

Supplementary Table 1. Sequencing stats

		Hd-rR	Hd-rR	Hd-rR	HNI	HNI	HNI	HSOK	HSOK	HSOK
		female	male	mixture of female & male	female	male	mixture of female & male	female	male	mixture of female & male
PacBio HiFi	Total bases	28,631,671,605	29,523,327,361	-	31,689,026,498	29,072,694,331	-	32,392,392,417	28,489,980,806	-
	Coverage	33.7	34.7	-	39.6	36.3	-	38.1	33.5	-
	Number of reads	2,322,255	2,254,969	-	2,047,759	2,094,990	-	2,220,443	1,747,613	-
	N50 length	12,571	13,385	-	15,563	13,736	-	14,360	16,408	-
ONT ultra-long (>50k), sequenced in 2023	Total bases	-	-	48,785,071,987	-	-	45,561,817,127	-	-	45,025,051,201
	Coverage	-	-	57.4	-	-	57	-	-	53
	Number of reads	-	-	534,463	-	-	448,982	-	-	535,872
	N50 length	-	-	94,748	-	-	109,748	-	-	85,314
ONT ultra-long (>100k), sequenced in 2023	Total bases	-	-	22,442,284,126	-	-	25,659,453,632	-	-	16,751,223,404
	Coverage	-	-	26.4	-	-	32.1	-	-	19.7
	Number of reads	-	-	154,417	-	-	165,398	-	-	122,495
	N50 length	-	-	142,788	-	-	154,711	-	-	133,508
ONT ultra-long (>50k), sequenced in 2021	Total bases	-	16,151,057,445	-	-	12,317,180,034	-	-	-	-
	Coverage	-	19	-	-	15.4	-	-	-	-
	Number of reads	-	137,819	-	-	109,846	-	-	-	-
	N50 length	-	133,348	-	-	125,493	-	-	-	-
ONT ultra-long (>100k), sequenced in 2021	Total bases	-	10,704,179,127	-	-	7,810,416,622	-	-	-	-
	Coverage	-	12.6	-	-	9.8	-	-	-	-
	Number of reads	-	60,608	-	-	45,920	-	-	-	-
	N50 length	-	181,761	-	-	173,616	-	-	-	-
		Hd-rR male	Hd-rR female x HNI male							
in situ Hi-C	Total bases	48,946,337,300	9,914,239,800							
	Coverage	57.6	11.7							
	Number of reads	489,463,373	66,094,932							
	N50 length	100	150							

NOTE: Coverage is calculated based on the estimated genome size by GeneScopeFK.

Supplementary Table 2. Assembly stats

		Number of sequences	Total base pairs	Scaffold max length	Scaffold N50 length	Contig max length	Contig N50 length	Mapping based QV	K-mer baesd QV	NOTE	
Hd-rR	v2.3	917	789,703,053	38,248,663	31,148,813	10,255,628	2,416,720	36.3	43.9		
	v2.3 (only chromosomal scaffolds)	24	734,040,372	38,248,663	31,218,526	10,255,628	2,530,934	-	-		
	v3.0.0 (uncrated)	355	871,026,354	51,670,418	36,038,857	51,595,255	35,561,884	49.1	53.6		
	v3.1	28	863,433,717	52,009,884	36,065,826	52,009,884	36,065,826	57.6	56.0		
	v3.1 (only chromosomal scaffolds)	28	863,433,717	52,009,884	36,065,826	52,009,884	36,065,826	-	-		chr1-24 + chrM + chr1_Y + chr1_Y_2 + chr1_Y_3
HNI	v2.3	1,474	749,060,063	35,737,580	28,784,337	6,798,599	1,303,079	38.8	45.9		
	v2.3 (only chromosomal scaffolds)	24	677,633,405	35,737,580	28,873,095	6,798,599	1,450,098	-	-		
	v3.0.0 (uncrated)	377	840,480,988	50,037,021	34,296,461	39,528,882	31,916,670	49.2	53.9		
	v3.1	182	835,773,411	43,986,858	34,297,563	43,986,858	33,354,181	49.2	53.9		
	v3.1 (only chromosomal scaffolds)	26	826,043,620	43,986,858	34,297,563	43,986,858	33,354,181	-	-		chr1-24 + chrM + chr1_Y
HSOK	v2.3	1,190	808,961,282	39,097,270	31,686,036	12,571,418	3,258,597	36.8	43.7		
	v2.3 (only chromosomal scaffolds)	24	744,414,398	39,097,270	32,853,055	12,571,418	3,516,609	-	-		
	v3.0.0 (uncrated)	611	882,466,574	52,269,905	36,194,818	32,661,471	15,487,369	47.6	51.6		
	v3.1	275	870,878,710	44,615,909	35,769,845	32,661,471	14,718,343	47.7	51.9		
	v3.1 (only chromosomal scaffolds)	26	849,092,814	44,615,909	36,194,818	32,661,471	15,487,369	-	-		chr1-24 + chrM + chr1_Y

Supplementary Table 3. Gene annotation of the T2T assembly of Hd-rR and near-T2T assemblies of HNI and HSOK

Hd-rR	v2.2.4 NCBI GFF	v3.1 complete genome			
		Liftoff	Helixer	BRAKER3	merged
gene	26,658	22,406	28,048	31,245	36,040
mRNA	44,767	45,485	28,048	40,031	60,420
exon	687,378	666,947	310,253	372,181	705,613
CDS	629,213	639,030	289,806	372,181	676,007
5' UTR	43,815	44,427	43,031	-	72,617
3' UTR	43,761	44,387	31,254	-	51,097
longest sequence (aa)	31,552	31,552	34,880	10,190	31,552
shortest sequence (aa)	23	5	33	2	20
mean sequence length (aa)	783	788	543	506	682
core genes (complete)	98.5%	98.5%	89.7%	97.5%	99.6%
core genes (missing)	1.5%	1.5%	4.7%	2.2%	0.3%

