

California MLPA North Coast Study Region
Genetic Connectivity Evaluation of External Marine Protected Area
Proposals
June 26, 2010 DRAFT

The mean change in genetic connectivity predicted for each of five species for Round 1 evaluations of external marine protected area (MPA) arrays using the University of California, Davis (UCD) bioeconomic model. Genetic connectivity between two MPAs is estimated by calculating the mean number of generations required for a so-called 'neutral' allele to spread from the origin MPA to the destination MPA. This calculation is made at equilibrium for the unsuccessful fishery management scenario (See *Draft Methods for Evaluation MPAs* for additional information about management scenarios). The change in genetic connectivity is calculated as the percent difference in connectivity relative to an unfished scenario, which has maximum connectivity. For ease of interpretation of results, only reductions in connectivity greater than -75% are shown; note that the color axis is on a logarithmic scale. The change in connectivity is shown for each pair of 'origin' and 'destination' MPAs in the north coast study region. The results are not symmetrical and that results are only shown for MPAs that are large enough to appear in the bioeconomic model analysis. For round 1 connectivity evaluations, five species were modeled: Black rockfish, brown rockfish, cabezon, red abalone, and red sea urchin. Redtail surfperch was excluded because it lacks larval dispersal and Dungeness crab was excluded because MPAs do not affect genetic connectivity in the male-only fishery. Due to limitations of the SAT's current evaluation methods, for round 1, proposed MPAs in external MPA array A were considered static rather than mobile. Traditional tribal uses were not integrated into round 1 evaluations of external MPA arrays due to the limited information about tribal uses.

Summary of results from round 1 genetic connectivity evaluation

The genetic connectivity results fall into four main categories:

1. External MPA arrays that show no substantial change in connectivity ($\leq 75\%$) relative to unfished state. Only ExH had this result.
2. External MPA arrays in which relatively distant MPAs showed decreased connectivity. For example, in ExA, there was decreased connectivity between the Point Cabrillo SMR and the Eureka SMCA, and in ExE there was decreased connectivity between the Point Cabrillo SMR and the False Klamath SMCA. This type of result could be corrected by reducing spacing in the network between those two focal MPAs. This type of result was observed for ExA, ExD, and ExE. However, it is worth noting that these proposed networks had more MPAs overall than ExH, which showed no change. This is likely because this metric is only calculated in locations where there are MPAs. That is, in ExH there was likely reduced genetic connectivity from the Point Cabrillo SMR to the region of the coastline near False Klamath cove (just as there was in ExE), but there was no MPA in that location in ExH for the reduced connectivity to be counted.
3. External MPA arrays in which closely spaced SMCAs had reduced connectivity. This type of result occurred in ExB, ExF, and ExG in the vicinity of Point Cabrillo and MacKerricher. In all cases the reduced connectivity appears to be a result of fishing inside an SMCA reducing the connectivity from that region to a nearby MPA, which would have been quite

high in the absence of fishing. This result illustrates a potential genetic consequence of MPAs that allow harvest, but has little bearing on MPA spacing recommendations.

4. External MPA arrays in which particular MPAs have very low connectivity to them. This occurred only in ExC, in which the Reading Rock Coastline SMCA had reduced connectivity from nearly all other MPAs in the network. This is a relatively clear case in which slight changes to the network would greatly improve predicted genetic connectivity: All other proposals had an MPA in the Reading Rock coast location, but only ExC exhibited reduced connectivity to that location. This appears to be a result of the large gap between Reading Rock and Punta Gorda to the south in ExC. In all other MPA proposals there is an additional MPA between Punta Gorda and Reading Rock, which appears to bolster connectivity to the Reading Rock coastline.

