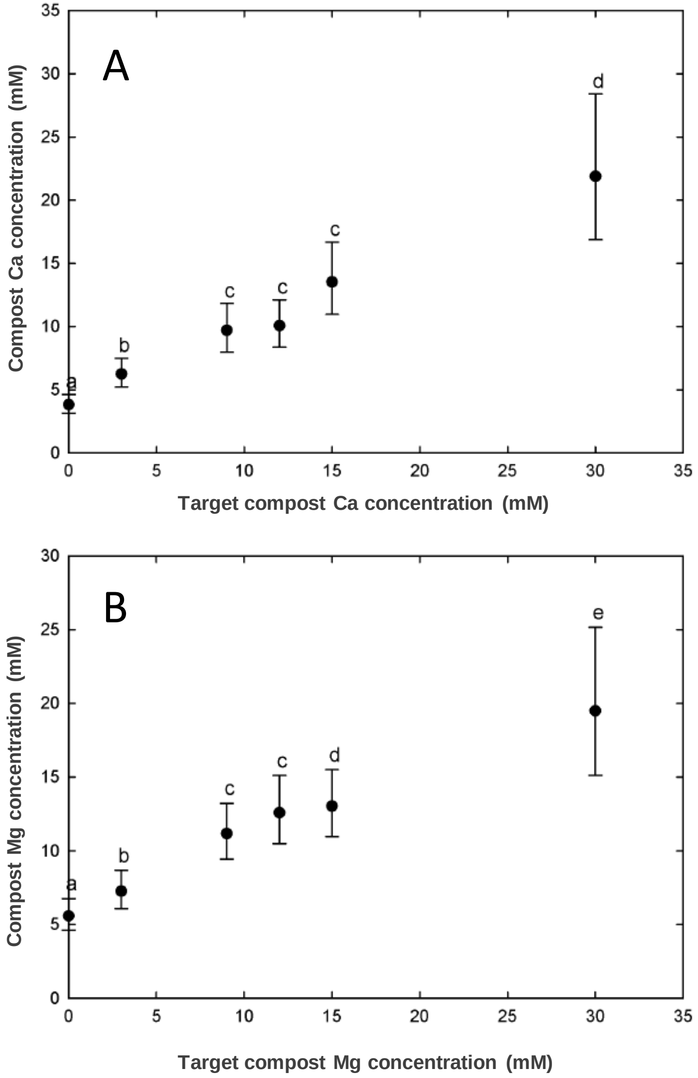
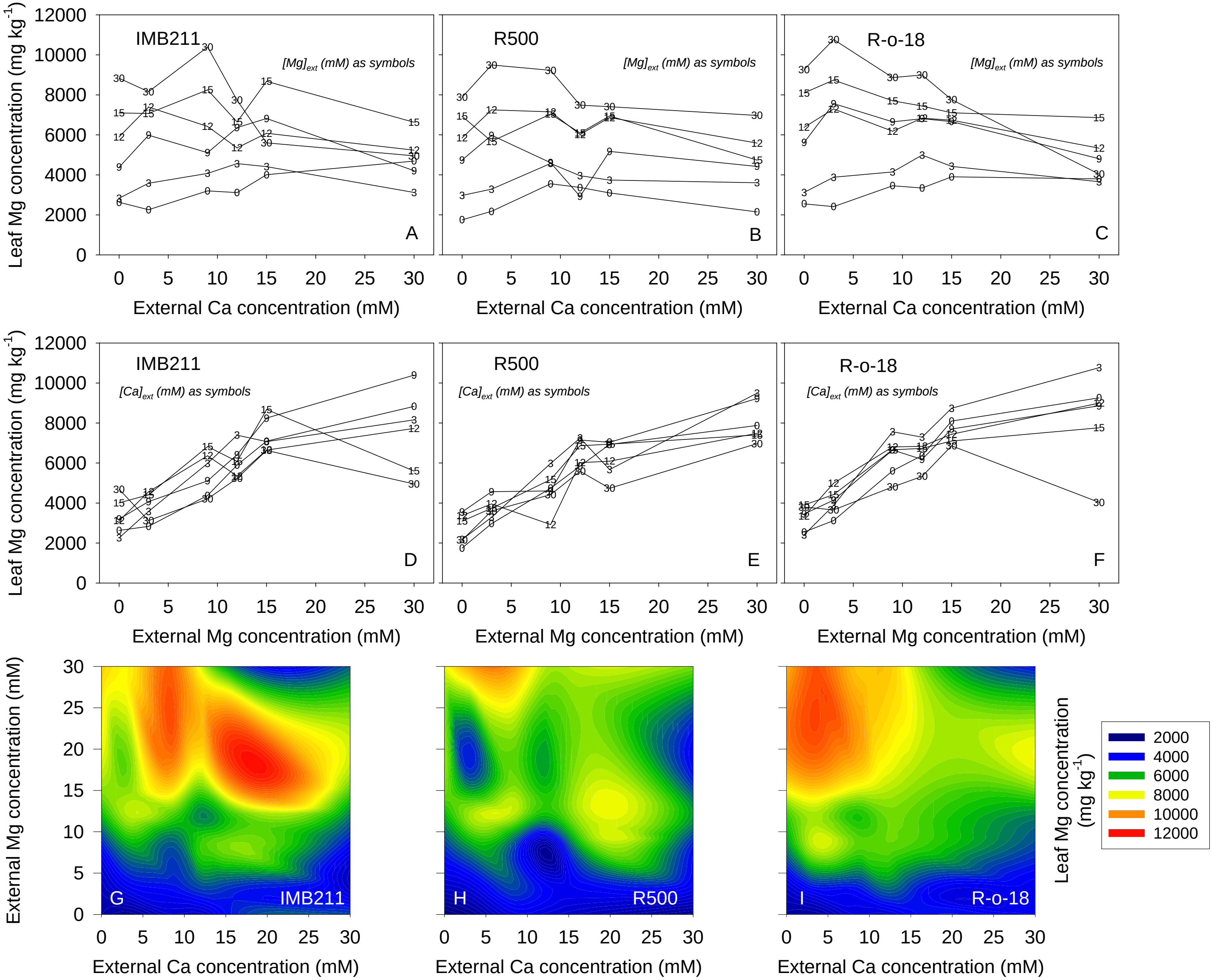
