Table S1: Seeds germinated in the greenhouse from the cores we collected.

Plot	p1	p2	p3	p4	p5	p6	p7	p8	p9	p10	p11	p12	p13	p14
Burn Severity (dNBR)	195	307	300	226	266	143	211	191	99	181	238	248	272	304
B. tectorum														
U_T2	162	87	70	437	453	5	15	40	16	35	8	225	129	176
U_B4	73	32	25	49	68	2	6	6	4	6	0	30	19	59
B_T2	48	19	4	29	1	0	1	0	15	5	3	9	11	34
B_B4	10	5	1	4	5	0	1	0	3	0	0	0	6	8
P. secunda														
U_T2	17	3	1	71	6	65	502	212	175	546	143	116	141	66
U_B4	13	0	0	18	2	10	55	24	19	49	29	19	29	51
B_T2	11	0	0	2	1	3	21	0	37	32	5	28	8	63
B_B4	3	0	0	0	0	0	4	1	4	4	2	6	18	35
A. tridentata														
U_T2	1	0	0	0	0	0	1	2	0	0	0	1	7	0
U_B4	0	0	0	0	0	0	0	3	0	0	2	0	6	1
B_T2	1	0	2	0	0	0	1	1	0	0	0	0	9	5
B_B4	0	0	0	0	0	0	0	1	0	0	0	0	1	2
A. desertorum														
U_T2	0	0	0	0	0	0	0	59	1	0	0	5	0	0
U_B4	0	0	0	0	0	0	0	8	0	0	1	1	0	0
B_T2	7	0	0	0	0	1	0	0	0	0	0	1	0	0
B_B4	2	0	0	0	0	3	0	0	0	0	0	0	0	0
C. testiculatum														
U_T2	24	0	0	0	0	0	2	28	30	0	1	2	3	0
U_B4	23	0	0	0	0	0	1	12	0	0	0	0	0	0
B_T2	6	0	0	0	0	0	0	0	0	0	0	0	0	0
B_B4	4	0	0	0	0	0	0	0	1	0	0	0	0	0
C. parviflora														
U_T2	0	0	0	0	0	6	10	0	0	3	0	0	1	0
U_B4	0	0	0	0	0	3	0	4	0	1	2	0	0	0
B_T2	0	0	0	0	0	0	2	0	0	3	0	0	0	0
B_B4	0	0	0	0	0	1	1	4	0	5	0	0	0	0
S. altissimum														
U_T2	0	20	23	0	0	0	0	1	0	1	0	0	0	1
U_B4	0	6	13	0	0	0	0	0	0	0	0	1	0	0
B_T2	0	1	14	1	0	0	0	0	0	0	0	0	0	15
B_B4	0	0	1	0	0	0	0	0	0	0	0	1	0	11
M. gracilis														
U_T2	0	0	0	1	0	1	0	0	0	0	0	0	0	0
U_B4	0	0	1	12	8	0	2	0	0	1	0	0	0	0
B_T2	0	0	0	0	0	0	0	0	0	2	0	0	0	0
B_B4	0	0	0	3	7	0	0	1	1	0	0	0	0	0
Other species														
All treatments	9	3	0	0	0	4	0	17	2	0	11	1	11	6

Note:

