Table S1. Top fifteen SNPs in the GWAS of ATDILI.

SNP	Chr (loci)	Alleles (RA)	11vs	22vs	1vs2	*P*_min	*P*_adj	OR (95% CI)	MAF	Nearest gene
rs10946739	6 (24993127)	A/G (A)	1.1×10^{-3}	2.5×10^{-4}	9.6×10^{-6}	9.6×10^{-6}	4.1×10^{-6}	3.4 (2.0-5.6)	0.19	*FAM65B*
rs7708937	5 (123169574)	T/C (T)	4.0×10^{-2}	1.1×10^{-5}	4.8×10^{-6}	4.8×10^{-6}	4.4×10^{-6}	4.0 (2.4-6.7)	0.11	*KRT18P16*
rs10946737	6 (24967240)	A/G (A)	1.2×10^{-1}	2.4×10^{-5}	2.0×10^{-5}	2.0×10^{-5}	9.7×10^{-6}	4.3 (2.5-7.4)	0.10	*FAM65B*
rs2089910	11 (1874404)	T/C (T)	1.2×10^{-2}	2.2×10^{-5}	5.3×10^{-6}	2.2×10^{-6}	4.2×10^{-5}	2.7 (1.8-4.2)	0.30	*LSP1*
rs4903067	14 (73286300)	T/C (C)	9.9×10^{-6}	2.9×10^{-1}	6.1×10^{-5}	9.9×10^{-6}	8.1×10^{-5}	3.0 (1.7-5.1)	0.17	*DPF3*
rs320035	1 (49089197)	A/G (G)	2.5×10^{-3}	4.9×10^{-5}	3.5×10^{-6}	3.5×10^{-6}	1.3×10^{-4}	2.4 (1.5-3.8)	0.48	*AGBL4*
rs393994	1 (49108745)	T/C (C)	2.5×10^{-3}	9.6×10^{-5}	6.1×10^{-6}	6.1×10^{-6}	1.7×10^{-4}	2.4 (1.5-3.7)	0.48	*AGBL4*
rs2069912	2 (128178191)	T/C (T)	2.9×10^{-5}	9.3×10^{-2}	1.2×10^{-5}	1.2×10^{-5}	1.7×10^{-4}	5.3 (2.2-12.5)	0.22	*PROC*
rs320003	1 (49126778)	A/G (A)	2.1×10^{-4}	2.6×10^{-3}	1.7×10^{-5}	1.7×10^{-5}	2.3×10^{-4}	2.3 (1.5-3.7)	0.48	*AGBL4*
rs319952	1 (49113622)	A/G (G)	2.5×10^{-3}	2.1×10^{-4}	1.1×10^{-5}	1.1×10^{-5}	2.8×10^{-4}	2.3 (1.5-3.6)	0.48	*AGBL4*
rs239319	22 (34120608)	A/G (G)	1.1×10^{-1}	3.7×10^{-5}	1.3×10^{-4}	3.7×10^{-6}	2.8×10^{-4}	2.3 (1.5-3.6)	0.39	*LARGE*
rs3959930	11 (15835975)	T/C (T)	7.8×10^{-1}	7.2×10^{-7}	5.4×10^{-4}	7.2×10^{-7}	1.1×10^{-3}	2.1 (1.4-3.3)	0.27	*SOX6*
rs3892834	12 (16486288)	A/G (A)	2.0×10^{-5}	4.0×10^{-1}	6.5×10^{-5}	2.0×10^{-5}	1.1×10^{-3}	3.1 (1.6-6.3)	0.26	*MGST1*
rs4733759	8 (128804840)	T/C (T)	1.0×10^{-5}	1.6×10^{-1}	6.1×10^{-4}	1.0×10^{-5}	1.6×10^{-3}	2.1 (1.3-3.2)	0.36	*PVT1*
rs2835109	21 (37107446)	A/G (A)	2.0×10^{-5}	3.7×10^{-1}	9.8×10^{-6}	9.8×10^{-6}	6.1×10^{-3}	16.1 (2.2-116)	0.14	*RPS20P1*

