

**Supplemental Table 3.** Post hoc power calculations for genetic association analyses of increase in ALT and AST and for occurrence of DILI.

Variant	Regression Coefficient <sup>1</sup>	Standard Error of Regression Coefficient	<i>P</i>	Power <sup>2</sup>	Adjusted Power <sup>3</sup>
<b>ALT</b>					
rs717620	-0.08	0.24	0.74	0.05	0.01
rs2273697	-0.08	0.28	0.78	0.05	0.01
rs1885301	-0.07	0.19	0.73	0.05	0.01
rs7910642	0.41	0.41	0.33	0.16	0.03
rs2804402	0.07	0.19	0.73	0.05	0.01
rs2287622	0.17	0.20	0.39	0.13	0.02
rs11045819	0.27	0.30	0.39	0.14	0.02
rs2306283	0.15	0.24	0.53	0.09	0.01
rs4149056	0.10	0.31	0.76	0.05	0.01
rs7311358	0.25	0.28	0.38	0.14	0.02
*2/rs1799853	0.78	0.34	0.03	0.62	0.26
*3/rs1057910	-0.49	0.39	0.21	0.24	0.05
<b>AST</b>					
rs717620	0.06	0.19	0.76	0.05	0.01
rs2273697	-0.21	0.22	0.34	0.16	0.03
rs1885301	0.03	0.15	0.82	0.04	0.00
rs7910642	0.07	0.33	0.82	0.04	0.00
rs2804402	-0.03	0.15	0.82	0.04	0.00
rs2287622	0.02	0.16	0.92	0.03	0.00
rs11045819	0.26	0.24	0.27	0.19	0.04

rs2306283	0.00	0.19	1.00	0.03	0.00
rs4149056	-0.17	0.24	0.48	0.10	0.02
rs7311358	0.14	0.22	0.52	0.09	0.01
*2/rs1799853	0.66	0.26	0.02	0.69	0.33
*3/rs1057910	-0.34	0.31	0.28	0.19	0.04

**DILI**

	<b>OR 95% CI</b>	<b>OR 95% CI</b>	<b>P</b>	<b>Power<sup>2</sup></b>	<b>Adjusted Power<sup>3</sup></b>
	<b>lower limit</b>	<b>upper limit</b>			
rs717620	0.11	23.52	0.64	0.04	0.00
rs2273697	0.01	6.18	0.64	0.03	0.00
rs1885301	0.14	103.22	1.00	0.01	0.00
rs7910642	0.00	8.41	1.00	0.00	0.00
rs2804402	0.02	4.21	0.23	0.19	0.03
rs2287622	0.03	6.74	0.59	0.09	0.01
rs11045819	0.30	71.49	0.17	0.29	0.06
rs2306283	0.15	111.62	1.00	0.01	0.00
rs4149056	0.01	7.26	1.00	0.01	0.00
rs7311358	0.02	11.25	1.00	0.01	0.00
*2/rs1799853	2.29	Infinite	0.003	0.81	0.60
*3/rs1057910	0.00	8.41	1.00	0.00	0.00

<sup>1</sup> The regression coefficient from a linear regression of the natural log transformed relative fold increase in ALT or AST from baseline with each SNP.

<sup>2</sup> The power of detecting an effect if the true effect is the observed effect.

<sup>3</sup> The power adjusted for 12 polymorphisms tested using Bonferroni correction.