

Strong maternal fidelity and natal philopatry shape genetic structure in North Pacific humpback whales

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Supplement. The Supplement includes the following figures and tables supporting the results and discussion of the primary article:

Fig. S1. Distribution of genetic sampling and approximate boundaries of the 18 geographic regions used in the analyses of population structure of humpback whales in the North Pacific

Fig. S2: Indicative results from the Bayesian clustering program STRUCTURE, for humpback whales in the North Pacific based on microsatellite genotypes

Fig. S3: Scatter plot of pair-wise F_{ST} values for microsatellite genotypes and mtDNA haplotypes for 18 regional samples of humpback whales in the North Pacific

Table S1: Genotype matches for individual humpback whales in the North Pacific, showing within-region replicates and between-regions ‘recaptures’

Table S2: Pair-wise Φ_{ST} values for mtDNA haplotypes of 18 regional samples of humpback whales in the North Pacific

Table S3: Pair-wise F_{ST} values for microsatellite genotypes of 18 regional samples of humpback whales in the North Pacific

Table S4: Pair-wise F'_{ST} values (F_{ST} adjusted for diversity) for microsatellite genotypes of 18 regional samples of humpback whales in the North Pacific

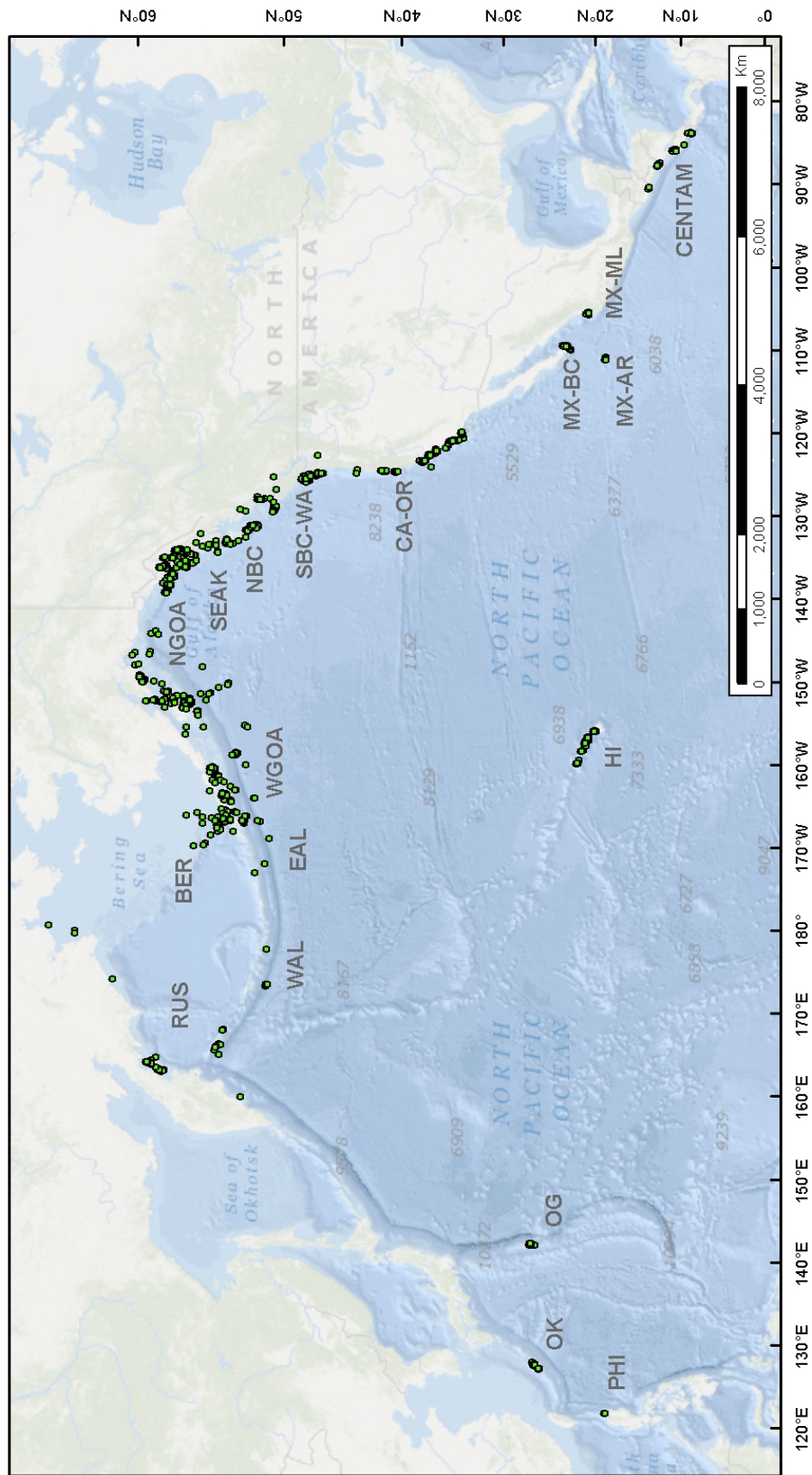
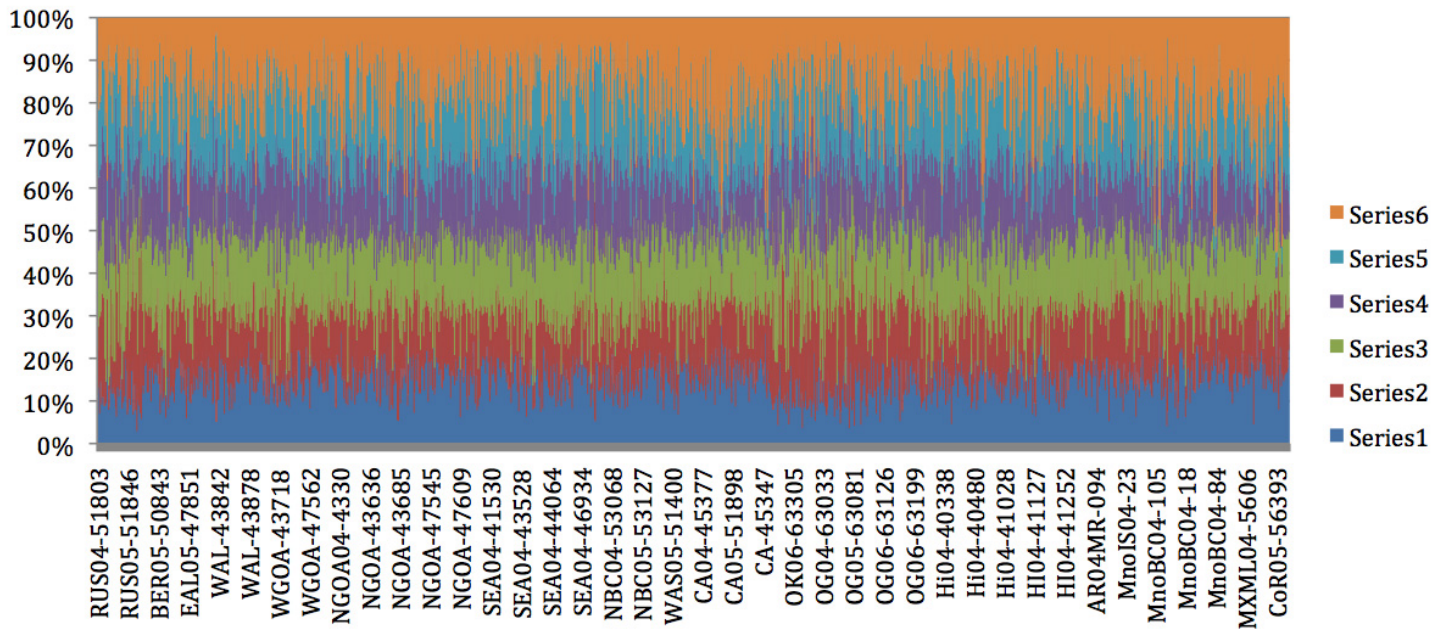


Fig. S1. *Megaptera novaeangliae*. Distribution of genetic sampling and approximate boundaries of the 18 geographic regions used in the analyses. Note that many samples are superimposed on each other. For a better indication of the density distribution of samples, see Fig. 2a of the main article. For abbreviations of geographic regions, see Table 2 of the main article.

