

**Table S2.** Sequencing data generated for *T. loennbergii* genome assembly.

Library type	Number of cells	Number of reads	Total read bases (bp)
PacBio	4	6,258,640	77,938,427,833
Hi-C		208,008,742	31,409,320,042
Iso-seq	2	1,211,859	63,927,996,589

**Table S3.** Lengths of *T. loennbergii* genome scaffolds (over 9 Mb).

No.	Scaffold name	Length (bp)
1	trescfv1_00002	48,466,630
2	trescfv1_00399	37,384,537
3	trescfv1_00006	33,625,553
4	trescfv1_00001	32,911,037
5	trescfv1_00023	31,988,177
6	trescfv1_00060	31,753,086
7	trescfv1_00127	31,057,693
8	trescfv1_00016	29,132,375
9	trescfv1_00056	28,046,923
10	trescfv1_00033	26,889,712
11	trescfv1_00103	26,707,442
12	trescfv1_00116	26,366,161
13	trescfv1_00086	25,980,741
14	trescfv1_00027	25,710,439
15	trescfv1_00014	25,647,304
16	trescfv1_00026	24,660,741
17	trescfv1_00066	24,182,687
18	trescfv1_00028	23,546,061
19	trescfv1_00012	23,285,647
20	trescfv1_00037	18,648,639
21	trescfv1_00017	16,915,034
22	trescfv1_00135	15,527,446
23	trescfv1_00055	9,913,305

**Table S4.** Statistics for annotated *T. loennbergii* transposable elements.

Class	Number of elements	Length occupied (bp)	Percentage of sequence (%)
SINEs:	32,294	5,826,086	0.48
MIRs	20,442	4,023,716	0.33
LINEs:	209,794	77,377,903	6.39
LINE1	7,383	5,114,973	0.42
LINE2	117,091	39,115,964	3.23
LTR elements:	76,230	41,535,962	3.43
ERV_classI	5,039	3,099,391	0.26
ERV_classII	139	41,606	0
DNA elements:	573,944	173,022,812	14.29
hAT-Charlie	54,620	16,633,540	1.37
Unclassified:	712,403	190,694,924	15.75
Total interspersed repeats:		488,457,687	40.35
Small RNA:	1,435	1,428,525	0.12
Satellites:	65,154	12,233,455	1.01
Simple repeats:	392,791	38,599,651	3.19
Low complexity:	34,868	2,207,534	0.18
GC level: (%)			41.12
Bases masked:		540,631,316	44.66

**Table S5.** Species information used in this study.

Common name	Species	Assembly
Antarctic scaly rockcod	<i>Trematomus loennbergii</i>	This study
Antarctic icefish	<i>Chaenocephalus aceratus</i>	Kim et al., 2019*
Antarctic dragonfish	<i>Parachaenichthys charcoti</i>	Ahn et al., 2017**
Antarctic bullhead notothen	<i>Notothenia coriiceps</i>	GCA_000735185
Stickleback	<i>Gasterosteus aculeatus</i>	BROAD S1
Spiny chromis	<i>Acanthochromis polyacanthus</i>	ASM210954v1
Midas cichlid	<i>Amphilophus citrinellus</i>	Midas_v5
Orange clownfish	<i>Amphiprion percula</i>	Nemo_v1
Climbing perch	<i>Anabas testudineus</i>	fAnaTes1.1
Pachon cavefish	<i>Astyanax mexicanus</i>	Astyanax_mexicanus-1.0.2
Atlantic herring	<i>Clupea harengus</i>	Ch_v2.0.2
Zebrafish	<i>Danio rerio</i>	GRCz11
Cod	<i>Gadus morhua</i>	gadMor1
Coelacanth	<i>Latimeria chalumnae</i>	LatCha1
Nile tilapia	<i>Oreochromis niloticus</i>	O_niloticus_UMD_NMBU
Japanese medaka HNI	<i>Oryzias latipes</i>	ASM223471v1
Amazon molly	<i>Poecilia formosa</i>	Poecilia_formosa-5.1.2
Yellowtail amberjack	<i>Seriola lalandi dorsalis</i>	Sedor1
Fugu	<i>Takifugu rubripes</i>	fTakRub1.2
Platyfish	<i>Xiphophorus maculatus</i>	X_maculatus-5.0-male

\* Kim et al., 2019, Nature Ecology & Evolution, 3, 469–478.; \*\* Ahn et al., 2017, GigaScience, 6, gix060.

