

Supplementary Materials

Supplementary Table S1 Sequencing data for *Platycephalus* sp.1 genome assembly

Sequencing technology	Library size (bp)	Raw data (Gb)	Clean data (Gb)	Coverage (X) [†]	Mean subread length (bp)	Average read length (bp)
Illumina	350	83.91	83.85	124.31	144	-
PacBio	20,000	138.12	-	204.63	20,099	31,100
Hi-C	350	245.62	72.02	363.88	144	-
RNA-seq	350	43.25	36.55	64.07	144	-

Supplementary Table S2 Reported genome assemblies of species in order Scorpaeniformes

Species	Family	Total length (Mb)	Scaffold number	Scaffold N50	Contig Number	Contig N50	Assembly level	Reference/GenBank assembly accession
<i>Platycephalus</i> sp.1	Platycephalidae	660.63	24	28.65 Mb	60	23.07 Mb	Chromosome	This study
<i>Cyclopterus lumpus</i>	Cyclopteridae	572.88	48	23.86 Mb	395	4.95 Mb	Chromosome	GCA_009769545.1
<i>Ophiodon elongatus</i>	Hexagrammidae	635.57	18,379	5.09 Mb	52,084	0.03 Mb	Scaffold	GCA_004358465.1
<i>Pseudoliparis</i> sp.	Liparidae	840.64	3,134	0.98 Mb	6,333	0.52 Mb	Scaffold	GCA_004335475.1
<i>Liparis tanakae</i>	Liparidae	498.98	27,878	0.38 Mb	97,972	9.90 Kb	Scaffold	GCA_006348945.1
<i>Sebastes aleutianus</i>	Sebastidae	899.65	10,489	0.34 Mb	110,635	10.83 Kb	Scaffold	GCA_001910805.2
<i>Sebastes nigrocinctus</i>	Sebastidae	746.04	15,872	0.12 Mb	89,356	13.47 Kb	Scaffold	GCA_000475235.3
<i>Sebastes rubrivinctus</i>	Sebastidae	756.30	68,206	0.03 Mb	136,109	13.54 Kb	Scaffold	GCA_000475215.1
<i>Sebastes norvegicus</i>	Sebastidae	717.74	75,627	0.02 Mb	117,709	9.47 Kb	Scaffold	GCA_900302655.1
<i>Sebastes koreanus</i>	Sebastidae	725.09	-	-	147,157	16.66 Kb	Contig	GCA_004335335.1
<i>Sebastes schlegelii</i>	Sebastidae	728.48	-	-	146,105	14.25 Kb	Contig	GCA_004335315.1
<i>Sebastes schlegelii</i>	Sebastidae	812.94	1,452	3.85 Mb	1,454	3.85 Mb	Chromosome	He et al., 2019
<i>Sebastes schlegelii</i>	Sebastidae	848.31	854	35.63 Mb	2,019	2.96 Mb	Chromosome	Liu et al., 2019
<i>Sebastes nudus</i>	Sebastidae	724.05	-	-	180,312	11.29 Kb	Contig	GCA_004335365.1
<i>Sebastes minor</i>	Sebastidae	681.65	166,448	7.68 Kb	812,852	1.90 Kb	Scaffold	GCA_001910765.2
<i>Sebastes steindachneri</i>	Sebastidae	648.01	279,232	4.29 Kb	1,089,366	1.31 Kb	Scaffold	GCA_001910785.2
<i>Myoxocephalus scorpius</i>	Cottidae	520.32	85,863	9.47 Kb	127,441	5.72 Kb	Scaffold	GCA_900312955.1
<i>Cottus rhenanus</i>	Cottidae	563.61	164,693	7.25 Kb	490,620	2.13 Kb	Scaffold	GCA_001455555.1
<i>Anoplopoma fimbria</i>	Anoplopomatidae	699.33	-	-	208,506	5.16 Kb	Contig	GCA_000499045.1

Supplementary Table S3 Quality assessment of *Platycephalus* sp.1 genome

Genomic characteristic	Percentage
Illumina reads mapping rate	97.64%
Illumina reads coverage	99.48%
CEGMA evaluation	94.76%
BUSCO evaluation	n = 2586
Complete BUSCOs	96.4%
Complete and single-copy BUSCOs	95.5%
Complete and duplicated BUSCOs	0.9%
Fragmented BUSCOs	1.7%
Missing BUSCOs	1.9%

Supplementary Table S4 Repetitive sequences in *Platycephalus* sp.1 genome

	Repeat size (bp)	Percentage of genome (%)
<i>Identification method</i>		
TRF	25,730,927	3.89
Repeatmasker	158,496,978	23.99
Proteinmask	12,563,434	1.9
Total	167,485,903	25.35
<i>Biological classification</i>		
DNA	20,582,135	3.12
LINE	9,052,614	1.37
SINE	306,702	0.05
LTR	111,043,241	16.81
Unknown	32,202,860	4.87
Total	159,810,468	24.19

Supplementary Table S5 Gene predictions in *Platycephalus* sp.1 genome

	Gene set	Gene number	Average transcript length (bp)	Average CDS length (bp)	Average exons per gene	Average exon length (bp)	Average intron length (bp)
<i>Ab initio</i>	Augustus	29,793	9,305.16	1,312.55	7.56	173.68	1,218.86
	GlimmerHMM	68,401	8,660.25	734.37	4.84	151.79	2,065.10
	SNAP	52,297	13,317.32	912.14	6.27	145.56	2,355.62
	GeneID	31,502	14,734.69	1,319.43	6.62	199.23	2,385.97
	GenScan	31,514	15,540.20	1,556.81	8.79	177.17	1,795.77
Homolog	<i>Gasterosteus_aculeatus</i>	18,919	11,205.88	1,489.70	8.96	166.28	1,220.81
	<i>Gadus_morhua</i>	18,210	10,481.30	1,406.75	8.34	168.59	1,235.62
	<i>Danio_rerio</i>	18,058	11,642.77	1,559.06	8.92	174.71	1,272.56
	<i>Larimichthys_crocea</i>	19,466	12,176.56	1,638.46	9.48	172.92	1,243.38
	<i>Oryzias_latipes</i>	18,375	10,571.58	1,463.01	8.65	169.06	1,190.06
RNAseq	PASA	35,863	12,963.71	1,389.34	8.47	164.01	1,549.26
	Transcripts	40,245	20,154.66	3,576.74	10.88	328.66	1,677.45
EVM		28,083	11,932.77	1,433.67	8.45	169.68	1,409.41
Final		22,743	14,190.20	1,650.16	9.85	167.50	1,416.70

Supplementary Table S6 Gene annotations in *Platycephalus* sp.1 genome

Database	Number	Percentage (%)
Total	22,743	-
Swissprot	20,320	89.3
Nr	21,522	94.6
KEGG	19,479	85.6
InterPro	20,650	90.8
GO	15,264	67.1
Pfam	18,828	82.8
Annotated	21,555	94.8
Unannotated	1,188	5.2

Supplementary Table S7 Non-coding genes in *Platycephalus* sp.1 genome

Type		Copy number	Average length (bp)	Total length (bp)	% of genome
miRNA		1,118	125.44	140,243	0.021229
tRNA		1,267	75.38	95,506	0.014457
rRNA	rRNA	92	171.66	15,793	0.002391
	18S	25	226.16	5,654	0.000856
	28S	34	189.59	6,446	0.000976
	5.8S	3	85	255	0.000039
	5S	30	114.6	3,438	0.00052
snRN	snRNA	399	141.36	56,404	0.008538
A	CD-box	140	115.43	16,160	0.002446
	HACA-bo	89	151.11	13,449	0.002036
	x				
	splicing	136	151.94	20,664	0.003128
	scaRNA	33	184.06	6,074	0.000919
Unknown		1	57	57	0.000009

Supplementary Table S8 Enriched GO terms for expanded genes in *Platycephalus*

sp.1 genome

GO_ID	GO_Term	GO_Class	P-value	Count
GO:0098609	cell-cell adhesion	BP	2.62E-20	28
GO:0016887	ATPase activity	MF	1.71E-14	32
GO:0007156	homophilic cell adhesion	BP	6.67E-13	27
GO:0004252	serine-type endopeptidase activity	MF	2.26E-09	22
GO:0005248	voltage-gated sodium channel activity	MF	8.17E-09	8
GO:0005488	binding	MF	2.06E-07	513
GO:0022804	active transmembrane transporter activity	MF	2.23E-06	26
GO:0001518	voltage-gated sodium channel complex	CC	3.51E-06	8
GO:0042623	ATPase activity, coupled	MF	2.11E-05	19
GO:0008092	cytoskeletal protein binding	MF	2.77E-05	39
GO:0004175	endopeptidase activity	MF	0.000125	34
GO:0016514	SWI/SNF complex	CC	0.000224	7
GO:0051015	actin filament binding	MF	0.000248	13
GO:0070603	SWI/SNF superfamily-type complex	CC	0.000267	11
GO:0035060	brahma complex	CC	0.000267	4
GO:0001784	phosphotyrosine binding	MF	0.000267	4
GO:0005315	inorganic phosphate transmembrane transporter activity	MF	0.000267	4
GO:0032420	stereocilium	CC	0.000267	4
GO:0043492	ATPase activity, coupled to movement of substances	MF	0.000352	16
GO:0030553	cGMP binding	MF	0.000577	5
GO:0032403	protein complex binding	MF	0.00063	28
GO:0015293	symporter activity	MF	0.000654	10
GO:0008017	microtubule binding	MF	0.000654	17
GO:0003713	transcription coactivator activity	MF	0.000861	11
GO:0003712	transcription cofactor activity	MF	0.000966	15
GO:0005247	voltage-gated chloride channel activity	MF	0.001748	5
GO:0016817	hydrolase activity, acting on acid anhydrides	MF	0.001841	53
GO:0017111	nucleoside-triphosphatase activity	MF	0.001947	51
GO:0010557	positive regulation of macromolecule biosynthetic process	BP	0.002034	10
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	BP	0.002034	10
GO:0003779	actin binding	MF	0.002034	21
GO:0016714	oxidoreductase activity, acting on paired	MF	0.002034	4

	donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen			
GO:0016462	pyrophosphatase activity	MF	0.002034	52
GO:0007399	nervous system development	BP	0.00211	19
GO:0031328	positive regulation of cellular biosynthetic process	BP	0.00211	10
GO:0032212	positive regulation of telomere maintenance via telomerase	BP	0.00211	3
GO:0007624	ultradian rhythm	BP	0.00211	3
GO:0009897	external side of plasma membrane	CC	0.00211	3
GO:0008233	peptidase activity	MF	0.002238	41
GO:0005254	chloride channel activity	MF	0.002676	6
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	MF	0.002676	12
GO:0051262	protein tetramerization	BP	0.002693	5
GO:0004800	thyroxine 5'-deiodinase activity	MF	0.002772	4
GO:0016589	NURF complex	CC	0.002772	4
GO:0048839	inner ear development	BP	0.002772	4
GO:0016787	hydrolase activity	MF	0.004625	123
GO:0006275	regulation of DNA replication	BP	0.005014	4
GO:0000723	telomere maintenance	BP	0.005547	5
GO:0015291	secondary active transmembrane transporter activity	MF	0.005638	14
GO:0000146	microfilament motor activity	MF	0.005966	3
GO:0030048	actin filament-based movement	BP	0.005966	3
GO:0032575	ATP-dependent 5'-3' RNA helicase activity	MF	0.005966	3
GO:0010735	positive regulation of transcription via serum response element binding	BP	0.005966	3
GO:0005515	protein binding	MF	0.006608	254
GO:0003714	transcription corepressor activity	MF	0.006744	6
GO:0015698	inorganic anion transport	BP	0.006946	10
GO:0071339	MLL1 complex	CC	0.006946	5
GO:0007600	sensory perception	BP	0.007158	13
GO:0006817	phosphate ion transport	BP	0.007158	4
GO:0030374	ligand-dependent nuclear receptor transcription coactivator activity	MF	0.007158	4
GO:0022857	transmembrane transporter activity	MF	0.007908	66
GO:0006338	chromatin remodeling	BP	0.00901	7
GO:0006508	proteolysis	BP	0.009136	38
GO:0015267	channel activity	MF	0.009163	36
GO:0010629	negative regulation of gene expression	BP	0.010281	11

