Supplementary Material

Contrasting impacts of climate change on protection forests of the Italian Alps

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S1. Extended Materials and Methods

S1.1 Site-specific inputs

For each simulated site, ForClim require site-specific parameters that are typically derived from measurements – if available – or site descriptions for each stand (Table S1). A slope and aspect correction factor (*kSlAsp*), with values ranging from -2 for steep north facing slopes to +2 for steep south facing slopes was derived from slope and exposition which were measured directly in the field (for sites based on sample plots) or derived with a DEM at 10 m resolution (for sites from angle count sampling; Table S1). Soil conditions are expressed by two input parameters such as soil water holding capacity (or bucket size, *kBS*) and soil available nitrogen (*kAvN*), which we derived from the descriptions of the forest types of South Tyrol (Autonomous Province of Bolzano/Bozen, 2010). In this publication, each local forest type has an associated estimate of soil water availability and nutrient availability. As these estimate were unitless and by classes with a range of uncertainty, we used the averages of the values of the upper and lower limits of the inner, darker box (see example in Figure S1) and converted into values within the typical ranges in ForClim used in previous application studies in the Alps (Rasche et al., 2011; Mina et al., 2017; Huber et al., 2021) (e.g., between 60 and 100 kg/ha*year for kAvN, where ~ 60 = poor soils, ~ 80 = normal soils, ~ 100 = nutrient-rich soils). In case a forest site was located at the edge between two different forest types, we averaged the estimates from the descriptions of both forest types.

Browsing pressure (*kBrPr*) is a parameter that affects seedling survival probability and accounts for the impacts of ungulates on regeneration at the local level (Didion et al., 2011). Despite a common browsing pressure parameter at site-level, regeneration of the tree species might be affected differently depending interspecific differences in species-specific palatability (Table S4). For our sites, *kBrPr*, expressed in %, was derived from assessments and field notes made during the collection of the forest data (i.e., severity of damage from ungulate to regeneration; low-medium-high) and from the descriptions in the publication of the forest types of South Tyrol.

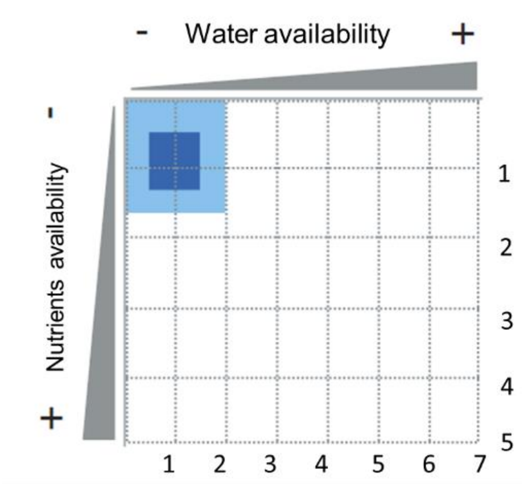

Figure S1. Site-specific table of distribution of water and nutrients of an example forest type of South Tyrol. Water availability is expressed in 7 classes (very low to very high water holding capacity), while nutrients availability is expressed in five classes (poor to rich soil in terms of available nitrogen). Modified from (Autonomous Province of Bolzano/Bozen, 2010).

Table S1. Additional information for the study sites: site-specific parameters given in ForClim (*kBS:* bucket size, *kAvN*: available nitrogen; *kBrPr*: browsing pressure, *kSlAsp*: slope and aspect correction factor), sampling method used for stand initialization and the sampling year (see section S1.2), and rock type and rock density needed for the calculation of the rockfall protection indices (see section 2.3 of the main manuscript).

Site	kBS (cm)	kAvN (kg/ha * year)	kBrPr (%)	kSlAsp (-)	Sampling method	Sampling year	Rock type	Rock density (kg/m³)
MON_SpF1	13	76	15	-1.7	Angle count	2016	Orthogneiss	2,700
MON_Ps	7	70	10	1.21	Sample plot	2022	Granite	2,600
MON_SpF2	11.5	78	10	-1.54	Sample plot*	2022	Granite	2,600
MON_B	9.5	76	10	1.58	Sample plot	2022	Dolomite	2,650
MON_SpFB	10	72	10	1.46	Sample plot	2021	Rhyolite	2,350
MON_Sp	13	78	10	-0.93	Sample plot	2021	Paragneiss	2,725
SUB_Sp1	12	76	10	-1.26	Angle count	2019	Paragneiss	2,725
SUB_Sp2	11	74	10	1.1	Sample plot	2021	Paragneiss	2,725
SUB_Sp3	11.5	74	25	0.28	Angle count	2012	Orthogneiss	2,700
SUB_LPc1	9	74	30	-1.81	Sample plot*	2022	Paragneiss	2,725
SUB_LPc2	14	74	10	-1.47	Sample plot	2021	Limestone	2,400

* sites initially selected from forest management plans but with missing a complete set of angle count sampling data, thus forest data was deliberately collected using a sample plot method.

S1.2 Forest stand initialization

To initialize ForClim from current forest conditions, forest stand data with information at the level of individual trees (i.e., species, diameters) are required. As reported in section 2.1 of the main manuscript, forest sites were selected from two province-wide datasets that used different methodologies to survey individual tree data in the field.

