

Supplementary Material 2. List of reference sequences used for phylogenetic analyses.

Gene	ID in phylogenetic trees ^{*1}	Lineage	DDBJ/EMBL/GenBank accession number	Reference ^{*2}
16S	16S_ONW4_LnA	A	AY247381	LM06
	16S_DH1_LnB	B	AY247289	LM06
	16S_CM01-143_LnB	B	OR340020	MD24
	16S_A-Sa01_LnC	C	AB748902	SY13
	16S_A-Sa02_LnC	C	AB748903	SY13
	16S_Smn3_LnD	D	AY247321	LM06
	16S_DH3_LnE	E	AY247328	LM06
	16S_G-Sa01_LnF	F	AB748908	SY13
	16S_CM01-495_LnF	F	OR340019	MD24
	16S_IRS07_LnG	G	LC111228	SY16
	16S_CM01-346_LnG	G	OR340011	MD24
	16S_IRS31_LnH	H	LC111250	SY16
	16S_IRS32_LnH	H	LC111251	SY16
	16S_IRF01_LnI	I	LC111209	SY16
	16S_CM01-680_LnI	I	OR340009	MD24
	16S_IRS01_LnJ	<i>S. spathulata</i> (J)	LC111222	SY16
	16S_CM01-452_LnJ	<i>S. spathulata</i> (J)	OR340003	MD24
	16S_iriomote-1_malab_Ln2	K (<i>S. malabonensis</i> lineage 2)	AB898229	HM14
	16S_iriomote-2_malab_Ln2	K (<i>S. malabonensis</i> lineage 2)	AB898230	HM14
	16S_ishigaki-11_malab_Ln2	K (<i>S. malabonensis</i> lineage 2)	AB898231	HM14
	16S_WNS02_kegaki	<i>S. kegaki</i>	LC111281	SY16
	16S_WNS03_kegaki	<i>S. kegaki</i>	LC111282	SY16
	16S_MRZ1_kegaki	<i>S. kegaki</i>	AY247315	LM06

^{*1}The lineages of complete mitogenomes (prefix "CompMT") were determined in the present study.

^{*2}References are abbreviated as follows:

HM14: Hamaguchi M, Shimabukuro H, Usuki H, Hori M. 2014. Occurrences of the Indo-West Pacific rock oyster *Saccostrea cucullata* in mainland Japan. *Mar Biodivers Rec* 7: e84.

LM06: Lam K, Morton B. 2006. Morphological and mitochondrial-DNA analysis of the Indo-West Pacific rock oysters (Ostreidae: *Saccostrea* species). *J Molluscan Stud* 72: 235–245.

LIU11: Liu J, Li Q, Kong L, Yu H, Zheng X. 2011. Identifying the true oysters (Bivalvia: Ostreidae) with mitochondrial phylogeny and distance-based DNA barcoding. *Mol Ecol Resour* 11: 820–830.

MD24: McDougall C, Nenadic N, Richardson M, Healy JM. 2024. Molecular identification of intertidal rock oyster species in north-eastern Australia reveals new candidates for aquaculture. *Aquaculture* 587: 740838.

MU22: Mu W. 2022. The complete mitochondrial genome of *Saccostrea malabonensis* (Ostreida: Ostreidae): characterization and phylogenetic position. *Mitochondrial DNA B Resour* 7: 1945–1947.

SY13: Sekino M, Yamashita H. 2013. Mitochondrial DNA barcoding for Okinawan oysters: a cryptic population of the Portuguese oyster *Crassostrea angulata* in Japanese waters. *Fish Sci* 79: 61–76

SY16: Sekino M, Yamashita H. 2016. Mitochondrial and nuclear DNA analyses of *Saccostrea* oysters in Japan highlight the confused taxonomy of the genus. *J Molluscan Stud* 82: 492–506.

