

Supplemental Figure. Relationships between each polymorphism and plasma efavirenz concentrations. Horizontal lines represent medians. Markers in each panel represent geometric means of paired efavirenz concentrations from each participant.

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Supplemental Table. Positions, frequencies, and associations between efavirenz concentrations and each polymorphism assayed in *CYP2A6*, *CYP2B6*, *ABCB1*, *CYP3A5* and *CYP3A4*.

Polymorphism	gene position	Chromosome position ^a	LD with 516G→T (r^2) ^b	LD with rs36118214 (r^2) ^b	MAF ^c		Efavirenz (ng/mL), median [IQR]		Efavirenz (ng/mL), median [IQR]		Efavirenz (ng/mL), median [IQR]	rho	P-value
CYP2A6													
rs28399433	Promoter	46048219	0.124	0.020	0.09	GG	-	GT	6073 [4170-7993]	TT	3066 [2307-5714]	-0.3494	0.0187
CYP2B6													
rs10411962	up-UTR ^d	46144052	0.004	0.143	0.16	AA	6402 [1194-11610]	AG	3143 [1782-4067]	GG	3305 [2502-6815]	0.0977	0.5230
rs8109818	up-UTR	46152461	0.266	0.443	0.30	AA	4170 [3294-7738]	AG	2963 [1772-4779]	GG	2725 [1893-3379]	-0.4218	0.0039
rs11671108	up-UTR	46173813	0	0.010	0.07	AA	3294 [2409-6815]	AC	3514 [2779-4664]	CC	2497 [2497- 2497]	-0.0592	0.6992
rs7251950	up-UTR	46174582	0.007	0.001	0.07	CC	3295 [2435-6914]	CT	3153 [2307-3614]	TT	-	-0.0956	0.5320
rs8105382	up-UTR	46180624	0.320	0.115	0.29	CC	2435 [1762-2813]	CT	3041 [2307-4067]	TT	4170 [3092-7681]	0.3578	0.0158
rs11083595	up-UTR	46180844	0.786	0.183	0.45	CC	8228 [6715-14829]	CG	3652 [3034-6473]	GG	2345 [1402-2691]	-0.6041	<0.0001 ^f
rs1808682	up-UTR	46181288	0.001	0	0.05	AA	-	AG	3514 [2779-4664]	GG	3219 [2409-6815]	0.0005	0.9680
rs892216	up-UTR	46181691	0.710	0.276	0.47	CC	1762 [1327-2435]	CT	3652 [3034-6473]	TT	7738 [3092-14829]	0.6065	<0.0001 ^f
rs10418990	up-UTR	46182244	0.017	0.007	0.02	CC	3315 [2383-6715]	CG	2830 [2569-3092]	GG	-	-0.0996	0.5149
rs7259758	up-UTR	46182927	0.102	0.043	0.11	GG	3365 [2307-6715]	GT	3053 [2684-5491]	TT	2435 [2435-2435]	-0.0996	0.5990
rs10419125	up-UTR	46183720	0.059	0.014	0.04	CC	3143 [2383-6473]	CT	3911 [3483-5926]	TT	-	0.1623	0.2867
rs8109525	up-UTR	46183758	0.007	0.038	0.11	AA	3143 [2383-6914]	AG	3514 [2892-4170]	GG	-	0.0329	0.8300
rs7254579	up-UTR	46186731	0.007	0.038	0.11	CC	-	CT	3514 [2892-4170]	TT	3143 [2383-6914]	-0.0329	0.8300
rs1962261	up-UTR	46187079	0.115	0.047	0.13	AA	2624 [2435-2813]	AG	3046 [2476-5491]	GG	3415 [2307-6715]	0.1259	0.4097
rs3760657	up-UTR	46187273	0.017	0	0.02	AA	3315 [2435-6715]	AG	2600 [2307-2892]	GG	-	-0.1578	0.3007
rs12721652	up-UTR	46187473	0.372	0.240	0.33	CC	3911 [3063-7709]	CT	3218 [2440-6016]	TT	1762 [1326-2435]	-0.3917	0.0078
rs2054675	up-UTR	46187595	0.831	0.194	0.46	CC	8718 [6715-14829]	CT	3533 [3034-6073]	TT	2345 [1402-2691]	-0.6338	<0.0001 ^f