11vs - Dominant or recessive-inheritance model of Fisher's exact test depending on inheritance mode of allele 1; 22vs - Dominant or recessive-inheritance model of Fisher's exact test depending on inheritance mode of allele 2; 1vs2 - Allelic model of Fisher's exact test; ATDILI - Anti-tuberculosis drugs induced liver injury; Chr (loci) - Chromosome, and chromosomal loci based on NCBI built 37; CI - Confidence interval; GWAS - Genome wide association study; MAF - Minor allele frequency; OR - Odds ratio; *P*_adj - Logistic *P*-value after adjustment for sex, HIV status, CD4 count and HIV viral load; *P*_min - Minimum *P*-value among the genetic models of Fisher's exact test; RA - Risk allele; SNP - Single nucleotide polymorphism

Table S2. Top fifteen SNPs in the replication study of ATDILI.

SNP	Chr (loci)	Alleles	11vs	22vs	1vs2	*P*_min	*P*_adj	OR (95% CI)	MAF	Nearest gene
rs319952	1 (49113622)	A/G	1.5x10^{-1}	1.3x10^{-2}	1.2x10^{-2}	1.2x10^{-2}	1.0x10^{-2}	2.3 (1.2-4.4)	0.50	*AGBL4*
rs320003	1 (49126778)	A/G	2.0x10^{-2}	3.0x10^{-1}	1.9x10^{-2}	1.9x10^{-2}	1.2x10^{-2}	2.3 (1.2-4.5)	0.50	*AGBL4*
rs320035	1 (49089197)	A/G	2.4x10^{-1}	4.2x10^{-3}	5.8x10^{-3}	4.2x10^{-3}	1.2x10^{-2}	2.2 (1.9-3.9)	0.50	*AGBL4*
rs1432988	5 (164771289)	A/G	3.0x10^{-2}	4.7x10^{-1}	4.9x10^{-2}	3.0x10^{-2}	1.3x10^{-2}	2.5 (1.2-5.2)	0.31	*LOC100507193*
rs393994	1 (49108745)	T/C	2.4x10^{-1}	7.9x10^{-3}	1.4x10^{-2}	7.9x10^{-3}	1.4x10^{-2}	2.1 (1.2-4.0)	0.50	*AGBL4*
rs10946737	6 (24967240)	A/G	1.0x10^{+0}	3.8x10^{-2}	5.0x10^{-2}	3.8x10^{-2}	8.6x10^{-2}	2.2 (0.9-5.4)	0.10	*FAM65B*
rs7708937	5 (123169574)	T/C	1.0x10^{+0}	1.5x10^{-1}	1.8x10^{-1}	1.5x10^{-1}	1.3x10^{-1}	2.6 (0.8-8.7)	0.12	*KRT18P16*
rs10946739	6 (24993127)	A/G	5.5x10^{-1}	1.1x10^{-1}	1.1x10^{-1}	1.1x10^{-1}	1.8x10^{-1}	1.7 (0.8-3.6)	0.18	*FAM65B*
rs2069912	2 (128178191)	T/C	1.0x10^{+0}	4.8x10^{-1}	4.0x10^{-1}	4.0x10^{-1}	2.5x10^{-1}	1.6 (0.7-3.5)	0.21	*PROC*
rs2089910	11 (1874404)	T/C	7.0x10^{-1}	5.2x10^{-1}	4.1x10^{-1}	4.1x10^{-1}	2.7x10^{-1}	1.5 (0.7-3.1)	0.31	*LSP1*
rs4903067	14 (73286300)	T/C	6.3x10^{-1}	1.0x10^{+0}	4.0x10^{-1}	4.0x10^{-1}	3.2x10^{-1}	1.6 (0.6-4.0)	0.15	*DPF3*
rs4733759	8 (128804840)	T/C	7.0x10^{-1}	1.0x10^{+0}	7.4x10^{-1}	7.0x10^{-1}	6.9x10^{-1}	1.2 (0.6-2.3)	0.32	*PVT1*
rs3892834	12 (16486288)	A/G	1.0x10^{+0}	4.8x10^{-1}	7.5x10^{-1}	4.8x10^{-1}	8.1x10^{-1}	1.1 (0.6-2.0)	0.28	*MGST1*
rs3959930	11 (15835975)	T/C	6.5x10^{-1}	8.4x10^{-1}	7.4x10^{-1}	6.5x10^{-1}	9.0x10^{-1}	1.1 (0.5-2.0)	0.90	*SOX6*
rs239319	22 (34120608)	A/G	8.2x10^{-1}	7.9x10^{-1}	1.0x10^{+0}	7.9x10^{-1}	9.5x10^{-1}	1.1 (0.6-1.8)	0.43	*LARGE*

