

Supplementary Table 1. Accession numbers and sizes of the scaffolds

Scaffold ID	Accession nos.	Length (bp)
Sc0000000_1	BLLK01000046	1,401,888
Sc0000000_2	BLLK01000047	4,456,483
Sc00000001	BLLK01000045	3,786,395
Sc00000002	BLLK01000022	3,682,818
Sc00000003	BLLK01000069	3,325,582
Sc00000004	BLLK01000020	2,427,249
Sc00000005	BLLK01000038	2,466,962
Sc00000006	BLLK01000062	2,448,919
Sc00000007	BLLK01000051	1,708,045
Sc00000008	BLLK01000019	1,557,594
Sc00000009	BLLK01000058	1,427,234
Sc00000010	BLLK01000023	1,324,147
Sc00000011	BLLK01000029	1,119,173
Sc00000012	BLLK01000074	898,138
Sc00000013	BLLK01000075	820,580
Sc00000014	BLLK01000057	796,113
Sc00000015	BLLK01000060	471,218
Sc00000016	BLLK01000052	459,726
Sc00000017	BLLK01000049	390,835
Sc00000018	BLLK01000056	353,616
Sc00000019	BLLK01000064	122,439
Sc00000020	BLLK01000001	75,078
Sc00000021	BLLK01000054	72,151
Sc00000022	BLLK01000034	56,547
Sc00000024	BLLK01000009	21,873
Sc00000025	BLLK01000067	8,026
xfSc00000000	BLLK01000055	240,635
xfSc00000001	BLLK01000014	89,933
xfSc00000002	BLLK01000068	72,226
xfSc00000004	BLLK01000076	59,726
xfSc00000005	BLLK01000033	52,213
xfSc00000007	BLLK01000048	35,414

xfSc0000008	BLLK01000083	31,890
xfSc0000009	BLLK01000004	30,766
xfSc0000013	BLLK01000015	24,073
xfSc0000015	BLLK01000017	20,284
xfSc0000016	BLLK01000002	13,235
xfSc0000017	BLLK01000010	8,965
xfSc0000018	BLLK01000041	8,172
xfSc0000020	BLLK01000035	4,234
xpSc0000023_1	BLLK01000039	165,750
xpSc0000023_2	BLLK01000040	902,213
xpSc0000024	BLLK01000027	883,853
xpSc0000025	BLLK01000025	441,269
xpSc0000026	BLLK01000032	329,341
xpSc0000027	BLLK01000061	299,809
xpSc0000028	BLLK01000072	229,945
xpSc0000029	BLLK01000013	192,834
xpSc0000030	BLLK01000028	142,297
xpSc0000031	BLLK01000077	130,342
xpSc0000032	BLLK01000071	119,343
xpSc0000033	BLLK01000082	105,001
xpSc0000034	BLLK01000078	103,065
xpSc0000035	BLLK01000042	74,774
xpSc0000036	BLLK01000016	69,767
xpSc0000037	BLLK01000066	53,032
xpSc0000038	BLLK01000079	41,318
xpSc0000039	BLLK01000036	34,663
xpSc0000040	BLLK01000012	34,430
xpSc0000041	BLLK01000050	31,955
xpSc0000042	BLLK01000081	26,297
xpSc0000043	BLLK01000005	24,083
xpSc0000046	BLLK01000003	20,481
xpSc0000047	BLLK01000037	20,058
xpSc0000050	BLLK01000070	15,833
xpSc0000053	BLLK01000065	14,005
xpSc0000054	BLLK01000021	13,957
xpSc0000056	BLLK01000059	12,086

xpSc0000059	BLLK01000007	11,102
xpSc0000061	BLLK01000044	10,160
xpSc0000062	BLLK01000063	10,148
xpSc0000065	BLLK01000024	9,117
xpSc0000066	BLLK01000084	8,793
xpSc0000070	BLLK01000031	7,900
xpSc0000072	BLLK01000006	6,564
xpSc0000074	BLLK01000080	6,087
xpSc0000078	BLLK01000030	4,807
xpSc0000080	BLLK01000008	4,590
xpSc0000085	BLLK01000018	4,265
xpSc0000091	BLLK01000011	3,564
xpSc0000094	BLLK01000043	3,076
xpSc0000096	BLLK01000073	2,963
xpSc0000097	BLLK01000085	2,940
xpSc0000101	BLLK01000026	1,753
xpSc0000104	BLLK01000053	1,063

Supplementary Table 2. Summary of BUSCO analysis

	<i>C. tenuissimus</i> NIES-3715	<i>T. pseudonana</i>	<i>T. oceanica</i>
Complete BUSCOs	82	75	54
Complete and single-copy BUSCOs	81	73	53
Complete and duplicated BUSCOs	1	2	1
Fragmented BUSCOs	1	2	1
Missing BUSCOs	151	157	179
Total BUSCO groups searched	234	234	234

