Supplementary Materials:

Supplemental Table S1: Raw dataset corresponding to all measurements made on 4 Arabidopsis accessions in 6 N supplies for three independent experiments.

Genotype	Experiment	Nutrition	SNO3	RNO3	SAA	RAA	SFM	RFM	SRFM	SRNO3	SRAA	RL	RT	SPA	N%	C%	C/N	SNH4	RNH4	SPC	Sstarch
Bur-0	1	0.01	45.84	7.94	23.91	14.00	49.30	32.80	1.50	5.77	1.71	20.50	1.60	2.44	2.51	41.25	16.42	1.44	1.45	2.39	61.10
Bur-0	1	0.01	96.44	14.61	NA	NA	34.87	14.07	2.48	6.60	NA	18.67	0.75	2.44	2.78	42.40	15.24	2.27	2.27	2.58	89.38
Bur-0	1	0.01	25.56	8.69	26.73	17.29	51.67	22.07	2.34	2.94	1.46	23.50	0.94	2.44	2.89	42.16	14.60	1.15	1.66	2.57	68.12
Bur-0	1	0.01	54.92	5.68	29.66	15.20	36.60	24.93	1.47	9.66	1.95	19.17	1.30	2.44	2.96	42.05	14.20	1.68	1.43	2.51	60.03
Col-0	1	0.01	45.14	69.60	28.05	23.56	23.97	10.07	2.38	0.65	1.06	20.73	0.49	1.05	2.91	41.53	14.27	1.61	3.81	NA	60.68
Col-0	1	0.01	105.77	19.77	33.35	22.20	22.80	13.03	1.75	5.35	1.50	18.40	0.71	1.05	3.00	41.88	13.98	1.78	2.09	NA	59.53
Col-0	1	0.01	NA	35.46	NA	24.00	17.10	5.70	3.00	NA	NA	16.73	0.34	1.05	2.98	42.36	14.23	2.84	2.36	NA	88.16
Col-0	1	0.01	NA	16.64	NA	23.86	13.83	7.27	1.90	NA	NA	17.77	0.41	1.05	2.82	42.23	14.96	2.15	3.35	NA	85.85
Cvi-0	1	0.01	73.74	11.04	22.33	15.65	45.70	14.47	3.16	6.68	1.43	16.83	0.86	2.40	2.76	39.87	14.46	1.39	1.98	2.28	42.00
Cvi-0	1	0.01	53.26	9.86	21.18	15.70	51.60	27.97	1.85	5.40	1.35	22.47	1.24	2.40	2.30	31.64	13.75	1.22	1.70	2.56	44.44
Cvi-0	1	0.01	39.49	12.37	18.58	15.57	53.23	16.10	3.31	3.19	1.19	14.90	1.08	2.40	4.66	65.42	14.04	1.04	2.82	3.12	48.41
Cvi-0	1	0.01	28.37	4.14	NA	14.56	52.35	21.30	2.46	6.85	NA	22.50	0.95	2.40	NA	NA	NA	NA	2.07	2.65	43.23
Ge-0	1	0.01	65.75	14.43	NA	18.01	34.80	16.17	2.15	4.56	NA	19.10	0.85	2.30	2.22	41.85	18.83	NA	3.14	NA	64.57
Ge-0	1	0.01	81.04	6.92	21.79	17.26	33.73	23.27	1.45	11.70	1.26	21.23	1.10	2.30	2.37	43.78	18.44	1.23	1.60	NA	60.62
Ge-0	1	0.01	61.91	10.09	22.70	17.78	35.57	18.57	1.92	6.14	1.28	20.63	0.90	2.30	2.46	41.61	16.93	1.23	2.23	2.84	61.00
Ge-0	1	0.01	92.19	7.16	26.08	17.20	30.83	17.70	1.74	12.87	1.52	21.53	0.82	2.30	2.43	42.39	17.48	1.84	2.47	NA	70.89
Bur-0	1	0.2	885.74	278.11	26.43	19.23	83.43	17.97	4.64	3.18	1.37	18.77	0.96	4.89	6.96	42.56	6.11	2.17	1.89	3.65	14.18
Bur-0	1	0.2	694.60	318.12	24.43	19.71	75.17	14.90	5.04	2.18	1.24	18.37	0.81	4.89	5.22	34.23	6.56	1.96	2.01	3.32	15.47
Bur-0	1	0.2	595.60	357.35	22.24	23.03	88.57	17.27	5.13	1.67	0.93	19.07	0.91	4.89	6.10	39.41	6.46	1.75	2.10	3.90	14.43
Bur-0	1	0.2	656.88	343.60	23.72	22.26	83.93	15.47	5.43	1.91	1.07	20.23	0.76	4.89	6.21	39.05	6.29	1.99	2.08	3.70	15.43
Col-0	1	0.2	547.74	303.01	22.26	36.11	29.80	5.30	5.62	1.87	0.57	17.43	0.30	1.85	5.75	36.42	6.33	1.54	4.57	3.69	15.46
Col-0	1	0.2	598.15	287.94	21.70	36.17	38.93	5.57	6.99	2.08	0.54	17.37	0.32	1.85	6.30	38.81	6.16	1.61	3.51	3.32	13.50
Col-0	1	0.2	700.32	359.68	23.66	33.13	30.80	5.50	5.60	1.95	0.71	14.07	0.39	1.85	6.76	42.88	6.35	1.85	4.58	4.07	13.44
Col-0	1	0.2	NA	371.89	NA	34.64	22.33	4.87	4.59	NA	NA	18.80	0.26	1.85	NA	NA	NA	2.95	4.51	3.69	18.43
Cvi-0	1	0.2	NA	314.12	27.12	24.22	79.63	18.57	4.29	NA	1.12	21.03	0.88	4.33	6.13	37.78	6.16	2.06	3.04	3.15	14.21
Cvi-0	1	0.2	676.72	336.98	21.38	17.25	75.27	12.20	6.17	2.01	1.24	22.87	0.53	4.33	5.96	35.26	5.91	1.63	2.46	3.41	13.40
Cvi-0	1	0.2	665.50	393.31	19.74	29.96	79.53	14.53	5.47	1.69	0.66	22.17	0.66	4.33	6.72	39.51	5.88	1.49	4.42	3.03	12.84
Cvi-0	1	0.2	600.89	447.75	20.03	27.61	84.60	15.77	5.37	1.34	0.73	22.53	0.70	4.33	6.56	37.60	5.73	1.42	3.88	3.13	13.37
Ge-0	1	0.2	601.89	262.68	19.73	17.42	79.40	28.30	2.81	2.29	1.13	21.43	1.32	4.58	6.08	39.05	6.42	1.13	2.37	3.07	14.95
Ge-0	1	0.2	617.17	279.37	19.83	19.75	67.93	20.60	3.30	2.21	1.00	19.37	1.06	4.58	5.88	39.44	6.70	1.58	3.12	3.46	14.55
Ge-0	1	0.2	731.96	328.02	22.68	17.60	69.53	22.60	3.08	2.23	1.29	20.57	1.10	4.58	6.19	38.59	6.23	1.79	2.57	3.42	16.21
Ge-0	1	0.2	883.47	313.76	25.92	18.09	72.03	22.40	3.22	2.82	1.43	20.23	1.11	4.58	6.08	39.27	6.46	2.95	2.51	3.52	15.60
Bur-0	1	1	NA	553.95	24.75	26.41	77.60	12.50	6.21	NA	0.94	19.90	0.63	5.14	6.38	38.19	5.99	2.10	2.39	3.64	14.78
Bur-0	1	1	671.43	648.68	20.67	28.47	76.00	13.03	5.83	1.04	0.73	18.50	0.70	5.14	6.48	39.01	6.02	1.64	1.54	3.61	15.86
Bur-0	1	1	673.71	534.92	21.81	24.74	103.23	15.43	6.69	1.26	0.88	21.47	0.72	5.14	6.45	38.65	6.00	1.72	2.29	4.06	17.05

