

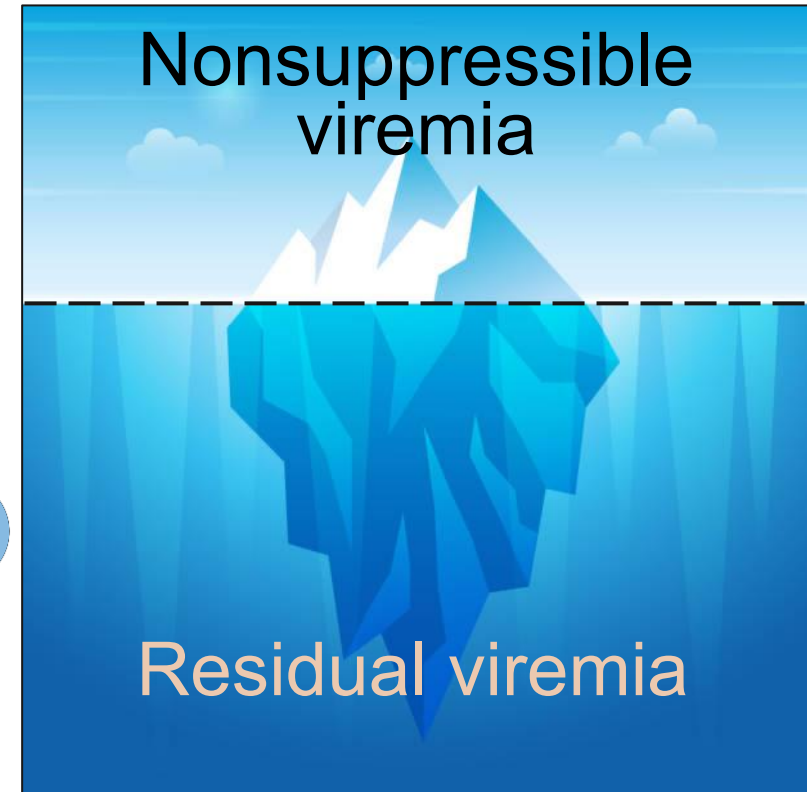
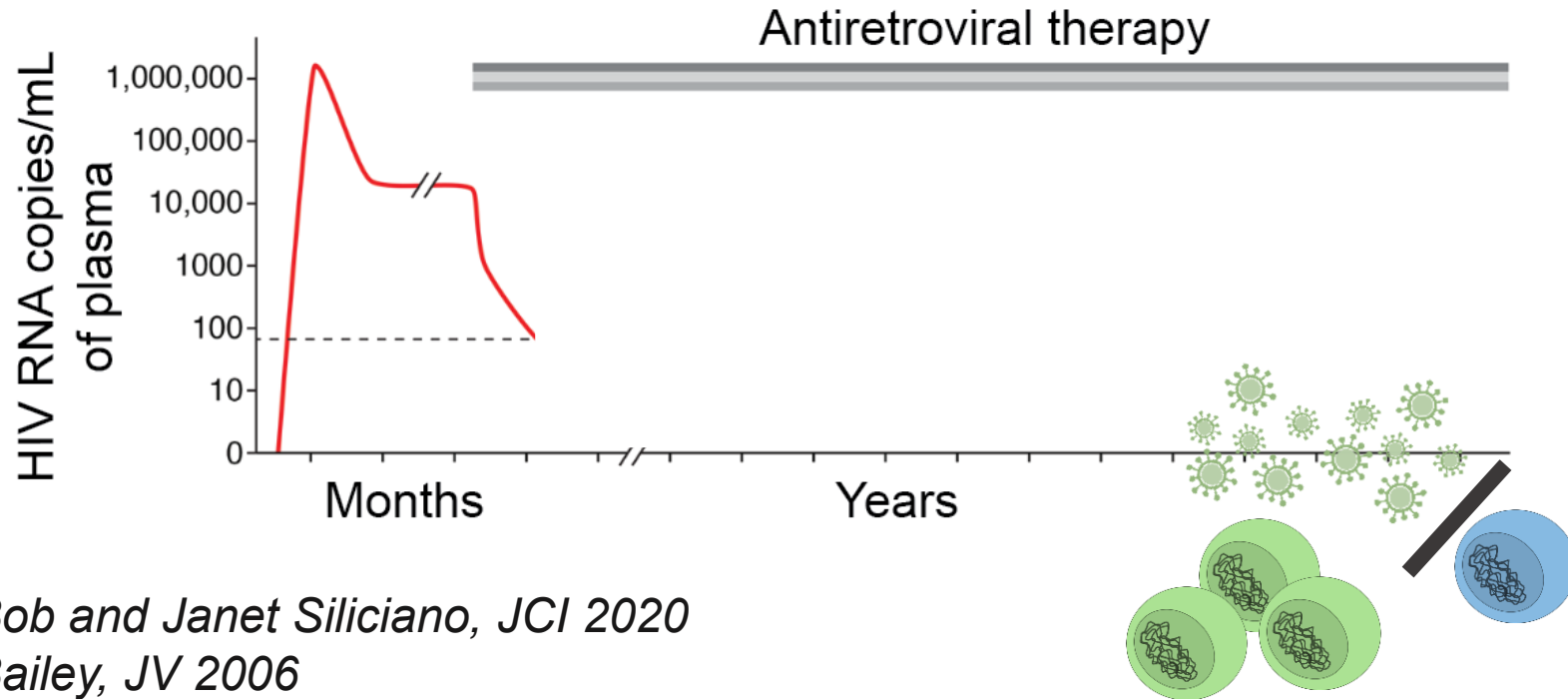
# 5'Leader-defective proviruses are a common source of persistent viremia despite effective ART

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I have received honoraria from Gilead to present at scientific conferences

