Supplement: Context-dependent effects of shifting large herbivore assemblages on plant structure and diversity

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Appendix S1 – Description of Site Selection and Exclosure Design

Site selection:

While we considered a number of locations in which to conduct this study, several conditions made Tejon a suitable case study both logistically and for producing generalizable results pertinent beyond the study site: (1) the Tejon Ranch Conservancy is supportive of this research and had a 10-year renewal permitting process, whereas public lands (e.g. Forest Service) had a 3year permit cycle; the longer permit duration period was a better match for the infrastructure cost and long intended duration of the experiment; (2) plants (Serra-Diaz et al 2016), large mammals (Ratcliff et al 2018, Teton et al 2016), and climatic conditions (Davis and Sweet 2012, Dingman et al 2013; McCullough et al 2016) at the site are the subjects of prior studies and well documented; (3) the baseline ecology of this ecosystem is representative of oak-dominated systems throughout the region- including the majority of California's rangelands; (4) the wild mammalian herbivores are numerous and as diverse as anywhere in the state and representative of species widespread throughout western North America; (5) the plant community is composed of native and exotic species common throughout California and the western U.S., and (6) it's location along the southern edge of the San Joaquin Valley makes it particularly exposed to climate change, as it's near the southern range extent for many plant species, allowing access to a strong gradient in climate over short distances (8 km) and relevance to regional conservation planning.

In the summer of 2015, we spent three months scouting potential sites prior to determining the final experimental location. Our study area had to be 1) within to the pre-existing downscaled climate grid (McCullough et al 2016), 2) of similar general vegetation: oak-dominated with a consistent understory of herbaceous vegetation, 3) of similar geologic parent material 4) accessible by 4wd vehicle (in order for movement and construction of fencing to be feasible), 5) on slopes <15%. Using mapping provided by the Tejon Ranch Conservancy and the Davis Lab UCSB, we identified a set of candidate sites that met these initial criteria. We then determined whether we could fit a full block (3 1ha plots) within each of those candidate sites; in many instances (~75% of sites that appeared suitable from satellite imagery and map layers) existing fencing, old roads, significant erosion, water troughs or salt blocks, ranching and hunting infrastructure, or other pre-existing disturbances made candidate sites non-viable after ground-truthing.

The remaining set of candidate sites were presented to the Ranch Company in January 2016. Final site selection was made by the Tejon Ranch Company (the landowner) to ensure that the experiment had no negative impact to Tejon's ranching or hunting activities, as well as to ensure that sites would be accessible by multiple entrance routes in case one road because washed out or otherwise unpassable, or in case of emergency (e.g. wildfire). This experiment was therefore located on a remote part of the ranch that receives very little visitation, thus minimizing the likelihood that human presence impacts wildlife or cattle movement. Ranchers were present at the sites only when actively moving cattle herds. Additionally, all experimental plots were situated within the boundaries of a single ranching lessee to avoid site differences due to different cattle management. Herd stocking density was approximately 0.13 cattle/ha (personal communication with Tejon Ranch Company, April 2016).

Due to these logistical considerations, the final arrangement of blocks was concentrated onto three aridity "levels", yielding three replicate blocks per level (rather than 9 blocks spread along a gradient). These final levels were selected 1) to have a climatic difference of ~2C mean temperature and 200-300 mm annual (water year) CWD between each level (but minimal differences within a level), 2) to have similar slopes, aspect, and parent soil material within each level, 3) to allow three blocks within level, and three plots within each block, and 4) in close spatial proximity to reduce unintended sources of environmental variation. Within a level, blocks were 120 to 350 m apart.

Exclosure fencing construction:

Fence construction began in September 2016 and was completed in November 2016. All twentyseven plots were within 0.4 km of dirt access roads. Repairs following heavy rains and snow December 2016- February 2017 were made in March and April 2017, and repairs were made as needed throughout the experiment. Fences were regularly patrolled monthly (spring, summer, fall) to bimonthly (winter) to find and repair any breaks in the fence, with damage typically due to fallen trees, branches, or soil erosion during winter storms. Any large herbivores (or their signs) seen in the plots during these patrols were recorded as incidental observations and were removed through the access gate if inside an exclosure meant to keep them out.

