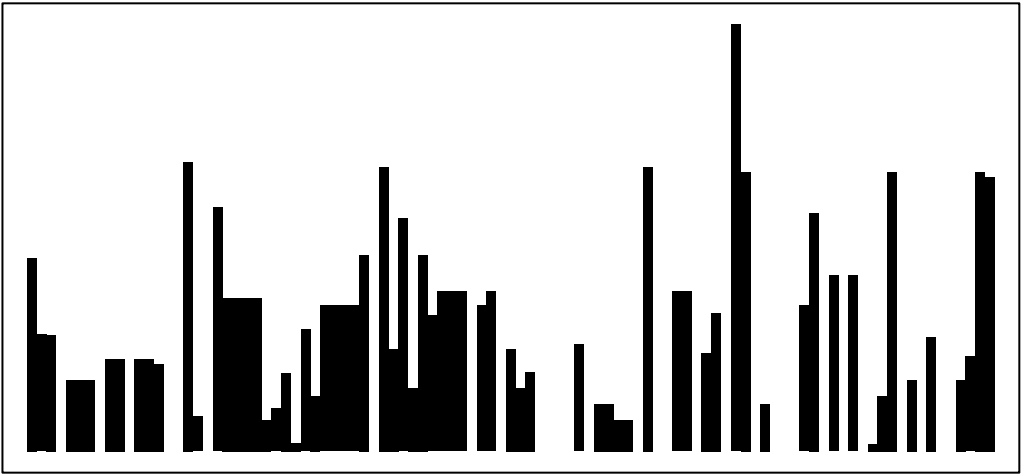


OTU_136.csv

Hypogastrura vernalis

Hypogastruridae

89.06



Hypogastrura vernalis 16S ribosomal RNA gene, part	JN970945	89.06	42.28	7.64734e-11	Hypogastruridae	Hypogastrura vernalis
Pogonognathellus cf. flavescens FZ-2014 voucher Po	KF591937	85.48	40.94	3.96142e-08	Tomoceridae	Pogonognathellus cf. flavescens FZ-2014
Podura aquatica mitochondrion, partial genome	AY639939	85.45	36.24	5.87927e-06	Poduridae	Podura aquatica
Isotoma viridis 16S ribosomal RNA gene, partial se	JN970946	78.79	44.3	7.16241e-05	Isotomidae	Isotoma viridis
Coecobrya communis 16S ribosomal RNA gene, partial	KC236218	83.33	32.21	0.00304554	Entomobryidae	Coecobrya communis
Coecobrya tenebricosa 16S ribosomal RNA gene, part	KC236191	83.33	32.21	0.00304554	Entomobryidae	Coecobrya tenebricosa
Buettikeria echinosa 16S ribosomal RNA gene, parti	EF487789	83.33	32.21	0.00304554	Scarabaeidae	Buettikeria echinosa
Schistosoma mattheei genome assembly S_mattheei_De	LM158611	79.69	42.95	0.01063	Schistosomatidae	Schistosoma mattheei
Congerina kusceri haplotype B 16S ribosomal RNA gen	JQ348915	84.31	32.89	0.01063	Dreissenidae	Congerina kusceri
Congerina kusceri isolate D10 16S ribosomal RNA gen	JX099439	84.31	32.89	0.01063	Dreissenidae	Congerina kusceri
Lepiserica sp. BMNH 671451 16S large subunit ribos	EF487924	78.46	42.28	0.01063	Scarabaeidae	Lepiserica sp. BMNH 671451
Congerina kusceri 16S ribosomal RNA gene, partial s	AF320601	84.31	32.89	0.01063	Dreissenidae	Congerina kusceri
Lotus japonicus genomic DNA, chromosome 4, clone:	AP006091	84.31	33.56	0.01063	Fabaceae	Lotus japonicus
Ovis canadensis canadensis isolate 43U chromosome	CP011891	84.09	29.53	0.0371022	Bovidae	Ovis canadensis canadensis
Strongyloides venezuelensis genome assembly S_vene	LM525031	76.81	44.97	0.0371022	Strongyloididae	Strongyloides venezuelensis
Strongyloides venezuelensis genome assembly S_vene	LM524996	76.81	44.97	0.0371022	Strongyloididae	Strongyloides venezuelensis
Clostridium scatologenes strain ATCC 25775, comple	CP009933	93.55	20.81	0.0371022	Clostridiales	Clostridium scatologenes
Strongyloides stercoralis genome assembly S_sterco	LL999054	81.63	32.89	0.0371022	Rhabditida	Strongyloides stercoralis
Schistosoma curassoni genome assembly S_curassoni_	LM068723	80	42.95	0.0371022	Strigeidida	Schistosoma curassoni
Wuchereria bancrofti genome assembly W_bancrofti_J	LM000688	91.43	22.15	0.0371022	Spirurida	Wuchereria bancrofti
Anomala varicolor isolate BM677826 16S ribosomal R	DQ680967	87.18	26.17	0.0371022	Coleoptera	Anomala varicolor
Anomala varicolor isolate BM671388 16S ribosomal R	DQ680892	87.18	26.17	0.0371022	Coleoptera	Anomala varicolor
Vitis vinifera contig VV78X008195.12, whole genome	AM446568	87.18	26.17	0.0371022	Vitales	Vitis vinifera
Vitis vinifera contig VV78X008195.18, whole genome	AM438115	87.18	26.17	0.0371022	Vitales	Vitis vinifera
