

SUPPLEMENTARY INFORMATION

Supplementary Text:

Phylogenetic tree data

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Fig. SI.2: Phylogenetic relationships of the 56 species in the data

Fig. SI.3: Directed acyclic graphs representing path model hypotheses

Fig. SI.4: Boxplots of three alternative estimations of community-weighted mean GS, including non-phylogenetic community-weighted mean GS.

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Fig. SI.6: Scatterplots showing associations between community-weighted mean C-strategy and community-weighted mean C-value

Fig. SI.7: Non-metric multidimensional scaling (NMDS) biplots showing species distributions

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Table SI.2: Species list: family, C-value (genome size), and C-strategy

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Table SI.4: CIC, C-statistics, p-values of path models

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Table SI.6: Model reduction assessing community-weighted mean genome size

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Table SI.11: Regression output for path models: $\pm$ Insects $\pm$ Molluscs

Table SI.12: Changes in species biomass with herbivore exclusion

SUPPLEMENTARY TEXT

Phylogenetic data (.tre format)

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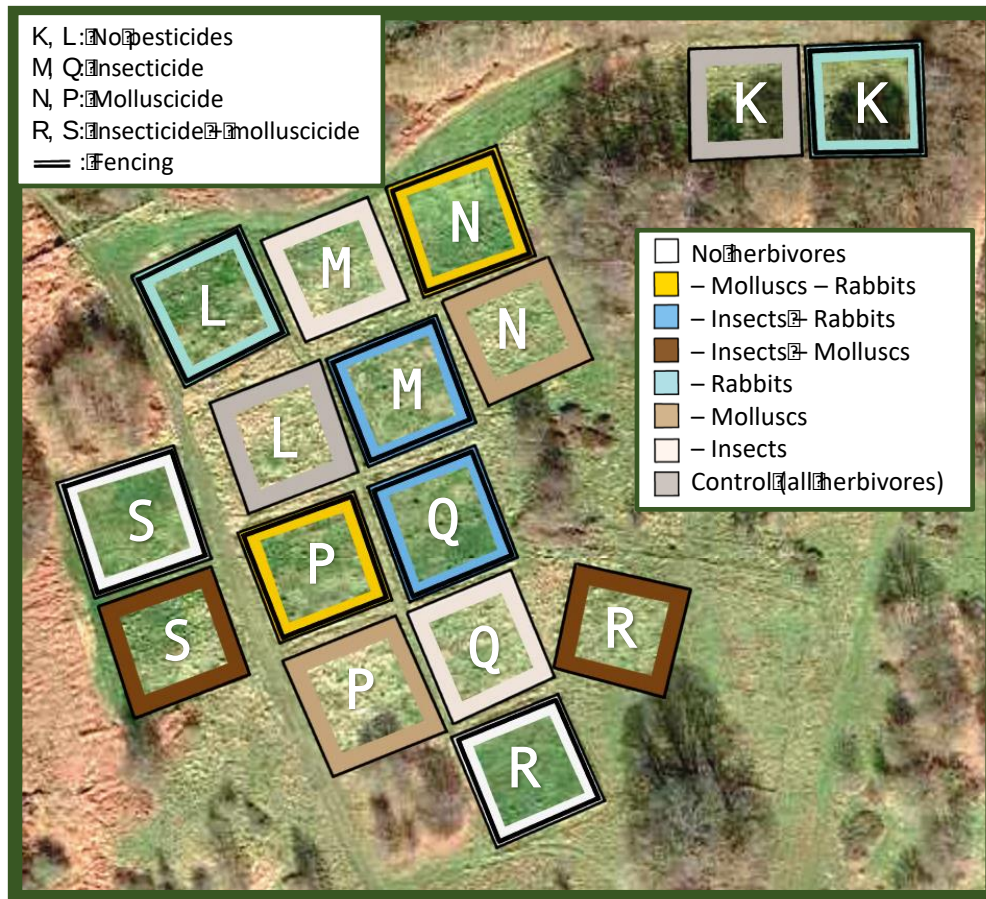


Fig. SI.1 Layout of experimental plots in Nash's Field, established in 1991 at Silwood Park (Imperial College, London). Further details are available at <http://www.imperial.ac.uk/silwood-park/research/silwood-lte/nashk-s/>.

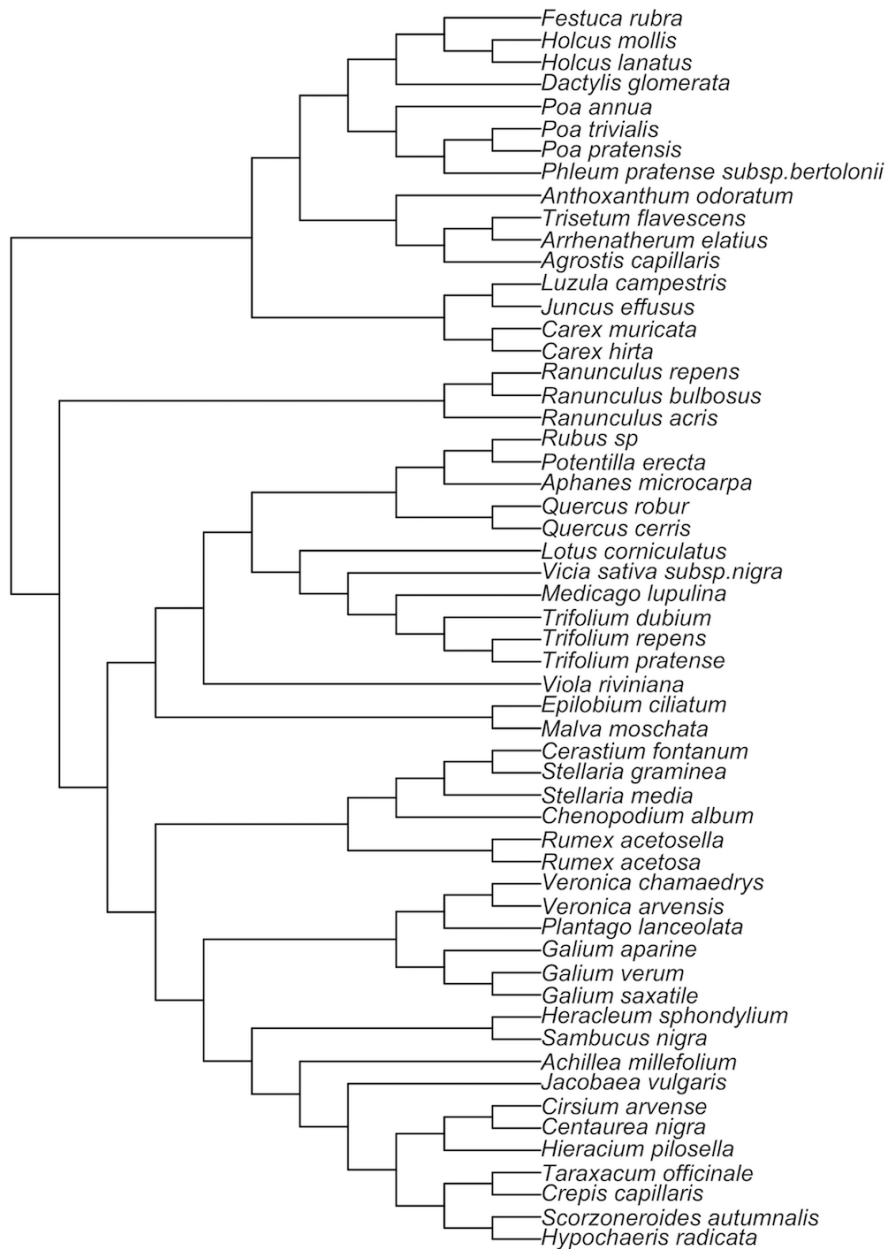


Fig. SI.2 Phylogenetic tree of the 56 species occurring on the 556 limed plots of Nash's Field, Silwood Park, UK.

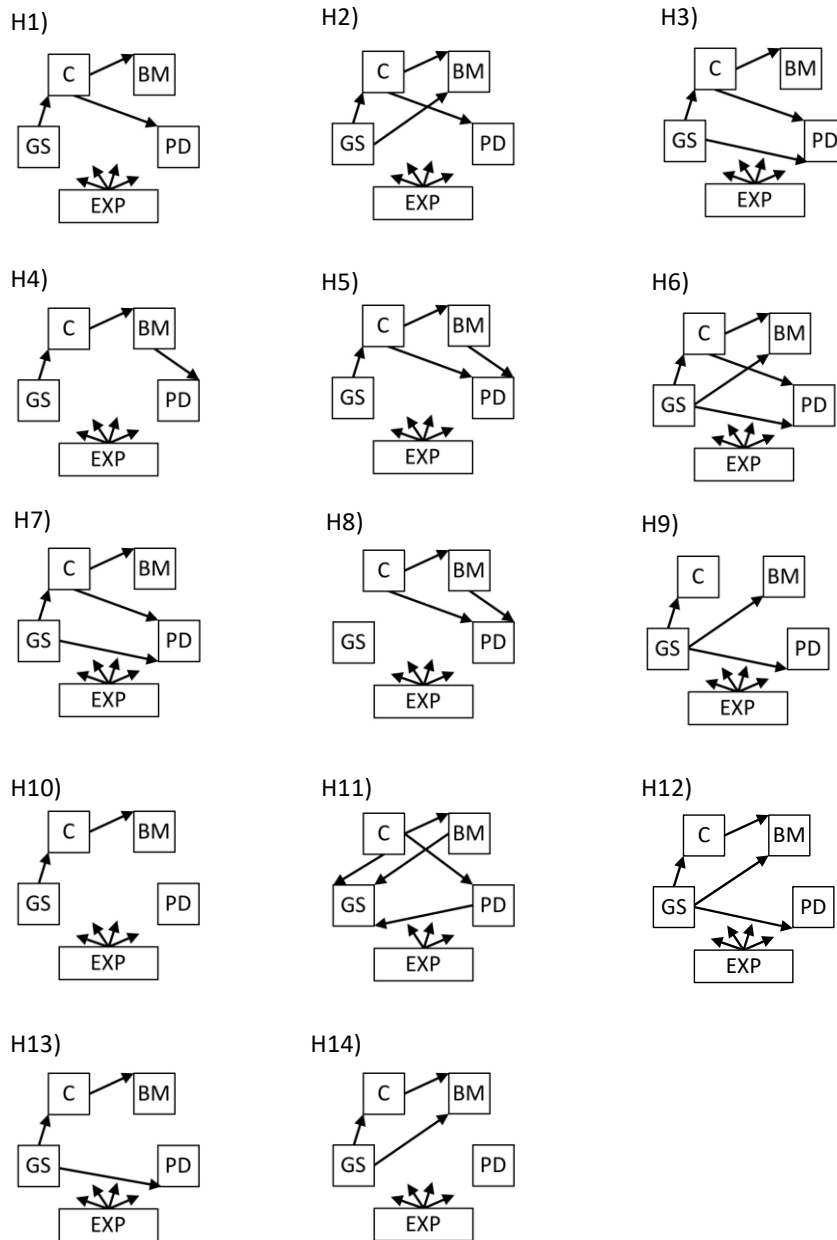


Fig. SI.3 Directed acyclic graphs representing path models investigating the effects exerted by the experiment on the four plant community parameters comprising (i) community-weighted mean genome size (GS), (ii) community-weighted mean competitive (C)-strategy (C), (iii) total community biomass (BM), and (iv) phylogenetic diversity (PD), and how these four properties are associated with each other. These hypotheses are built upon previous studies investigating the influence of GS on plant communities and from examining correlations present in the data. The small arrows pointing towards each variable represent the effect of experimental treatment (EXP: interactions between herbivore exclusion, N and P, plus K). An arrow originates from the experiment to each of the four community properties in all model hypotheses (diagrams H1-H14), except H11, where conditional independence was tested between the experiment and genome size (see also Table SI.3 for a more complete description of *d-sep* methods).

