

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	VCOV	AIC	BIC	VCOV	AIC	BIC		
ID	3063.959	3087.252	ID	2779.554	2826.140	ID	3368.388	3391.681	ID	3179.970	3255.672	ID	9533.019	9556.326	ID	9422.892	9469.507		
DIAG	3049.895	3090.658	DIAG	2719.693	2783.748	DIAG	3297.954	3338.716	DIAG	3148.916	3242.088	DIAG	9484.456	9525.243	DIAG	9408.044	9472.139		
CS	2803.479	2832.595	CS	2754.596	2807.005	CS	3258.909	3288.026	CS	3178.740	3250.266	CS	9474.068	9503.203	CS	9420.415	9472.857		
CS_{Het}	2794.751	2841.337	CS_{Het}	2709.854	2779.733	CS_{Het}	3200.774	3247.360	CS_{Het}	3149.236	3248.231	CS_{Het}	9435.728	9482.343	CS_{Het}	9409.021	9478.943		
AR1	2797.363	2826.479	AR1	2775.788	2828.197	AR1	3251.368	3280.484	AR1	3178.638	3260.164	AR1	9466.962	9496.097	AR1	NC	NC		
$AR1_{Het}$	2789.753	2836.339	$AR1_{Het}$	2708.930	2778.809	$AR1_{Het}$	3195.305	3241.891	$AR1_{Het}$	3148.321	3247.316	$AR1_{Het}$	9422.892	9469.507	$AR1_{Het}$	9406.941	9476.863		
Po	12104.230	12133.350	Po	2758.268	2810.677	Po	12416.700	12445.820	Po	3174.050	3255.576	Po	18560.660	18589.790	Po	9424.248	9476.689		
Po_{Het}	2779.554	2826.140	Po_{Het}	2719.181	2789.060	Po_{Het}	3196.917	3243.503	Po_{Het}	3148.092	3247.089	Po_{Het}	9426.396	9473.011	Po_{Het}	9408.675	9478.597		
US	2769.626	2845.329	US	2709.617	2808.612	US	3179.970	3255.672	US	3155.054	3283.166	US	9423.504	9499.253	US	9414.088	9513.145		
		LDM						RC						PLB					
G_L matrix		R_L matrix						G_L matrix						R_L matrix					
VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC	VCOV	AIC	BIC		
ID	53201.13	53227.23	ID	49748.58	49826.35	ID	4548.200	4574.304	ID	3487.264	3741.784	ID	28968.90	28994.99	ID	28255.82	28304.10		
DIAG	52447.27	52519.03	DIAG	48864.58	48988.52	DIAG	4513.644	4585.431	DIAG	3428.622	3728.825	DIAG	28288.59	28360.35	DIAG	28151.75	28275.69		
CS	51313.65	51346.26	CS	49103.34	49188.14	CS	3852.530	3885.161	CS	3451.710	3712.756	CS	28904.76	28937.38	CS	28202.86	28287.66		
CS_{Het}	50574.92	50653.19	CS_{Het}	NC	NC	CS_{Het}	3815.413	3893.727	CS_{Het}	3383.097	3689.826	CS_{Het}	28225.82	28304.10	CS_{Het}	28150.19	28280.65		
AR1	NC	NC	AR1	48979.35	49064.15	AR1	3706.684	3739.315	AR1	3458.770	3719.816	AR1	28968.69	29001.30	AR1	28227.66	28312.46		
$AR1_{Het}$	49939.84	50018.11	$AR1_{Het}$	NC	NC	$AR1_{Het}$	3674.901	3753.214	$AR1_{Het}$	3390.138	3696.867	$AR1_{Het}$	NC	NC	$AR1_{Het}$	28150.72	28281.18		
Po	81842.27	81874.88	Po	49130.54	49215.34	Po	33378.910	33411.540	Po	3450.158	3711.204	Po	57673.16	57705.78	Po	28225.28	28310.08		
Po_{Het}	49748.58	49826.85	Po_{Het}	48197.90	48328.36	Po_{Het}	3621.193	3699.507	Po_{Het}	3391.690	3698.419	Po_{Het}	28279.11	28357.39	Po_{Het}	28153.18	28283.64		
US	NC	NC	US	NC	NC	US	3487.264	3741.784	US	NC	NC	US	28169.81	28424.21	US	NC	NC		

