Supplementary Information for

Size, connectivity and edge effects of stream habitats explain spatio-temporal variation in brown trout (*Salmo trutta*) density

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This PDF file includes:

Figures S1 to S7
Tables S1 to S4

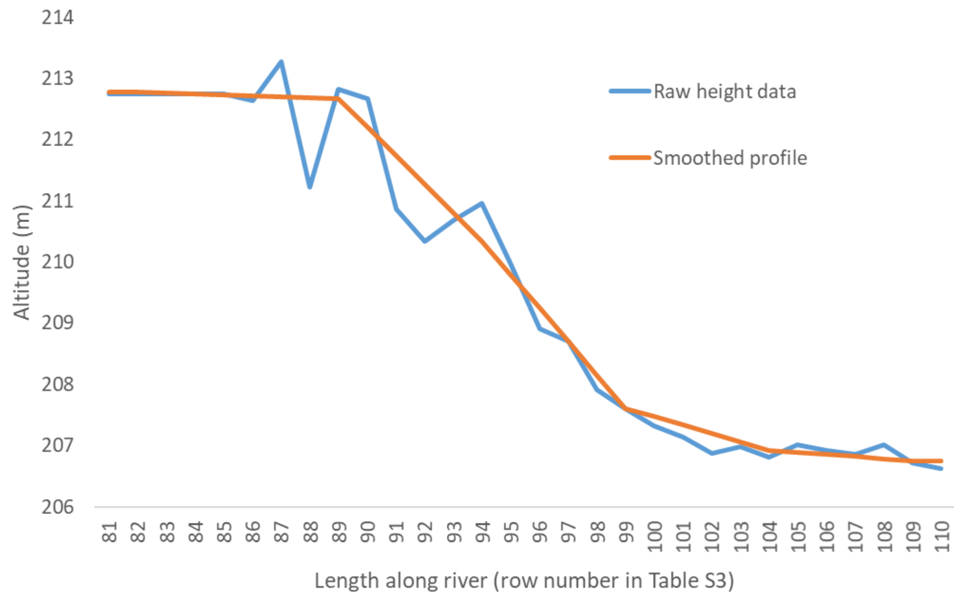

Fig. S1. An example of how the interpolating smoothing formula removed raw height data noise to facilitate calculation of location and lengths of lotic habitats. The formula is found in **Table S1**.

