

Supplementary Figures and Tables

First description of a widespread *Mytilus trossulus*-derived bivalve transmissible cancer lineage in *M. trossulus* itself

Maria Skazina^{1*}, Nelly Odintsova², Maria Maiorova², Angelina Ivanova¹,
Risto Väinölä³, Petr Strelkov¹

¹Saint-Petersburg State University, Saint-Petersburg 199178, Russia

²National Scientific Center of Marine Biology of the Far East Branch of the Russian Academy of Sciences, Vladivostok 690041, Russia

³Finnish Museum of Natural History, University of Helsinki, Helsinki P. O. Box 17, FI-00014, Finland

*Corresponding author m.skazina@spbu.ru

Supplementary figures

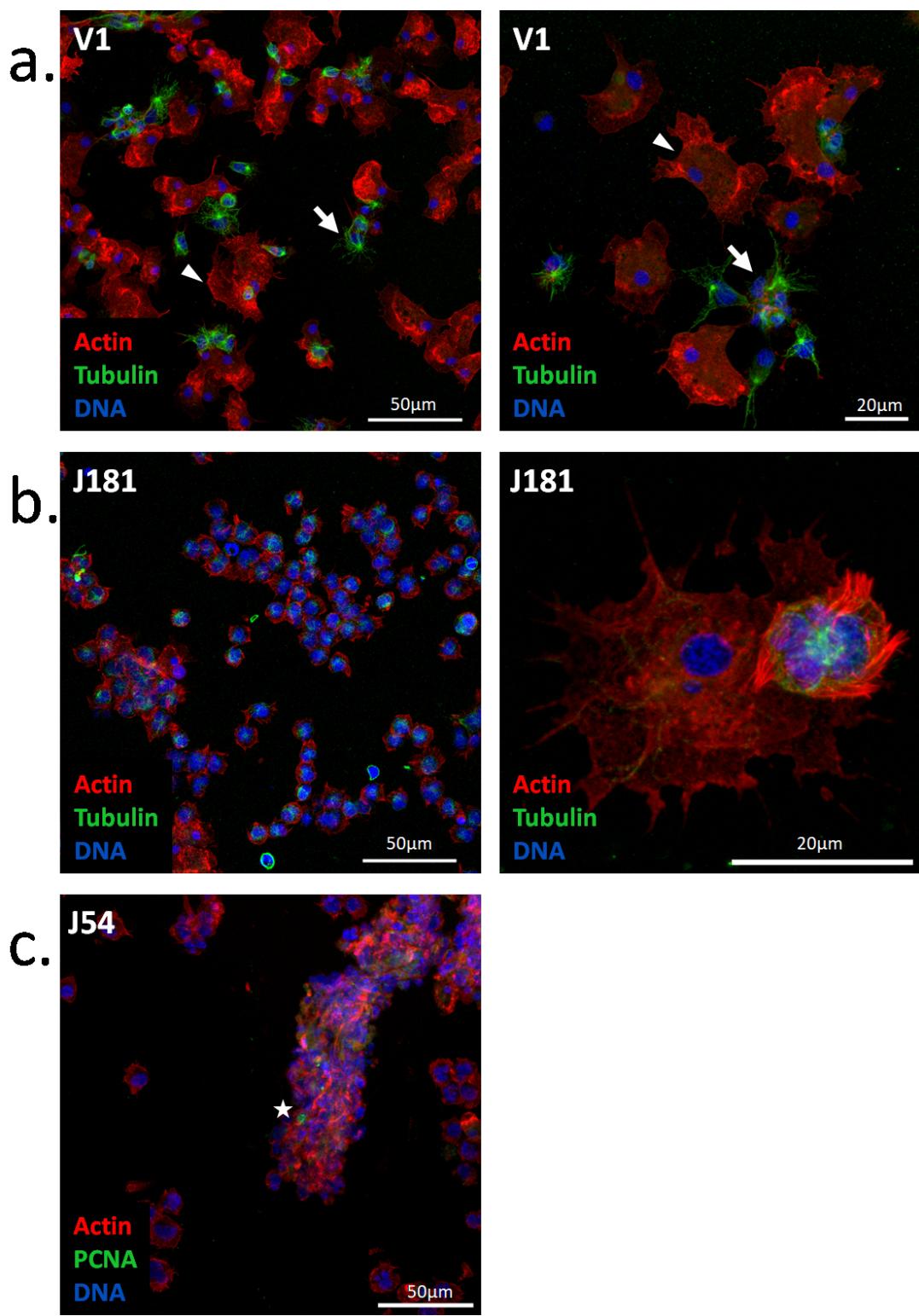


Figure S1. *Mytilus trossulus* hemocytes cultivated for 24 hours. Cells were stained with TRITC-labeled phalloidin (red), and the nuclei (chromatin) were stained by DAPI (blue). Hemocytes of a healthy individual V1 (**a**) and a diseased individual J181 (**b**) were stained with tubulin primary antibodies, hemocytes of a diseased individual J54 (**c**) were stained with PCNA antibodies (green). Arrows in pictures of V1 point to actively moving cells, while arrowheads point to adherent cells. Star in picture of J54 marks the cell positive for proliferation.

