

Table S4 Linkage analysis in SGRP-4X and two-parent crosses.

A. Genomic regions mapped by linkage analysis in the SGRP-4X that were previously detected in two parent crosses using the same founder strains (Cubillos et al, 2011).

Phenotype	Chromosome	Peak	Growth trait	-log10p	Nominal p-value	Strain	LOD (Cubillos et al, 2011)
Arsenite	III	302000	rate	3.5	0.12	SA	8.98
Arsenite	IV	1506000	rate	4	0.12	WA	14.21
Arsenite	VII	54000	rate	4.5	0.12	NA	3.66
Arsenite	XVI	899000	rate	3.3	0.12	NA	7.16
Arsenite	VI	196000	rate	2.9	0.26	WA	3.41
Arsenite	III	302000	efficiency	2.4	0.13	SA	9.26
Arsenite	IV	1506000	efficiency	3	0.069	WA	9.79
Arsenite	XVI	899000	efficiency	2.8	0.069	NA	4.81
Arsenite	VI	65000	efficiency	2.0	0.259	SA	3.15
Arsenite	III	302000	lag	3.3	0	WA	9.41
Arsenite	IV	1506000	lag	4.6	0	WA	11.82
Heat	XIII	875000	rate	5.7	0	WA	11.67
Heat	XIII	849000	efficiency	2.6	0.224	SA	3.31
Heat	VIII	336000	efficiency	3.8	0	WA	3.38
Paraquat	IV	625000	efficiency	3.1	0	WA	3.01
Paraquat	XII	606000	rate	3.0	0.18	WE	9.44

B. Number of QTLs mapped in both studies depending on LOD and FDR thresholds. Expected number of QTLs and FDR threshold values are indicated in () for each **P-value cutoff**.

F1 maximum LOD score	Total F1 QTLs with LOD	Replicated F1 QTLs at the below indicated <i>P</i> -value cutoff		
		0.01	0.12	0.3
0	26	5 (0.3, 0.05)	11 (3.1, 0.29)	16 (7.8, 0.49)
5	12	3 (0.1, 0.04)	7 (1.5, 0.21)	9 (3.6, 0.40)
9	7	3 (0.1, 0.02)	5 (0.8, 0.17)	7 (2.1, 0.30)