Supplementary Material 2. *Continued.*

Gene	ID in phylogenetic trees ^{*1}	Lineage	DDBJ/EMBL/GenBank accession number	Reference ^{*2}
<i>16S</i>	16S_glomerata	<i>S. glomerata</i>	AY247287	LM06
	16S_CM01-142_glomerata	<i>S. glomerata</i>	OR340032	MD24
	16S_mordaxA	<i>mordax</i> A	AY247314	LM06
	16S_mordaxB	<i>mordax</i> B	AY247326	LM06
	16S_Y-Sa02_mordaxC	<i>mordax</i> C	AB748916	SY13
	16S_CM01-133_mordoides	<i>mordax</i> C	OR339997	MD24
	CompMT_mordax	<i>mordax</i> B (complete mitogenome)	FJ841968	Wu X, Xu X, Yu Z (unpubl.)
	CompMT_cuccullata	B (complete mitogenome)	KT992045	Mu W., Liu X (unpubl.)
	CompMT_echinata	B (complete mitogenome)	NC_036478	Mu W, Liu X (unpubl.)
	CompMT_glomerata	B (complete mitogenome)	NC_036483	Mu W, Liu X (unpubl.)
	CompMT_kegaki	B (complete mitogenome)	KT936590	Mu W, Liu X (unpubl.)
	CompMT_mytiloides	B (complete mitogenome)	NC_036479	Mu W, Liu X (unpubl.)
	CompMT_malabonensis	F (complete mitogenome)	ON649706	MU22
	COX1_CM01-138_LnB	B	OR339841	MD24
<i>COX1</i>	COX1_CM01-141_LnB	B	OR339842	MD24
	COX1_A-Sa01_LnC	C	AB748824	SY13
	COX1_A-Sa02_LnC	C	AB748825	SY13
	COX1_G-Sa01_LnF	F	AB748830	SY13
	COX1_CM01-487_LnF	F	OR339835	MD24
	COX1_IRS07_LnG	G	LC110593	SY16
	COX1_CM01-307_LnG	G	OR339830	MD24
	COX1_IRS31_LnH	H	LC110615	SY16
	COX1_IRS32_LnH	H	LC110616	SY16
	COX1_IRF01_LnI	I	LC110574	SY16
	COX1_CM01_444_LnI	I	OR339819	MD24
	COX1_IRS01_LnJ	<i>S. spathulata</i> (J)	LC110587	SY16
	COX1_CM01-308_LnJ	<i>S. spathulata</i> (J)	OR339813	MD24
	COX1_WNS02_kegaki	<i>S. kegaki</i>	LC110646	SY16
	COX1_WNS03_kegaki	<i>S. kegaki</i>	LC110647	SY16
	COX1_CM01-33_glomerata	<i>S. glomerata</i>	OR339847	MD24
	COX1_CM01-199_glomerata	<i>S. glomerata</i>	OR339862	MD24
	COX1_Sm1_mordaxA	<i>mordax</i> A	HQ661025	LIU11
	COX1_SQ1_mordaxA	<i>mordax</i> A	EU816051	Xia J, Yu Z (unpubl.)
	COX1_BC4_mordaxB	<i>mordax</i> B	EU816064	Xia J, Yu Z (unpubl.)
	COX1_BC9_mordaxB	<i>mordax</i> B	EU816066	Xia J, Yu Z (unpubl.)
	COX1_CM01-132_mordoides	<i>mordax</i> C	OR339805	MD24
	COX1_Y-Sa01_mordaxC	<i>mordax</i> C	AB748837	SY13