GO:0005216	ion channel activity	MF	0.011132	34
GO:0017025	TBP-class protein binding	MF	0.011162	3
GO:0070897	DNA-templated transcriptional preinitiation complex assembly	BP	0.011162	3
GO:0005874	microtubule	CC	0.013724	7
GO:0006814	sodium ion transport	BP	0.014017	8
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	BP	0.014017	5
GO:0007224	smoothened signaling pathway	BP	0.014159	4
GO:0004675	transmembrane receptor protein serine/threonine kinase activity	MF	0.01674	5
GO:1901363	heterocyclic compound binding	MF	0.01674	225
GO:0048731	system development	BP	0.01674	25
GO:0005215	transporter activity	MF	0.01674	70
GO:0097159	organic cyclic compound binding	MF	0.01674	225
GO:0004652	polynucleotide adenylyltransferase activity	MF	0.01674	3
GO:0009892	negative regulation of metabolic process	BP	0.01674	13
GO:0007216	G-protein coupled glutamate receptor signaling pathway	BP	0.01674	2
GO:0010961	cellular magnesium ion homeostasis	BP	0.01674	2
GO:0032780	negative regulation of ATPase activity	BP	0.01674	2
GO:0035189	Rb-E2F complex	CC	0.01674	2
GO:0070876	SOSS complex	CC	0.01674	2
GO:0001843	neural tube closure	BP	0.01674	2
GO:0016048	detection of temperature stimulus	BP	0.01674	2
GO:0050951	sensory perception of temperature stimulus	BP	0.01674	2
GO:1900383	regulation of synaptic plasticity by receptor localization to synapse	BP	0.01674	2
GO:0002237	response to molecule of bacterial origin	BP	0.01674	2
GO:0034134	toll-like receptor 2 signaling pathway	BP	0.01674	2
GO:0050429	calcium-dependent phospholipase C activity	MF	0.01674	2
GO:0004363	glutathione synthase activity	MF	0.01674	2
GO:0031297	replication fork processing	BP	0.01674	2
GO:0036310	annealing helicase activity	MF	0.01674	2
GO:0035097	histone methyltransferase complex	CC	0.017157	6
GO:0070011	peptidase activity, acting on L-amino acid peptides	MF	0.017181	36
GO:0045893	positive regulation of transcription, DNA-templated	BP	0.017877	7
GO:0071900	regulation of protein serine/threonine kinase activity	BP	0.019239	4

GO:0030014	CCR4-NOT complex	CC	0.019239	4
GO:0051276	chromosome organization	BP	0.019239	17
GO:0005509	calcium ion binding	MF	0.020944	44
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	BP	0.020944	10
GO:0019894	kinesin binding	MF	0.022853	3
GO:0003950	NAD+ ADP-ribosyltransferase activity	MF	0.023694	5
GO:0009072	aromatic amino acid family metabolic process	BP	0.024781	4
GO:0006260	DNA replication	BP	0.025566	8
GO:0009628	response to abiotic stimulus	BP	0.029699	6
GO:0042995	cell projection	CC	0.029699	6
GO:0006821	chloride transport	BP	0.03409	6
GO:0016043	cellular component organization	BP	0.03799	64
GO:0009581	detection of external stimulus	BP	0.038118	4
GO:0009582	detection of abiotic stimulus	BP	0.038118	4
GO:0004947	bradykinin receptor activity	MF	0.038904	2
GO:0042030	ATPase inhibitor activity	MF	0.038904	2
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	BP	0.038904	2
GO:0070325	lipoprotein particle receptor binding	MF	0.038904	2
GO:1900542	regulation of purine nucleotide metabolic process	BP	0.039244	8
GO:0005871	kinesin complex	CC	0.0427	3
GO:0042393	histone binding	MF	0.0427	3
GO:0003785	actin monomer binding	MF	0.0427	3
GO:0050790	regulation of catalytic activity	BP	0.046126	12
GO:0008146	sulfotransferase activity	MF	0.04643	8
GO:0008134	transcription factor binding	MF	0.048837	5
GO:0000226	microtubule cytoskeleton organization	BP	0.048837	11
GO:0019220	regulation of phosphate metabolic process	BP	0.049602	12
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.049682	7

Supplementary Table S9 Enriched KEGG pathways for expanded genes in

Platycephalus sp.1 genome

Pathway ID	Pathway	P-value	Count
ko04141	Protein processing in endoplasmic reticulum	5.72E-05	31
ko04138	Autophagy - yeast	9.35E-05	17
ko00310	Lysine degradation	9.35E-05	18
ko02010	ABC transporters	0.000529	13
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	0.001088	6
ko00380	Tryptophan metabolism	0.001222	13
ko04136	Autophagy - other	0.004209	10
ko04145	Phagosome	0.010161	23
ko00360	Phenylalanine metabolism	0.029014	6
ko00562	Inositol phosphate metabolism	0.029014	16
ko04140	Autophagy - animal	0.047117	21
ko04391	Hippo signaling pathway - fly	0.047236	15
ko00633	Nitrotoluene degradation	0.047236	2

Supplementary Table S10 Enriched KEGG pathways for contracted genes in

Platycephalus sp.1 genome

Pathway ID	Pathway	P-value	Count
ko05134	Legionellosis	6.64E-05	7
ko04721	Synaptic vesicle cycle	9.45E-05	8
ko04727	GABAergic synapse	0.000208	8
ko03040	Spliceosome	0.000238	8
ko05416	Viral myocarditis	0.000298	6
ko04612	Antigen processing and presentation	0.002298	5
ko00053	Ascorbate and aldarate metabolism	0.003899	3
ko04530	Tight junction	0.004503	8
ko04260	Cardiac muscle contraction	0.009469	5
ko00040	Pentose and glucuronate interconversions	0.00998	3
ko00982	Drug metabolism - cytochrome P450	0.00998	3
ko00860	Porphyrin and chlorophyll metabolism	0.011642	3
ko00980	Metabolism of xenobiotics by cytochrome P450	0.012842	3
ko04012	ErbB signaling pathway	0.012842	5
ko04010	MAPK signaling pathway	0.017713	9
ko05231	Choline metabolism in cancer	0.019922	5
ko05204	Chemical carcinogenesis	0.020232	3
ko05320	Autoimmune thyroid disease	0.020232	3
ko05150	Staphylococcus aureus infection	0.020919	3
ko04213	Longevity regulating pathway - multiple species	0.020919	4
ko00140	Steroid hormone biosynthesis	0.024598	3
ko04725	Cholinergic synapse	0.037219	5
ko05322	Systemic lupus erythematosus	0.037219	3
ko00983	Drug metabolism - other enzymes	0.039692	3
ko00830	Retinol metabolism	0.039692	3
ko01521	EGFR tyrosine kinase inhibitor resistance	0.040527	4

Supplementary Table S11 Enriched GO terms for positively selected genes in
Platycephalus sp.1 genome

GO_ID	GO_Term	GO_Class	P-value	Count
GO:0006807	nitrogen compound metabolic process	BP	1.67E-06	189
GO:0090304	nucleic acid metabolic process	BP	1.67E-06	157
GO:0034641	cellular nitrogen compound metabolic process	BP	7.77E-06	177
GO:0006139	nucleobase-containing compound metabolic process	BP	1.20E-05	171
GO:0046483	heterocycle metabolic process	BP	1.88E-05	173
GO:0016070	RNA metabolic process	BP	1.90E-05	132
GO:0006725	cellular aromatic compound metabolic process	BP	1.90E-05	173
GO:1901360	organic cyclic compound metabolic process	BP	2.89E-05	174
GO:0010467	gene expression	BP	0.000326	140
GO:0003676	nucleic acid binding	MF	0.002875	181
GO:0006351	transcription, DNA-templated	BP	0.028386	93
GO:0043170	macromolecule metabolic process	BP	0.032786	271
GO:0008073	ornithine decarboxylase inhibitor activity	MF	0.033441	3
GO:0044237	cellular metabolic process	BP	0.035015	285
GO:0044260	cellular macromolecule metabolic process	BP	0.040005	238
GO:0034645	cellular macromolecule biosynthetic process	BP	0.046542	119

Supplementary Table S12 Identified positively selected genes with *Platycephalus* sp.1, *Scophthalmus maximus*, and *Cynoglossus semilaevis* as foreground species

Gene ID	P-value	Annotation
evm.model.HIC_ASM_21.952	0.005164	Major facilitator superfamily domain-containing protein 9 OS=Homo sapiens OX=9606 GN=MFSD9 PE=2 SV=2
evm.model.HIC_ASM_3.566	0.003928	Growth/differentiation factor 9 OS=Capra hircus OX=9925 GN=GDF9 PE=3 SV=1
evm.model.HIC_ASM_1.222	1.07E-06	Thyroid receptor-interacting protein 11 OS=Homo sapiens OX=9606 GN=TRIP11 PE=1 SV=3
evm.model.HIC_ASM_0.834	3.82E-09	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5
evm.model.HIC_ASM_22.996	1.34E-08	Clarin-3 OS=Mus musculus OX=10090 GN=Clrn3 PE=1 SV=1
evm.model.HIC_ASM_23.360	7.31E-09	Putative nuclease HARBI1 OS=Danio rerio OX=7955 GN=harbi1 PE=2 SV=1
evm.model.HIC_ASM_16.269.1	1.45E-06	60S ribosomal protein L27a OS=Xenopus laevis OX=8355 GN=rpl27a PE=2 SV=2
evm.model.HIC_ASM_7.959	0.001071	Sodium channel subunit beta-1 OS=Mus musculus OX=10090 GN=Scn1b PE=1 SV=1
evm.model.HIC_ASM_10.110	0.005076	Putative monooxygenase p33MONOX OS=Danio rerio OX=7955 GN=p33monox PE=1 SV=1
evm.model.HIC_ASM_9.663	0.003385	Matrilin-3 OS=Gallus gallus OX=9031 GN=MATN3 PE=2 SV=1
evm.model.HIC_ASM_5.948	0.000905	Transcription factor HES-1-A OS=Xenopus laevis OX=8355 GN=hes1-a PE=1 SV=1
evm.model.HIC_ASM_9.509.2	5.25E-07	Phospholipase ABHD3 OS=Homo sapiens OX=9606 GN=ABHD3 PE=1 SV=2
evm.model.HIC_ASM_12.414	3.56E-05	Mitochondrial import inner membrane translocase subunit TIM14 OS=Bos taurus OX=9913 GN=DNAJC19 PE=3 SV=3
evm.model.HIC_ASM_15.261	7.42E-06	Ras-related protein Ral-A OS=Homo sapiens OX=9606 GN=RALA PE=1 SV=1
evm.model.HIC_ASM_13.242	7.06E-07	Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens OX=9606 GN=SREK1 PE=1 SV=1
evm.model.HIC_ASM_20.1107	3.18E-10	Eukaryotic translation initiation factor 3 subunit B OS=Bos taurus OX=9913 GN=EIF3B PE=2 SV=1
evm.model.HIC_ASM_19.994.1	0.000138	CXADR-like membrane protein OS=Homo