Forest inventory plots. Data collected within the Biodiversity Monitoring South Tyrol (Hilpold et al., 2023) used small sample plots based on a simplified protocol of the third phase of the Italian National Forest Inventory (Gasparini et al., 2022). This consists in establishing concentric circles around the plot centre characterized by different levels (1 to 4) concerning the type of surveyed data (Figure S2). On level 1 (25 m radius), stand variables such as forest category, mixing degree, origin are assessed visually, in addition to morphological site characteristics such as slope and aspect. On level 2 and 3 (13 m and 4 m radius), all standing trees above 9.5 cm and 4.5 cm of diameter at breast height are recorded, together with the height and crown characteristics of a subset of trees. On these levels, lying and standing deadwood elements are also recorded. On level 4 (two subplots of 2 m radius at direction east and west from the centre) regeneration data is collected by species and height classes. For the purpose of initializing ForClim, standing tree data from level 2 (species, DBH) and site morphological characteristics from level 1 were used. Field notes indicating the presence of other tree species excluded from the sampling plot (i.e., because below DBH threshold or detected closely to the interpretation area) were also used to include other potential tree species in our simulations. The data was then assembled in a patch with an area of 531 m², representing the area formed by level 2 circle, and multiplied 200 times in order to replicate the same structure on the 200 ForClim patches.

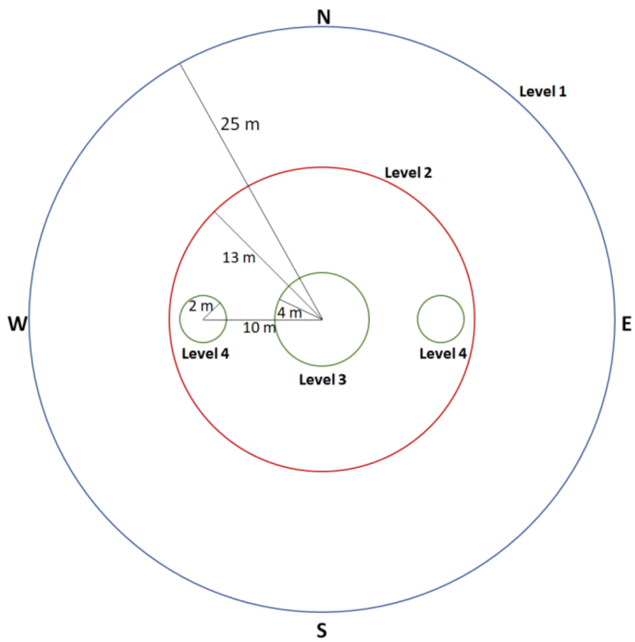

Figure S2. Sample plot design used in the Biodiversity Monitoring South Tyrol (Hilpold et al., 2023) and based on the Italian National Forest inventory. Blue circle (level 1) indicate the interpretation area of 25 m radius, red circle (level 2) the 530 m^2 for the survey of standing trees with DBH > 9.5 cm, the inner green circle (level 3) the 50.2 m^2 for the survey of standing trees with DBH >4.5 cm, and the two green circles (level 4) are the subplots for regeneration data (Gasparini et al., 2022).

Angle count sampling. This type of data is collected by the Province's Forest Services at the renewal of a decadal forest management plan but does not always cover an entire management unit or forest stand. Data from angle count sampling are collected using the mirror relascope. It uses an angle as proportion between diameter of the tree and distance of the tree from the sample point, where "*the tree diameter d will exceed the critical angle only if the distance to the tree is less than a proportional critical distance R, which is a multiple of the tree diameter*" (Bitterlich, 1980). From the sample point, each tree is observed through the relascope; trees fall into the sample if their DBH exceeds the basal area factor (k) of the scale in the mirror relascope (Figure S3). A sampled tree is then assessed in terms of tree species and DBH. Sample points are placed in a grid from 50x50 m to 150x150 m in the management unit of interest.

We retrieved data from all sampling plots covering the forest stands of our interest and grouped into classes of 5 cm per species (example in Table S2; column N Norway spruce and N silver fir state how many trees fall into each class), starting with the threshold value of 6 cm. For further calculation, the average of each class was used (e.g., 13 cm for class 11-15 cm). We then calculated the basal area in m² of each class (g_i). Since in angle count sampling every tree represents the basal area factor (k) used for the sampling ($k = 4$ is being used by the Office of Forest Planning in high forests in South Tyrol), there must be enough stems to add up to this basal area (Bitterlich, 1980). Hence, the representative basal area/hectare (RBA in Table S2) is derived by dividing the basal area factor k by the actual basal area g_i. The number of stems/species/DBH class per point (Norway spruce N/pts and silver fir N/pts) was then calculated by dividing the stem number/species (N Norway spruce and N silver fir) for each class by the number of points (12, as in the example). The result is average stems/species/DBH class per point (i.e., there is an average of 0.25 silver firs with a DBH class of 13 cm per sample point). Lastly, the number of stems/species/point of each class was multiplied by the representative stem number/ha (g_i), obtaining the number of stems/species/DBH class per hectare (Norway spruce N/ha and silver fir N/ha in Table S2). The data referred to the hectare were randomly distributed in 19 patches of 531 m² (10,000 m² / 531 m² ~ 19), which were then replicated ten times, reaching 190 patches. In case the stem number/ha did not fit evenly in 19 patches, random trees were added in random patches one by one until all trees/ha were placed in a patch. Ten additional patches were sampled randomly from the initial 19 patches to reach the total number of patches (200) needed for initializing ForClim.