All samples, K= 6



All samples, K=2

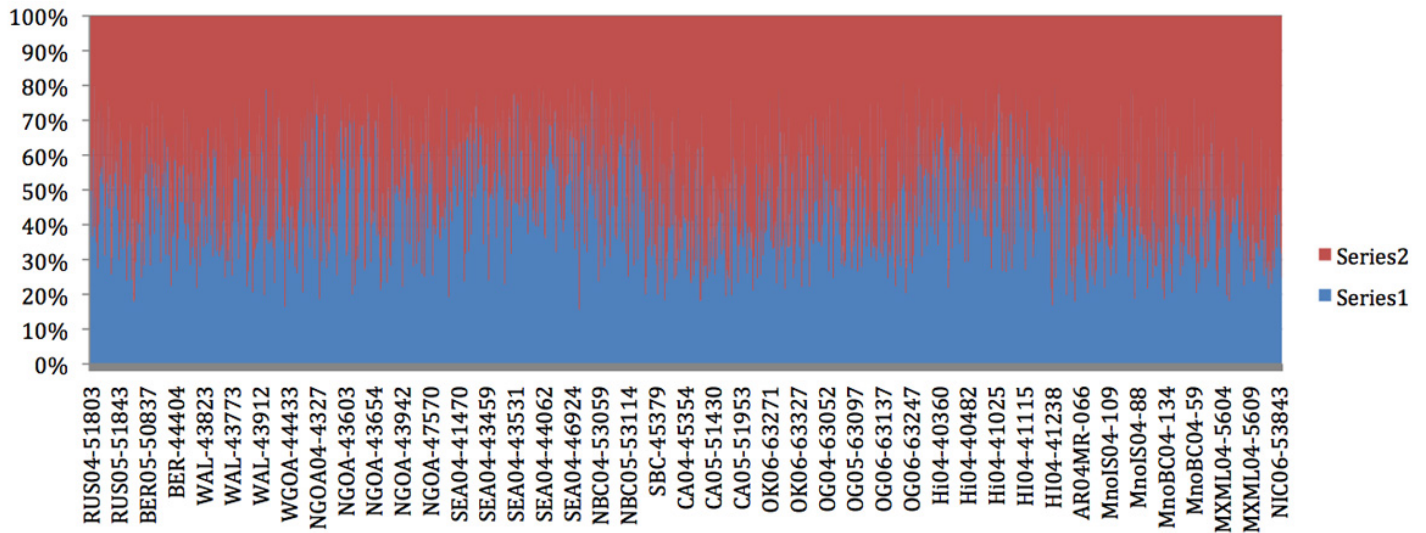


Fig. S2. *Megaptera novaeangliae*. Indicative results from the Bayesian clustering program STRUCTURE, for humpback whales in the North Pacific based on microsatellite genotypes. Each genotype is represented as a line partitioned into the membership coefficient for the putative number of populations (K = 6 and K = 2 shown here). Methods: We evaluated a range of potential populations from K = 1–6 using the admixture and correlated frequency model with 1 000 000 burn-ins and 10 000 000 runs and no location prior. STRUCTURE gave the highest likelihood to K = 1. For K > 1, the ΔK method described in Evanno et al. (2005) suggested K = 2 provided the best fit for the data. However, on inspection of the membership coefficients, all individuals were admixed for all tested values of K

