FINAL REPORT

Phylogeography of Geoduck Clams *Panopea generosa* in Southeastern Alaska

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Abstract: Geoduck clams *Panopea generosa* have supported commercial fisheries in Alaska for over two decades and subsistence harvests for much longer. Increasing demands for these clams have stimulated interest in enhancing production through hatchery rearing of larvae and out-planting of juveniles. Key components to stock management and supplementation are an understanding of genetic stock structure and the development of genetic guidelines for hatchery culture and out-planting. In this study, we examined genetic variability among geoduck clams from 16 localities in southeastern Alaska and in three samples of hatchery-reared juveniles. A 684 base-pair segment of the mitochondrial (mt) DNA cytochrome oxidase 1 gene produced 168 haplotypes in 1362 clams and showed a significant excess of low-frequency haplotypes overall (Tajima's D_T = -2.63; Fu's F_S = -29.01). Haplotype diversity (h = 0.708) and nucleotide diversity (θ_π = 0.0018) were moderate compared to other marine invertebrates. The analysis of molecular variance did not detect heterogeneity among samples (F_{ST} = 0.0008, P = 0.623, mean sample size N = 71.7 clams). Microsatellites showed low-frequency null alleles that produced pervasive departures from Hardy-Weinberg genotypic proportions and that distort estimates of genetic diversity. However, estimates of divergence between populations are relatively un affected because the null alleles were more or less evenly distributed among samples. An AMOVA detected significant heterogeneity for the 6 microsatellite loci (F_{ST} = 0.0027, P <0.0001, N = 76.5), which was attributable to differences among hatchery samples and not to differences among populations. The results for the analysis of quasi-neutral genetic markers indicate that geoduck clam populations are panmictic in southeastern Alaska and from a genetics' perspective can be considered a single management unit. Morphological or life-history variability, however, might indicate groups of populations that could be managed independently of one another.

Keywords: geoduck clams, *Panopea generosa*, mitochondrial DNA, microsatellite DNA, southeastern Alaska, shellfish hatchery

Introduction

Sea ranching and marine stock supplementation provide opportunities to augment the production of wild marine populations and to mitigate for over-exploited fisheries (Garibaldi 2012). For both fishery and stock supplementation, the protection of wild populations of marine organisms that are commercially harvested is a fundamental tenant of sustainable use of a marine biological resource. An important component of sustainable use is the protection of genetic diversity, which declines from the effects of genetic drift when overharvesting produces a drop in effective sizes of local populations (Grant et al. 2017). The preservation of genetic diversity is important because it underpins ontogenetic development, morphology, behavior and physiology. Together these variables affect the ability of a population to respond environmental challenges.

An essential goal of biological resource management is to maintain genetic diversity in wild populations of harvested and farmed species by preserving historical levels of effective population sizes of wild populations (Grant et al. 2017). The protection of genetic resources in Alaskan species is especially important because of continuing high-latitude environmental changes (Walther et al. 2002; Holland and Bitz 2003). The out-planting of hatchery-reared individuals can adversely influence the adaptive potential of wild populations by accelerating a drop in genetic diversity when inadequate numbers of brood stock are used to produced juveniles, or when out-planted individuals come from populations that are genetically different from the receiving local population.

Geoduck clams *Panopea generosa* are large bivalve mollusks that range along the west coast of North America from northern Mexico to Southeast Alaska. These large clams have shells reaching 20 cm in length and long extensible necks that are not accommodated by the shell. These burrowing clams are scattered among patches of suitable intertidal and subtidal habitats consisting of unconsolidated sand and mud (McDonald et al. 2015). Populations are connected by larval dispersal in near-shore currents, which leads to gene flow when larvae settle, mature, and spawn in non-natal habitat patches. Female geoduck clams can spawn as many as 40 million eggs in one spawning season (Beattie, 1992), which occurs in late spring in most areas. After external fertilization in the water, developing larval spend 40–50 days drifting in coastal currents before settling and burrowing into soft substrates (Goodwin and Pease 1991). The number of years to maturity of geoduck clams is unknown in Alaskan waters, but clams in British Columbia and Washington mature and spawn in their second or third year (Campbell and Ming 2003; Vadopalas et al. 2015). Geoduck clams can live as long as 168 years (Bureau et al. 2002).

An understanding of the genetic population structure of is vital to the management of geoduck clam harvests and to stock enhancement programs. Molecular markers can help to define independent demographic units for conservation and sustainable harvest (Begg et al. 1999). Stock definitions are needed to achieve sustainable harvests, because small, but demographically independent, populations may be depressed if they are included with larger more abundant populations in the setting of harvest quotas. Genetic markers can also be used to guide the development of brood stock (Ward, 2006), to monitor the effects of hatchery practices on genetic diversity in brood stock (Bartley et al. 1992; Evans et al. 2004b), and to monitor the genetic effects cultured individuals released into the wild (Gaffney et al. 1996).

In southeastern Alaska, geoduck clams are harvested by scuba divers and are farmed in some intertidal areas by the out-planting of hatchery-reared spat. Hatchery-origin clams are harvested at 6-7 years of age, presumably before the onset of sexual maturity. Sub-tidal aquatic farm permit holders are allowed to also harvest insignificant numbers of wild geoducks on the farm site (Alaska Department of Fish and Game 2009). Plans are underway to introduce geoduck clams for farming into areas beyond their natural geographic range in the western Gulf of Alaska, and an evaluation of the genetic population structure is needed to responsibly establish new populations.

Both short-term ecological processes and long-term evolutionary processes influence genetic variability in present-day populations. Hence, the objective of this project is to survey genetic variation in geoduck clams in southeastern Alaska with mitochondrial (mt) DNA, which has the potential to reveal imprints of historical population events, and microsatellite DNA markers, which are most influenced by mutation and contemporary processes affecting dispersal and population size. The assessment of genetic population structure is essential for defining stock boundaries for stock assessments and designing stock enhancement programs.

Materials and Methods

Sample collection and DNA extraction

Samples of geoducks *Panopea generosa* were collected by the Alaska Department of Fish and Game (ADF&G) for population analyses and by the Alaska Department of Environmental Conservation in small batches for the periodic testing of toxins, such as paralytic shell poisoning. The small samples from the DEC samples were pooled by location over years to achieve sample sizes ranging from 41 to 92 (Table 1). Pooling small numbers of individuals over years can be justified because geoduck clams are long lived, so little temporal variability in marker frequencies was expected over the period of the sample collections. Samples included geoduck clams from 16 locations in SE Alaska (Figure 1) and from three years of brood-stock offspring at Alutiiq Pride Shellfish Hatchery, Seward, Alaska. Brood stock for hatchery culture were collected at Vallanor Bay. Samples of the siphon muscle were freeze-dried for long-term storage and re-hydrated for DNA extraction. DNA was extracted from about 100 mg of tissue with NucleoSpin® 96 Tissue (Machery-Nagel Inc., Bethlehem, PA).

Mitochondrial DNA sequencing

A segment of mtDNA cytochrome oxidase subunit I (COI) was amplified with the polymerase chain reaction (PCR) using the universal primers LCO1490 (5'-GGTCAACAAATCATAAAGATATTGG-3') and HCO2198 (5'-TAAACTTCAGGGTGACCAAAAAATCA-3') (Folmer et al. 1994, Suarez-Moo et al. 2013). PCR cocktails consisted of a 50 µL mixture of 2.0 µL templates DNA in 1x Colorless GoTaq Flexi Buffer, 1.5 mM MgCl2, 0.2 mM of each dNTP, 0.4 µM of forward and reverse primers, and 1U GoTaq Flexi DNA polymerase. PCR amplification were conducted in ABI 9700 thermocyclers with an initial denaturation of 2 min at 95^{o}C, 35 cycles of 1 min at 95^{o}C, 1 min at primer annealing temperature 35 ^{o}C, and 1 min 30 sec at 72^{o}C; the final cycle was at 72^{o}C for 7 min. The PCR amplifications were sequenced in the forward and reverse directions by Genewiz Inc., South Plainfield, NJ. Representatives from different extraction plates were re-extracted and sequenced to check for handling errors. Forward and reverse sequences for all individuals were aligned and edited with MEGA 7.0.20 (Kumar et al. 2016) and Finch TV 1.4.0 (Geospiza Inc.) to produce 684 base-pair sequences for population analysis.

Microsatellite DNA

We used a suite of six microsatellite loci that had been developed previously for geoduck clams, including *Pab9* (Vadopalas et al. 2004), *Pab101*, *Pab105*, *Pab106*, *Pab112*, and *Pab117* (Kaukinen et al. 2004). The polymerase chain reaction was used to amplify microsatellite alleles with a Gene Amp PCR System 9700 (Applied Biosystems, Inc., Foster City, CA). Each 10 µL reaction mixture consisted of 2 µL template DNA (~0.1µg/µL) in 1x Colorless GoTaq Flexi Buffer (Promega Inc. Madison, WI), 2.3 mM $MgCl_2$ (Promega Inc. Madison, WI), 0.20 mM of each nucleotide (Applied Biogsytems, Inc.), 0.4 µM of forward and reverse primers, 0.1 mg/mL of BSA (Sigma Inc. St. Louis, MO), 0.05 U GoTaq Flexi DNA polymerase (Promega Inc. Madison, WI), and deionized water. Optimal thermal cycling profiles varied among loci (Table S1). Microsatellites were size fractionated in an Applied Biosystems 3730 capillary DNA sequencer. Genotypes were independently scored with GeneMapper 5.0 (Applied Biosystems) by two technicians.

Statistical analysis

The mtDNA haplotypes were examined in several ways to elicit various aspects of genetic population structure. We used TCS 1.21 (Clement et al. 2000) to construct a 95% plausible parsimony network of mtDNA haplotypes. ARLEQUIN 3.5.2.2 (Excoffier and Lisher 2010) was used to estimate haplotype (h), and nucleotide (θ_π) diversities and to test for departures from neutrality with Tajima's D_T (Tajima 1989) and Fu's F_S (Fu 1997) statistics with 10,000 randomizations to assess significance. Summary statistics, including the number of polymorphic nucleotide sites (N_{poly}), number of private haplotypes in a sample (N_{priv}), number of haplotypes (N_h), number of expected haplotypes given neutrality (N_{exp}), the numbers of transitions (ts) and tranversions (tv) were estimated from the sequences with ARLEQUIN.

Microsatellite genotypes were examined for stutter, large-allele dropout and null alleles with MICRO-CHECKER (van Oosterhout et al. 2004) and GENEPOP 4.6 (Rousset 2008). GENEPOP indicated the presence of null alleles from pervasive significant heterozygote deficits among samples detected with the 'U' test statistic and with 1,000 randomizations (Guo and Thompson 1992). Null-allele frequencies were estimated with GENEPOP and ML-NULLFREQ (Kalinowski and Taper 2006).

GENEPOP was used to estimate several summary statistics from microsatellite genotypic frequencies, including observed (H_O) and expected (H_E) heterozygosities and the inbreeding coefficients F_{IS} (based on genotypic frequencies) and Rho_{IS} (based on allelic frequencies and repeat distances between alleles). The number of alleles (A_N) and allelic richness (A_R) were calculated with HP-RARE (Kalinowski 2005) with a minimal sample size of 60 genes.

Genetic population structure reflected in mtDNA and microsatellites was assessed in several ways. Isolation by distance (IBD) between populations was tested with a Mantel's test between F_{ST} and shore-line geographic distances between pairs of samples (Wright 1943; Kimura and Weiss 1964). Geographic distances were estimated in kilometers with the path function in Google Earth and IBD was tested with the online facility IDBWS (http://ibdws.sdsu.edu/~ibdws/; Jensen et al. 2005),

Pairwise estimates of divergence were estimated with F_{ST} (Weir and Cockerham 1984) with 10,000 randomizations to estimate the probability that F_{ST} was greater than 0.0. Neighbor-joining trees (Saitou and Nei 1987) were constructed from pairwise values of F_{ST} with MEGA 7. Several models of population structure based on geography were tested with an AMOVA analysis in ARLEQUIN. The probability that F_{ST} (divergence between groups of populations) and F_{SC} (divergence between subpopulations within groups) was greater than 0.0 was estimated with 10,000 randomizations. While estimates of diversity are not reliable in datasets with null alleles because null-allele heterozygotes cannot be identified, the results for other analyses, such as AMOVA, are relatively unaffected with the null alleles are more or less even distributed among samples. We used the simulation model of Ryman and Palm (2006) to assess the statistical power that our sample design provided to be able to detect various levels of population structure.

Results

Mitochondrial DNA

Polymorphisms at 155 nucleotide sites along a 684 bp segment of mtDNA COI defined 168 haplotypes (Tables 1, S2, S3, Figure 2) in 1362 geoduck clams from 16 localities in southeastern Alaska and from 3 samples of juveniles cultured by the Alutiiq Pride Shellfish Hatchery. A haplotype network showing the mutational relationship among haplotypes depicted a high-frequency central haplotype (haplotype 1) with numerous singleton haplotypes removed by one or two mutations. In addition, 5 star-like clusters of haplotypes (2–5) were one or two mutations removed from the central haplotype.

The number of observed haplotypes per sample ranged from N_H = 13 to 28 and averaged 20.3 among samples (Table 1). The expected number of haplotypes under a model of neutrality ranged from N_{exp} = 4.33 to 6.60 and averaged 5.55 among samples. Gene diversity ranged from h = 0.629 to 0.810 and averaged 0.712 among samples. Total gene diversity in a sample pooled over locations was h = 0.708. Nucleotide diversity ranged from θ_π = 0.0012 to 0.0024 and averaged 0.0018. Total nucleotide diversity was θ_π = 0.179.

Tests for departure from neutrality indicated significant departures overall D_T = -2.63 and in all of the samples (range -2.02 to -2.47, mean -2.26) (Table 1). Fu's F_S also indicated significant departures from neutrality (overall F_S = -29.01) and in all of the samples (range -11.80 to -29.41, mean -19.45).

Geographic structure was tested in several ways. Pairwise estimates of divergence between samples ranged from F_{ST} = 0.0 (including all negative values) to 0.0198 between samples 10 and 12 (Table 2). A neighbor-joining tree of these F_{ST} values did not reveal meaningful geographical groupings of samples (Figure 3a). A one-sided test for IBD did not detect a significant correlation between pairwise F_{ST} and geographic distances between samples (r = -0.127, P = 0.914) (Figure 4a). A log transformation of geographic distances also did not produce a significant correlation (r = -0.029, P = 0.580).

No significant haplotype-frequency heterogeneity was detected overall with AMOVA, including (F_{ST} = -0.0008, P = 0.623), or excluding (F_{ST} = -0.0008, P = 0.625) the three samples of hatchery juveniles (Table 3). A three-group comparison among the northernmost sample from the Biorka-Legma-Elovoi-Symonds Islands (sample 1), northern samples (2–8), and southern samples (9–16) was not significant (F_{ST} = 0.0006, P = 0.266), and a comparison of populations within these groups was also not significant (F_{SC} = -0.0011, P = 0.661). No significant difference appeared between the three samples of hatchery juveniles (17–19) and the brood stock source population (14) (F_{ST} = -0.0040, P = 1.0), or among the three samples of hatchery juveniles (17–19) (F_{SC} = 0.0018, P = 0.308).

Microsatellite DNA

Allelic frequencies at six microsatellite loci were used to estimate various genetic parameters in populations of geoduck clams in southeastern Alaska (Table S4, S5). A summary of variability locus-by-locus indicated that the number of alleles pooled over samples ranged from A_N = 28 (*Pab9*) to 99 (*Pab106e*) (Table 4). Observed heterozygosities among loci ranged from H_O = 0.682 (*Pab105e*) to 0.974 (*Pab106e*), but expected heterozygosities were generally larger, ranging from H_O = 0.928 (*Pab9*) to 0.981 (*Pab106e*). The disparity between observed and expected pointed to the occurrence of null alleles at each locus.

The average number of alleles per sample ranged from A_N = 28.7 to 38.8 among samples, and allelic richness, based on 82 genes, ranged from A_R = 26.9 to 28.8 among samples (Table 5). Average observed heterozygosity ranged from H_O = 0.728 (hatchery sample 19) to 0.902 (hatchery sample 18), but expected heterozygosities ranged from H_E = 0.921 (sample 19) to 0.957 (samples 2, 3, 4) among samples. The difference between observed and expected heterozygosities was largely due to the presence of null alleles. Estimates of the mean null-allele frequencies over samples ranged from 0.002 (*Pab106e*) to 0.128 (*Pab105e*) among loci (Table 6). One sample had an estimate of null-alleles as large as 0.280 (hatchery juveniles sample 19). The apparent excess of homozygotes is due to the inability of standard methods to identify null-allele heterozygotes produced large values of the inbreeding coefficient, which ranged from F_{IS} = 0.045 (hatchery sample 18) to 0.125 (samples 10, 13), and Rho_{IS} ranged from -0.018 (sample 15) to 0.221 (sample 16). No geographic trends were apparent in the distributions of these statistics among populations.

Estimates of divergence between populations ranged from F_{ST} = 0.0, between 50 sample pairs, to 0.0029 (sample 9 vs 12) (Table 7). Seven of 171 (4.1%) comparisons between pairs of samples were significant, but there was no apparent geographical pattern to the distribution of the significances. None of the F_{ST} values were significant after Bonferroni correction for multiple comparisons. A neighbor-joining tree of F_{ST} showed no correspondence with geography (Figure

3b). A test for IBD among samples show a negative, non-significant correlation (r = -0.068, P = 0.708) (Figure 4b).

An AMOVA of the 19 samples indicated that 99.97% of the variability was contained among individuals within populations and only 0.03% was due to differences among samples, including the hatchery samples. Significant heterogeneity was detected among the 19 samples overall (F_{ST} = 0.0027, P <0.0001) (Table 8) but it could not be attributed to a particular geographic partition among samples. No significant difference was found in a three-group comparison among the northernmost sample from the Biorka-Legma-Elovoi-Symonds Islands (1), northern samples (samples 2–8), and southern samples (samples 9–16) (F_{ST} = -0.0001, P = 0.743) or within these groups (F_{SC} = 0.0011, P = 0.083). No significance difference appeared between the three pooled samples of hatchery juveniles (samples 17–19) and the brood-stock source population (sample 14) (-0.0058, P = 1.0), but significant heterogeneity appeared among the three samples of hatchery juveniles (samples 17–19) (F_{SC} = 0.0118, P = <0.0001).

