Functional diversity and community assembly of river invertebrates show globally consistent responses to decreasing glacier cover.

Article:

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Supplementary information

Supplementary Table 1. Study site information

Region	**Country(ies)**	**Climate**	**Mountain range** **[age M years]**	**Study period**	**Mean latitude of study rivers**	**N study rivers**	**N invertebrate taxa**	**Reference**
Alaska	USA	Temperate, coastal	Coast Mountains [115-130]	1978-2005	58°59’	1	18	(*1*)
European Alps	Austria, Italy	Temperate alpine	Alps [300]	1987-2013	46°59’	70	52	(*2-4*)
Greenland	Greenland	Subarctic, continental	Alángup Qáqai & Prince of Wales Range [1650-2940]	1999	68°00’	12	15	(*5*)
Iceland	Iceland	Temperate/sub-Arctic	Hofsjökull Ice Cap [3-15]	1996-98	65°02’	18	16	(*6*)
New Zealand	New Zealand	Temperate, coastal, alpine	Southern Alps [5-15]	1999-2005	43°49’	21	27	(*7, 8*)
Norway	Norway	Temperate, alpine	Jotunheimen [50]	1996-98	61°33’	15	31	(*9*)
Pyrenees	France	Temperate, alpine	Pyrenees [25-55]	2011	42°45’	26	41	(*10*)
Rocky Mountains	USA	Continental, alpine	Rockies [55-80]	2010	43°12’	9	15	(*11*)
Svalbard	Svalbard	Arctic	Spitsbergen [410-440]	2010-11	78°55’	7	4	(*12*)

Supplementary Table 2. Results of linear models showing the relationships of water temperature and Pfankuch channel stability index (PI) to glacier cover at the global level. Whilst the relationships at this scale are significant, strength would be enhanced with regional to local modifiers (e.g. latitude, altitude, river planform, discharge) which influence river thermal regime in addition to glacier cover.

Dependent variable	**n**	**Intercept**			**Glacier cover**			**R^2**
		β (SE)	***t***	**p**	**β (SE)**	***t***	**p**	
Water temperature	222	7.42 (0.31)	23.9	<2e-16	-0.07 (0.007)	-9.5	<2e-16	0.29
PI	286	27.01 (0.80)	33.75	<2e-16	0.25 (0.02)	12.78	<2e-16	0.37

Supplementary Table 3. Kendall correlation coefficients for fuzzy correspondence analysis (FCA) axis scores and community weighted trait abundance. Correlations r>0.7 are highlighted in bold and P values are adjusted for multiple comparisons using the sequential Holm-Bonferroni method.

		FCA 1		**FCA 2**	
	% variance explained	**43**		**18**	
		Kendal tau	**P adj.**	**Kendal tau**	**P adj.**
Body size	Small	-0.07	1	0.32	<0.0001
	Large	0.07	1	-0.32	<0.0001
Life cycle	Semivoltine	-0.66	<0.0001	-0.05	1
	Univoltine	**-0.77**	<0.0001	0.00	1
	Multivoltine	**0.84**	<0.0001	0.03	1
Pupation	None	**-0.70**	<0.0001	-0.28	<0.0001
	Water	**0.81**	<0.0001	0.11	0.0635
	Land	-0.38	<0.0001	0.57	<0.0001
Adult stage	Aquatic	0.07	1	-0.24	<0.0001
	Aerial (Terrestrial)	-0.09	0.464	0.23	<0.0001
Respiration	Tegument	0.46	<0.0001	-0.20	<0.0001
	Gill	-0.23	<0.0001	-0.25	<0.0001
	Plastron	-0.22	<0.0001	0.07	1
	Spiracle	-0.35	<0.0001	0.58	<0.0001
Locomotion/attachment	Swimmer	-0.17	<0.0001	-0.36	<0.0001
	Crawler	-0.46	<0.0001	0.19	<0.0001
	Burrower	0.54	<0.0001	0.13	0.0087
	Attached	0.16	0.0002	-0.23	<0.0001
Diet	POM deposit	0.61	<0.0001	-0.12	0.0234
	CPOM	**-0.70**	<0.0001	0.06	1
	Algae	-0.46	<0.0001	-0.13	0.0068
	POM suspended	0.58	<0.0001	0.04	1
	Animal	-0.10	0.145	0.16	0.0002
Resistance elements	Eggs	0.24	<0.0001	-0.12	0.0184
	Diapause	-0.14	<0.0001	-0.28	<0.0001
	None	0.04	1	0.33	<0.0001

Supplementary Table 4. Results for GAMM models with optimal random effects structures.

