

Supplementary Material

Table S1. Functional categorization of the annotated sequences

SeqName	Description	Length	#Hits	e-Value	sim mean	#GO	GO Names list
Anguilla_japonica_contig_21789	kinesin-like protein kif1c isoform x1	8360	20	1.60E-176	83.10%	10	F:microtubule motor activity; F:microtubule binding; P:posterior lateral line ganglion development; P:axon extension; C:microtubule; P:posterior lateral line nerve development; F:ATP binding; P:microtubule-based movement; P:intracellular mRNA localization; C:kinesin complex
Anguilla_japonica_contig_136591	c-c chemokine receptor type 5-like	7329	20	2.60E-141	56.40%	22	P:axon guidance; P:tissue migration; P:G-protein coupled receptor signaling pathway; P:germ cell migration; P:tissue morphogenesis; P:tissue regeneration; P:heart development; F:coreceptor activity; P:response to bacterium; P:regulation of chemotaxis; P:cell migration involved in gastrulation; P:posterior lateral line neuromast primordium migration; P:sprouting angiogenesis; P:gastrulation with mouth forming second; P:regulation of multicellular organismal process; P:striated muscle cell development; C:integral component of membrane; F:chemokine binding; F:chemokine receptor activity; P:leukocyte migration involved in immune response; P:vasculogenesis; P:chemokine-mediated signaling pathway

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Anguilla_japonica_contig_74215	transcription factor sp3 isoform x2	3331	20	1.90E-113	72.10%	11	F:double-stranded DNA binding; P:post-anal tail morphogenesis; P:anterior/posterior pattern specification; P:embryonic pectoral fin morphogenesis; P:regulation of transcription, DNA-templated; P:positive regulation of fibroblast growth factor receptor signaling pathway; P:hindbrain development; P:Wnt signaling pathway; P:notochord development; P:mesoderm formation; P:embryonic limb morphogenesis
Anguilla_japonica_contig_24402	partitioning defective 6 homolog gamma	9854	18	6.40E-94	78.11%	14	P:apical protein localization; P:neural tube formation; P:pronephros development; P:cloaca development; P:embryonic heart tube development; C:cytoplasm; C:cleavage furrow; P:regulation of ARF protein signal transduction; P:spinal cord development; F:ARF guanyl-nucleotide exchange factor activity; P:positive regulation of GTPase activity; P:regulation of collateral sprouting in absence of injury; C:nucleus; C:apical plasma membrane
Anguilla_japonica_contig_46045	fat storage-inducing transmembrane protein 1	12607	4	1.60E-66	68.50%	3	C:integral component of membrane; C:endoplasmic reticulum; C:proteasome activator complex
Anguilla_japonica_contig_188109	heparan-sulfate 6-o-sulfotransferase 3	7350	5	4.00E-63	82.20%	20	F:1-phenanthrol sulfotransferase activity; F:trans-9R,10R-dihydrodiolphenanthrene sulfotransferase activity; F:hydroxyjasmonate sulfotransferase activity; F:2-phenanthrol sulfotransferase activity; C:integral component of membrane; F:9-phenanthrol sulfotransferase activity; F:3-phenanthrol sulfotransferase activity; F:4-phenanthrol sulfotransferase activity; P:embryonic eye morphogenesis; F:cholesterol sulfotransferase activity; F:proteoglycan sulfotransferase activity; F:heparan sulfate 2-O-sulfotransferase activity; F:N-acetylgalactosamine 4-O-sulfotransferase activity; F:trans-3,4-