# Persistent viremia complicates HIV clinical care



*Bob and Janet Siliciano, JCI 2020*

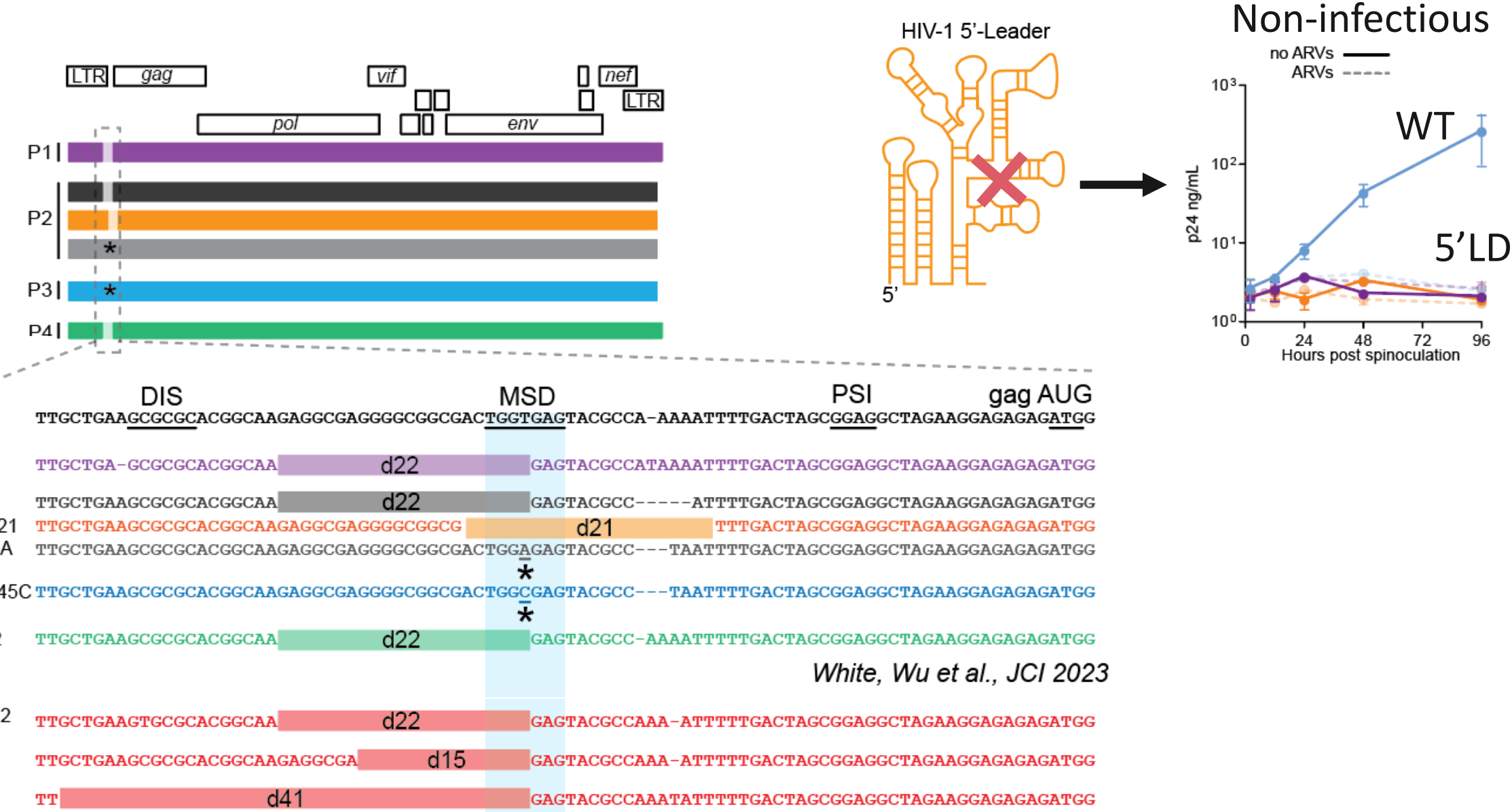
*Bailey, JV 2006*

*Simonetti, PNAS 2016*

*Halvas, JCI 2020*

Determining virus and host drivers of persistent viremia can improve clinical care and our understanding of HIV persistence

# Proviruses with 5'Leader Defects can cause NSV



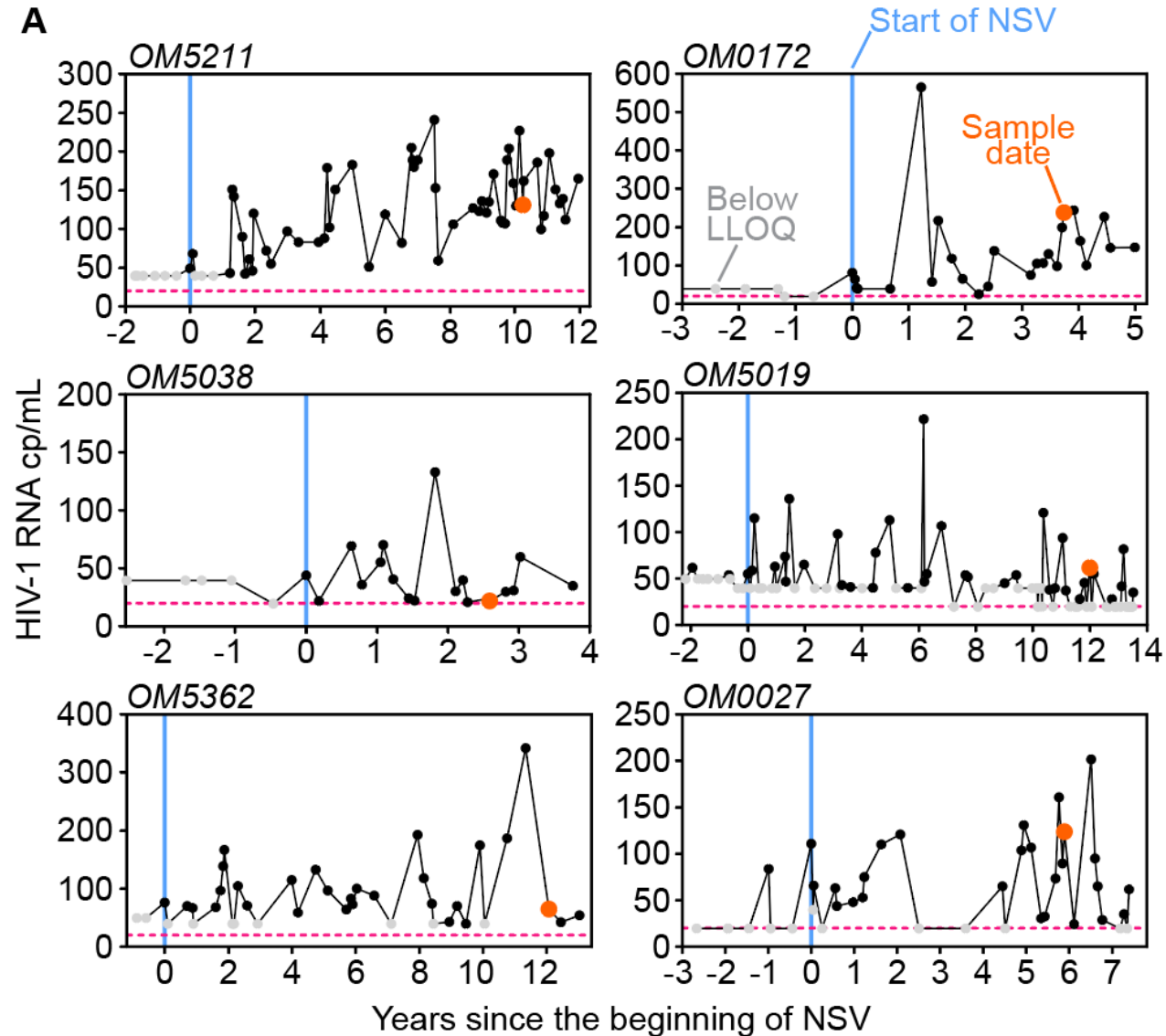
White, Wu et al., JCI 2023

Mohammadi et al., Nature Med 2023

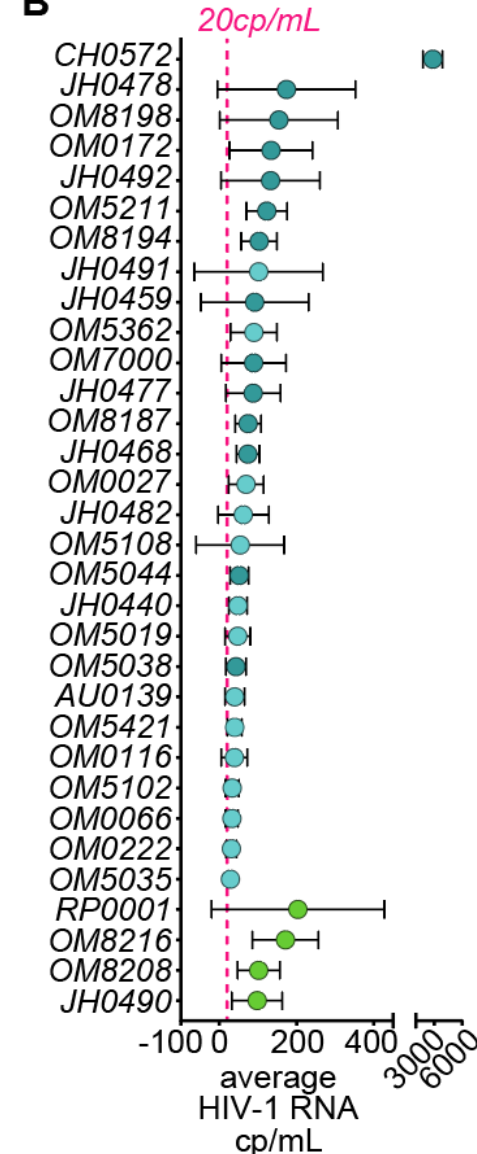
# To which extent do 5'L defects contribute to NSV?

