Accessory Publication

Table S1.   Significant and suggestive MTA for single-dose markers inherited from Q165, the male parent of the mapping population

Direction, scale (r^2) and significance of each association is shown. Single marker regression was performed on trait data from 168 segregating F_1 siblings grown under high or low N supply in glasshouse conditions. MTA are significant at $*P < 0.05$, $**P < 0.01$ and $***P < 0.005$

Marker[A]	HG/LG[B]	Shoot dry weight		Root dry weight		Total shoot N		iNUE		Leaf soluble protein		Leaf GS activity	
		High	Low	High	Low	High	Low	High	Low	High	Low	High	Low
Aggcac12	1/17	−6***		−3*				−4*					
Acacat25	1/19									−6***		−6***	
M179b	1/42										+7***		−3*
Acccat34	1/47						+5**				−7***		+3*
Accctc19	1/50									−6***		−6***	
Acgcac16	1/81				+5***								
M36d	1/114					−4*					+5**		−6***
Acccat38	2/8									+4*		+5**	+6***
Aaccag13	2/11									−5**		−6***	
M12f	2/12a	+6***	+4*	+7***		+4*			+3*				
Aaccat4	2/14												−6***
MM28b	2/16	−6***				−6***							
Aggcag27	2/22												+6***
Aggcac34	2/38	−12***		−5**		−11***		−7***	−5**				
Acgctt27	2/38	−5**	−4*				−3*		−4*	−12***	+5**		
Acgcag10	3/3	−3*		−6***									
Acccat12	3/4									−8***		−8***	
Accctc1	3/7	−8***	−6***	−5**	−6***	−4*	−5**	−5**					+4*
Aggcac17	3/11		−8***		−8***	−3*	−9***						
Agccat20	3/15		+4*	+5***					+4*				
Aagcaa19	3/41	−4*	−6***		−3*	−3*	−6***	−5**	−4*				
Actcat8	3/41										+8***		
Acccta31	3/41								+9***				

Marker[A]	[B]										
Acccac22	3/69					+6***					
Agcctc24	4/47	−7***		−5**	−4*	−3*		−5**			
Acgcta30	4/48							−6***		+4*	
M34a	5/57		+4*		+5**		+6***				
K091	6/82	+4*				+6***	+4*				−4*
Acccta14	u/u[C]		+4*		+5***		+4*				
La1814d	u/u							−4*			+8***
M32i	u/u		+4*				+7***		+3*		
Agcctc3y	u/u	+4*		+3*		+6***	+5*				
M286h	u/u		−3*	−3*	−7***						

[A]The most significant marker of the group of markers associated with the trait.

[B]The homology and linkage group from Aitken *et al.* (2005).

[C]Unknown location.

Table S2.   Significant and suggestive MTA for single-dose markers inherited from IJ76-514, the female parent of the mapping population

Direction, scale (r^2) and significance of each association is shown. Single marker regression was performed on trait data from 168 segregating F_1 siblings grown under high or low N supply in glasshouse conditions. MTA are significant at *P < 0.05, **P < 0.01 and ***P <0.005