In each plot enclosed by these barriers, there was a metal, hinged gate to allow entry to researchers. Total exclosure treatments were fully fenced using 2m high barbed wire fencing (wires 220 mm apart; the lowermost wire is smooth, to facilitate passage by small and mediumbodied wildlife (such as squirrels, rabbit), as well as carnivores (bobcat, coyote, mountain lion); partial exclosures use semi-permeable barriers made of 1.07 m high barbed wire spaced 300 mm apart and connected to short metal T-posts (this construction is the same as all fences across the ranch used to limit cattle movement while enabling passage by wild ungulates that can readily jump over or crawl under the barriers). Open plots are fully permeable and completely unfenced, with 1 m high t-posts demarcating plot boundaries. While it would be ideal to have a fully factorial design, a treatment that excluded wild ungulates but was open to cattle was not feasible given free-roaming cattle in this system and the additional burden on ranchers to actively move cattle in and out of plots was not practical here. The central 0.25 ha of each plot was used for short-visit, descriptive data collection (e.g. composition surveys); more manipulative activities (biomass clipping, soil sampling) were restricted to the plot edges. The 1ha plot size allowed us to minimize edge effects and granted more confidence in the observed patterns.

To ensure plot locations accurately captured measured and modeled CWD, blocks were cosituated with weather stations used by McCullough et al (2016). CWD, calculated as potential evapotranspiration minus actual evapotranspiration, can be thought of as a surrogate for plant water demand in a Mediterranean climate: changes in CWD effectively quantify the supplemental amount of water needed to maintain current water balance given projected increases in air temperature and evaporative demand, and CWD is a good predictor of plant distributions (Anderegg et al., 2015; Lutz, Wagtendonk, & Franklin, 2010; Stephenson, 1990). While MAP (mean annual precipitation) is a commonly used proxy for productivity in many systems, other factors such as solar radiation, slope and aspect may be equally if not more important in driving plant production, especially in California's topographically heterogeneous landscapes (Bartolome et al., 2007), with significant impacts on plant community diversity and composition (Olff & Ritchie, 1998; Osem et al., 2002). CWD helps account for this by spanning climate-mediated variation in soil fertility, soil water holding capacity, and slope and aspect variation (Figure 2) over a relatively small (8.5 km) spatial scale.

These sites also roughly represent present, future, and far-future climate scenarios. Estimates of future scenarios are based on projections (McCullough et al., 2016) which predict upslope migration of drought-tolerant oak species, particularly *Q. douglasii*, and declines in *Q. kelloggii* in response to net increases in aridity. These predictions are consistent with both recent historical trends and dynamic vegetation models, indicating that more mesic areas are likely to transition toward communities currently present downslope (Kelly & Goulden, 2008; Lenihan, Bacheler, Neilson, & Drapek, 2008; McIntyre et al., 2015). While rarely, if ever, is there enough information to predict with certainty how species assemblages will shift with climate change, our experimental sites represent one plausible data-driven scenario of future trajectories in this system, and are therefore useful both for understanding present heterogeneity as well as predicting future change.

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S1-Figure 1. Exclosures were situated adjacent to a pre-existing weather stations and landscape climate loggers to capitalize on climate data presented in McCullough et al (2016). Top: schematic of Mesic Block 1 in relation to existing weather station. Bottom: Photo of weather station adjacent to Arid blocks; infrastructure has little to no effect on wildlife behavior. Photo credit: Ian McCullough.

Appendix S2 – Establishing a Relationship Between Aridity and Productivity

To determine whether our three aridity levels also correspond to different levels of primary productivity—thus enabling us to consider our work in the context of prior research on herbivore effects on richness-productivity relationships—we established that aridity and productivity covary in our system. We used three proxies for primary productivity (Fig 2). First, we extracted the Normalized Difference Vegetation Index (NDVI) for each climate level using the USGS Modis satellite image database (https://lpdaac.usgs.gov/tools/usgs-earthexplorer/), and recorded the 5-year (2010-2015) maximum NDVI values of each block (taken prior to exclosure installation, n = 9 satellite NDVI value grids per level). Second, we collected aboveground standing biomass from 5 haphazardly selected (subject to their having continuous understory vegetation and no tree basal area) .5m² quadrats per plot in June 2016 prior to exclosure installation. Biomass was clipped at the soil surface, bagged, dried for 48 hr at 38 °C, and weighed (n = 15 quadrats per block, 45 per level). Third, in July 2016, we estimated standing biomass using a modified point-intercept method (Robel et al 1970, Frank and McNaughton 1990): using three 50m transects established in the inner .25ha of each plot, we recorded total hits along a 5-point pin frame (n = 300 pin drops per plot).

For each metric, we investigated whether the three levels differed significantly using ANOVA for NDVI and Kruskal-Wallis tests for pin hits and biomass in R. Mean max NDVI was significantly different among the three levels ($F_{2,24} = 630.5$, P = <.001), with lowest values at Arid and highest at Mesic. Pin hit data were significantly different between Arid and the other two levels, but not between Intermediate and Mesic ($\chi^2 = 0.92114$, df = 2, P < .001). Aboveground biomass was significant different across all levels ($\chi^2 = 86.161$, df = 2, P < .001), again, with greatest aboveground standing biomass at Mesic and least at Arid.