U = Unburned

B = Burned

T2 = Top 2 cm

B4 = Bottom 4 cm

Table S2: Model performance metrics

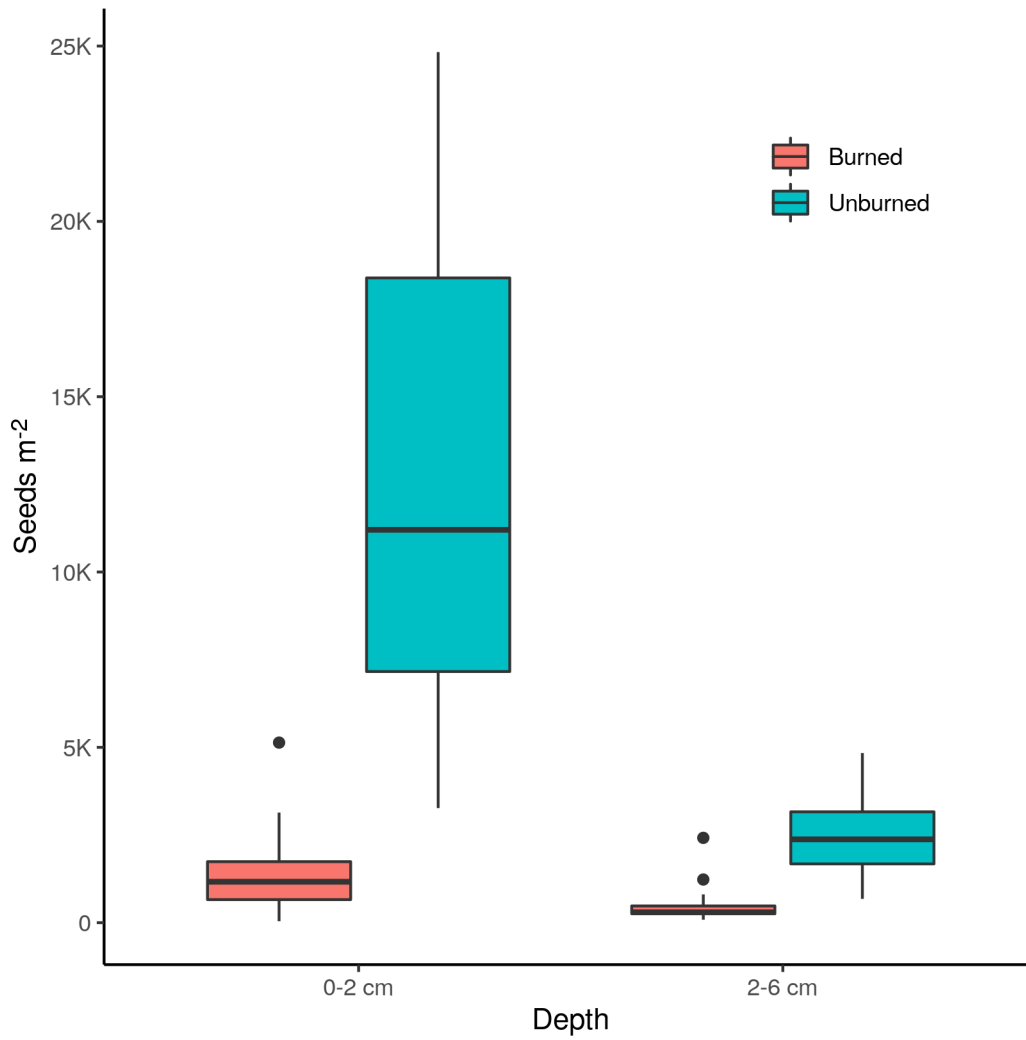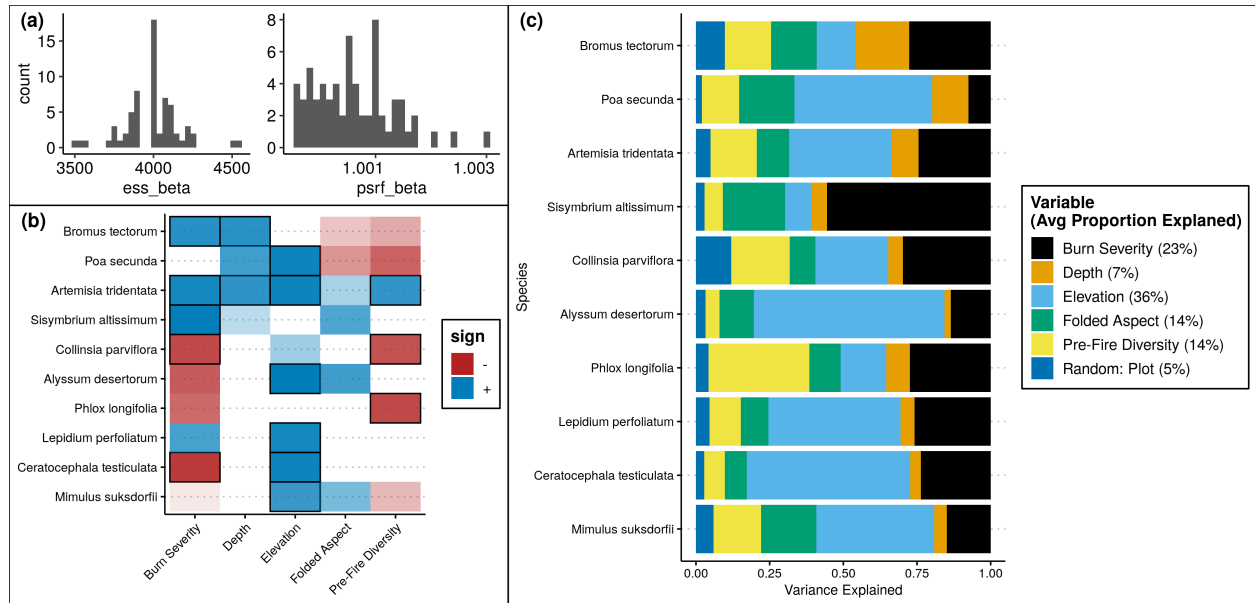| Model	R2	R2_adjusted	Sign
H1: TVC ~ NDSVI + Green NDVI	0.35		+
H1: dNBR ~ TVC(modelled)	0.42	0.42	+
H1: dNBR ~ TVC(in situ)	0.27	0.20	+
H3: Post-Fire Fuel Connectivity ~ # Cheatgrass Seeds + covariates	0.84	0.75	+
H4: Post-Fire Diversity ~ Post-Fire Fuel Connectivity	0.92	0.89	-

Figure S1: Total seed counts per plot.