HNI & HSOK	HNI (250306) 1-24	HNI (250306) Y	HSOK (250306) 1-24	HSOK (250306) Y
Number of genes	28,161	858	29,340	315
Number of mRNAs	28,183	861	29,366	315
BUSCO completeness (%)	99.6	-	99.8	-
Number of core genes (complete)	3,627	108	3,632	30
Number of missing genes	10	-	7	-

OrthoDB v10: Actinopterygii

BUSCO v5.1.2 (gVolante)

Supplementary Table 4. Centromeres on the assembled genomes

	Hd-rR						HNI						HSOK					
Chr	begin	end	gapless?	Total number of centromeric repeat units	Total base pairs of centromeric repeats	Centromeric position	begin	end	gapless?	Total number of centromeric repeat units	Total base pairs of centromeric repeats	Centromeric position	begin	end	gapless?	Total number of centromeric repeat units	Total base pairs of centromeric repeats	Centromeric position
1	14,904,965	15,178,160	Y	2,103	293,165	submeta	13,875,317	14,299,346	Y	3,290	443,982	submeta	15,005,164	16,162,900	N	7,028	1,001,676	submeta
2	17,199,271	17,672,961	Y	3,638	493,106	submeta	13,565,548	13,977,447	Y	3,135	432,007	submeta	13,485,282	14,099,303	Y	3,788	522,616	submeta
3	9,163,934	9,588,668	Y	3,217	444,659	subtelo	8,898,041	9,607,393	Y	4,080	571,199	subtelo	9,336,435	10,038,253	N	4,950	721,937	subtelo
4	144,477	1,475,732	Y	8,842	1,351,182	acro	20,717	902,127	Y	5,096	777,830	acro	29,499	1,089,506	Y	5,949	900,191	acro
5	166,848	549,761	Y	2,693	402,792	acro	33,807	62,831	Y	335	49,034	di	61,471	1,037,855	Y	6,556	996,425	acro
	-	-	-	-	-	-	2,056,376	2,713,871	Y	4,527	677,394	-	-	-	-	-	-	-
6	19,543	831,521	Y	5,478	832,050	acro	26,961	90,035	Y	554	82,999	di	6	128,528	Y	933	138,538	acro
	-	-	-	-	-	-	3,915,074	4,753,190	Y	4,677	709,987	-	-	-	-	-	-	-
7	30,717	646,741	Y	4,244	635,939	acro	71,255	300,794	Y	1,633	249,449	di	0	248,659	Y	1,717	258,657	acro
	-	-	-	-	-	-	3,590,311	4,417,176	Y	4,498	677,144	-	-	-	-	-	-	-
8	9,965,976	10,375,435	Y	3,011	429,490	submeta	9,435,326	10,130,129	Y	4,090	560,305	submeta	10,267,772	11,998,151	N	10,010	1,441,502	submeta
9	12,063,280	13,163,654	Y	8,219	1,120,160	submeta	11,930,170	12,647,673	N	4,630	625,100	submeta	12,359,449	13,268,791	N	6,324	929,515	submeta
10	87,312	876,652	Y	5,318	809,218	acro	37,220	802,058	Y	3,012	449,459	di	174,518	1,324,725	Y	5,582	842,527	acro
	-	-	-	-	-	-	8,789,790	9,820,526	Y	2,021	304,421	-	-	-	-	-	-	-
11	86,626	309,308	Y	1,662	242,682	acro	50,166	593,344	Y	3,700	563,181	acro	59,907	584,059	Y	3,594	544,043	acro
12	11,006,064	11,573,351	Y	4,080	586,969	submeta	10,037,511	11,117,359	Y	5,356	816,398	submeta	11,086,293	11,859,679	N	4,566	648,622	submeta
13	120,808	565,998	Y	3,077	465,144	acro	1	340,952	Y	2,339	351,020	acro	92,461	436,813	Y	2,436	364,366	acro
14	215,764	580,779	Y	2,638	385,110	acro	67,383	863,592	Y	5,391	816,287	acro	136,385	341,155	Y	1,465	224,739	acro
15	69,279	1,208,513	Y	7,611	1,159,273	acro	101,026	920,153	Y	5,520	839,326	acro	24,187	648,544	Y	4,250	644,246	acro
16	52,807	899,068	Y	5,756	866,466	acro	87,691	168,382	Y	664	100,810	di	0	481,450	Y	3,298	491,483	acro
	-	-	-	-	-	-	4,416,071	5,724,809	Y	4,880	731,339	-	-	-	-	-	-	-
17	15,018	1,336,626	Y	8,786	1,341,563	acro	4,115	405,701	Y	2,752	415,569	acro	258,075	1,044,210	Y	4,152	624,686	acro
18	14,739,988	15,643,359	Y	5,898	923,254	submeta	11,933,018	12,915,527	Y	5,627	864,986	submeta	12,342,689	13,012,756	N	3,880	587,358	submeta
19	9,525,668	10,794,607	Y	7,005	968,913	submeta	9,089,222	9,898,430	N	5,868	829,017	submeta	8,973,106	9,675,671	N	4,930	722,356	submeta
20	7,336,485	8,283,094	Y	6,504	967,458	subtelo	7,053,823	7,803,476	N	4,648	771,348	subtelo	7,753,430	8,082,062	N	2,392	348,614	subtelo
21	16,462,281	17,142,877	Y	3,154	463,887	meta	14,634,826	15,431,579	Y	5,616	816,595	meta	15,881,196	16,687,796	Y	3,549	511,473	meta
22	40,816	211,669	Y	1,371	190,894	acro	40,168	567,551	Y	3,634	547,332	acro	1	105,442	N	799	115,545	acro
23	11,021,153	11,686,900	Y	4,752	685,782	submeta	10,412,788	10,946,612	Y	3,863	553,721	submeta	11,042,713	12,295,035	N	6,413	934,607	submeta
24	109,668	748,730	Y	4,355	658,827	acro	88,826	613,450	Y	3,685	544,633	acro	29,192	223,292	Y	1,431	214,100	acro

NOTE:

Centromeric positions highlighted in blue are those updated from the prior (v2.2.4) assemblies.