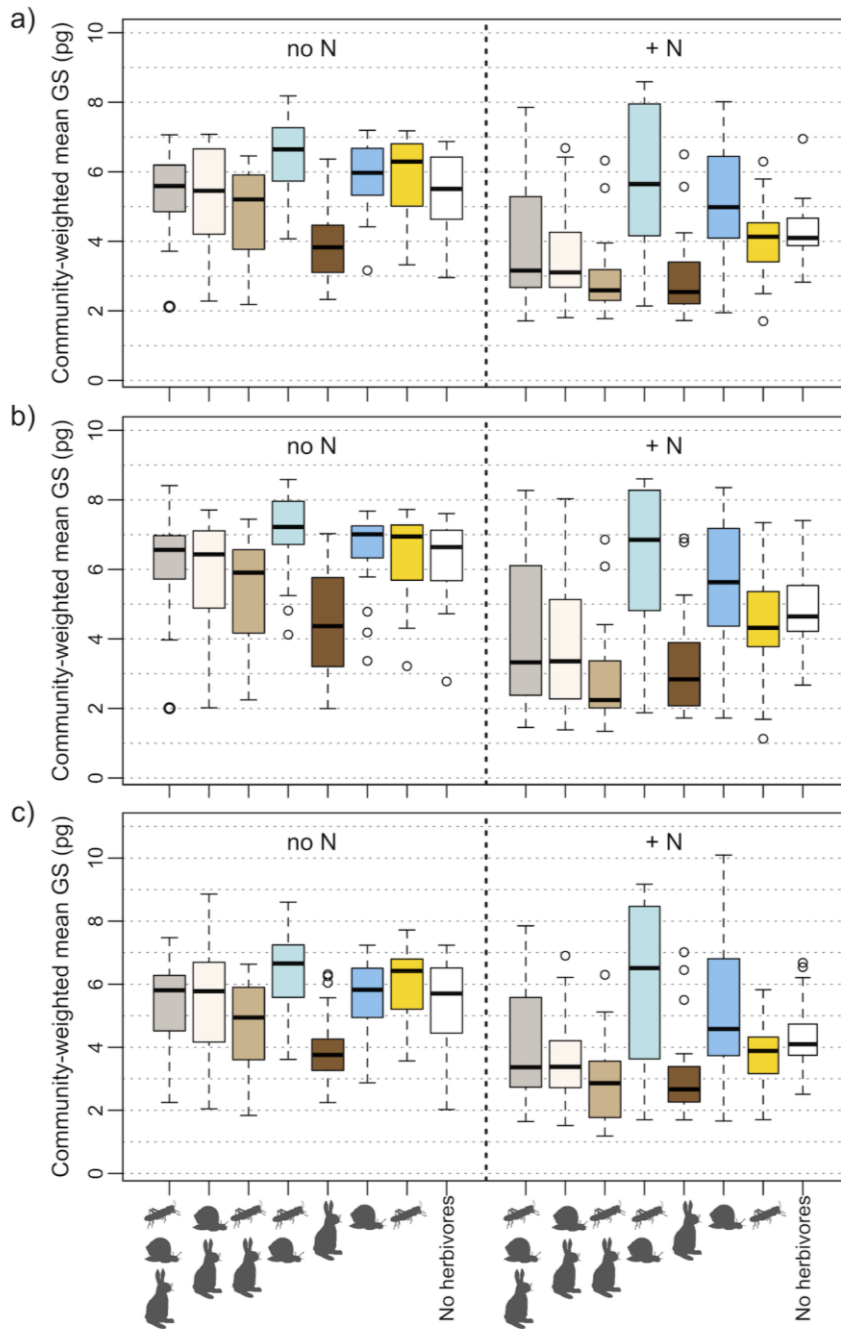


Fig. SI.4 Three alternative estimations of community-weighted mean GS (1C-value in picograms): **a)** simple weighted mean GS, without accounting for phylogenetic non-independence. As in the main text, species GS were log10-transformed, and the weighted mean back-transformed; **b)** estimated with PGLS assuming a Brownian motion of evolution structure (as described in the main text); however GS was *not* transformed; **c)** estimated with PGLS with lambda optimisation, thus relaxing the assumptions of Brownian motion of evolution. As in the main text, species GS were log10-transformed, and the community-weighted mean back-transformed. See also Table SI.9 for significance of experimental treatments (N fertilizer and herbivore exclusions) on community-weighted mean GS.

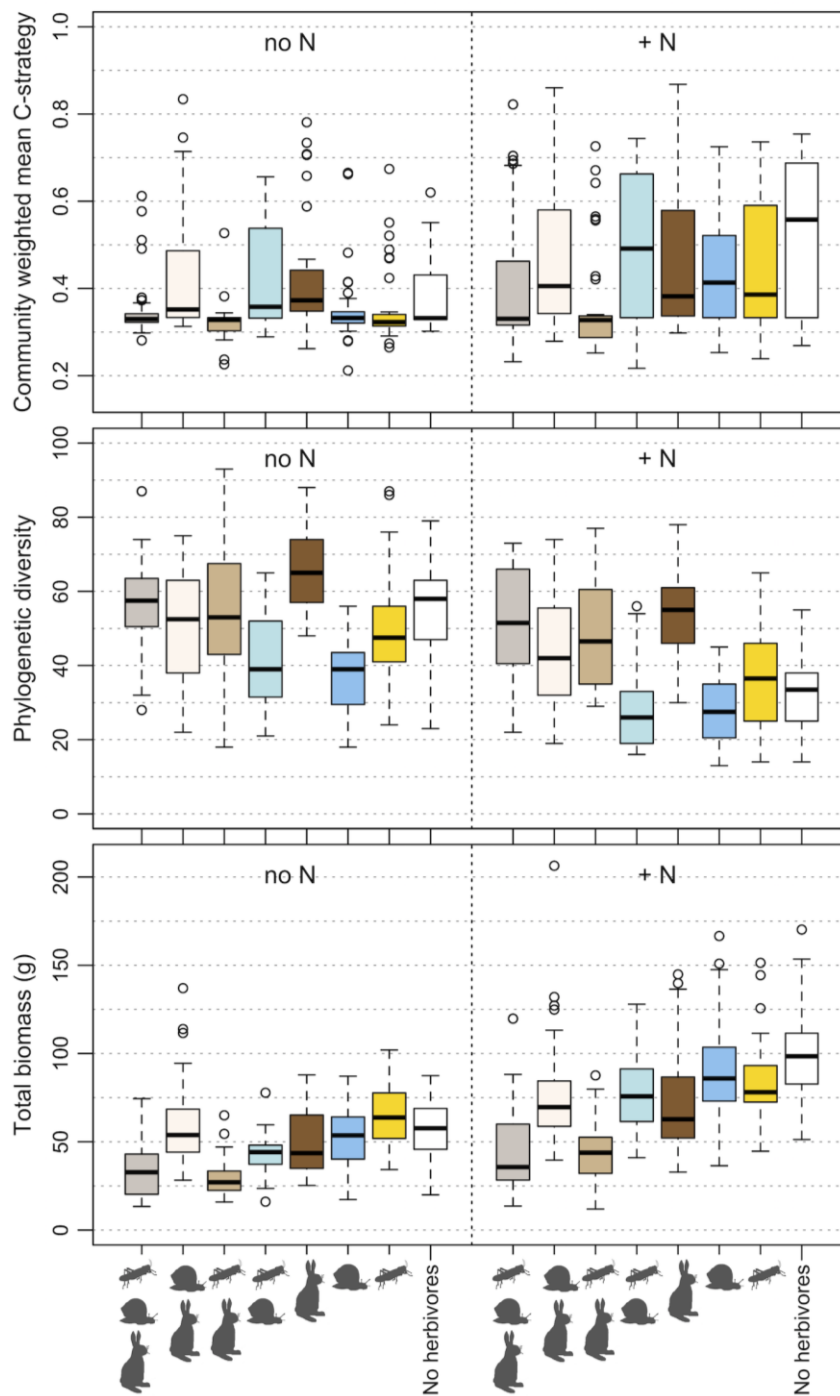


Fig. SI.5 Community-weighted mean competitive (C)-strategy; phylogenetic diversity (Faith's PD [1]), and total community biomass (dry weight g/m²) (n = 556), shown according to herbivore treatment. Herbivore treatments, in order as shown above are: 1) control (all herbivores present); 2) – insects; 3) – molluscs; 4) – rabbits; 5) rabbits only (– insects, – molluscs); 6) molluscs only (– insects, – rabbits); 7) insects only (– molluscs, – rabbits); 8) no herbivores. See also Table SI.8.

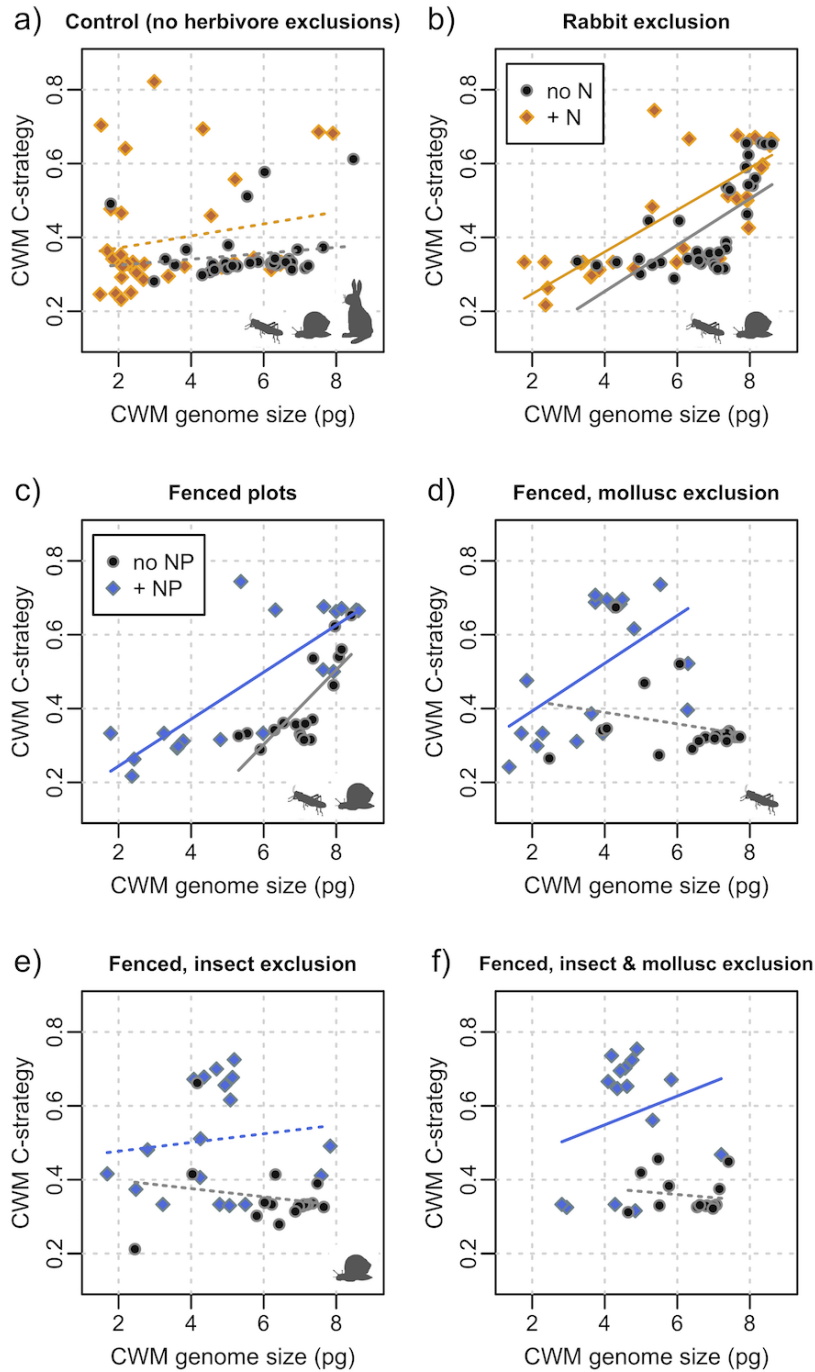


Fig. SI.6 Associations between community-weighted mean (CWM) C-strategy (CWM C-strategy) and CWM GS under different herbivore exclusion treatments and $\pm$ N input. Herbivore exclusion treatments correspond to those of the path analyses: effects of rabbit herbivory (**a, b**); and effects of molluscs and insects on fenced plots (**c-f**). The rabbit herbivory path analysis showed that N input (but not P) had a significant influence on CWM GS and CWM C-strategy. In the path analysis on mollusc and insect herbivory, the 4-way interaction [–insects –molluscs N P] was significant, thus shown in **c-f** are plots without N and P input, and with both N and P input. Both community properties were estimated with PGLS, taking phylogeny into account. Trend lines were estimated with a simple bivariate linear model. A solid line shows a significant association ($p < 0.05$), a dashed line shows non-significance.

