

Supplemental material 1 Climate data of the site in South Africa (Alma) and the two sites in Switzerland (Delley and Avenches). The two sites in Switzerland were situated close to each other and were subjected to the same climatic conditions. In South Africa, the field was irrigated due to the low precipitation level (*).

Flowering	Site	Year	Temp. daily mean (°C)	Temp. max (°C)	Temp. min (°C)	Precipitation daily mean (mm)	Precipitation max (mm)	Days with a minimum lower or equal		Days with a maximum higher or equal		
								6°C	12°C	24°C	30°C	35°C
before	Switzerland	2013	15.0	34.4	-0.5	2.79	53.4	27	79	44	13	0
after	Switzerland	2013	15.9	30.1	4.5	2.69	26.6	4	39	19	1	0
before	South Africa	2013	22.5	31.9	11.2	0.06*	8.4	0	3	54	16	1
after	South Africa	2013	22.7	35.1	11.3	0.02*	9.0	0	0	32	17	0
before	Switzerland	2014	15.4	33.7	0.5	2.04	22.0	18	74	39	7	0
after	Switzerland	2014	15.3	29.8	1.6	2.07	32.2	5	48	27	0	0
before	South Africa	2014	22.3	34.5	12.8	0.08*	14.8	0	0	49	21	0
after	South Africa	2014	22.4	32.6	10.9	0.09*	34	0	0	27	9	0

Supplemental material 3 Traits measured with the REST software and presented in the manuscript. Abbreviations: ROI: Region of Interest (Expansion of the root system after correction for outstanding roots).

Trait	Abbreviation	Description
Root angle opening	RoA	opening of the angle between left and right
Area convex hull [cm ²]	AcH	area of the convex hull
Area [cm ²]	area	area of all root derived pixels within the convex hull
0.95 quantile depth [cm]	depth	height of 90% ROI
Maximal width [cm]	mW	width of 90% ROI
total projected structure length [cm]	tpSL	total projected structure length within convex hull
median fractal dimension	mfD	fractal dimension derived from a box-count algorithm
Fill factor	Ff	Number of root derived pixels within convex hull divided by number of pixels within convex hull.
number of gaps [counts]	NoG	total number of gaps enclosed by root derived pixels
Median gap size [cm ²]	mGS	contains the summary statistics of background patches which are enclosed by root-derived pixel visualized
Medium structure width	mSW	distance of structure to background

Supplemental material 4 A: Prediction of mean values under either HN or LN conditions. B: Prediction of mean values across different environments (site + year + N fertilization level). C: Reduction under LN compared to HN in %. D: Genotypic mean values across environments and honest significant difference (HSD). E: Genotypic mean values under HN across environments of traits with a significant genotype by treatment interaction (GXT) and the reduction under LN compared to HN in %. Abbreviations: AVEN: Avenches, DEL: Delley, SA: Alma, South Africa, RoA: Root opening angle, mW: maximal width, mFD: median fractal dimension, area: area of root derived pixels, AcH: area of convex hull, Ff: fill factor, depth: 95 % quantile depth, tpSL: total projected structure length, mSW: medium structure width, mGS: median gap size, NoG: number of gaps, Shoot: Shoot fresh weight, SPAD: leaf greenness, Silage: Silage yield, % DM: percent dry matter, kernel: kernel yield and height: plant height.