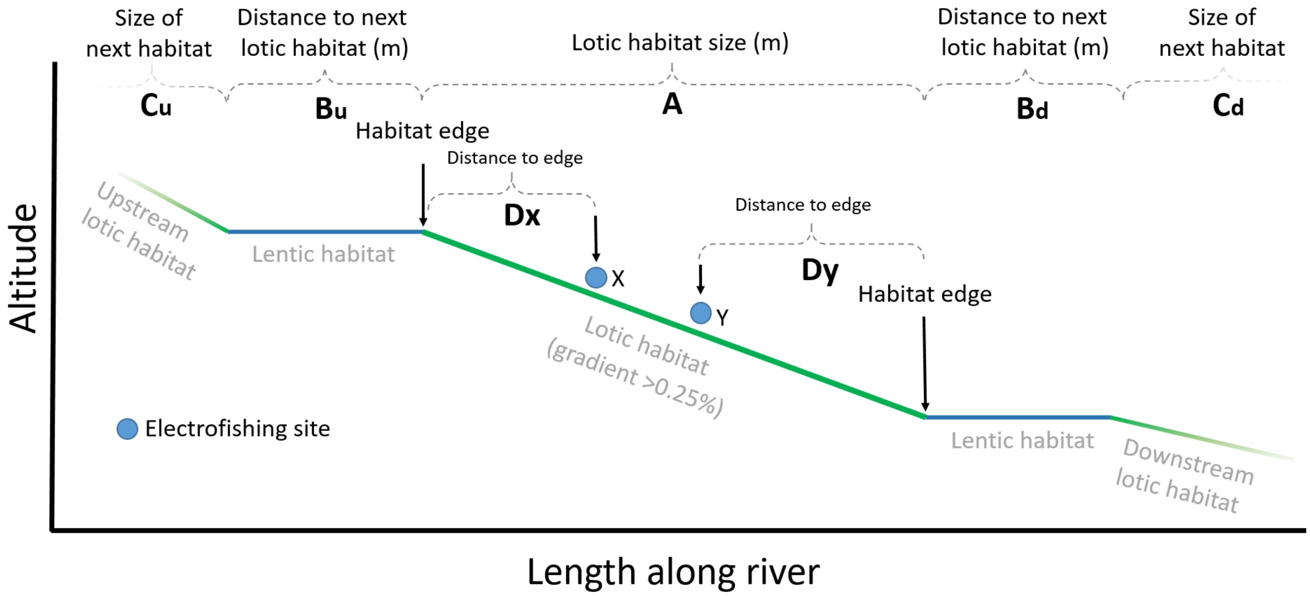

Fig. S2. Schematic illustration of the data. Lotic habitats are identified by finding consecutive stretches of river with a gradient of at least 0.25%, the length of these are calculated as habitat size (**A**). From this habitat, the distance is measured to the next lotic habitat upstream (**B$_u$**) and downstream (**B$_d$**) – connectivity (or rather isolation) is measured as the distance to whichever of these is shortest. The size of the closest habitat is measured (**C$_u$** or **C$_d$**). Additionally, the distance to the closest edge is measured for each electrofishing site – for site X, the distance is shorter to the upstream edge (**D$_x$**). For site Y, the distance is shorter to the downstream edge (**D$_y$**). Measurements A, B and C are used for **Model 1**, while A, B, C, and D are used for the extended **Model 2** (see **Table 2** in main manuscript and **Tables S3** and **S4**).

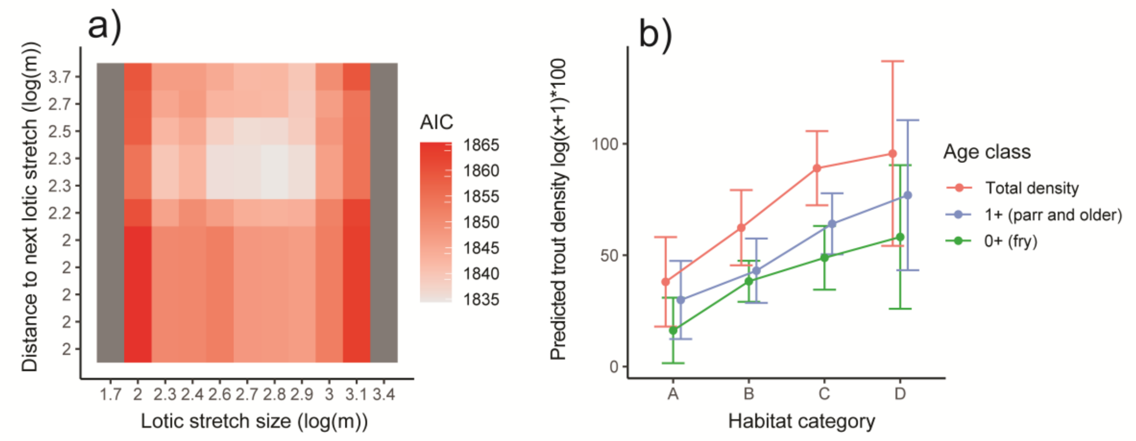

Fig. S3. Results from sensitivity analysis used to evaluate effect of cutoff points for delineation of habitats into four biogeographic categories. a) Iteration of the delineation of the lotic habitat categories (A – D in **Fig. 1**) in the two dimensions 'lotic stretch length' and 'distance to next lotic stretch'. The numbers on the X- and Y-axis indicate the values located on the 10-percentiles between 0 and 100% of variables 'lotic stretch length' and 'distance to next lotic stretch', respectively. The (grey-red) shade indicate the model fit (AIC) for the habitat category model (**Table 1**) with the delineations as specified at each respective percentile. The most parsimonious model was found at 2.8 (102.8 = 600 meters) for lotic stretch length and 2.3 (102.3) = 200 meters) for distance to next lotic stretch. **b)** Predicted means with 95% confidence intervals as acquired from zero-inflated negative binomial mixed model using delineations demonstrated in a) are illustrated in green (0+, fry), blue (>0+, parr and older) and red (pooled ages).