Bur-0	1	1	623.35	563.78	18.83	21.12	89.03	12.50	7.12	1.11	0.89	19.57	0.64	5.14	6.37	39.41	6.19	1.48	1.42	3.61	13.92
Col-0	1	1	620.34	490.72	18.82	23.74	34.83	8.83	3.94	1.26	0.79	16.03	0.55	1.86	6.41	40.93	6.38	1.21	3.77	5.22	15.17
Col-0	1	1	708.87	565.49	21.75	33.79	31.80	6.00	5.30	1.25	0.50	15.70	0.38	1.86	6.35	38.97	6.14	1.58	3.67	NA	16.37
Col-0	1	1	939.35	531.16	28.68	32.50	26.43	5.33	4.96	1.77	0.88	15.93	0.33	1.86	6.59	39.49	5.99	1.78	2.81	NA	16.75
Cvi-0	1	1	NA	471.42	23.50	15.49	96.60	21.67	4.46	NA	1.52	26.60	0.81	5.21	6.06	36.33	5.99	1.72	8.52	2.78	13.14
Cvi-0	1	1	659.56	466.62	20.69	38.80	94.80	13.60	6.97	1.16	0.42	22.00	0.62	5.21	6.40	37.09	5.79	1.50	1.70	2.94	14.46
Cvi-0	1	1	594.17	435.48	20.52	11.20	109.27	21.33	5.12	1.40	2.23	27.50	0.78	5.21	6.24	36.87	5.91	1.35	3.30	2.63	15.69
Cvi-0	1	1	615.42	481.68	18.07	NA	74.05	11.05	6.70	1.28	NA	21.30	0.52	5.21	6.02	35.95	5.97	1.30	0.68	3.08	12.59
Ge-0	1	1	623.93	462.62	19.59	20.04	82.80	22.63	3.66	1.35	0.98	21.07	1.07	4.80	6.18	38.48	6.22	1.31	2.77	3.29	13.56
Ge-0	1	1	718.31	480.22	20.32	22.95	80.17	22.50	3.56	1.50	0.89	20.30	1.11	4.80	6.28	38.53	6.13	1.38	2.14	3.09	13.78
Ge-0	1	1	952.16	487.72	27.92	25.69	73.80	20.63	3.58	1.95	1.09	22.77	0.91	4.80	6.03	37.73	6.25	2.17	2.57	3.30	17.65
Ge-0	1	1	997.46	482.28	28.84	27.05	54.60	12.57	4.34	2.07	1.07	17.80	0.71	4.80	6.21	38.90	6.26	1.76	2.91	3.49	17.88
Bur-0	1	4	1237.24	456.90	NA	22.42	NA	16.57	NA	2.71	NA	19.57	0.85	5.90	6.59	38.99	5.92	2.99	2.20	NA	14.80
Bur-0	1	4	941.80	467.89	24.42	27.37	81.57	15.03	5.43	2.01	0.89	19.77	0.76	5.90	6.50	38.57	5.93	2.07	2.42	NA	13.00
Bur-0	1	4	784.11	470.31	21.88	25.45	95.73	16.63	5.76	1.67	0.86	20.00	0.83	5.90	13.23	77.74	5.88	2.03	2.92	NA	12.79
Bur-0	1	4	883.45	511.91	25.48	NA	65.70	8.05	8.16	1.73	NA	14.65	0.55	5.90	11.78	68.09	5.78	2.32	2.42	NA	15.28
Col-0	1	4	1137.29	518.15	22.96	38.13	28.23	5.20	5.43	2.19	0.60	13.53	0.38	1.42	6.60	38.76	5.87	1.56	4.19	NA	14.69
Col-0	1	4	873.02	620.46	20.25	37.39	29.13	3.83	7.60	1.41	0.54	14.83	0.26	1.42	6.55	38.83	5.93	1.08	5.17	NA	13.02
Col-0	1	4	NA	521.10	NA	NA	14.87	1.47	10.14	NA	NA	13.57	0.11	1.42	6.16	38.67	6.28	1.89	4.70	NA	46.71
Col-0	1	4	1059.76	487.44	NA	NA	16.50	1.53	10.76	2.17	NA	13.53	0.11	1.42	5.12	40.08	7.82	3.24	6.22	NA	35.99
Cvi-0	1	4	1049.47	371.74	25.20	20.23	93.10	19.93	4.67	2.82	1.25	22.57	0.88	4.95	6.40	37.43	5.85	1.95	2.83	3.82	11.79
Cvi-0	1	4	852.49	387.99	20.75	21.65	91.57	18.80	4.87	2.20	0.96	25.70	0.73	4.95	6.18	36.90	5.97	1.68	1.96	3.18	11.03
Cvi-0	1	4	1021.65	368.42	23.78	25.30	84.10	14.67	5.73	2.77	0.94	17.97	0.82	4.95	6.48	37.34	5.76	1.92	3.82	3.19	14.40
Cvi-0	1	4	781.69	392.58	16.44	21.62	89.13	19.17	4.65	1.99	0.76	25.13	0.76	4.95	6.36	37.01	5.82	1.48	3.26	3.54	13.22
Ge-0	1	4	966.37	432.90	22.41	23.08	89.63	18.67	4.80	2.23	0.97	25.20	0.74	5.69	6.48	38.10	5.88	1.75	2.33	3.44	13.29
Ge-0	1	4	992.42	488.42	21.31	27.67	91.23	18.23	5.00	2.03	0.77	24.37	0.75	5.69	6.41	38.23	5.96	1.74	2.66	3.23	13.07
Ge-0	1	4	1177.53	538.19	27.26	31.73	90.77	13.77	6.59	2.19	0.86	19.17	0.72	5.69	6.51	38.70	5.95	2.23	3.73	4.30	16.51
Ge-0	1	4	1307.86	506.31	30.80	28.58	82.47	12.87	6.41	2.58	1.08	18.87	0.68	5.69	6.28	37.73	6.01	2.35	3.56	3.68	14.24
Bur-0	1	10	1087.13	459.96	31.09	28.53	93.40	12.73	7.34	2.36	1.09	17.70	0.72	5.39	6.41	39.09	6.10	2.66	3.33	3.84	18.40
Bur-0	1	10	941.04	444.25	25.64	31.02	90.67	12.40	7.31	2.12	0.83	17.20	0.72	5.39	6.35	38.52	6.07	2.12	3.02	3.72	15.55
Bur-0	1	10	894.49	576.42	22.88	24.49	84.33	10.90	7.74	1.55	0.93	17.30	0.63	5.39	6.29	38.91	6.18	2.01	3.11	4.58	14.40
Bur-0	1	10	851.22	488.83	26.21	22.57	97.17	11.33	8.57	1.74	1.16	19.07	0.59	5.39	6.20	38.42	6.19	2.29	2.15	3.15	15.68
Col-0	1	10	936.02	908.19	27.08	NA	20.40	2.13	9.56	1.03	NA	10.87	0.20	1.80	6.25	39.00	6.24	1.23	12.80	NA	22.60
Col-0	1	10	1046.79	490.54	27.46	27.48	32.23	4.80	6.72	2.13	1.00	15.27	0.31	1.80	6.38	37.15	5.82	1.43	5.92	NA	16.99
Col-0	1	10	1351.38	769.58	31.87	22.63	39.80	7.07	5.63	1.76	1.41	15.57	0.45	1.80	6.75	47.09	6.98	1.98	4.43	4.18	16.20
Col-0	1	10	1556.07	899.94	NA	25.59	22.67	2.50	9.07	1.73	NA	12.83	0.19	1.80	5.89	38.66	6.56	2.26	6.78	NA	25.02
Cvi-0	1	10	1176.05	445.59	28.17	22.62	94.80	19.43	4.88	2.64	1.25	24.47	0.79	5.26	6.41	37.10	5.79	2.24	3.25	3.16	15.65
Cvi-0	1	10	1087.30	504.45	28.00	NA	81.57	12.67	6.44	2.16	NA	21.70	0.58	5.26	5.94	36.96	6.22	2.01	4.59	2.86	16.30
Cvi-0	1	10	895.13	535.42	23.51	20.34	80.57	18.23	4.42	1.67	1.16	23.17	0.79	5.26	6.43	37.26	5.79	1.67	4.28	3.14	13.81
Cvi-0	1	10	1495.40	665.54	32.33	22.39	117.40	25.55	4.59	2.25	1.44	26.60	0.96	5.26	6.17	37.01	6.00	3.84	3.89	2.17	15.17
Ge-0	1	10	1511.78	543.05	33.51	28.32	92.60	15.77	5.87	2.78	1.18	20.07	0.79	5.16	6.59	38.60	5.86	3.19	3.33	4.68	18.13
Ge-0	1	10	1111.37	548.70	28.84	34.30	85.63	11.40	7.51	2.03	0.84	18.97	0.60	5.16	6.36	38.39	6.03	1.79	4.10	3.51	19.45
Ge-0	1	10	1066.25	771.35	26.18	36.14	69.87	10.40	6.72	1.38	0.72	18.87	0.55	5.16	6.21	36.51	5.88	1.74	4.40	3.56	16.70
Ge-0	1	10	1351.06	734.92	30.15	34.86	71.20	11.03	6.45	1.84	0.86	19.43	0.57	5.16	6.38	38.52	6.04	2.19	4.19	3.18	20.21
Bur-0	1	50	1504.38	729.47	38.85	28.53	71.53	15.03	4.76	2.06	1.36	20.37	0.74	3.35	6.32	37.03	5.86	2.99	3.82	3.89	20.85