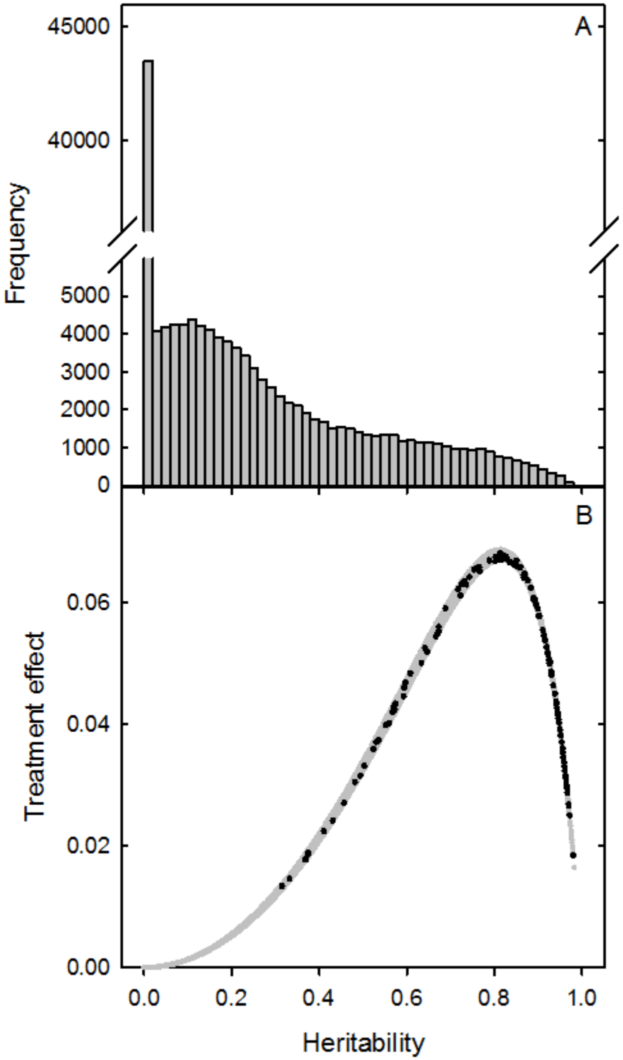


