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Supplemental Table S1. Nutrients used in the multivariate steps and sample removal rates for forages

Supplemental Table S1. Nutrients used in the multivariate steps and sample removal rates for forages  Additional Start N <sup>3</sup> Removal rate, <sup>4</sup> % Final							
Feed <sup>1</sup>	Additional nutrients used <sup>2</sup>	Start N <sup>3</sup>	UNI	Final clusters <sup>5</sup>			
Alfalfa hay	Ash, LIG	6,929	1.5	PCA 1.4	CLS 4.9	Total 7.6	2
Alfalfa hay	Ash, LIG	1,247	2.7	0.8	0.0	3.5	1
Alfalfa hay, western	Ash, LIG	718	3.9	1.4	6.9	11.8	3
Alfalfa silage	Ash, LIG	13,276	4.3	0.9	0.0	5.1	2 <sup>a</sup>
Alfalfa silage	Ash, LIG	816	3.3	0.7	4.4	8.2	2
Barley hay	Ash, LIG, STA	112	5.4	0.9	12.1	17.6	2
Barley silage	Ash, LIG, STA	4,123	5.5	1.9	0.0	7.3	2
Coastal bermudagrass hay	Ash	120	3.3	0.8	0.0	4.2	1
Coastal bermudagrass silage	Ash	75	4.0	0.0	0.0	4.0	2
Corn silage	Ash, LIG, STA	109,190	3.9	1.7	0.0	5.5	1
Corn silage	Ash, LIG, STA	49,021	3.6	1.4	8.4	12.9	1
Corn silage, BMR	Ash, LIG, STA	8,677	3.5	1.5	0.0	4.9	2
Corn silage, BMR	Ash, LIG, STA	1,006	3.0	0.8	9.1	12.5	3
Corn plants, fresh	Ash, LIG, STA	21,502	2.8	1.2	0.4	4.4	2
Corn silage, sweet corn	Ash	99	3.0	2.1	0.0	5.0	1
Corn stalks	Ash	363	7.2	2.8	0.0	9.8	3
Corn stalks	Ash	161	2.5	0.6	45.6	47.3	2
Fescue hay	Ash	234	3.4	0.4	14.8	18.1	2
Fescue silage	Ash	94	2.1	1.1	7.5	10.5	2 <sup>a</sup>
Grass hay, unclassified	Ash, LIG	16,709	4.5	1.5	3.6	9.2	2
Grass hay, unclassified	Ash, LIG	4,494	3.3	1.0	0.0	4.3	2
Grass silage	Ash, LIG	10,007	3.7	1.1	0.0	4.8	3
Grass silage	Ash, LIG	1,133	3.8	0.6	4.3	8.5	2
Haycrop hay, unclassified	Ash, LIG	61,637	3.6	1.0	8.9	13.1	4
Haycrop silage, unclassified	Ash, LIG	166,545	3.8	0.8	0.3	4.9	5
Legume hay	Ash, LIG	4,675	2.5	1.4	0.0	3.8	3
Legume silage	Ash, LIG	3,829	3.6	0.7	0.0	4.3	2
Mixed hay	Ash, LIG	22,602	2.0	1.0	0.0	3.0	1
Mixed silage	Ash, LIG	64,094	3.3	1.1	0.5	4.9	2
Oat hay	Ash, LIG	1,426	3.5	1.2	12.3	16.4	2
Oat hay	Ash, LIG	167	1.8	0.0	7.3	9.0	2
Oat silage	Ash, LIG	3,966	6.8	0.9	0.0	7.6	2
Oat silage	Ash, LIG	517	3.5	0.6	6.1	9.9	2
Orchard grass hay	Ash, LIG	676	3.7	1.2	9.8	14.2	3
Orchard grass silage	Ash, LIG	255	2.4	0.8	5.2	8.2	2 <sup>a</sup>
Pasture hay	Ash, LIG	161	5.0	1.9	0.0	6.8	2 <sup>a</sup>
Pasture silage	Ash, LIG	847	4.5	1.6	7.1	12.6	3 <sup>b</sup>
Rye hay	Ash, LIG	652	5.2	1.2	4.7	10.8	2 <sup>a</sup>