Index	Optimal structure	n	Intercept			s(Glacier cover)			R^2adj
			β (SE)	*t*	p	edf	*F*	p	
Taxonomic richness	Region, basin, site	363	1.75 (0.15)	11.97	<2e-16	3.20	62.82	<2e-16	0.27
FRic	Region, basin, site	271	2.03 (0.14)	14.38	<2e-16	2.36	30.00	1.08e-13	0.17
FDiv	Region	271	0.70 (0.02)	29.79	<2e-16	5.35	4.62	3.50e-4	0.08
FEve	Region	271	0.72 (0.02)	32.01	<2e-16	3.51	31.5	<2e-16	0.28
FDis	Region	363	1.08 (0.09)	12.23	<2e-16	3.94	69.92	<2e-16	0.47
FEnt	Region	363	2.44 (0.14)	17.16	<2e-16	3.95	79.39	<2e-16	0.44
FCA1	Region, basin, site	363	0.026 (0.06)	0.42	0.68	3.94	28.4	<2e-16	0.26
FCA2	Basin, site	363	-0.01 (0.02)	-0.54	0.59	1.0	1.91	0.17	-0.007
Dispersal B-C resid.	Region, site	238	0.23 (0.02)	13.26	<2e-16	2.91	5.67	6.20e-4	0.09
Trait selection B-C resid.	Region	238	-0.012 (0.016)	--0.80	0.43	2.47	17.60	1.51e-8	0.13
Mixed model B-C resid.	Region	238	0.12 (0.02)	7.58	8.04e-13	2.10	8.49	2.75e-4	0.08
FG1*	Region, basin	363	0.11 (0.46)	0.244	0.81	2.44	8.94	8.25e-5	0.58
FG3*	Region	363	-1.10 (0.47)	-2.36	0.02	2.13	5.75	0.004	0.36

*Parametric term for region also included in model

Supplementary Table 5. Functional Group (FG) allocation for each taxon

Taxon	FG	Taxon	FG	Taxon	FG
Agapetus	**1**	Elmis	**9**	Pediciini	**7**
Allomyia	**2**	Empididae	**9**	Perla	**6**
Alloperla	**3**	Epeorus	**9**	Perlidae	**6**
Ameletus	**3**	Ephemerella	**3**	Perlodes	**6**
Amphinemura	**4**	Eriopterini	**4**	Philopotamus	**8**
Amphipoda	**5**	Esolus	**9**	Physa	**5**
Aotopsyche	**2**	Gammaridae	**9**	Plectrocnemia	**8**
Apatania	**1**	Gyraulus	**5**	Podonominae	**8**
Arcynopteryx	**6**	Haliplus	**5**	Polycelis	**5**
Atherix	**7**	Helicopsyche	**9**	Polycentropus	**8**
Austrosimulium	**1**	Hydora	**1**	Potamophylax	**2**
Baetis	**3**	Hydraena	**9**	Potamopyrgus	**5**
Blepharicera	**1**	Hydrobiosis	**8**	Prodiamesinae	**1**
Brachycentrus	**8**	Hydroporus	**9**	Protonemura	**4**
Brachyptera	**4**	Hydropsyche	**8**	Psilochorema	**8**
Capnia	**4**	Isoperla	**6**	Psychodidae	**9**
Capnioneura	**4**	Leuctra	**4**	Pycnocentrodes	**1**
Centroptilum	**5**	Limnophila	**7**	Rhabdiopteryx	**4**
Ceratopogonidae	**1**	Limonia	**7**	Rhithrogena	**3**
Chaetopteryx	**2**	Limoniini	**9**	Rhyacophila	**8**
Chironominae	**1**	Liponeura	**1**	Seratella	**3**
Chloroperla	**4**	Lithax	**1**	Sericostoma	**2**
Chloroperlidae/ Kathoperla	**3**	Lymnaea	**5**	Simuliidae	**1**
Cinygmula	**3**	Maoridiamesa	**1**	Siphlonurus	**3**
Corixidae	**5**	Metanoea	**2**	Siphonoperla	**4**
Costachorema	**8**	Micrasema	**1**	Stenoperla	**6**
Crenobia	**5**	Muscidae	**9**	Suwallia	**3**
Deleatidium	**3**	Nemoura	**4**	Tabanidae	**7**
Diamesinae	**1**	Neocurupira	**1**	Taeniopteryx	**4**
Dicranota	**7**	Nesameletus	**1**	Tanypodinae	**8**
Dictyogenus	**6**	Neurochorema	**8**	Thaumaleidae	**2**
Dinocras	**6**	Oligochaeta	**3**	Tipulidae	**7**
Diura	**6**	Onocosmoecus	**2**	Tricladida	**5**
Dixa/Dixella	**9**	Orthocladiinae	**1**	Utaperla	**3**
Drusus	**2**	Orthocladiinae (NZ)	**1**	Zapada	**3**
Ecclisiopteryx	**2**	other Limnephilini	**2**	Zelandobius	**3**
Ecclisomyia	**2**	Oxyethira	**1**	Zelandoperla	**5**
Ecdyonurus	**3**	Pachyleuctra	**6**		