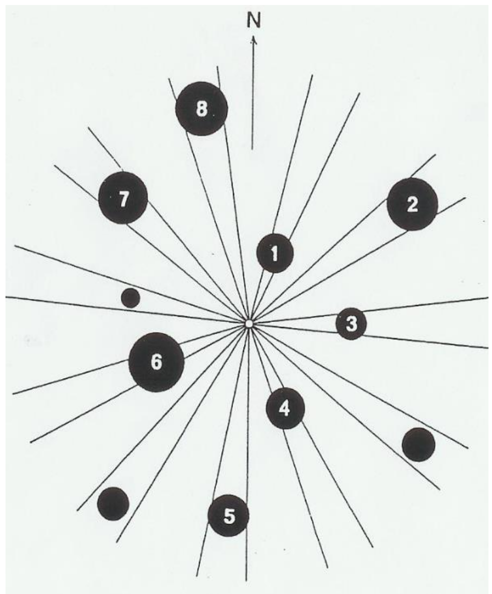

Figure S3. Functioning of the mirror relascope in angle count sampling (Bitterlich, 1980). Trees with a DBH exceeding the critical angle (numbered circles) fall into the sample, while threes with a smaller DBH do not (unnumbered circles).

Table S2. Example of calculating stems/ha using shortened data from site MON_SpF1, where $\boldsymbol{g_i}$= representative basal area per class, N = number of stems. Number of sample points = 12.

Class	N Norway spruce	N silver firs	g_i [m²]	RBA	Norway spruce N/pts	Silver fir N/pts	Norway spruce N/ha	Silver fir N/ha
8	0	2	0.0050	796		0.17		133
13	0	3	0.0133	301		0.25		75
18	2	3	0.0254	157	0.17	0.25	26	39
23	2	7	0.0415	96	0.17	0.58	16	56
28	4	5	0.0616	65	0.33	0.42	22	27
33	2	14	0.0855	47	0.17	1.17	8	55
38	1	18	0.1134	35	0.08	1.50	3	53
43	2	9	0.1452	28	0.17	0.75	5	21

In each site, simulations were run with a selected number of species (i.e., not all 30+ species parameterised in ForClim). In addition to the tree species surveyed in the field and present in the stand initialization, we allowed a few other species according to the forest types of South Tyrol (Autonomous Province of Bolzano/Bozen, 2010), which include a description of the presence of sporadic species (e.g., *Sorbus aria, Sorbus aucuparia, Popolus tremula, Betula pendula, Corylus avellana*) in each forest category. These species were allowed to establish in those sites where descriptions recoded their presence; however, given the timeframe of our simulations (ca. 80 years) their effect was negligible and were merged under *Other species* in Fig. 4 and Fig. S8.

S1.3 Model testing and parameterization

Although ForClim has been extensively tested and validated in its ability to reproduce forest structure and composition in Central European and Alpine forests (Bugmann, 1996; Wehrli, 2005; Rasche et al., 2011), this study represents the first application of the model in the Italian Alps. Before running the simulation experiment, we evaluated the behaviour of ForClim to assess whether the model was able to maintain current the forest composition and productivity under baseline climate and without the effect of management. In the absence of long-term forest records such as yield tables and multi-decadal forest inventory datasets (e.g. as done in Irauschek et al., 2021), we evaluated model performance by testing its ability to maintain current species composition and productivity under current climate.

First tests from initialized stands under baseline climate showed sudden decreases of Norway spruce and European beech basal area in a few sites only (e.g., MON_B and MON_SpFB in the external Alps and MON_SpF1 and SUB_Sp3 in the inner Alps; Figure S4). This was due to an overestimated drought-induced mortality as both species have been parameterised on conditions that are typical of Central Europe (Bugmann, 1994). Our stand data and records from management plans, instead, showed values of basal area and growth for Norway spruce and European beech that are typical for mountain forests with medium-high productivity (e.g., 50 m^2/ha in site MON_B and 54 m^2/ha in site MON_SpFB). To avoid an unrealistic reduction of these species at the onset of the simulation and to assure that the model was able to maintain the same levels of current basal area under baseline climate, we calibrated the species-specific drought tolerance parameter (*kDrTol*, Table S4) for Norway spruce and European beech. We simulated forest development from initialized stands in sites MON_B, MON_SpFB, MON_SpF1 and SUB_Sp3 and increased the *kDrTol* for spruce and beech in steps of 0.01 but maintaining the parameter in the same range of drought tolerance compared to the other species using the ranking reported by Niinemets and Valladares (2006). *kDrTol* was eventually modified from 0.15 to 0.19 for Norway spruce and from 0.25 to 0.29 for European beech (see Table S4). For consistency, we applied these changes to all simulation sites; differences in simulation outputs in terms of species-specific basal area for the remaining sites before and after calibration were negligible. The calibrated parameters still yielded a reduction in the long-term of both Norway spruce and European beech in some the tested forest sites (e.g., MON_B, MON_SpFB; see Figure S4), which is not unrealistic given current structure in these two sites but avoiding the sudden collapse of basal area due to a likely initial mismatch between the computed drought index and drought-tolerance parameter. The (slightly) modified parameters also reflected possible phenological adaptations of these two species, as shown in past studies. For example, the Eastern Alps feature a variation in haplotypes of Norway spruce (Mengl et al., 2009; Konrad et al., 2011). Kapeller et al., (2012) found that Norway spruce populations in Austria exhibit large genetic variation with a natural developed adaptation to different climatic optima. Also in the Trentino-South Tyrol region, genetic differentiation between populations were found to be significant and biologically important, depending on their geographical location (Di Pierro et al., 2017). European beech also showed co-variation of significance between environmental and genetic gradients in the French Alps (Capblancq et al., 2020). The issue of parameterization with ForClim for tree species and possible genotypical adaptations for regions outside their original range of calibration, however, requires further investigations (see also section 4.3 of the main manuscript).

