

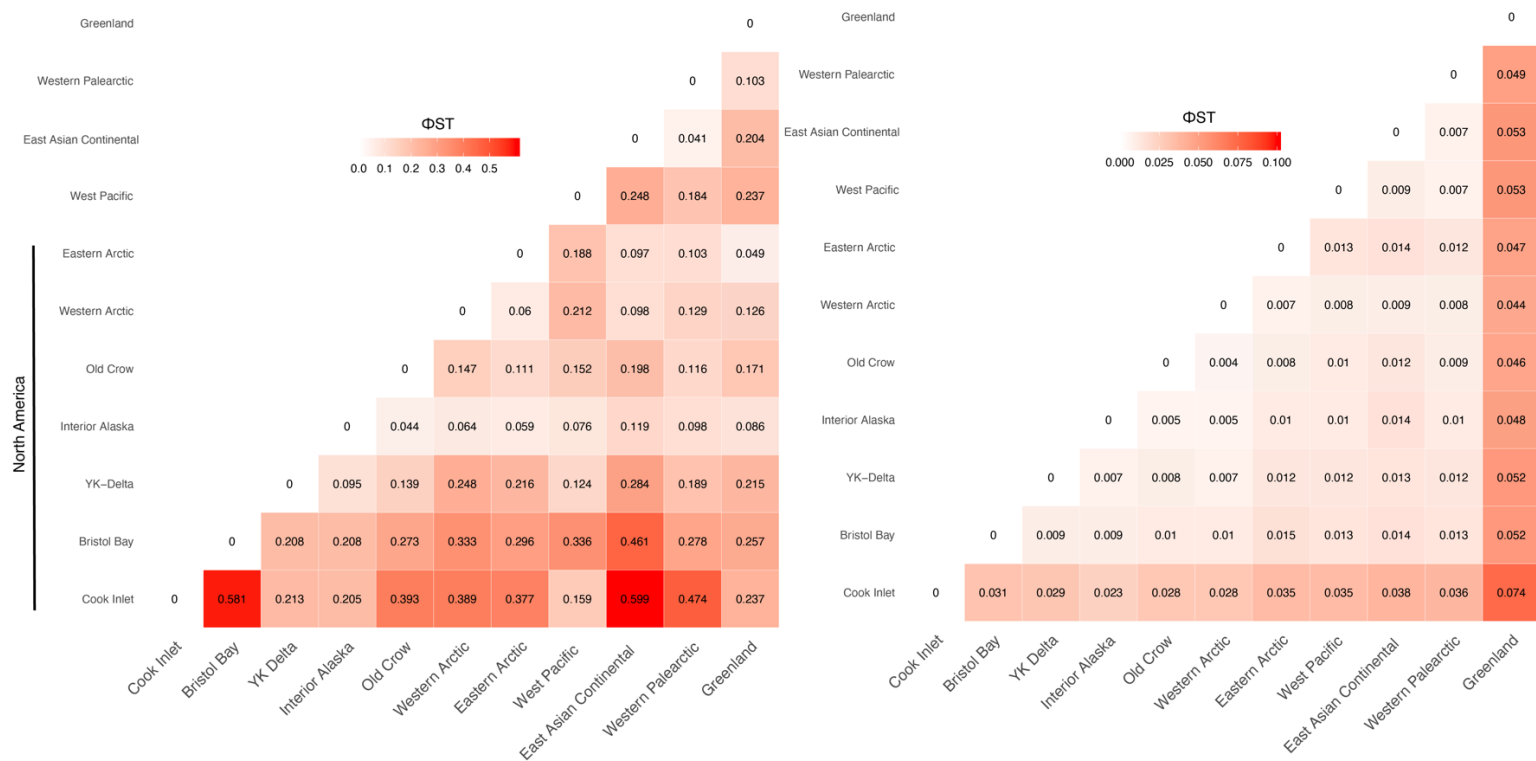
Supplemental Table S1. Summary of COLONY analysis results showing familial relationships among samples of greater white-fronted geese (*Anser albifrons*) from the same nesting area.