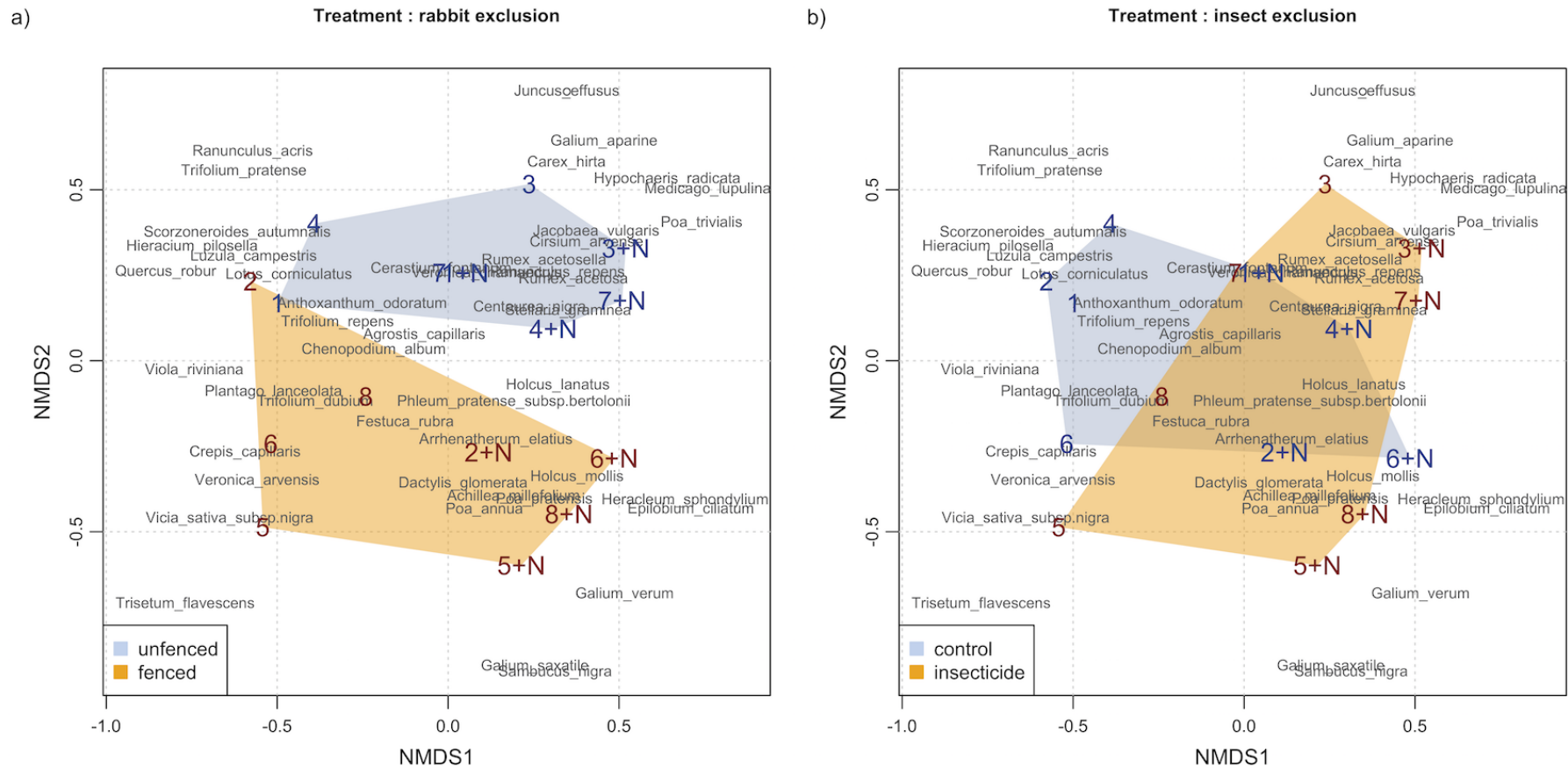


Fig. SI.7 Non-metric multidimensional scaling (NMDS) biplots showing species abundances in two-dimensional space. Stress = 0.173. Experimental treatments are coded as follows: 1 = control (no treatments); 2 = fencing; 3 = insecticide; 4 = molluscicide; 5 = insecticide + fencing; 6 = molluscicide + fencing; 7 = insecticide + molluscicide; 8 = no herbivores (insecticide + molluscicide + fencing). For each treatment, there is also an equivalent with N fertilizer (+ N). Convex hull polygons delineate experimental treatments and the plant species found within them: **a)** $\pm$ fencing (rabbit exclusion); **b)** $\pm$ insect exclusion; **c)** $\pm$ mollusc exclusion; and **d)** $\pm$ N fertilizer. See Table SI.12 for species lists with mean percent change in biomass.

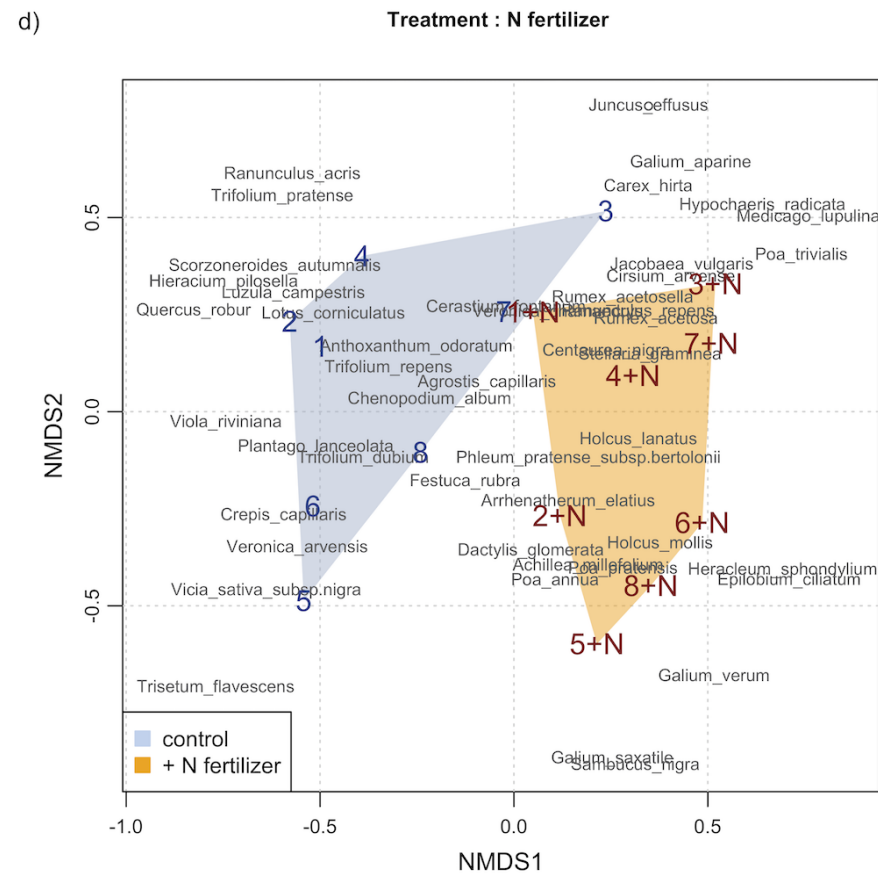
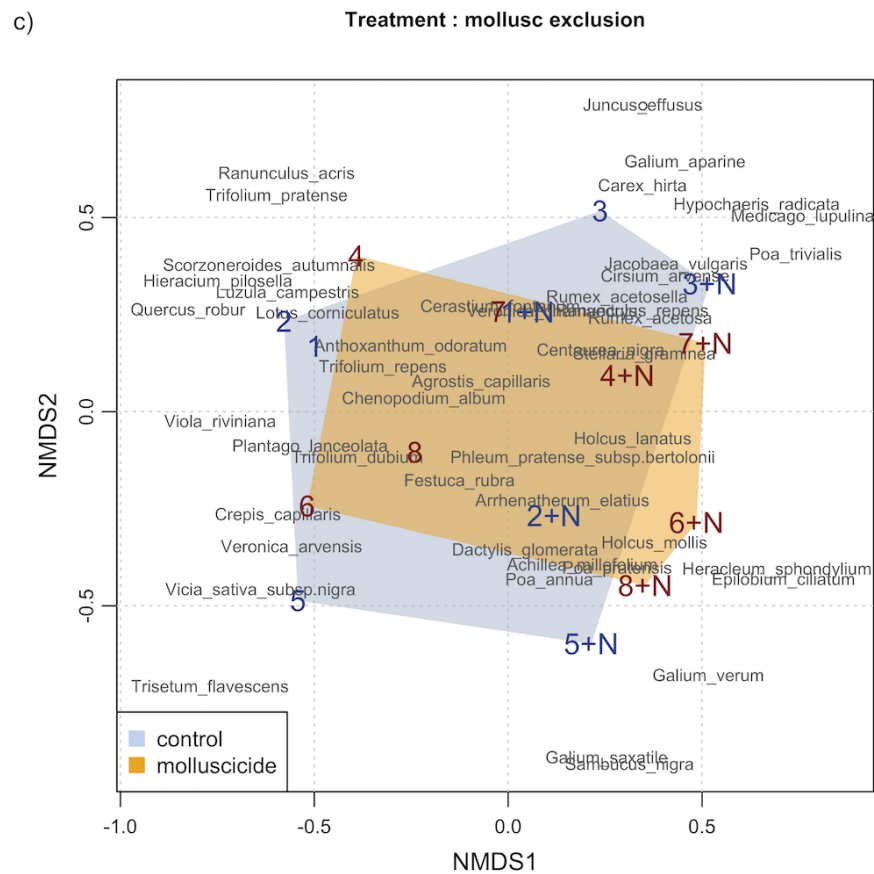


Table SI.1 (A) Flow cytometry results for 36 species collected at Nash’s field, Silwood Park, showing the mean estimated 1C-value in picograms (pg) obtained, number of plants measured (n), standard deviation in 1C-value (sdev), and mean target and standard coefficients of variation (CoV). 1C-values were estimated using a Partec CyFlow Space flow cytometer fitted with a Cobalt Samba green (532 nm, 100 mW) laser. Internal standards were either parsley (*Petroselinum crispum* “Champion Moss Curled”; 1C=2.22 pg), pea (*Pisum sativum* “Minerva Maple”; 1C=4.86 pg), tomato (*Solanum lycopersicum*, 1C=0.98 pg), or rice (*Oryza sativa*; 1C = 0.5 pg) (the 1C-values for the calibration standards were taken from Pellicer and Leitch [2]), and samples were prepared with Galbraith’s or LB01 buffers. For some species several flow cytometry runs were made using different calibration standards. These are indicated in the final column below, while the results of all individual flow cytometry runs used to calculate the Mean 1C-values together with the calibration standard used are given in Table SI.1 (B). Note that for species with a high CoV (e.g. > 5 - 8 %), we used the Prime C-value from the Plant DNA C-values database [3]. See Table SI.1 (B) for flow cytometry output of each sample run. The species’ C-values used in the statistical analyses are shown in Table SI.2.

Taxon	Mean 1C-value (pg)	n	Sdev	Mean target CoV	Mean standard CoV	Calibration standard(s)
<i>Achillea millefolium</i>	7.98	3	0.03	3.16	3.40	Pea
<i>Agrostis capillaris</i>	3.60	8	0.25	4.43	4.37	Parsley, pea
<i>Anthoxanthum odoratum</i>	7.28	3	0.36	4.05	4.27	Parsley, pea
<i>Arrhenatherum elatius</i>	8.58	3	0.47	3.73	4.71	Parsley, pea
<i>Carex muricata</i>	0.38	7	0.01	6.52	4.61	Parsley, rice, tomato
<i>Centaurea nigra</i>	2.13	2	0.29	7.17	6.23	Pea
<i>Cerastium fontanum</i>	3.23	2	0.20	4.29	3.68	Parsley, pea
<i>Chenopodium album</i>	1.95	1	NA	6.76	6.84	Rice
<i>Cirsium arvense</i>	1.48	1	NA	4.64	3.74	Pea
<i>Crepis capillaris</i>	2.45	2	0.13	8.50	5.81	Pea
<i>Dactylis glomerata</i>	4.44	2	0.21	4.60	5.20	Parsley
<i>Festuca rubra</i>	7.31	2	0.02	5.25	5.46	Pea
<i>Galium aparine</i>	1.11	1	NA	6.88	5.14	Parsley
<i>Galium saxatile</i>	1.72	1	NA	4.21	2.44	Pea
<i>Galium verum</i>	2.25	1	NA	6.99	8.67	Pea
<i>Heracleum sphondylium</i>	2.46	2	0.15	5.09	5.26	Rice, pea
<i>Hieracium pilosella</i>	3.52	2	0.05	6.46	6.95	Parsley
<i>Holcus lanatus</i>	1.70	1	NA	4.14	2.94	Parsley
<i>Holcus mollis</i>	4.03	3	0.04	6.30	7.31	Parsley
<i>Jacobaea vulgaris</i>	2.30	3	0.11	4.21	4.46	Rice, pea
<i>Juncus effusus</i>	0.28	2	0.02	5.37	4.61	Parsley, rice
<i>Lotus corniculatus</i>	1.30	4	0.05	4.75	4.41	Parsley, rice
<i>Luzula campestris</i>	0.40	2	0.01	5.54	4.32	Parsley, tomato
<i>Medicago lupulina</i>	0.55	1	NA	15.07	4.82	Parsley
<i>Phleum pratense</i> subsp. <i>bertolonii</i>	1.88	3	0.08	3.13	3.54	Parsley, pea, rice
<i>Plantago lanceolata</i>	1.43	2	0.03	4.99	4.79	Parsley, rice
<i>Poa trivialis</i>	2.01	4	0.02	4.41	3.68	Pea
<i>Ranunculus acris</i>	4.98	2	0.13	3.79	4.24	Parsley
<i>Ranunculus repens</i>	11.06	2	0.14	5.68	5.69	Pea

Table SI.1 (A) continued

Taxa	Mean 1C-value (pg)	n	Sdev	Mean target CoV	Mean standard CoV	Calibration standard(s)
<i>Rubus</i> sp.	0.87	1	NA	19.0	6.72	Parsley
<i>Rumex acetosella</i>	1.07	2	0.01	7.50	6.00	Parsley
<i>Stellaria graminea</i>	1.01	4	0.05	4.22	4.59	Rice, pea
<i>Trifolium repens</i>	1.12	2	0.02	6.41	6.11	Parsley
<i>Veronica chamaedrys</i>	2.16	2	0.02	5.02	3.80	Pea
<i>Vicia sativa</i> subsp. <i>nigra</i>	2.21	2	0.02	6.71	5.80	Pea
<i>Viola riviniana</i>	1.48	2	0.15	6.93	4.08	Parsley, pea

Table SI.1 (B) Flow cytometry output of individual samples run to estimate the mean 1C-values (pg) of the 36 species given in Table SI.1 (A). It gives the peak values of the target and standard obtained from the flow histograms. The table shows the standard used in each sample and the 1C-value (pg) of the calibration standard used. The target 1C-value is estimated as: (target peak/standard peak) x standard 1C-value. Also shown are the coefficients of variation (CoV) of the target and standard peaks, the estimated genome size (1C-value in pg) of the target.

