Supplementary data

Supplementary Table S1. Details of amino acid sequences used in the phylogenetic and rate-shift analyses.

Supplementary Fig. S1. A. Nucleotide sequence alignment of 8 salmonid *akirin1*(*1*) family members that could not be split into two monophyletic clades using phylogenetic analysis with amino acid sequences (see Fig. 1, discussed in main article). Sites underlined in red font highlight fixed substitutions and indels, which demarcate the sequences into two distinct family members inherited from a common ancestor. B. Neighbour joining tree produced using nucleotide data excluding *akirin2* sequences splits salmonid *akirin1*(*1*) family members into two monophyletic clades representing two paralogues. Details of sequences used are in Supplementary Table S1.

Supplementary Fig. S2. Matrix of Pearson's R-values, demonstrating the strength and direction of linear relationships in transcript abundances between the 28 non-reference genes measured across the experimental model altering nutritional state in Arctic charr skeletal muscle. Values highlighted in bold blue and red font represent R-values exceeding 0.7 and 0.8 respectively.

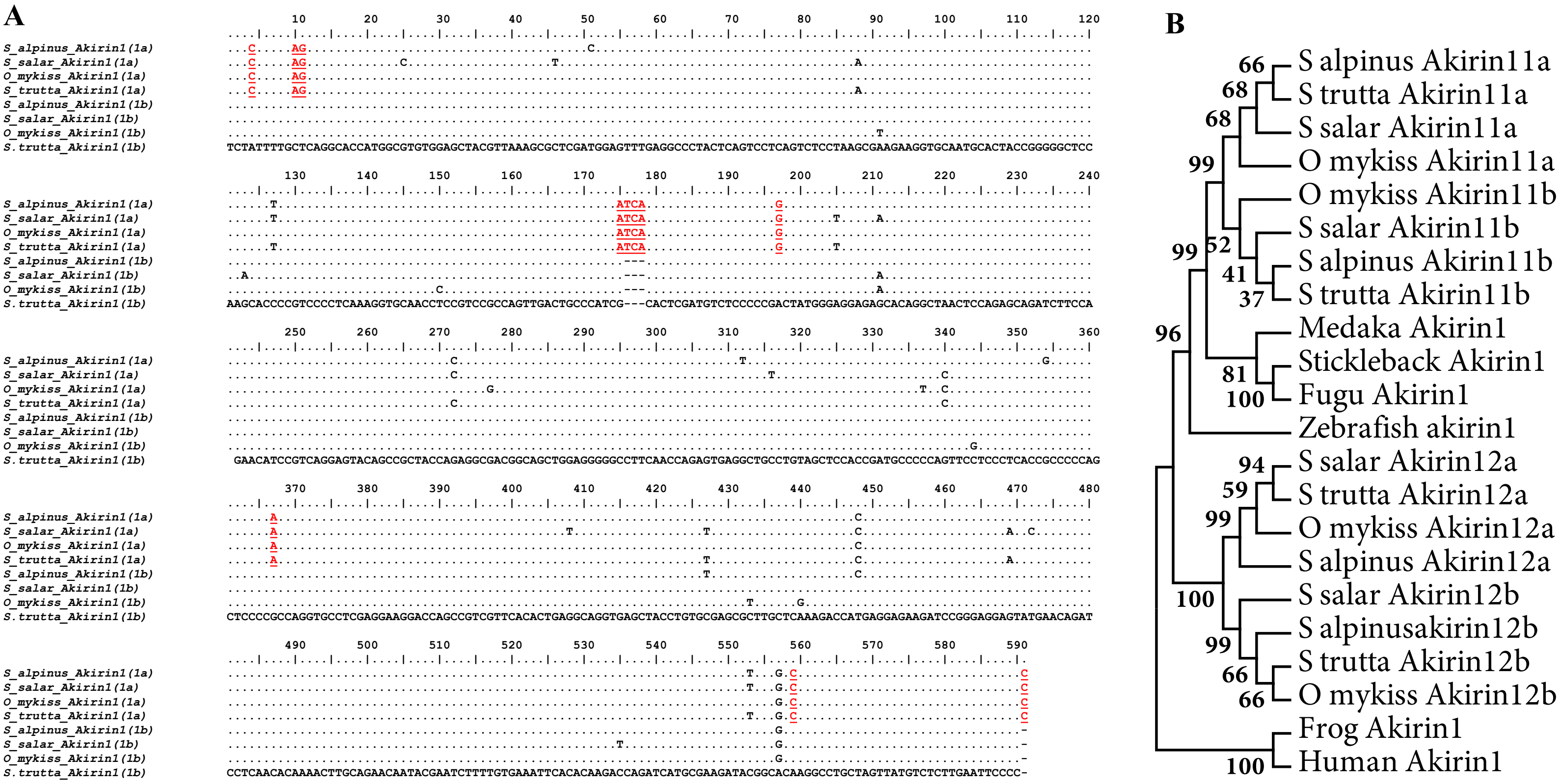
Supplementary Table S1. Details of amino acid sequences used for phylogenetic and rate-shift analyses

