

**Comparison of susceptibility call between 3F and Reference on unseen data for ATV, AZT and ETR.**

ATV				AZT				ETR			
reference				reference				reference			
	MA	RE	MI		MA	RE	MI		MA	RE	MI
3F	5100	44	0	3F	4685	73	0	3F	4967	312	0
	57	1291	129		63	2401	178		294	2366	103
	0	163	1927		0	150	1148		MI (1)	92	358
% Concordant			95.49%	% Concordant			94.67%	% Concordant			90.56%
% Minor discordant			4.51%	% Minor discordant			5.33%	% Minor discordant			9.43%
% Major discordant			0.00%	% Major discordant			0.00%	% Major discordant			0.01%

Susceptibility calls using vircoTYPE 4.2 clinical cutoffs: FC ≤ CCO1: MA= maximal response, CCO1 < FC ≤ CCO2: RE= reduced response, FC > CCO2: MI= minimal response.  
 ATV: CCO1= 2.5, CCO2= 32.5; AZT: CCO1= 1.5, CCO2= 11.4; ETR: CCO1= 1.6, CCO2= 27.6  
 Minor discordances: MA(3F)-RE(reference), RE-MA, RE-MI or MI-RE.  
 Major discordances: MA(3F)-MI(reference) or MI-MA.

**Genotype with major discordance for ETR between 3F and Reference.**

RT Mutations			Reference		
37L, 41L, 43K/Q, 44D, 49R, 53D, 58N, 64R, 67N, 69A, 74I, 75S, 98S, <b>101Q, 108I</b> , 118I, 123N, 135M, 162D, 169D, 177E, 178L, <b>179F, 181C</b> , 184V, <b>190A</b> , 196E, 203K, 210W, 211K, 214F, 215Y, 219D, 223Q, 272A, 277K, 293V, 297A, 322T, 334L, 342F, 356K, 366R, 376S, 377L, 386I, 390R, 395R, 399D			intercept	no mutations	-0.08
				<b>49R &amp; 190A</b>	0.11
				49R & 214F	-0.08
			single_2	67N	-0.08
				74I & 184V	0.04
				<b>101Q</b>	0.06
				<b>108I</b>	0.06
Pheno Fold Change (FC) 72.0			int_2	118I & 214F	-0.09
			single_4	178L	0.07
				<b>179F</b>	0.99
				<b>179F &amp; 184V</b>	0.41
				<b>179F &amp; 376S</b>	-0.79
				<b>179F &amp; 395R</b>	-0.61
			single_5	<b>181C</b>	0.80
			int_4	<b>181C &amp; 184V</b>	-0.20
				<b>181C &amp; 190A</b>	-0.12
				<b>181C &amp; 214F</b>	-0.10
			single_6	184V	-0.04
				184V & 223Q	-0.14
			single_7	203K	-0.06
			single_8	214F	0.16
			single_9	215Y	-0.31
			single_10	219D	0.32
			single_11	356K	-0.04
			single_12	376S	0.06
			single_13	386I	-0.11
			single_14	395R	-0.08
				399D	0.03
			log FC	log FC	0.19
			FC	FC	1.55

Known NNRTI mutations are indicated in bold. Pheno call is resistant (FC > BCO of 3.2) and 3F calls Minimal Response (FC > CCO2 of 27.6) for this sample. The Reference call is discordant by predicting Maximal Response (FC ≤ 1.6). In the Reference linear model the overall contribution for mutation 179F is zero, taking the interactions into account (0.99 + 0.41 - 0.79 - 0.61). Linear model coefficients (log FC) are summed to calculate the genotype resistance (log FC).