Overall, all three measures showed the same trend, with productivity proxies mostly increasing from Arid to Mesic, supporting variation in productivity across our three sites paralleling changes in CWD. We therefore consider the three categorical climate levels (Arid, Intermediate, Mesic) as also representative of distinct primary productivity levels (low, medium, high) and reference literature on both climate and productivity when discussing our experiment and results.

Examining Soil Properties:

To assess whether soil properties differed across experimental units, we collected 15-cm deep soil cores every 10 m along two transects paralleling the periphery of the central .25ha of each plot. Samples from each plot were dried (60 C for 72 hours), homogenized into one sample per transect (n=2 per plot), and sieved through 2-mm mesh, and sent to Brookside Laboratories (New Knoxville, OH) for analysis of pH, organic matter (derived from loss on ignition), NH₄-N, NO₃-N, K, P, Fe, Na, and total exchange capacity (TEC). Gravimetric water content, measured as the difference between the wet weight and dry weight of soils, was collected for a subset of samples (n=18). We investigated whether the three levels differed significantly for each metric using MANOVA.

Total exchange capacity (TEC), gravimetric water content (GWC), organic matter, NH₄-N, NO₃-N, P, and Fe were significantly different among climate levels, with mesic sites generally

exhibiting higher resource availability, a pattern consistent with expectations of climatemediated resource variation (one-way ANOVA, p < 0.001; Table 1 and 2). There was no significant difference in pH, Na, or K.

Level	Organic	Gravimetric	Total	pH	NH ₄	NO ₃	Р	K	Fe	Na
	matter	water	exchange							
		content	capacity							
		(GWC)	(TEC)							
Arid	14.334	0.185	15.202	7.133	12.122	12.200	59.000	445.278	105.167	24.278
Intermediate	6.517	0.25	18.537	7.166	15.74	18.763	102.722	555.111	160.500	24.944
Mesic	11.001	0.456	21.625	7.055	26.872	27.439	156.778	551.778	171.500	24.833

Table S2-1. Mean values of soil properties measured per aridity level.

Soil Property	Aridity Level		
	F value	Pr(> <i>F</i>)	
	(df =2, 51)		
Organic matter	35.02	<.001	
GWC	13.95	<.001	
TEC	21.14	<.001	
pH	.396	.675	
NH4	16.41	<.001	
NO3	10.55	.0001	
Na	.301	0.741	
Р	54.08	<.001	
Κ	1.127	.332	
Fe	57.29	<.001	

Table S2-2. Significant differences in soil properties across the three levels reflect differences we would expect due to climate variation. There were no significant differences in pH, sodium, or potassium.



S2- Figure 1. NMDS ordination of soil samples by aridity level. The distance between points represents Bray-Curtis dissimilarity. Mesic and Intermediate soils appear more homogeneous (clustered most strongly) than Arid soils. Mesic and Intermediate soils also appear more similar to each other than to Arid, likely reflecting the geographic spread of sites (Mesic and Intermediate blocks were geographically closer, approx. 0.6 km apart, than either was to Arid, approx. 8 km).

Variation in Tree Canopy Cover Across Experimental Plots

We estimated tree canopy cover using the program ImageJ (Shneider et al 2012) to calculate canopy area from aerial satellite imagery of each plot (Google Earth) collected between 2007 and 2015.

Climate Level	Block	Treatment	% Canopy Cover
Arid	1	Control	21.115
Arid	1	Partial	24.017
Arid	1	Full	24.431
Arid	2	Control	15.820
Arid	2	Partial	21.006
Arid	2	Full	35.503
Arid	3	Control	52.572
Arid	3	Partial	30.552
Arid	3	Full	22.608
Intermediate	1	Control	18.736
Intermediate	1	Partial	37.699
Intermediate	1	Full	20.418
Intermediate	2	Control	50.641
Intermediate	2	Partial	33.349
Intermediate	2	Full	41.772
Intermediate	3	Control	44.117
Intermediate	3	Partial	44.275
Intermediate	3	Full	34.368
Mesic	1	Control	57.818
Mesic	1	Partial	59.721
Mesic	1	Full	50.778
Mesic	2	Control	53.937
Mesic	2	Partial	35.727
Mesic	2	Full	45.467
Mesic	3	Control	33.047
Mesic	3	Partial	33.467
Mesic	3	Full	33.947

Table S2-3. Estimated percent canopy cover for each experimental block.

1. Schneider, C.A., Rasband, W.S., Eliceiri, K.W. "NIH Image to ImageJ: 25 years of image analysis". Nature Methods 9, 671-675, 2012.