Bur-0	1	50	1408.86	1033.31	36.51	32.69	68.27	14.90	4.58	1.36	1.12	20.43	0.73	3.35	6.46	37.48	5.80	2.77	3.25	3.30	17.56
Bur-0	1	50	1277.05	817.66	32.64	25.10	58.90	11.80	4.99	1.56	1.30	19.33	0.61	3.35	6.25	37.69	6.03	2.68	2.73	3.30	22.02
Bur-0	1	50	1227.62	753.53	31.04	26.80	51.53	10.83	4.76	1.63	1.16	18.80	0.58	3.35	6.12	37.20	6.07	2.46	2.92	3.50	19.30
Col-0	1	50	2356.79	960.82	44.31	31.13	19.67	2.80	7.02	2.45	1.42	11.10	0.25	1.09	6.38	34.77	5.45	3.81	6.86	2.91	27.38
Cvi-0	1	50	1383.74	649.62	30.82	22.36	78.47	21.27	3.69	2.13	1.38	21.57	0.99	4.19	6.43	35.08	5.45	2.14	3.50	2.47	18.71
Cvi-0	1	50	1443.73	680.68	32.45	21.84	88.43	20.37	4.34	2.12	1.49	22.60	0.90	4.19	6.26	34.73	5.55	2.26	3.93	2.14	20.79
Cvi-0	1	50	1645.21	741.83	36.06	23.01	83.43	19.47	4.29	2.22	1.57	25.37	0.77	4.19	6.52	35.23	5.41	2.59	2.90	2.16	19.23
Cvi-0	1	50	1791.66	754.16	36.43	NA	64.93	13.00	4.99	2.38	NA	19.97	0.65	4.19	6.72	33.31	4.96	2.86	3.31	1.85	14.02
Ge-0	1	50	1741.63	881.42	40.20	26.36	61.30	13.10	4.68	1.98	1.53	17.87	0.73	4.07	6.83	37.52	5.49	3.08	3.76	2.51	18.05
Ge-0	1	50	1697.49	871.48	36.25	31.90	64.87	13.00	4.99	1.95	1.14	20.77	0.63	4.07	6.64	37.40	5.63	3.05	2.44	2.91	16.90
Ge-0	1	50	1334.20	830.88	32.16	33.65	65.47	13.10	5.00	1.61	0.96	19.53	0.67	4.07	6.65	37.38	5.62	2.31	3.86	2.90	17.32
Ge-0	1	50	1386.58	967.31	31.31	31.13	63.00	12.80	4.92	1.43	1.01	19.03	0.67	4.07	6.52	36.74	5.64	2.37	5.06	2.47	17.79
Bur-0	2	0.01	109.95	12.45	23.49	17.37	44.67	18.57	2.41	8.83	1.28	17.37	1.07	2.60	4.13	42.00	10.18	1.56	1.19	2.75	NA
Bur-0	2	0.01	182.85	13.46	27.03	16.17	34.70	13.87	2.50	13.58	1.67	17.30	0.80	2.60	4.36	41.41	9.49	2.12	1.23	2.92	NA
Bur-0	2	0.01	151.12	10.01	26.76	15.02	41.47	18.10	2.29	15.10	1.78	16.50	1.10	2.60	4.03	39.35	9.77	3.08	1.40	2.20	NA
Bur-0	2	0.01	160.39	25.35	27.88	14.77	22.43	6.27	3.58	6.33	1.89	15.30	0.41	2.60	4.13	41.89	10.14	2.81	3.73	2.62	NA
Col-0	2	0.01	47.78	13.68	18.15	20.76	18.50	8.37	2.21	3.49	0.87	13.60	0.62	1.29	3.84	43.46	11.32	1.72	NA	NA	NA
Col-0	2	0.01	55.73	19.53	19.77	11.81	21.43	11.83	1.81	2.85	1.67	16.20	0.73	1.29	3.75	40.63	10.84	1.82	1.62	NA	NA
Col-0	2	0.01	49.96	15.61	17.72	15.42	17.43	7.33	2.38	3.20	1.15	12.13	0.60	1.29	3.78	42.67	11.30	1.81	1.06	NA	NA
Col-0	2	0.01	57.32	20.36	20.52	20.90	16.77	6.17	2.72	2.82	0.98	16.53	0.37	1.29	3.99	42.57	10.67	1.64	NA	NA	NA
Cvi-0	2	0.01	247.06	14.77	21.56	14.57	35.97	17.03	2.11	16.73	1.48	20.53	0.83	2.57	4.52	39.30	8.70	1.52	1.28	2.79	NA
Cvi-0	2	0.01	225.24	12.64	19.37	10.24	40.57	19.93	2.04	17.82	1.89	16.77	1.19	2.57	4.32	36.63	8.48	1.44	0.97	3.41	NA
Cvi-0	2	0.01	345.76	16.91	21.39	14.76	42.33	13.43	3.15	20.44	1.45	17.17	0.78	2.57	4.93	42.48	8.62	1.91	1.40	3.10	NA
Ge-0	2	0.01	44.09	5.95	21.52	13.13	44.30	25.77	1.72	7.40	1.64	16.57	1.56	3.32	3.62	40.90	11.31	1.69	1.05	2.61	NA
Ge-0	2	0.01	51.04	16.33	22.68	17.08	30.77	12.93	2.38	3.12	1.33	20.07	0.64	3.32	3.55	43.00	12.11	1.84	2.16	1.49	NA
Ge-0	2	0.01	55.09	13.20	19.72	15.19	39.20	18.00	2.18	4.17	1.30	21.10	0.85	3.32	3.78	42.07	11.12	1.41	1.43	2.58	NA
Ge-0	2	0.01	38.90	10.41	15.15	15.22	34.93	17.53	1.99	3.74	1.00	18.27	0.96	3.32	3.64	41.05	11.29	1.15	0.87	2.23	NA
Bur-0	2	0.2	1305.72	134.42	27.59	14.00	111.93	29.70	3.77	9.71	1.97	21.20	1.40	5.22	6.50	38.84	5.98	2.27	1.26	3.37	NA
Bur-0	2	0.2	748.29	146.05	19.41	13.46	104.57	29.93	3.49	5.12	1.44	19.80	1.51	5.22	6.59	39.11	5.94	1.57	1.42	3.25	NA
Bur-0	2	0.2	480.56	137.49	NA	11.58	110.60	26.83	4.12	3.50	NA	18.60	1.44	5.22	6.41	38.20	5.96	1.07	1.20	3.50	NA
Bur-0	2	0.2	1019.70	83.37	26.87	11.30	NA	NA	NA	12.23	2.61	18.37	NA	5.22	6.23	39.14	6.28	2.83	1.10	3.32	NA
Col-0	2	0.2	950.78	136.02	18.48	13.60	43.67	13.97	3.13	6.99	1.36	17.67	0.79	2.10	6.34	38.17	6.02	2.55	1.95	3.66	NA
Col-0	2	0.2	874.29	188.90	23.29	9.45	35.20	7.57	4.65	4.63	2.46	13.10	0.58	2.10	6.55	39.53	6.04	2.01	1.54	3.49	NA
Col-0	2	0.2	875.73	171.22	24.94	12.01	32.23	6.93	4.65	5.11	2.08	15.57	0.45	2.10	6.47	40.50	6.26	1.86	2.88	3.58	NA
Cvi-0	2	0.2	945.71	170.49	18.01	10.21	87.10	28.60	3.05	5.55	1.76	22.33	1.28	3.93	6.72	37.49	5.58	1.98	1.57	3.05	NA
Cvi-0	2	0.2	1099.55	166.99	18.86	NA	83.53	24.67	3.39	6.58	NA	23.17	1.06	3.93	6.47	36.15	5.59	2.34	1.66	2.91	NA
Cvi-0	2	0.2	1024.06	203.61	20.52	11.33	76.97	20.30	3.79	5.03	1.81	21.37	0.95	3.93	6.50	36.76	5.66	1.92	1.81	2.61	NA
Cvi-0	2	0.2	623.51	163.38	NA	13.06	73.90	19.43	NA	3.82	NA	24.00	0.81	3.93	6.69	37.68	5.64	1.36	2.15	3.05	NA
Ge-0	2	0.2	949.09	133.28	28.90	10.96	76.90	18.10	4.25	7.12	3.22	21.97	0.82	4.42	6.66	38.19	5.73	2.69	1.72	2.77	NA
Ge-0	2	0.2	963.80	122.68	33.78	11.77	76.77	20.87	3.68	7.86	2.87	23.33	0.89	4.42	6.48	38.33	5.91	3.04	1.71	2.70	NA
Ge-0	2	0.2	891.09	129.08	28.75	NA	77.73	20.83	3.73	6.90	NA	20.53	1.01	4.42	6.48	38.23	5.90	2.52	1.71	3.26	NA
Ge-0	2	0.2	563.06	200.19	NA	13.06	58.90	16.40	3.73	2.81	NA	20.50	0.80	4.42	6.40	38.29	5.98	1.53	2.06	3.26	NA
Bur-0	2	1	1098.56	281.51	27.81	12.67	78.57	24.33	3.23	3.90	2.38	19.97	1.22	5.32	6.64	37.21	5.60	2.67	2.06	3.08	NA
Bur-0	2	1	1136.53	233.28	25.38	12.90	127.63	36.53	3.49	4.87	1.97	21.23	1.72	5.32	6.69	37.33	5.58	2.54	1.76	3.03	NA
Bur-0	2	1	1084.45	236.41	27.66	16.83	105.90	26.80	3.95	4.59	1.64	19.77	1.36	5.32	6.62	37.76	5.70	2.23	2.10	3.11	NA

