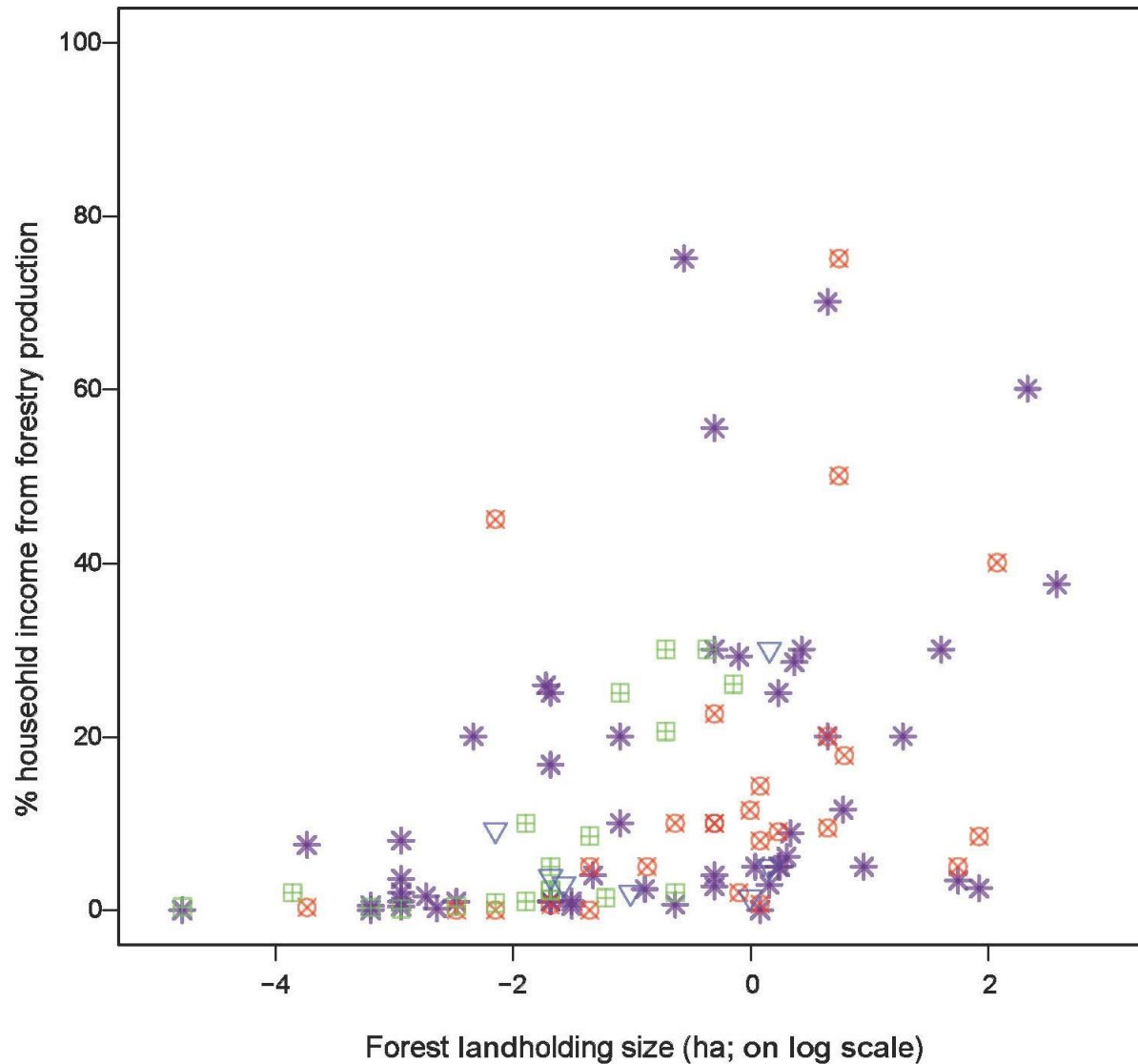
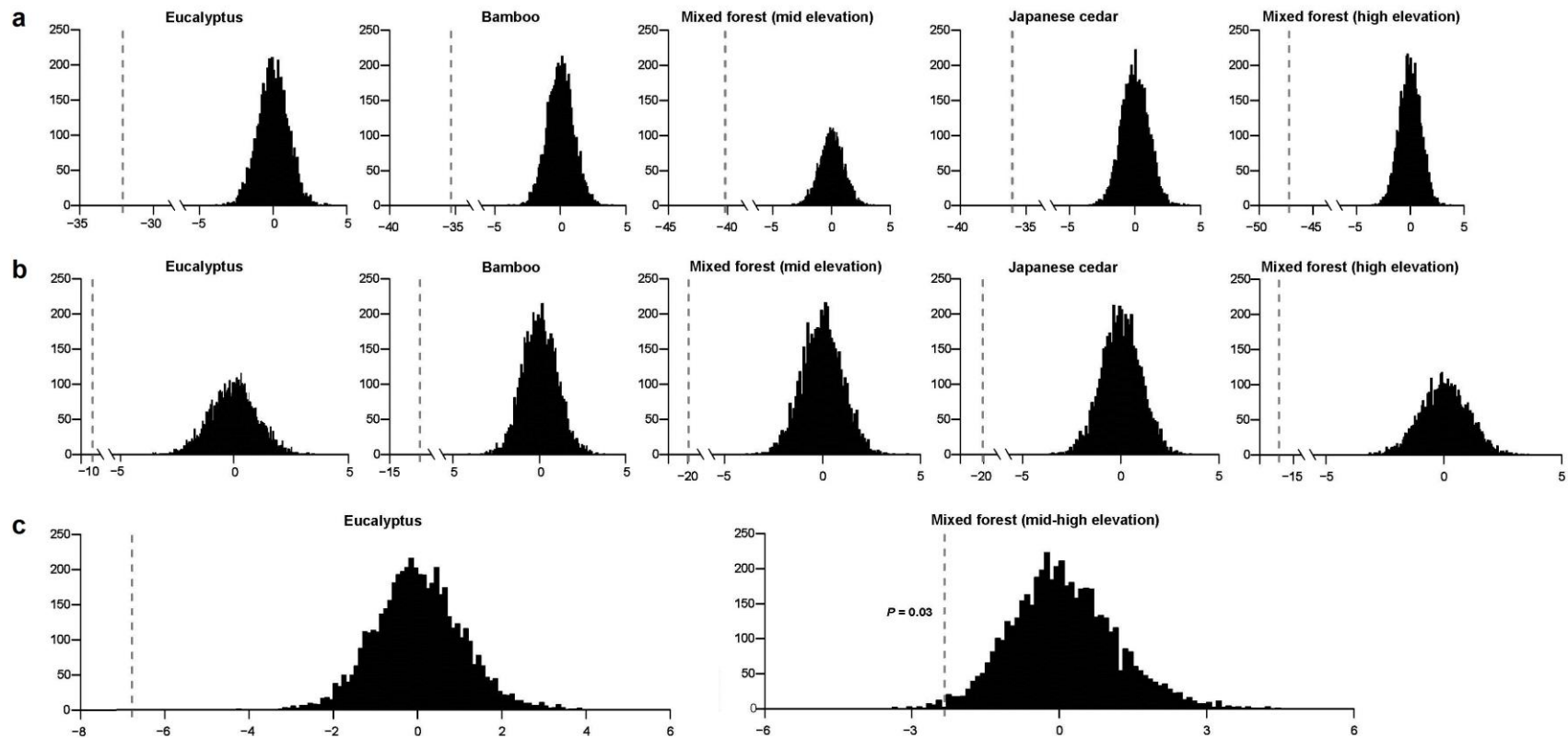