Figure S2: a) Model convergence diagnostics. On the left is the effective sample size after adjusting for autocorrelation (ideally 4,000), and on the right is the Gelman diagnostic, ideally 1. b) Predictor variables that had at least 80% support. Variables with 95% support are outlined in black. The level of transparency corresponds to the level of support. c) Variance partitioning by species. Average across all species per variable is given in the legend. Species are ordered by prevalence.
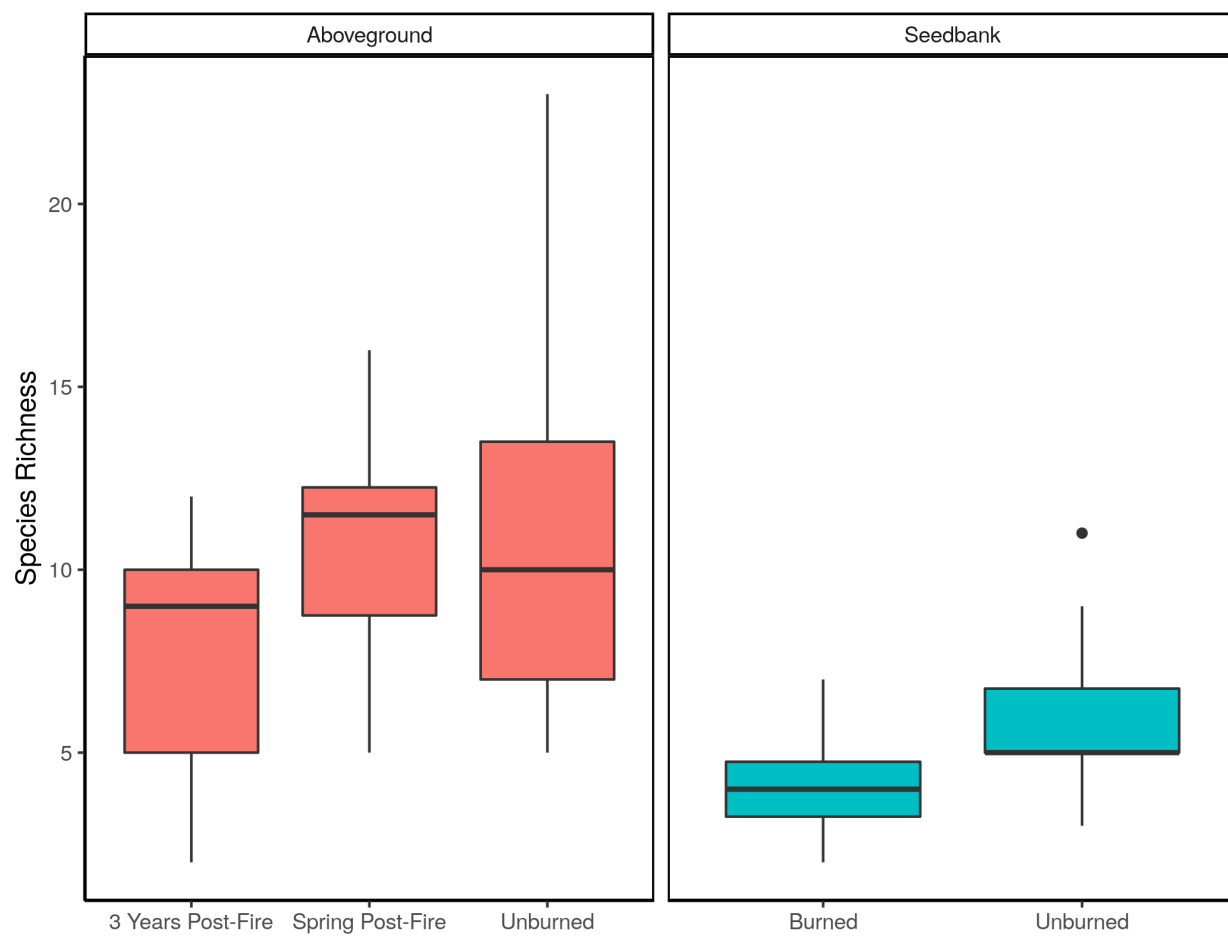
Figure S3: Species richness at different sampling times and locations.