

## Supporting Information

### Leveraging private lands to meet 2030 biodiversity targets in the United States

All code to run analysis and reproduce main text figures is available at: <https://github.com/milliechapman/easements-biodiversity>

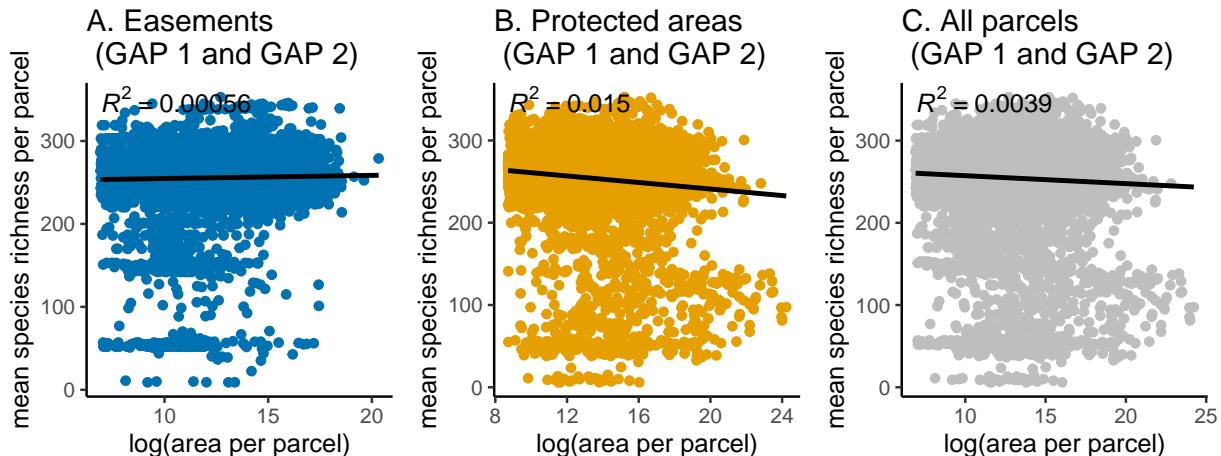
**Table S1:** Total area and number of parcels of conservation easements and fee owned protected areas per GAP status code.

```
kable(t_management)
```

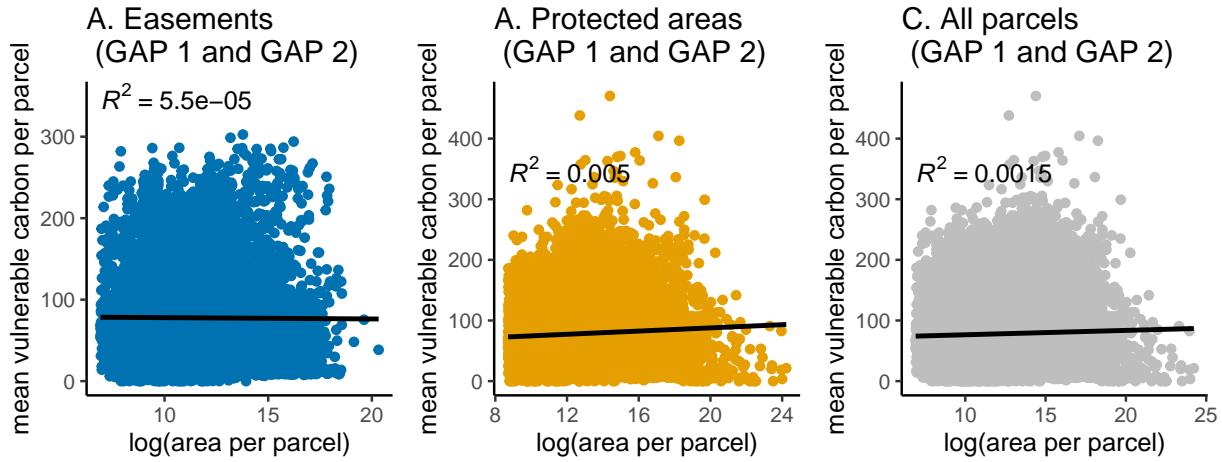
Category	GAP_Stats	area	number
Easement	1	3.049056	4491
Easement	2	15.203632	16382
fee	1	320.525412	1362
fee	2	152.286359	21502

