**Introduction para:** Low-coverage whole-genome sequencing analysis of 429 samples of Pacific cod from known spawning aggregations indicated population structure similar to what was previously known, but with finer resolution and greater due to a 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 distinct differences in the genes coding for the zona pellucida gene region ZP3 (Spies et al. 2021). Also notable is the lack of strong genetic differentiation among spawning cod from the eastern Gulf of Alaska (Unimak) and the western Gulf of Alaska.



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