A	Mean values under either LN or HN conditons																			
Environment	RoA	mW	mFD	area	AcH	Ff	depth	tpSL	mSW	mGS	NoG	Shoot	SPAD	vigor	lodging	staygreen	silage	% DM	kernel	height
High	82.8	12.18	1.80	100	190	0.551	16.97	903	0.166	0.0031	1092	1154.3	56.9	2.7	1.9	3.7	146.08	32.26	99.72	161.62
Low	75.5	11.22	1.79	83	172	0.509	16.55	788	0.147	0.0030	936	977.1	47.3	2.9	1.7	5.2	122.57	32.94	50.55	138.94
HSD	8.6	1.16	0.02	15	21	0.051	1.25	97	0.032	0.0007	165	187.8	9.0	0.2	0.2	0.6	6.52	0.55	12.53	2.01
B	Mean values of each environment-treatment combination																			
Environment	RoA	mW	mFD	area	AcH	Ff	depth	tpSL	mSW	mGS	NoG	Shoot	SPAD	vigor	lodging	staygreen	silage	% DM	kernel	height
AVEN_2013_H	94.1	14.35	1.79	125	279	0.451	21.90	1147	0.136	0.0033	1207	1241.4	56.8	2.2	2.7	5.1	155.92	34.92	NA	NA
AVEN_2013_L	94.5	14.39	1.77	115	272	0.420	21.19	1067	0.131	0.0034	1073	1101.5	51.0	2.6	2.2	5.4	138.79	35.73	NA	NA
AVEN_2014_H	87.1	12.57	1.78	96	224	0.433	19.41	1052	0.116	0.0020	1311	2024.0	60.5	3.0	1.5	4.7	140.90	31.08	NA	NA
DEL_2013_H	90.8	11.62	1.80	110	192	0.575	16.27	792	0.200	0.0056	753	912.0	59.5	2.8	1.9	2.5	141.13	30.00	NA	NA
DEL_2013_L	80.6	13.35	1.79	87	162	0.539	15.74	660	0.181	0.0047	617	739.1	53.8	3.1	1.8	4.9	105.37	29.72	NA	NA
DEL_2014_H	81.0	11.77	1.79	93	181	0.520	16.89	918	0.137	0.0023	1180	1693.1	60.3	2.8	1.4	2.4	146.36	33.04	NA	NA
DEL_2014_L	74.1	11.56	1.78	86	172	0.511	17.31	827	0.146	0.0022	1056	1503.8	54.4	2.7	1.3	4.3	128.73	34.54	NA	NA
SA_2013_H	80.7	10.87	1.82	104	159	0.654	14.99	784	0.229	0.0033	903	303.6	51.4	NA	NA	NA	NA	NA	88.73	165.86
SA_2013_L	72.0	11.72	1.81	88	143	0.613	15.01	709	0.198	0.0035	830	264.4	40.3	NA	NA	NA	NA	NA	63.02	164.07
SA_2014_H	62.8	10.69	1.83	72	106	0.672	12.33	723	0.174	0.0020	1201	751.9	53.1	NA	NA	NA	NA	NA	110.71	157.38
SA_2014_L	51.7	9.52	1.80	44	77	0.581	11.04	530	0.130	0.0021	885	407.0	33.6	NA	NA	NA	NA	NA	38.09	113.80
HSD	12.3	1.48	0.02	16	28	0.05	1.40	125	0.02	0.0005	188	160.5	5.1	1.0	1.0	1.6	19.65	1.73	70.45	16.66
C	Decrease under LN compared to HN in each environment (%)																			
Environment	RoA	mW	mFD	area	AcH	Ff	depth	tpSL	mSW	mGS	NoG	Shoot	SPAD	vigor	lodging	staygreen	silage	% DM	kernel	height
AVEN_2013	0.4	0.3	-1.1	-8.2	-2.5	-6.7	-3.2	-6.9	-3.4	2.2	-11.1	-11.3	-10.2	16.9	-16.5	6.6	-11.0	2.3	NA	NA
DEL_2013	-12.6	13.0	-0.4	-26.9	-18.5	-6.7	-3.4	-20.1	-10.9	-19.8	-22.0	-23.4	-10.5	10.4	-5.1	48.7	-33.9	-0.9	NA	NA
DEL_2014	-9.2	-1.8	-0.4	-7.5	-5.3	-1.7	2.4	-11.0	6.0	-0.6	-11.7	-12.6	-10.8	-1.0	-7.0	44.3	-13.7	4.4	NA	NA
SA_2013	-12.1	7.3	-1.0	-18.2	-11.4	-6.7	0.1	-10.6	-15.6	6.3	-8.7	-14.8	-27.6	NA	NA	NA	NA	NA	-40.8	-1.1
SA_2014	-21.6	-12.3	-1.8	-62.1	-38.4	-15.6	-11.6	-36.6	-33.8	3.5	-35.7	-84.7	-58.0	NA	NA	NA	NA	NA	-190.7	-38.3