Common name	Species	Gene	NCBI Accession number	Ensembl Identifier	Size (amino acids), status [1]	Chromosomal location
Arctic charr	*Salvelinus alpinus*	*akirin1*(*1a*)	GQ247756	N/A	187, complete	N/A
		akirin1(*1b*)	GQ247757	N/A	186, complete	N/A
		akirin1(*2a*)	GQ247758	N/A	187, complete	N/A
		akirin1(*2b*)	GQ247759	N/A	181, complete	N/A
		akirin2(*1a*)	GQ247760	N/A	184, complete	N/A
		akirin2(*1b*)	GQ247761	N/A	184, complete	N/A
		akirin2(*2a*)	GQ247762	N/A	181, complete	N/A
		akirin2(*2b*)	GQ247763	N/A	180, complete	N/A
Atlantic salmon	*Salmo salar*	*akirin1*(*1a*)	GQ247764	N/A	187, complete	N/A
		akirin1(*1b*)	GQ247765	N/A	186, complete	N/A
		akirin1(*2a*)	GQ247766	N/A	187, complete	N/A
		akirin1(*2b*)	GQ247767	N/A	187, complete	N/A
		akirin2(*1a*)	GQ247768	N/A	184, complete	N/A
		akirin2(*1b*)	GQ247769	N/A	184, complete	N/A
		akirin2(*2a*)	GQ247770	N/A	181, complete	N/A
		akirin2(*2b*)	GQ247771	N/A	180, complete	N/A
Brown trout	*Salmo trutta*	*akirin1*(*1a*)	GQ247772	N/A	187, complete	N/A
		akirin1(*1b*)	GQ247773	N/A	186, complete	N/A
		akirin1(*2a*)	GQ247774	N/A	187, complete	N/A
		akirin1(*2b*)	GQ247775	N/A	187, complete	N/A
		akirin2(*1a*)	GQ247776	N/A	184, complete	N/A
		akirin2(*1b*)	GQ247777	N/A	184, complete	N/A
		akirin2(*2a*)	GQ247778	N/A	181, complete	N/A
		akirin2(*2b*)	GQ247779	N/A	180, complete	N/A
Rainbow trout	*Oncorhynchus mykiss*	*akirin1*(*1a*)	GQ247780	N/A	187, complete	N/A
		akirin1(*1b*)	GQ247781	N/A	186, complete	N/A
		akirin1(*2a*)	GQ247782	N/A	191, complete	N/A
		akirin1(*2b*)	GQ247783	N/A	187, complete	N/A
		akirin2(*1a*)	GQ247784	N/A	184, complete	N/A
		akirin2(*1b*)	GQ247785	N/A	180, complete	N/A
		akirin2(*2a*)	GQ247786	N/A	178, complete	N/A
		akirin2(*2b*)	GQ247787	N/A	180, complete	N/A
Common roach	*Rutilus rutilus*	*akirin1*(*1*)	EG540958	N/A	188, complete	N/A
		akirin2(*1*)	EG546460	N/A	162, partial	N/A
Zebrafish	*Danio rerio*	*akirin1*(*1*)	NM_001007186	ENSDARG0000003996	188, complete	Chr 16
		akirin2(*1*)	BC065319	ENSDARG00000058729	180, complete	Chr 20
Fathead minnow	*Pimephales promelas*	*akirin1*(*1*)	DT245087	N/A	188, complete	N/A
		akirin2(*1*)	DT344888	N/A	178, complete	N/A
Blue catfish	*Ictalurus furcatus*	*akirin2*(*2*)	FD160843	N/A	162, partial	N/A
Channel catfish	*Ictalurus punctatus*	*akirin2*(*2*)	FD344768	N/A	188, complete	N/A
Atlantic cod	*Gadus morhua*	*akirin2*(*1*)	EX736334	N/A	186, complete	N/A
		akirin2(*2*)	ES470970	N/A	180, complete	N/A
Three-spined stickleback	*Gasterosteus Aculeatus*	*akirin1*(*1*)	N/A	ENSGACG00000013657	188, complete	Group 20
		akirin2(*1*)	N/A	ENSGACG00000008247	180, complete	Group 18
		akirin2(*2*)	N/A	ENSGACG00000009179	185, complete	Group 15
Japanese medaka	*Oryzias latipes*	*akirin1*(*1*)	N/A	ENSORLG00000014770	187, complete	Chr 16
		akirin2(*1*)	N/A	ENSORLG00000011455	180, complete	Chr 24
		akirin2(*2*)	N/A	ENSORLG00000014760	181, complete	Chr 22