## J. Dairy Sci. 97:5645-5656 http://dx.doi.org/10.3168/jds.2013-7724

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Rye silage	Ash, LIG	357	4.5	2.0	0.0	6.4	2
Rye silage	Ash, LIG	7,849	8.2	1.0	5.4	14.0	3 <sup>b</sup>
Small grain hay	Ash, LIG	351	3.1	1.4	5.8	10.1	2
Small grain hay	Ash, LIG	125	6.4	4.1	0.0	10.2	2
Small grain silage	Ash, LIG	5,285	4.7	0.8	0.0	5.5	3
Small grain silage	Ash, LIG	1,800	4.9	0.6	5.3	10.5	2
Sorghum hay	Ash	466	3.2	0.9	15.9	19.3	2
Sorghum silage	Ash, LIG, STA	3,277	4.9	1.3	0.0	6.1	2
Sorghum silage BMR	Ash, LIG	438	4.1	0.9	0.0	5.0	3
Sorghum Sudan BMR silage	Ash, LIG	101	5.0	2.0	0.0	6.9	2
Sorghum Sudan silage	Ash, LIG, STA	468	4.3	1.5	0.0	5.8	1
Sorghum Sudan silage	Ash, LIG	237	6.8	0.9	0.0	7.6	3
Soybean silage	Ash	439	3.4	0.5	23.1	26.1	3
Straw	Ash, LIG	2,033	7.6	3.1	0.0	10.4	2
Straw	Ash, LIG	710	7.7	2.4	0.0	9.9	2
Sudan hay	Ash	116	1.7	0.9	0.0	2.6	3
Sudan silage	Ash, LIG	392	4.8	2.1	0.0	6.8	2 <sup>a</sup>
Timothy hay	Ash	1,909	1.9	0.7	0.0	2.6	2
Triticale and peas silage	STA	98	4.1	1.0	0.0	5.1	3
Triticale hay	Ash, LIG, STA	262	4.2	1.6	0.0	5.7	3
Triticale silage	Ash, LIG	3,049	5.1	1.1	0.0	6.2	3
Triticale silage	Ash, LIG	218	6.0	0.5	7.1	13.0	1
Wheat hay	Ash, LIG, STA	837	3.7	1.5	10.9	15.4	2
Wheat silage	Ash, LIG	5,371	6.1	0.7	0.0	6.7	2 <sup>a</sup>
Wheat silage	Ash, LIG	239	3.3	0.4	0.0	3.8	2

<sup>&</sup>lt;sup>1</sup>Feed names as provided by laboratories. If rows have identical feed names, data within each row were provided by different laboratories.

<sup>2</sup>Additional nutrients as % of DM (all forages used DM, NDF, and CP) used in multivariate procedures;

Additional nutrients as % of DM (all forages used DM, NDF, and CP) used in multivariate procedures; LIG = lignin; STA = starch.

<sup>&</sup>lt;sup>3</sup>Starting N = number of records within a specific feed classification provided by a laboratory.

<sup>&</sup>lt;sup>4</sup>Removal rates for univariate (UNI), principal components analysis (PCA), and clustering (CLS) steps. Removal rates = (number of records to which the step was applied – number of records remaining after the step)/number of records to which the step was applied × 100. Total removal = (starting number of records – final number)/starting records × 100.

<sup>&</sup>lt;sup>5</sup>Number of clusters that were retained and combined into the final dataset.

<sup>&</sup>lt;sup>a</sup>Based on average nutrient composition of the clusters, the 2 clusters were tentatively identified as less mature and more mature.

<sup>&</sup>lt;sup>b</sup>Based on average nutrient composition of the clusters, the 3 clusters were tentatively identified as immature, mid-maturity, and mature.

