

Table 2. Parametric and Nonparametric Measures of Reproducibility of Susceptibility Tests Performed on HIV-1 Isolates with Matching Patterns of Drug-Resistance Mutations: Comparison of the Antivirogram (AV) and PhenoSense (PS) Assays

Drug	No. patterns	No. isolate		Mean*		Standard Deviation			Median*		Median Absolute Deviance			
		AV	PS	AV	PS	AV	PS	p [†]	AV	PS	AV	PS	p [†]	
<i>Nucleoside RT Inhibitors</i>														
3TC	10	93	58	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
ABC	9	70	61	0.8 – 4.4	1.0 – 8.4	0.33	0.12	2E-12	0.9 – 6.0	1.0 – 8.0	0.19	0.08	9E-07	
D4T	10	90	60	0.5 – 2.8	0.8 – 3.5	0.30	0.08	<1E-18	0.6 – 2.8	0.8 – 3.3	0.15	0.05	3E-10	
DDC	8	84	50	0.9 – 4.7	1.1 – 3.1	0.32	0.09	2E-15	0.8 – 4.2	1.1 – 3.1	0.20	0.04	2E-10	
DDI	10	89	58	0.4 – 3.9	0.9 – 2.2	0.35	0.07	<1E-18	0.4 – 4.0	0.9 – 2.1	0.23	0.04	2E-11	
ZDV	10	93	58	0.8 – 68	0.5 – 354	0.35	0.26	2E-02	0.8 – 68	0.4 – 354	0.16	0.10	2E-02	
<i>Protease Inhibitors</i>														
APV	24	91	112	0.4 – 5.7	0.1 – 19	0.36	0.26	5E-03	0.4 – 6.0	0.1 – 21	0.19	0.12	5E-03	
IDV	28	134	160	0.4 – 45	0.7 – 49	0.38	0.27	3E-04	0.4 – 45	0.7 – 53	0.17	0.11	1E-02	
LPV	15	65	46	0.5 – 23	0.5 – 33	0.29	0.27	6E-01	0.5 – 24	0.3 – 33	0.15	0.09	1E-01	
NFV	27	125	159	0.5 – 48	1.5 – 78	0.33	0.32	8E-01	0.5 – 48	1.5 – 74	0.18	0.16	9E-01	
RTV	25	127	148	0.3 – 96	0.6 – 98	0.41	0.23	9E-09	0.3 – 134	0.6 – 83	0.24	0.10	4E-07	
SQV	28	136	161	0.3 – 130	0.5 – 241	0.42	0.28	1E-05	0.3 – 130	0.5 – 241	0.16	0.13	3E-02	
<i>Nonnucleoside RT Inhibitors</i>														
DLV	12	72	64	0.8 – 167	0.2 – 75	0.33	0.29	4E-01	0.6 – 157	0.2 – 89	0.18	0.15	1E-01	
EFV	10	51	59	0.7 – 141	0.3 – 76	0.35	0.24	1E-02	0.7 – 141	0.3 – 76	0.19	0.10	3E-02	
NVP	12	90	67	1.2 – 413	0.3 – 299	0.35	0.25	1E-02	0.9 – 414	0.32 – 249	0.16	0.12	9E-02	

*Mean and median were calculated independently for each pattern of drug-resistance mutations. Results for the patterns with the lowest and highest mean and median are shown. †F-test was used to determine whether there were significant differences in the standard deviation of results of the Antivirogram (AV) and PhenoSense (PS) assays. To test whether the variance of the two assays were the same across different mutation patterns, we used an F-test based on the mean-squared error for two one-way ANOVA models on log-fold resistance, one model for each assay. Fligner's test was used to determine whether there were significant differences in the median absolute deviance of results of the AV and PS assays. Both tests, as well as the mean, median, standard deviation, and median absolute deviance were performed on the log-transformed values of fold-resistance. The antilog of the mean and median are shown in the table. Significant results ($p < 0.0033$), based on a Bonferroni adjustment for 15 comparisons, are shown in bold. 3TC – lamivudine, ABC – abacavir, D4T – stavudine, DDC – zalcitibine, DDI – didanosine, ZDV – zidovudine, APV – amprenavir, IDV – indinavir, LPV – lopinavir, NFV – nelfinavir, RTV – ritonavir, SQV – saquinavir, DLV – delavirdine, EFV – efavirenz, NVP – nevirapine