Figure 1. Genetic connectivity result for Proposal 0

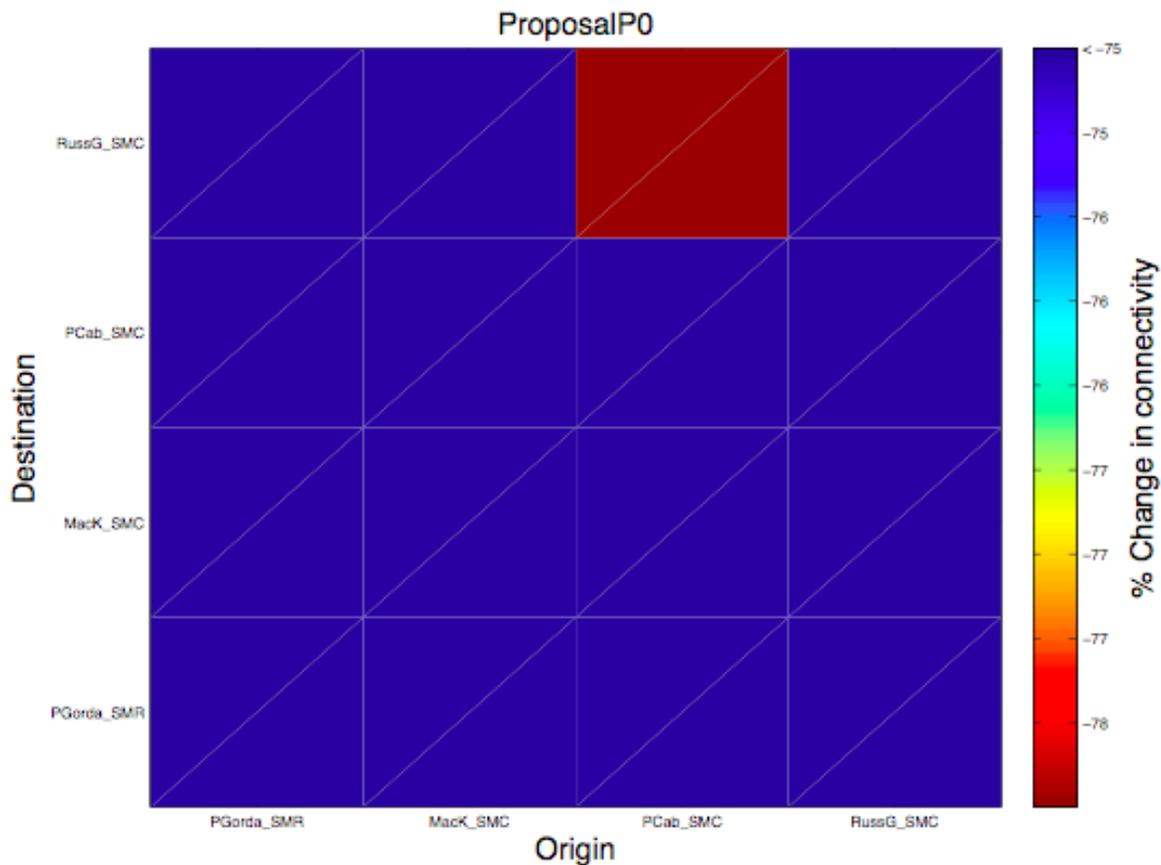


Figure 2. Genetic connectivity result for Proposal ExA

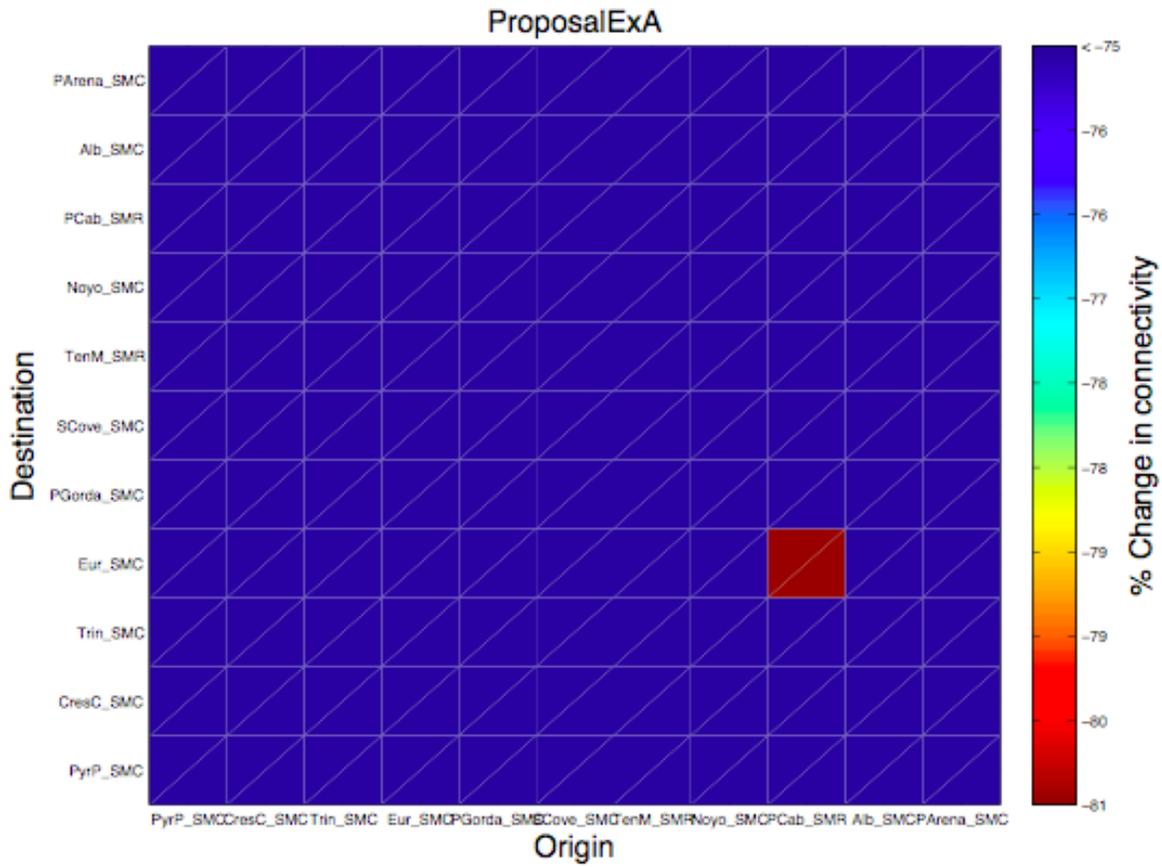