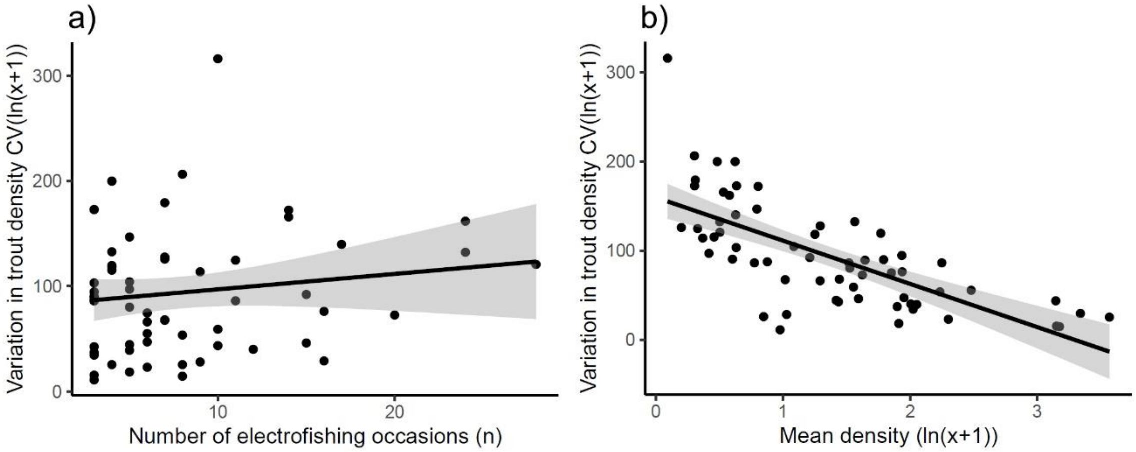

Fig. S4. The coefficient of variation in brown trout density was not associated with **a)** number of electrofishing occasions on a site but **b)** negatively related with the mean density.

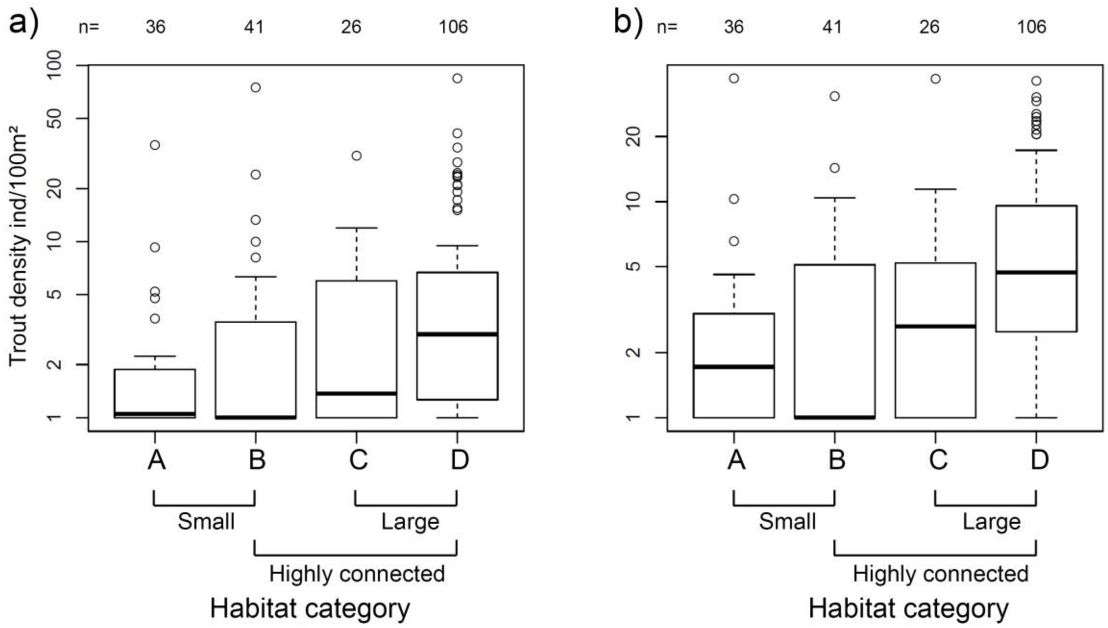

Fig. S5. Boxplots showing mean brown trout density of age classes **a)** 0+, fry, and **b)** >0+, parr and older, per electrofishing site depending on habitat category (A = small, far; B = small, near; C = large, far; D = large, close, see **Fig. 1**). The data points represent raw data, not model outputs. Note the logarithmic scale on the y-axis. Values above represent sample sizes.

