Virco®TYPE HIV-1 Phenotype

(what's inside the box?)

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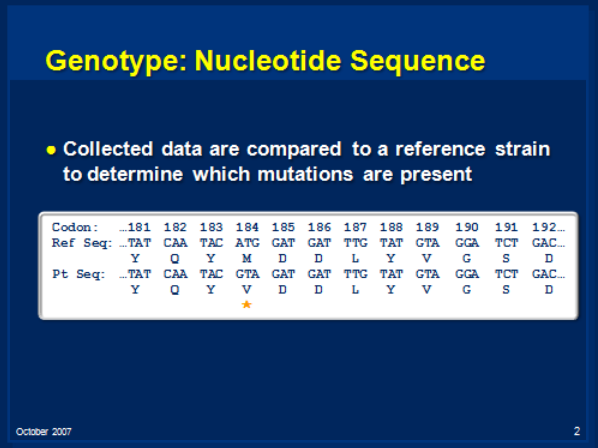
November 6, 2009

Outline

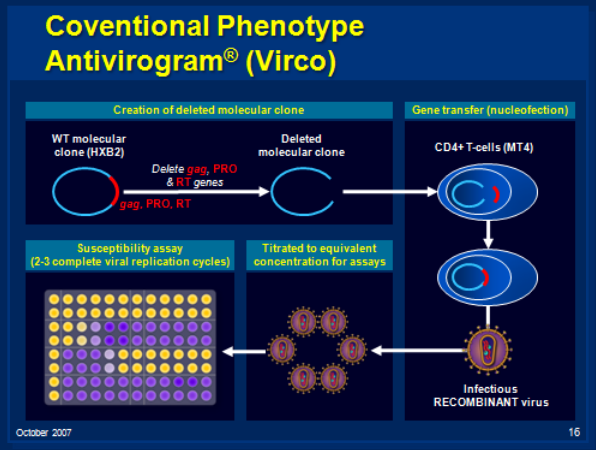
- Estimating fold-change from genotypic data
  - Vermeiren H et al. J Virol Methods (2007); 145:47-45
- Comparable results Phenosense™
  - Van Houtte M et al. J Med Virol (2009); 81:1702-1709
- An example
  - Mixtures, mutation pairs (184V, 65R) and non-IAS mutations

Mechanics of Resistance

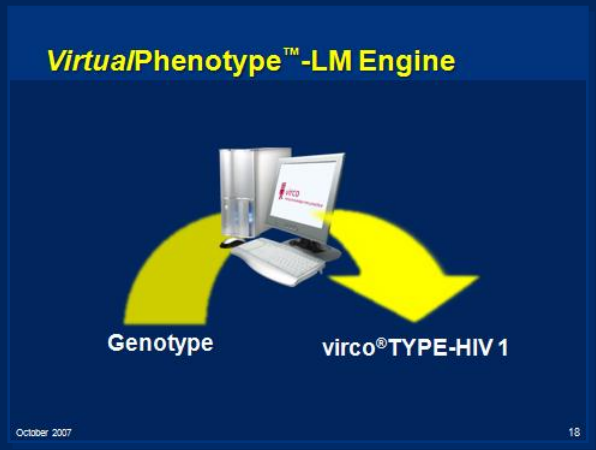
- Change in the molecular target of a drug
  - HIV RT enzyme: 400 codons
  - Protease enzyme: 99 codons



Genotypic Sequence



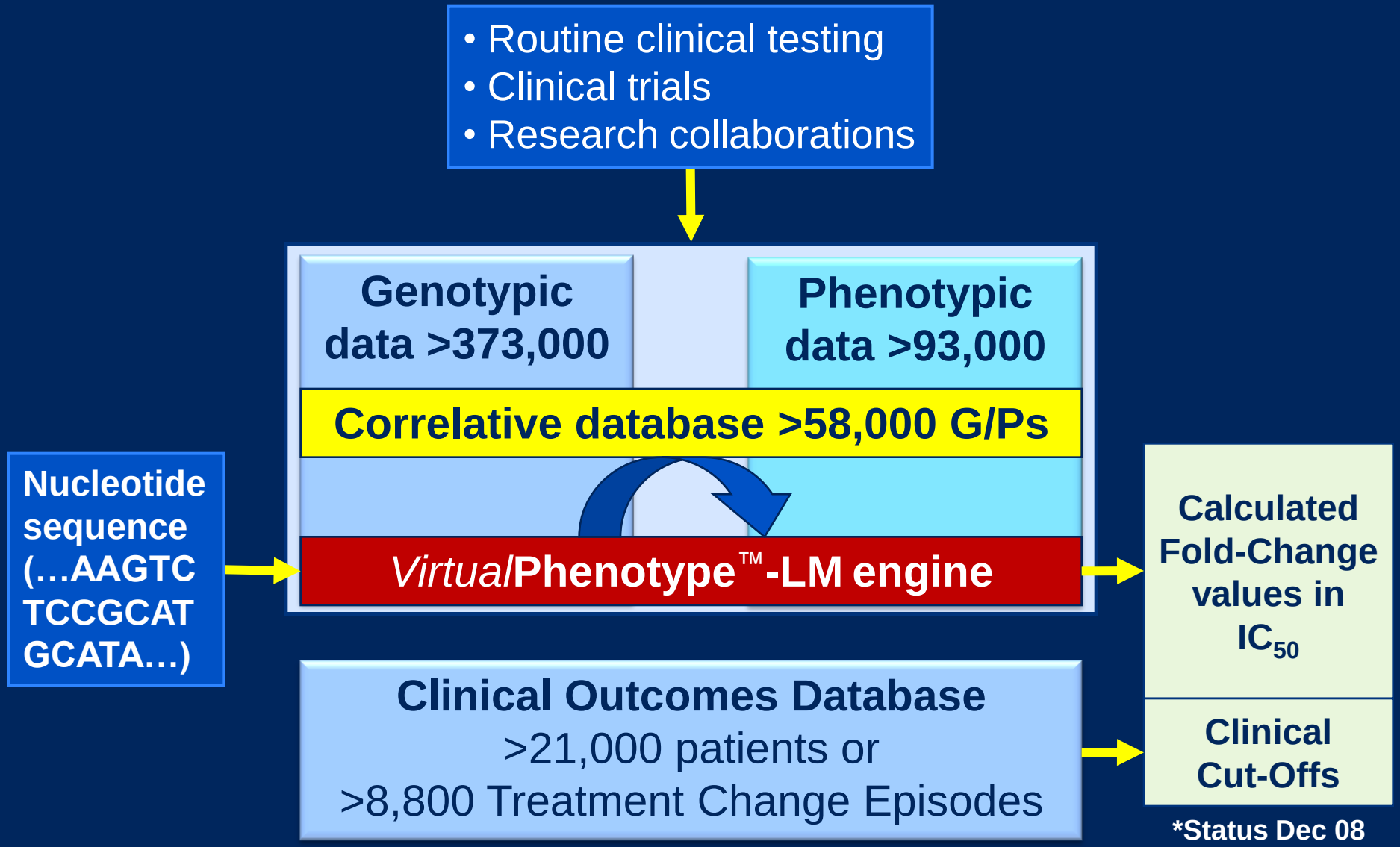
Measured Fold Change (FC)



Calculated Fold Change (FC)

Estimated fold change from genotypic data

Vermeiren H et al. J Virol Methods 2007; 145:47-5500



Linear Regression Model

- General Formula: $y = \beta_o + \beta_1 x_1 + e$

- Estimating SBP from demographic factors
  - y (dependent variable) = SBP (mmHg)
  - B_o = mean SBP in general population
  - $B_1 x_1$ = (weight factor) x (risk factor, i.e. age, gender, etc)

- Estimating FC from mutations
  - y (dependent variable) = Fold Change (FC)
  - B_o = FC of wild-type virus
  - $B_1 x_1$ = (weight factor) x (mutation)