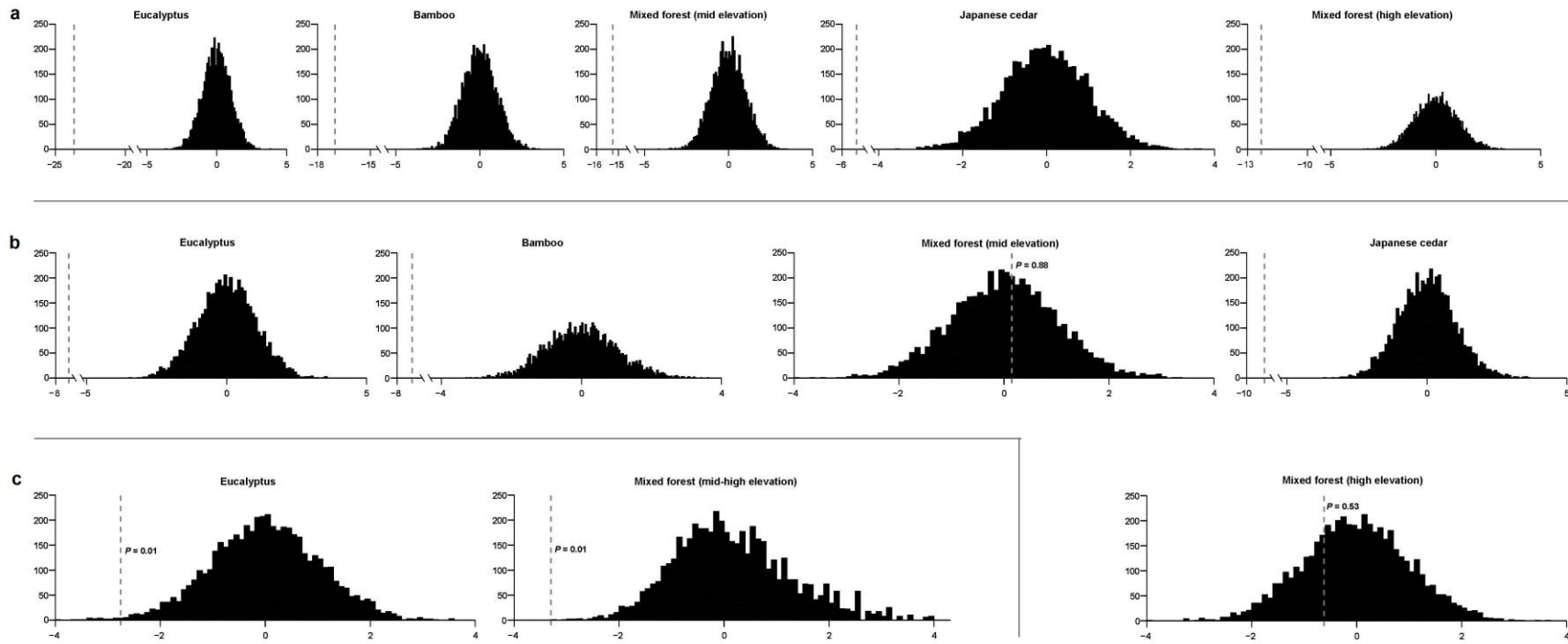
Supplementary Figures



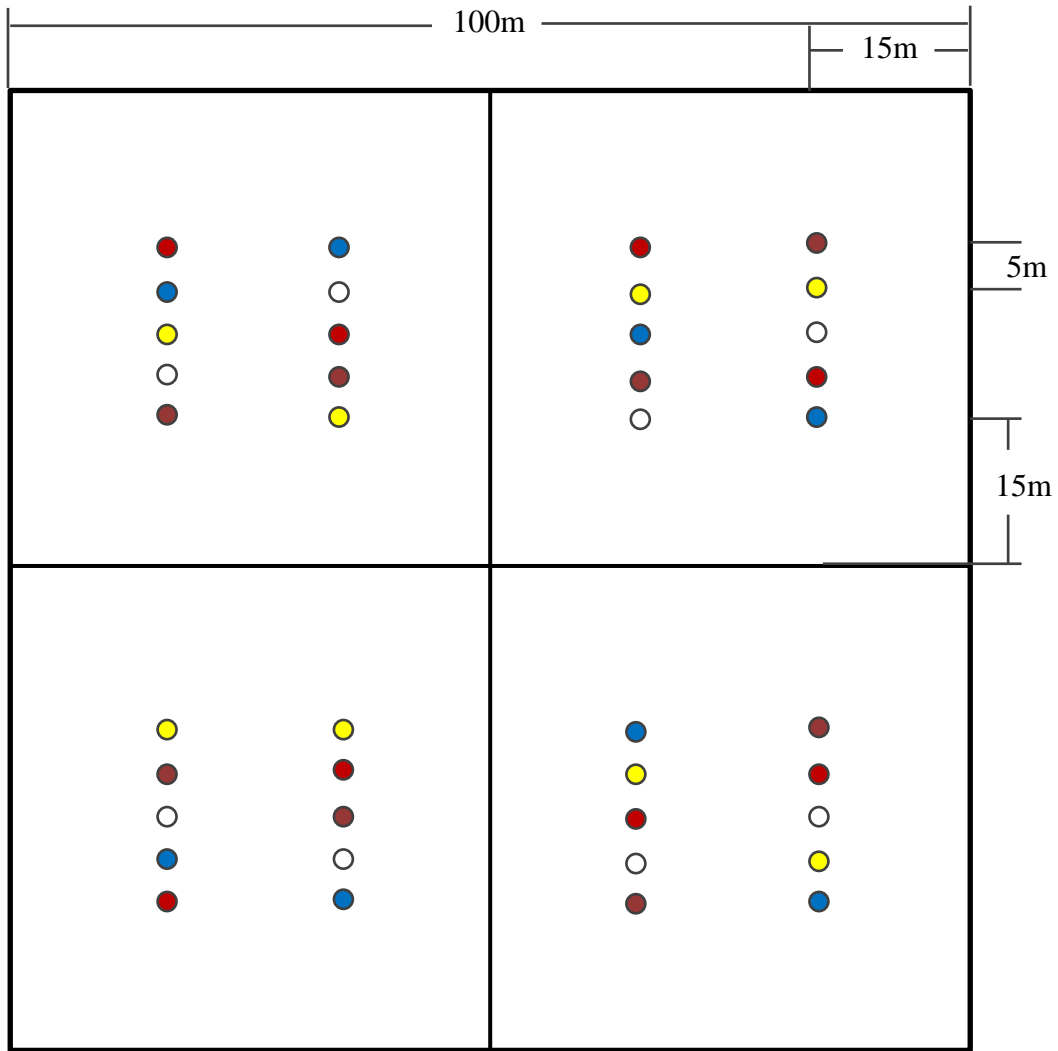
Supplementary Figure 1. Distribution of respondent households in terms of the percentage of household income from forest production against forest landholding size. Symbols of different shapes and colors represent households managing different types of forest: green crossed square - eucalyptus monoculture, blue triangle - bamboo monoculture, red crossed circle - Japanese cedar monoculture, and purple asterisk - mixed forest. Forest landholding size is displayed on a log scale. The percentage of household income from forest production is positively correlated with forest landholding size ($\beta = 4.20$, $SE = 1.17$, 95% confidence interval = [1.91, 6.49]).



Supplementary Figure 2. Community compositional differences between GFPG forests and cropland based on PERMANOVA analysis of community dissimilarity under 5000 permutations. Graphs are 100-bin histograms (black) with X axis displaying the t-test statistic score that compares (1) community dissimilarity (using Bray-Curtis dissimilarity index) within the GFPG forest type in question against (2) community dissimilarity between the GFPG forest type in question and cropland, and Y axis displaying the number of permutations yielding each bin of t-test statistic score; grey dotted lines display the observed t-test statistic score. Panels display analyses for birds during the breeding (a) and nonbreeding seasons (b), and bees (c). All PERMANOVA tests where grey dotted line does not overlap with black histogram have $P < 0.001$; P-values are displayed for tests where $P \geq 0.001$.