Bur-0	2	1	954.52	206.07	24.83	12.85	103.20	30.70	3.36	4.63	1.93	20.50	1.50	5.32	6.57	37.61	5.72	2.17	1.93	3.64	NA
Col-0	2	1	1098.02	251.77	25.10	NA	37.70	7.53	5.00	4.36	NA	17.30	0.44	2.11	6.79	38.98	5.74	1.40	2.40	3.33	NA
Col-0	2	1	992.34	182.80	24.73	12.26	52.97	12.53	4.23	5.43	2.20	16.53	0.76	2.11	6.75	38.67	5.73	2.23	1.56	3.52	NA
Col-0	2	1	1094.13	233.78	24.14	16.33	44.83	10.50	4.27	4.68	1.48	14.27	0.74	2.11	6.85	38.72	5.66	1.66	1.62	3.56	NA
Col-0	2	1	916.88	252.29	20.86	15.02	43.40	10.45	4.15	3.63	1.39	16.50	0.63	2.11	6.32	38.64	6.11	1.40	2.38	3.47	NA
Cvi-0	2	1	1111.69	210.14	25.14	13.42	90.10	23.57	3.82	5.29	1.87	22.33	1.06	3.74	6.54	37.57	5.74	2.21	2.51	3.28	NA
Cvi-0	2	1	1191.13	173.22	21.53	14.29	77.90	26.50	2.94	6.88	1.51	23.73	1.12	3.74	6.73	39.75	5.91	2.54	1.95	3.65	NA
Cvi-0	2	1	1105.10	190.96	21.87	17.96	79.53	23.30	3.41	5.79	1.22	25.73	0.91	3.74	6.72	38.09	5.67	1.84	2.62	3.66	NA
Cvi-0	2	1	1278.08	203.63	25.34	18.15	113.05	29.40	3.85	6.28	1.40	21.47	1.37	3.74	6.61	37.87	5.73	2.42	3.11	3.94	NA
Ge-0	2	1	1180.83	229.94	34.86	16.87	81.93	21.70	3.78	5.14	2.07	24.03	0.90	4.79	6.67	38.15	5.72	3.00	3.11	4.13	NA
Ge-0	2	1	1138.24	207.71	30.62	15.08	79.13	19.50	4.06	5.48	2.03	23.77	0.82	4.79	6.62	38.45	5.81	2.80	2.85	4.20	NA
Ge-0	2	1	1128.92	216.54	32.96	14.41	89.23	21.30	4.19	5.21	2.29	23.17	0.92	4.79	6.64	38.77	5.84	3.21	2.19	3.26	NA
Ge-0	2	1	1200.73	217.24	33.46	20.82	82.37	21.93	3.76	5.53	1.61	24.17	0.91	4.79	6.68	38.85	5.82	2.65	1.85	2.74	NA
Bur-0	2	4	1215.93	242.88	26.37	19.75	129.70	26.33	4.93	5.01	1.34	22.30	1.18	6.54	6.45	37.87	5.87	2.63	2.45	3.15	NA
Bur-0	2	4	1275.90	266.81	28.66	16.78	126.53	31.50	4.02	4.78	1.71	21.53	1.46	6.54	6.54	37.41	5.72	2.71	1.73	3.56	NA
Bur-0	2	4	1217.96	283.44	29.03	17.29	118.83	25.07	4.74	4.30	1.68	20.47	1.22	6.54	6.62	38.04	5.74	2.65	1.54	3.78	NA
Bur-0	2	4	1105.00	313.20	24.67	25.21	99.00	11.05	8.96	3.53	0.98	18.55	0.60	6.54	6.40	37.74	5.90	2.84	3.17	3.35	NA
Col-0	2	4	1094.52	198.88	21.21	17.92	60.00	10.33	5.81	5.50	1.18	17.30	0.60	3.03	6.68	38.41	5.75	1.71	2.53	3.04	NA
Col-0	2	4	1126.45	282.00	22.76	19.00	55.47	12.43	4.46	3.99	1.20	17.13	0.73	3.03	6.71	38.96	5.80	1.79	2.47	3.05	NA
Col-0	2	4	1136.09	293.83	20.77	21.37	44.87	7.73	5.80	3.87	0.97	17.43	0.44	3.03	6.71	38.25	5.70	1.65	1.09	3.89	NA
Col-0	2	4	1223.71	258.66	23.73	21.74	55.00	9.73	5.65	4.73	1.09	16.60	0.59	3.03	6.81	38.67	5.68	2.01	2.83	2.83	NA
Cvi-0	2	4	1181.58	228.61	24.18	18.06	84.20	24.77	3.40	5.17	1.34	23.10	1.07	4.37	6.47	37.76	5.84	2.39	2.19	3.69	NA
Cvi-0	2	4	1304.02	258.08	28.48	NA	75.83	13.00	5.83	5.05	NA	21.90	0.59	4.37	6.46	37.70	5.84	2.56	1.17	2.54	NA
Cvi-0	2	4	1126.13	253.00	22.72	20.32	73.03	19.10	3.82	4.45	1.12	23.97	0.80	4.37	6.38	37.04	5.81	2.14	2.09	3.05	NA
Cvi-0	2	4	1100.27	229.94	22.56	18.02	74.83	21.47	3.49	4.79	1.25	23.97	0.90	4.37	6.48	37.85	5.84	2.35	1.89	3.60	NA
Ge-0	2	4	1328.96	219.97	33.83	NA	85.07	20.17	4.22	6.04	NA	22.67	0.89	5.30	6.85	38.02	5.55	3.15	1.58	4.05	NA
Ge-0	2	4	1226.49	257.95	34.78	22.25	79.33	17.27	4.59	4.75	1.56	23.30	0.74	5.30	6.77	37.36	5.52	3.19	1.84	2.73	NA
Ge-0	2	4	1208.09	276.95	31.37	23.96	81.47	18.33	4.44	4.36	1.31	21.03	0.87	5.30	6.86	37.68	5.50	2.92	2.41	2.86	NA
Ge-0	2	4	1359.93	282.16	37.14	23.09	76.57	16.37	4.68	4.82	1.61	22.90	0.71	5.30	6.81	37.75	5.54	3.37	1.19	3.23	NA
Bur-0	2	10	1197.97	270.42	28.25	16.93	85.23	19.17	4.45	4.43	1.67	17.50	1.10	5.82	6.55	37.75	5.76	2.84	1.54	3.10	NA
Bur-0	2	10	NA	295.96	NA	22.57	102.80	16.17	6.36	NA	NA	19.27	0.84	5.82	NA	NA	NA	1.39	1.74	3.23	NA
Bur-0	2	10	1127.09	325.03	23.11	19.33	96.57	18.73	5.15	3.47	1.20	19.27	0.97	5.82	6.53	37.76	5.79	2.63	1.42	2.88	NA
Bur-0	2	10	1080.52	309.61	23.68	19.70	74.00	15.97	4.63	3.49	1.20	18.90	0.84	5.82	6.45	39.18	6.08	2.57	1.93	3.71	NA
Col-0	2	10	NA	283.52	NA	21.96	46.73	7.90	5.92	NA	NA	16.93	0.47	2.90	1.85	68.97	37.21	1.12	2.75	2.62	NA
Col-0	2	10	NA	262.58	NA	21.16	49.53	9.57	5.18	NA	NA	16.70	0.57	2.90	NA	NA	NA	1.91	2.68	2.77	NA
Col-0	2	10	NA	293.05	NA	22.75	49.10	8.47	5.80	NA	NA	14.93	0.57	2.90	NA	NA	NA	1.13	2.80	3.37	NA
Col-0	2	10	1278.18	268.05	26.29	19.67	47.50	9.37	5.07	4.77	1.34	17.07	0.55	2.90	6.96	38.01	5.46	1.57	2.36	2.92	NA
Cvi-0	2	10	1091.82	226.95	23.74	19.39	80.80	18.43	4.38	4.81	1.29	22.90	0.80	3.71	6.30	34.93	5.54	2.24	1.66	2.76	NA
Cvi-0	2	10	1230.94	219.32	23.92	15.39	78.53	22.27	3.53	5.61	1.66	20.60	1.08	3.71	6.70	37.11	5.54	2.37	0.93	2.55	NA
Cvi-0	2	10	1253.00	239.14	21.69	16.03	63.47	23.90	2.66	5.24	1.35	21.13	1.13	3.71	6.55	37.13	5.67	2.25	1.15	2.92	NA
Cvi-0	2	10	1283.21	225.94	20.06	17.48	108.00	27.90	3.87	5.68	1.22	22.57	1.24	3.71	6.64	37.21	5.61	2.34	1.55	2.93	NA
Ge-0	2	10	1410.90	228.08	34.19	16.53	84.00	16.20	5.19	6.19	2.20	22.23	0.73	5.23	6.88	37.28	5.42	3.42	1.94	2.59	NA
Ge-0	2	10	1465.05	270.42	31.50	19.42	80.13	17.27	4.64	5.42	1.62	23.40	0.74	5.23	6.79	37.64	5.54	3.13	1.84	3.11	NA
Ge-0	2	10	1313.17	287.53	30.25	22.21	91.33	13.47	6.78	4.57	1.36	18.93	0.71	5.23	6.77	37.44	5.53	2.93	2.36	3.33	NA
Ge-0	2	10	1428.01	295.56	29.72	19.15	68.73	14.27	4.82	4.83	1.73	20.07	0.71	5.23	6.76	37.74	5.59	3.00	2.14	3.42	NA