Calculating the Fold-Change: Tipranavir Example

Protease Mutations Detected

3I, 10I, 14R, 19I, 24I, 37N, 41K, 46I, 53Y, 54V, 55R, 63P, 64V, 71V, 82T, 84V

From page 2 of the virco®TYPE HIV-1 Report

All Mutations Detected (HXB2 Reference Sequence)	
PR:	3I, 10I, 14R, 19I, 24I, 37N, 41K, 46I, 53Y, 54V, 55R, 63P, 64V, 71V, 82T, 84V
RT:	20R, 35I, 41L, 74V, 103N, 169D, 181C, 184V, 200A, 214F, 215Y, 272A, 286A, 288S, 293V, 376A, 390R

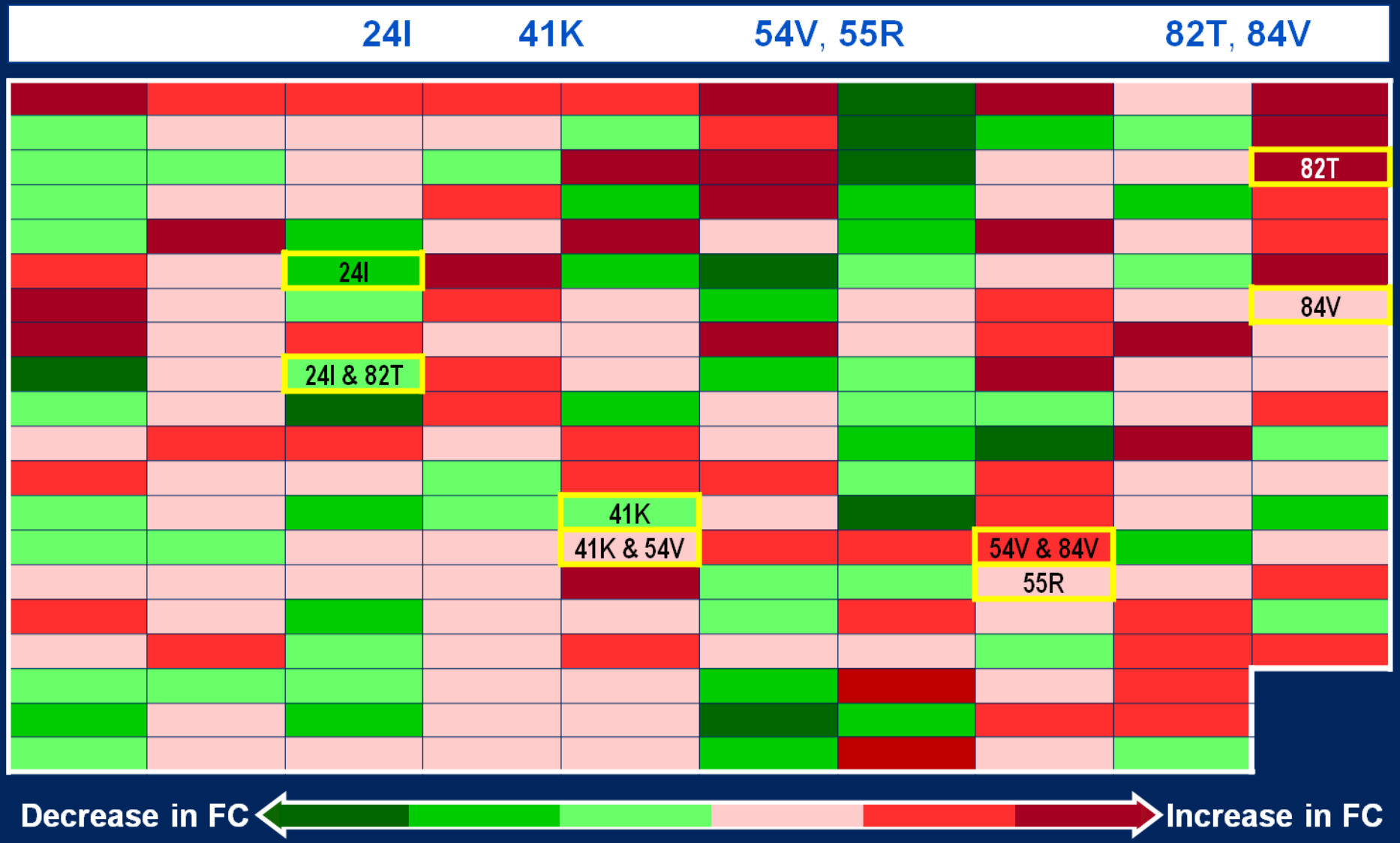
*DB0802 implemented on DEC 2008; report #ASJ001979

FC Assessment: Example of Tipranavir Protease Mutation Analysis

3I, 10I, 14R, 19I, 24I, 37N, 41K, 46I, 53Y, 54V, 55R, 63P, 64V, 71V, 82T, 84V

10C & 33F	13A & 47V	20T & 73T	33I & 35G	35N	43T & 85L	48Q	54A & 84V	60E	82L
10F	13V & 15V	20T & 84V	33I & 36I	35N & 43T	45I	48S	54L	60E & 71V	82S
10F & 47V	13V & 34Q	20V	33I & 82A	35N & 70E	45Q	48V	54L & 76V	60E & 82A	82T
10F & 54M	13V & 36I	22V	33I & 95F	35N & 82F	45V	48V & 54A	54L & 82A	60E & 95V	83D
10F & 58E	13V & 43S	24F & 60E	33V	36A	46L	48V & 54S	54L & 82S	66V	83D & 84V
10F & 82C	13V & 71L	24I	33V & 43T	36I & 83D	46L & 48M	48V & 54V	54M	69K	84A
10F & 82F	13V & 71V	24I & 33F	33V & 54V	36I & 84V	46L & 50L	48V & 71V	54M & 83D	71V & 73T	84V
10F & 82L	13V & 82F	24I & 50V	34D	36L & 53L	46L & 80I	48V & 82A	54M & 88D	71V & 74E	85V
10F & 84A	13V & 84V	24I & 82T	34D & 58E	36L & 84V	46L & 82L	48V & 84V	54S	74A	88D
10F & 84V	14T	30N	34N & 82A	36V & 82F	46L & 84V	50L	54S & 74S	74P	88G
10I & 13A	15V & 43I	30N & 50V	34Q & 36I	36V & 84V	47V	50V	54S & 82A	74P & 82S	88S
10I & 33M	15V & 95F	30N & 88D	34Q & 54V	38W	47V & 54M	50V & 58E	54S & 84V	74P & 84V	89M
10I & 82F	16A	33.1Q	35D	41K	47V & 54V	50V & 70E	54T & 82T	74S	89V & 95L
10I & 82I	18H	33F	35D & 36I	41K & 54V	47V & 69K	50V & 76V	54V & 84V	76V	90M
10V	20R & 35D	33F & 36L	35D & 36V	41T & 70E	47V & 82A	53L	55R	79S	91P
10V & 34A	20R & 53L	33F & 48A	35D & 54M	43I & 55R	47V & 82I	53L & 82F	55R & 60E	82C	95F
10V & 84V	20R & 70E	33F & 50V	35D & 54V	43Q & 73T	47V & 84V	53L & 82I	55R & 95F	82C & 95F	95V
10V & 88D	20T & 33F	33F & 60E	35D & 84V	43T	48A	54A	58E	82F & 89V	
10Y & 13V	20T & 41K	33F & 66L	35D & 89V	43T & 82F	48E	54A & 82A	58E & 80I	82G	
12S & 69K	20T & 53L	33F & 82F	35G	43T & 82T	48M	54A & 82F	58E & 89V	82I & 89V	