Supplementary Figure 3. Community compositional differences between GFGP forests and native forest based on PERMANOVA analysis of community dissimilarity under 5000 permutations. Graphs are 100-bin histograms (black) with X axis displaying the t-test statistic score that compares (1) community dissimilarity (using Bray-Curtis dissimilarity index) within the GFGP forest type in question against (2) community dissimilarity between the GFGP forest type in question and native forest, and Y axis displaying the number of permutations yielding each bin of t-test statistic score; grey dotted lines display the observed t-test statistic score. Panels display analyses for birds during the breeding (a) and nonbreeding seasons (b), and bees (c). All PERMANOVA tests where grey dotted line does not overlap with black histogram have $P < 0.001$; P-values are displayed for tests where $P \geq 0.001$.



Supplementary Figure 4. Schematic illustration of pan trap layout in a trapping plot. Color dots represent individual pan traps of different colors (dyed with fluorescent spray paint).

Supplementary Tables

Supplementary Table 1. Information synopsis on six target land-cover types included in field study in south-central Sichuan Province.

Land-cover category	Land-cover type	Forest structure/main crop	Elevation	Note on condition and production mode
GFGP forest	Eucalyptus	Broadleaf	≤ 650 m (low)	• Monoculture; for timber production.
	Bamboo†	Bamboo	530-1000 m (mid)	• Monoculture; for timber and bamboo shoot production.
	Japanese cedar	Coniferous	≥ 830 m (high)	• Monoculture; for timber production.
	Mixed forest	Mixed broadleaf and coniferous	≥ 530 m (mid & high)	• Compositionally simple, involving 2-5 tree species and predominantly a bi-mixture of bamboo and Japanese cedar; for timber and bamboo shoot production.
Baseline land cover	Cropland	Seasonally rotational rice, corn, vegetables	All elevations	• Non-mechanized, generally low-intensity farming; proxy for GFGP-replaced cropland.
	Native forest	Broadleaf	All elevations	• Disturbed, often with regular extraction of (non)timber forest products; proxy for the most conservation-friendly forest form conforming to the production, unprotected nature of GFGP forests.