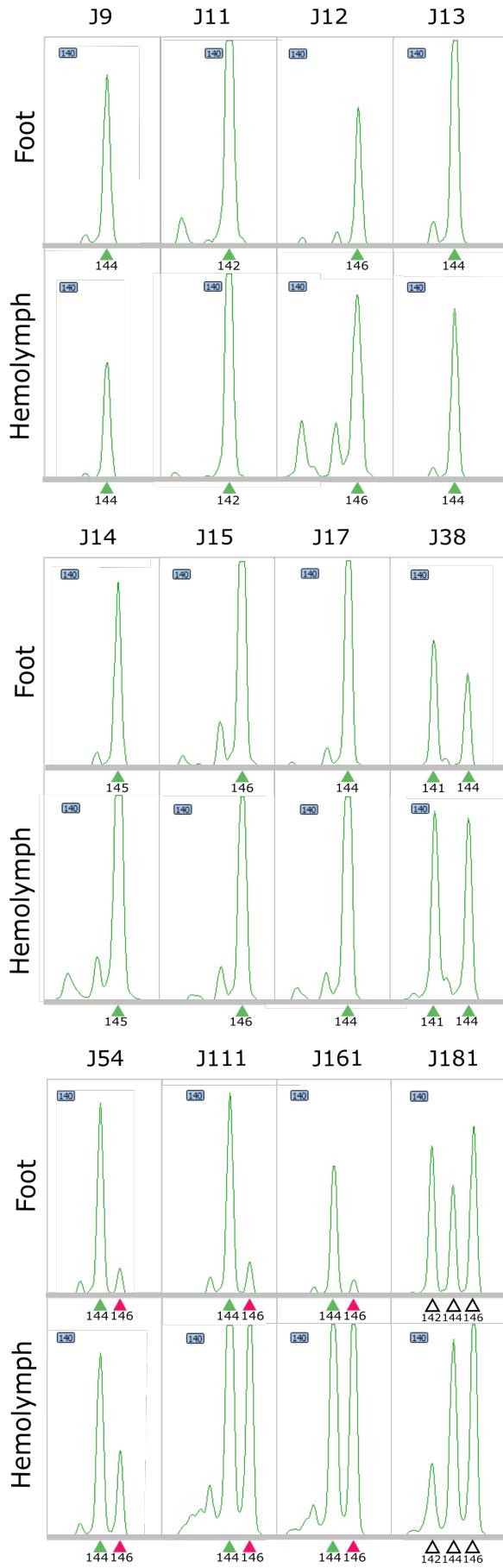


Figure S2. Fragment analysis of *Mg μ 3* microsatellite locus from the hemolymph and the foot tissues of eight healthy mussels (control) and four DN-suggested mussels. Colored triangles designate putatively host-derived *Mg μ 3* fragments (green), putatively cancer-derived *Mg μ 3* fragments (violet); open triangles mark unrecognized fragments. The patterns of *Mg μ 3* fragments in the hemolymph and the foot tissues coincide in healthy mussels; an additional peak is present in the hemolymph of DN-suggested mussels.