Supplementary Table 3. Gene numbers and functional domains in orthogroup

Orthogroup	Number of genes in OG				PfamID	Description
	Cte*	Tps	Ptr	Cme		
OG0000	385 (376)	1	0	0	IPR026906	Leucine rich repeat 5
OG0001	111 (110)	56	51	3	IPR000232	Heat shock factor (HSF)-type, DNA-binding
OG0003	89 (52)	16	5	0	IPR008752	Peptidase M11, gametolysin
OG0004	83 (36)	5	4	0	IPR013103	Reverse transcriptase, RNA-dependent DNA polymerase
OG0005	69 (12)	2	1	2	IPR001841	Zinc finger, RING-type
OG0007	54 (52)	5	7	2	IPR001841	Zinc finger, RING-type
OG0016	42 (39)	0	0	1	IPR002893	Zinc finger, MYND-type
OG0006	30 (10)	2	41	0	IPR013103	Reverse transcriptase, RNA-dependent DNA polymerase
OG0021	27 (17)	0	5	0	IPR013103	Reverse transcriptase, RNA-dependent DNA polymerase
OG0024	26 (3)	2	1	0	IPR000477	Reverse transcriptase domain
OG0026	24 (24)	2	1	1	IPR000917	Sulfatase
OG0033	21 (21)	1	1	0	IPR000917	Sulfatase
OG0065	15 (2)	0	1	0	IPR000477	Reverse transcriptase domain
OG0040	15 (15)	3	4	0	IPR021134	Bestrophin/UPF0187
OG0079	14 (13)	0	0	1	IPR001005	SANT/Myb domain
OG0034	13 (10)	5	3	2	IPR005331	Sulfotransferase
OG0022	12 (12)	8	11	0	IPR022796	Chlorophyll A-B binding protein
OG0121	10 (9)	0	2	0	IPR013103	Reverse transcriptase, RNA-dependent DNA polymerase
OG0008	62 (39)	0	0	0	IPR000800	Notch domain
OG0052	20 (19)	0	0	0	IPR000719	Protein kinase domain
OG0058	19 (19)	0	0	0	IPR001254	Peptidase S1
OG0061	18 (14)	0	0	0	IPR027806	Harbinger transposase-derived nuclease domain
OG0094	14 (7)	0	0	0	IPR000477	Reverse transcriptase domain
OG0125	12 (-)	0	0	0	-	No domain
OG1743	4 (2)	0	0	0	IPR000408	Regulator of chromosome condensation, RCC1
OG3531	3 (3)	0	0	0	IPR029526	PiggyBac transposable element-derived protein

*Number of genes possessing the functional domain were shown in parentheses.

Supplementary Table 4. Accession numbers of replication associated protein sequence using the ML tree

Accession number	Species
Cten2-10_frame-shift	
Cten2-6_DNAVirus:g8095.t1	
YP_009345086.1	Amphibola crenata associated bacilladnavirus 2
YP_009345107.1	Amphibola crenata associated bacilladnavirus 1
AXH78029.1	Bacilladnaviridae sp.
AXH73196.1	Bacilladnaviridae sp.
BAL05205.1	Chaetoceros virus YT-2008
YP_473359.1	Chaetoceros protobacilladnavirus 1
YP_004046698.1	Chaetoceros protobacilladnavirus 4
BAP99817.1	Chaetoceros tenuissimus DNA virus type-II
YP_009111348.1	Chaetoceros tenuissimus DNA virus type-II
BBE21064.1	Chaetoceros tenuissimus DNA virus SS12-43V
YP_009001777.1	Chaetoceros sp. DNA virus 7
AUF34978.1	uncultured virus
YP_009109635.1	Bacillariodnavirus LDMD-2013
AUF34977.1	uncultured virus
YP_009345097.1	Avon-Heathcote estuary associated bacilladnavirus
YP_004286322.1	Chaetoceros protobacilladnavirus 3
BAN59850.1	Thalassionema nitzschioides DNA virus
P0DOK4.1	Chaetoceros diatodnavirus 1
BAH66307.1	Chaetoceros debilis DNA virus
BCD41518_V	Chaetoceros tenuissimus DNA virus sp.
BCD41526.1_V	Chaetoceros tenuissimus DNA virus sp.
BCD41525_V	Chaetoceros tenuissimus DNA virus sp.
BCD41529_V	Chaetoceros tenuissimus DNA virus sp.
BCD41513_T	Chaetoceros tenuissimus DNA virus sp.
BCD41521_T	Chaetoceros tenuissimus DNA virus sp.
BCD41517_T	Chaetoceros tenuissimus DNA virus sp.
BCD41530_T	Chaetoceros tenuissimus DNA virus sp.
69-1_stopcodon	
69-4_F1_s144	
I-All_frame-shift	
H-1_frame-shift	
A-0_frame-shift_stopcodon	
72-1_F3_s151	
72-8_F1_s144	
36-1_frame-shift3-1-2	
36-3_frame-shift_stopcodon	
45-1_frame-shift	
45-2_frame-shift_stopcodon	
YP_009021875.1	Porcine stool-associated circular virus 4
APG55817.1	unidentified circular ssDNA virus