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%)

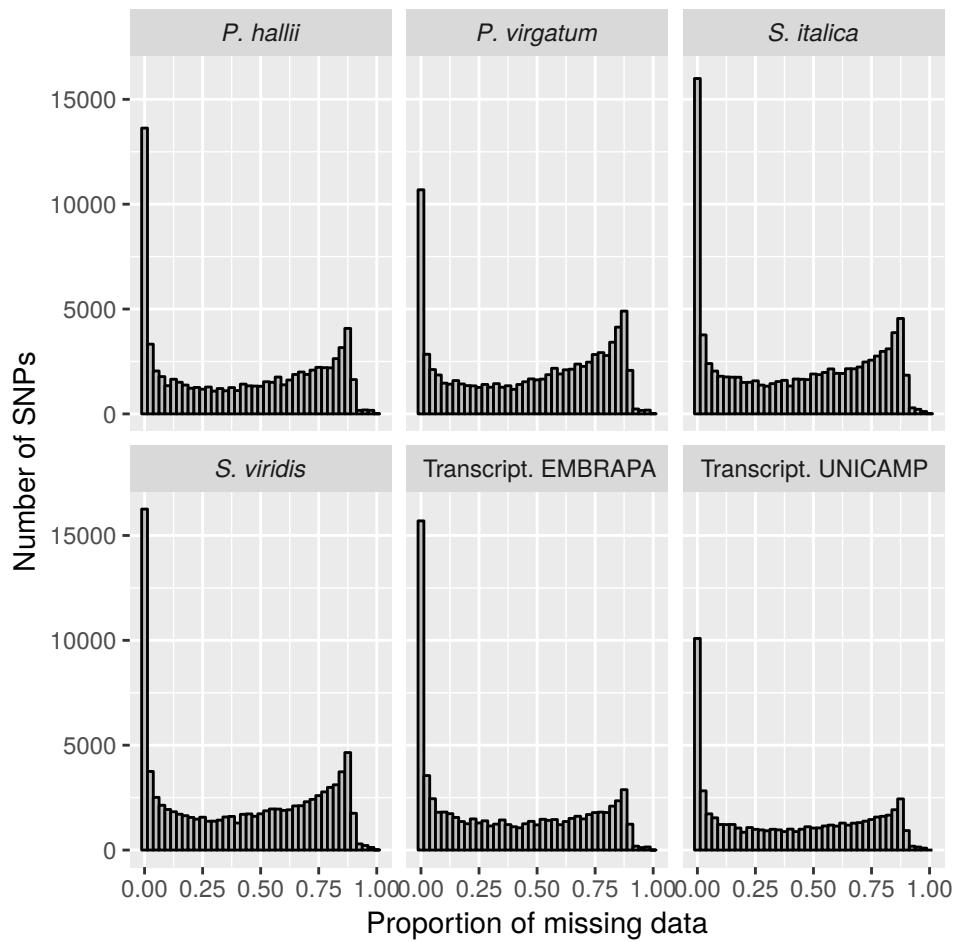


Figure S2 Proportion of missing data in GBS markers using *Panicum hallii*, *Panicum virgatum*, *Setaria italica*, *Setaria viridis*, and two transcriptomes of *Panicum maximum* (obtained by EMBRAPA and UNICAMP research groups) as reference genomes.