Taxon	Standard	Standard 1C-value	Target peak	Standard peak	Target 1C-value	Target CoV	Standard Cov
<i>Achillea millefolium</i>	pea	4.86	385.12	235.34	7.95	3.58	3.48
<i>Achillea millefolium</i>	pea	4.86	392.75	239.76	7.96	3.64	3.14
<i>Achillea millefolium</i>	pea	4.86	415.56	251.92	8.02	2.27	3.57
<i>Agrostis capillaris</i>	parsley	2.22	163.54	110.84	3.28	4.58	4.72
<i>Agrostis capillaris</i>	parsley	2.22	287.30	188.10	3.39	3.83	3.60
<i>Agrostis capillaris</i>	parsley	2.22	262.84	166.78	3.50	4.89	5.15
<i>Agrostis capillaris</i>	parsley	2.22	314.98	199.81	3.50	4.51	4.35
<i>Agrostis capillaris</i>	parsley	2.22	198.60	124.31	3.55	4.51	4.51
<i>Agrostis capillaris</i>	parsley	2.22	182.58	111.21	3.64	4.17	4.95
<i>Agrostis capillaris</i>	pea	4.86	201.59	248.93	3.94	4.20	4.23
<i>Agrostis capillaris</i>	pea	4.86	135.91	166.02	3.98	4.77	3.44
<i>Anthoxan. odoratum</i>	parsley	2.22	345.25	110.73	6.92	3.52	4.42
<i>Anthoxan. odoratum</i>	parsley	2.22	346.00	105.60	7.27	4.86	3.56
<i>Anthoxan. odoratum</i>	pea	4.86	289.27	184.06	7.64	3.77	4.82
<i>Arrhenatherum elatius</i>	parsley	2.22	373.76	99.72	8.32	3.50	7.50
<i>Arrhenatherum elatius</i>	parsley	2.22	214.89	55.02	8.67	2.66	3.01
<i>Arrhenatherum elatius</i>	pea	4.86	253.04	140.42	8.76	5.03	3.63
<i>Carex muricata</i>	tomato	0.98	28.60	77.04	0.36	6.37	5.05
<i>Carex muricata</i>	rice	0.50	106.00	140.35	0.38	6.70	4.74
<i>Carex muricata</i>	rice	0.50	108.35	142.57	0.38	6.55	4.44
<i>Carex muricata</i>	parsley	2.22	18.01	104.53	0.38	6.35	4.97
<i>Carex muricata</i>	parsley	2.22	18.21	105.08	0.38	6.79	4.80
<i>Carex muricata</i>	parsley	2.22	18.14	104.03	0.39	6.52	4.91
<i>Carex muricata</i>	rice	0.50	44.81	57.70	0.39	6.36	3.36
<i>Centaurea nigra</i>	pea	4.86	54.17	137.08	1.92	6.41	5.44
<i>Centaurea nigra</i>	pea	4.86	82.71	172.37	2.33	7.93	7.01
<i>Cerastium fontanum</i>	parsley	2.22	96.75	69.51	3.09	5.00	4.52
<i>Cerastium fontanum</i>	pea	4.86	100.63	144.80	3.38	3.57	2.83
<i>Chenopodium album</i>	rice	0.50	143.70	36.78	1.95	6.76	6.84
<i>Cirsium arvense</i>	pea	4.86	58.16	191.51	1.48	4.64	3.74
<i>Crepis capillaris</i>	pea	4.86	100.14	206.88	2.35	10.37	6.06
<i>Crepis capillaris</i>	pea	4.86	78.48	150.03	2.54	6.63	5.55
<i>Dactylis glomerata</i>	parsley	2.22	232.63	120.30	4.29	5.05	5.55
<i>Dactylis glomerata</i>	parsley	2.22	192.52	93.11	4.59	4.15	4.84
<i>Festuca rubra</i>	pea	4.86	267.44	178.24	7.29	5.27	5.34
<i>Festuca rubra</i>	pea	4.86	247.31	164.12	7.32	5.22	5.94

Table SI.1 (B) continued

Taxon	Standard	Standard 1C-value	Target peak	Standard peak	Target 1C-value	Target CoV	Standard Cov
<i>Galium aparine</i>	parsley	2.22	68.14	136.37	1.11	6.88	5.14
<i>Galium saxatile</i>	pea	4.86	172.61	488.13	1.72	4.21	2.44
<i>Galium verum</i>	pea	4.86	67.42	145.49	2.25	6.99	8.67
<i>Heracleum sphondylium</i>	rice	0.50	232.10	49.37	2.35	4.72	5.25
<i>Heracleum sphondylium</i>	pea	4.86	78.63	148.95	2.57	5.46	5.26
<i>Hieracium pilosella</i>	parsley	2.22	221.55	141.21	3.48	6.98	8.36
<i>Hieracium pilosella</i>	parsley	2.22	247.57	154.92	3.55	5.94	5.54
<i>Holcus lanatus</i>	parsley	2.22	147.43	192.18	1.70	4.14	2.94
<i>Holcus mollis</i>	parsley	2.22	245.02	136.48	3.99	6.48	6.43
<i>Holcus mollis</i>	parsley	2.22	121.87	66.82	4.05	5.91	7.51
<i>Holcus mollis</i>	parsley	2.22	244.91	133.96	4.06	6.52	7.99
<i>Jacobaea vulgaris</i>	pea	4.86	72.75	161.09	2.19	4.55	2.60
<i>Jacobaea vulgaris</i>	rice	0.50	113.51	24.88	2.28	4.03	4.93
<i>Jacobaea vulgaris</i>	pea	4.86	97.01	194.88	2.42	4.05	5.86
<i>Juncus effusus</i>	rice	0.50	48.33	88.89	0.27	5.66	5.58
<i>Juncus effusus</i>	parsley	2.22	13.78	103.51	0.30	5.08	3.63
<i>Lotus corniculatus</i>	parsley	2.22	119.58	212.15	1.25	5.34	4.94
<i>Lotus corniculatus</i>	parsley	2.22	140.90	243.72	1.28	4.27	3.17
<i>Lotus corniculatus</i>	rice	0.50	142.91	54.75	1.31	6.17	5.13
<i>Lotus corniculatus</i>	parsley	2.22	153.43	248.56	1.37	3.20	4.40
<i>Luzula campestris</i>	tomato	0.98	24.97	63.08	0.39	5.51	5.16
<i>Luzula campestris</i>	parsley	2.22	21.58	119.88	0.40	5.56	3.48
<i>Medicago lupulina</i>	parsley	2.22	37.89	153.10	0.55	15.07	4.82
<i>Phleum pratense</i> subsp. <i>bertolonii</i>	parsley	2.22	111.21	135.99	1.82	4.31	3.54
<i>Phleum pratense</i> subsp. <i>bertolonii</i>	rice	0.50	223.27	59.97	1.86	2.32	3.89
<i>Phleum pratense</i> subsp. <i>bertolonii</i>	pea	4.86	57.84	142.53	1.97	2.76	3.18
<i>Plantago lanceolata</i>	rice	0.50	112.71	39.86	1.41	4.81	5.84
<i>Plantago lanceolata</i>	parsley	2.22	73.44	112.44	1.45	5.17	3.73
<i>Poa trivialis</i>	pea	4.86	82.92	204.13	1.97	4.37	3.57
<i>Poa trivialis</i>	pea	4.86	82.49	198.88	2.02	4.84	3.74
<i>Poa trivialis</i>	pea	4.86	87.99	212.11	2.02	4.97	4.60
<i>Poa trivialis</i>	pea	4.86	118.46	283.72	2.03	3.47	2.81
<i>Ranunculus acris</i>	parsley	2.22	213.90	97.20	4.89	4.01	3.84
<i>Ranunculus acris</i>	parsley	2.22	186.99	81.93	5.07	3.57	4.63
<i>Ranunculus repens</i>	pea	4.86	251.80	111.63	10.96	6.81	7.18
<i>Ranunculus repens</i>	pea	4.86	545.29	237.58	11.15	4.54	4.19
<i>Rubus</i> sp.	parsley	2.22	14.93	38.12	0.87	19.00	6.72
<i>Rumex acetosella</i>	parsley	2.22	67.70	141.90	1.06	7.03	4.50
<i>Rumex acetosella</i>	parsley	2.22	90.73	186.81	1.08	7.97	7.49
<i>Stellaria grmainea</i>	pea	4.86	53.99	244.42	1.07	3.87	3.44
<i>Stellaria grmainea</i>	rice	0.50	125.98	65.74	0.96	4.91	4.75
<i>Stellaria grmainea</i>	rice	0.50	117.22	58.72	1.00	4.30	5.58
<i>Stellaria grmainea</i>	rice	0.50	105.17	52.09	1.01	3.80	4.57

Table SI.1 (B) continued

Taxon	Standard	Standard 1C-value	Target peak	Standard peak	Target 1C-value	Target CoV	Standard Cov
<i>Trifolium repens</i>	parsley	2.22	71.51	143.44	1.11	6.51	6.53
<i>Trifolium repens</i>	parsley	2.22	75.88	148.80	1.13	6.30	5.68
<i>Veronica chamaedrys</i>	pea	4.86	88.21	199.93	2.14	4.65	3.30
<i>Veronica chamaedrys</i>	pea	4.86	112.32	250.77	2.18	5.39	4.29
<i>Vicia sativa</i> subsp. <i>nigra</i>	pea	4.86	86.23	191.09	2.19	7.20	6.15
<i>Vicia sativa</i> subsp. <i>nigra</i>	pea	4.86	90.78	198.60	2.22	6.21	5.44
<i>Viola riviniana</i>	parsley	2.22	92.46	150.05	1.37	5.96	3.31
<i>Viola riviniana</i>	pea	4.86	60.17	185.61	1.58	7.90	4.84

Table SI.2 Angiosperm Phylogeny Group IV family [4], genome size (1C-value), C-S-R type and competitive (C)-strategy for each species in the dataset (n=56). In bold are the 12 species with $\geq 1\%$ mean biomass on at least two herbivore exclusion treatment plots, and which comprise the data analysed using PGLMMs. Where applicable, the column “Dif.” shows the difference between the C-value that we used to analyse our data, and the C-value that we obtained with flow cytometry. When empty, this indicates we estimated the taxon’s C-value by flow cytometry following field sampling at Nash’s field, Silwood Park. The remaining 1C-values were obtained from the Plant DNA C-values database [3] (The original reference for the GS data if taken from the C-values database are given in the column labelled ‘Ref.’). They were taken from the database when our coefficient of variations were $>5\%$, or when we were unable to estimate a C-value with flow cytometry (difference = NA).

Taxon	Family (n=25)	C-S-R type	C-strategy	1C-value (pg)	Dif. (pg)	Ref.*
<i>Achillea millefolium</i>	Aster.	CSR	0.333	7.98	-	-
<i>Agrostis capillaris</i>	Poa.	CSR	0.333	3.60	-	-
<i>Anthoxanthum odoratum</i>	Poa.	SR/CSR	0.117	7.28	-	-
<i>Aphanes microcarpa</i>	Rosa.	SR	0	0.58	NA	1
<i>Arrhenatherum elatius</i>	Poa.	C/CSR	0.667	8.58	-	-
<i>Carex hirta</i>	Cyper.	C/CSR	0.667	0.53	NA	2
<i>Carex muricata</i>	Cyper.	S/CSR	0.167	0.38	-	-
<i>Centaurea nigra</i>	Aster.	CSR	0.333	1.80	0.33	3
<i>Cerastium fontanum</i>	Caryophy.	R/CSR	0.167	3.24	-	-
<i>Chenopodium album</i>	Amaranth.	CR	0.5	1.63	0.32	4
<i>Cirsium arvense</i>	Aster.	C	1	1.42	0.06	5
<i>Crepis capillaris</i>	Aster.	R/SR	0	2.10	0.35	6
<i>Dactylis glomerata</i>	Poa.	C/CSR	0.667	4.40	0.04	7, 8
<i>Epilobium ciliatum</i>	Onagr.	R/CSR	0.167	0.53	NA	9
<i>Festuca rubra</i>	Poa.	CSR	0.333	7.31	-	-
<i>Galium aparine</i>	Rubia.	CR	0.5	1.03	0.08	10
<i>Galium saxatile</i>	Rubia.	S/CSR	0.167	1.45	0.27	10
<i>Galium verum</i>	Rubia.	SC/CSR	0.417	1.89	0.36	11
<i>Heracleum sphondylium</i>	Api.	C/CSR	0.667	2.19	0.27	12
<i>Hieracium pilosella</i>	Aster.	S/CSR	0.167	3.45	0.07	13
<i>Holcus lanatus</i>	Poa.	CSR	0.333	1.70	-	-
<i>Holcus mollis</i>	Poa.	C/CSR	0.667	4.03	-	-
<i>Hypochaeris radicata</i>	Aster.	CSR	0.333	1.34	NA	14
<i>Jacobaea vulgaris</i>	Aster.	R/CR	0.417	2.25	0.05	10
<i>Juncus effusus</i>	Junca.	C/SC	0.75	0.3	-0.02	15
<i>Lotus corniculatus</i>	Faba.	S/CSR	0.167	1.3	-	-
<i>Luzula campestris</i>	Cyper.	S/CSR	0.167	0.49	-0.1	16
<i>Malva moschata</i>	Malva.	C/CSR	0.667	1.10	NA	28, 29
<i>Medicago lupulina</i>	Faba.	R/CSR	0.167	0.65	-0.1	11
<i>Phleum pratense</i> subsp. <i>bertolonii</i>	Poa.	CSR	0.167	1.88	-	-
<i>Plantago lanceolata</i>	Planta.	CSR	0.333	1.43	-	-
<i>Poa annua</i>	Poa.	R	0	2.88	NA	-

