Table S4 Biallelic SNPs with p-values less than 0.01 for both gemcitabine toxicity and methotrexate toxicity within the GB1 candidate gene region (see Table S2).

chr	base	GEM %V_T	MTX %V_T	GEM P	MTX P	GEM %V_G	MTX %V_G	GEM MAF	MTX MAF
3L	3325388	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326092	3.0	2.3	0.0005	0.008	4.7	3.6	40.0	57.1
3L	3326126	4.3	2.2	2.6E-05	0.01	6.8	3.4	26.7	28.5
3L	3326147	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326157	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326171	2.0	2.9	0.004	0.003	3.2	4.5	20.0	21.4
3L	3326188	2.0	2.9	0.004	0.003	3.2	4.5	20.0	21.4
3L	3326189	2.0	2.9	0.004	0.003	3.2	4.5	20.0	21.4
3L	3326419	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326597	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326672	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326690	1.8	2.3	0.007	0.008	2.8	3.5	6.7	7.1
3L	3326933	1.8	2.9	0.006	0.003	2.9	4.6	20.0	21.4
3L	3327091	1.7	2.5	0.009	0.006	2.7	3.8	40.0	50.0
3L	3329269	1.8	2.3	0.007	0.008	2.8	3.6	6.7	7.1
3L	3329532	1.6	2.3	0.010	0.008	2.6	3.6	6.7	7.1

Note: chr=chromosome, base=base position in chromosome, GEM = gemcitabine, MTX = methotrexate, %V_T=percent of total variation explained by SNP, P=p-value, %V_G=percent of genetic variation explained by SNP, MAF = minor allele frequency= number of founder chromosomes having minor allele represented at this position/total number of founder chromosomes. Shaded rows are SNPs with p-values less than 0.001 for gemcitabine toxicity.