Appendix S3- Monitoring Large Herbivore Activity

An overview of dung patterns is presented in the main text. Here, we describe the dung count analyses and results, as well as differences in activity among individual wildlife species.

Wildlife dung: We used generalized mixed models with a poisson distribution for wildlife dung patterns. Models included treatment (n=3), climate level (n = 3), year (n=2), and their interactions as fixed effects, and block (n=9) and transect (n = 4/plot) as nested random effects (Zuur et al. 2009). We built all models in the lme4 package in R (R version 3.5.0, lme4 v 1.1-17, Bates et al. 2015). We selected the best fitting model by minimizing AICc values (MuMIn package v 1.42.1, (Burnham & Anderson 2002) and generated p-values of the final models using parametric bootstrapping with 10,000 iterations (pbkrtest package v 0.4-7, Halekoh & Hojsgaard 2014). We verified that model assumptions were met using the DHARMa package (version 0.2.0; Hartig 2018). When a fixed effect with more than two levels was statistically significant (P<0.05), we examined pairwise differences using Tukey's Honestly Significant Difference (HSD) post-hoc tests (package emmeans). Significant effects of level in these models reflect variation in activity levels across treatment types.

GLMM results indicate that treatments were effective at excluding target wildlife from total exclosures, but may have either had the unintended effect of reducing activity within partial exclosures as well, or else wildlife preferentially selected sites that had been previously grazed by cattle. There was a significant difference (p <.001) among all three treatment types in wildlife dung abundance. Activity appears bimodal, with highest activity levels at Mesic and Arid, but significantly lower activity at Intermediate (p <.01). Our best fit model for wildlife activity included treatment, climate level, their interaction with year ($R^2m = 0.997$, $R^2c = 0.9998$; AICc = 3222; Δ AICc = 94) and both random effects terms, though upon further investigation, there was not a significant overall difference between herbivore activity in 2017 and 2018 (p = 0.153).

Cattle dung: Because visual inspection of the data showed exclosures clearly functioned as intended for removing cattle from partial and total exclosures (S3-Figure 1b), we investigated effects of level, year, and their interaction on cattle dung abundance for open plots only. Our best fit model for cattle dung included climate level, year, and their interaction ($R^2m = 0.003$, $R^2c = 0.826$; AICc = 2740 ; Δ AICc = 30). Cattle dung was significantly different (p <.001) at Arid relative to Intermediate and Mesic, and dung abundance differed across all sites between 2017 and 2018, suggesting there was a change of some kind in management over that period.



S3-Figure 1. Summary graphs for dung counts (mean and standard deviation) for all wildlife (top) and cattle (bottom). There was a significant difference in dung abundance across treatment types, indicating that treatments operated successfully and kept intended herbivore groups from entering. However, there was a slight decrease in wildlife activity in partial exclosures vs. open plots at Arid (p < 0.05), indicating that fencing may have unintentionally deterred some wildlife.



S3-Figure 2. Activity (dung counts) of wildlife species varied by plot and aridity level. Elk and pig were more active in open than partial exclosures at Arid; pigs were more active in open plots at all sites.

Appendix S4- Plant Species Composition

To understand which species could be driving diversity changes, we examined rank abundance curves (vegan package), and used the package mvabund (Wang et al 2012) to examine differences in species composition, fitting generalized linear models with a negative binomial distribution to each species and then used resampling to test for significant community level and species level responses. This is an alternative approach to perMANOVA that better handles a wider range of multivariate data and is not based on distance matrices, allowing for easier interpretation of results. Because our intention was not to examine changes in community composition across climate levels (as species assemblages differ, with high species turnover across sites), we modeled each of the three sites separately for composition analyses.

We found that plant community composition differed across treatments at Arid (LRT = $230_{2.6}$, p < 0.01), and Mesic (207_{2.6}, p= 0.011), but did not differ significantly across treatments at Intermediate (LRT = $60.34_{2.6}$; p = 0.152). Composition varied significantly by block at two levels (interm: LRT = 80_{2,6}, p = 0.043, mesic: LRT = 116_{2,6}; p = .01), but not at arid (22.78_{2,6}; p = 0.685). At Arid, the community was dominated by *Bromus diandrus* and *Bromus hordeaceus*, two invasive annual grasses; at intermediate, Bromus diandrus and Ericamera nauseosa, a native woody shrub; and at mesic, the two most abundant species were *Ribes roezlii*, a thorny native shrub, and Galium aparine, an annual native forb. At Arid, these shifts were driven by significant changes in abundance of 2 grasses, Bromus diandrus (p=0.017) and Bromus hordeaceus (p=0.049), which increased within total exclosures and partial exclosures, and one forb, Acmispon wrangelianus (p=0.051) which was marginally more abundant in open plots. Several species were detected only inside exclosures-Lupinus nanus, Triteleia laxa-while several others were never or rarely detected within either exclosure type (Leptosiphon spp. Broidea coronata). At Intermediate, though there was not a significant overall treatment effect, we did observe a trend towards increasing B. diandrus cover inside exclosures relative to open plots. At Mesic, there were significant changes in abundance of 4 forbs: Keckiella breviflora (p= 0.003), Galium aparine (p= 0.005), Collinsia parviflora (p= 0.039), increased inside partial and total exclosures, while Ranunculus californicus (p= 0.005) was substantially more abundant in open plots.

