

ThyroSeq[®] International

Molecular test for cytologically indeterminate thyroid nodules empowering individualized patient management



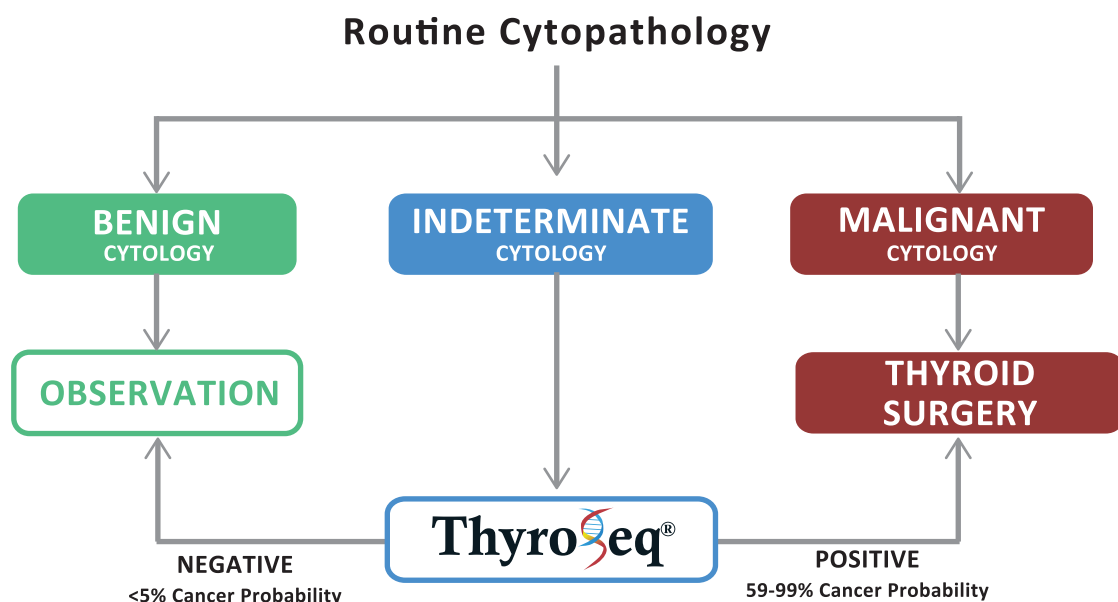
- ▶ Cutting-edge next-generation sequencing technology
- ▶ Most rigorously validated test on the market
- ▶ Reliable detection of all types of thyroid tumors
- ▶ Highest reduction in number of diagnostic surgeries
- ▶ Reports comprehensive detailed molecular profile with cancer risk assessment
- ▶ Every test reported by licensed physician

94%
Sensitivity

82%
Specificity

97%
NPV

66%
PPV





✓ LEADING PLATFORM FOR COMPREHENSIVE GENOTYPING OF THYROID NODULES

ThyroSeq interrogates 112 genes across 5 classes of genomic alterations, providing information on >12,000 mutation hotspots and >150 gene fusion types.

✓ MOST RIGOROUSLY VALIDATED TEST ON THE MARKET

ThyroSeq was validated in the largest, prospective, double-blind, multicenter study (Steward et al. *JAMA Oncol.* 2019.) of any commercially available molecular test for indeterminate thyroid nodules.¹

✓ HIGHEST NPV AND PPV AMONG WELL-VALIDATED TESTS

ThyroSeq has the highest negative predictive value at 97% (rule-out) and positive predictive value (rule-in) at 64% among well-validated tests for thyroid nodules.¹

✓ HIGHEST REDUCTION IN DIAGNOSTIC SURGERIES

ThyroSeq allows for avoidance of diagnostic surgery in up to 61% of patients with indeterminate nodules, and up to 82% of all benign nodules with indeterminate cytology.¹ Most cost-effective test on the market.⁵

