

Is HCV drug resistance an issue?

**5TH ASIAN CONFERENCE ON
HEPATITIS&AIDS
NANJING, CHINA • 28-29 MAY 2016
FROM BASIC SCIENCE TO
CLINICAL PRACTIC**

**Jürgen Kurt Rockstroh
Department of Medicine I,
University Hospital Bonn,
Bonn, Germany**



Conflict of Interest

Jürgen Rockstroh has received:

- Honoraria for lectures and/or consultancies from Abbott, AbbVie, Bionor, BMS, Cipla, Gilead, Janssen, Merck and ViiV.
- Research grants from Dt. Leberstiftung, DZIF, NEAT ID.

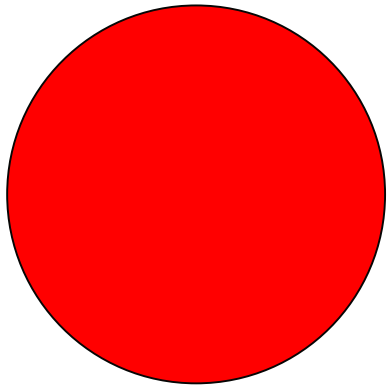
Deutsche
_Leberstiftung

 DZIF

neatid

Mechanisms of resistance

Mechanisms of Resistance