Discussion

The goal of this study was to use genetic markers to resolve the genetic population structure of geoduck clams in southeastern Alaska. The results of a survey of populations in 16 areas with mtDNA and microsatellite markers showed that these populations were genetically homogeneous over a distance of about 400 km. Additionally, all of the populations showed similar levels of mtDNA and microsatellite DNA diversity. While three samples from the hatchery (2007–2009) were not significantly different from the donor population at Vallenar Bay (sample 9), microsatellite allelic frequencies were significantly different among the three juvenile hatchery samples.

Before discussing these results in more detail we offer two comments on the ability of our methods to resolve genetic population structure of geoduck clams in southeastern Alaska. First, the number of localities sampled and sample sizes were most adequate to detect levels of differentiation among populations that would be useful to resource managers. The power to detect a particular level of differentiation between populations for particular samples sizes and numbers of genetic markers can be estimated with the Ryman and Palm (2006) simulations. For a single (mtDNA) or a few loci unreasonably large sample sizes would be needed to provide power to detect low levels of differentiation between pairs of populations observed in this study (mtDNA: F_{ST} = 0.0 to 0.015). Our use of six microsatellite loci and average sample sizes of about 72 clams provided power of about 0.22 of detecting the observed level of differentiation of F_{ST} = 0.003. The small allele- and haplotype-frequency differences among populations observed in our study likely represent sample error or short-term genetic drift and are not of use to harvest managers. However, our samples sizes were adequate to detect differences among larger groups of populations. The pooled samples used to search for regional differences exceeded N = 200 clams and provided at least a probability of 0.80 of detecting small differences on the order of F_{ST} = 0.001.

Second, genotypic frequencies for some microsatellite loci were affected by the presence of null alleles with estimated frequencies averaging from 0.002 (*Pab106e*) to 0.146 (*Pab105e*) over samples among loci (Table 6). The presence of null alleles led to a strong contrast between estimates of observed and expected heterozygosity. Observed heterozygosity is based on counts of heterozygous genotypes, some of which cannot be identified, while expected heterozygosity is calculated from allele frequencies. Hence, estimates of observed diversity can be used to make relative comparisons among populations, but only expected heterozygosity is appropriate for making comparisons with other species. Estimates of divergence between populations are also calculated from allelic frequencies, and when null alleles are more or less evenly distributed among samples, which for the most part they were. Hence, we are confident that the patterns of divergence estimated with F_{ST} are reliable for making inferences about genetic population structure.

Despite these caveats, the analyses of mtDNA and microsatellite markers provide insights into the biology and population structure of geoduck clams in southeastern Alaska. The central outcome of this study was the apparent lack of genetic population structure (panmixia) among geoduck clam populations in southeastern Alaska. Genetic homogeneity can arise from the effects of several mechanisms. One is from the effects of gene flow between populations. Adult geoducks are sedentary and do not move after metamorphosis from the larval to miniature adult phases and settlement to the bottom. Movement between populations can occur only during planktonic stages when larvae move passively in nearshore currents. Females spawn as many as 40 million eggs in late spring (Beattie 1992), and larvae drift in currents for as long as 6–7 weeks before settling and burrowing into soft substrates. Recruitment into a new population and successful reproduction leads to gene flow. Larval dispersal between the populations in energetic currents may account for the weak genetic structure among geoduck clams in southeastern Alaska. The lack of isolation by distance for both mtDNA and microsatellite markers (Figure 4) may indicate that gene flow between populations is substantial.

Over a long time, the presence of only a few migrants per year can prevent extensive divergence between populations that are demographically independent of one another. Simulations indicate populations with migration rates as large as 10% can still be demographically independent of one another (Hastings 1993; Waples and Gaggiotti 2006). This large rate of migration would produce genetic homogeneity, and hence demographic independence between stocks would not be detectable with genetic markers. The finding of genetic differences indicates demographic differences between populations, but the lack of genetic differences does not conclusively indicate demographic interdependence among populations.

A second related hypothesis is that larvae originate from northern British Columbia in northward-flowing coastal currents and are not produced locally in southeastern Alaska. A demographic profile skewed toward older clams provides support for this hypothesis. The absence of younger individuals in the populations suggests only periodic spawning and recruitment or migration from other populations into this sink group of populations (J. Hetrick, Alutiiq Pride Shellfish Hatchery, Seward, personal communication). Cool waters in southeastern Alaska may prevent geoducks from spawning and from supplying local individuals for recruitment. If recruitment occurs only rarely, the commercial harvests of the standing biomass has to be carefully regulated to prevent population declines from overharvesting.

A third hypothesis invokes a recent population expansion into southeastern Alaska from a single source population. Several statistics indicated that the genetic profiles of geoduck clam populations in southeastern Alaska depart significantly from neutrality and these departures are due to excesses of low frequency haplotypes and alleles, which are characteristic of populations that have recently expanded (Fu 1997). New mutations are retained to a greater extent in rapidly growing populations than they are in stable or declining populations (McInerny et al. 2009).

However, the timing of an expansion is difficult to estimate, as calibrations of genetic signals with time are hampered by the inability to accurately estimate mutation rate (Grant 2015).

Both long- and short-term processes may promote population expansions. Climate in the North Pacific varies on long and short time scales. On long time scales, periodic coastal glaciations during Pleistocene glacial maxima led to local extinctions and post glacial expansions for numerous marine species in the Northeastern Pacific (e.g. red king crab, Grant and Cheng 2012; Vulstek et al. 2013). Geoduck populations may have expanded after inshore habitats became available in southeastern Alaska after the last glacial maximum (Hewitt 2004; Davies et al. 2011). However, we cannot exclude the possibility that the geographically marginal geoduck populations in southeastern Alaska are part of a larger southern population that expands and contracts in response to multidecadal or centennial climate cycles (Wilson et al. 2007).

Three samples of hatchery juveniles were included in our study. None of these samples showed depressed levels of genetic diversity. In fact, some low-frequency mtDNA haplotypes and microsatellite alleles appeared in these samples that were not present in the wild donor populations. This was likely due to sample error from estimating diversity from finite samples. Additionally, none of the three hatchery cohorts had diverged from the donor population. The overall implication for stock supplementation and farming is that any of the geoduck clam populations in southeastern Alaska can serve as hatchery brood stock and hatchery-reared offspring can be out-planted at any ecologically suitable location in southeastern Alaska. Nevertheless, brood-stock sizes should be as large as possible given the economic constraints of the hatchery facilities to conserve genetic diversity (Ryman and Laikre 1991; Grant et al. 2017).

The results of our study of geoduck clams indicated little genetic population structure. In other areas, the results of several studies of geoduck clam genetic population structure show that populations are structured. Phelps (1993; unpublished report WA Department of Fish and Wildlife; cited in Feldman et al. 2004) examined allozyme variability for 15 loci in samples from Puget Sound and concluded that populations in Hood Canal, South Puget Sound, and Port Townsend, separated by about 100 km, were genetically distinct from one another. However, this conclusion was weak, because of poor sample quality (Feldman et al. 2004). Another study used mitochondrial DNA sequences to survey genetic variability in 39 individuals from 6 localities in

British Columbia, but an analysis of molecular variance showed no significant frequency divergences between samples (VanKoeveringe 1998). However, the statistical powers of these tests were low, because each population was represented by only 6.5 individuals, on average.

Another study examined genetic variability with seven microsatellite and 11 allozyme markers among 16 samples from Puget Sound, Georgia Strait, and the Strait of Juan de Fuca (Vadopalas et al. 2004). Both marker classes were highly polymorphic and revealed significant, but low, levels of differentiation among populations on several spatial scales. Although year-class strength can be variable, a subsequent study showed little frequency variability among year classes in most populations (Vadopalas et al. 2012). The genetic variability among these populations in Puget Sound appeared to be hap-hazard and did not follow the island or isolation-by-distance model of differentiation.

Lastly, a fourth study surveyed variability in eight microsatellite loci in 16 samples collected over a broader geographic scale, including Southeast Alaska, British Columbia, and Puget Sound (Miller et al. 2006). In contrast to geoduck clam populations in Puget Sound, significant isolation-by-distance geographic structure was detected in British Columbia, as well as significant differences between populations on a larger geographic scale.

In conclusion, the experimental design of our genetic survey was adequate to be able to detect genetic differences among subpopulations of geoduck clams in southeastern Alaska that would be useful to resource managers. However, we found no significant differentiation among populations separated by as much as 400 km. The reason for the lack of structure remains uncertain, but could be due to high levels of gene flow, or to recruitment from a single source population to south. Levels of genetic diversity were similar among subpopulations. Notably, the samples of juveniles over three years did not show a drop in genetic diversity, nor divergence from the donor population, indicating that brood stock numbers were adequate. The lack of genetic differentiation among subpopulations indicates that subpopulations in this area can be managed as a single population for stock supplementations and farming. Nevertheless, since geoducks are long lived and recruitment is sporadic, local populations should be likely be managed individually to ensure sustained harvests.

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Figure captions

Figure 1. Map of southeastern Alaska showing locations of samples of geoduck clams (*Panopea generosa*) used for genetic analyses. Location numbers correspond to sample numbers in Table 1.

Figure 2. Network of relationships among haplotypes of mitochondrial DNA cytochrome oxidase I (684 base pairs) in 1362 geoduck clams (*Panopea generosa*) from southeastern Alaska.

Figure 3. Neighbor-joining trees of pairwise F_{ST} between samples of geoduck clams (*Panopea generosa*) from southeastern Alaska. Sample numbers correspond to numbers in Figure 1 and Table 1. (a) mitochondrial DNA sequences. (b) microsatellite allelic frequencies.

Figure 4. Isolation by distance between populations of geoduck clams (*Panopea generosa*). (a) mitochondrial DNA Mantel's correlation r = -0.127, P = 0.914. (b) microsatellite DNA r = 0.068, P = 0.708.

Table 1. Locations, dates, and summary statistics for sequence variability along a 684 base pair fragment of mitochondrial DNA cytochrome oxidase I in Pacific geoduck clams from SE Alaska.

Location(s)	Year(s)	latitude	longitude	N	N_{poly}	N_{priv}	ts	tv	N_H	N_{exp}	h	Θ_π %	D_T	F_S
1. Biorka, Legma, Elovoi, Symonds	2007, 2008, 2010, 2012, 2013, 2014, 2015, 2016	56.81	-136.43	90	23	1	19	4	22	5.79	0.694	0.177	-2.19	-21.46
2. Warren Is., Warren Channel	2009, 2010, 2011, 2013, 2014, 2015, 2016	55.90	-133.85	89	21	3	17	6	22	5.47	0.709	0.164	-2.16	-22.86
3. Port Alice, Cone Bay	2007, 2009, 2010, 2011, 2013, 2014, 2015, 2016	55.83	-133.62	85	19	5	12	7	16	5.40	0.697	0.161	-2.07	-11.80
4. Maurelle Is.	2011, 2013, 2014, 2015, 2016	55.60	-133.70	87	25	7	20	5	25	6.25	0.810	0.120	-2.19	-25.82
5. Portillo Channel	2009, 2011, 2013, 2014, 2015	55.48	-133.42	92	27	4	22	5	23	6.02	0.706	0.186	-2.31	-22.52
6. Bucareli Bay	2007, 2009, 2011, 2013, 2015	55.40	-133.50	66	19	5	15	4	18	5.57	0.735	0.184	-2.08	-15.18
7. Tlevak Narrows	2007	55.26	-133.12	75	27	7	22	5	25	5.61	0.697	0.179	-2.43	-28.31
8. Kaigani Strait	2007, 2009, 2011, 2013, 2015, 2016	54.82	-132.78	57	23	4	19	4	18	5.51	0.753	0.191	-2.35	-15.67
9. Vallenar Bay	2009, 2013, 2014	55.38	-131.86	81	29	10	24	5	26	5.52	0.650	0.167	-2.47	-29.41
10. Nehenta Bay, SW Gravina Is.	2012, 2013, 2014, 2016	55.32	-131.87	62	21	4	15	6	20	5.36	0.667	0.163	-2.20	-19.43
11. Annette Is., Area 4	2008, 2009, 2010, 2014, 2015, 2016	55.00	-131.50	48	22	5	18	4	20	4.96	0.658	0.158	-2.40	-21.83
12. Percy Is.	2009, 2011, 2012, 2013, 2015	55.31	-131.60	90	16	3	15	1	16	5.19	0.762	0.186	-2.02	-13.32
13. Vegas Is.	2007, 2012	54.96	-131.46	65	23	6	19	4	17	5.35	0.682	0.174	-2.35	-14.11
14. Kelp Is., South Duke Is.	2007, 2009, 2011, 2013, 2015, 2016	55.20	-131.40	41	13	4	11	2	13	4.33	0.692	0.148	-2.07	-10.83
15. Foggy Bay	2008, 2010, 2012, 2014, 2016	54.96	-130.95	78	32	3	26	6	28	6.60	0.796	0.224	-2.41	-28.05

16. Lord Is., Nakat Bay, Cape Fox	2007, 2008, 2009, 2011, 2013, 2015, 2016	54.88	-130.72	76	23	3	17	6	18	5.29	0.629	0.164	-2.33	-15.92
17. Alutiiq Pride Hatchery-Vallenar stock	2007			83	20	5	16	4	19	5.47	0.651	0.167	-2.12	-16.97
18. Alutiiq Pride Hatchery-Vallenar stock	2008			41	24	8	14	10	20	5.82	0.765	0.236	-2.39	-19.76
19. Alutiiq Pride Hatchery-Vallenar stock	2009			57	25	4	22	3	19	5.87	0.769	0.210	-2.36	-16.36
Mean	–	–	–	71.7	22.7	4.8	18.1	4.8	20.3	5.55	0.712	0.177	-2.26	-19.45
Total	–	–	–	1362	155	–	112	51	168	12.80	0.708	0.179	-2.63	-29.01

Samples collected over years at a location were pooled because the extreme longevity of geoduck clams produces year-class overlap, so that temporal samples are not expected to show genetic differences. Samples were also pooled between nearby areas, so that the latitude and longitudes are approximate. N = sample size. N_{poly} = number of polymorphic nucleotide sites. N_{priv} = number of private haplotype occurring only in one sample. ts = number of transitional mutations. tv = number of transversal mutations. N_h = number of haplotypes. N_{Exp} = expected number of haplotypes under neutrality. h = gene diversity (based on haplotype frequencies and ranges from 0.0–1.0). θ_π % = nucleotide diversity (based on both haplotype frequencies and sequence divergence between haplotypes). D_T = Tajima's measure of neutrality. F_S= Fu's measure of neutrality.

Table 2. Pairwise F_{ST} for mtDNA (lower triangle) and geographic distance in kilometers (upper triangle) between samples of geoduck clams (*Panopea generosa*) from southeastern Alaska.

	Sample number															
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	–	150	170	180	200	218	243	291	419	396	289	409	393	389	411	412
2	0.0038	–	15	39	51	76	99	150	326	308	248	318	254	248	273	273
3	0.0067	-0.0024	–	27	39	70	94	144	275	259	244	265	249	244	267	267
4	0.0059	-0.0001	-0.0065	–	17	39	62	110	244	288	227	234	219	213	237	237
5	-0.0035	-0.0043	-0.0032	-0.0010	–	28	48	96	244	226	212	233	215	311	234	234
6	-0.0055	0.0051	0.0097	0.0096	-0.0025	–	40	90	220	205	190	210	193	188	213	213
7	0.0009	-0.0033	-0.0014	0.0017	-0.0057	-0.0008	–	54	190	271	155	177	161	155	179	179
8	-0.0060	-0.0014	0.0040	0.0010	-0.0048	-0.0057	-0.0022	–	141	125	108	129	114	108	132	132
9	0.0022	0.0010	0.0054	0.0113	-0.0004	0.0015	-0.0018	0.0015	–	19	56	62	72	82	105	107
10	0.0148	0.0006	-0.0049	-0.0033	0.0011	0.0140	0.0014	0.0069	0.0121	–	44	38	57	65	87	90
11	-0.0025	0.0027	0.0080	0.0100	-0.0023	-0.0021	-0.0026	-0.0035	-0.0026	0.0128	–	45	14	34	58	61
12	-0.0022	0.0079	0.0129	0.0109	-0.0007	-0.0058	-0.0003	0.0032	0.0058	0.0198	0.0010	–	58	65	88	91
13	-0.0022	0.0002	0.0025	0.0045	-0.0035	-0.0003	-0.0036	-0.0036	-0.0041	0.0105	-0.0037	0.0042	–	38	26	43
14	0.0026	-0.0077	-0.0084	-0.0062	-0.0066	0.0043	-0.0079	-0.0024	-0.0028	-0.0062	0.0018	0.0045	-0.0035	–	24	29
15	0.0002	-0.0039	-0.0054	-0.0061	-0.0049	0.0019	-0.0023	-0.0041	0.0032	-0.0044	0.0016	0.0037	-0.0009	-0.0089	–	29
16	-0.0033	-0.0032	-0.0021	0.0003	-0.0061	-0.0013	-0.0055	-0.0056	-0.0041	0.0039	-0.0050	0.0037	-0.0076	-0.0065	-0.0048	–

Table 3. Analysis of molecular variance (AMOVA) of mitochondrial cytochrome oxidase I sequence variability (684 bp) among samples of geoduck clams (*Panopea generosa*) from the southeastern Alaska. Sample numbers as in Figure 1 and Table 1. Asterisks represent groups for analysis.

Sample location																			Divergence			
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	F_{ST}	*P*	F_{SC}	*P*
[*	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	***]**	-0.0008	0.6232	–	–
[*	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	***]**				-0.0008	0.6250	–	–
[*]	**[***	*****	*****	*****	*****	*****	***]**	**[*]**	**[***	*****	*****	*****	*****	*****	***]**				0.0006	0.2660	-0.0011	0.6609
													[*]			**[***	*****	***]**	-0.0040	1.0000	0.0018	0.3080

Table 4. Summary statistics for 6 microsatellite in 19 samples of geoduck clams (*Panopea generosa*) from southeastern Alaska. *N* is sample size for each locus. A_N is the number of alleles (including a null allele for each locus). A_P is the number of alleles occurring in only one sample (sometimes in multiple copies). H_O and H_E are observed and expected heterozygosities pooled over samples. *P* is the probability of exact G-test of allele-frequency differences between samples for each microsatellite locus. Default values of 10,000 burn-in, 20 batches of 5000 iterations each. The distribution of allele-frequencies heterogeneity among samples across loci was not significant Fisher's test: X^2 = 15.386, *P* = 0.221.