Figure 3. Genetic connectivity result for Proposal ExB

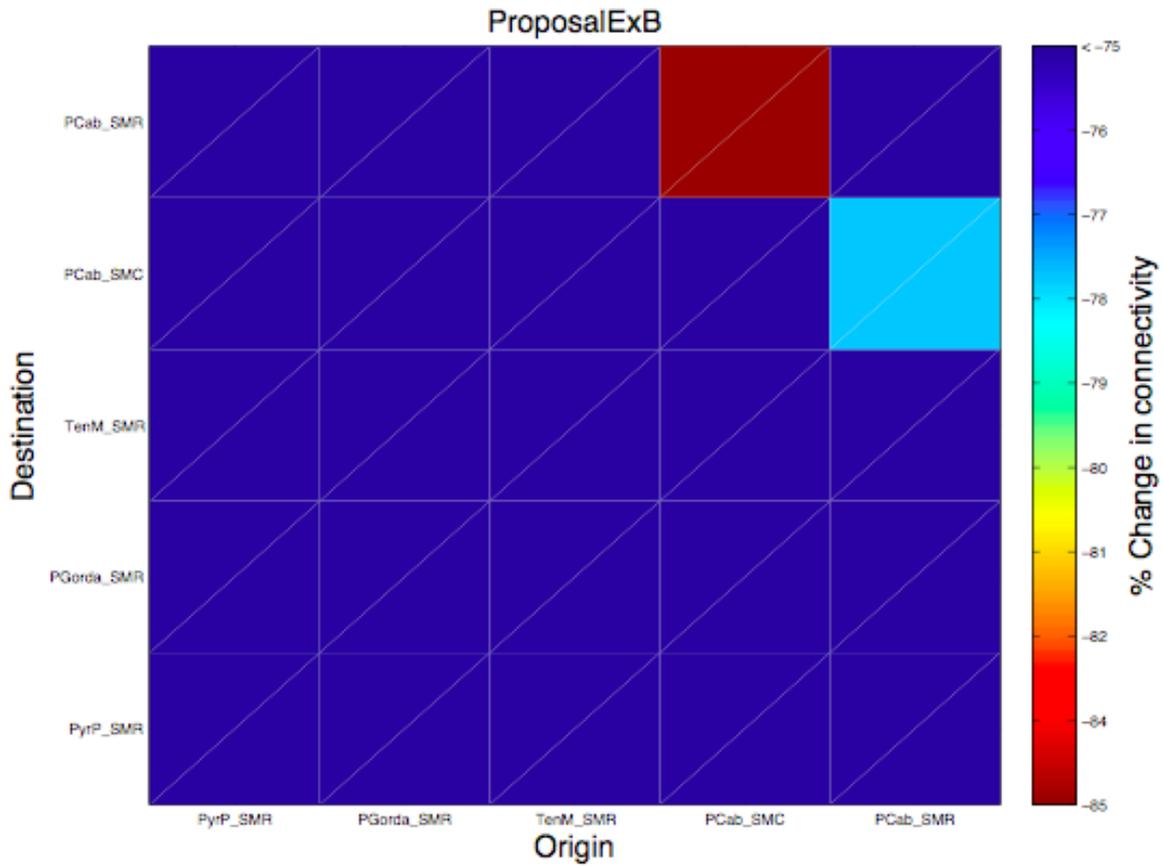


Figure 4. Genetic connectivity result for Proposal ExC.