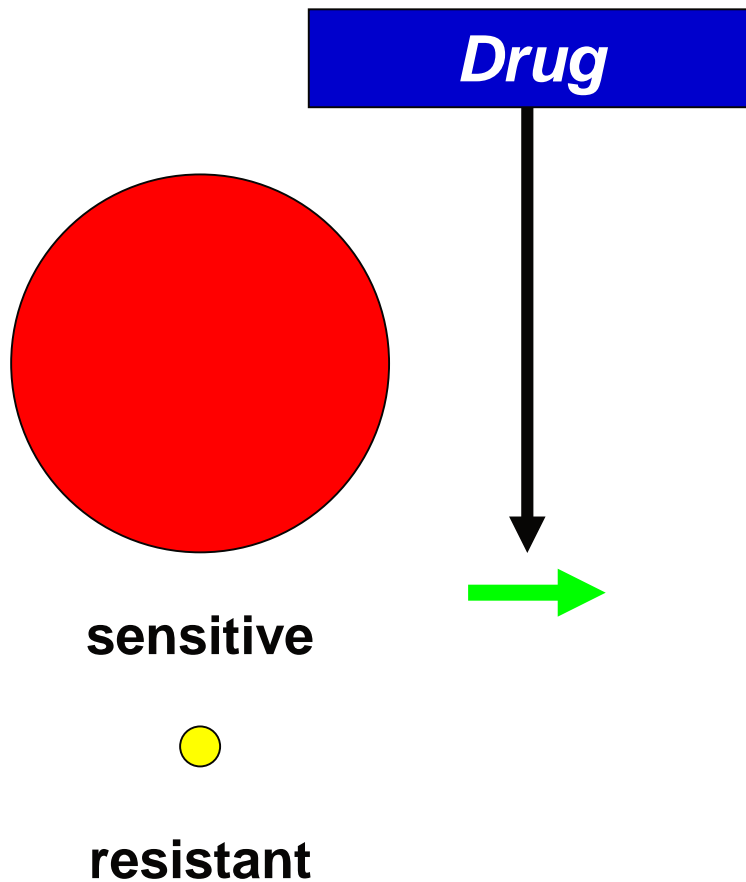
sensitive



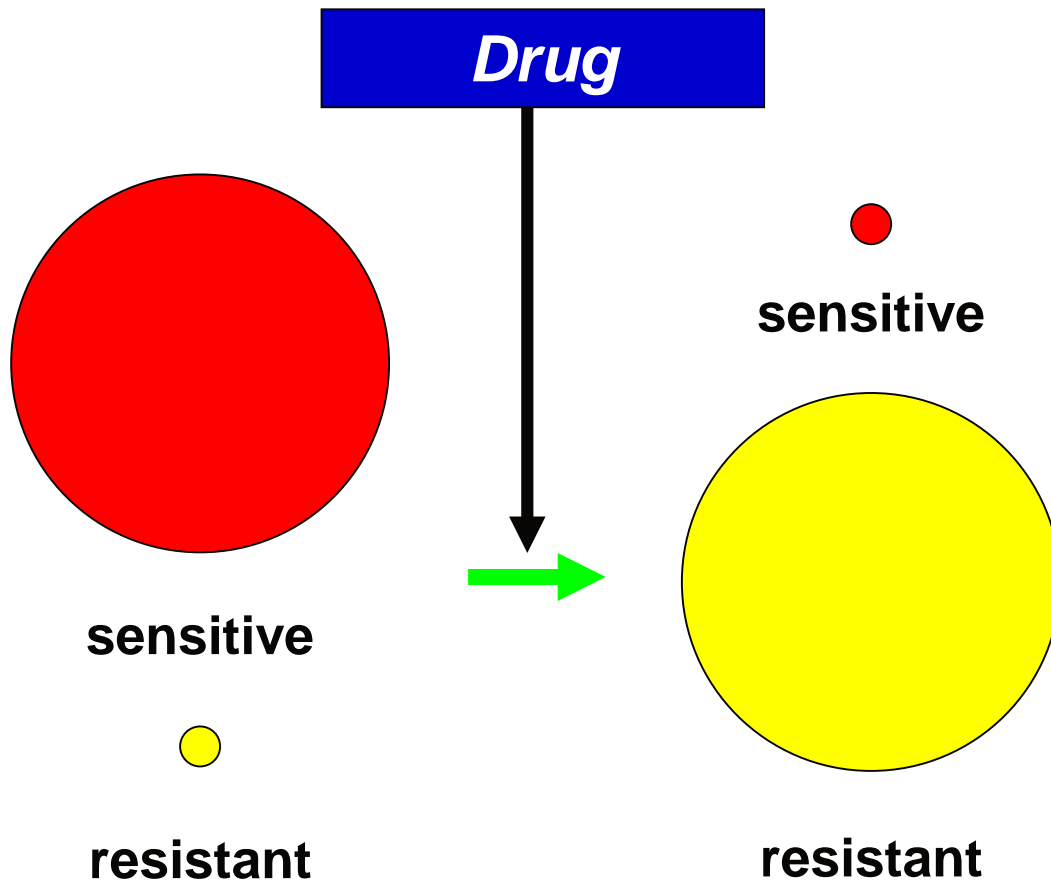
resistant

JM Pawlotsky IAS 2015

Mechanisms of Resistance

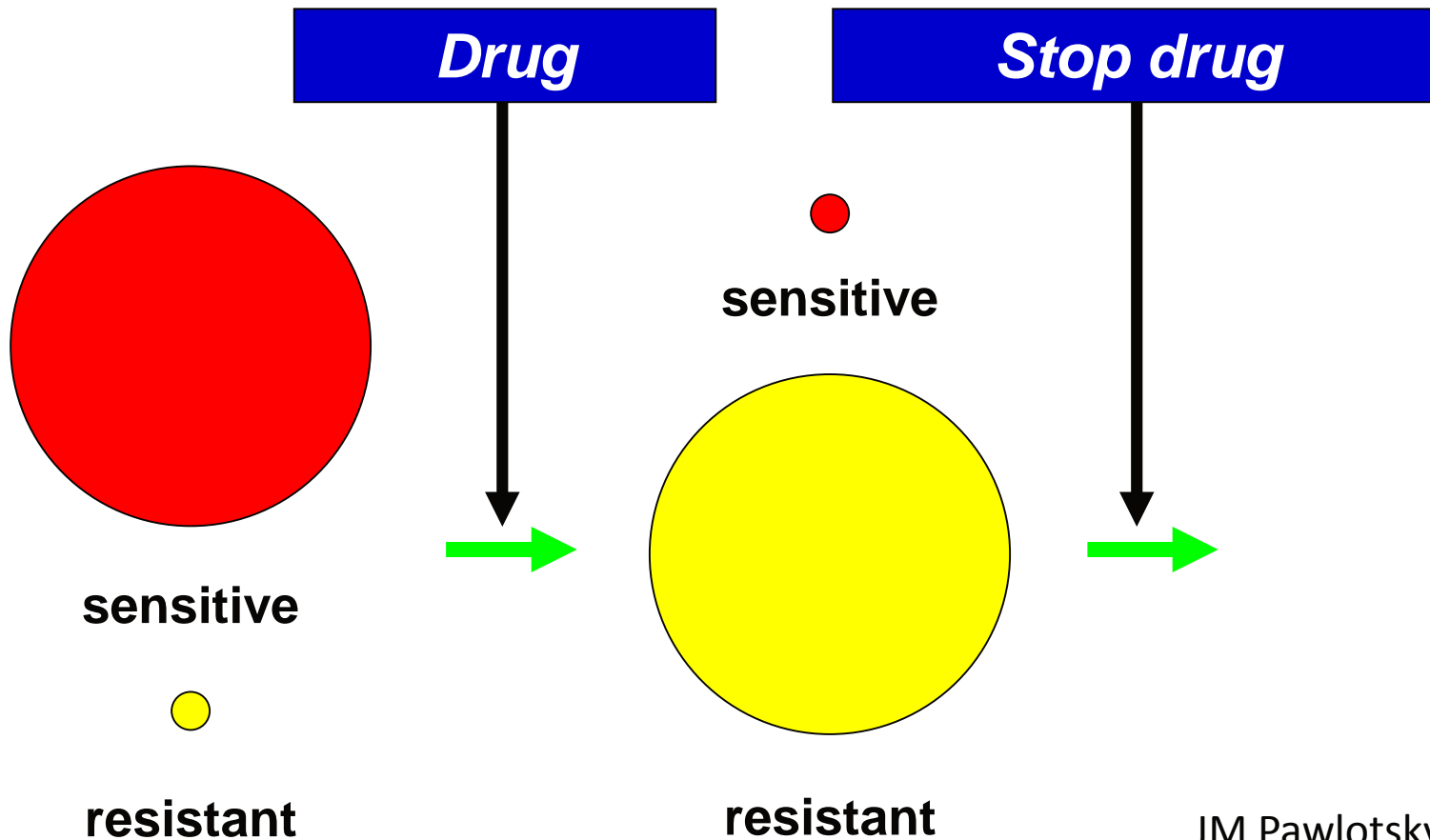


Mechanisms of Resistance



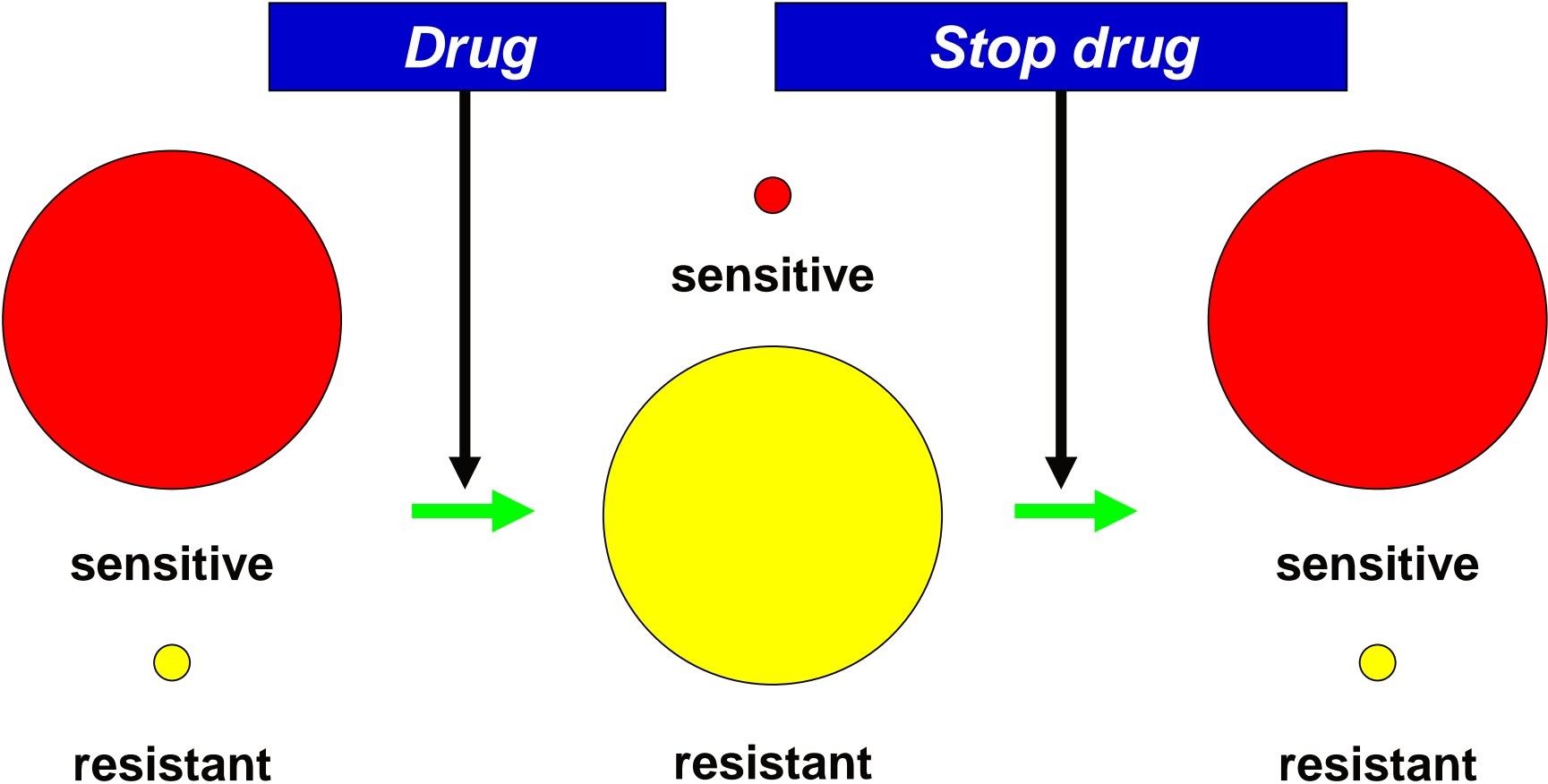
JM Pawlotsky IAS 2015

Mechanisms of Resistance

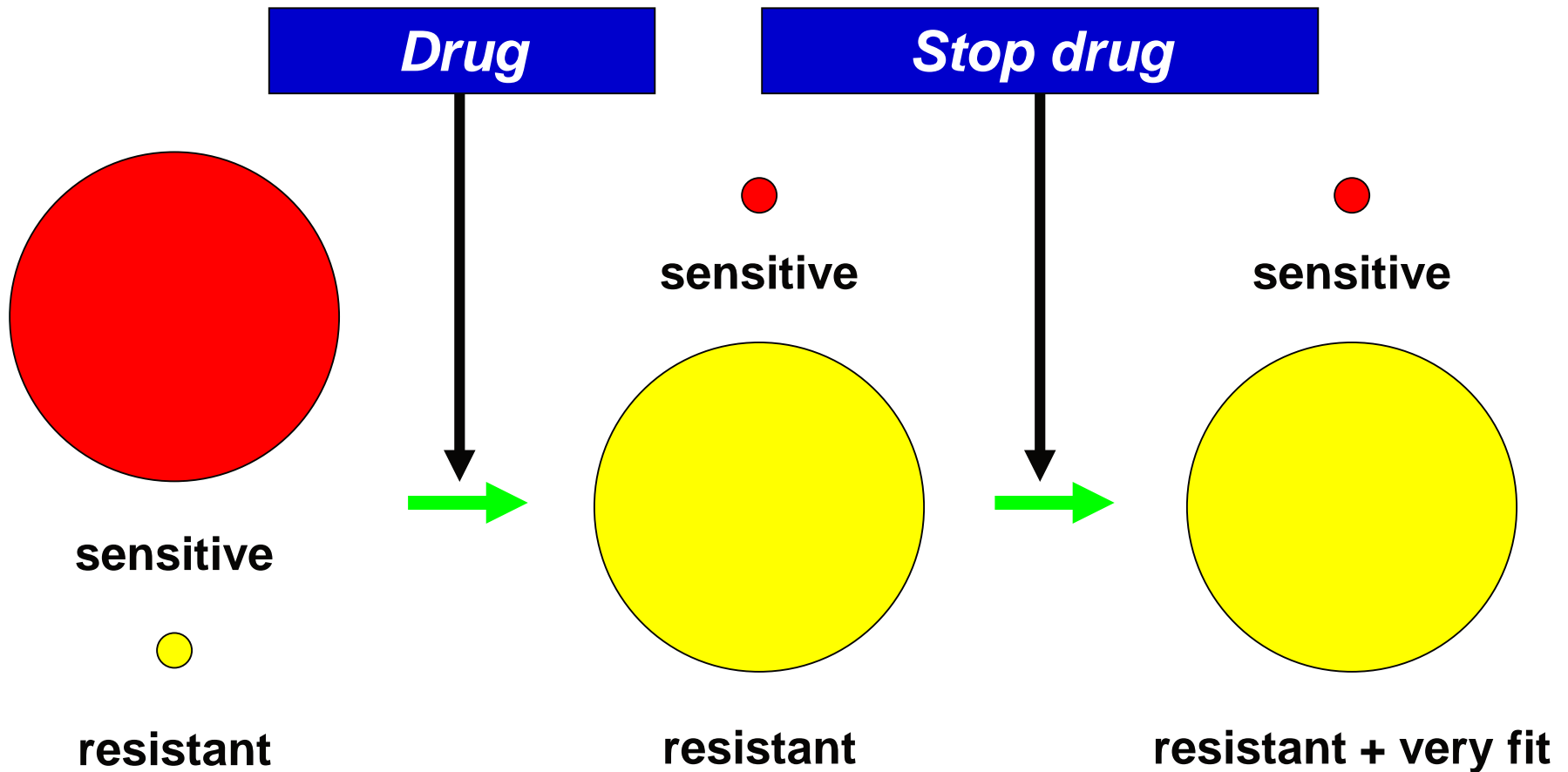


JM Pawlotsky IAS 2015

Mechanisms of Resistance


























Mechanisms of Resistance



General aspects of DAA resistance

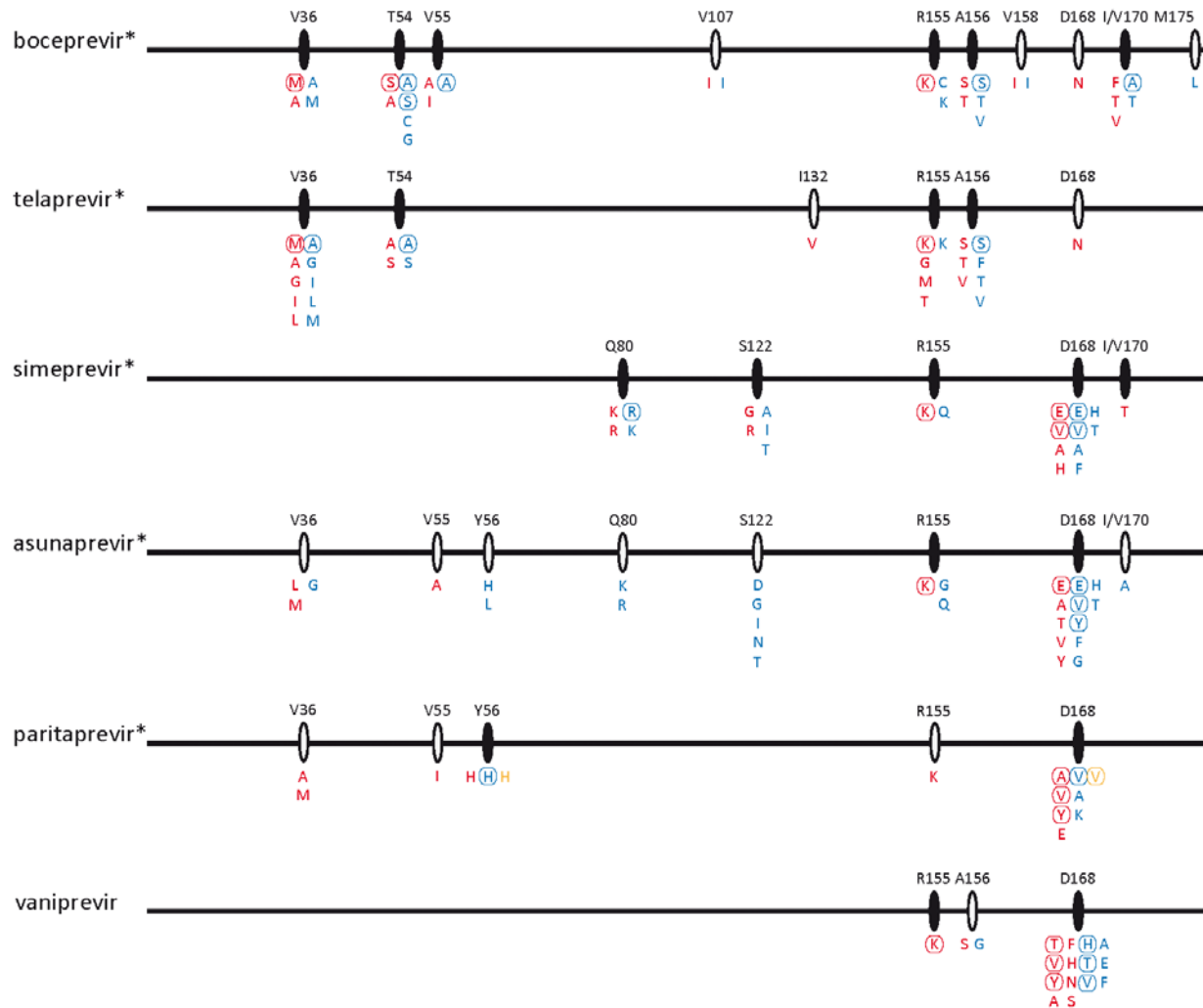
Not All Direct-Acting Antivirals are Created Equal