1. Wang, Y. I., Naumann, U., Wright, S. T., & Warton, D. I. (2012). mvabund–an R package for model-based analysis of multivariate abundance data. Methods in Ecology and Evolution, 3(3), 471-474.

Appendix S4- Phylogeny construction: We used all species from vegetation surveys to create a phylogenetic tree using the Phylomatic tool, version 3 (http://phylodiversity.net/phylomatic/) (Webb & Donoghue, 2005) and based on the APG III (2009) phylogeny. If species were not available in the tree, we used genus-level classification. We then used Phylocom 4.2 to add branch lengths to the phylogeny (Gastauer & Meira-Neto, 2013).

S4-Table 1: Arid Species List

Family	Genus	Genus_species
Asteraceae	Achillea	Achillea_millefolium
Fabaceae	Acmispon	Acmispon_wrangelianus
Boraginaceae	Amsinckia	Amsinckia_menziesii
Fabaceae	Astragalus	Astragalus_didymocarpus
Poaceae	Avena	Avena_fatua
Poaceae	Avena	Avena_barbata
Brassicaceae	Brassica	Brassica_tournefortii
Themidaceae	Brodiaea	Brodiaea_coronaria
Poaceae	Bromus	Bromus_diandrus
Poaceae	Bromus	Bromus_hordeaceus
Poaceae	Bromus	Bromus_tectorum
Poaceae	Bromus	Bromus_madritensis
Montiaceae	Calandrinia	Calandrinia_menziesii
Brassicaceae	Capsella	Capsella_bursa-pastoris
Orobanchaceae	Castilleja	Castilleja_attenuata
Caryophyllacea	eCerastium	Cerastium_glomeratum
Montiaceae	Claytonia	Claytonia_perfoliata
Apiaceae	Daucus	Daucus_pusillus
Asparagaceae	Dichelostemma	Dichelostemma_capitatum
Brassicaceae	Draba	Draba_cuneifolia
Poaceae	Elymus	Elymus_cinereus
Geraniaceae	Erodium	Erodium_botrys
Geraniaceae	Erodium	Erodium_circutarium
Poaceae	Festuca	Festuca_myuros
Rubiaceae	Galium	Galium_aparine
Geraniaceae	Geranium	Geranium_molle
Polemoniaceae	Gilia	Gilia_tricolor
Poaceae	Hordeum	Hordeum_murinum
Asteraceae	Hypochaeris	Hypochaeris_glabra
Polemoniaceae	Leptosiphon	Leptosiphon_ciliatus
Fabaceae	Lupinus	Lupinus_bicolor
Fabaceae	Lupinus	Lupinus_nanus
Asteraceae	Madia	Madia_elegans
Fabaceae	Medicago	Medicago_polymorpha
Boraginaceae	Phacelia	Phacelia_congdonii
Boraginaceae	Plagiobothrys	Plagiobothrys_nothofulvus
Caryophyllacea	e Stellaria	Stellaria_media
Poaceae	Stipa	Stipa_pulchra
Fabaceae	Trifolium	Trifolium_albopurpureum
Themidaceae	Triteleia	Triteleia_ixioides
Themidacea	Triteleia	Triteleia_laxa

S4-Table 2: Intermediate Species List

Genus Family Fabaceae Acmispon Acmispon Fabaceae Apocynaceae Asclepias Asteraceae Asteraceae Poaceae Bromus Poaceae Bromus Poaceae Bromus Poaceae Bromus Portulacaceae Calandrinia Onagraceae Camissonia Collinsia Plantaginaceae Euphorbiaceae Croton Poaceae Elymus Poaceae Elymus Asteraceae Ericameria Polygonaceae Eriogonum Geraniaceae Erodium Onagraceae Eulobus Poaceae Festuca Onagraceae Gayophytum Gilia Polemoniaceae Polemoniaceae Gilia Polemoniaceae Gilia Poaceae Hordeum Polemoniaceae Leptosiphon Fabaceae Medicago Boraginaceae Nemophila Boraginaceae Plagiobothrys Grossulariaceae Ribes Urticaceae Urtica Violaceae Viola