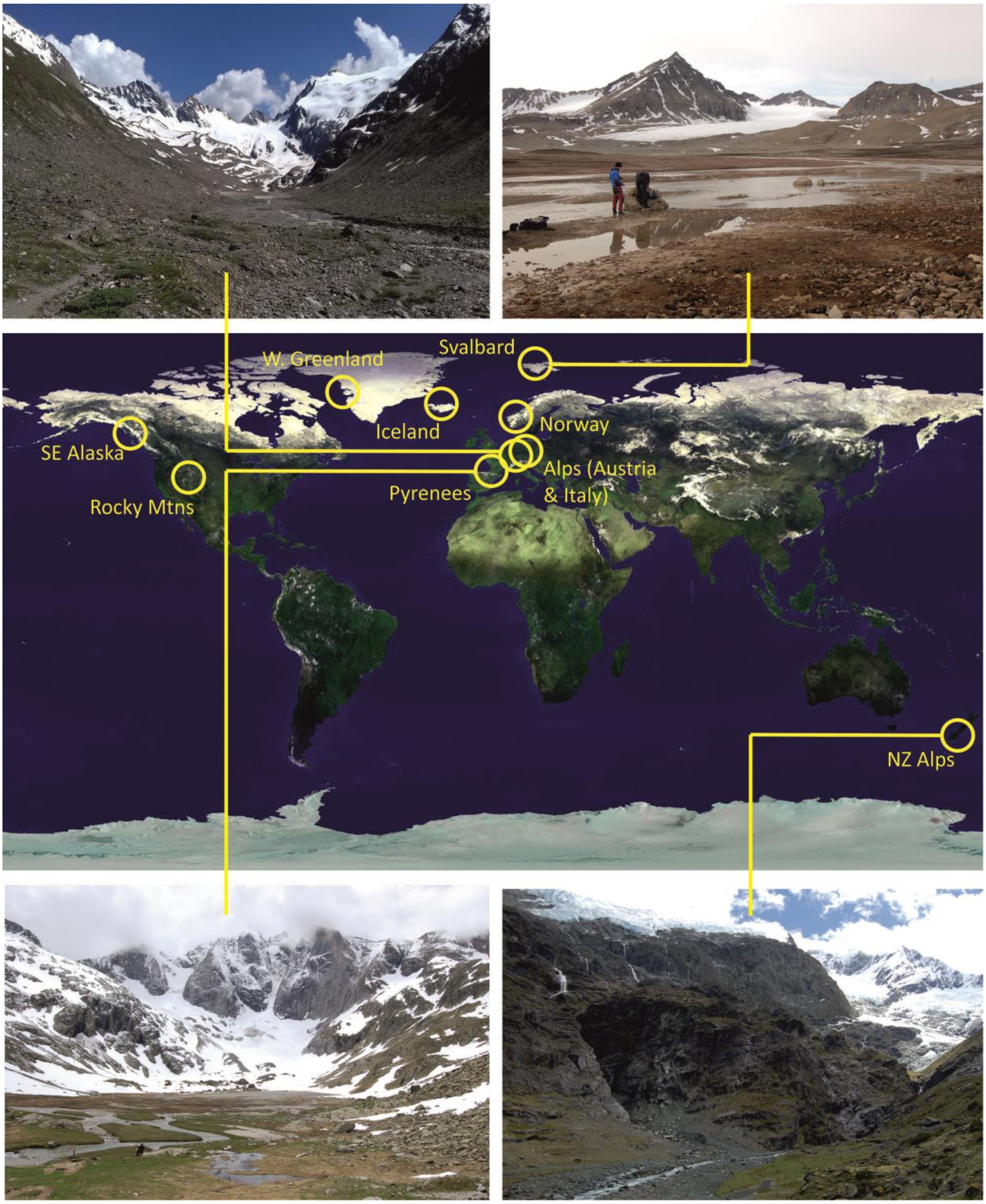
Supplementary Table 6. Results of general linear models for mean latitude at the region level.

Index	n	Intercept			Latitude			R^2
		$\hat{y}$ (SE)	t	p	$\hat{y}$ (SE)	t	p	
FRic	8	21.48 (9.20)	2.33	0.06	-0.23 (0.17)	-1.38	0.22	0.24
FDiv	8	1.03 (0.10)	10.32	4.83e-5	-5.91e-3 (1.82e-3)	-3.24	0.02	0.64
FEve	8	1.08 (0.04)	22.97	1.38e-7	-6.48e-3 (7.05e-4)	-9.20	9.32e-5	0.93
FDis	9	6.43 (0.76)	8.48	6.27e-5	-0.06 (0.01)	-4.27	3.71e-3	0.72
FEnt	9	32.15 (4.69)	6.85	2.42e-4	-0.33 (0.08)	-4.03	5.01e-3	0.70
FCA1	9	-0.71 (0.15)	-4.89	1.77e-3	0.01 (2.52e-3)	5.01	1.55e-3	0.78