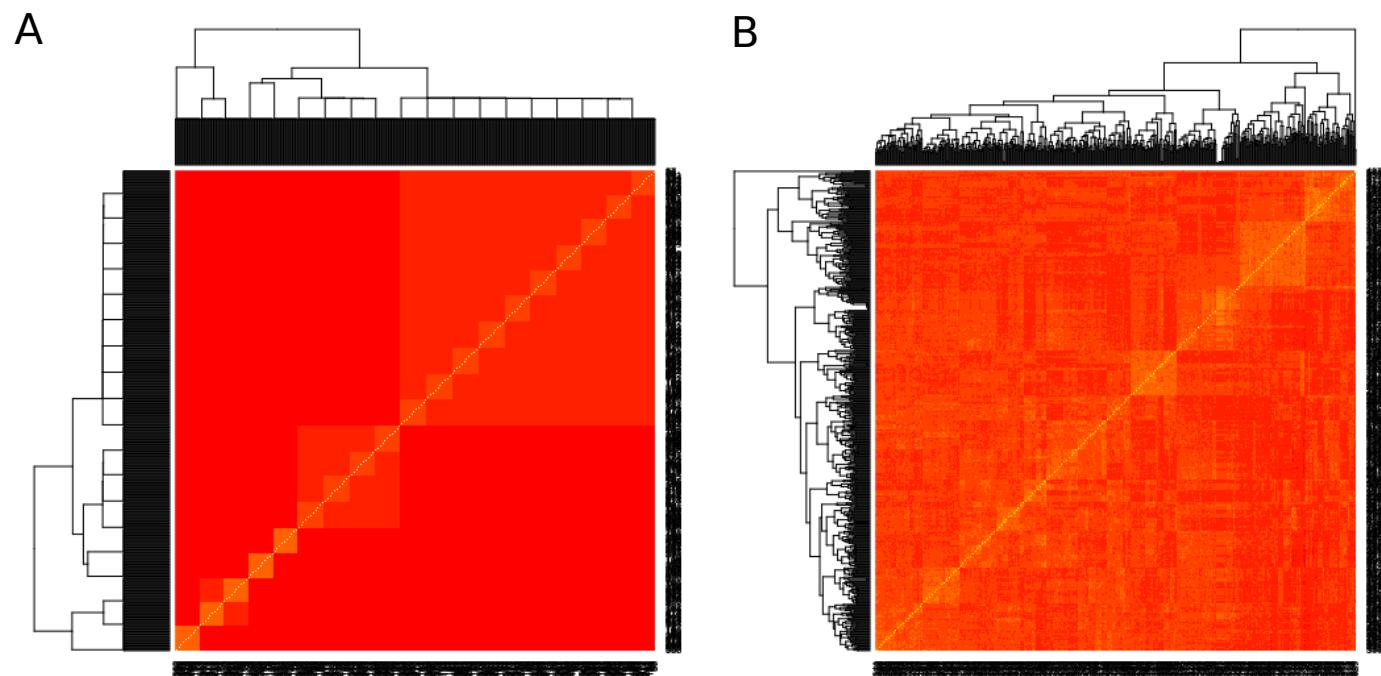


Figure S3 Heatmaps of relationship matrices for 530 individuals using: (A) additive relationship matrix based on pedigree information; and (B) genomic relationship matrix based on molecular markers.

