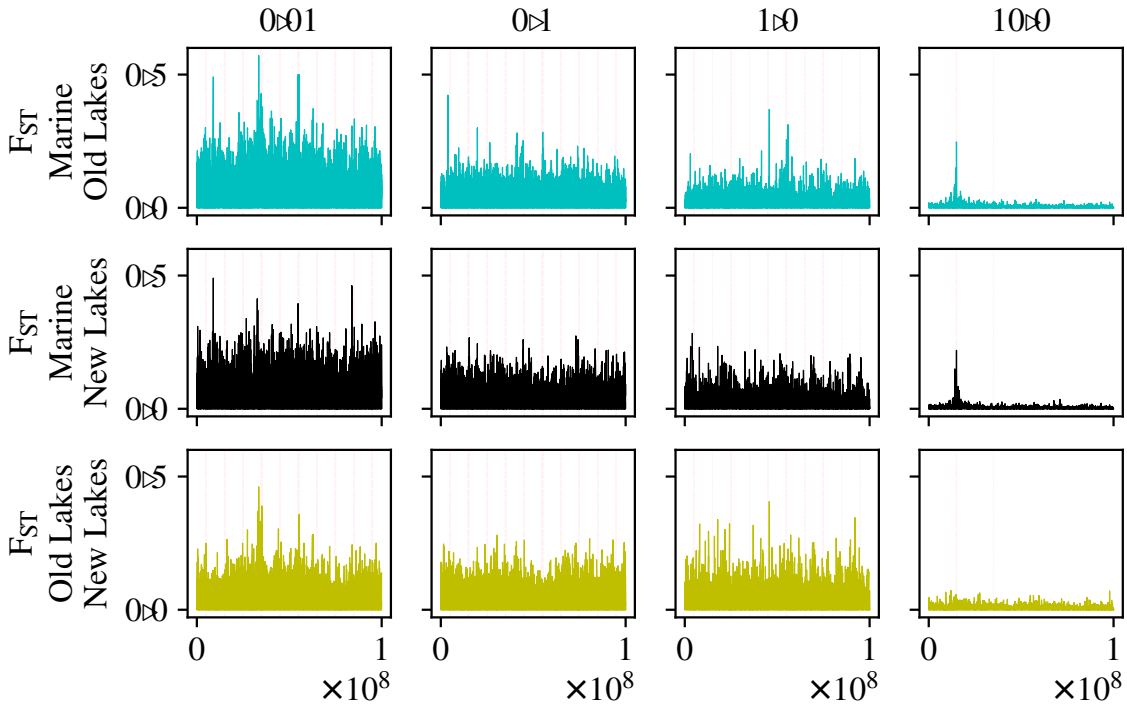

Figure S4: Average F_{ST} in windows of 500Mb between: (top) marine habitat and old lakes; (middle) marine habitat and new lakes; and (bottom) old and new lakes. Each plot shows F_{ST} values for a separate simulation, with columns corresponding to increasing gene f ow from left to right. F_{st} is calculated between all marine individuals with spatial location ≤ 5▷0, and the f ve corresponding lakes. All locations of pre-existing freshwater adapted alleles have been highlighted by partially transparent pink dashed vertical lines, so darker shades of blue imply more freshwater adapted alleles at that location.