Characteristic	Protease Inhibitor*	Protease Inhibitor**	NS5A Inhibitor	Nuc Polymerase Inhibitor	Non-Nuc Polymerase Inhibitor
Resistance profile					
Pangenotypic efficacy					
Antiviral potency					
Adverse events					

 Good profile
  Average profile
  Least favorable profile

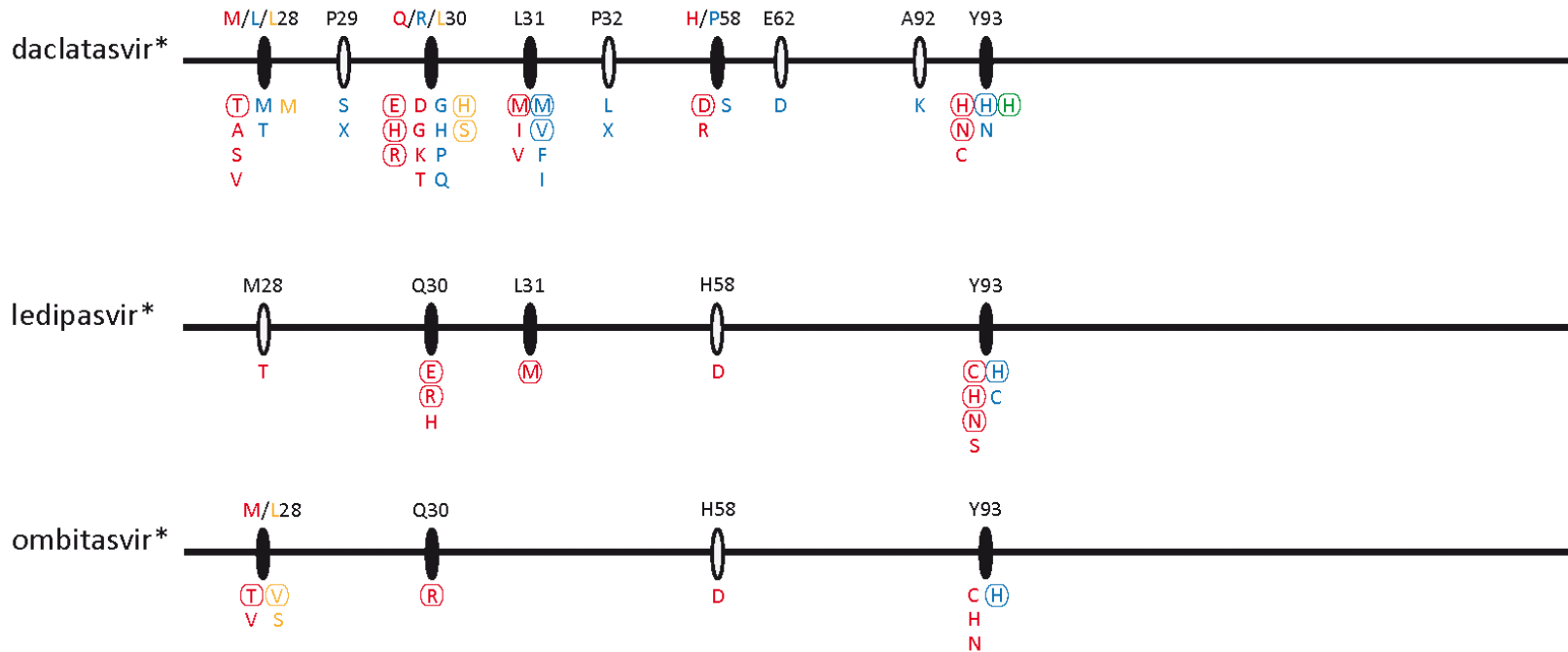
*First generation. **Second generation.

Protease Inhibitor Resistance



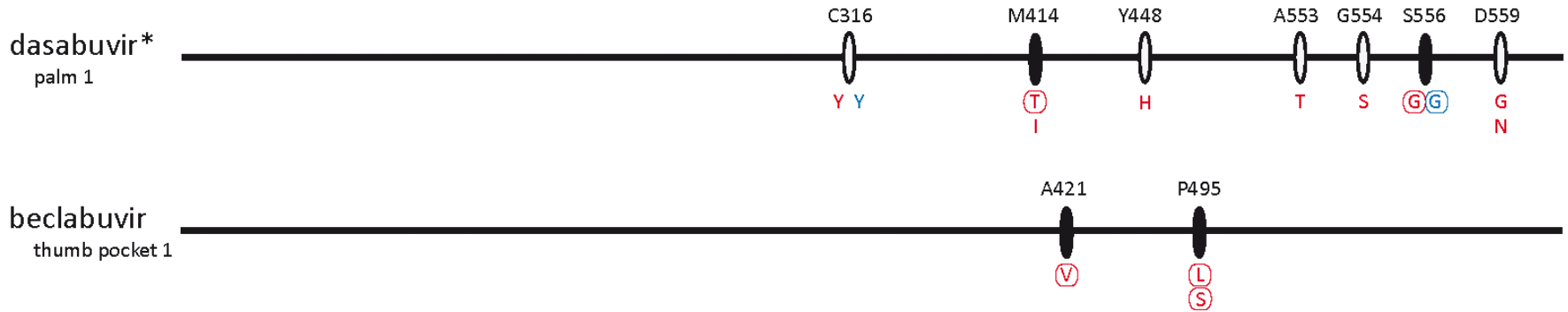
Genotype and subtype designations: 1a - red, 1b - blue, 4d - orange

NS5A Inhibitor Resistance



Genotype and subtype designations: 1a - red, 1b - blue, 3a - green, X - amino acid deletion
 4 - orange (daclatasvir - genotype 4, ombitasvir - genotype 4d)

Non-Nucleoside Inhibitor Resistance



Genotype and subtype designations: 1a - red, 1b - blue, 2 - brown, 3a - green

Nucleotide Analogue Resistance



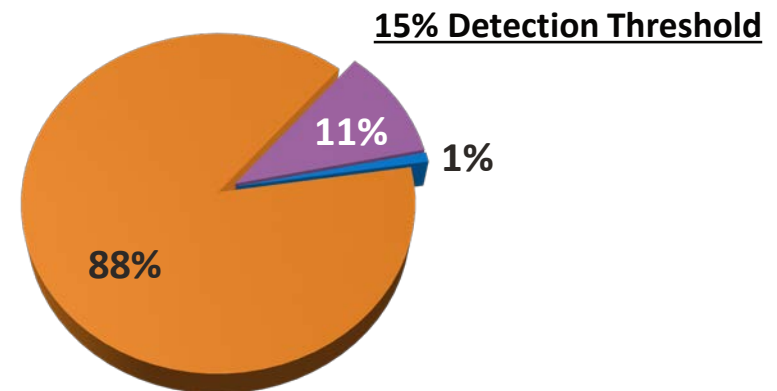
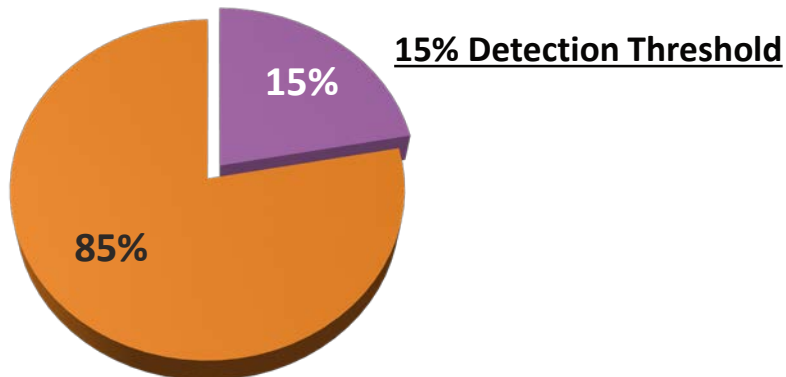
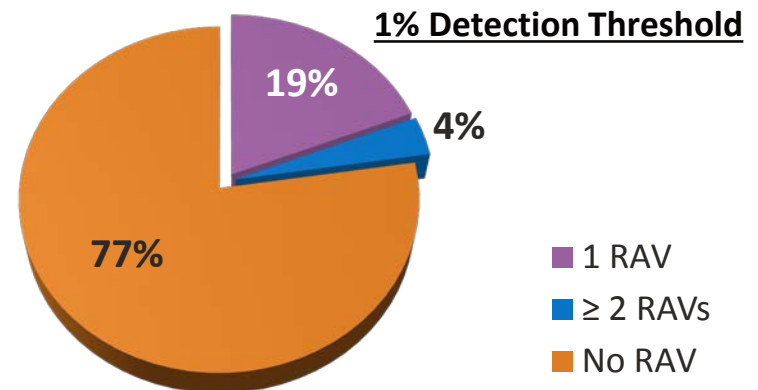
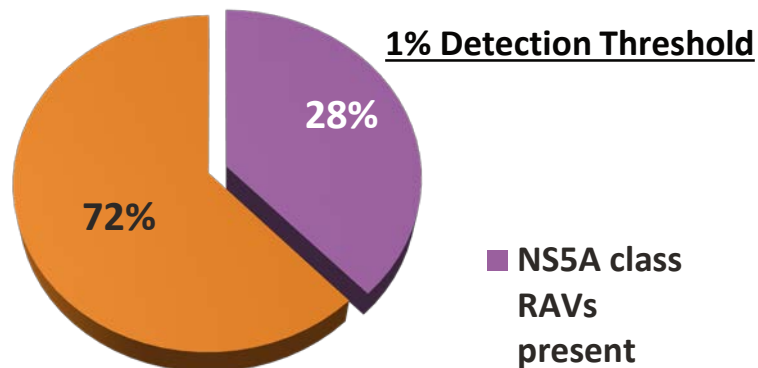
Prevalence of Baseline GT1a NS5A RAVs: Impact of RAV Definition and Sensitivity of Detection