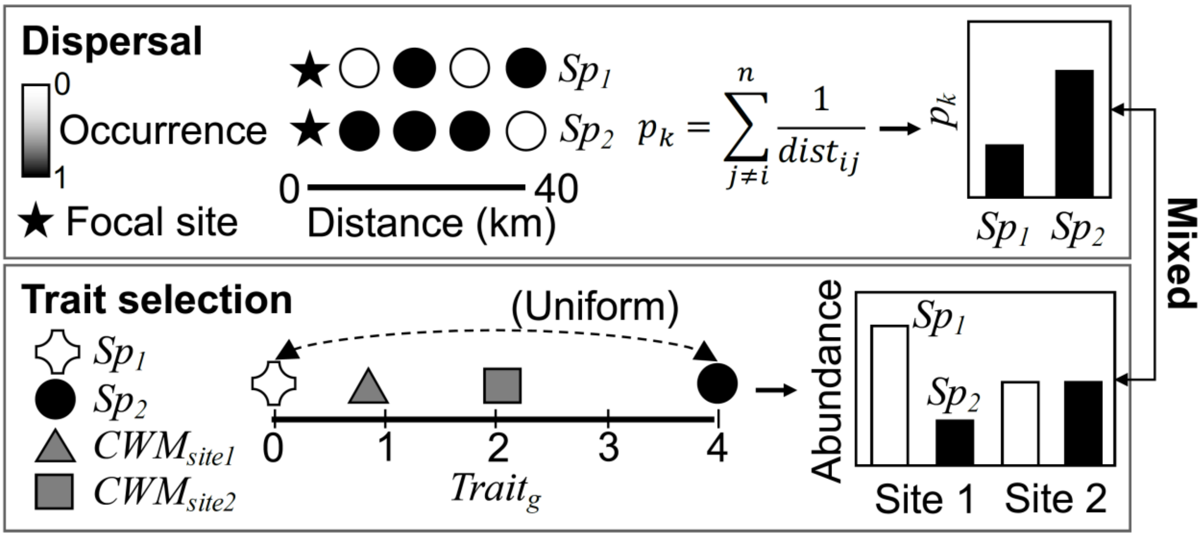
Supplementary Table 7. Regression parameters describing the relationships between glacier cover and FCA1 scores, taxonomic richness and log10 invertebrate abundance for samples collected in Iceland and the European Alps. Seven kick samples from lake-outlet rivers with zero glacier cover in the Alps were omitted as comparable river types were not represented in the Surber sample dataset.