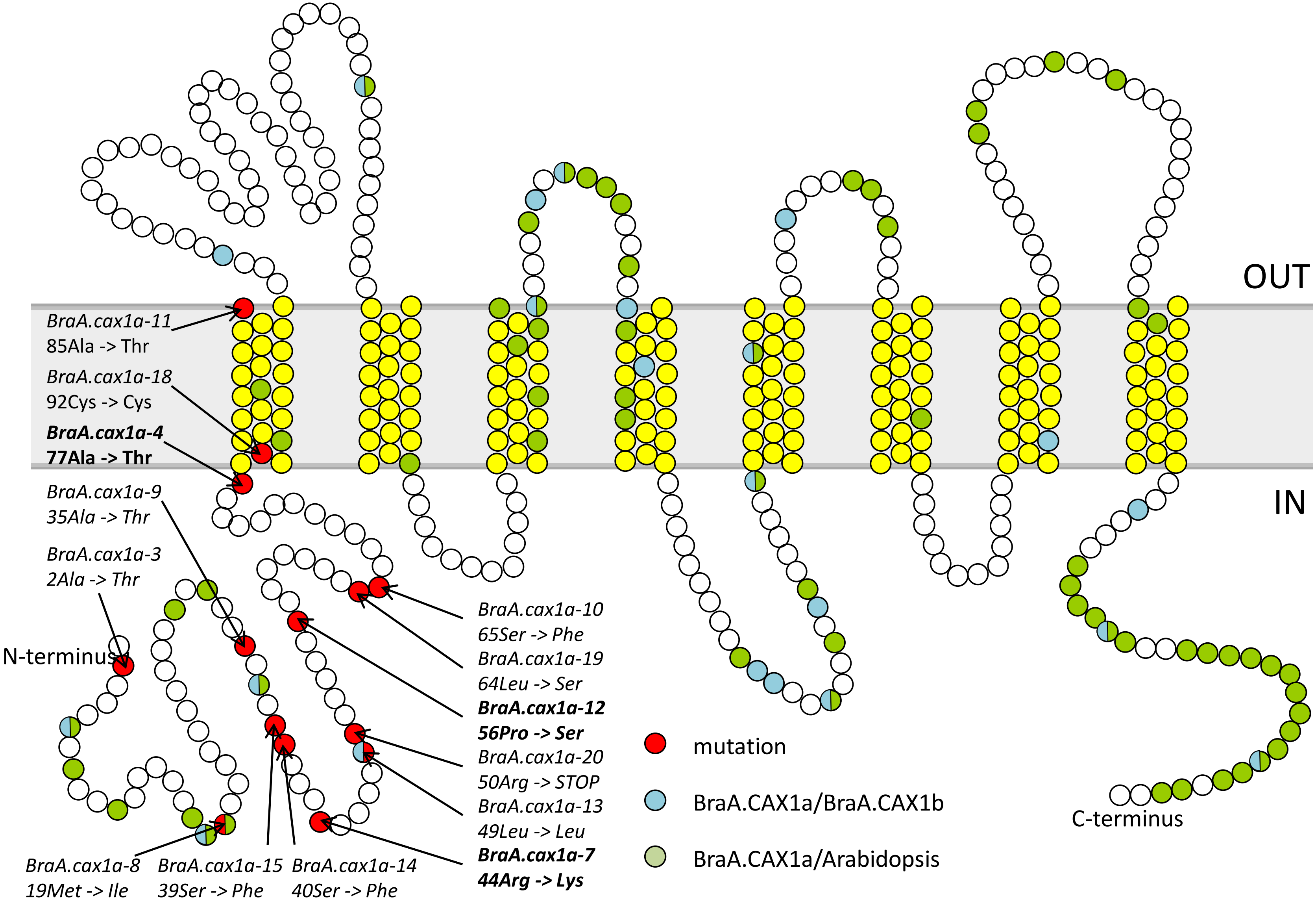
Supplemental Figure 1. Target and measured $[Ca]_{ext}$ and $[Mg]_{ext}$ in compost. Aqueous solutions of $CaCl_2$ or $MgCl_2$ were added to compost. Data are means ±95% confidence interval (n=18). Data sharing the same letter within a plot are statistically indistinguishable (*P*=0.05).