rs4802100	up-UTR	46187865	0.017	0	0.02	CC	3315 [2435-6715]	CG	2600 [2307-2892]	GG	-	-0.1578	0.3007
rs4802101	up-UTR	46188301	0.017	0.007	0.02	CC	3315 [2383-6715]	CT	2830 [2569-3092]	TT	-	-0.0996	0.5149
rs28723610	up-UTR	46188665	0.059	0.014	0.04	AA	-	AG	3911 [3483-5926]	GG	3143 [2383-6473]	-0.1623	0.2867
rs34223104	up-UTR	46188969	0.044	0.033	0.05	CC	1145 [1145-1145]	CT	3034 [1478-3295]	TT	3415 [2497-2496]	0.2697	0.0732
rs28739581	intron	46189415	0.380	0.257	0.32	AA	1762 [1327-2435]	AT	3294 [2497-6473]	TT	3911 [3063-7709]	0.3807	0.0108
rs2099361	intron	46190188	0.017	0.007	0.02	GG	-	GT	2830 [2569-3092]	TT	3315 [2383-6715]	0.0996	0.5149
rs8100458	intron	46192053	0.029	0.079	0.10	CC	-	CT	2892 [2142-3614]	TT	3305 [2533-7225]	0.2224	0.1419
rs7250873	intron	46195462	0.656	0.086	0.49	AA	2409 [1762-2813]	AG	3652 [2891-6073]	GG	7227 [3034-13528]	0.4389	0.0026
rs3786547	intron	46198031	0.831	0.194	0.46	CC	8718 [6715-14829]	CT	3533 [3034-6073]	TT	2345 [1402-2691]	-0.6338	<0.0001 ^f
rs4803417	intron	46199860	0.127	0.052	0.14	AA	3514 [2307-6715]	AC	3092 [2799-4067]	CC	2502 [2435-2569]	-0.1366	0.3709
rs1987236	intron	46200873	0.187	0.076	0.20	AA	3633 [2307-7536]	AG	3218 [2806-5070]	GG	2435 [2383-2569]	-0.1853	0.2229
rs35490259	intron	46201012	0.174	0.500	0.19	CC	-	CT	2497 [1762-3614]	TT	3859 [2963-7298]	0.3706	0.0122
rs1872121	intron	46202502	0.228	0.941	0.23	AA	1402 [750-1565]	AG	3041 [2307-5558]	GG	3826 [2853-7298]	0.4144	0.0047
rs4803419	intron	46204632	0.054	0.001	0.07	CC	3315 [2497-6914]	CT	2637 [2307-3614]	TT	-	-0.1611	0.2905
rs3745274	516G→T (exon 4)	46204681	-	0.242	0.44	GG	2142 [1478-2569]	GT	3826 [3092-6473]	TT	8228 [6214-14178]	0.7242	<0.0001 ^f
rs10401737	intron	46206263	0.592	0.264	0.44	CC	7198 [3911-11123]	CT	3118 [2569-5558]	TT	1762 [1478-2307]	-0.5913	<0.0001 ^f
rs2279343	785A→G (exon 5)	46207103	0.957	0.231	0.42	AA	2225 [1565-2691]	AG	4000 [3092-6473]	GG	8228 [6214-14178]	0.7141	<0.0001 ^f
rs2279344	intron	46207323	0.127	0.052	0.14	AA	3514 [2307-6715]	AG	3092 [2799-4067]	GG	2502 [2435-2569]	-0.1366	0.3709
rs2279345	intron	46207542	0.228	0.093	0.23	CC	3614 [2307-7536]	CT	3315 [2383-4170]	TT	2569 [2435-2813]	-0.1587	0.2978
rs12721649	intron	46207677	0.165	0.668	0.18	AA	-	AG	2225 [1565-3379]	GG	4033 [2963-7298]	0.4461	0.0024
rs6508965	intron	46209528	0.228	0.093	0.23	CC	3614 [2307-7536]	CT	3315 [2383-4170]	TT	2569 [2435-2813]	-0.1587	0.2978
rs7246456	intron	46209918	0.957	0.231	0.42	CC	2142 [1478-2569]	CT	4000 [3092-6914]	TT	7738 [5714-14829]	0.7012	<0.0001 ^f
rs28399499	983T→C (exon 7)	46210061	0.026	0.107	0.03	CC	-	CT	6473 [3143-11610]	TT	3294 [2383-6073]	-0.1921	0.2062
rs8192719	intron	46210613	0.957	0.231	0.42	CC	2142 [1478-2569]	CT	4000 [3092-6914]	TT	7738 [5714-14829]	0.7012	<0.0001 ^f
rs36118214	intron	46211146	0.242	-	0.24	AA	1402 [750-1565]	AG	3037 [2142-5558]	GG	4000 [2892-7681]	0.4803	0.0008 ^f

