**Introduction para:** Two genetics studies using Restriction-site Associated DNA sequencing have indicated significant genetic differentiation among spawning stocks of Pacific cod in the GOA and the EBS (Drinan *et al.* 2018; Spies *et al.* 2019). The most recent genomic analysis of Pacific cod includes a new publication that used pooled whole genome sequencing (Pool-Seq; Spies et al. 2022), as well as a new study conducted during 2021 and 2022 that used low coverage whole genome sequencing (lcWGS). Low-coverage whole-genome sequencing analysis of 429 samples of Pacific cod from known spawning regions during spawning season indicated population structure similar to what was previously known, but with finer resolution and greater power owing to the larger number of markers. Using 1,922,927 polymorphic SNPs (Fig. 2.3), the pattern of population structure mostly resembles isolation-by-distance, in which samples from proximate spawning areas are more genetically similar than samples from more distant areas. Isolation-by-distance was observed from western Gulf of Alaska (Kodiak and the Shumagin Islands) through Unimak Pass and the eastern Aleutian Islands. Previous studies have reported an isolation-by-distance pattern in Pacific cod using microsatellite markers (Cunningham et al. 2009 and Spies 2012) and reduced-representation sequencing (Drinan et al. 2018). Within the isolation-by-distance pattern, there were some distinct breaks in the population structure. The most significant genetic break occurs between western and eastern Gulf of Alaska (GOA) spawning samples (Fig. 2.3), and was supported by previous research that highlighted the zona pellucida gene region (Spies et al. 2021).



##### Figure 2.3. Principal components analysis of 1,922,927 polymorphic SNPs from the lcWGS dataset.