

**Supplementary Table 3.** Significant (Bonferroni corrected  $P=0.01$ ,  $-\log_{10}P=6.41$ ) markers for SnTox3 sensitivity identified in the AM panel by GWAS, using SNP GENE-3324\_338 as a cofactor in the analysis. Physical map positions determined by BLASTn. TGACv1 gene models prefixed with TRIAE\_CS42\_5BS\_TGACv1\_. †SNP previously been shown to be located on chromosome 5B by using the genetically unmapped SNP as a trait, and localising to a chromosome by trait mapping (Gardner *et al.* 2016). Chr = chromosome.

Marker name	$-\log_{10}P$	IWGSC RefSeq v1.0 chr, position (bp)	IWGSC RefSeq v1.0 gene model	TGACv1 chr, position (bp)	TGACv1 gene model
<b>A</b>					
Excalibur_c13833_570	15.88	5A, 2897270 <sup>†</sup>	TraesC5A01G004200	5A, 3748	729465_AA2172150
BS00066144_51	14.31	U, 318919829 <sup>†</sup>	TraesCSU01G215500	5B, 2228	none
w SNP_Ex_c9301_15450818	13.43	U, 65429392 <sup>†</sup>	TraesCSU01G073200	5B, 24489	424411_AA1389470
IACX7443	13.43	U, 96543638 <sup>†</sup>	TraesCSU01G073300	5B, 17484	424411_AA1389460
Ra_c68425_1406	13.11	U, 65431410 <sup>†</sup>	TraesCSU01G073200	5B, 22472	424411_AA1389470
Ra_c68425_1419	13.11	U, 65431423 <sup>†</sup>	TraesCSU01G073200	5B, 22497	424411_AA1389470
RAC875_c7582_680	6.960	5D, 72270 <sup>†</sup>	none	5D, 72270	456971_AA1480450
Ku_c10387_272	6.960	5B, 232228 <sup>†</sup>	TraesCS5B01G00060	5B, 9061	424586_AA1390720
BS00032003_51	6.327	5B, 2559430 <sup>†</sup>	TraesCS5B01G00160	5B, 122519	423227_AA1371660