NS5A Inhibitor Class RAVs detected in this study at amino acid positions:

M28(all), Q30(all), L31(all), P32L, H58D/R, and Y93(all)

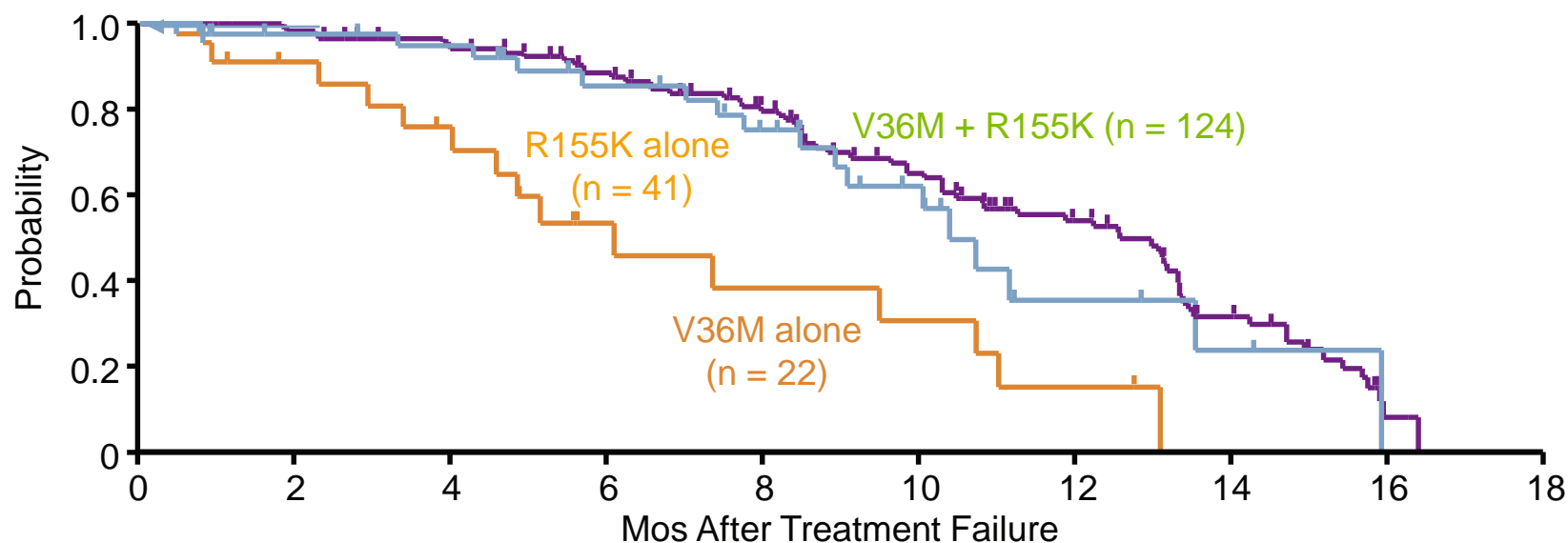
Ombitasvir-specific RAVs detected in this study:

M28T/V, Q30E/R, H58D, Y93C/F/H/L/N



Stopping Rules—The Facts: Multiple Mutations May Be More Troublesome

Loss of detectable resistance in patients with resistant variant(s) at failure of TVR + pegIFN/RBV (analysis includes only patients with follow-up data)



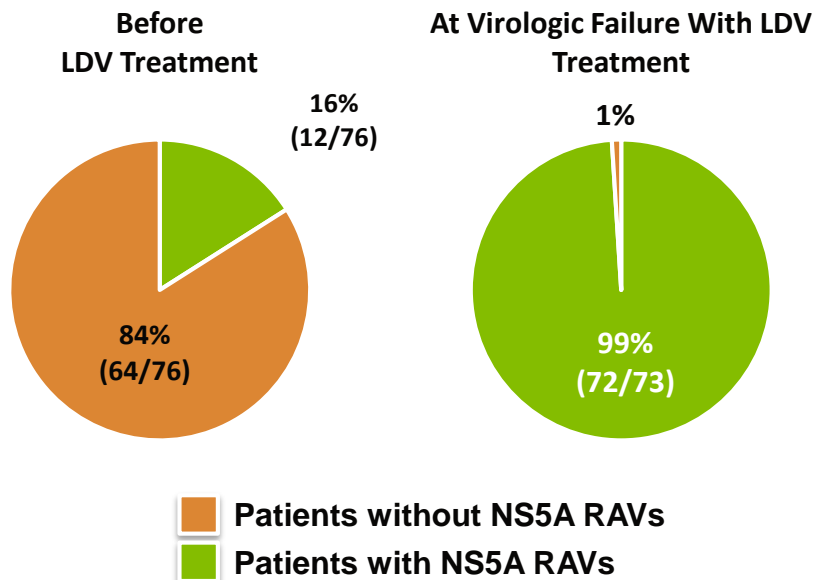
	V36M Alone*	R155K Alone†	V36M + R155K
% of 1a failures (WT: 16%)	10	20	46
Median mos to loss (95% CI)	6 (4-9)	10 (9-13)	13 (10-13)

*Comparison of V36M vs V36M + R155K: $P < .0001$. †Comparison of R155K vs V36M + R155K: $P = .48$.

Long-Term Persistence of HCV NS5A Variants After Treatment With LDV

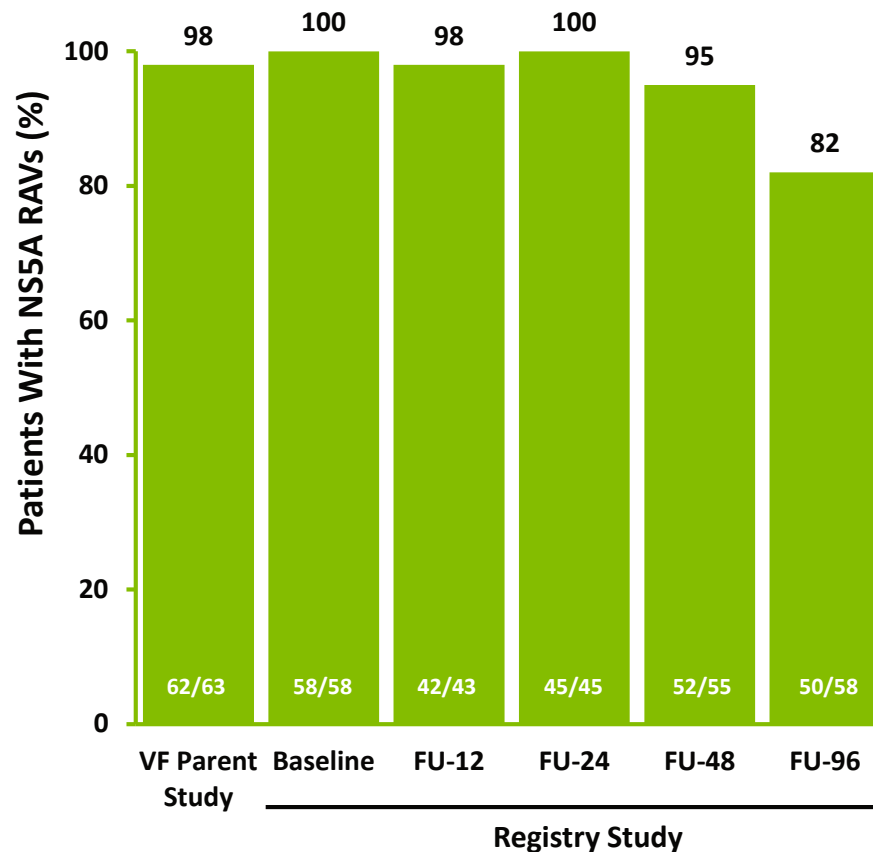
NS5A RAVs in patients who failed HCV treatment with ledipasvir (LDV) in the absence SOF

- Positions 24, 28, 30, 31, 32, 58, 93 that confer >2.5-fold reduced susceptibility to LDV *in vitro* were included