D		Genotypic mean values across environments													
EuRoot_ID	Genotype	mFD	AcH	Ff	depth	tpSL	mSW	mGS	NoG	shoot	SPAD	vigor	lodging	%DM	kernel
1	B73	1.80	177	0.535	17.23	833.94	0.156	0.0030	1001	1184.1	54.6	2.8	1.5	31.07	81.87
2	UH250	1.79	180	0.535	16.74	842.54	0.162	0.0028	1025	991.1	52.0	2.2	1.3	37.13	76.32
3	Mo17	1.80	182	0.562	17.15	869.33	0.164	0.0031	1034	1073.7	55.2	3.8	1.7	30.88	73.15
4	EC169	1.79	177	0.513	16.45	859.21	0.148	0.0029	1051	944.2	51.6	2.0	1.5	37.71	67.86
5	F98902	1.80	187	0.562	17.22	903.30	0.167	0.0030	1117	1042.2	51.1	2.4	1.3	33.66	71.60
6	FV353	1.79	190	0.514	16.86	874.17	0.152	0.0034	1036	962.9	51.8	2.3	1.3	36.13	85.25
7	MS153	1.80	178	0.534	16.15	827.72	0.168	0.0028	981	1128.9	50.6	2.5	1.8	31.87	73.69
8	F7028	1.79	176	0.517	16.57	803.15	0.153	0.0031	940	893.1	52.9	3.4	1.6	37.19	74.12
9	EZ47	1.79	192	0.502	16.55	830.34	0.155	0.0029	957	1151.9	52.4	3.2	2.0	29.23	75.31
10	EZ37	1.79	174	0.518	16.42	805.62	0.153	0.0031	949	1001.7	52.1	2.6	2.0	34.06	71.26
11	ABA-	1.80	176	0.543	16.31	855.14	0.152	0.0031	1058	1042.7	49.7	2.8	2.2	32.59	71.82
12	ABA+	1.80	177	0.548	16.11	874.87	0.152	0.0031	1085	1082.2	49.9	3.4	2.3	31.94	73.76
13	EZ11A	1.80	181	0.524	17.32	831.53	0.158	0.0029	984	1216.8	51.9	2.7	2.3	29.41	76.07
14	LH38	1.80	185	0.536	16.64	904.12	0.154	0.0030	1142	981.5	52.0	2.6	1.7	32.95	95.67
15	Pa405	1.79	174	0.519	16.27	800.89	0.156	0.0030	943	1035.0	52.0	2.7	1.6	33.61	72.85
16	Oh33	1.80	177	0.549	16.92	853.08	0.159	0.0029	1049	1127.6	51.8	2.3	1.7	33.44	73.26
17	OH43	1.80	176	0.553	16.93	842.65	0.165	0.0029	1018	1014.9	50.8	2.9	1.7	31.70	72.79
18	FC1890	1.79	189	0.521	17.14	841.81	0.157	0.0030	973	988.5	53.4	2.8	1.5	33.72	75.47