Note: † - In this study, bamboo stands involving multiple bamboo species were considered as bamboo monoculture because of the similar and consistently simple forest structure associated with all bamboo species concerned in this study.

Supplementary Table 2. Thresholds of elevation for assigning elevation bands and the number of sampling units shared between neighboring elevation bands.

Field season	Elevation band	Elevation bound (m)		Number of survey units shared with the next higher neighboring band		
		Lower	Upper	Land cover	Bird point count/mixed-species flock	Bee trapping plots
Avian breeding	Low	342	647	Cropland	17	0
				Native forest	13	4
	Mid	529	1017	Cropland	14	--
				Native forest	9	--
				Mixed forest	12	--
	High	878	1429	Cropland	--	--
				Native forest	--	--
				Mixed forest	--	--
	Avian nonbreeding	Low	315	648	Cropland	11/2
Native forest					27/7	--
Mid		532	1102	Cropland	32/1	--
				Native forest	37/7	--
				Mixed forest	26/4	--
High		829	1314	Cropland	--	--
				Native forest	--	--
				Mixed forest	--	--

Supplementary Table 3. Tally of bird and bee survey sample size.

Taxon	Elevation band	Land-cover type	Sample size†	
			Avian breeding season	Avian nonbreeding season§
Bird	Low	Cropland	53	48/3
		Native forest	35	28/7
		Eucalyptus forest	57	54/5
	Mid	Cropland	46	43/3
		Native forest	46	80/19
		Bamboo forest	55	49/4
		Mixed forest	66	59/8
	High	Cropland	46	49/1
		Native forest	67	77/23
		Japanese cedar forest	72	57/8
		Mixed forest	84	65/5
	Bee	Low	Cropland	6‡
Native forest			5	--
Eucalyptus forest			10	--
Mid-high		Cropland	9	--
		Native forest	15‡	--
		Bamboo forest	8‡	--
		Japanese cedar forest	12	--
		Mixed forest	10	--

Note: † - Sample size is in terms of the numbers of point counts (birds), trapping plots (bees) and mixed-species flocks recorded (birds), by land-cover type and season. ‡ - Based on Tietjen-Moore test ($P < 0.05$), we removed two cropland plots in low elevation, as well as one native forest plot and two bamboo plots in mid-high elevation as outliers. § - Numbers before and after the slash refer to the numbers of point counts and mixed-species flocks observed, respectively.

Supplementary Table 4. Tally of household interview sample size by GFGP forest type.

GFGP forest type	Sample size (number of households)		
	Percentage of household income from forest production	Production profit	Labor intensity
Eucalyptus	20	20	14
Bamboo	7	12	14
Japanese cedar	26	10	43
Mixed forest	52	12	41
Total	105	54	112

Note: Household interview sample size is in terms of the numbers of estimates obtained for production profit, labor intensity, and percentage of household income coming from forest production.

Supplementary Table 5. The number of species shared between each type of GFPG forest and baseline land cover that had different abundances[†] between each type of GFPG forest and baseline land cover.

Taxon	Season	Type of GFPG forest	Baseline land cover					
			Cropland			Native forest		
			Higher	Lower	No difference	Higher	Lower	No difference
Bird	Breeding	Eucalyptus	2	1	29	0	0	31
		Bamboo	5	6	21	3	4	25
		Mixed forest – mid elevation	7	8	20	4	2	28
		Japanese cedar	5	3	25	2	8	29
		Mixed forest – high elevation	7	3	23	2	7	31
	Nonbreeding	Eucalyptus	0	2	22	0	2	18
		Bamboo	0	0	16	0	1	18
		Mixed forest – mid elevation	0	0	23	0	0	30
		Japanese cedar	0	0	19	0	3	20
		Mixed forest – high elevation	0	0	22	2	5	23
Bee	NA	Eucalyptus	0	1	2	1	1	1
		Bamboo	0	1	2	0	1	0
		Japanese cedar	0	1	2	0	0	1
		Mixed forest	0	2	1	0	1	1

Note: † - For a given species/genus, the abundance analysis compares its abundance in each type of GFPG forest against that in each type of baseline land cover. “Lower” and “higher” abundances therefore refer to lower and higher abundance in GFPG forest than in baseline land cover, respectively.

Supplementary Table 6. Comparison of forest annual profit (US\$ ha⁻¹ yr⁻¹) and labor intensity (Days ha⁻¹ yr⁻¹) under different discount rates.

Discount rate	Comparison in	Forest type	β	SE	<i>P</i> (difference from mixed forest)
0.05	Forest profit	Bamboo	425.56	82.65	0.586
		Eucalyptus	497.71	70.78	0.211
		Japanese cedar	288.54	91.37	0.542
		Mixed forest	362.77	79.13	--
	Labor intensity	Bamboo	5.73	4.19	0.062
		Eucalyptus	13.70	3.54	0.832
		Japanese cedar	9.55	2.34	0.111
		Mixed forest	14.58	2.07	--
0	Forest profit	Bamboo	695.70	135.40	0.812
		Eucalyptus	726.10	116.00	0.934
		Japanese cedar	607.70	149.70	0.506
		Mixed forest	740.60	129.70	--
	Labor intensity	Bamboo	8.39	6.41	0.068
		Eucalyptus	15.27	5.42	0.315
		Japanese cedar	14.33	3.59	0.131
		Mixed forest	21.61	3.17	--
0.0125	Forest profit	Bamboo	610.39	117.10	0.985
		Eucalyptus	660.52	100.30	0.755
		Japanese cedar	499.18	129.40	0.508

		Mixed forest	613.37	112.09	--
	Labor intensity	Bamboo	7.56	5.71	0.066
		Eucalyptus	14.84	4.83	0.416
		Japanese cedar	12.82	3.19	0.126
		Mixed forest	19.40	2.82	--
0.025	Forest profit	Bamboo	538.46	102.83	0.850
		Eucalyptus	601.01	88.06	0.501
		Japanese cedar	412.92	113.68	0.516
		Mixed forest	511.44	98.45	--
	Labor intensity	Bamboo	6.85	5.12	0.065
		Eucalyptus	14.44	4.33	0.539
		Japanese cedar	11.55	2.86	0.121
		Mixed forest	17.53	2.53	--

Supplementary Table 7. Results of multiple linear model analysis of the percentage of household income coming from forest production.