**Figure S1:** There is no significant correlation between parcel area and mean richness value in either (a) conservation easements ( $r^2 < 0.01$ ) or (b) protected areas ( $r^2 < 0.01$ ) (GAP 1 and GAP 2). Similarly, (c) there is no significant trend when considering all of the data ( $r^2 < 0.01$ ).

```
## [1] 6.907755
```



**Figure S2:** There is no significant correlation between parcel area and mean vulnerable carbon in either (a) conservation easements ( $r^2 < 0.01$ ) or (b) protected areas ( $r^2 < 0.01$ ) (GAP 1 and GAP 2). Similarly, (c) there is no significant trend when considering all of the data ( $r^2 < 0.01$ ).



## Statistical significance of differences in mean values

First, we provide a weighted-t test of parcels, where we compare the mean of fee-owned protected area parcels relative to conservation easement parcels (GAP1-2) weighted by the area of the parcel

**Table S2:** Area weighted t-test of species richness per parcel

```
wtt1 <- wtd.t.test(x=fee_summary$`richness_all`,  
                     y=ease_summary$`richness_all`,  
                     weight=fee_summary$area,  
                     weighty=ease_summary$area,  
                     samedata=FALSE)  
wtt1  
  
## $test  
## [1] "Two Sample Weighted T-Test (Welch)"  
##  
## $coefficients  
##   t.value      df    p.value  
## -189.7935 34775.9102    0.0000  
##  
## $additional  
##   Difference     Mean.x     Mean.y    Std. Err  
## -106.5315318 148.7947741 255.3263058 0.5613024
```

**Table S3:** Area weighted t-test of vulnerable per parcel

```
wtt2 <- wtd.t.test(x=fee_summary$`richness_all`,  
                     y=ease_summary$`richness_all`,  
                     weight=fee_summary$area,  
                     weighty=ease_summary$area,  
                     samedata=FALSE)  
wtt2  
  
## $test  
## [1] "Two Sample Weighted T-Test (Welch)"  
##  
## $coefficients  
##   t.value      df    p.value  
## -189.7935 34775.9102    0.0000  
##  
## $additional  
##   Difference     Mean.x     Mean.y    Std. Err  
## -106.5315318 148.7947741 255.3263058 0.5613024
```

## Effect of parcel size on overall patterns

While our paper focuses on richness and carbon values overall, whether or not these patterns hold true on a per parcel basis might be of interest, particularly when trying to account for the potential influence of difference in parcel area on conservation targeting.

We use propensity score matching to estimate the average marginal difference of mean species richness and carbon density between conservation easements and protected areas parcels accounting for the potentially confounding effect of area of parcels.

```

m.out1 <- matchit(type ~ area, data = match_df, method = "nearest", distance = "glm")
m.data1 <- match.data(m.out1)
#plot(m.out1, type = "jitter", interactive = FALSE)

```

**Table S4:** Easements have significantly higher mean richness values on a per parcel basis compared to fee owned protected areas when accounting for the potential confounding effect of parcel size.

```

fit1 <- lm(richness_all ~ type + area, data = m.data1, weights = weights)
kable(coefest(fit1, vcov. = vcovCL, cluster = ~subclass)[1:2,])

```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	255.4734727	0.2652952	962.9782858	0.0000000
type	-0.0656273	0.3763282	-0.1743886	0.8615613

**Table S5:** Easements have significantly higher mean vulnerable carbon density on a per parcel basis compared to fee owned protected areas when accounting for the potential confounding effect of parcel size.

```

fit2 <- lm(carbon_vulnerable ~ type + area, data = m.data1, weights = weights)
kable(coefest(fit2, vcov. = vcovCL, cluster = ~subclass)[1:2,])

```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	77.8753669	0.3179573	244.9239659	0.0000000
type	-0.2826074	0.4817849	-0.5865843	0.5574874