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1 **The effect of buffer strip width and selective logging on streamside polypore communities**

2

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19 **Abstract**

20 Preserving streamside forest habitats or buffer strips is considered to reduce forestry related  
21 biodiversity loss in commercial forest landscapes. However, it is still unclear what type of  
22 management in and near streamside forests can be undertaken without compromising their  
23 biodiversity and its natural change through succession. We tested the before-after-control impacts  
24 of forested buffer strips (15 or 30 m wide, with or without selective logging) preserved after clear-  
25 cutting, on the changes of polypore communities in streamside boreal forests in Finland.  
26 Manipulations in 28 sites produced four treatment classes, the community compositions of which  
27 were compared with 7 unmanaged controls before and 12 years after the manipulations. The  
28 polypore community composition in 15 m wide buffer strips changed differently than that in  
29 controls, and resembled the community composition typically found in production forests.  
30 Moreover, selective logging tended to homogenize polypore communities. These responses of  
31 polypore communities indicate that the natural biodiversity and succession of streamside forests  
32 was disturbed in both 15 m wide and selectively logged buffer strips. Streamside forests in non-  
33 logged 30 m wide buffer strips seemed to retain the natural polypore community composition and  
34 succession, at least during the 12 years period.

35

36 **Key words:** buffer zone, dead wood, key habitat, partial harvesting, riparian forest

37

## 38 **1 Introduction**

39 Most of the boreal forests are under timber production, which has decreased their biodiversity  
40 values by homogenizing forest structures and species compositions (Esseen et al. 1997;  
41 Kuuluvainen and Gauthier 2018). Preserving small-scaled forest patches, which provide valuable  
42 habitat for specialized and red-listed species, is considered to reduce forestry related biodiversity  
43 loss in forest landscapes (Ericsson et al. 2005; Timonen et al. 2010, 2011). These assumed  
44 biodiversity-hotspots are called woodland key habitats and they are protected by law or forest  
45 certification in most Fennoscandian countries (Timonen et al. 2010). However, it is still unclear  
46 what type of management, if any, can be allowed in and near these habitats without disturbing their  
47 biodiversity in the long term (Marczak et al. 2010; Timonen et al. 2010, 2011; Hylander and  
48 Weibull 2012; Kuglerová et al. 2014). Streamside forests represent one of the most common key  
49 habitat types in Fennoscandia (Timonen et al. 2010; Selonen and Kotiaho 2013) and their retention  
50 is a part of sustainable forest management internationally (e.g., Lee et al. 2004; Sweeney and  
51 Newbold 2014).

52 Most commercial boreal forests are still managed under rotation forestry with clear-cuts  
53 (Kuuluvainen and Gauthier 2018), while streamside forests are retained by leaving a forested buffer  
54 strip between the stream and the clear-cut area (Timonen et al. 2010; Kuglerová et al. 2014). The  
55 width of the strip varies but they can be narrow (from few meters to tens of meters) (Lee et al. 2004;  
56 Selonen and Kotiaho 2013) and prone to strong edge effects (Murcia 1995), which extend at least  
57 20-50 m into the forest from the edge (Aune et al. 2005; Ylisirniö et al. 2016). Edges are exposed to  
58 disturbances and they are usually warmer and drier than inland forests (Murcia 1995). Moreover,  
59 many common generalist species in boreal forests favor edges and outcompete specialized species  
60 that require closed forest structures (Ruete et al. 2016). Therefore, the area of natural streamside  
61 habitat, which is not under the edge effect, can be very small or non-existent (Aune et al. 2005).

62 Previous studies in streamside habitats have suggested that the width of the buffer strips should be  
63 at least 30 to 45 m to preserve the natural microclimatic conditions and community composition of  
64 the streamside habitat biodiversity (Selonen and Kotiaho 2013; Sweeney and Newbold 2014; Oldén  
65 et al. 2019a, 2019b).

66 The forests in the immediate surroundings of streams have a special microclimate and forest  
67 structure that provide habitats for a diverse range of species (Naiman and Décamps 1997). The  
68 amount and diversity of dead wood, which is a critical resource for many forest-dwelling species,  
69 can be higher in streamside habitats than in other production forests (Siitonen et al. 2009; Sweeney  
70 and Newbold 2014). In Fennoscandia, the average amount of dead wood in managed forests is 5 m<sup>3</sup>  
71 ha<sup>-1</sup> or below, whereas for many dead wood dependent species the critical threshold may be around  
72 20 m<sup>3</sup>ha<sup>-1</sup> (Junninen and Komonen 2011). Siitonen et al. (2009) reported that the average volume of  
73 dead wood in streamside habitats in southern Finland was 11.7 m<sup>3</sup> ha<sup>-1</sup> and that only 15% of  
74 streamside forests fulfilled the threshold of 20 m<sup>3</sup> ha<sup>-1</sup>.

75 Dead wood dependent polypores are pathogens of living trees and decomposers of dead trees and  
76 therefore crucial for forest ecosystems' natural functioning and succession (Junninen and Komonen  
77 2011; Stokland et al. 2012). In addition, as polypores are sensitive to changes in substrate quality  
78 and abiotic conditions, they are widely used as biological indicators in ecological research (Halme  
79 et al. 2017). Findings about the importance of streamside forests in supporting polypore  
80 communities are controversial (Junninen and Kouki 2006; Hottola and Siitonen 2008). Streamside  
81 habitats can support polypore species richness but their function in the conservation of threatened  
82 polypores is uncertain. In general, key habitats, such as streamside forests, are often too small in  
83 size and isolated to preserve viable populations of specialized and rare species, especially if  
84 surrounded by clear-cuts (Sippola et al. 2005; Ylisirniö et al. 2016). Several studies have reported

85 that the composition of polypore communities changes near forest edges (Snäll and Jonsson 2001;  
86 Siitonen et al. 2005; Ruete et al. 2016).

87

88 Streamside forests are often productive and thus interesting from the economic point of view  
89 (Lundström et al. 2018). Therefore, leaving wide buffer strips next to clear-cuts can evoke  
90 significant costs. The Finnish Forest Act (*Forest act* 2013) allows selective logging in the  
91 streamside key habitats, provided their characteristic features, i.e. natural forest structure,  
92 microclimatic conditions and growing conditions, are not altered. If selective logging can be  
93 performed without altering these characteristic features, it could be a way to decrease the costs of  
94 retaining wider buffer strips. Relative to clear-cutting, selective logging can reduce forestry related  
95 biodiversity loss (Joelsson et al. 2017; Vanha-Majamaa et al. 2017; Oldén et al. 2019a), but it  
96 nevertheless is likely to disturb microclimatic conditions and species composition relative to  
97 unmanaged old-growth forests (Bader et al. 1995; Sippola et al. 2001; Oldén et al. 2019b).  
98 However, the impacts of selective logging on the changes of species community composition are  
99 still poorly understood.