We studied **32 people on ART** with persistent (or intermittent) viremia >20 cp/mL

**A**

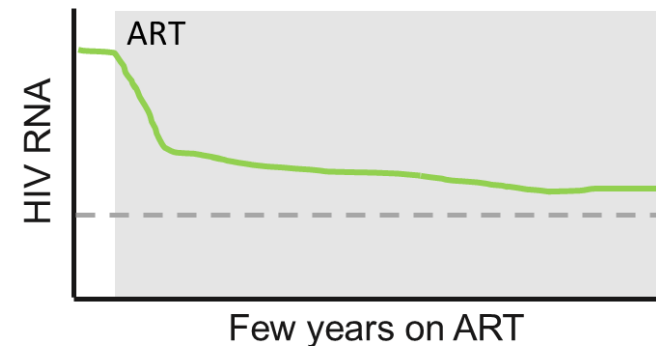
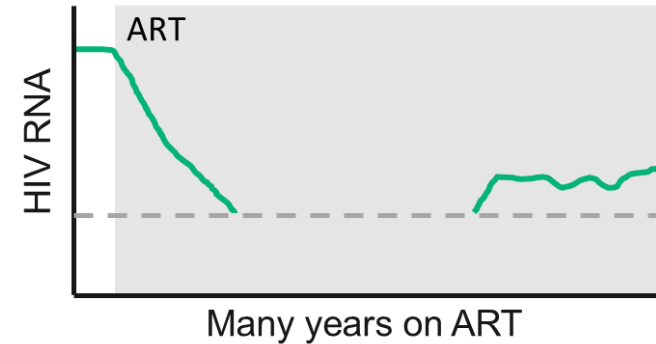


