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## Identifying Genotype-by-Environment Interactions in the Metabolism of Germinating Arabidopsis Seeds Using Generalized Genetical Genomics

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Supplemental table 1. Shared QTLs when using overlapping 95% confidence intervals.

a) Main QTL effect

The number of overlapping QTLs (main effect LOD > 4) between pairs of models					
	Model PD	Model AR	Model 6H	Model RP	Full Model
Model PD	45	32	24	25	35
Model AR	32	37	22	24	29
Model 6H	24	22	38	22	28
Model RP	25	24	22	43	29
Full Model	35	29	28	29	101
Number of model specific QTLs	3	1	8	14	54

b) Interacting QTL effect

The number of overlapping QTLs (G:E effect LOD > 5) between pairs of models							
	PD:AR	PD:6H	PD:RP	AR:6H	AR:RP	6H:RP	Full model
PD:AR	0	0	0	0	0	0	0
PD:6H	0	6	4	3	2	1	4
PD:RP	0	4	11	3	6	2	6
AR:6H	0	3	3	6	2	3	1
AR:RP	0	2	6	2	10	2	3
6H:RP	0	1	2	3	2	10	1
Full model	0	4	6	1	3	1	15
Number of model specific QTLs	0	0	0	0	2	4	8

Shared QTLs when using overlapping 95% confidence intervals (compared to the results shown in Fig. 2 where the definition of overlapping of QTLs was based on the chromosome arm approach). Using the 95% confidence intervals we find:  $54+8 = 62$  main effects and G:E interactions, respectively, only found when using the full model. Furthermore there are  $3+1+8+14 = 26$  main effects that are only found in the single environment mapping (PD, AR, 6H and RP). The overlap between models is  $57+7 = 64$ . We also show the overlap between QTLs in all the different models used. These results only differ slightly from the results obtained using the different approach of summarizing the data (shown in Fig. 2).