

Phenotypic Susceptibility Assays for HCV Polymerase and Protease Inhibitors

HCV Drug Resistance Advisory Group,
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Purpose

- Review state of the art, strengths and weaknesses
 - Replicons, enzymatic assays
 - Genotype (subtype) issues
- Frame discussion on role for phenotypic assays
 - Drug development
 - Patient care

Why Phenotype?

- Before drug approval (pharma)
 - Structure-function studies
 - Confirm role of mutations observed in cell culture selection expts. and clinical samples
 - Determine extent and importance of natural variability in susceptibility in clinical isolates
- After drug approval (patient care)
 - Assess cross-resistance to 2nd line drug(s) after 1st line failure (therapy guidance)
 - Assess reasons for 1st line failure
 - Expand knowledge base (*in vitro* studies and small clinical trials are incomplete)

Danger of Not (or Limited) Phenotyping

- Over-confident interpretation of genotypes
 - *in vitro* selected mutations not observed in patients, ergo “no resistance”
- Little information about partial drug activity
- Miss rare but important novel pathways to development of resistance
 - HIV-1 examples: V106M, K101P and NNRTIs; I47A and lopinavir
- Under-appreciation for cross-resistance or suppressive effects on other drugs
 - HIV-1 examples: TAMs and NRTIs, M184V and ZDV, d4T, TDF

Strengths of Phenotypic Assays

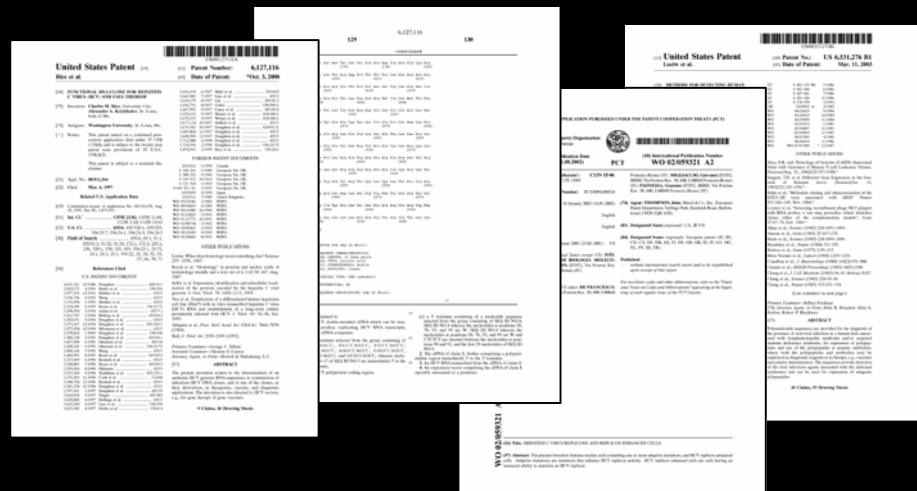
- Quantitative measurement
- Intuitive interpretation (?); more familiar to physicians
- It is what it is – doesn't matter how it got there
- Not limited by knowledge about resistance mutations
- Able to test new drugs immediately
- Generates replication capacity data

Limitations of Phenotype Assays

- Relatively slow and expensive
- Relatively complex (harder to assure quality and to standardize)
- Typically performed in reference laboratory only
- Sensitivity for **minority species** dependent on resistant virus genotype and on drug MOA
- **Cutoffs, cutoffs, cutoffs!**

IP is an Important Problem

- Companies must protect their IP with patents and/or keep details secret
- Raises the cost of R&D and the threshold for positive ROI
- Encourages development of alternative assays – sets up the standardization problem



Phenotyping HCV

- Replicon-based systems
 - Transfer of patient virus sequences
 - Populations and/or clones
 - Evaluation of specific mutations (SDMs) observed in patients
- Chimeric cell-based systems
 - Drug target expression, alternative activity readout
- Enzyme (cell-free) systems
 - *In vitro* enzyme expression & assay

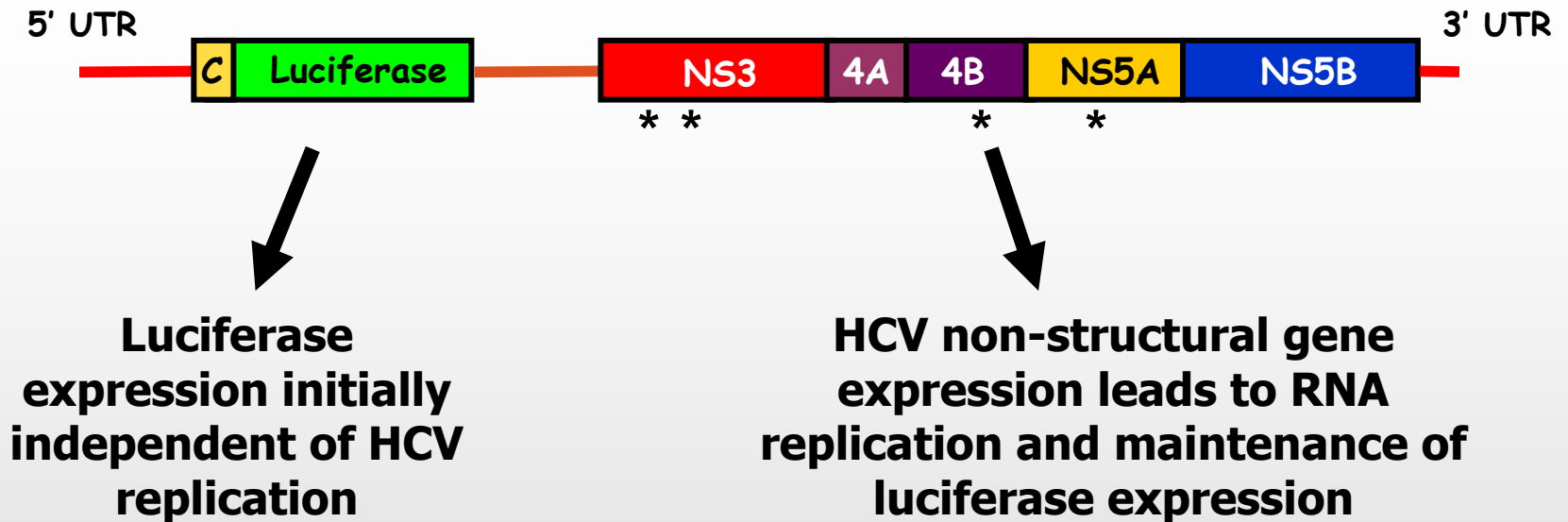
Replicon-Based Systems

- Cell lines (G418): Colony formation or RNA copy number readout
 - not suitable for evaluation of large numbers of patient isolates
- Transient transfection: reporter gene readout (luciferase, SEAP, β -lactamase)
 - NS5B Polymerase
 - Patient sequence transfer feasible (60-90%)
 - NS3/4A Protease
 - Appears to be more technically challenging
 - Dependent on adapted replicons and “cured” cell lines

Who is Doing What? (An Incomplete List!)