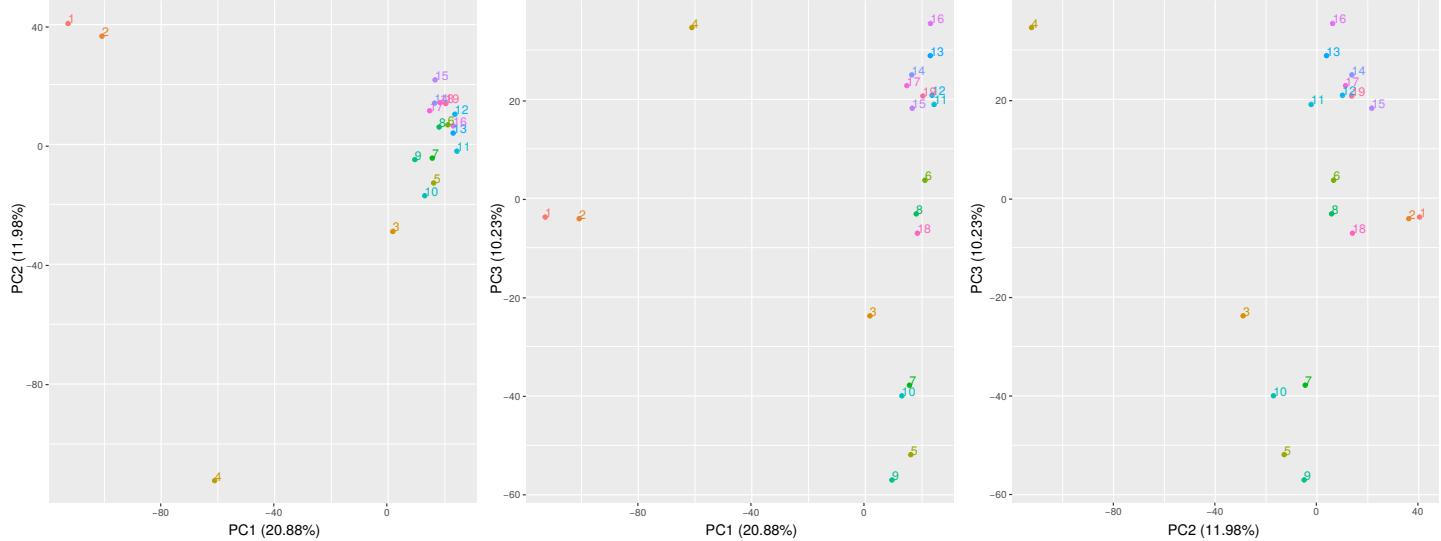