FC Assessment: Example of Tipranavir Protease Mutation Analysis



Calculating the Fold-Change: Example of Tipranavir Mutation Analysis

PI Mutations Detected **and Evaluated**
3I, 10I, 14R, 19I, **24I**, 37N, **41K**, 46I, 53Y, **54V**, **55R**, 63P, 64V, 71V, **82T**, **84V**

Mutations	RWF
24I	-0.18198
41K	-0.06075
55R	0.05418
82T	0.36480
84V	0.16181
24I & 82T	-0.10545
41K & 54V	0.03803
54V & 84V	0.20493
Intercept (no mutations)	-0.06039

Resistance Weight Factor: weight and direction for mutations which **impact** TPV

Log(FC) = 0.415

FC = $10^{0.415}$ = 2.6

A Direct Comparison between VirtualPhenotype™-LM & Phenosense™

- Used phenotypic and genotypic data in Stanford Database to compare FC values estimated by Virco™ linear model with FC values measured by the Monogram Phenosense™ assay
  - HIV drugs with 287 to 902 genotype-phenotype data pairs
  - Sequences exhibiting amino acid mixtures
- Pearson's correlation coefficient to compare estimated FC with measured FC

Van Houtte M, et al. J Med Virol 2009; 81:1702-1709

Pearson's Correlation: NRTI & NNRTI

ZDV

3TC

DDI

D4T

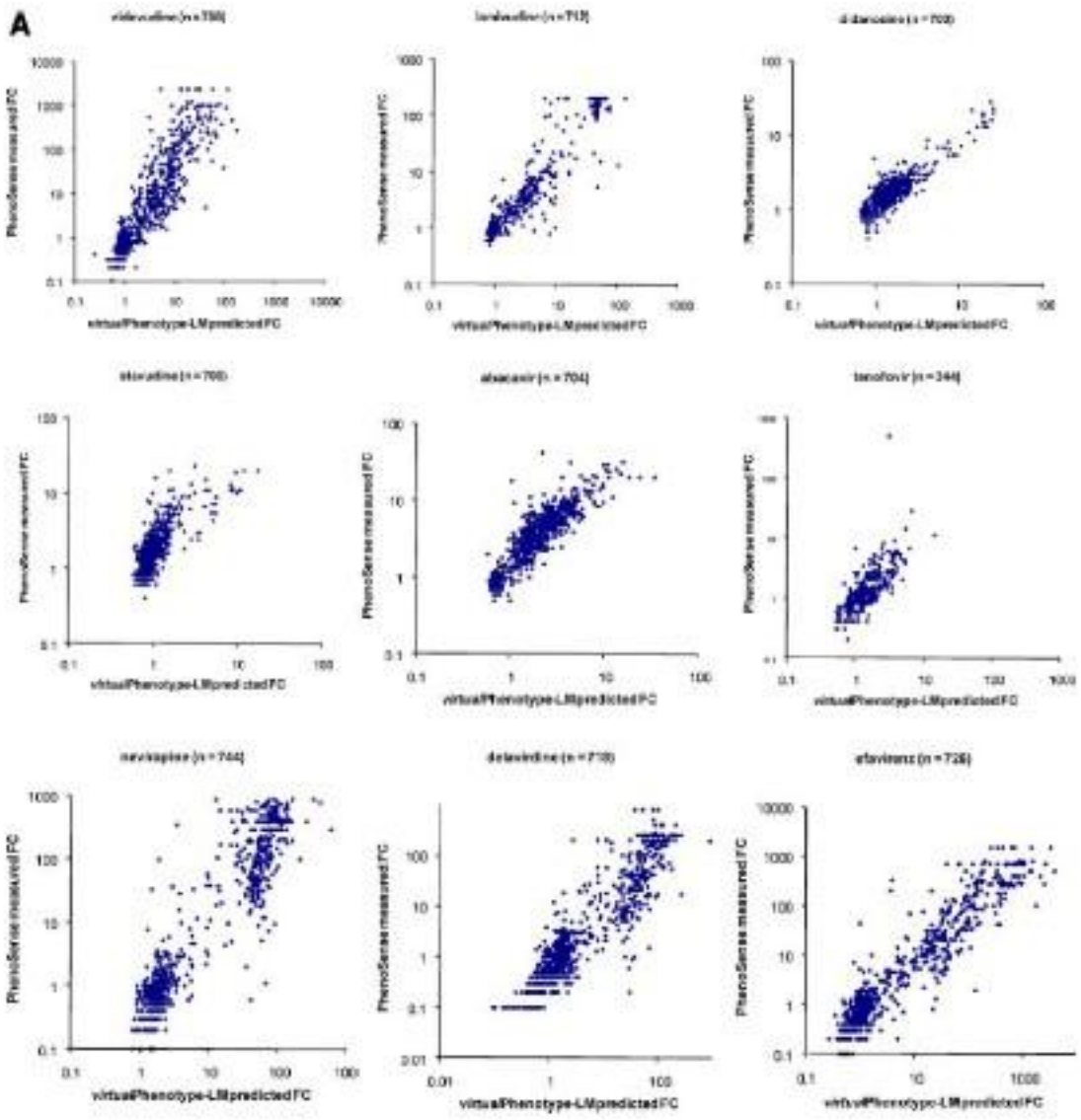
ABC

TDF

NVP

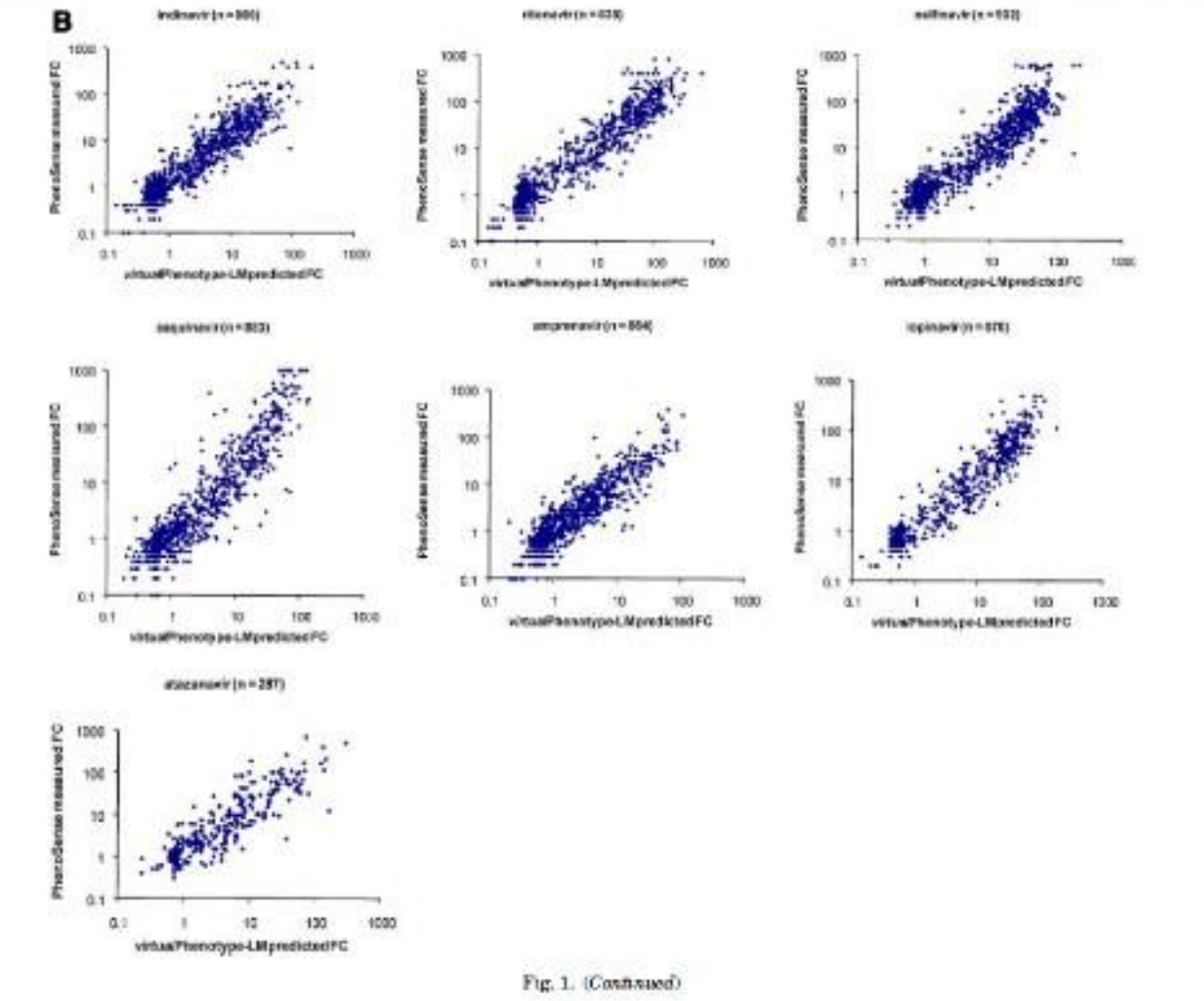
DLV

EFV



Pearson's Correlations: PIs

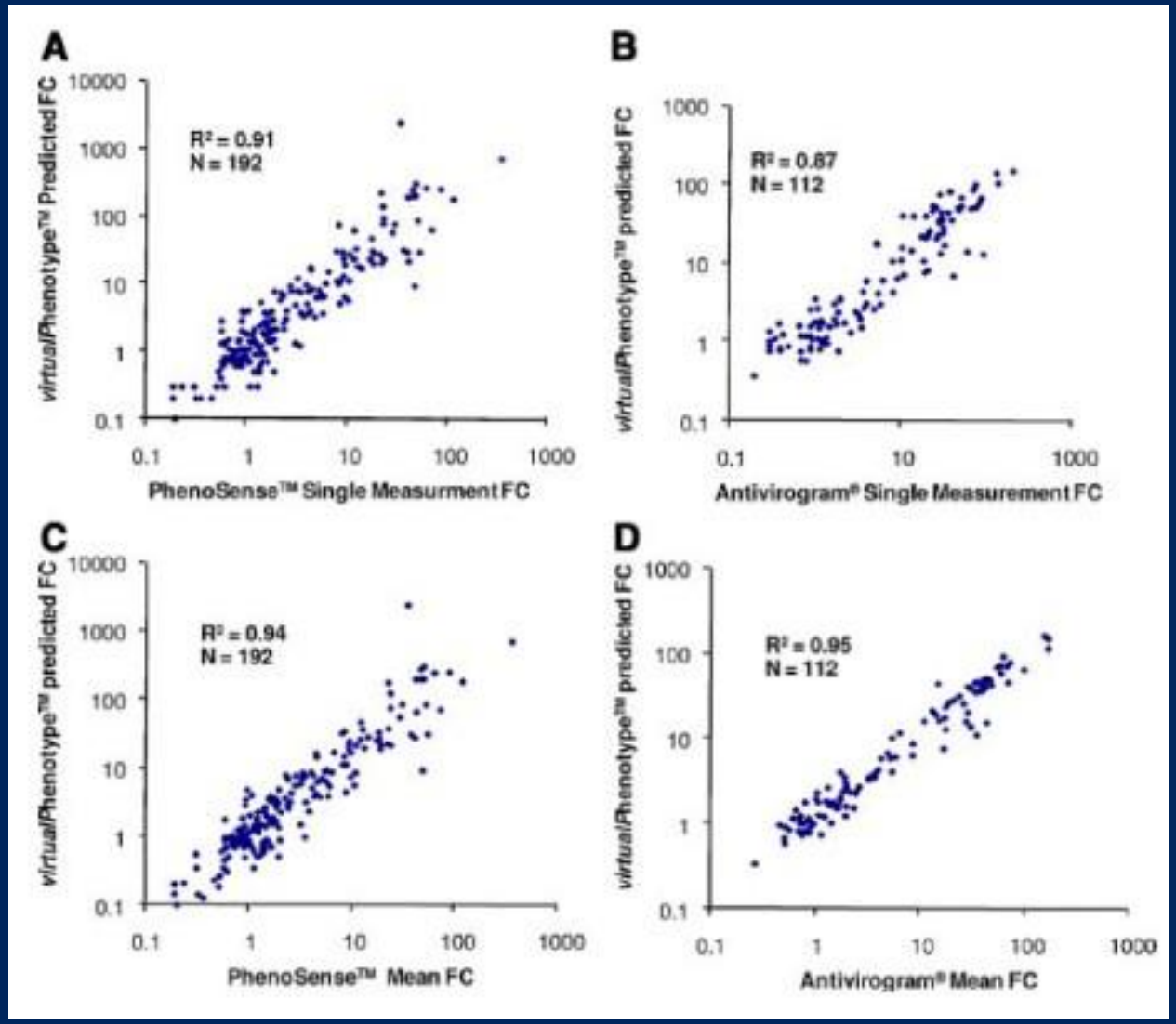
- IDV
- RTV
- NLF
- SQV
- APV
- LPV
- ATV



Predicted vs. Measured FC (Phenosense™ and Antivirogram®)

Single FC measurements

Mean of Multiple FC measurements



Interpretation of resistance

Drug class	Drug	Pearson's correlation coefficient (R)	Clinical or biological cut-offs[a]		Major discordances (%)	No. discordant calls with VT/PS FC ratio ≤0.4 or ≥2.5[b]
			virco®TYPE HIV-1	PhenoSense™		
NRTI	AZT	0.90	2.7	1.9	9.6	30|4
	3TC	0.97	**1.0–3.4**	3.5	2.4	0|9
	ddI	0.89	**0.9–2.6**	1.3–2.2	0.0	0|0
	d4T	0.76	**0.9–2.0**	1.7	6.3	18|0
	ABC	0.89	**0.8–1.9**	4.5–6.5	8.1	0|0
