

Supplementary Figures

Supplementary Figure S1. Climatological water balances using the available water capacity (AWC = 100 mm) on a 10-day scale from November 2012 to January 2014 at the Brazilian Agricultural Research Corporation (Embrapa) Beef Cattle (EBC) station in Campo Grande, Mato Grosso do Sul State, Brazil ($20^{\circ}27^{\circ}S$, $54^{\circ}37^{\circ}W$, 530 m).



Supplementary Figure S2. Box plots of the scaled phenotype clippings. DM, LDM, SDM, GM and RG represent dry matter, leaf dry matter, stem dry matter, green matter and regrowth, respectively.

LDM_T	0.66	0.82	0.93	0.89	0.93	0.96	0.92	0.88	0.98	0.72	0.66	0.92	0.89	0.94	0.96	0.91	0.87	0.98	0.71	0.86	0.81	0.8	0.8	0.74	0.77	0.66	0.9	0.4	0.71	0.86	0.83	0.92	1	
LDM_5	0.39	0.64	0.87	0.99	0.96	0.91	0.83	0.85	0.88	0.46	0.47	0.85	0.99	0.94	0.89	0.8	0.84	0.89	0.56	0.84	0.72	0.85	0.71	0.56	0.71	0.63	0.81	0.15	0.9	0.81	0.59	1	0.92	
LDM_2	0.94	0.89	0.77	0.55	0.65	0.78	0.8	0.66	0.84	0.97	0.75	0.81	0.55	0.69	0.79	0.81	0.67	0.82	0.82	0.67	0.78	0.57	0.69	0.76	0.55	0.51	0.75	0.74	0.29	0.71	1	0.59	0.83	
SDM_T	0.65	0.67	0.74	0.81	0.8	0.81	0.71	0.71	0.84	0.71	0.49	0.72	0.81	0.79	0.8	0.67	0.7	0.82	0.6	0.64	0.63	0.74	0.63	0.5	0.62	0.54	0.74	0.6	0.73	1	0.71	0.81	0.86	
SDM_5	0.12	0.37	0.66	0.93	0.83	0.69	0.56	0.67	0.65	0.19	0.2	0.61	0.93	0.78	0.66	0.52	0.65	0.66	0.34	0.64	0.47	0.78	0.48	0.26	0.54	0.48	0.58	-0.02	1	0.73	0.29	0.9	0.71	
SDM_2	0.87	0.56	0.32	0.14	0.23	0.36	0.33	0.21	0.43	0.89	0.46	0.36	0.14	0.25	0.36	0.32		0.38	0.55	0.18	0.41	0.25	0.31	0.38		0.19	0.35	1	-0.02	0.6	0.74	0,15	0.4	
RG_T	0.59	0.76	0.87	0.78	0.86	0.9	0.91	0.86	0.92	0.64	0.66	0.89	0.77	0.87	0.9	0.9	0.84	0.93	0.66	0.8	0.77	0.73	0.79	0.8	0.79	0.72	1	0.35	0.58	0.74	0.75	0.81	0.9	
RG_9	0.38	0.56	0.72	0.61	0.66	0.66	0.71	0.72	0.68	0.42	0.47	0.71	0.62	0.67	0.66	0.7	0.71	0.69	0.44	0.61	0.54	0.46	0.57	0.54	0.68	1	0.72	0.19	0.48	0.54	0.51	0.63	0.66	
RG_8	0.38	0.63	0.73	0.68	0.74	0.8	0.8	0.87	0.81	0.43	0.55	0.71	0.68	0.75	0.78	0.77	0.86	0.81	0.39	0.63	0.53	0.56	0.78	0.64	1	0.68	0.79	0.15	0.54	0.62	0.55	0.71	0.77	
RG_7	0.63	0.71	0.75	0.5	0.63	0.76	0.85	0.74	0.77	0.67	0.64	0.79	0.52	0.68	0.77	0.86	0.74	0.78	0.58	0.7	0.67	0.52	0.78	1	0.64	0.54	0.8	0.38	0.26	0.5	0.76	0.56	0.74	
RG_6	0.55	0.73	0.76	0.66	0.76	0.86	0.84	0.8	0.82	0.59	0.62	0.78	0.67	0.78	0.88	0.82	0.79	0.83	0.52	0.68	0.63	0.66	1	0.78	0.78	0.57	0.79	0.31	0.48	0.63	0.69	0.71	0.8	
RG_5	0.44	0.58	0.77	0.85	0.85	0.8	0.72	0.72	0.76	0.48	0.43	0.77	0.85	0.84	0.78	0.69	0.72	0.76	0.54	0.75	0.68	1	0.66	0.52	0.56	0.46	0.73	0.25	0.78	0.74	0.57	0.85	0.8	