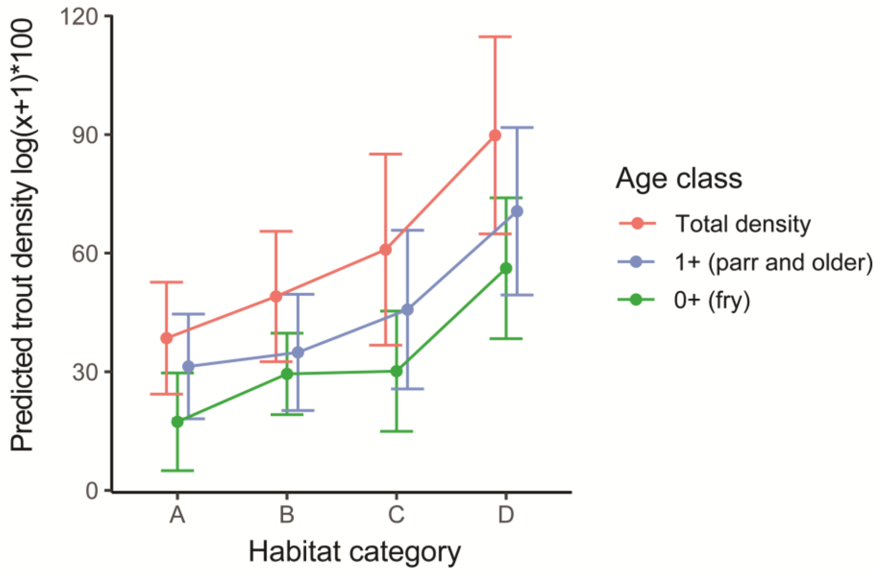

Fig. S6. Effect plot (predicted mean with 95 % CI) of island biogeographic categories (A = small, far; B = small, near; C = large, far; D = large, close, see **Fig. 1** for context) on brown trout density modelled by mixed zero-inflated negative binomial distribution models (**Table 1**). Green shows 0+, fry, blue shows 1+, parr and older, and red shows pooled data (as in **Fig. 1e** in main paper).

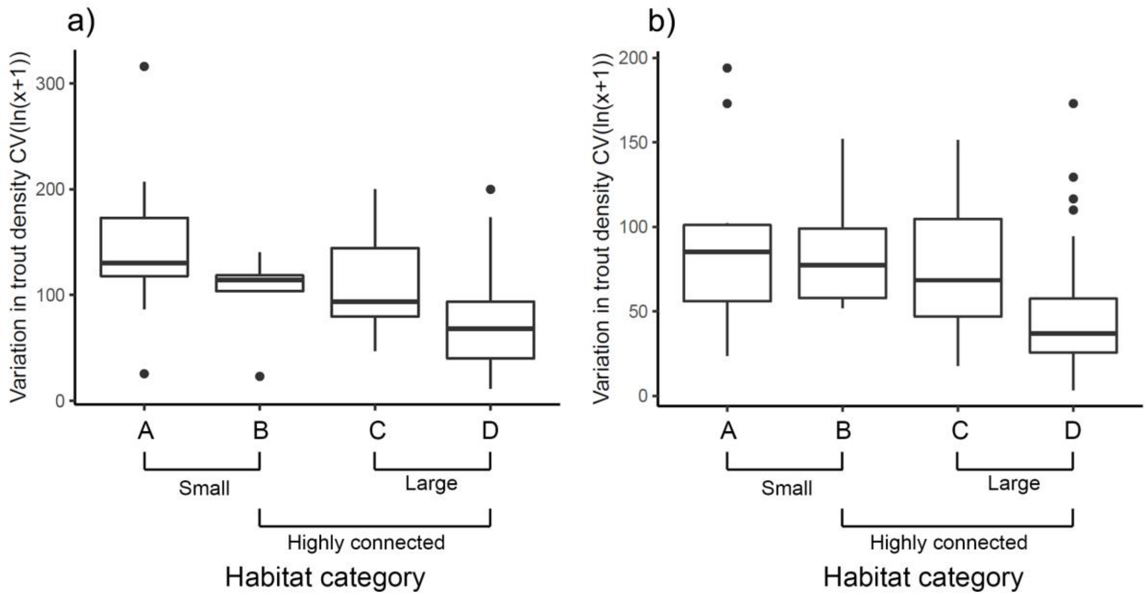

Fig. S7. Abundance fluctuations of brown trout vary according to length and isolation of lotic habitats. Coefficient of variation representing over-time sample variation in **a)** 0+, fry, and **b)** >0+, parr and older, brown trout density on electrofishing sites (with at least three sampling occasions) per island biography category.

Table S1. The Excel formula with which raw height data noise was removed to facilitate calculation of location and lengths of lotic stretches. The raw height data and smoothed profile is illustrated in **Fig S1**.