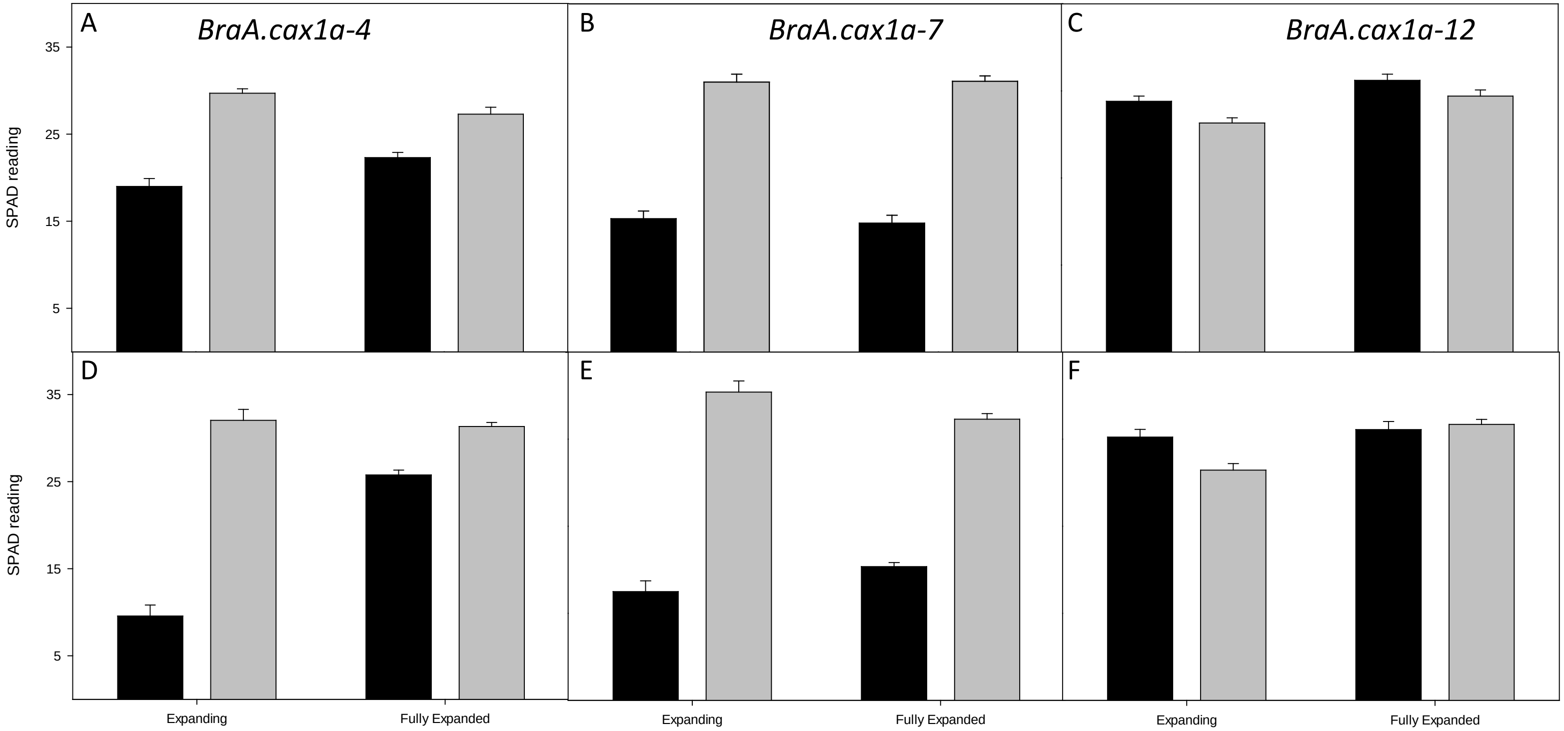
Supplemental Figure 2. Leaf Mg concentration of three genotypes of *Brassica rapa* (IMB211, R500, R-o-18) as functions of external $CaCl_2$ and $MgCl_2$ supply. Plants were grown in compost for 18 d. Data are means of 3 replicates analysed using a genotype/($[Ca]_{ext}$*$[Mg]_{ext}$) treatment structure within an analysis of variance. In plots A-C, there are 6 $[Mg]_{ext}$ treatment levels per $[Ca]_{ext}$ treatment level; these are indicated as numerical symbols for each data point. Similarly, in plots D-F there are 6 $[Ca]_{ext}$ treatment levels per $[Mg]_{ext}$ treatment level. Plots G-I are ternary plots showing interpolated data for all 36 Ca*Mg treatment combinations. Error terms ($LSD_{P=0.05}$) are: 389, 953 and 2334 mg kg^{-1} for genotype, $[Ca]_{ext}$ or $[Mg]_{ext}$, and genotype/($[Ca]_{ext}$*$[Mg]_{ext}$) terms, respectively.