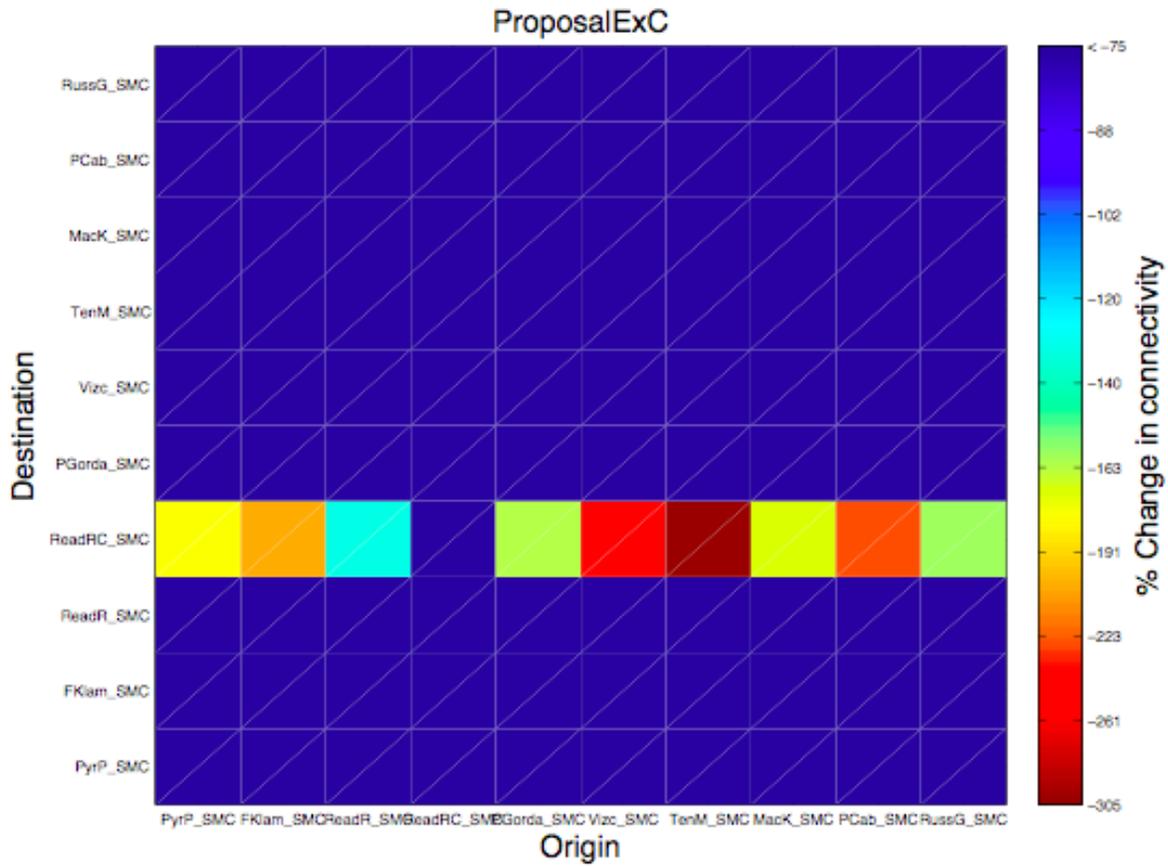


Figure 5. Genetic connectivity result for Proposal ExD

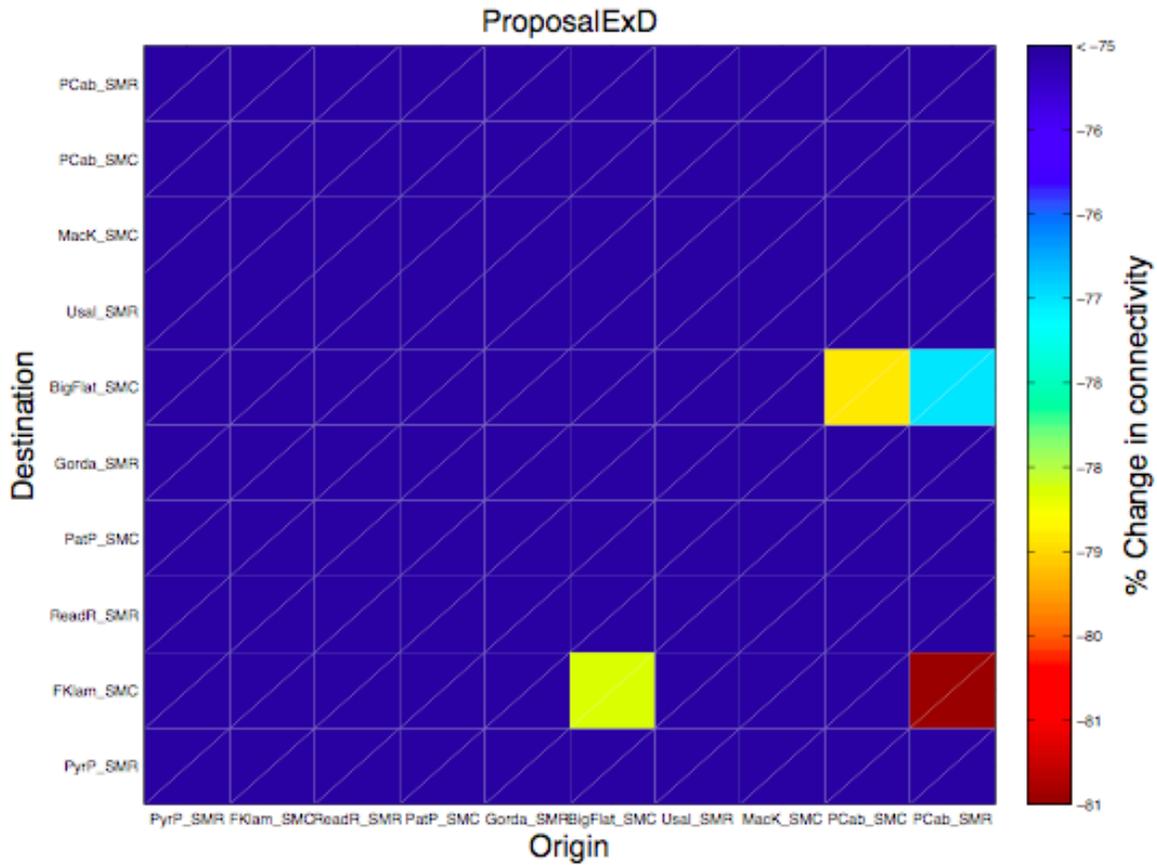