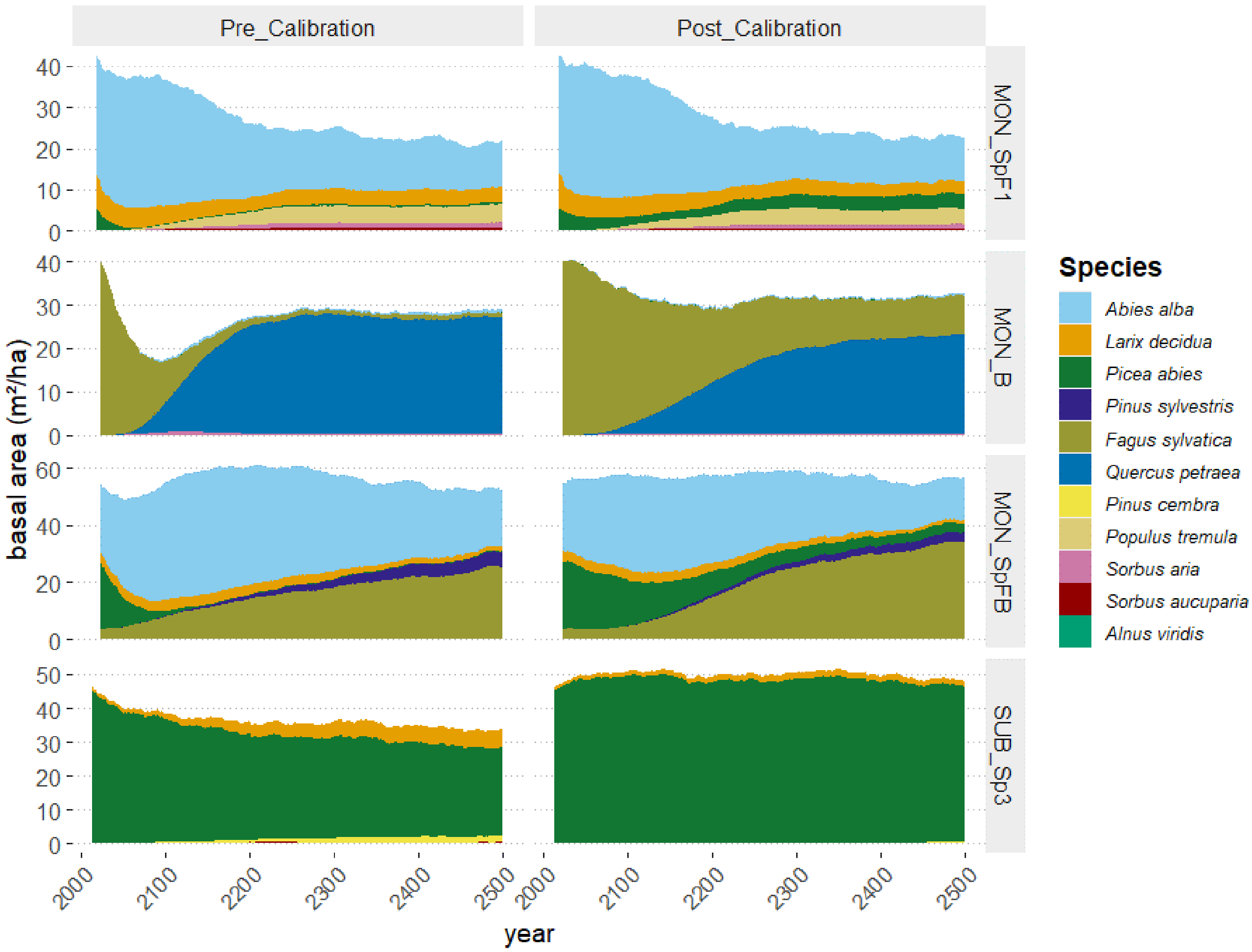

Figure S4. Test simulations on three sites used for calibration of *kDrTol* parameter for European beech and Norway spruce. The figure shows long-term simulations (500 years) from initialized forest conditions under baseline climate and without management.

S1.4 Forest management scenario

In order to create scenarios as realistic as possible, each site was given a specific management regime (Table S3). Information about current management interventions were taken, when available, from the respective forest management plans in each forest site. Management plans contain information about maximum allowed yield volume over the decade following the renewal (or creation) of the plan, as well as descriptions of the type of harvesting to be executed. Since not all of the sites possessed a detailed management plan, additional information on silvicultural interventions were taken from the forest types of South Tyrol (Autonomous Province of Bolzano/Bozen, 2010) and from expert knowledge in consultation with the Office of Forest Planning. Each forest type features a corresponding description of typical management strategies, silvicultural felling and expected growth and productivity, which we used as baseline information to derive a current management regime to be implemented in ForClim. Two subalpine sites (SUB_LPc1, SUB_LPc2) were simulated without any silvicultural interventions, since harvesting is typically not carried out in these high-elevation forests due to difficulties in accessibility and prohibitive costs of timber extraction (Office of Forest Planning of the Autonomous Province of South Tyrol – personal communication, June 2022).

We simulated future silvicultural interventions using two harvesting algorithms implemented in the management submodel of ForClim, such as mountain forest plentering (MFP) and target cutting. MFP mimic a groupwise removal of trees eligible for harvesting in small patches. The aim is to induce regeneration and improve the heterogenous structure of the forest by removing trees in small patches above a defined target diameter until a target percentage of the standing volume is reached (Thrippleton et al., 2020). Harvesting is only executed of a sufficient timber volume given the criteria is present; an intensity parameter denotes the number of trees per cohort to be removed and a cycle length parameter the time step of interventions. The target cutting function, instead, removes trees – of all or only certain species – that have reached a certain diameter (Rasche et al., 2011). Here the intensity parameter denotes the proportion of trees to be removed within the patches. Details of the parameters of the management scenarios for each site where we simulated harvesting are given in Table S3.