	A	B	C
Row #	**Raw height data**	**Smoothed profile**	**Formula**
…	**…**	**…**	**…**
81	212.75	212.78	=B79-((B79-B84)/5)*2
82	212.75	212.77	=B79-((B79-B84)/5)*3
83	212.75	212.76	=B79-((B79-B84)/5)*4
84	212.75	212.75	=IF(MEDIAN(A82:A86)>B79;IF((MEDIAN(B79;(MEDIAN(A82:A90))))>B79;B79;(MEDIAN(B79;(MEDIAN(A82:A90)))));MEDIAN(A82:A86))
85	212.75	212.73	=B84-((B84-B89)/5)*1
86	212.64	212.72	=B84-((B84-B89)/5)*2
87	213.27	212.70	=B84-((B84-B89)/5)*3
88	211.23	212.69	=B84-((B84-B89)/5)*4
89	212.82	212.67	=IF(MEDIAN(A87:A91)>B84;IF((MEDIAN(B84;(MEDIAN(A87:A95))))>B84;B84;(MEDIAN(B84;(MEDIAN(A87:A95)))));MEDIAN(A87:A91))
90	212.67	212.20	=B89-((B89-B94)/5)*1
91	210.86	211.74	=B89-((B89-B94)/5)*2
92	210.34	211.27	=B89-((B89-B94)/5)*3
93	210.68	210.81	=B89-((B89-B94)/5)*4
94	210.96	210.34	=IF(MEDIAN(A92:A96)>B89;IF((MEDIAN(B89;(MEDIAN(A92:A100))))>B89;B89;(MEDIAN(B89;(MEDIAN(A92:A100)))));MEDIAN(A92:A96))
95	209.98	209.79	=B94-((B94-B99)/5)*1
96	208.91	209.25	=B94-((B94-B99)/5)*2
97	208.71	208.70	=B94-((B94-B99)/5)*3
98	207.92	208.16	=B94-((B94-B99)/5)*4
99	207.61	207.61	=IF(MEDIAN(A97:A101)>B94;IF((MEDIAN(B94;(MEDIAN(A97:A105))))>B94;B94;(MEDIAN(B94;(MEDIAN(A97:A105)))));MEDIAN(A97:A101))
100	207.32	207.47	=B99-((B99-B104)/5)*1
101	207.14	207.34	=B99-((B99-B104)/5)*2
102	206.87	207.20	=B99-((B99-B104)/5)*3
103	206.99	207.07	=B99-((B99-B104)/5)*4
104	206.81	206.93	=IF(MEDIAN(A102:A106)>B99;IF((MEDIAN(B99;(MEDIAN(A102:A110))))>B99;B99;(MEDIAN(B99;(MEDIAN(A102:A110)))));MEDIAN(A102:A106))
105	207.02	206.89	=B104-((B104-B109)/5)*1
106	206.93	206.86	=B104-((B104-B109)/5)*2
107	206.86	206.82	=B104-((B104-B109)/5)*3
108	207.02	206.79	=B104-((B104-B109)/5)*4
109	206.72	206.75	=IF(MEDIAN(A107:A111)>B104;IF((MEDIAN(B104;(MEDIAN(A107:A115))))>B104;B104;(MEDIAN(B104;(MEDIAN(A107:A115)))));MEDIAN(A107:A111))
110	206.62	206.75	=B109-((B109-B114)/5)*1
…	…	…	…

Table S2. Results from mixed zero-inflated binomial distribution model on the effects of the habitat categories (A = small, far; B = small, close; C = large, far, and D = large, close, see **Fig. 1**) on occurrence and density (count) of **a)** brown trout fry (0+) and **b)** brown trout parr and older (>0+).

	A. Age class: 0+ (fry)				**B. Age class: 1+ (parr and older)**			
Predictors	*Estimate*	*std. Error*	*Z-value*	*p*	*Estimate*	*std. Error*	*Z-value*	*p*
Count Part								
(Intercept)	3.57	0.19	19.14	**<0.001**	3.84	0.14	28.27	**<0.001**
Habitat category [B]	0.67	0.22	3.03	**0.002**	0.42	0.16	2.70	**0.007**
Habitat category [C]	0.50	0.24	2.11	**0.035**	0.36	0.16	2.22	**0.027**
Habitat category [D]	0.70	0.19	3.61	**<0.001**	0.51	0.13	3.79	**<0.001**
Zero-Inflated Part								
(Intercept)	0.06	0.46	0.12	0.904	-0.73	0.63	-1.16	0.247
Habitat category [B]	0.26	0.57	0.46	0.643	0.75	0.59	1.27	0.203
Habitat category [C]	-0.10	0.65	-0.15	0.879	-0.05	0.72	-0.07	0.946
Habitat category [D]	-1.35	0.53	-2.54	**0.011**	-1.62	0.68	-2.39	**0.017**