11vs - Dominant or recessive-inheritance model of Fisher's exact test depending on inheritance mode of allele 1; 22vs - Dominant or recessive-inheritance model of Fisher's exact test depending on inheritance mode of allele 2; 1vs2 - Allelic model of Fisher's exact test; ATDILI - Anti-tuberculosis drugs induced liver injury; Chr (loci) - Chromosome, and chromosomal loci based on NCBI built 37; CI - Confidence interval; MAF - Minor allele frequency; OR - Odds ratio; *P*_adj - Logistic *P*-value after adjustment for sex, HIV status, CD4 count and HIV viral load; *P*_min - Minimum *P*-value among the genetic models of Fisher's exact test; RA - Risk allele; SNP - Single nucleotide polymorphism

Table S3. Top SNPs in the GWAS of the pattern of ATDILI.

DILI Pattern	SNP	Chr (loci)	Alleles	Case/control	*P*_min	*P*_adj	OR (95% CI)	MAF	Nearest gene
Cholestatic	rs10182566	2 (29287708)	T/C	19/354	1.2x10^{-6}	4.1x10^{-6}	6.0 (2.8-12.8)	0.24	*C2orf71*
	rs12969241	18 (12842480)	T/G	19/354	1.9x10^{-4}	6.8x10^{-6}	18.2 (5.1-64.4)	0.03	*PTPN2*
	rs9507038	13 (23737972)	A/C	19/354	4.1x10^{-6}	1.5x10^{-5}	6.2 (2.7-14.0)	0.34	*SGCG*
	rs10504112	8 (52101444)	T/C	19/354	1.0x10^{-5}	4.0x10^{-5}	4.6 (2.2-9.6)	0.18	*PXDNL*
	rs3176320	6 (36646788)	T/C	19/354	4.5x10^{-6}	3.7x10^{-4}	9.1 (2.7-30.7)	0.42	*CDKN1A*
	rs2388757	10 (131939898)	A/G	19/354	8.0x10^{-6}	1.5x10^{-3}	3.1 (1.5-6.3)	0.35	*GLRX3*
Hepatocellular	rs1990046	7 (83747642)	A/G	10/354	1.0x10^{-6}	3.7x10^{-6}	28.4 (6.9-117.3)	0.05	*SEMA3A*
	rs7183361	15 (57343199)	A/C	10/354	9.8x10^{-6}	1.4x10^{-5}	11.6 (3.8-35.1)	0.06	*TCF12*
	rs10865177	2 (41829089)	A/G	10/354	3.9x10^{-6}	2.0x10^{-5}	8.1 (3.1-21.2)	0.06	*LDHAP3*
	rs7615167	3 (107514134)	A/G	10/354	6.9x10^{-6}	3.7x10^{-5}	8.8 (3.1-24.8)	0.08	*BBX*
	rs1926559	10 (114052917)	A/G	10/354	7.7x10^{-6}	4.6x10^{-5}	7.2 (2.8-18.5)	0.11	*TECTB*
	rs9982437	21 (40123424)	T/C	10/354	1.7x10^{-7}	1.0x10^{+0}	NA	0.48	*LINC00114*
Mixed	rs12603186	17 (11218707)	A/G	19/354	4.8x10^{-6}	8.1x10^{-6}	7.2 (3.0-17.2)	0.11	*SHISA6*
	rs2089910	11 (1874404)	T/C	19/354	3.9x10^{-7}	9.5x10^{-6}	5.8 (2.7-12.6)	0.29	*LSP1*
	rs1432988	5 (164771289)	A/G	19/353	2.7x10^{-6}	1.3x10^{-5}	5.5 (2.6-11.8)	0.32	*LOC100507193*
	rs8039957	15 (74664851)	A/G	19/354	2.8x10^{-6}	1.3x10^{-5}	5.6 (2.6-12.2)	0.16	*CYP11A1*
	rs1983476	7 (102065322)	T/C	19/354	7.7x10^{-6}	1.7x10^{-5}	7.3 (2.9-18.1)	0.05	*LOC100630923*
	rs1413611	10 (36466891)	A/G	19/354	8.1x10^{-6}	2.1x10^{-5}	4.8 (2.3-9.8)	0.19	*NAMPTL*