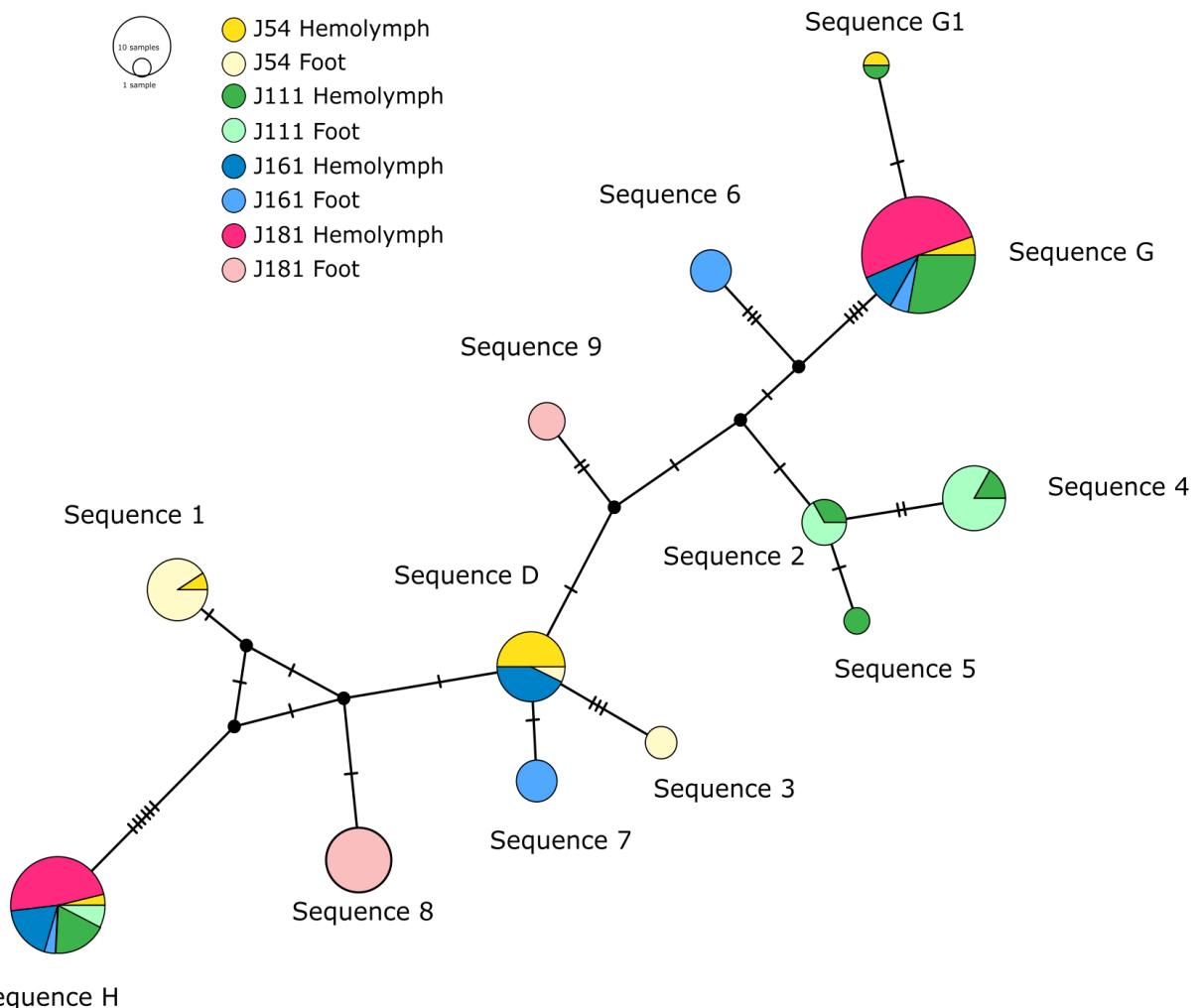


Figure S3. TCS network representing EF1 α sequences obtained by molecular cloning. Sequences from individual mussels and from different tissues (hemolymph and foot) are color-coded (see legend on the top). All minor sequences represented by a single bacterial colony have been removed.