Genus species Acmispon_argophyllus Acmispon_wrangelianus Asclepias_eriocarpa Eriophyllum Bromus_diandrus Bromus hordeaceus Bromus_madritensis Bromus_tectorum Calandrinia menziesii Camissonia_contorta Collinsia_parviflora Croton setiger Elymus_cinereus Elymus_tricoides Ericameria_nauseosa Erigononum_sp Erodium_cicutarium Eulobus_californicus Festuca_myuros Gayophytum_diffusum Gilia latiflora Gilia_minor Gilia_tricolor Hordeum_murinum Leptosiphon_pygmaeus Medicago_polymorpha Nemophila_menziesii Plagiobothrys_nothofulvus Ribes_roezlii var. roezlii Urtica_dioica Viola_purpurea

S4-Table 3: Mesic Species List

Family	Genus	Species
Grossulariaceae	Ribes	Ribes_roezlii
Fabaceae	Acmispon	Acmispon_argophyllus
Alliaceae	Allium	Allium_campanulatum
Rosaceae	Aphanes	Aphanes_occidentalis
Apocynaceae	Asclepias	Asclepias_eriocarpa
Poaceae	Bromus	Bromus_arenarius
Poaceae	Bromus	Bromus_diandrus
Poaceae	Bromus	Bromus_hordeaceus
Poaceae	Bromus	Bromus_tectorum
Onagraceae	Camissonia	Camissonia_contorta
Onagraceae	Clarkia	Clarkia_unguiculata
Montiaceae	Claytonia	Claytonia_perfoliata
Plantaginaceae	Collinsia	Collinsia_parviflora
Asparagaceae	Dichelostemma	Dichelostemma_capitatum
Brassicaceae	Erysimum	Erysimum_capitatum
Phrymaceae	Erythranthe	Erythranthe_sierrae
Poaceae	Festuca	Festuca_myuros
Rubiaceae	Galium	Galium_aparine
Onagraceae	Gayophytum	Gayophytum_diffusum
Poaceae	Hordeum	Hordeum_murinum
Fabaceae	Hosackia	Hosackia_crassifolia
Plantaginaceae	Keckiella	Keckiella_breviflora
Polemoniaceae	Leptosiphon	Leptosiphon_bicolor
Poaceae	Melica	Melica_imperfecta
Plantaginaceae	Penstemon	Penstemon_centranthifolius
Plantaginaceae	Penstemon	Penstemon_laetus
Boraginaceae	Phacelia	Phacelia_douglasii
Boraginaceae	Pholistoma	Pholistoma_auritum
Boraginaceae	Cryptantha	Cryptantha_affinis
Rosaceae	Potentilla_gracilis	Potentilla_gracilis
Rosaceae	Prunus	Prunus_virginiana
Ranunculaceae	Ranunculus	Ranunculus_californicus
Poaceae	Stipa	Stipa_pulchra
Caprifoliaceae	Symphoricarpos	Symphoricarpos_albus
Themidaceae	Triteleia	Triteleia_ixioides
Themidaceae	Triteleia	Triteleia_laxa

Phylogenetic trees:

arid_tree =

"((((((((achillea_millefolium:15.000000,madia_elegans:17.000000):11.000000,hypochaeris_gla bra:32.000000)asteraceae:6.000000,daucus_pusillus:9.000000):2.000000,((amsinckia_menziesii: 0.666667, phacelia_congdonii: 37.666668, plagiobothrys_nothofulvus: 37.666668) boraginaceae: 0. 333333,castilleja_attenuata:12.000000,galium_aparine:38.000000):2.000000):1.000000,(gilia_tri color:37.000000,leptosiphon_ciliatus:37.000000)polemoniaceae:4.000000)ericales_to_asterales: 2.000000,((calandrinia_menziesii:0.666667,claytonia_perfoliata:32.666668)montiaceae:5.33333 3,(cerastium_glomeratum:0.6666667,stellaria_media:36.666668)caryophyllaceae:1.333333):5.000 000):3.000000,(((acmispon_wrangelianus:7.000000,(astragalus_didymocarpus:7.000000,(medic ago_polymorpha:2.000000,trifolium_albopurpureum:2.000000):5.000000):2.000000):4.000000,(lupinus_bicolor:0.500000,lupinus_nanus:19.500000)lupinus:9.500000):14.000000,((brassica_tou rnefortii:0.666667,capsella bursa pastoris:27.6666666,draba cuneifolia:27.6666666)brassicaceae: 14.333334,((erodium_botrys:0.333333,erodium_circutarium:39.333336)erodium:0.3333333,geran ium_molle:39.666668)geraniaceae:2.333333)malvids:1.000000):3.000000):6.000000,(((((avena_ fatua:0.500000,avena_barbata:25.500000)avena:0.500000,(bromus_diandrus:0.500000,bromus_ hordeaceus:24.500000,bromus tectorum:24.500000,bromus madritensis:24.500000)bromus:1.5 00000):3.000000,stipa_pulchra:5.000000):9.000000,elymus_cinereus:38.000000,festuca_myuros :38.000000, hordeum murinum: 38.000000) poaceae: 8.000000, dichelostemma capitatum: 9.00000 0):6.00000)poales to asterales:6.000000);\n"