Almost all patients developed NS5A RAVs at treatment failure

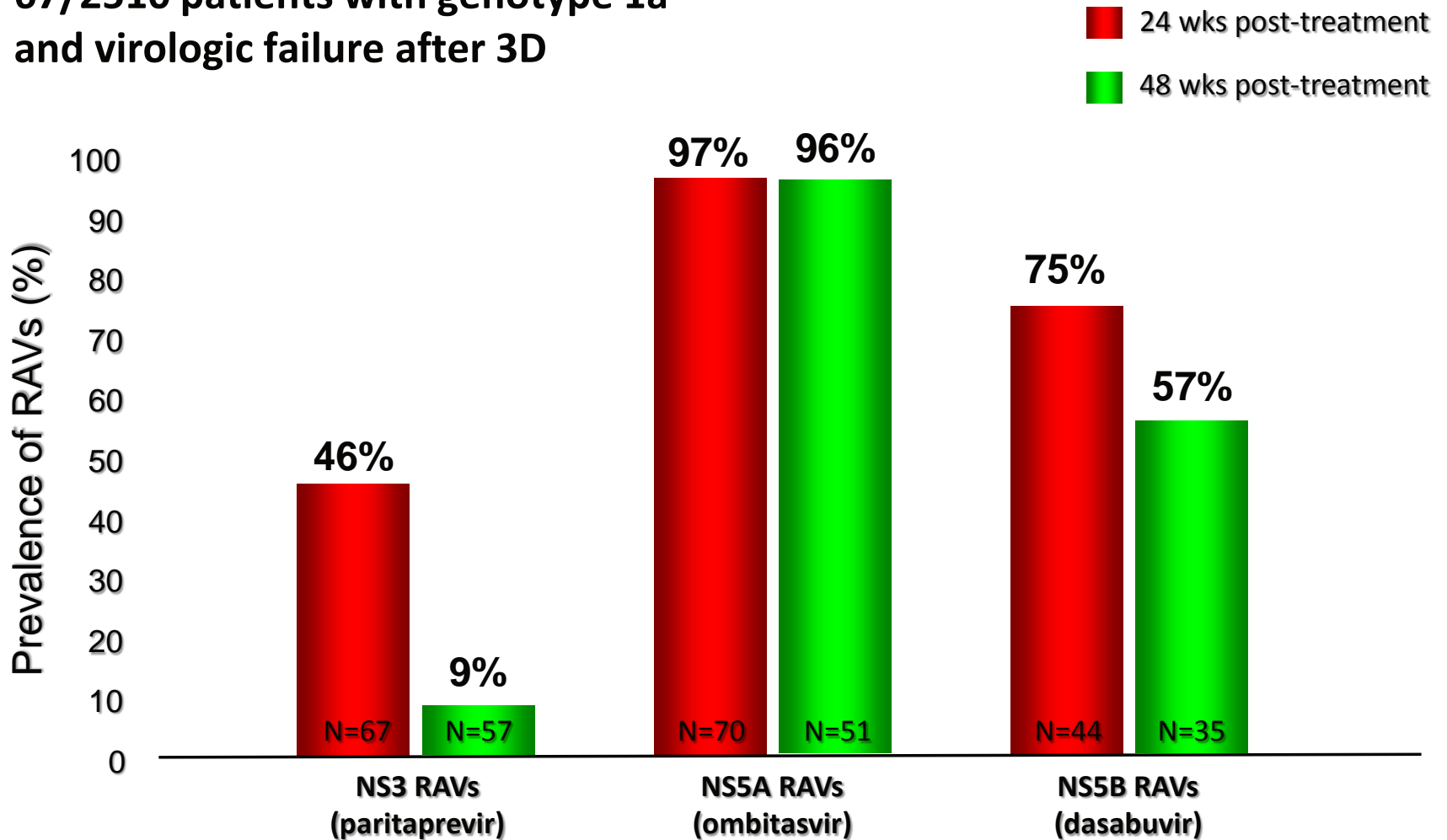
Majority of RAVs Detected After 96 Weeks (> 1% of Population)



NS5A RAVs persisted in majority of patients for 96 weeks

Persistence of RAVs in Patients who Relapsed after 3D

67/2510 patients with genotype 1a
and virologic failure after 3D



What do the guidelines say?

EASL Recommendations on Treatment of Hepatitis C 2015

European Association for the Study of the Liver *

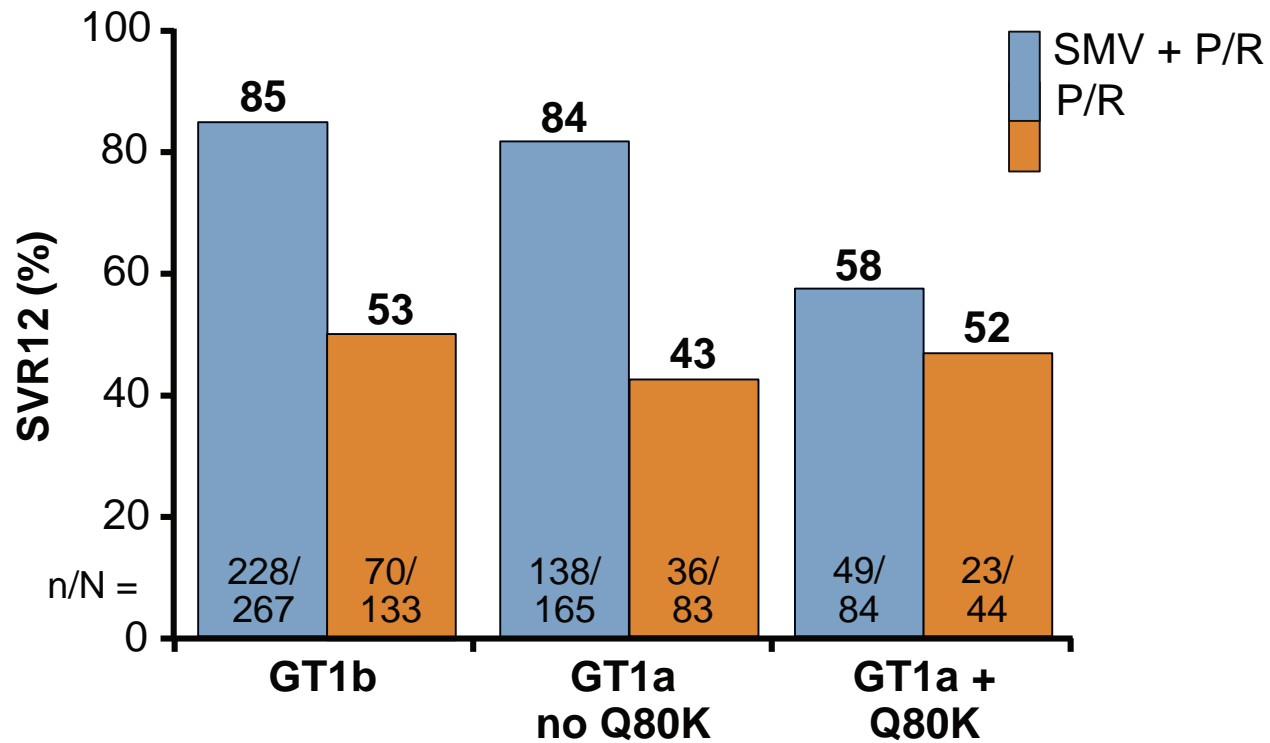
- The HCV genotype and genotype 1 subtype (1a/1b) must be assessed prior to treatment initiation and will determine the choice of therapy (A1)
- *IL28B* genotyping has no role in the indication for treating hepatitis C with the new DAAs (A1)
- HCV resistance testing should not be performed prior to therapy, because the SVR rates are very high both in patients without and with detectable amounts of resistance-associated variants by means of population sequencing at baseline (with the exception of patients infected with subtype 1a who receive the combination of PegIFN- α , ribavirin and simeprevir) (A1)
- The utility of HCV resistance testing (i.e. the determination of the sequence of the DAA target region) prior to retreatment in patients who failed on any of the DAA-containing treatment regimens is unknown (B2)

**What does the label
say?**

What does the label say?

- **When considering OLYSIO (Siemprevir) combination treatment with peginterferon alfa and ribavirin in HCV genotype 1a patients, patients should be tested for the presence of virus with the NS3 Q80K polymorphism before starting treatment**
- **Zepatier label USA: Genotype 1a: Testing for the presence of virus with NS5A**
- **resistance-associated polymorphisms is recommended.**

QUEST: No Benefit of Simeprevir if Q80K Positive



Q80K present in 34% of GT1a patients
No benefit of simeprevir if Q80K positive

C-EDGE TN + C-EDGE CO-INFECTION: universitäts klinikum bonn

NS3/4A Resistance Associated Variants

Resistance analysis population (290 GT1a; 172 GT1b)†

	RAV Status in Patients with Baseline Sequence % (n/m)		SVR12 All Patients % (N/n)		SVR12 NS3 RAVs ≤5-fold potency loss		SVR12 NS3 RAVs >5-fold potency loss	
Genotype 1a RAVS								
Baseline NS3 RAVS	53.4	(155/290)	96.1	(149/155)	96.1	(149/155)	0	0/0
No baseline NS3	46.6	(135/290)	93.3	(126/135)	—	—	—	—
Genotype 1b RAVS								
Baseline NS3 RAVS	17.4	(30/172)	96.7	(29/30)	96.1	(25/26)	100	(4/4)
No baseline NS3 RAVs	82	(142/172)	99.3	(141/142)	—	—	—	—

†The resistance analysis population includes all patients from the full analysis set who have sequencing data available and who either achieved SVR12 or met criteria for virologic failure

N = number of patients who achieved SVR12

m = number of patients with evaluable baseline sequence

n = number of patients with or without a baseline RAV

Signature NS3 loci included the substitutions V36A/G/L/M/I, I54A/C/G/S, V55A/I, Y56H, Q80K/R, V107I, I22A/G/R, I132V, R155X, A156S/T/V/F/G/L, V158I, D168X, I/V170A/F/T/V, and M175L.

The following NS3 RAV(s) are considered to have >5-fold resistance to GZR based on GT1a replicons: Y56H, R155G/T/W, A156G/T/V/L, D168A/G/T/V/L/I/F/Y/E/H/K/R.