evm.model.HIC_ASM_13.612	0	sapiens OX=9606 GN=CLMP PE=1 SV=1 NF-kappa-B inhibitor-like protein 1 OS=Homo sapiens OX=9606 GN=NFKBIL1 PE=1 SV=1
evm.model.HIC_ASM_12.1168	0.001936	Cystathionine gamma-lyase OS=Bos taurus OX=9913 GN=CTH PE=2 SV=1
evm.model.HIC_ASM_2.900	0.006456	Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=3
evm.model.HIC_ASM_0.434	6.32E-07	Fibroblast growth factor 7 OS=Canis lupus familiaris OX=9615 GN=FGF7 PE=2 SV=1
evm.model.HIC_ASM_20.433	4.33E-10	Sodium-independent sulfate anion transporter OS=Homo sapiens OX=9606 GN=SLC26A11 PE=2 SV=2
evm.model.HIC_ASM_8.325	0.005101	5-hydroxytryptamine receptor 3A OS=Cavia porcellus OX=10141 GN=HTR3A PE=1 SV=1
evm.model.HIC_ASM_11.906	3.75E-06	Chymotrypsin-like protease CTRL-1 OS=Homo sapiens OX=9606 GN=CTRL PE=2 SV=1
evm.model.HIC_ASM_0.586	0	NA
evm.model.HIC_ASM_13.596	0.000741	Calcium-binding protein 1 OS=Homo sapiens OX=9606 GN=CABP1 PE=1 SV=5
evm.model.HIC_ASM_22.153	0	Probable G-protein coupled receptor 142 OS=Homo sapiens OX=9606 GN=GPR142 PE=2 SV=1
evm.model.HIC_ASM_15.104.1	0.006695	Ras-responsive element-binding protein 1 OS=Gallus gallus OX=9031 GN=RREB1 PE=2 SV=2
evm.model.HIC_ASM_16.298	1.36E-07	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3 OS=Homo sapiens OX=9606 GN=ALKBH3 PE=1 SV=1
evm.model.HIC_ASM_7.54	0	Proteasome subunit beta type-4 (Fragment) OS=Xenopus laevis OX=8355 GN=psmb4 PE=2 SV=2
evm.model.HIC_ASM_20.877	1.72E-06	NA
evm.model.HIC_ASM_11.597	1.99E-09	Ubiquitin-like protein ATG12 OS=Bos taurus OX=9913 GN=ATG12 PE=2 SV=1
evm.model.HIC_ASM_11.761	0.002079	Protein virilizer homolog OS=Mus musculus OX=10090 GN=Virma PE=1 SV=1
evm.model.HIC_ASM_5.455	6.76E-08	Alanine aminotransferase 2 OS=Xenopus tropicalis OX=8364 GN=gpt2 PE=2 SV=1
evm.model.HIC_ASM_15.554	0	Methionine synthase reductase OS=Mus musculus OX=10090 GN=Mtrr PE=1 SV=2
evm.model.HIC_ASM_15.223	0.006184	Otospiralin OS=Homo sapiens OX=9606

		GN=OTOS PE=2 SV=1
evm.model.HIC_ASM_9.700	0.000219	TATA box-binding protein-associated factor RNA polymerase I subunit A OS=Homo sapiens OX=9606 GN=TAF1A PE=1 SV=1
evm.model.HIC_ASM_2.134	0	N-acylglucosamine 2-epimerase OS=Sus scrofa OX=9823 GN=RENBPE PE=1 SV=2
evm.model.HIC_ASM_8.101	1.34E-06	DNA-3-methyladenine glycosylase OS=Mus musculus OX=10090 GN=Mpg PE=2 SV=3
evm.model.HIC_ASM_4.370	1.17E-05	Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2
evm.model.HIC_ASM_0.118	0	Zinc finger protein 507 OS=Mus musculus OX=10090 GN=Znf507 PE=2 SV=2
evm.model.HIC_ASM_21.458	0	HSPB1-associated protein 1 homolog OS=Danio rerio OX=7955 GN=hspbp1 PE=2 SV=2
evm.model.HIC_ASM_7.563	3.20E-13	Protein Abitram OS=Danio rerio OX=7955 GN=abitram PE=2 SV=1
evm.model.HIC_ASM_13.1087	1.58E-07	RNA/RNP complex-1-interacting phosphatase OS=Homo sapiens OX=9606 GN=DUSP11 PE=1 SV=2
evm.model.HIC_ASM_16.610	7.01E-07	43 kDa receptor-associated protein of the synapse OS=Gallus gallus OX=9031 GN=RAPSN PE=2 SV=3
evm.model.HIC_ASM_9.411	0.000291	G patch domain-containing protein 2 OS=Homo sapiens OX=9606 GN=GPATCH2 PE=1 SV=1
evm.model.HIC_ASM_4.838	0	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Homo sapiens OX=9606 GN=ARFGEF3 PE=1 SV=3
evm.model.HIC_ASM_19.752	0.005431	Out at first protein homolog OS=Gallus gallus OX=9031 GN=oaf PE=2 SV=1
evm.model.HIC_ASM_12.181	8.99E-09	Aldo-keto reductase family 1 member A1-B OS=Danio rerio OX=7955 GN=akr1a1b PE=2 SV=1
evm.model.HIC_ASM_11.808	6.20E-14	Uridine phosphorylase 1 OS=Mus musculus OX=10090 GN=Upp1 PE=1 SV=2
evm.model.HIC_ASM_8.706	2.34E-05	Cytoglobin-1 OS>Oryzias latipes OX=8090 GN=cygb1 PE=2 SV=1
evm.model.HIC_ASM_2.736.1	3.89E-15	mRNA-decapping enzyme 1A OS=Sus scrofa OX=9823 GN=DCP1A PE=1 SV=1
evm.model.HIC_ASM_5.456	0.000185	ATP-dependent RNA helicase DHX30 OS=Gallus gallus OX=9031 GN=DHX30 PE=2 SV=1

evm.model.HIC_ASM_8.187	0.003225	Caveolae-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cavin1 PE=1 SV=1
evm.model.HIC_ASM_6.1223	0	Bridging integrator 2 OS=Rattus norvegicus OX=10116 GN=Bin2 PE=1 SV=1
evm.model.HIC_ASM_2.355	2.69E-06	Pre-mRNA-processing factor 6 OS=Mus musculus OX=10090 GN=Prpf6 PE=1 SV=1
evm.model.HIC_ASM_10.8	0.002765	Prefoldin subunit 1 OS=Danio rerio OX=7955 GN=pfdn1 PE=2 SV=1
evm.model.HIC_ASM_21.163	0.000337	RING finger protein 17 OS=Mus musculus OX=10090 GN=Rnf17 PE=1 SV=2
evm.model.HIC_ASM_8.1122	0.000571	F-box/LRR-repeat protein 16 OS=Mus musculus OX=10090 GN=Fbxl16 PE=1 SV=1
evm.model.HIC_ASM_9.318	9.75E-10	Pre-mRNA-processing factor 39 OS=Danio rerio OX=7955 GN=prpf39 PE=2 SV=2
evm.model.HIC_ASM_20.199	0	Zinc finger protein Aiolos OS=Homo sapiens OX=9606 GN=IKZF3 PE=1 SV=2
evm.model.HIC_ASM_1.995	0.000521	Pinin OS=Pongo abelii OX=9601 GN=PNN PE=2 SV=1
evm.model.HIC_ASM_21.609	7.99E-07	Myosin light chain 1, skeletal muscle isoform OS=Chelon ramada OX=30804 PE=1 SV=1
evm.model.HIC_ASM_14.1057	2.55E-07	Doublesex- and mab-3-related transcription factor 2 OS=Homo sapiens OX=9606 GN=DMRT2 PE=2 SV=2
evm.model.HIC_ASM_20.774	0.001807	Interleukin-8 OS=Gallus gallus OX=9031 GN=CXCL8 PE=2 SV=1
evm.model.HIC_ASM_13.607	2.20E-06	Calsenilin OS=Rattus norvegicus OX=10116 GN=Kcnip3 PE=1 SV=1
evm.model.HIC_ASM_14.41	0.000531	Beta-ureidopropionase OS=Pongo abelii OX=9601 GN=UPB1 PE=2 SV=1
evm.model.HIC_ASM_14.821	4.25E-12	Sperm flagellar protein 2 OS=Rattus norvegicus OX=10116 GN=Spef2 PE=1 SV=2
evm.model.HIC_ASM_9.273	0	Tribbles homolog 2 OS=Bos taurus OX=9913 GN=TRIB2 PE=2 SV=1
evm.model.HIC_ASM_2.598	0.000447	Deleted in malignant brain tumors 1 protein OS=Mus musculus OX=10090 GN=Dmbt1 PE=1 SV=2
evm.model.HIC_ASM_1.523	0.004909	Cell cycle control protein 50B OS=Mus musculus OX=10090 GN=Tmem30b PE=2 SV=1
evm.model.HIC_ASM_11.1049	0.000364	Ethylmalonyl-CoA decarboxylase OS=Danio rerio OX=7955 GN=echdc1 PE=3 SV=2

evm.model.HIC_ASM_12.47	0	Growth arrest and DNA damage-inducible protein GADD45 beta OS=Homo sapiens OX=9606 GN=GADD45B PE=1 SV=1
evm.model.HIC_ASM_7.202	8.55E-06	Neurochondrin OS=Xenopus laevis OX=8355 GN=ncdn PE=2 SV=1
evm.model.HIC_ASM_0.887	4.29E-07	Protein ELYS OS=Mus musculus OX=10090 GN=Ahtcf1 PE=1 SV=1
evm.model.HIC_ASM_2.1097	0.000127	Lysophosphatidic acid receptor 4 OS=Mus musculus OX=10090 GN=Lpar4 PE=2 SV=2
evm.model.HIC_ASM_14.1026	0.002654	Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2
evm.model.HIC_ASM_5.660	8.98E-08	Serine/threonine-protein kinase STK11 OS=Gallus gallus OX=9031 GN=STK11 PE=2 SV=1
evm.model.HIC_ASM_1.462	4.44E-16	Four and a half LIM domains protein 2 OS=Homo sapiens OX=9606 GN=FHL2 PE=1 SV=3
evm.model.HIC_ASM_16.861	0	Fibroleukin OS=Mus musculus OX=10090 GN=Fgl2 PE=1 SV=1
evm.model.HIC_ASM_10.367	0.003577	Protein-tyrosine sulfotransferase 1 OS=Homo sapiens OX=9606 GN=TPST1 PE=1 SV=1
evm.model.HIC_ASM_22.646	1.33E-10	Ubiquitin-conjugating enzyme E2 D4 OS=Homo sapiens OX=9606 GN=UBE2D4 PE=1 SV=1
evm.model.HIC_ASM_14.891	5.51E-10	Follistatin-A OS=Danio rerio OX=7955 GN=fsta PE=2 SV=2
evm.model.HIC_ASM_1.960	0	Protein tyrosine phosphatase type IVA 2 OS=Rattus norvegicus OX=10116 GN=Ptp4a2 PE=2 SV=1
evm.model.HIC_ASM_21.459	0.003321	Solute carrier family 49 member 4 homolog OS=Xenopus laevis OX=8355 GN=slc49a4 PE=2 SV=1
evm.model.HIC_ASM_16.548	0.005987	Transcription factor 12 OS=Homo sapiens OX=9606 GN=TCF12 PE=1 SV=1
evm.model.HIC_ASM_1.17	0.000482	Inositol-3-phosphate synthase 1-A OS=Xenopus laevis OX=8355 GN=isyna1-a PE=2 SV=1
evm.model.HIC_ASM_17.336	5.44E-14	TERF1-interacting nuclear factor 2 OS=Homo sapiens OX=9606 GN=TINF2 PE=1 SV=1
evm.model.HIC_ASM_12.281	0.002444	NACHT domain- and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=NWD1 PE=1 SV=3
evm.model.HIC_ASM_18.888	0.000135	Splicing factor 1 OS=Homo sapiens