Bur-0	2	50	1532.93	300.94	30.77	19.49	77.30	16.63	4.65	5.09	1.58	19.97	0.83	3.71	6.40	36.56	5.71	3.59	2.20	2.05	NA
Bur-0	2	50	1413.54	308.69	28.55	24.33	78.87	14.53	5.43	4.58	1.17	20.00	0.73	3.71	6.54	37.38	5.71	3.40	2.70	3.26	NA
Bur-0	2	50	1516.77	315.43	33.68	27.16	39.93	8.13	4.91	4.81	1.24	15.33	0.53	3.71	6.04	34.27	5.68	3.56	2.04	2.70	NA
Col-0	2	50	1682.69	449.31	24.78	24.97	39.10	6.77	5.78	3.75	0.99	12.97	0.52	2.30	6.53	36.34	5.56	2.13	3.26	2.84	NA
Col-0	2	50	1538.65	369.67	24.87	NA	36.77	3.93	9.35	4.16	NA	13.37	0.29	2.30	6.88	37.47	5.44	1.83	4.85	1.99	NA
Col-0	2	50	1439.86	335.39	24.09	19.27	36.97	8.47	4.37	4.29	1.25	14.43	0.59	2.30	6.85	37.12	5.42	1.69	1.66	2.80	NA
Cvi-0	2	50	1602.87	297.50	28.73	16.30	72.70	22.57	3.22	5.39	1.76	22.83	0.99	3.91	6.64	35.92	5.41	2.81	1.87	2.50	NA
Cvi-0	2	50	1418.63	271.66	21.88	18.03	67.17	19.70	3.41	5.22	1.21	23.47	0.84	3.91	6.62	35.62	5.38	2.91	2.40	2.01	NA
Cvi-0	2	50	1453.27	269.63	25.84	15.77	66.27	21.43	3.09	5.39	1.64	20.87	1.03	3.91	6.65	36.07	5.43	2.46	1.65	2.01	NA
Cvi-0	2	50	1462.90	303.12	25.53	17.22	66.67	18.63	3.58	NA	1.48	22.13	0.84	3.91	6.76	36.04	5.33	3.53	1.35	1.52	NA
Ge-0	2	50	1434.39	316.32	35.04	22.67	59.07	12.50	4.73	4.53	1.55	19.57	0.64	4.04	6.95	36.59	5.27	2.73	2.94	2.18	NA
Ge-0	2	50	1516.20	410.48	38.88	25.38	54.70	9.73	5.62	3.69	1.53	19.00	0.51	4.04	6.88	37.54	5.46	2.92	3.13	2.79	NA
Ge-0	2	50	1425.24	383.68	39.32	24.85	56.03	7.80	7.18	3.71	1.58	19.23	0.41	4.04	6.67	37.95	5.69	3.10	3.40	3.17	NA
Ge-0	2	50	1485.13	359.15	37.91	22.24	52.90	9.90	5.34	4.14	1.70	18.70	0.53	4.04	6.98	37.68	5.40	2.22	2.52	2.71	NA
Bur-0	3	0.01	171.69	37.26	25.20	NA	61.37	13.13	4.67	4.61	NA	18.80	0.70	2.60	4.22	39.55	9.37	3.39	3.93	2.99	28.86
Bur-0	3	0.01	191.54	27.57	25.81	17.85	52.47	20.13	2.61	6.95	1.45	18.23	1.10	2.60	4.41	40.13	9.10	3.59	2.85	3.17	30.81
Bur-0	3	0.01	146.61	18.30	30.74	18.22	49.97	14.07	3.55	8.01	1.60	18.27	0.77	2.60	4.04	40.49	10.02	3.16	2.53	3.32	33.94
Bur-0	3	0.01	121.16	11.60	23.17	18.02	41.77	11.87	3.52	10.45	1.29	15.23	0.78	2.60	4.14	40.30	9.73	3.50	2.55	3.25	35.03
Col-0	3	0.01	38.20	42.34	23.36	NA	22.00	4.83	4.55	0.90	NA	15.53	0.31	1.29	4.28	42.88	10.03	4.04	6.30	NA	52.19
Col-0	3	0.01	41.80	21.59	19.89	23.18	25.07	8.43	2.97	1.94	0.82	14.53	0.58	1.29	4.21	41.43	9.84	3.07	3.21	3.71	42.93
Col-0	3	0.01	47.41	22.76	18.08	23.16	19.30	7.43	2.60	2.08	0.75	14.20	0.52	1.29	4.21	42.16	10.00	2.75	3.15	NA	44.65
Col-0	3	0.01	NA	NA	NA	NA	21.30	3.80	5.61	NA	NA	12.20	0.31	1.29	3.89	41.36	10.64	NA	9.47	NA	NA
Cvi-0	3	0.01	130.46	51.45	20.24	23.73	46.07	11.73	3.93	2.54	0.66	23.97	0.49	2.57	4.32	40.00	9.25	2.50	3.90	2.03	34.94
Cvi-0	3	0.01	98.87	23.33	22.68	22.66	42.53	11.20	3.80	4.24	0.96	21.17	0.53	2.57	3.87	39.40	10.17	2.64	2.77	3.08	34.66
Cvi-0	3	0.01	144.15	29.98	22.20	23.51	48.83	13.77	3.55	4.81	0.78	20.90	0.66	2.57	4.38	39.67	9.05	2.39	3.42	2.07	27.06
Cvi-0	3	0.01	155.13	18.19	28.04	20.71	43.60	13.87	3.14	8.53	1.35	21.53	0.64	2.57	4.27	39.25	9.20	2.63	2.74	2.72	28.40
Ge-0	3	0.01	57.82	12.31	24.33	16.35	39.13	22.13	1.77	4.70	1.49	19.13	1.16	3.32	3.85	41.07	10.68	2.91	2.15	3.59	42.48
Ge-0	3	0.01	31.18	16.44	30.76	16.82	38.90	17.87	2.18	1.90	1.83	19.30	0.93	3.32	3.60	41.25	11.47	2.45	2.00	3.59	34.36
Ge-0	3	0.01	15.50	14.95	28.96	14.51	37.17	18.10	2.05	1.04	2.00	16.30	1.11	3.32	3.86	40.88	10.58	2.43	1.64	3.48	39.77
Ge-0	3	0.01	41.23	15.39	30.60	18.79	38.43	19.53	1.97	2.68	1.63	19.67	0.99	3.32	3.52	40.14	11.39	3.15	2.22	3.70	39.61
Bur-0	3	0.2	NA	296.43	22.67	18.82	92.23	19.67	4.69	NA	1.21	21.83	0.90	5.22	6.09	37.89	6.22	2.64	3.39	2.93	31.31
Bur-0	3	0.2	NA	271.67	27.83	17.24	88.10	19.67	4.48	NA	1.61	19.27	1.02	5.22	6.35	38.15	6.01	2.68	2.68	2.73	33.98
Bur-0	3	0.2	810.26	265.78	28.68	19.48	83.77	15.63	5.36	3.05	1.47	20.90	0.75	5.22	6.22	38.19	6.14	3.57	3.40	3.56	20.38
Bur-0	3	0.2	787.35	258.10	27.88	17.80	81.37	17.47	4.66	3.05	1.57	21.43	0.81	5.22	6.36	38.40	6.04	3.45	2.92	3.20	20.33
Col-0	3	0.2	871.25	265.81	30.61	21.78	34.90	9.17	3.81	3.28	1.41	17.33	0.53	2.10	6.01	36.84	6.13	2.37	4.18	4.90	23.06
Col-0	3	0.2	888.10	219.36	28.37	23.06	36.23	7.07	5.13	4.05	1.23	16.13	0.44	2.10	6.41	38.62	6.02	2.59	5.40	4.11	24.48
Col-0	3	0.2	753.64	259.00	28.00	25.07	31.20	5.77	5.41	2.91	1.12	13.33	0.43	2.10	6.04	39.34	6.51	2.13	4.50	4.87	29.98
Col-0	3	0.2	876.82	263.78	30.00	NA	26.30	4.50	5.84	3.32	NA	13.65	0.33	2.10	6.21	38.84	6.25	2.13	5.69	4.63	24.88
Cvi-0	3	0.2	768.91	324.77	24.01	27.07	65.23	13.83	4.72	2.37	0.89	25.10	0.55	3.93	6.47	37.95	5.86	2.65	4.69	2.87	20.42
Cvi-0	3	0.2	876.18	301.10	24.57	24.83	65.23	13.17	4.95	2.91	0.99	20.07	0.66	3.93	6.74	37.96	5.63	2.92	4.48	2.85	20.87
Cvi-0	3	0.2	847.37	262.88	24.03	31.54	68.57	10.37	6.61	3.22	0.76	20.63	0.50	3.93	6.02	36.62	6.08	2.67	7.21	3.49	19.05
Cvi-0	3	0.2	775.09	288.22	23.40	20.00	60.57	13.07	4.64	2.69	1.17	22.20	0.59	3.93	6.28	37.87	6.03	2.55	4.37	3.52	20.83
Ge-0	3	0.2	816.48	222.01	32.76	15.20	68.43	17.57	3.90	3.68	2.16	17.77	0.99	4.42	6.23	38.43	6.17	3.09	2.06	4.87	19.10
Ge-0	3	0.2	990.60	228.56	38.63	14.59	66.87	25.00	2.67	4.33	2.65	20.83	1.20	4.42	6.11	38.14	6.24	4.32	2.13	3.05	26.58
Ge-0	3	0.2	822.15	273.09	35.25	21.39	64.17	17.80	3.60	3.01	1.65	17.60	1.01	4.42	6.10	38.54	6.32	3.07	3.53	3.75	21.04