**B**



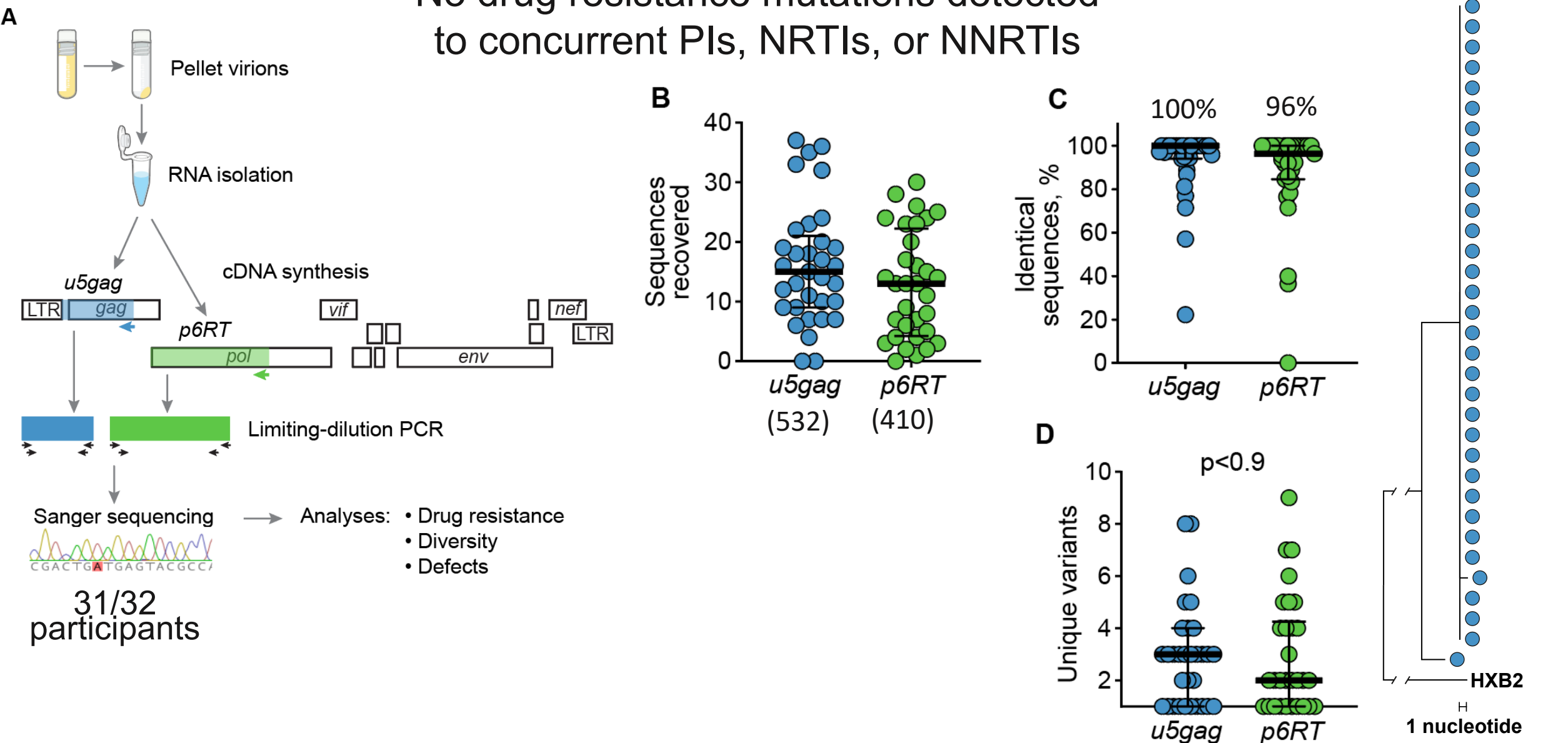
NSV type

- Persistent
- Intermittent
- Short-term ART



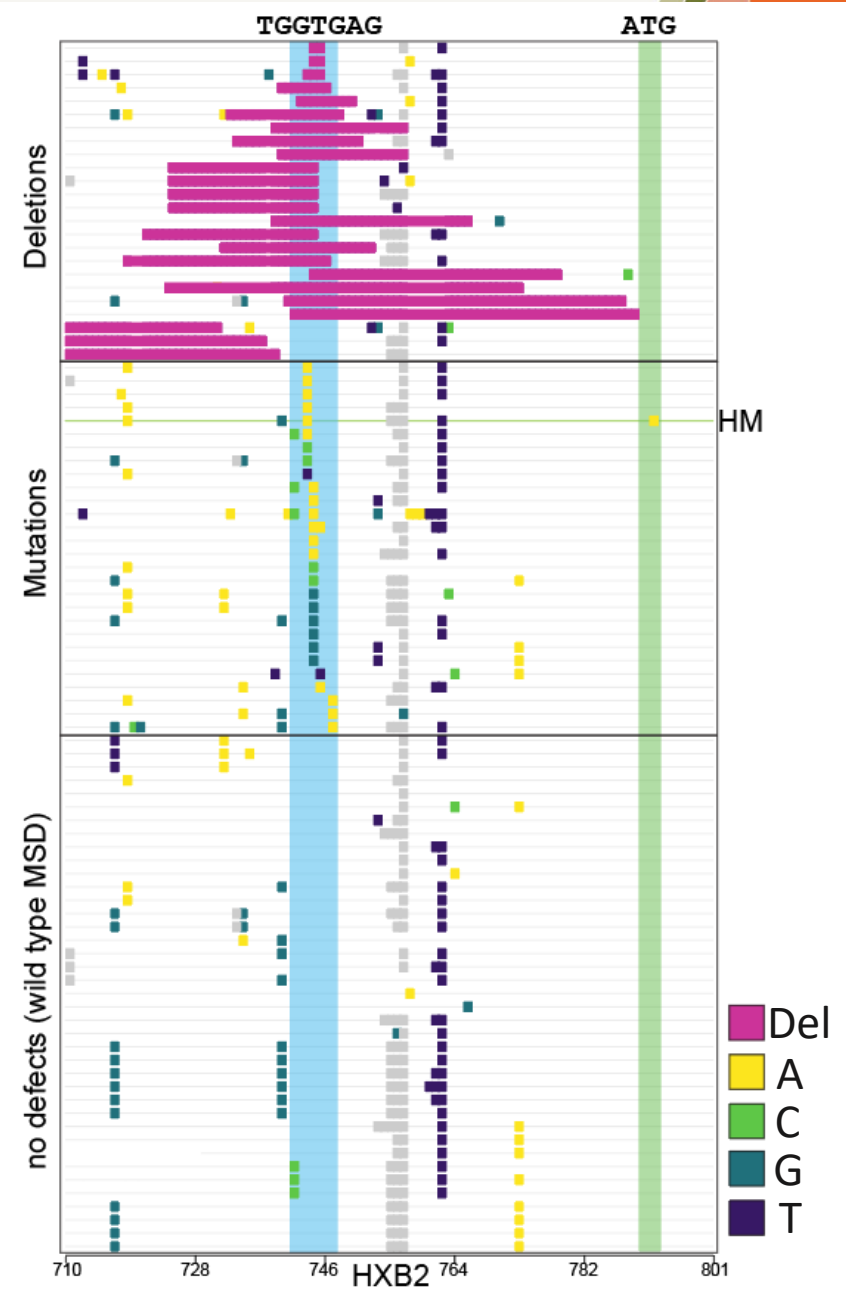
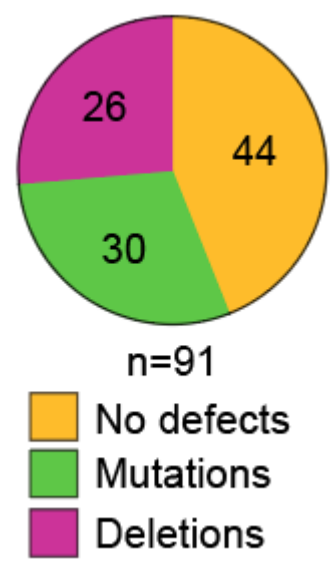
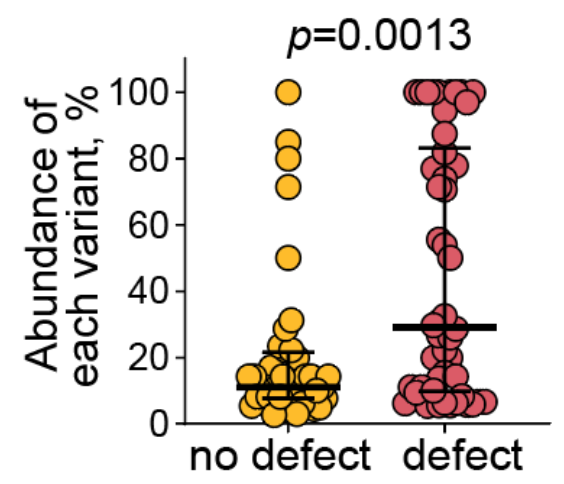
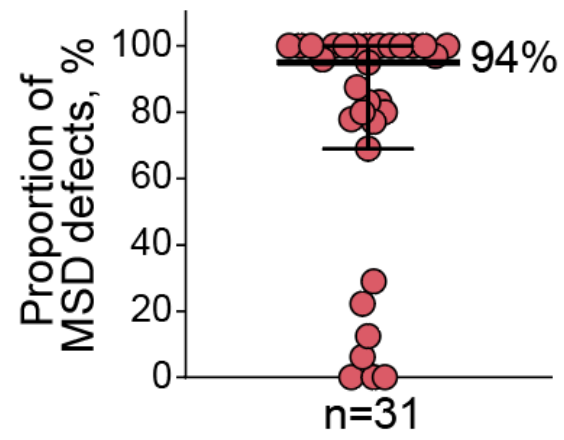
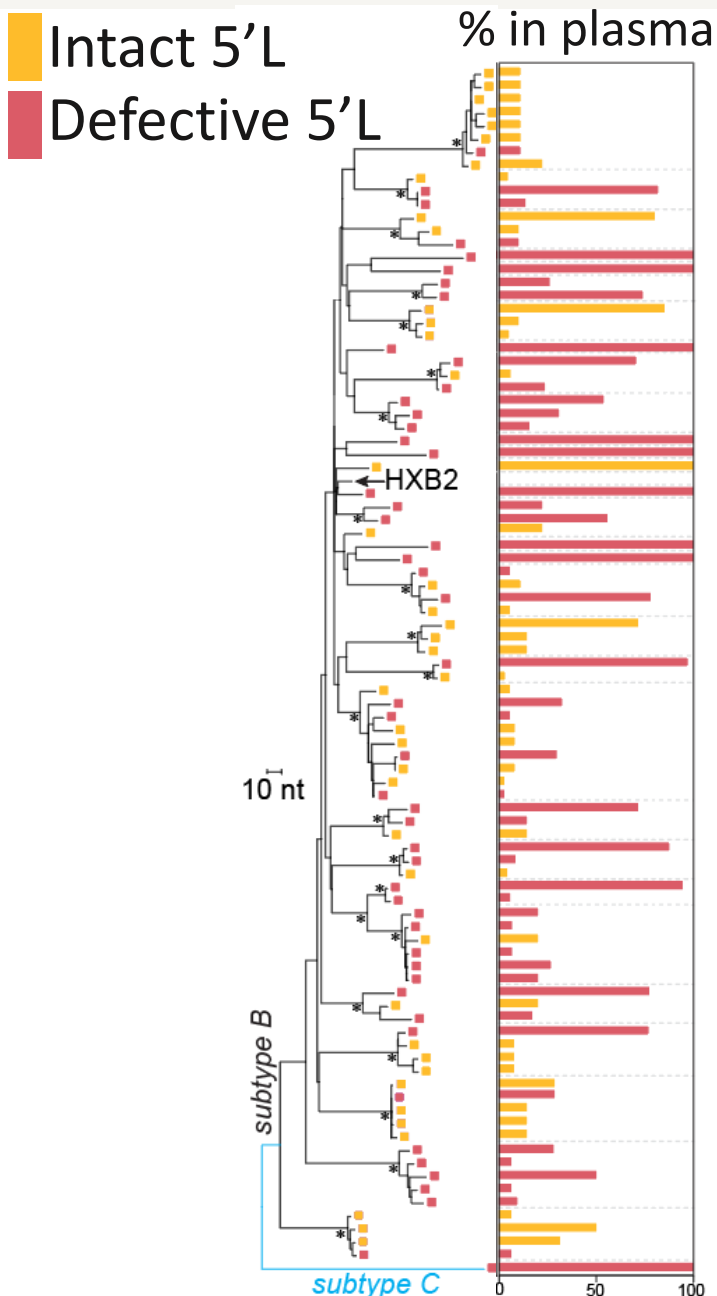
# HIV-1 variants contributing to NSV are highly clonal