								dihydrodiolphenanthrene sulfotransferase activity; F:N-acetylglucosamine 6-O-sulfotransferase activity; F:heparan sulfate 6-O-sulfotransferase activity; P:patterning of blood vessels; F:HNK-1 sulfotransferase activity; F:galactose 3-O-sulfotransferase activity; F:1-hydroxypyrene sulfotransferase activity
Anguilla_japonica_contig_155111	kinesin light chain 3 isoform x1	3898	14	5.70E-51	84.50%	2	F:microtubule motor activity; C:kinesin complex	
Anguilla_japonica_contig_140360	transmembrane protein c5orf28 homolog isoform 1	1758	2	5.90E-49	90%	1	C:integral component of membrane	
Anguilla_japonica_contig_178342	solute carrier family 25 member 36-a	3164	6	1.40E-44	79.83%	4	C:mitochondrial inner membrane; P:transmembrane transport; P:mitochondrial transport; C:integral component of membrane	
Anguilla_japonica_contig_14671	eukaryotic translation initiation factor 3 subunit b	9664	2	1.40E-43	81.50%	7	F:translation initiation factor activity; P:translational initiation; P:heart rudiment development; C:eukaryotic translation initiation factor 3 complex; P:neural crest cell development; F:nucleotide binding; F:translation initiation factor binding	
Anguilla_japonica_contig_33451	1-phosphatidylinositol - bisphosphate phosphodiesterase epsilon-1 isoform x1	4864	20	1.50E-43	68.95%	6	F:phosphatidylinositol phospholipase C activity; F:signal transducer activity; P:lipid catabolic process; P:small GTPase mediated signal transduction; F:guanyl-nucleotide exchange factor activity; P:glomerular basement membrane development	

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Anguilla_japonica_contig_76117	serine threonine-protein kinase wnk1 isoform x1	9835	20	2.90E-39	81%	4	P:protein phosphorylation; F:ATP binding; P:posterior lateral line neuromast development; F:protein serine/threonine kinase activity
Anguilla_japonica_contig_57722	neurotrophin-7 isoform x1	9376	14	2.00E-37	55.21%	2	P:dopaminergic neuron differentiation; P:brain development
Anguilla_japonica_contig_110528	atp-binding cassette sub-family g member 1	11677	6	3.60E-37	77.83%	7	P:defense response to bacterium; F:ATPase activity; P:regulation of cholesterol efflux; F:ATP binding; C:integral component of membrane; C:extracellular region; P:sprouting angiogenesis
Anguilla_japonica_contig_150907	abhydrolase domain containing 17aa	6343	4	1.40E-36	95.25%	3	F:coenzyme F390-A hydrolase activity; F:GPI-anchor transamidase activity; F:coenzyme F390-G hydrolase activity
Anguilla_japonica_contig_36470	phospholipid-transporting atpase id 0	1289	9	4.60E-36	70.11%	5	F:ATP binding; F:phospholipid-translocating ATPase activity; F:magnesium ion binding; C:integral component of membrane; P:phospholipid transport
Anguilla_japonica_contig_36562	c-terminal-binding protein 2 isoform 1	15214	7	3.60E-35	96%	9	P:retinoic acid receptor signaling pathway; F:NAD binding; P:camera-type eye development; P:oxidation-reduction process; P:clustering of voltage-gated calcium channels; F:oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; P:synapse assembly involved in innervation; P:regulation of melanocyte differentiation; C:basolateral plasma membrane

Anguilla_japonica_contig_14180	tyrosine-protein phosphatase non-receptor type 9	2197	9	5.10E-33	46.67%	3	P:erythrocyte maturation; F:phosphatase activity; P:primitive hemopoiesis
Anguilla_japonica_contig_311315	dcc-interacting protein 13-beta	10582	3	1.10E-32	96.67%	2	F:protein binding; C:early endosome
Anguilla_japonica_contig_119265	la-related protein 6	18188	2	1.40E-32	89%	6	F:RNA binding; C:ribonucleoprotein complex; C:nucleus; P:somitogenesis; F:nucleotide binding; P:RNA processing
Anguilla_japonica_contig_112873	methyl- -binding protein 2 isoform x1	3536	2	1.90E-29	78%	1	P:locomotory behavior
Anguilla_japonica_contig_314498	fibroblast growth factor receptor 3 isoform x1	1447	20	2.30E-29	82.55%	31	P:determination of heart left/right asymmetry; P:apoptotic process; C:integral component of plasma membrane; P:positive regulation of cell proliferation; P:determination of pancreatic left/right asymmetry; P:skeletal system development; F:heparin binding; P:anatomical structure homeostasis; P:peptidyl-tyrosine phosphorylation; P:cilium assembly; P:positive regulation of MAP kinase activity; P:positive regulation of phospholipase C activity; P:posterior lateral line development; P:cardiac muscle tissue development; C:endomembrane system; F:fibroblast growth factor binding; P:determination of left/right asymmetry in lateral mesoderm; C:intracellular membrane-bounded organelle; P:olfactory nerve formation; P:fin regeneration; F:fibroblast growth factor-activated receptor activity; P:cell proliferation in midbrain; P:post-anal tail morphogenesis; P:skin morphogenesis; P:negative regulation of endodermal cell fate specification; F:ATP binding; P:dorsal/ventral

