

Supplementary Information

Maximising recombination across macadamia populations to generate linkage maps for genome anchoring.

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Table S1. Paternity assignment of progeny from mapping populations using SNP markers

Putative Cross	n	Cross	# based on paternity assignment	% expected cross	% Self	% unexpected cross
741 x A268	60	741xA268	34	56.7	3.3	43.3
		741xA4	23			
		741x741	2			
		unassigned	1			
741 x A4	36	741xA4	34	94.4	5.6	5.6
		741x741	2			
A268 x 741	97	A268x741	90	92.8	0	7.2
		unassigned	7			
741 x 741	70	741x741	49	70	70	30
		unassigned	21			

n number of progeny

Table S2. Data filtering parameters and statistics for codominant SNP and dominant PAV markers

Markers	Codominant SNP								Dominant PAV		SNP and PAV										
Section	1. Segregating SNP		2. parental genotype inconsistency			3. Mendelian inconsistency			4. Segregating PAV		5. SNP and PAV	6. Missing data >10%			7. PIC, call rate, reproducibility			8. Segregation type			9. Mapped Markers
Cross	proportion of total SNPs	number	proportion of available SNPs	excluded	retained	proportion of available SNPs	excluded	retained	proportion of total PAVs	number	available	proportion of available markers	excluded	retained	proportion of available markers	excluded	retained	1:2:1	1:1	3:1	number of markers mapped
741 x 741	0.18	1069	0.06	64	1005			1005		0	1005	0.03	30	975	0.075	74	901	901	0	0	884
741 x A4	0.40	2440	0.12	293	2147	0.47	1009	1138	0.37	3703	4841	0.12	581	4260	0.14	587	3673	132	654	2887	3139
741 x A268	0.38	2318	0.15	348	1970	0.47	926	1044	0.36	3585	4629	0.14	648	3981	0.11	448	3533	131	590	2812	2674
A268 x 741	0.38	2318	0.15	348	1970	0.47	926	1044	0.36	3585	4629	0.25	1157	3472	0.24	822	2650	128	404	2118	2395

Section Marker filtering

- 1 Identification of informative segregating codominant SNP markers
- 2 Markers filtered based on inconsistency between parental replicates
- 3 Markers filtered based on Mendelian inconsistency in progeny given parental genotypes
- 4 Identification of informative segregating dominant PAV markers
- 5 Available and informative SNP and PAV markers
- 6 Markers filtered with >10% missing data
- 7 Markers filtered with <90% reproducibility, <90% call rate, <0.25 polymorphic information content (PIC)
- 8 Segregation type of available markers
- 9 Final number of markers mapped

Table S3. Heat map of coupling and repulsion phase marker ratios

LG	Map 2	Map 3	Map 4	Map 5	Map 6	Map 7
1	1.5	3.5	10.0	1.9	3.4	5.6
2	1.9	2.6	1.6	1.5	2.9	8.6
3	1.8	1.9	1.5	1.8	2.5	1.9
4	1.7	2.0	1.4	1.9	5.1	2.7
5	1.8	1.1	2.1	1.4	2.2	2.9
6	1.3	1.5	1.4	1.8	3.5	2.0
7	1.3	0.8	2.7	1.5	3.3	2.2
8	1.5	1.4	2.6	1.7	2.7	3.3
9	1.7	2.0	2.5	2.3	3.3	6.4
10	1.7	1.8	2.7	2.6	3.2	2.9
11	1.3	1.5	1.4	2.1	0.7	2.2
12	3.3	N/A	5.5	2.1	7.7	12.3
13	1.0	2.5	1.3	1.9	2.8	2.1
14	0.7	2.3	N/A	2.0	5.3	4.5
Average	1.6	1.9	2.8	1.9	3.5	4.2

Map	Cross
2. 741 ♀	741 x A4
3. 741 ♀	741 x A268
4. 741 ♂	A268 x 741
5. A4 ♂	741 x A4
6. A268 ♂	741 x A268
7. A268 ♀	A268 x 741

Table S4. Spearman's rank correlation co-efficient of marker order between genetic linkage maps

LG	Map 1 v Map 2		Map 1 v Map3		Map 1 v Map4		Map 1 v Map 8		Map 5 v Map 6		Map 5 v Map 7		Map 6 v Map 7	
	ρ	n	ρ	n	ρ	n	ρ	n	ρ	n	ρ	n	ρ	n
1	0.83**	20	0.94**	9	0.98**	9	1.00**	70	0.98*	8	0.95**	13	0.88**	36
2	0.97**	12	0.97**	11	0.97**	9	1.00**	67	0.96**	69	0.84**	52	0.86**	121
3	0.94**	16	0.97**	18	0.97**	14	1.00**	54	0.98**	42	0.60**	28	0.65**	131
4	0.98**	23	0.94**	20	0.98**	16	0.99**	73	0.82**	61	0.80**	61	0.68**	152
5	0.99**	20	0.22	16	0.77*	12	1.00**	62	0.94**	16	0.87*	10	0.87**	123
6	0.93**	13	0.62	10	0.99**	10	1.00**	89	0.83**	59	0.91**	40	0.85**	116
7	0.99**	28	0.97**	19	0.80**	14	1.00**	73	0.86**	20	0.67*	12	0.71**	98
8	0.91**	21	0.98**	13	0.69	9	0.98**	23	0.98**	45	0.92**	32	0.94**	136
9	0.99**	20	0.74*	12	0.97*	8	1.00**	63	0.52**	27	0.03	16	0.95**	118
10	0.85**	13	0.49	13	0.44	12	1.00**	62	0.86**	64	0.91**	34	0.92**	101
11	0.97**	11	1.00**	11	0.20	4	1.00**	56	0.96	7	0.92**	39	0.93**	11
12	0.87**	12	0.71*	11	0.00	5	1.00**	54	N/A	2	0.30	14	0.23	21
13	0.96**	11	0.93	7	1.00	5	0.97**	37	0.91**	47	0.79**	37	0.80**	98
14	0.85*	9	1.00	6	1.00	5	0.99**	39	0.93**	47	0.92**	26	0.96**	128
Average	0.93		0.82		0.77		1.00		0.82		0.75		0.80	
Total		229		176		132		822		514		414		1390