		OX=9606 GN=SF1 PE=1 SV=4
evm.model.HIC_ASM_9.479	5.92E-13	Basic leucine zipper transcriptional factor ATF-like OS=Danio rerio OX=7955 GN=batf PE=3 SV=1
evm.model.HIC_ASM_16.759	0	Phosphatidylinositol phosphatase PTPRQ OS=Homo sapiens OX=9606 GN=PTPRQ PE=1 SV=2
evm.model.HIC_ASM_19.1044.1	4.96E-10	G2/mitotic-specific cyclin-B2 OS=Rana japonica OX=8402 GN=CCNB2 PE=2 SV=1
evm.model.HIC_ASM_16.160	0.000408	IQ and ubiquitin-like domain-containing protein OS=Macaca fascicularis OX=9541 GN=IQUB PE=2 SV=2
evm.model.HIC_ASM_7.580	0.000283	Interleukin-6 OS=Paralichthys olivaceus OX=8255 GN=il6 PE=2 SV=1
evm.model.HIC_ASM_4.823	0	Solute carrier family 22 member 15-like OS=Xenopus laevis OX=8355 GN=slc22a15b PE=2 SV=1
evm.model.HIC_ASM_1.1140	1.69E-05	NA
evm.model.HIC_ASM_9.222.2	1.91E-11	Transcription initiation factor IIA subunit 1 OS=Homo sapiens OX=9606 GN=GTF2A1 PE=1 SV=1
evm.model.HIC_ASM_15.146	8.40E-05	Myoneurin OS=Danio rerio OX=7955 GN=mynn PE=2 SV=1
evm.model.HIC_ASM_0.522	0.000179	RING finger protein 219 OS=Mus musculus OX=10090 GN=Rnf219 PE=1 SV=2
evm.model.HIC_ASM_20.946	0.001333	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus OX=10090 GN=Aimp1 PE=1 SV=2
evm.model.HIC_ASM_9.157	1.71E-06	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6
evm.model.HIC_ASM_19.518	0.001616	Synergism gamma OS=Homo sapiens OX=9606 GN=SYNRG PE=1 SV=2
evm.model.HIC_ASM_14.320	2.58E-08	Major facilitator superfamily domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Mfsd3 PE=2 SV=1
evm.model.HIC_ASM_13.1006	0	WD repeat-containing protein 36 OS=Homo sapiens OX=9606 GN=WDR36 PE=1 SV=1
evm.model.HIC_ASM_5.83	6.62E-08	Vasoactive intestinal polypeptide receptor 2 OS=Rattus norvegicus OX=10116 GN=Vipr2 PE=2 SV=1
evm.model.HIC_ASM_0.479	6.53E-10	U2 small nuclear ribonucleoprotein auxiliary

		factor 35 kDa subunit-related protein 2 OS=Homo sapiens OX=9606 GN=ZRSR2 PE=1 SV=2
evm.model.HIC_ASM_23.209	0.000181	Lectin OS=Pleurodeles waltl OX=8319 GN=LEC PE=1 SV=1
evm.model.HIC_ASM_12.563	0.000176	Axonemal dynein light chain domain-containing protein 1 OS=Homo sapiens OX=9606 GN=AXDND1 PE=2 SV=1
evm.model.HIC_ASM_12.985	8.65E-07	SAC3 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SAC3D1 PE=1 SV=2
evm.model.HIC_ASM_1.12	2.10E-06	Phospholipid phosphatase 2 OS=Bos taurus OX=9913 GN=PLPP2 PE=2 SV=1
evm.model.HIC_ASM_22.661	1.40E-07	Beta-tectorin OS=Mus musculus OX=10090 GN=Tectb PE=2 SV=2
evm.model.HIC_ASM_19.288	3.09E-05	V-set and transmembrane domain-containing protein 5 OS=Homo sapiens OX=9606 GN=VSTM5 PE=3 SV=1
evm.model.HIC_ASM_20.735	2.35E-13	Osteocalcin 2 OS=Diplodus sargus OX=38941 GN=bglap2 PE=1 SV=1
evm.model.HIC_ASM_16.89.1	1.94E-10	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Homo sapiens OX=9606 GN=COQ9 PE=1 SV=1
evm.model.HIC_ASM_10.548	6.77E-05	Layilin OS=Cricetulus griseus OX=10029 GN=LAYN PE=1 SV=1
evm.model.HIC_ASM_19.731	4.10E-07	Mediator of RNA polymerase II transcription subunit 29 OS=Danio rerio OX=7955 GN=med29 PE=2 SV=1
evm.model.HIC_ASM_16.502	2.49E-14	Tumor protein p53-inducible protein 11 OS=Mus musculus OX=10090 GN=Trp53i11 PE=1 SV=1
evm.model.HIC_ASM_14.819	5.91E-07	Centrosomal protein of 78 kDa OS=Mus musculus OX=10090 GN=Cep78 PE=2 SV=1
evm.model.HIC_ASM_12.806	0.004491	Interleukin-12 receptor subunit beta-2 OS=Sus scrofa OX=9823 GN=IL12RB2 PE=2 SV=1
evm.model.HIC_ASM_5.399	0	Coiled-coil domain-containing protein 13 OS=Homo sapiens OX=9606 GN=CCDC13 PE=1 SV=2
evm.model.HIC_ASM_3.112	5.68E-05	Pro-epidermal growth factor OS=Sus scrofa OX=9823 GN=EGF PE=1 SV=2
evm.model.HIC_ASM_9.802	2.14E-06	Transcription factor AP-2-delta OS=Homo

evm.model.HIC_ASM_16.137	6.46E-12	sapiens OX=9606 GN=TFAP2D PE=2 SV=1 DET1 homolog OS=Homo sapiens OX=9606 GN=DET1 PE=1 SV=2
evm.model.HIC_ASM_13.792	3.77E-06	5'-AMP-activated protein kinase subunit beta-1 OS=Mus musculus OX=10090 GN=Prkab1 PE=1 SV=2
evm.model.HIC_ASM_7.898	0.006245	Uncharacterized protein KIAA0895 OS=Mus musculus OX=10090 GN=Kiaa0895 PE=2 SV=2
evm.model.HIC_ASM_8.479	9.73E-10	Heme oxygenase 2 OS=Rattus norvegicus OX=10116 GN=Hmox2 PE=1 SV=1
evm.model.HIC_ASM_16.1087	1.10E-11	Probable fructose-2,6-bisphosphatase TIGAR A OS=Danio rerio OX=7955 GN=tigara PE=2 SV=1
evm.model.HIC_ASM_11.1404	1.75E-05	T-cell activation inhibitor, mitochondrial OS=Homo sapiens OX=9606 GN=TCAIM PE=2 SV=2
evm.model.HIC_ASM_8.561	0.001905	RING finger protein 151 OS=Bos taurus OX=9913 GN=RNF151 PE=2 SV=1
evm.model.HIC_ASM_16.169	2.14E-13	Sorting nexin-22 OS=Homo sapiens OX=9606 GN=SNX22 PE=1 SV=1
evm.model.HIC_ASM_14.91	4.15E-12	T-box transcription factor TBX1 OS=Danio rerio OX=7955 GN=tbx1 PE=2 SV=1
evm.model.HIC_ASM_3.639	2.41E-08	Proheparin-binding EGF-like growth factor OS=Gallus gallus OX=9031 GN=HBEGF PE=1 SV=1
evm.model.HIC_ASM_5.1017	0.000328	Gamma-interferon-inducible lysosomal thiol reductase OS=Danio rerio OX=7955 GN=ifi30 PE=1 SV=1
evm.model.HIC_ASM_10.473	0.000339	Solute carrier family 46 member 3 OS=Gallus gallus OX=9031 GN=SLC46A3 PE=2 SV=1
evm.model.HIC_ASM_19.979	0.002625	Cilia- and flagella-associated protein 45 OS=Homo sapiens OX=9606 GN=CFAP45 PE=2 SV=2
evm.model.HIC_ASM_12.1030	9.67E-06	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens OX=9606 GN=DNTTIP2 PE=1 SV=2
evm.model.HIC_ASM_12.832	7.74E-07	DNA-binding protein RFXANK OS=Homo sapiens OX=9606 GN=RFXANK PE=1 SV=2
evm.model.HIC_ASM_10.844	2.18E-05	Drebrin OS=Rattus norvegicus OX=10116 GN=Dbn1 PE=1 SV=3

