

# (LBSAT255) Real World Performance of the Afirma Genomic Sequencing Classifier (GSC) - A Meta-analysis

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\*Potential conflict of interest may exist. Refer to the Meeting App.

## BACKGROUND

- The Afirma GSC aids in the clinical decision making for patients with indeterminate thyroid nodule cytology (ITN). The 2018 GSC validation study was based on a cohort of ITN samples collected prospectively from multiple community and academic centers. All patients underwent surgery without known genomic information and were assigned a histopathology diagnosis by an expert panel blinded to all genomic information.
- The results showed (at a 24% cancer prevalence – point estimate and 95% CI):
  - Sensitivity (SN) - 91% (79-98)
  - Specificity (SP) - 68% (60-76)
  - Negative Predictive Value (NPV) - 96% (90-99)
  - Positive Predictive Value (PPV) - 47% (36-58)
- Thirteen independent GSC post-validation studies have been published. This study's objective is to compare the real world (RW) GSC performance to the clinical validation (CV) study metrics.

## META-ANALYSIS RULES AND ASSUMPTIONS

- At least one patient with molecular benign results must have surgery for that study to be included in SN, SP and NPV analysis and in these studies, molecular benign results without surgical histology are considered true negatives (TN) (as are the molecular benign results with benign surgical histology).
- Patients with suspicious results that do not have surgery are either excluded from the analysis (generating an observed PPV (oPPV) and observed SP (oSP)) or assumed as histology negatives (i.e. false positives), generating a conservative PPV (cPPV) and conservative SP (cSP).
- NIFTP is considered malignant as surgical resection is required to make the diagnosis.

## METHODS

- Babazadeh et al and Wei et al were excluded from SN, SP and NPV analysis.
- Data from all studies were pooled using a random-effects model.
- All analyses were done using R package meta (version 4.18-2).

## RESULTS

- Figure 1 shows the benign call rate (BCR), SN, NPV, oPPV and % operated where the data is available for each independent, post-validation study.
  - The BCR overall is 67% (65%, 69%).
- In RW studies, the GSC demonstrates (Table 1):
  - SN – 97%
  - NPV – 99%
  - oSP – 88%, cSP – 80%
  - oPPV – 65%, cPPV – 49%
- Statistically significantly improved over the CV study for oSP, cSP, oPPV, and NPV (p<0.05).

- Figures 2 and 3 show the SN and oSP for each included study.
- Figure 4 shows the SN, SP, PPV, NPV and BCR comparing the validation study to the real-world experience (observed – unoperated GSC-S excluded; conservative – unoperated GSC-S considered benign).

## DISCUSSION

- RW studies of the Afirma GSC show an improved performance in SP and show a higher ROM in GSC-S nodules than the CV demonstrated (65% vs 47%).
- The RW SP translates to a high benign call rate (as reflected by the RW BCR of 67%), which likely increases the overall rate of clinical observation in lieu of surgery.
- When making the extreme assumption that unoperated GSC-S lesions are all benign, the cPPV matches the CV study (49% vs 47%).
- Possible reasons for this improved performance include:
  - An overrepresentation of Hürthle subtypes in the validation study (20% Hürthle carcinoma (HCC) of malignant histology and 11% Hürthle adenoma of benign histology) relative to RW estimates of HCC prevalence (<7%)<sup>14</sup> along with other histology subtype differences.
  - An enrichment of malignancy in the operated cohort based upon the selection of patients with GSC-S nodules that have surgery (higher clinical risk or more worrisome ultrasound features compared to GSC-S nodules without surgical follow-up).
- In summary, RW GSC data in ITN indicates significantly better performance on several metrics as compared to the validation study, most notably on cSP, oSP and oPPV.