FCA1 scores

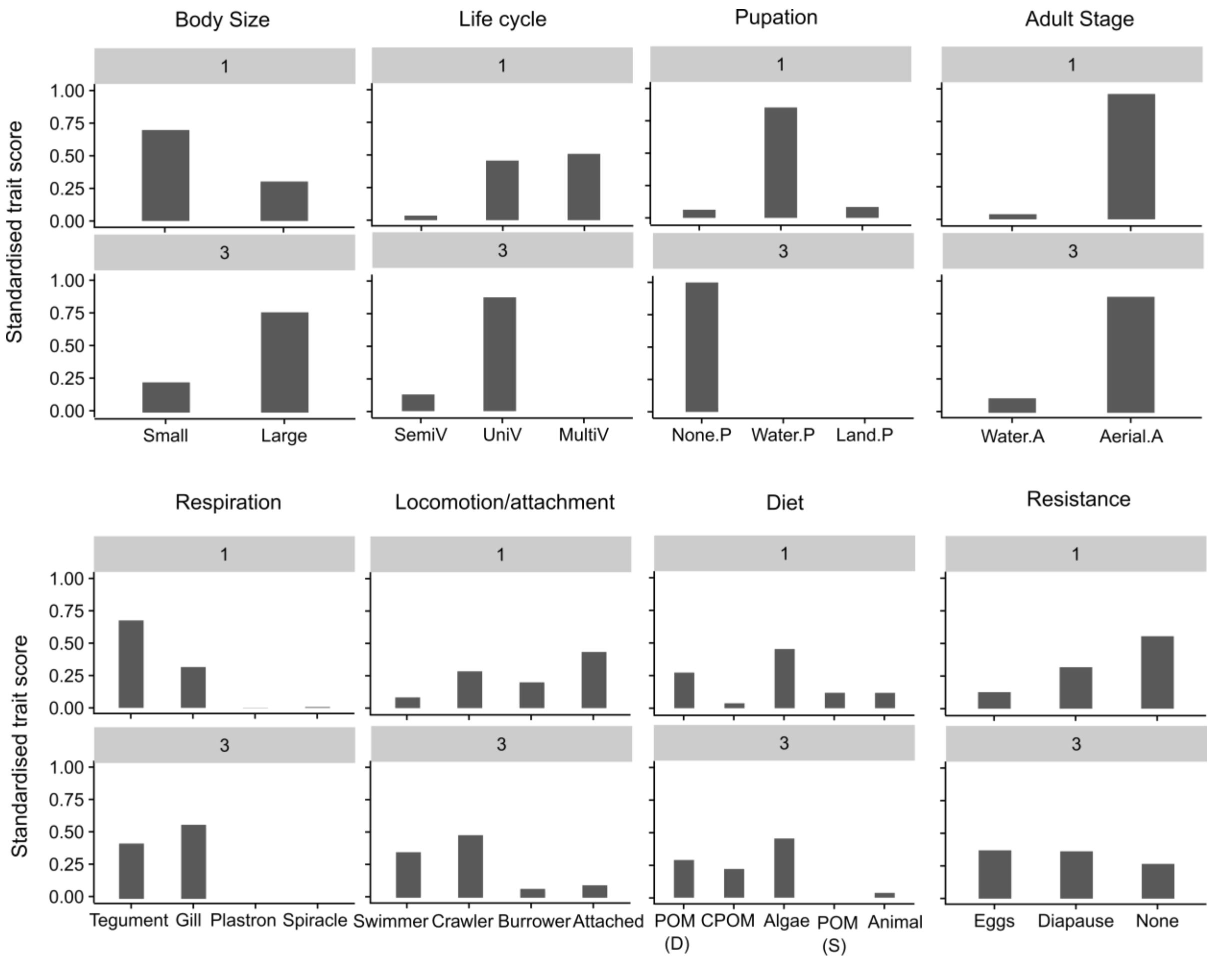
Sample type (region)	**n**	**Glacier Cover**			**Intercept**			**Null dev. (df)**	**Residual dev. (df)**
		β (95% CI)	***t***	**p**	**β (95% CI)**	***t***	**p**		
Iceland									
Stones	58	0.0023 (0.0018, 0.0029)	9.0	1.87e-12	0.14 (0.12, 0.17)	11.8	< 2e-16	0.59 (57)	0.24 (56)
Kick	11	0.0027 (0.0011, 0.0043)	3.4	0.00826	0.13 (0.04, 0.21)	3.0	0.016	0.11 (10)	0.05 (9)
Surber (Alps)	46	0.006 (0.004, 0.008)	5.9	4.3e-07	-0.38 (-0.44, -0.33)	-13.0	< 2e-16	1.59 (45)	0.88 (44)
Kick (Alps)	66	0.007 (0.004, 0.008)	5.5	8.50e-07	-0.32 (-0.44 ,-0.33)	-6.4	2.33e-08	4.41 (65)	3.01 (64)
Taxonomic richness									
Iceland									
Stones	58	-0.068 (-0.081, -0.056)	-10.8	< 2.36e-15	7.63 (7.07, 8.20)	26.5	< 2e-16	428.4 (57)	138.5 (56)
Kick	11	-0.058 (-0.093, -0.022)	-3.1	0.0119	7.21 (5.32, 9.1)	7.5	3.72e-05	52.5 (10)	25.1 (9)
Alps									
Surber	46	-0.14 (-0.20, -0.08)	-4.8	1.69e-05	14.7 (13.0, 16.3)	17.7	< 2e-16	1077.9 (45)	704.5 (44)
Kick	66	-0.22 (-0.29, -0.14)	-5.8	2.11e-7	18.3 (15.5, 21.2)	12.6	< 2e-16	3804.5 (65)	2489.7 (64)
Abundance									
Iceland									
Stones	58	-0.018 (-0.022, -0.015)	-11.0	1.31e-15	4.09 (3.94/4.24)	52.7	< 2e-16	31.8 (57)	10.1 (56)
Kick	11	-0.012 (-0.02, 0.0006)	-1.9	0.0937	2.79 (2.14/3.44)	8.4	1.57e-05	4.2 (10)	3.0 (9)
Alps									
Surber	46	-0.008 (-0.018, 0.001)	-1.7	0.0896	3.72 (3.46, 3.99)	27.1	< 2e-16	20.6 (45)	19.3 (44)
Kick	66	-0.017 (-0.023, -0.011)	-5.8	2.62e-07	3.36 (3.13, 3.58)	29.2	< 2e-16	23.6 (65)	15.6 (64)