		Repeat						*Heterogeneity*	
Locus	***N***	**motif**	A_N	A_P	H_O	H_E	**S.E.**	***P***	***S.E.***
Pab101e	1088	3	44	2	0.914	0.933	0.022	0.256	0.018
Pab105e	1109	4	35	0	0.682	0.937	0.276	0.164	0.019
Pab106e	1102	3	99	2	0.974	0.981	0.008	0.384	0.036
Pab112e	1110	4	75	1	0.964	0.975	0.013	0.271	0.029
Pab117	1125	2	79	0	0.810	0.972	0.161	0.162	0.024
Pab9	1111	4	28	2	0.824	0.928	0.113	0.642	0.018

Table 5. Summary of measures of genetic variability of 6 microsatellite loci in samples of geoduck clams (*Panopea generosa*) from Southeastern Alaska. N is sample size. A_N is the average number alleles across loci. A_R is allelic richness (based on $2n = 82$). H_O is observed and H_E expected heterozygosity averaged over 6 loci. F_{IS} is the inbreeding coefficient based on allelic frequencies. Rho_{IS} is the inbreeding coefficient based on allelic size in addition to allelic frequencies. Sample numbers as in Figure 1 and Table 1.

Sample	N	A_N	A_R	H_O	H_E	F_{IS}	Rho_{IS}
1	92	38.33	28.84	0.862	0.956	0.087	0.100
2	80	37.00	27.95	0.842	0.957	0.093	-0.008
3	86	37.00	28.09	0.871	0.957	0.074	0.007
4	85	38.67	28.59	0.843	0.957	0.107	0.143
5	94	38.83	28.52	0.832	0.956	0.110	0.039
6	78	35.00	27.46	0.835	0.952	0.113	0.083
7	84	35.67	26.87	0.837	0.950	0.080	0.038
8	61	33.17	27.60	0.874	0.951	0.071	0.048
9	41	28.67	27.51	0.846	0.954	0.092	0.115
10	80	37.83	28.04	0.811	0.955	0.125	0.111
11	88	37.50	28.00	0.845	0.956	0.093	0.016
12	84	37.17	27.77	0.839	0.952	0.094	0.133
13	88	37.00	28.22	0.814	0.956	0.125	0.158
14	50	33.00	27.96	0.836	0.955	0.087	-0.016
15	85	36.50	27.91	0.844	0.956	0.087	-0.018
16	69	34.50	27.75	0.838	0.954	0.108	0.221
17	92	35.83	26.92	0.839	0.952	0.094	0.067
18	44	30.50	28.60	0.902	0.955	0.045	0.128
19	73	32.50	27.01	0.728	0.921	0.124	0.043
Mean	76.5	35.51	27.87	0.839	0.953	0.095	0.074
Total	1454	59.17	28.96	0.860	0.953	0.097	0.076

Table 6. Estimates of null alleles at 6 microsatellite loci in samples of geoduck clams (*Panopea generosa*) from southeastern Alaska. Estimates in left column are from GenePop and in the right column from ML-NULLFREQ.

Sample	***Pab101e***		***Pab105e***		***Pab106e***		***Pab112e***		***Pab117***		***Pab9***	
1	0.0	0.0	0.1215	0.144	0.0030	0.003	0.0061	0.006	0.0790	0.087	0.0406	0.044
2	0.0007	0.001	0.1184	0.141	0.0032	0.003	0.0021	0.002	0.0520	0.056	0.0801	0.091
3	0.0	0.0	0.0990	0.115	0.0083	0.008	0.0137	0.014	0.0503	0.054	0.0332	0.036
4	0.234	0.017	0.1701	0.180	0.0085	0.009	0.0153	0.015	0.0422	0.045	0.0505	0.050
5	0.0321	0.035	0.1353	0.157	0.0	0.0	0.0	0.000	0.0898	0.101	0.0564	0.063
6	0.0088	0.009	0.1664	0.192	0.0003	0.000	0.0109	0.011	0.0651	0.058	0.0588	0.066
7	0.0097	0.010	0.0600	0.067	0.0044	0.004	0.0	0.000	0.0613	0.067	0.0729	0.083
8	0.0	0.0	0.1195	0.119	0.0	0.0	0.0	0.000	0.0451	0.048	0.0387	0.042
9	0.0034	0.003	0.0778	0.090	0.0	0.0	0.0	0.000	0.1141	0.132	0.0561	0.062
10	0.0	0.0	0.1746	0.205	0.0	0.0	0.0	0.000	0.1224	0.143	0.0684	0.077
11	0.0	0.0	0.1245	0.148	0.0022	0.002	0.0002	0.000	0.0591	0.064	0.0545	0.060
12	0.0058	0.006	0.1392	0.151	0.009	0.000	0.0	0.000	0.0997	0.112	0.0244	0.026
13	0.0	0.0	0.1347	0.158	0.0	0.0	0.0132	0.014	0.1500	0.171	0.0518	0.057
14	0.0	0.0	0.1162	0.126	0.0	0.0	0.0	0.000	0.0719	0.079	0.0756	0.085
15	0.0	0.0	0.1715	0.211	0.0020	0.002	0.0152	0.016	0.0374	0.039	0.0447	0.049
16	0.163	0.016	0.1705	0.212	0.0	0.0	0.0	0.000	0.0601	0.065	0.0557	0.062
17	0.0235	0.023	0.1139	0.119	0.0027	0.003	0.0170	0.018	0.0747	0.083	0.0219	0.023
18	0.0	0.0	0.0969	0.097	0.0	0.0	0.0030	0.000	0.0175	0.018	0.0032	0.003
19	0.0	0.0	0.1225	0.145	0.0	0.0	0.0	0.000	0.2141	0.280	0.0808	0.092
Mean	0.0253	0.006	0.1280	0.146	0.0023	0.002	0.0051	0.005	0.0793	0.090	0.0510	0.056

Table 7. Estimates of F_{ST} based on 6 microsatellite loci between samples of geoduck clams (*Panopea generosa*) from southeastern Alaska.

	Sample number														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	–														
2	0.0	–													
3	0.0	0.0	–												
4	0.0	0.0	0.0	–											
5	0.0	0.0	0.0	0.0009	–										
6	0.0	0.0	0.0	0.0002	0.0009	–									
7	0.0004	0.0	0.0002	0.0017	0.0001	0.0000	–								
8	0.0002	0.0002	0.0	0.0007	0.0007	0.0010	0.0020	–							
9	0.0013	0.0007	0.0	0.0006	0.0007	0.0009	0.0013	0.0002	–						
10	0.0	0.0	0.0	0.0001	0.0004	0.0	0.0	0.0005	0.0009	–					
11	0.0002	0.0	0.0	0.0002	0.0	0.0	0.0	0.0003	0.0002	0.0	–				
12	0.0003	0.0	0.0	0.0006	0.0	0.0013	0.0024	0.0007	0.0029	0.0013	0.0006	–			
13	0.0004	0.0	0.0	0.0001	0.0002	0.0	0.0005	0.0004	0.0004	0.0	0.0	0.0015	–		
14	0.0015	0.0	0.0	0.0007	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0010	0.0004	–	
15	0.0018	0.0	0.0	0.0012	0.0005	0.0021	0.0014	0.0005	0.0	0.0006	0.0	0.0019	0.0005	0.0	–
16	0.0	0.0	0.0001	0.0011	0.0007	0.0019	0.0019	0.0006	0.0013	0.0008	0.0013	0.0	0.0013	0.0012	0.0009

Table 8. Analysis of molecular variance (AMOVA) of microsatellite allele-frequency variability among samples of geoduck clams (*Panopea generosa*) from the Northeastern Pacific Ocean. Sample location numbers as in Figure 1 and Table 1. Analyses were made on allelic frequencies unadjusted for null alleles, except that PCR failures for individuals with at least one successful locus were coded as null-allele homozygotes.

Sample location																			Divergence			
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	F_{ST}	*P*	F_{SC}	*P*
[*	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	***]**	0.0027	<0.0001	–	–
[*	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	***]**				0.0010	0.100	–	–
[*]	**[***	*****	*****	*****	*****	*****	***]**	**[*]**	*****	*****	*****	*****	*****	*****	***]**				-0.0001	0.743	0.0011	0.083
													[*]			**[***	*****	***]**	-0.0058	1.000	0.0118	<0.0001

[The magnitudes of divergences between the groups and the pattern of significance were similar to AMOVAs of allele frequencies unadjusted for null alleles.]

Figure 1

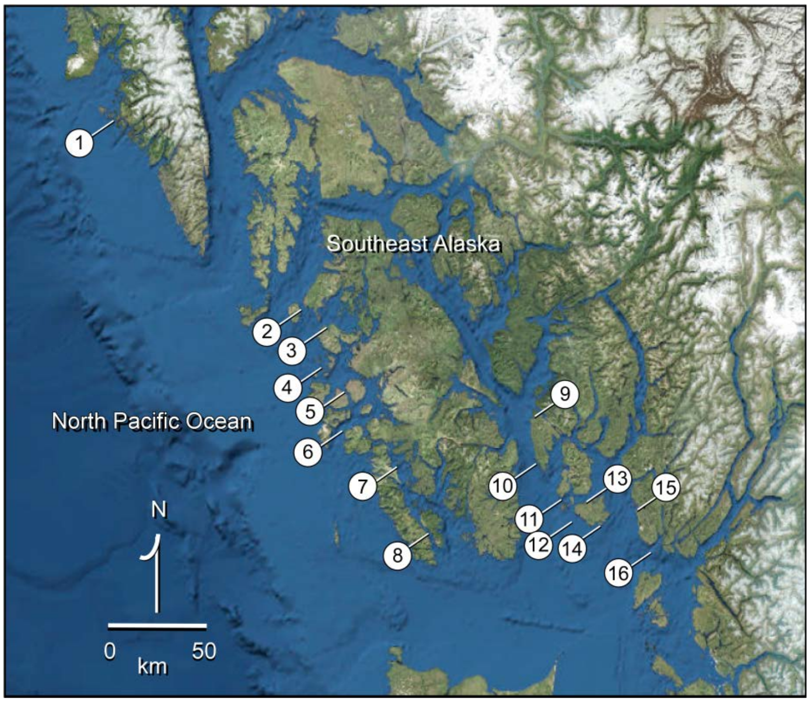

Southeast Alaska
North Pacific Ocean
N
0
50
km
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16

Figure 2

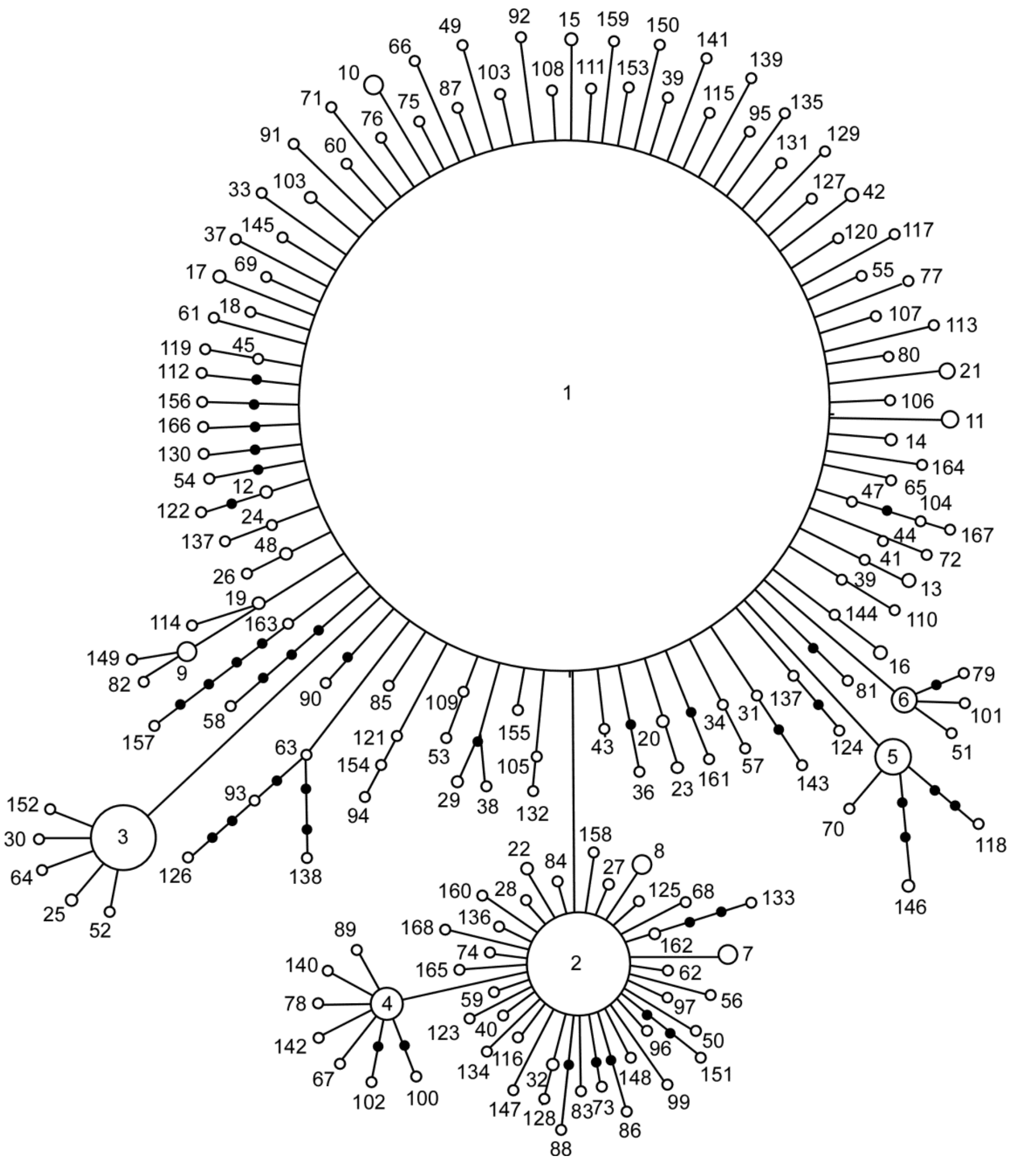

1
2
3
4
5
6
7
92 15 159 150 49 141 66 139 10 103 108 111 153 39 87 115 135 71 75 95 76 131 129 91 60 127 42 33 103 120 117 37 145 55 77 17 69 107 113 61 18 80 21 119 45 112 106 11 156 166 14 130 164 54 65 12 47 104 122 24 44 167 137 48 41 72 26 39 13 19 144 110 114 163 16 149 79 9 81 82 101 90 85 109 137 157 58 31 34 51 155 20 63 121 53 43 124 105 57 154 36 23 161 143 94 29 38 132 70 118 93 152 30 64 25 52 126 138 146 158 22 84 27 8 160 28 125 68 133 168 136 162 89 140 74 165 62 78 59 97 56 123 40 50 142 67 102 100 134 116 32 148 96 151 147 128 83 73 99 88 86

Figure 3

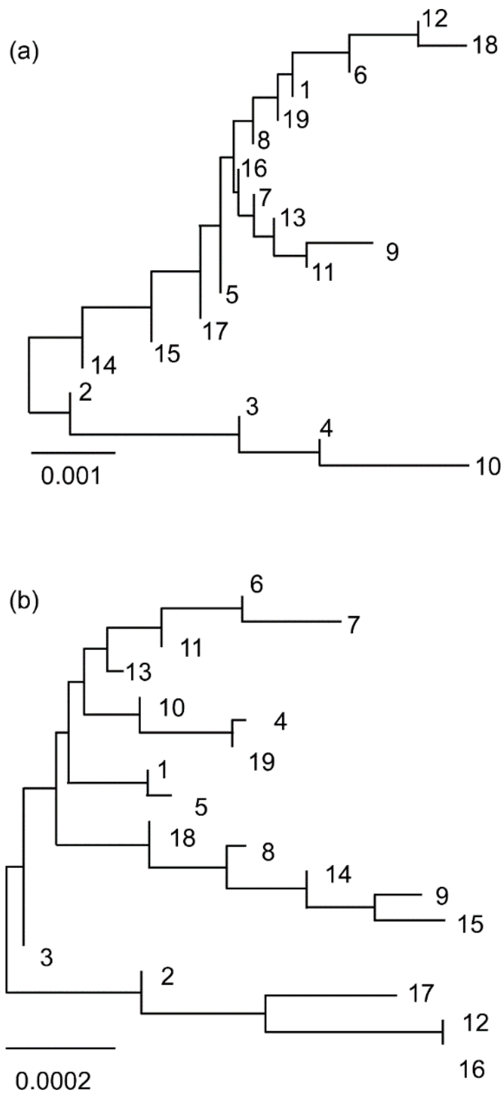
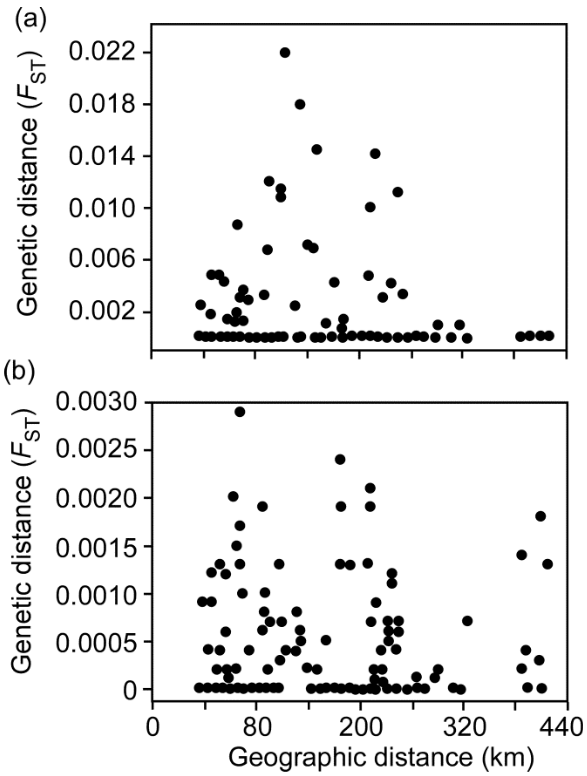

(a)
12
18
6
1
19
8
16
7
13
9
11
5
17
15
14
2
3
4
10
0.001
(b)
6
7
11
13
10
4
19
1
5
18
8
14
9
15
3
2
17
12
16
0.0002

Figure 4


(a)
Genetic distance (F_{ST})
0.022
0.018
0.014
0.010
0.006
0.002
(b)
Genetic distance (F_{ST})
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0
0
80
200
320
440
Geographic distance (km)

Supplemental tables S1–S5: Grant & Templin: Saltonstall-Kennedy Final Report, Phylogeography of geoduck clams in southeastern Alaska.

