

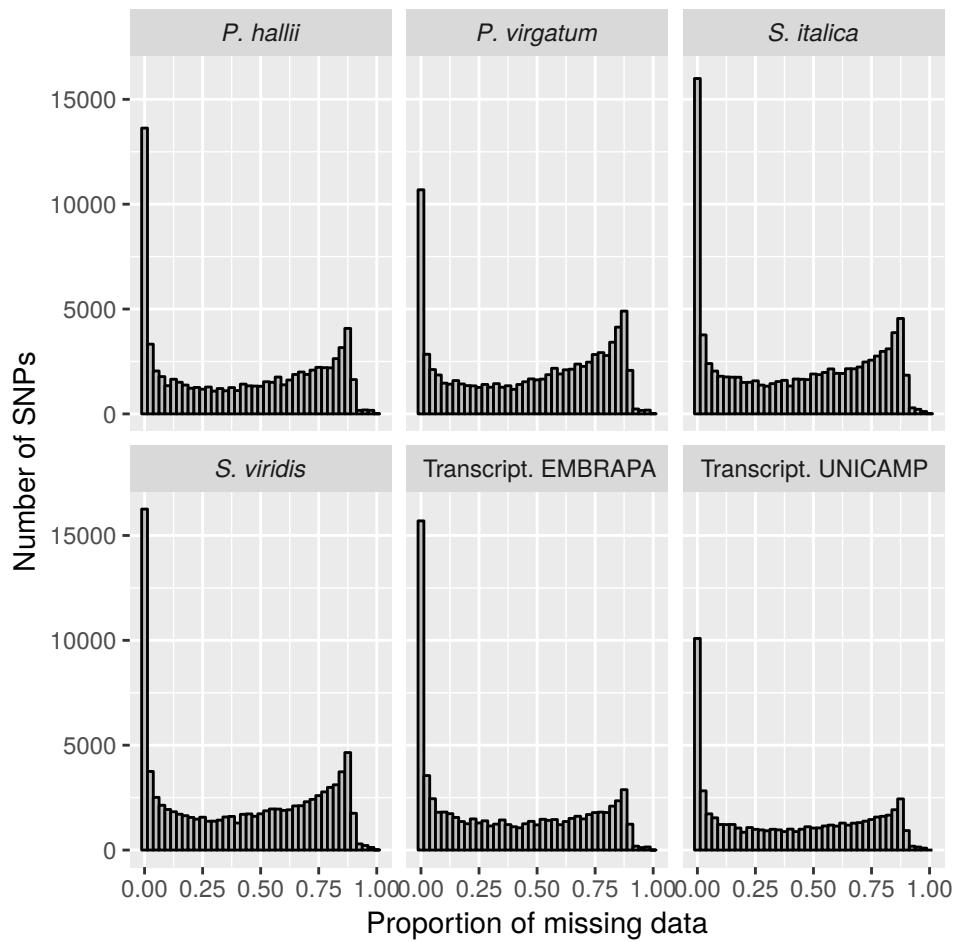
**Figure S1** Illustrative scheme of the experimental design. Empty circles are individuals from half-sib progenies from 19 female parents (P1 to P19) and solid circles are clones of three apomictic cultivars (T1 to T3). Individual genotypes are numbered from 1 to 570.

**Table S1** Values of AIC and BIC for  $G_L$  and  $R_L$  matrices for organic matter (OM), crude protein (CP), *in vitro* digestibility of organic matter (IVD), leaf dry matter (LDM), regrowth capacity (RC), and percentage of leaf blade (PLB). The lowest values and selected variance and covariance (VCOV) structures are indicated in bold.