100

101 The aim of this study was to determine the impact of forested buffer strip width and the impact of  
102 selective logging of the buffer strips on the formation of dead wood and on the succession of  
103 polypore species community composition in streamside habitats in Finnish boreal forests. The  
104 streamside habitat was assumed to be the forested area from 0 to 15 m from the stream, which is  
105 included in the buffer strips. The width of the buffer strip between a stream and a clear-cut area (15  
106 or 30 m) and selective logging within it were manipulated forming four buffer strip treatments,  
107 which were compared with unmanaged controls 12 years after treatment loggings. Study forests  
108 were 80–100 years old mature forests and expected to slowly change towards natural old-growth  
109 forest structure and species composition. Therefore, natural changes were likely to occur also in the

110 control sites and our aim was to determine whether the treatments disturb the natural succession.  
111 We tested for differences in changes over time in the formation of dead wood, the number of  
112 polypore species and individuals, the polypore community composition, and the homogenization of  
113 the polypore communities among sites, between treatments and in relation to controls.

114

## 115 **2 Materials and methods**

### 116 **2.1 Study design**

117 Our 35 study sites, representing spruce (*Picea abies*) dominated and mature streamside forests,  
118 were located in production forest landscapes in southern and middle boreal region (Oldén et al.  
119 2019a). There was only one study site along each stream. All of the sites were classified as Forest  
120 Act Habitats meaning that streamside forests were in a natural or nearly natural state. Before the  
121 treatment manipulations, the minimum distance to the nearest clear-cut area was 80 m, sites had not  
122 been managed during recent decades and the dominant trees were 80-100 years old. Thus, forests  
123 were expected to slowly develop towards old-growth conditions. In treatment manipulations, 7 sites  
124 were left as unmanaged control sites and loggings were conducted in 28 sites during the winter  
125 2005-2006. As part of the logging operations, the adjacent upland forest on one side of the stream  
126 was clear-cut and one of four buffer strip treatments was applied between the stream and the clear-  
127 cut area: 30 m wide buffer strip without selective logging (5 sites), 30 m wide buffer strip with  
128 selective logging (8 sites), 15 m wide buffer strip without selective logging (6 sites) or 15 m wide  
129 buffer strip with selective logging (9 sites) (Fig. 1a). In selective loggings, 30% of the basal area of  
130 the forested buffer strip was evenly logged from the whole buffer strip width. The logged trees were  
131 mainly the largest trees. More information on study design and sites is found in Oldén et al. (2019a,  
132 2019b).

133

### 134 **2.2 Data collection**

135 Dead wood and polypores were inventoried in late September – early November 2004 before the  
136 treatments and the inventory was repeated in late September – early November 2017, i.e. 12  
137 growing seasons after the treatments. Dead wood was measured from 0.045 ha study plots and  
138 polypores from 0.1 ha plots (Fig. 1b). In this study, the immediate surrounding of a stream (from 0  
139 to 15 m from a stream) was considered to be the actual streamside key habitat. Therefore in  
140 treatments with a 15 m wide buffer strip, the clear-cut was immediately next to study area whereas  
141 in treatments with a 30 m wide buffer strip, there was a 15 m wide strip (from 15 to 30 m from a  
142 stream) between the study area and the clear-cut (Fig. 1a). We did not have the dead wood data  
143 from 5 sites (one control site, two 30 m wide buffer strip sites with selective logging, and one 15 m  
144 wide buffer strip site with and one without selective logging), so the number of sites with dead  
145 wood data was 30.

146

147 Dead trees and their fragments with a diameter  $\geq 5$  cm and length  $\geq 1.3$  m were inventoried (thus  
148 excluding stumps). For each trunk and a fragment of a trunk, the length, diameter, tree species and  
149 decay stage was recorded. For the whole trunks, the diameter at 1.3 m height was measured, and for  
150 the fragments of the trunks the diameter at the middle of the fragment. The decay stages 1–5 were  
151 classified as follows (Renvall 1995): (1) hard, a knife penetrates by pushing only a few mm into the  
152 wood; (2) relatively hard, knife penetrates 1–2 cm in depth; (3) relatively soft, knife penetrates 3–5  
153 cm in depth, (4) soft throughout, (5) very soft, can be moulded by hand. Volumes of whole dead  
154 trees were calculated based on the volume formulas of spruce (*Picea abies*), pine (*Pinus sylvestris*)  
155 and birch (*Betula pendula* and *pubescens*), the latter of which was applied for all deciduous tree  
156 species (Laasasenaho and Snellman 1983). Volumes of dead tree fragments were calculated using  
157 the formula of a cylinder.

158



159 Polypores were surveyed by observing their fruiting bodies from the dead and living trees with  
160 length  $\geq 1.3$  m and diameter  $\geq 5$  cm at 1.3 m height. Several fruiting bodies of the same species in  
161 one dead or living tree trunk or fragment of a trunk were considered as one individual. Only living  
162 fruiting bodies of perennial species were recorded but both living and dead fruiting bodies of annual  
163 species were recorded. If species identification in the field was not possible, a specimen was  
164 collected and identified under a microscope. The nomenclature and division of species follows  
165 Niemelä (2016) but *Phellinus igniarius* coll. included species *P. igniarius*, *P. alni* and *P. cinereus*,  
166 and *Postia leucomallella* coll. included species *P. calvenda* and *P. rufsecens*. We classified red-  
167 listed species according to Kotiranta et al. (2019).

168

169 Treatment loggings have caused changes in abiotic microclimatic conditions (Oldén et al. 2019b)  
170 and can disturb biotic conditions through altered dead wood dynamics (Mäenpää et al.  
171 unpublished). Early colonizers can produce fruiting bodies soon after the colonization and on the  
172 other hand, the fruiting success of existing species can be disturbed due to changed abiotic  
173 conditions (Jönsson et al. 2008; Moore et al. 2008). Therefore, the early impacts of altered abiotic  
174 and biotic conditions on polypore community succession can be detected after 12 years.