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pattern formation; P:determination of liver left/right asymmetry; P:olfactory placode morphogenesis; C:cytoplasmic part; P:fibroblast growth factor receptor signaling pathway

Anguilla_japonica_contig_119270	threonine--trna cytoplasmic isoform 1	5993	5	3.10E-29	87.40%	6	P:protein phosphorylation; F:protein serine/threonine kinase activity; P:threonyl-tRNA aminoacylation; F:threonine-tRNA ligase activity; F:ATP binding; C:cytoplasm
Anguilla_japonica_contig_158308	lanc-like protein 2 isoform x1	10141	3	6.60E-27	87.33%	6	C:cytoplasm; C:integral component of plasma membrane; P:G-protein coupled receptor signaling pathway; F:zinc ion binding; F:catalytic activity; F:glutathione binding
Anguilla_japonica_contig_320986	glycosyltransferase-like protein large1 isoform x1	3040	4	2.80E-26	95.50%	4	F:transferase activity, transferring glycosyl groups; C:Golgi apparatus; P:protein glycosylation; C:integral component of membrane
Anguilla_japonica_contig_25735	cadherin-4 isoform 1 precursor	4803	11	6.30E-26	67.64%	39	P:post-anal tail morphogenesis; P:regulation of eye photoreceptor cell development; P:neuron cell-cell adhesion; P:ectoderm development; P:midbrain development; P:embryonic eye morphogenesis; C:catenin complex; P:adherens junction organization; P:tissue regeneration; P:embryonic pectoral fin morphogenesis; P:motor neuron migration; P:neuronal stem cell maintenance; C:presynaptic membrane; P:hindbrain development; P:odontogenesis; P:cartilage condensation; P:homophilic cell adhesion via plasma membrane adhesion molecules; F:calcium ion binding; P:neural crest cell migration; P:establishment of epithelial cell apical/basal polarity; P:dorsal convergence; P:lateral line system development; P:axial mesoderm structural organization; P:peripheral nervous system development; P:cranial nerve development; P:dorsal fin morphogenesis; P:semicircular canal morphogenesis;

								P:pigment cell development; C:integral component of membrane; P:embryonic retina morphogenesis in camera-type eye; P:cell-cell adhesion mediated by cadherin; P:glial cell differentiation; P:axonal fasciculation; P:cell migration involved in somitogenic axis elongation; C:perinuclear region of cytoplasm; P:auditory receptor cell stereocilium organization; P:cardioblast differentiation; P:synapse assembly; P:neural tube development
Anguilla_japonica_contig_16443	nesprin-1 isoform x1	4725	14	1.40E-25	84.71%	4		C:integral component of membrane; P:photoreceptor cell maintenance; F:actin binding; P:establishment of nucleus localization
Anguilla_japonica_contig_266176	kelch-like protein 17	2217	20	2.90E-25	70.20%	9		P:vesicle-mediated transport; C:intracellular membrane-bounded organelle; P:skeletal muscle fiber development; P:anterior/posterior pattern specification; P:swimming; C:cytoplasmic vesicle; P:Wnt signaling pathway; C:endomembrane system; P:convergent extension involved in axis elongation
Anguilla_japonica_contig_229580	neuromedin-k receptor	3928	7	5.10E-25	82%	6		P:synaptic transmission; C:plasma membrane; P:tachykinin receptor signaling pathway; F:tachykinin receptor activity; C:integral component of membrane; P:neuropeptide signaling pathway
Anguilla_japonica_contig_179294	tripartite motif containing 3b isoform x1	7560	11	1.60E-23	93.09%	18		P:protein autoubiquitination; F:zinc ion binding; P:negative regulation of translation involved in gene silencing by miRNA; F:ubiquitin-protein transferase activity; F:protein-glycine ligase activity; P:primitive hemopoiesis; F:miRNA binding; P:regulation of gene silencing by miRNA; P:stem cell proliferation; P:myeloid cell differentiation; P:G1/S transition of mitotic cell cycle; P:miRNA metabolic process; C:cytoplasmic mRNA processing body; F:protein-glutamic