- Patient sequence populations in replicon vector
 - Abbott, Gilead, Monogram, Roche
- “Representative” clone(s) in replicon vector
 - Merck, Pfizer, Tibotec, Vertex
- Biochemical assay, with “representative” clone(s)
 - Tibotec, Vertex
- Other
 - Gilead

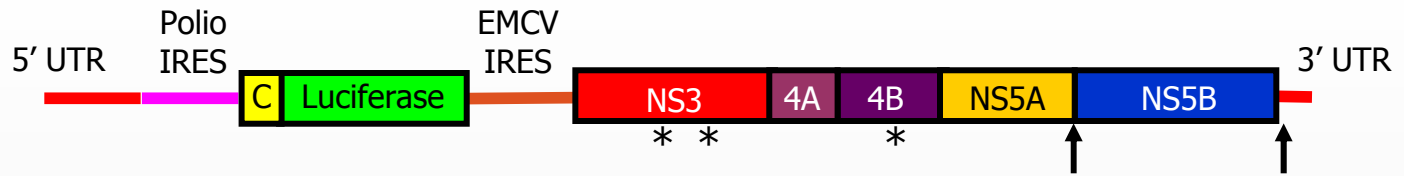
Luciferase HCV Replicon



* Adaptive mutations

HCV Resistance Test Vectors (RTV)

For NS5B:



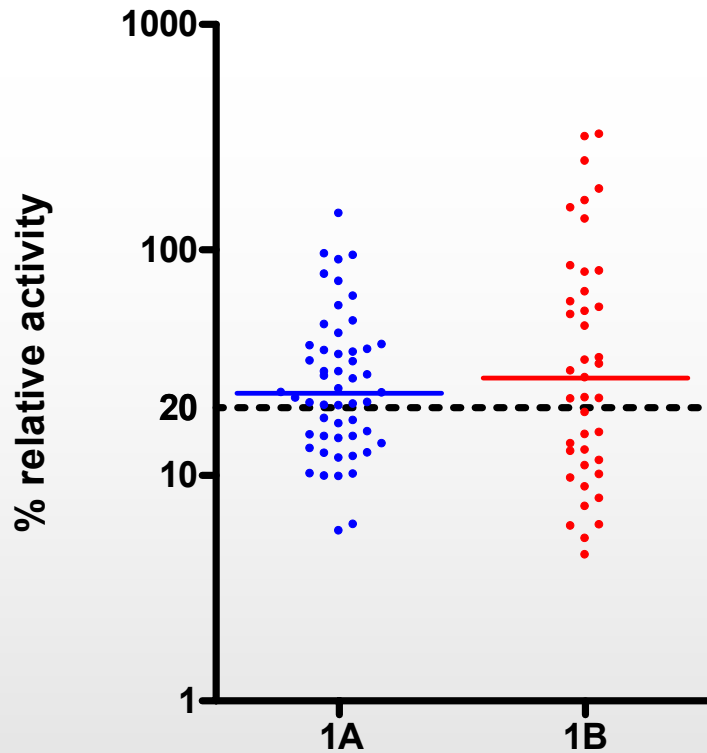
For NS3:



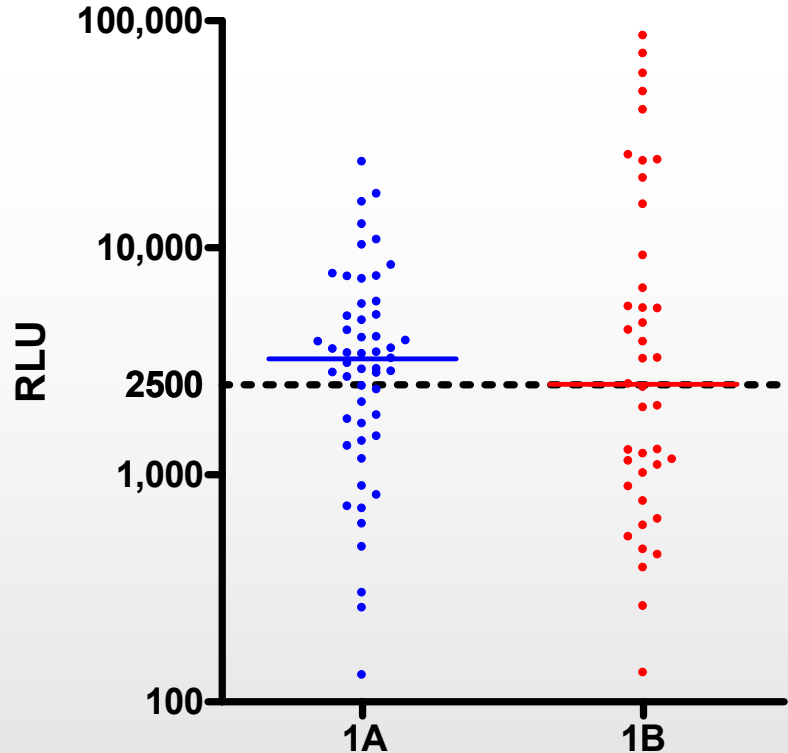
↑ Patient sequence acceptor sites (PSAS)

* Adaptive mutations

Patient Sample RTV Activity

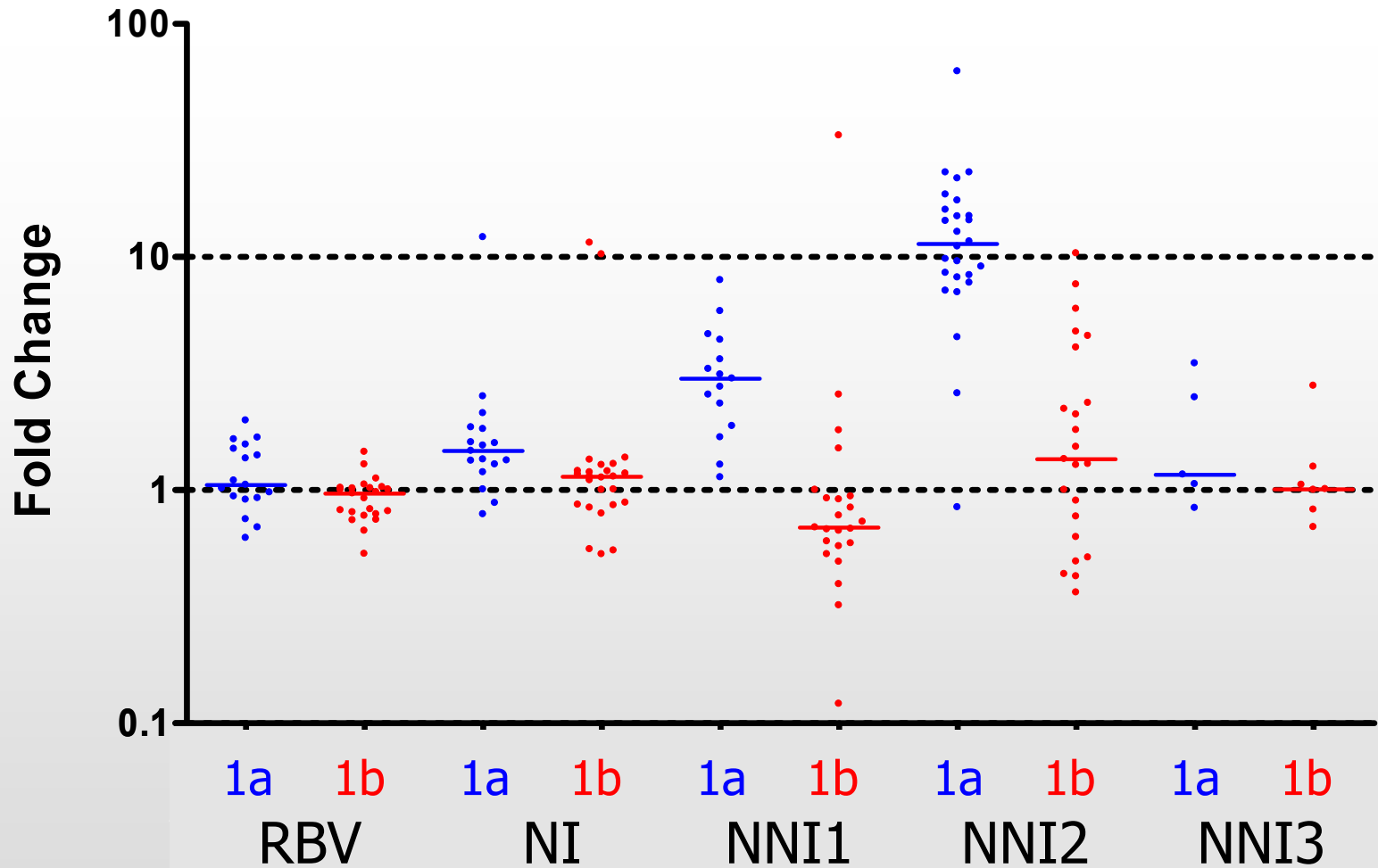


	ALL	1a	1b
n tested	94	53	41
N > 20%	57	33	24
N > 50%	23	8	15
% > 20%	61%	62%	59%
% > 50%	24%	15%	37%