Ge-0	3	0.2	795.73	279.06	33.46	18.71	59.73	19.10	3.13	2.85	1.79	19.80	0.96	4.42	NA	NA	NA	2.95	3.16	3.89	17.17
Bur-0	3	1	1090.20	429.84	24.80	24.28	106.90	23.33	4.58	2.54	1.02	21.70	1.08	5.32	6.49	37.91	5.84	3.54	2.81	3.85	NA
Bur-0	3	1	976.07	370.63	24.05	20.39	96.20	16.97	5.67	2.63	1.18	21.50	0.79	5.32	6.30	38.28	6.07	3.52	2.58	3.73	21.24
Bur-0	3	1	959.50	381.80	23.44	18.73	102.47	20.00	5.12	2.51	1.25	21.37	0.94	5.32	6.38	38.11	5.98	3.13	2.74	2.85	17.86
Bur-0	3	1	789.74	365.32	27.23	16.64	77.73	14.17	5.49	2.16	1.64	20.17	0.70	5.32	5.85	38.99	6.66	3.34	2.68	4.94	20.55
Col-0	3	1	1148.89	483.63	28.02	NA	42.10	9.30	4.53	2.38	NA	16.37	0.57	2.11	6.57	38.73	5.90	2.43	4.86	4.70	23.14
Col-0	3	1	1038.14	400.08	30.17	30.06	32.43	4.87	6.66	2.59	1.00	14.37	0.34	2.11	6.31	39.17	6.20	2.03	4.74	4.31	24.01
Col-0	3	1	1043.47	389.65	27.37	24.90	35.73	5.43	6.58	2.68	1.10	11.60	0.47	2.11	6.57	38.73	5.89	2.51	4.89	3.10	20.45
Col-0	3	1	NA	422.80	32.03	29.45	30.43	3.67	8.30	NA	1.09	12.10	0.30	2.11	6.10	39.01	6.40	2.41	5.23	3.69	17.52
Cvi-0	3	1	1034.68	388.11	31.52	25.57	74.00	16.83	4.40	2.67	1.23	21.83	0.77	3.74	6.37	37.57	5.90	2.65	4.28	3.55	21.71
Cvi-0	3	1	910.81	334.55	22.49	18.05	74.40	17.43	4.27	2.72	1.25	21.40	0.81	3.74	6.29	37.25	5.93	2.43	2.93	3.71	22.19
Cvi-0	3	1	944.03	383.38	25.20	18.88	62.00	13.57	4.57	2.46	1.33	19.27	0.70	3.74	6.49	37.75	5.81	2.59	3.29	3.77	21.91
Cvi-0	3	1	953.28	381.56	26.68	NA	55.03	9.60	5.73	2.50	NA	19.17	0.50	3.74	6.31	38.23	6.06	2.05	4.42	4.04	22.26
Ge-0	3	1	1152.15	441.58	34.55	17.59	66.93	18.27	3.66	2.61	1.96	18.87	0.97	4.79	6.27	37.45	5.97	3.43	3.68	3.45	20.39
Ge-0	3	1	1131.80	424.31	44.42	21.25	72.03	18.43	3.91	2.67	2.09	21.33	0.86	4.79	6.34	38.53	6.08	3.39	3.06	4.01	20.29
Ge-0	3	1	1032.43	447.81	31.75	18.03	63.03	13.93	4.52	2.31	1.76	20.23	0.69	4.79	6.30	38.42	6.10	3.55	2.45	3.91	20.49
Ge-0	3	1	1074.59	432.95	34.48	18.15	53.03	12.57	4.22	2.48	1.90	18.90	0.66	4.79	6.20	38.14	6.15	3.09	2.42	3.79	19.24
Bur-0	3	4	942.61	437.03	29.68	15.38	122.17	22.60	5.41	2.16	1.93	20.10	1.12	6.54	5.92	34.69	5.86	4.49	2.29	3.38	23.18
Bur-0	3	4	1135.69	453.52	33.10	19.71	98.23	20.23	4.86	2.50	1.68	20.00	1.01	6.54	6.39	37.73	5.90	4.75	3.79	4.08	24.03
Bur-0	3	4	1308.80	432.14	41.32	17.74	104.43	23.00	4.54	3.03	2.33	19.93	1.15	6.54	6.51	38.02	5.84	5.52	3.00	3.55	23.08
Bur-0	3	4	1077.38	428.52	34.78	17.57	103.13	21.33	4.83	2.51	1.98	20.20	1.06	6.54	6.44	38.07	5.91	4.39	3.02	3.66	20.26
Col-0	3	4	1266.66	475.78	32.87	NA	55.47	7.60	7.30	2.66	NA	17.40	0.44	3.03	6.36	36.26	5.71	3.30	5.16	2.74	19.78
Col-0	3	4	1090.21	500.77	27.95	23.98	53.23	10.37	5.14	2.18	1.17	18.57	0.56	3.03	6.63	37.49	5.65	2.80	3.33	3.52	23.46
Col-0	3	4	1149.79	410.48	32.35	NA	39.60	4.33	9.14	2.80	NA	15.47	0.28	3.03	6.47	37.95	5.86	2.39	5.47	3.46	21.36
Col-0	3	4	1158.74	NA	32.64	NA	50.45	4.50	11.21	NA	NA	17.35	0.26	3.03	6.36	37.73	5.93	3.85	5.55	4.47	22.84
Cvi-0	3	4	1135.06	398.74	19.36	22.14	57.97	9.60	6.04	2.85	0.87	20.97	0.46	4.37	6.54	37.94	5.81	3.60	3.69	2.45	22.84
Cvi-0	3	4	1070.88	394.46	22.71	19.89	75.40	13.17	5.73	2.71	1.14	24.80	0.53	4.37	6.41	36.25	5.65	3.66	3.20	2.89	22.98
Cvi-0	3	4	1116.89	396.11	19.74	19.05	68.97	12.00	5.75	2.82	1.04	21.23	0.57	4.37	6.23	36.20	5.81	4.29	3.53	3.06	28.76
Cvi-0	3	4	1002.26	397.60	30.15	NA	45.07	7.70	5.85	2.52	NA	20.57	0.37	4.37	6.01	37.54	6.25	4.38	5.47	3.88	24.40
Ge-0	3	4	1268.85	453.62	37.27	17.49	65.77	18.20	3.61	2.80	2.13	22.53	0.81	5.30	6.54	36.91	5.65	5.01	2.84	3.34	23.96
Ge-0	3	4	1160.76	446.68	35.29	16.22	80.87	21.97	3.68	2.60	2.18	22.83	0.96	5.30	6.73	38.28	5.69	4.81	2.57	2.77	24.51
Ge-0	3	4	1261.62	464.31	35.12	16.03	73.43	19.57	3.75	2.72	2.19	19.80	0.99	5.30	NA	NA	NA	4.74	2.66	2.73	20.64
Ge-0	3	4	1331.20	483.37	41.26	NA	69.87	11.03	6.33	2.75	NA	20.37	0.54	5.30	6.55	37.84	5.78	4.65	2.68	2.25	23.28
Bur-0	3	10	1143.39	497.54	38.55	19.29	93.00	18.87	4.93	2.30	2.00	18.07	1.04	5.82	6.18	36.87	5.96	3.98	2.95	2.28	22.56
Bur-0	3	10	NA	450.66	39.88	19.19	90.93	16.40	5.54	NA	2.08	19.53	0.84	5.82	6.72	38.38	5.71	5.29	2.73	2.13	28.62
Bur-0	3	10	1139.58	447.77	34.72	NA	99.20	20.13	4.93	2.55	NA	19.30	1.04	5.82	6.28	37.18	5.92	4.60	3.29	1.74	20.83
Bur-0	3	10	1303.23	462.87	36.28	19.53	92.97	16.30	5.70	2.82	1.86	18.23	0.89	5.82	6.50	37.06	5.70	4.36	3.62	2.09	22.69
Col-0	3	10	1473.74	474.62	37.13	34.66	44.80	5.93	7.55	3.11	1.01	15.37	0.39	2.90	6.70	38.50	5.74	3.55	5.77	2.87	24.28
Col-0	3	10	1262.27	530.44	37.26	34.01	41.00	6.40	6.41	2.38	1.10	13.33	0.48	2.90	4.80	28.07	5.85	3.88	5.72	3.00	26.01
Col-0	3	10	1478.44	457.35	38.91	26.20	55.87	8.50	6.57	3.23	1.49	16.57	0.51	2.90	6.68	38.11	5.71	4.56	4.14	2.87	24.15
Col-0	3	10	1441.94	523.12	41.65	37.46	52.10	5.97	8.73	2.76	1.11	16.07	0.37	2.90	6.29	38.69	6.15	3.35	6.75	3.24	22.70
Cvi-0	3	10	1270.80	412.75	32.64	17.38	59.10	18.77	3.15	3.08	1.88	22.17	0.85	3.71	6.30	36.81	5.85	4.10	3.60	3.01	25.80
Cvi-0	3	10	1142.47	498.21	27.95	26.65	66.20	12.20	5.43	2.29	1.05	23.80	0.51	3.71	6.39	37.69	5.90	3.79	6.30	3.04	22.89
Cvi-0	3	10	1201.87	408.40	31.19	18.77	61.30	10.10	6.07	2.94	1.66	17.37	0.58	3.71	6.56	38.82	5.92	4.46	4.42	3.05	27.57
Cvi-0	3	10	1160.15	387.34	32.73	22.64	46.35	10.40	4.46	3.00	1.45	21.50	0.48	3.71	6.81	38.90	5.71	4.21	5.54	3.32	25.64

Ge-0	3	10	1407.78	472.51	42.23	19.03	77.87	17.43	4.47	2.98	2.48	19.43	0.90	5.23	6.24	38.08	6.10	4.35	2.71	3.09	20.99
Ge-0	3	10	1407.63	498.69	44.10	15.80	78.00	19.47	4.01	2.82	2.79	18.63	1.04	5.23	6.46	37.90	5.86	4.77	2.30	2.66	22.32
Ge-0	3	10	1296.26	481.56	39.59	15.91	82.27	19.17	4.29	2.69	2.85	20.97	0.91	5.23	6.59	38.24	5.81	4.74	2.14	2.57	21.52
Ge-0	3	10	1358.90	495.02	46.33	19.50	67.80	15.87	4.27	2.75	2.38	18.87	0.84	5.23	6.50	39.01	6.00	4.60	3.35	2.66	23.18
Bur-0	3	50	1286.40	519.55	37.47	25.71	83.40	16.53	5.04	2.48	1.46	18.83	0.88	NA	6.05	37.41	6.19	5.17	3.13	2.69	25.97
Bur-0	3	50	1313.24	476.71	37.48	24.27	80.03	14.00	5.72	2.75	1.54	20.10	0.70	NA	5.92	35.77	6.05	5.54	3.82	2.69	24.85
Bur-0	3	50	1358.73	475.31	42.02	24.94	67.90	14.77	4.60	2.86	1.69	19.43	0.76	NA	4.64	26.36	5.68	5.80	3.78	3.42	27.02
Bur-0	3	50	1318.08	455.55	39.17	28.25	64.10	12.13	5.28	2.89	1.39	19.10	0.64	NA	5.90	36.54	6.19	5.12	3.44	2.64	26.50
Col-0	3	50	1492.64	441.00	31.23	35.80	41.07	6.07	6.77	3.38	0.87	11.27	0.54	NA	6.43	37.36	5.81	3.13	4.32	2.92	25.22
Col-0	3	50	1502.23	494.29	29.60	NA	29.07	4.33	6.71	3.04	NA	12.27	0.35	NA	6.17	35.00	5.67	4.34	4.26	NA	25.47
Col-0	3	50	1324.62	564.43	24.61	NA	27.37	3.30	8.29	2.35	NA	10.13	0.33	NA	6.59	37.56	5.70	3.14	4.73	NA	26.33
Cvi-0	3	50	1410.69	467.73	35.99	35.27	56.13	9.80	5.73	3.02	1.02	22.40	0.44	NA	6.51	36.20	5.56	4.81	5.03	2.85	52.32
Cvi-0	3	50	1407.68	480.65	34.30	30.00	47.97	9.37	5.12	2.93	1.14	20.97	0.45	NA	7.21	43.43	6.02	4.92	4.85	2.81	46.57
Cvi-0	3	50	1436.59	527.36	40.58	35.20	52.17	8.97	5.82	2.72	1.15	16.27	0.55	NA	6.41	36.79	5.74	4.94	4.98	3.27	49.13
Cvi-0	3	50	1408.48	543.90	31.49	35.35	47.23	6.60	7.16	2.59	0.84	17.13	0.39	NA	6.40	36.09	5.64	4.52	6.46	2.65	49.29
Ge-0	3	50	1511.52	517.19	57.42	27.27	54.23	15.30	3.54	2.92	2.11	18.43	0.83	NA	6.02	36.09	6.00	5.74	3.10	3.05	50.34
Ge-0	3	50	1510.00	568.44	40.62	26.17	48.23	11.83	4.08	2.66	1.55	17.33	0.68	NA	6.73	37.39	5.56	5.19	4.05	2.17	46.91
Ge-0	3	50	1446.04	553.24	39.64	30.95	46.33	9.07	5.11	2.61	1.28	15.80	0.57	NA	6.50	37.18	5.72	4.44	3.33	2.60	44.75
Ge-0	3	50	1559.92	544.01	49.71	34.43	43.37	8.87	4.89	2.87	1.40	13.67	0.65	NA	NA	NA	NA	5.03	3.25	2.51	51.20

Supplemental Table S2: Percentage of explained variance of investigated traits.