RG_4	0.65	0.76	0.88	0.7	0.71	0.8	0.8	0.68	0.81	0.69	0.72	0.88	0.71	0.74	0.8	0.8	0.67	0.82	0.71	0.86	1	0.68	0.63	0.67	0.53	0.54	0.77	0.41	0.47	0.63	0.78	0.72	0.81	
RG_3	0.47	0.7	0.91	0.82	0.82	0.82	0.84	0.78	0.83	0.53	0.67	0.91	0.83	0.85	0.82	0.83	0.77	0.86	0.64	1	0.86	0.75	0.68	0.7	0.63	0.61	0.8	0.18	0.64	0.64	0.67	0.84	0.86	
RG_2	0.76	0.84	0.69	0.55	0.6	0.67	0.64	0.54	0.71	0.77	0.68	0.73	0.54	0.62	0.69	0.66	0.55	0.69	1	0.64	0.71	0.54	0.52	0.58	0.39	0.44	0.66	0.55	0.34	0.6	0.82	0.56	0.71	Pearson Correlation
DM_T	0.65	0.84	0.93	0.86	0.92	0.98	0.96	0.92	0.99	0.7	0.72	0.94	0.86	0.94	0.97	0.95	0.91	1	0.69	0.86	0.82	0.76	0.83	0.78	0.81	0.69	0.93	0.38	0.66	0.82	0.82	0.89	0.98	Coefficient
DM_9	0.47	0.72	0.86	0.8	0.87	0.92	0.93	1	0.9	0.54	0.58	0.85	0.81	0.88	0.92	0.9	1	0.91	0.55	0.77	0.67	0.72	0.79	0.74	0.86	0.71	0.84	0.22	0.65	0.7	0.67	0.84	0.87	0.75
DM_8	0.63	0.81	0.92	0.76	0.85	0.93	0.99	0.9	0.94	0.68	0.69	0.93	0.77	0.89	0.93	1	0.9	0.95	0.66	0.83	0.8	0.69	0.82	0.86	0.77	0.7	0.9	0.32	0.52	0.67	0.81	0.8	0.91	0.50
DM_7	0.63	0.82	0.91	0.85	0.91	1	0.94	0.92	0.97	0.68	0.66	0.91	0.85	0.93	1	0.93	0.92	0.97	0.69	0.82	0.8	0.78	0.88	0.77	0.78	0.66	0.9	0.36	0.66	0.8	0.79	0.89	0.96	0.00
DM_6	0.51	0.73	0.91	0.93	0.99	0.94	0.9	0.89	0.93	0.57	0.58	0.91	0.91	1	0.93	0.89	0.88	0.94	0.62	0.85	0.74	0.84	0.78	0.68	0.75	0.67	0.87	0.25	0.78	0.79	0.69	0.94	0.94	
DM_5	0.37	0.61	0.85	0.99	0.93	0.88	0.8	0.83	0.85	0.43	0.44	0.82	1	0.91	0.85	0.77	0.81	0.86	0.54	0.83	0.71	0.85	0.67	0.52	0.68	0.62	0.77	0.14	0.93	0.81	0.55	0.99	0.89	
DM_4	0.64	0.83	0.99	0.82	0.88	0.91	0.93	0.85	0.93	0.69	0.71	1	0.82	0.91	0.91	0.93	0.85	0.94	0.73	0.91	0.88	0.77	0.78	0.79	0.71	0.71	0.89	0.36	0,61	0.72	0.81	0.85	0.92	
DM_3	0.67	0.83	0.66	0.44	0.55	0.64	0.66	0.56	0.7	0.68	1	0.71	0.44	0.58	0.66	0.69	0.58	0.72	0.68	0.67	0.72	0.43	0.62	0.64	0.55	0.47	0.66	0.46	0.2	0.49	0.75	0.47	0.66	
DM_2	0.97	0.82	0.65	0.43	0.53	0.67	0.67	0.53	0.73	1	0.68	0.69	0.43	0.57	0.68	0.68	0.54	0.7	0.77	0.53	0.69	0.48	0.59	0.67	0.43	0.42	0.64	0.89	0.19	0.71	0.97	0.46	0.72	
GM_T	0.7	0.85	0.92	0.85	0.91	0.98	0.95	0.91	1	0.73	0.7	0.93	0.85	0.93	0.97	0.94	0.9	0.99	0.71	0.83	0.81	0.76	0.82	0.77	0.81	0.68	0.92	0.43	0.65	0.84	0.84	0.88	0.98	
GM_9	0.46	0.71	0.88	0.82	0.88	0.93	0.93	1	0.91	0.53	0.56	0.85	0.83	0.89	0.92	0.9	1	0.92	0.54	0.78	0.68	0.72	0.8	0.74	0.87	0.72	0.86	0.21	0.67	0.71	0.66	0.85	0.88	
GM_8	0.62	0.8	0.93	0.79	0.87	0.95	1	0.93	0.95	0.67	0.66	0.93	0.8	0.9	0.94	0.99	0.93	0.96	0.64	0.84	0.8	0.72	0.84	0.85	0.8	0.71	0.91	0.33	0.56	0.71	0.8	0.83	0.92	