Marker[A]	HG/LG[B]	Shoot dry weight		Root dry weight		Total shoot N		iNUE		Leaf soluble protein		Leaf GS activity	
		High	Low	High	Low	High	Low	High	Low	High	Low	High	Low
Single-dose markers													
aggctg21	1/4	+3*	+4*	+4*	+7***								
aagctc9	1/15	−6***		−5**		−6***							
aagctc55	2/10								−6***				
actctg27	2/10	+5**	+7***		+4*	+4*	+4*	+4*	+4*				
agcctg31	2/18							−6***					
acgctt24	2/22						−7***					+3*	+3*
acccac1	2/23	−5**				−6***	−5*		−3*				
m1b	2/23								−7***				
m42c	3a/3								−7***				
m1068f	3a/8	+6***		+3*	+4*			+9***	+5*				
accta22	3a/11		−6***			−3*	−9***						
acccag32	3a/12							+6***				−3*	−3*
aagctc61	4−b/4	+19***	+14***	+9**	+16***	+9*	+8*						
acgcag2	5/6										+7***	−5**	+7***
m16e	7/1	−4*	−4*		−7***	−3*	−4*			+3*			
aggcta28	8/1								−6***				
m1527c	u/u[C]	−4*				−5*				+6***			
aagctc16	u/8		−8***		−4*		−8***						
aggctg23	u/9	−7***		−3*		−6**							
Multi-dose markers													
acccat41	2/18	−3*						−6***					
acacat12	3a/6			−5***									
accta5	4-b/4	+6***		+3*		+4*							
agccat27	u/8	−3*	−10***		−6***		−12***		−4*				
aggctg33	u/11	−4*	−4*			−4*		−3*	−8***				
aggctc36	u/13	−4*				−6***	−3*	−5*					
m66a	u/u	−4*	−6***		−4*	−3*	−3*						
aagcaa27	u/u										+6***	−3*	+6***
m32b	u/u		+3*					+5*			−4*	−6***	−6***
la12322	u/u												−6***	−6***

la12326	u/u								+6***			−3*		−3*
aagctc33	u/u	−4**	−4*	−4*	−5**	−8***	−4*		−4*					
aacctc26	u/u	+7***		+4*		+7***		+3*	−4*					
actctg2	u/u		+3*		+3*				+6***			−4*		−4*
m37e	u/u								+10***					
m1493f	u/u		+4*						+11***					
m334c	u/u	+3*	+5***	+3*	+5***		+6***							
acacat2	u/u				+6***							−5**		−5**
m74a	u/u										+7***		+3*	+3*
m548	u/u											−7***		−7***

[A]The most significant marker of the group of markers associated with the trait.

[B]The homology and linkage group from Aitken *et al.* (2005).

[C]Unknown location.

Table S3.   Significant and suggestive associations for markers inherited from both parents of the mapping population (those displaying

3 : 1 segregation)

Direction, scale (r^2) and significance of each association is shown. Single marker regression was performed on trait data from 168 segregating F_1 siblings grown under high or low N supply in glasshouse conditions. MTA are significant at *$P < 0.05$, **$P < 0.01$ and ***$P < 0.005$

Marker[A]	HG/LG[B]	Shoot dry weight		Root dry weight		Total shoot N		iNUE		Leaf soluble protein		Leaf GS activity	
		High	Low	High	Low	High	Low	High	Low	High	Low	High	Low
x1527e	8/2		+6***	+3*	+5**	+3*	+4*						
x1527b	8/3									+10***			
xgccta31	u/u[c]	+5**		+6***	+3*					+3*			
xagctc60	u/u	−4*				−6***							
xagcta39	u/u	+3*	+10***	+5**	+13***		+6***	+3*	+4*	−3*			
xagcta46	u/u									+6***			
xcgcta37	u/u		−4*						−7***		+5**		+5**
xggcag20	u/u	−4*		−5***	−3*	−5**							
xgccat46	u/u	−3*	−4*			−6***	−4*						
x1527f	u/u								+7***				
xcacat23	u/u									+8***			
xcgctt28	u/u	+5**		+7***		+5**							
xcgctt34	u/u									−6***		−3*	−3*
xgccag2	u/u					+7***							
xgccag19	u/u	+8***				+5**	+3*	+5**					
xAB0414	u/u			+3*						+4*	−3*	+6***	−3*
xM24a	u/u					−6***							

[A]The most significant marker of the group of markers associated with the trait.

[B]The homology and linkage group from Aitken *et al.* (2005).

[C]Unknown location.

Reference

Aitken K, Jackson P, McIntyre C (2005) A combination of AFLP and SSR markers provides extensive map coverage and identification of homo(eo)logous linkage groups in a sugarcane cultivar. *Theoretical and Applied Genetics* **110**, 789–801. doi:10.1007/s00122-004-1813-7