Supplementary Materials

Table S1. Descriptive statistics for measured dry matter yield (DMY [kg ha⁻¹]) across different ploidy levels and three different cuts; reported DMY mean values over the cuts were used as a reference for relative root mean square error (rRMSE).

	Dry Matter Yield [kg DM ha⁻¹]							
	diploid				tetraploid			
	mean	sd	min	max	mean	sd	min	max
cut 1	4058	854	2308	6506	5520	761	3626	7595
cut 4	1395	197	785	2469	2014	230	1446	2687
cut 5	882	160	433	1319	1193	185	733	1802
mean	2112	1485	433	6506	2905	1935	733	7595

Table S2. Results of Linear Model (LM), Partial Least Square Regresssion (PLSR), Random Forest (RF), and Support Vector Machines (SVM) methods for DMY estimation. Lowest root mean square error (RMSE) and relative RMSE per group are underlined.

group	dataset	RMSE [kg ha⁻¹] (rRMSE)			
		LM	PLSR	RF	SVM
all	1.CHMrgb	897 (35.9%)	NA	NA	NA
	2.CHMms	743 (29.7%)	NA	NA	NA
	3.VIrgb	NA	824 (33%)	536 (21.5%)	767 (30.7%)
	4.VIrgb+HIS	NA	828 (33.1%)	527 (21.1%)	770 (30.8%)
	5.VIms	NA	478 (19.1%)	431 (17.2%)	444 (17.8%)
	6.CHMrgb+VIrgb	NA	545 (21.8%)	414 (16.6%)	523 (20.9%)
	7.CHMrgb+VIrgb+HIS	NA	544 (21.8%)	412 (16.5%)	516 (20.7%)
	8.CHMms+VIms	NA	417 (16.7%)	382 (15.3%)	397 (15.9%)
diploid	1.CHMrgb	654 (31%)	NA	NA	NA
	2.CHMms	591 (28%)	NA	NA	NA
	3.VIrgb	NA	667 (31.6%)	465 (22%)	651 (30.8%)
	4.VIrgb+HIS	NA	667 (31.6%)	445 (21.1%)	633 (30%)
	5.VIms	NA	452 (21.4%)	414 (19.6%)	442 (20.9%)
	6.CHMrgb+VIrgb	NA	440 (20.8%)	345 (16.3%)	423 (20%)
	7.CHMrgb+VIrgb+HIS	NA	438 (20.7%)	345 (16.3%)	416 (19.7%)
	8.CHMms+VIms	NA	347 (16.5%)	308 (14.6%)	326 (15.4%)
tetraploid	1.CHMrgb	986 (34%)	NA	NA	NA
	2.CHMms	821 (28.2%)	NA	NA	NA
	3.VIrgb	NA	695 (23.9%)	492 (16.9%)	680 (23.4%)
	4.VIrgb+HIS	NA	705 (24.3%)	500 (17.2%)	681 (23.5%)
	5.VIms	NA	478 (16.4%)	432 (14.9%)	444 (15.3%)
	6.CHMrgb+VIrgb	NA	528 (18.2%)	397 (13.6%)	507 (17.5%)
	7.CHMrgb+VIrgb+HIS	NA	512 (17.6%)	396 (13.6%)	479 (16.5%)
	8.CHMms+VIms	NA	416 (14.3%)	380 (13.1%)	397 (13.7%)

(a)

1	2	3	4	5	6	7	8	dataset
-	****	****	****	****	****	****	****	1
	-	****	****	****	****	****	****	2
		-	ns	****	****	****	****	3
			-	****	****	****	****	4
				-	ns	ns	***	5
					-	ns	**	6
						-	**	7
							-	8

(b)

1	2	3	4	5	6	7	8	dataset
-	****	****	****	****	****	****	****	1
	-	****	****	****	****	****	****	2
		-	ns	****	****	****	****	3
			-	*	****	****	****	4
				-	****	****	****	5
					-	ns	***	6
						-	****	7
							-	8

(c)

1	2	3	4	5	6	7	8	dataset
-	****	****	****	****	****	****	****	1
	-	****	****	****	****	****	****	2
		-	ns	****	****	****	****	3
			-	****	****	****	****	4
				-	*	**	****	5
					-	ns	ns	6
						-	ns	7
							-	8

the significance level of adjusted p-values

****	≤ 0.0001
***	≤ 0.001
**	≤ 0.01
*	≤ 0.05
ns	> 0.05

dataset:
1. CH_{RGB}
2. CH_{MS}
3. VI_{RGB}
4. $VI_{RGB}+HIS$
5. VI_{MS}
6. $CH_{RGB}+VI_{RGB}$
7. $CH_{RGB}+VI_{RGB}+HIS$
8. $CH_{MS}+VI_{MS}$

Figure S1. Wilcoxon Signed Rank Test results showing significance levels of adjusted p-value between compared datasets for (a) all plots, (b) diploid, and (c) tetraploid plots.