Vitis vinifera contig VV78X134311.9, whole genome	AM459239	81.48	36.24	0.0371022	Vitales	Vitis vinifera
Onychiurus orientalis mitochondrion, partial genom	AY639938	82	33.56	0.0371022	Onychiuridae	Onychiurus orientalis
Medicago truncatula clone mth2-34b13, complete seq	AC130799	83.67	30.87	0.0371022	Fabaceae	Medicago truncatula
Arabidopsis thaliana srp30 gene, exons 1-12	AJ131214	80.39	34.23	0.0371022	Brassicales	Arabidopsis thaliana
Ovis canadensis canadensis isolate 43U chromosome	CP011888	85.71	30.87	0.129499	Bovidae	Ovis canadensis canadensis
Strongyloides venezuelensis genome assembly S_vene	LM525123	82.61	30.87	0.129499	Strongyloididae	Strongyloides venezuelensis
PREDICTED: Linepithema humile neuroparsin-A-like (XM_012361527	86.84	25.5	0.129499	Formicidae	Linepithema humile
PREDICTED: Linepithema humile neuroparsin-A-like (XM_012361526	86.84	25.5	0.129499	Formicidae	Linepithema humile
PREDICTED: Linepithema humile neuroparsin-A-like (XM_012361525	86.84	25.5	0.129499	Formicidae	Linepithema humile
PREDICTED: Linepithema humile neuroparsin-A-like (XM_012361524	86.84	25.5	0.129499	Formicidae	Linepithema humile
PREDICTED: Linepithema humile pro-corazonin-like (XM_012359878	89.19	24.16	0.129499	Formicidae	Linepithema humile
Strongyloides stercoralis genome assembly S_sterco	LL999050	79.25	35.57	0.129499	Strongyloididae	Strongyloides stercoralis
Strongyloides stercoralis genome assembly S_sterco	LL999048	93.33	20.13	0.129499	Strongyloididae	Strongyloides stercoralis
Schistosoma rodhaini genome assembly S_rodhaini_Bu	LL958232	84.78	28.86	0.129499	Schistosomatidae	Schistosoma rodhaini
Syphacia muris genome assembly S_muris_Valencia_s	LK998325	90.91	22.15	0.129499	Oxyuridae	Syphacia muris
Syphacia muris genome assembly S_muris_Valencia_s	LK996050	82.98	31.54	0.129499	Oxyuridae	Syphacia muris
Strongyloides papillosus genome assembly S_papillo	LM525569	89.19	24.16	0.129499	Strongyloididae	Strongyloides papillosus
Cyprinus carpio genome assembly common carp genome	LM590968	86.36	28.86	0.129499	Cyprinidae	Cyprinus carpio
Plasmodium yoelii genome assembly PY17X01, chromos	LM993663	87.5	26.85	0.129499	Plasmodiidae	Plasmodium yoelii
Plasmodium yoelii genome assembly PYYM01, chromoso	LK934637	87.5	26.85	0.129499	Plasmodiidae	Plasmodium yoelii
Plasmodium berghei ANKA genome assembly PBANKA01,	LK023124	87.5	26.85	0.129499	Plasmodiidae	Plasmodium berghei ANKA
Eurys sp. SS2 voucher AE065 16S ribosomal RNA gene	KF318477	78.33	39.6	0.129499	Pergidae	Eurys sp. SS2
Callistethus sp. 6 VF-2014 voucher CEUA00105818 16	KF738015	86.84	25.5	0.129499	Scarabaeidae	Callistethus sp. 6 VF-2014
PREDICTED: Apis mellifera zinc finger protein 516-	XM_006567475	87.5	26.85	0.129499	Apis mellifera	Apis mellifera
Folsomia quadrioculata 16S ribosomal RNA gene, par	KC236199	78.18	36.91	0.129499	Isotomidae	Folsomia quadrioculata