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Supplemental Table S2. Nutrients used in the multivariate steps and sample removal rates for byproduct feeds

product feeds	Additional	Start	Removal rate, <sup>4</sup> %				Final
Feed <sup>1</sup>	nutrients used <sup>2</sup>	$N^3$	UNI	PCA	CLS	Total	clusters <sup>5</sup>
Almond hulls	NDF, ash	448	8.7	3.8	6.4	17.8	2
Bakery By-product	NDF, ash, fat	588	5.4	2.3	5.6	12.8	2
Beet pulp, dry	NDF, ash	243	6.2	1.7	14.3	21.0	2
Beet pulp, wet	NDF, ash	160	8.1	2.6	8.1	17.7	1
Blood meal	Ash	183	9.3	2.3	4.8	15.7	1
Brewers grains, wet	NDF, ash	1,010	3.0	1.1	4.6	8.4	3
Candy meal	NDF, ash	125	2.4	2.5	22.7	26.4	1
Cereal By-product	NDF, ash	153	5.2	0.7	0.0	5.9	1
Chocolate By-product	NDF, ash	118	2.5	4.3	8.2	14.4	2
Citrus pulp dried	NDF, ash	189	7.4	3.9	19.9	28.7	1
Corn gluten feed, dry	NDF, ash	438	4.8	2.4	14.5	20.5	2
Corn gluten feed, wet	NDF, ash	213	3.3	1.4	14.0	18.0	2
Corn gluten feed, wet	NDF, ash	63	4.8	4.9	0.0	9.4	2
Corn gluten meal	NDF, ash	127	3.1	2.4	46.7	50.4	2
Corn screenings	NDF, ash	92	9.8	3.4	0.0	12.9	1
Corn screenings	NDF, ash, STA	276	4.7	2.3	0.0	6.9	4
Cotton gin	NDF, ash	71	5.6	0.0	9.0	14.1	1
Cottonseed hulls	NDF, ash	197	4.6	3.2	57.1	60.9	1
Distillers grains syrup	NDF, ash, fat	645	11.2	3.2	0.0	14.0	3
Distillers grains syrup	Ash	297	1.7	1.0	11.3	13.7	3
Distillers grains, wet	NDF, ash, fat	1,674	2.6	1.6	0.0	4.2	2
Distillers grains, wet	NDF, ash, fat	1,082	8.3	2.8	38.9	45.6	2 <sup>a</sup>
Distillers grains, dry	NDF, ash, fat	1,610	5.8	2.1	17.0	23.5	2
Distillers grains, dry	NDF, ash, fat, NDICP	2,384	9.3	5.3	6.3	19.5	2 <sup>b</sup>
Feather meal	Fat	260	1.5	0.0	4.7	6.1	3
Hominy	NDF, ash	93	5.4	1.1	0.0	6.4	2
Hominy	NDF, ash, STA, fat	144	4.9	4.3	9.0	17.2	2 <sup>c</sup>
Pomace, tomato	NDF, ash	150	4.0	2.0	15.3	20.3	1
Meat and bone meal, porcine	Ash, fat	472	5.3	3.6	0.0	8.7	2
Potato by-product waste	NDF, ash, fat	144	6.9	5.2	10.2	20.7	2
Poultry meal	Ash, fat	574	0.3	0.7	28.2	28.9	7
Wheat red dog	Ash	1,884	1.8	0.8	23.1	25.1	2
Soybean hulls	NDF, ash	327	6.4	4.5	5.3	15.4	3
Vegetables, mixed	NDF, ash	220	3.6	1.4	14.7	18.9	3
Wheat middlings	Ash	4,510	1.4	1.1	27.5	29.3	4
Whey by-product, wet	NDF, ash, sugar	115	7.0	3.6	0.0	10.3	3

### J. Dairy Sci. 97:5645-5656 http://dx.doi.org/10.3168/jds.2013-7724

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<sup>3</sup>Starting N = number of records within a specific feed classification provided by a laboratory.

<sup>&</sup>lt;sup>1</sup>Feed names as provided by laboratories. If rows have identical feed names, data within each row were provided by different laboratories.

<sup>&</sup>lt;sup>2</sup>Additional nutrients as % of DM (used in multivariate procedures; STA = starch (all by-products used DM and CP).