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acid ligase activity; P:embryonic body morphogenesis; P:fibroblast growth factor receptor signaling pathway; P:regulation of neural precursor cell proliferation; P:neural tube development

Anguilla_japonica_contig_172308	protein scribble homolog isoform x4	8023	13	1.00E-22	93%	19	P:convergent extension involved in gastrulation; P:apoptotic process involved in morphogenesis; P:activation of GTPase activity; P:negative regulation of mitotic cell cycle; P:motor neuron migration; P:positive chemotaxis; P:secondary neural tube formation; C:presynaptic membrane; C:cell-cell adherens junction; P:cell proliferation; P:establishment of mitotic spindle orientation; C:cytoplasm; F:protein heterodimerization activity; C:postsynaptic membrane; C:cell leading edge; P:establishment of planar polarity; P:establishment of apical/basal cell polarity; P:positive regulation of apoptotic process; P:single organismal cell-cell adhesion
Anguilla_japonica_contig_139771	protocadherin fat 1 isoform x2	7651	19	1.20E-22	57.05%	7	P:morphogenesis of a branching structure; P:anterior/posterior axon guidance; P:positive regulation of axon extension; P:endocardial progenitor cell migration to the midline involved in heart field formation; P:negative regulation of axon extension; P:central nervous system projection neuron axonogenesis; P:axonal defasciculation
Anguilla_japonica_contig_331970	tubulin delta chain isoform x1	3705	2	4.60E-22	80%	7	C:microtubule; P:protein polymerization; P:obsolete GTP catabolic process; P:microtubule-based process; F:GTPase activity; F:structural constituent of cytoskeleton; F:GTP binding

Anguilla_japonica_contig_33983	cytohesin 4	8684	20	8.60E-22	76.75%	3	P:positive regulation of GTPase activity; F:ARF guanyl-nucleotide exchange factor activity; P:regulation of ARF protein signal transduction
Anguilla_japonica_contig_246953	ankyrin repeat and soxs box protein 5	4287	7	1.20E-21	83.43%	2	P:protein ubiquitination; P:intracellular signal transduction
Anguilla_japonica_contig_92585	mitogen-activated protein kinase kinase 7 isoform x1	6477	3	6.80E-21	93%	6	P:blood vessel morphogenesis; P:protein phosphorylation; F:ATP binding; F:magnesium ion binding; F:MAP kinase kinase kinase activity; P:signal transduction
Anguilla_japonica_contig_27604	thrombospondin-1 isoform x2	3018	13	5.20E-20	80.69%	8	P:negative regulation of angiogenesis; C:sarcoplasmic reticulum; C:extracellular space; F:heparin binding; P:tendon development; C:extracellular matrix; P:cell adhesion; F:calcium ion binding
Anguilla_japonica_contig_361441	trace amine-associated receptor 13c-like	1792	20	1.10E-19	68.35%	3	C:membrane; P:signal transduction; F:G-protein coupled receptor activity
Anguilla_japonica_contig_190350	deoxyribonuclease gamma-like isoform x1	6653	9	1.20E-19	78.11%	3	F:endonuclease activity; P:DNA catabolic process; F:deoxyribonuclease activity
Anguilla_japonica_contig_265560	acetyl- carboxylase 1 isoform x4	639	18	1.20E-19	93.83%	5	P:fatty acid biosynthetic process; F:metal ion binding; F:ATP binding; F:biotin carboxylase activity; F:acetyl-CoA carboxylase activity