Centromeric positions in bold texts are those different from positions in the other strains (i.e. five dicentric chromosomes in HNI) .

Coordinates are 0-indexed, begin-close, end-open (same as BED file).

Supplementary Table 5. List of 6-mers enriched in hypo-/hyper-methylated representative centromere units

SF type	K-mer	Most frequent position in representative units	Enriched in	P-value (chi-square, Bonferroni)	# observed (hypo)	n (hypo)	# observed (hyper)	n (hyper)
SF1	GCATAT	11	hypo	3.6E-07	37	38	11	43
SF1	CATATT	12	hypo	2.9E-05	37	38	15	43
SF1	ATATTG	13	hypo	3.6E-07	37	38	11	43
SF1	TATTGT	14	hypo	6.0E-07	36	38	10	43
SF1	ATTGTA	15	hypo	2.9E-05	35	38	12	43
SF1	TTGTAC	16	hypo	2.6E-03	34	38	15	43
SF1	GTACAT	18	hypo	2.6E-03	34	38	15	43
SF1	TACATA	19	hypo	2.6E-03	34	38	15	43
SF1	ACATAA	20	hypo	3.6E-04	34	38	13	43
SF1	ATAAAA	22	hypo	2.9E-05	37	38	15	43
SF1	TAAAAA	23	hypo	6.4E-04	35	38	15	43
SF3	ATAGCG	75	hypo	2.6E-04	22	35	1	37
SF3	TAGCGT	76	hypo	1.3E-03	22	35	2	37

Merged k-mer motifs:

SF1	GCATATTGTACATAAAAA	11	hypo	4.80E-06	33	38	7	43
SF3	ATAGCGT	75	hypo	3.90E-04	22	35	1	37

Supplementary Table 6. List of Tetatorn copies in the three medaka strains and their QC metrics.