19	F912	1.80	189	0.555	16.76	908.73	0.160	0.0030	1098	1083.1	51.9	2.6	1.3	33.24	73.73
20	W64A	1.79	172	0.522	16.31	789.98	0.153	0.0031	942	984.0	52.3	2.9	1.6	33.86	67.07
21	B84	1.79	180	0.533	16.85	831.27	0.160	0.0032	981	1215.5	51.1	2.7	1.9	29.43	76.17
22	MS71	1.79	199	0.519	16.94	899.66	0.155	0.0033	1065	1125.1	50.4	3.3	1.4	30.20	74.52
23	LAN496	1.80	190	0.548	16.25	901.98	0.162	0.0030	1118	1221.7	50.3	3.1	1.2	29.94	76.59
24	B100	1.80	183	0.548	16.74	834.88	0.170	0.0030	975	1041.4	53.4	2.7	1.4	30.87	74.07
25	N6	1.79	168	0.535	17.05	802.20	0.153	0.0031	979	1007.2	53.4	4.0	2.2	29.64	74.98
26	N25	1.80	176	0.539	16.57	826.57	0.158	0.0030	1008	1147.5	52.3	3.5	1.9	29.16	73.68
27	A310	1.80	186	0.527	17.17	876.67	0.154	0.0030	1070	1086.8	47.8	2.6	2.9	32.96	75.38
28	EP52	1.79	185	0.514	17.35	836.85	0.152	0.0031	965	1247.3	52.0	3.5	2.3	29.46	77.06
29	F894	1.80	185	0.525	16.85	844.57	0.157	0.0030	988	1153.1	50.5	2.1	1.2	32.73	73.06
30	PB40R	1.79	177	0.491	16.94	787.81	0.148	0.0030	929	1026.0	53.9	2.2	2.5	31.32	74.18
31	PHK76	1.79	187	0.527	16.49	894.03	0.153	0.0031	1094	1017.1	53.1	3.7	1.1	33.05	77.96
32	A347	1.79	181	0.540	16.50	898.25	0.152	0.0031	1139	979.8	54.5	3.0	2.6	35.50	74.60
33	PH207	1.78	180	0.484	16.91	770.28	0.149	0.0034	848	851.0	53.7	2.5	1.3	35.02	72.59
34	F1808	1.80	181	0.556	16.75	869.38	0.164	0.0029	1065	1114.7	53.1	2.3	1.7	34.00	75.85
35	B89	1.79	178	0.495	17.09	802.15	0.148	0.0030	944	1046.0	52.8	2.9	1.8	34.29	74.12
36	B97	1.79	172	0.541	16.73	811.39	0.157	0.0029	964	1155.1	54.3	2.8	2.2	30.63	77.17
Mean		1.80	181	0.530	16.76	845.56	0.157	0.0030	1014	1065.7	52.1	2.8	1.8	32.60	75.14
HSD		0.02	22	0.043	1.22	97.76	0.016	0.0004	143	135.7	3.5	0.8	0.9	1.30	46.33