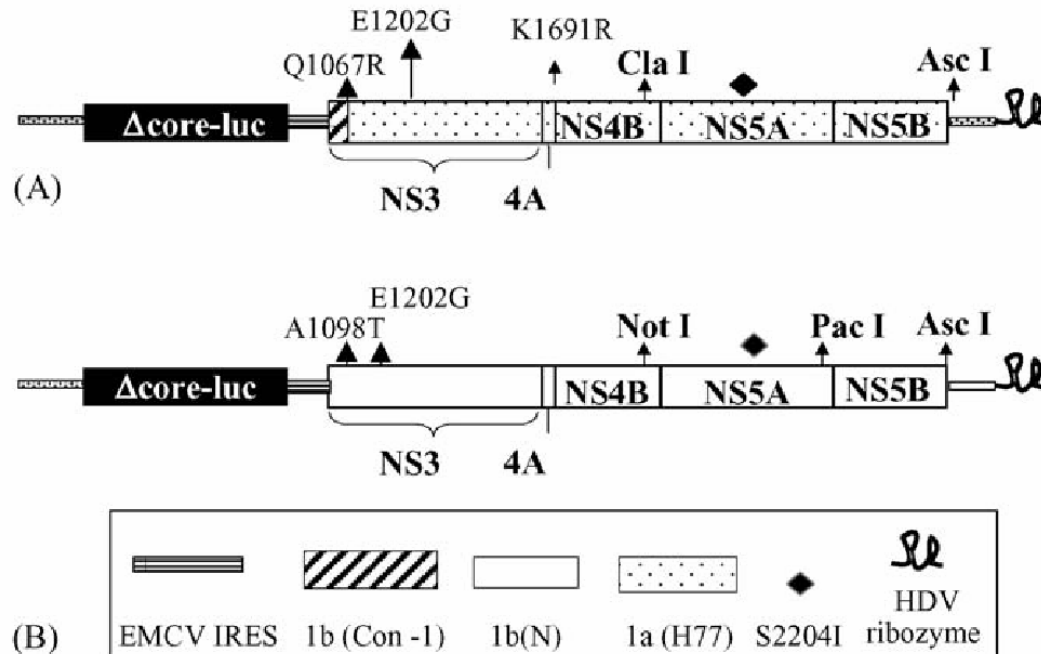


	ALL	1a	1b
N tested	94	53	41
N > 2500	55	34	21
% > 2500	59%	64%	51%

Patient Sample RTV Drug Susceptibility

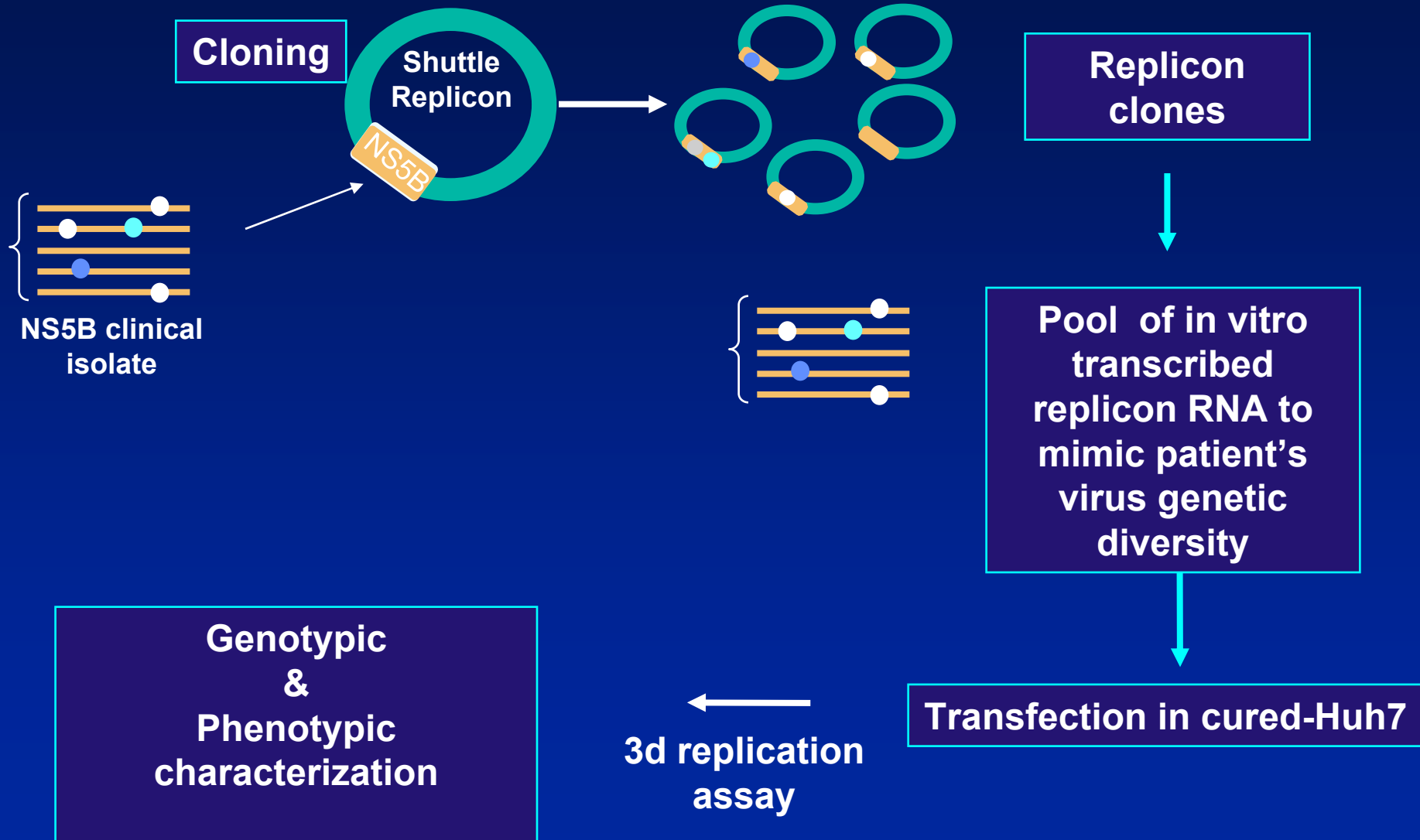


NS5A/B Replicon Vector

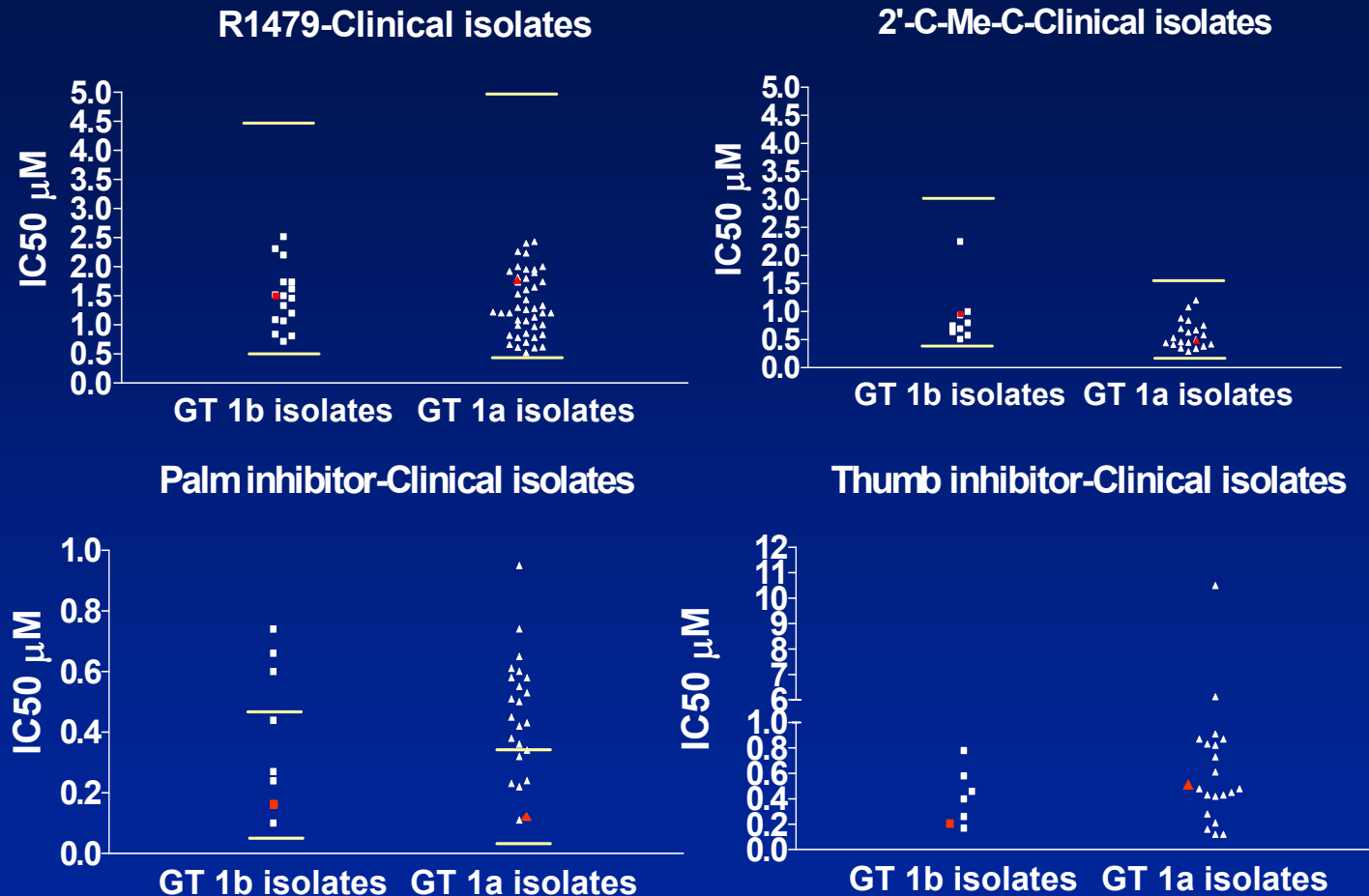


	NS5A/5B	NS5A	NS5B
1a	5/5	nt	nt
1b	4/7 (low)	7/7	7/7

Phenotypic and Genotypic Characterization of NS5B Clinical Isolates



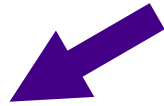
Variable potency of NNI but not NI across clinical isolates



92% of clinical isolates replicate to levels that allow determination of drug sensitivity