Supplementary Table S1. Continued.

Common name	Species	Gene	NCBI Accession number	Ensembl Identifier	Size (amino acids), status [1]	Chromosomal location
Tiger pufferfish	*Takifugu rubripes*	*akirin2*(*1*)	N/A	ENSTRUG00000017799	183, complete	scaffold_94
		akirin2(*2*)	N/A	ENSTRUG00000006920	186, complete	scaffold_10
Human	*Homo sapiens*	*akirin1*	NM_024595	ENSG00000174574	192, complete	Chr 1
		akirin2	NM_018064	ENSG00000135334	204, complete	Chr 6
Mouse	*Mus musculus*	*akirin1*	NM_023423	ENSMUSG00000023075	192, complete	Chr 4
		akirin2	NM_00100758	ENSMUSG00000028291	202, complete	Chr 4
Chicken	*Gallus gallus*	*akirin2*	BX934526	ENSGALG00000015791	190, complete	Chr 3
Zebra finch	*Taeniopygia guttata*	*akirin2*	DQ213345	ENSTGUG00000012437	194, complete	Chr 3
Western clawed frog	*Xenopus tropicalis*	*akirin1*	BC090594	ENSXETG00000005271	187, complete	scaffold_76
		akirin2	NM_203583	ENSXETG00000019800		
Sea pineapple	*Halocynthia roretzi*	*akirin*	DB608126	N/A	212, complete	N/A
Florida lancelet	*Branchiostoma floridae*	*akirin*	XM_002223114	N/A	216, complete	N/A
Purple sea urchin	*Strongylocentrotus purpuratus*	*akirin*	XM_001182037	N/A	212, complete	N/A

[1] informs the reader the size of the protein sequence and whether it is complete (i.e. has a stop and start codon)


A
S_alpinus_Akirin1(1a)
S_salar_Akirin1(1a)
O_mykiss_Akirin1(1a)
S_trutta_Akirin1(1a)
S_alpinus_Akirin1(1b)
S_salar_Akirin1(1b)
O_mykiss_Akirin1(1b)
S.trutta_Akirin1(1b)
B
S alpinus Akirin11a
S trutta Akirin11a
S salar Akirin11a
O mykiss Akirin11a
O mykiss Akirin11b
S salar Akirin11b
S alpinus Akirin11b
S trutta Akirin11b
Medaka Akirin1
Stickleback Akirin1
Fugu Akirin1
Zebrafish akirin1
S salar Akirin12a
S trutta Akirin12a
O mykiss Akirin12a
S alpinus Akirin12a
S salar Akirin12b
S alpinusakirin12b
S trutta Akirin12b
O mykiss Akirin12b
Frog Akirin1
Human Akirin1
66
68
68
99
99
52
41
37
96
81
100
94
59
99
100
99
66
66
100

