

INTRODUCTION

Next-generation sequencing-based multiplex testing is standard for detecting driver mutations in lung cancer. Conventional assays such as Oncomine Dx Target Test (ODxTT) and AmoyDx generally require tissue samples. The newly insurance-approved multigene testing system (MINtS) improves success rates and shortens turnaround time^{1,2}.

METHODS

We evaluated the utility of MINtS compared with existing multiplex assays (ODxTT, AmoyDx, Compact Panel). Patients with NSCLC diagnosed at our hospital between July and December 2024 whose specimens (cytology, aspiration fluid from histology) were submitted for MINtS were analyzed. Target genes included *EGFR*, *ALK*, *ROS1*, *BRAF*, *MET*, *RET*, *KRAS*, *HER2* and *NTRK*.

Specimen processing procedure for MINtS

- Aspirate 5–10 mL of saline into a 20 mL syringe.
- Place the biopsy specimen in the saline and apply negative pressure to release tumor cells into the solution.
- Fix the biopsy specimen in formalin and repeat the procedure for each biopsy.
- After all procedures, add bronchial lavage fluid and brush washing fluid to the saline to create a cell specimen mixture.
- Divide the mixture into two equal parts; submit one to MINtS.
- Centrifuge the remaining sample, discard the supernatant, and keep the pellet.
- Add RNA stabilization buffer to the pellet and mix by tapping.



Procedure 2



Procedure 6



Procedure 7

CONCLUSION

MINtS achieved detection rates comparable to existing multiplex assays with complete concordance. Its high nucleic acid yield supports its utility as a reliable multiplex platform, even with tissue-derived cytology specimens.

REFERENCES & ACKNOWLEDGEMENTS

REFERENCES

- Fujita K, et al. Cancer Science. 2023;114(8):3342–3351.
- Goto Y, et al. Lung Cancer. 2025;202:180505.

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Table 1: Patient characteristics

		Overall n=59	%
Age, median (range)		73 (35–89)	
Sex	Male	46	78%
	Female	13	22%
Stage	I	14	24%
	II	6	10%
	III	13	22%
	IV	24	41%
	Recurrence	2	3%
Tissue type	Adenocarcinoma	32	54%
	Squamous	21	36%
	Other	6	10%
Procedure	EBUS-GS+TBB	7	12%
	EBUS-GS	26	44%
	EBUS-TBNA	23	39%
	Other	3	5%
Multiplex gene-panel testing (n=40)			
ODxTT		32	80%
	AmoyDx	2	5%
	Compact Panel	6	15%
Presence of genetic mutation (n=40)			
Yes		17	43%
	No	23	58%

		Histology	
		Positive	Negative
Cytology	Positive	51 cases → Category 1	0
	Negative	8 cases → Category 2	0

Table 2: Concordance of driver mutation detection between MINtS and other multiplex assays

		MINtS	
Existing multiplex		Negative	Positive
	Negative	28 cases	0
	Positive	0	12 cases