Methods for Phenotypic Analyses of Variants

Phenotypic analyses



Replicon analysis



Enzymatic analysis



Structural analysis

Genotype 1b



Inhibition of HCV
replication by telaprevir

Genotype 1a



Inhibition of HCV
protease by telaprevir

Genotype 1a



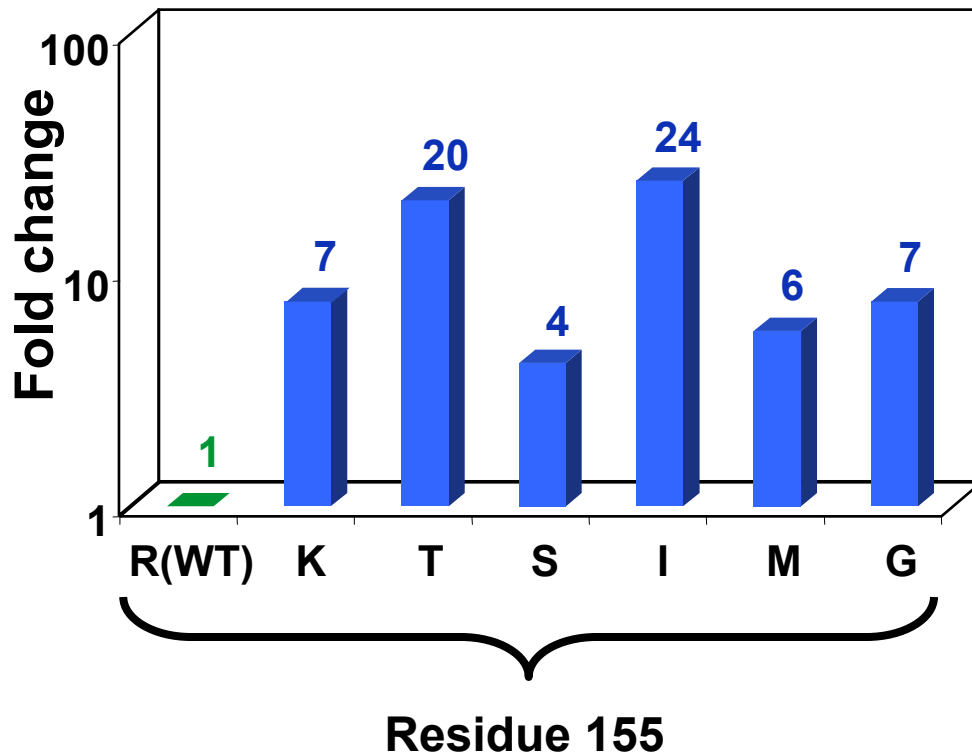
Binding of telaprevir to
HCV protease

Definition of resistance (in fold change)

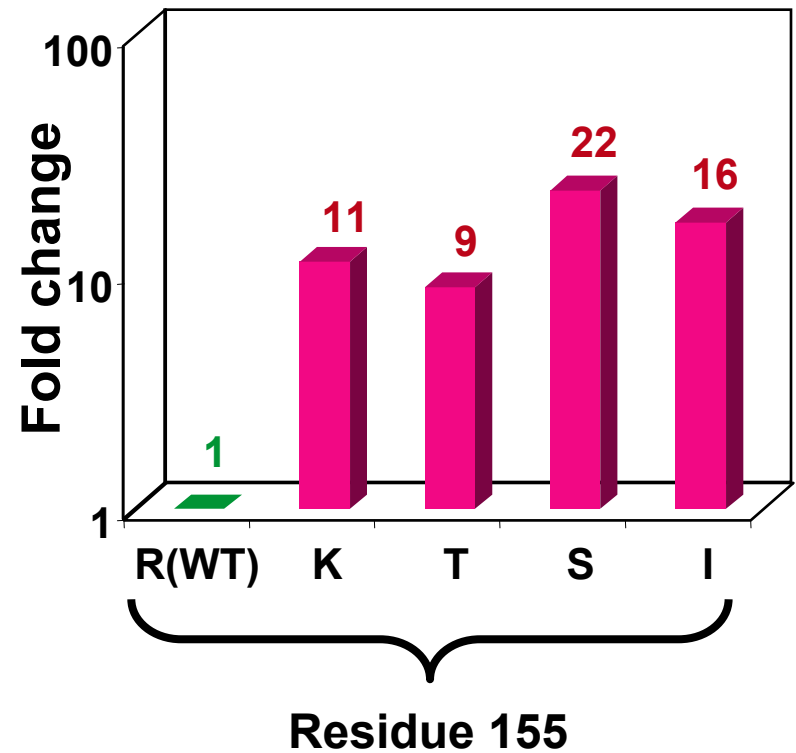
< 3-fold	(no resistance)
3- to 25-fold	(low-level resistance)
25- to 50-fold	(intermediate-level resistance)
>50-fold	(high-level resistance)