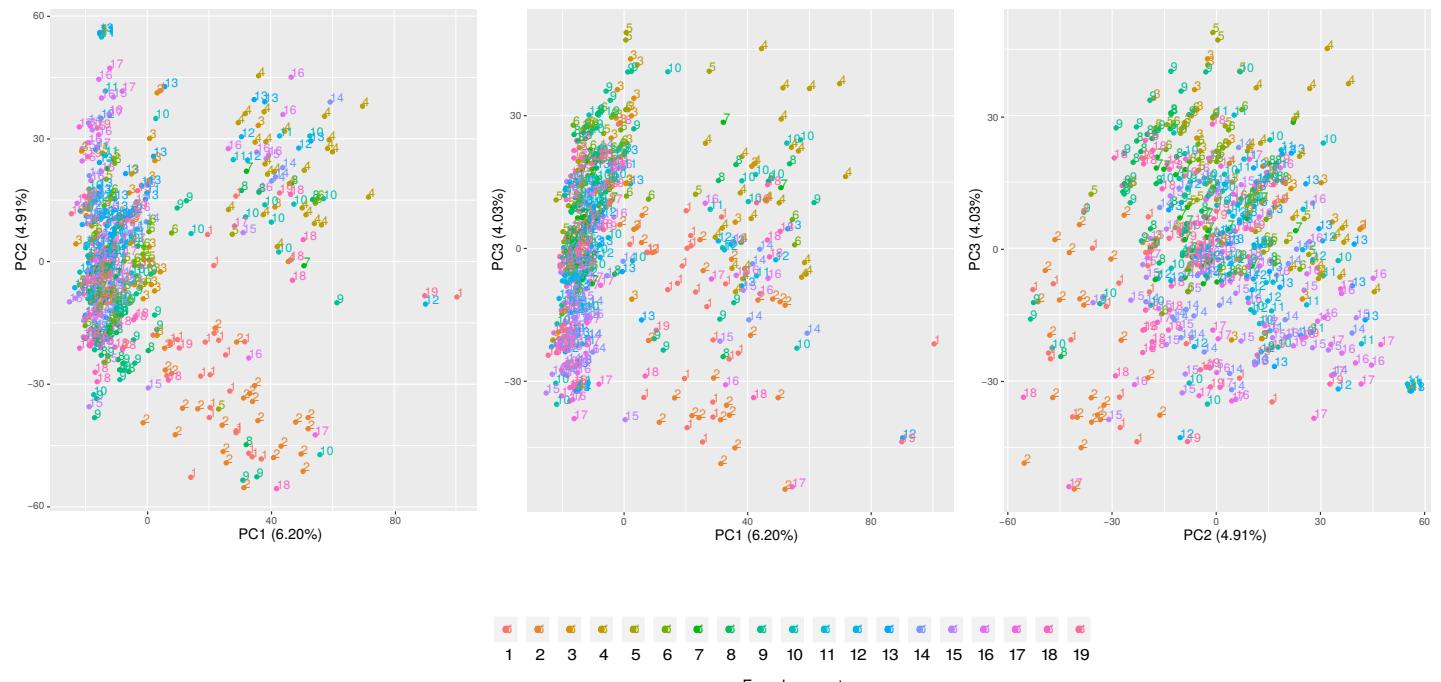
A**B**