Name	Sequence Name	Start	End	Strand	Number of sequence gaps	Number of read coverage drops	Number of SNVs	Status
Hd-rR_teratorm1_chr1_1	chr1	6,226,018	6,408,873	-	0	0	0	OK
Hd-rR_teratorm1_chr2_1	chr2	265,868	451,529	-	0	0	0	OK
Hd-rR_teratorm1_chr2_2	chr2	1,175,652	1,346,024	+	0	0	0	OK
Hd-rR_teratorm1_chr2_3	chr2	30,057,932	30,242,572	+	0	0	0	OK
Hd-rR_teratorm1_chr2_4	chr2	45,525,551	45,715,623	+	0	0	0	OK
Hd-rR_teratorm1_chr3_1	chr3	17,417,950	17,592,464	+	0	0	0	OK
Hd-rR_teratorm1_chr4_1	chr4	12,695,741	12,881,963	+	0	0	0	OK
Hd-rR_teratorm1_chr4_2	chr4	19,000,761	19,181,920	-	0	0	0	OK
Hd-rR_teratorm1_chr5_1	chr5	5,636,321	5,819,689	+	0	0	0	OK
Hd-rR_teratorm1_chr5_2	chr5	12,596,292	12,778,871	-	0	0	0	OK
Hd-rR_teratorm1_chr5_3	chr5	15,759,782	15,950,616	+	0	0	0	OK
Hd-rR_teratorm1_chr7_1	chr7	5,445,283	5,643,438	-	0	0	0	OK
Hd-rR_teratorm1_chr7_2	chr7	20,932,212	21,092,626	-	0	0	0	OK
Hd-rR_teratorm1_chr8_1	chr8	14,976,966	15,151,499	+	0	0	0	OK
Hd-rR_teratorm1_chr9_1	chr9	8,129,249	8,311,034	-	0	0	0	OK
Hd-rR_teratorm1_chr9_2	chr9	22,099,330	22,280,464	-	0	0	0	OK
Hd-rR_teratorm1_chr9_3	chr9	23,666,312	23,858,179	+	0	0	0	OK
Hd-rR_teratorm1_chr10_1	chr10	22,347,235	22,519,600	-	0	0	0	OK
Hd-rR_teratorm1_chr12_1	chr12	6,914,199	7,106,314	+	0	0	0	OK
Hd-rR_teratorm1_chr12_3	chr12	33,395,679	33,585,957	+	0	0	0	OK
Hd-rR_teratorm1_chr12_4	chr12	34,443,732	34,637,426	-	0	0	0	OK
Hd-rR_teratorm1_chr16_1	chr16	19,531,899	19,714,546	+	0	0	0	OK
Hd-rR_teratorm1_chr16_2	chr16	25,184,618	25,377,939	-	0	0	0	OK
Hd-rR_teratorm1_chr17_1	chr17	13,268,866	13,395,697	+	0	0	0	OK
Hd-rR_teratorm1_chr17_2	chr17	15,964,418	16,147,582	-	0	0	0	OK
Hd-rR_teratorm1_chr17_3	chr17	16,940,170	17,119,179	+	0	0	0	OK
Hd-rR_teratorm1_chr18_1	chr18	17,365,086	17,537,942	-	0	0	0	OK
Hd-rR_teratorm1_chr19_1	chr19	8,111,549	8,305,198	+	0	0	0	OK
Hd-rR_teratorm1_chr19_4	chr19	22,743,029	22,928,263	+	0	0	0	OK
Hd-rR_teratorm1_chr20_1	chr20	24,610,897	24,789,252	-	0	0	0	OK
Hd-rR_teratorm1_chr21_1	chr21	16,774,038	17,030,904	+	0	0	0	OK
Hd-rR_teratorm1_chr21_2	chr21	26,193,411	26,373,036	+	0	0	0	OK
Hd-rR_teratorm1_chr22_1	chr22	17,320,134	17,501,007	-	0	0	0	OK
Hd-rR_teratorm1_chr23_1	chr23	21,389,984	21,583,062	-	0	0	0	OK
Hd-rR_teratorm2_chr12_2	chr12	20,838,914	21,013,369	-	0	0	0	OK
Hd-rR_teratorm2_chr19_2	chr19	9,833,003	10,017,878	+	0	0	0	OK
Hd-rR_teratorm2_chr19_3	chr19	10,273,824	10,448,929	-	0	0	0	OK
Hd-rR_teratorm2_chr3_1	chr3	3,726,376	3,908,841	+	0	0	0	OK
Hd-rR_teratorm2_chr8_2	chr8	16,292,882	16,476,888	-	0	0	0	OK
HNI_teratorm1_chr1_3	chr1	15,646,357	15,837,557	+	0	0	0	OK
HNI_teratorm1_chr1_4	misplaced_1	521,725	711,935	+	0	0	0	OK
HNI_teratorm1_chr1_Y_1	chr1_Y	642,537	819,507	+	0	0	0	OK
HNI_teratorm1_chr1_Y_2	chr1_Y	18,962,098	19,143,927	+	0	0	0	OK
HNI_teratorm1_chr1_Y_3	chr1_Y	23,476,045	23,659,563	+	0	0	2	WARN
HNI_teratorm1_chr2_2	chr2	17,725,730	17,900,921	+	0	0	0	OK
HNI_teratorm1_chr2_3	chr2	26,828,588	27,008,356	-	0	0	0	OK
HNI_teratorm1_chr3_1	chr3	8,900,222	9,056,129	+	0	0	0	OK
HNI_teratorm1_chr3_2	chr3	18,481,881	18,656,329	+	0	0	0	OK
HNI_teratorm1_chr4_1	chr4	684,348	819,424	-	0	0	0	OK
HNI_teratorm1_chr4_2	chr4	11,755,172	11,941,088	+	0	0	0	OK
HNI_teratorm1_chr4_3	chr4	20,733,011	20,912,142	-	0	0	0	OK
HNI_teratorm1_chr4_4	chr4	21,046,522	21,226,527	+	0	0	1	WARN
HNI_teratorm1_chr4_5	chr4	25,862,692	26,027,281	-	0	0	1	WARN
HNI_teratorm1_chr7_1	chr7	3,751,643	3,941,337	-	0	0	0	OK
HNI_teratorm1_chr7_2	chr7	32,738,940	32,910,424	-	0	0	1	WARN
HNI_teratorm1_chr8_2	chr8	12,483,669	12,655,412	-	0	0	0	OK
HNI_teratorm1_chr9_2	chr9	12,106,596	12,238,680	+	0	0	0	OK
HNI_teratorm1_chr12_1	chr12	10,077,259	10,243,533	-	0	0	0	OK
HNI_teratorm1_chr12_2	chr12	10,602,086	10,759,254	-	0	0	0	OK
HNI_teratorm1_chr12_3	chr12	12,975,819	13,165,504	+	0	0	2	WARN
HNI_teratorm1_chr12_4	chr12	17,889,023	18,013,911	-	0	0	0	OK
HNI_teratorm1_chr12_5	chr12	18,066,699	18,276,073	+	0	0	1	WARN
HNI_teratorm1_chr14_1	chr14	11,860,257	12,020,638	-	0	0	0	OK
HNI_teratorm1_chr15_1	chr15	1,131,803	1,315,778	+	0	0	0	OK
HNI_teratorm1_chr16_1	chr16	168,384	350,491	-	0	0	0	OK
HNI_teratorm1_chr16_2	chr16	4,550,285	4,736,362	+	0	0	0	OK
HNI_teratorm1_chr16_3	chr16	4,959,938	5,142,426	+	0	0	0	OK
HNI_teratorm1_chr16_4	chr16	5,455,796	5,627,410	+	0	0	0	OK
HNI_teratorm1_chr17_2	chr17	10,146,676	10,321,955	-	0	0	0	OK
HNI_teratorm1_chr18_1	chr18	12,342,251	12,499,875	+	0	0	2	WARN
HNI_teratorm1_chr20_1	chr20	18,781,304	18,970,850	+	0	0	0	OK