	TDF	0.77	**0.9–2.1**	1.4–4.0	1.2	0|1
NNRTI	NVP	0.94	5.5	4.5	3.1	7|12
	DLV	0.91	10.5	6.2	7.1	15|28
	EFV	0.94	3.4	3.0	4.1	6|13
PI	IDV	0.93	2.4	2.1	7.4	18|4
	IDV/r		**10.6–40.1**	10	8.1	38|1
	RTV	0.95	2.3	2.5	4.5	15|6
	NFV	0.93	2.2	3.6	8.0	5|14
	SQV	0.92	1.8	1.7	9.0	16|15
	SQV/r		**7.1–26.5**	**2.3–12.0**	2.7	22|0
	FPV	0.91	2.2	2.0	10.3	24|9
	FPV/r		**1.3–11.4**	**4.0–11.0**	0.5	0|4
	LPV/r	0.95	**9.7–56.1**	**9.0–55.0**	0.0	0|0
	ATV/r	0.88	**2.7–32.9**	5.2	3.8	10|1
Overall		0.90				

- Overall major discordances low for all drugs (≤3.8%)
  - Higher for D4T (6.3%), ABC (8.1%), AZT (9.6%), IDV/r (8.1%)

Biologic vs. Clinical Cut-off values

- **Biologic Cut-off (BCO) define what is resistant and non-resistant based on how the patient's virus responds to a drug *in vitro***

- **Clinical Cut-off (CCO) values refer to the fold-change of virus susceptibility above which the drug has less activity *in-vivo***

Uniform and Consistent 4-Step Methodology to Define Clinical Cut-Off Values for All Drugs

Step 1: Collect clinical outcome data and create analysis datasets (one per drug)

Step 2: Develop models (one per drug) of virologic response as a function of baseline FC as predicted by virco®TYPE HIV-1 and other variables

Step 3: Define clinical cut-offs

- **“**Lower” — FC at which response begins to be lost
- “Upper” — FC at which response is essentially gone

Step 4: Validation

Bart W et al. J Virol Method 2009; [Epub]

Case Study: Patient BH: (First-line Treatment Failure)

This case study is for discussion and education purposes only and does not constitute professional medical advice. The information provided in the case study should not be relied upon as the basis for making patient management decisions. This case study is not intended to show that any line of therapy is any more or less effective than any other therapy.

