

## Supplementary material

**Table S1** Number of *Araucaria angustifolia* adults, females, males, juveniles, and seedlings sampled (*n*), and logging intensity (LI) in blocks in scenarios of pre-logging (Pre), logged, and post-logging (Post) in three sample blocks (B13, B15, B20) and total sample of a remnant of Araucaria Forest located in Fernandes Pinheiro County, Parana state, Brazil.

Scenario	Sample size ( <i>n</i> )			DBH (cm)			Sample size ( <i>n</i> )		Total
	Adults	Females	Males	Adults	Females	Males	Juveniles	Seedlings	
B13									136
Pre	68	35	33	48.6	52.4	44.6	25	-	93
Logged	22	12	10	53.6	56.1	50.6	-	-	22
LI (%)	32.3	34.3	30.3	-	-	-	-	-	-
Post	46	23	23	46.2	50.5	42	25	43	114
B15									121
Pre	51	20	31	44.3	46.3	43	30	-	174
Logged	16	2	14	48.6	55.4	47.6	-	-	16
LI (%)	31.4	10	45.2	-	-	-	-	-	-
Post	35	18	17	42.3	45.2	39.2	30	40	105
B20									93
Pre	38	19	19	47.3	50.2	44.4	23	-	61
Logged	7	3	4	53.2	51.7	54.4	-	-	7
LI (%)	18.4	15.8	22.1	-	-	-	-	-	-
Post	31	16	15	46	49.7	41.4	23	32	86
Total									350
Pre	157	74	83	46.8	50.2	43.9	78	115	235
Logged	45	17	28	51.8	55.2	49.6	-	-	45
LI (%)	28.7	23	33.7	-	-	-	-	-	-
Post	112	57	55	44.9	46.8	41	78	115	305

DBH is the mean of diameter at breast height.

**Table S2** Sample size ( $n$ ) and number of pairs ( $N_{\text{pairs}}$ ) of adults (A), adults + juveniles (A+J) and adults + juveniles + seedlings (A+J+S) pre- and post-logging by distance classes used in the analysis of the spatial genetic structure in blocks B13, B15 and B20.

Sample	$n$		Distance classes (m)				Total
B13			-	0-25	25-50	50-136	
Pre: Adults (A)	68	$N_{\text{pairs}}$	-	374	824	1080	2278
Post: Adults (A)	46	$N_{\text{pairs}}$	-	160	366	509	1035
B15			-	0-25	25-50	50-132	
Pre: Adults (A)	51	$N_{\text{pairs}}$	-	198	486	591	1275
Post: Adults (A)	35	$N_{\text{pairs}}$	-	98	246	251	595
B20			-	0-25	25-50	50-141	
Pre: Adults (A)	38	$N_{\text{pairs}}$	-	130	191	382	703
Post: Adults (A)	31	$N_{\text{pairs}}$	-	75	131	259	465
B13			0-15	15-25	25-50	50-136	
Pre: A+J	93	$N_{\text{pairs}}$	277	450	1520	2031	4278
Post: A+J+S	114	$N_{\text{pairs}}$	249	371	1195	4626	6441
B15			0-15	15-25	25-50	50-132	
Pre: A+J	81	$N_{\text{pairs}}$	209	327	1140	1564	3240
Post: A+J+S	105	$N_{\text{pairs}}$	454	625	1794	2587	5460
B20			0-15	15-25	25-50	50-141	
Pre: A+J	61	$N_{\text{pairs}}$	162	148	503	1017	1830
Post: A+J+S	86	$N_{\text{pairs}}$	364	411	999	1881	3655

**Table S3** Mean, minimum, and maximum distance between females (FF), males (MM), and females and males (FM) within and among blocks B13, B15 and B20 in pre- (Pre) and post-logging (Post) sceneries.