Figure 6. Genetic connectivity result for Proposal ExE

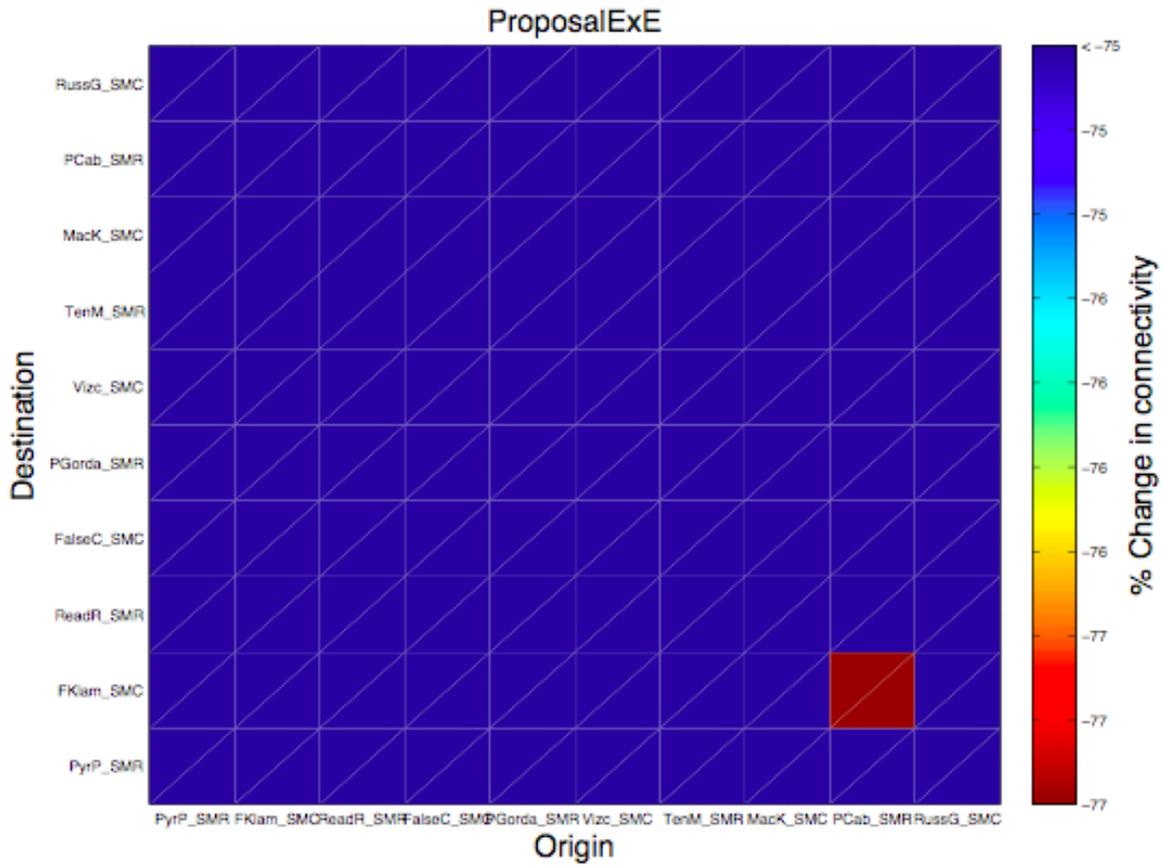