Table S3. Specifics of the management scenarios per site with harvest type, target diameter, intensity parameter, target volume, cycle length and harvested species.

Site	Harvest type	Target DBH [cm]	Intensity [-]	Target volume [%]	Cycle length [y]	Harvested species
MON_SpF1	MPF	60	0.1	8	30	*P. abies, A. alba, L. decidua*
MON_Ps	MPF	40	0.3	7	30	*P. sylvestris*
MON_SpF2	MPF	60	0.8	8	20	*A. alba, P. abies*
MON_B	TC	70	0.2*	-	40	*F. sylvatica*
MON_SpFB	MPF	55	0.5	7	40	*P. abies, A. alba, F. sylvatica*
MON_Sp	MPF	60	0.5	9	20	*P. abies*
SUB_Sp1	MPF	60	1	8	10	*P. abies, L. decidua*
SUB_Sp2	MPF	60	1	7	20	*P. abies*
SUB_Sp3	MPF	55	0.5	7	20	*P. abies, L. decidua, P. cembra*

**Intensity in site MON_B (harvest type TC) indicates the percentage of trees harvested within the patch (differently from harvest type MPF where intensity denotes number of trees per cohort).*

Table S4. Species-specific parameters in ForClim used in this simulation study. kType = Crown type [D = deciduous, E = evergreen, describes the relationship between DBH and foliage weight], kHMax = Maximum possible tree height [m], kAMax = Maximum age [yr], kDMax = Maximum DBH [cm], kG = growth rate parameter [cm/yr], kDDMin = Minimal annual degree-day sum [°C*days], kWiTN = Minimum winter temperature tolerated [°C], kWiTX = Maximum winter temperature tolerated [°C], kDrTol = Drought tolerance parameter [unitless, scale 0 to 1], kNTol = Nitrogen tolerance parameter [unitless, scale 1 to 3], kBrow = Browsing sensivity [unitless, scale 1 to 5], kLy = Light requirement of tree saplings [unitless, scale 1 to 9], kLa = Light requirement of adult trees [unitless, scale 1 to 9], kLQ = Leaf litter quality [1-3, fast to slow litter decay], kRedMax = Maximal reduction of kHmax [%], kWD = Wood density [t/m³].

For more information on ForClim species parameters see (Bugmann, 1994).

kID	kName	kSName	kType	kHMax	kAMax	kDMax	kG	kDDMin	kWiTN	kWiTX	kDrTol	kNTol	kBrow	kLy	kLa	kLQ	kRedMax	kWD
0	*Abies alba*	AAlb	E5	60	700	200	296	650	-6	6	0.23	3	5	0.03	1	2	44	0.4
1	*Larix decidua*	LDec	D2	54	1000	250	400	350	-11	-1	0.25	2	4	0.5	9	3	38	0.46
2	*Picea abies*	PAbi	E5	63	930	200	342	350	-99	-1	0.19	2	2	0.05	5	3	34	0.4
3	*Pinus cembra*	PCem	E5	26	1050	200	198	350	-11	-6	0.23	1	4	0.075	5	3	38	0.42
4	*Pinus montana*	PMon	E5	23	300	50	239	500	-99	-3	0.37	1	3	0.5	9	3	38	0.42
5	*Pinus sylvestris*	PSyl	E4	48	760	150	393	500	-99	1	0.37	1	3	0.4	8	3	38	0.42
6	*Taxus baccata*	TBac	E5	22	2110	350	175	1050	-5	8	0.3	3	5	0.03	1	2	38	0.67
7	*Acer campestre*	ACam	D2	25	300	150	210	950	-99	8	0.33	3	4	0.2	6	2	80	0.52
8	*Acer platanoides*	APla	D3	35	380	200	360	850	-17	10	0.25	4	4	0.075	4	2	58	0.52
9	*Acer pseudoplatanus*	APse	D3	40	600	250	338	650	-99	8	0.25	4	4	0.05	3	2	50	0.52
10	*Alnus glutinosa*	AGlu	D2	40	240	150	380	750	-16	11	0.08	4	1	0.2	6	1	68	0.45
11	*Alnus incana*	AInc	D2	25	150	100	218	500	-99	7	0.16	1	1	0.2	7	1	68	0.45
12	*Alnus viridis*	AVir	D2	6	110	25	476	350	-99	-6	0.16	2	1	0.3	7	1	68	0.45
13	*Betula pendula*	BPen	D1	30	220	100	448	425	-99	9	0.25	1	2	0.5	9	2	63	0.51
14	*Carpinus betulus*	CBet	D3	35	300	150	360	950	-9	9	0.16	3	3	0.075	4	1	56	0.63
15	*Castanea sativa*	CSat	D3	35	500	350	375	1050	-99	10	0.33	1	2	0.1	5	2	40	0.48
16	*Corylus avellana*	CAve	D3	15	100	50	245	850	-16	9	0.33	3	2	0.2	6	1	68	0.58
17	*Fagus sylvatica*	FSyl	D3	52	500	250	307	850	-4	9	0.29	3	2	0.03	1	2	43	0.58
18	*Fraxinus excelsior*	FExc	D2	42	300	250	363	850	-17	8	0.25	5	3	0.075	5	1	40	0.57