C-EDGE TN + C-EDGE CO-INFECTION: NS5A Resistance Associated Variants

Resistance analysis population (294 GT1a; 173 GT1b)[†]

	RAV Status in Patients with Baseline Sequence % (n/m)		SVR12 All Patients % (N/n)		SVR12 NS5A RAVs ≤5-fold potency loss		SVR12 NS5A RAVs >5-fold potency loss	
Genotype 1a RAVS								
Baseline NS5A RAVS	9.9	(29/294)	65.5	(19/29)	87.5	(14/16)	38.5	(5/13)
No baseline NS5A RAVs	90.1	(265/294)	98.1	(260/265)	—	—	—	—
Genotype 1b RAVS								
Baseline NS5A RAVS	13.3	(23/173)	95.7	(22/23)	100	(1/1)	95.5	(21/22)
No baseline NS5A RAVs	86.7	(150/173)	99.3	(149/150)	—	—	—	—

[†]The resistance analysis population includes all patients from the full analysis set who have sequencing data available and who either achieved SVR12 or met criteria for virologic failure

N = number of patients who achieved SVR12

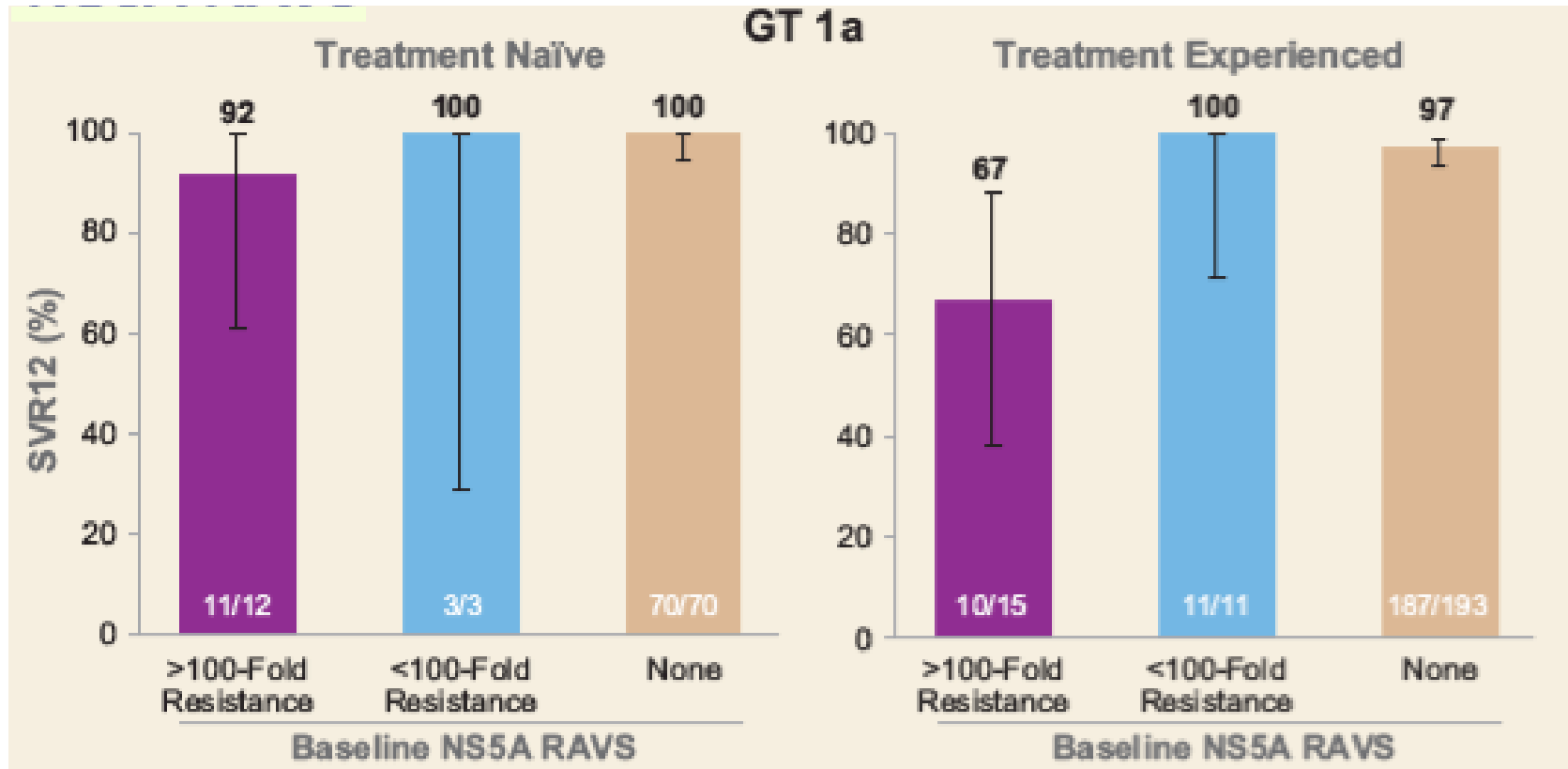
m = number of patients with evaluable baseline sequence

n = number of patients with or without a baseline RAV

Signature NS5A loci included the substitutions M28T/V/A, Q30E/H/R/G/K/L/D, L31M/V/F, H58D, and Y93C/H/N/S for GT1a and the substitutions L28T/V/A, R30E/H/G/K/L/D, L31M/V/F, P58D and Y93C/H/N/S for GT1b.

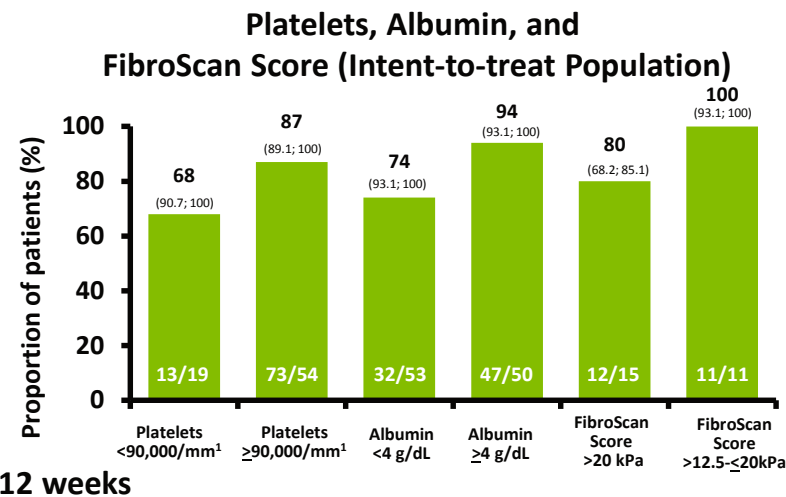
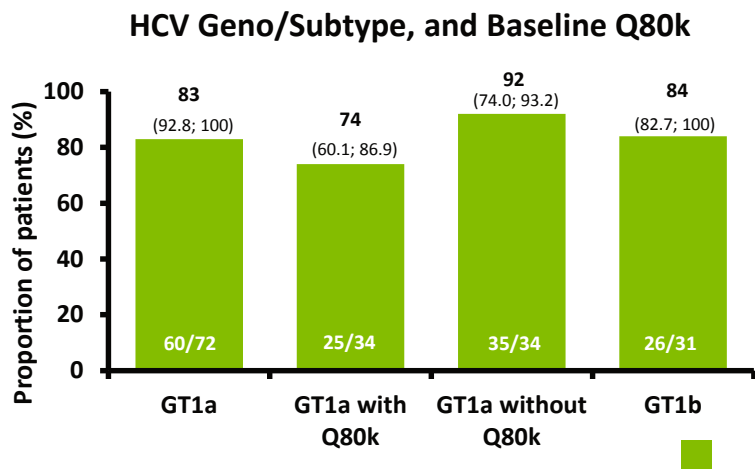
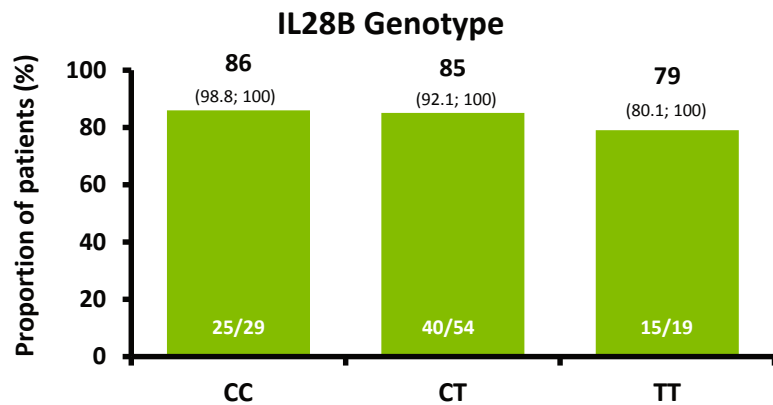
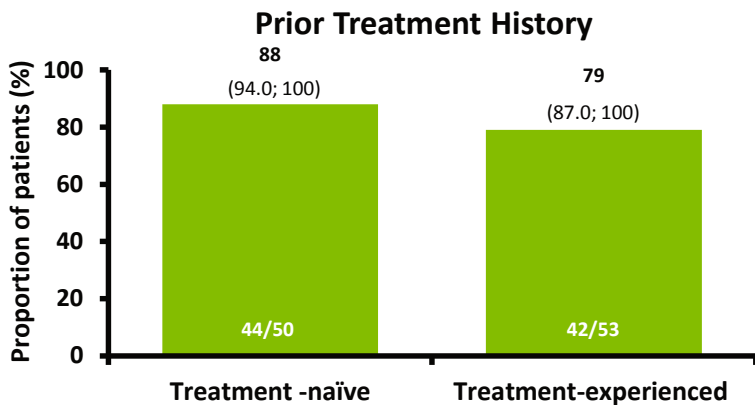
Based on the available GT1a replicon data, the following variants are considered to have >5-fold resistance to EBR: M/L28T/A, Q/R30E/H/R/G/K/L/D, L31M/V/F, H58D, Y93C/H

SVR to Sofosbuvir/Ledipasvir According to NS5A RAVs (513 cirrhotic patients)