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Anguilla_japonica_contig_207147	epithelial membrane protein 1 isoform x2	5912	15	2.20E-19	69.33%	5	C:cytoplasm; P:positive regulation of cell proliferation; P:regulation of glomerular filtration; C:integral component of membrane; C:nucleus
Anguilla_japonica_contig_162838	ankyrin neuronal	3231	20	2.20E-18	97%	3	P:signal transduction; P:proteolysis; F:aspartic-type endopeptidase activity
Anguilla_japonica_contig_134750	disks large homolog 1 isoform x12	4649	20	4.90E-18	96.80%	13	F:phosphatase binding; C:basolateral plasma membrane; P:actin filament organization; C:postsynaptic membrane; P:single organismal cell-cell adhesion; C:cell junction; P:cortical actin cytoskeleton organization; P:endothelial cell proliferation; C:postsynaptic density; F:protein kinase binding; F:protein heterodimerization activity; C:endoplasmic reticulum; P:negative regulation of mitotic cell cycle
Anguilla_japonica_contig_251146	structural maintenance of chromosomes protein 6 isoform x1	3776	6	1.10E-17	72%	2	C:Smc5-Smc6 complex; P:double-strand break repair via homologous recombination
Anguilla_japonica_contig_207939	ethanolamine-phosphate phospho-lyase	1829	3	1.40E-17	85.33%	5	F:pyridoxal phosphate binding; P:embryonic hemopoiesis; F:ethanolamine-phosphate phospho-lyase activity; F:transaminase activity; C:mitochondrion
Anguilla_japonica_contig_12782	lethal malignant brain tumor-like protein 4 isoform x2	3323	20	6.00E-17	77.25%	4	P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity; C:nucleus; F:zinc ion binding

Anguilla_japonica_contig_96579	transmembrane protease serine 2	9647	20	2.00E-16	68.40%	4	F:serine-type endopeptidase activity; P:epidermis development; P:proteolysis; C:membrane
Anguilla_japonica_contig_369337	serine palmitoyltransferase 3 isoform x1	4107	6	3.60E-16	72.17%	2	P:metabolic process; F:catalytic activity
Anguilla_japonica_contig_281979	dynein regulatory complex protein 1	2536	1	1.80E-15	77%	4	P:cilium-dependent cell motility; C:axoneme; P:bacterial-type flagellum-dependent cell motility; P:axonemal dynein complex assembly
Anguilla_japonica_contig_285894	choline transporter-like protein 1	6934	5	8.00E-15	84.60%	1	C:integral component of membrane
Anguilla_japonica_contig_59973	monofunctional c1-tetrahydrofolate mitochondrial isoform x1	15736	7	6.10E-14	85.14%	5	P:oxidation-reduction process; F:methylenetetrahydrofolate dehydrogenase (NADP+) activity; P:folic acid-containing compound biosynthetic process; F:ATP binding; F:formate-tetrahydrofolate ligase activity
Anguilla_japonica_contig_154121	protein fam65b isoform x1	18788	3	6.90E-13	100%	2	P:skeletal muscle fiber development; P:sensory perception of sound
Anguilla_japonica_contig_228634	protein crumbs homolog 1	9442	2	7.70E-13	92.50%	3	P:establishment or maintenance of epithelial cell apical/basal polarity; F:calcium ion binding; C:protein complex

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Anguilla_japonica_contig_17883	grb2-related adaptor protein	7886	4	2.40E-11	83.50%	1	C:membrane
Anguilla_japonica_contig_33774	transmembrane serine 13a	940	5	2.40E-11	69.80%	3	C:membrane; P:proteolysis; F:serine-type endopeptidase activity
Anguilla_japonica_contig_316214	latent-transforming growth factor beta-binding protein partial	2763	1	2.10E-10	88%	2	F:calcium ion binding; C:extracellular region
Anguilla_japonica_contig_42928	coronin-2b isoform x1	5289	2	3.80E-09	97%	3	P:actin cytoskeleton organization; C:membrane; F:actin filament binding
Anguilla_japonica_contig_114037	cadherin-7 isoform x2	7868	3	4.70E-09	69.33%	2	P:notochord cell differentiation; C:membrane
Anguilla_japonica_contig_352934	glycosyltransferase-like protein large1	3958	2	1.30E-08	91%	3	C:integral component of membrane; C:Golgi apparatus; F:transferase activity, transferring glycosyl groups
Anguilla_japonica_contig_124304	cyclic amp-dependent transcription factor atf-1	5889	1	4.60E-08	89%	4	P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity; F:sequence-specific DNA binding; C:nucleus

Anguilla_japoni ca_contig_2051 64	microtubule- associated serine threonine-protein kinase 4 isoform x5	14643	2	1.10E-07	63%	1	F:transferase activity, transferring phosphorus-containing groups
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