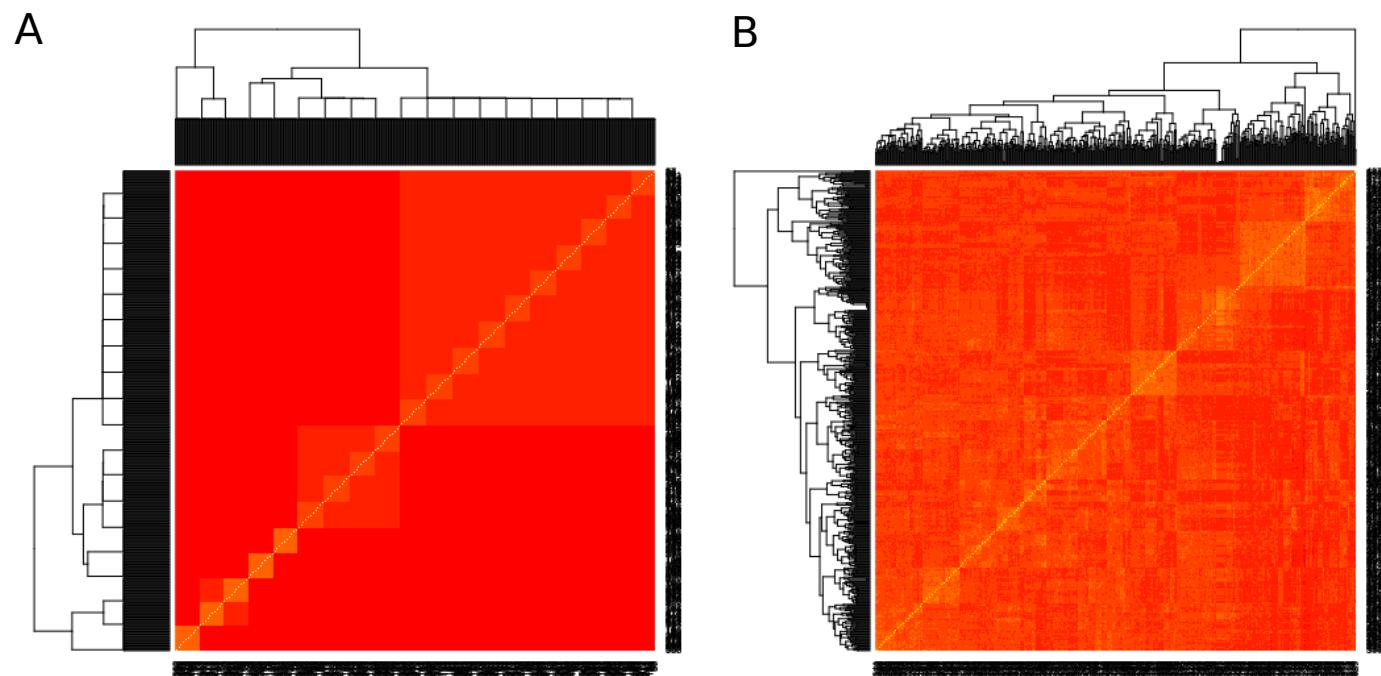
OM			CP			IVD					
$G_L$ matrix			$R_L$ matrix			$G_L$ matrix			$R_L$ matrix		
VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC
ID	3050.437	3079.553	ID	2782.262	2817.201	ID	3361.000	3390.117	ID	3192.723	3245.723
DIAG	3039.441	3086.027	DIAG	2714.927	2767.337	DIAG	3291.024	3337.610	DIAG	3140.123	<b>3210.002</b>
CS	2794.329	2829.269	CS	2767.056	2807.819	CS	3255.887	3290.827	CS	NC	NC
$CS_{Het}$	2788.671	2841.080	<b>CS<sub>Het</sub></b>	<b>2707.356</b>	<b>2765.589</b>	$CS_{Het}$	3198.476	3250.885	$CS_{Het}$	3140.954	3216.656
AR1	2789.073	2824.012	AR1	2776.316	2817.079	AR1	3248.110	3283.050	AR1	3192.149	3250.381
$AR1_{Het}$	2784.013	2836.422	$AR1_{Het}$	2708.434	2766.667	$AR1_{Het}$	3192.723	<b>3245.132</b>	$AR1_{Het}$	<b>3139.881</b>	3215.583
Po	2782.262	<b>2817.201</b>	Po	NC	NC	Po	3247.358	3282.298	Po	3182.825	3241.058
$Po_{Het}$	<b>2774.400</b>	2826.809	$Po_{Het}$	NC	NC	$Po_{Het}$	3194.377	3246.786	$Po_{Het}$	3141.987	3217.689
US	NC	NC	US	2708.135	2795.484	US	<b>3177.022</b>	3258.548	US	NC	NC
LDM			RC			RC			$G_L$ matrix		
$G_L$ matrix			$R_L$ matrix			$G_L$ matrix			$R_L$ matrix		
VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC
ID	53176.31	53202.40	ID	49748.58	49826.85	ID	4535.698	4568.329	ID	3486.283	3747.330
DIAG	52440.24	52505.47	DIAG	NC	NC	DIAG	4505.830	4582.143	DIAG	3427.027	3735.756
CS	51308.98	51341.60	CS	49105.14	49196.47	CS	3844.131	3883.288	CS	3449.976	3717.549
$CS_{Het}$	50574.92	50653.19	$CS_{Het}$	NC	NC	$CS_{Het}$	3808.653	3893.493	$CS_{Het}$	NC	$CS_{Het}$
AR1	50821.60	50860.74	<b>AR1</b>	<b>48979.23</b>	<b>49070.55</b>	AR1	3697.371	3736.527	AR1	3457.433	3725.006
$AR1_{Het}$	49939.84	50018.11	$AR1_{Het}$	NC	NC	$AR1_{Het}$	3665.877	3750.717	$AR1_{Het}$	NC	$AR1_{Het}$
Po	NC	NC	Po	NC	NC	Po	3650.286	<b>3689.443</b>	Po	3448.822	<b>3716.395</b>
$Po_{Het}$	49748.58	<b>49826.85</b>	$Po_{Het}$	NC	NC	$Po_{Het}$	3612.722	3697.562	$Po_{Het}$	NC	$Po_{Het}$
US	<b>49671.64</b>	49932.55	US	NC	NC	<b>US</b>	<b>3486.283</b>	3747.330	US	<b>3404.527</b>	3893.989