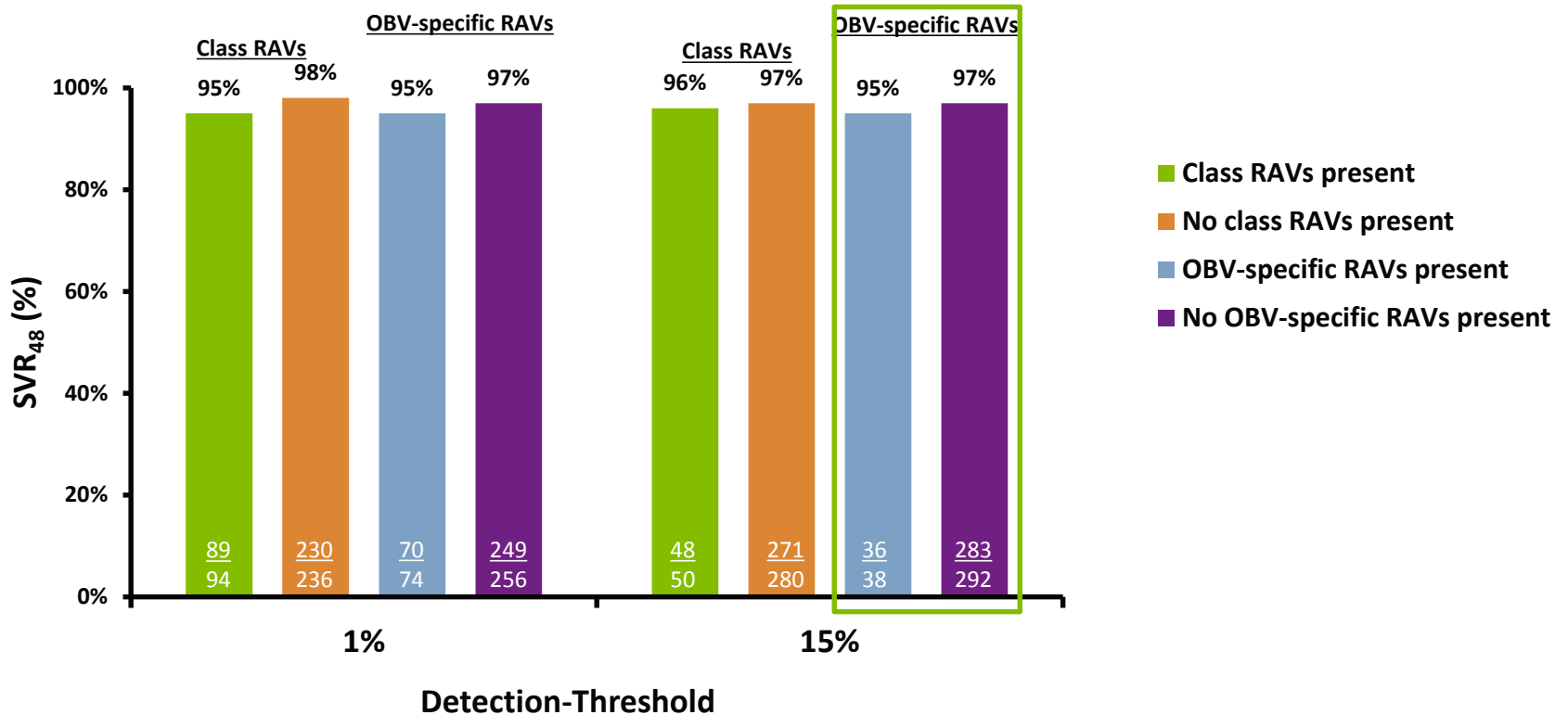
OPTIMIST 2: SMV + SOF in HCV Mono-Infx with GT1 and Cirrhosis

SVR12 Rates (95% CI) by:



■ SMV + SOF 12 weeks

Impact of Baseline GT1a NS5A Class RAVs and Ombitasvir-specific RAVs on SVR Rate



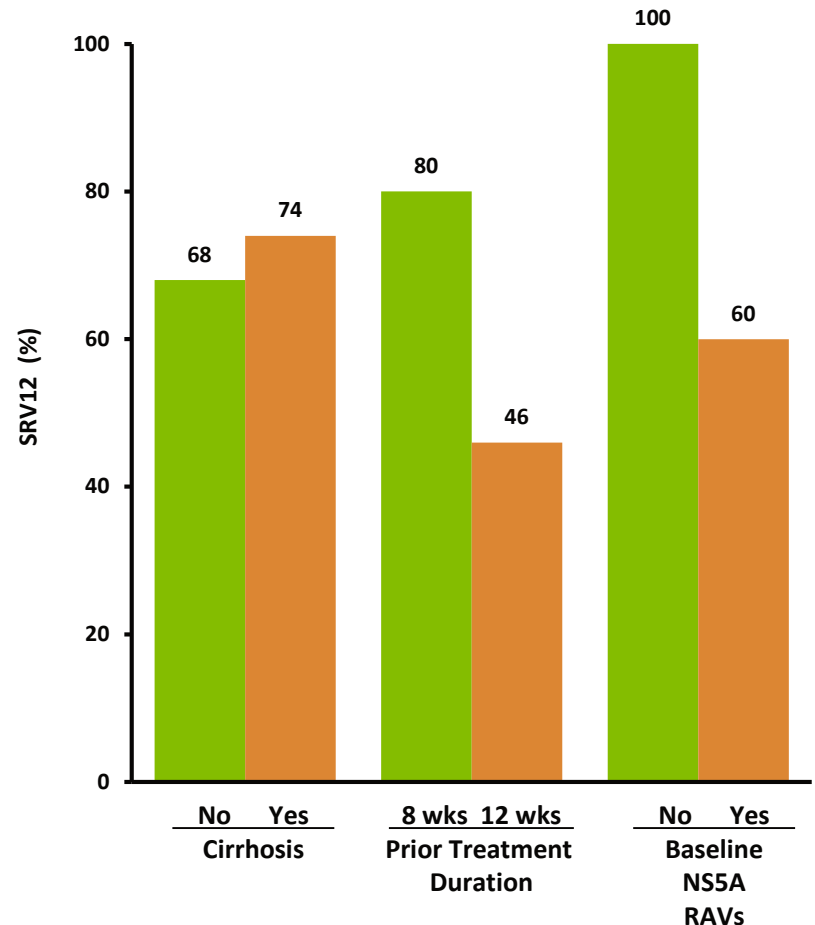
Similar SVR rates were observed irrespective of the presence or absence of baseline variants

**Can a resistance test
guide treatment
decision making in
patients with prior
failure of DAA based
therapy?**

Retreatment of Patients Who Failed 8 or 12 Weeks of LDV/SOF-Based Regimens With LDV/SOF for 24 Weeks

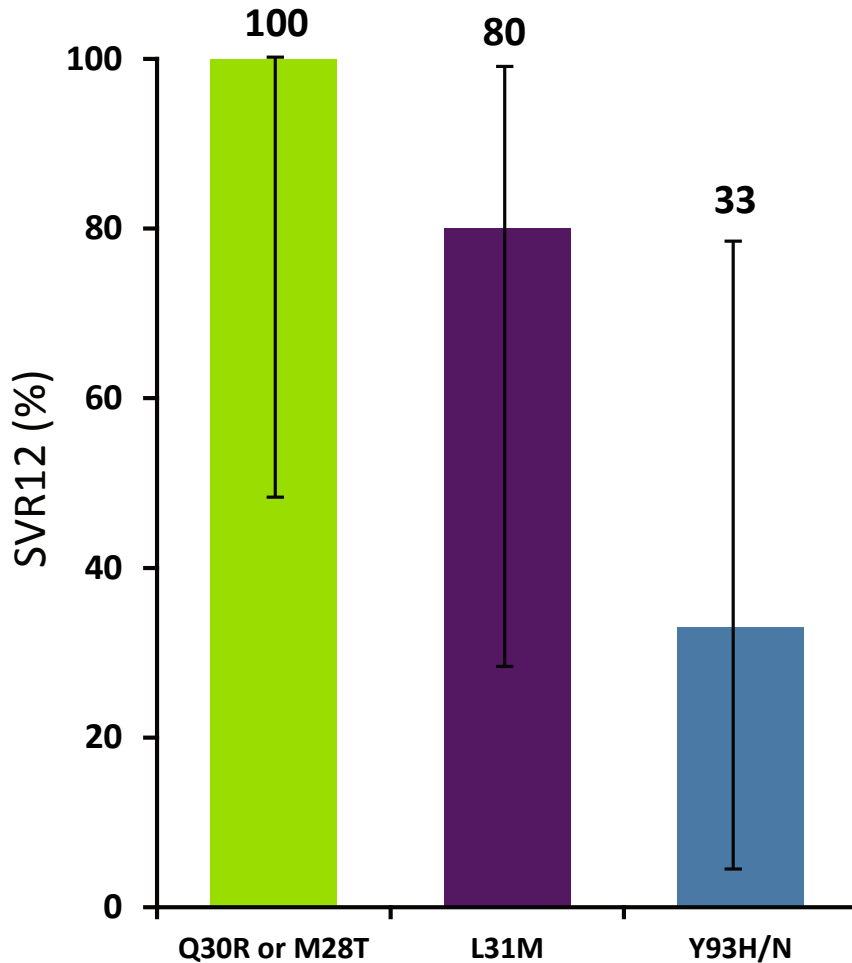
LDV/SOF 24 Weeks N=41	
Mean age, y (range)	58 (35-71)
Male, n (%)	34 (83)
Black/African American, n (%)	10 (24)
IL28B non-CC, n (%)	38 (93)
GT 1a, n (%)	34 (83)
Mean HCV RNA, log ₁₀ IU/mL (range)	6.2 (4.5-7.4)
Cirrhosis, n (%)	19 (46)
Presence of NS5A RAVs	15 (79)
Prior HCV treatment, n (%)	
LDV/SOF ± RBV	33 (80)
LDV/SOF + GS-9669	8 (20)
Prior HCV treatment duration, n (%)	
8 weeks	30 (73)
Presence of NS5A RAVs	19 (63)
12 weeks	11 (27)
Presence of NS5A RAVs	11 (100)

SVR according to baseline parameters



Results and Analysis

SVR12 by Baseline NS5A RAVs
GT 1 Retreatment



Prior to re-treat

- No NS5B resistance associated (S282T) or treatment-emergent (L159F, V321A) variants were detected

At second virologic failure

- 4 of 12 (33%) patients had NS5B variants detected
 - S282T (n=2)
 - L159F (n=1)
 - Double-mutant S282T + L159F (n=1)

Retreatment of Patients Who Failed DAA-combination Therapies - Real-world Experience From a Large Hepatitis C Resistance Database

Subset of the European resistance database (n=3549) with persons who failed DAAs outside of clinical trials (N=310) – drug-class specific RASs (NS3, NS5A, NS5B) associated with > 2-fold increase in EC50