Table S4. (Continued)

kID	kName	kSName	kType	kHMax	kAMax	kDMax	kG	kDDMin	kWiTN	kWiTX	kDrTol	kNTol	kBrow	kLy	kLa	kLQ	kRedMax	kWD
19	*Populus nigra*	PNig	D2	40	300	250	394	750	-99	12	0.16	5	2	0.3	7	2	78	0.35
20	*Populus tremula*	PTre	D2	42	200	150	390	425	-99	9	0.25	1	2	0.3	7	2	72	0.35
21	*Quercus petraea*	QPet	D3	50	1000	350	378	950	-5	9	0.33	2	4	0.2	7	2	43	0.58
22	*Quercus pubescens*	QPub	D3	25	500	150	226	1150	-99	9	0.41	1	4	0.3	8	2	42	0.58
23	*Quercus robur*	QRob	D3	52	2000	350	376	1050	-17	9	0.25	3	4	0.2	7	2	42	0.58
24	*Salix alba*	SAlb	D1	35	200	250	403	650	-99	12	0.08	5	2	0.3	7	2	68	0.35
25	*Sorbus aria*	SAri	D2	23	200	100	230	750	-99	12	0.33	3	4	0.3	8	1	68	0.64
26	*Sorbus aucuparia*	SAuc	D1	27	140	100	205	500	-99	7	0.25	1	4	0.1	6	1	68	0.64
27	*Tilia cordata*	TCor	D3	40	1000	350	365	750	-19	8	0.33	3	4	0.075	5	2	40	0.43
28	*Tilia platyphyllos*	TPla	D3	40	1000	350	365	850	-99	8	0.25	4	4	0.075	5	2	40	0.43
29	*Ulmus glabra*	UGla	D3	43	500	300	361	850	-16	11	0.16	5	3	0.075	5	1	40	0.56
30	*Pseudotsuga menziesii*	PMen	E3	54	700	200	403	633	-15	-5	0.4	3	1	0.22	7	3	49	0.4

S2. Supplementary Figures and Tables

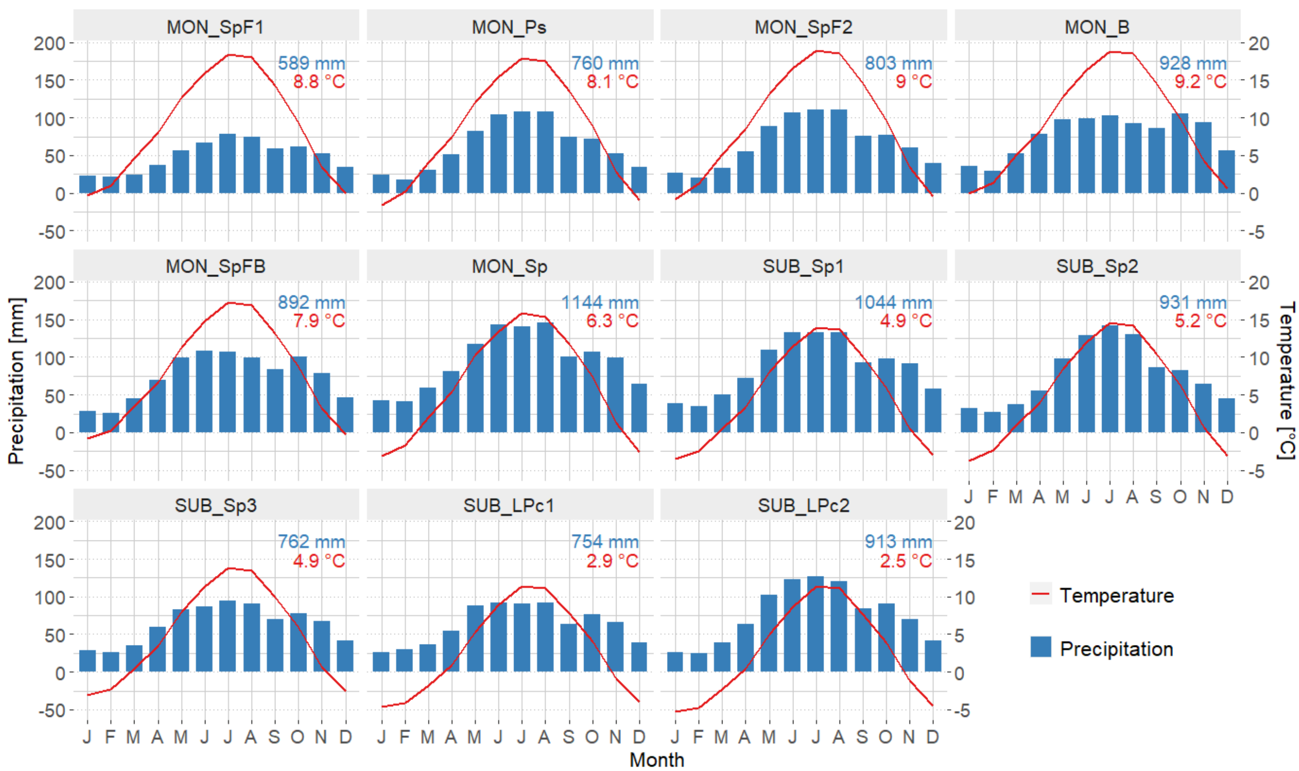

Figure S5. Long-term means (1980-2010) of average temperatures and precipitation sums for the selected sites. Values on the top right of each panel represent mean annual temperature (red) and total annual precipitation (blue).