**Table S2 Bowtie2 alignment results of 6,596,939 GBS tags in absolute and relative (in parenthesis) values.**

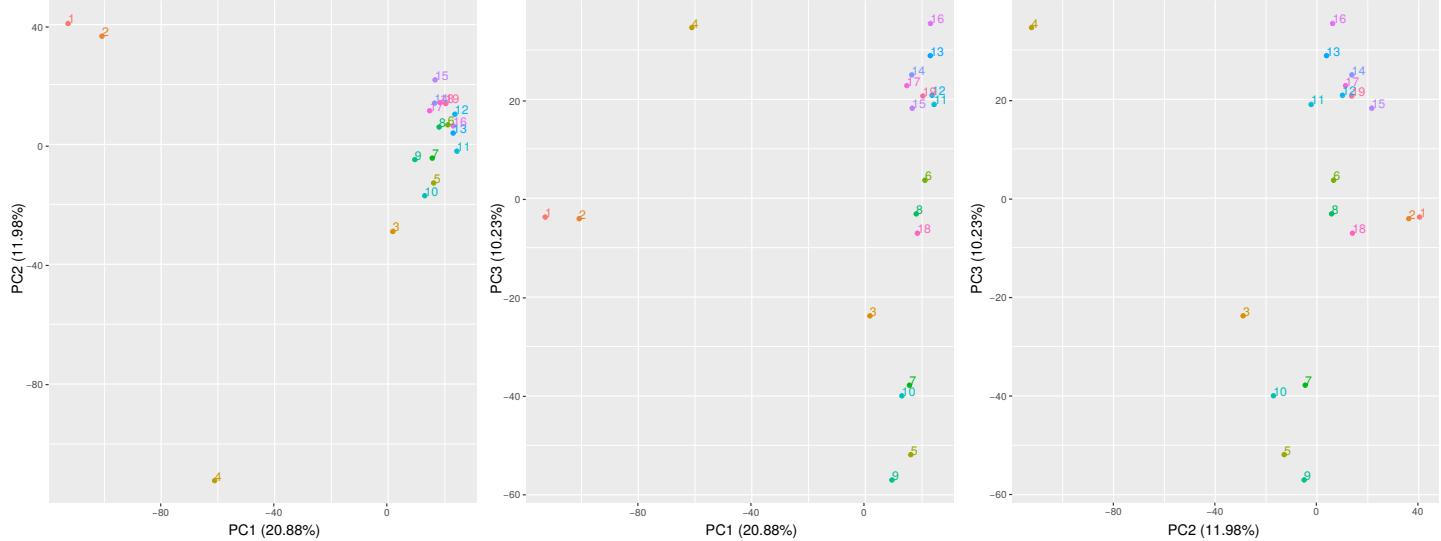
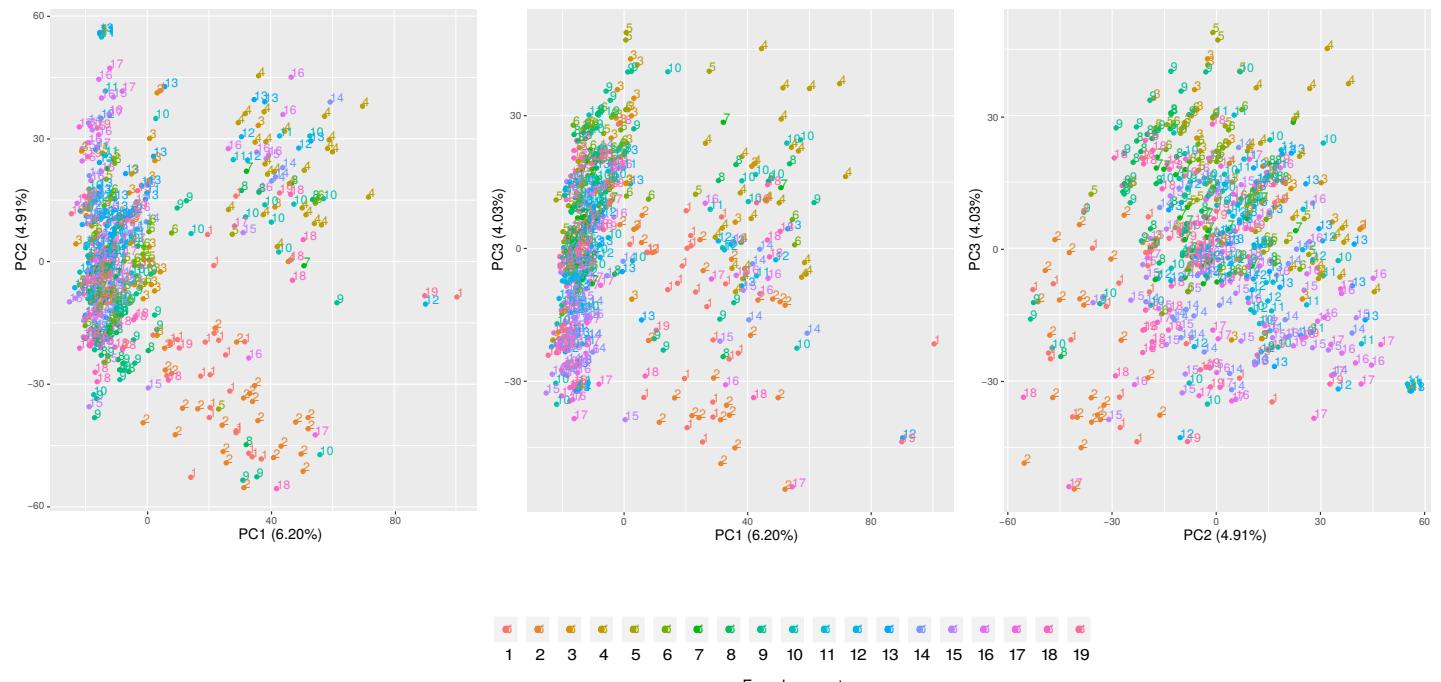
Reference Genome	Non-aligned		Aligned tags	
	tags	Overall alignment	Unique alignment	Non-unique alignment
<i>Panicum hallii</i> genome	5,340,535 (80.95%)	1,256,404 (19.05%)	1,002,261 (15.19%)	254,143 (3.85%)
<i>Panicum virgatum</i> genome	5,101,776 (77.34%)	1,495,163 (22.66%)	503,124 (7.63%)	992,039 (15.04%)
<i>Setaria italica</i> genome	5,143,121 (77.96%)	1,453,818 (22.04%)	1,149,693 (17.43%)	304,125 (4.61%)
<i>Setaria viridis</i> genome	5,141,196 (77.93%)	1,455,743 (22.07%)	1,164,462 (17.65%)	291,281 (4.42%)
Transcriptome (EMBRAPA)	4,997,950 (75.76%)	1,326,602 (20.11%)	1,244,861 (18.87%)	81,741 (1.24%)
Transcriptome (UNICAMP)	5,270,337 (79.89%)	1,598,989 (24.24%)	839,084 (12.72%)	759,905 (11.52%)