Predictor variable	Tree species concerned	β	SE	95% CI
Forest type	Eucalyptus	7.72	3.69	[0.49, 14.95]
	Bamboo	5.52	6.09	[-6.42, 17.46]
	Japanese cedar	9.48	3.45	[2.72, 16.24]
	Mixed forest	9.67	2.58	[4.61, 14.73]
Area of forest holding	--	4.20	1.17	[1.91, 6.49]

Supplementary Table 8. The coverage (birds[†]) and sample size (bees[‡]) sampling data were extrapolated to in the analysis of species richness.

Taxon	Low elevation	Mid elevation	High elevation
Birds (breeding)	98.8%	97.9%	98.8%
Birds (nonbreeding)	98.4%	99.4%	99.3%
Bees	10	--	16 (Mid-high elevation)

Note: † - Coverage is a measure of the completeness with which sampling data represent the species richness of a community; specifically, it is defined as the percentage of the total number of individuals in a community that belong to species represented in the sample¹. ‡ - Sample size refers to the number of trapping plots.

Supplementary Notes

Supplementary Note 1. Details on the vegetative make-up of the six target land-cover types

Eucalyptus forest. The tree species used in eucalyptus monoculture forests is *Eucalyptus grandis* W. Hill ex Maiden, which is not native to China. Individual trees are typically spaced 2 m apart, and harvested using clear-cuts every six to seven years. Forest stands are typically managed with chemical weeding and fertilization, which results in a highly limited understory structure, although on the rare occasions that forest stands are subject to less management, they usually have a well-developed understory.

Bamboo forest. Tree species used in bamboo monoculture forests mostly include *Neosinocalamus affinis* (Rendle) Keng f, *Pleioblastus amarus* (Keng) Keng, and *Phyllostachys pubescens* Mazel ex H. de Lehaie. All species are native to the region. Spacing between individual plants varies depending on the species. Typically, *Neosinocalamus affinis* and *Phyllostachys pubescens* bamboo forests are selectively harvested every one to two years for timber, while *Pleioblastus amarus* forests are maintained for bamboo shoot production. Forest stands are typically managed with chemical fertilization; minimal weeding is needed because the strong water-absorbing ability of bamboo plants discourages the growth of other plants. In all cases, understory structure is minimal.

Japanese cedar forest. The tree species used in Japanese cedar monoculture forests is *Cryptomeria japonica* var. *sinensis* Miquel, which is native to the region. Young plantations are started at high densities, and trees are then selectively removed until a harvest density of two to three meters apart. The mode of selective harvest (i.e., timing and number of harvests) tends to vary among households. Forest stands are typically managed with chemical fertilization. Weeding is only done before canopy closure, after which the stands self-maintain minimal

understory structure because of extremely low light levels in the understory. Clear-cut typically happens at 18-20 years.

Mixed forest. Mixed GFGP forests consist of up to five, although most typically two or three tree species, including alder (*Alnus cremastogyne* Burk), Japanese cedar (*Cryptomeria japonica* var. *sinensis* Miquel), bamboo (*Neosinocalamus affinis*, *Pleioblastus amarus*, *Phyllostachys pubescens*), toona (*Toona ciliata* Roem), and happy tree (*Camptotheca acuminata* Decne). All species are native to the region. Stands can follow one of two levels of species mixture: mixture of individual trees/plants (hereafter “tree-level mixture”), or mixture at the scale of small patches of monocultures (hereafter “patch-level mixture”). Plots consisting of a patch-level mixture tend to be managed in the same way as monoculture forest described above. Spacing between individual trees varies between species. For tree-level mixtures, forest stands are sometimes managed with chemical weeding and fertilization. Stands are typically selectively harvested on cycles specific to different species. Understory structure is typically reasonably developed for forests with tree-/plant-level mixture, and understory structure of patch-level mixture generally resembles that of the corresponding monoculture plots.

Cropland. Croplands included in our field study are invariably distributed ≤ 5 km from the surveyed forest expanses and on relatively flat terrain, and are predominantly managed in a low-intensity way that involves minimal mechanization. Crops at the time of the avian breeding season surveys were predominantly rice, corn, and vegetables; crops at the time of avian nonbreeding season surveys were predominantly fallow rice paddies (no crop) and vegetables.

Native forest. Native forest in the region is mostly broadleaf subtropical evergreen forest, dominated by tree species in the families Lauraceae, Fagaceae, Theaceae and Symplocaceae, with well-developed herbaceous understory. Native forests sites in our field study consisted of

sites in and around the Emei Mountain Forest Park (> 98% of survey efforts) and the Xiang'er Buddhist temple in Pengshan County of Meishan Municipality (Fig. 2). The vast majority of forests surveyed were subject to considerable levels of disturbance and resource extraction including timber and herbal medicine collection. Notably, forests outside of Emei Mountain Forest Park are routinely dotted with small, scattered stands of monoculture plantations that have replaced former native forest cover.

Supplementary Methods

Compilation of peer-reviewed literature on GFGP forest type. To search the English literature on Web of Science (www.webofknowledge.com), we checked all publications cited in and citing four “anchor” publications on GFGP: two generic review articles ^{2,3}, one meta-analysis on soil carbon levels ⁴, and one generic book ⁵. We additionally searched for publications about biodiversity under GFGP, using the search terms “China”, “grain for green”, and “biodiversity”. Importantly, we used all six variants of GFGP’s English translation that have occurred in the literature, including “grain for green”, “grain-for-green”, “grain to green” (e.g. ²), “grain-to-green”, “sloping land conversion” (e.g. ⁶), and “returning farmland to forest program” (e.g. ⁷). For our search of the Mandarin literature on the China Knowledge Resource Integrated Database (www.cnki.net), we used the Mandarin term “tui geng huan lin” (“退耕还林”, the official name of GFGP in Mandarin) as the only search term. Of all publications we retrieved, we retained only those that provided information on the type of GFGP forests (i.e. composition of tree species, or at least if the forest was monoculture or mixed forest).