HNI_teratom1_chr24_1	chr24	8,927,635	9,094,960	+	0	0	0	OK
HNI_teratom2_chr1_1	chr1	7,955,935	8,153,514	+	0	0	1	WARN
HNI_teratom2_chr1_2	chr1	13,522,106	13,711,484	-	0	0	2	WARN
HNI_teratom2_chr2_1	chr2	15,017,620	15,197,047	-	0	0	0	OK
HNI_teratom2_chr2_4	chr2	40,476,474	40,659,263	-	0	0	0	OK
HNI_teratom2_chr6_1	chr6	4,148,256	4,316,435	+	0	0	0	OK
HNI_teratom2_chr8_1	chr8	9,630,623	9,805,112	-	0	0	0	OK
HNI_teratom2_chr9_1	chr9	4,197,320	4,370,186	+	0	0	0	OK
HNI_teratom2_chr9_3	chr9	25,827,336	26,005,866	-	0	0	0	OK
HNI_teratom2_chr10_1	chr10	160,909	353,953	+	0	0	2	WARN
HNI_teratom2_chr10_2	chr10	449,759	632,211	+	0	0	2	WARN
HNI_teratom2_chr10_3	chr10	10,001,998	10,190,131	-	0	0	0	OK
HNI_teratom2_chr13_1	chr13	18,662,569	18,827,155	-	0	0	0	OK
HNI_teratom2_chr17_1	chr17	486,853	668,312	+	0	0	1	WARN
HNI_teratom2_chr22_1	chr22	23,910,969	24,108,400	+	0	0	0	OK
HNI_teratom2_chr24_2	chr24	12,986,055	13,170,931	-	0	0	2	WARN
HNI_teratom1_chr12_partial	misplaced_4	153,057	185,887	-	0	0	1	WARN
HNI_teratom1_chr13_partial	chr13	87,901	108,545	-	0	0	0	OK
HNI_teratom1_chr18_partial	chr18	11,985,327	12,009,266	-	0	0	5	WARN
HNI_teratom1_chr23_partial	chr23	10,985,174	10,986,345	-	0	0	0	OK
HSOK_teratom1_chr1_1	chr1	15,245,885	15,441,852	+	0	0	0	OK
HSOK_teratom1_chr1_2	chr1	19,700,872	19,944,732	+	1	16	3	NG
HSOK_teratom1_chr1_Y_1	chr1_Y	1,081,640	1,273,507	+	0	0	0	OK
HSOK_teratom1_chr1_Y_2	chr1_Y	2,600,991	2,802,902	+	1	14	0	NG
HSOK_teratom1_chr2_1	chr2	26,125,475	26,291,974	-	0	12	8	NG
HSOK_teratom1_chr3_3_del	chr3	19,903,729	19,936,648	+	1	1	0	NG
HSOK_teratom1_chr3_1	chr3	35,689,342	35,898,205	+	1	2	9	NG
HSOK_teratom1_chr3_2	chr3	38,960,785	39,141,527	+	0	0	0	OK
HSOK_teratom1_chr4_1	chr4	809,387	1,009,116	-	0	0	1	WARN
HSOK_teratom1_chr4_2	chr4	14,435,112	14,625,422	-	1	17	164	NG
HSOK_teratom1_chr4_3	chr4	23,113,239	23,293,855	+	1	12	30	NG
HSOK_teratom1_chr4_4	chr4	26,814,849	26,971,216	+	1	2	78	NG
HSOK_teratom1_chr4_5_del	chr4	34,116,274	34,201,274	+	1	1	0	NG
HSOK_teratom1_chr5_1	chr5	12,201,861	12,414,077	-	1	1	0	NG
HSOK_teratom1_chr6_3	chr6	2,790,583	3,097,115	-	2	3	15	NG
HSOK_teratom1_chr6_4_del	chr6	26,337,664	26,375,966	+	1	1	0	NG
HSOK_teratom1_chr6_1	chr6	26,592,063	26,893,450	+	1	1	3	NG
HSOK_teratom1_chr6_2	chr6	28,575,920	28,747,221	+	1	0	6	NG
HSOK_teratom1_chr7_3_del	chr7	7,099,743	7,199,419	+	1	1	0	NG
HSOK_teratom1_chr7_1	chr7	22,078,869	22,250,381	+	0	0	0	OK
HSOK_teratom1_chr7_2	chr7	27,495,818	27,673,703	-	1	15	4	NG
HSOK_teratom1_chr8_1	chr8	5,634,041	5,869,252	+	1	1	30	NG
HSOK_teratom1_chr8_2	chr8	7,065,231	7,224,437	+	0	0	0	OK
HSOK_teratom1_chr8_3	chr8	8,366,972	8,543,979	+	0	0	0	OK
HSOK_teratom1_chr8_4	chr8	9,705,297	9,890,477	+	0	0	0	OK
HSOK_teratom1_chr8_5	chr8	10,539,352	10,703,785	+	0	0	0	OK
HSOK_teratom1_chr8_6	chr8	10,775,505	10,959,942	+	0	0	0	OK
HSOK_teratom1_chr8_7	chr8	23,172,222	23,350,892	-	1	1	3	NG
HSOK_teratom1_chr9_1	chr9	6,215,087	6,416,287	+	1	1	1	NG
HSOK_teratom1_chr9_3	chr9	18,198,916	18,393,905	+	1	0	0	NG
HSOK_teratom1_chr9_4_del	chr9	20,927,272	21,010,746	-	1	1	9	NG
HSOK_teratom1_chr10_1	chr10	624,025	809,560	-	0	0	12	WARN
HSOK_teratom1_chr10_2	chr10	842,223	1,024,262	+	0	0	1	WARN
HSOK_teratom1_chr10_3	chr10	15,435,927	15,627,202	-	0	13	33	NG
HSOK_teratom1_chr10_4	chr10	27,280,516	27,466,621	-	0	0	0	OK
HSOK_teratom1_chr10_5	chr10	32,544,022	32,708,734	-	1	0	30	NG
HSOK_teratom1_chr11_1	chr11	22,255,456	22,448,506	-	1	1	1	NG
HSOK_teratom1_chr11_2	chr11	28,138,033	28,355,658	-	1	13	2	NG
HSOK_teratom1_chr12_1	chr12	10,454,980	10,656,750	+	1	1	1	NG
HSOK_teratom1_chr12_2	chr12	11,643,319	11,808,115	+	0	0	0	OK
HSOK_teratom1_chr13_4_del	chr13	2,380,847	2,427,073	+	1	1	0	NG
HSOK_teratom1_chr13_1	chr13	19,370,471	19,513,389	+	1	9	5	NG
HSOK_teratom1_chr13_2	chr13	21,168,677	21,357,469	-	0	10	5	NG
HSOK_teratom1_chr13_3	chr13	29,287,118	29,482,039	-	0	1	0	NG
HSOK_teratom1_chr14_1	chr14	0	136,385	+	0	0	2	WARN
HSOK_teratom1_chr14_2	chr14	15,655,718	15,850,766	+	1	12	35	NG
HSOK_teratom1_chr15_1	chr15	16,973,977	17,142,684	+	1	0	22	NG
HSOK_teratom1_chr15_2	chr15	19,896,989	20,086,038	+	1	1	0	NG
HSOK_teratom1_chr15_3	chr15	21,505,796	21,705,209	+	0	0	0	OK
HSOK_teratom1_chr15_4	chr15	23,919,807	24,111,859	-	0	4	1	NG
HSOK_teratom1_chr15_5	chr15	25,789,612	25,980,347	+	0	0	0	OK
HSOK_teratom1_chr15_6	chr15	28,175,222	28,353,142	+	0	0	0	OK
HSOK_teratom1_chr16_1	chr16	9,247,321	9,400,059	-	0	1	1	NG
HSOK_teratom1_chr16_2	chr16	15,024,428	15,147,911	+	0	0	0	OK