No drug resistance mutations detected to concurrent PIs, NRTIs, or NNRTIs



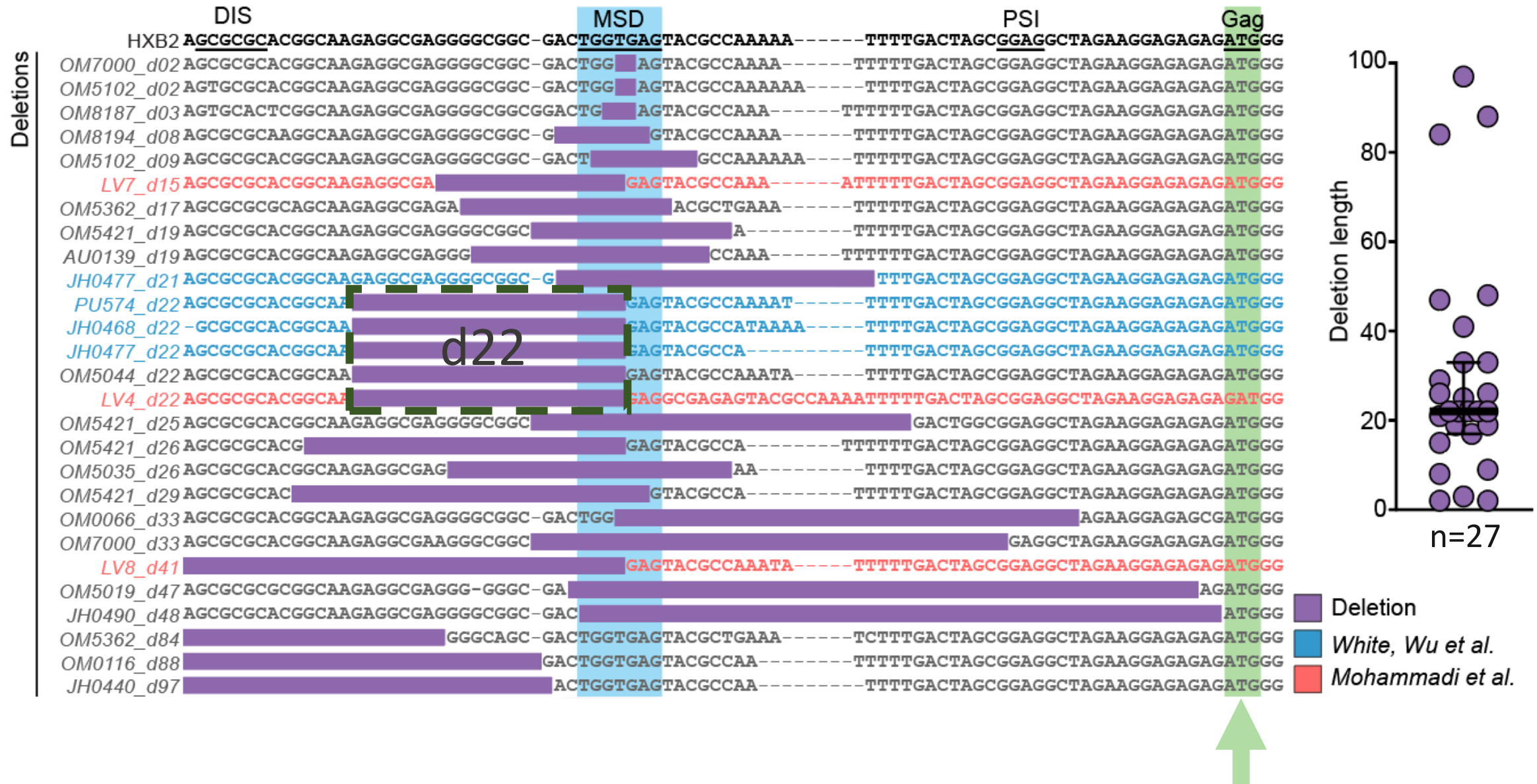


# >90% of virus in plasma has 5'Leader defects



Box, et al., in preparation

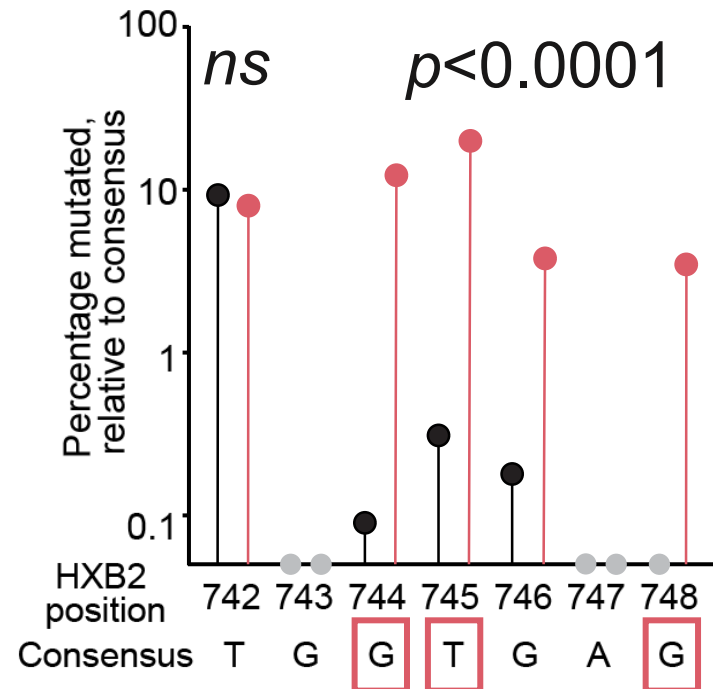
# Deletions involve the Major Splicing Donor



# Specific MSD mutations are enriched in NSV

Mutations

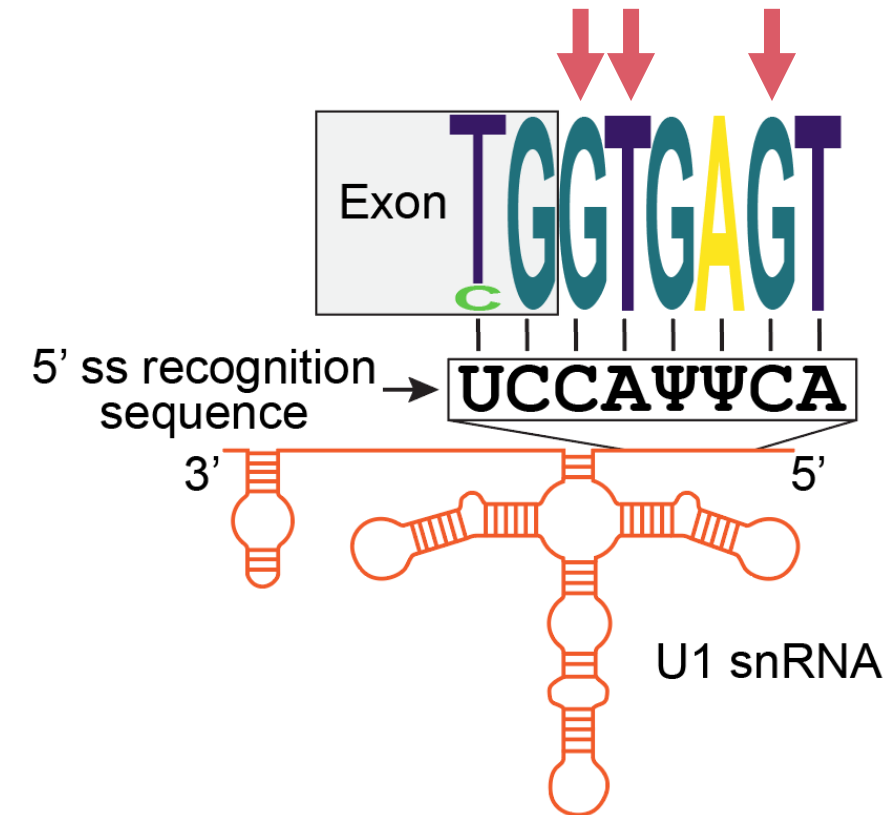
	MSD	
HXB2	GCGACTGGTGAAGTACGCC	
JH0492_G744A	GCGACTGATGAGTACGCC	A
OM5038_G744A	GCGACTGATGAGTACGCC	C
OM8194_G744A	GCGACTGATGAGTACGCC	G
JH0440_G744A	GCGACTGATGAGTACGCC	T
OM0116_G744A	GCGCTGATGAGTACGCC	
OM5211_G744A	GCGACCGATGAGTACGCC	
JH0482_G744C	GCGACTCGTGAAGTACGCC	
OM5019_G744C	GCGACTCGTGAAGTACGCC	
OM0222_G744T	GCGACTGTTGAAGTACGCC	
OM5211_T745A	GCGACCGGAGAGTACGCC	
JH0477_T745A	GCGACTGGGAGAGTACGCC	
JH0491_T745A	GCGAAGCGAGAGTACGCC	
AU0139_T745A	GCGACTGGAAAGTACGCC	
OM5108_T745A	GCGACTGGAGAGTACGCC	
OM5421_T745A	GCGACTGGAGAGTACGCC	
JH0478_T745C	GCGACTGGGAGTACGCC	
RP0001_T745C	GCGACTGGGAGTACGCC	
JH0440_T745G	GCGACTGGGAGTACGCC	
JH0440_T745G	GCGACTGGGAGTACGCC	
OM8208_T745G	GCGGCTGGGAGTACGCC	
OM7000T745G	GCGACTGGGAGTACGCC	
OM0172_T745G	GCGACTGGGAGTACGCC	
OM0172_T745G	GCGACTGGGAGTACGCC	
JH0477_G746T	GCTACTGGTTAGTACGCC	
AU0139_G746A	GCGACTGGTAAAGTACGCC	
JH0440_G748A	GCGACTGGTGAAATACGCC	
OM5035_G748A	GCGCTGGTGAAATACGCC	
OM8208_G748A	GCGCTGGTGAAATACGCC	