Continent	Flyway	Nesting Area	Sample Relationship
North America	Pacific	USA (Alaska): Yukon-Kuskokwim Delta	H_04_21 is mother of H_45_19
North America	Pacific	USA (Alaska): Yukon-Kuskokwim Delta	H_6J9 is mother of H_R29
North America	Pacific	USA (Alaska): Yukon-Kuskokwim Delta	H_R28/H_60_30F are half-sib pair
North America	Pacific	USA (Alaska): Yukon-Kuskokwim Delta	H_R28/H_60_30MF are half-sib pair
North America	Pacific	USA (Alaska): Bristol Bay	A_A40/A_89_20 are half-sib pair
North America	Pacific	USA (Alaska): Cook Inlet	B_6 is father of B_2, B_3 and B_61805805, which are three full sibs
North America	Central/Mississippi	Canada (Nunavut): Victoria Island	L_A24 is mother of L_A23
North America	Central/Mississippi	Canada (Nunavut): Queen Maud Gulf	M_49714 and M_49719 are full sibs
North America	Western Palearctic	Greenland	P_DI/P_F2F/P_F4F are full sibs
North America	Western Palearctic	Greenland	P_D5U/P_D1T are full sibs
North America	Western Palearctic	Greenland	P_D4T is father of P_D3T
North America	Western Palearctic	Greenland	P_F2H is father of P_F7F
North America	Western Palearctic	Greenland	P_F0F is mother of P_F7F
Asia	East Asian Continental Palearctic	Russia: Lena River	S_95_6/S_95_10 are half-sibs or equivalent

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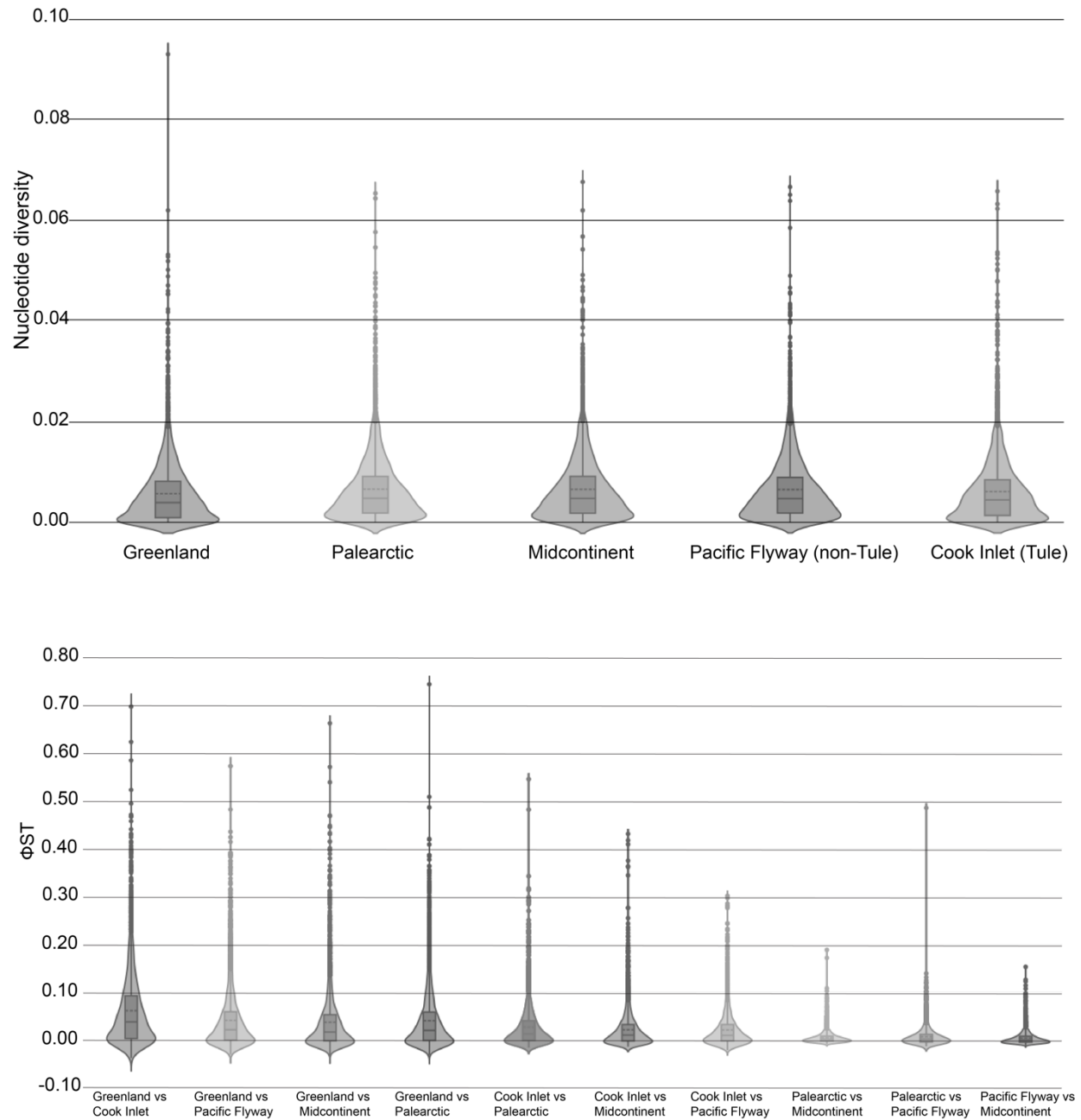
Asia	West Pacific Palearctic	Russia: Magadan	T_I/ T_II are full sib pairs
Asia	West Pacific Palearctic	Russia: Magadan	T_III/ T_IV are full sib pairs