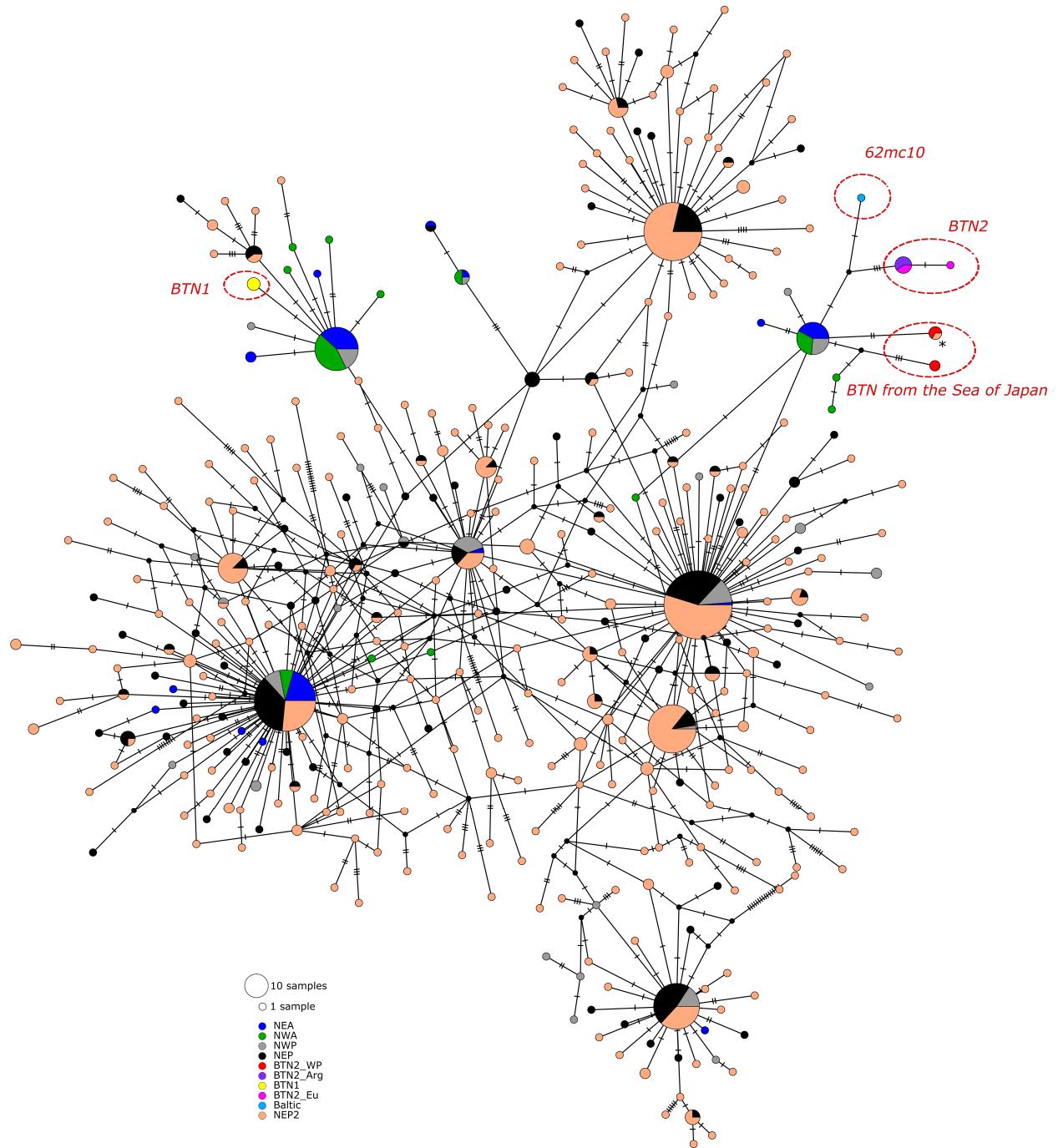


Figure S4. *M. trossulus* and BTN COI haplotype network from the TCS analysis of 542-bp alignment of 843 sequences. The data come from a reanalysis of the results (Fig. 5) with additional 493 sequences from Crego-Prieto *et al.*⁵⁴. Each circle represents a single allele. The size of the circle is proportional to the number of individuals found to bear the allele. Bars indicate mutations between alleles. Small black circles indicate hypothetical haplotypes predicted by the model. The alignment is available as Supplementary Data S5. The geographical origin of samples is color-coded. Samples corresponding to BTN1 (British Columbia) are in yellow, to BTN2 in pink (Europe, BTN2_Eu) and purple (Argentina, BTN2_Arg), to BTN from the SOJ in red (BTN2_WP). Reference *M. trossulus* samples from the Northwest Pacific (NWP) are in grey, from Northeast Pacific (NEP), in black, from Northwest Atlantic (NWA), in green, from Northeast Atlantic (NEA), in dark blue, and from the Baltic Sea (a single sample 62mc10), in light blue (Baltic). The data from Northeast Pacific from Crego-Prieto *et al.*⁵⁴ are in orange (NEP2). The asterisk mark the putatively cancer sequence (NCBI accession number KF931805) from Crego-Prieto *et al.*⁵⁴