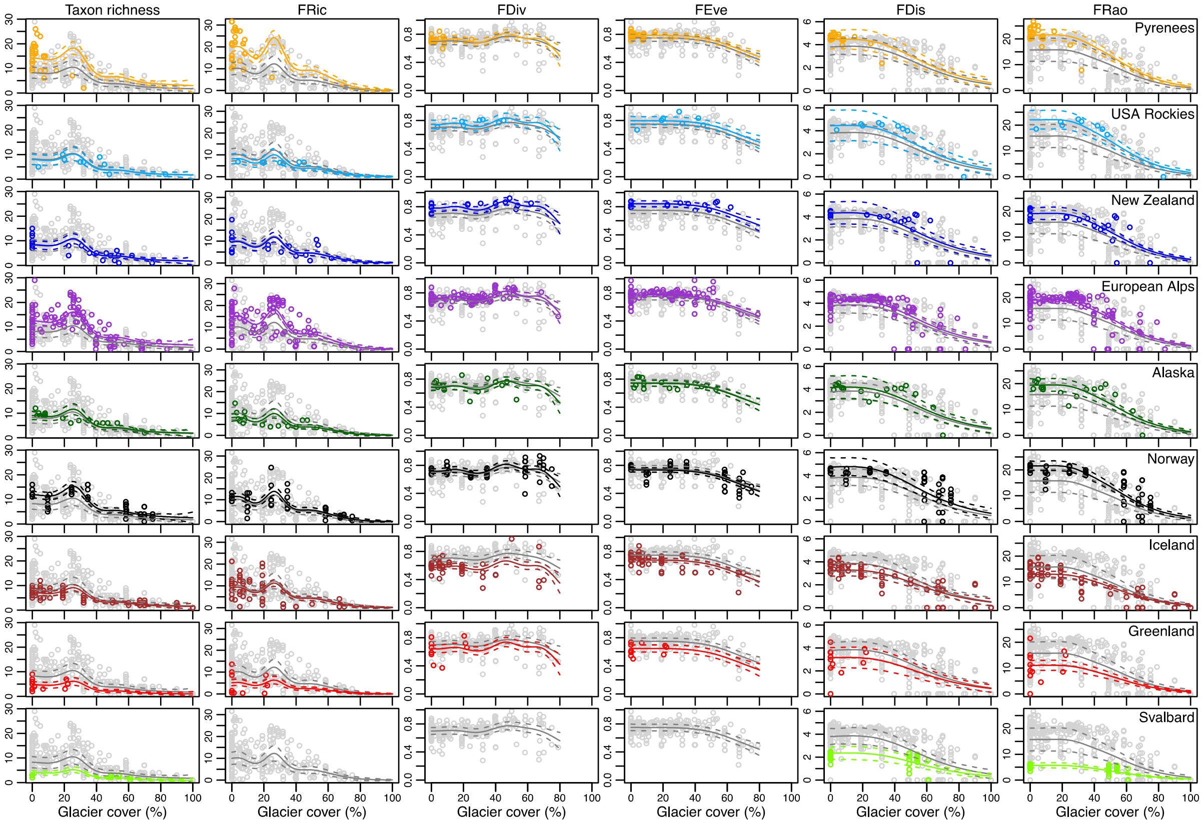
Supplementary Figure 1. Location of study rivers. Samples were collected from ten locations spanning nine biogeographically distinct mountain ranges around the world. Image credits: photographs taken by Lee Brown; Earth image created by Dave Pape using copyright-free AVHRR Pathfinder images (http://flatplanet.sourceforge.net/maps/natural.html accessed 10/11/2018).



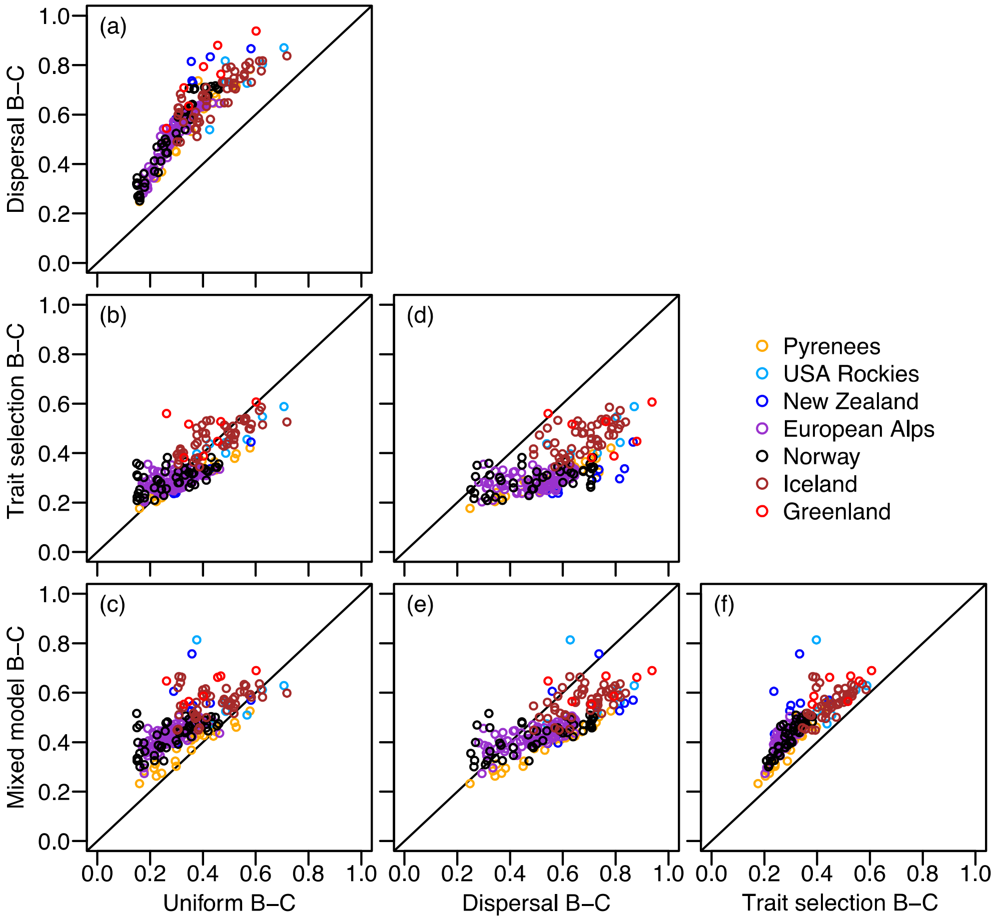
Supplementary Figure 2. Simplified representations of the community assembly model with two species, two sites and one trait. In the dispersal component, occurrences of the k^{th} species (*Sp*) at sites $j=1..n$ in the metacommunity and their distances from the focal site (*i*) determine a probability weighting (p_k) for selection of the species from the pool. In the trait selection component, species are sampled from the pool at random and abundances assigned iteratively until the community weighted mean (*CWM*) for the g^{th} trait satisfies $CWM_{pick}=CWM_{site}\pm T$, where T is a threshold (typically 2.5%) to reduce computational intensity. The mixed component combines dispersal-based occurrences with trait-based abundances. A 'uniform' model is generated by randomly selecting taxa from the species pool, effectively removing the effect of traits (*13*). Species richness is fixed at observed values.