E		Genotypic mean values across environments and reduction under low N of traits with significant GXT interaction											
EuRoot_ID	Genotype	RoA		mW		area		staygreen		silage		height	
		high N	reduction	high N	reduction	high N	reduction	high N	reduction	high N	reduction	high N	reduction
1	B73	79.4	-12.3	11.49	-10.7	98.0	-18.3	3.8	44.2	157.17	-14.9	169.66	-12.7
2	UH250	82.8	-7.9	12.15	-6.3	99.2	-15.4	4.6	36.7	147.32	-13.3	164.35	-13.3
3	Mo17	77.8	-7.9	11.67	-6.4	104.4	-13.5	3.5	41.0	129.59	-16.0	160.77	-13.6
4	EC169	83.4	-10.8	12.14	-10.0	96.9	-17.7	5.1	25.4	153.29	-16.6	154.87	-14.6
5	F98902	79.7	-9.0	11.99	-7.9	109.8	-16.3	4.0	33.3	156.45	-14.7	163.80	-14.7
6	FV353	88.3	-9.6	12.92	-9.7	105.4	-19.2	4.4	32.7	155.11	-14.6	166.59	-13.6
7	MS153	87.5	-8.6	12.69	-8.2	100.2	-17.8	3.3	44.3	147.50	-16.5	161.46	-13.0
8	F7028	78.8	-7.9	11.83	-6.2	93.4	-16.1	4.4	38.7	136.49	-18.8	160.24	-14.5
9	EZ47	87.2	-6.5	12.95	-5.8	98.2	-14.6	2.9	59.7	137.60	-16.6	166.80	-13.2
10	EZ37	79.2	-9.8	12.04	-10.3	96.1	-20.5	3.8	34.3	150.13	-16.0	160.38	-14.1
11	ABA-	83.3	-6.7	12.11	-6.4	100.3	-16.5	4.6	25.8	136.13	-14.4	158.97	-15.1
12	ABA+	85.4	-8.2	12.66	-8.3	102.8	-17.5	4.1	33.5	131.53	-17.6	162.49	-14.7
13	EZ11A	79.4	-10.2	11.76	-9.9	98.5	-16.2	3.7	48.4	161.92	-17.6	172.98	-13.0
14	LH38	88.8	-12.2	12.71	-9.8	105.1	-19.7	3.3	52.3	147.11	-19.8	157.89	-15.0
15	Pa405	82.7	-9.3	12.31	-8.3	94.5	-17.8	4.3	30.7	143.35	-16.5	161.17	-14.8
16	Oh33	79.3	-7.5	11.74	-6.6	99.0	-16.2	4.3	30.0	144.56	-15.7	159.72	-13.8
17	OH43	79.2	-12.1	11.73	-10.4	101.4	-17.7	2.5	62.2	145.95	-17.2	159.13	-14.1
18	FC1890	85.3	-11.1	12.72	-9.7	101.3	-15.7	3.4	46.1	153.11	-15.0	166.27	-13.6
19	F912	86.9	-6.1	12.67	-6.1	108.6	-14.2	3.5	47.1	151.61	-16.0	160.90	-14.1
20	W64A	77.5	-6.3	11.79	-6.2	90.6	-15.8	3.7	35.3	146.03	-16.0	154.98	-14.4
21	B84	81.5	-9.2	11.93	-7.9	101.5	-18.1	2.8	66.3	159.99	-17.3	161.16	-14.9
22	MS71	92.9	-7.0	13.41	-6.2	108.1	-15.5	2.6	59.8	137.34	-17.1	155.92	-14.0
23	LAN496	92.9	-9.6	13.47	-9.3	107.4	-16.3	3.1	62.2	144.67	-17.6	162.50	-14.2
24	B100	81.9	-6.5	12.19	-6.3	102.5	-15.0	3.3	43.2	150.28	-15.2	161.31	-14.1
25	N6	74.1	-10.5	10.89	-8.3	93.0	-16.4	3.2	44.6	132.94	-13.0	153.93	-14.0
26	N25	79.2	-7.8	11.82	-7.2	98.2	-17.1	3.9	51.8	136.43	-21.9	159.57	-13.5
27	A310	84.5	-6.1	12.05	-5.2	102.3	-16.4	4.1	33.2	132.04	-14.3	160.34	-15.2
28	EP52	81.8	-9.8	12.20	-8.9	99.3	-15.7	3.9	43.5	164.24	-17.9	162.65	-14.0
29	F894	83.1	-9.0	12.31	-7.7	100.4	-17.3	3.4	59.7	166.09	-18.8	171.09	-14.2
30	PB40R	76.2	-6.7	11.62	-5.3	89.4	-16.5	3.0	49.9	128.10	-11.4	155.75	-13.5
31	PHK76	88.9	-8.6	12.87	-8.1	105.2	-18.5	2.8	67.6	139.26	-16.6	156.11	-15.4
32	A347	86.5	-9.8	12.42	-7.2	102.2	-15.8	4.1	35.4	138.45	-16.7	159.28	-13.8
33	PH207	83.5	-10.7	12.24	-10.2	92.5	-18.8	3.6	33.4	142.12	-11.5	160.25	-13.8
34	F1808	83.6	-9.6	12.10	-6.8	102.3	-14.4	4.4	36.8	160.42	-13.3	171.22	-13.4
35	B89	79.1	-9.1	11.63	-8.1	91.7	-18.2	4.1	33.6	145.94	-15.8	161.01	-13.7
36	B97	77.5	-7.3	11.21	-6.2	94.6	-17.1	3.0	47.8	148.54	-16.3	162.71	-14.1
Mean		82.8	-8.8	12.18	-7.83	99.8	-16.8	3.7	43.6	146.08	-16.07	161.62	-14.04
HSD		9.4		1.10		12		1.0		12.73		13.92	