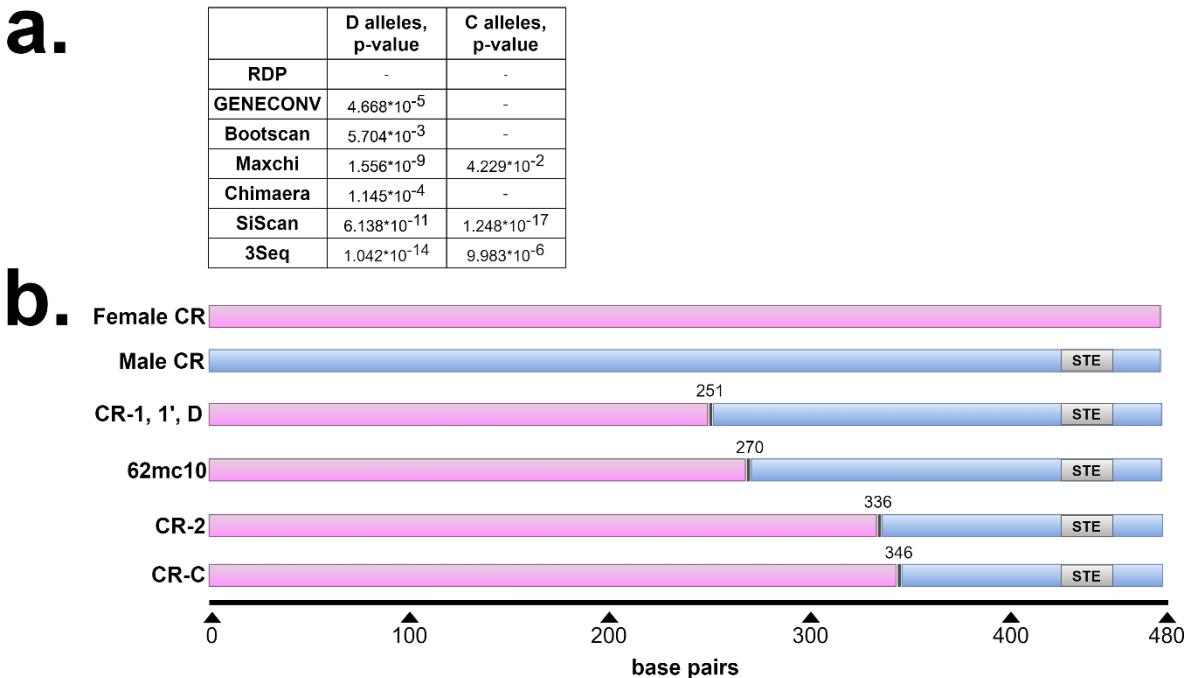


Figure S5. (a) 479 bp long alignment subjected to recombination essay in RDP4 package with default parameters included CR alleles of cancerous mussels detected in this study and in the study of Yonemitsu *et al.* (2019), CR of 62mc10 individual from the Baltic Sea and the set of reference male and female CR (see Accession numbers in the alignment included as Supplementary Data S6). The RDP4 package detected two recombination events in the region around 249-263 nucleotide position of alignment in CR-D, D1, D2, D3, 1, 1' and 62mc10 and in the region of 333-360 nucleotide position in CR-C, C1 and 2. RDP4 output p-values (cutoff of 0.05) are represented in the table. (b) The putative breakpoints marked at schematically depicted alignment of CR used in the recombination analysis. Each bar represents a sequence. Pink color designates standard F-mtDNA, blue color, standard M-mtDNA. The putative breakpoints are marked with black vertical lines, designated by the nucleotide position from the start of alignment. Sperm transmissible element is marked with a grey box.

Supplementary tables

Table S1. The list of *Mytilus trossulus* and BTN COI sequences used for creating TCS haplotype networks.

NCBI Accession numbers	N of sequences	Source
AY823625	1	Breton et al., 2006
KF643248, KF643275, KF643297, KF643331, KF643385, KF643387, KF643419, KF643426, KF643427, KF643460, KF643487, KF643497, KF643502, KF643600, KF643628, KF643676, KF643701, KF643735, KF643750, KF643757, KF643770, KF643789, KF643795, KF643812, KF643820, KF643889, KF643915, KF643952, KF643955, KF643956, KF644043, KF644059, KF644073, KF644107, KF644123, KF644190, KF644206, KF644232, KF644263, KF644321, KF644327	41	Layton et al., 2014
GQ902548-GQ902685	138	Marko et al., 2010
MN546832-MN546835, MN546842, MN546848, MN546852-MN546858	15	Yonemitsu et al., 2019
KM192133	1	Zbawicka et al., 2014
MN119673	1	Chung et al., 2019
MG422062	1	deWaard et al., 2019
MT736560-MT736683	124	Laakkonen et al., 2020
KF931763-KF931851, KF931854-KF931898, KF931901-KF931939, KF931943-KF932262	493	Crego-Prieto et al., 2015
MW191702-MW191719, MT857958-MT857963, MW150800-MW150801	28	This study

Table S2. The list of EF1 α and CR sequences revealed by molecular cloning.