Supplemental Figure 3. Summary of heritability (H^2) and treatment effect variance components for all 135k *Brassica* array probe sets. A, frequency distribution for the H^2 of gene expression. B, treatment effect variance components as a function of H^2; black circles are the 134 gene expression markers (GEMs) which were used to generate the linkage map for the BraIRRI mapping population.



Supplemental Figure 4. Putative structure of BraA.CAX1a. Red circles, mutations for which M_3 seed were obtained. Green circles, amino acid differences between BraA.CAX1a and AtCAX1. Blue circles, amino acid differences between BraA.CAX1a and BraA.CAX1b. Yellow circles, amino acids within transmembrane domains, predicted using Krogh, A., Larsson B., von Hejine, G., Sonnhammer, E.L.L. (2001). Predicting transmembrane protein topology with a hidden Markov model: Application to complete genomes. *J. Mol. Biol.* **305:** 567-580.



Supplemental Figure 5. Single-photon avalanche diode (SPAD) measurements of expanding and fully expanded leaves of three independent homozygous *BraA.cax1a* lines (BC_1S_2s, black bars), and their segregating wild-types (WT; BC_1S_2s, grey bars) grown in compost for 4 (A,B,C) or 5 (D,E,F) weeks.

Supplemental Table 1. Comparative analysis of non-responsive eQTL hotspots from this study and Hammond et al. (2011). Lists of Brassica rapa probe-sets with non-responsive eQTL for individual markers along B. rapa linkage groups A01, A02, A06, and A07 from this study and from Hammond et al. (2011) were loaded in Virtual Plant 1.3 (Katari et al., 2010). Pairwise comparisons between lists were made to identify significant overlaps between lists and z-scores calculated. Data represent z-score values for individual pairwise comparisons

A01

		Markers from Hammond et al. (2011)																				
	Marker	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Markers from this study	1	6.6	20.8	5.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0	0.0	0.0	0.0	6.3	0.0
	2	13.9	25.4	1.6	1.3	2.8	2.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	2.4	0.0	0.0	0.0	0.8
	3	10.1	5.2	16.5	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	0.0	0.7	5.1	0.0	0.0	0.0	0.0	0.0
	4	8.0	3.2	12.6	4.5	2.7	0.0	3.9	0.0	0.8	2.0	4.8	0.0	3.9	0.0	1.1	1.7	2.2	0.0	0.0	0.0	0.7
	5	0.0	0.0	4.9	4.2	2.1	0.0	0.0	4.6	2.2	5.6	2.8	0.0	0.0	4.0	0.9	3.9	1.6	0.0	0.0	0.0	1.8
	6	0.0	0.0	3.0	9.1	10.5	2.5	0.0	2.2	3.4	0.0	1.1	0.0	0.0	0.0	0.0	0.0	0.0	3.9	0.0	0.0	0.0
	7	2.4	2.1	0.7	0.0	11.6	13.4	2.3	4.8	3.1	0.0	4.2	4.0	0.0	2.5	0.8	0.0	0.0	0.0	0.0	0.0	0.0
	8	0.0	0.0	0.0	3.5	1.3	1.5	6.5	6.5	12.7	22.1	1.6	4.0	0.0	2.4	2.9	0.0	1.0	2.4	0.0	0.0	1.9
	9	0.0	0.0	0.0	1.2	0.0	0.0	0.0	0.0	3.7	19.0	3.2	4.3	0.0	0.0	1.2	0.0	2.1	4.2	0.0	0.0	0.0
	10	0.0	0.0	0.0	1.5	0.0	6.5	0.0	0.0	1.1	1.0	10.5	10.3	6.8	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.0
	11	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.3	0.0	8.6	4.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	12	0.0	0.0	2.5	0.5	1.9	1.7	0.0	1.6	0.2	2.3	0.7	0.0	0.0	16.8	6.0	4.7	0.0	3.0	0.0	0.0	2.4
	13	0.0	0.0	1.1	0.8	0.0	0.0	0.0	0.0	1.7	0.3	0.0	7.4	0.0	0.0	0.7	10.5	11.6	23.0	2.9	0.0	1.6
	14	0.0	0.0	0.0	0.0	0.0	0.0	2.3	0.0	0.0	1.4	0.0	2.7	0.0	0.0	3.5	2.6	3.3	10.2	0.0	4.6	14.3