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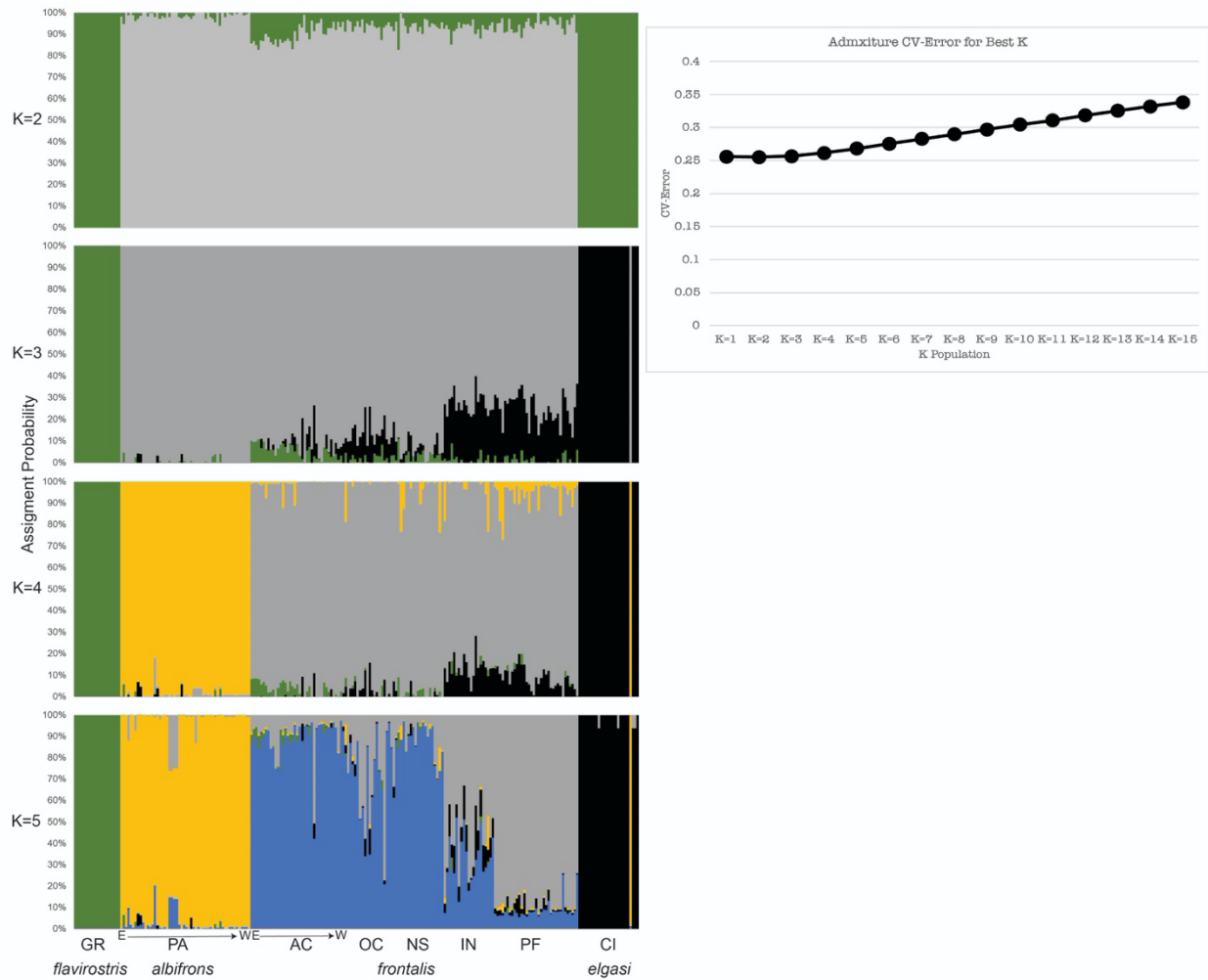


Supplemental Figure S1. Pairwise  $\Phi_{ST}$  comparisons for mitochondrial control region (376 base pairs, left) and ddRAD-seq loci (3,888 loci, right). Values for mtDNA between Greenland, Bristol Bay, Cook Inlet, YK-Delta, and Old Crow are taken from Wilson et al. 2018<sup>1</sup>.