Map	Cross	ρ	Spearman's Rank correlation
Map 1	741 Self	741 x 741	n Number of common markers
Map 2	741 ♀	741 x A4	* P < 0.05
Map 3	741 ♀	741 x A268	** P < 0.01
Map 4	741 ♂	A268 x 741	1.00 Perfect Correlation
Map 5	A4 ♂	741 x A4	0.9 < 1.0 Very High Correlation
Map 6	A268 ♂	741 x A268	0.7 < 0.9 High Correlation
Map 7	A268 ♀	A268 x 741	0.5 < 0.7 Moderate Correlation
Map 8	Integrated 741		0.3 < 0.5 Low Correlation

Table S5. Summary of apparent chiasmata across linkage groups for each map.

Cross	741 x 741					741 x A4										741 x A268										A268 x 741									
Progeny	116					51										35										97									
	Map 1. '741' Self					Map 2. 741 ♀					Map 5. A4 ♂					Map 3. 741 ♀					Map 6. A268 ♂					Map 7. A268 ♀					Map 4. 741 ♂				
LG	0	1	2	3	≥ 4	0	1	2	3	≥ 4	0	1	2	3	≥ 4	0	1	2	3	≥ 4	0	1	2	3	≥ 4	0	1	2	3	≥ 4	0	1	2	3	≥ 4
1	34	50	31	1	0	23	19	7	1	1	22	15	2	5	7	20	9	2	4	0	25	10	0	0	0	38	21	19	11	8	35	56	6	0	0
2	16	59	32	8	1	24	20	5	1	1	15	19	9	3	5	21	12	1	1	0	15	16	3	1	0	29	13	23	6	26	29	17	16	17	18
3	22	61	30	3	0	23	20	1	6	1	11	27	5	5	3	12	15	1	6	1	14	14	2	5	0	29	6	16	16	30	30	37	14	6	10
4	31	46	32	7	0	24	15	5	3	4	20	16	6	5	4	18	11	2	4	0	16	8	8	1	2	26	16	13	11	31	38	30	12	6	11
5	32	50	30	3	1	23	23	1	3	1	16	18	8	4	5	18	4	8	4	1	18	11	3	2	1	26	20	24	12	15	38	16	17	13	13
6	20	44	41	11	0	18	21	3	6	3	12	21	8	7	3	14	15	2	4	0	14	5	8	2	6	26	20	15	15	21	36	29	12	9	11
7	26	61	27	2	0	20	26	3	0	2	18	23	8	1	1	21	13	0	1	0	17	10	1	6	1	29	18	19	12	19	37	24	18	11	7
8	18	60	32	6	0	28	11	6	1	5	12	21	11	4	3	18	12	2	3	0	16	8	5	4	2	19	27	8	24	19	33	33	18	7	6
9	17	55	32	11	1	19	25	2	4	1	18	8	14	4	7	13	16	2	4	0	10	19	2	3	1	28	20	17	25	7	26	36	24	7	4
10	33	41	34	8	0	22	20	4	4	1	21	16	11	1	2	16	5	13	1	0	19	10	2	2	2	32	24	11	14	16	28	31	23	9	6
11	27	63	23	3	0	26	18	3	3	1	20	18	5	5	3	16	19	0	0	0	21	13	0	1	0	21	27	22	12	15	38	38	15	5	1
12	24	53	35	4	0	23	10	13	3	2	20	13	10	6	2	30	3	1	1	0	33	2	0	0	0	27	12	21	10	27	29	27	27	7	7
13	36	49	25	6	0	32	19	0	0	0	20	12	15	3	1	16	7	8	3	1	17	8	7	2	1	30	31	10	18	8	41	36	12	5	3
14	32	66	18	0	0	20	25	5	1	0	16	11	13	6	5	19	15	1	0	0	11	21	2	1	0	38	23	13	8	15	43	48	4	2	0
Total	368	758	422	73	3	325	272	58	36	23	241	238	125	59	51	252	156	43	36	3	246	155	43	30	16	398	278	231	194	257	481	458	218	104	97
Proportion	0.2	0.5	0.3	0.0	0.0	0.5	0.4	0.1	0.1	0.0	0.3	0.3	0.2	0.1	0.1	0.5	0.3	0.1	0.1	0.0	0.5	0.3	0.1	0.1	0.0	0.3	0.2	0.2	0.1	0.2	0.4	0.3	0.2	0.1	0.1

LG Linkage group