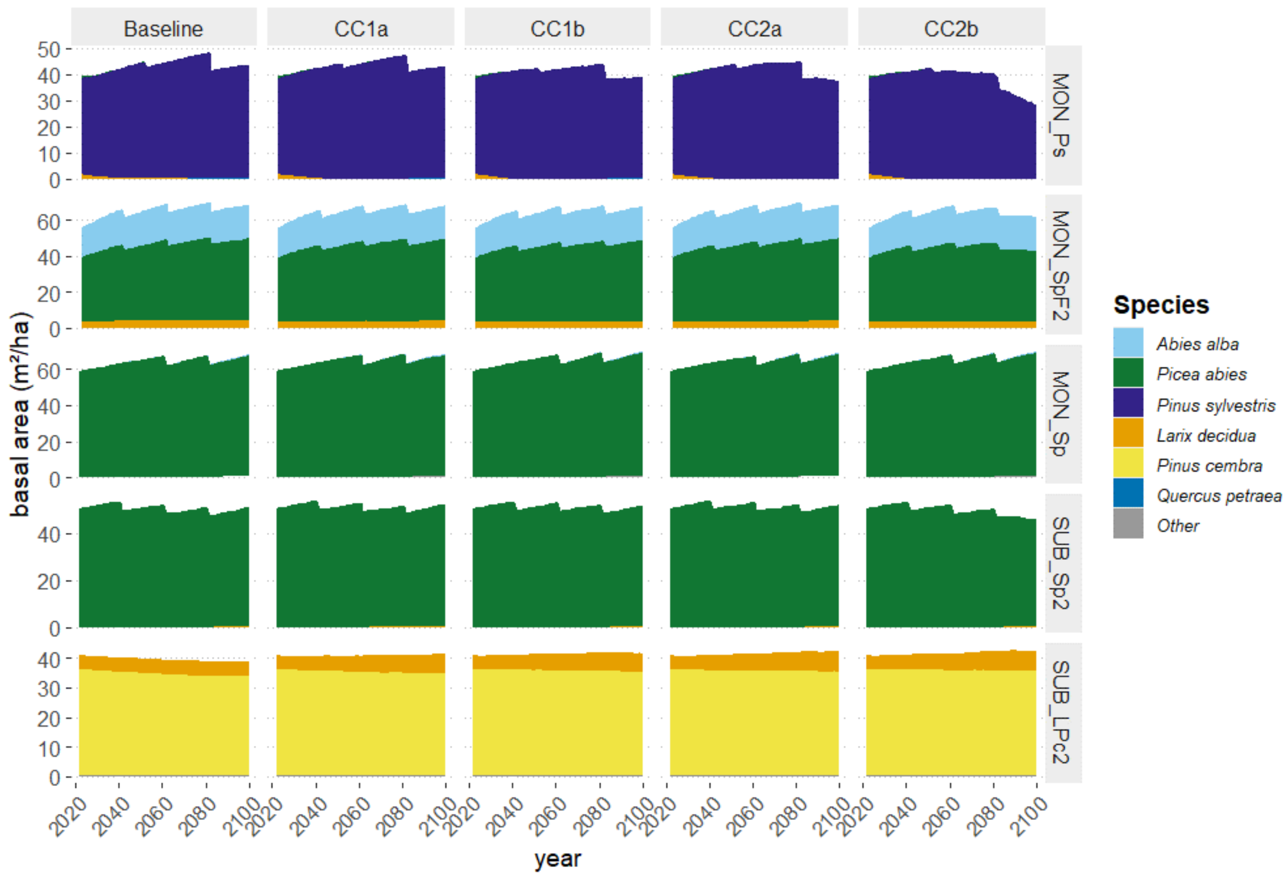

Figure S6. Simulated change in species-specific basal area under baseline and climate change scenarios for the remaining forest sites not displayed in Figure 4.