175

## 176 **2.3 Statistical analyses**

### 177 **2.3.1 Dead wood and numbers of polypore species and individuals**

178 Most polypore species are specialized with regards to the tree species, size, mortality factor and  
179 decay stage of the trees (Junninen and Komonen 2011; Stokland et al. 2012). However in this study,  
180 our aim was not to deeply explore the dead wood profile and its impacts on polypore communities,  
181 and thus we only divided the resources between fresh (decay stages 1,2) and old dead wood (decay  
182 stages 3,4,5). We calculated the change in the volume of fresh and old dead wood between 2004  
183 and 2017 separately for each site. The change of fresh decaying wood indicates the change in the

184 formation of new dead wood, which is the one that can mainly be altered due to buffer strip  
185 treatments during the 12 years.

186

187 Similarly, we calculated the changes in the number of polypore species and the number of  
188 individuals for each site by subtracting the numbers observed in 2004 from those observed in 2017.  
189 These changes were calculated for all species as a group, in addition to which they were calculated  
190 separately for red-listed species as a group.

191

192 The calculated changes were not normally distributed so to test if there were differences in the  
193 changes among treatments we conducted non-parametric Anova, Kruskal-Wallis tests by ranks  
194 (function *kurskal.test* in R-package stats). To further test if the changes in buffer strip treatments  
195 differed from the control treatment we conducted Dunn's multiple comparison tests by ranks  
196 (function *dunn.test* in R-package dunn.test)

197

### 198 **2.3.2 Polypore communities**

199 To estimate the differences in polypore communities among sites and years we calculated and  
200 tested for differences in their semi-metric abundance-based (i.e., taking the number of individuals  
201 into account) Bray-Curtis dissimilarity measures (function *vegdist* in R-package Vegan). This  
202 dissimilarity measure is widely used and shown to be good in detecting ecological gradients. The  
203 measure varies between 0 and 1, with 1 meaning total dissimilarity between communities (no  
204 shared species). In addition, we repeated the analyses applying presence-absence based Sørensen  
205 measure. Polypore fruiting bodies were not detected at all from three sites before the treatment  
206 manipulations (one control site, one 30 m wide buffer strip site with selective logging and one 15 m  
207 wide buffer strip without selective logging), so we removed these sites from the community-level  
208 analyses. Due to this one polypore species (*Heterobasidion parviporum*) was not included in the

209 community-level analyses as it was detected only in one site in 2017 and this site did not have  
210 fruiting bodies in 2004.

211

212 First, we analysed the impacts of buffer treatments on the mean community composition. We  
213 compared separately the mean community composition of each buffer treatment with the  
214 composition of control before and after the treatment manipulations using a permutational Manova,  
215 Permanova (function *adonis2* in R-package *Vegan*, a multivariate analog of analysis of variance).  
216 Explanatory factors were the four treatment contrasts: each buffer strip treatment compared with the  
217 control treatment. To test if the treatments change polypore communities differently compared with  
218 controls we ran a Permanova where we used the interactions of each treatment contrast and year as  
219 explanatory variables. We used study site as a strata to constrain permutations within sites. To  
220 directly test the effect of selective logging and to compare the effects of different buffer strip widths  
221 on the change of polypore community composition, we also analyzed data without the controls. In  
222 these analyzes, explanatory factors were the width of the buffer strip (15 m or 30 m), selective  
223 logging (yes or no), year and their interactions.

224

225 Second, we studied the impacts of buffer treatments on the dispersion in community composition.  
226 Decreased dispersion in community composition indicates homogenization, i.e. sites become more  
227 similar to each other in community composition. We compared the dispersion of each buffer  
228 treatment with the dispersion of control before and after the treatment manipulations using the  
229 analysis of multivariate homogeneity of group dispersions (*betadisper* in R-package *Vegan*, a  
230 multivariate analogue of Levene's test for homogeneity of variances) and permutations  
231 (*permutest.betadisper* in R-package *Vegan*). To test if buffer treatments changed the dispersion of  
232 communities differently than controls, we first used *betadisper* to extract the distance of each site to  
233 the centroid of the sites of the same treatment and year. *Betadisper* does not allow using more than

234 one explanatory variable in the analysis, so we extracted the distances and used Anova (with Type  
235 II sums of squares) to test for the effects of the interaction between each treatment contrast and year  
236 (*Anova* in R-package *car*). As in the Permanova-analyses above, we also analyzed the data without  
237 controls to test for the effects of buffer strip width and selective logging among the buffer strip  
238 sites.

239

240 We also illustrated these community changes in different treatments with ordination using non-  
241 metric multidimensional scaling (NMDS, function *metaMDS* in R-package *Vegan*). Moreover, we  
242 tested if there were species associated with specific treatments before and after the treatment  
243 manipulations using multi-level pattern analysis (function *multipatt* in R-package *Indicspecies*).

244

245 The results of all community analyses above are reported with Bray-Curtis dissimilarity measures in  
246 the main text, but the results of the same analyses with Sørensen dissimilarity are fully reported in  
247 the Supplementary material. In all permutation tests, significances were tested using a  
248 randomization test with 9999 permutations. All statistical analyses were performed using R version  
249 3.5.1 (R Development Core Team 2014). The references for the R-packages are available in Table  
250 S1.

251

## 252 **3 Results**

### 253 **3.1 Dead wood**

254 The formation of fresh dead wood (decay stages 1,2) tended to increase during the study period in  
255 all treatments (Figure 2a). The average volume of fresh dead wood was on average ( $\pm$  SD)  $5.4 \pm$   
256  $5.6 \text{ m}^3 \text{ ha}^{-1}$  in 2004 and  $20.0 \pm 22.2 \text{ m}^3 \text{ ha}^{-1}$  in 2017. However, compared with controls, the  
257 formation of fresh dead wood increased less in 30 m wide buffer strips with selective logging  
258 (Dunn's test:  $Z_{df=1,12} = -2.62$ ,  $p = 0.044$ ). The volume of old dead wood (decay stages 3,4,5) tended to

259 remain at similar levels in 2004 and 2017 in all treatments (Figure 2b). The average volume ( $\pm$  SD)  
260 of old dead wood (decay stages 3,4,5) was  $9.9 \pm 21.4 \text{ m}^3 \text{ ha}^{-1}$  in 2004 and  $6.7 \pm 8.0 \text{ m}^3 \text{ ha}^{-1}$  in 2017.  
261 There were no significant differences among treatments in the change of old dead wood volume  
262 (Kruskal-Wallis:  $\text{Chi-square}_{df=2.104, 27}$ ,  $p=0.718$ ).