rs33967301	intron	46211408	0.017	0	0.02	CC	-	CT	3572 [3143-4000]	TT	3295 [2383-6715]	-0.0249	0.871
rs11671243	intron	46211555	0.228	0.093	0.23	AA	2569 [2435-2813]	AC	3314 [2383-4170]	CC	3614 [2307-7536]	0.1587	0.2978
rs10853744	intron	46213779	0.956	0.236	0.42	GG	2142 [1478-2569]	GT	4033 [3092-6914]	TT	7738 [5714-14829]	0.7019	<0.0001 ^f
rs7260525	dn-UTR ^e	46215094	0.017	0.071	0.02	AA	3295 [2435-6715]	AG	2878 [2142-3614]	GG	-	-0.0913	0.5507
rs7246465	dn-UTR	46215143	0.032	0.112	0.25	CC	3826 [2799-7536]	CT	2813 [1478-3614]	TT	4808 [2169-9042]	-0.281	0.0615
rs34128717	dn-UTR	46215592	0.100	0.040	0.11	AA	3415 [2307-6715]	AG	3053 [2684-5491]	GG	2435 [2435-2435]	-0.1090	0.4812
rs34789700	dn-UTR	46216573	0.123	0.050	0.13	GG	3365 [2225-6394]	GT	3218 [2684-6694]	TT	-	0.0118	0.9396
rs1552222	dn-UTR	46217744	0.025	0.004	0.26	AA	3605 [2435-6473]	AT	2806 [2263-5264]	TT	3415 [2497-6715]	0.0989	0.5182
Composite 516/983						EXT	1962 [1478-2435]	INT	3415 [3092-5558]	SLO	8228 [6473-13528]	0.7578	<0.0001 ^f
ABCB1													
rs1045642	3435C→T	86976581			0.17	CC	3295 [2307-6073]	CT	3315 [3092-6914]	TT	3143 [1194-7681]	0.0895	0.5589
rs2032582	2677G→T	86998554			0.06	GG	3143 [2307-6073]	GT	3614 [3315-6914]	TT	-	0.1396	0.3660
rs1128503	1236C→T	87017537			0.16	CC	3415 [2307-6715]	CT	3218 [3034-6473]	TT	-	0.0037	0.9808
CYP3A5													
rs776746	6986A→G	87017537			0.20	AA	3193 [2307-6073]	AG	4085 [2805-7225]	GG	3652 [3034-8718]	0.1975	0.1934
CYP3A4													
rs2740574	-392A→G	99108475			0.22	AA	4064 [2569-5558]	AG	3118 [1772-5542]	GG	3315 [2497-6715]	0.0969	0.5265

^a Positions map to genome build 36.3.

^a Linkage disequilibrium (LD) r^2 values were generated using Haploview [23].

^c MAF indicates minor allele frequency.

^d up-UTR indicates upstream untranslated region.

^e dn-UTR indicates downstream untranslated region.

^f These P values are significant after Bonferroni correction for multiple comparisons.