Table S3. Associations of 0+ (fry) brown trout density with continuous variables lotic stretch size, distance to next lotic stretch, the direction (upstream or downstream) and the size of the next lotic stretch, distance to edge of nearest lentic stretch, and pike presence/absence. Results from mixed zero-inflated binomial distribution model of the effects of continuous data on size and isolation of lotic river habitats on occurrence and density of 0+ (fry) brown trout on the spatial only model (Model 1) or extended model with edge and predator effects (Model 2).

	Model 1: Only spatial variables (AIC=1588)				**Model 2: Added predator and edge effects (AIC=1581)**			
Predictors	*Estimate*	*std. Error*	*Z-value*	*p*	*Estimate*	*std. Error*	*Z-value*	*p*
Count Part								
(Intercept)	4.92	1.08	4.56	**<0.001**	5.01	1.07	4.69	**<0.001**
Distance to next habitat	-0.19	0.17	-1.15	0.249	-0.21	0.16	-1.28	0.200
Upstream	0.11	1.04	0.11	0.913	-0.66	1.04	-0.64	0.525
Size of habitat	0.11	0.07	1.63	0.103	0.17	0.08	2.05	**0.040**
Size of neighbouring habitat	-0.10	0.06	-1.71	0.087	-0.06	0.06	-1.05	0.294
Distance to next habitat * Upstream	-0.01	0.20	-0.03	0.977	0.14	0.20	0.70	0.481
Distance to edge					-0.10	0.06	-1.76	0.078
Pike presence (1)					-0.98	0.37	-2.64	**0.008**
Distance to edge * Pike presence (1)					0.13	0.08	1.71	0.087
Zero-Inflated Part								
(Intercept)	0.56	2.16	0.26	**0.796**	0.55	2.16	0.26	**0.799**
Size of habitat	-0.57	0.22	-2.62	**0.009**	-0.57	0.22	-2.61	**0.009**
Distance to next habitat	0.45	0.28	1.62	0.106	0.45	0.28	1.62	0.105

Table S4. Associations of >0+ (parr and older) brown trout abundance with continuous variables lotic stretch size, distance to next lotic stretch, the direction (upstream or downstream) and the size of the next lotic stretch, distance to edge of nearest lentic stretch, and pike presence/absence. Results from mixed zero-inflated binomial distribution model of the effects of continuous data on size and isolation of lotic river habitats on occurrence and density of 1+ (parr and older) brown trout on the spatial only model (Model 1) or extended model with edge and predator effects (Model 2).

	Model 1: Only spatial variables (AIC=1722)				**Model 2: Added predator and edge effects (AIC=1719)**			
Predictors	*Estimate*	*std. Error*	*Z-value*	*p*	*Estimate*	*std. Error*	*Z-value*	*p*
Count Model								
(Intercept)	4.52	0.79	5.69	**<0.001**	4.83	0.81	5.94	**<0.001**
Distance to next habitat	-0.18	0.11	-1.68	0.094	-0.20	0.11	-1.86	**0.063**
Upstream	-0.17	0.70	-0.24	0.811	-0.61	0.72	-0.84	0.403
Size of habitat	0.13	0.06	2.28	**0.023**	0.11	0.07	1.69	0.092
Size of neighbouring habitat	-0.04	0.04	-0.91	0.364	-0.02	0.04	-0.41	0.685
Distance to next habitat * Upstream	0.06	0.14	0.46	0.647	0.14	0.14	1.03	0.301
Distance to edge					-0.04	0.04	-0.97	0.330
Pike presence (1)					-0.73	0.30	-2.41	**0.016**
Distance to edge * Pike presence (1)					0.11	0.06	1.86	0.063
Zero-Inflated Model								
(Intercept)	5.01	2.77	1.80	0.071	5.00	2.77	1.80	0.071
Size of habitat	-0.96	0.29	-3.27	**0.001**	-0.96	0.29	-3.28	**0.001**
Distance to next habitat	-0.09	0.33	-0.28	0.777	-0.09	0.33	-0.28	0.779