Supplementary Material 2. *Continued.*

Gene	ID in phylogenetic trees ^{*1}	Lineage	DDBJ/EMBL/GenBank accession number	Reference ^{*2}
<i>COXI</i>	CompMT_mordax	<i>mordax</i> B (complete mitogenome)	FJ841968	Wu X, Xu X, Yu Z (unpubl.)
	CompMT_cuccullata	B (complete mitogenome)	KT992045	Mu W., Liu X (unpubl.)
	CompMT_echinata	B (complete mitogenome)	NC_036478	Mu W, Liu X (unpubl.)
	CompMT_glomerata	B (complete mitogenome)	NC_036483	Mu W, Liu X (unpubl.)
	CompMT_kegaki	B (complete mitogenome)	KT936590	Mu W, Liu X (unpubl.)
	CompMT_mytiloides	B (complete mitogenome)	NC_036479	Mu W, Liu X (unpubl.)
	CompMT_malabonensis	F (complete mitogenome)	ON649706	MU22
<i>COX3</i>	COX3_A-Sa01_LnC	C	LC110777	SY16
	COX3_A-Sa02_LnC	C	LC110778	SY16
	COX3_G-Sa01_LnF	F	LC110783	SY16
	COX3_G-Sa02_LnF	F	LC110784	SY16
	COX3_IRS07_LnG	G	LC110809	SY16
	COX3_IRS18_LnG	G	LC110819	SY16
	COX3_IRS31_LnH	H	LC110831	SY16
	COX3_IRS32_LnH	H	LC110832	SY16
	COX3_IRF01_LnI	I	LC110790	SY16
	COX3_IRF02_LnI	I	LC110791	SY16
	COX3_IRS01_LnJ	<i>S. spathulata</i> (J)	LC110803	SY16
	COX3_IRS02_LnJ	<i>S. spathulata</i> (J)	LC110804	SY16
	COX3_WNS02_kegaki	<i>S. kegaki</i>	LC110862	SY16
	COX3_WNS03_kegaki	<i>S. kegaki</i>	LC110863	SY16
	CompMT_mordax	<i>mordax</i> B (complete mitogenome)	FJ841968	Wu X, Xu X, Yu Z (unpubl.)
	CompMT_cuccullata	B (complete mitogenome)	KT992045	Mu W., Liu X (unpubl.)
	CompMT_echinata	B (complete mitogenome)	NC_036478	Mu W, Liu X (unpubl.)
	CompMT_glomerata	B (complete mitogenome)	NC_036483	Mu W, Liu X (unpubl.)
	CompMT_kegaki	B (complete mitogenome)	KT936590	Mu W, Liu X (unpubl.)
	CompMT_mytiloides	B (complete mitogenome)	NC_036479	Mu W, Liu X (unpubl.)
	CompMT_malabonensis	F (complete mitogenome)	ON649706	MU22
<i>NAD3</i>	NAD3_A-Sa01_LnC	C	LC110993	SY16
	NAD3_A-Sa02_LnC	C	LC110994	SY16
	NAD3_G-Sa01_LnF	F	LC110999	SY16
	NAD3_G-Sa02_LnF	F	LC111000	SY16
	NAD3_IRS07_LnG	G	LC111025	SY16
	NAD3_IRS18_LnG	G	LC111035	SY16
	NAD3_IRS31_LnH	H	LC111047	SY16
	NAD3_IRS32_LnH	H	LC111048	SY16