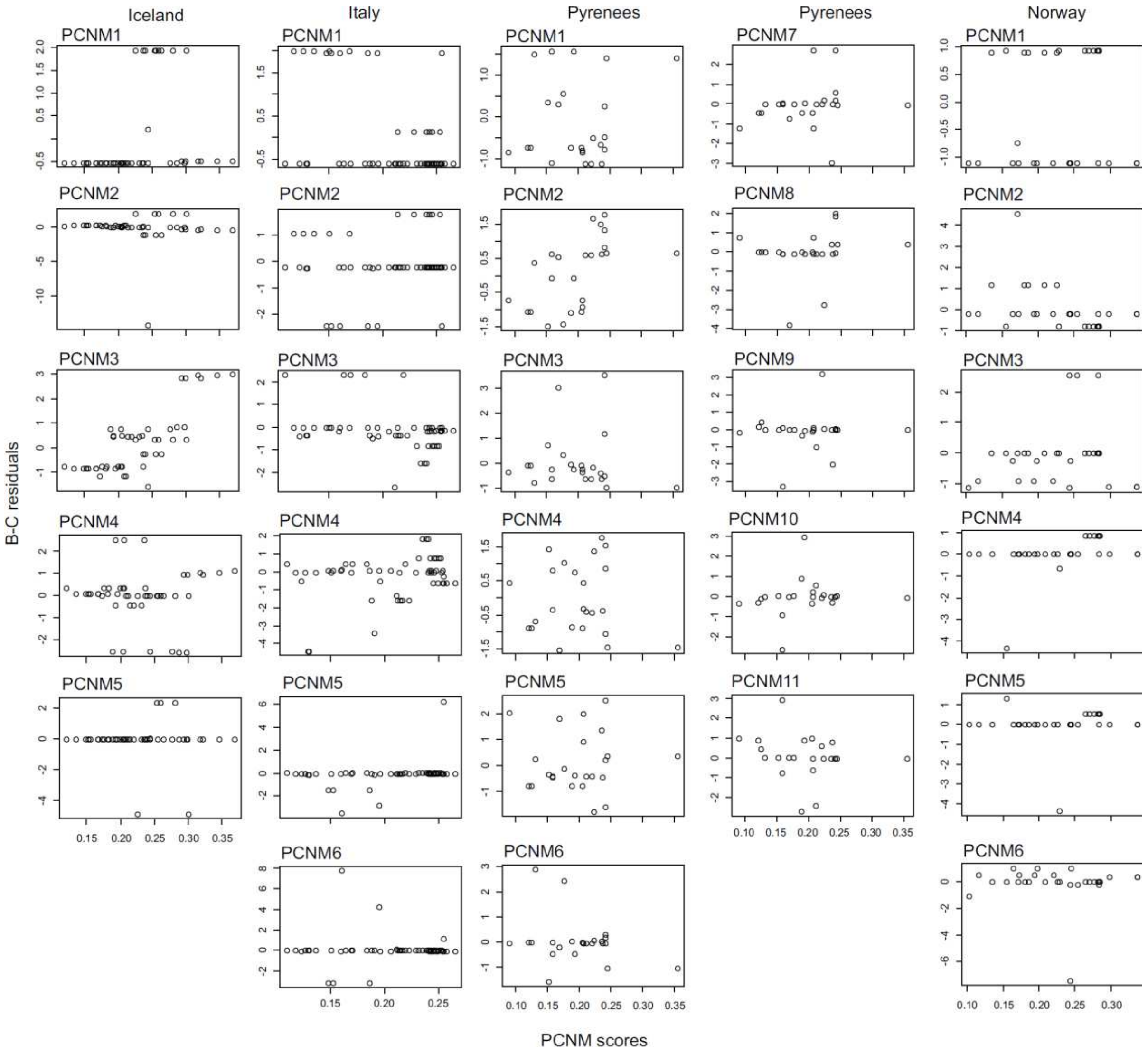
Supplementary Figure 3. Mean trait profiles for the two most common functional groups (FG 1 and 3) represented as average standardised taxon scores.