Figure 1 - Afirma GSC Real-World Independent Clinical Utility Studies<sup>1-13</sup>

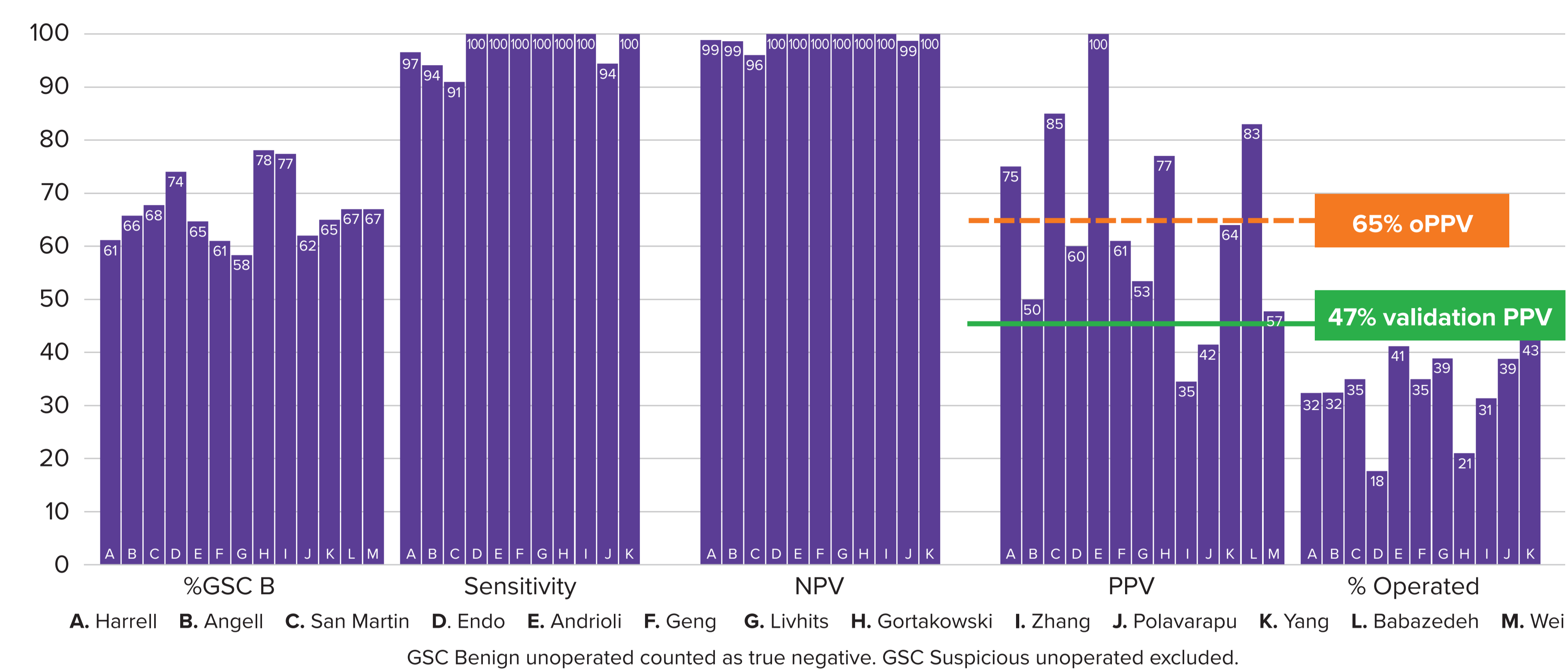


Figure 2 - Sensitivity

