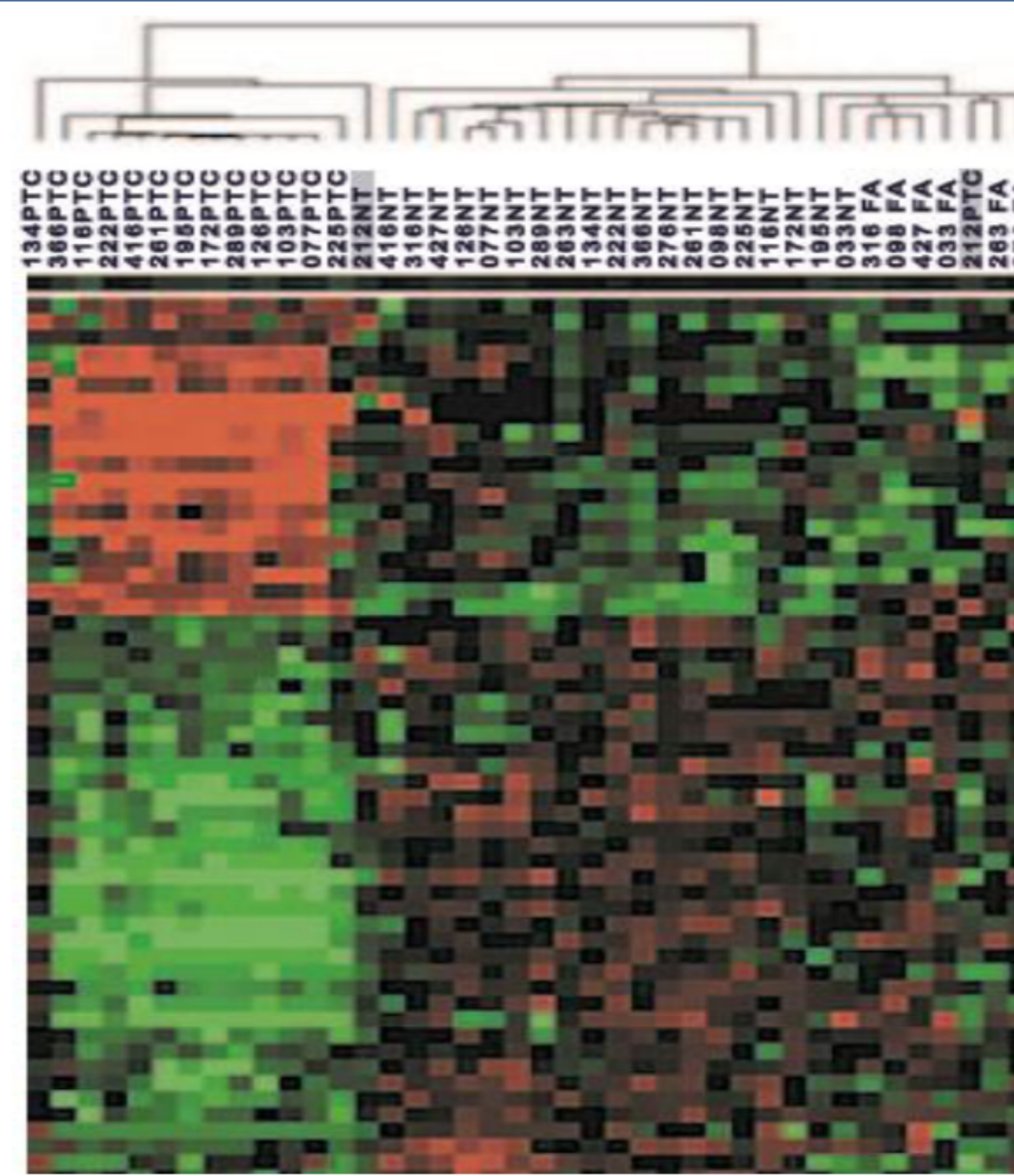
The **Study Population** consisted of patients with available cytological (Bethesda classification), histological and molecular result.

Method : transcriptomic analysis

We performed a transcriptomic analysis of 20 genes selected from a previous study (1) using qPCR on FNA material.