evm.model.HIC_ASM_20.797	0.000683	Replication factor C subunit 1 OS=Homo sapiens OX=9606 GN=RFC1 PE=1 SV=4
evm.model.HIC_ASM_3.697	0	LON peptidase N-terminal domain and RING finger protein 1 OS=Homo sapiens OX=9606 GN=LONRF1 PE=1 SV=2
evm.model.HIC_ASM_10.1076.1	1.28E-08	Zinc finger HIT domain-containing protein 3 OS=Mus musculus OX=10090 GN=Znhit3 PE=1 SV=1
evm.model.HIC_ASM_20.947	1.66E-08	Dickkopf-related protein 2 OS=Homo sapiens OX=9606 GN=DKK2 PE=2 SV=1
evm.model.HIC_ASM_9.986	4.16E-09	Tyrosine-protein kinase FRK OS=Homo sapiens OX=9606 GN=FRK PE=1 SV=1
evm.model.HIC_ASM_14.595	0.000632	D-amino-acid oxidase OS=Macaca fascicularis OX=9541 GN=DAO PE=2 SV=1
evm.model.HIC_ASM_19.972	9.53E-08	Mitochondrial intermediate peptidase OS=Pongo abelii OX=9601 GN=MIPEP PE=2 SV=1
evm.model.HIC_ASM_16.580	0.001278	Protein saal1 OS=Danio rerio OX=7955 GN=saal1 PE=2 SV=2
evm.model.HIC_ASM_18.304	0	RELT-like protein 1 OS=Gallus gallus OX=9031 GN=RELL1 PE=2 SV=1
evm.model.HIC_ASM_17.564	1.52E-09	ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1
evm.model.HIC_ASM_9.880	9.76E-12	General transcription factor 3C polypeptide 2 OS=Mus musculus OX=10090 GN=Gtf3c2 PE=2 SV=2
evm.model.HIC_ASM_11.832	0	Protein lifeguard 1 OS=Homo sapiens OX=9606 GN=GRINA PE=2 SV=1
evm.model.HIC_ASM_21.928	2.64E-11	Immunoglobulin-like domain-containing receptor 2 OS=Mus musculus OX=10090 GN=Illdr2 PE=1 SV=2
evm.model.HIC_ASM_17.791	6.11E-10	Uncharacterized protein KIAA0930 homolog OS=Xenopus laevis OX=8355 PE=2 SV=2
evm.model.HIC_ASM_19.862	9.19E-11	Paired mesoderm homeobox protein 2A OS=Mus musculus OX=10090 GN=Phox2a PE=2 SV=1
evm.model.HIC_ASM_19.509	2.85E-10	Group 3 secretory phospholipase A2 OS=Bos taurus OX=9913 GN=PLA2G3 PE=2 SV=1
evm.model.HIC_ASM_10.317	0	Homeobox protein MSH-D OS=Danio rerio OX=7955 GN=msxd PE=3 SV=1
evm.model.HIC_ASM_9.533	1.26E-05	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Danio rerio OX=7955 GN=cmtr1 PE=2 SV=1

evm.model.HIC_ASM_1.758	2.14E-11	Iron-sulfur cluster assembly 2 homolog, mitochondrial OS=Homo sapiens OX=9606 GN=ISCA2 PE=1 SV=2
evm.model.HIC_ASM_11.626	7.44E-11	Cdc42 effector protein 5 OS=Mus musculus OX=10090 GN=Cdc42ep5 PE=1 SV=2
evm.model.HIC_ASM_22.710	4.44E-15	Homeobox protein Hox-B1b OS=Takifugu rubripes OX=31033 GN=hoxb1b PE=3 SV=1
evm.model.HIC_ASM_4.396	5.15E-05	Stonin-1 OS=Homo sapiens OX=9606 GN=STON1 PE=1 SV=2
evm.model.HIC_ASM_22.287	4.75E-14	N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo sapiens OX=9606 GN=GNPTG PE=1 SV=1
evm.model.HIC_ASM_7.550	1.72E-07	EF-hand calcium-binding domain-containing protein 1 OS=Xenopus laevis OX=8355 GN=efcab1 PE=2 SV=1
evm.model.HIC_ASM_11.1052	0.000171	R-spondin-3 OS=Danio rerio OX=7955 GN=rspondin3 PE=2 SV=2
evm.model.HIC_ASM_8.354.1	3.27E-09	Meteorin-like protein OS=Danio rerio OX=7955 GN=metrnl PE=2 SV=1
evm.model.HIC_ASM_6.29	6.22E-15	Podocalyxin-like protein 2 OS=Homo sapiens OX=9606 GN=PODXL2 PE=1 SV=1
evm.model.HIC_ASM_10.507	0.001101	PAX3- and PAX7-binding protein 1 OS=Homo sapiens OX=9606 GN=PAXBP1 PE=1 SV=2
evm.model.HIC_ASM_14.1378	0.000828	PHD finger protein 19 OS=Mus musculus OX=10090 GN=Phf19 PE=1 SV=1
evm.model.HIC_ASM_12.918	4.70E-13	Uncharacterized protein C1orf21 homolog OS=Mus musculus OX=10090 PE=1 SV=1
evm.model.HIC_ASM_12.912.1	0.002032	Vesicle-trafficking protein SEC22b-B OS=Danio rerio OX=7955 GN=sec22bb PE=2 SV=1
evm.model.HIC_ASM_14.650	0.001368	Zinc finger CCHC domain-containing protein 8 OS=Xenopus laevis OX=8355 GN=zcchc8 PE=2 SV=1
evm.model.HIC_ASM_19.976.1	1.02E-10	40S ribosomal protein S25 OS=Danio rerio OX=7955 GN=rps25 PE=2 SV=1
evm.model.HIC_ASM_5.1232	0.003967	Ubiquitin-like-conjugating enzyme ATG10 OS=Mus musculus OX=10090 GN=Atg10 PE=1 SV=1
evm.model.HIC_ASM_19.580	5.23E-07	Synaptotagmin-like protein 2 OS=Mus musculus OX=10090 GN=Sytl2 PE=1 SV=2
evm.model.HIC_ASM_11.1112	0.000529	DEP domain-containing protein 1B OS=Mus musculus OX=10090 GN=Depdc1b PE=2 SV=1

evm.model.HIC_ASM_19.337	0.002756	Interferon regulatory factor 2-binding protein 1 OS=Danio rerio OX=7955 GN=irf2bp1 PE=2 SV=1
evm.model.HIC_ASM_21.877	2.51E-06	Leucine-rich repeat-containing protein 58 OS=Xenopus laevis OX=8355 GN=lrrc58 PE=2 SV=1
evm.model.HIC_ASM_8.57	4.61E-05	Histone-lysine N-methyltransferase KMT5C OS=Xenopus laevis OX=8355 GN=kmt5c PE=2 SV=1
evm.model.HIC_ASM_21.370	0.000669	U3 small nucleolar RNA-associated protein 14 homolog A OS=Bos taurus OX=9913 GN=UTP14A PE=2 SV=1
evm.model.HIC_ASM_3.1007	0.005985	Ganglioside GM2 activator OS=Mus musculus OX=10090 GN=Gm2a PE=1 SV=2
evm.model.HIC_ASM_0.545	1.60E-05	Protein-lysine methyltransferase METTL21E OS=Bos taurus OX=9913 GN=METTL21E PE=2 SV=1
evm.model.HIC_ASM_22.206	1.29E-05	Dynein assembly factor 3, axonemal OS=Danio rerio OX=7955 GN=dnaaf3 PE=2 SV=2
evm.model.HIC_ASM_7.818	3.00E-15	Collagen alpha-1(XXII) chain OS=Homo sapiens OX=9606 GN=COL22A1 PE=2 SV=2
evm.model.HIC_ASM_2.1107	7.77E-16	Telomere zinc finger-associated protein OS=Mus musculus OX=10090 GN=Zbtb48 PE=1 SV=1
evm.model.HIC_ASM_9.90	1.99E-05	Beta-taxilin OS=Gallus gallus OX=9031 GN=TXLNB PE=2 SV=1
evm.model.HIC_ASM_15.504	2.22E-16	COP9 signalosome complex subunit 5 OS=Xenopus tropicalis OX=8364 GN=cops5 PE=2 SV=1
evm.model.HIC_ASM_1.691	0	Receptor expression-enhancing protein 1 OS=Homo sapiens OX=9606 GN=REEP1 PE=1 SV=1
evm.model.HIC_ASM_20.928	1.52E-06	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Pan troglodytes OX=9598 GN=NDUFB6 PE=2 SV=3
evm.model.HIC_ASM_13.658	0.001811	MORN repeat-containing protein 5 OS=Danio rerio OX=7955 GN=morn5 PE=2 SV=1
evm.model.HIC_ASM_7.532	0	R3H domain-containing protein 2 OS=Mus musculus OX=10090 GN=R3hdm2 PE=1 SV=2
evm.model.HIC_ASM_3.332	0	Girdin OS=Mus musculus OX=10090

		GN=Ccdc88a PE=1 SV=2
evm.model.HIC_ASM_8.754	1.10E-09	Desumoylating isopeptidase 1 OS=Rattus norvegicus OX=10116 GN=Desi1 PE=2 SV=1
evm.model.HIC_ASM_1.37	2.62E-06	Serine/threonine-protein kinase ATR OS=Homo sapiens OX=9606 GN=ATR PE=1 SV=3
evm.model.HIC_ASM_10.740	1.94E-05	Ras-related GTP-binding protein A OS=Rattus norvegicus OX=10116 GN=Rraga PE=1 SV=1
evm.model.HIC_ASM_11.13	0.000408	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6 OS=Bos taurus OX=9913 GN=NDUFAF6 PE=2 SV=1
evm.model.HIC_ASM_23.206	0.000447	STE20-related kinase adapter protein beta OS=Mus musculus OX=10090 GN=Stradb PE=2 SV=1
evm.model.HIC_ASM_11.792	4.45E-06	FAST kinase domain-containing protein 4 OS=Xenopus laevis OX=8355 GN=tbgr4 PE=2 SV=1
evm.model.HIC_ASM_13.675	0.001871	Dopamine beta-hydroxylase OS=Bos taurus OX=9913 GN=DBH PE=1 SV=2
evm.model.HIC_ASM_11.245	0.005261	Membrane progesterin receptor delta OS=Homo sapiens OX=9606 GN=PAQR6 PE=1 SV=2
evm.model.HIC_ASM_0.378	2.52E-09	Cilia- and flagella-associated protein 70 OS=Homo sapiens OX=9606 GN=CFAP70 PE=2 SV=3
evm.model.HIC_ASM_10.1095	9.42E-06	P2X purinoceptor 5 OS=Rattus norvegicus OX=10116 GN=P2rx5 PE=2 SV=1
evm.model.HIC_ASM_11.615	0	Beta-2-glycoprotein 1 OS=Pan troglodytes OX=9598 GN=APOH PE=2 SV=1
evm.model.HIC_ASM_1.1200	4.16E-13	AP-4 complex subunit sigma-1 OS=Bos taurus OX=9913 GN=AP4S1 PE=2 SV=1
evm.model.HIC_ASM_1.214	0.000486	Legumain OS=Macaca fascicularis OX=9541 GN=LGMN PE=2 SV=1
evm.model.HIC_ASM_1.404	1.51E-05	Lipid droplet-associated hydrolase OS=Gallus gallus OX=9031 GN=LDAH PE=2 SV=2
evm.model.HIC_ASM_4.330	0	McKusick-Kaufman/Bardet-Biedl syndromes putative chaperonin OS=Homo sapiens OX=9606 GN=MKKS PE=1 SV=1
evm.model.HIC_ASM_2.464	3.38E-13	Homeobox protein Hox-C9 OS=Orizias latipes OX=8090 GN=hoxc9 PE=2 SV=1
evm.model.HIC_ASM_9.588	0.001446	Probable inactive peptidyl-prolyl cis-trans