		Distance (m)					
		FF	FF	MM	MM	FM	FM
		Pre	Post	Pre	Post	Pre	Post
Within B13	Mean	52	52	48	50	49	50
Within B13	Minimum	5	6	3	3	2	2
Within B13	Maximum	116	116	117	117	122	119
Within B15	Mean	55	52	47	40	52	51
Within B15	Minimum	8	8	2	9	4	9
Within B15	Maximum	122	117	113	99	126	126
Within B20	Mean	51	52	54	57	52	54
Within B20	Minimum	5	5	4	6	2	5
Within B20	Maximum	145	105	113	113	121	121
Among blocks	Mean	282	276	279	283	280	280
Among blocks	Minimum	153	153	124	124	124	124
Among blocks	Maximum	403	402	433	433	425	424

**Table S4** Results of P-values for linkage genotypic disequilibrium for all *Araucaria angustifolia* samples (adults + juveniles + seedlings).

Pairs of loci	All samples	Pairs of loci	All samples
Aang1 x Aang12	0.00353	Aang15 x Ag20	0.18526
Aang1 x Aang14	0.17981	Aang15 x Ag56	0.06154
Aang1 x Aang15	0.00865	Aang15 x Ag62	0.23782
Aang1 x Aang27	0.48718	Aang27 x Aang28	0.1016
Aang1 x Aang28	0.21987	Aang27 x Aang37	0.63141
Aang1 x Aang37	0.73718	Aang27 x Aang43	0.62949
Aang1 x Aang43	0.00256	Aang27 x Aa1774	0.38814
Aang1 x Aa1774	0.61154	Aang27 x Aa5332	0.37244
Aang1 x Aa5332	0.01891	Aang27 x Ag20	0.57436
Aang1 x Ag20	0.90256	Aang27 x Ag56	0.50865
Aang1 x Ag56	0.22115	Aang27 x Ag62	0.06891
Aang1 x Ag62	0.50032	Aang28 x Aang37	0.07276
Aang12 x Aang14	0.01026	Aang28 x Aang43	0.12949
Aang12 x Aang15	0.00481	Aang28 x Aa1774	0.29487
Aang12 x Aang27	0.225	Aang28 x Aa5332	0.1
Aang12 x Aang28	0.16026	Aang28 x Ag20	0.47115
Aang12 x Aang37	0.73814	Aang28 x Ag56	0.51506
Aang12 x Aang43	0.27949	Aang28 x Ag62	0.01571
Aang12 x Aa1774	0.09744	Aang37 x Aang43	0.22115
Aang12 x Aa5332	0.00353	Aang37 x Aa1774	0.06667
Aang12 x Ag20	0.24455	Aang37 x Aa5332	0.12436
Aang12 x Ag56	0.29776	Aang37 x Ag20	0.12853
Aang12 x Ag62	0.00128	Aang37 x Ag56	0.22244
Aang14 x Aang15	0.67083	Aang37 x Ag62	0.01122
Aang14 x Aang27	0.3734	Aang43 x Aa1774	0.05929
Aang14 x Aang28	0.45865	Aang43 x Aa5332	0.0016
Aang14 x Aang37	0.90353	Aang43 x Ag20	0.0016
Aang14 x Aang43	0.33942	Aang43 x Ag56	0.0484
Aang14 x Aa1774	0.21218	Aang43 x Ag62	0.10513
Aang14 x Aa5332	0.50417	Aa1774 x Aa5332	0.81218
Aang14 x Ag20	0.80641	Aa1774 x Ag20	0.00064
Aang14 x Ag56	0.62821	Aa1774 x Ag56	0.19167
Aang14 x Ag62	0.37179	Aa1774 x Ag62	0.01186
Aang15 x Aang27	0.05577	Aa5332 x Ag20	0.51699
Aang15 x Aang28	0.41891	Aa5332 x Ag56	0.04712
Aang15 x Aang37	0.30737	Aa5332 x Ag62	0.11282
Aang15 x Aang43	0.12532	Ag20 x Ag56	0.01218
Aang15 x Aa1774	0.22436	Ag20 x Ag62	0.00705
Aang15 x Aa5332	0.16122	Ag56 x Ag62	0.07308

P-value for genotypic disequilibrium based on 4680 permutations. Adjusted P-value for 5% significance level was 0.000321.