Supplementary Figure 4. GAMM results for functional diversity indices with region-level random effects structure. Mean global fit shown with solid grey line and 95% confidence intervals shown with dashed grey line. Coloured lines show mean fit (solid) and 95% confidence intervals (dashed) for each region. FRic, FDiv and FEve could not be calculated for Svalbard due to insufficient taxonomic richness.



Supplementary Figure 5. Pairwise comparisons of outputs from four community assembly models (Uniform, Dispersal, Trait selection, Mixed). Points are mean Bray-Curtis (B-C) similarity between observed and mean of null communities from each individual model. Points plot above the solid (1:1) line when observed communities were more similar under the model on the vertical axis. Alaska and Svalbard were not included as the former was a time series at one site, and the latter had insufficient taxonomic richness.



Supplementary Figure 6. Plots of PCNM (Principal Coordinates of Neighbourhood Matrix) scores against 1-Bray-Curtis (B-C) residuals from the dispersal based null model.

References

1. A. M. Milner, A. Robertson, K. Monaghan, A. J. Veal, E. A. Flory, Colonization and development of a stream community over 28 years; Wolf Point Creek in Glacier Bay, Alaska. *Frontiers in Ecology and the Environment* **6**, 413-419 (2008).
2. B. Maiolini, V. Lencioni, Longitudinal distribution of macroinvertebrate assemblages in a glacially influenced stream system in the Italian Alps. *Freshw. Biol.* **46**, 1625-1640 (2001).
3. V. Lencioni, B. Rossaro, Microdistribution of chironomids (Diptera: Chironomidae) in Alpine streams: an autoecological perspective. *Hydrobiologia* **533**, 61-76 (2005).
4. L. Füreder, Life at the edge: habitat condition and bottom fauna of Alpine running waters. *International Review of Hydrobiology* **92**, 492-513 (2007).
5. N. Friberg, A. M. Milner, L. M. Svendsen, C. Lindegaard, S. E. Larsen, Macroinvertebrate stream communities along regional and physico-chemical gradients in Western Greenland. *Freshw. Biol.* **46**, 1753-1764 (2001).
6. G. M. Gíslason, H. Adalsteinsson, I. Hansen, J. S. Olafsson, K. Svavarsdottir, Longitudinal changes in macroinvertebrate assemblages along a glacial river system in central Iceland. *Freshw. Biol.* **46**, 1737-1752 (2001).
7. A. M. Milner, R. C. Taylor, M. J. Winterbourn, Longitudinal distribution of macroinvertebrates in two glacier-fed New Zealand rivers. *Freshw. Biol.* **46**, 1765-1776 (2001).
8. S. L. Cadbury, A. M. Milner, D. M. Hannah, Hydroecology of a New Zealand glacier-fed river: linking longitudinal zonation of physical habitat and macroinvertebrate communities. *Ecohydrology* **4**, 520-531 (2011).
9. J. E. Brittain *et al.*, The macroinvertebrate communities of two contrasting Norwegian glacial rivers in relation to environmental variables. *Freshw. Biol.* **46**, 1723-1736 (2001).
10. K. Khamis, L. E. Brown, D. M. Hannah, A. M. Milner, Glacier–groundwater stress gradients control alpine river biodiversity. *Ecohydrology* **9**, 1263-1275 (2016).
11. C. Thompson, E. David, M. Freestone, C. T. Robinson, Ecological patterns along two alpine glacial streams in the Fitzpatrick Wilderness, Wind River Range, USA. *West. N. Am. Nat.* **73**, 137-147 (2013).
12. P. J. Blaen, L. E. Brown, D. M. Hannah, A. M. Milner, Environmental drivers of macroinvertebrate communities in high Arctic rivers (Svalbard). *Freshw. Biol.* **59**, 378-391 (2014).
13. B. Shipley, Measuring and interpreting trait-based selection versus meta-community effects during local community assembly. *J. Veg. Sci.* **25**, 55-65 (2014).