**Table S6.** Summary of gene families of *Trematomus loennbergii* and other fish species.

	Number of genes	Number of genes in orthogroups	Number of unassigned genes	Percentage of genes in orthogroups	Percentage of unassigned genes	Number of orthogroups containing species	Percentage of orthogroups containing species	Number of species-specific orthogroups	Number of genes in species-specific orthogroups	Percentage of genes in species-specific orthogroups
<i>T. loennbergii</i>	29,900	28,556	1,344	95.5	4.5	15,668	62.9	229	895	3.0
<i>N. coriiceps</i>	32,661	29,240	3,421	89.5	10.5	18,396	73.8	114	269	0.8
<i>P. charcoti</i>	32,713	31,571	1,142	96.5	3.5	18,617	74.7	79	421	1.3
<i>C. aceratus</i>	30,773	28,505	2,268	92.6	7.4	17,057	68.5	229	847	2.8
<i>A. polyacanthus</i>	24,027	23,626	401	98.3	1.7	15,771	63.3	66	155	0.6
<i>A. citrinellus</i>	23,696	23,349	347	98.5	1.5	15,305	61.4	18	46	0.2
<i>A. percula</i>	23,926	23,379	547	97.7	2.3	15,458	62.1	20	93	0.4
<i>A. testudineus</i>	24,643	24,270	373	98.5	1.5	15,378	61.7	41	136	0.6
<i>A. mexicanus</i>	26,698	25,403	1,295	95.1	4.9	15,543	62.4	135	632	2.4
<i>C. harengus</i>	24,095	23,349	746	96.9	3.1	14,430	57.9	110	493	2.0
<i>D. rerio</i>	30,313	29,443	870	97.1	2.9	15,205	61.0	207	1,782	5.9
<i>G. morhua</i>	20,095	19,503	592	97.1	2.9	13,904	55.8	17	70	0.3
<i>G. aculeatus</i>	20,787	20,225	562	97.3	2.7	14,149	56.8	16	47	0.2
<i>L. chalumnae</i>	19,569	18,923	646	96.7	3.3	13,305	53.4	124	986	5.0
<i>O. niloticus</i>	28,189	27,440	749	97.3	2.7	15,334	61.6	100	616	2.2
<i>O. latipes</i>	22,127	21,515	612	97.2	2.8	14,522	58.3	34	229	1.0
<i>P. formosa</i>	23,615	23,433	182	99.2	0.8	15,164	60.9	25	87	0.4
<i>S. lalandidorsalis</i>	24,755	24,224	531	97.9	2.1	15,793	63.4	61	131	0.5
<i>T. rubripes</i>	21,411	20,804	607	97.2	2.8	14,120	56.7	50	201	0.9
<i>X. maculatus</i>	23,774	23,291	483	98.0	2.0	15,288	61.4	36	140	0.6

**Table S7.** Gene Ontology of expanded genes families in the *T. loennbergii* genome among twenty fishes.

Category*	GO ID	GO Name	No. genes	P-Value
B	GO:0050907	detection of chemical stimulus involved in sensory perception	32	5.00E-13
B	GO:0020027	hemoglobin metabolic process	16	5.60E-13
B	GO:0009593	detection of chemical stimulus	32	8.10E-12
B	GO:0010605	negative regulation of macromolecule metabolic process	103	1.10E-11
B	GO:0032269	negative regulation of cellular protein metabolic process	61	2.70E-11
B	GO:0051248	negative regulation of protein metabolic process	61	2.70E-11
B	GO:0043086	negative regulation of catalytic activity	59	6.80E-11
B	GO:0051172	negative regulation of nitrogen compound metabolic process	91	9.80E-11
B	GO:0050906	detection of stimulus involved in sensory perception	32	1.20E-10
B	GO:0031324	negative regulation of cellular metabolic process	91	2.50E-10
B	GO:0044092	negative regulation of molecular function	60	7.00E-10
B	GO:0051336	regulation of hydrolase activity	84	6.00E-09
B	GO:0006956	complement activation	19	2.60E-08
B	GO:0032268	regulation of cellular protein metabolic process	97	3.20E-08
B	GO:0051246	regulation of protein metabolic process	99	4.00E-08
B	GO:0098868	bone growth	7	4.10E-08
B	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	7	4.10E-08
B	GO:0003422	growth plate cartilage morphogenesis	7	4.10E-08
B	GO:0003417	growth plate cartilage development	7	4.10E-08
B	GO:0003418	growth plate cartilage chondrocyte differentiation	7	4.10E-08
B	GO:0003429	growth plate cartilage chondrocyte morphogenesis	7	4.10E-08
B	GO:0003416	endochondral bone growth	7	4.10E-08
B	GO:0003433	chondrocyte development involved in endochondral bone morphogenesis	7	4.10E-08
B	GO:0098660	inorganic ion transmembrane transport	89	7.50E-08
B	GO:0000041	transition metal ion transport	17	1.60E-07
B	GO:1902476	chloride transmembrane transport	19	2.00E-07
B	GO:0006821	chloride transport	22	6.20E-07
B	GO:0050790	regulation of catalytic activity	106	6.60E-07
B	GO:0060255	regulation of macromolecule metabolic process	261	9.80E-07
B	GO:0006959	humoral immune response	19	1.20E-06
B	GO:0090171	chondrocyte morphogenesis	7	1.30E-06
B	GO:0034453	microtubule anchoring	9	2.00E-06
B	GO:1902600	proton transmembrane transport	29	2.90E-06
B	GO:0061737	leukotriene signaling pathway	6	3.00E-06
B	GO:0002191	cap-dependent translational initiation	6	3.00E-06