Figure 7. Genetic connectivity result for Proposal ExF

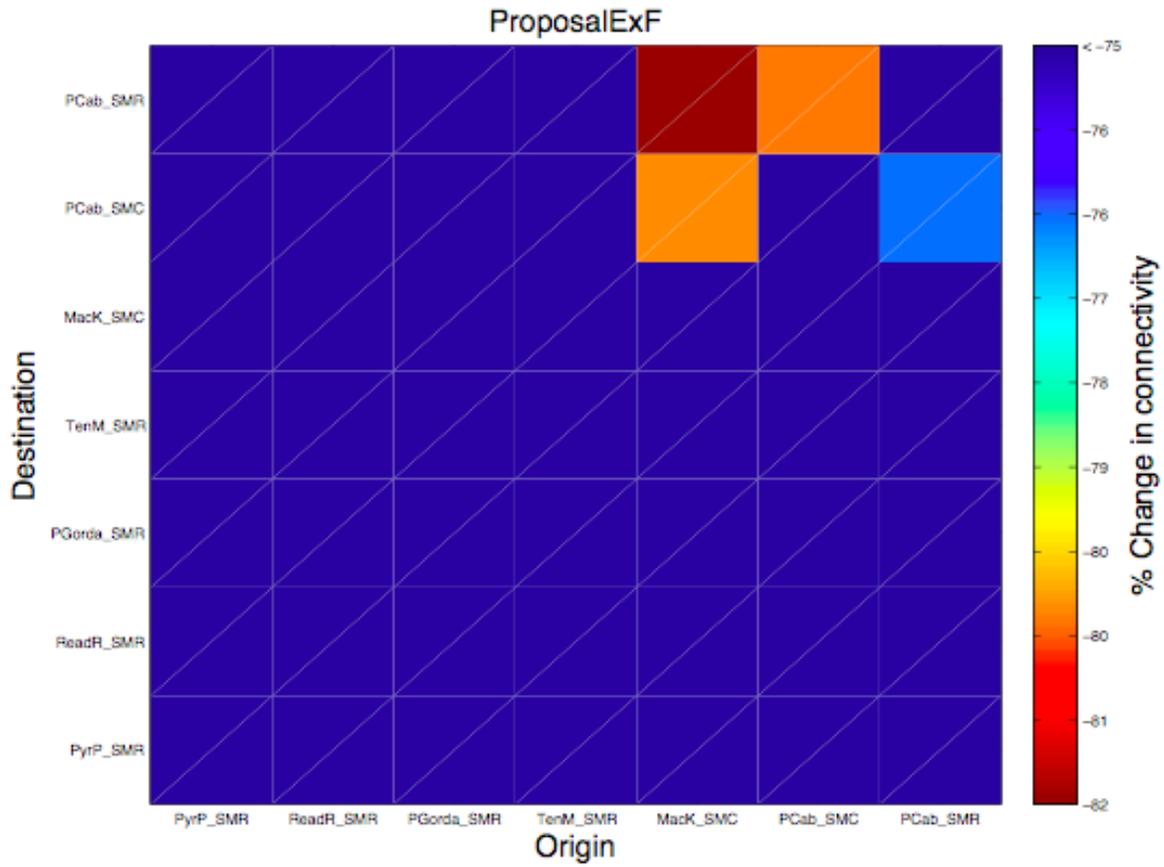


Figure 8. Genetic connectivity