Table SI.2 continued

Taxon	Family (n=25)	C-S-R type	C-strategy	1C-value (pg)	Dif. (pg)	Ref.
<i>Poa pratensis</i>	Poa.	CSR	0.333	4.24	NA	17
<i>Poa trivialis</i>	Poa.	R/CSR	0.167	2.01	-	-
<i>Potentilla erecta</i>	Rosa.	S/CSR	0.167	0.45	NA	18
<i>Quercus cerris</i>	Faga.	SC	0.5	0.95	NA	19
<i>Quercus robur</i>	Faga.	SC	0.5	0.93	NA	20
<i>Ranunculus acris</i>	Ranun.	CSR	0.333	4.98	-	-
<i>Ranunculus bulbosus</i>	Ranun.	SR	0	5.63	NA	21
<i>Ranunculus repens</i>	Ranun.	CR	0.5	11.2	-0.14	21
<i>Rubus</i> sp.	Rosa.	SC	0.5	0.7	0.17	12, 30
<i>Rumex acetosa</i>	Polygon.	CSR	0.333	1.65	NA	22
<i>Rumex acetosella</i>	Polygon.	SR/CSR	0.117	1.68	-0.61	23
<i>Sambucus nigra</i>	Adoxa.	C	1	15.25	NA	24
<i>Scorzoneroideis autumnalis</i>	Aster.	R/CSR	0.167	1.16	NA	12
<i>Stellaria graminea</i>	Caryophy.	CSR	0.333	1.01	-	-
<i>Stellaria media</i>	Caryophy.	R	0	1.05	NA	1
<i>Taraxacum officinale</i>	Aster.	R/CSR	0.167	1.28	NA	23
<i>Trifolium dubium</i>	Faba.	R/SR	0	0.73	NA	25
<i>Trifolium pratense</i>	Faba.	CSR	0.333	0.43	NA	25
<i>Trifolium repens</i>	Faba.	CR/CSR	0.417	1.12	-	25
<i>Trisetum flavescens</i>	Poa.	CSR	0.333	2.55	NA	10
<i>Veronica arvensis</i>	Planta.	SR	0	0.33	NA	26
<i>Veronica chamaedrys</i>	Planta.	CSR	0.333	2.16	-	-
<i>Vicia sativa</i> subsp. <i>nigra</i>	Faba.	R/CSR	0.25	2.25	-0.04	27
<i>Viola riviniana</i>	Viola.	S/CSR	0.167	1.35	0.12	3

Notes:

Dactylis glomerata: two references listed in the Plant DNA C-values database, both with the same C-value of 1C = 4.4 pg.

Malva moschata: mean of *M. parviflora* (28) and *M. sylvestris* (29).

Rubus sp.: mean of *R. chamaemorus* (30), *R. idaeus* (12), and of own measurement.

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Table SI.3 Conditional independence claims tested in the context of path analyses. Each number refers to a hypothetical directed acyclic path diagram (Fig. SI.3).

The *d-sep* path analysis method tests conditional independence between parameters in a path diagram. For example, the conditional independence between community-weighted mean genome size and community-weighted mean C-strategy, given the experimental treatment (i.e. herbivory and nutrient input), can be drawn as genome size $\leftarrow$ treatment $\rightarrow$ competition, and written as: (genome size, competition) | {treatment}[3]. Independence between these two community properties is tested while holding experimental treatment constant i.e.: community-weighted mean C-strategy is a function of herbivory, nutrient treatment, and community-weighted mean genome size (competition $\sim$ treatment + genome size). If the p-value for the coefficient of community-weighted mean genome size is below the alpha level ($p \leq 0.05$), this indicates that genome size and C-strategy are not independent of each other for a given experimental treatment.

Each conditional independence claim (set of parameters *not* connected by a path) in a path model is tested in this way to calculate its p-value. A variable may function as a dependent variable (e.g. C-strategy as a function of genome size and the experimental treatments), or as predictor (e.g. C-strategy as a predictor of total biomass). Fisher's C-statistic [5] is calculated from the p-values of the conditional independencies and the Chi-square distributed parameter k , which is equal to the number of conditional independencies in the model. The hypothetical path model is rejected when the C-statistic is below the alpha p-value, meaning that useful information is contained in one or more of the missing paths. Another goodness-of-fit statistic is the C-statistic Information Criterion (CICc) [6, 7] which takes into account sample size and the number of parameters in the model.

The experimental treatments were fitted as N x P x herbivore exclusion + K + herbicide (where each is a binary factor, except for herbicide, which is a three-level factor). In terms of the coefficients and p-values returned for each community property, this is equivalent to scoring the experiment as a single factor variable with eight levels in the rabbit exclusion experiment and 16 levels in the $\pm$ insects $\pm$ molluscs experiment, with additional information on their interactions, while controlling for K and herbicide treatments. We thus have a total of five parameters: the experiment, community-weighted mean genome size, community-weighted mean C-strategy, total biomass, and phylogenetic diversity.

Shown below are the p-values obtained for each conditional independence claim, which were tested with generalised least squares (GLS) with ten different variance structures (varID): 1) plot; 2) N; 3) P; 4) herbivore treatment (HT); 5) N + herbivore treatment; 6) N + P; 7) plot * N; 8) herbivore treatment * N; 9) plot * herbivore treatment * N; 10) herbivore treatment * P * N; and, 11) no variance structure. If the varID column = na, no variance structures were applied. This was assessed by whether it contributed to 1) a lower AICc, and 2) whether the difference in AICc was significant ($p \leq 0.05$) with an ANOVA test. GS= community-weighted mean

genome size of each plot, PD= phylogenetic diversity, BM= total plot biomass, C = mean weighted competitive (C)- strategy of each plot also estimated by PGLS; exp = experimental treatment, i.e.: herbivore * N * P + K. HT = herbivore treatment.

Table SI.3 (A) ± Rabbits:

± Rabbits						
No.	Conditional independence claim	Claim test	p-value: LME	p-value: LME + varID	varID	ANOVA
1	(GS, PD) exp, C	PD ~ exp + C + GS	0.3594	na	na	na
	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
	(BM, PD) exp, C	PD ~ exp + C + BM	0.5556	na	na	na
2	(GS, PD) exp, C	PD ~ exp + C + GS	0.3594	na	na	na
	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.5664	na	na	na
3	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.5664	na	na	na
4	(GS, PD) exp, BM	PD ~ exp + BM + GS	0.1101	na	na	na
	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
	(C, PD) exp, GS, BM	PD ~ exp + GS + BM + C	0.3084	na	na	na
5	(GS, PD) exp, C, BM	PD ~ exp + C + BM + GS	0.3799	na	na	na
	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
6	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.5664	na	na	na
7	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001

Table SI.3 (A) continued $\pm$ Rabbits

8	(GS, PD) exp, C	PD ~ exp + C + GS	0.3594	na	na	na
	(GS, C) exp	C ~ exp + GS	<0.0001	0.0043	plot*HT*N	<0.0001
	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
9	(BM, PD) exp, C	PD ~ exp + C + BM	0.5556	na	na	na
	(C, PD) exp, GS	PD ~ exp + GS + C	0.1547	na	na	na
	(C, BM) exp, GS	BM ~ exp + GS + C	0.0055	0.0088	N+P	<0.0001
10	(GS, PD) exp	PD ~ exp + GS	0.0485	na	na	na
	(BM, PD) exp, C	PD ~ exp + C + BM	0.5556	na	na	na
	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
	(C, PD) exp, GS	PD ~ exp + GS + C	0.1547	na	na	na
11	(BM, PD) exp, C	PD ~ exp + C + BM	0.5556	na	na	na
	(exp, GS) PD, C, BM	GS ~ PD + C + BM + exp	<0.0001	<0.0001	plot*HT*N	<0.0001
12	(C, PD) exp, GS	PD ~ exp + GS + C	0.1547	na	na	na
	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.5664	na	na	na
13	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.5664	na	na	na
	(GS, BM) exp, C	BM ~ exp + C + GS	0.5934	0.7363	N+P	<0.0001
	(C, PD) exp, GS	PD ~ exp + GS + C	0.1547	na	na	na
14	(GS, PD) exp	PD ~ exp + GS	0.0485	na	na	na
	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.5664	na	na	na
	(C, PD) exp, GS	PD ~ exp + GS + C	0.1547	na	na	na

Table SI.3 (B) Conditional independence claim tests on plots with $\pm$ insects $\pm$ molluscs. See Fig. SI.3 for path diagrams being tested below.

$\pm$ insects $\pm$ molluscs						
No.	Conditional independence claim	Claim test	p-value: LME	p-value: LME + varID	varID	ANOVA
1	(GS, PD) exp, C	PD $\sim$ exp + C + GS	0.1395	0.0648	HT	0.0163
	(GS, BM) exp, C	BM $\sim$ exp + C + GS	0.0625	0.5167	N*P	<0.0001
	(BM, PD) exp, C	PD $\sim$ exp + C + BM	0.2439	0.2556	HT	0.0322
2	(GS, PD) exp, C	PD $\sim$ exp + C + GS	0.1395	0.0648	HT	0.0163
	(BM, PD) exp, GS, C	PD $\sim$ exp + GS + C + BM	0.1625	0.1778	HT	0.0163
3	(GS, BM) exp, C	BM $\sim$ exp + C + GS	0.0625	0.5167	N*P	<0.0001
	(BM, PD) exp, GS, C	PD $\sim$ exp + GS + C + BM	0.1625	0.1778	HT	0.0163
4	(GS, PD) exp, BM	PD $\sim$ exp + BM + GS	0.0587	0.1018	HT	0.0161
	(GS, BM) exp, C	BM $\sim$ exp + C + GS	0.0625	0.5167	N*P	<0.0001
	(C, PD) exp, GS, BM	PD $\sim$ exp + GS + BM + C	0.7011	0.7335	HT	0.0163
5	(GS, PD) exp, C, BM	PD $\sim$ exp + C + BM + GS	0.1025	0.0473	HT	0.0163
	(GS, BM) exp, C	BM $\sim$ exp + C + GS	0.0625	0.5167	N*P	<0.0001
6	(BM, PD) exp, GS, C	PD $\sim$ exp + GS + C + BM	0.1625	0.1778	HT	0.0163
7	(GS, BM) exp, C	BM $\sim$ exp + C + GS	0.0625	0.5167	N*P	<0.0001

Table SI.3 (B) continued $\pm$ insects $\pm$ molluscs

8	(GS, PD) exp, C	PD ~ exp + C + GS	0.1395	0.0648	HT	0.0163
	(GS, C) exp	C ~ exp + GS	<0.0001	0	plot*N*P	<0.0001
	(GS, BM) exp, C	BM ~ exp + C + GS	0.0625	0.5167	N*P	<0.0001
9	(BM, PD) exp, C	PD ~ exp + C + BM	0.2439	0.2556	HT	0.0322
	(C, PD) exp, GS	PD ~ exp + GS + C	0.3676	0.8739	HT	0.0163
	(C, BM) exp, GS	BM ~ exp + GS + C	<0.0001	0	N*P	<0.0001
10	(GS, PD) exp	PD ~ exp + GS	0.0593	0.0449	HT	0.0116
	(BM, PD) exp, C	PD ~ exp + C + BM	0.2439	0.2556	HT	0.0322
	(GS, BM) exp, C	BM ~ exp + C + GS	0.0625	0.5167	N*P	<0.0001
	(C, PD) exp, GS	PD ~ exp + GS + C	0.3676	0.8739	HT	0.0163
11	(BM, PD) exp, C	PD ~ exp + C + BM	0.2439	0.2556	HT	0.0322
	(exp, GS) PD, C, BM	GS ~ PD + C + BM + exp	<0.0001	<0.0001	plot+N	0.0006
12	(C, PD) exp, GS	PD ~ exp + GS + C	0.3676	0.8739	HT	0.0163
	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.1625	0.1778	HT	0.0163
13	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.1625	0.1778	HT	0.0163
	(GS, BM) exp, C	BM ~ exp + C + GS	0.0625	0.5167	N*P	<0.0001
	(C, PD) exp, GS	PD ~ exp + GS + C	0.3676	0.8739	HT	0.0163
14	(GS, PD) exp	PD ~ exp + GS	0.0593	0.0449	HT	0.0116
	(BM, PD) exp, GS, C	PD ~ exp + GS + C + BM	0.1625	0.1778	HT	0.0163
	(C, PD) exp, GS	PD ~ exp + GS + C	0.3676	0.8739	HT	0.0163

Table SI.4 Summary path model goodness-of-fit statistics: Fisher's C-statistic and CICc (C-statistic information criterion) and p-values. P-values above the alpha value (0.05) indicate the conditional independencies are satisfied and the model is a plausible model. The column "V, A" shows the number of vertices and number of arrows for each acyclic path diagram.