263

### 264 **3.2 Numbers of polypore species and individuals**

265 In total 62 different polypore species were recorded, of which 41 species were found in 2004 and 50  
266 in 2017 (Table S2). The total number of individuals had doubled during the study period, as it was  
267 320 in 2004 and 656 in 2017. The number of species per site (Fig. 2c) and the number of  
268 individuals per site (Fig. 2d) tended to increase in all treatments. The site-level number of species  
269 increased similarly among all treatments (Kruskal-Wallis:  $\text{Chi-square}_{df=4.714, 32}$ ,  $p=0.320$ ).  
270 However, compared with controls, the site-level number of polypore individuals increased more in  
271 15 m wide buffer strips with selective logging (Dunn's test:  $Z_{df=-2.621, 16}$ ,  $p= 0.009$ ).

272

273 One red list species was observed in 2004, and seven in 2017, of which five different species were  
274 found in controls, two in 30 m wide strips without selective logging, two in 30 m wide strips with  
275 selective logging and two in 15 m wide strips with selective logging (Table S2). There were many  
276 sites without red-listed species and variation among sites was high so there were no significant  
277 differences among treatments in the change of site-level number of red-listed species (Kruskal-  
278 Wallis:  $\text{Chi-squared}_{df= 5.134, 32}$ ,  $p = 0.280$ ) or individuals (Kruskal-Wallis:  $\text{Chi-squared}_{df= 4.634, 32}$ ,  
279  $p = 0.330$ ).

280

### 281 **3.3 Polypore communities**

#### 282 **3.3.1 Community composition**

283 The mean community composition was similar to controls in all buffer strip treatments before the  
284 manipulations in 2004 (Table 1a, Fig. 3a). In contrast, the mean community composition was

285 similar to controls only in non-logged 30 m wide buffer strips after the manipulations in 2017, and  
286 differed from the controls in both types of 15 m wide buffer strips and in 30 m wide buffer strips  
287 with selective logging (Table 1a, Fig. 3a).

288

289 The community composition of polypores had changed between years 2004 and 2017 in all sites  
290 (Fig. 3b). However, communities in both types of 15 m wide buffer strips showed changes that  
291 deviated from the changes in controls (Fig. 3). In controls, the changes tended to be inconsistent in  
292 direction whereas in 15 m wide buffer strips, changes tended to be more directional and towards  
293 species not found in the controls. (Fig. 3b). However, mean changes in community composition  
294 differed significantly from the controls only in 15 m wide buffer strips with selective logging (Table  
295 2a). In non-logged 15 m wide buffer strips, the directions of change in community composition  
296 were less consistent (Fig. 3b) and the number of sites within the treatment was the smallest so the  
297 deviation from the control was not captured by Permanova. The mean community composition in  
298 selectively logged 30 m wide buffer strips changed roughly to the same direction as the composition  
299 in controls (Fig. 3b), and therefore these changes were not statistically different, although the  
300 compositions themselves differed in 2017 (Table 1a, Fig. 3a). Moreover, communities in 15 m and  
301 30 m wide buffer strips changed differently but selective logging did not affect the change in mean  
302 community composition at either buffer strip width (Table 3a).

303

### 304 **3.3.2 Community dispersion**

305 The dispersion in community composition among sites was similar to controls in all treatments  
306 before the treatment manipulations in 2004 (Table 1b, Fig. 3a). After the manipulations in 2017, the  
307 dispersion in community composition was still similar to the controls in all treatments with the  
308 exception of the 15 m wide buffer strips with selective logging where the dispersion was smaller  
309 (Table 1b, Fig. 3a). Despite this, the dispersion in community composition changed differently than

310 in controls in 15 m wide buffers without selective logging (Table 2b), where the dispersion seemed  
311 to be slightly increased compared to other treatments (Fig. 3a). The dispersion in community  
312 composition decreased in both buffer treatments with selective logging (Table 3b, Fig. 3a).  
313 However, the change of dispersion in buffer strip treatments with selective logging did not differ  
314 significantly from the change of dispersion in controls as it seemed to decrease slightly as well.  
315 Nevertheless, when the sites with different buffer strips were compared, selective logging caused a  
316 decrease in dispersion, while buffer strip width did not impact the change in dispersion (Table 3b).

317

### 318 **3.3.3 Species associated with treatments**

319 Except for one species (*Phellinus punctatus*) that was associated with controls, there were no  
320 species associated with treatments prior to treatment manipulations (Table S3). After the  
321 manipulations in 2017, there were three species (*Gloeophyllum sepiarium*, *Antrodia serialis* and  
322 *Postia tephroleuca*), which were associated with both types of 15 m wide buffer strips (Table S3).  
323 In addition, *Postia caesia* was associated with all buffer strip treatments, except the non-logged 30  
324 m wide buffer strips (Table S2). These associated polypore species are mostly generalist species  
325 and typically found in production forests (Niemelä 2016). The direction of change of community  
326 composition in both types of 15 m wide buffer strips tended to be towards these species (Fig. 3). In  
327 addition, even though not significantly associated with the 15 m wide buffers, the abundance of two  
328 generalist species (*Fomitopsis pinicola* and *Trichaptum abietinum*) increased in 15 m wide buffer  
329 strips after treatment manipulations (Table S2). Moreover, in 2017 three species (*Phellinus*  
330 *tremulae*, *Postia ptychogaster* and *Trichaptum fuscoviolaceum*) were associated with 15 m wide  
331 buffer strips without selective logging and one species (*Antrodiella pallescens*) was associated with  
332 30 m wide buffer strips without selective logging (Table S3).

333

### 334 **3.3.4 Species presence vs. abundance**

335 Communities were similar in buffer strip treatments and controls before the treatment  
336 manipulations in 2004 also when species presence-absence (Sørensen dissimilarity) was only  
337 considered (Table S4). After the manipulations in 2017, fewer buffer strip treatment differed from  
338 the control when species presence-absence was only considered than when abundance (Bray-Curtis  
339 dissimilarity) was considered. In 2017, only 15 m wide buffer strips differed from the controls in  
340 the mean community composition and 15 m wide buffer strips with selective logging in the  
341 dispersion of community composition (Table S4). The changes in mean composition and dispersion  
342 did not differ between any logging treatment and the control (Table S5). Similarly, the width of the  
343 buffer strip or selective logging did not affect the changes in mean composition and dispersion  
344 (Table S6). Therefore, the largest effects of management on communities were captured via  
345 increased abundance of certain species, such as species associated with specific treatments in 2017  
346 (Table S3).