RESULTS

Figure 1: Detection of driver mutations by category

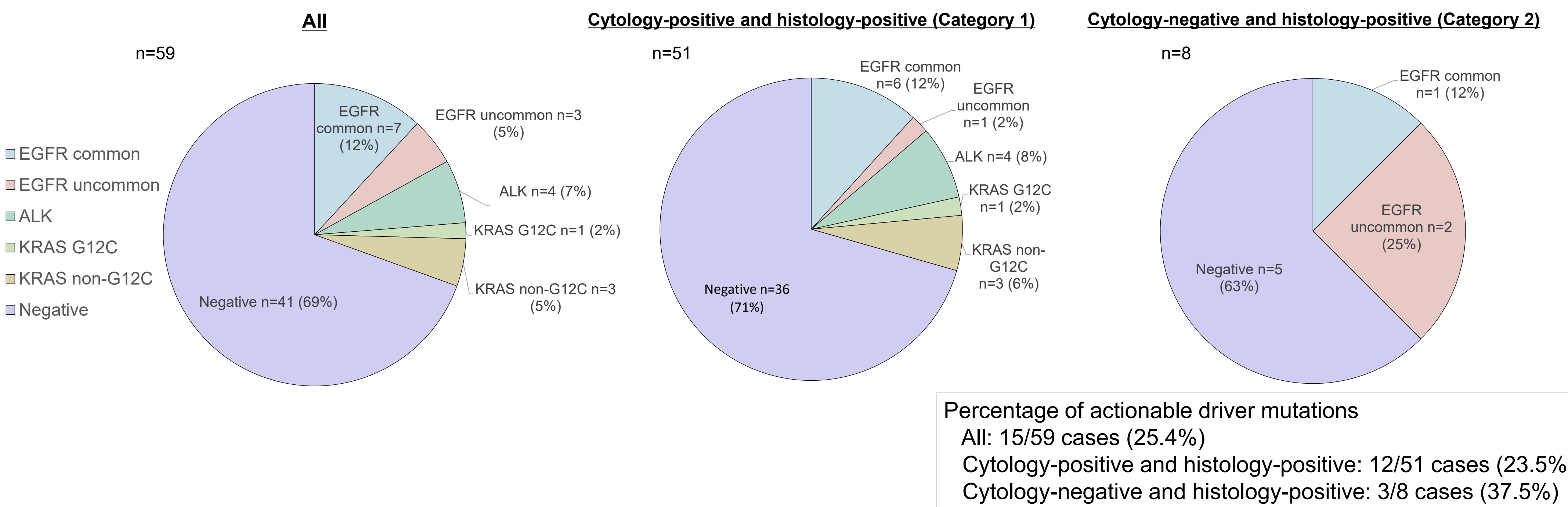


Figure 2: Comparison of nucleic acid yield between Category 1 and 2

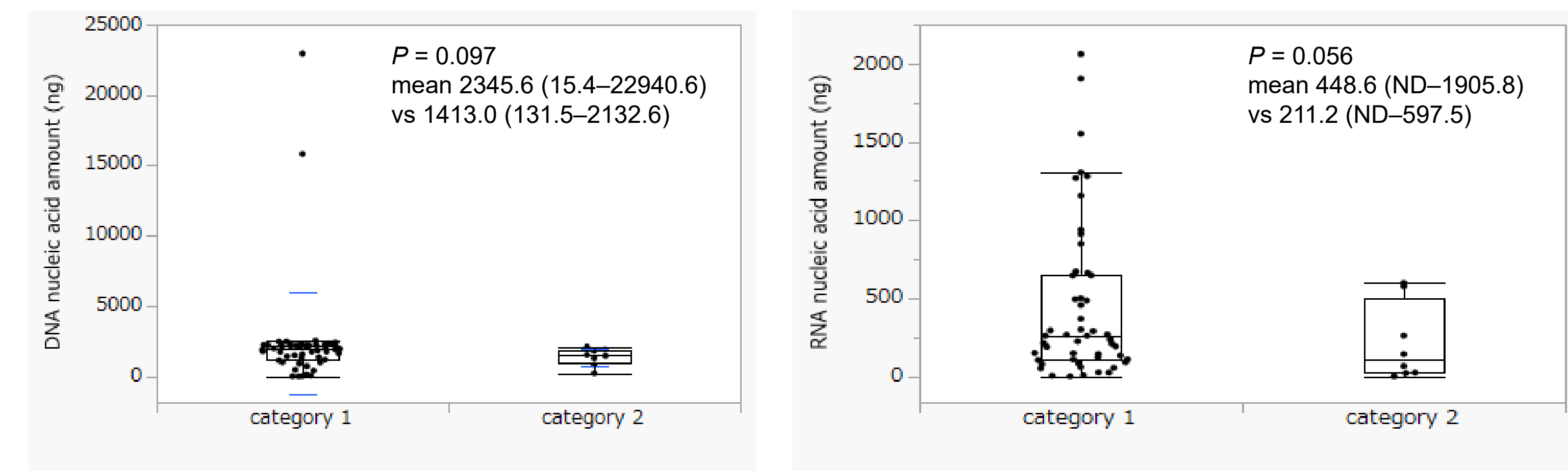


Figure 3: Comparison of nucleic acid quality parameters between Category 1 and 2

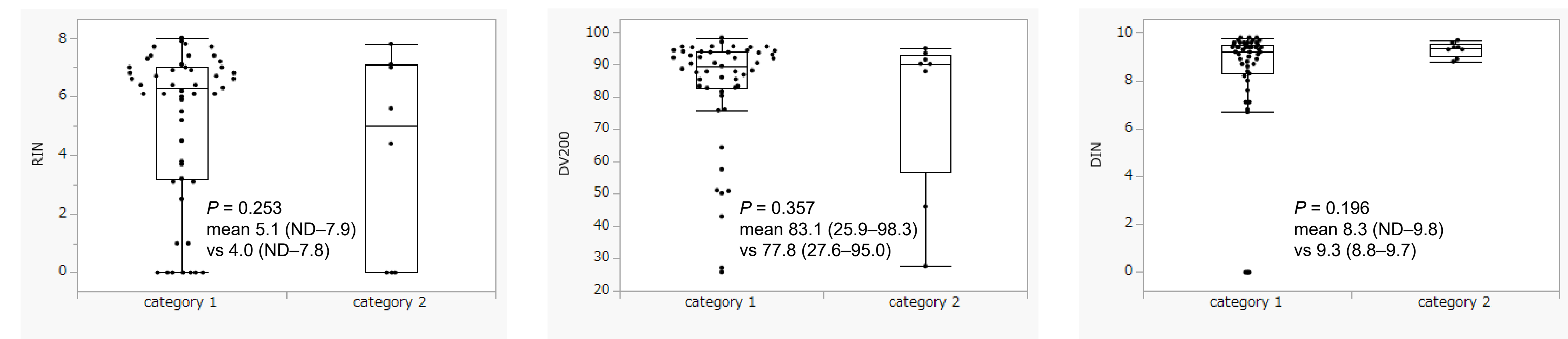