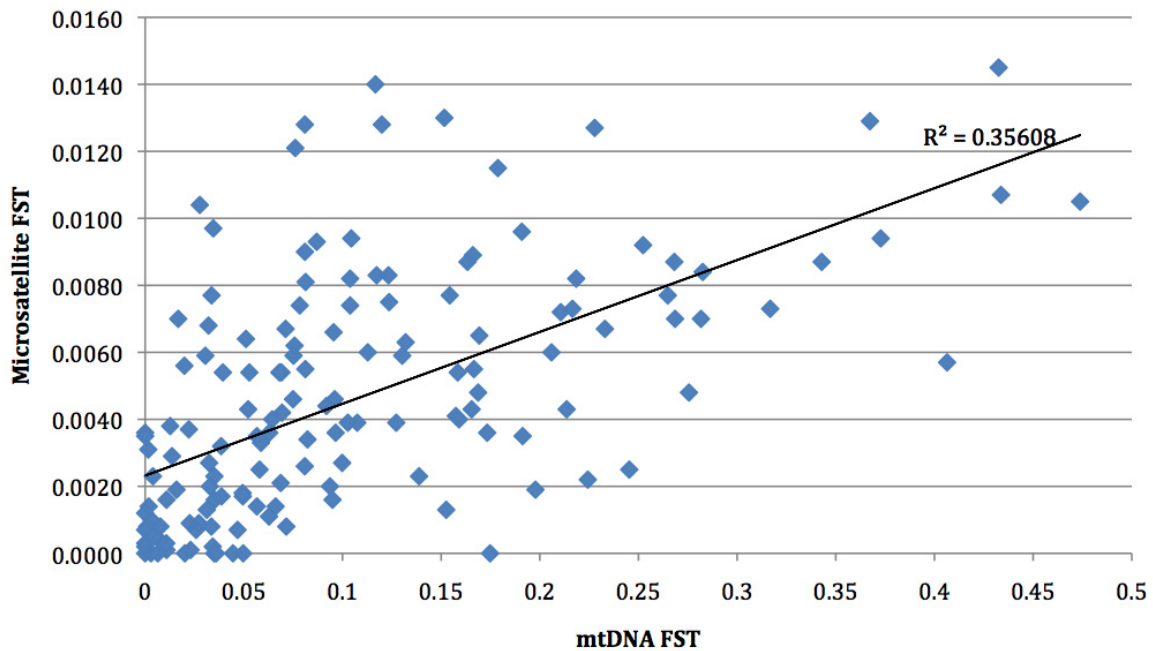


Fig. S3. *Megaptera novaeangliae*. Pair-wise F_{ST} values for microsatellite genotypes (y-axis) and mitochondrial (mt) DNA haplotypes (x-axis) for 18 regional samples of humpback whales in the North Pacific. A Mantel test of the relationship ($r = 0.609$, $p < 0.001$) was implemented in GENODIVE (Meirmans & Van Tienderen 2004)

Table S1. *Megaptera novaeangliae*. Number of genotype matches for individual humpback whales in the North Pacific, showing within-region replicates (on diagonal) and between-regions ‘recaptures’ (below diagonal). Regional abbreviations are explained in Table 1 and adjacent numbers in parentheses refer to the individuals genotyped in each region (see NI in Table 1)

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC-WAS	CA-OR	PHI	OK	OG	HI	MXAR	MXBC	MXML	CENTAM
RUS (72)	7																	
WAL (8)		0																
BER (119)			10															
EAL (36)			1	1														
WGOA (98)					12													
NGOA (237)					1	10												
SEA (186)							13											
NBC (108)							1	14										
SBC-WAS (51)									6									
CA-OR (125)									1	9								
PHI (13)	1										0							
OK (72)	4											18						
OG (163)	4											2	59					
HI (231)			1			1	2	4						14				
MXAR (115)			2		1	2			1						26			
MXBC (120)			1			3									2	17		
MXML (62)			1			1			1	2					1	9	13	
CENAM (39)										2								2

Table S2. *Megaptera novaeangliae*. Pair-wise Φ_{ST} values for mitochondrial (mt) DNA haplotypes of North Pacific humpback whales for (a) feeding grounds, (b) breeding and feeding grounds and (c) breeding grounds. Values* indicate significance at <0.05, values** significance at <0.01 and values*** significant at <0.001, unadjusted for multiple comparisons. **Bolded** values were significant after adjustment for the false discovery rate. Φ_{ST} indices and significance of pair-wise differences (10 000 permutations) were calculated with the program ARLEQUIN (Excoffier & Lischer 2010). Shaded rows and columns with *italics* indicate low sample sizes for comparisons involving Western Aleutians (WAL) or Philippines (PHI)

(a) Feeding to feeding

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC/WA	CA/OR
RUS	–									
WAL	<i>0.000</i>	–								
BER	0.092***	<i>0.000</i>	–							
EAL	0.109***	<i>0.000</i>	0.000	–						
WGOA	0.038*	<i>0.000</i>	0.013	0.008	–					
NGOA	0.102***	<i>0.000</i>	0.013	0.006	0.014	–				
SEA	0.389***	0.449**	0.247***	0.345***	0.223***	0.117***	–			
NBC	0.283***	0.315**	0.172***	0.239***	0.145***	0.079***	0.004	–		
SBC/WA	0.041**	<i>0.008</i>	0.092***	0.104***	0.035*	0.078***	0.319***	0.217***	–	
CA/OR	0.265***	<i>0.111</i>	0.153***	0.108**	0.198***	0.225***	0.478***	0.396***	0.268***	–