Supplemental tables S1–S5: Grant & Templin: Saltonstall-Kennedy Final Report, Phylogeography of geoduck clams in southeastern Alaska. These tables report 1) Table S1: PCR profiles for microsatellite DNA amplifications (those for mtDNA are in the Materials and Methods section of the text), 2) Tables S2–S3: mtDNA haplotypes and frequencies among samples and, and 3) Tables S4–S5: microsatellite genotypes and frequencies among samples.

Table S1. Microsatellite loci surveyed in Pacific geoduck clam (*Panopea generosa)* and associated thermal profiles.

Locus	Thermal profile
Pab9	95 ºC/3 min; 5 cycles of (94 ºC/30 sec + 52 ºC/30 sec + 72 ºC/30 sec); 26 cycles of (94 ºC/15 sec + 52 ºC/15 sec + 72 ºC/30 sec); 72 ºC 10 min
Pab101	95 ºC/3 min; 31 cycles of (94 ºC/30 sec + 52 ºC/30 sec + 72 ºC/45 sec); 72 ºC 10 min
Pab105	95 ºC/3 min; 30 cycles of (94 ºC/30 sec + 50 ºC/30 sec + 72 ºC/45 sec); 72 ºC 10 min
Pab106	95 ºC/3 min; 31 cycles of (94 ºC/30 sec + 52 ºC/30 sec + 72 ºC/45 sec); 72 ºC 10 min
Pab112	95 ºC/3 min; 30 cycles of (94 ºC/30 sec + 50 ºC/30 sec + 72 ºC/45 sec); 72 ºC 10 min
Pab117	95 ºC/3 min; 30 cycles of (94 ºC/30 sec + 50 ºC/30 sec + 72 ºC/45 sec); 72 ºC 10 min

Table S2. Haplotype frequencies of partial sequences (684 base pairs) of mitochondrial DNA Cytochrome oxidase I in samples of geoduck clams (*Panopea generosa*) collected in southeastern Alaska. Sample numbers correspond to those in Table 1.

Haplotype number	Sample number																		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	49	46	46	35	49	33	41	27	51	45	36	23	36	22	34	45	48	20	26
2	5	14	14	13	8	7	6	7	8	13	5	4	6	7	8	8	10	1	6
3	8	4	4	6	6	6	3	7	1	2	4	3	4	1	6	5	5	3	8
4	3	1	6	5	4	1	1	1	1	5	1	1	1	1	3	2	3	1	1
5	3	3	5	4	2	1	2	1	3	1	1		5	1	3	2	2	1	1
6	3	1	2	4	2		1	1	1			3	1	2	2	1	1		1
7	1	2	1	2	2	1	1	1	2		1	1				1	1	1	1
8	2	2	1		2		1	2	1		1		2	1	1				1
9	2	1	1		3	2						2			1		2	1	1
10		1	1			2	1	1	2			1		1		1		1	1
11			1	1		2	3					2	1						
12	2		2	1	1				1						1				
13		1			1		1			1					1				1
14		3		1											1				1
15	1	1									1	1			1				
16					1								1				1		2
17						2			1						1		1		
18		1	1														1	1	
19				1		1						1					1		
20					1				1	1						1			
21	1									1					1				
22				1								1			1				
23									1										
24						2		1		1									
25									1	1							1		
26	1	1																	
27	1	1																	
28	1									1									
29	1			1															
30	1					1													
31	1				1														
32																1			
33		1						1											
34		1								1									
35				1														1	
36				1									1						
37				1									1						
38					1			1											
39					1								1						
40					1										1				
41											1								
42							1									1			
43							1							1					
44										1						1			

Table S2. – continued Page 2 of 4

Haplotype number	Sample number																		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
45										1					1				
46									1		1								
47												2							
48									1										1
49													1		1				
50														1	1				
51	1																		
52	1																		
53	1																		
54		1																	
55		1																	
56		1																	
57		1																	
58			1																
59			1																
60			1																
61				1															
62				1															
63				1															
64				1															
65				1															
66				1															
67				1															
68				1															
69				1															
70					1														
71					1														
72					1		1												
73					1														
74					1														
75					1														
76						1													
77						1													
78						1													
79						1													
80							1												
81							1												
82							1												
83							1												
84							1												
85							1												
86							1												
87							1												
88							1												
89							1												
90							1												
91								1											

Table S2. – continued Page 3 of 4

Haplotype number	Sample number																		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
92								1											
93								1											
94								1											
95								1											
96										1									
97										1									
98										1									
99										1									
100										1									
101										1									
102											1								
103											1								
104											1								
105											1								
106											1								
107											1								
108											1								
109											1								
110											1								
111											1								
112												1							
113												1							
114												1							
115									1										
116									1										
117									1										
118									1										
119									1										
120									1										
121									1										
122									1										
123									1										
124									1										
125													1						
126													1						
127													1						
128													1						
129														1					
130														1					
131														1					
132															1				
133															1				
134															1				
135															1				
136															1				
137															1				
138															1				

Table S2. – continued Page 4 of 4

Haplotype number	Sample number 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
139															1				
140															1				
141																1			
142																1			
143																1			
144																1			
145																1			
146																1			
147																	1		
148																	1		
149																	1		
150																	1		
151																	1		
152																	1		
153																		1	
154																		1	
155																		1	
156																		1	
157																		1	
158																		1	
159																		1	
160																		1	
161																		1	
162																		1	
163																		1	
164																			1
165																			1
166																			1
167																			1
168																			1

S3. Arlequin formatted sequences of mitochondrial DNA cytochrome oxidase I (684 bp) in geoduck clams, *Panopea generosa*. The body of table consists of haplotype sequences and the haplotype frequencies in 19 samples appear at the end of the table. Sample numbers correspond to those in Table 1.

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    NbSamples=19
    GenotypicData=0
    DataType=DNA
    LocusSeparator=NONE
[Data]
     [[HaplotypeDefinition]]
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        HaplList={
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GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
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003
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TGTTCATTTGTTTTGATTTTTTGGTCAC
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CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
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GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
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TGTTCACTTGTTTTGATTTTTTGGTCAC
010
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TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
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012
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013
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TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTGGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACCACTGGGAATATACCGCCAGAAATTATA
GAATTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCGATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
158
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATCGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTATCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
159
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATTGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGGGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
160
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATCGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATTACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
161
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATTGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC

CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGGTACCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
162
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATCGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTACCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
163
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATTGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACCGCCAGAAATTATA
GAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
164
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATTGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGCGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
165
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATCGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGTTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
166
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATTGTGACTGCGCATTCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCCCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG

```
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
167
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATACTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATTGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTTTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTTGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTCTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
GAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
168
AAAGATATTGGAGTCTTATATTTTATCTTTGCTATTTGAGCTGGTATAGTTGGTACAGCTTTTAGAATATTAATTCGAATAG
AGTTAGCACGTCCTGGGGCATTTTTAGGAGATGATCATCTCTATAATGTAATCGTGACTGCGCATGCCTTTGTTATAATTTT
TTTTCTGGTGATACCTATAATAGTGGGTGGTTTTGGGAATTTTTTAGTTCCTTTGATACTTTCTGCTCCTGATATGGCATTC
CCTCGAATAAATAACATGAGGTTTTGGCTTTTACCTATGGCAGTTTTGTTACTTTTAAGGTCAGCTTTTGTCGAGAGAGGTG
TTGGTACTGGGTGAACAGTCTATCCTCCCCTTTCTTCAAATGTTGCCCATAGAGGCGGCTCTGTTGATTATGGGATTTTTTC
TCTTCATCTGGCGGGGGTATCTTCTATTTTGGGGGCTATTAATTTCATTTCTACAACTGTGAATATACGGCCAGAAATTATA
AAGTTAAAGCGAGTTAGCTTATTTGTATGGTCAGTTGCTATCACTGCTTTTTTGCTGGTGCTTGCTATGCCTGTGTTGGCGG
GGGCTATTACAATATTATTAACAGATCGTAATTTTAATACCTCATTTTTTGATCCGTCGGGCGGTGGGGACCCAATTCTTTT
TGTTCATTTGTTTTGATTTTTTGGTCAC
}
    [[Samples]]
        SampleName="1-biorka"
        SampleSize=90
        SampleData={
001 49
002  5
003  8
004  3
005  3
006  3
007  1
008  2
009  2
012  2
015  1
021  1
026  1
027  1
028  1
029  1
030  1
031  1
032  1
051  1
052  1
053  1
}
        SampleName="2-warren"
        SampleSize=89
        SampleData={
001 46
```

```
002 14
003  4
004  1
005  3
006  1
007  2
008  2
009  1
010  1
013  1
014  3
015  1
018  1
026  1
027  1
033  1
034  1
054  1
055  1
056  1
057  1
}
        SampleName="3-ptalice"
        SampleSize=88
        SampleData={
001 46
002 14
003  4
004  6
005  5
006  2
007  1
008  1
009  1
010  1
011  1
012  2
018  1
058  1
059  1
060  1
}
        SampleName="4-maur"
        SampleSize=87
        SampleData={
001 35
002 13
003  6
004  5
005  4
006  4
007  2
011  1
012  1
```

```
014  1
019  1
022  1
029  1
035  1
036  1
037  1
061  1
062  1
063  1
064  1
065  1
066  1
067  1
068  1
069  1
}
        SampleName="5-port"
        SampleSize=92
        SampleData={
001 49
002  8
003  6
004  4
005  2
006  2
007  2
008  2
009  3
012  1
013  1
016  1
020  1
031  1
038  1
039  1
040  1
070  1
071  1
072  1
073  1
074  1
075  1
}
        SampleName="6-bucar"
        SampleSize=66
        SampleData={
001 33
002  7
003  6
004  1
005  1
007  1
009  2
```

```
010  2
011  2
017  2
019  1
023  2
024  1
030  1
076  1
077  1
078  1
079  1
}

        SampleName="7-telvak"
        SampleSize=75
        SampleData={
001 41
002  6
003  3
004  1
005  2
006  1
007  1
008  1
010  1
011  3
013  1
042  1
043  1
072  1
080  1
081  1
082  1
083  1
084  1
085  1
086  1
087  1
088  1
089  1
090  1
}
        SampleName="8-kaig"
        SampleSize=57
        SampleData={
001 27
002  7
003  7
004  1
005  1
006  1
007  1
008  2
010  1
```

```
013  1
024  1
033  1
038  1
091  1
092  1
093  1
094  1
095  1
}
        SampleName="9-foggy"
        SampleSize=87
        SampleData={
001 51
002  8
003  1
004  1
005  3
006  1
007  2
008  1
010  2
012  1
017  1
020  1
023  1
025  1
046  1
048  1
115  1
116  1
117  1
118  1
119  1
120  1
121  1
122  1
123  1
124  1
}
        SampleName="10-percy"
        SampleSize=81
        SampleData={
001 45
002 13
003  2
004  5
005  1
013  1
020  1
021  1
024  1
025  1
028  1
```

```
034  1
044  1
045  1
096  1
097  1
098  1
099  1
100  1
101  1
}
        SampleName="11-vegas"
        SampleSize=62
        SampleData={
001 36
002  5
003  4
004  1
005  1
007  1
008  1
015  1
041  1
046  1
102  1
103  1
104  1
105  1
106  1
107  1
108  1
109  1
110  1
111  1
}
        SampleName="12-kelp"
        SampleSize=48
        SampleData={
001 23
002  4
003  3
004  1
006  3
007  1
009  2
010  1
011  2
015  1
019  1
022  1
047  2
112  1
113  1
114  1
}
```

```
        SampleName="13-lord"
        SampleSize=65
        SampleData={
001 36
002  6
003  4
004  1
005  5
006  1
008  2
011  1
016  1
036  1
037  1
039  1
049  1
125  1
126  1
127  1
128  1
}
        SampleName="14-vall"
        SampleSize=41
        SampleData={
001 22
002  7
003  1
004  1
005  1
006  2
008  1
010  1
043  1
050  1
129  1
130  1
131  1
}
        SampleName="15-nehent"
        SampleSize=78
        SampleData={
001 34
002  8
003  6
004  3
005  3
006  2
008  1
009  1
012  1
013  1
014  1
015  1
017  1
```

```
021  1
022  1
040  1
045  1
049  1
050  1
132  1
133  1
134  1
135  1
136  1
137  1
138  1
139  1
140  1
}
        SampleName="16-ann"
        SampleSize=75
        SampleData={
001 45
002  8
003  5
004  2
005  2
006  1
007  1
010  1
020  1
032  1
042  1
044  1
133  1
141  1
142  1
143  1
145  1
146  1
}
        SampleName="17-APSH07"
        SampleSize=83
        SampleData={
001 48
002 10
003  5
004  3
005  2
006  1
007  1
009  2
016  1
017  1
018  1
019  1
025  1
```

```
147  1
148  1
149  1
150  1
151  1
152  1
}
        SampleName="18-APSH08"
        SampleSize=41
        SampleData={
001 20
002  1
003  3
005  1
007  1
009  1
010  1
018  1
035  1
153  1
154  1
155  1
156  1
157  1
158  1
159  1
160  1
161  1
162  1
163  1
}
        SampleName="19-APSH09"
        SampleSize=57
        SampleData={
001 26
002  6
003  8
004  1
005  1
006  1
007  1
008  1
009  1
010  1
013  1
014  1
016  2
048  1
164  1
165  1
166  1
167  1
168  1
}
```

```
[[Structure]]

    StructureName="geo-19-pops"
    NbGroups=1

    Group={
        "1-biorka"
        "2-warren"
        "3-ptalice"
        "4-maur"
        "5-port"
        "6-bucar"
        "7-telvak"
        "8-kaig"
        "9-foggy"
        "10-percy"
        "11-vegas"
        "12-kelp"
        "13-lord"
        "14-vall"
        "15-nehent"
        "16-ann"
        "17-APSH07"
        "18-APSH08"
        "19-APSH09"
    }
```