		isomerase-like 6 OS=Bos taurus OX=9913 GN=PPIL6 PE=2 SV=1
evm.model.HIC_ASM_2.1106	2.97E-13	Kelch-like protein 21 OS=Danio rerio OX=7955 GN=klhl21 PE=2 SV=1
evm.model.HIC_ASM_22.703	0.002058	39S ribosomal protein L10, mitochondrial OS=Danio rerio OX=7955 GN=mrpl10 PE=2 SV=1
evm.model.HIC_ASM_14.1122	1.36E-12	Protein FAM102A OS=Homo sapiens OX=9606 GN=FAM102A PE=1 SV=2
evm.model.HIC_ASM_14.601	1.16E-06	Protein adenylyltransferase FICD OS=Danio rerio OX=7955 GN=ficd PE=2 SV=1
evm.model.HIC_ASM_19.831	0	Alkylated DNA repair protein alkB homolog 8 OS=Homo sapiens OX=9606 GN=ALKBH8 PE=1 SV=2
evm.model.HIC_ASM_22.262	5.23E-06	Meteorin OS=Mus musculus OX=10090 GN=Metrn PE=1 SV=2
evm.model.HIC_ASM_7.991	0	Integrator complex subunit 8 OS=Homo sapiens OX=9606 GN=INTS8 PE=1 SV=1
evm.model.HIC_ASM_3.892	8.54E-05	Nucleotide exchange factor SIL1 OS=Homo sapiens OX=9606 GN=SIL1 PE=1 SV=1
evm.model.HIC_ASM_4.588	1.90E-09	Protein Wnt-8b OS=Danio rerio OX=7955 GN=wnt8b PE=2 SV=1
evm.model.HIC_ASM_22.270	1.65E-08	Retinol dehydrogenase 13 OS=Homo sapiens OX=9606 GN=RDH13 PE=1 SV=2
evm.model.HIC_ASM_4.841	1.54E-07	Gonadotropin subunit beta-2 OS=Morone saxatilis OX=34816 GN=cgbb PE=2 SV=2
evm.model.HIC_ASM_19.549	1.56E-05	2-(3-amino-3-carboxypropyl)histidine synthase subunit 1 OS=Danio rerio OX=7955 GN=dph1 PE=2 SV=1
evm.model.HIC_ASM_0.436	0	Selenocysteine insertion sequence-binding protein 2-like OS=Homo sapiens OX=9606 GN=SECISBP2L PE=1 SV=3
evm.model.HIC_ASM_11.874	1.00E-11	Steroid 21-hydroxylase OS=Homo sapiens OX=9606 GN=CYP21A2 PE=1 SV=1
evm.model.HIC_ASM_8.1083	0	Homeobox protein Hox-B5a OS=Takifugu rubripes OX=31033 GN=hoxb5a PE=3 SV=1
evm.model.HIC_ASM_15.309	3.06E-06	Ubiquitin thioesterase otulin OS=Homo sapiens OX=9606 GN=OTULIN PE=1 SV=3
evm.model.HIC_ASM_10.860	0.003894	CCR4-NOT transcription complex subunit 8 OS=Homo sapiens OX=9606 GN=CNOT8 PE=1 SV=1
evm.model.HIC_ASM_21.941	5.30E-07	Vertebrate ancient opsin OS=Salmo salar OX=8030 PE=1 SV=1
evm.model.HIC_ASM_2.1138	3.57E-05	Inter-alpha-trypsin inhibitor heavy chain H6

		OS=Homo sapiens OX=9606 GN=ITIH6 PE=2 SV=1
evm.model.HIC_ASM_17.309	1.39E-06	Troponin I, slow skeletal muscle OS=Oryctolagus cuniculus OX=9986 GN=TNNI1 PE=1 SV=1
evm.model.HIC_ASM_22.1120	5.57E-07	Cyclin N-terminal domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CNTD1 PE=2 SV=2
evm.model.HIC_ASM_1.868	0.003892	Coiled-coil domain-containing protein 28B OS=Mus musculus OX=10090 GN=Ccdc28b PE=1 SV=3
evm.model.HIC_ASM_13.191	3.79E-09	Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus OX=10090 GN=Hnrnpd PE=1 SV=2
evm.model.HIC_ASM_12.1147	2.77E-13	Uricase OS=Danio rerio OX=7955 GN=uox PE=1 SV=1
evm.model.HIC_ASM_22.422	0.000442	Josephin-1 OS=Pongo abelii OX=9601 GN=JOSD1 PE=2 SV=1
evm.model.HIC_ASM_20.354	0.000799	5-demethoxyubiquinone hydroxylase, mitochondrial OS=Bos taurus OX=9913 GN=COQ7 PE=2 SV=1
evm.model.HIC_ASM_2.980	4.95E-14	Protein phosphatase 1 regulatory subunit 3A OS=Oryctolagus cuniculus OX=9986 GN=PPP1R3A PE=1 SV=1
evm.model.HIC_ASM_22.397	9.45E-06	ATP synthase mitochondrial F1 complex assembly factor 2 OS=Mus musculus OX=10090 GN=Atpaf2 PE=1 SV=1
evm.model.HIC_ASM_11.1155	0.001515	PR domain zinc finger protein 13 OS=Homo sapiens OX=9606 GN=PRDM13 PE=2 SV=2
evm.model.HIC_ASM_19.679	0	Zinc transporter 10 OS=Mus musculus OX=10090 GN=Slc30a10 PE=1 SV=1
evm.model.HIC_ASM_16.246	0.000109	ALX homeobox protein 1 OS=Danio rerio OX=7955 GN=alx1 PE=2 SV=1
evm.model.HIC_ASM_7.361	0.005814	39S ribosomal protein L9, mitochondrial OS=Papio anubis OX=9555 GN=MRPL9 PE=3 SV=1
evm.model.HIC_ASM_5.749	0	E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens OX=9606 GN=TRIM21 PE=1 SV=1
evm.model.HIC_ASM_4.966	0.00262	Tetratricopeptide repeat protein 27 OS=Gallus gallus OX=9031 GN=TTC27 PE=2 SV=1
evm.model.HIC_ASM_23.218	0.000653	DNA annealing helicase and endonuclease ZRANB3 OS=Bos taurus OX=9913

		GN=ZRANB3 PE=3 SV=3
evm.model.HIC_ASM_7.474	1.11E-16	Nuclear pore complex protein Nup153 OS=Homo sapiens OX=9606 GN=NUP153 PE=1 SV=2
evm.model.HIC_ASM_19.1015	0.004549	Signal recognition particle receptor subunit alpha OS=Mus musculus OX=10090 GN=Srpra PE=1 SV=1
evm.model.HIC_ASM_2.146	0	Methyl-CpG-binding protein 2 OS=Macaca fascicularis OX=9541 GN=MECP2 PE=2 SV=1
evm.model.HIC_ASM_16.1142	4.83E-06	PSME3-interacting protein OS=Mus musculus OX=10090 GN=Fam192a PE=1 SV=1
evm.model.HIC_ASM_17.584	0.003529	Transmembrane 7 superfamily member 3 OS=Mus musculus OX=10090 GN=Tm7sf3 PE=2 SV=2
evm.model.HIC_ASM_7.232	0.000534	Probable thiopurine S-methyltransferase OS=Danio rerio OX=7955 GN=tpmt PE=2 SV=1
evm.model.HIC_ASM_2.926	1.02E-11	Eukaryotic translation initiation factor 4E type 3 OS=Danio rerio OX=7955 GN=eif4e3 PE=2 SV=1
evm.model.HIC_ASM_1.89	0.001026	Cysteine-rich protein 2 OS=Mus musculus OX=10090 GN=Crip2 PE=1 SV=1
evm.model.HIC_ASM_4.374	0	Calcium uniporter protein, mitochondrial OS=Danio rerio OX=7955 GN=mcu PE=1 SV=1
evm.model.HIC_ASM_14.867	5.74E-11	DNA polymerase beta OS=Danio rerio OX=7955 GN=polb PE=2 SV=2
evm.model.HIC_ASM_9.991	2.51E-09	Myristoylated alanine-rich C-kinase substrate OS=Gallus gallus OX=9031 GN=MARCKS PE=1 SV=2
evm.model.HIC_ASM_13.425	6.66E-16	Prolactin receptor OS=Oreochromis niloticus OX=8128 GN=prlr PE=2 SV=1
evm.model.HIC_ASM_14.714	8.53E-12	Coiled-coil domain-containing protein 112 OS=Macaca fascicularis OX=9541 GN=CCDC112 PE=2 SV=1
evm.model.HIC_ASM_16.284	1.11E-16	40S ribosomal protein S13 OS=Ictalurus punctatus OX=7998 GN=rps13 PE=2 SV=3
evm.model.HIC_ASM_21.1058	2.87E-08	Ceramide kinase-like protein OS=Homo sapiens OX=9606 GN=CERKL PE=1 SV=1
evm.model.HIC_ASM_19.67	0.002942	Bifunctional polynucleotide phosphatase/kinase OS=Homo sapiens OX=9606 GN=PNKP PE=1 SV=1

evm.model.HIC_ASM_5.998	0	Plasmalemma vesicle-associated protein OS=Mus musculus OX=10090 GN=Plvap PE=1 SV=1
evm.model.HIC_ASM_6.146	0.000685	Deoxynucleotidyltransferase terminal-interacting protein 1 OS=Homo sapiens OX=9606 GN=DNTTIP1 PE=1 SV=2
evm.model.HIC_ASM_12.121	0.000879	Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens OX=9606 GN=DDX10 PE=1 SV=2
evm.model.HIC_ASM_4.962	4.19E-08	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens OX=9606 GN=AHNAK PE=1 SV=2
evm.model.HIC_ASM_2.951	5.27E-09	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus OX=10090 GN=Tmpo PE=1 SV=4
evm.model.HIC_ASM_12.483	0.00181	KN motif and ankyrin repeat domain-containing protein 4 OS=Homo sapiens OX=9606 GN=KANK4 PE=1 SV=1
evm.model.HIC_ASM_9.281	0.001192	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens OX=9606 GN=TRMT6 PE=1 SV=1
evm.model.HIC_ASM_21.661	0	Transmembrane protein 41A-A OS=Danio rerio OX=7955 GN=tmem41aa PE=2 SV=1
evm.model.HIC_ASM_16.200	2.22E-16	Ornithine decarboxylase antizyme 2 OS=Mus musculus OX=10090 GN=Oaz2 PE=1 SV=2
evm.model.HIC_ASM_16.245	1.52E-06	Ras association domain-containing protein 9 OS=Homo sapiens OX=9606 GN=RASSF9 PE=2 SV=2
evm.model.HIC_ASM_16.1286	0.000356	Nuclear pore complex protein Nup160 OS=Mus musculus OX=10090 GN=Nup160 PE=1 SV=2
evm.model.HIC_ASM_1.1238.1	7.94E-07	AT-rich interactive domain-containing protein 4A OS=Homo sapiens OX=9606 GN=ARID4A PE=1 SV=3
evm.model.HIC_ASM_22.465	4.67E-06	MMS19 nucleotide excision repair protein homolog OS=Danio rerio OX=7955 GN=mms19 PE=3 SV=1
evm.model.HIC_ASM_18.513	0.00167	NEDD4-binding protein 1 OS=Gallus gallus OX=9031 GN=N4BP1 PE=2 SV=1
evm.model.HIC_ASM_1.997	0.001565	Gem-associated protein 2 OS=Mus musculus OX=10090 GN=Gemin2 PE=2 SV=1
evm.model.HIC_ASM_18.880	0.001543	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial

		OS=Danio rerio OX=7955 GN=ecsit PE=2 SV=1
evm.model.HIC_ASM_21.272	1.61E-10	Lanosterol synthase OS=Rattus norvegicus OX=10116 GN=Lss PE=1 SV=2
evm.model.HIC_ASM_20.1170	0	ERI1 exoribonuclease 2 OS=Xenopus laevis OX=8355 GN=eri2 PE=2 SV=1
evm.model.HIC_ASM_2.239	1.54E-09	Calcium-responsive transactivator OS=Mus musculus OX=10090 GN=Ss18l1 PE=1 SV=1
evm.model.HIC_ASM_21.655	0	E3 ubiquitin-protein ligase MARCH4 OS=Danio rerio OX=7955 GN=march4 PE=2 SV=1
evm.model.HIC_ASM_7.312	0.000201	Secretory carrier-associated membrane protein 3 OS=Bos taurus OX=9913 GN=SCAMP3 PE=2 SV=1
evm.model.HIC_ASM_16.265	4.60E-05	Wee1-like protein kinase OS=Homo sapiens OX=9606 GN=WEE1 PE=1 SV=2
evm.model.HIC_ASM_7.677	0	Stromal membrane-associated protein 2 OS=Gallus gallus OX=9031 GN=SMAP2 PE=2 SV=1
evm.model.HIC_ASM_11.954	1.44E-06	G patch domain-containing protein 3 OS=Mus musculus OX=10090 GN=Gpatch3 PE=2 SV=1
evm.model.HIC_ASM_2.687	0	Probable G-protein coupled receptor 153 OS=Mus musculus OX=10090 GN=Gpr153 PE=2 SV=2
evm.model.HIC_ASM_3.727	3.26E-13	Zinc finger C4H2 domain-containing protein OS=Danio rerio OX=7955 GN=zc4h2 PE=2 SV=1
evm.model.HIC_ASM_22.393	0.00045	Disks large-associated protein 5 OS=Homo sapiens OX=9606 GN=DLGAP5 PE=1 SV=2
evm.model.HIC_ASM_15.368	0.000356	RNA-binding protein 33 OS=Mus musculus OX=10090 GN=Rbm33 PE=1 SV=2
evm.model.HIC_ASM_19.458	1.66E-10	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Pan troglodytes OX=9598 GN=BCKDHA PE=2 SV=1
evm.model.HIC_ASM_3.549	1.11E-07	Cyclin-J OS=Mus musculus OX=10090 GN=Ccnj PE=2 SV=2
evm.model.HIC_ASM_1.1223.1	1.11E-16	MAX gene-associated protein OS=Mus musculus OX=10090 GN=Mga PE=2 SV=1
evm.model.HIC_ASM_8.843	7.46E-05	GTPase IMAP family member 5 OS=Homo sapiens OX=9606 GN=GIMAP5 PE=1 SV=1
evm.model.HIC_ASM_15.311	3.92E-05	POU domain, class 6, transcription factor 2 OS=Homo sapiens OX=9606 GN=POU6F2

		PE=1 SV=3
evm.model.HIC_ASM_21.785	0	Homeobox protein Hox-D11a OS=Takifugu rubripes OX=31033 GN=hoxd11a PE=3 SV=1
evm.model.HIC_ASM_20.84	1.24E-07	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus OX=10116 GN=Arhgdia PE=1 SV=1
evm.model.HIC_ASM_11.776	2.34E-05	Protein transport protein Sec61 subunit beta OS=Pongo abelii OX=9601 GN=SEC61B PE=3 SV=3
evm.model.HIC_ASM_11.893	0	Nephrin OS=Homo sapiens OX=9606 GN=NPFS1 PE=1 SV=1
evm.model.HIC_ASM_2.380	0.003364	Zinc finger protein SNAI2 OS=Rattus norvegicus OX=10116 GN=Snai2 PE=2 SV=2
evm.model.HIC_ASM_0.290	0.000955	Forkhead box protein N5 OS=Xenopus tropicalis OX=8364 GN=foxn5 PE=2 SV=1
evm.model.HIC_ASM_19.882.1	1.15E-14	B-cell CLL/lymphoma 7 protein family member B-B OS=Danio rerio OX=7955 GN=bcl7bb PE=2 SV=1
evm.model.HIC_ASM_9.352	0	DDB1- and CUL4-associated factor 4 OS=Homo sapiens OX=9606 GN=DCAF4 PE=1 SV=3
evm.model.HIC_ASM_10.765	0	Zinc finger protein-like 1 OS=Danio rerio OX=7955 GN=zfpl1 PE=2 SV=1
evm.model.HIC_ASM_5.296	0.002427	Translocation protein SEC62 OS=Gallus gallus OX=9031 GN=SEC62 PE=2 SV=1
evm.model.HIC_ASM_10.187	1.81E-14	Serine/threonine-protein kinase pim-1 OS=Homo sapiens OX=9606 GN=PIM1 PE=1 SV=4
evm.model.HIC_ASM_10.361	0	CREB3 regulatory factor OS=Homo sapiens OX=9606 GN=CREBRF PE=1 SV=2
evm.model.HIC_ASM_8.724	3.14E-07	Epithelial membrane protein 2 OS=Danio rerio OX=7955 GN=emp2 PE=2 SV=2
evm.model.HIC_ASM_9.1050	2.01E-10	N-alpha-acetyltransferase 20 OS=Danio rerio OX=7955 GN=naa20 PE=2 SV=1
evm.model.HIC_ASM_22.33	3.66E-14	Renalase OS=Homo sapiens OX=9606 GN=RNLS PE=1 SV=1
evm.model.HIC_ASM_0.655	9.65E-14	Vitamin D 25-hydroxylase OS=Mus musculus OX=10090 GN=Cyp2r1 PE=1 SV=1
evm.model.HIC_ASM_17.538	0.001741	ADP-ribosylation factor-like protein 1 OS=Bos taurus OX=9913 GN=ARL1 PE=2 SV=1

evm.model.HIC_ASM_2.508	0.006711	Neurogenic differentiation factor 4 OS=Gallus gallus OX=9031 GN=NEUROD4 PE=2 SV=1
evm.model.HIC_ASM_7.552	0.002424	Peroxisome biogenesis factor 1 OS=Homo sapiens OX=9606 GN=PEX1 PE=1 SV=1
evm.model.HIC_ASM_22.601	0.000507	Galactokinase OS=Bos taurus OX=9913 GN=GALK1 PE=2 SV=2
evm.model.HIC_ASM_20.192	7.56E-07	Keratin, type I cytoskeletal 42 OS=Rattus norvegicus OX=10116 GN=Krt42 PE=3 SV=1
evm.model.HIC_ASM_19.921	1.22E-13	Sodium channel subunit beta-4 OS=Rattus norvegicus OX=10116 GN=Scn4b PE=1 SV=1
evm.model.HIC_ASM_18.508	0.004204	Lysophospholipid acyltransferase LPCAT4 OS=Xenopus laevis OX=8355 GN=lpcat4 PE=2 SV=2
evm.model.HIC_ASM_22.712	5.60E-07	Homeobox protein Hox-B5b OS=Takifugu rubripes OX=31033 GN=hoxb5b PE=3 SV=1
evm.model.HIC_ASM_8.235	0.000466	Prohibitin OS=Gallus gallus OX=9031 GN=PHB PE=1 SV=1
evm.model.HIC_ASM_7.1007	1.97E-09	Elongin-A OS=Rattus norvegicus OX=10116 GN=Eloa PE=1 SV=1
evm.model.HIC_ASM_16.702	0.000563	Proline-serine-threonine phosphatase-interacting protein 1 OS=Mus musculus OX=10090 GN=Pstpip1 PE=1 SV=1
evm.model.HIC_ASM_2.289	0.001181	28S ribosomal protein S25, mitochondrial OS=Bos taurus OX=9913 GN=MRPS25 PE=1 SV=2
evm.model.HIC_ASM_22.288	8.88E-16	Ribosome biogenesis protein TSR3 homolog OS=Mus musculus OX=10090 GN=Tsr3 PE=1 SV=1
evm.model.HIC_ASM_4.594	5.27E-06	GTP-binding protein SAR1b OS=Cricetulus griseus OX=10029 GN=SAR1B PE=1 SV=1
evm.model.HIC_ASM_7.660	0.000378	Homeobox protein Hox-A10 OS=Morone saxatilis OX=34816 GN=hoxa10 PE=3 SV=1
evm.model.HIC_ASM_11.473	0	Multiple epidermal growth factor-like domains protein 8 OS=Rattus norvegicus OX=10116 GN=Megf8 PE=1 SV=2
evm.model.HIC_ASM_14.658	0.001101	General transcription factor IIH subunit 3 OS=Bos taurus OX=9913 GN=GTF2H3 PE=2 SV=1
evm.model.HIC_ASM_0.743	0.001647	Inactive serine/threonine-protein kinase VRK3 OS=Mus musculus OX=10090

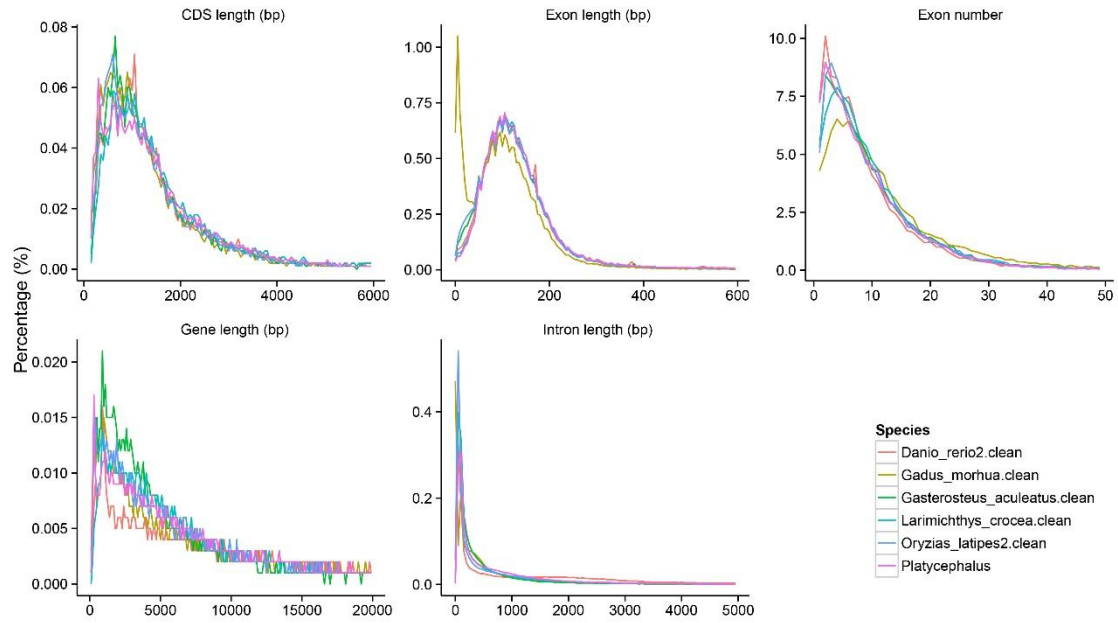
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evm.model.HIC_ASM_16.630	9.95E-08	Protein zwilch homolog OS=Danio rerio OX=7955 GN=zwilch PE=2 SV=1
evm.model.HIC_ASM_21.847	0.002485	Ankyrin repeat and SOCS box protein 9 OS=Mus musculus OX=10090 GN=Asb9 PE=1 SV=2
evm.model.HIC_ASM_10.28.1	0.000769	Steroid receptor RNA activator 1 OS=Homo sapiens OX=9606 GN=SRA1 PE=1 SV=1
evm.model.HIC_ASM_18.154	0	Ras-like protein family member 11A-like OS=Danio rerio OX=7955 GN=zgc:110179 PE=2 SV=1
evm.model.HIC_ASM_12.180	1.01E-13	Serine/threonine-protein kinase Kist OS=Rattus norvegicus OX=10116 GN=Uhmk1 PE=1 SV=1
evm.model.HIC_ASM_3.761	0	Probable G-protein coupled receptor 174 OS=Mus musculus OX=10090 GN=Gpr174 PE=2 SV=1
evm.model.HIC_ASM_10.670	7.55E-07	Solute carrier family 25 member 35 OS=Danio rerio OX=7955 GN=slc25a35 PE=2 SV=1
evm.model.HIC_ASM_7.482	0.000187	Protein lifeguard 1 OS=Homo sapiens OX=9606 GN=GRINA PE=2 SV=1
evm.model.HIC_ASM_4.884	2.66E-15	DNA helicase MCM8 OS=Gallus gallus OX=9031 GN=MCM8 PE=1 SV=1
evm.model.HIC_ASM_2.467	2.22E-16	Homeobox protein Hox-C12a OS=Takifugu rubripes OX=31033 GN=hoxc12a PE=3 SV=1
evm.model.HIC_ASM_16.322	0.000799	High choriolytic enzyme 1 OS=Oryzias latipes OX=8090 GN=hcea PE=1 SV=1
evm.model.HIC_ASM_19.77	1.74E-05	F-box only protein 46 OS=Homo sapiens OX=9606 GN=FBXO46 PE=1 SV=3
evm.model.HIC_ASM_19.674	2.62E-11	Homeobox protein SIX4 OS=Mus musculus OX=10090 GN=Six4 PE=1 SV=1
evm.model.HIC_ASM_13.411	1.91E-05	Endothelial cell-specific molecule 1 OS=Rattus norvegicus OX=10116 GN=Esm1 PE=2 SV=1
evm.model.HIC_ASM_14.552	1.67E-09	Putative phospholipase B-like 2 OS=Bos taurus OX=9913 GN=PLBD2 PE=2 SV=1
evm.model.HIC_ASM_1.669	5.92E-05	Probable sodium-coupled neutral amino acid transporter 6 OS=Danio rerio OX=7955 GN=slc38a6 PE=2 SV=1
evm.model.HIC_ASM_7.606	0.002576	Probable acyl-CoA dehydrogenase 6 OS=Caenorhabditis elegans OX=6239 GN=acdh-6 PE=3 SV=2