B	GO:0098655	cation transmembrane transport	83	3.90E-06
B	GO:0006508	proteolysis	137	3.90E-06
B	GO:0098661	inorganic anion transmembrane transport	19	4.10E-06
B	GO:0009617	response to bacterium	23	4.20E-06
B	GO:0098662	inorganic cation transmembrane transport	76	5.60E-06
B	GO:0030001	metal ion transport	77	5.70E-06
B	GO:0051171	regulation of nitrogen compound metabolic process	244	6.30E-06
B	GO:0080090	regulation of primary metabolic process	247	6.80E-06
B	GO:0015672	monovalent inorganic cation transport	62	9.80E-06
C	GO:0060077	inhibitory synapse	7	4.10E-08
C	GO:0005858	axonemal dynein complex	11	6.80E-07
C	GO:0015630	microtubule cytoskeleton	56	2.20E-06
M	GO:0061135	endopeptidase regulator activity	55	2.20E-18
M	GO:0030414	peptidase inhibitor activity	54	1.10E-16
M	GO:0061134	peptidase regulator activity	56	1.80E-16
M	GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	18	2.10E-15
M	GO:0004857	enzyme inhibitor activity	56	3.40E-13
M	GO:0031404	chloride ion binding	12	2.60E-12
M	GO:0005247	voltage-gated chloride channel activity	17	3.90E-12
M	GO:0004067	asparaginase activity	12	1.60E-11
M	GO:0008308	voltage-gated anion channel activity	17	8.80E-11
M	GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	38	1.00E-10
M	GO:0005254	chloride channel activity	21	2.20E-10
M	GO:0005253	anion channel activity	21	1.90E-09
M	GO:0003777	microtubule motor activity	37	5.20E-09
M	GO:0015108	chloride transmembrane transporter activity	22	2.20E-08
M	GO:0015299	solute:proton antiporter activity	15	8.50E-08
M	GO:0015078	proton transmembrane transporter activity	32	1.80E-07
M	GO:0043178	alcohol binding	11	1.90E-07
M	GO:0004132	dCMP deaminase activity	6	4.60E-07
M	GO:0019842	vitamin binding	27	6.20E-07
M	GO:0098808	mRNA cap binding	6	3.00E-06
M	GO:0004974	leukotriene receptor activity	6	3.00E-06
M	GO:0070679	inositol 1,4,5 trisphosphate binding	7	3.90E-06
M	GO:0004692	cGMP-dependent protein kinase activity	8	6.60E-06
M	GO:0005540	hyaluronic acid binding	14	8.10E-06

\*B, Biological process; C, Cellular component; M, Molecular function

**Table S8.** Gene Ontology of contracted genes families in the *T. loennbergii* genome among twenty fishes.

Category	GO ID	GO Name	No. genes	P-Value
B	GO:0006796	phosphate-containing compound metabolic process	52	1.10E-10
B	GO:0006793	phosphorus metabolic process	52	1.40E-10
B	GO:0048731	system development	49	2.00E-09
B	GO:0036211	protein modification process	48	2.30E-08
B	GO:0006464	cellular protein modification process	48	2.30E-08
B	GO:0070887	cellular response to chemical stimulus	23	6.50E-08
B	GO:0043412	macromolecule modification	48	1.10E-07
B	GO:1901564	organonitrogen compound metabolic process	70	1.50E-07
B	GO:0044260	cellular macromolecule metabolic process	80	1.60E-07
B	GO:0044267	cellular protein metabolic process	55	3.30E-07
B	GO:0016043	cellular component organization	43	4.10E-07
B	GO:0048368	lateral mesoderm development	5	6.30E-07
B	GO:0006996	organelle organization	32	1.10E-06
B	GO:0006468	protein phosphorylation	26	1.20E-06
B	GO:0016310	phosphorylation	34	1.40E-06
B	GO:1990778	protein localization to cell periphery	6	2.10E-06
B	GO:0080090	regulation of primary metabolic process	42	2.30E-06
B	GO:0009889	regulation of biosynthetic process	34	3.70E-06
B	GO:0031323	regulation of cellular metabolic process	42	3.80E-06
B	GO:2000112	regulation of cellular macromolecule biosynthetic process	33	3.90E-06
B	GO:0019538	protein metabolic process	59	4.30E-06
B	GO:0048513	animal organ development	33	5.10E-06
B	GO:0072659	protein localization to plasma membrane	5	6.00E-06