Patient 1: Treatment History

Date	Meds	CD4	HIV RNA	Comments
2002	None	441	92,526	Treatment deferred
2003	None	265	110,611	Start AZT/3TC, LPV/r; claims good adherence, tolerance; Makes most appointments; Episodes of >6 months w/o labs
Wk 24	AZT/3TC, LPV/r	>400	2,615	Pt preference: no changes; Provider: tolerate low level viremia given immunologic response
10/2006	AZT/3TC, LPV/r	>400	~2,600	
01/2007	AZT/3TC, LPV/r	>500	~2,600	Patient declines Hep C therapy; Resistance testing obtained

Patient 1: Resistance Test Report Page 1

virco

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vircoTYPE HIV-1

powered by VirtualPhenotype-LM

The Complete Resistance Analysis

CONFIDENTIAL

Patient/Sample Details			Physician Details
Patient Name	Sample ID	318299	
	Collection Date		
Patient ID	Received by Virco		
National Identifier	Project	101024	
Date of birth	Report Date		Physician:
Gender	Virco ID	VRN000857	

SUMMARY REPORT

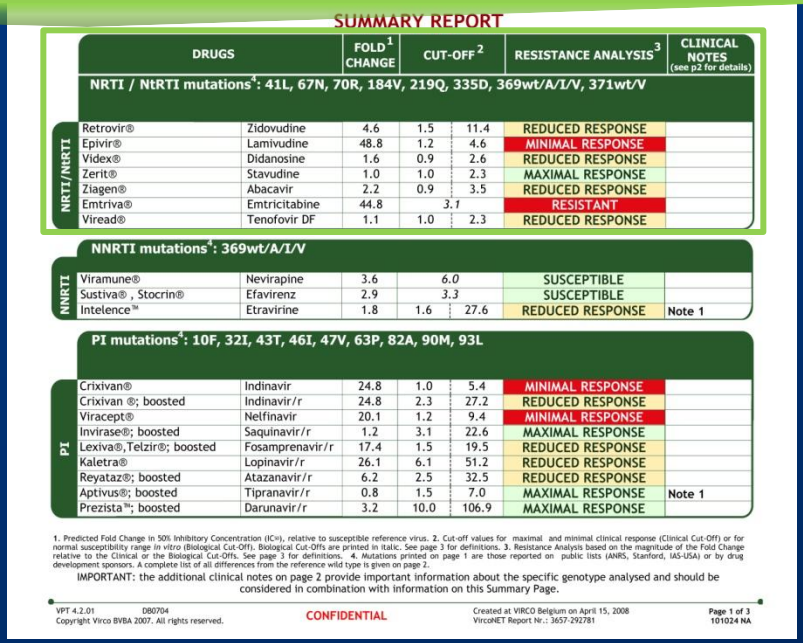
	DRUGS		FOLD[1] CHANGE	CUT-OFF[2]		RESISTANCE ANALYSIS[3]	CLINICAL NOTES (see p2 for details)
	NRTI / NtRTI mutations[4]: 41L, 67N, 70R, 184V, 219Q, 335D, 369wt/A/I/V, 371wt/V						
NRTI/NtRTI	Retrovir®	Zidovudine	4.6	1.5	11.4	REDUCED RESPONSE	
	Epivir®	Lamivudine	48.8	1.2	4.6	MINIMAL RESPONSE	
	Videx®	Didanosine	1.6	0.9	2.6	REDUCED RESPONSE	
	Zerit®	Stavudine	1.0	1.0	2.3	MAXIMAL RESPONSE	
	Ziagen®	Abacavir	2.2	0.9	3.5	REDUCED RESPONSE	
	Emtriva®	Emtricitabine	44.8	*3.1*		RESISTANT	
	Viread®	Tenofovir DF	1.1	1.0	2.3	REDUCED RESPONSE	
	NNRTI mutations[4]: 369wt/A/I/V						
NNRTI	Viramune®	Nevirapine	3.6	*6.0*		SUSCEPTIBLE	
	Sustiva® , Stocrin®	Efavirenz	2.9	*3.3*		SUSCEPTIBLE	
	Intelence™	Etravirine	1.8	1.6	27.6	REDUCED RESPONSE	Note 1
	PI mutations[4]: 10F, 32I, 43T, 46I, 47V, 63P, 82A, 90M, 93L						
PI	Crixivan®	Indinavir	24.8	1.0	5.4	MINIMAL RESPONSE	
	Crixivan ®; boosted	Indinavir/r	24.8	2.3	27.2	REDUCED RESPONSE	
	Viracept®	Nelfinavir	20.1	1.2	9.4	MINIMAL RESPONSE	
	Invirase®; boosted	Saquinavir/r	1.2	3.1	22.6	MAXIMAL RESPONSE	
	Lexiva®,Telzir®; boosted	Fosamprenavir/r	17.4	1.5	19.5	REDUCED RESPONSE	
	Kaletra®	Lopinavir/r	26.1	6.1	51.2	REDUCED RESPONSE	
	Reyataz®; boosted	Atazanavir/r	6.2	2.5	32.5	REDUCED RESPONSE	
	Aptivus®; boosted	Tipranavir/r	0.8	1.5	7.0	MAXIMAL RESPONSE	Note 1
	Prezista™; boosted	Darunavir/r	3.2	10.0	106.9	MAXIMAL RESPONSE	

1. Predicted Fold Change in 50% Inhibitory Concentration (IC_{50}), relative to susceptible reference virus. 2. Cut-off values for maximal and minimal clinical response (Clinical Cut-Off) or for normal susceptibility range *in vitro* (Biological Cut-Off). Biological Cut-Offs are printed in italic. See page 3 for definitions. 3. Resistance Analysis based on the magnitude of the Fold Change relative to the Clinical or the Biological Cut-Offs. See page 3 for definitions. 4. Mutations printed on page 1 are those reported on public lists (ANRS, Stanford, IAS-USA) or by drug development sponsors. A complete list of all differences from the reference wild type is given on page 2.

IMPORTANT: the additional clinical notes on page 2 provide important information about the specific genotype analysed and should be considered in combination with information on this Summary Page.

Patient 1: Resistance Test Report Page 1 (NRTI/NtRTI)

	DRUGS		FOLD CHANGE [1]	CUT-OFF [2]		RESISTANCE ANALYSIS [3]	CLINICAL NOTES (see p2 for details)
	NRTI / NtRTI mutations[4]: 41L, 67N, 70R, 184V, 219Q, 335D, 369wt/A/I/V, 371wt/V						
NRTI/NtRTI	Retrovir®	Zidovudine	4.6	1.5	11.4	REDUCED RESPONSE	
	Epivir®	Lamivudine	48.8	1.2	4.6	MINIMAL RESPONSE	
	Videx®	Didanosine	1.6	0.9	2.6	REDUCED RESPONSE	
	Zerit®	Stavudine	1.0	1.0	2.3	MAXIMAL RESPONSE	
	Ziagen®	Abacavir	2.2	0.9	3.5	REDUCED RESPONSE	
	Emtriva®	Emtricitabine	44.8	*3.1*		RESISTANT	
	Viread®	Tenofovir DF	1.1	1.0	2.3	REDUCED RESPONSE	