HIV sequence database (plasma RNA, all subtypes) n=2238

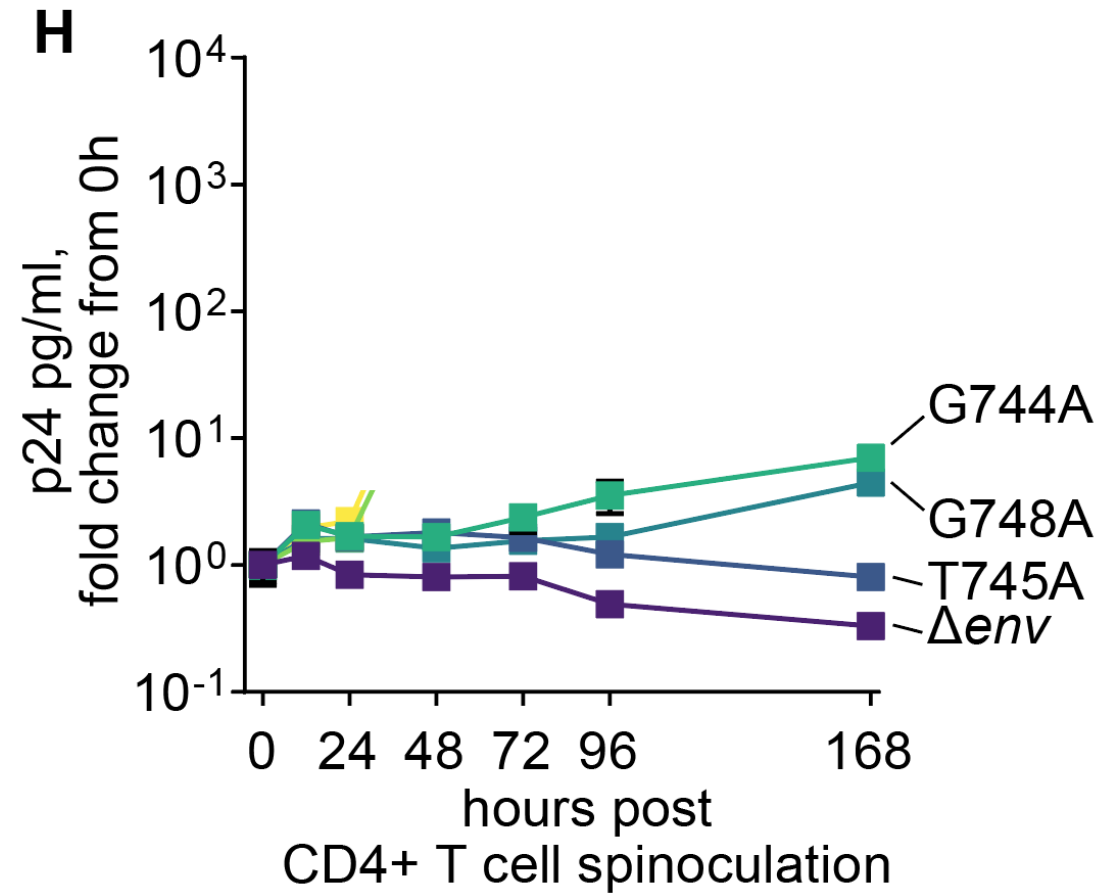
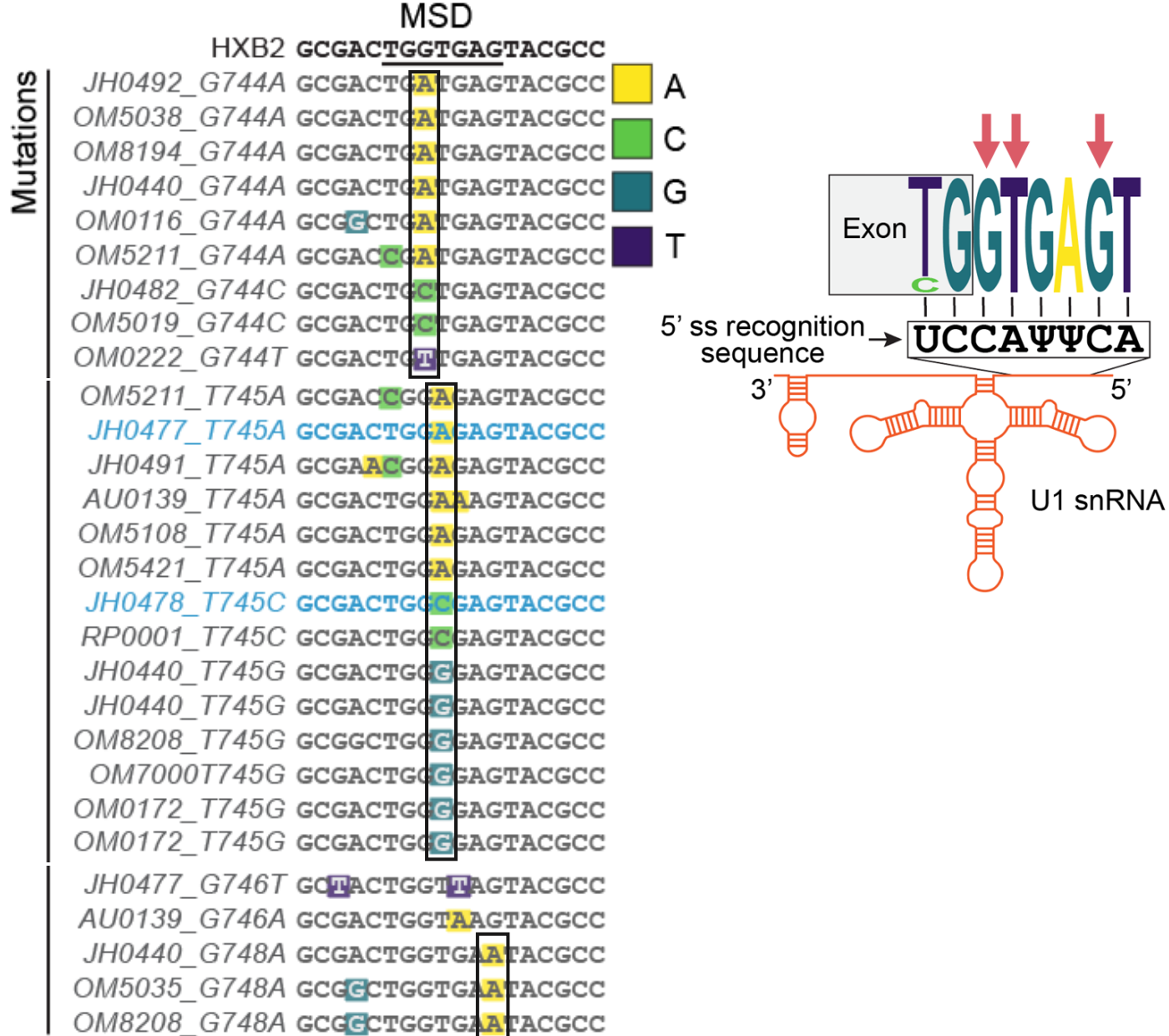
$\chi^2$  test