347

## 348 **4 Discussion**

### 349 **4.1 The width of the buffer strips**

350 Species richness and number of individuals tended to increase in all treatments 12 years after the  
351 manipulations. However, the community composition in 15 m wide buffer strips changed  
352 differently than that in controls and 30 m wide buffer strips, and after the manipulations, resembled  
353 the composition typically found in production forests. These results were not surprising, as narrow  
354 buffer strips are prone to strong edge effects, which has been identified in these sites also as  
355 increased abundance of windthrows (Mäenpää et al. unpublished) and as altered microclimatic  
356 conditions (Oldén et al. 2019b). In this study, we did not separate the impacts of substrate  
357 availability and abiotic conditions on polypores but the occurrence and increased abundances of  
358 certain species in narrow buffer strips indicate that polypore communities were disturbed through  
359 changes in both of them. *G. sepiarium* favours open and warm habitats (Snäll and Jonsson 2001;



360 Siitonen et al. 2005) provided by these narrow strips (Oldén et al. 2019b). *F. pinicola*, *T. abietinum*,  
361 *T. fuscoviolaceum* and *A. serialis* colonize recently felled dead trees in early and intermediate  
362 decay stages (Jönsson et al. 2008; Niemelä 2016), which were common in our narrow buffer strips  
363 due to the high number of windthrows (Mäenpää et al. unpublished). Moreover, two *Postia* species,  
364 which are common also in production forests (Niemelä 2016), were abundant in 15 m wide buffer  
365 strips. These responses of polypore species community support earlier conclusions the natural  
366 species composition of streamside habitats is disturbed in narrow buffer strips (Selonen and Kotiaho  
367 2013; Sweeney and Newbold 2014; Oldén et al. 2019a, 2019b).

368

369 The natural like succession of streamside polypore communities appeared not to be disturbed if the  
370 width of the forested buffer strip between the stream and the clear-cut was 30 m wide and not  
371 selectively logged. In this case, the outer half of the buffer strip (from 15 to 30 m from the stream)  
372 seemed to protect the streamside habitat (from 0 to 15 m from the stream) from the strongest edge  
373 effect. However, an edge effect often travels deeper than 15 m into the forest (Murcia 1995;  
374 Ylisirniö et al. 2016) and the moisture conditions were found to be altered also in 30 m wide buffer  
375 strips in these study sites (Oldén et al. 2019b). Polypore communities are sensitive to these changes  
376 in microclimate even if their substrate availability is not disturbed (Moore et al. 2008). Moreover,  
377 negative responses of species can be slow due to extinction debt and thus may not yet be visible  
378 after 12 years (Junninen and Komonen 2011; Hylander and Weibull 2012). Therefore, based on our  
379 study it is too early to conclude that 30 m wide buffer strips would be wide enough to preserve the  
380 natural biodiversity of streamside habitats in the long term.

381

382 To retain biodiversity in streamside habitats, several studies have suggested that the width of buffer  
383 strip between a stream and a clear-cut area should be more than 30 m, depending on the features of  
384 the site and its surrounding landscape (Wenger 1999; Kuglerová et al. 2014; Sweeney and Newbold

385 2014; Oldén et al. 2019b). We did not explore other environmental factors in this study but, for  
386 example, the structure of the surrounding forest (Oldén et al. 2019b), topography (Wenger 1999;  
387 Sweeney and Newbold 2014) and the width of the moist habitat area (Kuglerová et al. 2014) can  
388 influence the needed width of the buffer strip to protect the biodiversity of streamside habitats.

389

#### 390 **4.2 Selective logging**

391 Selective logging seemed to cause the homogenization of polypore communities when compared to  
392 buffer strips that had not been selectively logged. Such decreased variation in communities among  
393 sites with selective logging indicates that selective logging disturbed the natural variation in  
394 polypore communities, which is typically high in natural forests (Abrego et al. 2014). Moreover,  
395 compared with unmanaged controls, the formation of fresh dead wood was smaller in 30 m wide  
396 buffer strips with selective logging. This indicates that the continuity and diversity of dead wood  
397 resources in the future can be disturbed. These negative impacts of selective logging were not  
398 surprising either as previous studies in boreal forests have reported that selective logging can reduce  
399 the availability of dead wood resources and the richness of polypore species even decades after  
400 loggings (Bader et al. 1995; Sippola et al. 2001).

401

402 In narrow buffer strips with selective logging, the edge effect is strong and the direct impact of  
403 selective logging is probably smaller than the impact of the edge. In wider buffer strips with  
404 selective logging, the selective logging can affect the streamside habitat in two ways: directly by  
405 changing the forest structure in the streamside key habitat (from 0 to 15 m from the stream in this  
406 study) and indirectly by increasing the edge effect through the selectively logged outer half of the  
407 buffer (from 15 to 30 m from the stream). In any case, based on this and previous research in  
408 streamside forests, selective logging should not be applied, at least in the actual key habitat, if the

409 aim is to retain the natural biodiversity and its succession (Lundström et al. 2018; Oldén et al.  
410 2019b).

411

412 However, if selective logging is applied in surrounding forests beyond the 30 m instead of clear-  
413 cutting, this could reduce the negative effects of the adjacent loggings on streamside habitats  
414 (Braithwaite and Mallik 2012). In this case, the non-logged buffer strip between the stream and the  
415 production forest stand could be potentially narrower than 30 m. Despite the increased interest  
416 towards the possibilities of continuous cover forestry, such as selective logging, to reduce forestry  
417 related biodiversity loss in boreal commercial forests (Joelsson et al. 2017; Vanha-Majamaa et al.  
418 2017), the strength of edge effect between an ecologically valuable habitat and a forest managed  
419 with continuous cover forestry has not been measured. However, continuous cover forestry affects  
420 microclimate less than clear-cuts at the stand scale (Zheng et al. 2000) and continuous cover  
421 forestry applied at the landscape scale can reduce the occurrence of windthrows (Pukkala et al.  
422 2016). Therefore, the edge effect of continuous cover forestry is likely less severe than the effect of  
423 clear-cuts. This alternative forestry method has been suggested to be economically profitable  
424 (Tahvonen et al. 2010). Hence, managing forest stands next to a streamside habitat under  
425 continuous cover forestry could be beneficial from both economic and ecological perspectives.  
426 Future studies should explore more the possibilities of alternative forestry methods in the  
427 surrounding landscape to reduce negative edge effects on streamside habitats.