SUMMARY REPORT

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NRTI/NtRTI	Retrovir®	Zidovudine	4.6	1.5	11.4	REDUCED RESPONSE	
	Epivir®	Lamivudine	48.8	1.2	4.6	MINIMAL RESPONSE	
	Videx®	Didanosine	1.6	0.9	2.6	REDUCED RESPONSE	
	Zerit®	Stavudine	1.0	1.0	2.3	MAXIMAL RESPONSE	
	Ziagen®	Abacavir	2.2	0.9	3.5	REDUCED RESPONSE	
	Emtriva®	Emtricitabine	44.8	*3.1*		RESISTANT	
	Viread®	Tenofovir DF	1.1	1.0	2.3	REDUCED RESPONSE	
	NNRTI mutations[4]: 369wt/A/I/V						
NNRTI	Viramune®	Nevirapine	3.6	*6.0*		SUSCEPTIBLE	
	Sustiva® , Stocrin®	Efavirenz	2.9	*3.3*		SUSCEPTIBLE	
	Intelence™	Etravirine	1.8	1.6	27.6	REDUCED RESPONSE	Note 1
	PI mutations[4]: 10F, 32I, 43T, 46I, 47V, 63P, 82A, 90M, 93L						
PI	Crixivan®	Indinavir	24.8	1.0	5.4	MINIMAL RESPONSE	
	Crixivan ®; boosted	Indinavir/r	24.8	2.3	27.2	REDUCED RESPONSE	
	Viracept®	Nelfinavir	20.1	1.2	9.4	MINIMAL RESPONSE	
	Invirase®; boosted	Saquinavir/r	1.2	3.1	22.6	MAXIMAL RESPONSE	
	Lexiva®,Telzir®; boosted	Fosamprenavir/r	17.4	1.5	19.5	REDUCED RESPONSE	
	Kaletra®	Lopinavir/r	26.1	6.1	51.2	REDUCED RESPONSE	
	Reyataz®; boosted	Atazanavir/r	6.2	2.5	32.5	REDUCED RESPONSE	
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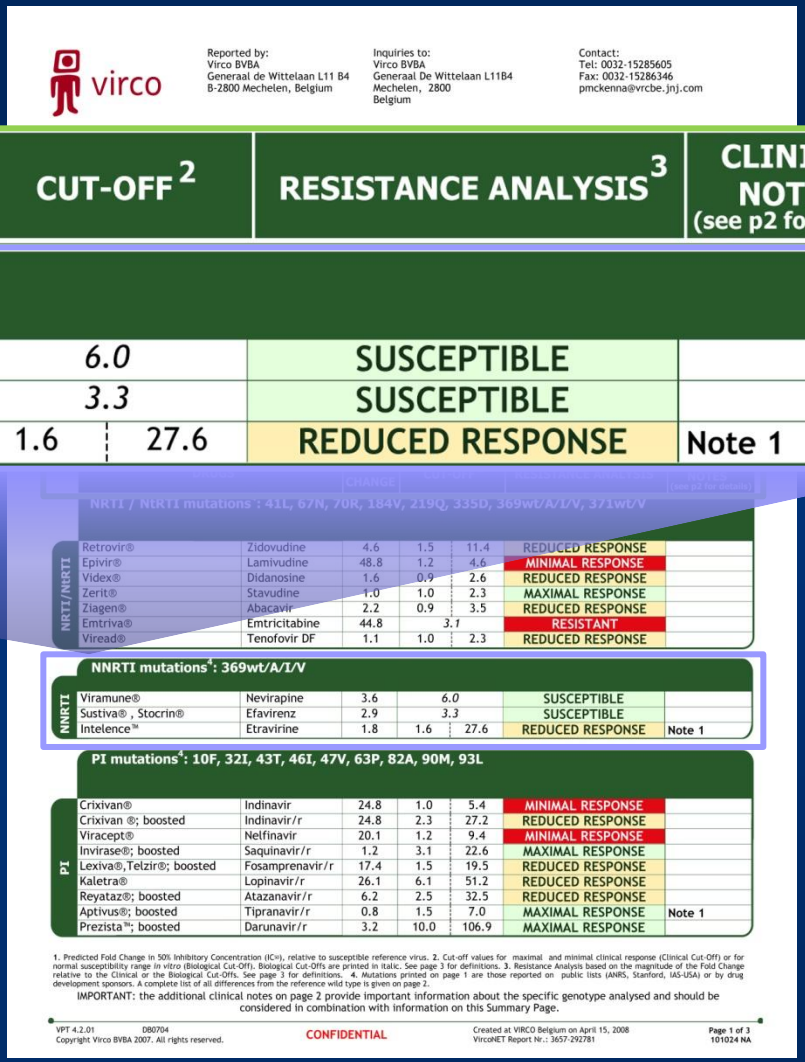
Patient 1: Resistance Test Report Page 1 (NNRTI)



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NNRTI	Sustiva® , Stocrin®	Efavirenz	2.9	*3.3*		SUSCEPTIBLE	
NNRTI	Intelence™	Etravirine	1.8	1.6	27.6	REDUCED RESPONSE	Note 1
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NRTI/NtRTI	Videx®	Didanosine	1.6	0.9	2.6	REDUCED RESPONSE	
NRTI/NtRTI	Zerit®	Stavudine	1.0	1.0	2.3	MAXIMAL RESPONSE	
NRTI/NtRTI	Ziagen®	Abacavir	2.2	0.9	3.5	REDUCED RESPONSE	
NRTI/NtRTI	Emtriva®	Emtricitabine	44.8	*3.1*		RESISTANT	
NRTI/NtRTI	Viread®	Tenofovir DF	1.1	1.0	2.3	REDUCED RESPONSE	
	NNRTI mutations[4]: 369wt/A/I/V						
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NNRTI	Sustiva® , Stocrin®	Efavirenz	2.9	*3.3*		SUSCEPTIBLE	
NNRTI	Intelence™	Etravirine	1.8	1.6	27.6	REDUCED RESPONSE	Note 1
	PI mutations[4]: 10F, 32I, 43T, 46I, 47V, 63P, 82A, 90M, 93L						
PI	Crixivan®	Indinavir	24.8	1.0	5.4	MINIMAL RESPONSE	
PI	Crixivan ®; boosted	Indinavir/r	24.8	2.3	27.2	REDUCED RESPONSE	
PI	Viracept®	Nelfinavir	20.1	1.2	9.4	MINIMAL RESPONSE	
PI	Invirase®; boosted	Saquinavir/r	1.2	3.1	22.6	MAXIMAL RESPONSE	
PI	Lexiva®,Telzir®; boosted	Fosamprenavir/r	17.4	1.5	19.5	REDUCED RESPONSE	
PI	Kaletra®	Lopinavir/r	26.1	6.1	51.2	REDUCED RESPONSE	
PI	Reyataz®; boosted	Atazanavir/r	6.2	2.5	32.5	REDUCED RESPONSE	
PI	Aptivus®; boosted	Tipranavir/r	0.8	1.5	7.0	MAXIMAL RESPONSE	Note 1
PI	Prezista™; boosted	Darunavir/r	3.2	10.0	106.9	MAXIMAL RESPONSE	

1. Predicted Fold Change in 50% Inhibitory Concentration (IC50), relative to susceptible reference virus. 2. Cut-off values for maximal and minimal clinical response (Clinical Cut-Off) or for normal susceptibility range in vitro (Biological Cut-Off). Biological Cut-Offs are printed in italic. See page 3 for definitions. 3. Resistance Analysis based on the magnitude of the Fold Change relative to the Clinical or the Biological Cut-Offs. See page 3 for definitions. 4. Mutations printed on page 1 are those reported on public lists (ANRS, Stanford, IAS-USA) or by drug development sponsors. A complete list of all differences from the reference wild type is given on page 2.

IMPORTANT: the additional clinical notes on page 2 provide important information about the specific genotype analysed and should be considered in combination with information on this Summary Page.