± Rabbits					± insect ± molluscs				
No.	V, A	C	p-value	CIC	No.	V, A	C	p-value	CIC
1	5, 7	4.266	0.641	30.648	1	5, 7	12.306	0.055	37.47
2	5, 8	3.184	0.528	31.984	2	5, 8	7.573	0.109	34.937
3	5, 8	2.181	0.703	30.981	3	5, 8	9.178	0.057	36.542
4	5, 7	7.808	0.931	34.19	4	5, 7	11.926	0.064	37.09
5	5, 8	2.979	0.561	31.779	5	5, 8	10.101	0.039	37.464
6	5, 9	1.137	0.566	32.393	6	5, 9	3.634	0.163	33.213
7	5, 9	1.044	0.593	32.3	7	5, 9	5.545	0.163	35.123
8	5, 7	21.511	0.001	47.893	8	5, 7	32.51	<0.0001	57.674
9	5, 7	15.328	0.018	41.71	9	5, 7	27.85	<0.0001	53.014
10	5, 6	12.005	0.151	36.005	10	5, 6	16.019	0.042	39
11	5, 8	19.596	0.001	48.396	11	5, 8	21.243	<0.0001	48.606
12	5, 8	4.869	0.301	32.232	12	5, 8	5.636	0.228	32.999
13	5, 7	5.913	0.433	32.295	13	5, 7	11.18	0.083	36.344
14	5, 7	10.923	0.091	36.087	14	5, 7	11.286	0.08	36.45

Table SI.5 (A) Logistic PGLMM: MCMCglmm output where absence/presence (0/1) of the abundant species (n=12) were fitted as a function of genome size (GS), herbivore and nutrient treatment. Insect, rabbit and mollusc exclusion, N, P, and K are scored as $\pm$ binary factors. Baseline levels are the untreated plots (i.e. without fencing, without insecticide, without molluscicide and without fertilizer). Random effects (G-structure) account for experimental design, repeated measurements, and phylogenetic correlation. The posterior mean shows the log odds; and means (categorical variables) and slopes (continuous variables) were estimated as the sum of the posterior means for all parameters involved: e.g.: the slope of $-\text{rabbits} : \text{GS} = [\text{GS} + (-\text{rabbits}:\text{GS})]$. These values were transformed with inverse logit [4] to obtain the probability. “:” in the fixed effects denotes an interaction.

G-structure:	Posterior mean	95% Credible intervals	Eff. sample size			
plot	0.614	3.11E-04, 2.10	4940			
plot : fencing	0.327	2.77E-04, 1.06	4940			
species	5.291	3.57E-04, 13.38	4940			
phylogeny	5.781	2.02E-04, 25.07	4940			

Fixed effects:	Posterior mean	95% Credible intervals	Eff. sample size	pMCMC	Mean or slope	Probability
Intercept	-0.659	-4, 2.99	4940	0.6332	-0.659	0.341
GS	-0.028	-0.84, 0.72	4940	0.9490	-0.028	0.493
– insects	2.127	0.24, 4.27	4940	0.0425	1.469	0.813
N	-0.401	-1.04, 0.25	4572	0.2304	-1.060	0.257
– molluscs	0.782	-1.2, 2.7	4550	0.3818	0.123	0.531
– rabbits	-1.207	-2.61, 0.06	4940	0.0664	-1.866	0.134
P	0.061	-0.34, 0.48	4940	0.7696	-0.598	0.355
K	-0.241	-0.52, 0.04	4940	0.0850	-0.900	0.289
– insects : GS	-0.032	-0.2, 0.14	5153	0.6988	-0.060	0.485
GS : N	0.140	-0.12, 0.41	5288	0.2988	0.113	0.528
– insects : N	-0.431	-1, 0.19	4940	0.1672	0.636	0.654
– molluscs : GS	-0.266	-0.44, -0.11	4940	0.0020	-0.294	0.427
– molluscs : N	0.357	-0.2, 0.96	4913	0.2308	0.079	0.520
– rabbits : GS	0.322	0.15, 0.49	4940	< 0.0002	0.294	0.573
– rabbits : N	-0.269	-0.8, 0.36	4940	0.3563	-2.537	0.073
GS : P	0.096	-0.08, 0.26	4940	0.2502	0.068	0.517
N : P	-0.247	-0.84, 0.29	4940	0.3968	-1.246	0.223
– insects – molluscs	-1.149	-3.96, 1.52	4687	0.3458	1.102	0.751
– molluscs – rabbits	0.920	-1.21, 2.61	4940	0.2413	-0.164	0.459
– insects – rabbits	-0.784	-2.88, 0.97	4940	0.3057	-0.523	0.372
– insects : N : GS	0.124	-0.11, 0.36	4940	0.3008	0.205	0.551
– molluscs : N : GS	-0.018	-0.26, 0.2	4940	0.8656	-0.172	0.457
– rabbits : GS : N	0.054	-0.18, 0.28	4940	0.6526	0.488	0.620
GS : N : P	-0.121	-0.35, 0.12	4940	0.3219	0.088	0.522
–insects –molluscs –rabbits	0.375	-2.15, 3.17	4940	0.7194	0.405	0.600

Table SI.5 (B) Linear PGLMM: MCMCglmm output in which species biomass > 0 was fitted with a Gaussian distribution. Biomass was log-transformed. G-structure shows the variance of the random effects. R-structure = residual variance. GS = genome size. The effects of each category were estimated as the combined effect of all posterior means (coefficients) involved; e.g. change in slope for GS:N:P = GS:N + GS:P + GS:N:P. These effect values were then exponentiated to estimate percent change, where change in percent = $100(\exp(\text{effect}) - 1)$.

G-structure:	Posterior mean	95% Credible intervals	Eff. sample size			
plot	0.041	1.49E-04, 0.17	4940			
plot : fencing	0.145	1.85E-04, 0.42	4940			
species	0.391	1.79E-04, 1.75	4940			
phylogeny	1.826	3.73E-04, 4.56	4598			
R-structure:	Posterior mean	95% Credible intervals	Eff. sample size			
units	3.797	3.46, 4.14	5284			
Fixed effects:	Posterior mean	95% Credible intervals	Eff. sample size	pMCMC	Effect	exp(Effect)
Intercept	-0.955	-2.8, 0.71	4940	0.2397	-0.955	0.3850
GS	0.482	0.17, 0.86	4940	0.0057	0.482	1.6187
– insects	0.240	-0.74, 1.3	4940	0.6061	0.240	1.2716
N	0.845	0.21, 1.53	4940	0.0105	0.845	2.3291
– molluscs	0.667	-0.31, 1.73	4423	0.1575	0.667	1.9479
– rabbits	-0.740	-1.7, 0.31	5049	0.1458	-0.740	0.4772
P	0.217	-0.19, 0.6	4940	0.2858	0.217	1.2428
K	-0.172	-0.42, 0.07	4940	0.1891	-0.172	0.8423
– insects : GS	-0.108	-0.26, 0.04	4940	0.1640	-0.108	0.8976
GS : N	-0.268	-0.5, -0.03	4940	0.0243	-0.268	0.7653
– insects : N	0.085	-0.53, 0.62	4940	0.7806	1.171	3.2245
– molluscs : GS	-0.150	-0.31, -0.01	4940	0.0466	-0.150	0.8604
– molluscs : N	-0.459	-1.04, 0.11	4940	0.1178	1.053	2.8660
– rabbits : GS	0.191	0.05, 0.33	4940	0.0117	0.191	1.2099
– rabbits : N	-0.108	-0.68, 0.46	4940	0.7130	-0.002	0.9977
GS : P	-0.053	-0.2, 0.09	4940	0.4830	-0.053	0.9484
N : P	0.238	-0.35, 0.81	5100	0.4198	1.301	3.6735
– insects – molluscs	-0.190	-1.54, 1.11	4940	0.7696	0.717	2.0489
– molluscs – rabbits	0.206	-1.13, 1.53	4940	0.7235	0.133	1.1417
– insects – rabbits	-0.035	-1.43, 1.25	4940	0.9696	-0.535	0.5859
– insects : N : GS	0.012	-0.18, 0.23	4940	0.9154	-0.364	0.6952
– molluscs : N : GS	-0.124	-0.32, 0.09	4940	0.2296	-0.542	0.5815
– rabbits : GS : N	0.156	-0.05, 0.36	4940	0.1304	0.079	1.0827
GS : N : P	-0.183	-0.4, 0.01	4940	0.0781	-0.503	0.6045
– insects – molluscs – rabbits	0.238	-1.57, 2.1	5148	0.7814	0.386	1.4711

Table SI.6 Step-wise model reduction with AIC and p-values of each assessed parameter in testing community-weighted mean genome size. This table shows interactions and variables that have been removed because they do not have a significant influence on the dependent variable. The beginning, most complex model included all four-way interactions between herbivore exclusion treatments and the fertilizers N and P.

Parameter	change in AIC	p-value
K	2	0.8217
Mg	2	0.8801
slope	2.1	0.3934
herbicide	1.1	0.2313
– rabbits – molluscs – insects : N	2	0.9931
– rabbits – molluscs – insects : P	1.9	0.7825
– rabbits – molluscs: N : P	1.3	0.3900
– rabbits – insects : N : P	1.6	0.5406
– molluscs – insects : N : P	1.8	0.6457
– rabbits – molluscs – insects	1.4	0.4503
– rabbits – insects : N	0.9	0.2899
– rabbits – molluscs: P	2	0.9833
– rabbits – insects : P	2	0.9911
– molluscs – insects : P	0.6	0.2342
– rabbits : N : P	1.1	0.3468
– molluscs : N : P	0.1	0.1699
– insects : N : P	1.1	0.3400
– rabbits – insects	2	0.8222
– rabbits : P	-0.5	0.1124
– molluscs : P	-0.7	0.0992
– insects : P	1.9	0.7700
N : P	1.4	0.4489

Table SI.7 Effects of experimental treatment (herbivore exclusion and N and P input) on community-weighted mean genome size (CWM GS). CWM GS (1C-value) on plots with all herbivores and no nutrient input (control plots) = 5.76 pg. The model shows a significant decrease in CWM GS with N fertilizer and rabbit and mollusc exclusion (= +N plots with insect grazing only) to 4.22 pg; and with N fertilizer and mollusc and insect exclusion (= +N plots with rabbit grazing only) to 3.03 pg. CI= 95% confidence intervals. CWM GS estimated using PGLS.

	LME					ANOVA		
	Coef.	CI	Std. error	t-value	p-value	CWM GS (pg)	F value	Pr(>F)
Intercept	5.759	5.02, 6.50	0.453	12.721	< 0.00001	5.76	na	na
– rabbits	1.106	0.26, 1.95	0.485	2.280	0.0538	6.86	27.265	0.0019
– molluscs	-1.013	-2.05, 0.02	0.636	-1.593	0.1465	4.75	6.971	0.0566
– insects	-0.285	-1.15, 0.58	0.534	-0.533	0.6174	5.47	0.474	0.5283
+ N	-1.868	-2.42, -1.32	0.281	-6.636	< 0.00001	3.89	184.67	< 0.00001
+ P	-0.312	-0.54, -0.08	0.117	-2.669	0.0078	5.45	7.125	0.0078
– rabbits – molluscs	0.679	-0.52, 1.88	0.690	0.985	0.3544	6.53	0.017	0.9007
– rabbits : N	1.097	0.46, 1.73	0.325	3.374	0.0008	6.09	4.588	0.0327
– molluscs: N	-0.355	-1.14, 0.43	0.401	-0.885	0.3765	2.52	0.989	0.3206
– molluscs – insects	-0.330	-1.55, 0.90	0.760	-0.434	0.6826	4.13	0.286	0.6207
– insects : N	-0.315	-0.95, 0.32	0.325	-0.969	0.3329	3.29	2.927	0.0877
– rab – mol: N	-1.190	-2.10, -0.28	0.468	-2.540	0.0114	4.22	6.453	0.0114
– mol – ins : N	1.433	0.52, 2.35	0.469	3.054	0.0024	3.03	9.327	0.0024

Table SI.8 Means and standard deviations of community-weighted mean genome size (CWM GS) (1C-value, pg), total biomass, number of species and phylogenetic diversity of plots, shown for each of eight herbivore treatments and $\pm$ nitrogen (N) treatment (n = the number of plots included in the analysis of each treatment, out of a total of 556 plots). Control = no treatment (i.e. all herbivores present and no fertilizer input).