HSOK_teratomn1_chr16_3	chr16	17,647,919	17,830,841	-	0	1	0	NG
HSOK_teratomn1_chr16_4	chr16	31,789,421	31,954,879	+	2	4	5	NG
HSOK_teratomn1_chr17_1	chr17	55,714	226,725	+	0	0	5	WARN
HSOK_teratomn1_chr17_2	chr17	262,296	439,596	+	0	0	0	OK
HSOK_teratomn1_chr17_3	chr17	3,690,837	3,879,904	+	0	0	1	WARN
HSOK_teratomn1_chr17_4	chr17	21,200,223	21,332,714	+	1	9	121	NG
HSOK_teratomn1_chr17_5	chr17	31,158,033	31,372,859	+	1	1	0	NG
HSOK_teratomn1_chr18_1	chr18	12,449,594	12,572,236	-	1	1	0	NG
HSOK_teratomn1_chr18_2	chr18	12,877,926	13,073,921	-	2	8	9	NG
HSOK_teratomn1_chr19_1	chr19	15,700,880	15,905,543	-	1	1	5	NG
HSOK_teratomn1_chr19_2	chr19	18,066,073	18,248,095	+	0	0	0	OK
HSOK_teratomn1_chr19_3_del	chr19	23,386,333	23,436,466	-	1	1	0	NG
HSOK_teratomn1_chr21_1	chr21	16,150,725	16,339,435	-	0	0	1	WARN
HSOK_teratomn1_chr21_2	chr21	16,479,244	16,645,682	-	0	6	1	NG
HSOK_teratomn1_chr21_3	chr21	21,539,096	21,738,293	-	0	0	0	OK
HSOK_teratomn1_chr21_4	chr21	24,276,115	24,326,999	-	1	1	0	NG
HSOK_teratomn1_chr22_2_del	chr22	23,725,450	23,794,119	+	1	1	3	NG
HSOK_teratomn1_chr22_1	chr22	24,601,066	24,857,584	-	2	2	29	NG
HSOK_teratomn1_chr23_3_del	chr23	1,754,820	1,792,522	-	1	1	0	NG
HSOK_teratomn1_chr23_1	chr23	11,309,877	11,505,964	+	0	14	1	NG
HSOK_teratomn1_chr23_2	chr23	11,865,669	12,046,681	-	0	0	1	WARN
HSOK_teratomn1_chr24_1	chr24	10,143,698	10,322,120	+	0	0	0	OK
HSOK_teratomn1_chr24_2	chr24	13,876,042	14,048,949	-	0	0	0	OK
HSOK_teratomn1_chr24_3	chr24	18,425,405	18,601,922	+	0	0	0	OK
HSOK_teratomn1_chr24_4	chr24	21,999,130	22,193,600	+	0	0	1	WARN
HSOK_teratomn1_chr24_5	misplaced_9	0	176,496	-	2	4	15	NG
HSOK_teratomn1_ptg000092l_1	ptg000092l	537,076	726,905	+	0	0	1	WARN
HSOK_teratomn1_ptg00131l_1	ptg000131l	71,206	252,326	-	0	0	1	WARN
HSOK_teratomn2_chr9_2	chr9	13,268,792	13,409,918	+	0	0	0	OK
HSOK_teratomn1_chr1_partial3	chr1	22,300,408	22,301,177	+	0	0	0	OK
HSOK_teratomn1_chr1_partial1	chr1	25,299,520	25,328,909	-	0	0	0	OK
HSOK_teratomn1_chr1_partial2	misplaced_1	14,673	16,929	+	0	1	0	NG
HSOK_teratomn1_chr2_partial1	chr2	29,331,199	29,331,971	-	0	0	0	OK
HSOK_teratomn1_chr4_partial1	chr4	25,798,509	25,814,883	-	0	3	0	NG
HSOK_teratomn1_chr4_partial2	misplaced_3	817,861	833,779	-	0	0	0	OK
HSOK_teratomn1_chr6_partial1	chr6	22,516,561	22,555,081	+	1	1	1	NG
HSOK_teratomn1_chr8_partial1	chr8	11,626,272	11,627,375	+	0	0	0	OK
HSOK_teratomn1_chr11_partial1	chr11	55,678	57,068	-	0	0	0	OK
HSOK_teratomn1_chr12_partial1	chr12	11,085,410	11,086,293	+	0	0	0	OK
HSOK_teratomn1_chr13_partial3	chr13	91,690	92,461	+	0	0	0	OK
HSOK_teratomn1_chr13_partial2	chr13	26,673,993	26,675,195	+	0	0	0	OK
HSOK_teratomn1_chr13_partial1	chr13	29,527,405	29,543,844	-	0	0	0	OK
HSOK_teratomn1_chr18_partial1	chr18	15,180,018	15,220,890	+	0	0	0	OK
HSOK_teratomn1_chr21_partial1	chr21	14,169,007	14,210,754	-	0	0	0	OK
HSOK_teratomn1_chr22_partial1	chr22	99,364	100,135	+	0	0	0	OK
subtype1_leftTIR	chr24	14,453	29,190	-	0	0	0	OK
ptg000026l_teratomn1_partial	ptg000026l	67,564	102,097	-	0	0	0	OK
ptg000154l_teratomn1_partial	ptg000154l	150,932	179,728	-	0	0	0	OK
ptg000115l_teratomn1_partial	ptg000115l	38,296	64,914	-	0	0	0	OK
ptg000141l_teratomn1_partial	ptg000141l	97,942	115,877	-	0	1	1	NG
ptg000202l_teratomn1_partial	ptg000202l	86,965	92,225	-	0	0	0	OK
ptg000203l_teratomn1_partial	ptg000181l	69,712	70,483	+	0	1	0	NG
ptg000204l_teratomn1_partial	ptg000158l	17,768	18,539	+	0	0	0	OK
ptg000205l_teratomn1_partial	ptg000130l	15,863	16,634	+	0	0	0	OK
ptg000206l_teratomn1_partial	ptg000106l	19,850	20,621	+	0	0	0	OK
ptg000207l_teratomn1_partial	ptg000109l	19,217	19,876	+	0	0	0	OK
ptg000208l_teratomn1_partial	ptg000143l	32,403	33,046	-	0	0	0	OK