VPT 4.2.01 DB0704

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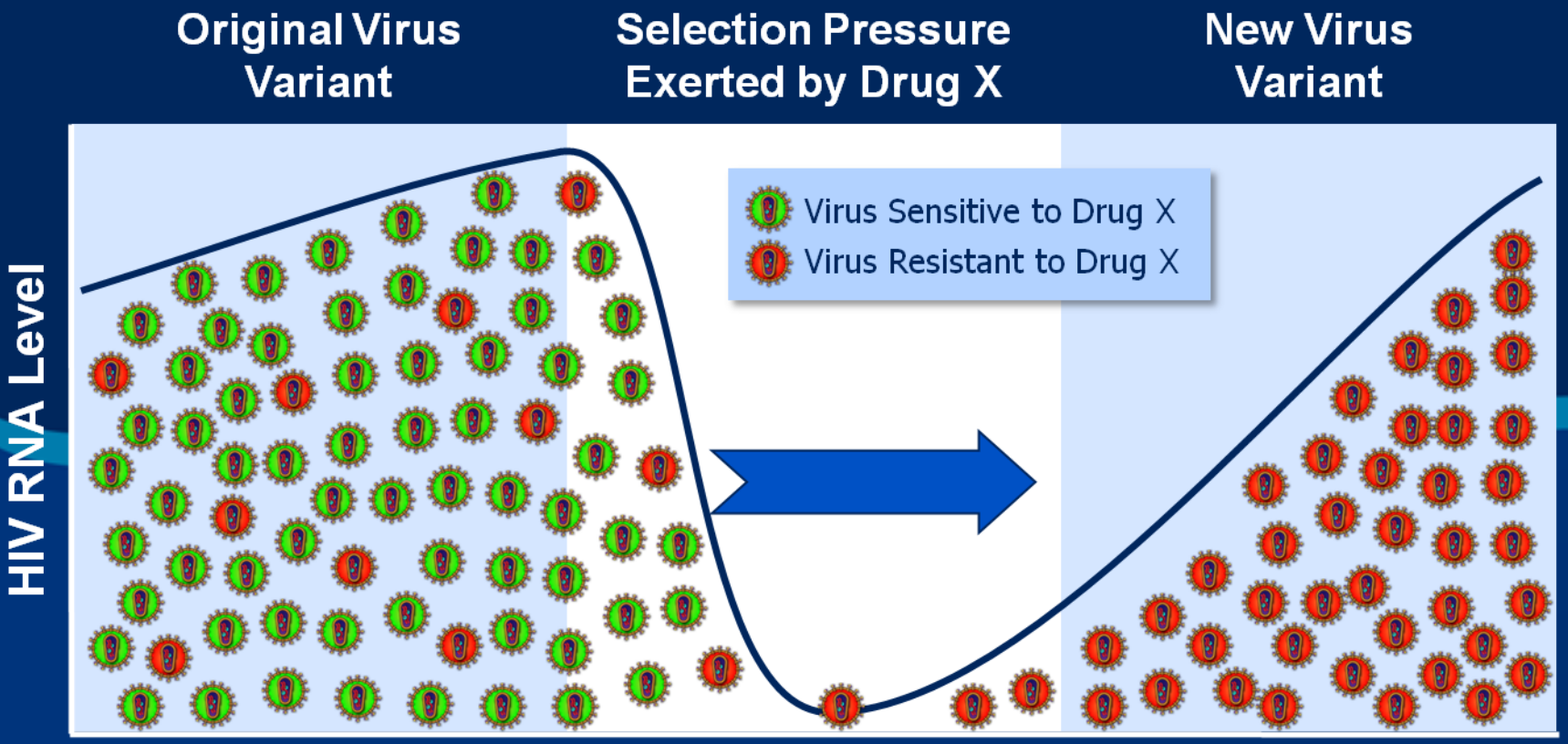
Created at VIRCO Belgium on April 15, 2008
VircoNET Report Nr.: 3657-292781

1. Non-IAS mutation
2. Mixtures

Issue: Mixtures and Phenotype Tests

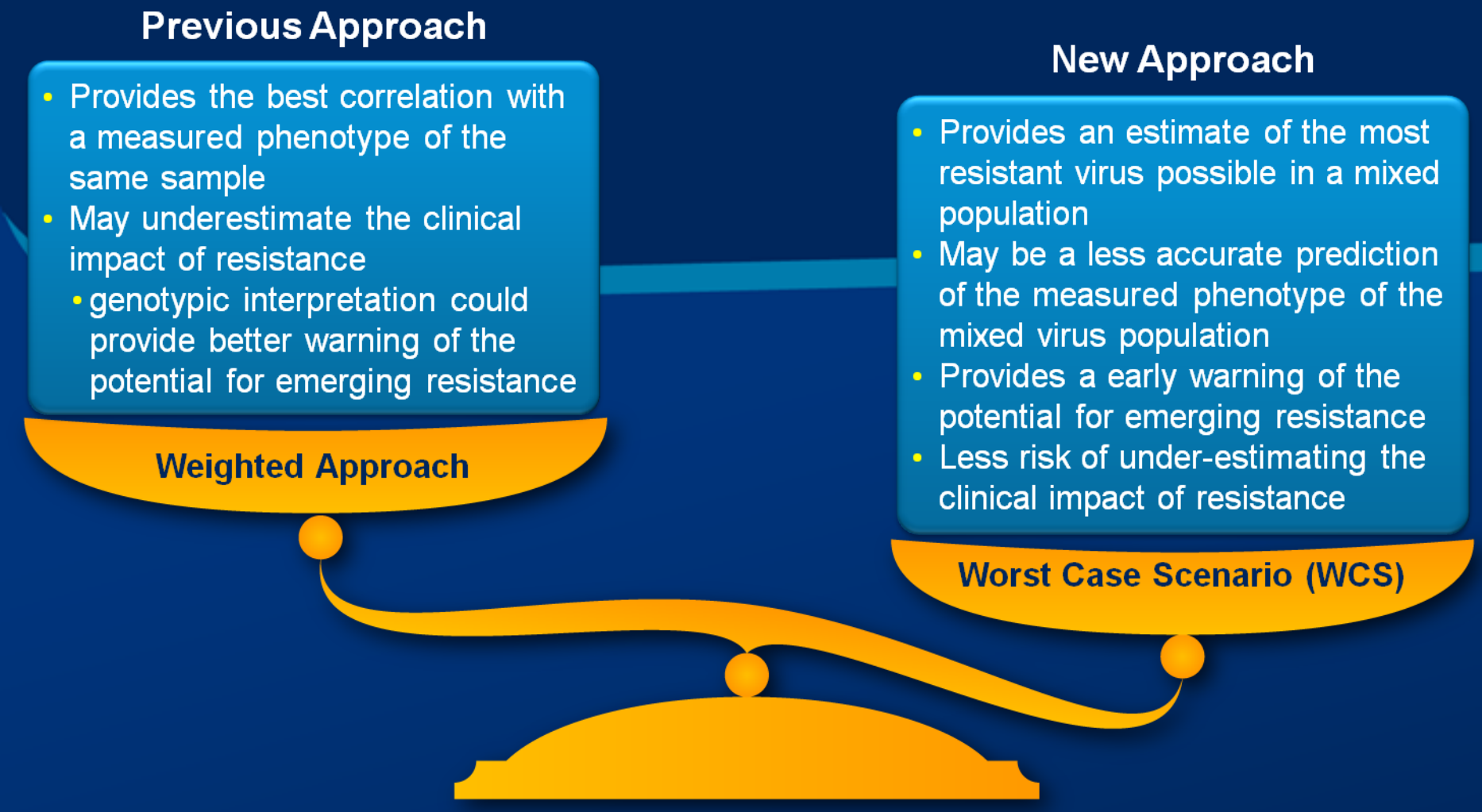


"Dilution effect"