R155 Substitutions Confer Low-level Resistance to Telaprevir

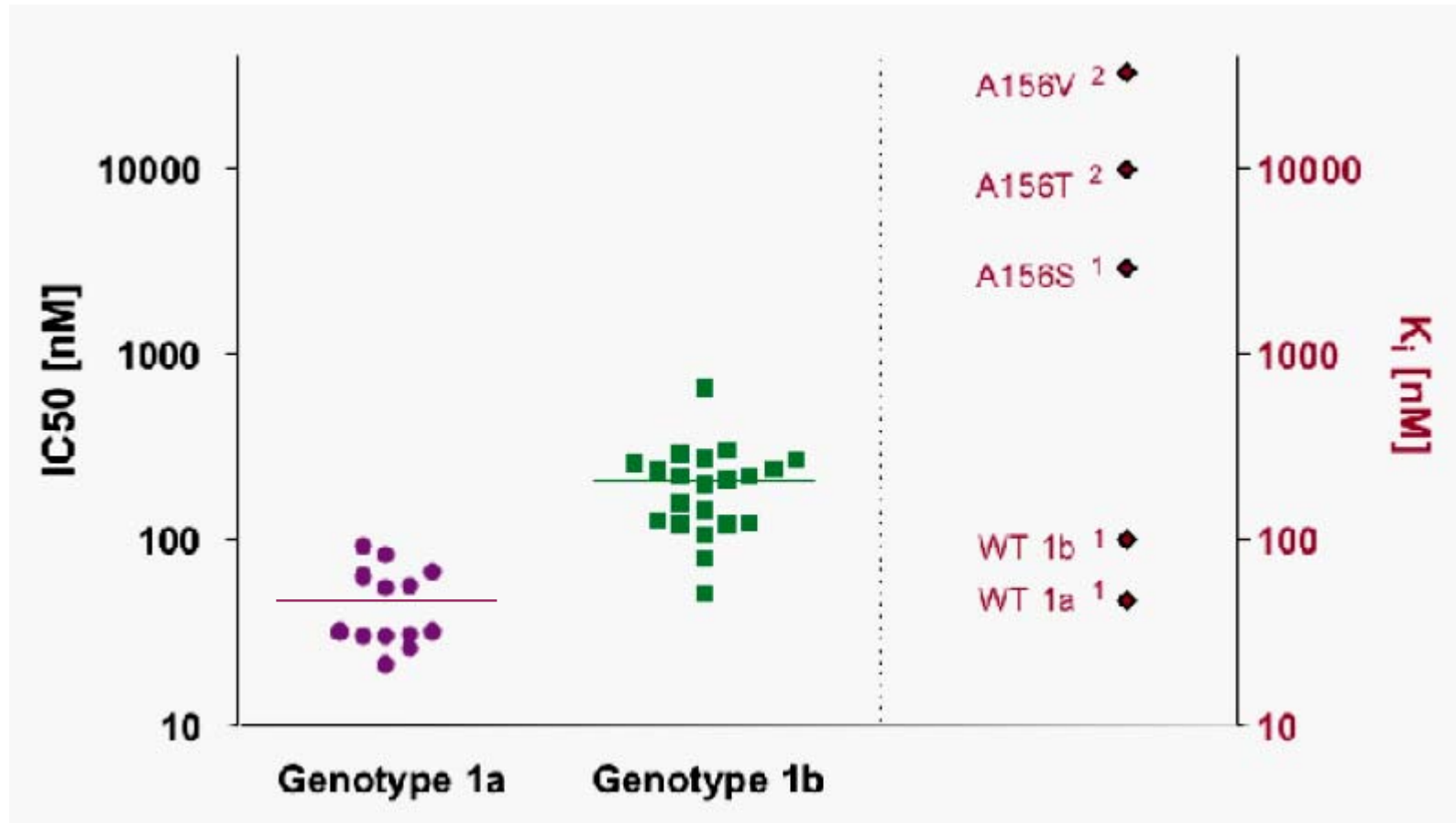
Replicon IC_{50}



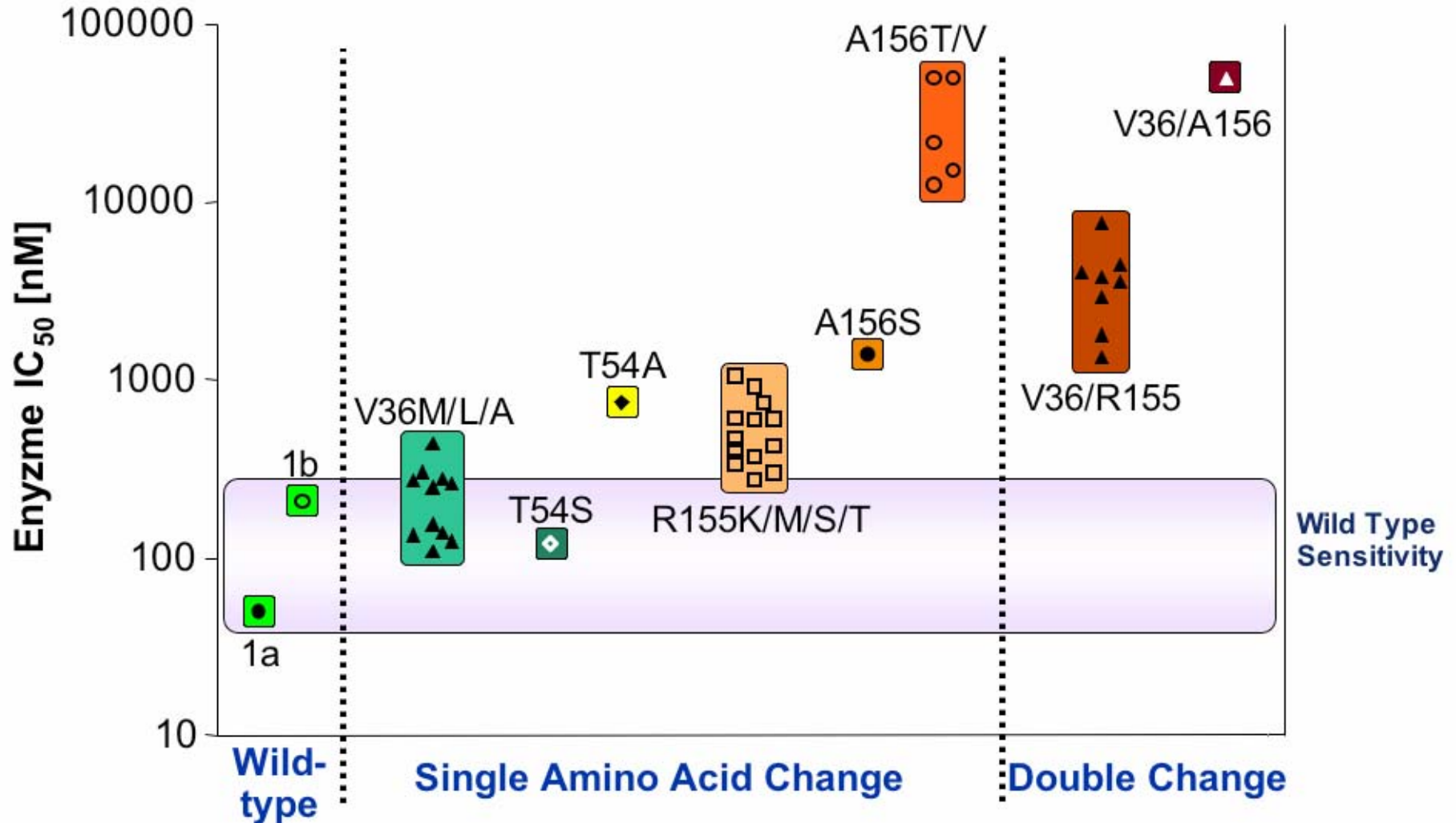
Enzyme K_i



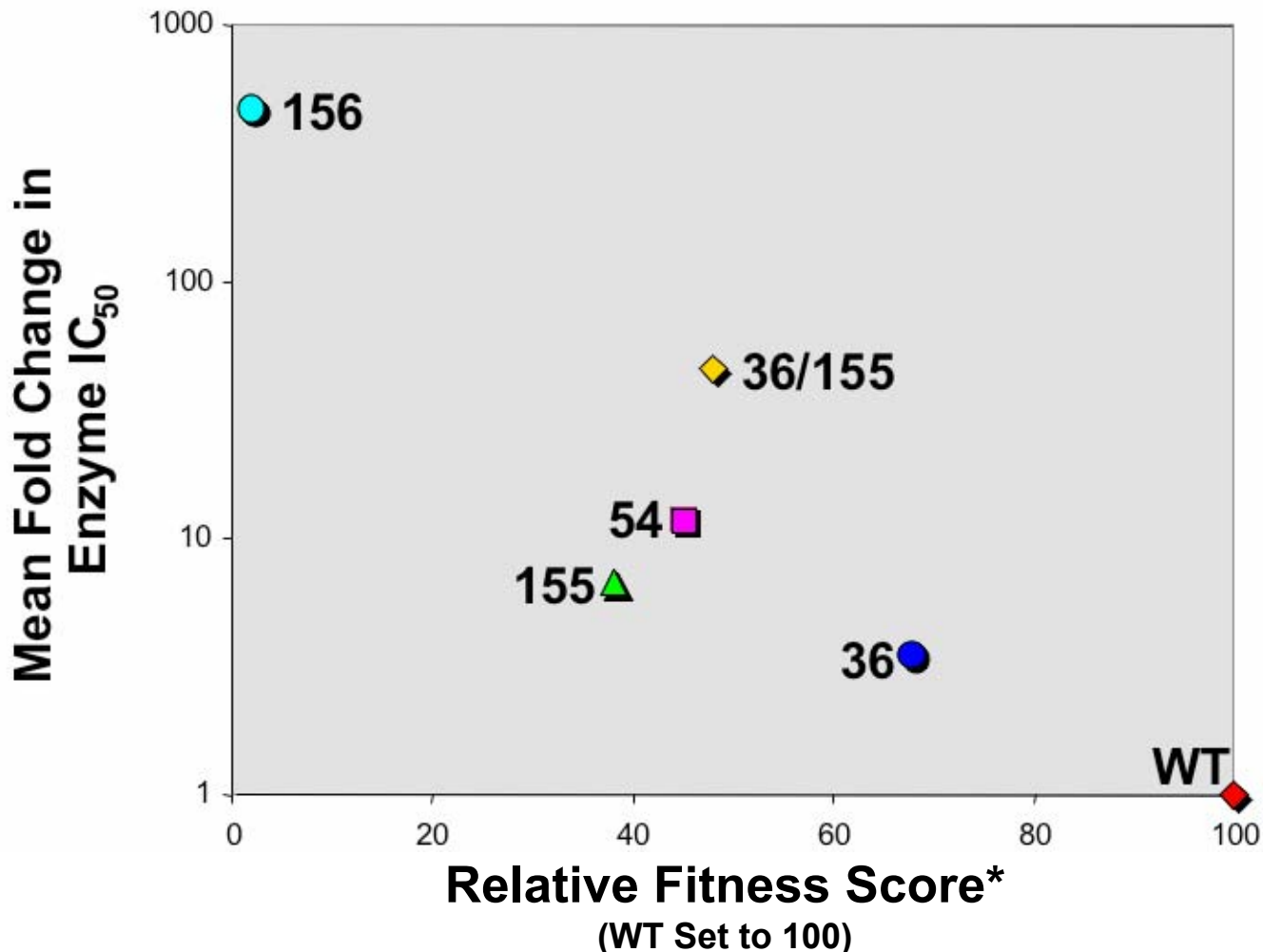
Baseline Variability in Susceptibility to VX-950