428

### 429 **4.3 Key habitats and buffer strips as conservation tools**

430 In general, the function of small retained forest patches, such as key habitats or buffer strips, as a  
431 conservation tool has been questioned, especially, from the perspective of red-listed species  
432 (Marczak et al. 2010; Timonen et al. 2011). Hottola et al. (2008) found that the number of red-listed  
433 polypore species was not significantly larger in streamside habitats than in spruce-dominated

434 mature production forests in the same regions. However, some of their study sites were younger  
435 than in our study, all streamside habitats did not fulfill the criteria of key habitats defined by the  
436 Finnish Forest Act, and the forest management in and near streamside habitats was not controlled.  
437 In our study, only one red-listed species was found in 2004 when the volume of dead wood was  
438 small in many sites. However, in 2017 many sites fulfilled the threshold of 20 m<sup>3</sup> ha<sup>-1</sup> dead wood  
439 (Junninen and Komonen 2011) and seven different red-listed species were found, whereof five  
440 species were found in the control sites. Thus, our study suggests that streamside key habitats, at  
441 least those defined by the Finnish Forest Act, and when allowed to develop through natural  
442 succession, can provide important habitats for red-listed polypores in forest landscapes. However,  
443 their long-term capacity to support the populations of sensitive species is not known (Junninen and  
444 Komonen 2011; Timonen et al. 2011).

445

446 Previous research suggests that while different types of key habitats or retained buffer strips can  
447 provide habitats for dead wood dependent species (Jönsson and Jonsson 2007; Siitonen et al. 2009;  
448 Hylander and Weibull 2012; Sverdrup-Thygeson et al. 2014), they may be too isolated and small in  
449 size to preserve viable populations of sensitive and specialized species in the long term (Junninen  
450 and Kouki 2006; Hottola and Siitonen 2008; Junninen and Komonen 2011; Ylisirniö et al. 2016).  
451 On the other hand, retained habitat patches or buffer strips themselves can support existing  
452 conservation networks by increasing the habitat connectivity at least for species with moderate  
453 dispersal ability (Laita et al. 2010). Nevertheless, in the case of streamside habitats, fragmentation  
454 may not be as problematic as, for example, in the case of old-growth forest patches, since streams  
455 form connected networks of habitats if forested buffer strips are wide enough and retained  
456 continuously. However, to guarantee the effectiveness of limited conservation efforts in commercial  
457 forest landscapes, small-scale efforts, such as retention trees in neighboring stands (Gustafsson et  
458 al. 2012) and less intensive forestry methods could be allocated to the vicinity of key habitats or

459 buffer strips to protect them more from the negative impacts of forest management in the  
460 surrounding landscape.

461

#### 462 **4.4 Conclusions**

463 We studied the management of streamside habitats in boreal Fennoscandia by manipulating the  
464 width of the forested buffer strip and selective logging within the buffer strips. The responses in  
465 polypore communities and dead wood formation 12 years after the manipulations showed that the  
466 natural biodiversity and its succession was disturbed in 15 m wide buffer strips and in selectively  
467 logged buffer strips. The disturbance was mainly detected in the changed species composition and  
468 not in terms of overall species diversity. Streamside habitats in non-logged 30 m wide buffer strips  
469 seemed to retain the natural like polypore community composition and its succession. However,  
470 based on previous studies, it is too early to conclude that 30 m wide strips would be wide enough to  
471 safeguard the preservation of natural biodiversity in streamside habitats in the long term. Therefore,  
472 large-scale spatial planning, which takes into account the adjacent forests next to streamside  
473 habitats, is needed to secure their effectiveness in conservation.

474

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481

482

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623

624

625 **Tables**

626

627 **Table 1** Each buffer strip treatment compared with control separately in 2004 and in 2017 with  
 628 Bray-Curtis dissimilarity in a) mean community composition (Permanova) and in b) dispersion in  
 629 community composition (Betadisper).

Explanatory factor	a) Community composition		b) Dispersion	
	Pseudo-F <sub>df</sub>	p	F <sub>df</sub>	p
<b>2004</b>				
30m vs Control	0.70 <sub>1,31</sub>	0.763	0.14 <sub>1,31</sub>	0.717
30mSL vs Control	0.85 <sub>1,31</sub>	0.621	0.52 <sub>1,31</sub>	0.487
15m vs Control	1.14 <sub>1,31</sub>	0.302	0.21 <sub>1,31</sub>	0.656
15mSL vs Control	0.59 <sub>1,31</sub>	0.880	0.01 <sub>1,31</sub>	0.934
<b>2017</b>				
30m vs Control	0.80 <sub>1,31</sub>	0.628	0.17 <sub>1,31</sub>	0.693
30mSL vs Control	<b>2.20</b> <sub>1,31</sub>	<b>0.017</b>	0.23 <sub>1,31</sub>	0.639
15m vs Control	<b>2.81</b> <sub>1,31</sub>	<b>0.004</b>	0.83 <sub>1,31</sub>	0.387
15mSL vs Control	<b>3.31</b> <sub>1,31</sub>	<b>0.003</b>	<b>5.03</b> <sub>1,31</sub>	<b>0.043</b>

630 *Statistically significant effects ( $p < 0.05$ ) are indicated in bold.*

631

632

633 **Table 2** The effects of year, each buffer strip treatment compared with control, and their  
 634 interactions with Bray-Curtis dissimilarity in a) mean community composition (Permanova) and in  
 635 b) dispersion in community composition (Betadisper).

Explanatory factor	a) Community composition		b) Dispersion	
	Pseudo-F <sub>df</sub>	p	F <sub>df</sub>	p
Year	<b>3.51</b> <sub>1,62</sub>	<b>0.002</b>	<b>22.46</b> <sub>1,62</sub>	<b>&lt;0.001</b>
30m vs Control	1.26 <sub>1,62</sub>	0.23	1.87 <sub>1,62</sub>	0.178
30mSL vs Control	1.69 <sub>1,62</sub>	0.061	0.70 <sub>1,62</sub>	0.406
15m vs Control	<b>2.32</b> <sub>1,62</sub>	<b>0.012</b>	2.52 <sub>1,62</sub>	0.119
15mSL vs Control	1.20 <sub>1,62</sub>	0.26	1.78 <sub>1,62</sub>	0.187
Year*30m vs Control	0.70 <sub>1,62</sub>	0.76	0.13 <sub>1,62</sub>	0.718
Year*30mSL vs Control	1.14 <sub>1,62</sub>	0.33	1.23 <sub>1,62</sub>	0.272
Year*15m vs Control	0.64 <sub>1,62</sub>	0.82	<b>6.63</b> <sub>1,62</sub>	<b>0.013</b>
Year*15mSL vs Control	<b>2.12</b> <sub>1,62</sub>	<b>0.014</b>	1.31 <sub>1,62</sub>	0.258