evm.model.HIC_ASM_19.686	8.85E-07	Prostacyclin receptor OS=Homo sapiens OX=9606 GN=PTGIR PE=1 SV=1
evm.model.HIC_ASM_20.1169	0.000414	RNA exonuclease 5 OS=Homo sapiens OX=9606 GN=REXO5 PE=2 SV=1
evm.model.HIC_ASM_20.653	0.000137	NA
evm.model.HIC_ASM_7.1024	1.12E-08	Bone morphogenetic protein 8B OS=Homo sapiens OX=9606 GN=BMP8B PE=2 SV=2
evm.model.HIC_ASM_0.748	0	Prolyl 3-hydroxylase OGFOD1 OS=Pongo abelii OX=9601 GN=OGFOD1 PE=2 SV=1
evm.model.HIC_ASM_20.1137	0.001363	Pentatricopeptide repeat-containing protein 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ptd1 PE=2 SV=1
evm.model.HIC_ASM_1.675	9.07E-09	Homeobox protein SIX6 OS=Homo sapiens OX=9606 GN=SIX6 PE=1 SV=2
evm.model.HIC_ASM_3.249	0.000198	Transmembrane protein 35A OS=Danio rerio OX=7955 GN=tmem35a PE=2 SV=1
evm.model.HIC_ASM_15.484	0.002128	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Bos taurus OX=9913 GN=ABHD10 PE=2 SV=1
evm.model.HIC_ASM_14.1029	2.30E-07	X-box-binding protein 1 OS=Bos taurus OX=9913 GN=XPB1 PE=2 SV=1
evm.model.HIC_ASM_18.587	9.81E-14	G-protein coupled receptor 26 OS=Mus musculus OX=10090 GN=Gpr26 PE=2 SV=1
evm.model.HIC_ASM_13.588	0	Transmembrane protein 120B OS=Danio rerio OX=7955 GN=tmem120b PE=2 SV=1
evm.model.HIC_ASM_0.934	5.30E-14	Tetraspanin-3 OS=Pongo abelii OX=9601 GN=TPAN3 PE=2 SV=1
evm.model.HIC_ASM_19.626	3.61E-07	Intraflagellar transport protein 80 homolog OS=Rattus norvegicus OX=10116 GN=Ifit80 PE=2 SV=1
evm.model.HIC_ASM_12.897	0.000761	Ornithine decarboxylase antizyme 1 OS=Danio rerio OX=7955 GN=oaz1a PE=2 SV=1
evm.model.HIC_ASM_21.212	5.04E-07	Fas apoptotic inhibitory molecule 1 OS=Mus musculus OX=10090 GN=Faim PE=1 SV=1
evm.model.HIC_ASM_12.578	1.11E-06	Probable ATP-dependent RNA helicase DDX49 OS=Homo sapiens OX=9606 GN=DDX49 PE=1 SV=1
evm.model.HIC_ASM_1.1255	8.44E-05	TNF receptor-associated factor 3 OS=Mus musculus OX=10090 GN=Traf3 PE=1 SV=2
evm.model.HIC_ASM_0.614	3.92E-09	Protein lin-7 homolog C OS=Rattus norvegicus OX=10116 GN=Lin7c PE=1 SV=1
evm.model.HIC_ASM_7.505	4.67E-09	Deubiquitinase OTUD6B OS=Danio rerio

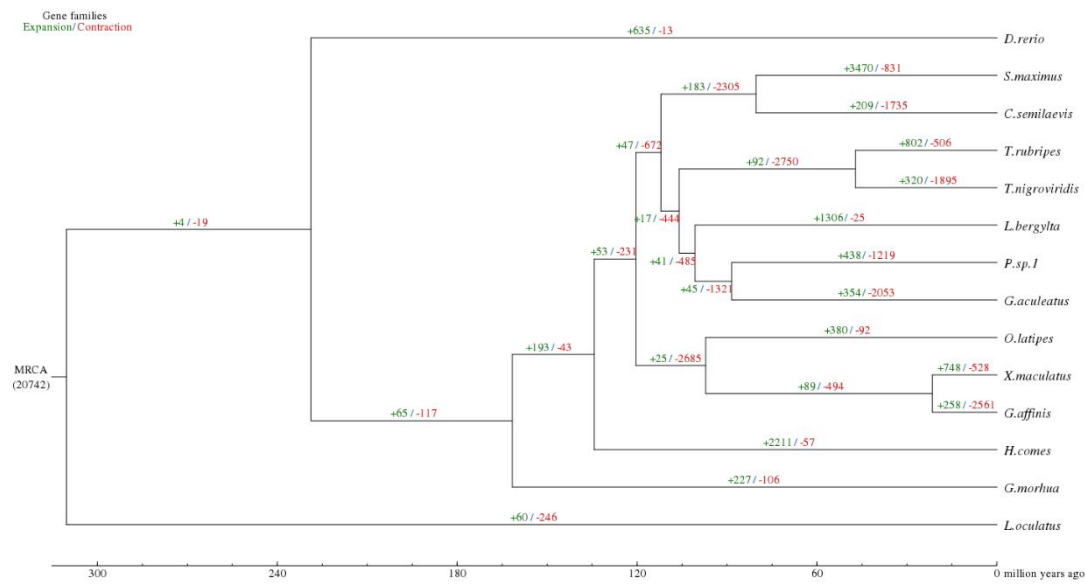
		OX=7955 GN=otud6b PE=2 SV=1
evm.model.HIC_ASM_13.422	0.003654	O-acyltransferase like protein OS=Mus musculus OX=10090 GN=Oacyl PE=2 SV=1
evm.model.HIC_ASM_20.1483	8.23E-07	DNA-directed RNA polymerase III subunit RPC6 OS=Mus musculus OX=10090 GN=Polr3f PE=1 SV=1
evm.model.HIC_ASM_20.324	9.45E-08	Peroxiredoxin-1 OS=Gallus gallus OX=9031 GN=PRDX1 PE=1 SV=1
evm.model.HIC_ASM_2.88	0.002651	AP-4 complex subunit beta-1 OS=Mus musculus OX=10090 GN=Ap4b1 PE=1 SV=2
evm.model.HIC_ASM_20.1312	0.00514	Puromycin-sensitive aminopeptidase OS=Mus musculus OX=10090 GN=Npepps PE=1 SV=2
evm.model.HIC_ASM_22.278	0.004848	Rhomboid-related protein 1 OS=Mus musculus OX=10090 GN=Rhbd1l PE=2 SV=1
evm.model.HIC_ASM_7.579	0	Hyccin OS=Danio rerio OX=7955 GN=fam126a PE=2 SV=1
evm.model.HIC_ASM_12.834	2.69E-09	Transmembrane protein 221 OS=Homo sapiens OX=9606 GN=TMEM221 PE=4 SV=3
evm.model.HIC_ASM_9.820	7.65E-05	Lymphokine-activated killer T-cell-originated protein kinase homolog OS=Danio rerio OX=7955 GN=pbk PE=2 SV=1
evm.model.HIC_ASM_17.492	1.35E-05	Cysteine-rich with EGF-like domain protein 2 OS=Danio rerio OX=7955 GN=creld2 PE=2 SV=2
evm.model.HIC_ASM_7.380	0.001653	Cilia- and flagella-associated protein 20 OS=Xenopus tropicalis OX=8364 GN=cfap20 PE=2 SV=1
evm.model.HIC_ASM_12.470.1	0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens OX=9606 GN=DDAH1 PE=1 SV=3
evm.model.HIC_ASM_0.766	8.14E-06	Kinesin-like protein kif7 OS=Danio rerio OX=7955 GN=kif7 PE=1 SV=1
evm.model.HIC_ASM_0.895	8.55E-06	Spermatogenesis-associated protein 17 OS=Homo sapiens OX=9606 GN=SPATA17 PE=2 SV=1

Supplementary Table S13 Enriched GO terms of positively selected genes with *Platycephalus* sp.1, *Scophthalmus maximus*, and *Cynoglossus semilaevis* as foreground species

GO_ID	GO_Term	GO_Class	P-value	Count
GO:0001510	RNA methylation	BP	0.00376	7
GO:0008168	methyltransferase activity	MF	0.023555	18
GO:0032259	methylation	BP	0.023555	11
GO:0008173	RNA methyltransferase activity	MF	0.026041	7
GO:0006396	RNA processing	BP	0.026041	26
GO:0043414	macromolecule methylation	BP	0.026041	10
GO:0003690	double-stranded DNA binding	MF	0.042477	6



Supplementary Figure S1 Comparisons of predicted gene models between *Platycephalus* sp.1 and other teleost species



Supplementary Figure S2 Gene family expansion and contraction in 14 selected teleost species