Supplemental material 5 Correlations across all sites (A), within Switzerland (B) or within Alma (C). All traits that were a result of a visual rating are marked with *. Significant correlations ($p \leq 0.05$) are highlighted.

[illegible]

[illegible]

C	RoA	FFonArc	mFD	area	AcH	Ff	depth	mW	tpSL	mSW	mGS	NoG	Shoot	SPAD	Kernel	Height
RoA	1	0.08	0.35	0.75	0.89	0.01	0.19	0.94	0.84	0.10	0.11	0.73	0.15	-0.27	0.25	0.06
FFonArc		1	0.56	0.60	0.18	0.80	0.44	-0.01	0.40	0.69	-0.36	0.44	0.31	0.48	0.31	0.28
mFD			1	0.63	0.22	0.77	-0.06	0.21	0.48	0.70	-0.61	0.54	0.46	0.17	0.18	0.28
area				1	0.82	0.53	0.45	0.68	0.88	0.57	-0.19	0.76	0.36	0.01	0.36	0.30
AcH					1	-0.04	0.51	0.90	0.87	0.08	0.24	0.68	0.15	-0.20	0.29	0.15
Ff						1	0.06	-0.13	0.26	0.88	-0.68	0.35	0.41	0.33	0.20	0.32
depth							1	0.17	0.42	0.11	0.21	0.29	0.18	0.18	0.28	0.30
mW								1	0.79	-0.02	0.25	0.66	0.05	-0.28	0.22	-0.01
tpSL									1	0.18	-0.10	0.94	0.25	-0.16	0.42	0.18
mSW										1	-0.55	0.17	0.38	0.29	0.09	0.34
mGS											1	-0.23	-0.26	-0.01	-0.07	-0.13
NoG												1	0.24	-0.08	0.46	0.11
Shoot													1	0.26	0.18	0.62
SPAD														1	0.19	0.17
Kernel															1	0.20
Height																1

Supplemental material 6 Correlation between the reduction in % of root and shoot traits under low N compared to high N.

	RoA	mFD	area	AcH	Ff	mW	tpSL	mSW	mGS	NoG
Biomass	0.16	0.24	0.25	0.15	0.27	0.12	0.28	0.37	-0.35	0.30
SPAD	-0.21	-0.19	0.12	-0.02	0.27	-0.05	0.11	-0.07	0.05	0.14
vigor	0.06	-0.21	-0.01	-0.08	0.01	0.11	0.06	-0.07	-0.01	0.08
lodging	0.11	0.06	0.06	0.25*	-0.17	0.20	0.08	-0.26	-0.12	0.13
staygreen	-0.07	-0.15	0.02	0.13	0.02	-0.03	0.02	0.25	-0.07	-0.05
Silo_dt_ha	0.08	-0.06	0.12	0.13	0.08	0.13	0.06	-0.10	0.15	0.06
% DM	-0.03	-0.13	0.18	0.16	0.18	-0.01	0.14	0.19	0.13	0.06
Kernel	0.08	0.24**	0.33	0.18	0.17	0.06	0.27*	0.24*	-0.37***	0.24*
Height	-0.15	0.04	0.24	0.00	0.49***	-0.11	0.12	0.20	-0.19	0.12