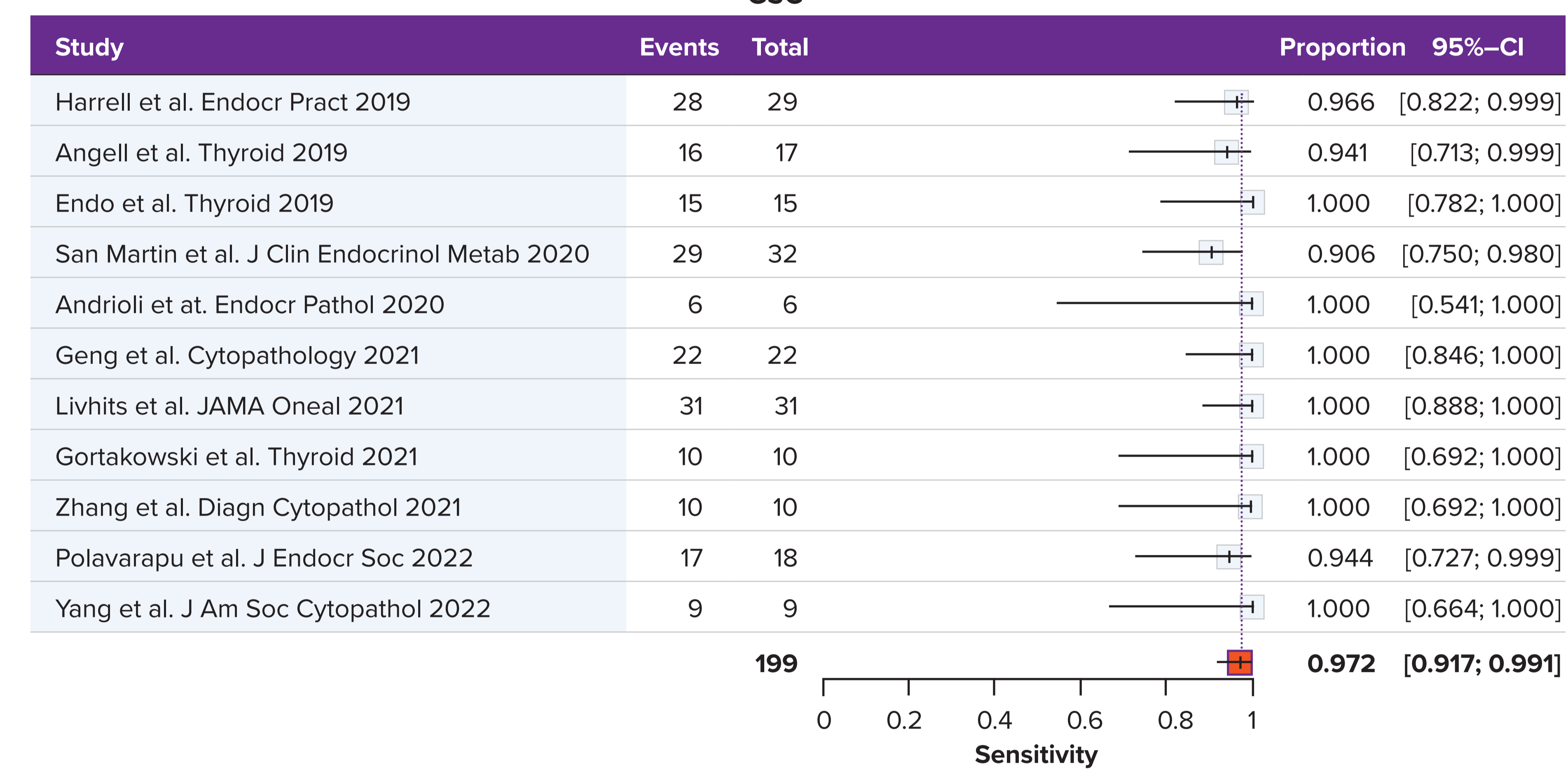


Figure 3 - Observed Specificity