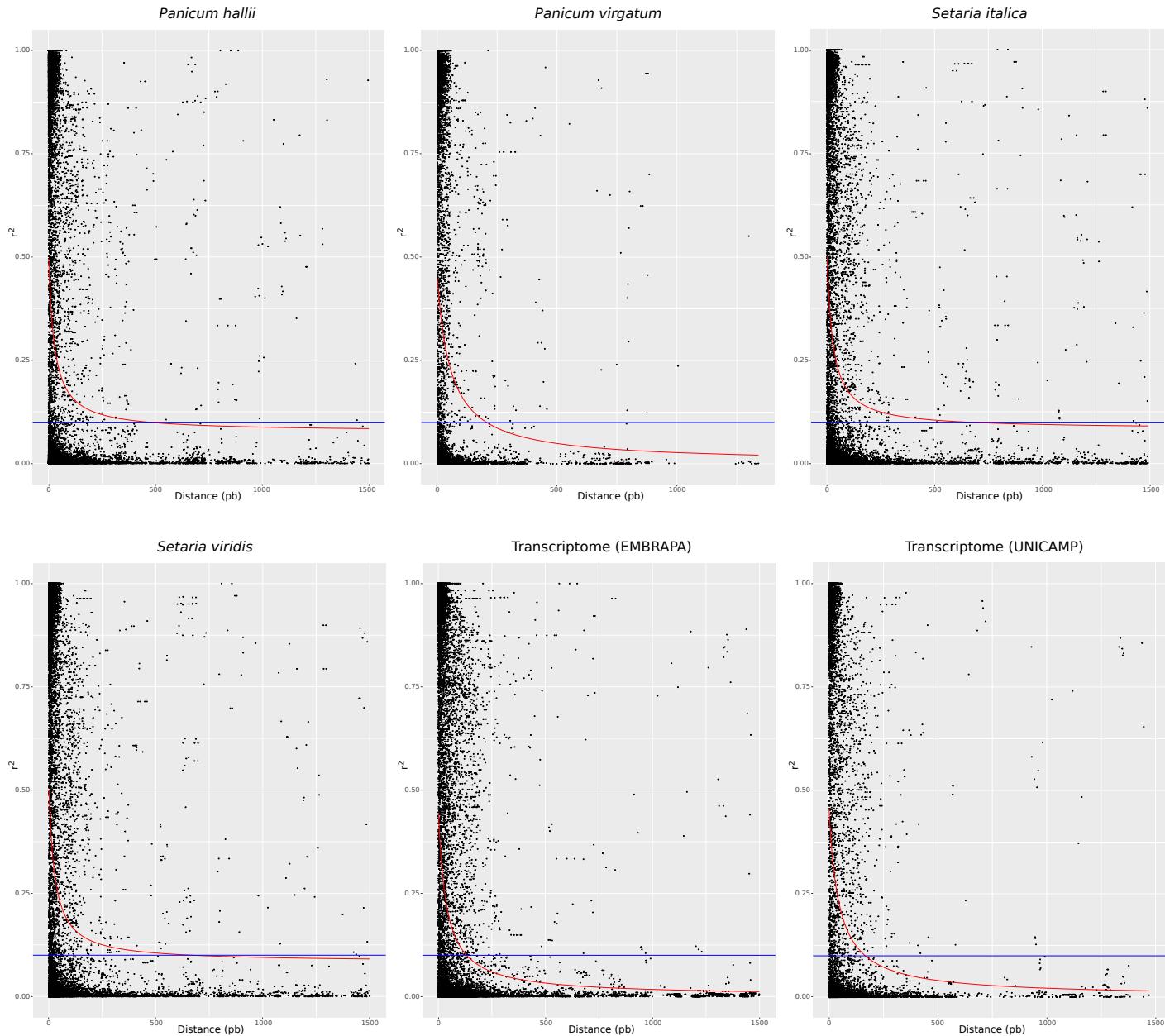
**Figure S2** Proportion of missing data in GBS markers using *Panicum hallii*, *Panicum virgatum*, *Setaria italica*, *Setaria viridis*, and two transcriptomes of *Panicum maximum* (obtained by EMBRAPA and UNICAMP research groups) as reference genomes.



**Figure S3** Heatmaps of relationship matrices for 530 individuals using: (A) additive relationship matrix based on pedigree information; and (B) genomic relationship matrix based on molecular markers.