NSV dataset n= 94

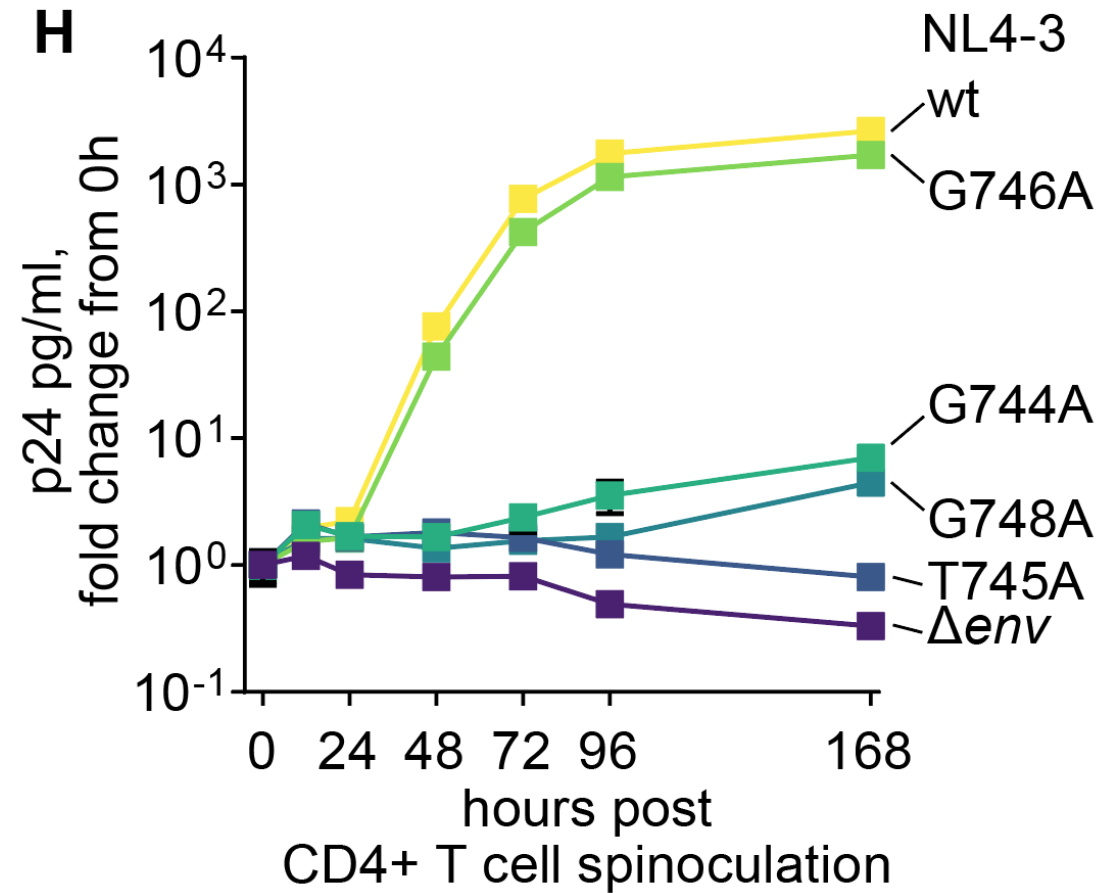
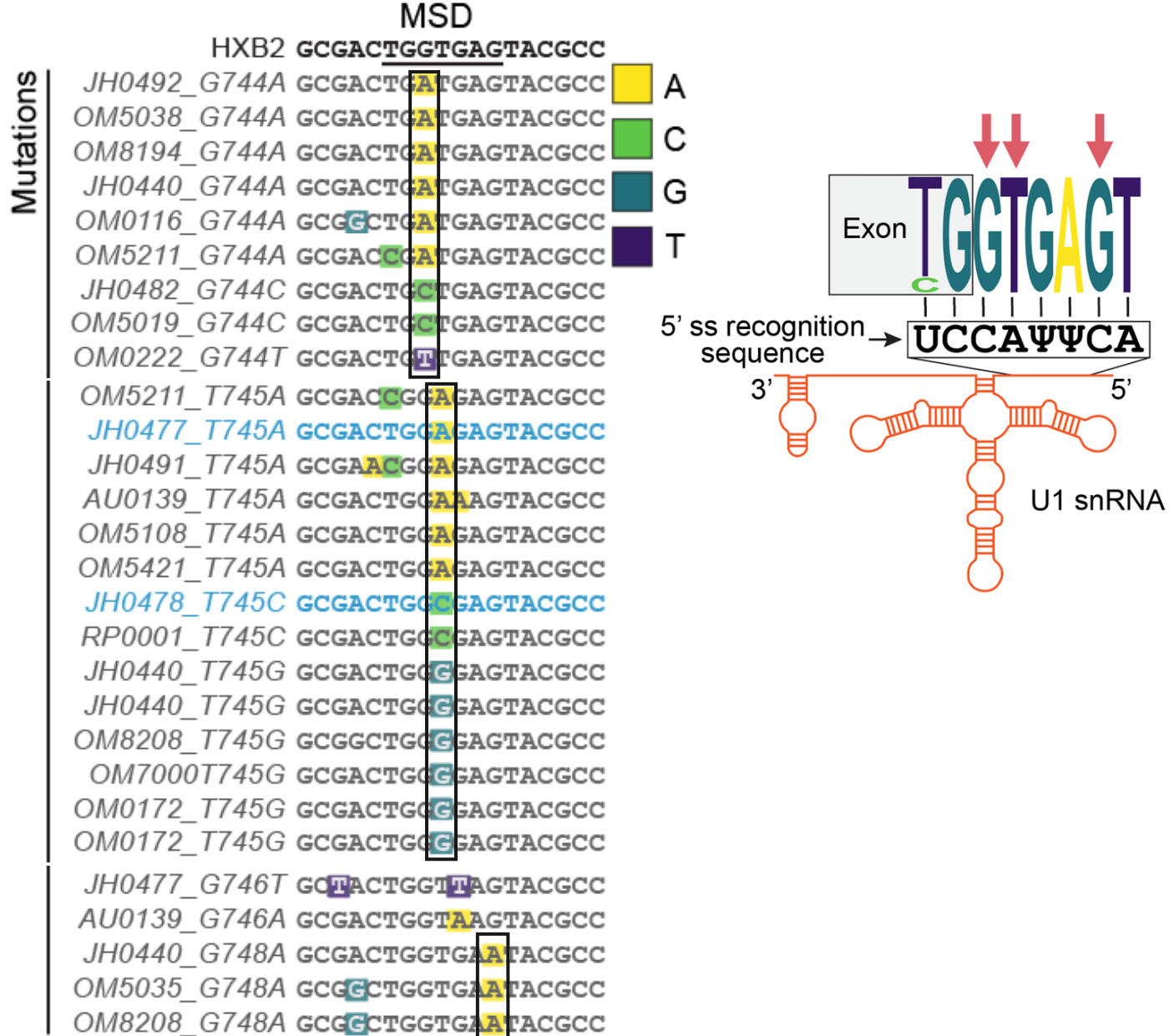