Biodiversity sampling. All bird point count stations and bee trapping plots were ≥ 50 m from the edge of the focal land-cover type. We conducted all surveys at lower elevations before moving to higher elevations with the exception of a small subset of breeding season point counts and ~25% of the bee trapping plots at low elevations during the avian breeding season, which we surveyed toward the latter half of the field season. We determined the required effort level of point count surveys for each land-cover type based on the leveling of species accumulation curves. Pan trapping efforts were limited by time and personnel; we had a minimum of ten trapping plots for each land-cover type. For both birds and bees, survey effort was higher for the more biodiverse land-cover types (according to our field experience).

For bird point count surveys, we used a 150-m radius, avoiding double-counts to the best of our ability. We divided each 12-minute survey into four 3-min subintervals and recorded individual-/group-level detections (using visual and auditory cues) for each subinterval⁸, excluding flying individuals. In the nonbreeding season, when there were many mixed-species flocks, we additionally quantified the composition of flocks encountered during the point counts and/or during travel between point counts. To characterize mixed-species flocks during the nonbreeding season, we recorded the species identity and number of all individuals in the flocks that we encountered. Observers were allowed to move up to 10 m from the routes between point count stations, which we considered a realistic distance for the auditory detection of passing flocks, and to spend up to five minutes observing each flock. In situations where a flock passed through during a point count period, we stopped the point count and instead focused on recording the flock, before restarting the point count from the beginning. Breeding season surveys were conducted between 30 minutes before dawn and 10:30 am, and nonbreeding season surveys between 8:30 am and 4:30 pm. Two different groups consisting of four surveyors each conducted the breeding and nonbreeding season surveys. We minimized observer bias with regard to land-cover type by ensuring that each land-cover type was covered by all observers, and that observer identity was considered in subsequent analysis (see “Statistical analysis” below). Supplementary Table 3 lists the number of point counts conducted for each land-cover type and season, divided into elevation bands (see elevation band delineation below and in Supplementary Table 2).

For bee surveys, we divided each trapping plot into four equal quadrats, within each of which we systematically set up two parallel lines of five fluorescent pan traps of different colors spaced 5 m apart and 15 m from quadrat edges; each trapping plot thus had 40 traps (Supplementary Fig. 4). We used 96 ml plastic pans (3.25-ounce translucent plastic soufflé

portion cups; www.cuptainers.com) that we fluorescent-dyed with white, red, yellow, blue and purple, respectively. We set up all pans on 1-m poles to improve visibility, filled each pan two thirds full with 2% scentless liquid detergent as a surfactant ⁹, and operated them for 24 hours on days without rain. We collected all captured individuals (including bees and other insects) and stored them in 99.99% ethanol at $\leq 4^{\circ}\text{C}$ before DNA extraction. All samples were stored at -20°C within five days of field collection until the time of lab work. Seven out of the total 74 plots were changed to a rectangular shape of equivalent area due to terrain constraints.

Supplementary Table 3 lists the number of trapping plots surveyed for each land-cover type, divided into elevation bands (see elevation band delineation below and in Supplementary Table 2).

DNA barcoding. For each individual, we extracted DNA from one leg following protocols in ¹⁰, and amplified the mtCOI gene using the corbiculate bee primers BarbeeF (5'-CAACAAATCATAAAAATATTGG-3') and MtD9 (5'-CCCGGTAAAATTTAAAATATAAACTTC-3' ¹¹). Our PCR used 13.5ul reaction volumes that contained 1.25ul 10x buffer (Mg^{2+} plus), 0.2mM dNTPs, 0.25uM of each primer, 0.3U Taq DNA polymerase (TaKaRa Biotechnology (Dalian) Co., Ltd.), and ~60ng pooled genomic DNA. We implemented PCR amplifications with Mastercycler Pro (Eppendorf, Germany), starting with an initial denaturation process at 94°C for 5 min, followed by 35 cycles, each comprising 94°C for 1 min, 38°C for 80s and 64°C for 2 min, and finished with 64°C for 10 min. We used the ABI 3730xl DNA Analyser (Applied Biosystems, Carlsbad, California, USA) for sequencing; after sequence quality control, pairwise alignment and a translation check, we obtained 734 Sanger sequences. We then used MOLE-BLAST (www.blast.ncbi.nlm.nih.gov/moleblast/moleblast.cgi; accessed July 30th 2015) to filter out non-bee sequences, and obtained 546 bee sequences.

For all mtCOI Sanger sequences, we conducted single-threshold GMYC species delineation¹². We constructed an ultrametric gene tree under a relaxed log-normal molecular clock with BEAST 2.3.0, generated the BEAST input file with BEAUti 2.3.0¹³ and used the GTR substitution model, which we selected using jModelTest2 2.1.7^{14,15}. We set mean substitution rate to one, and estimated the proportion invariant and base frequencies. We chose a birth-death model as a single coalescent cluster constituting the GMYC null model. We set the AG transition rate prior to a gamma distribution with Alpha = 2 and Beta = 0.5 and all the other transition-rate parameters to gamma distribution with Alpha = 2 and Beta = 0.25. We set the uclMean prior to 0.0176, which is the mean substitution rate for arthropods. We defined three Crabronidae COI sequences as the outgroup. We ran the MCMC chains for 20 million generations and sampled every 1000 generations. We visualized run convergence using Tracer version 1.6.0¹⁶, and discarded the first 10% of the trees as burn-in. We ran TreeAnnotator 1.8.2¹⁶ to produce a single tree for GMYC analysis using maximum clade credibility tree, with the Node Heights option set to Keep Target Heights. We applied single-threshold GMYC models to DNA barcodes using the package *splits* (1.0-19¹⁷; in R 3.2.0¹⁸; see enclosed R script: bees_GMYC_BEAST2.R).