Clostridium saccharoperbutylacetonicum N1-4(HMT),	CP004121	84.78	28.86	0.129499	Clostridiaceae	Clostridium saccharoperbutylacetonicum N1-4(HMT)
Podura aquatica 16S ribosomal RNA gene, partial se	JN970977	82.98	30.87	0.129499	Poduridae	Podura aquatica
Megalothorax sp. EA040003-cs17 16S ribosomal RNA g	JN970951	83.72	28.86	0.129499	Neelidae	Megalothorax sp. EA040003-cs17
Myrmecolax sp. 5 DPM-2011 16S large subunit riboso	JN082867	74.36	49.66	0.129499	Myrmecolacidae	Myrmecolax sp. 5 DPM-2011
Myrmecolax sp. 4 DPM-2011 16S large subunit riboso	JN082866	74.36	49.66	0.129499	Myrmecolacidae	Myrmecolax sp. 4 DPM-2011
Homo sapiens T-box 20 (TBX20) gene, complete cds	HM015599	77.61	44.3	0.129499	Hominidae	Homo sapiens
Homo sapiens T-box 20 (TBX20), RefSeqGene on chrom	NG_015805	77.61	44.3	0.129499	Hominidae	Homo sapiens
Psychotria acuminata voucher STRI:BCI 711071 photo	GQ982336	85	26.85	0.129499	Rubiaceae	Psychotria acuminata
Zebrafish DNA sequence from clone CH73-15N15 in li	FP102191	79.03	40.27	0.129499	Cypriniformes	Danio rerio
Maladera sp. BMNH 671449 16S large subunit ribosom	EF487929	82.22	30.2	0.129499	Coleoptera	Maladera sp. BMNH 671449
Lepiserica sp. BMNH 671452 16S large subunit ribos	EF487925	82.22	30.2	0.129499	Coleoptera	Lepiserica sp. BMNH 671452
Phytophthora ramorum strain CBS 101553 mitochondri	EU427470	81.48	36.24	0.129499	Peronosporales	Phytophthora ramorum
Phytophthora ramorum mitochondrion, complete genom	DQ832718	81.48	36.24	0.129499	Peronosporales	Phytophthora ramorum
Vitis vinifera, whole genome shotgun sequence, con	AM480418	76.81	45.64	0.129499	Vitales	Vitis vinifera
Taeniopygia guttata chromosome UNK clone TGMCBa-9H	AC188314	93.33	20.13	0.129499	Passeriformes	Taeniopygia guttata
Homo sapiens chromosome 7 clone RP11-178P2, comple	AC009531	77.61	44.3	0.129499	Primates	Homo sapiens
Homo sapiens clone SCb-41A3 from 7p14-15, complete	AC005826	77.61	44.3	0.129499	Primates	Homo sapiens
Plasmodium yoelii yoelii str. 17XNL hypothetical p	XM_724929	87.5	26.85	0.129499	Plasmodiidae	Plasmodium yoelii yoelii 17XNL
Plasmodium berghei strain ANKA hypothetical protei	XM_663995	87.5	26.85	0.129499	Plasmodiidae	Plasmodium berghei ANKA
Homo sapiens BAC clone RP11-456N16 from 7p15.1-p13	AC006379	77.61	44.3	0.129499	Hominidae	Homo sapiens
Fusobacterium nucleatum subsp. vincentii ChDC F8 s	CP012714	84.62	26.17	0.451997	Fusobacteriales	Fusobacterium nucleatum subsp. vincentii ChDC F8
Drosophila busckii chromosome 3R sequence	CP012526	86.49	24.83	0.451997	Diptera	Drosophila busckii
Spiroplasma litorale strain TN-1, complete genome	CP012357	75.71	46.31	0.451997	Entomoplasmatales	Spiroplasma litorale
Pomacea maculata mitochondrion, complete genome	KR350466	100	16.11	0.451997	Ampullariidae	Pomacea maculata
Ovis canadensis canadensis isolate 43U chromosome	CP011886	93.1	19.46	0.451997	Bovidae	Ovis canadensis canadensis