Supplementary Material 2. *Continued.*

Gene	ID in phylogenetic trees ^{*1}	Lineage	DDBJ/EMBL/GenBank accession number	Reference ^{*2}
<i>NAD3</i>	NAD3_IRF01_LnI	I	LC111006	SY16
	NAD3_IRF02_LnI	I	LC111007	SY16
	NAD3_IRS01_LnJ	<i>S. spathulata</i>	LC111019	SY16
	NAD3_IRS02_LnJ	<i>S. spathulata</i>	LC111020	SY16
	NAD3_WNS02_kegaki	<i>S. kegaki</i>	LC111078	SY16
	NAD3_WNS03_kegaki	<i>S. kegaki</i>	LC111079	SY16
	CompMT_mordax	<i>mordax</i> B (complete mitogenome)	FJ841968	Wu X, Xu X, Yu Z (unpubl.)
	CompMT_echinata	B (complete mitogenome)	NC_036478	Mu W, Liu X (unpubl.)
	CompMT_glomerata	B (complete mitogenome)	NC_036483	Mu W, Liu X (unpubl.)
	CompMT_kegaki	B (complete mitogenome)	KT936590	Mu W, Liu X (unpubl.)
	CompMT_mytiloides	B (complete mitogenome)	NC_036479	Mu W, Liu X (unpubl.)
	CompMT_malabonensis	F (complete mitogenome)	ON649706	MU22
Concatenated	Cat_A-Sa01_LnC	C	<i>16S</i> , AB748902; <i>COX1</i> , AB748824; <i>COX3</i> , LC110777; <i>NAD3</i> , LC110993	<i>16S/COX1</i> , SY13; <i>COX3/NAD3</i> , SY16
	Cat_A-Sa02_LnC	C	<i>16S</i> , AB748903; <i>COX1</i> , AB748825; <i>COX3</i> , LC110778; <i>NAD3</i> , LC110994	<i>16S/COX1</i> , SY13; <i>COX3/NAD3</i> , SY16
	Cat_G-Sa01_LnF	F	<i>16S</i> , AB748908; <i>COX1</i> , AB748830; <i>COX3</i> , LC110783; <i>NAD3</i> , LC110999	<i>16S/COX1</i> , SY13; <i>COX3/NAD3</i> , SY16
	Cat_G-Sa02_LnF	F	<i>16S</i> , AB748909; <i>COX1</i> , AB748831; <i>COX3</i> , LC110784; <i>NAD3</i> , LC111000	<i>16S/COX1</i> , SY13; <i>COX3/NAD3</i> , SY16
	Cat_IRS07_LnG	G	<i>16S</i> , LC111228; <i>COX1</i> , LC110593; <i>COX3</i> , LC110809; <i>NAD3</i> , LC111025	SY16
	Cat_IRS18_LnG	G	<i>16S</i> , LC111238; <i>COX1</i> , LC110603; <i>COX3</i> , LC110819; <i>NAD3</i> , LC111035	SY16
	Cat_IRS31_LnH	H	<i>16S</i> , LC111250; <i>COX1</i> , LC110615; <i>COX3</i> , LC110831; <i>NAD3</i> , LC111047	SY16
	Cat_IRS32_LnH	H	<i>16S</i> , LC111251; <i>COX1</i> , LC110616; <i>COX3</i> , LC110832; <i>NAD3</i> , LC111048	SY16
	Cat_IRF01_LnI	I	<i>16S</i> , LC111209; <i>COX1</i> , LC110574; <i>COX3</i> , LC110790; <i>NAD3</i> , LC111006	SY16
	Cat_IRF02_LnI	I	<i>16S</i> , LC111210; <i>COX1</i> , LC110575; <i>COX3</i> , LC110791; <i>NAD3</i> , LC111007	SY16
	Cat_IRS01_LnJ	<i>S. spathulata</i> (J)	<i>16S</i> , LC111222; <i>COX1</i> , LC110587; <i>COX3</i> , LC110803; <i>NAD3</i> , LC111019	SY16
	Cat_IRS02_LnJ	<i>S. spathulata</i> (J)	<i>16S</i> , LC111223; <i>COX1</i> , LC110588; <i>COX3</i> , LC110804; <i>NAD3</i> , LC111020	SY16
	Cat_WNS02_kegaki	<i>S. kegaki</i>	<i>16S</i> , LC111281; <i>COX1</i> , LC110646; <i>COX3</i> , LC110862; <i>NAD3</i> , LC111078	SY16
	Cat_WNS03_kegaki	<i>S. kegaki</i>	<i>16S</i> , LC111282; <i>COX1</i> , LC110647; <i>COX3</i> , LC110863; <i>NAD3</i> , LC111079	SY16
	CompMT_mordax	<i>mordax</i> B (complete mitogenome)	FJ841968	Wu X, Xu X, Yu Z (unpubl.)
	CompMT_echinata	B (complete mitogenome)	NC_036478	Mu W, Liu X (unpubl.)
	CompMT_glomerata	B (complete mitogenome)	NC_036483	Mu W, Liu X (unpubl.)
	CompMT_kegaki	B (complete mitogenome)	KT936590	Mu W, Liu X (unpubl.)
	CompMT_mytiloides	B (complete mitogenome)	NC_036479	Mu W, Liu X (unpubl.)
	CompMT_malabonensis	F (complete mitogenome)	ON649706	MU22