Assess HCV guidelines approach to re-treatment:

1. Use active DAAs
2. Add RBV
3. Longer duration

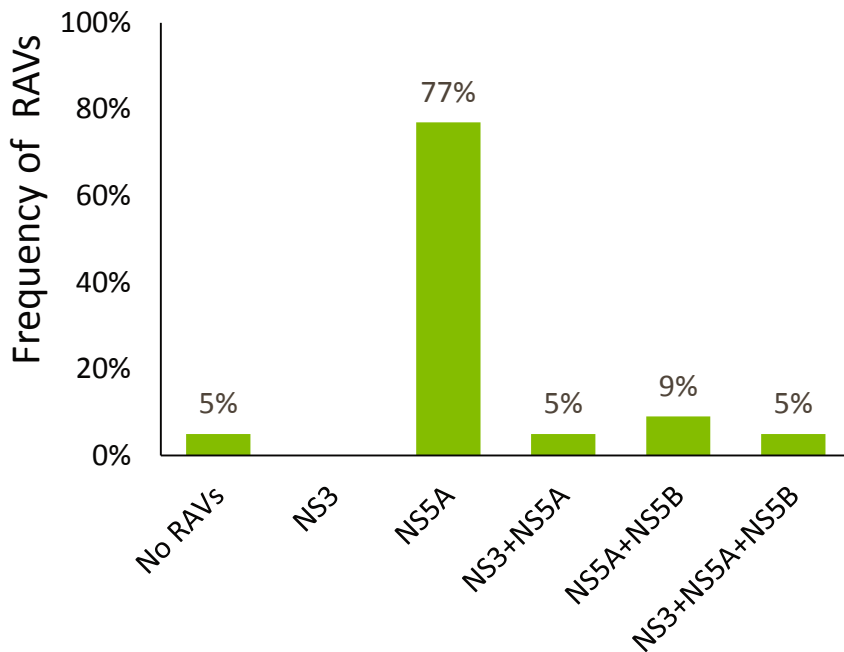
N = 310	SMV/SOF ± RBV N=55	LDV/SOF ± RBV n=114	DCV/SOF ± RBV n=51	RTV/OBV ± RBV n=30	SOF + RBV n=60
Mean age, y (range)	58 (43-75)	57 (34-77)	55 (31-71)	55 (34-58)	52 (27-65)
Men, n (%)	43 (78)	94 (82)	42 (82)	26 (87)	47 (78)
Cerrhosis, n (%)	37 (71)	62 (57)	33 (70)	11 (37)	21 (44)
+RBV, n (%)	10 (55)	39 (34)	8 (16)	19 (63)	60 (100)
Prior IFN Therapy	39 (76)	67 (67)	20 (76)	21 (70)	27 (63)
G, n (%)					
1	49 (89)	90 (79)	29 (57)	27 (90)	-
2	-	-	-	-	27 (45)
3	1 (2)	15 (13)	20 (39)	-	33 (55)
4	5 (9)	9 (8)	2 (4)	3 (10)	-
Treatment duration 8/12/24 weeks, n	-/53/1	12/80/20	-/25/26	-/29/1	-/26/29

Retreatment after DAA Failure

22 of 119 patients with **G1 and NS5A treatment failure** (DCV or LDV + SOF)

Retreatment with with PI containing regimen

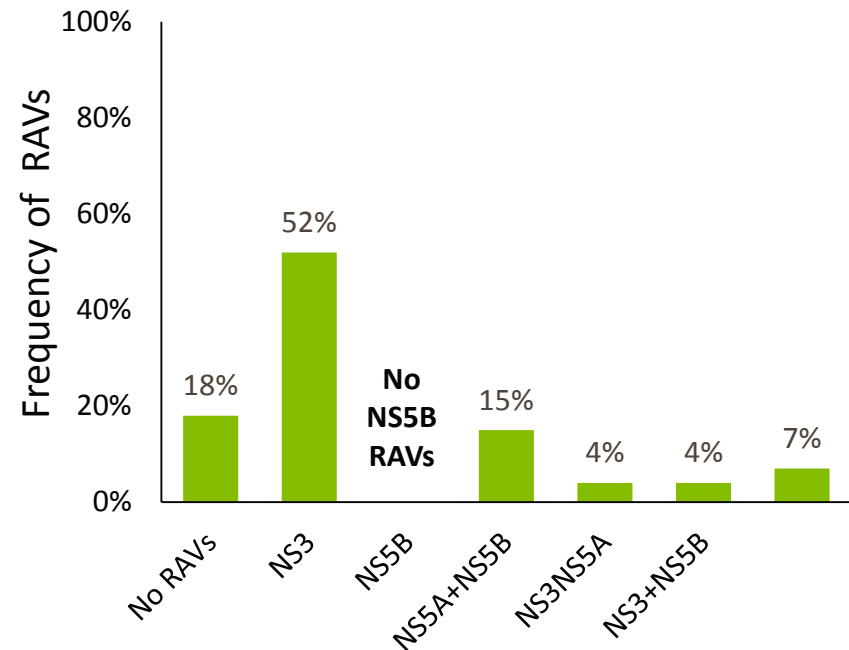
- SMV/SOF +/- RBV or 3D +/- RBV for 12 or 24 weeks
- SVR12 in 6 of 7 patients (limited data)



27 of 49 patients with **G1 and SMV/SOF treatment failure**

Retreatment with NS5A containing regimen

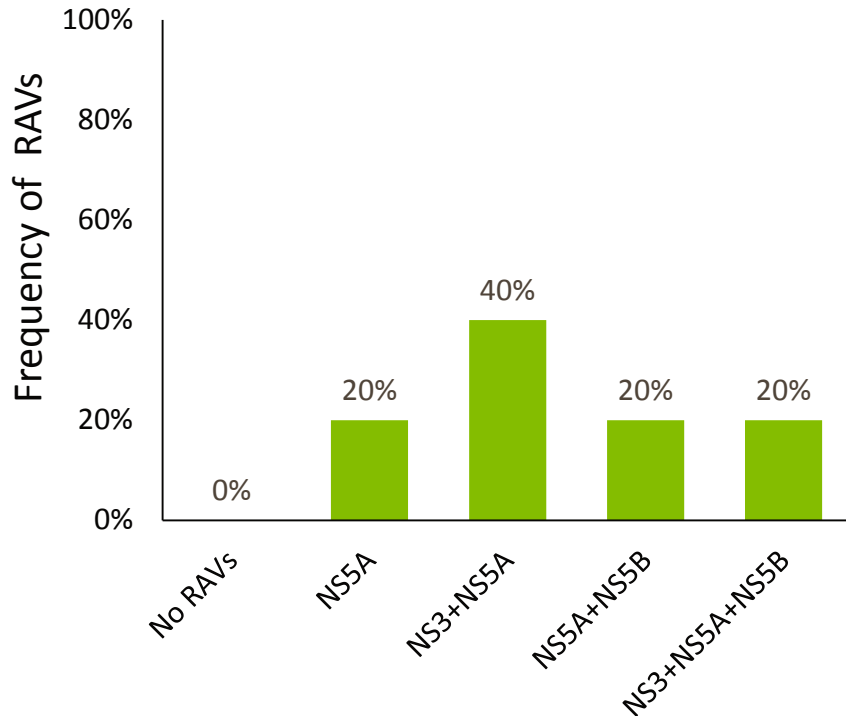
- LDV/SOF (n=23) or 3D (n=4) +/- RBV
- SVR12 in 20 of 22 patients



Retreatment after DAA Failure (cont'd)

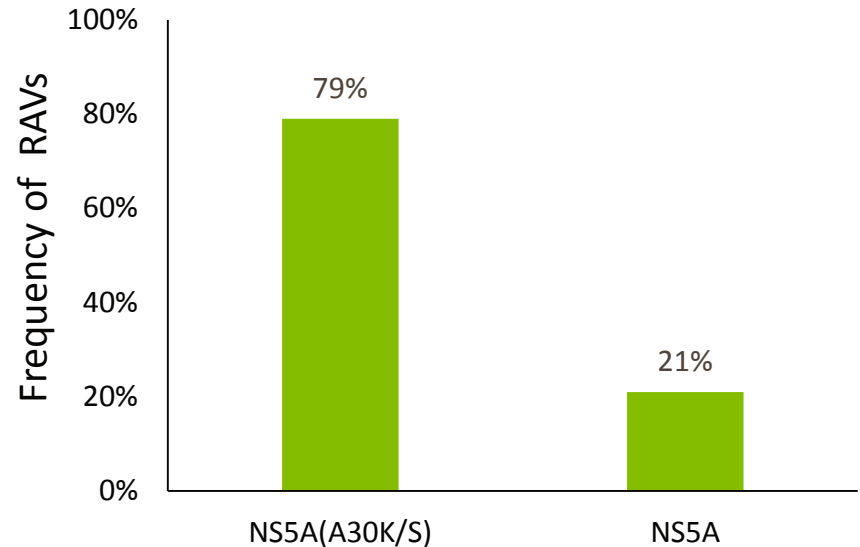
5 of 27 patients with G1 and 3D treatment failure

- Retreatment with SOF based regimen
- No data on outcomes



14 of 23 patients with genotype 3 and SOF/RBV treatment failure

- Retreatment with DCV (n=13) or LDV (n=1) + SOF +/- RBV
- SVR12 in 7 of 7



- DAA failures – male sex, cirrhosis, prior PR
- 73 patients (28%) started RAS-driven retreatment
- Preliminary data promising

Summary

- **After IFN-free treatment failure, HCV variants resistant to protease inhibitors progressively disappear by population sequencing, replaced by wild-type virus**
- **In contrast, viruses resistant to NS5A inhibitors and to NNIs persist for years, maybe for ever, as dominant species already in place to prevent onward transmission and re-infection**
- **In most (if not all) patients who fail to achieve an SVR on an IFNfree regimen, viruses that are resistant to one or more of the DAAs administered are present as the dominant species at the time of relapse**
- **The detection, by means of population sequencing, of HCV RAVs at baseline has an impact on the rate of SVR with IFN-free regimens in patients with negative host factors**
- **The addition of ribavirin appears to minimize the impact of preexisting RAVs on SVR**