(b) Breeding to feeding

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC/WA	CA/OR
PHI	<i>0.000</i>	<i>0.000</i>	<i>0.069*</i>	<i>0.067</i>	<i>0.020</i>	0.097*	0.550***	0.425***	<i>0.045</i>	0.196**
OK	0.032**	0.192**	0.200***	0.274***	0.130***	0.196***	0.580***	0.490***	0.122***	0.353***
OG	0.002	<i>0.000</i>	0.102***	0.115***	0.041**	0.110***	0.332***	0.249***	0.028*	0.292***
HI	0.128***	<i>0.014</i>	0.027*	0.023	0.030**	0.000	0.099***	0.065***	0.095***	0.249***
MX-AR	0.034*	<i>0.000</i>	0.015	0.014	0.000	0.024**	0.243***	0.162***	0.041**	0.212***
MX-BC	0.040**	<i>0.000</i>	0.014	0.001	0.000	0.030**	0.249***	0.172***	0.044**	0.150***
MX-ML	0.076**	<i>0.000</i>	0.014	0.000	0.022	0.053**	0.362***	0.260***	0.086**	0.088***
CENAM	0.313***	<i>0.108</i>	0.173***	0.117***	0.227***	0.256***	0.638***	0.533***	0.320***	0.000

(c) Breeding to breeding

	PHI	OK	OG	HI	MX-AR	MX-BC	MX-ML	CENAM
PHI	–							
OK	<i>0.033</i>	–						
OG	<i>0.000</i>	0.031**	–					
HI	0.131*	0.230***	0.136***	–				
MX-AR	<i>0.018</i>	0.119***	0.038**	0.044***	–			
MX-BC	<i>0.011</i>	0.119***	0.043***	0.050***	0.003	–		
MX-ML	<i>0.031</i>	0.185***	0.080***	0.077***	0.030*	0.001	–	
CENAM	0.202*	0.461***	0.341***	0.289***	0.244***	0.158***	0.087*	–

Table S3. *Megaptera novaeangliae*. Pair-wise F_{ST} values for microsatellite genotypes of North Pacific humpback whales for (a) feeding grounds, (b) breeding and feeding grounds and (c) breeding grounds. Values and significance calculated with modified Fisher's exact test in GENEPOP (Rousset 2008). Values* indicate significance at <0.05, values** significance at <0.01 and values*** significant at <0.001, unadjusted for multiple comparisons. **Bold** values were significant after adjustment for the false discovery rate. Rows and columns in *italics* indicate low sample size for comparisons involving Western Aleutians (WAL) or Philippines (PHI)

(a) Feeding to feeding

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC/WA	CA/OR
RUS	–									
WAL	<i>0.0035</i>	–								
BER	0.0055***	<i>0.0036</i>	–							
EAL	<i>0.0042*</i>	<i>0.0000</i>	0.0000	–						
WGOA	0.0020*	<i>0.0000</i>	0.0001	0.0000	–					
NGOA	0.0060***	<i>0.0070</i>	0.0017**	0.0003***	0.0009	–				
SEA	0.0073***	<i>0.0070</i>	0.0025**	0.0022***	0.0019*	0.0016***	–			
NBC	0.0092***	<i>0.0060</i>	0.0000	0.0013*	0.0023**	0.0014**	0.0010*	–		
SBC/WA	0.0062***	<i>0.0029</i>	0.0018***	0.0002**	0.0000	0.0023***	0.0035***	0.0039***	–	
CA/OR	0.0128***	<i>0.0008</i>	0.0034***	0.0054**	0.0021**	0.0075***	0.0087***	0.0084***	0.0039**	–

(b) Breeding to feeding

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC/WA	CA/OR
PHI	<i>0.0000</i>	<i>0.0017</i>	<i>0.0043</i>	<i>0.004</i>	<i>0.002</i>	<i>0.0082</i>	0.0105*	<i>0.0057</i>	0.0089**	<i>0.0083*</i>
OK	0.0000	<i>0.0000</i>	0.0055***	0.0036***	0.0027***	0.0073***	0.0107***	0.0094***	0.0065**	0.013***
OG	0.0019***	<i>0.0000</i>	0.004***	0.0043***	0.0013***	0.0036***	0.007***	0.0072***	0.0036***	0.009***
HI	0.0054***	<i>0.0054</i>	0.0011*	0.0000	0.0025	0.0005	0.0008*	0.0008	0.0035***	0.0087***
MX-AR	0.0077***	<i>0.0000</i>	0.0016	0.0012	0.0003	0.0054***	0.0067***	0.0048***	0.0027**	0.0014**
MX-BC	0.0104***	<i>0.0000</i>	0.0016**	0.0004	0.0007	0.0032***	0.0043***	0.0041***	0.0009*	0.0007
MX-ML	0.0097***	<i>0.0000</i>	0.0038***	0.0031**	0.0001	0.0064***	0.0077***	0.0096***	0.0007*	0.0000
CENAM	0.0121***	<i>0.0000</i>	0.0063***	0.0094**	0.0044**	0.0115***	0.0145***	0.0129***	0.0077*	0.0000