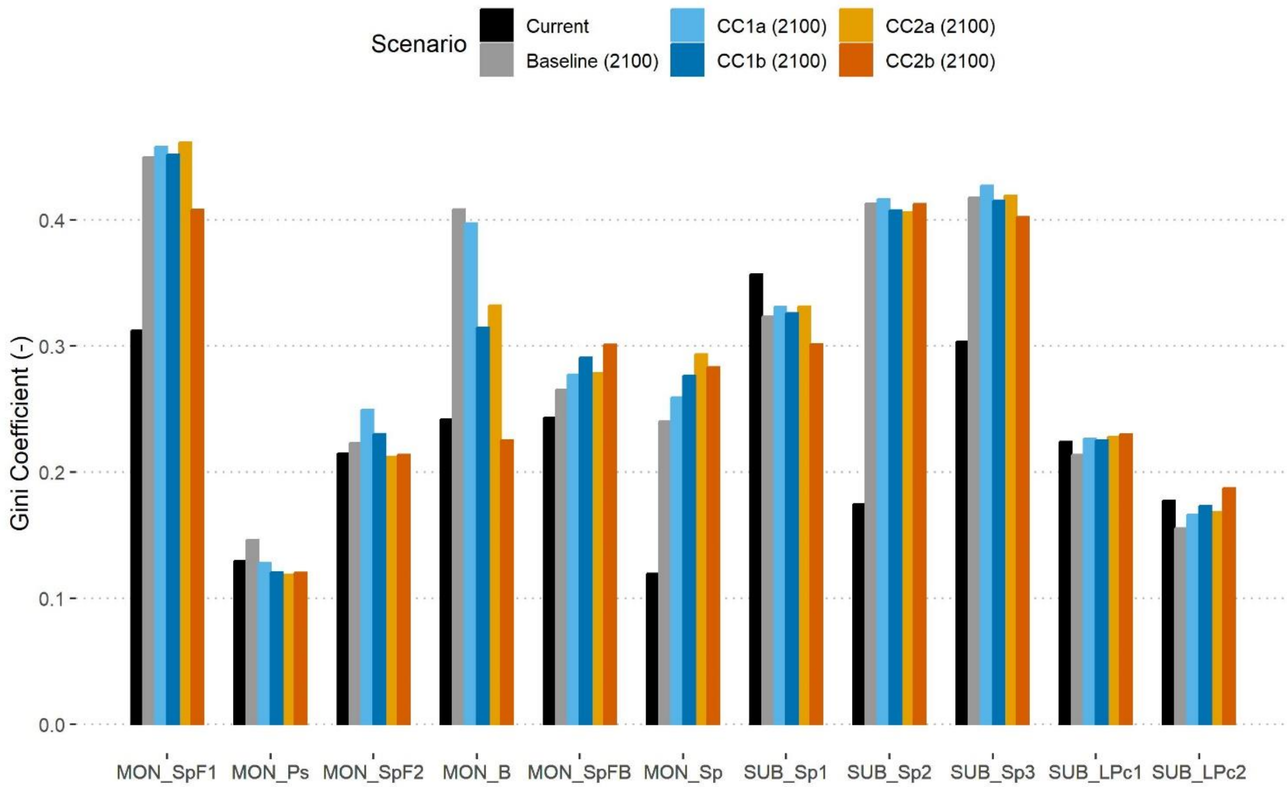

Figure S7. Projected changes of the Gini coefficient of tree size inequality (unitless) for all forest sites under baseline climate and four climate change scenarios compared to simulation start (Current). The higher the values of the Gini coefficient, the higher the tree size diversity within the forest stand.

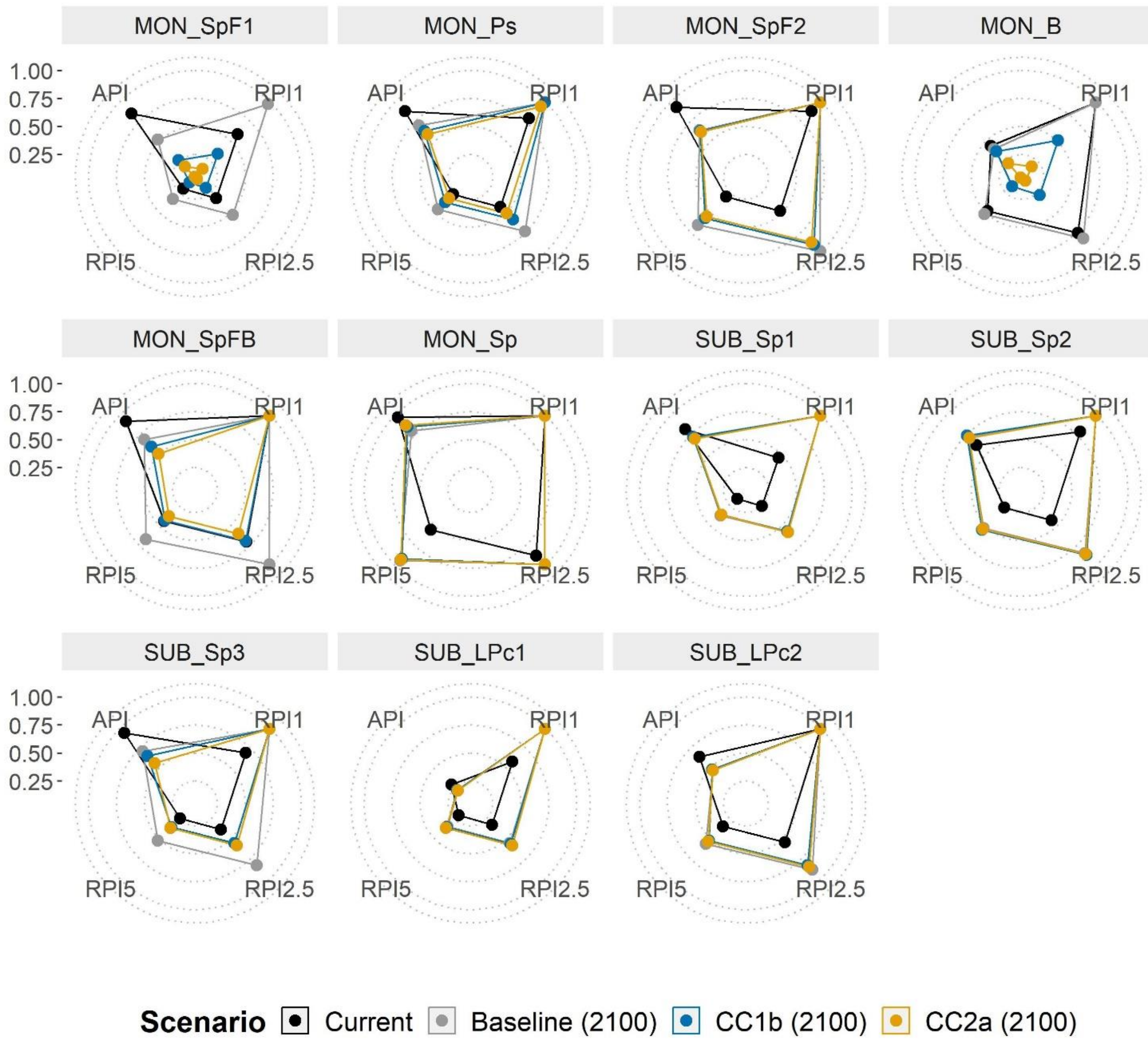

Figure S8. Projected changes in protection indexes for the forest sites under baseline climate and the remaining two intermediate climate change scenarios (CC1b, CC2a) compared to simulation start (Current). API = Avalanche Protection Index, RPI = Rockfall Protection Index (see section 2.3 for explanations of differences between RPI1, RPI2.5 and RPI5).

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