Locus	Individual	Tissue	Clone	Haplotype
EF1 α	J17	Hemolymph	2	D
EF1 α	J17	Hemolymph	3	D
EF1 α	J17	Hemolymph	5	D
EF1 α	J17	Hemolymph	8	D
EF1 α	J17	Hemolymph	9	D'
EF1 α	J17	Hemolymph	10	D'
EF1 α	J17	Hemolymph	18	D'
EF1 α	J17	Hemolymph	24	D'
EF1 α	J17	Hemolymph	26	D'
EF1 α	J17	Hemolymph	27	D'
EF1 α	J17	Hemolymph	30	D'
EF1 α	J17	Hemolymph	32	D
EF1 α	J17	Hemolymph	33	D'
EF1 α	J17	Hemolymph	34	D'
EF1 α	J17	Hemolymph	35	D'
EF1 α	J17	Hemolymph	36	D
EF1 α	J38	Hemolymph	1	10
EF1 α	J38	Hemolymph	2	10
EF1 α	J38	Hemolymph	3	10
EF1 α	J38	Hemolymph	4	10
EF1 α	J38	Hemolymph	6	10
EF1 α	J38	Hemolymph	9	10
EF1 α	J38	Hemolymph	10	10
EF1 α	J38	Hemolymph	11	10
EF1 α	J38	Hemolymph	13	10
EF1 α	J38	Hemolymph	15	10
EF1 α	J38	Hemolymph	16	10
EF1 α	J38	Hemolymph	17	10
EF1 α	J38	Hemolymph	18	10
EF1 α	J38	Hemolymph	19	10
EF1 α	J38	Hemolymph	21	10
EF1 α	J38	Hemolymph	27	10
EF1 α	J54	Hemolymph	1	MINOR
EF1 α	J54	Hemolymph	2	D
EF1 α	J54	Hemolymph	5	MINOR
EF1 α	J54	Hemolymph	6	H
EF1 α	J54	Hemolymph	9	MINOR
EF1 α	J54	Hemolymph	11	MINOR
EF1 α	J54	Hemolymph	15	MINOR
EF1 α	J54	Hemolymph	16	D
EF1 α	J54	Hemolymph	17	D
EF1 α	J54	Hemolymph	18	MINOR
EF1 α	J54	Hemolymph	19	D
EF1 α	J54	Hemolymph	20	D
EF1 α	J54	Hemolymph	21	D
EF1 α	J54	Hemolymph	24	MINOR
EF1 α	J54	Hemolymph	26	D
EF1 α	J54	Hemolymph	31	G1
EF1 α	J54	Hemolymph	33	G
EF1 α	J54	Hemolymph	41	1
EF1 α	J54	Hemolymph	49	G

EF1 α	J54	Foot	3	1
EF1 α	J54	Foot	4	1
EF1 α	J54	Foot	5	1
EF1 α	J54	Foot	6	1
EF1 α	J54	Foot	7	MINOR
EF1 α	J54	Foot	8	1
EF1 α	J54	Foot	9	D
EF1 α	J54	Foot	10	3
EF1 α	J54	Foot	11	3
EF1 α	J54	Foot	12	1
EF1 α	J54	Foot	13	1
EF1 α	J54	Foot	14	1
EF1 α	J54	Foot	15	3
EF1 α	J54	Foot	19	1
EF1 α	J54	Foot	17	1
EF1 α	J54	Foot	18	MINOR
EF1 α	J111	Hemolymph	2	G
EF1 α	J111	Hemolymph	3	G
EF1 α	J111	Hemolymph	7	G
EF1 α	J111	Hemolymph	9	G
EF1 α	J111	Hemolymph	11	MINOR
EF1 α	J111	Hemolymph	12	5
EF1 α	J111	Hemolymph	13	G
EF1 α	J111	Hemolymph	14	H
EF1 α	J111	Hemolymph	15	5
EF1 α	J111	Hemolymph	17	H
EF1 α	J111	Hemolymph	18	G
EF1 α	J111	Hemolymph	19	4
EF1 α	J111	Hemolymph	20	G
EF1 α	J111	Hemolymph	24	G
EF1 α	J111	Hemolymph	25	H
EF1 α	J111	Hemolymph	27	G
EF1 α	J111	Hemolymph	28	G
EF1 α	J111	Hemolymph	29	2
EF1 α	J111	Hemolymph	30	H
EF1 α	J111	Hemolymph	31	G1
EF1 α	J111	Hemolymph	32	2
EF1 α	J111	Hemolymph	33	G
EF1 α	J111	Hemolymph	34	MINOR
EF1 α	J111	Hemolymph	35	4
EF1 α	J111	Hemolymph	37	H
EF1 α	J111	Foot	3	4
EF1 α	J111	Foot	4	4
EF1 α	J111	Foot	5	4
EF1 α	J111	Foot	9	4
EF1 α	J111	Foot	14	4
EF1 α	J111	Foot	16	4
EF1 α	J111	Foot	17	4
EF1 α	J111	Foot	18	H
EF1 α	J111	Foot	19	2
EF1 α	J111	Foot	20	2
EF1 α	J111	Foot	25	4
EF1 α	J111	Foot	27	2
EF1 α	J111	Foot	33	H
EF1 α	J111	Foot	34	4