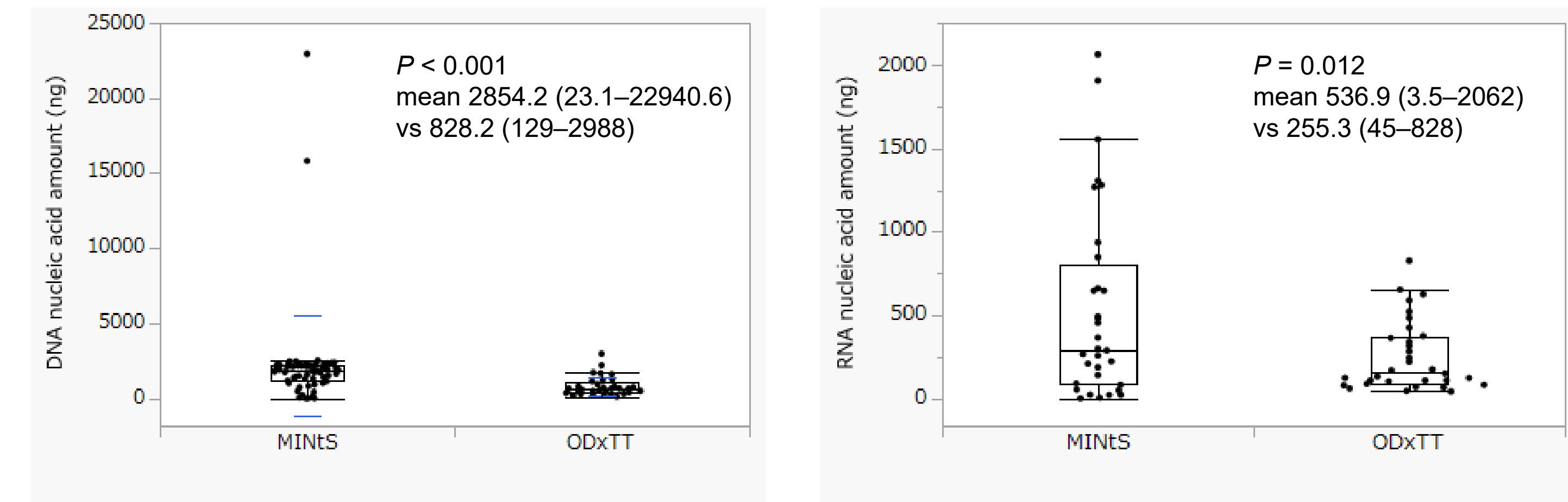


Figure 4: Comparison of nucleic acid yield between MINtS and ODxTT



Figures 2 and 3: There were no significant differences in the nucleic acid quality parameters between Category 1 and Category 2.

Figure 4: Compared with ODxTT, MINtS had significantly higher DNA and RNA yields.

ND, not detected.