GM_7	0.62	0.8	0.92	0.88	0.93	1	0.95	0.93	0.98	0.67	0.64	0.91	0.88	0.94	1	0.93	0.92	0.98	0.67	0.82	0.8	0.8	0.86	0.76	0.8	0.66	0.9	0.36	0.69	0.81	0.78	0.91	0.96	
GM_6	0.47	0.7	0.89	0.95	1	0.93	0.87	0.88	0.91	0.53	0.55	0.88	0.93	0.99	0.91	0.85	0.87	0.92	0.6	0.82	0.71	0.85	0.76	0.63	0.74	0.66	0.86	0.23	0.83	0.8	0.65	0.96	0.93	
GM_5	0.36	0.61	0.85	1	0.95	0.88	0.79	0.82	0.85	0.43	0.44	0.82	0.99	0.93	0.85	0.76	0.8	0.86	0.55	0.82	0.7	0.85	0.66	0.5	0.68	0.61	0.78	0.14	0.93	0.81	0.55	0.99	0.89	
GM_4	0.59	0.8	1	0.85	0.89	0.92	0.93	0.88	0.92	0.65	0.66	0.99	0.85	0.91	0.91	0.92	0.86	0.93	0.69	0.91	0.88	0.77	0.76	0.75	0.73	0.72	0.87	0.32	0.66	0.74	0.77	0.87	0.93	
GM_3	0.81	1	0.8	0.61	0.7	0.8	0.8	0.71	0.85	0.82	0.83	0.83	0.61	0.73	0.82	0.81	0.72	0.84	0.84	0.7	0.76	0.58	0.73	0.71	0.63	0.56	0.76	0.56	0.37	0.67	0.89	0.64	0.82	
GM_2	1	0.81	0.59	0.36	0.47	0.62	0.62	0.46	0.7	0.97	0.67	0.64	0.37	0.51	0.63	0.63	0.47	0.65	0.76	0.47	0.65	0.44	0.55	0.63	0.38	0.38	0.59	0.87	0.12	0.65	0.94	0.39	0.66	
	GM_2	GM_3	GM_4	GM_5	GM_6	GM_7	GM_8	GM_9	GM_T	DM_2	DM_3	DM_4	DM_5	DM_6	DM_7	DM_8	DM_9	DM_T	RG_2	RG_3	RG_4	RG_5	RG_6	RG_7	RG_8	RG_9	RG_T	SDM_2	SDM_5	SDM_T	LDM_2	LDM_5	LDM_T	

Supplementary Figure S3. Heatmap showing the correlation between all trait clippings. Red lines separate different phenotypes. DM, LDM, SDM, GM and RG represent dry matter, leaf dry matter, stem dry matter, green matter and regrowth, respectively.



Supplementary Figure S4. Principal component analysis scatter plot of the family phenotypes. The axes represent the first and second principal components, which explain 75.7% and 9.5% of the variance, respectively.



Supplementary Figure S5. Principal component analysis scatter plot of family genotyping, with a total of 28,106 markers. The axes represent the first and second principal components, which explain 38.9% and 18.3% of the variance, respectively.



Supplementary Figure S6. Principal component analysis scatter plot of family genotyping, considering only the major importance markers (69 markers). The axes represent the first and second principal components, which explain 58% and 9.5% of the variance, respectively.



Supplementary Figure S7. Venn diagrams showing the logical relationship among the sets of markers identified for each phenotype. (A) A total of 283 markers from the FI-2 dataset and (B) 69 markers selected by the Gini importance condition. DM, LDM, SDM, GM and RG represent dry matter, leaf dry matter, stem dry matter, green matter and regrowth, respectively.



Supplementary Figure S8. Urochloa ruziziensis gene coexpression network (GCN).