Table S4. Microsatellite genotypes 19 in samples of geoduck clams (*Panopea generosa*) in GENEPOP format. Sample 'popX' numbers correspond to in Table 1 and Figure 1.

```
"Geoducks"
Pab101e
Pab105e
Pab106e
Pab112e
Pab117
Pab9
Pop
GDPSP07_16     ,  218222 134150 123196 121149 276312 214230
GDPSP07_17     ,  178222 154162 193201 173197 264292 222230
GDPSP07_18     ,  222230 154154 195219 169305 292317 222254
GDPSP07_37     ,  190218 146166 207213 249309 321346 214254
GDPSP07_38     ,  202206 134134 127259 141145 334354 214254
GDPSP07_39     ,  202234 154174 127211 181217 000000 222226
GDPSP07_52     ,  226246 134194 213266 173217 300300 246278
GDPSP07_53     ,  210214 142142 158270 145225 358383 222238
GDPSP07_54     ,  190218 142162 225233 129217 304321 234250
GDDEC08_259    ,  210222 138138 000000 213253 198300 206242
GDDEC08_260    ,  194202 166178 115233 145345 272346 222246
GDDEC08_261    ,  194218 154154 142205 193309 292296 222226
GDDEC08_301    ,  206222 154176 199209 229229 276276 254254
GDDEC08_302    ,  210222 162174 142201 161297 308346 206242
GDDEC08_303    ,  166226 158162 123193 137221 325338 242258
GDDEC08_307    ,  210226 138158 134197 113129 243288 242246
GDDEC08_308    ,  202218 154166 107146 153361 358358 218242
GDDEC08_309    ,  210218 170170 107123 149193 317338 234246
GDDEC10_13     ,  186202 138162 219229 201297 280292 206234
GDDEC10_14     ,  178210 162194 185215 141237 300338 238250
GDDEC10_15     ,  194222 154154 154251 149197 375395 198210
GDDEC10_139    ,  218230 134166 154221 129205 288404 234246
GDDEC10_140    ,  206214 170186 127229 181193 362362 226238
GDDEC10_141    ,  194210 166190 197229 133169 300329 234258
GDDEC12_123155 ,  214226 162186 138174 165169 300334 218270
GDDEC12_123156 ,  202230 142170 199219 157161 284300 238258
GDDEC12_123157 ,  174202 150170 103205 153177 354358 210234
GDDEC12_123164 ,  186206 134194 211259 309357 321379 246266
GDDEC12_123165 ,  222226 146158 134274 153165 251292 246250
GDDEC12_123166 ,  230234 134194 131185 165233 276276 238238
GDDEC08_187    ,  174202 138138 134211 121221 296296 246258
GDDEC08_188    ,  202210 146146 115123 125149 321342 226250
GDDEC08_189    ,  190218 000000 162249 137285 308308 210238
GDDEC08_400    ,  202222 134158 193237 165209 354375 222246
GDDEC12_123143 ,  194210 154186 111201 185201 260280 230230
GDDEC12_123144 ,  194214 158170 193261 129245 288383 242242
GDDEC12_123145 ,  194222 126162 170239 229253 288300 214222
GDDEC12_123188 ,  198206 158158 127127 141197 239350 218242
GDDEC12_123189 ,  206226 166190 119187 149177 272296 222226
GDDEC12_123190 ,  210258 162166 203298 209225 276276 246250
GDDEC13_171740 ,  194210 186190 119142 157217 325362 214234
GDDEC13_171741 ,  186210 162170 219227 209373 366366 246246
GDDEC13_171742 ,  210230 146194 142193 161229 260338 234270
GDDEC14_214722 ,  210210 134134 115197 309349 274342 238250
```

```
GDDEC14_214723 ,  226230 170170 217231 133197 358358 230234
GDDEC14_214724 ,  218230 174174 166223 205249 375383 214214
GDDEC14_214734 ,  194214 000000 178219 161165 317350 218242
GDDEC14_214735 ,  210218 166182 115231 181333 276346 238250
GDDEC14_214736 ,  182218 154218 107223 185213 300371 234246
GDDEC14_214743 ,  194202 170206 115223 213357 342404 234238
GDDEC14_214744 ,  190206 126162 134217 329329 292342 222222
GDDEC14_214745 ,  202234 150186 127142 165165 255308 214250
GDDEC15_312784 ,  182198 170170 142209 149305 350379 222238
GDDEC15_312785 ,  178230 138138 249261 129137 358400 226238
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GDDEC11_111280	,	202228	142158	211259	185337	329362	242254
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GDDEC13_171759	,	198226	166198	146239	229313	296354	218258
GDDEC13_171760	,	208226	158194	166215	257361	276317	230234
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GDAPSH07_22	,	226226	190190	166189	321349	304308	214234
GDAPSH07_23	,	198206	162166	201237	165233	304404	206226
GDAPSH07_24	,	186210	182182	213229	145145	317362	230242
GDAPSH07_25	,	210238	154158	142172	189201	325383	234242
GDAPSH07_26	,	202208	154170	115142	125213	272304	218250
GDAPSH07_27	,	202210	162170	193247	129173	321321	226246
GDAPSH07_28	,	210222	166166	207243	185317	304366	230258
GDAPSH07_29	,	206226	150170	150209	133225	000000	210238
GDAPSH07_30	,	190218	150186	131138	129185	264350	218234
GDAPSH07_31	,	206234	178182	146197	145161	280391	246250
GDAPSH07_32	,	198214	138202	111154	121237	284308	226262
GDAPSH07_33	,	198238	158182	193225	201341	325366	210250
GDAPSH07_34	,	214214	162182	127134	121177	292350	258258
GDAPSH07_35	,	210222	166170	111146	141313	000000	238242
GDAPSH07_36	,	210218	166166	127205	133397	334334	234250
GDAPSH07_37	,	186202	138158	107119	201217	329348	222234
GDAPSH07_38	,	198202	126186	201223	145161	346358	234246
GDAPSH07_39	,	198230	150206	154211	121189	255334	234274
GDAPSH07_40	,	194208	142166	127134	113201	292292	226234
GDAPSH07_41	,	194208	142166	127134	113201	292292	226234
GDAPSH07_42	,	162190	178178	185249	145145	312321	238238
GDAPSH07_43	,	202222	150174	266266	189205	255292	246254
GDAPSH07_44	,	198198	178182	131162	125181	000000	238250
GDAPSH07_45	,	198230	150206	154211	121189	255334	234274
GDAPSH07_46	,	162194	158174	119249	189189	272300	206242
GDAPSH07_47	,	214234	170186	131227	141201	276288	222250
GDAPSH07_48	,	222226	134170	134245	117237	260260	206246
GDAPSH07_49	,	194242	134166	189193	125129	325387	210250
GDAPSH07_50	,	202210	134170	146150	157169	321338	222246
GDAPSH07_51	,	198226	182182	115209	133193	276300	206210
GDAPSH07_52	,	194218	154170	138174	129281	276304	234238
GDAPSH07_53	,	198206	158186	219239	121213	379408	210250
GDAPSH07_54	,	206226	138138	142207	165201	292292	234254
GDAPSH07_55	,	186206	158158	131142	137185	325358	246246
GDAPSH07_56	,	166190	146162	227233	137185	329371	218242
GDAPSH07_57	,	222226	158158	197207	173185	379379	214214
GDAPSH07_58	,	206222	126162	185201	181213	292292	000000
GDAPSH07_59	,	190226	158182	138266	113153	284358	250254
GDAPSH07_60	,	218228	146154	134227	133189	276325	266266
GDAPSH07_61	,	186234	166166	127245	193357	292304	242246
GDAPSH07_62	,	214230	154174	166193	157157	296371	214242
GDAPSH07_63	,	198222	170170	138227	201293	272272	210262
GDAPSH07_64	,	182214	150150	131193	145185	000000	000000
GDAPSH07_65	,	218230	170174	146229	125189	334400	222258
GDAPSH07_67	,	186198	138142	164215	149213	000000	242254
GDAPSH07_68	,	210210	166178	205205	193209	288346	246258
GDAPSH07_70	,	202214	170170	119249	121145	280292	246258
GDAPSH07_71	,	194206	178178	142229	133309	239395	218246

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GDAPSH07_72    ,  194226 134154 131213 141153 292329 210242
GDAPSH07_73    ,  198198 170174 119259 141141 371391 234234
GDAPSH07_74    ,  202222 170170 142201 000000 000000 000000
GDAPSH07_76    ,  190210 146150 146205 193205 260329 226250
GDAPSH07_77    ,  190214 166166 138229 105129 272304 238250
GDAPSH07_78    ,  206210 142150 193229 141169 358366 246262
GDAPSH07_79    ,  198234 166186 231278 145209 304317 226242
GDAPSH07_80    ,  226254 146170 203268 153157 317383 238254
GDAPSH07_81    ,  210262 000000 131247 117353 321325 214246
GDAPSH07_82    ,  206218 154182 134134 121149 218304 226266
GDAPSH07_83    ,  222222 158158 127134 217225 338354 238242
GDAPSH07_84    ,  206218 226226 197207 193217 247304 250254
GDAPSH07_85    ,  186230 134162 231237 137213 308308 206222
GDAPSH07_86    ,  182226 158174 123142 133213 272308 226234
GDAPSH07_87    ,  214214 138154 146195 177257 284321 246262
GDAPSH07_88    ,  202222 166170 142203 197265 251362 234238
GDAPSH07_89    ,  222230 174178 207225 133217 321350 210250
GDAPSH07_90    ,  210214 170182 134229 117213 000000 254258
GDAPSH07_91    ,  206206 170170 107262 173261 296296 242242
GDAPSH07_92    ,  186200 162190 197235 161209 000000 218230
GDAPSH07_93    ,  186218 162162 138189 133185 296387 214214
GDAPSH07_94    ,  222222 162166 115131 145357 346346 214238
GDAPSH07_95    ,  206226 126150 123127 157337 296304 218254
Pop
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GDAPSH08_2     ,  178230 126162 207251 185289 375404 206238
GDAPSH08_3     ,  206212 158166 000000 137261 260304 238242
GDAPSH08_4     ,  214230 142178 119166 121157 292292 254258
GDAPSH08_5     ,  186218 146170 197229 185265 329391 214226
GDAPSH08_6     ,  210214 126170 174231 145197 308428 226238
GDAPSH08_7     ,  230250 170190 134154 121153 260312 214254
GDAPSH08_8     ,  190210 158166 123223 133337 317346 230242
GDAPSH08_9     ,  218230 134158 154237 137141 321346 210246
GDAPSH08_10    ,  222226 174186 138261 137137 334350 222226
GDAPSH08_11    ,  198222 142170 243259 261325 260371 238246
GDAPSH08_12    ,  198214 170178 154233 169233 276280 210250
GDAPSH08_13    ,  202202 154154 131166 117197 329329 206230
GDAPSH08_14    ,  210274 162162 119201 145217 292346 214234
GDAPSH08_15    ,  202206 170186 154193 273317 288312 206246
GDAPSH08_16    ,  182218 154154 123197 165185 276296 222250
GDAPSH08_17    ,  210210 158190 185227 145225 321395 238242
GDAPSH08_18    ,  174218 146158 146174 141189 325334 234234
GDAPSH08_19    ,  210214 154190 185227 137153 375379 238242
GDAPSH08_20    ,  198214 134166 231280 125157 274300 222258
GDAPSH08_22    ,  194210 186186 229270 125205 268300 206246
GDAPSH08_23    ,  174198 138178 138213 237345 300304 234242
GDAPSH08_24    ,  194198 126126 178201 193205 300312 226238
GDAPSH08_25    ,  186226 158158 243251 133197 288292 230250
GDAPSH08_26    ,  190206 142158 134249 141301 321329 234254
GDAPSH08_27    ,  198206 166166 185201 121325 317321 230254
GDAPSH08_28    ,  206214 154158 162170 189261 276321 218238
GDAPSH08_29    ,  214226 126126 193211 297357 260342 230246
GDAPSH08_30    ,  218218 142170 158268 137149 243243 210262
GDAPSH08_31    ,  214214 202202 150189 221345 288387 238242
GDAPSH08_32    ,  182218 174206 134178 205205 375416 214226
GDAPSH08_33    ,  206226 158182 170227 177325 304329 210254
GDAPSH08_34    ,  170198 126150 154233 137225 362383 222222
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GDAPSH08_36    ,  194202 178178 138205 201213 317325 226266
GDAPSH08_37    ,  202250 134158 138185 161205 288379 242246
GDAPSH08_38    ,  206234 146166 107166 149185 260276 230238
GDAPSH08_39    ,  214238 138166 142150 221333 288391 254254
GDAPSH08_41    ,  202250 134158 138185 161205 000000 242246
GDAPSH08_42    ,  210222 134170 193233 149181 000000 238246
GDAPSH08_43    ,  210222 134158 164229 153405 296350 214250
GDAPSH08_44    ,  182230 154174 215221 109137 300366 214238
GDAPSH08_46    ,  202206 126134 195251 173277 325342 230238
GDAPSH08_47    ,  198222 134182 131181 265277 308321 226230
GDAPSH08_48    ,  190226 142174 209257 133349 304338 246270
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GDAPSH09_3     ,  214218 134170 193243 125313 296296 262262
GDAPSH09_4     ,  198222 140174 150191 177181 280280 222250
GDAPSH09_5     ,  198222 140174 150191 177181 000000 222250
GDAPSH09_6     ,  198222 140174 150191 177181 280304 222250
GDAPSH09_7     ,  214218 138174 131229 000000 000000 214226
GDAPSH09_8     ,  186206 000000 211249 000000 000000 234258
GDAPSH09_9     ,  206250 134158 123185 181209 325325 238242
GDAPSH09_10    ,  214230 134134 197247 173201 000000 210258
GDAPSH09_11    ,  194210 158158 193247 217249 255300 242250
GDAPSH09_12    ,  218222 150162 193229 141349 268387 226242
GDAPSH09_13    ,  206226 182182 205261 137141 243312 230242
GDAPSH09_14    ,  178186 138182 174201 193205 000000 234238
GDAPSH09_15    ,  194210 174186 162207 141205 000000 234250
GDAPSH09_17    ,  178202 134178 150255 137185 272375 206250
GDAPSH09_18    ,  210210 142142 138160 201309 304358 226234
GDAPSH09_19    ,  186210 154174 134138 129197 264264 250250
GDAPSH09_20    ,  170178 154174 181215 129153 334334 246246
GDAPSH09_21    ,  190210 000000 127237 000000 000000 000000
GDAPSH09_22    ,  202230 158166 178183 133149 000000 238242
GDAPSH09_23    ,  182210 206206 119235 145289 260284 262262
GDAPSH09_24    ,  202242 170190 127197 149189 000000 234258
GDAPSH09_25    ,  194202 142158 191195 141193 284296 210226
GDAPSH09_26    ,  206214 194194 111223 141373 321338 226226
GDAPSH09_27    ,  190198 126142 123197 000000 000000 230242
GDAPSH09_28    ,  206234 126126 111154 133261 329329 226250
GDAPSH09_29    ,  214226 146154 000000 000000 000000 234234
GDAPSH09_30    ,  198226 170170 131185 141203 000000 234246
GDAPSH09_31    ,  000000 158162 178193 225233 000000 242266
GDAPSH09_32    ,  222222 134174 229266 149193 272272 206206
GDAPSH09_33    ,  202210 134154 166199 137145 280280 000000
GDAPSH09_34    ,  210234 154174 213219 141177 251304 238238
GDAPSH09_35    ,  182198 146158 115154 137149 000000 222230
GDAPSH09_36    ,  194202 170194 154189 145209 329329 254262
GDAPSH09_37    ,  210234 146170 142229 133197 338338 222226
GDAPSH09_38    ,  214238 170198 142239 129149 000000 210226
GDAPSH09_39    ,  222226 158198 000000 113181 000000 238258
GDAPSH09_40    ,  210226 134162 158193 189237 304304 202250
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GDAPSH09_43    ,  198210 134170 154174 145181 000000 238254
GDAPSH09_44    ,  198210 134170 154174 145181 000000 238254
GDAPSH09_45    ,  194210 154174 162185 000000 000000 214226
GDAPSH09_46    ,  190202 142142 185205 121285 000000 238242
GDAPSH09_47    ,  210214 170178 123209 217257 000000 234234
GDAPSH09_48    ,  210210 134158 181225 000000 000000 222230
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GDAPSH09_50    ,  162190 134134 146197 137193 304321 234234
GDAPSH09_51    ,  194206 146146 235255 149273 000000 230238
GDAPSH09_52    ,  194206 146146 235255 149273 276346 230238
GDAPSH09_53    ,  214222 206206 142255 185189 000000 218218
GDAPSH09_54    ,  198230 150174 154231 185209 000000 238242
GDAPSH09_55    ,  186202 146146 154189 213249 268268 210210
GDAPSH09_56    ,  182202 158158 127199 193201 000000 246246
GDAPSH09_57    ,  190246 134134 154241 121141 288288 222254
GDAPSH09_58    ,  190210 162190 201233 141157 260300 000000
GDAPSH09_59    ,  178218 162162 201237 253313 404404 226254
GDAPSH09_60    ,  182214 000000 221284 000000 000000 246262
GDAPSH09_61    ,  174186 134178 131253 129297 000000 230250
GDAPSH09_62    ,  198206 122154 138239 129133 000000 230234