ATDILI - Anti-tuberculosis drugs induced liver injury; Chr (loci) - Chromosome, and chromosomal loci based on NCBI built 37; CI - Confidence interval; DILI - Drugs induced liver injury; GWAS - Genome wide association study; MAF - Minor allele frequency; NA - Not applicable; OR - Odds ratio; *P*_adj - Logistic *P*-value after adjustment for sex, HIV status, CD4 count and HIV viral load; *P*_min - Minimum *P*-value among the genetic models (dominant, recessive and allelic) of Fisher's exact test; RA - Risk allele; SNP - Single nucleotide polymorphism

Table S4. Top SNPs for GWAS of ATDILI in genes related to autoimmune diseases, oxidative stress, pharmacokinetic, and HLA region.

SNP	Chrloc	Alleles	P_min	P_adj	OR (95% CI)	MAF	Nearest gene
rs12969241	**18 (12842480)**	**T/G**	**1.3×10^{-4}**	**1.1×10^{-5}**	**9.1 (3.3-24.9)**	**0.03**	***PTPN2***
rs7958375	**12 (111640017)**	**A/G**	**8.8×10^{-5}**	**1.2×10^{-5}**	**11.3 (3.8-33.5)**	**0.02**	***CUX2***
rs2103025	**3 (188070570)**	**A/G**	**1.7×10^{-4}**	**4.9×10^{-4}**	**2.9 (1.6-5.2)**	**0.32**	***LPP***
rs404046	**6 (29923817)**	**T/C**	**2.0×10^{-3}**	**1.2×10^{-3}**	**2.7 (1.5-5.0)**	**0.18**	***HLA-W***
rs4479187	**15 (38711486)**	**T/C**	**7.2×10^{-4}**	**1.3×10^{-3}**	**2.1 (1.3-3.3)**	**0.37**	***FAM98B***
rs885622	**1 (97691005)**	**T/C**	**2.2×10^{-3}**	**2.3×10^{-3}**	**2.7 (1.5-5.0)**	**0.20**	***DPYD***
rs4148328	**2 (234677659)**	**A/G**	**4.3×10^{-3}**	**4.6×10^{-3}**	**1.9 (1.2-3.0)**	**0.26**	***UGT1A8***
rs2842997	**6 (160063852)**	**A/G**	**5.1×10^{-3}**	**7.1×10^{-3}**	**5.5 (1.6-19.0)**	**0.35**	***SOD2***
rs2758331	**6 (160105070)**	**T/G**	**8.8×10^{-3}**	**7.7×10^{-3}**	**5.3 (1.6-17.9)**	**0.34**	***SOD2***
rs9348834	**6 (29864497)**	**A/G**	**1.0×10^{-3}**	**8.3×10^{-3}**	**5.1 (1.6-16.4)**	**0.13**	***HLA-T***
rs12543818	**8 (18271912)**	**A/C**	**1.9×10^{-3}**	**1.1×10^{-2}**	**3.4 (1.7-6.9)**	**0.37**	***NAT2***
rs2248927	**6 (29702709)**	**T/C**	**2.5×10^{-3}**	**2.5×10^{-2}**	**2.7 (1.4-5.0)**	**0.50**	***HLA-F-AS1***
rs7670819	**4 (70481880)**	**T/C**	**2.9×10^{-3}**	**4.5×10^{-1}**	**1.2 (0.8-1.8)**	**0.45**	***UGT2A1***

ATDILI - Anti-tuberculosis drugs induced liver injury; Chr (loci) - Chromosome, and chromosomal loci based on NCBI built 37; CI - Confidence interval; GWAS - Genome wide association study; HLA - Human leukocyte antigen; MAF - Minor allele frequency; OR - Odds ratio; *P*_adj - Logistic *P*-value after adjustment for sex, HIV status, CD4 count and HIV viral load; *P*_min - Minimum *P*-value among the genetic models (dominant, recessive or allelic) of Fisher's exact test; SNP - Single nucleotide polymorphism