A02

		Markers from Hammond et al. (2011)									
	Marker	1	2	3	4	5	6	7	8	9	10
Markers from this study	1	5.5	8.0	0.0	3.2	0.0	2.1	2.1	3.9	0.0	0.0
	2	7.9	0.0	4.3	2.5	0.0	1.6	3.7	0.0	0.0	1.1
	3	10.5	10.2	0.0	4.8	0.0	0.0	2.7	2.4	3.3	0.0
	4	5.8	22.7	4.1	0.0	4.0	4.1	3.7	0.0	0.0	0.0
	5	2.8	0.0	10.8	26.2	2.4	2.5	5.5	0.0	0.0	0.0
	6	0.0	0.0	2.2	6.9	0.0	6.2	0.0	0.0	0.0	0.0
	7	0.0	0.0	0.0	2.2	7.5	12.3	0.0	0.0	0.0	0.0
	8	4.8	4.3	0.0	0.0	0.0	3.6	32.8	4.0	0.0	0.0
	9	3.3	5.7	0.0	0.0	0.0	8.1	4.3	19.4	0.0	0.0
	10	1.6	4.8	0.0	0.0	0.0	0.0	4.1	9.1	0.0	3.7
	11	0.0	0.0	0.0	3.5	0.0	0.0	0.0	6.6	26.1	11.9
	12	0.0	0.0	3.5	0.0	0.0	0.0	0.0	0.0	0.0	7.6

A06

		Markers from Hammond et al. (2011)												
	Marker	1	2	3	4	5	6	7	8	9	10	11	12	13
Markers from this study	1	11.5	1.5	3.1	0.0	0.0	2.0	0.0	2.3	0.0	0.0	0.0	0.0	0.0
	2	10.0	3.2	19.7	0.0	0.0	0.0	0.0	2.0	0.0	0.0	0.0	0.0	0.0
	3	1.6	1.1	14.5	8.9	1.7	0.0	0.0	6.8	0.0	0.0	0.0	0.0	0.0
	4	3.3	1.0	5.3	19.5	1.6	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	5	0.7	0.8	3.6	11.1	5.5	0.8	1.4	4.3	0.0	0.0	0.0	0.0	0.0
	6	6.5	1.0	0.0	1.1	37.7	10.4	0.0	4.1	0.0	0.0	2.8	1.1	2.7
	7	8.9	17.3	7.4	4.8	10.0	15.1	19.2	13.3	0.0	0.3	2.6	5.0	4.2
	8	1.1	6.9	1.9	2.1	0.0	1.1	15.4	7.2	0.0	0.0	4.5	0.0	0.0
	9	1.2	0.0	0.0	0.0	3.1	0.0	2.1	5.8	22.4	32.7	0.0	2.6	0.0
	10	0.0	2.1	0.0	0.0	0.0	0.0	0.0	1.7	0.0	14.9	19.3	5.7	5.4
	11	0.0	0.0	0.0	0.0	0.0	5.4	0.0	0.0	0.0	0.0	0.0	17.5	6.9

A07

		Markers from Hammond et al. (2011)									
	Marker	1	2	3	4	5	6	7	8	9	10
Markers from this study	1	6.1	0.0	5.3	2.0	6.3	0.0	0.0	0.0	0.0	0.0
	2	9.0	0.0	3.3	26.3	0.0	2.5	0.0	0.0	0.0	0.0
	3	0.0	3.1	0.0	15.8	3.7	3.1	0.0	2.1	0.0	5.6
	4	0.0	3.6	3.4	2.2	18.3	0.0	0.0	0.0	0.0	1.9
	5	0.0	0.0	0.0	2.7	0.0	0.0	0.0	0.0	1.6	0.7
	6	1.2	0.0	0.0	5.3	1.3	2.6	0.0	3.7	0.6	1.9
	7	3.4	0.6	0.6	2.0	0.0	3.0	1.6	2.5	1.2	1.7
	8	0.0	3.1	0.0	4.5	0.0	3.2	0.0	18.4	2.3	0.0
	9	0.0	1.9	0.0	5.6	0.0	0.0	0.0	19.9	20.1	2.2
	10	0.0	4.0	0.0	1.0	4.4	4.2	0.0	0.0	22.8	2.1
	11	0.0	0.0	3.7	4.0	0.0	14.7	0.0	2.7	2.9	11.7
	12	0.0	0.0	0.0	0.0	0.0	7.5	0.0	0.0	0.0	25.7
	13	0.0	0.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	18.2
	14	0.0	0.0	0.0	0.0	0.0	3.0	0.0	0.0	0.0	3.6
	15	0.0	0.0	6.0	0.0	0.0	0.0	0.0	0.0	0.0	3.2
	16	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0