Supplementary Table 7. List of genes on the chr1_Y_3 region of Hd-rR.

mRNA name (predicted)	aa length	protein	aa length	protein name	species	gene	GeneID	bit score	%identity	Query cover (%)
Orylat36035.t1	220	XP_061784775	222	(uncharacterized)	Nerophis lumbriciformis		133575888	258	64.25	87.73
Orylat36036.t1	939	XP_004066287	939	metal transporter CNNM2 isoform X1	<i>Oryzias latipes</i>	cnm2	101175055	1936	99.57	100.00
		NP_060119	875	metal transporter CNNM2 isoform 1	<i>Homo sapiens</i>	CNNM2	54805	1320	79.06	85.30
Orylat36036.t2	918	XP_011477780	918	metal transporter CNNM2 isoform X2	<i>Oryzias latipes</i>	cnm2	101175055	1894	99.56	100.00
		NP_951058	853	metal transporter CNNM2 isoform 2	<i>Homo sapiens</i>	CNNM2	54805	1290	78.98	84.97
Orylat36037.t1	379	XP_020561162	379	arsenite methyltransferase	<i>Oryzias latipes</i>	as3mt	101161375	782	99.47	100.00
		NP_065733	375	arsenite methyltransferase	<i>Homo sapiens</i>	AS3MT	57412	438	57.75	96.31
Orylat36038.t1	366	XP_023815815	366	WW domain binding protein 1-like isoform X4	<i>Oryzias latipes</i>	wbp1l	101174809	733	98.63	100.00
Orylat36039.t1	577	XP_004066233	577	DNA polymerase lambda isoform X1	<i>Oryzias latipes</i>	poll	101161125	1200	100.00	100.00
		NP_037406	575	DNA polymerase lambda isoform a	<i>Homo sapiens</i>	POLL	27343	637	58.08	100.00
Orylat36040.t1	175	XP_023815842	207	protein DPCD	<i>Oryzias latipes</i>	dpcd	101174567	367	100.00	100.00
		NP_056263	203	protein DPCD isoform 2	<i>Homo sapiens</i>	DPCD	25911	197	56.73	97.14

Supplementary Table 8. List of genes on the chr1_Y_2 region of Hd-rR.

mRNA name (predicted)	aa length	protein	aa length	protein name	species	gene	GeneID	bit score	%identity	Query cover (%)
Orylat35992.t1	387	XP_011477694	387	keratin, type I cytoskeletal 13 isoform X1	Oryzias latipes	LOC101160141	101160141	795	100.00	100.00
		NP_002267	400	keratin, type I cytoskeletal 19	Homo sapiens	KRT19	3880	403	62.58	80.10
Orylat35993.t1	396	XP_004066229	396	keratin, type I cytoskeletal 13	Oryzias latipes	LOC101159894	101159894	804	100.00	100.00
Orylat35994.t1	439	XP_004066228	439	keratin, type I cytoskeletal 13	Oryzias latipes	LOC101159648	101159648	882	100.00	100.00
		NP_000413	432	keratin, type I cytoskeletal 17	Homo sapiens	KRT17	3872	383	55.37	80.64
Orylat35995.t1	408	XP_004066227	408	keratin, type I cytoskeletal 19	Oryzias latipes	LOC101159418	101159418	828	99.51	100.00
Orylat35996.t1	98	ALD51259	98	gastrin, partial	Oryzias latipes	GAST		199	100.00	100.00
Orylat35997.t1	813	XP_023810588	813	trafficking kinesin-binding protein 1, partial	Oryzias latipes	LOC101173611	101173611	1635	98.89	100.00
		NP_001336175	932	trafficking kinesin-binding protein 1 isoform 7	Homo sapiens	TRAK1	22906	619	50.90	83.27
Orylat35999.t1	591	XP_023815745	733	junction plakoglobin	Oryzias latipes	LOC101173369	101173369	1222	99.49	100.00
		XP_047291895	745	junction plakoglobin isoform X2	Homo sapiens	JUP	3728	864	72.73	98.31
Orylat36000.t1	253	XP_004066225	253	Kv channel-interacting protein 2	Oryzias latipes	LOC101158830	101158830	525	100.00	100.00
		NP_775284	252	A-type potassium channel modulatory protein KCNIP2 isoform 3	Homo sapiens	KCHIP2	30819	377	69.17	100.00
Orylat36001.t1	689	XP_004066223	689	UPF0668 protein C10orf76 homolog	Oryzias latipes	armh3	101158585	1426	99.86	100.00
		NP_078817	689	armadillo-like helical domain-containing protein 3	Homo sapiens	ARMH3	79591	1198	84.76	100.00
Orylat36003.t1	262	XP_023815738	262	thymidine kinase 2, mitochondrial	Oryzias latipes	tk2	101158333	540	99.62	100.00
		NP_004605	265	thymidine kinase 2, mitochondrial isoform 1 precursor	Homo sapiens	TK2	7084	304	57.81	96.18
Orylat36004.t1	414	XP_023815711	414	LIM domain-binding protein 1 isoform X1	Oryzias latipes	LOC101158085	101158085	867	99.76	100.00
		NP_001106878	411	LIM domain-binding protein 1 isoform 1	Homo sapiens	LDB1	8861	779	93.80	97.34
Orylat36005.t1	997	KAK3506165	996	hypothetical protein QTP70_000859	Hemibagrus guttatus			1693	84.15	100.00
Orylat36006.t1	161	KAK3507903	177	hypothetical protein QTP70_002520	Hemibagrus guttatus			116	50.34	80.12
Orylat36007.t2	950	XP_023815696	950	peroxisome proliferator-activated receptor gamma coactivator-related protein 1 isoform X1	Oryzias latipes	LOC101173124	101173124	1905	99.58	100.00
Orylat36008.t1	688	XP_023815677	688	protein O-GlcNAcase	Oryzias latipes	LOC101172880	101172880	1432	100.00	100.00
Orylat36009.t1	426	XP_023815682	426	soluble calcium-activated nucleotidase 1 isoform X1	Oryzias latipes	LOC101172636	101172636	870	99.77	100.00
		NP_620148	401	soluble calcium-activated nucleotidase 1	Homo sapiens	CANT1	124583	490	60.74	93.66
Orylat36010.t1	291	XP_023815660	291	kynurenine formamidase isoform X1	Oryzias latipes	afmid	101157840	602	100.00	100.00
Orylat36011.t1	223	XP_004066219	223	thymidine kinase, cytosolic	Oryzias latipes	tk1	101157597	460	99.55	100.00
		NP_003249	234	thymidine kinase, cytosolic isoform 1	Homo sapiens	TK1	7083	296	69.68	95.52
Orylat36012.t1	238	XP_004066218	238	synaptogyrin-2	Oryzias latipes	LOC101157351	101157351	488	100.00	100.00
Orylat36013.t1	553	XP_011477543	553	hemicentin-2-like isoform X1	Oryzias latipes	LOC105354740	105354740	1141	99.64	100.00
Orylat36014.t1	530	XP_024115802	522	Fc receptor-like protein 5	Oryzias melastigma	LOC112137619	112137619	766	78.81	91.51
Orylat36015.t1	705	XP_023815637	702	transmembrane channel-like protein 7 isoform X1	Oryzias latipes	LOC101172389	101172389	1438	99.57	100.00
Orylat36016.t1	260	XP_023815670	260	(uncharacterized)	Oryzias latipes	LOC111948188	111948188	541	100.00	100.00
Orylat36017.t1	829	XP_011477534	829	transmembrane channel-like protein 6	Oryzias latipes	tmc6	101157113	1714	99.88	100.00
Orylat36018.t1	570	XP_023815617	563	tether containing UBX domain for GLUT4	Oryzias latipes	aspscr1	101172137	1123	98.25	100.00
		NP_001238817	647	tether containing UBX domain for GLUT4 isoform 2	Homo sapiens	ASPSCR1	79058	414	50.10	81.40
Orylat36019.t1	310	XP_011477527	310	myeloid-associated differentiation marker-like protein 2	Oryzias latipes	LOC101171891	101171891	620	99.68	100.00
		NP_001138585	307	myeloid-associated differentiation marker-like protein 2	Homo sapiens	MYADML2	255275	326	55.92	97.42
		XP_004066216	321	pyrroline-5-carboxylate reductase 1, mitochondrial	Oryzias latipes	LOC101156872	101156872	649	100.00	100.00