GENE	*Akirin1(1a)*																										
Akirin1(1b)	0.472	*Akirin1(1b)*																									
Akirin1(2a)	0.131	0.073	*Akirin1(2a)*																								
Akirin1(2b)	0.348	**0.716**	0.243	*Akirin1(2b)*																							
Akirin2(1a)	0.525	**0.754**	0.088	**0.835**	*Akirin2(1a)*																						
Akirin2(1b)	0.42	0.247	0.398	0.542	0.561	*Akirin2(1b)*																					
Akirin2(2a)	0.478	-0.216	-0.024	-0.262	-0.109	0.262	*Akirin2(2a)*																				
Akirin2(2b)	0.234	-0.386	0.429	-0.073	-0.107	0.62	0.631	*Akirin2(2b)*																			
IGF1	0.329	0.592	0.23	0.325	0.298	0.148	0.044	-0.034	*IGF1*																		
IGF2	0.379	0.384	0.14	0.166	0.388	0.317	0.204	0.074	0.414	*IGF2*																	
BP2(1)	0.407	0.352	0.141	-0.013	0.165	0.059	0.287	-0.077	0.411	0.61	*BP2(1)*																
BP2(2)	0.051	0.203	0.128	0.153	0.144	0.229	0.024	0.159	0.369	0.17	-0.034	*BP2(2)*															
BP6	0.3	-0.029	0.142	-0.13	0.008	0.138	0.254	0.289	0.328	0.505	0.306	0.115	*BP6*														
Mafbx	0.142	-0.546	0.28	-0.406	-0.345	0.324	0.586	**0.79**	-0.102	0.06	0.068	0.149	0.377	*Mafbx*													
Mstn1a	0.275	0.292	-0.144	0.363	0.528	0.317	0.01	-0.076	-0.112	0.308	0.018	0.325	0.013	-0.17	*Mstn1a*												
IGF-IR1a	0.053	-0.448	0.353	-0.492	-0.468	0.152	0.494	0.637	0.085	0.152	0.272	0.019	0.332	**0.791**	-0.48	*IGF1R1a*											
P65	0.199	-0.5	0.29	-0.417	-0.333	0.331	0.571	**0.779**	-0.119	0.099	0.058	0.037	0.386	**0.911**	-0.162	**0.822**	*P65*										
IGF-IR1b	0.021	-0.398	0.383	-0.259	-0.279	0.363	0.336	0.663	0.075	0.064	-0.039	0.291	0.365	**0.792**	-0.218	0.692	**0.78**	*igf1r1b*									
14-3-3G1	0.071	0.675	0.035	0.681	0.63	0.055	-0.526	-0.54	0.237	0.173	0.067	0.2	-0.207	-0.67	0.512	-0.719	-0.669	-0.539	*14-3-3G1*								
14-3-3G2	0.111	**0.768**	-0.206	0.653	0.645	-0.087	-0.556	**-0.738**	0.254	0.115	0.051	0.047	-0.275	**-0.852**	0.413	**-0.831**	**-0.84**	**-0.709**	**0.892**	*14-3-3G2*							
14-3-3B2	0.389	0.579	0.309	**0.765**	0.649	0.576	0.032	0.26	0.307	0.246	-0.034	0.272	0.01	-0.059	0.379	-0.168	-0.013	0.028	0.458	0.339	*14-3-3B2*						
BP4	-0.015	0.517	0.119	0.214	0.146	-0.203	-0.348	-0.52	0.574	0.205	0.436	0.026	-0.009	-0.38	-0.235	-0.076	-0.38	-0.221	0.415	0.457	-0.049	*BP4*					
pappa-1a	0.091	0.336	0.032	0.083	0.173	0.024	-0.018	-0.163	0.607	0.313	0.437	0.13	0.156	-0.067	-0.095	0.131	-0.16	0.001	0.111	0.168	-0.064	0.57	*pappa-1a*				
BP5(2)	0.531	0.511	0.033	0.204	0.417	0.254	0.225	0.03	0.571	0.514	0.535	0.207	0.326	0.093	0.141	0.199	0.149	0.041	0.153	0.127	0.267	0.326	0.46	*BP5(2)*			
Murf1	-0.111	-0.601	0.267	-0.614	-0.606	0.096	0.439	0.642	-0.097	-0.042	0.058	0.083	0.23	**0.859**	-0.405	**0.855**	**0.834**	**0.788**	**-0.747**	**-0.885**	-0.252	-0.248	-0.019	-0.044	*Murf1*		
Stat3	-0.159	-0.126	**0.712**	-0.014	-0.274	0.217	0.015	0.462	0.237	0.079	0.032	0.151	0.073	0.358	-0.385	0.578	0.382	0.424	-0.192	-0.386	0.223	0.093	0.046	-0.107	0.515	*Stat3*	
UBE2H1	-0.109	-0.612	0.366	-0.406	-0.432	0.331	0.408	**0.787**	-0.133	-0.065	-0.051	0.051	0.171	**0.811**	-0.315	**0.823**	**0.863**	**0.764**	-0.658	**-0.853**	-0.05	-0.358	-0.177	-0.101	**0.832**	0.561	*UBE2H1*
UBE2H2	0.021	-0.677	0.209	-0.551	-0.454	0.292	0.522	**0.737**	-0.219	-0.005	-0.004	-0.011	0.291	**0.843**	-0.21	**0.781**	**0.883**	**0.73**	**-0.717**	**-0.882**	-0.276	-0.401	-0.088	-0.015	**0.813**	0.278	**0.882**