ANOVA Factor	SFM	RFM	SRFM	RL	RT	SPC	SNO3	RNO3	SRNO3	SAA	RAA	SRAA	N%	C%	C/N	SNH4	RNH4	SPA	SStarch
Genotype	49.5	55.7	14.6	69.8	49.0	8.8	0.8	0.9	3.6	18.0	8.0	15.8	0.0	4.3	2.1	6.5	27.9	55.7	0.7
Experiment	1.4	8.1	7.1	1.7	9.4	4.0	1.3	24.2	28.7	17.6	32.0	23.3	0.6	3.7	1.7	52.9	40.7	0.2	0.9
Nutrition	33.3	7.5	50.9	8.6	8.1	36.6	91.2	62.9	25.2	32.7	17.2	0.0	80.6	21.9	56.4	21.5	11.2	35.2	41.5
Gen*Exp	6.1	8.8	6.1	2.4	12.0	4.7	0.6	0.4	4.8	8.7	10.2	18.8	1.5	9.9	3.6	3.9	12.9	0.0	2.8
Gen*Nut	4.6	4.9	8.5	5.2	5.4	7.4	1.8	1.3	15.6	4.6	5.7	7.2	4.9	16.5	9.1	4.2	0.0	8.9	3.5
Exp*Nut	1.8	7.2	5.9	4.8	6.2	12.0	3.0	8.9	4.5	11.3	10.3	23.6	5.5	11.4	15.1	7.4	7.3	0.0	44.3
Gen*Exp*Nut	3.3	7.8	6.8	7.4	10.0	26.5	1.3	1.4	17.7	7.1	16.6	11.2	6.9	32.2	12.1	3.8	0.0	0.0	6.3

Supplemental Table S3: Nutrition indexes of different N pools in the 4 Arabidopsis accessions.

Genotype	Nutrition	Experiment	NNI	NO3NI	RNO3NI	SAANI	RAA NI
Bur-0	0.01	1	0.23	0.03	0.01	0.63	0.33
Bur-0	0.01	2	0.20	0.04	0.02	0.29	0.24
Bur-0	0.01	3	0.32	0.07	0.03	0.36	0.49
Bur-0	0.2	1	0.98	0.83	0.69	1.03	0.86
Bur-0	0.2	2	0.92	0.65	0.46	0.79	0.59
Bur-0	0.2	3	0.79	0.55	0.46	0.62	0.84
Bur-0	1	1	1.07	0.83	1.33	0.96	1.07
Bur-0	1	2	0.91	0.78	0.76	0.85	0.61
Bur-0	1	3	0.88	0.77	0.79	0.64	1.02
Bur-0	4	1	1.00	1.00	1.00	1.00	1.00

Bur-0	4	2	1.00	1.00	1.00	1.00	1.00
Bur-0	4	3	1.00	1.00	1.00	1.00	1.00
Bur-0	10	1	1.11	1.22	1.15	1.25	1.20
Bur-0	10	2	0.77	0.68	0.82	0.66	0.75
Bur-0	10	3	0.88	0.95	0.95	0.95	0.97
Bur-0	50	1	0.76	1.20	1.33	1.12	0.87
Bur-0	50	2	0.55	0.81	0.73	0.72	0.66
Bur-0	50	3	0.61	0.82	0.76	0.78	1.01
Col-0	0.01	1	0.40	0.07	0.08	NA	0.54
Col-0	0.01	2	0.21	0.02	0.02	0.30	0.30
Col-0	0.01	3	0.29	0.02	0.03	0.29	0.43
Col-0	0.2	1	1.35	0.81	0.78	1.21	1.27
Col-0	0.2	2	0.69	0.54	0.44	0.69	0.40
Col-0	0.2	3	0.62	0.47	0.35	0.60	0.63
Col-0	1	1	1.41	0.93	1.23	1.16	1.11
Col-0	1	2	0.87	0.74	0.72	0.89	0.60
Col-0	1	3	0.71	0.68	0.68	0.66	0.83
Col-0	4	1	1.00	1.00	1.00	1.00	1.00
Col-0	4	2	1.00	1.00	1.00	1.00	1.00
Col-0	4	3	1.00	1.00	1.00	1.00	1.00
Col-0	10	1	1.28	1.40	1.70	1.43	0.87
Col-0	10	2	0.62	0.98	0.92	1.05	0.96
Col-0	10	3	0.93	1.18	1.05	1.20	1.34
Col-0	50	1	0.88	0.95	1.42	0.78	0.73
Col-0	50	2	0.74	0.81	1.04	0.59	0.77
Col-0	50	3	0.65	0.03	0.71	0.54	0.98
Cvi-0	0.01	1	0.29	0.10	0.01	0.44	0.39
Cvi-0	0.01	2	0.37	0.09	0.03	0.74	0.36
Cvi-0	0.01	3	0.48	0.62	0.06	0.91	0.81
Cvi-0	0.2	1	0.88	0.82	0.92	0.84	0.99
Cvi-0	0.2	2	1.08	0.79	0.76	1.10	0.64
Cvi-0	0.2	3	1.05	0.70	0.78	1.01	1.33
Cvi-0	1	1	1.01	1.16	1.34	1.12	1.03
Cvi-0	1	2	1.22	0.95	0.94	1.24	0.99
Cvi-0	1	3	1.07	1.00	1.01	1.00	1.10
Cvi-0	4	1	1.00	1.00	1.00	1.00	1.00
Cvi-0	4	2	1.00	1.00	1.00	1.00	1.00
Cvi-0	4	3	1.00	1.31	1.00	1.36	1.00
Cvi-0	10	1	1.02	1.11	1.48	0.98	1.03
Cvi-0	10	2	1.10	1.04	1.01	1.27	0.98
Cvi-0	10	3	0.96	1.49	1.01	1.39	0.99
Cvi-0	50	1	0.89	1.12	1.64	0.92	0.89
Cvi-0	50	2	0.92	1.08	1.04	1.27	0.79
Cvi-0	50	3	0.85	0.03	1.05	0.35	1.37
Ge-0	0.01	1	0.14	0.02	0.01	0.27	0.24
Ge-0	0.01	2	0.26	0.02	0.02	0.41	0.30
Ge-0	0.01	3	0.31	0.52	0.02	0.71	0.53

Ge-0	0.2	1	0.77	0.59	0.49	0.85	0.54
Ge-0	0.2	2	0.92	0.61	0.51	0.84	0.47
Ge-0	0.2	3	0.86	0.61	0.49	0.78	0.94
Ge-0	1	1	0.79	0.94	0.80	0.99	0.71
Ge-0	1	2	1.07	0.77	0.87	0.86	0.75
Ge-0	1	3	0.86	1.00	0.83	1.00	1.00
Ge-0	4	1	1.00	1.00	1.00	1.00	1.00
Ge-0	4	2	1.00	1.00	1.00	1.00	1.00
Ge-0	4	3	1.00	1.02	1.00	1.05	1.00
Ge-0	10	1	0.90	1.10	1.19	0.92	1.08
Ge-0	10	2	1.07	1.15	1.05	1.22	0.84
Ge-0	10	3	1.06	1.00	1.11	0.99	1.12
Ge-0	50	1	0.75	0.79	1.30	0.76	0.80
Ge-0	50	2	0.74	0.80	0.98	0.83	0.71
Ge-0	50	3	0.66	NA	0.78	NA	1.19

Supplemental Table S4: ANOVA of the 5 nutrition indexes in 4 Arabidopsis accessions growing in 6 different N supplies in 3 independent experiments. Three factors were tested in the ANOVA model: Genotype (accessions), Nutrition (nitrate supplies) and Experiment. For each index, the sum of squares (SCR) and p-value of each factors, SCR of residuals and global p-value of the ANOVA model are given. Groups of genotype significantly different following the Newman and Keuls tests are shown in brackets.

	Genotype		**Nutrition**		**Experiment**		**Residual**	**Model**	**Newman and Keuls test**
Index	SCR	p-value	SCR	p-value	SCR	p-value	SCR	p-value	groups
NNI	0.43	0.0008	3.14	< 0.0001	0.37	0.0007	5.36	< 0.0001	*(Cvi-0) and (Bur-0, Col-0, Ge-0)*
NO3NI in Shoot	0.20	0.0113	8.98	< 0.0001	0.10	0.0557	1.02	< 0.0001	*(Cvi-0) and (Bur-0, Col-0, Ge-0)*
NO3NI in Roots	0.27	0.0122	10.46	< 0.0001	0.95	< 0.0001	1.41	< 0.0001	*(Cvi-0) and (Bur-0, Col-0, Ge-0)*
AANI in Shoot	0.43	0.0008	3.14	< 0.0001	0.37	0.0007	1.32	< 0.0001	*(Cvi-0) and (Bur-0, Col-0, Ge-0)*
AANI in Roots	0.21	0.0389	2.94	< 0.0001	0.81	< 0.0001	1.45	< 0.0001	*(Cvi-0) and (Bur-0, Col-0, Ge-0)*

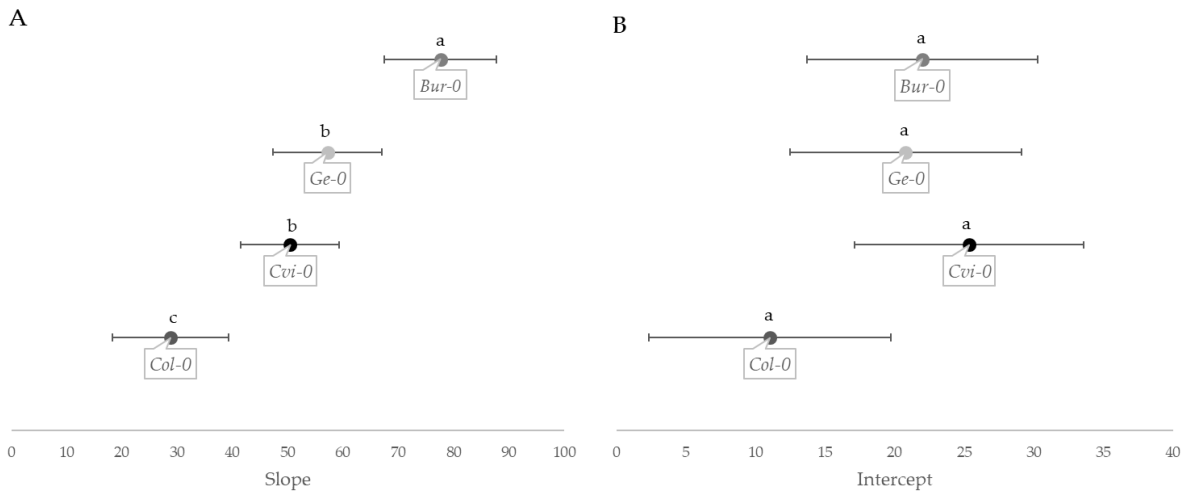
Supplemental Table S5: Pearson's correlation matrix of investigated traits. Colours indicate correlation values used for building-up the descriptive model (**Figure 7**). For each trait in rows, the dark and light greys highlight the first and second highest significant correlations with the other traits. The extreme right column and the down row contain the correlations between nutrition and each of the investigated traits. Numbers in bold represent significant correlation values ($P \leq 0.05$).