GDAPSH09_63    ,  218226 142194 207229 117221 284292 206234
GDAPSH09_64    ,  218218 170170 131243 121225 000000 222222
GDAPSH09_65    ,  182226 150170 131215 125177 272321 246250
GDAPSH09_66    ,  214234 162170 138223 153317 304325 210234
GDAPSH09_67    ,  194226 150162 134189 157333 338338 238246
GDAPSH09_68    ,  214222 000000 134185 000000 000000 258262
GDAPSH09_69    ,  178182 146182 127134 205205 251251 246258
GDAPSH09_70    ,  222246 150186 197199 000000 000000 250262
GDAPSH09_71    ,  194194 158166 150219 217301 408408 218266
GDAPSH09_72    ,  210218 154170 174261 121133 387387 202234
GDAPSH09_73    ,  210218 142190 119193 125301 292304 222222
GDAPSH09_74    ,  226226 142142 000000 213273 288342 226242
GDAPSH09_75    ,  202214 142142 154213 153221 000000 222226
GDAPSH09_76    ,  210218 166166 205239 129185 284292 222242
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Table S5. Allelic frequencies of 6 microsatellite loci in geoduck clams (*Panopea generosa*). BETAa is the probability that allele-frequency distortion in a sample is due to something other than null alleles. NULL is the maximum likelihood estimate of null alleles. Results from ML-NULLFREQ (Kalinowski 2006).

Sample	Pab101e															
	BETA	NULL	154	158	162	166	170	174	178	182	186	190	194	196	198	200	202
1	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.011	0.033	0.022	0.022	0.038	0.092	0.000	0.033	0.000	0.109
2	0.011	0.001	0.000	0.000	0.005	0.005	0.005	0.016	0.027	0.027	0.037	0.080	0.037	0.000	0.043	0.000	0.096
3	0.000	0.000	0.000	0.000	0.006	0.000	0.011	0.011	0.034	0.028	0.039	0.039	0.073	0.006	0.056	0.000	0.067
4	0.010	0.017	0.000	0.005	0.000	0.005	0.011	0.000	0.032	0.053	0.029	0.053	0.084	0.005	0.048	0.000	0.057
5	0.009	0.035	0.000	0.000	0.000	0.005	0.021	0.000	0.016	0.021	0.032	0.078	0.043	0.000	0.064	0.000	0.059
6	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.006	0.019	0.013	0.038	0.056	0.083	0.000	0.064	0.000	0.076
7	0.011	0.010	0.000	0.000	0.000	0.000	0.000	0.011	0.022	0.027	0.022	0.056	0.065	0.000	0.065	0.000	0.121
8	0.000	0.000	0.000	0.000	0.000	0.008	0.016	0.041	0.008	0.025	0.000	0.033	0.066	0.000	0.074	0.000	0.049
9	0.000	0.003	0.000	0.000	0.000	0.000	0.024	0.000	0.012	0.037	0.073	0.000	0.049	0.000	0.061	0.000	0.024
10	0.011	0.000	0.005	0.000	0.000	0.000	0.011	0.005	0.037	0.021	0.021	0.043	0.074	0.000	0.064	0.000	0.069
11	0.011	0.000	0.000	0.000	0.011	0.006	0.011	0.006	0.029	0.029	0.017	0.080	0.063	0.000	0.080	0.006	0.086
12	0.011	0.006	0.000	0.000	0.000	0.000	0.016	0.000	0.043	0.027	0.022	0.080	0.047	0.005	0.075	0.005	0.081
13	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.057	0.051	0.074	0.057	0.000	0.057	0.000	0.091
14	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.017	0.000	0.042	0.008	0.042	0.076	0.000	0.076	0.000	0.059
15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.021	0.058	0.016	0.047	0.079	0.000	0.068	0.000	0.084
16	0.000	0.016	0.000	0.000	0.007	0.000	0.007	0.007	0.051	0.036	0.051	0.033	0.072	0.000	0.070	0.007	0.092
17	0.000	0.023	0.000	0.000	0.011	0.005	0.000	0.005	0.005	0.022	0.043	0.043	0.068	0.000	0.083	0.005	0.076
18	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.023	0.011	0.034	0.023	0.034	0.034	0.000	0.091	0.000	0.080
19	0.027	0.000	0.000	0.000	0.007	0.000	0.007	0.007	0.035	0.042	0.035	0.049	0.070	0.000	0.077	0.000	0.070

204	206	208	210	212	214	216	218	220	222	226	228	230	232	234	236	238	240
0.000	0.082	0.000	0.130	0.000	0.071	0.000	0.087	0.000	0.082	0.054	0.000	0.065	0.000	0.027	0.000	0.011	0.000
0.000	0.101	0.005	0.096	0.000	0.069	0.000	0.096	0.005	0.090	0.053	0.000	0.043	0.000	0.011	0.000	0.021	0.000
0.000	0.084	0.006	0.112	0.000	0.101	0.006	0.096	0.000	0.073	0.051	0.000	0.056	0.000	0.017	0.000	0.028	0.000
0.000	0.100	0.000	0.116	0.011	0.058	0.000	0.084	0.000	0.084	0.027	0.000	0.048	0.000	0.016	0.000	0.011	0.000
0.000	0.067	0.005	0.114	0.000	0.061	0.005	0.116	0.000	0.070	0.078	0.005	0.038	0.000	0.005	0.000	0.016	0.005
0.000	0.102	0.000	0.133	0.000	0.102	0.006	0.095	0.000	0.045	0.050	0.000	0.032	0.000	0.026	0.000	0.013	0.006
0.000	0.097	0.000	0.065	0.000	0.131	0.000	0.070	0.000	0.065	0.063	0.000	0.043	0.005	0.016	0.000	0.032	0.000
0.000	0.082	0.000	0.139	0.000	0.115	0.000	0.115	0.000	0.107	0.041	0.000	0.041	0.000	0.016	0.000	0.000	0.008
0.000	0.134	0.012	0.097	0.000	0.122	0.000	0.098	0.000	0.061	0.073	0.000	0.035	0.000	0.037	0.000	0.037	0.000
0.000	0.106	0.000	0.096	0.000	0.133	0.000	0.074	0.000	0.074	0.043	0.011	0.059	0.000	0.016	0.000	0.000	0.000
0.000	0.075	0.000	0.080	0.000	0.121	0.000	0.092	0.000	0.040	0.069	0.006	0.029	0.006	0.023	0.000	0.017	0.006
0.005	0.038	0.000	0.160	0.000	0.065	0.000	0.091	0.000	0.070	0.054	0.005	0.032	0.000	0.019	0.000	0.038	0.005
0.000	0.091	0.006	0.108	0.000	0.102	0.000	0.085	0.000	0.062	0.028	0.000	0.040	0.000	0.040	0.000	0.017	0.000
0.008	0.085	0.008	0.093	0.017	0.127	0.000	0.127	0.000	0.085	0.042	0.000	0.042	0.000	0.034	0.000	0.000	0.000
0.000	0.074	0.000	0.058	0.000	0.121	0.000	0.079	0.005	0.095	0.058	0.005	0.032	0.000	0.037	0.000	0.037	0.000

0.000	0.085	0.000	0.122	0.000	0.072	0.000	0.048	0.000	0.085	0.029	0.007	0.022	0.000	0.022	0.007	0.029	0.000
0.000	0.085	0.016	0.089	0.000	0.083	0.000	0.060	0.000	0.092	0.068	0.005	0.043	0.000	0.027	0.000	0.022	0.000
0.000	0.091	0.000	0.102	0.011	0.125	0.000	0.080	0.000	0.068	0.057	0.000	0.057	0.000	0.011	0.000	0.011	0.000
0.000	0.063	0.000	0.148	0.000	0.085	0.000	0.070	0.000	0.077	0.070	0.000	0.021	0.000	0.028	0.000	0.007	0.000

242	246	250	254	258	262	266	270	274	292
0.016	0.005	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000
0.005	0.021	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.016	0.016	0.005	0.005	0.000	0.000	0.000	0.000	0.000	0.005
0.011	0.011	0.005	0.000	0.000	0.005	0.000	0.000	0.005	0.000
0.019	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.016	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.008	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.021	0.000	0.005	0.005	0.000	0.000	0.000	0.005	0.000	0.000
0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000
0.000	0.000	0.005	0.005	0.000	0.000	0.000	0.000	0.000	0.000
0.023	0.000	0.000	0.006	0.006	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.021	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.007	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.007	0.000
0.005	0.000	0.000	0.005	0.000	0.005	0.000	0.000	0.000	0.000
0.000	0.000	0.034	0.000	0.000	0.000	0.000	0.000	0.011	0.000
0.007	0.014	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Sample Pab105e

	BETA	NULL	122	126	130	134	138	140	142	146	150	154	156	158	160	162	166	168
1	0.001	0.144	0.000	0.022	0.000	0.079	0.046	0.000	0.034	0.039	0.039	0.092	0.000	0.045	0.000	0.098	0.066	0.000
2	0.023	0.141	0.000	0.022	0.000	0.069	0.038	0.000	0.044	0.027	0.039	0.066	0.000	0.079	0.000	0.117	0.055	0.000
3	0.009	0.115	0.000	0.017	0.000	0.059	0.023	0.000	0.053	0.046	0.058	0.092	0.000	0.065	0.000	0.052	0.082	0.000
4	0.000	0.180	0.000	0.016	0.005	0.076	0.049	0.005	0.088	0.022	0.026	0.048	0.000	0.049	0.000	0.088	0.049	0.000
5	0.000	0.157	0.000	0.033	0.000	0.050	0.016	0.005	0.043	0.038	0.065	0.091	0.005	0.063	0.000	0.100	0.054	0.005
6	0.000	0.192	0.000	0.040	0.000	0.087	0.033	0.000	0.060	0.006	0.006	0.047	0.006	0.088	0.006	0.053	0.086	0.000
7	0.028	0.067	0.000	0.016	0.000	0.069	0.011	0.000	0.056	0.016	0.038	0.106	0.000	0.103	0.000	0.111	0.081	0.000
8	0.000	0.119	0.000	0.025	0.000	0.078	0.000	0.000	0.071	0.025	0.033	0.112	0.000	0.074	0.000	0.041	0.052	0.008
9	0.016	0.090	0.000	0.012	0.000	0.050	0.037	0.000	0.086	0.037	0.074	0.122	0.000	0.039	0.000	0.012	0.025	0.000
10	0.000	0.205	0.005	0.048	0.000	0.038	0.048	0.000	0.060	0.032	0.038	0.048	0.000	0.054	0.000	0.048	0.060	0.000
11	0.012	0.148	0.000	0.018	0.000	0.078	0.036	0.000	0.060	0.054	0.053	0.052	0.000	0.054	0.000	0.071	0.071	0.000
12	0.000	0.151	0.000	0.016	0.000	0.055	0.033	0.005	0.032	0.037	0.055	0.049	0.000	0.072	0.000	0.095	0.053	0.000
13	0.000	0.158	0.000	0.040	0.000	0.063	0.017	0.006	0.060	0.017	0.066	0.064	0.000	0.053	0.000	0.046	0.072	0.000

14	0.018	0.126	0.000	0.009	0.000	0.055	0.000	0.000	0.075	0.046	0.043	0.060	0.009	0.112	0.000	0.073	0.086	0.000
15	0.000	0.211	0.000	0.016	0.000	0.037	0.026	0.000	0.075	0.027	0.077	0.043	0.000	0.079	0.000	0.038	0.054	0.000
16	0.000	0.212	0.000	0.036	0.000	0.043	0.052	0.000	0.015	0.030	0.037	0.067	0.000	0.045	0.007	0.091	0.052	0.000
17	0.000	0.119	0.000	0.016	0.000	0.038	0.033	0.000	0.022	0.038	0.066	0.054	0.000	0.063	0.000	0.062	0.093	0.000
18	0.000	0.097	0.000	0.074	0.000	0.091	0.023	0.000	0.057	0.034	0.011	0.062	0.000	0.141	0.000	0.038	0.071	0.000
19	0.034	0.145	0.007	0.015	0.000	0.105	0.014	0.021	0.069	0.053	0.035	0.057	0.000	0.074	0.000	0.051	0.036	0.000

170	174	176	178	180	182	183	186	190	194	196	198	202	206	210	214	218	226
0.092	0.045	0.005	0.028	0.000	0.017	0.000	0.038	0.022	0.039	0.000	0.000	0.000	0.005	0.000	0.000	0.005	0.000
0.080	0.066	0.000	0.044	0.000	0.038	0.000	0.016	0.032	0.005	0.000	0.011	0.005	0.000	0.000	0.005	0.000	0.000
0.080	0.051	0.000	0.068	0.000	0.048	0.000	0.023	0.017	0.017	0.000	0.006	0.017	0.006	0.000	0.006	0.000	0.000
0.055	0.067	0.000	0.037	0.005	0.021	0.005	0.027	0.021	0.032	0.000	0.016	0.000	0.005	0.005	0.000	0.000	0.000
0.032	0.032	0.000	0.032	0.005	0.032	0.000	0.032	0.032	0.021	0.000	0.021	0.016	0.011	0.000	0.005	0.000	0.000
0.069	0.058	0.000	0.078	0.000	0.013	0.000	0.020	0.000	0.006	0.000	0.020	0.000	0.026	0.000	0.000	0.000	0.000
0.081	0.064	0.000	0.064	0.000	0.022	0.000	0.027	0.000	0.005	0.000	0.023	0.005	0.011	0.005	0.011	0.005	0.000
0.126	0.061	0.000	0.025	0.000	0.042	0.000	0.017	0.042	0.008	0.008	0.016	0.008	0.000	0.008	0.000	0.000	0.000
0.109	0.062	0.000	0.095	0.000	0.050	0.000	0.062	0.000	0.012	0.000	0.000	0.000	0.012	0.012	0.000	0.000	0.000
0.060	0.085	0.000	0.053	0.000	0.032	0.005	0.027	0.021	0.005	0.005	0.005	0.011	0.000	0.005	0.000	0.000	0.000
0.061	0.064	0.006	0.053	0.000	0.023	0.000	0.017	0.029	0.017	0.006	0.006	0.012	0.000	0.006	0.006	0.000	0.000
0.114	0.071	0.000	0.027	0.000	0.032	0.000	0.016	0.021	0.027	0.000	0.011	0.011	0.011	0.005	0.000	0.000	0.000
0.046	0.070	0.000	0.052	0.006	0.070	0.000	0.023	0.023	0.011	0.000	0.006	0.011	0.006	0.011	0.000	0.000	0.000
0.071	0.069	0.000	0.062	0.000	0.026	0.000	0.026	0.018	0.009	0.000	0.009	0.000	0.009	0.000	0.000	0.000	0.009
0.064	0.059	0.000	0.043	0.000	0.044	0.000	0.038	0.027	0.011	0.000	0.011	0.011	0.005	0.005	0.000	0.000	0.000
0.091	0.059	0.000	0.022	0.000	0.052	0.000	0.015	0.022	0.022	0.000	0.014	0.007	0.000	0.007	0.000	0.000	0.000
0.131	0.071	0.000	0.040	0.000	0.070	0.000	0.027	0.023	0.000	0.000	0.005	0.011	0.011	0.000	0.000	0.000	0.006
0.091	0.045	0.000	0.048	0.000	0.023	0.000	0.036	0.034	0.000	0.000	0.000	0.012	0.011	0.000	0.000	0.000	0.000
0.096	0.078	0.000	0.021	0.000	0.022	0.000	0.014	0.021	0.029	0.000	0.014	0.000	0.015	0.000	0.007	0.000	0.000

Sample	Pab106e																
	BETA	NULL	103	107	111	115	119	123	127	129	131	133	134	136	138	142	146
1	0.011	0.003	0.005	0.016	0.005	0.044	0.027	0.027	0.038	0.000	0.022	0.000	0.038	0.000	0.022	0.038	0.011
2	0.021	0.003	0.016	0.016	0.005	0.032	0.043	0.032	0.048	0.000	0.048	0.000	0.038	0.000	0.032	0.011	0.032
3	0.000	0.008	0.006	0.006	0.006	0.011	0.011	0.039	0.017	0.000	0.028	0.000	0.028	0.000	0.022	0.017	0.022
4	0.010	0.009	0.000	0.021	0.011	0.027	0.000	0.011	0.032	0.000	0.035	0.000	0.057	0.000	0.021	0.021	0.048
5	0.021	0.000	0.005	0.000	0.005	0.038	0.049	0.022	0.027	0.000	0.033	0.000	0.022	0.000	0.038	0.022	0.033
6	0.000	0.000	0.000	0.006	0.013	0.038	0.019	0.013	0.013	0.000	0.051	0.000	0.051	0.000	0.070	0.038	0.032
7	0.000	0.004	0.005	0.005	0.005	0.027	0.043	0.016	0.016	0.000	0.043	0.000	0.021	0.000	0.027	0.011	0.025
8	0.016	0.000	0.000	0.008	0.017	0.033	0.033	0.050	0.033	0.000	0.033	0.000	0.017	0.000	0.033	0.017	0.025
9	0.024	0.000	0.000	0.013	0.013	0.025	0.025	0.038	0.038	0.000	0.063	0.000	0.038	0.000	0.013	0.038	0.013

10	0.000	0.000	0.016	0.016	0.011	0.011	0.037	0.032	0.026	0.000	0.032	0.000	0.042	0.000	0.042	0.026	0.037
11	0.011	0.002	0.000	0.006	0.023	0.006	0.034	0.040	0.029	0.000	0.046	0.000	0.022	0.000	0.017	0.034	0.029
12	0.032	0.000	0.000	0.016	0.016	0.005	0.049	0.027	0.049	0.005	0.022	0.000	0.055	0.000	0.027	0.049	0.049
13	0.000	0.000	0.006	0.011	0.017	0.028	0.040	0.028	0.028	0.000	0.017	0.000	0.040	0.000	0.023	0.017	0.006
14	0.017	0.000	0.000	0.009	0.009	0.034	0.026	0.052	0.043	0.000	0.034	0.009	0.026	0.000	0.043	0.009	0.026
15	0.000	0.002	0.005	0.000	0.011	0.021	0.032	0.032	0.026	0.000	0.020	0.000	0.016	0.005	0.026	0.021	0.047
16	0.014	0.000	0.007	0.015	0.015	0.037	0.044	0.007	0.059	0.000	0.022	0.000	0.066	0.000	0.007	0.029	0.022
17	0.011	0.003	0.000	0.016	0.016	0.016	0.044	0.016	0.044	0.000	0.044	0.000	0.060	0.000	0.038	0.049	0.033
18	0.023	0.000	0.000	0.012	0.000	0.000	0.023	0.023	0.000	0.000	0.023	0.000	0.035	0.000	0.058	0.012	0.012
19	0.041	0.000	0.000	0.007	0.014	0.021	0.014	0.021	0.029	0.000	0.036	0.000	0.029	0.000	0.029	0.021	0.007

150	154	156	158	160	162	164	166	168	170	172	174	176	178	180	181	183	185
0.021	0.033	0.000	0.016	0.000	0.016	0.000	0.005	0.000	0.011	0.000	0.011	0.000	0.011	0.000	0.005	0.005	0.022
0.048	0.016	0.000	0.005	0.000	0.016	0.000	0.005	0.000	0.011	0.005	0.022	0.005	0.022	0.000	0.000	0.022	0.022
0.039	0.011	0.000	0.022	0.000	0.028	0.000	0.006	0.000	0.011	0.000	0.006	0.000	0.017	0.000	0.028	0.011	0.011
0.027	0.027	0.000	0.005	0.000	0.021	0.000	0.011	0.000	0.005	0.000	0.000	0.005	0.021	0.000	0.027	0.005	0.021
0.005	0.011	0.000	0.016	0.000	0.022	0.000	0.016	0.005	0.000	0.000	0.022	0.000	0.011	0.000	0.011	0.000	0.000
0.026	0.026	0.000	0.000	0.000	0.019	0.000	0.013	0.000	0.019	0.000	0.026	0.013	0.045	0.000	0.019	0.000	0.013
0.021	0.037	0.005	0.048	0.000	0.005	0.000	0.021	0.000	0.000	0.005	0.043	0.000	0.032	0.000	0.021	0.000	0.011
0.033	0.025	0.000	0.058	0.000	0.000	0.000	0.017	0.008	0.042	0.000	0.017	0.000	0.000	0.000	0.017	0.008	0.017
0.025	0.025	0.000	0.025	0.013	0.013	0.000	0.000	0.000	0.025	0.000	0.013	0.000	0.013	0.000	0.050	0.000	0.000
0.016	0.042	0.000	0.021	0.000	0.021	0.000	0.011	0.000	0.016	0.000	0.000	0.000	0.011	0.005	0.016	0.011	0.016
0.006	0.023	0.000	0.029	0.000	0.011	0.000	0.017	0.000	0.006	0.000	0.011	0.006	0.034	0.000	0.029	0.006	0.017