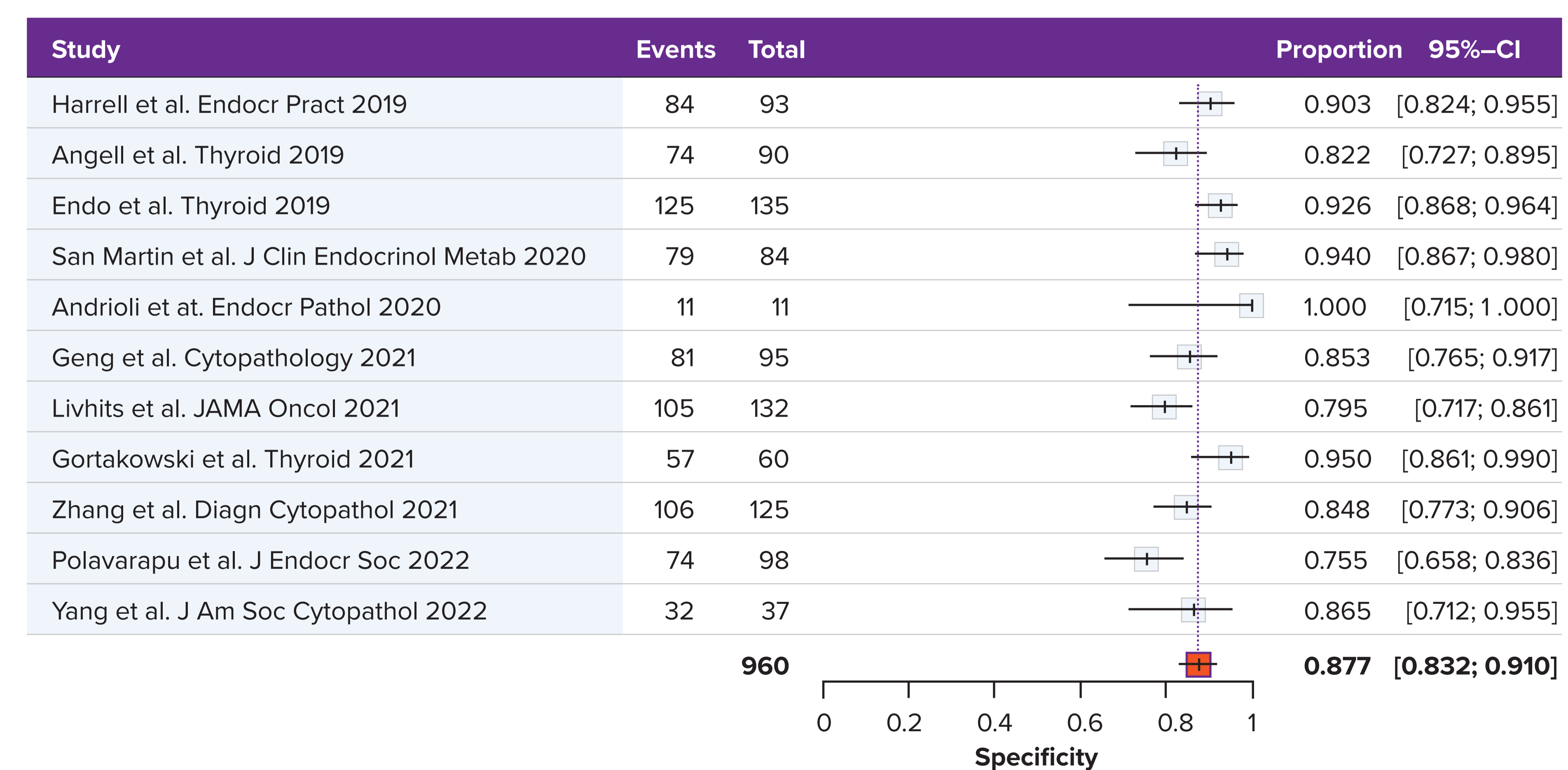
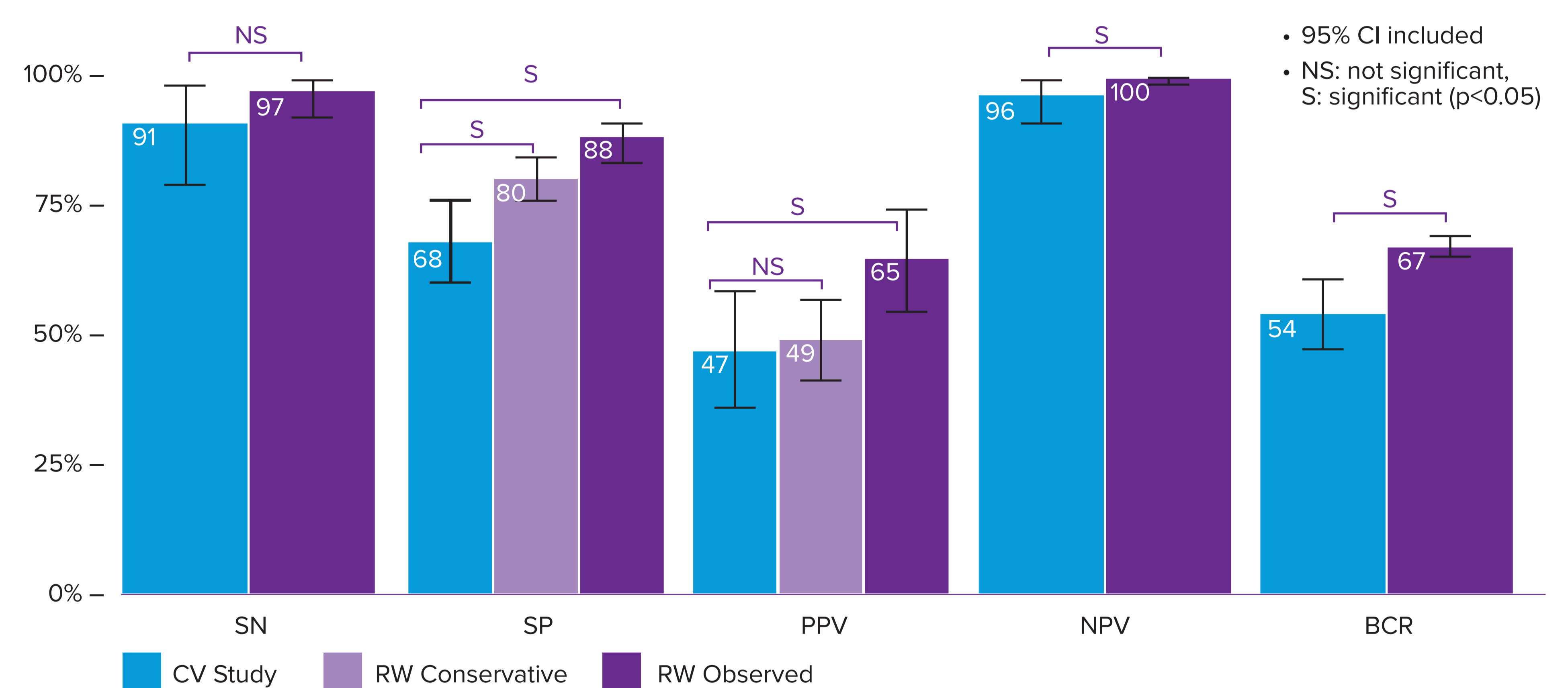