Sensitivity of Variant Proteases to VX-950



Reduced VX-950 Sensitivity is Associated with Low Relative Fitness Score

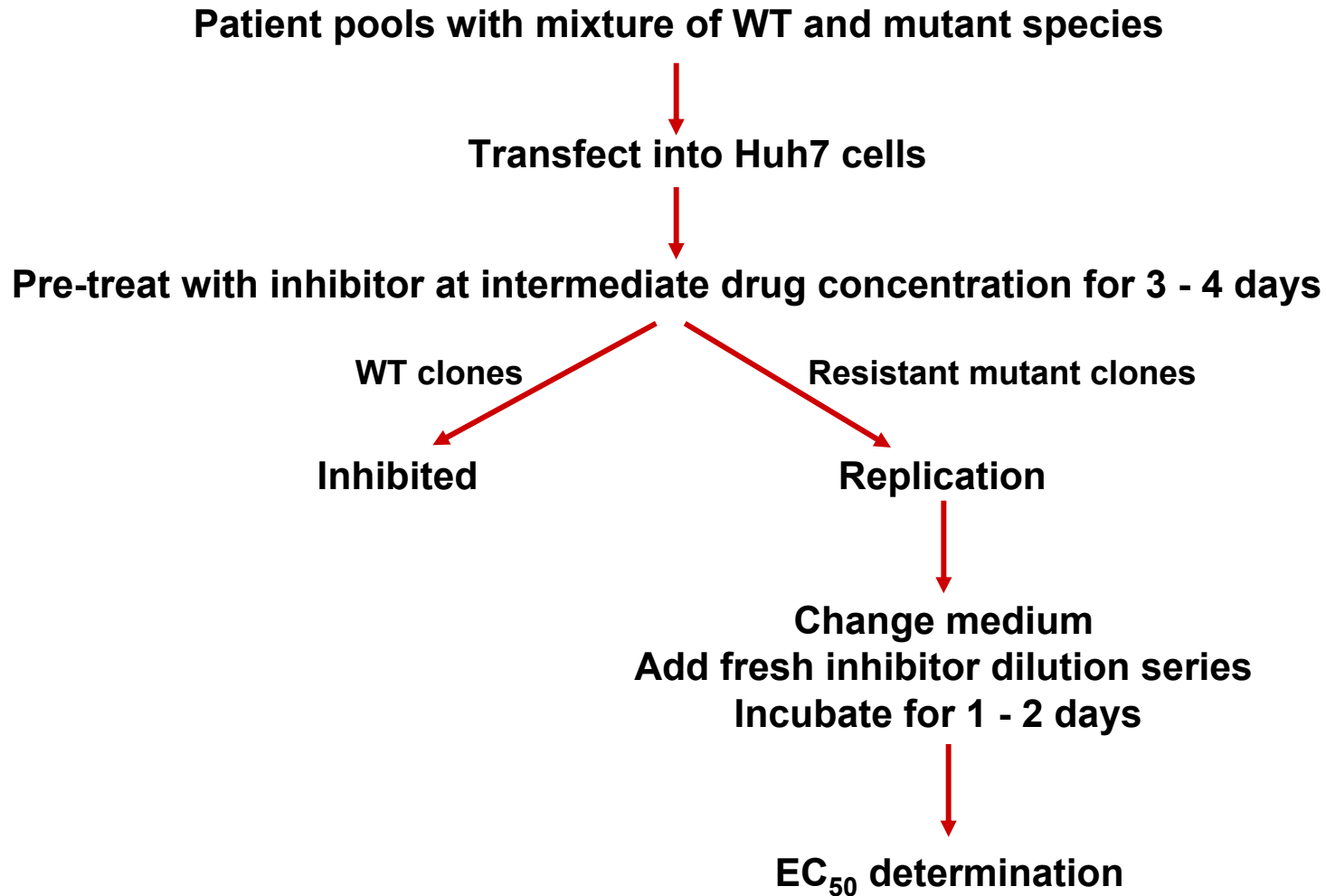


*as measured by the relative rate of replication for individual variants from end of dosing to 7-10 day F/U