A **logistic regression model** using genes expression levels as linear covariates generated the **molecular predictor**.

A **gene selection** was made using Bootstrap method and Akaike information Criterion.



7 genes predicted the best malignancy

| Gene | Adjusted OR [95% CI] | p-value * |
|------------|----------------------|-----------|
| FN1 | 2.01 [1.12; 3.58] | 0.015 |
| CITED2 | 0.31 [0.17; 0.58] | <0.001 |
| CITED1 | 2.60 [1.45; 4.65] | <0.001 |
| CHI3L1 | 0.50 [0.29; 0.87] | 0.012 |
| TFF3 | 0.46 [0.26; 0.82] | 0.005 |
| CDKN1A | 1.71 [0.99; 2.98] | 0.046 |
| CSGALNACT1 | 1.79 [0.98; 3.28] | 0.047 |

* log-likelihood ratio test

Results : cytology and histology

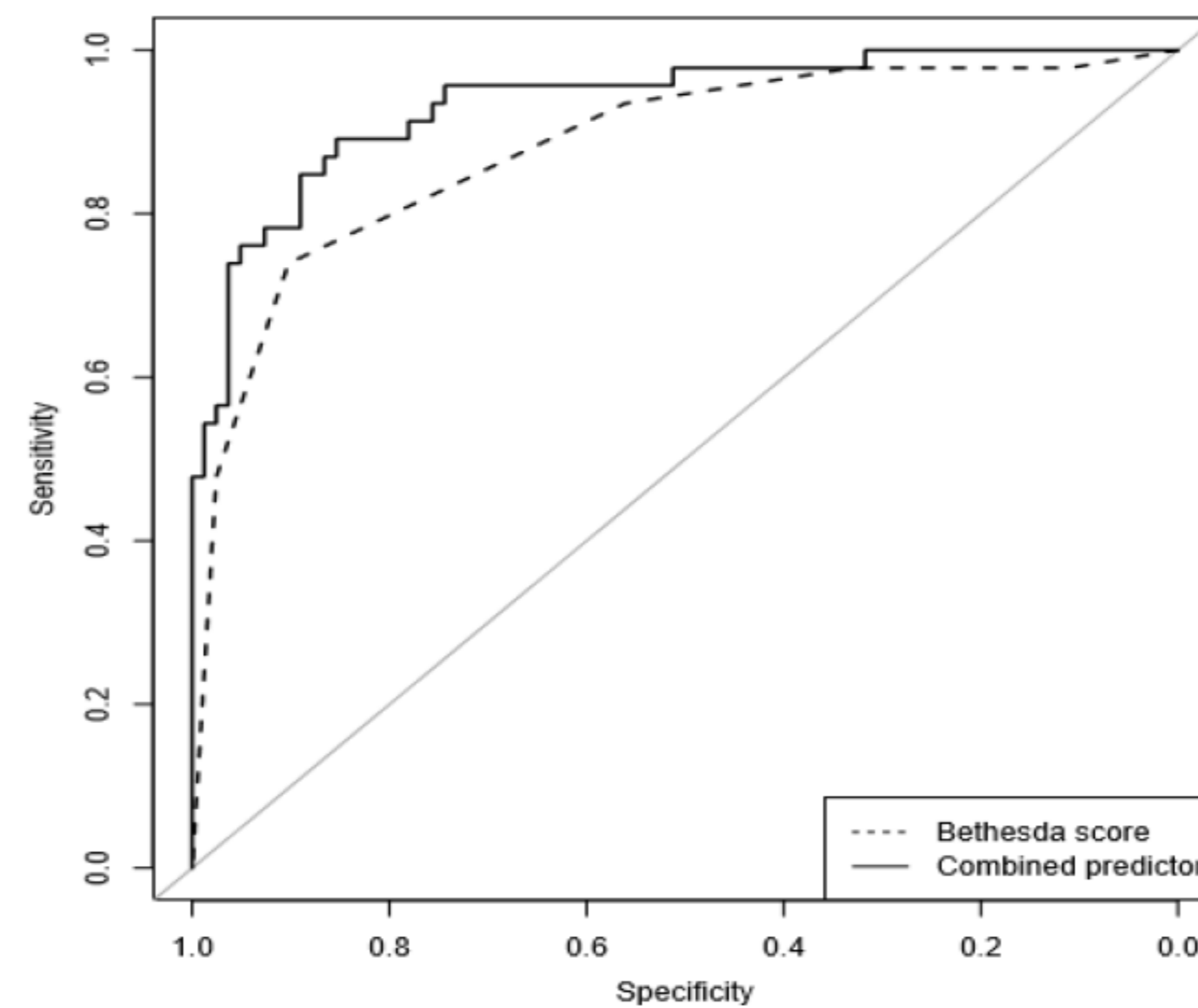
The malignancy prevalence among Bethesda categories was similar to the rates reported in literature (2).