EF1 α	J111	Foot	37	4
EF1 α	J111	Foot	38	2
EF1 α	J161	Hemolymph	1	H
EF1 α	J161	Hemolymph	3	G
EF1 α	J161	Hemolymph	6	D
EF1 α	J161	Hemolymph	7	D
EF1 α	J161	Hemolymph	9	G
EF1 α	J161	Hemolymph	10	G
EF1 α	J161	Hemolymph	13	H
EF1 α	J161	Hemolymph	15	G
EF1 α	J161	Hemolymph	18	MINOR
EF1 α	J161	Hemolymph	20	G
EF1 α	J161	Hemolymph	21	MINOR
EF1 α	J161	Hemolymph	22	D
EF1 α	J161	Hemolymph	23	G
EF1 α	J161	Hemolymph	24	MINOR
EF1 α	J161	Hemolymph	25	D
EF1 α	J161	Hemolymph	26	D
EF1 α	J161	Hemolymph	27	G
EF1 α	J161	Hemolymph	28	MINOR
EF1 α	J161	Hemolymph	29	MINOR
EF1 α	J161	Hemolymph	30	H
EF1 α	J161	Hemolymph	31	H
EF1 α	J161	Hemolymph	33	MINOR
EF1 α	J161	Hemolymph	34	D
EF1 α	J161	Hemolymph	35	H
EF1 α	J161	Foot	1	MINOR
EF1 α	J161	Foot	2	MINOR
EF1 α	J161	Foot	5	7
EF1 α	J161	Foot	6	G
EF1 α	J161	Foot	7	6
EF1 α	J161	Foot	10	G
EF1 α	J161	Foot	11	7
EF1 α	J161	Foot	14	MINOR
EF1 α	J161	Foot	18	7
EF1 α	J161	Foot	20	H
EF1 α	J161	Foot	21	6
EF1 α	J161	Foot	23	6
EF1 α	J161	Foot	28	6
EF1 α	J161	Foot	33	7
EF1 α	J161	Foot	35	MINOR
EF1 α	J161	Foot	36	6
EF1 α	J181	Hemolymph	1_pJet	G
EF1 α	J181	Hemolymph	2_pJet	G
EF1 α	J181	Hemolymph	3_pJet	G
EF1 α	J181	Hemolymph	4_pJet	G
EF1 α	J181	Hemolymph	5_pJet	G
EF1 α	J181	Hemolymph	6_pJet	G
EF1 α	J181	Hemolymph	7_pJet	G
EF1 α	J181	Hemolymph	8_pJet	MINOR
EF1 α	J181	Hemolymph	9_pJet	H
EF1 α	J181	Hemolymph	10_pJet	G
EF1 α	J181	Hemolymph	11_pJet	H
EF1 α	J181	Hemolymph	12_pJet	G
EF1 α	J181	Hemolymph	13_pJet	G

EF1 α	J181	Hemolymph	14 pJet	G
EF1 α	J181	Hemolymph	15 pJet	H
EF1 α	J181	Hemolymph	16 pJet	MINOR
EF1 α	J181	Hemolymph	1	MINOR
EF1 α	J181	Hemolymph	2	G
EF1 α	J181	Hemolymph	5	MINOR
EF1 α	J181	Hemolymph	6	H
EF1 α	J181	Hemolymph	7	H
EF1 α	J181	Hemolymph	8	G
EF1 α	J181	Hemolymph	9	H
EF1 α	J181	Hemolymph	10	G
EF1 α	J181	Hemolymph	12	G
EF1 α	J181	Hemolymph	13	G
EF1 α	J181	Hemolymph	15	G
EF1 α	J181	Hemolymph	16	G
EF1 α	J181	Hemolymph	18	H
EF1 α	J181	Hemolymph	22	G
EF1 α	J181	Hemolymph	23	H
EF1 α	J181	Hemolymph	24	G
EF1 α	J181	Hemolymph	25	H
EF1 α	J181	Hemolymph	26	H
EF1 α	J181	Hemolymph	28	H
EF1 α	J181	Hemolymph	29	H
EF1 α	J181	Hemolymph	30	MINOR
EF1 α	J181	Hemolymph	31	G
EF1 α	J181	Hemolymph	32	G
EF1 α	J181	Hemolymph	33	G
EF1 α	J181	Hemolymph	34	MINOR
EF1 α	J181	Hemolymph	35	G
EF1 α	J181	Hemolymph	36	H
EF1 α	J181	Foot	2	8
EF1 α	J181	Foot	4	8
EF1 α	J181	Foot	6	8
EF1 α	J181	Foot	16	8
EF1 α	J181	Foot	17	9
EF1 α	J181	Foot	20	9
EF1 α	J181	Foot	23	8
EF1 α	J181	Foot	24	9
EF1 α	J181	Foot	28	8
EF1 α	J181	Foot	29	8
EF1 α	J181	Foot	30	8
EF1 α	J181	Foot	31	8
EF1 α	J181	Foot	39	9
EF1 α	J181	Foot	47	8
EF1 α	J181	Foot	51	8
EF1 α	J181	Foot	58	8
CR	J54	Hemolymph	1	1
CR	J54	Hemolymph	2	1
CR	J54	Hemolymph	4	1
CR	J54	Hemolymph	5	1
CR	J54	Hemolymph	6	1
CR	J54	Hemolymph	7	1
CR	J54	Hemolymph	8	1
CR	J54	Hemolymph	10	1
CR	J54	Hemolymph	11	1