interm_tree =

"(((((((acmispon_argophyllus:0.500000,acmispon_wrangelianus:18.500000)acmispon:6.50000 0,medicago_polymorpha:9.000000):15.000000,urtica_dioica:7.000000):1.000000,(croton_setige r:2.000000,viola_purpurea:4.000000)malpighiales:3.000000):2.000000,((camissonia_contorta:0. 666667,eulobus_californicus:37.666668,gayophytum_diffusum:37.666668)onagraceae:3.333333 ,erodium_cicutarium:2.000000):2.000000):2.000000,ribes_roezlii:6.000000):1.000000,((((asclep ias_eriocarpa:38.000000,collinsia_parviflora:7.000000,(nemophila_menziesii:0.666667,plagiobo thrys_nothofulvus:37.666668)boraginaceae:0.333333):2.000000,(ariophyllum:32.000000,ericam eria_nauseosa:32.000000)asteraceae:8.000000):1.000000,((gilia_latiflora:18.500000,gilia_minor :18.500000,gilia_tricolor:18.500000)gilia:18.500000,leptosiphon_pygmaeus:37.000000)polemon iaceae:4.000000)ericales_to_asterales:2.000000,(calandrinia_menziesii:12.000000,erigononum_ sp:4.000000)caryophyllales:1.000000):3.000000):6.000000,((bromus_diandrus:0.500000,bromus_ hordeaceus:24.500000,bromus_madritensis:24.500000,bromus_tectorum:24.500000)polemons:13 .500000,(elymus_cinereus:19.000000,elymus_tricoides:19.000000)elymus:19.000000,festuca_m yuros:38.000000,Hordeum_murinum:38.000000)poaceae:14.000000)poales_to_asterales:6.0000 00);\n"

mesic_tree =

"((((((((asclepias_eriocarpa:37.000000,galium_aparine:37.000000)gentianales:1.000000,(pholist

oma_auritum:0.666667,cryptantha_affinis:37.666668,phacelia_douglasii:37.666668)boraginacea e:0.333333,(erythranthe_sierrae:6.000000,(collinsia_parviflora:0.666667,keckiella_breviflora:31 .666666,(penstemon_centranthifolius:15.833333,penstemon_laetus:15.833333)penstemon:15.83 3333)plantaginaceae:0.333333):6.000000):2.000000,symphoricarpos_albus:7.000000):1.000000, leptosiphon_bicolor:41.000000)ericales_to_asterales:2.000000,claytonia_perfoliata:11.000000): 3.000000,(((erysimum_capitatum:15.000000,(clarkia_unguiculata:0.666667,camissonia_contorta :37.666668,gayophytum_diffusum:37.666668)onagraceae:4.33333)malvids:1.000000,((acmisp on_argophyllus:3.000000,hosackia_crassifolia:4.000000):19.000000,(aphanes_occidentalis:37.0 00000,potentilla_gracilis:37.000000,prunus_virginiana:6.000000)rosaceae:3.000000):3.000000): 2.000000,ribes_roezlii:6.000000):1.000000):4.000000,ranunculus_californicus:6.000000):3.000000): 2.000000,dichelostemma_capitatum:9.000000,((((bromus_arenarius:0.500000,bromus_diandr us:24.500000,bromus_hordeaceus:24.500000,bromus_tectorum:24.500000)bromus:4.500000,sti pa_pulchra:5.000000):2.000000,melica_imperfecta:2.000000):7.000000,festuca_myuros:38.000 000,hordeum_murinum:38.000000)poaceae:8.000000):6.000000)poales_to_asterales:6.000000)e uphyllophyte:1.000000;\r\n"

Appendix S5- Change in Exotic species richness and diversity

To better understand the role of exotic species in observed richness and diversity patterns, we conducted a follow-up analysis for exotic species only. We followed similar linear mixed effect model procedures to those previously described for the response variables exotic species richness and exotic species Shannon diversity. Our best fit model for exotic species richness included climate level, herbivore treatment, and their interaction (exotic richness: $R^2m = 00.5165$, $R^2c = 0.7345$; AICc = 2740 ; Δ AICc = 11.315). Our best fit model for exotic Shannon diversity also included climate level, herbivore treatment, and their interaction (exotic richness: $R^2m = 0.8587$, $R^2c = 0.927$; Δ AICc = -1019.8351).