0.049	0.027	0.000	0.011	0.000	0.016	0.000	0.011	0.005	0.016	0.005	0.022	0.000	0.000	0.000	0.016	0.011	0.022
0.017	0.017	0.000	0.017	0.006	0.011	0.000	0.017	0.000	0.023	0.006	0.011	0.000	0.006	0.000	0.023	0.000	0.034
0.026	0.009	0.000	0.000	0.000	0.026	0.000	0.009	0.017	0.000	0.009	0.026	0.000	0.009	0.009	0.009	0.026	0.009
0.021	0.016	0.000	0.016	0.000	0.016	0.000	0.011	0.000	0.011	0.000	0.005	0.000	0.000	0.000	0.021	0.015	0.011
0.015	0.007	0.000	0.029	0.000	0.022	0.007	0.029	0.000	0.029	0.000	0.007	0.000	0.015	0.000	0.007	0.007	0.015
0.011	0.022	0.000	0.000	0.000	0.005	0.005	0.011	0.000	0.005	0.005	0.011	0.000	0.011	0.000	0.011	0.000	0.016
0.023	0.058	0.000	0.012	0.000	0.012	0.012	0.035	0.000	0.023	0.000	0.023	0.000	0.023	0.000	0.012	0.000	0.058
0.036	0.064	0.000	0.007	0.007	0.014	0.000	0.007	0.000	0.000	0.000	0.029	0.000	0.021	0.000	0.014	0.007	0.036

187	189	191	193	195	196	197	199	200	201	203	205	207	209	211	213	215	217
0.005	0.005	0.005	0.033	0.005	0.005	0.016	0.016	0.000	0.022	0.005	0.011	0.005	0.022	0.016	0.022	0.022	0.027
0.005	0.011	0.000	0.032	0.011	0.000	0.016	0.016	0.000	0.022	0.005	0.022	0.016	0.005	0.000	0.016	0.011	0.011
0.006	0.022	0.006	0.062	0.000	0.006	0.028	0.017	0.000	0.022	0.011	0.028	0.006	0.006	0.007	0.028	0.034	0.011
0.000	0.000	0.016	0.037	0.016	0.000	0.016	0.016	0.000	0.016	0.016	0.037	0.005	0.011	0.013	0.027	0.016	0.011
0.000	0.016	0.011	0.038	0.016	0.000	0.005	0.000	0.000	0.033	0.005	0.016	0.011	0.027	0.011	0.011	0.027	0.022
0.000	0.006	0.000	0.045	0.006	0.000	0.006	0.000	0.000	0.019	0.000	0.006	0.013	0.013	0.000	0.026	0.000	0.019
0.005	0.005	0.005	0.027	0.016	0.000	0.000	0.021	0.000	0.016	0.000	0.016	0.000	0.021	0.000	0.016	0.011	0.011

0.000	0.025	0.008	0.033	0.000	0.000	0.033	0.017	0.000	0.008	0.017	0.025	0.000	0.017	0.042	0.017	0.000	0.008
0.000	0.038	0.000	0.038	0.000	0.000	0.025	0.013	0.000	0.013	0.000	0.025	0.013	0.013	0.000	0.038	0.038	0.000
0.011	0.021	0.005	0.021	0.005	0.000	0.016	0.005	0.000	0.026	0.011	0.026	0.021	0.016	0.005	0.026	0.000	0.016
0.000	0.016	0.011	0.029	0.017	0.000	0.029	0.017	0.006	0.023	0.006	0.011	0.011	0.034	0.011	0.023	0.017	0.011
0.000	0.011	0.005	0.027	0.005	0.000	0.033	0.011	0.005	0.016	0.000	0.005	0.016	0.000	0.011	0.022	0.011	0.011
0.006	0.017	0.011	0.045	0.017	0.000	0.023	0.006	0.000	0.028	0.006	0.045	0.023	0.006	0.023	0.028	0.000	0.006
0.017	0.017	0.000	0.034	0.026	0.000	0.009	0.017	0.000	0.052	0.000	0.009	0.017	0.034	0.009	0.017	0.009	0.000
0.005	0.042	0.005	0.032	0.005	0.000	0.021	0.016	0.000	0.026	0.026	0.026	0.021	0.011	0.026	0.026	0.011	0.026
0.000	0.044	0.000	0.029	0.007	0.000	0.037	0.000	0.000	0.000	0.007	0.044	0.007	0.007	0.007	0.022	0.015	0.029
0.005	0.016	0.000	0.038	0.005	0.000	0.033	0.000	0.000	0.033	0.022	0.032	0.027	0.011	0.022	0.016	0.005	0.000
0.000	0.012	0.000	0.035	0.012	0.000	0.023	0.012	0.000	0.035	0.000	0.012	0.012	0.012	0.023	0.012	0.012	0.000
0.000	0.021	0.029	0.043	0.007	0.000	0.036	0.021	0.000	0.021	0.000	0.021	0.014	0.007	0.007	0.014	0.014	0.007

219	221	223	225	227	229	231	233	235	237	239	241	243	245	247	249	251	253
0.027	0.016	0.026	0.011	0.016	0.027	0.011	0.011	0.005	0.016	0.016	0.011	0.000	0.000	0.005	0.011	0.005	0.005
0.022	0.032	0.016	0.011	0.022	0.027	0.000	0.016	0.014	0.005	0.031	0.005	0.000	0.005	0.000	0.000	0.005	0.005
0.028	0.026	0.017	0.017	0.006	0.022	0.022	0.011	0.000	0.011	0.011	0.006	0.026	0.017	0.006	0.006	0.011	0.006
0.037	0.005	0.005	0.016	0.021	0.011	0.005	0.005	0.021	0.021	0.016	0.011	0.005	0.005	0.000	0.005	0.019	0.011
0.016	0.016	0.022	0.011	0.005	0.027	0.005	0.027	0.016	0.022	0.005	0.016	0.027	0.005	0.011	0.016	0.005	0.005
0.006	0.013	0.013	0.026	0.019	0.019	0.013	0.013	0.013	0.000	0.025	0.013	0.013	0.013	0.006	0.013	0.006	0.000
0.016	0.016	0.016	0.021	0.032	0.043	0.011	0.021	0.016	0.005	0.025	0.005	0.016	0.021	0.021	0.005	0.005	0.000
0.008	0.008	0.025	0.000	0.042	0.008	0.025	0.017	0.000	0.000	0.008	0.008	0.000	0.000	0.000	0.008	0.008	0.000
0.050	0.013	0.025	0.000	0.013	0.037	0.013	0.025	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.013	0.000
0.011	0.005	0.011	0.000	0.021	0.032	0.021	0.011	0.005	0.021	0.032	0.000	0.011	0.000	0.005	0.011	0.000	0.005
0.011	0.029	0.023	0.011	0.011	0.023	0.011	0.011	0.000	0.006	0.006	0.023	0.017	0.011	0.006	0.006	0.000	0.017
0.038	0.022	0.011	0.000	0.005	0.016	0.016	0.016	0.011	0.005	0.005	0.011	0.016	0.000	0.005	0.005	0.000	0.000
0.011	0.017	0.017	0.017	0.040	0.023	0.006	0.023	0.006	0.028	0.017	0.006	0.000	0.011	0.011	0.006	0.000	0.000
0.009	0.017	0.017	0.034	0.017	0.017	0.000	0.009	0.009	0.000	0.000	0.017	0.009	0.000	0.017	0.009	0.000	0.000
0.011	0.011	0.011	0.005	0.021	0.032	0.026	0.011	0.000	0.011	0.011	0.011	0.016	0.005	0.011	0.005	0.005	0.000
0.015	0.000	0.000	0.007	0.037	0.022	0.007	0.029	0.000	0.000	0.007	0.015	0.022	0.000	0.007	0.007	0.000	0.000
0.016	0.000	0.005	0.016	0.022	0.038	0.016	0.005	0.005	0.011	0.005	0.000	0.011	0.011	0.016	0.016	0.000	0.000
0.000	0.012	0.012	0.000	0.035	0.035	0.023	0.035	0.000	0.012	0.000	0.000	0.023	0.000	0.000	0.012	0.035	0.000
0.014	0.007	0.014	0.007	0.000	0.036	0.007	0.014	0.021	0.014	0.021	0.007	0.014	0.000	0.014	0.007	0.000	0.007

255	257	259	261	262	264	266	268	270	272	274	276	278	280	282	284	286	288
0.000	0.000	0.011	0.011	0.000	0.000	0.011	0.000	0.005	0.005	0.005	0.011	0.000	0.000	0.005	0.000	0.000	0.000
0.005	0.000	0.011	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.006	0.000	0.000	0.000	0.006	0.011	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.006	0.000

0.000	0.021	0.011	0.000	0.000	0.005	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000
0.005	0.016	0.005	0.000	0.000	0.000	0.011	0.000	0.005	0.005	0.011	0.000	0.005	0.000	0.000	0.000	0.000	0.000
0.000	0.013	0.000	0.013	0.000	0.000	0.006	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.011	0.000	0.020	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.008	0.000	0.000	0.008	0.000	0.008	0.000	0.000
0.013	0.013	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.011	0.016	0.000	0.005	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.005
0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.005	0.000	0.000	0.000	0.011	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.006	0.011	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.009	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000
0.005	0.011	0.005	0.005	0.000	0.005	0.000	0.005	0.000	0.000	0.000	0.000	0.005	0.011	0.000	0.005	0.000	0.000
0.000	0.015	0.000	0.000	0.007	0.007	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.005	0.000	0.005	0.000	0.015	0.005	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000
0.000	0.012	0.012	0.012	0.000	0.000	0.000	0.012	0.012	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
0.029	0.000	0.000	0.014	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000

290	298	300	306	308	311	313	315	317	327	333	347
0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.005	0.000
0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.005
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.009	0.009	0.000
0.000	0.005	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Sample		Pab112e															
	BETA	NULL	105	109	113	117	121	125	129	133	137	141	145	149	153	157	161
1	0.000	0.006	0.000	0.000	0.016	0.005	0.016	0.016	0.043	0.016	0.027	0.033	0.027	0.054	0.027	0.022	0.027
2	0.032	0.002	0.005	0.000	0.000	0.027	0.022	0.038	0.033	0.038	0.038	0.054	0.043	0.022	0.022	0.022	0.027
3	0.011	0.014	0.000	0.000	0.011	0.019	0.017	0.034	0.011	0.051	0.043	0.040	0.072	0.023	0.040	0.028	0.028
4	0.000	0.015	0.000	0.000	0.005	0.016	0.021	0.026	0.026	0.047	0.021	0.034	0.047	0.029	0.032	0.042	0.021
5	0.021	0.000	0.005	0.005	0.011	0.005	0.016	0.043	0.038	0.011	0.027	0.043	0.043	0.060	0.016	0.033	0.022
6	0.000	0.011	0.000	0.006	0.006	0.026	0.006	0.006	0.045	0.026	0.083	0.051	0.019	0.036	0.071	0.019	0.038
7	0.074	0.000	0.000	0.006	0.006	0.017	0.017	0.052	0.046	0.075	0.023	0.034	0.040	0.057	0.034	0.023	0.011
8	0.016	0.000	0.000	0.000	0.008	0.008	0.008	0.042	0.008	0.025	0.050	0.042	0.083	0.042	0.025	0.025	0.042
9	0.000	0.000	0.012	0.000	0.000	0.024	0.012	0.037	0.037	0.037	0.049	0.024	0.012	0.037	0.037	0.049	0.024
10	0.011	0.000	0.000	0.000	0.005	0.005	0.037	0.021	0.037	0.043	0.074	0.037	0.064	0.053	0.021	0.016	0.011
11	0.023	0.000	0.000	0.000	0.006	0.000	0.006	0.023	0.035	0.023	0.081	0.070	0.081	0.023	0.052	0.023	0.012
12	0.011	0.000	0.000	0.000	0.011	0.005	0.022	0.038	0.005	0.027	0.048	0.054	0.054	0.054	0.038	0.027	0.016
13	0.034	0.014	0.000	0.000	0.018	0.018	0.006	0.029	0.018	0.024	0.065	0.055	0.041	0.012	0.047	0.045	0.012
14	0.034	0.000	0.000	0.000	0.018	0.035	0.009	0.035	0.035	0.018	0.061	0.044	0.061	0.026	0.035	0.035	0.000
15	0.042	0.016	0.000	0.000	0.013	0.022	0.005	0.016	0.038	0.030	0.049	0.055	0.066	0.030	0.027	0.038	0.022
16	0.000	0.000	0.000	0.000	0.022	0.022	0.029	0.014	0.051	0.022	0.036	0.014	0.072	0.043	0.036	0.022	0.051
17	0.011	0.018	0.005	0.011	0.022	0.022	0.044	0.022	0.038	0.044	0.033	0.030	0.085	0.016	0.027	0.045	0.016
18	0.000	0.000	0.000	0.011	0.000	0.011	0.034	0.023	0.000	0.034	0.091	0.034	0.034	0.034	0.034	0.023	0.023
19	0.137	0.000	0.000	0.000	0.008	0.008	0.040	0.032	0.056	0.040	0.040	0.071	0.048	0.056	0.024	0.016	0.000

Sample	165	169	173	177	181	185	189	193	197	201	203	205	209	213	217	221	225	229
1	0.042	0.022	0.022	0.033	0.027	0.033	0.005	0.027	0.033	0.011	0.000	0.027	0.022	0.033	0.033	0.016	0.011	0.031
2	0.016	0.011	0.016	0.027	0.027	0.049	0.016	0.033	0.027	0.016	0.000	0.027	0.033	0.021	0.016	0.038	0.027	0.005
3	0.017	0.000	0.011	0.034	0.045	0.006	0.023	0.040	0.023	0.041	0.000	0.011	0.023	0.034	0.023	0.049	0.023	0.011
4	0.021	0.026	0.011	0.037	0.068	0.021	0.037	0.011	0.042	0.021	0.000	0.026	0.016	0.021	0.032	0.026	0.016	0.005
5	0.022	0.033	0.033	0.027	0.011	0.038	0.022	0.038	0.065	0.011	0.000	0.016	0.027	0.027	0.016	0.027	0.000	0.027
6	0.006	0.032	0.032	0.006	0.022	0.013	0.043	0.022	0.006	0.032	0.000	0.019	0.006	0.026	0.026	0.013	0.019	0.006
7	0.029	0.011	0.011	0.029	0.017	0.046	0.017	0.029	0.034	0.034	0.000	0.046	0.046	0.006	0.017	0.029	0.006	0.006
8	0.008	0.017	0.017	0.025	0.017	0.025	0.058	0.025	0.033	0.042	0.000	0.050	0.017	0.017	0.000	0.025	0.025	0.017
9	0.024	0.024	0.049	0.012	0.024	0.037	0.049	0.012	0.061	0.000	0.000	0.012	0.012	0.012	0.024	0.012	0.000	0.024
10	0.032	0.000	0.021	0.021	0.043	0.027	0.011	0.016	0.043	0.021	0.000	0.005	0.021	0.011	0.021	0.037	0.021	0.011
11	0.017	0.000	0.029	0.012	0.052	0.017	0.029	0.041	0.029	0.017	0.006	0.012	0.035	0.029	0.017	0.006	0.012	0.017
12	0.022	0.016	0.032	0.027	0.016	0.027	0.022	0.032	0.043	0.032	0.000	0.038	0.016	0.038	0.016	0.032	0.011	0.022
13	0.018	0.024	0.006	0.014	0.020	0.024	0.047	0.018	0.035	0.029	0.000	0.041	0.018	0.018	0.000	0.012	0.024	0.006
14	0.009	0.000	0.044	0.009	0.026	0.018	0.018	0.026	0.026	0.026	0.000	0.026	0.018	0.026	0.000	0.018	0.000	0.000
15	0.027	0.011	0.016	0.038	0.030	0.027	0.038	0.022	0.022	0.027	0.000	0.033	0.016	0.022	0.024	0.027	0.005	0.000
16	0.029	0.029	0.022	0.007	0.022	0.029	0.036	0.014	0.007	0.022	0.000	0.029	0.014	0.029	0.043	0.014	0.036	0.007
17	0.011	0.011	0.016	0.011	0.011	0.038	0.053	0.038	0.005	0.044	0.000	0.022	0.016	0.038	0.027	0.000	0.011	0.005

0.011	0.011	0.011	0.011	0.011	0.057	0.023	0.011	0.045	0.011	0.000	0.068	0.000	0.011	0.011	0.023	0.023	0.000
0.000	0.000	0.008	0.040	0.056	0.032	0.032	0.040	0.016	0.024	0.008	0.032	0.024	0.016	0.024	0.024	0.016	0.000

233	237	241	245	249	253	257	261	265	269	273	277	281	285	289	293	297	301
0.011	0.005	0.000	0.016	0.016	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.011	0.000	0.000	0.022	0.000
0.016	0.016	0.005	0.005	0.005	0.005	0.016	0.005	0.000	0.011	0.011	0.000	0.000	0.005	0.005	0.005	0.000	0.000
0.006	0.000	0.006	0.006	0.006	0.000	0.000	0.006	0.000	0.000	0.006	0.006	0.006	0.011	0.000	0.000	0.006	0.000
0.005	0.005	0.000	0.000	0.000	0.005	0.005	0.005	0.000	0.011	0.005	0.005	0.000	0.011	0.011	0.021	0.000	0.005
0.005	0.016	0.000	0.005	0.005	0.011	0.005	0.000	0.000	0.000	0.000	0.005	0.005	0.000	0.005	0.000	0.000	0.016
0.006	0.006	0.013	0.006	0.000	0.006	0.000	0.019	0.006	0.006	0.013	0.000	0.000	0.006	0.000	0.006	0.006	0.000
0.011	0.011	0.006	0.000	0.006	0.006	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.006	0.006	0.017	0.000
0.017	0.017	0.008	0.008	0.000	0.000	0.008	0.000	0.000	0.008	0.000	0.000	0.017	0.008	0.000	0.017	0.008	0.000
0.024	0.024	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.012	0.000	0.000	0.024	0.012	0.000	0.012	0.000	0.000
0.011	0.005	0.000	0.016	0.011	0.005	0.005	0.011	0.005	0.005	0.000	0.011	0.005	0.000	0.016	0.005	0.005	0.011
0.029	0.012	0.006	0.012	0.012	0.012	0.000	0.006	0.000	0.006	0.000	0.000	0.006	0.000	0.000	0.006	0.006	0.006
0.011	0.000	0.011	0.005	0.005	0.016	0.005	0.000	0.011	0.000	0.000	0.005	0.000	0.011	0.000	0.016	0.005	0.005
0.006	0.012	0.006	0.006	0.000	0.000	0.000	0.006	0.006	0.000	0.006	0.006	0.006	0.006	0.018	0.012	0.006	0.006
0.018	0.009	0.018	0.000	0.018	0.000	0.026	0.000	0.018	0.000	0.000	0.009	0.000	0.000	0.000	0.026	0.018	0.026
0.005	0.000	0.000	0.005	0.000	0.000	0.005	0.005	0.000	0.005	0.000	0.011	0.005	0.005	0.000	0.000	0.022	0.005
0.014	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.007	0.000	0.000	0.000	0.029
0.005	0.011	0.000	0.000	0.000	0.000	0.005	0.005	0.005	0.005	0.000	0.000	0.005	0.000	0.000	0.005	0.000	0.000
0.011	0.011	0.000	0.000	0.000	0.000	0.000	0.034	0.023	0.000	0.011	0.023	0.000	0.000	0.011	0.000	0.011	0.011
0.008	0.008	0.000	0.000	0.016	0.008	0.008	0.008	0.000	0.000	0.024	0.000	0.000	0.008	0.008	0.000	0.008	0.016

305	309	313	317	321	325	329	333	337	341	345	349	353	357	361	365	369	373
0.011	0.027	0.005	0.005	0.000	0.000	0.007	0.011	0.011	0.000	0.005	0.011	0.011	0.011	0.016	0.000	0.000	0.005
0.016	0.005	0.011	0.005	0.005	0.015	0.000	0.000	0.000	0.005	0.005	0.016	0.000	0.000	0.000	0.000	0.000	0.000
0.028	0.006	0.000	0.000	0.011	0.011	0.000	0.006	0.000	0.011	0.000	0.000	0.000	0.006	0.006	0.000	0.000	0.000
0.011	0.011	0.016	0.000	0.005	0.005	0.006	0.000	0.011	0.005	0.005	0.000	0.000	0.005	0.000	0.005	0.000	0.000
0.005	0.005	0.005	0.005	0.005	0.005	0.016	0.005	0.016	0.011	0.000	0.000	0.005	0.000	0.011	0.000	0.000	0.000
0.038	0.019	0.000	0.000	0.000	0.000	0.006	0.013	0.006	0.000	0.013	0.006	0.000	0.000	0.013	0.000	0.000	0.000