CR	J54	Hemolymph	12	1
CR	J54	Hemolymph	14	1
CR	J54	Hemolymph	15	1
CR	J54	Hemolymph	16	1
CR	J54	Hemolymph	19	1
CR	J54	Hemolymph	20	1
CR	J54	Hemolymph	21	1
CR	J111	Hemolymph	1	2
CR	J111	Hemolymph	3	2
CR	J111	Hemolymph	6	2
CR	J111	Hemolymph	12	2
CR	J111	Hemolymph	15	2
CR	J111	Hemolymph	2	4
CR	J111	Hemolymph	7	4
CR	J111	Hemolymph	10	4
CR	J111	Hemolymph	13	4
CR	J111	Hemolymph	14	4
CR	J111	Hemolymph	16	4
CR	J111	Hemolymph	8	MINOR
CR	J111	Hemolymph	4	MINOR
CR	J111	Hemolymph	11	MINOR
CR	J111	Hemolymph	17	MINOR
CR	J111	Hemolymph	5	MINOR
CR	J161	Hemolymph	1	1
CR	J161	Hemolymph	2	1'
CR	J161	Hemolymph	3	1'
CR	J161	Hemolymph	4	1
CR	J161	Hemolymph	5	1
CR	J161	Hemolymph	6	1
CR	J161	Hemolymph	7	1
CR	J161	Hemolymph	8	1
CR	J161	Hemolymph	9	1'
CR	J161	Hemolymph	10	1
CR	J161	Hemolymph	11	1'
CR	J161	Hemolymph	13	1
CR	J161	Hemolymph	14	1'
CR	J161	Hemolymph	15	1
CR	J161	Hemolymph	16	1
CR	J161	Hemolymph	17	MINOR
CR	J181	Hemolymph	1	2
CR	J181	Hemolymph	5	2
CR	J181	Hemolymph	6	2
CR	J181	Hemolymph	10	2
CR	J181	Hemolymph	11	2
CR	J181	Hemolymph	12	2
CR	J181	Hemolymph	15	2
CR	J181	Hemolymph	16	2
CR	J181	Hemolymph	17	2
CR	J181	Hemolymph	4	6
CR	J181	Hemolymph	7	6
CR	J181	Hemolymph	9	6
CR	J181	Hemolymph	2	MINOR
CR	J181	Hemolymph	13	MINOR
CR	J181	Hemolymph	20	MINOR
CR	J181	Hemolymph	14	MINOR

Table S3. NCBI accession numbers of cancer and host sequences generated in this study.

Sequence	Suggested origin	NCBI Accession Number
COI-1	Cancer	MT857958
COI-2	Cancer	MT857959
COI-3	Host	MT857960
COI-4	Host	MT857961
COI-5	Host	MT857962
COI-6	Host	MT857963
COI-7	Host	MW150800
COI-8	Host	MW150801
CR-1	Cancer	MT877229
CR-1'	Cancer	MT877228
CR-2	Cancer	MT877230
CR-3	Host	MT877231
CR-4	Host	MT877233
CR-5	Host	MT877232
CR-6	Host	MT877234
CR-7	Host	MW013817
CR-8	Host	MW013818
EF1 α -1	Host	MW187821
EF1 α -2	Host	MW187822
EF1 α -3	Host	MW187823
EF1 α -4	Host	MW187824
EF1 α -5	Host	MW187825
EF1 α -6	Host	MW187826
EF1 α -7	Host	MW187827
EF1 α -8	Host	MW187828
EF1 α -9	Host	MW187829
EF1 α -D	Host	MW187831
EF1 α -D'	Host	MW187832
EF1 α -G1	Cancer	MW187833
EF1 α -H	Cancer	MW187834
EF1 α -G	Cancer	MW187835
COI-R7	Host	MW191702
COI-R11	Host	MW191703
COI-R13	Host	MW191704
COI-R14	Host	MW191705
COI-J10	Host	MW191706
COI-J11	Host	MW191707
COI-J12	Host	MW191708
COI-J13	Host	MW191709
COI-J14	Host	MW191710
COI-J15	Host	MW191711
COI-J16	Host	MW191712
COI-J2	Host	MW191713
COI-J3	Host	MW191714
COI-J4	Host	MW191715
COI-J6	Host	MW191716
COI-J7	Host	MW191717
COI-J8	Host	MW191718
COI-J9	Host	MW191719