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

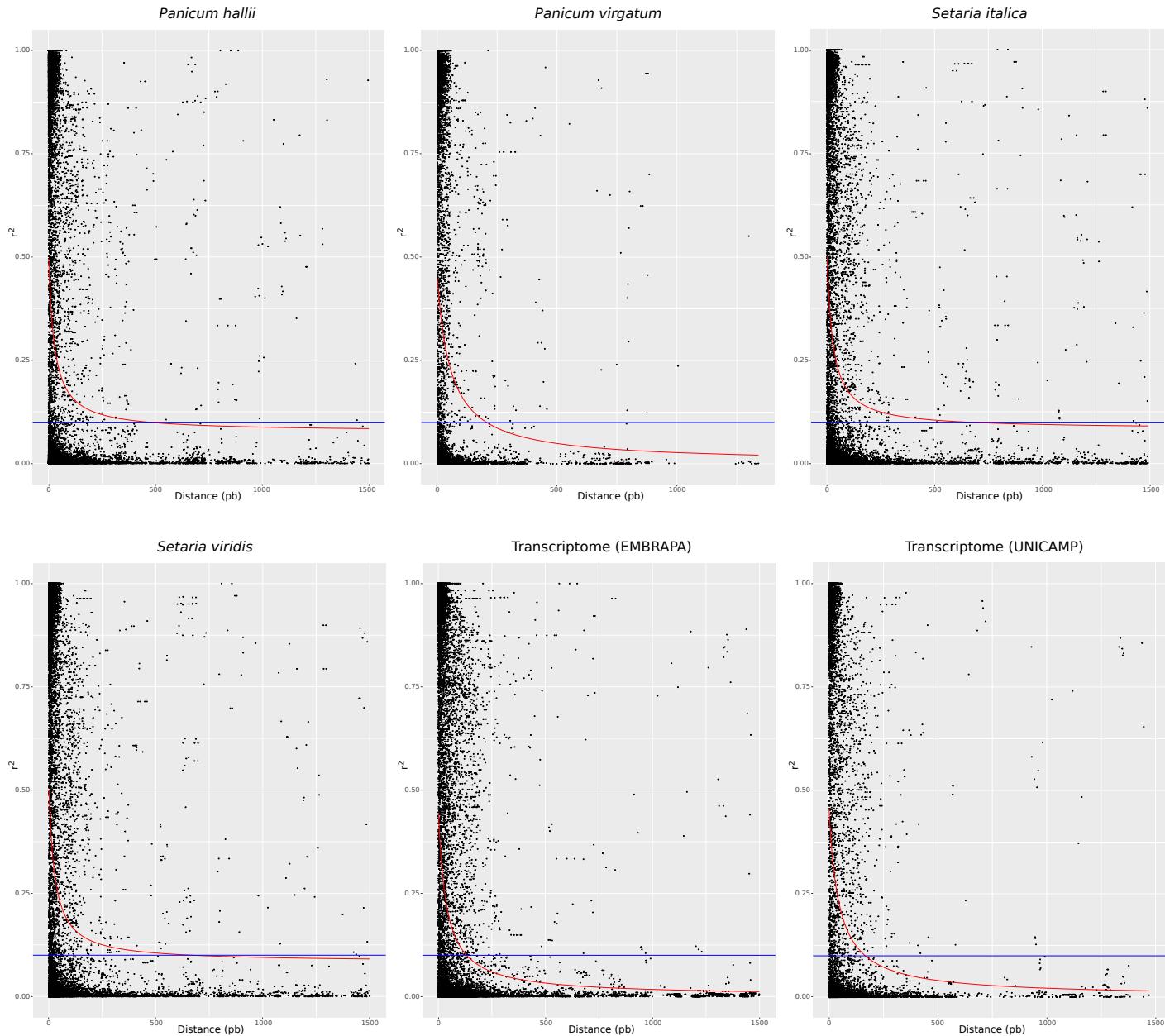


Figure S5 Linkage disequilibrium (LD) calculated as squared Pearson correlation, r^2 , *Panicum hallii*, *Panicum virgatum*, *Setaria italica*, *Setaria viridis*, and two transcriptomes of *Panicum maximum* (obtained by EMBRAPA and UNICAMP research groups) as reference genomes. Red lines are LD decay 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	92.9435	100.2830	435.2424	28026.20	103.2576	5112.803
BRR-TD	92.7964	100.4924	437.8210	28669.28	102.7981	5114.345
BA-TD	92.8276	101.3066	442.9697	29268.08	102.9785	5156.154
BB-TD	92.5074	100.7038	439.2393	28542.16	102.8898	5134.251
BC-TD	92.7423	100.4191	437.2531	28394.85	102.8985	5115.418
BL-TD	92.9028	100.2947	436.4833	29006.38	102.9359	5107.220