Table S5-1. ANOVA results of 1) herbivore treatment effect on richness of exotic species and 2) differences in exotic species richness across aridity levels.

D	f	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	2	36	18.236	3.388	0.0342 *
Residuals 96	9	5215	5.382		
Signif. codes:	0 '***	' 0.001 '**' 0.0	01 '*' 0.05 '.' ().1 ' ' 1	
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Aridity Level	2	3378	1689.2	873.9	<0.0001 ***
Residuals	969	1873	1.9		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table S5-2. Results of fixed effects tests from mixed models testing for differences in exotic species richness across treatments and aridity levels. When there were significant main effects, we used Tukey's multiple comparisons to test for differences among treatments within levels, with degrees of freedom calculated following the Kenward-roger method.

Level = Arid:				
contrast	estimate	SE	df	t.ratio p.value
Open - Partial	0.5278	0.184	957	2.871 0.0117 *
Open - Total	1.0370	0.184	957	5.641 <.0001 ***
Partial - Total	0.5093	0.184	957	2.770 0.0158 *
Level = Intermediate :				
contrast	estimate	SE	df	t.ratio p.value
Open - Partial	0.3056	0.184	957	1.662 0.2205
Open - Total	0.1944	0.184	957	1.058 0.5407
Partial - Total	-0.1111	0.184	957	-0.604 0.8178
Level = Mesic:				
contrast	estimate	SE	df	t.ratio p.value
Open - Partial	0.3241	0.184	957	1.763 0.1828
Open - Total	0.0645	0.184	957	0.351 0.9343
Partial - Total -0.259	5 0.184 957 -1	.412 0	.3353	



S5-Figure 1. Summary graphs for exotic species richness (top) and exotic species Shannon diversity (bottom). There were significant treatment differences at Arid, but not Intermediate or Mesic. However, there were treatment effects at all levels for Shannon diversity.

Exotic Species Shannon Diversity:

Table S5-3. ANOVA results of 1) herbivore treatment effect and 2) aridity level on Shannon diversity exotic species.

Effect of Herbivore Treatment

	Df	Sum Sc	Mean S	Sq F value	Pr(>F)
Treatment	2	9.24	4.619	20.07 2.88	8e-09 ***
Residuals	968	3 222.74	0.230		

Effect of Aridity Level (Site)

Df	Sum Sq Mean Sq F value Pr(>F)

Level	2	196.42	98.21	2673 <2e-16 ***
Residuals	968	35.57	0.04	

Table S5-4. Results of fixed effects tests from mixed models testing for differences in exotic species shannon diversity across treatments and aridity levels. When there were significant main effects, we used Tukey's multiple comparisons to test for differences among treatments within levels, with degrees of freedom calculated following the Kenward-roger method.

Level = Arid:

contrast	estimate	SE	df	t.rat	io p.value
Open - Partial	0.3059	0.0186	956 1	6.484	<.0001 ***
Open - Total	0.5193	0.0186	5 956 2'	7.981	<.0001 ***
Partial - Total	0.2133	0.0186	956 1	1.496	<.0001 ***

Level = Intermediate :

contrast	estima	ate SE df t.ratio p.value
Open - Partial	0.0332	0.0186 956 1.783 0.1758
Open - Total	0.0583	0.0186 956 3.140 0.0050 **
Partial - Total	0.0251	0.0186 956 1.349 0.3682

Level = Mesic:

contrast	estimate SE df t.ratio p.value			
Open - Partial	0.0881	0.0186 9	956 4.747	<.0001 ***
Open - Total	0.1347	0.0186 9	956 7.258	<.0001 ***
Partial - Total	0.0466	0.0186 9	956 2.512	0.0326 *

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 3 estimates



Appendix S6- Correlation among diversity metrics

Figure S6- Pearson's correlation among (top left) richness and Shannon diversity; (top right) richness and dominance; (bottom left) richness and MPD. Richness and Shannon diversity were significantly positively correlated; richness and dominance were negatively correlated, but not significantly so; and richness and MPD were positively correlated, but not the relationship was not significant.





Linear models exploring the relationship between dominance and richness across (A) all herbivores [ln(full exclosure/open control)], (B) large herbivores only [ln(partial exclosure/open control)], or (C) small herbivores [ln(full exclosure/open control)] on plant species richness. The shaded area shows the 95% confidence interval of the predicted relationship around the regression line. None of the effect size relationships were significant (p > 0.05).