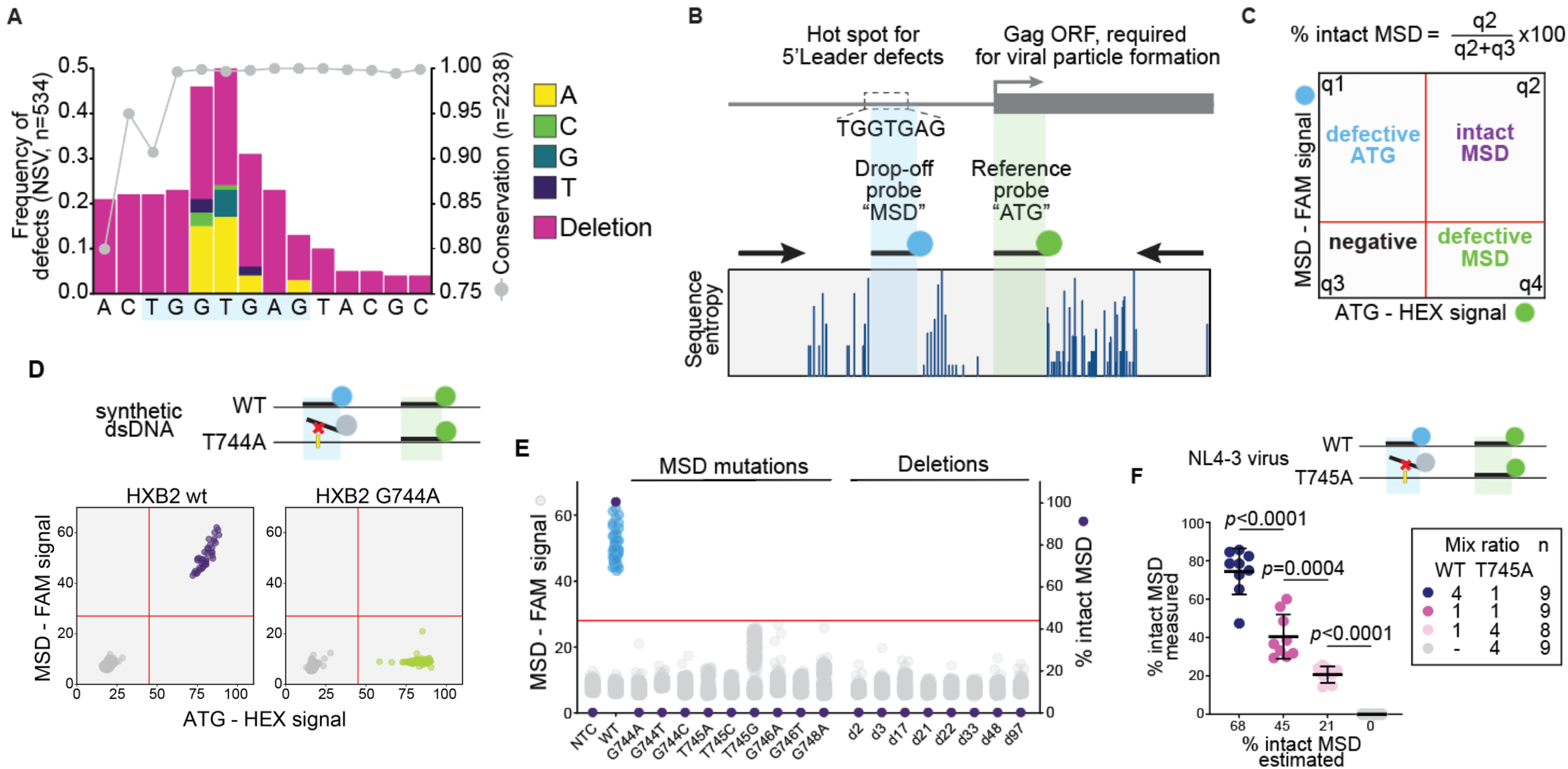
# Mutations affect RNA binding to splicing machinery



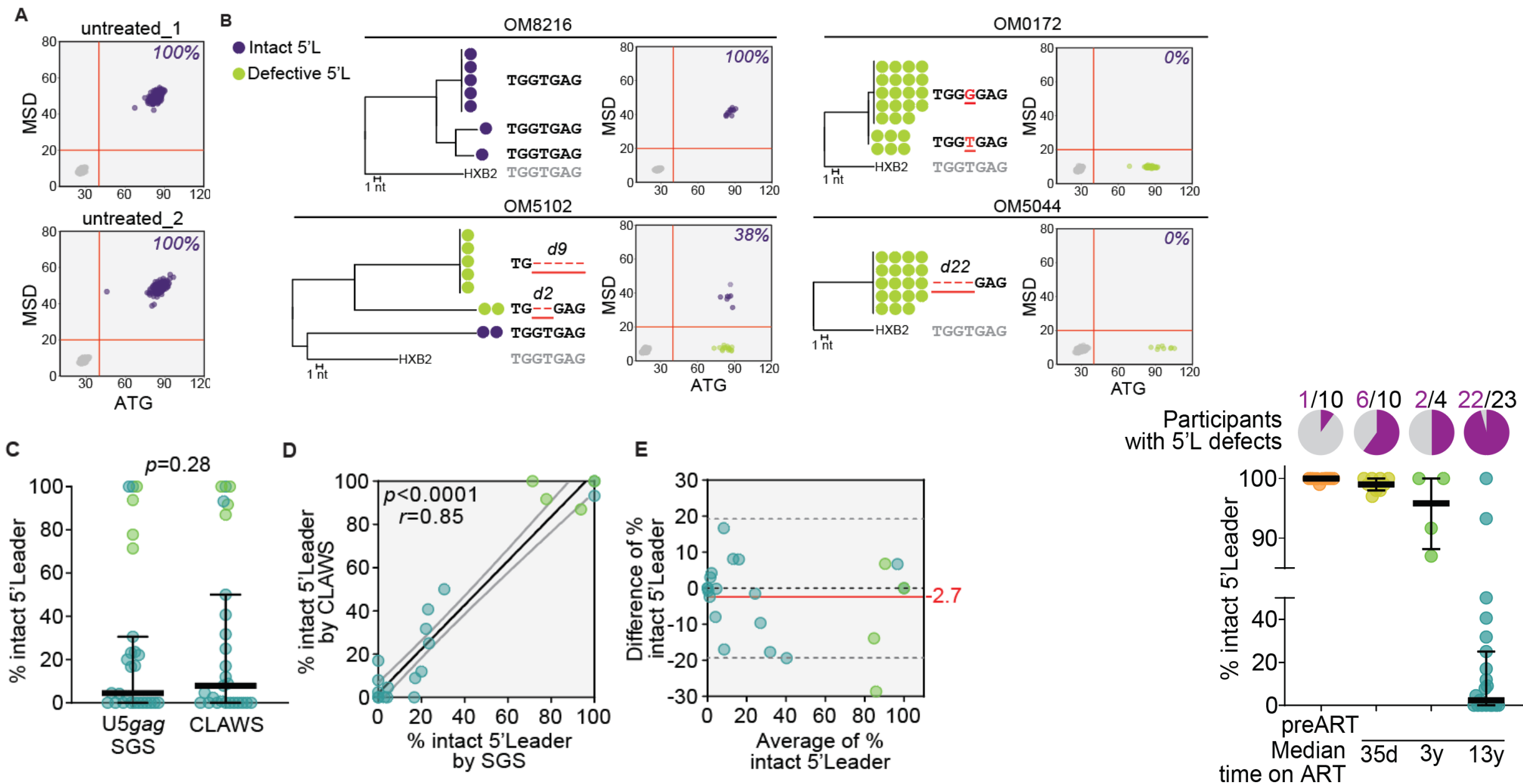
# Mutations affect RNA binding to splicing machinery



# Capturing 5' L Anomalies Without Sequencing



# CLAWS strongly correlates with 5'L sequencing





# Conclusions

The new onset of persistent viremia despite no issues in adherence and drug efficacy is driven by virus production from expanded infected clones, and not replication.

Proviruses with small defects in the 5'Leader region are a common cause detectable viremia, complicating ART management.

These defects result in non-infectious virus, due to inefficient HIV splicing

→ differential selection pressure compared to intact proviruses?

→ These results allow a *better clinical interpretation of detectable viral load*

→ Sequencing data informed the design of a *simpler, targeted assay* that can distinguish intact from defective viral RNA

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