Household interview. We obtained ≥ 50 interviews for each GFGP forest type, except for eucalyptus monoculture, for which we obtained 30 interviews (total number of households included was 166). Supplementary Table 4 lists the number of households interviewed for each land-cover type whose data contributed to our economic analyses. In each household, we first asked what forest types the household managed. For each forest type, we then asked about the management/production costs per unit area per production cycle, breaking the costs down into discrete processes, including the establishment, maintenance and harvesting of forests, and to

discrete components including costs of seedlings, chemicals, hired and self-labor, equipment and transportation. We also asked respondents about the yield and market price for forest products per unit area per production cycle, covering both timber and non-timber products. These questions allowed us to calculate the yield and profit of different GFGP forest types. Importantly, because of China's registration system that ties parcels of rural land to particular households, respondents generally know the sizes of their land-holdings with considerable accuracy. While government subsidies on seedlings and fertilizer could result in underestimations of production costs, there is no reason to expect this underestimation to systematically vary with GFGP forest type in a way that would bias our conclusions on profit from forest products. We additionally asked respondents to estimate what percentage of their household income came from forest production.

Statistical analysis. Considering the likely inadequate sampling of bees, we first eliminated plots identified as outliers of anomalous trapping patterns. To identify outlier plots, we tallied the total number of individuals trapped from each survey plot, and used the Tietjen-Moore test for outliers¹⁹ to identify plots with excessively low or high number of captures ($P < 0.05$). This resulted in the removal of five survey plots (Supplementary Table 3). We stratified biodiversity analysis into three elevation categories using the natural elevation range of the three monoculture forests (eucalyptus, bamboo, and Japanese cedar; Supplementary Note 1): eucalyptus defining low elevation, bamboo mid elevation, and Japanese cedar high elevation. For the analysis of bees, we combined data for mid and high elevations because of limited sample size. We assigned survey data for each monoculture to their respective elevation bands, and survey data for cropland, native forest and mixed GFGP forest, three land-cover types that spanned more than one elevation bands, to elevation bands according to the threshold elevation values provided in

Supplementary Table 2; a portion of these data was used in more than one elevation bands because of the overlap between bands (Supplementary Table 2).

For species richness analysis using coverage-/sample-based extrapolation, we extrapolated to two times the minimum sample size or the largest sample size, whichever was greater²⁰ (Supplementary Table 8). We used PERMANOVA to test community compositional turnover between each type of GFGP forest and baseline land-cover types, by permutating the site-level (with a site being a point count station for birds, and a trapping plot for bees) Bray-Curtis distance of community composition 5000 times^{21,22}. For bees, no PERMANOVA was conducted for bamboo and Japanese cedar GFGP forests because both forest types involved only two plots that yielded at least one bee individual, thus involving only one community dissimilarity measure. We followed del Hoyo et al.²³ and MacKinnon et al.²⁴ in classifying bird species into forest-dependent, generalist, and open-country guilds. A species was classified as forest-dependent if it is predominantly associated with forested habitat, i.e. its association with forested habitat was cited by the sources as being stronger than “occasional” or “sometimes”. Similarly, a species was classified as open-country if its association with open habitat was cited by sources as being stronger than “occasional” or “sometimes”. We classified the remaining species in between these two association categories into the generalist guild (Supplementary Data 6).

For N-mixture modeling of bird species abundance, we treated only species with ≥ 10 total detections of individuals or groups as standalone species, and collapsed the remaining species into their respective genera only when the genus satisfied the 10-detection requirement. Abundance modeling for species living in groups estimated the abundance of groups rather than individuals. The rationale for using this 10-detection requirement lay in the fact that N-mixture

models entail modeling both the “true” abundance and the detection probability of each species, involving a maximum of ten covariates in the most complete models (i.e. global models; see below). The convergence of these N-mixture models, particularly when involving a large number of covariates, depends upon a reasonable number of detections to provide sufficient information to tease apart the contribution of true abundance and detection to the observed abundance of the species. Because we are unaware of well-established guidelines for “a reasonable number of detections”, we chose a minimum of ten detections; it was found to work well for the purposes of our models.

For all species/genera, the model’s abundance component included land-cover type as the only candidate covariate and used a log link and Poisson error distribution. The detection probability component included land-cover type (in binary form of forest versus non-forest), observer identity and day of year (we considered May 3rd and December 1st as day 1 for avian breeding and nonbreeding seasons, respectively) as candidate covariates, and time as a nuisance covariate, and used a log link and binomial error distribution. Models for the nonbreeding season were simultaneously parameterized with data from mixed-species flocks, because flocks accounted for a considerable proportion of the bird individuals detected during the nonbreeding season (see below). We assumed closed population and constant detection probability during each point count ⁸. For each species/taxon, we generated a full set of sub-models from the global model (i.e. using all combinations of candidate covariates), and ranked these models based on the AIC (Akaike’s information criterion ²⁵) score. For the model with the lowest AIC score, we checked its estimates to gauge whether they were generally consistent with our biological knowledge of the species/genus. If they were, we would select the model with the lowest AIC score as the best model; otherwise, we would move to the model with the next lowest AIC score

and conduct such check again, until we identified the model with the lowest AIC score that produced estimates consistent with our biological knowledge, as the best model. The reason for including our biological knowledge of the species/genus was that in some situations, the particular data structure could cause the models to produce unrealistic abundance and detection probability estimates even if they converged (e.g. exceedingly high densities of populations). Our biological knowledge of the species'/genera's likely abundance from our field experiences therefore serves as a safeguard against such unrealistic estimates. For GLMs of bee species abundance, we followed the same 10-capture criterion in identifying standalone bee species, and collapsed the rest into one taxon. All GLM models included land-cover type as the only covariate and used a log link and Poisson error distribution.