Trait	SNO3	RNO3	SAA	RAA	SFM	RFM	SRFM	SRNO3	SRAA	RL	RT	N%	C%	C/N	SNH4	RNH4	SPC	SPA	SRNH4	nutrition
SNO3		0.70	0.55	0.24	0.34	-0.07	0.49	-0.24	0.11	0.03	-0.13	0.81	-0.56	-0.78	0.44	0.28	-0.07	0.38	0.14	0.60
RNO3	0.70		0.41	0.61	0.20	-0.28	0.61	-0.57	-0.22	-0.06	-0.33	0.60	-0.41	-0.60	0.25	0.49	0.09	0.29	-0.22	0.50
SAA	0.55	0.41		0.17	0.06	-0.08	0.14	-0.13	0.44	-0.06	-0.07	0.23	-0.26	-0.23	0.72	0.27	-0.11	0.20	0.28	0.48
RAA	0.24	0.61	0.17		-0.25	-0.60	0.57	-0.46	-0.70	-0.31	-0.62	0.17	-0.11	-0.18	0.09	0.61	0.14	-0.15	-0.44	0.34
SFM	0.34	0.20	0.06	-0.25		0.69	0.06	-0.09	0.25	0.64	0.60	0.47	-0.37	-0.46	0.14	-0.30	-0.05	0.88	0.30	-0.05
RFM	-0.07	-0.28	-0.08	-0.60	0.69		-0.58	0.29	0.46	0.67	0.95	-0.03	-0.11	0.05	-0.03	-0.59	-0.18	0.53	0.43	-0.19
SRFM	0.49	0.61	0.14	0.57	0.06	-0.58		-0.43	-0.37	-0.32	-0.61	0.51	-0.27	-0.52	0.13	0.58	0.19	0.14	-0.32	0.20
SRNO3	-0.24	-0.57	-0.13	-0.46	-0.09	0.29	-0.43		0.33	0.04	0.35	-0.30	0.18	0.31	-0.11	-0.43	-0.21	-0.17	0.36	-0.14
SRAA	0.11	-0.22	0.44	-0.70	0.25	0.46	-0.37	0.33		0.21	0.49	0.05	-0.07	-0.03	0.32	-0.38	-0.18	0.26	0.57	-0.04
RL	0.03	-0.06	-0.06	-0.31	0.64	0.67	-0.32	0.04	0.21		0.45	0.11	-0.20	-0.09	0.02	-0.33	-0.20	0.53	0.21	-0.11
RT	-0.13	-0.33	-0.07	-0.62	0.60	0.95	-0.61	0.35	0.49	0.45		-0.10	-0.04	0.11	-0.04	-0.63	-0.16	0.46	0.46	-0.19
N%	0.81	0.60	0.23	0.17	0.47	-0.03	0.51	-0.30	0.05	0.11	-0.10		-0.40	-0.96	0.22	0.17	0.15	0.49	0.06	0.27
C%	-0.56	-0.41	-0.26	-0.11	-0.37	-0.11	-0.27	0.18	-0.07	-0.20	-0.04	-0.40		0.54	-0.28	-0.13	0.17	-0.35	-0.09	-0.41
C/N	-0.78	-0.60	-0.23	-0.18	-0.46	0.05	-0.52	0.31	-0.03	-0.09	0.11	-0.96	0.54		-0.27	-0.20	-0.14	-0.48	-0.08	-0.28
SNH4	0.44	0.25	0.72	0.09	0.14	-0.03	0.13	-0.11	0.32	0.02	-0.04	0.22	-0.28	-0.27		0.28	-0.16	0.27	0.48	0.37
RNH4	0.28	0.49	0.27	0.61	-0.30	-0.59	0.58	-0.43	-0.38	-0.33	-0.63	0.17	-0.13	-0.20	0.28		0.19	-0.25	-0.61	0.22
SPC	-0.07	0.09	-0.11	0.14	-0.05	-0.18	0.19	-0.21	-0.18	-0.20	-0.16	0.15	0.17	-0.14	-0.16	0.19		-0.06	-0.26	-0.36
SPA	0.38	0.29	0.20	-0.15	0.88	0.53	0.14	-0.17	0.26	0.53	0.46	0.49	-0.35	-0.48	0.27	-0.25	-0.06		0.35	0.01
SRNH4	0.14	-0.22	0.28	-0.44	0.30	0.43	-0.32	0.36	0.57	0.21	0.46	0.06	-0.09	-0.08	0.48	-0.61	-0.26	0.35		0.07
nutrition	0.60	0.50	0.48	0.34	-0.05	-0.19	0.20	-0.14	-0.04	-0.11	-0.19	0.27	-0.41	-0.28	0.37	0.22	-0.36	0.01	0.07	

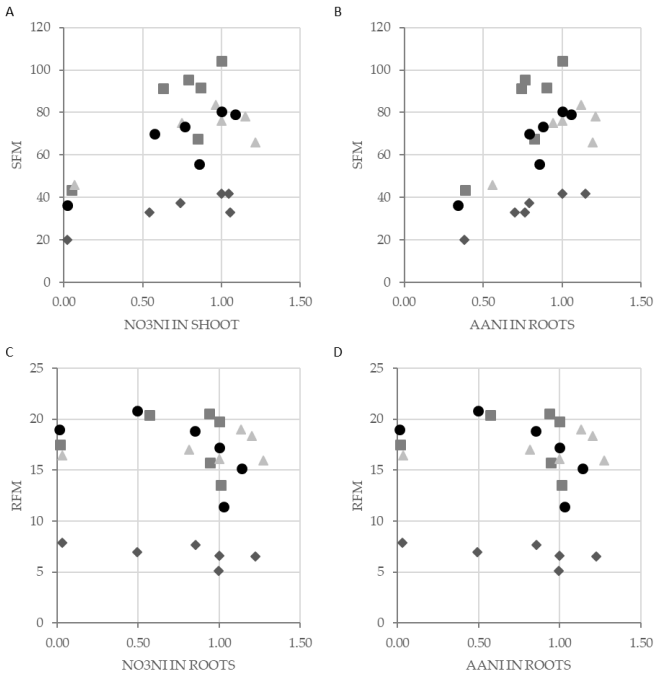
Supplemental Table S6: Parameters of the descriptive model for the estimation of morphological traits according to N nutrition. The parameters are obtained for each accession in the three independent experiments.

	Experiment 1				**Experiment 2**				**Experiment 3**			
	Bur-0	**Col-0**	**Cvi-0**	**Ge-0**	**Bur-0**	**Col-0**	**Cvi-0**	**Ge-0**	**Bur-0**	**Col-0**	**Cvi-0**	**Ge-0**
A1	84	101	72	97	38	40	29	40	55	60	53	63
A2	432	492	399	446	204	211	185	203	332	350	325	351
B1	0.016	-0.001	0.013	0.019	0.022	0.018	0.019	0.030	0.008	0.017	0.005	0.013
B2	16.70	31.73	16.39	16.30	12.65	14.03	11.79	11.85	17.22	21.64	23.01	14.74
C1	-0.74	-0.26	-0.21	-0.66	-0.94	-0.19	-0.37	-0.41	-0.42	-0.06	-0.26	-0.44
C2	3.13	1.24	1.45	2.96	3.74	1.10	2.00	1.96	2.13	0.63	1.40	2.17
D1	21.51	19.34	19.38	22.17	22.40	16.73	20.17	17.77	20.31	17.04	21.80	20.68
D2	-1.67	-1.10	2.41	-1.44	-3.15	-0.60	1.84	2.73	-0.57	-0.98	-0.37	-1.32

E1	-0.34	0.24	0.17	-0.09	0.83	0.50	0.82	0.32	0.98	0.39	0.36	0.26
E2	5.20	2.84	3.88	4.43	1.90	2.56	1.76	3.29	1.63	2.86	3.15	3.33
F1	0.06	0.03	0.05	0.05	0.04	0.04	0.02	0.04	0.06	0.05	0.03	0.05
F2	0.42	0.84	0.48	0.70	1.71	0.55	2.44	2.12	-0.12	0.42	1.61	1.69



Supplemental Figure S1: Slope (A) and intercept (B) of linear regression of SFM against NNI for the 4 Arabidopsis accessions. The confidence intervals were computed with an alpha risk of 5%. Different letters indicate values significantly different at $P < 0.05$.



Supplemental Figure S2: Nutrition Use Efficiency in 4 Arabidopsis accessions. Shoot fresh matter (SFM, A and B) and root fresh matter (RFM, C and D) of the 4 accessions are plotted against their Nitrate Nutrition Index (NO3NI, A and C) and their Amino Acids Nutrition Index (AANI, B and C). Accessions are showed by squares, diamonds, triangles and circles in different shades of grey for *Bur-0*, *Col-0*, *Cvi-0* and *Ge-0*, respectively.