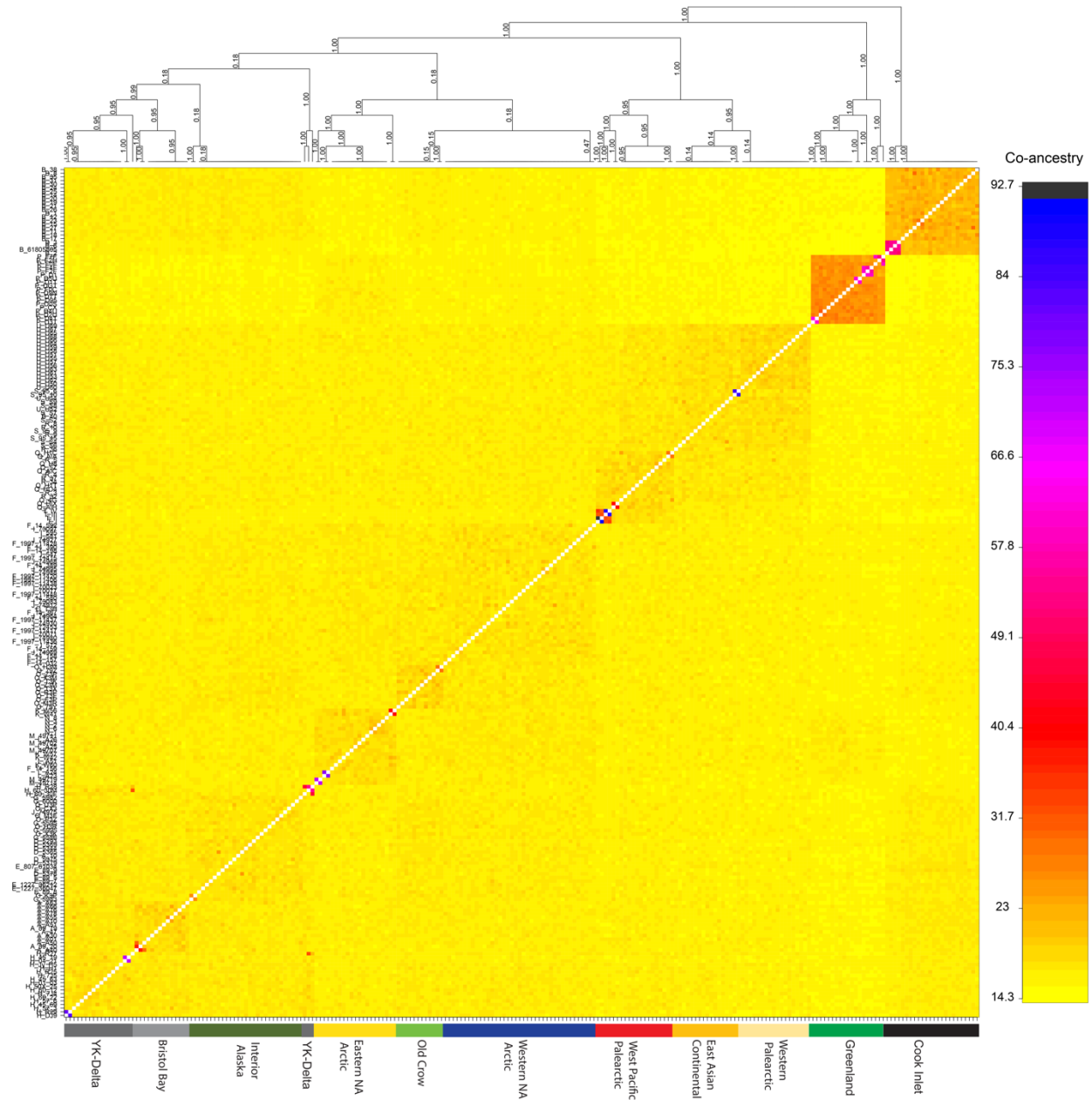
<sup>1</sup>Wilson RE, Ely CR, and Talbot SL. 2018. Flyway structure in a circumpolar greater white-fronted goose. *Ecology and Evolution* 8: 8490–8507.