For the parameterization of N-mixture models for the nonbreeding season, we combined data from both point count and mixed-species flock observation (see “Biodiversity sampling” above for methods of flock observation). The combination of these two datasets to inform N-mixture models was based on two assumptions. (1) For a given species/genus, the same population density underlay the pattern of the species'/genus' detection during both point count and mixed-species flock observation; in other words, the numbers of individuals detected during point count and flock observation were the representation of the same underlying density of the species/genus. (2) Unlike during point counts, bird individuals in flocks had a perfect detection probability; in other words, we considered the identity and number of bird individuals recorded in mixed-species flocks to be an adequate representation of the composition of the flocks. We consider this assumption to largely hold because of the high activity levels and visibility of flocks. As with the breeding season, N-mixture modeling for species living in groups estimated

the abundance of groups rather than individuals; for this purpose, flock observation of these group-living species recorded the number of groups rather than individuals.

Given these two assumptions, for a given species/genus, the expected number of individuals/groups detected during point count and flock observation could be expressed mathematically based on parameters of population density, land area surveyed, and, for point counts, detection probability. This expression involves (1) multiplying population density with land area surveyed to express the “super” population associated with the land-cover type²⁶, (2) conducting Poisson draws from this super population to express the number of individuals/groups that were present, and thus available, to be detected by point count or encountered by flock observation, and for point count, (3) conducting binomial draws using detection probability to express the number of individuals/groups detected during point count. Parameters pertaining to population density and detection probability were estimated by N-mixture models, while those pertaining to the land area surveyed were known (see below). N-mixture modeling thus hinged on using the maximum likelihood estimate approach to estimate the unknown parameters by fitting the mathematical expressions of the expected number of detections to the observed data.

For each point count, the land area surveyed (represented as A_{pc}) was calculated as the area of the circle covered by the 150 m radius; it is thus:

$$\begin{aligned} A_{\text{point count}} &= \pi \times 150 \text{ m}^2 \\ &= 7.07 \times 10^4 \text{ m}^2 \end{aligned}$$

For mixed-species flock observation, because the observation was not conducted at clear-cut sampling units, we considered an overall rectangular area covered by the total effort of flock observation for each land-cover type, as an approximation of the area surveyed for flocks within

the land-cover type in question. Correspondingly, we combined flock data within each land-cover type to tally the total number of individuals/groups detected in flocks for a given species/genus. The length of this rectangular area (represented as L) was determined by (1) the total number of point count stations for the land-cover type in question (represented as n, which was known; Supplementary Table 3), (2) the typical inter-station distance of 250 m, and (3) an additional 10 m on either end of the rectangle to represent the 10 m distance observers were allowed to wander off the point count station for flock observation. The width of this rectangular area was 20 m, because observers were allowed to wander off 10 m on each side of the travel route between point count stations to observe flocks. L is thus expressed as:

$$L = (n-1) \times 250 + 10 + 10 \text{ m}$$

The overall land area surveyed for flocks within each land-cover type (represented as A_f) is thus expressed as:

$$\begin{aligned} A_f &= L \times 20 \text{ m}^2 \\ &= 20 \times [(n-1) \times 250 + 20] \text{ m}^2 \end{aligned}$$

With known A_{pc} and A_f , we were thus able to mathematically express the expected number of individuals/groups detected during point count and flock observation using parameters pertaining to population density and detection probability, and estimate these parameters by fitting the expressions to observed data using the maximum likelihood approach.

For the analysis of household interview data, we first calculated the annual per ha sale and cost (in US\$ and labor days) for each household, GFGP forest type and tree species, based on forest product yield and unit price, length of production cycle, and various aspects of production cost during initial forest establishment and subsequent maintenance. We in turn calculated the annual per ha profit by subtracting all available aspects of production cost from

the annualized gross rents, including initial cost of forest establishment, annual maintenance cost as directly reported by households, and harvest cost. We applied a discount rate of 5% ($r=0.05$) to production sale, cost and labor input based on the 2015 one-year lending rate of the People's Bank of China (range 4.35-6%²⁷). For data from households with mixed forests that provided information on more than one species, such calculation involved all species for which data were available through weighted sum based on the production area of each species. We did not use mixed forest-owning households that provided production or labor estimates for only one tree species to estimate the profit or labor intensity of mixed forest.

Among the three main tree species used in GFGP in the study region, bamboo is generally harvested every year, while eucalyptus and Japanese cedar have a harvest (i.e. clear-cut) cycle of around seven years and 20 years, respectively. For households that did not report the number of years it took for bamboo to start producing, we assumed harvest started in the third year after forest establishment and used a 20 year time span of which production happened in 18 years to calculate average annual sale. For bamboo and eucalyptus forests, we calculated the annualized net rent and labor input over the harvest cycles (harvest cycle of eucalyptus was directly reported by respondent households) with the 5% discount rate. For Japanese cedar forest, forest production typically entailed a one-time clear-cut at the end of each production cycle, with 2-3 rounds of selective harvest before the final clear-cut. We assumed that selective harvesting of these forests happened at the mid-point of the reported production cycle. The net rent was therefore a summation of the net present value (NPV) for the clear-cut (full production cycle) and the NPV of the reported selective harvest. As with bamboo and eucalyptus, we applied the discount rate of 5% to calculate annualized net rent and labor input.

We conducted all analyses using multiple linear models. For the self-reported percentage of household income contributed by forest production, visualization of the distribution of the self-reported percentages suggested possible outliers toward the high end of the values. We thus used the Tietjen-Moore test for outliers ¹⁹ to identify estimates with excessively high percentages ($P < 0.05$) and eliminated these outliers. This resulted in the removal of four data points (all 100% despite very small household land-holding size). We then tested for the difference in this percentage among different types of GFGP forest, but additionally included forest area as a nuisance covariate because of its obvious relationship to the response variable. For annual per ha profit and labor intensity, we included forest type as the only covariate. To avoid the specific discount rates driving our conclusions, we additionally used alternative discount rates ($r=0$, 0.0125, and 0.025; one-year interest rate for personal saving was 1.35-1.75% as of October 24th, 2015 ²⁷) for the full set of analysis. Results based on all discount rates are presented in Supplementary Table 6.

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