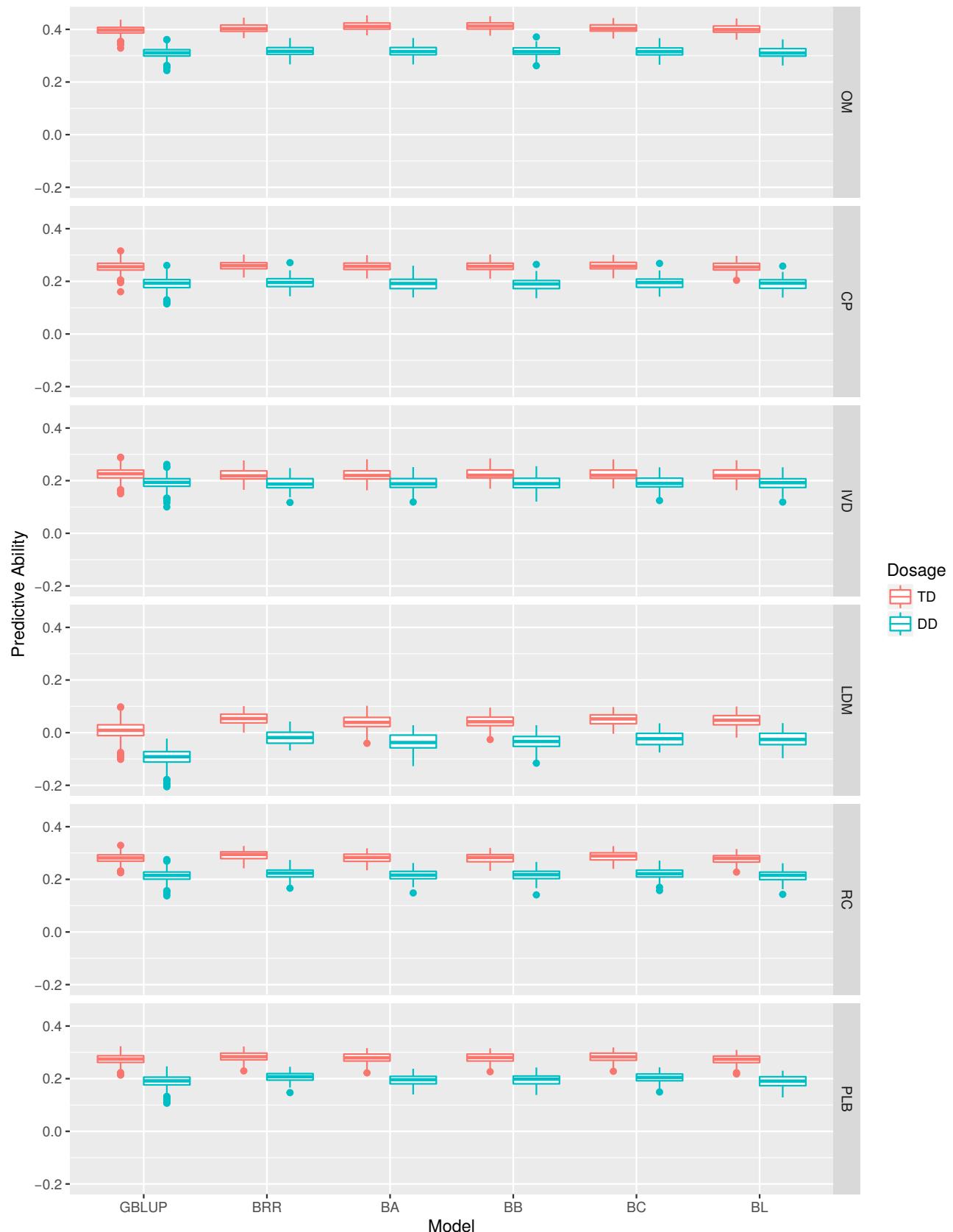


Figure S6 Comparison between genomic selection models using tetraploid dosage (GS-TD) and diploid dosage (GS-DD), for organic matter (OM), crude protein (CP), *in vitro* digestibility of organic matter (IVD), leaf dry matter (LDM), regrowth capacity (RC), and percentage of leaf blade (PLB). Molecular matrices containing 1,223 markers for each data set.

Table S4 Mean predictive ability of genomic selection models using tetraploid dosage (GS-TD) and diploid dosage (GS-DD) 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). GS-TD and GS-DD models with the highest mean predictive ability for each trait are indicated in bold. Molecular matrices containing 1,223 markers for each data set.

Model	OM	CP	IVD	LDM	RC	PLB
GBLUP-TD	0.3969	0.2548	0.2259	0.0086	0.2804	0.2740
GBLUP-DD	0.3106	0.1906	0.1931	-0.0928	0.2138	0.1904
BRR-TD	0.4042	0.2590	0.2209	0.0529	0.2907	0.2835
BRR-DD	0.3165	0.1955	0.1900	-0.0171	0.2216	0.2056
BA-TD	0.4127	0.2559	0.2226	0.0392	0.2820	0.2790
BA-DD	0.3161	0.1909	0.1901	-0.0353	0.2159	0.1949
BB-TD	0.4139	0.2558	0.2247	0.0394	0.2802	0.2795
BB-DD	0.3161	0.1892	0.1910	-0.0341	0.2168	0.1949
BC-TD	0.4049	0.2585	0.2242	0.0493	0.2865	0.2827
BC-DD	0.3153	0.1939	0.1924	-0.0219	0.2211	0.2040
BL-TD	0.4004	0.2538	0.2235	0.0462	0.2778	0.2728
BL-DD	0.3120	0.1903	0.1918	-0.0252	0.2140	0.1898
Average GS-TD	0.4055	0.2563	0.2236	0.0393	0.2829	0.2786
Average GS-DD	0.3144	0.1917	0.1914	-0.0377	0.2172	0.1966