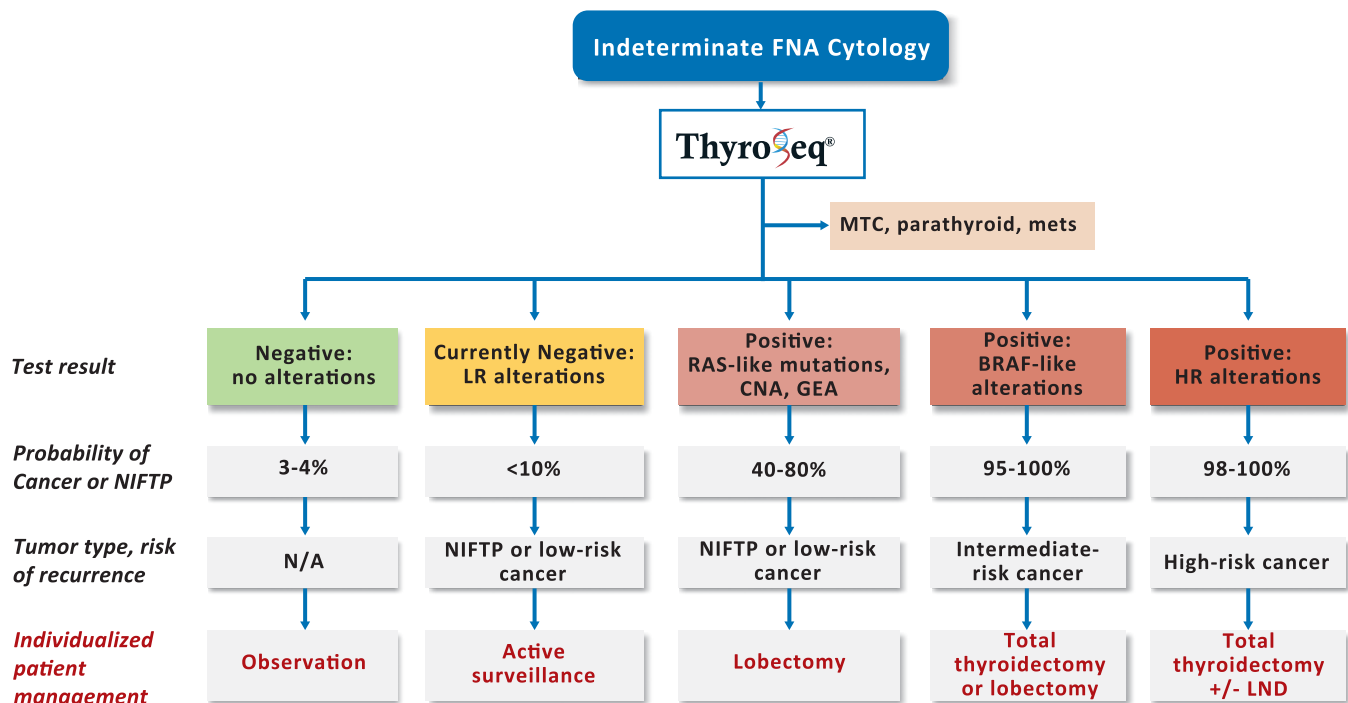
✓ COMPREHENSIVE TUMOR PROFILING WITH CANCER RISK ASSESSMENT

ThyroSeq tests all main types of genetic alterations, providing patient-specific probability of cancer and prediction of risk of cancer recurrence, allowing physicians to individualize patient management.

✓ RELIABLE DETECTION OF HCC, MTC, PARATHYROID, AND METS

ThyroSeq has demonstrated reliable detection of Hurthle cell cancer, medullary thyroid cancer, and non-thyroidal tumors.^{1,2,3,4}

EMPOWERING INDIVIDUALIZED PATIENT MANAGEMENT



MTC-medullary thyroid carcinoma, LR-low risk, HR-high risk, CNA-copy number alterations, GEA-gene expression alterations, LND-lymph node dissection

References: 1. Steward DL, et al. *JAMA Oncol* 2019. 2. Nikiforova MN, et al. *Cancer*. 2018. 3. Schatz-Siemers N, et al. *Diagn Cytopathol*. 2019. 4. Cho M, et al. *Cancer Cytopathol*. 2017. 5. Nicholson KJ, et al. *Thyroid*. 2019.