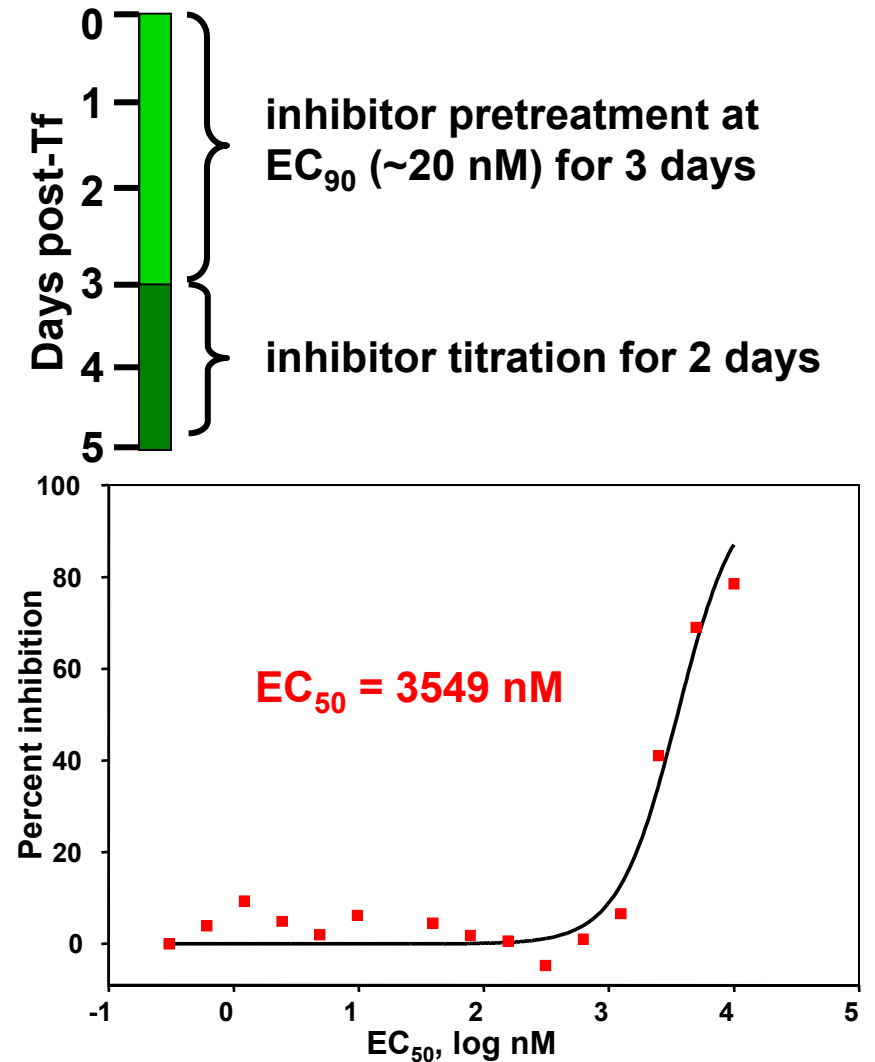
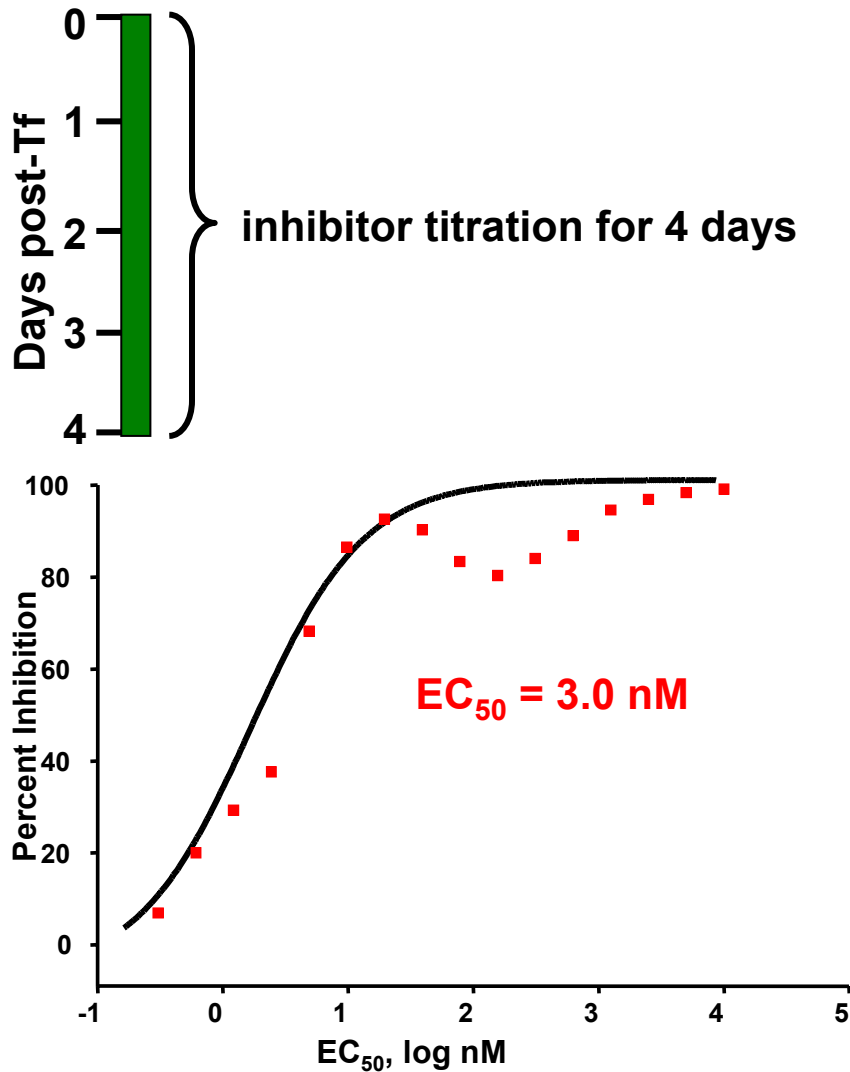
Minority Species

- All single and many double mutants (vs. patient's consensus) pre-exist at important frequencies
- Drug selection pressure enriches for variants with reduced susceptibility to varying extents
- Population-based genotype and phenotype assays miss low levels of specific variants (<5-10% or higher)
- Clinically appropriate sensitivity not yet defined, even for HIV-1

Isolation of resistant mutant species from mixed pools by drug pretreatment



Phenotype of A-837093-resistant mutants from day 5 HCV genotype 1a-infected chimpanzee pool



Interpretation Issues

- IC_{50} , IC_{90} etc.
 - *In vitro* IC_{50} does not necessarily reflect *in vivo* potency
 - Dependent on cell line used (esp. NIs)
 - Need to interpret relative to free drug level in plasma or liver, etc.
 - Important for TDM, IQ calculation
- Fold-change (FC)
 - More reproducible assay “deliverable”
 - Internally controlled
 - More comparable across assays
 - What reference virus to use (GT-specific?)

Interpretation Issues

- Cutoffs

- Before correlations between FC and clinical response are known, cannot claim “activity” or “resistance” based on arbitrary criteria
 - HIV-1 examples: tipranavir, tenofovir
- Describe data in relative terms i.e. “reduced susceptibility vs. control”
- Just because a mutation selected *in vitro* confers high level resistance does not mean less (or more) dramatic reductions in susceptibility are not relevant
 - HIV-1 examples: M184V and lamivudine; K103N and NNRTIs

