

Supplementary Data

SUPPLEMENTARY TABLE S1. TOP SINGLE NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH DRUG-INDUCED HEPATOTOXICITY IN THE GENOME-WIDE ASSOCIATION STUDY OF ANTIRETROVIRAL DRUG-ALONE AND ANTIRETROVIRAL AND ANTI-TUBERCULOSIS DRUGS CO-TREATMENT GROUPS

Group	SNP	Chr (loci)	Allele I/2 (RA)	I1vs	22vs	Ivs2	p_{min}	p_{adj}	OR (95% CI)	MAF	Gene/loci
ARV	rs199650082	17 (62121526)	T/C (T)	4.6×10^{-2}	2.6×10^{-5}	4.3×10^{-6}	4.3×10^{-6}	2.3×10^{-6}	21.4 (7.5 – 60.6)	0.03	ERNI
	rs32498	5 (55548797)	A/G (A)	7.1×10^{-6}	2.1×10^{-2}	8.8×10^{-6}	7.1×10^{-6}	2.6×10^{-5}	11.5 (4.6 – 28.9)	0.38	ANKRD55
	rs7196606	16 (15941025)	T/C (C)	5.6×10^{-4}	1.9×10^{-3}	2.9×10^{-5}	2.9×10^{-5}	2.8×10^{-5}	9.6 (3.3 – 27.8)	0.07	MYH11
	rs7804397	7 (116857547)	A/C (A)	1.8×10^{-2}	4.4×10^{-5}	7.3×10^{-6}	7.3×10^{-6}	3.0×10^{-5}	7.1 (3.1 – 16.2)	0.09	ST7
	rs16947045	17 (61770954)	T/C (T)	1.1×10^{-2}	3.1×10^{-4}	1.5×10^{-5}	1.5×10^{-5}	4.7×10^{-5}	7.4 (2.9 – 18.7)	0.05	MAP3K3
	rs7206999	17 (61733668)	A/G (A)	1.1×10^{-2}	3.1×10^{-4}	1.5×10^{-5}	1.5×10^{-5}	4.7×10^{-5}	7.4 (2.8 – 19.4)	0.05	MAP3K3
	rs2305599	8 (121210250)	A/G (A)	7.5×10^{-4}	9.0×10^{-4}	3.6×10^{-5}	3.6×10^{-5}	6.6×10^{-5}	6.1 (2.5 – 14.8)	0.19	COL14A1
	rs152343	5 (55560577)	T/C (T)	1.6×10^{-6}	4.0×10^{-2}	4.6×10^{-6}	1.6×10^{-6}	7.3×10^{-5}	10.5 (3.6 – 30.5)	0.43	PSMCIP4
	rs12632280	3 (87722254)	T/C (C)	5.0×10^{-2}	1.7×10^{-5}	6.5×10^{-5}	1.7×10^{-5}	2.0×10^{-4}	4.9 (2.1 – 11.4)	0.26	PSMCIP6
	rs7615453	3 (17490952)	T/C (C)	2.4×10^{-6}	5.1×10^{-2}	6.4×10^{-4}	2.4×10^{-4}	3.6×10^{-4}	4.6 (1.9 – 10.8)	0.22	NAALADL2
	rs7487755	12 (7631190)	A/C (A)	9.0×10^{-6}	9.8×10^{-2}	2.5×10^{-4}	9.0×10^{-6}	5.0×10^{-4}	5.0 (2.0 – 10.0)	0.27	CD163
	rs17064971	5 (165015242)	A/G (G)	5.3×10^{-1}	3.9×10^{-6}	3.1×10^{-4}	3.9×10^{-6}	8.9×10^{-4}	5.9 (2.1 – 16.9)	0.48	LOC574080
	rs971048	4 (13955163)	A/G (A)	1.4×10^{-5}	5.8×10^{-1}	1.1×10^{-3}	1.4×10^{-5}	1.2×10^{-3}	3.3 (1.7 – 10.0)	0.37	LOC391636
	rs937303	15 (33940768)	T/C (C)	7.0×10^{-1}	8.5×10^{-6}	2.1×10^{-4}	8.5×10^{-6}	1.8×10^{-3}	11.6 (2.5 – 54.3)	0.39	RYR3
	rs4842407	12 (79201073)	T/C (C)	1.1×10^{-5}	3.4×10^{-5}	2.3×10^{-7}	2.3×10^{-7}	7.2×10^{-6}	5.9 (2.7 – 12.8)	0.44	LOC642550
	rs10862812	12 (84464616)	T/C (T)	4.2×10^{-4}	1.6×10^{-3}	4.5×10^{-5}	4.5×10^{-5}	2.0×10^{-5}	4.7 (2.6 – 8.5)	0.27	LOC100128335