**Table S5** Genetic diversity per locus and mean loci, estimate of frequency of null alleles ( $Freq_{(null)}$ ) and the fixation index uncorrected ( $F$ ) and corrected for null alleles ( $F_{null}$ ) for 13 microsatellite loci analyzed in pre- and post-logging scenarios in an *Araucaria angustifolia* population located in Fernandes Pinheiro County, Parana state, Brazil.

Locus	$n$	$K$	$H_o$	$H_e$	$F$	$Freq_{(null)} \pm 1.96SE$	$F_{null}$
<b>Adults</b>							
Aang01	154	18	0.882	0.925	0.047	-	0.047
Aang12	147	21	0.8	0.933	0.143*	0.155 $\pm$ 0.088*	0.053
Aang14	155	8	0.89	0.829	-0.073	-	-0.073
Aang15	153	17	0.94	0.931	-0.01	-	0.01
Aang27	156	6	0.881	0.82	-0.074	-	-0.074
Aang28	157	5	0.874	0.729	-0.199*	-	-0.199
Aang37	156	3	0.663	0.513	-0.293	-	-0.293
Aang43	156	12	0.782	0.661	-0.183	-	-0.183
Aa1774	157	4	0.596	0.444	-0.343*	-	-0.343*
Aa5332	151	18	0.887	0.908	0.023	-	0.023
Ag20	155	8	0.754	0.735	-0.026	-	-0.026
Ag56	157	6	0.857	0.764	-0.122	-	-0.122
Ag62	155	14	0.822	0.836	0.017	-	0.017
Mean	-	10.8	0.818	0.771	-0.06*	-	-0.068
SD	-	6.2	0.098	0.156	0.14	-	0.128
<b>Juveniles</b>							
Aang01	78	16	0.964	0.92	-0.048	-	-
Aang12	75	18	0.846	0.925	0.085	-	-
Aang14	78	7	0.891	0.841	-0.06	-	-
Aang15	77	16	0.963	0.909	-0.059	-	-
Aang27	78	6	0.891	0.825	-0.08	-	-
Aang28	78	5	0.873	0.742	-0.176	-	-
Aang37	78	3	0.581	0.547	-0.063	-	-
Aang43	78	10	0.709	0.639	-0.11	-	-
Aa1774	78	4	0.346	0.333	-0.038	-	-
Aa5332	77	18	0.944	0.889	-0.062	-	-
Ag20	78	7	0.818	0.745	-0.098	-	-
Ag56	78	6	0.818	0.76	-0.076	-	-
Ag62	78	13	0.818	0.794	-0.033	-	-
Mean	-	9.6	0.805	0.759	-0.06	-	-
SD	-	5.5	0.174	0.17	0.058	-	-
<b>Seedlings</b>							
Aang01	115	16	0.965	0.924	-0.044	-	-
Aang12	106	20	0.908	0.929	0.023	-	-
Aang14	115	8	0.879	0.839	-0.048	-	-
Aang15	114	17	0.951	0.912	-0.043	-	-
Aang27	115	6	0.891	0.814	-0.095	-	-
Aang28	114	5	0.88	0.72	-0.222	-	-
Aang37	115	3	0.41	0.484	0.115	-	-
Aang43	115	12	0.626	0.608	-0.03	-	-
Aa1774	115	3	0.373	0.364	-0.025	-	-
Aa5332	115	19	0.964	0.909	-0.061	-	-
Ag20	115	8	0.819	0.775	-0.057	-	-
Ag56	115	6	0.844	0.757	-0.115	-	-
Ag62	115	14	0.783	0.749	-0.045	-	-
Mean	-	10.5	0.972	0.753	-0.052*	-	-
SD	-	6.1	0.199	0.175	0.083	-	-

$n$  is the sample size;  $K$  is the total number of alleles;  $H_o$  and  $H_e$  are the observed and expected heterozygosity, respectively; SE is the 95% confidence interval; SD is the standard error; \*P< 0.05.