HIV Drug Resistance Cutoffs

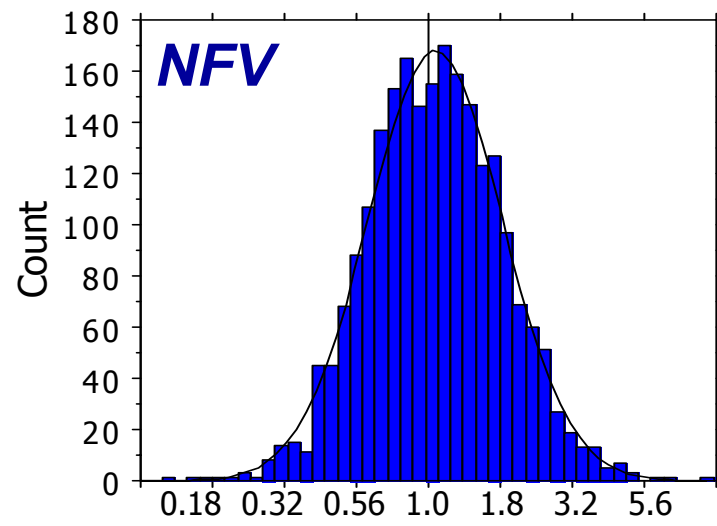
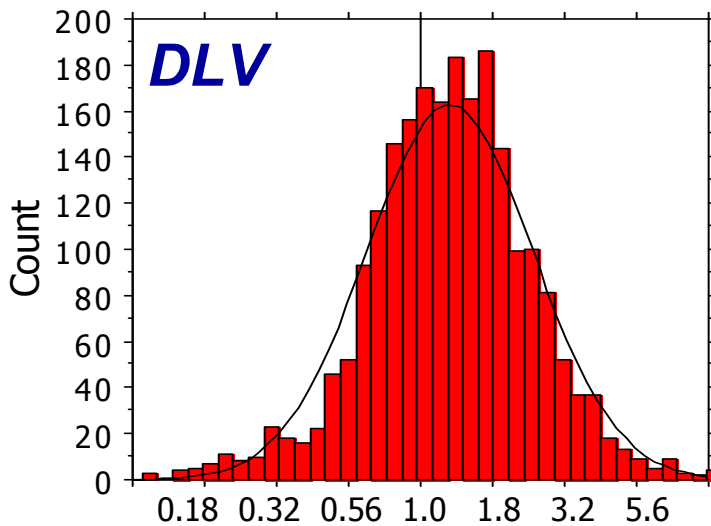
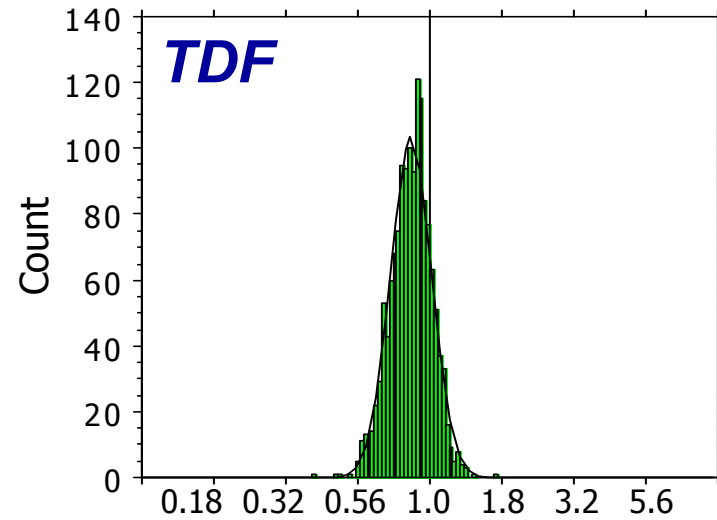
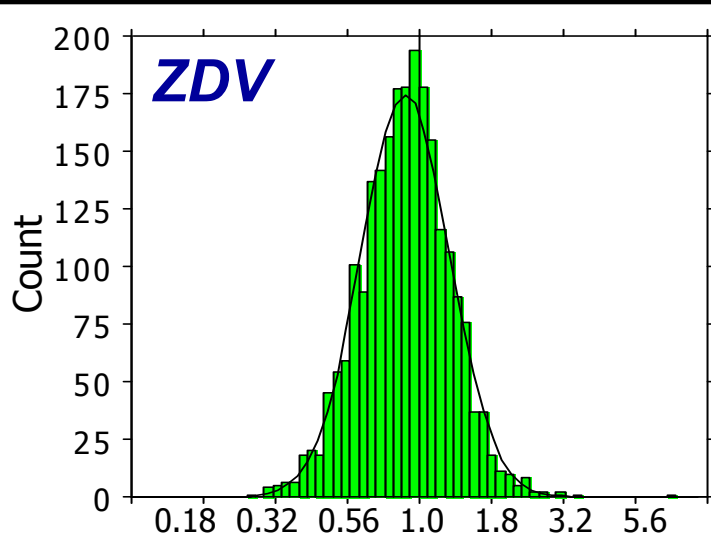
- Clinical cutoffs :
 - based on outcome data from clinical trials
- Biological cutoffs :
 - based on natural variability of wild-type viruses from patients
- Technical cutoffs :
 - based on assay variability with repeated testing of patient samples

Clinical Relevance

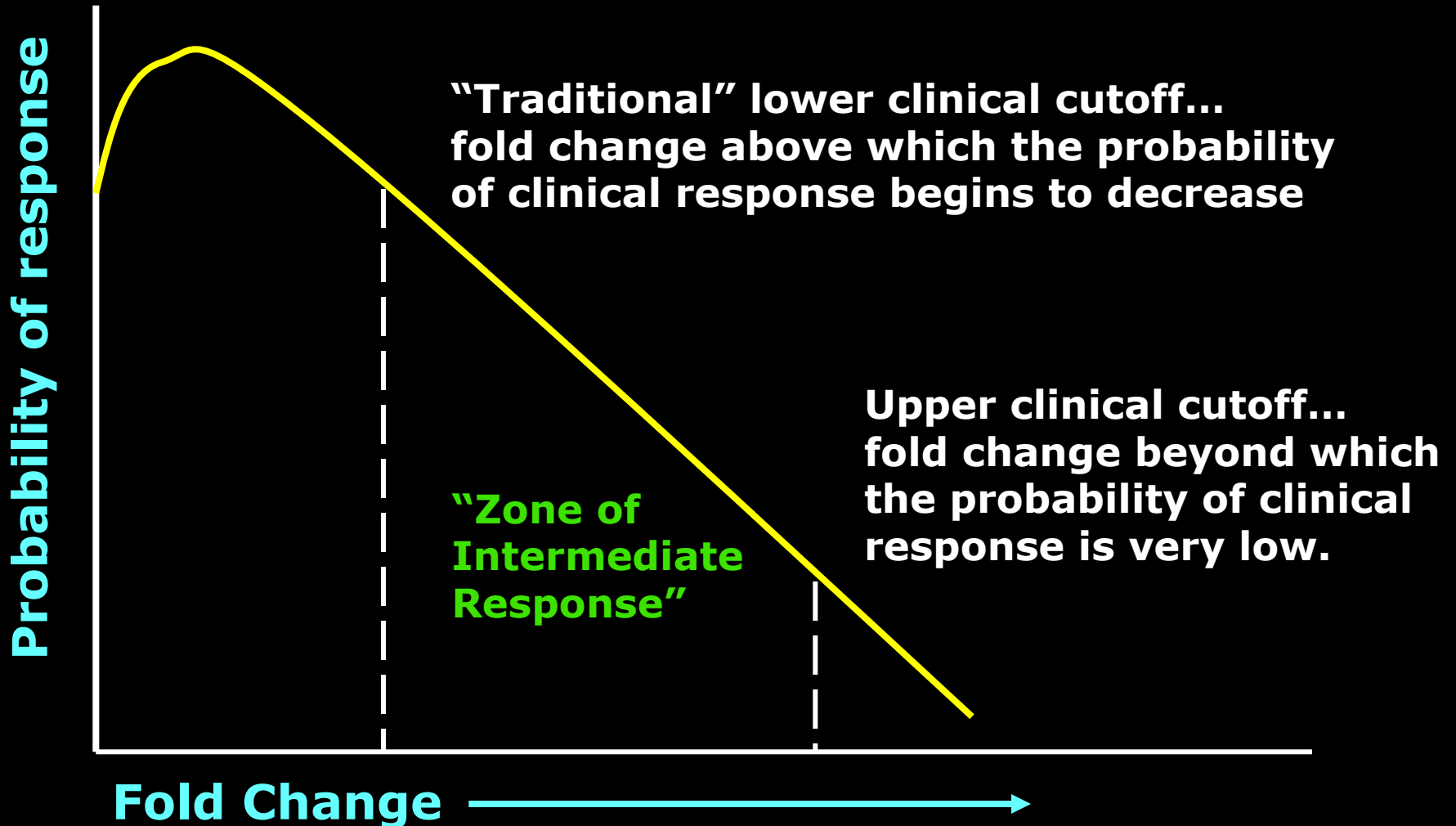
Highest

Moderate

Natural Variation in Drug Susceptibility



Clinical Cutoffs



Replicon-Based Systems: Questions

- Effect(s) on replication and/or drug susceptibility of patient virus chimeras of...
 - Cell culture adaptive mutations?
 - Cured cell lines?
 - Patient sequence/vector compatibility? (subtype/genotype mismatch)
 - 1a, 1b, 2a – does it matter?
 - Boundaries of patient-derived sequence
 - NS5B (need 3'UTR?)
 - NS3 (need helicase, NS4A?)
 - Lack of structural proteins, NS2, p7?

Questions

- Sensitivity of replication efficiency to patient-vector incompatibility
 - Must use caution when interpreting activity data, ≠ “fitness”
- Minority species assays
 - HIV-1 experience: still evolving, technology moving faster than clinical correlates
 - Cost issues
 - Sensitivity: how low can you go? How low do you need to go?

Summary

- Replicon-based phenotyping looks feasible
 - NS5B: 60-90% or GT1 patient samples OK
 - NNI variability observed
 - Non-GT1??
 - NS3/4A: limited data, may have to limit amplicon to PR
- Minority species
 - Are they more important than in HIV-1?
 - Routine detection would require a paradigm shift
- Interpretation is key
 - Learn from HIV-1 experience

Acknowledgements

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