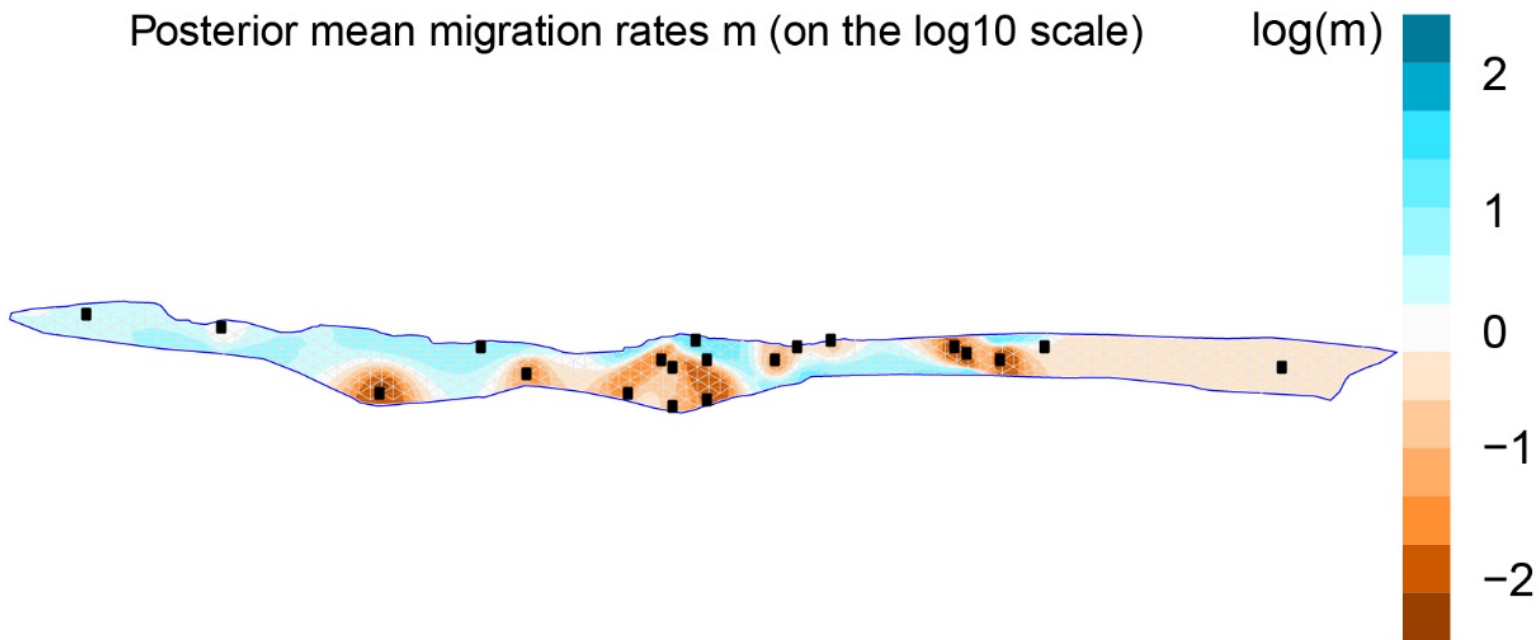
Supplemental Figure S2. Violin plots of the distribution of nucleotide diversity (top) and  $\phi_{ST}$  values (bottom) across 3,888 ddRAD-seq loci. Pacific Flyway group excludes the Cook Inlet (Tule) samples that also use the Pacific Flyway.



Supplemental Figure S3. Average assignment probabilities for K = 2-5 clusters inferred from ddRAD-seq data in ADMIXTURE using all biallelic single nucleotide polymorphisms (SNPs) with subspecies designation indicated. Abbreviations are GR = Greenland, PA = Palearctic, AC = Arctic Canada, OC = Old Crow, NS = North Slope, Alaska, IN = Interior Alaska, PF = Pacific Flyway (non-Tule), CI = Cook Inlet (Tule). East (E) and west (W) designate locations within Arctic Canada and Palearctic. CV = cross-validation.



Supplemental Figure S4. FineRADstructure results with co-ancestry values uncapped. Color blocks on bottom correspond to the geographic region the majority of samples were collected. Interior Alaska group includes portion of Old Crow and western Arctic individuals and East Asian Continental includes both Western and West Pacific Palearctic individuals in addition to individuals from the central region of the Lena River.



Supplemental Figure S5. Estimated Effective Migration Surface (EEMS) posterior mean effective migration surface based on 500 demes. Orange areas represent area of low migration relative to average (barrier) and blue indicates higher migration (connectivity).