Orylat36020.t1	321	NP_008838	319	pyrroline-5-carboxylate reductase 1, mitochondrial isoform 1	Homo sapiens	PYCR1	5831	524	88.62	90.34
Orylat36021.t1	171	XP_004066215	171	transcription factor MafG	Oryzias latipes	LOC101156633	101156633	341	100.00	100.00
		NP_002350	162	transcription factor MafG	Homo sapiens	MAFG	4097	275	84.30	100.00
Orylat36022.t2	1051	XP_023815554	1051	(uncharacterized)	Oryzias latipes	LOC101171642	101171642	2123	99.72	100.00
Orylat36023.t1	408	XP_023815574	408	NAD-dependent protein deacetylase sirtuin-7	Oryzias latipes	sirt7	101156229	836	99.75	100.00
		NP_057622	400	NAD-dependent protein deacetylase sirtuin-7	Homo sapiens	SIRT7	51547	516	65.19	97.79
Orylat36024.t1	396	XP_023815577	396	ethanolamine-phosphate cytidyltransferase	Oryzias latipes	pcyt2	101171141	830	100.00	100.00
		NP_002852	389	ethanolamine-phosphate cytidyltransferase isoform 2	Homo sapiens	PCYT2	5833	639	77.92	99.24
Orylat36025.t1	363	XP_004066212	363	guanine nucleotide-binding protein G(o) subunit alpha	Oryzias latipes	LOC101155991	101155991	746	99.45	100.00
Orylat36026.t1	257	XP_037399505	254	(uncharacterized)	Pygocentrus nattereri	LOC119264775	119264775	354	66.40	97.28
Orylat36027.t1	130	XP_004066211	130	neuropeptide B	Oryzias latipes	npb	101155748	266	100.00	100.00
Orylat36028.t1	523	XP_004066210	523	N-sulphoglucosamine sulphonylase isoform X1	Oryzias latipes	sgsh	101155495	1083	99.81	100.00
		NP_000190	502	N-sulphoglucosamine sulphonylase isoform 1 precursor	Homo sapiens	SGSH	6448	746	71.26	98.47
Orylat36029.t1	580	XP_020560983	580	sodium-independent sulfate anion transporter	Oryzias latipes	slc26a11	101170906	1182	100.00	100.00
		NP_775897	606	sodium-independent sulfate anion transporter	Homo sapiens	SLC26A11	284129	643	60.28	96.38
Orylat36030.t1	71	XP_004066209	71	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	Oryzias latipes	LOC101155257	101155257	140	100.00	100.00
		NP_005265	68	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	Homo sapiens	GNG5	2787	94.4	65.67	94.37
Orylat36031.t2	432	XP_011477433	432	afadin- and alpha-actinin-binding protein B isoform X1	Oryzias latipes	LOC101170653	101170653	883	100.00	100.00