B	GO:0006355	regulation of transcription, DNA-templated	31	6.30E-06
B	GO:0043170	macromolecule metabolic process	86	6.70E-06
B	GO:0035295	tube development	16	7.10E-06
B	GO:0010556	regulation of macromolecule biosynthetic process	33	7.10E-06
B	GO:0071310	cellular response to organic substance	17	7.30E-06
B	GO:0007399	nervous system development	23	7.40E-06
B	GO:0035690	cellular response to drug	6	8.60E-06
B	GO:0031326	regulation of cellular biosynthetic process	33	9.00E-06
B	GO:0051171	regulation of nitrogen compound metabolic process	40	9.10E-06
C	GO:0043227	membrane-bounded organelle	65	1.50E-06
C	GO:0009898	cytoplasmic side of plasma membrane	5	4.10E-06
C	GO:0098562	cytoplasmic side of membrane	5	7.10E-06
C	GO:0031332	RNAi effector complex	3	7.30E-06
C	GO:0016442	RISC complex	3	7.30E-06
M	GO:0004715	non-membrane spanning protein tyrosine kinase activity	7	2.70E-09
M	GO:0019003	GDP binding	6	8.20E-08
M	GO:0004672	protein kinase activity	23	2.90E-06
M	GO:0016773	phosphotransferase activity, alcohol group as acceptor	24	4.70E-06
M	GO:0000287	magnesium ion binding	8	5.50E-06
M	GO:0035198	miRNA binding	3	7.30E-06
M	GO:0004674	protein serine/threonine kinase activity	14	7.60E-06

**Table S9.** Gene Ontology of specific genes families in the *T. loennbergii* genome among four Antarctic fishes.

Category	GO ID	GO Name	No. genes	P-Value
B	GO:0001890	placenta development	6	7.50E-05
B	GO:0022904	respiratory electron transport chain	12	4.80E-05
B	GO:0019646	aerobic electron transport chain	12	3.30E-07
B	GO:0006119	oxidative phosphorylation	12	1.40E-04
B	GO:0042773	ATP synthesis coupled electron transport	12	2.10E-05
B	GO:0021517	ventral spinal cord development	13	1.20E-04
B	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	12	3.30E-07
B	GO:0021515	cell differentiation in spinal cord	13	2.00E-04
B	GO:0021522	spinal cord motor neuron differentiation	13	5.90E-06
B	GO:0038007	netrin-activated signaling pathway	6	2.50E-05
B	GO:0006259	DNA metabolic process	64	3.60E-06
B	GO:0042775	mitochondrial ATP synthesis coupled electron transport	12	1.10E-05
B	GO:0015074	DNA integration	48	3.70E-19
B	GO:0006310	DNA recombination	22	6.50E-07
B	GO:0001701	in utero embryonic development	9	1.30E-05
M	GO:0009055	electron transfer activity	15	8.70E-05
M	GO:0016675	oxidoreductase activity, acting on a heme group of donors	15	3.30E-08
M	GO:0030246	carbohydrate binding	38	2.90E-06
M	GO:0015002	heme-copper terminal oxidase activity	15	3.30E-08
M	GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	10	8.80E-05
M	GO:0016676	oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor	15	3.30E-08
M	GO:0016886	ligase activity, forming phosphoric ester bonds	6	1.80E-04
M	GO:0008452	RNA ligase activity	6	2.50E-05
M	GO:0004129	cytochrome-c oxidase activity	15	3.30E-08
M	GO:0005042	netrin receptor activity	6	4.50E-05
M	GO:0017166	vinculin binding	6	4.50E-05
M	GO:0003972	RNA ligase (ATP) activity	6	2.50E-05
M	GO:0008234	cysteine-type peptidase activity	29	2.40E-04
M	GO:0015078	proton transmembrane transporter activity	19	2.90E-04
M	GO:0005506	iron ion binding	26	9.50E-06
C	GO:0005746	mitochondrial respirasome	12	5.80E-05
C	GO:0098803	respiratory chain complex	12	3.20E-05
C	GO:0072669	tRNA-splicing ligase complex	6	1.20E-04
C	GO:0045277	respiratory chain complex IV	12	9.00E-07
C	GO:0005751	mitochondrial respiratory chain complex IV	12	6.50E-07
C	GO:0070069	cytochrome complex	12	1.70E-06