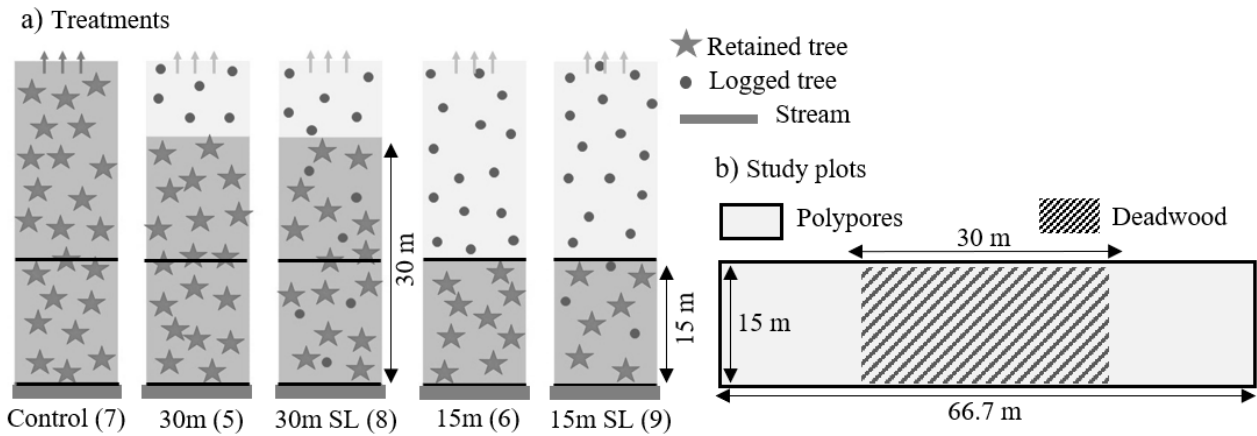
636 *Statistically significant effects ( $p < 0.05$ ) are indicated in bold.*  
637

638 **Table 3** The effects of year, width of the strip, selective logging, and their interactions with Bray-  
639 Curtis dissimilarity in a) mean community composition (Permanova) and in b) dispersion in  
640 community composition (Betadisper).

Explanatory factor	a) Community composition		b) Dispersion	
	Pseudo- $F_{df}$	p	$F_{df}$	p
Year	<b>4.08</b> <sub>1,50</sub>	<b>0.001</b>	<b>18.57</b> <sub>1,50</sub>	<b>&lt;0.001</b>
Width	1.56 <sub>1,50</sub>	0.091	2.39 <sub>1,50</sub>	0.129
Selective logging	1.13 <sub>1,50</sub>	0.335	3.40 <sub>1,50</sub>	0.072
Year*Width	<b>1.90</b> <sub>1,50</sub>	<b>0.032</b>	0.39 <sub>1,50</sub>	0.538
Year*Selective logging	0.74 <sub>1,50</sub>	0.717	<b>6.79</b> <sub>1,50</sub>	<b>0.013</b>
Width*Selective logging	<b>2.26</b> <sub>1,50</sub>	<b>0.015</b>	0.73 <sub>1,50</sub>	0.398
Year*Width*Selective logging	0.58 <sub>1,50</sub>	0.871	1.55 <sub>1,50</sub>	0.220

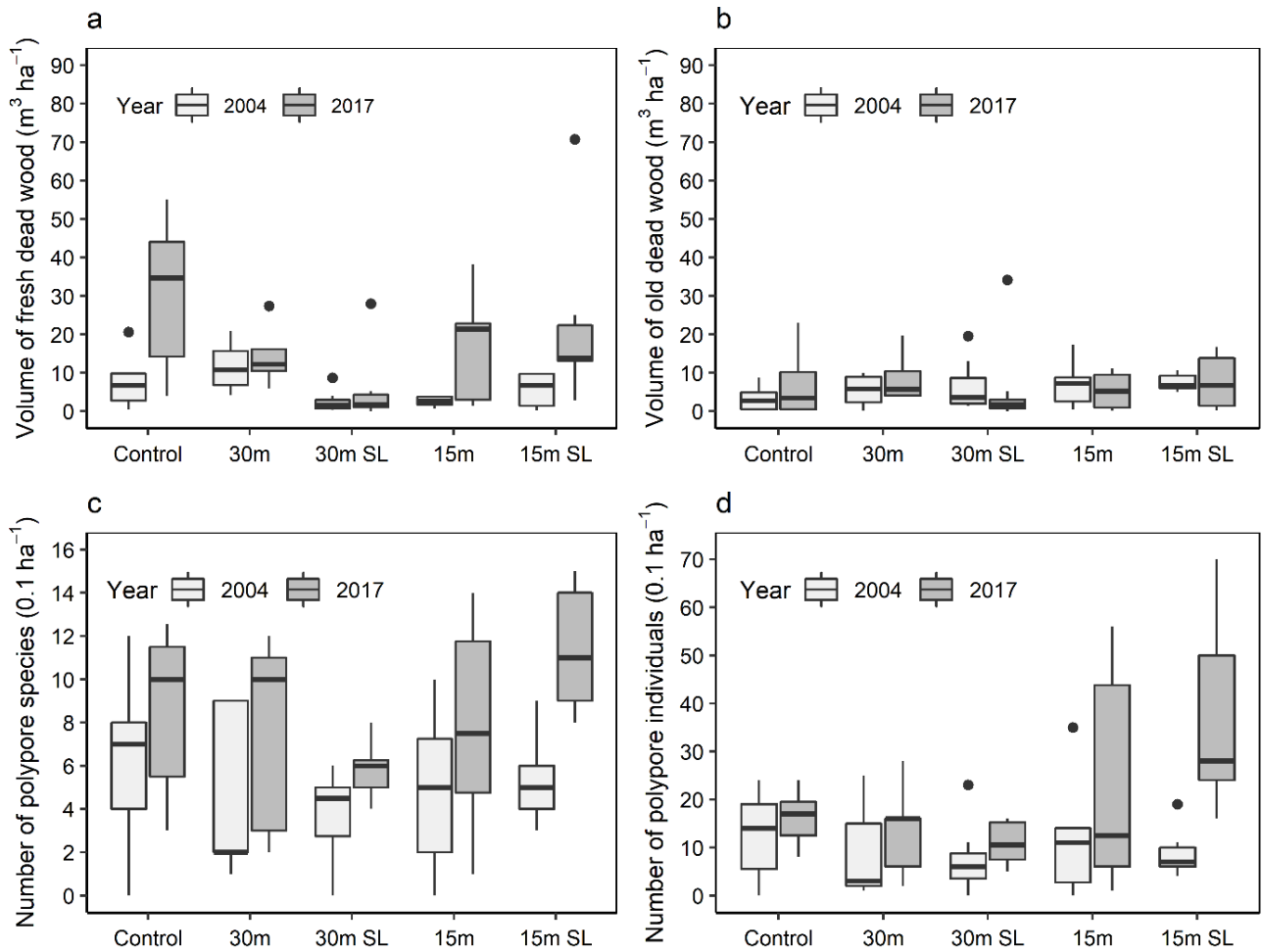
641 *Statistically significant effects ( $p < 0.05$ ) are indicated in bold.*  
642