- Mixture of susceptible and resistant strains
- IC_{50} of pre-treatment population may be low and result in a 'sensitive' call

- Selection of resistant variant by Drug X
- Viral breakthrough despite "sensitive" pre-treatment phenotype

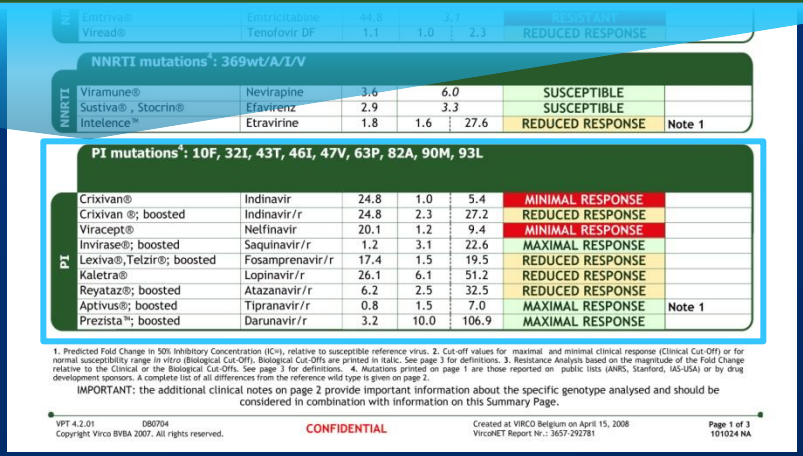
Two Approaches to Mixtures



Patient 1: Resistance Test Report Page 1 (PI)

	DRUGS		FOLD CHANGE [1]	CUT-OFF [2]		RESISTANCE ANALYSIS [3]	CLINICAL NOTES (see p2 for details)
	PI mutations[4]: 10F, 32I, 43T, 46I, 47V, 63P, 82A, 90M, 93L						
PI	Crixivan®	Indinavir	24.8	1.0	5.4	MINIMAL RESPONSE	
	Crixivan ®; boosted	Indinavir/r	24.8	2.3	27.2	REDUCED RESPONSE	
	Viracept®	Nelfinavir	20.1	1.2	9.4	MINIMAL RESPONSE	
	Invirase®; boosted	Saquinavir/r	1.2	3.1	22.6	MAXIMAL RESPONSE	
	Lexiva®,Telzir®; boosted	Fosamprenavir/r	17.4	1.5	19.5	REDUCED RESPONSE	
	Kaletra®	Lopinavir/r	26.1	6.1	51.2	REDUCED RESPONSE	
	Reyataz®; boosted	Atazanavir/r	6.2	2.5	32.5	REDUCED RESPONSE	
	Aptivus®; boosted	Tipranavir/r	0.8	1.5	7.0	MAXIMAL RESPONSE	Note 1
	Prezista™; boosted	Darunavir/r	3.2	10.0	106.9	MAXIMAL RESPONSE	

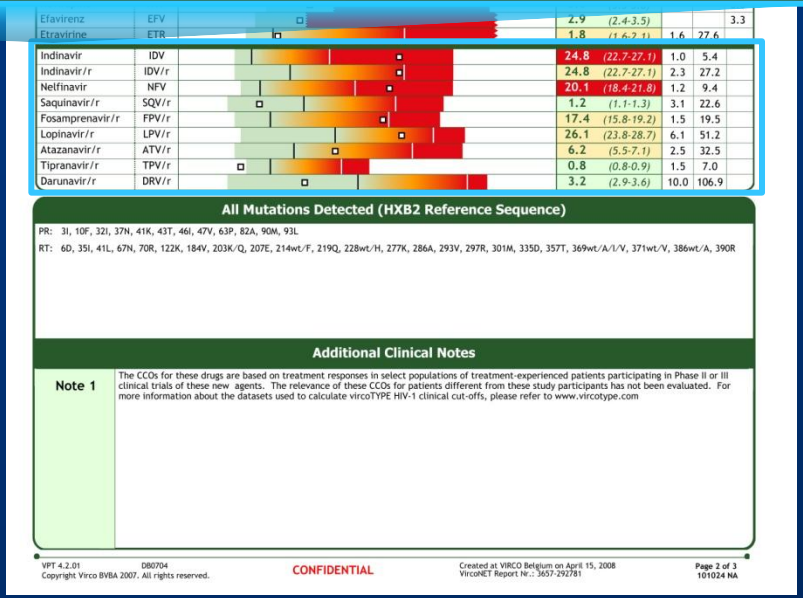
Note 1: The CCOs for these drugs are based on treatment responses in select populations of treatment-experienced patients participating in Phase II or III clinical trials of these new agents. The relevance of these CCOs for patients different from these study participants has not been evaluated. For more information about the datasets used to calculate virco®TYPE HIV-1 clinical cut-offs, please refer to www.vircotype.com



Patient 01: Resistance Test Report Page 2 (PI)

Cut-off for maximal virologic response (CCO1)
Cut-off for minimal virologic response (CCO2)
Cut-off for in vitro susceptibility (BCO)
Patient Sample Fold Change in IC_{50}
maximal virologic response
reduced virologic response
minimal virologic response

DRUGS		0.3 1 10 100 200 (>200)	FC	(95% confidence limits)	CCO 1	CCO 2	BCO
Indinavir	IDV		24.8	(22.7-27.1)	1.0	5.4	
Indinavir/r	IDV/r		24.8	(22.7-27.1)	2.3	27.2	
Nelfinavir	NFV		20.1	(18.4-21.8)	1.2	9.4	
Saquinavir/r	SQV/r		1.2	(1.1-1.3)	3.1	22.6	
Fosamprenavir/r	FPV/r		17.4	(15.8-19.2)	1.5	19.5	
Lopinavir/r	LPV/r		26.1	(23.8-28.7)	6.1	51.2	
Atazanavir/r	ATV/r		6.2	(5.5-7.1)	2.5	32.5	
Tipranavir/r	TPV/r		0.8	(0.8-0.9)	1.5	7.0	
Darunavir/r	DRV/r		3.2	(2.9-3.6)	10.0	106.9	



Efavirenz EFV 2.9 (2.4-3.5) 3.3
Etravirine ETR 1.8 (1.6-2.1) 1.6 27.6

Indinavir	IDV	24.8	(22.7-27.1)	1.0	5.4
Indinavir/r	IDV/r	24.8	(22.7-27.1)	2.3	27.2
Nelfinavir	NFV	20.1	(18.4-21.8)	1.2	9.4
Saquinavir/r	SQV/r	1.2	(1.1-1.3)	3.1	22.6
Fosamprenavir/r	FPV/r	17.4	(15.8-19.2)	1.5	19.5
Lopinavir/r	LPV/r	26.1	(23.8-28.7)	6.1	51.2
Atazanavir/r	ATV/r	6.2	(5.5-7.1)	2.5	32.5
Tipranavir/r	TPV/r	0.8	(0.8-0.9)	1.5	7.0
Darunavir/r	DRV/r	3.2	(2.9-3.6)	10.0	106.9

All Mutations Detected (HXB2 Reference Sequence)

PR: 3I, 10F, 32I, 37N, 41K, 43T, 46I, 47V, 63P, 82A, 90M, 93L

RT: 6D, 35I, 41L, 67N, 70R, 122K, 184V, 203K/Q, 207E, 214wt/F, 219Q, 228wt/H, 277K, 286A, 293V, 297R, 301M, 335D, 357T, 369wt/A/I/V, 371wt/V, 386wt/A, 390R

Additional Clinical Notes

Note 1: The CCOs for these drugs are based on treatment responses in select populations of treatment-experienced patients participating in Phase II or III clinical trials of these new agents. The relevance of these CCOs for patients different from these study participants has not been evaluated. For more information about the datasets used to calculate vircoTYPE HIV-1 clinical cut-offs, please refer to www.vircotype.com

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Questions/Comment??