result for Proposal ExG

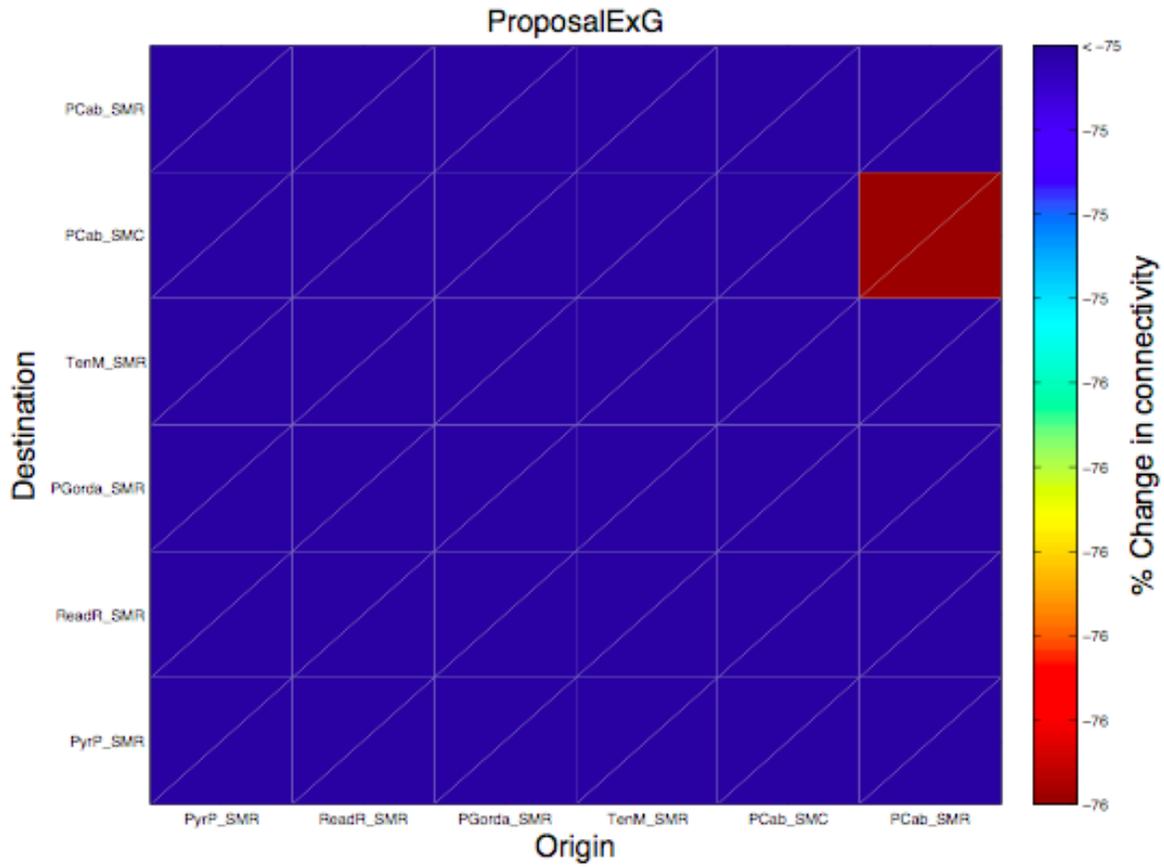


Figure 9. Genetic connectivity result for Proposal ExH