643 **Figure captions**



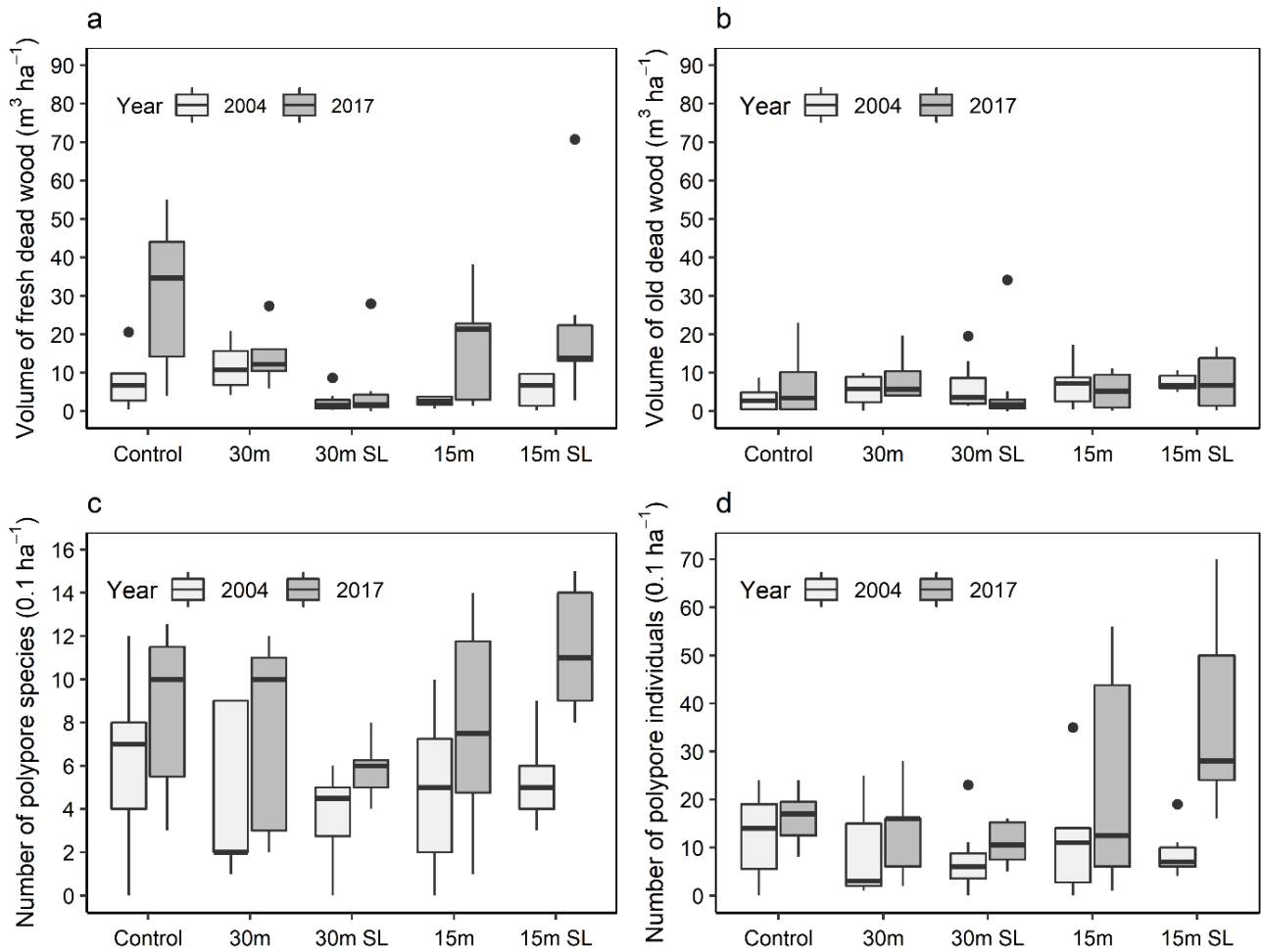
644

645 **Fig 1.** a) Study design of treatments modified from Oldén et al. (2019a). Streams are at the bottom  
646 of the figure, arrows above indicate continuous forest cover in the controls and continuing clear-cut  
647 area in buffer strip treatments. The treatments are: control, 30 m wide buffer strip with or without  
648 selective logging (SL), and 15 m wide buffer strip with or without selective logging. The number of  
649 sites per treatment are given in parentheses. b) The study plots for dead wood and polypores.



650

651 **Fig. 2** The volume of fresh dead wood (a), the volume of old dead wood (b), the number of  
 652 polypore species (c), and the number of polypore individuals (d) on sites of different treatments  
 653 before the treatment manipulations in 2004 and after the manipulations in 2017. Please note that the  
 654 scales of y-axis are different in figures c and d. One outlier was removed from the figure b ( $120 \text{m}^3$   
 655  $\text{ha}^{-1}$  in control site 2004).



656

657 **Fig. 3** Non-metric multidimensional scaling plots of polypore species (n=61) communities based on  
 658 Bray-Curtis dissimilarities (stress=19%). Treatments are indicated by colours. a) Treatment  
 659 centroids with 95% confidence interval ellipses in 2004 and in 2017 are indicated by dashed and  
 660 solid lines, respectively. b) Arrows indicate sites, the beginning of the arrow is the composition of  
 661 the polypore community of the site in 2004 and the end of the arrow is the composition of the  
 662 polypore community of the site in 2017. Species associated with more than one treatment in 2017  
 663 (Table S3) are indicated by black symbols.