Strongyloides venezuelensis genome assembly S_vene	LM525114	76.12	43.62	0.451997	Strongyloididae	Strongyloides venezuelensis
Strongyloides venezuelensis genome assembly S_vene	LM525008	82.22	30.2	0.451997	Strongyloididae	Strongyloides venezuelensis
Sinothela sp. XUX-2011-217 16S ribosomal RNA gene,	KP230154	80	36.24	0.451997	Liphistiidae	Sinothela sp. XUX-2011-217
Vinathela abca voucher XUX-2013-047 16S ribosomal	KP230086	78.57	37.58	0.451997	Araneae	Vinathela abca
Heptathela higoensis voucher XUX-2013-468 16S ribo	KP230064	78.57	35.57	0.451997	Araneae	Heptathela higoensis
Elizabethkingia sp. BM10, complete genome	CP011059	86.84	25.5	0.451997	Flavobacteriales	Elizabethkingia sp. BM10
Campylobacter volucris LMG 24379, complete genome	CP007774	91.18	22.15	0.451997	Campylobacteriales	Campylobacter volucris LMG 24379
Cucumis melo genomic chromosome, chr_11	LN713265	78.95	36.24	0.451997	Cucurbitales	Cucumis melo
Cucumis melo genomic chromosome, chr_6	LN713260	88.24	22.82	0.451997	Cucurbitales	Cucumis melo
Cucumis melo genomic scaffold, anchoredscaffold000	LN681921	78.95	36.24	0.451997	Cucurbitales	Cucumis melo
Cucumis melo genomic scaffold, anchoredscaffold000	LN681860	88.24	22.82	0.451997	Cucurbitales	Cucumis melo
Parastrongyloides trichosuri genome assembly P_tri	LM523525	79.59	32.89	0.451997	Rhabditida	Parastrongyloides trichosuri
Toxocara canis genome assembly T_canis_Ecuador_sc	LM038155	80.36	36.24	0.451997	Ascaridida	Toxocara canis
Strongyloides stercoralis genome assembly S_sterco	LL999108	82.61	30.87	0.451997	Rhabditida	Strongyloides stercoralis
Strongyloides stercoralis genome assembly S_sterco	LL999053	93.1	19.46	0.451997	Rhabditida	Strongyloides stercoralis
Onchocerca ochengi genome assembly O_ochengi_Ngaou	LL518239	75.71	46.98	0.451997	Spirurida	Onchocerca ochengi
Heligmosomoides polygyrus genome assembly H_bakeri	LL195820	83.33	28.19	0.451997	Rhabditida	Heligmosomoides polygyrus
Dracunculus medinensis genome assembly D_medinensi	LK978194	76.56	42.95	0.451997	Spirurida	Dracunculus medinensis
Brugia pahangi genome assembly B_pahangi_Glasgow ,	LK973504	85.37	26.85	0.451997	Spirurida	Brugia pahangi
Brugia pahangi genome assembly B_pahangi_Glasgow ,	LK968273	76.06	46.98	0.451997	Spirurida	Brugia pahangi
Brugia pahangi genome assembly B_pahangi_Glasgow ,	LK966974	77.27	43.62	0.451997	Spirurida	Brugia pahangi
Brugia pahangi genome assembly B_pahangi_Glasgow ,	LK965037	83.33	28.19	0.451997	Spirurida	Brugia pahangi
Protopolystoma xenopodis genome assembly P_xenopod	LM990169	84.44	29.53	0.451997	Polystomatidae	Protopolystoma xenopodis
Toxocara canis genome assembly T_canis_Ecuador_sc	LM041102	93.1	19.46	0.451997	Ascaridida	Toxocara canis
Ovis canadensis canadensis isolate 43U chromosome	CP011887	92.86	18.79	1.57763	Bovidae	Ovis canadensis canadensis
Ovis canadensis canadensis isolate 43U chromosome	CP011905	72.31	41.61	1.57763	Bovidae	Ovis canadensis canadensis