Herbivore treatment	N	CWM GS (pg)	Total biomass (g)	Number of species	Phylogenetic diversity	n
Control (all herbivores)	–	5.59 $\pm$ 1.43	33.14 $\pm$ 15.17	9 $\pm$ 2	57.03 $\pm$ 12.56	36
– insects	–	5.33 $\pm$ 1.68	59.79 $\pm$ 23.72	8 $\pm$ 3	50.42 $\pm$ 14.12	36
– molluscs	–	4.77 $\pm$ 1.53	29.79 $\pm$ 10.34	9 $\pm$ 3	54.03 $\pm$ 16.64	36
– rabbits	–	6.72 $\pm$ 1.34	43.29 $\pm$ 11.23	7 $\pm$ 2	41.36 $\pm$ 13.05	36
– molluscs – rabbits	–	6.19 $\pm$ 1.42	65.79 $\pm$ 15.97	8 $\pm$ 3	49.5 $\pm$ 15.23	36
– insects – molluscs	–	3.78 $\pm$ 1.33	48.72 $\pm$ 18.59	11 $\pm$ 2	65.37 $\pm$ 11	30
– insects – rabbits	–	6.42 $\pm$ 1.2	52.93 $\pm$ 17.3	6 $\pm$ 2	37.86 $\pm$ 9.75	36
No herbivores	–	5.92 $\pm$ 1.26	57.58 $\pm$ 15.11	9 $\pm$ 2	55.76 $\pm$ 12.86	33
All herbivores present	+	3.6 $\pm$ 1.96	46.4 $\pm$ 24.39	8 $\pm$ 3	50.97 $\pm$ 15.13	36
– insects	+	3.27 $\pm$ 1.7	78.23 $\pm$ 31.46	7 $\pm$ 3	43.61 $\pm$ 14.87	36
– molluscs	+	2.44 $\pm$ 1.09	43.61 $\pm$ 16.7	8 $\pm$ 3	48.72 $\pm$ 14.54	36
– rabbits	+	6.07 $\pm$ 2.33	76.92 $\pm$ 21.44	5 $\pm$ 2	28.42 $\pm$ 11.19	36
– molluscs – rabbits	+	3.98 $\pm$ 1.46	83.85 $\pm$ 23.41	6 $\pm$ 2	36.25 $\pm$ 13.73	36
– insects – molluscs	+	2.82 $\pm$ 1.27	74.63 $\pm$ 31.13	8 $\pm$ 2	54.07 $\pm$ 12.08	29
– insects – rabbits	+	5.21 $\pm$ 1.81	90.3 $\pm$ 30.56	5 $\pm$ 1	27.36 $\pm$ 8.96	36
no herbivores	+	4.62 $\pm$ 1.28	100.83 $\pm$ 26.24	6 $\pm$ 2	33.47 $\pm$ 10.54	32

Table SI.9 Most reduced linear mixed effect model output showing the effects of experimental treatments on three alternative estimations of community-weighted mean genome size (CWM GS). Prior to model reduction, CWM GS was estimated for each plot: **A)** CWM GS was estimated without accounting for phylogenetic non-independence (i.e. it is simply weighted by species biomass). Similar to the community-weighted means estimated in the main text, GS was log10-transformed prior to the estimation, and back-transformed for ease of interpretation and comparison; **B)** CWM GS estimated with PGLS as described in the text, however GS was *not* log-transformed; **C)** CWM GS was log10-transformed and estimated with PGLS, however the lambda parameter was allowed to be estimated (rather than fixed at 1 which assumes a Brownian motion of evolution). The last column contains the estimated CWM GS (1C-value in pg) of plots under each of the treatments on left. This table shows that LME output is very similar between different estimations, the key results remaining unchanged. See also Fig. SI.4.

A)	CWM GS, without phylogeny					
	Coef.	CI	Std. error	t-value	p-value	Mean GS (pg)
Intercept	5.669	5.02, 6.31	0.387	14.644	< 0.0001	5.67
– rabbits	0.962	0.21, 1.71	0.447	2.154	0.0650	6.63
– molluscs	-0.751	-1.65, 0.15	0.541	-1.388	0.1987	4.92
– insects	-1.530	-1.94, -1.12	0.213	-7.196	< 0.0001	4.14
+ N	-0.287	-1.02, 0.45	0.443	-0.648	0.5477	5.38
+ P	-0.197	-0.44, 0.05	0.126	-1.568	0.1175	5.47
– rabbits – molluscs	0.442	-0.60, 1.48	0.622	0.711	0.4997	6.32
– rabbits : N	1.050	0.57, 1.53	0.246	4.277	< 0.0001	7.39
– molluscs: N	-0.470	-1.06, 0.12	0.303	-1.554	0.1208	4.16
– molluscs – insects	-0.429	-1.47, 0.62	0.629	-0.683	0.5266	2.96
– insects : N	-0.365	-0.84, 0.11	0.246	-1.487	0.1376	3.49
– rabbits : P	-0.390	-0.73, -0.05	0.177	-2.208	0.0277	6.04
– rab – mol : N	-1.021	-1.71, -0.33	0.354	-2.885	0.0041	5.59
– mol – ins : N	1.188	0.50, 1.88	0.355	3.352	0.0009	3.02

B)	CWM GS estimated with PGLS, GS untransformed					
	Coef.	CI	Std. error	t-value	p-value	Mean GS (pg)
Intercept	6.419	5.73, 7.11	0.410	15.676	< 0.0001	6.42
– rabbits	0.810	0.03, 1.59	0.469	1.728	0.1087	7.23
– molluscs	-0.996	-1.96, -0.03	0.575	-1.732	0.1078	5.42
– insects	-0.307	-2.55, -1.53	0.469	-0.654	0.5248	6.11
+ N	-2.040	-1.09, 0.48	0.263	-7.76	< 0.0001	4.38
+ P	-0.352	-0.56, -0.14	0.109	-3.217	0.0014	6.07
– rabbits – molluscs	0.643	-0.48, 1.76	0.667	0.964	0.3530	6.88
– rabbits : N	1.297	0.70, 1.89	0.304	4.272	< 0.0001	6.49
– molluscs: N	-0.517	-1.25, 0.21	0.374	-1.381	0.1680	2.87
– molluscs – insects	-0.250	-1.37, 0.87	0.667	-0.375	0.7136	4.87
– insects : N	-0.284	-0.88, 0.31	0.304	-0.935	0.3503	3.79
– rab – mol : N	-0.980	-1.83, -0.13	0.438	-2.241	0.0255	4.64
– mol – ins : N	1.309	0.46, 2.16	0.438	2.988	0.0029	3.33

Table SI.9 continued

c)	CWM GS estimated with PGLS, lambda parameter optimised					
	Coef.	CI	Std. error	t-value	p-value	Mean GS (pg)
Intercept	5.598	4.86, 6.33	0.445	12.569	< 0.0001	5.60
– rabbits	0.890	0.04, 1.74	0.493	1.806	0.1081	6.49
– molluscs	-0.981	-1.99, 0.03	0.615	-1.593	0.1462	4.62
– insects	-0.405	-1.24, 0.43	0.511	-0.793	0.4658	5.19
+ N	-1.300	-1.85, -0.75	0.282	-4.613	< 0.0001	4.30
+ P	0.041	-0.32, 0.40	0.186	0.222	0.8246	5.64
– rabbits – molluscs	0.806	-0.36, 1.97	0.682	1.182	0.2737	6.31
– rabbits : N	1.086	0.51, 1.66	0.298	3.650	0.0003	6.27
– molluscs: N	-0.252	-0.97, 0.47	0.370	-0.680	0.4965	3.07
– molluscs – insects	-0.223	-1.40, 0.96	0.725	-0.308	0.7713	3.99
– insects : N	-0.193	-0.77, 0.39	0.298	-0.649	0.5168	3.70
– rabbits : P	-0.497	-0.92, -0.08	0.215	-2.315	0.0210	6.03
+ N + P	-0.507	-0.92, -0.09	0.215	-2.355	0.0189	3.83
– rab – molluscs: N	-1.484	-2.32, -0.65	0.430	-3.450	0.0006	4.36
– mol – insects: N	1.065	0.23, 1.91	0.431	2.470	0.0139	5.18

Table SI.10 Linear model output for each for the community properties in the path analysis model in Fig. 2 ($\pm$ rabbits). CW = community-weighted.

Community-weighted mean genome size (1C-value, pg)					
	Estimate	Std. Error	95% CI	t value	Pr(> t)
Intercept	5.124	1.020	3.24, 7.06	5.021	0.0188
– rabbits	1.339	1.277	-1.08, 3.76	1.049	0.4664
N	-1.694	0.404	-2.47, -0.92	-4.195	0.0001
P	-0.100	0.412	-0.9, 0.7	-0.243	0.8088
K	-0.137	0.247	-0.61, 0.34	-0.552	0.5820
– grass (herbicide)	0.741	0.511	-0.24, 1.72	1.45	0.1973
– forbs (herbicide)	1.025	0.511	0.04, 2.01	2.007	0.0916
– rabbits : N	1.344	0.466	0.44, 2.24	2.881	0.0047
– rabbits : P	-0.433	0.466	-1.33, 0.47	-0.928	0.3550
N : P	-0.594	0.466	-1.49, 0.31	-1.274	0.2049

Community-weighted mean C-strategy					
	Estimate	Std. Error	95% CI	t value	Pr(> t)
Intercept	0.365	0.069	0.21, 0.52	5.311	0.0693
– rabbits	0.042	0.032	-0.02, 0.1	1.308	0.2034
N	0.089	0.028	0.04, 0.15	3.22	0.0016
P	0.011	0.027	-0.04, 0.06	0.43	0.6681
K	0.030	0.016	0, 0.06	1.84	0.0681
– grass (herbicide)	-0.063	0.028	-0.11, -0.01	-2.207	0.0648
– forbs (herbicide)	-0.002	0.029	-0.05, 0.05	-0.057	0.9560
CW mean genome size	0.025	0.005	0.02, 0.04	4.674	< 0.0001
– rabbits : N	-0.023	0.031	-0.09, 0.03	-0.743	0.4590
– rabbits : P	0.001	0.030	-0.06, 0.06	0.025	0.9799
N : P	0.009	0.030	-0.05, 0.07	0.286	0.7756

Total biomass (g/m²)					
	Estimate	Std. Error	95% CI	t value	Pr(> t)
Intercept	14.037	10.186	-5.47, 34.86	1.378	0.2688
– rabbits	10.212	8.795	-9.14, 29.35	1.161	0.4068
N	8.978	4.172	0.98, 16.92	2.152	0.0332
P	5.427	4.219	-2.63, 13.48	1.287	0.2005
K	3.614	2.551	-1.28, 8.47	1.417	0.1589
– grass (herbicide)	3.522	2.972	-2.23, 9.34	1.185	0.2381
– forbs (herbicide)	0.293	2.937	-5.45, 6	0.1	0.9207
CW mean C-strategy	37.640	12.292	14.06, 62.69	3.062	0.0027
– rabbits : N	19.974	4.773	10.85, 29.08	4.185	0.0001
– rabbits : P	-5.440	4.773	-14.55, 3.68	-1.14	0.2565
N : P	5.272	4.772	-3.83, 14.39	1.105	0.2713

Table SI.10 continued

Phylogenetic diversity

	Estimate	Std. Error	95% CI	t value	Pr(> t)
Intercept	65.081	4.336	56.05, 72	15.009	< 0.0001
– rabbits	-15.477	3.656	-22.16, -9.54	-4.233	0.0003
N	-3.143	3.240	-9.63, 2.88	-0.97	0.3339
P	-0.101	3.284	-6.5, 6.21	-0.031	0.9756
K	-2.653	1.981	-6.61, 1.05	-1.339	0.1830
– grass (herbicide)	7.998	3.042	3.77, 12.66	2.629	0.0398
– forbs (herbicide)	-5.469	3.027	-10, -1.18	-1.807	0.1223
CW mean C-strategy	-21.259	8.239	-30.36, -2.28	-2.58	0.0139
– rabbits : N	-6.666	3.715	-13.9, 0.47	-1.794	0.0752
– rabbits : P	2.620	3.715	-4.52, 9.85	0.705	0.4821
N : P	-3.964	3.714	-11.12, 3.25	-1.067	0.2879

Table SI.11 Linear mixed effect model output for each of the community properties in the path analysis in Fig. 3 ($\pm$ insects $\pm$ molluscs). CW= community-weighted, CI = confidence intervals.