**A****B**

**Figure S4** Principal component analysis (PCA) using: (A) parental molecular data; and (B) progeny molecular data.



**Figure S5** Linkage disequilibrium (LD) calculated as squared Pearson correlation,  $r^2$ , using *Panicum hallii*, *Panicum virgatum*, *Setaria italica*, *Setaria viridis*, and two transcriptomes of *Panicum maximum* (obtained by EMBRAPA and UNICAMP research groups) as reference genomes. Red lines are LD decay and blue lines are  $r^2 = 0.1$ .

**Table S3 Predicted residual error sum of squares (PRESS) of genomic selection models using tetraploid dosage (GS-TD) for organic matter (OM), crude protein (CP), *in vitro* digestibility of organic matter (IVD), leaf dry matter (LDM), regrowth capacity (RC), and percentage of leaf blade (PLB). Molecular data contains 41,424 markers.**

Model	OM	CP	IVD	LDM	RC	PLB
GBLUP-TD	90.4495	98.0999	435.4498	2603994	116.7085	2476.148
BRR-TD	90.2800	98.2686	438.0750	2616551	115.7767	2503.678
BA-TD	90.3069	99.0743	443.2646	2644412	115.7348	2541.937
BB-TD	89.9856	98.4550	439.5213	2618234	115.8339	2505.119
BC-TD	90.2337	98.1835	437.4437	2610263	115.9343	2494.210
BL-TD	90.3840	98.0920	436.7276	2778360	116.0370	2507.217

**Table S4 Mean predictive ability of genomic selection models using tetraploid dosage (GS-TD models) for organic matter (OM), crude protein (CP), *in vitro* digestibility of organic matter (IVD), leaf dry matter (LDM), regrowth capacity (RC), and percentage of leaf blade (PLB). Lower and upper limits are in parentheses. GS-TD models with the highest mean predictive ability for each trait are indicated in bold. Molecular data contains 41,424 markers.**

Model	OM	CP	IVD	LDM	RC	PLB
GBLUP-TD	0.4170 (0.39; 0.45)	0.2301 (0.19; 0.27)	0.2369 (0.19; 0.29)	0.1786 (0.14; 0.22)	0.2667 (0.22; 0.30)	<b>0.1915</b> (0.16; 0.23)
BRR-TD	0.4189 (0.39; 0.45)	<b>0.2341</b> (0.21; 0.27)	0.2367 (0.19; 0.29)	<b>0.1812</b> (0.13; 0.21)	0.2818 (0.24; 0.33)	0.1844 (0.15; 0.22)
BA-TD	0.4206 (0.39; 0.45)	0.2322 (0.20; 0.27)	0.2322 (0.19; 0.29)	0.1762 (0.13; 0.22)	<b>0.2889</b> (0.24; 0.34)	0.1737 (0.13; 0.21)
BB-TD	<b>0.4229</b> (0.39; 0.45)	0.2331 (0.20; 0.27)	0.2348 (0.19; 0.29)	0.1789 (0.12; 0.21)	0.2829 (0.24; 0.33)	0.1829 (0.14; 0.22)
BC-TD	0.4194 (0.39; 0.45)	0.2337 (0.20; 0.27)	0.2367 (0.19; 0.29)	0.1809 (0.12; 0.21)	0.2793 (0.24; 0.32)	0.1863 (0.15; 0.22)
BL-TD	0.4173 (0.39; 0.45)	0.2335 (0.20; 0.27)	<b>0.2377</b> (0.20; 0.30)	0.1610 (0.11; 0.21)	0.2773 (0.24; 0.32)	0.1826 (0.14; 0.22)
Average	0.4194	0.2328	0.2358	0.1761	0.2795	0.1836

**Table S5 Comparison between the predictions of individual plant values based on their half-sib family means and the genomic prediction of the individuals for organic matter (OM), crude protein (CP), *in vitro* digestibility of organic matter (IVD), leaf dry matter (LDM), regrowth capacity (RC), and percentage of leaf blade (PLB).**

Model	OM	CP	IVD	LDM	RC	PLB
Prediction of individuals	0.3466	0.2642	0.3085	0.1786	0.2731	0.2628
Only maternal effects	0.0758	0.0478	0.0552	0.1843	0.0668	0.0452