| Bethesda level | Malignant tumors in the study* | |
|----------------|--------------------------------|---------|
| | frequencies | percent |
| I | 1/10 | 10.0 |
| II | 0/18 | 0.0 |
| III | 2/21 | 9.5 |
| IV | 9/37 | 24.3 |
| V | 12/18 | 66.7 |
| VI | 22/24 | 91.7 |
| Total | 46/128 | 36.0 |

* Malignant tumors (46)

papillary thyroid carcinomas (39) anaplastic thyroid cancer (1)
 follicular thyroid carcinomas (3) poorly differentiated carcinoma (1)
 medullary thyroid carcinomas (2)

Results : combined predictor performances



A **logistic regression model** using two covariates, molecular result (7 genes) and cytological Bethesda category, generated the **combined predictor**.

The Area under the curve of the combined predictor was **significantly higher than those of Bethesda classification** (DeLong test p = 0,004).

In our data-set (36% prevalence of malignancy), the combined predictor achieved a **high specificity** :

Sensitivity : 76,1 % [65.22; 97.83]
Specificity : 95,1 % [85.37; 100.00]

Results : clinical situations and performances

Thyroid cancer prevalence being around 7% among generic aspirated nodules (2), we optimized the performances **considering this prevalence and 2 different benefit-to-harm ratios**.

Thus, the combined predictor still harboured a high specificity together with an acceptable sensitivity.

| Probability of malignant tumor* | Ratio* | Sensitivity | Specificity |
|---------------------------------|--------|------------------------|------------------------|
| In our dataset | | | |
| 36% | 4: 1 | 95.7% [86.96 ; 100.00] | 74.4% [66.43; 93.90] |
| 36% | 1: 1 | 76.1% [65.22; 97.83] | 95.1% [85.37; 100.00] |
| 36% | 1: 4 | 73.9% [39.13; 86.96] | 96.3% [95.12; 100.00] |
| In a virtual population | | | |
| 7% | 4: 1 | 73.9% [52.17; 89.13] | 96.3% [92.04; 100.00] |
| 7% | 1: 1 | 47.8% [35.82; 82.61] | 100% [98.78 ; 100.00] |
| 7% | 1: 4 | 47.8% [34.78; 71.74] | 100% [100.00 ; 100.00] |

* The combined predictor model gave a probability of malignancy. The cut-off probability to classify a nodule as malignant or non malignant was set taking into account the malignancy prevalence. Then, we introduced the benefit-to-harm ratio concept by weighting the number of false negative and false positive results.

Conclusion: We present the development of a **very specific molecular test** that may improve the pre-operative diagnosis of thyroid nodules. Moreover, its performances optimization according to the prevalence of the disease may avoid a reduction in its performances into clinical practice and enables an adaptation to the population of use.

1. Durand S, Ferraro-Peyret C, Selmi-Ruby S, Paulin C, El Atifi M, Berger F, Berger-Dutrieux N, Decaussin M, Peix JL, Bournaud C, Orgiazzi J, Borson-Chazot F, Rousset B. Evaluation of gene expression profiles in thyroid nodule biopsy material to diagnose thyroid cancer. The Journal of clinical endocrinology and metabolism 2008; 93:1195-1202
 2. Bongiovanni M, Spitale A, Faquin WC, Mazzucchelli L, Baloch ZW. The Bethesda System for Reporting Thyroid Cytopathology: a meta-analysis. Acta cytologica 2012; 56:333-339