<sup>&</sup>lt;sup>4</sup>Removal rates for univariate (UNI), principal components analysis (PCA), and clustering (CLS) steps. Removal rates = (number of records to which the step was applied – number of records remaining after the step)/number of records to which the step was applied × 100. Total removal = (starting number of records – final number)/starting records × 100.

<sup>&</sup>lt;sup>5</sup>Number of clusters that were retained and combined into the final dataset.

<sup>&</sup>lt;sup>a</sup>Based on average nutrient composition of the clusters, the 2 clusters were tentatively identified as modified wet distillers grains (i.e., additional water removed) and conventional wet distillers grains.

<sup>b</sup>Based on average nutrient composition of the clusters, the 2 clusters were tentatively identified as samples in which NDF and NDICP were determined with and without sodium sulfite (NDF assay without sodium sulfite results in greater concentrations of NDICP and NDF).

<sup>&</sup>lt;sup>c</sup>Based on average nutrient composition of the clusters, the 2 clusters were tentatively identified as lowand high-fat hominy.

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Supplemental Table S3. Nutrients used in the multivariate steps and sample removal rates for grains, oilseeds, and oilseed meals

	Additional	Start	Removal rate, <sup>4</sup> %				Final
Feed <sup>1</sup>	nutrients used <sup>2</sup>	N <sup>3</sup>	UNI	PCA	CLS	Total	clusters <sup>5</sup>
Grains							
Barley	NDF, ash, STA	399	5.3	1.8	0.0	7.0	2
Corn ear, high moisture	NDF, STA	1,437	1.7	0.5	14.8	16.6	4
Corn earlage, high moisture	NDF, STA	1,391	1.9	1.6	12.4	15.5	5
Corn, dry	NDF, ash, STA	696	5.5	3.2	5.6	13.6	2
Corn, dry	NDF, ash, STA	4876	5.7	3.8	14.5	23.1	2
Corn, high moisture	NDF, ash, STA	17,788	4.3	1.5	0.0	5.7	2
Corn, high moisture	NDF, ash, STA	8,376	2.1	1.0	0.0	3.2	2
Corn snaplage	NDF, STA	1,209	1.7	0.6	0.0	2.2	3
Corn snaplage	NDF, ash, STA	4,697	3.2	2.2	7.9	12.7	2
Oats	NDF, ash	162	4.9	0.6	10.1	15.1	1
Small grains, unclassified	NDF, STA	402	5.0	1.8	15.9	21.5	2
Small grains, unclassified	NDF, ash	229	4.4	2.3	0.0	6.5	2
Wheat	NDF, ash, STA	920	2.9	2.7	10.1	15.1	2
Oilseeds and meals							
Canola meal	NDF, ash	642	5.5	3.2	12.1	19.5	1
Cottonseed meal, solvent	NDF, ash	69	7.2	3.1	12.9	21.7	1
Cottonseed, whole	NDF, ash, fat	359	10.0	3.6	5.3	17.8	2
Soybean meal, solvent	None	247	5.3	2.5	0.0	7.6	2
Soybean meal, expellers	Fat	1,228	3.2	2.3	30.4	34.1	2
Soybeans, whole roasted	NDF, ash, fat	170	8.2	0.0	7.9	15.5	2
Soybeans, whole	Fat	85	7.1	1.2	0.0	8.2	1

<sup>&</sup>lt;sup>1</sup>Feed names as provided by laboratories. If rows have identical feed names, data within each row were

provided by different laboratories.

Additional nutrients as % of DM (used in multivariate procedures); STA = starch (all feeds in table used DM and CP).

<sup>&</sup>lt;sup>3</sup>Starting N = number of records within a specific feed classification provided by a laboratory.

<sup>&</sup>lt;sup>4</sup>Removal rates for univariate (UNI), principal components analysis (PCA), and clustering (CLS) steps. Removal rates = (number of records to which the step was applied - number of records remaining after the step)/number of records to which the step was applied × 100. Total removal = (starting number of records – final number)/starting records × 100.

<sup>&</sup>lt;sup>5</sup>Number of clusters that were retained and combined into the final dataset.