0.011	0.000	0.006	0.006	0.006	0.006	0.006	0.000	0.006	0.000	0.000	0.006	0.011	0.006	0.000	0.000	0.000	0.000
0.008	0.000	0.000	0.017	0.008	0.000	0.008	0.000	0.000	0.008	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000
0.000	0.024	0.012	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.024	0.000	0.000	0.000	0.012	0.000	0.000
0.005	0.011	0.011	0.016	0.005	0.000	0.000	0.000	0.000	0.011	0.005	0.005	0.000	0.005	0.000	0.000	0.000	0.005
0.012	0.006	0.012	0.000	0.006	0.000	0.006	0.000	0.006	0.012	0.000	0.000	0.006	0.000	0.006	0.000	0.000	0.000
0.005	0.000	0.016	0.000	0.005	0.005	0.005	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.005	0.000	0.005	0.000
0.012	0.012	0.018	0.006	0.012	0.006	0.006	0.012	0.000	0.006	0.012	0.012	0.000	0.006	0.000	0.012	0.006	0.006

0.018	0.009	0.026	0.009	0.000	0.000	0.018	0.000	0.000	0.009	0.000	0.009	0.000	0.000	0.009	0.000	0.000	0.000
0.011	0.011	0.027	0.005	0.016	0.011	0.000	0.011	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.007	0.014	0.000	0.000	0.014	0.014	0.000	0.007	0.022	0.000	0.014	0.000	0.007	0.000	0.000	0.000	0.000	0.000
0.005	0.011	0.016	0.005	0.005	0.000	0.005	0.000	0.011	0.012	0.005	0.005	0.005	0.011	0.005	0.000	0.000	0.000
0.000	0.000	0.000	0.011	0.000	0.034	0.000	0.011	0.011	0.000	0.023	0.011	0.000	0.011	0.000	0.000	0.000	0.000
0.000	0.008	0.016	0.008	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.008

377	381	397	401	405
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.006	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.005	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.009	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.007	0.000	0.000	0.000
0.000	0.000	0.005	0.000	0.000
0.000	0.000	0.000	0.000	0.011
0.000	0.000	0.000	0.000	0.000

Sample		Pab117															
	BETA	NULL	198	206	210	218	222	226	230	235	239	243	247	251	255	260	264
1	0.014	0.087	0.006	0.000	0.000	0.006	0.000	0.000	0.006	0.006	0.006	0.011	0.000	0.017	0.011	0.011	0.011
2	0.029	0.056	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.005	0.011	0.023	0.022	0.005
3	0.020	0.054	0.000	0.000	0.000	0.000	0.011	0.006	0.000	0.006	0.000	0.000	0.006	0.017	0.006	0.011	0.023
4	0.019	0.045	0.000	0.005	0.000	0.000	0.000	0.005	0.011	0.000	0.011	0.000	0.016	0.011	0.000	0.021	0.016
5	0.033	0.101	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.016	0.011	0.011	0.016
6	0.000	0.058	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.019	0.006	0.013	0.019	0.013	0.013
7	0.113	0.067	0.000	0.000	0.006	0.000	0.006	0.000	0.000	0.000	0.000	0.006	0.006	0.012	0.031	0.031	0.012
8	0.014	0.048	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.009	0.008	0.017	0.018	0.008	0.008	0.000

9	0.057	0.132	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013
10	0.033	0.143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.011	0.016	0.011	0.022	0.017	0.022
11	0.053	0.064	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.018	0.000	0.000	0.006	0.012	0.012	0.042
12	0.041	0.112	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.006	0.006	0.006	0.000	0.006	0.017	0.017	0.028
13	0.000	0.171	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.011	0.000	0.006	0.017	0.017	0.012	0.000	0.006
14	0.062	0.079	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.009	0.028	0.009	0.000	0.028	0.009
15	0.104	0.039	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.006	0.012	0.006	0.018	0.018	0.012	0.012
16	0.010	0.065	0.000	0.000	0.000	0.000	0.000	0.007	0.007	0.000	0.000	0.000	0.007	0.007	0.007	0.015	0.015
17	0.092	0.083	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.006	0.000	0.012	0.006	0.018	0.012	0.018
18	0.045	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.000	0.000	0.000	0.060	0.000
19	0.420	0.280	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.024	0.012	0.024	0.024

268	272	274	276	280	282	284	288	290	292	296	300	302	304	306	308	312	314
0.011	0.017	0.006	0.030	0.040	0.000	0.006	0.028	0.000	0.033	0.040	0.069	0.000	0.006	0.000	0.034	0.011	0.000
0.033	0.033	0.000	0.016	0.023	0.000	0.034	0.049	0.000	0.038	0.035	0.016	0.000	0.028	0.000	0.050	0.038	0.000
0.046	0.017	0.000	0.036	0.057	0.000	0.017	0.029	0.000	0.053	0.029	0.040	0.006	0.017	0.000	0.011	0.040	0.000
0.011	0.027	0.000	0.032	0.032	0.000	0.038	0.061	0.000	0.011	0.059	0.023	0.000	0.027	0.000	0.056	0.039	0.000
0.044	0.033	0.000	0.028	0.045	0.000	0.034	0.028	0.000	0.038	0.027	0.045	0.000	0.056	0.000	0.039	0.051	0.000
0.006	0.006	0.000	0.033	0.058	0.006	0.013	0.019	0.000	0.026	0.028	0.042	0.000	0.047	0.000	0.032	0.032	0.006
0.036	0.012	0.006	0.013	0.036	0.000	0.031	0.050	0.000	0.018	0.048	0.064	0.000	0.048	0.000	0.024	0.042	0.000
0.017	0.008	0.000	0.053	0.050	0.000	0.033	0.008	0.000	0.027	0.100	0.033	0.000	0.033	0.000	0.025	0.025	0.000
0.014	0.026	0.000	0.041	0.000	0.000	0.041	0.054	0.000	0.054	0.052	0.013	0.000	0.039	0.000	0.014	0.039	0.000
0.040	0.016	0.000	0.028	0.039	0.000	0.016	0.033	0.000	0.044	0.027	0.044	0.000	0.033	0.000	0.022	0.017	0.000
0.024	0.018	0.000	0.058	0.036	0.000	0.030	0.044	0.012	0.030	0.030	0.025	0.000	0.026	0.006	0.042	0.018	0.000
0.011	0.028	0.000	0.017	0.055	0.000	0.022	0.039	0.000	0.034	0.046	0.028	0.000	0.017	0.006	0.028	0.028	0.000
0.011	0.023	0.000	0.023	0.046	0.000	0.006	0.048	0.000	0.034	0.035	0.058	0.000	0.035	0.000	0.036	0.023	0.006
0.018	0.027	0.000	0.036	0.000	0.000	0.094	0.027	0.000	0.018	0.054	0.038	0.000	0.038	0.000	0.009	0.045	0.000
0.035	0.023	0.000	0.047	0.043	0.000	0.065	0.035	0.000	0.037	0.018	0.006	0.000	0.047	0.000	0.043	0.037	0.000
0.007	0.007	0.007	0.044	0.015	0.000	0.037	0.051	0.000	0.059	0.059	0.061	0.008	0.022	0.000	0.037	0.022	0.000
0.000	0.051	0.000	0.024	0.018	0.000	0.024	0.024	0.000	0.067	0.043	0.024	0.000	0.072	0.000	0.049	0.018	0.000
0.012	0.000	0.012	0.048	0.012	0.000	0.000	0.060	0.000	0.055	0.024	0.060	0.000	0.048	0.000	0.036	0.036	0.000
0.024	0.036	0.000	0.012	0.037	0.000	0.047	0.024	0.000	0.035	0.036	0.024	0.000	0.084	0.000	0.000	0.012	0.000

317	319	321	325	327	329	334	338	340	342	346	348	350	354	356	358	362	364
0.028	0.000	0.028	0.022	0.006	0.028	0.040	0.033	0.000	0.028	0.022	0.006	0.033	0.017	0.000	0.035	0.023	0.000
0.045	0.000	0.033	0.028	0.000	0.011	0.033	0.033	0.000	0.027	0.022	0.000	0.016	0.016	0.005	0.012	0.022	0.000
0.034	0.006	0.012	0.018	0.000	0.017	0.040	0.017	0.000	0.024	0.025	0.000	0.036	0.036	0.000	0.024	0.011	0.000
0.027	0.000	0.021	0.047	0.005	0.006	0.021	0.016	0.000	0.005	0.041	0.005	0.021	0.028	0.000	0.027	0.027	0.000
0.027	0.000	0.057	0.028	0.000	0.027	0.028	0.028	0.000	0.017	0.016	0.000	0.006	0.022	0.000	0.011	0.005	0.000

0.027	0.000	0.045	0.019	0.000	0.040	0.051	0.019	0.000	0.026	0.019	0.000	0.019	0.019	0.000	0.019	0.013	0.000
0.036	0.000	0.032	0.036	0.000	0.036	0.012	0.031	0.000	0.018	0.006	0.000	0.018	0.036	0.000	0.012	0.006	0.000
0.067	0.000	0.036	0.036	0.000	0.033	0.025	0.025	0.000	0.008	0.042	0.000	0.025	0.008	0.000	0.017	0.008	0.000
0.027	0.000	0.026	0.039	0.000	0.026	0.026	0.000	0.000	0.013	0.013	0.000	0.039	0.013	0.000	0.054	0.039	0.000
0.045	0.005	0.011	0.022	0.000	0.046	0.033	0.034	0.000	0.022	0.016	0.005	0.028	0.016	0.000	0.011	0.000	0.000
0.018	0.000	0.042	0.066	0.000	0.024	0.018	0.037	0.000	0.018	0.019	0.000	0.036	0.031	0.000	0.006	0.006	0.000
0.028	0.000	0.011	0.034	0.000	0.011	0.023	0.044	0.000	0.023	0.035	0.000	0.017	0.051	0.006	0.011	0.006	0.006
0.012	0.000	0.051	0.011	0.000	0.028	0.028	0.006	0.000	0.029	0.028	0.000	0.029	0.017	0.000	0.023	0.012	0.000
0.047	0.000	0.045	0.047	0.000	0.038	0.018	0.018	0.009	0.018	0.000	0.009	0.018	0.018	0.000	0.018	0.009	0.000
0.029	0.000	0.019	0.006	0.000	0.018	0.043	0.053	0.006	0.029	0.049	0.000	0.029	0.012	0.000	0.012	0.029	0.000
0.061	0.000	0.023	0.015	0.000	0.024	0.007	0.015	0.000	0.015	0.022	0.000	0.015	0.066	0.000	0.038	0.015	0.000
0.030	0.000	0.049	0.063	0.000	0.030	0.025	0.018	0.000	0.000	0.019	0.006	0.018	0.006	0.000	0.024	0.018	0.000
0.036	0.000	0.071	0.036	0.000	0.055	0.024	0.012	0.000	0.024	0.036	0.000	0.024	0.000	0.000	0.000	0.012	0.000
0.012	0.000	0.035	0.024	0.000	0.025	0.012	0.049	0.000	0.012	0.012	0.000	0.000	0.000	0.000	0.012	0.000	0.000

366	368	371	373	375	379	383	387	391	393	395	400	404	408	412	416	420	424
0.017	0.000	0.011	0.000	0.039	0.017	0.017	0.017	0.000	0.000	0.006	0.006	0.011	0.000	0.000	0.006	0.000	0.006
0.027	0.000	0.005	0.000	0.022	0.016	0.022	0.006	0.011	0.000	0.011	0.005	0.000	0.000	0.011	0.000	0.000	0.016
0.011	0.000	0.046	0.000	0.006	0.029	0.017	0.000	0.017	0.000	0.017	0.000	0.000	0.006	0.006	0.000	0.000	0.006
0.005	0.000	0.011	0.000	0.021	0.038	0.000	0.011	0.005	0.005	0.005	0.005	0.011	0.000	0.011	0.005	0.005	0.000
0.016	0.000	0.005	0.000	0.005	0.005	0.000	0.000	0.017	0.000	0.005	0.005	0.000	0.000	0.005	0.005	0.000	0.000
0.032	0.000	0.019	0.000	0.019	0.013	0.006	0.032	0.006	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.019
0.032	0.000	0.012	0.000	0.006	0.012	0.013	0.000	0.000	0.000	0.000	0.006	0.000	0.006	0.000	0.006	0.012	0.012
0.017	0.000	0.008	0.000	0.008	0.017	0.018	0.000	0.008	0.000	0.017	0.000	0.008	0.000	0.008	0.000	0.008	0.008
0.026	0.000	0.013	0.000	0.000	0.013	0.013	0.000	0.041	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000
0.011	0.005	0.005	0.000	0.005	0.027	0.011	0.006	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.005	0.000
0.018	0.000	0.042	0.006	0.006	0.012	0.012	0.006	0.006	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000
0.011	0.000	0.000	0.000	0.006	0.017	0.017	0.017	0.011	0.000	0.011	0.011	0.000	0.011	0.011	0.000	0.000	0.006
0.012	0.000	0.000	0.000	0.000	0.017	0.011	0.000	0.017	0.000	0.000	0.006	0.000	0.006	0.000	0.006	0.011	0.006
0.009	0.000	0.018	0.009	0.009	0.000	0.028	0.009	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.019	0.000	0.012	0.000	0.006	0.012	0.000	0.000	0.023	0.000	0.000	0.006	0.000	0.006	0.006	0.006	0.006	0.000
0.000	0.000	0.037	0.000	0.007	0.000	0.007	0.000	0.000	0.000	0.007	0.015	0.015	0.000	0.000	0.015	0.007	0.007
0.018	0.000	0.018	0.000	0.000	0.012	0.012	0.012	0.019	0.000	0.006	0.006	0.006	0.006	0.006	0.000	0.000	0.000
0.012	0.000	0.012	0.000	0.036	0.024	0.012	0.012	0.024	0.000	0.012	0.000	0.012	0.000	0.000	0.012	0.000	0.000
0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.012	0.012	0.000	0.000	0.000	0.000

428	433	437	441	445	449	454	458	487
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

0.005	0.000	0.000	0.000	0.005	0.005	0.000	0.011	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000
0.000	0.005	0.005	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.006	0.000	0.000	0.006	0.000	0.000	0.006
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.013	0.000	0.013	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000
0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000
0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Sample Pab9

	BETA	NULL	194	198	202	206	210	214	218	222	226	230	234	238	242	246	248
1	0.009	0.044	0.000	0.005	0.005	0.051	0.016	0.074	0.033	0.079	0.051	0.042	0.088	0.118	0.105	0.085	0.000
2	0.024	0.091	0.000	0.000	0.000	0.027	0.061	0.050	0.043	0.022	0.077	0.041	0.077	0.083	0.105	0.084	0.000
3	0.044	0.036	0.000	0.000	0.018	0.031	0.088	0.041	0.035	0.067	0.037	0.067	0.073	0.067	0.103	0.089	0.000
4	0.019	0.050	0.000	0.000	0.006	0.021	0.056	0.038	0.035	0.080	0.066	0.043	0.066	0.121	0.096	0.099	0.000
5	0.007	0.063	0.000	0.000	0.005	0.037	0.037	0.033	0.027	0.037	0.059	0.061	0.077	0.079	0.140	0.109	0.000
6	0.034	0.066	0.000	0.007	0.007	0.020	0.066	0.046	0.033	0.028	0.092	0.053	0.099	0.126	0.088	0.099	0.000
7	0.015	0.083	0.005	0.000	0.005	0.032	0.065	0.058	0.022	0.038	0.033	0.077	0.103	0.096	0.073	0.115	0.000
8	0.015	0.042	0.000	0.000	0.008	0.075	0.042	0.018	0.017	0.062	0.075	0.050	0.067	0.062	0.101	0.075	0.000
9	0.021	0.062	0.000	0.000	0.000	0.025	0.085	0.050	0.050	0.040	0.050	0.145	0.062	0.075	0.100	0.105	0.000
10	0.058	0.077	0.000	0.000	0.006	0.034	0.035	0.040	0.029	0.041	0.034	0.028	0.113	0.097	0.117	0.145	0.000
11	0.008	0.060	0.000	0.006	0.006	0.077	0.057	0.040	0.023	0.047	0.053	0.087	0.082	0.114	0.085	0.080	0.000
12	0.042	0.026	0.000	0.000	0.000	0.022	0.067	0.039	0.022	0.047	0.098	0.061	0.096	0.058	0.177	0.094	0.000
13	0.077	0.057	0.000	0.000	0.006	0.068	0.037	0.040	0.032	0.043	0.098	0.043	0.127	0.098	0.080	0.107	0.000
14	0.078	0.085	0.000	0.000	0.000	0.009	0.030	0.057	0.046	0.019	0.028	0.067	0.095	0.055	0.118	0.105	0.000
15	0.008	0.049	0.000	0.000	0.005	0.027	0.058	0.076	0.037	0.033	0.053	0.090	0.050	0.074	0.109	0.048	0.011
16	0.011	0.062	0.000	0.000	0.007	0.023	0.037	0.082	0.015	0.015	0.051	0.084	0.106	0.069	0.166	0.046	0.000
17	0.032	0.023	0.000	0.000	0.000	0.039	0.056	0.051	0.045	0.039	0.062	0.034	0.122	0.082	0.099	0.119	0.000
18	0.000	0.003	0.000	0.000	0.000	0.045	0.045	0.068	0.011	0.056	0.080	0.091	0.056	0.148	0.102	0.102	0.000
19	0.033	0.092	0.000	0.000	0.014	0.022	0.051	0.014	0.015	0.090	0.087	0.057	0.100	0.094	0.078	0.062	0.000

250	254	258	262	266	270	274	278	282	286	298	302
0.074	0.040	0.033	0.022	0.011	0.011	0.005	0.005	0.000	0.000	0.000	0.000
0.086	0.056	0.033	0.043	0.017	0.000	0.000	0.000	0.000	0.000	0.005	0.000
0.076	0.061	0.043	0.023	0.012	0.006	0.006	0.012	0.000	0.006	0.000	0.000
0.061	0.059	0.059	0.016	0.000	0.021	0.000	0.000	0.000	0.000	0.000	0.005
0.076	0.061	0.033	0.028	0.021	0.011	0.000	0.000	0.000	0.005	0.000	0.000
0.057	0.048	0.033	0.020	0.007	0.007	0.000	0.000	0.000	0.000	0.000	0.000
0.055	0.068	0.027	0.011	0.022	0.005	0.000	0.005	0.000	0.000	0.000	0.000
0.104	0.087	0.083	0.025	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.050	0.025	0.027	0.025	0.012	0.000	0.000	0.000	0.000	0.012	0.000	0.000
0.078	0.049	0.034	0.017	0.017	0.006	0.000	0.000	0.006	0.000	0.000	0.000
0.055	0.063	0.023	0.017	0.006	0.011	0.000	0.000	0.000	0.006	0.000	0.000
0.047	0.061	0.033	0.033	0.011	0.000	0.000	0.000	0.000	0.006	0.000	0.000
0.037	0.064	0.026	0.006	0.006	0.018	0.006	0.000	0.000	0.000	0.000	0.000
0.086	0.089	0.028	0.046	0.018	0.018	0.000	0.000	0.000	0.000	0.000	0.000
0.095	0.078	0.032	0.048	0.016	0.011	0.000	0.000	0.000	0.000	0.000	0.000
0.091	0.059	0.051	0.007	0.015	0.000	0.007	0.000	0.007	0.000	0.000	0.000
0.079	0.056	0.036	0.028	0.018	0.000	0.011	0.000	0.000	0.000	0.000	0.000
0.057	0.079	0.023	0.011	0.011	0.011	0.000	0.000	0.000	0.000	0.000	0.000
0.087	0.035	0.042	0.045	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.000