(c) Breeding to breeding

	PHI	OK	OG	HI	MX-AR	MX-BC	MX-ML	CENAM
PHI	–							
OK	<i>0.0000</i>	–						
OG	0.0054**	0.0033***	–					
HI	<i>0.0048</i>	0.0087***	0.0059***	–				
MX-AR	<i>0.0039</i>	0.0074***	0.0059***	0.0059***	–			
MX-BC	<i>0.0066</i>	0.0082***	0.0068***	0.0046***	0.0014	–		
MX-ML	<i>0.0083*</i>	0.0128***	0.0056***	0.0081***	0.0023*	0.0008	–	
CENAM	<i>0.0074</i>	0.014***	0.0093***	0.0127***	0.0046***	0.0067*	0.0026	–

Table S4. *Megaptera novaeangliae*. Pair-wise F'_{ST} values (F_{ST} adjusted for diversity) for microsatellite genotypes of North Pacific humpback whales for (a) feeding grounds, (b) breeding and feeding grounds and (c) breeding grounds. Values were calculated with GENODIVE (Meirmans & Van Tienderen 2004). Rows and columns in *italics* indicate low sample size for comparisons involving Western Aleutians (WAL) or Philippines (PHI)

(a) Feeding to feeding

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC/WA	CA/OR
RUS	–									
WAL	<i>0.0098</i>	–								
BER	0.0188	<i>0.0019</i>	–							
EAL	0.0129	<i>0.0000</i>	0.0000	–						
WGOA	0.0054	<i>0.0000</i>	0.0000	0.0000	–					
NGOA	0.0216	<i>0.0237</i>	0.0058	0.0002	0.0025	–				
SEA	0.0245	<i>0.0136</i>	0.0080	0.0046	0.0053	0.0054	–			
NBC	0.0325	<i>0.0110</i>	0.0000	0.0010	0.0064	0.0048	0.0021	–		
SBC/WA	0.0212	<i>0.0054</i>	0.0047	0.0000	0.0000	0.0081	0.0105	0.0124	–	
CA/OR	0.0458	<i>0.0010</i>	0.0120	0.0183	0.0065	0.0276	0.0306	0.0305	0.0137	–

(b) Breeding to feeding

	RUS	WAL	BER	EAL	WGOA	NGOA	SEA	NBC	SBC/WA	CA/OR
PHI	<i>0.0000</i>	<i>0.0002</i>	<i>0.0086</i>	<i>0.0060</i>	<i>0.0000</i>	<i>0.0288</i>	<i>0.0306</i>	<i>0.0140</i>	<i>0.0289</i>	<i>0.0288</i>
OK	0.0000	<i>0.0000</i>	0.0178	0.0045	0.0055	0.0257	0.0357	0.0315	0.0186	0.0461
OG	0.0043	<i>0.0000</i>	0.0132	0.0102	0.0020	0.0126	0.0236	0.0247	0.0098	0.0313
HI	0.0181	<i>0.0082</i>	0.0031	0.0000	0.0076	0.0014	0.0018	0.0017	0.0109	0.0313
MX-AR	0.0278	<i>0.0000</i>	0.0050	0.0032	0.0000	0.0199	0.0235	0.0175	0.0095	0.0050
MX-BC	0.0380	<i>0.0000</i>	0.0052	0.0002	0.0014	0.0119	0.0151	0.0148	0.0027	0.0025
MX-ML	0.0302	<i>0.0000</i>	0.0108	0.0016	0.0000	0.0217	0.0239	0.0315	0.0000	0.0000
CENAM	0.0413	<i>0.0096</i>	0.0205	0.0295	0.0119	0.0408	0.0480	0.0447	0.0260	0.0000

(c) Breeding to breeding

	PHI	OK	OG	HI	MX-AR	MX-BC	MX-ML	CENAM
PHI	–							
OK	<i>0.0000</i>	–						
OG	<i>0.0071</i>	0.0082	–					
HI	<i>0.0107</i>	0.0296	0.0205	–				
MX-AR	<i>0.0131</i>	0.0256	0.0205	0.0210	–			
MX-BC	<i>0.0238</i>	0.0290	0.0238	0.0163	0.0051	–		
MX-ML	<i>0.0085</i>	0.0383	0.0155	0.0265	0.0060	0.0004	–	
CENAM	<i>0.0227</i>	0.0437	0.0286	0.0431	0.0160	0.0237	0.0018	–

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