Table 1 - Performance Analysis of the Afirma GSC When Excluding Unoperated GSC-S Lesions or Considering Them Benign (False Positives)

	Validation Study	Meta-analysis Excluding Validation Study GSC-S unoperated excluded	Meta-analysis Excluding Validation Study GSC-S unoperated considered benign	Post-validation vs CV P-value of Difference GSC-S unoperated excluded	Post-validation vs CV P-value of Difference GSC-S unoperated considered benign
<b>Sensitivity</b>	0.911 (0.788, 0.975)	0.972 (0.917, 0.991)	0.972 (0.917, 0.991)	0.122	0.122
<b>Specificity</b>	0.683 (0.6, 0.757)	0.877 (0.832, 0.91)	0.804 (0.759, 0.842)	<b>3.09e-06</b>	<b>0.004</b>
<b>PPV</b>	0.471 (0.363, 0.581)	0.649 (0.544, 0.741)	0.493 (0.413, 0.574)	<b>0.019</b>	0.748
<b>NPV</b>	0.961 (0.904, 0.989)	0.995 (0.98, 0.999)	0.995 (0.98, 0.999)	<b>0.018</b>	<b>0.018</b>

Figure 4 - Performance Comparison: CV vs RW Studies



## References

- Harrell, R.M., et al., *Statistical Comparison of Afirma GSC and Afirma GEC Outcomes in a Community Endocrine Surgical Practice: Early Findings*. Endocr Pract, 2019. **25**(2): p. 161-164.
- Endo, M., et al., *Afirma Gene Sequencing Classifier Compared with Gene Expression Classifier in Indeterminate Thyroid Nodules*. Thyroid, 2019. **29**(8): p. 1115-1124.
- Angell, T.E., et al., *Independent Comparison of the Afirma Genomic Sequencing Classifier and Gene Expression Classifier for Cytologically Indeterminate Thyroid Nodules*. Thyroid, 2019. **29**(5): p. 650-656.
- San Martin, V.T., et al., *Real-world Comparison of Afirma GEC and GSC for the Assessment of Cytologically Indeterminate Thyroid Nodules*. J Clin Endocrinol Metab, 2020. **105**(3).
- Wei, S., et al., *Performance of the Afirma genomic sequencing classifier versus gene expression classifier: An institutional experience*. Cancer Cytopathol, 2019. **127**(1): p. 720-724.
- Andrioli, M., et al., *Testing for Afirma in Thyroid Nodules with High-Risk Indeterminate Cytology (TIR3B): First Italian Experience*. Endocr Pathol, 2020. **31**(1): p. 46-51.
- Geng, Y., J.S. Aguilera-Jakthong, and N.A. Moatamed, *Comparison of Afirma Gene Expression Classifier with Gene Sequencing Classifier in Indeterminate thyroid nodules: A single-institutional experience*. Cytopathology, 2021. **32**(2): p. 187-191.
- Livhits, M.J., et al., *Effectiveness of Molecular Testing Techniques for Diagnosis of Indeterminate Thyroid Nodules: A Randomized Clinical Trial*. JAMA Oncol, 2021. **7**(1): p. 70-77.
- Gortakowski, M., K. Feghalli, and I. Osakwe, *Single Institution Experience with Afirma and Thyroseq Testing in Indeterminate Thyroid Nodules*. Thyroid, 2021. **31**(9): p. 1376-1382.
- Zhang, L., et al., *Performance of Afirma genomic sequencing classifier vs gene expression classifier in Bethesda category III thyroid nodules: An institutional experience*. Diagn Cytopathol, 2021. **49**(8): p. 921-927.
- Polavarapu, P., et al., *Comparison of Afirma GEC and GSC to Nodules Without Molecular Testing in Cytologically Indeterminate Thyroid Nodules*. J Am Soc Cytopathol, 2021. **5**(1): p. bvab148.
- Babazadeh, N.T., et al., *Thyroid nodule molecular profiling: The clinical utility of Afirma Xpression Atlas for nodules with Afirma Genomic Sequencing Classifier-suspicious results: Surgery*. 2022. **17**(1): p. 155-159.
- Yang, Z., et al., *Performance of Afirma Gene Sequencing Classifier versus Gene Expression Classifier in thyroid nodules with indeterminate cytology*. J Am Soc Cytopathol, 2022. **11**(2): p. 74-78.
- Goffredo et al., *Hürthle cell carcinoma: a population-level analysis of 3311 patients*. Cancer, 2013. **119**(3): p. 504-511.