Community-weighted mean genome size (1C-value, pg)					
	Estimate	Std. Error	95% CI	t-value	p-value
Intercept	6.943	0.777	5.70, 8.18	8.934	0.0001
– insects	-0.771	1.075	-2.48, 0.94	-0.718	0.5035
– molluscs	-0.938	1.075	-2.65, 0.77	-0.873	0.4208
N	-0.483	0.446	-1.34, 0.37	-1.084	0.2796
P	-0.697	0.449	-1.56, 0.16	-1.55	0.1223
K	-0.043	0.169	-0.37, 0.28	-0.253	0.8004
– grass (herbicide)	0.158	0.264	-0.36, 0.67	0.6	0.5583
– forbs (herbicide)	0.274	0.268	-0.24, 0.80	1.021	0.3244
– insects – molluscs	1.073	1.528	-1.37, 3.50	0.702	0.5117
– insects : N	-0.014	0.630	-1.22, 1.19	-0.023	0.9819
– molluscs : N	-1.448	0.630	-2.66, -0.24	-2.298	0.0224
– insects : P	0.938	0.630	-0.27, 2.15	1.489	0.1379
– molluscs : P	0.824	0.630	-0.38, 2.03	1.308	0.1922
N : P	-0.329	0.630	-1.54, 0.88	-0.523	0.6018
– insects – molluscs : N	0.155	0.907	-1.58, 1.90	0.171	0.8646
– insects – molluscs : P	-1.957	0.905	-3.69, -0.22	-2.162	0.0316
– insects : N : P	-1.096	0.891	-2.8, 0.61	-1.229	0.2202
– molluscs : N : P	-0.224	0.891	-1.93, 1.48	-0.252	0.8016
– insects – molluscs : N : P	2.571	1.284	0.10, 5.02	2.002	0.0464

Community-weighted mean C-strategy					
	Estimate	Std. Error	95% CI	t-value	p-value
Intercept	0.406	0.057	0.31, 0.50	7.106	0.0006
– insects	-0.041	0.079	-0.17, 0.08	-0.524	0.6223
– molluscs	-0.031	0.079	-0.16, 0.09	-0.395	0.7089
N	0.088	0.031	0.03, 0.15	2.827	0.0051
P	0.040	0.032	-0.02, 0.10	1.252	0.2118
K	0.014	0.012	-0.01, 0.04	1.207	0.2287
CW mean genome size	0.025	0.004	0.02, 0.03	5.77	0.0000
– grass (herbicide)	-0.088	0.017	-0.12, -0.05	-5.082	0.0002
– forbs (herbicide)	0.000	0.018	-0.04, 0.03	-0.022	0.9829
– insects – molluscs	0.048	0.112	-0.13, 0.23	0.427	0.6862
– insects : N	-0.041	0.044	-0.12, 0.04	-0.92	0.3583
– molluscs : N	-0.009	0.045	-0.09, 0.08	-0.213	0.8318
– insects : P	-0.043	0.044	-0.13, 0.04	-0.975	0.3306
– molluscs : P	-0.049	0.044	-0.13, 0.04	-1.1	0.2724
N : P	-0.036	0.044	-0.12, 0.05	-0.814	0.4165
– insects – molluscs : N	0.125	0.063	0, 0.25	1.966	0.0504
– insects – molluscs : P	0.105	0.064	-0.02, 0.23	1.647	0.1008
– insects : N : P	0.187	0.063	0.07, 0.31	2.987	0.0031
– molluscs : N : P	0.171	0.062	0.05, 0.29	2.745	0.0065
– insects – molluscs : N : P	-0.283	0.090	-0.46, -0.11	-3.129	0.0020

Table SI.11 continued ± insects ± molluscs

Total biomass (g/m²)					
	Estimate	Std. Error	95% CI	t-value	p-value
Intercept	14.923	6.949	2.46, 28.01	2.147	0.0339
– insects	9.157	6.737	-3.23, 21.48	1.359	0.1769
– molluscs	26.591	6.744	14.2, 38.93	3.943	0.0001
N	25.264	6.270	13.38, 37.33	4.029	0.0001
P	-2.659	6.265	-14.59, 9.35	-0.424	0.6717
K	3.595	2.348	-0.87, 8.09	1.531	0.1270
CW mean C-strategy	65.655	11.309	43.63, 85.97	5.806	0.0000
CW mean genome size	-1.570	0.866	-3.17, 0.08	-1.814	0.0709
– grass (herbicide)	4.147	3.638	-2.26, 10.49	1.14	0.2678
– forbs (herbicide)	0.023	3.560	-6.20, 6.24	0.006	0.9950
– insects – molluscs	-23.151	9.747	-41.01, -5.25	-2.375	0.0192
– insects : N	1.492	8.741	-15.25, 18.15	0.171	0.8646
– molluscs : N	-23.804	8.804	-40.62, -7.00	-2.704	0.0073
– insects : P	9.271	8.778	-7.54, 25.99	1.056	0.2919
– molluscs : P	-0.815	8.774	-17.63, 15.9	-0.093	0.9261
N : P	7.572	8.741	-9.16, 24.24	0.866	0.3872
– insects – molluscs : N	24.815	12.639	0.82, 49.08	1.963	0.0507
– insects – molluscs : P	-2.824	12.695	-26.92, 21.53	-0.222	0.8241
– insects : N : P	-2.374	12.567	-26.18, 21.82	-0.189	0.8503
– molluscs : N : P	6.648	12.499	-17.05, 30.69	0.532	0.5953
– insects – molluscs : N : P	-2.636	18.211	-37.68, 31.78	-0.145	0.8850
Phylogenetic diversity					
	Estimate	Std. Error	95% CI	t-value	p-value
Intercept	45.363	4.942	37.37, 53.36	9.179	0.0000
– insects	-5.111	6.654	-15.79, 5.57	-0.768	0.4711
– molluscs	7.722	6.654	-2.96, 18.40	1.16	0.2893
N	-12.111	3.353	-18.54, -5.68	-3.612	0.0004
P	1.584	3.380	-4.90, 8.06	0.469	0.6397
K	-3.585	1.272	-6.02, -1.15	-2.818	0.0052
– grass (herbicide)	-0.740	2.503	-5.61, 4.13	-0.295	0.7721
– forbs (herbicide)	-8.265	2.535	-13.18, -3.33	-3.261	0.0056
– insects – molluscs	8.768	9.490	-6.53, 23.99	0.924	0.3896
– insects : N	3.389	4.742	-5.70, 12.48	0.715	0.4755
– molluscs : N	3.167	4.742	-5.92, 12.26	0.668	0.5049
– insects : P	3.222	4.742	-5.87, 12.31	0.68	0.4975
– molluscs : P	0.833	4.742	-8.26, 9.92	0.176	0.8606
N : P	-1.667	4.742	-10.76, 7.42	-0.351	0.7255
– insects – molluscs : N	-10.602	6.827	-23.65, 2.52	-1.553	0.1217
– insects – molluscs : P	1.010	6.817	-12.00, 14.13	0.148	0.8823
– insects : N : P	-1.889	6.706	-14.74, 10.97	-0.282	0.7784
– molluscs : N : P	-6.944	6.706	-19.80, 5.91	-1.036	0.3014
– insects – molluscs : N : P	-1.797	9.674	-20.43, 16.65	-0.186	0.8528

Table SI.12 Change in species mean percent of above-ground biomass, measured as dry weight, per herbivore exclusion treatment, relative to the control plots (plots without herbivore exclusion i.e. plots with rabbits, molluscs, and insects), and by N treatment. Mean percentages were rounded, thus plants with very low biomass may equal to 0.

	– rab	– rab	– rab	– rab	– mol	– mol	– ins	– ins	– ins	– ins	– all	– all	– ins	– ins
	no N	+ N	no N	+ N	no N	+ N	no N	+ N	no N	+ N	no N	+ N	no N	+ N
<i>Achillea millefolium</i>	0.4	0	-0.3	-0.2	0.1	-0.2	-0.6	-0.6	-0.6	-0.5	1.9	3.9	-0.6	-0.5
<i>Agrostis capillaris</i>	-7.1	-10.6	-8.5	-12.1	0.9	-1.7	-8.1	-11.8	-8.7	-10.6	-5	-11.9	-6.5	-10.3
<i>Anthoxanthum odoratum</i>	-0.4	-0.8	-0.7	-0.8	0.4	-0.3	-0.6	-0.7	-0.7	-0.8	-0.2	-0.8	-0.8	-0.7
<i>Aphanes microcarpa</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Arrhenatherum elatius</i>	17.9	26.6	-3.3	-5.9	-3.3	-8.1	-0.5	0.6	6.3	2.1	0.7	-3.7	-1.6	-3
<i>Carex hirta</i>	0	0	0	0	0	0	0	0	0.3	0	0	0	0	0
<i>Carex muricata</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Centaurea nigra</i>	0.3	0	0	0	0	1.1	0	0	0	0	0	0	0	0
<i>Cerastium fontanum</i>	0	-0.2	0	-0.2	0	-0.1	0	-0.2	0	-0.2	0	-0.2	0	-0.2
<i>Chenopodium album</i>	-0.3	0	-0.3	0.1	-0.3	0	-0.3	0	-0.3	0	-0.3	0	-0.3	0
<i>Cirsium arvense</i>	-1.1	-4.3	-0.2	-3.5	-1	-2.2	-1.1	-4	3.7	2.6	-0.8	-4	2.8	-0.6
<i>Crepis capillaris</i>	0	-0.1	1.3	-0.1	0.2	0	0.2	-0.1	0	0	0.2	-0.1	0	-0.1
<i>Dactylis glomerata</i>	0.3	0.3	7	7.4	0	0	3	2.7	2.8	0.8	2.3	1.8	0.1	0
<i>Epilobium ciliatum</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Festuca rubra</i>	-5.4	5.2	8.4	2.5	-6	-13.2	7.6	15	-4.5	-8.3	-7.6	-7.6	-24.3	-21.1
<i>Galium aparine</i>	0	0	0	0	0	0	0	0	0.2	0.1	0	0	0	0
<i>Galium saxatile</i>	0	0	0	0	0	0	0.7	2.3	0	0	0	0	0	0
<i>Galium verum</i>	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
<i>Heracleum sphondylium</i>	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
<i>Hieracium pilosella</i>	0	0	-0.1	0	-0.1	0	-0.1	0	-0.1	0	-0.1	0	-0.1	0
<i>Holcus lanatus</i>	-3.8	-13	-3.8	-4.1	6	18.2	-1.9	-15.3	1	3.3	1.1	-11.5	7.1	7.3
<i>Holcus mollis</i>	1.1	1.8	1.9	17.6	1.5	6.4	3	14.4	-0.5	7.4	6.7	34.5	8.1	15.9

Table SI.12 continued

	– rab no N	– rab + N	– rab – mol no N	– rab – mol + N	– mol no N	– mol + N	– ins – rab no N	– ins – rab + N	– ins no N	– ins + N	– all no N	– all + N	– ins – mol no N	– ins – mol + N
<i>Hypochaeris radicata</i>	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0
<i>Jacobaea vulgaris</i>	-1.3	-0.6	-1.3	-0.6	-1	-0.5	-1.3	-0.6	1.5	4	-1.3	-0.6	12.1	13
<i>Juncus effusus</i>	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0
<i>Lotus corniculatus</i>	0.5	0	-0.1	0	-0.1	0	-0.1	0	-0.1	0	0.1	0	0.4	0
<i>Luzula campestris</i>	-0.7	-0.1	-1.3	-0.1	-0.5	-0.1	-1.3	-0.1	-1.3	-0.1	-1.3	-0.1	-1	-0.1
<i>Malva moschata</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Medicago lupulina</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Phleum pratense</i> subsp. <i>bertolonii</i>	0	0	0.1	1.7	3.1	1.3	0	0.5	0.1	0.3	1.2	1.7	0.7	0
<i>Plantago lanceolata</i>	-0.4	-0.2	0.3	-0.1	-0.4	-0.2	0.2	-0.2	-0.4	-0.2	-0.1	-0.2	-0.3	-0.2
<i>Poa annua</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Poa pratensis</i>	0.7	0.1	-0.1	1.4	-0.1	0.4	0	2.1	0	0.9	0.8	1.7	0.6	0.3
<i>Poa trivialis</i>	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0
<i>Potentilla erecta</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Quercus cerris</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Quercus robur</i>	0.3	0	0.1	0	0	0	0	0	0	0	0	0	0	0
<i>Ranunculus acris</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Ranunculus bulbosus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Ranunculus repens</i>	-0.3	-0.1	-0.2	0	-0.2	0	-0.3	-0.1	-0.1	0.1	-0.3	-0.1	0.2	0.8
<i>Rubus fruticosus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Rumex acetosa</i>	-0.1	-0.3	-0.1	-0.2	0.5	1.1	0	-0.1	0.9	1.3	0.2	-0.3	0.5	0.2
<i>Rumex acetosella</i>	-0.2	-2.2	-0.2	-2.2	-0.2	-1.1	-0.2	-2.2	-0.2	-2	-0.2	-2.2	0.5	-1.5
<i>Sambucus nigra</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Scorzoneroide autumnalis</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Stellaria graminea</i>	0.1	-0.2	0	0.1	0.4	0.2	-0.1	-0.3	0	-0.1	0.1	-0.2	0.2	1.1

Table SI.12 continued

	– rab	– rab	– rab – mol	– rab – mol	– mol	– mol	– ins – rab	– ins – rab	– ins	– ins	– all	– all	– ins – mol	– ins – mol
	no N	+ N	no N	+ N	no N	+ N	no N	+ N	no N	+ N	no N	+ N	no N	+ N
<i>Stellaria media</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Taraxacum officinale</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Trifolium dubium</i>	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0
<i>Trifolium pratense</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Trifolium repens</i>	0	0	0	0	0.3	0	0	0	0	0	0.4	0	0.1	0
<i>Trisetum flavescens</i>	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0
<i>Veronica arvensis</i>	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0
<i>Veronica chamaedrys</i>	-0.9	-1.2	0.3	-1.1	-0.6	-0.9	-0.8	-1.2	0.6	0	-0.3	-0.8	2	-0.1
<i>Vicia sativa</i> subsp. <i>nigra</i>	0.3	0.1	1.1	0	0.1	0	2.6	0	0	0	1.7	0	0.2	0
<i>Viola riviniana</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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