	rs868567	10 (129266910)	T/G (G)	6.3×10^{-4}	2.3×10^{-4}	1.4×10^{-5}	1.4×10^{-5}	3.3×10^{-5}	4.8 (2.3 – 10.1)	0.29	DOCK1
	rs16870561	6 (84230450)	T/C (C)	4.5×10^{-5}	1.0×10^0	7.8×10^{-5}	4.5×10^{-5}	4.5×10^{-5}	10.6 (3.4 – 32.8)	0.04	PRSS35
	rs11012476	10 (21292923)	A/G (A)	1.0×10^{-0}	5.7×10^{-5}	8.7×10^{-5}	5.7×10^{-5}	5.1×10^{-5}	13.7 (4.3 – 43.5)	0.03	NEBL
	rs2835071	21 (37032177)	T/C (C)	1.2×10^{-4}	1.8×10^{-3}	1.7×10^{-5}	1.7×10^{-5}	5.4×10^{-5}	4.4 (2.2 – 9.1)	0.30	EZH2P1
rs251891	5 (115050362)	A/C (A)	2.0×10^{-2}	5.6×10^{-4}	1.2×10^{-4}	1.2×10^{-4}	6.0×10^{-5}	5.8 (2.7 – 12.2)	0.10	TMED7-TICAM2	
rs10809892	9 (1315843)	A/C (A)	2.4×10^{-5}	3.2×10^{-2}	8.0×10^{-6}	8.0×10^{-6}	1.4×10^{-4}	6.2 (2.7 – 14.0)	0.40	RPS27AP14	
rs714046	8 (97631573)	A/C (A)	1.6×10^{-1}	2.2×10^{-5}	9.2×10^{-5}	2.2×10^{-5}	1.4×10^{-4}	4.1 (2.0 – 8.3)	0.21	SDC2	
rs7044362	9 (1316816)	A/G (G)	8.5×10^{-2}	5.4×10^{-6}	5.1×10^{-6}	5.1×10^{-6}	1.9×10^{-4}	7.1 (2.5 – 19.9)	0.35	RPS27AP14	
rs2270476	2 (211525764)	A/G (A)	5.5×10^{-1}	7.4×10^{-6}	5.3×10^{-5}	7.4×10^{-6}	2.0×10^{-4}	4.1 (1.9 – 8.3)	0.13	CPS1	
rs2597553	4 (121786273)	A/G (A)	3.9×10^{-5}	3.7×10^{-1}	6.9×10^{-5}	3.9×10^{-5}	3.9×10^{-4}	5.0 (2.5 – 10.0)	0.29	PRDM5	
rs7149043	14 (95116292)	A/G (A)	4.6×10^{-1}	1.3×10^{-5}	5.8×10^{-4}	1.3×10^{-5}	4.1×10^{-4}	3.3 (1.7 – 5.0)	0.29	SERPINA13	
rs10809893	9 (1315952)	T/C (T)	2.0×10^{-5}	2.9×10^{-2}	3.6×10^{-6}	3.6×10^{-6}	8.0×10^{-4}	10.0 (2.5 – 98.0)	0.30	RPS27AP14	

I1vs, dominant or recessive-inheritance model of Fisher's exact test depending on inheritance mode of allele 1; Ivs2, allelic model of Fisher's exact test; 22vs, dominant or recessive-inheritance model of Fisher's exact test depending on inheritance mode of allele 2; ARV, antiretroviral; ARV-ATD, antiretroviral and anti-tuberculosis drugs co-treatment; Chr (loci), chromosome, and chromosomal loci based on NCBI build 37; CI, confidence interval; DIH, drug-induced hepatotoxicity; ERNI, endoplasmic reticulum to nucleus signaling-1; MAF, minor allele frequency; OR, odds ratio; p_{adj} , logistic p -value after adjustment for covariates; p_{min} , minimum p -value among the genetic models of Fisher's exact test; RA, risk allele; SNP, single nucleotide polymorphism.